# STOCK IDENTIFICATION METHODS WORKING GROUP (SIMWG)

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# Contents

# i Executive summary

The Stock Identification Methods Working Group (SIMWG) reviews new methods for the definition and investigation of stock structure and provides recommendations to other ICES expert groups on how to interpret patterns of population structure.

In 2024, SIMWG has continued providing annual updates on recent applications of stock identification methods to species assessed by ICES and on advances in stock identification methods. Based on the wide expertise of SIMWG members, we provide reviews of recent literature on genetics, growth marks in calcified structures, life history parameters, morphometrics/meristics, tagging, otolith shape, otolith chemistry, parasites and interdisciplinary approaches.

A key activity of SIMWG is to address requests by ICES working groups for technical recommendations on issues of stock identity. In the current term, we reviewed working documents (WDs) by the Working Group on the Biology and Assessment of Deep-sea Fisheries Resources (WGDEEP) on the stock structure of blue ling and by the Benchmark Workshop on Horse Mackerel and Boarfish stocks (WKBHMB) on northern and western horse mackerel. During the SIMWG online meeting, the group assessed WDs on the stock boundaries of anchovy (request by the Working Group on Southern Horse Mackerel, Anchovy, and Sardine (WGHANSA)) and Baltic dab, flounder and plaice (joint request by the Baltic Fisheries Assessment Working Group (WGBFAS) and the Working Group on the Assessment of Demersal Stocks in the North Sea and Skagerrak (WGNSSK)).

Moreover, SIMWG members co-chaired and participated in the Third Workshop on Stock Identification and Allocation of Catches of Herring to Stocks (WKSIDAC3). There also is a strong link to the Working Group on the Application of Genetics for Fisheries and Aquaculture (WGAGFA).

SIMWG contributes to the general understanding of the biological features of the north Atlantic ecosystem through its work to describe fish population structure. Additionally, SIMWG annual reviews on advances in stock identification methods keep ICES members abreast of best practices in this field of study. SIMWG expert reviews on questions of stock structure for particular ICES species are directly relevant to the appropriate definition of stock and contribute to the accuracy of stock assessment and effectiveness of management actions. We see an important role for SIMWG in the future as ICES copes with the shifting distributions of fishery resources and questions regarding the appropriate definition of fish stocks. Understanding stock structure is a fundamental requirement before any assessment or modelling on a stock can be contemplated and SIMWG will continue to work with ICES expert groups to address pressing stock identification issues.

# ii Expert group information

| | |
|---|---|
| **Expert group name** | Stock Identification Methods Working Group (SIMWG) |
| **Expert group cycle** | Multiannual |
| **Year cycle started** | 2023 |
| **Reporting year in cycle** | 2/3 |
| **Chair** | Christoph Stransky, Germany |
| **Meeting venues and dates** | By correspondence in 2023 |
| | 17–19 June 2024; Online meeting |

# 1 Review recent advances in stock identification methods (ToR a)

Over the past years, there has been a wide use of applications of stock identification methods to ICES stocks, as well as several notable advances in stock identification methods with many results relevant to ICES science and advice. SIMWG has committed to providing annual updates on recent applications of stock identification methods to ICES species and on advances in stock identification methods. The group has focused on summarizing research in the focal areas listed below:

a) Genetics

b) Growth marks in calcified structures

c) Life history parameters

d) Morphometrics/meristics

e) Tagging

f) Otolith shape

g) Otolith chemistry

h) Parasites

i) Interdisciplinary approaches

SIMWG annual reviews on advances in stock identification methods keep ICES members abreast of best practices in this field of study. This review activity has served as a valuable contribution to the field and has formed the foundational material for two editions of the book "Stock Identification Methods: Applications in Fishery Science". This book was published first in 2005 and again in 2014. SIMWG members S. Cadrin, L. Kerr and S. Mariani edited the 2nd edition and several SIMWG members contributed chapters to this book. A 3rd edition is planned for 2025/2026, again involving several SIMWG members.

The details of annual reviews of advances in stock identification methods are summarized in Annex 3.

# 2 Technical reviews and expert opinion on matters of stock identification (ToR b)

SIMWG provides ICES expert groups and working groups expert feedback on questions of stock structure for ICES stocks. In 2024, SIMWG has contributed to ICES advisory needs by providing expert feedback on the status of stock structure of:

- blue ling in Subareas 1, 2, 8, 9, 12 and Divisions 3a and 4.a (bli.27.nea), Subarea 14 and Division 5a (bli.5a14) and 3) and Subarea 6-7 and Division 5b (bli.5b67);
- horse mackerel in Subarea 8 and Divisions 2.a, 5.b, 6.a, 7.a-c, and 7.e-k and 3.a & 4.a in quarters 3 and 4 (Western stock, hom.27.2a4a5b6a7a-ce-k8) and in Divisions 4.b-c, 7.d and 3.a & 4.a in quarters 1 and 2 (North Sea stock, hom.27.3a4bc7d);
- anchovy in Division 9a (ane.27.9a);
- dab in the Baltic Sea (dab.27.22-32) and in the North Sea (dab.27.3a4);
- flounder in the Belt Seas and the Sound (fle.27.22-23) and in the North Sea (fle.27.3a4); and
- plaice in the Kattegat, Belt Seas and the Sound (ple.27.21-23) and in the Baltic Sea, excluding the Sound and Belt Seas (ple.27.24-32).

The detailed reviews are provided in Annex 4.

Moreover, SIMWG members co-chaired and participated in the Third Workshop on Stock Identification and Allocation of Catches of Herring to Stocks (WKSIDAC3).

SIMWG expert reviews on questions of stock structure for ICES stocks are directly relevant to the appropriate definition of stock and contribute to the accuracy of stock assessment and effectiveness of management actions. Understanding stock structure is a fundamental requirement before any assessment or modelling on a stock can be contemplated and SIMWG will continue to work with ICES expert groups to address pressing stock identification issues. We see an important role for SIMWG in the future as ICES copes with the shifting distributions of fishery resources and questions regarding the appropriate definition of fish stocks.

SIMWG recommendations have been well received by the requesting groups and there are a growing number of requests from different groups which speaks to the service that SIMWG provides to the ICES community. SIMWG expertise should be continued to be used to address on specific questions of stock structure and should be considered in the advisory process in the context of whether the stock units are appropriate for accurate assessment and sustainable management of ICES fishery resources.

# 3 Advances in mixed-stock analysis (ToR c)

The group discussed examples of ongoing applications, offering practical recommendations for implementing mixed stock composition analysis, as follow-up of section 3 in the SIMWG 2022 report (ICES 2022).

## North-East Atlantic cod (NEAC) and Norwegian coastal cod (NCC) stocks

The Institute of Marine Research (IMR) in Norway uses real-time genomic analyses to manage a mixed-fishery during spawning season of the abundant North-East Atlantic cod (NEAC) stock and the much smaller northern Norwegian coastal cod (NCC) stock (Johansen *et al.* 2018). The NEAC stock is the single largest cod stock worldwide, with an annual total allowable catch of approximately 450 000 tonnes, worth millions of Euros to the Norwegian economy (Bertheussen *et al.*, 2020; Dahle *et al.*, 2018). IMR uses the Pan I*B allele, which is present in NEAC but is almost absent in NCC stocks, as population marker to assess their relative abundances within two selected the spawning areas. Atlantic cod have been sampled three times per week to test for the presence of these genomic markers in Lofoten (Dahle *et al.*, 2018) and Møre (Johansen *et al.* 2018). Only when the frequency of Pan IB allele is high enough to assume that the NEAC have arrived on fishing grounds does the Norwegian Directorate of Fisheries open the sector for fishing. Sampling continues throughout until the Pan I alleles frequency decreases, signalling the departure of NEAC. In the recent years, NEAC was highly abundant and thus, only few samples were needed before the fishing ground in Lofoten was opened. However, an important area in Lofoten (Henningsvær) was not opened for the first time in 2024. On the other hand, very small amounts of NEAC were observed on the fishing ground in Møre which is closed to commercial fishing since 2016 during the entire spawning season to protect the NCC.

## Baltic cod

Mixed-stock analysis is conducted using otoliths or genetics; stock composition integrated into assessment and management. Catches in Subdivision 25 in both western and eastern Baltic are split. DTU-Aqua (Denmark) developed a SNPchip for North Sea and Baltic cod.

## North Sea cod

WKNSCodID (ICES 2020) provided recommendations for genetic sampling to support stock composition analysis. There are still uncertainties with regard to the three stock components (“Viking”, ”Dogger”, ”Celtic”) and a new project (GenDC) will address increased genetic sampling.

## US Atlantic cod stock structure

Four populations including sympatric populations in the western Gulf of Maine are misaligned with 2 management units. There is potential for stock composition analysis using genetics or otolith structure (Dean *et al.* 2019, Kerr *et al.* in press), but otolith processing was not available for the Atlantic Cod Research Track Working Group (ACRTWG) assessment, so the western Gulf of Maine stock is currently assessed a mixed population unit, with potential for future stock composition analysis. The management procedure being developed is a challenge.

## Greenland cod

There is a year-round genetic monitoring of mixed-stock fishery, with implications for management (Christensen *et al.* 2022).

### Salmon in the Baltic Sea

Mixed-stock catches of the salmon in the Baltic Sea have been analyzed using a combination of microsatellite markers and smolt-age data since the early 2000s. The results of the mixed-stock analysis have been used to guide area and temporal management of the salmon fishery in the Baltic Sea. To increase cost-effectiveness, SNPs are now being used.

### West Greenland salmon

There is an international sampling program developed by ICES to determine the continent of origin and biological characteristics of Atlantic salmon collected at West Greenland (Sheehan *et al.* 2021). Sampling includes continent and region of origin from genetic analysis of tissue samples.

### Herring

WKSIDAC2 (ICES, 2024b) concluded that genetic stock identification was the most appropriate and robust method for population assignment modelling of survey and commercial caught Atlantic herring, including the estimation of samples population of origin. A new "population code" (https://vocab.ices.dk/?CodeID=249075)was added to the ICES databases to distinguish between stocks (management units) and genetically distinct populations (biological units). It was recommended that common, standardised methods for analysing genetic samples should be developed, as well as guidelines for the storage and accessibility of genotype data.

Currently, genetic stock identification is applied in two area, ICES Div. 6a and the eastern part of the North Sea. In Div. 6.a, genetic splits are implemented on the Malin Shelf herring acoustic survey (MSHAS) which can now be split and provide stock specific biomass estimates. The split survey time series is available from 2014 onwards. Commercial catches in 6.a S are also genetically assigned using the same assignment model as on the MSHAS samples. In the eastern part of the North Sea, the Skagerrak and the Kattegat, both scientific surveys and commercial catches are split based on genetics. Traditional methods like mena vertebral counts or otolith microstructure have been replaced since 2022. However, even though genetic stock identification is applied, and several populations observed, all herring are finally lumped as either North Sea autumn-spawning herring or Western Baltic spring-spawning herring. Future work is need on how to deal with herring populations that certainly belong to different stocks. A genetic assignment model has also been developed to distinguish the Irish Sea autumn spawning stock from the herring in the Celtic Seas. Samples collected on the 2021–2023 Irish Sea Herring Acoustic Survey (ISAS) and on the 2021 Irish Sea Commercial Acoustic Survey (ISSS) have now been analysed and assigned with the model, indicating a significant mixing of adjacent stocks. However, the survey biomass estimates have yet to be slit between the different stocks.

The development of a Universal Assignment Model (UAM) was discussed at WKSIDAC3 in 2024 and concluded to be a critical objective requiring development prior to the next WKSIDAC meeting. To achieve this objective, it was concluded that a sub-group of WKSIDAC should be established for development and implementation of a UAM. A Roadmap for the development of the UAM is also to be included in the WKSIDAC3 report. One requirement for such an UAM is a common, shared, and open-access database. Such a database should ideally be able to store all the individual genotypes, rather than just pure assignment results as currently possible.

## Horse mackerel

Fuentes-Pardo *et al.* (2023) identified, for the first time, the existence of three locally adapted biological units of horse mackerel in the northeast Atlantic and developed a panel of genetic markers capable of differentiating the three biological units under-lying the three horse mackerel stocks; Western, North Sea and Southern. These markers were recently included on a multi-species Axiom® SNP genotyping array to enable high throughput genotyping of large numbers of samples The results of the large-scale largescale genotyping of both baseline and mixed samples collected from 2015–2023 (145 samples, 3075 individuals) across the three stock areas, on an Axiom® SNP genotyping array (see Andersson *et al.*, 2024), indicated that the current delineation of the three horse mackerel stocks was not appropriate for the purposes of data collection and collation for stock assessment (Farrell *et al.*, 2024). A support vector machine learning (*svm*) based assignment model was developed in the *R* package *assignPOP* (Chen *et al.*, 2018) to distinguish individuals from the Western and North Sea biological units and to assign individuals of unknown origin, from potentially mixed samples caught in these stock areas, to either biological unit. Widescale application of the model to mixed samples from the Western and North Sea stock areas revealed a clear spatial pattern of the distribution of individuals assigned to either the Western or North Sea biological units. The North Sea individuals were primarily restricted to the southern part of 4.b, 4.c and 7.d. There was little evidence of North Sea individuals in divisions 3.a or 4.a, where samples comprised primarily individuals from the Western biological unit. The patterns of assignment in the channel (Divisions 7.d and 7.e) also indicated a significant issue with the current delineation of the North Sea stock. Due to the small number of baseline samples from the Southern biological unit it was not possible to develop an assignment model to distinguish the Southern and Western biological units. However, it was possible to conclude that there was mixing of the Western and Southern units along the Portuguese coast but the majority of the Southern individuals were caught south of Lisbon.

The results were presented to the ICES Benchmark workshop on horse mackerel and boarfish stocks (WKBHMB) and resulted in changes to the North Sea and Western assessment areas (ICES, 2024a). A five year research plan was also developed as part of the benchmark process to further develop the genetic assignment models including developing an assignment model to distinguish the Western and Southern biological units in mixed catches.

## Blue whiting

Genome sequencing is used to determine the north-south split in the NE Atlantic.

## Anglerfish

Genetic analyses have revealed that what is labelled as white anglerfish and has a white peritoneum (the morphological characteristic used to distinguish between black and white anglerfish) can either be white anglerfish, black anglerfish or a hybrid between the two (Aguirre-Sarabia, 2019). Thus, although the issue in this case is about species identification, it can be treated as a stock-mixing scenario since catches need to be allocated to species using an appropriate tool for it. A qPCR assay for identifying the three types (black, white or hybrid) has been developed and applied to about 1500 white anglerfish labelled samples. Results show that the southern stock is mostly affected by misidentification (25% of the white labelled samples are black) and the northern stock is mostly affected by hybrids (14%of the white labelled samples are hybrid); the northern platform stock, where no morphological species identification is performed (all specimens are considered white) no issues were observed. These results have been shared with WGBIE (ICES. 2023) and simulations have been performed for the norther stock to assess the effect considering the effect of hybrids on the recommended TAC.

## Atlantic bluefin tuna

Genetic analyses based on thousand SNP markers suggest homing behaviour followed by extensive mixing of eastern and western populations in Atlantic bluefin tuna (Rodriguez-Ezpeleta *et al.* 2019), which calls for a stock identification tool that allows assigning catches to stocks. Genetic stock assignments based on a 96 highly informative SNP panel (Rodriguez-Ezpeleta *et al.* 2019) together with otolith microchemistry-based assignments (Artetxe-Arrate *et al.* 2023) are now used as part of the ICCAT Management Strategy Evaluation (MSE, Carruthers & Butterworth, 2021), which includes mixing for Operating Models. Although the current model reflects the population dynamics of bluefin tuna much better than the previous assumption of using the 45º W meridian as stock boundary, the lack of agreement of genetics and otolith microchemistry in some samples (Brophy *et al.* 2020) claimed for additional analyses. Using an expanded dataset, Díaz-Arce *et al.* (2024) revealed that the two bluefin tuna stocks are connected through a unidirectional trans-Atlantic gene flow, which is most likely mediated by a mixed spawning area. Several sources of evidence indicate that this westward gene-flow is recent, which calls for monitoring population connectivity and its effects in the genetic diversity and conservation of western population. For this aim, a new SNP array containing 7000 SNPs (neutral, adaptive, sex markers, mitochondrial markers) has been developed and is currently being applied to thousands of reference and feeding aggregate Atlantic bluefin tuna samples (Díaz-Arce *et al.* 2023) in order to further inform about stock mixing and potentially merging.

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# 4 Update on stock ID book (3rd edition)

Elsevier invited a 3rd edition of the SIMWG book (Stock Identification Methods: Applications in Fishery Science) with substantial revisions and new information. In 2022, SIIMWG confirmed that there have been advances in many of the topics covered in the 2nd edition (e.g., genomics, spatial Management Strategy Evaluation, spatial integration of multidisciplinary information), and climate change is an emergent topic that influences several aspects of stock identification. The editors and SIMWG proposed a substantial revision to consolidate some current chapters and add some new chapters.

All chapters will be revised to deemphasize traditional or outdated methods, retaining brief descriptions to support integration, and consider challenges of climate change. Additional topics within existing chapters:

- Mitochondrial genetics chapter on will include metabarcoding and eDNA
- Nuclear genetics chapter on will include recent stock identification applications of genomics
- Simulation chapter will include spatial Management Strategy Evaluation
- Interdisciplinary Evaluation chapter will include spatial integration

Four new chapters are proposed on:

- Managing Fisheries to Conserve Spatially Complex Populations
- Movement Patterns of Fish Populations
- Tag-Integrated Stock Assessment to Account for Spatial Structure and Movement
- Stock Composition Analysis to Support Assessment and Management of Sympatric Populations

SIMWG offered recommendations to consider reviving and updating the subsection from the first edition on statistical analyses (e.g., including classification models, machine learning, and ensemble modelling). The chapter on otolith chemistry might be expanded to include broader applications (e.g., contaminants in soft tissues). The previous chapters on life history and bandings patterns might also be combined if there have not been active applications (but there have been many recent applications in schlerochronology for stock ID).

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# Annex 2: SIMWG resolution

The **Stock Identification Methods Working Group** (SIMWG), chaired by Christoph Stransky, Germany, will work on ToRs and generate deliverables as listed in the Table below.

| | MEETING DATES | VENUE | REPORTING DETAILS | COMMENTS (CHANGE IN CHAIR, ETC.) |
|---|---|---|---|---|
| Year 2023 | By correspondence | | Interim report by 15 August | |
| Year 2024 | 17–20 June | Faro, Portugal | Interim report by 15 August | |
| Year 2025 | By correspondence | | Final report by 15 August to ACOM & SCICOM | |

**ToR descriptors**

| TOR | DESCRIPTION | BACKGROUND | SCIENCE PLAN CODES | DURATION | EXPECTED DELIVERABLES |
|---|---|---|---|---|---|
| a | Review recent advances in stock identification methods. | a) Tracks best practices in stock ID<br>b) Promotes new technologies relevant to all ICES species | 1.4, 1.8, 5.2 | 3 years (and continued) | EG report, revised stock ID book chapters |
| b | Provide technical reviews and expert opinions on matters of stock identification, as requested by specific Working Groups and ACOM. | Ad hoc advice requests to be addressed at short notice | 1.4, 1.8, 5.2 | 3 years (and continued) | EG report, contribution to ASC |
| c | Review and report on advances in mixed stock analysis, and assess their potential role in improving precision of stock assessment. | | 1.4, 1.8, 5.2, 5.4 | 3 years (and continued) | EG report |
| d | Review of the suggested splitting of the West Greenland inshore stock (cod) into two separate stock units, based on available biological (tagging), catch trends and survey trends. | Advisory requirement | 1.4, 1.8, 5.2 | 1 year | Bief review report provided to NWWG and ACOM (clear response required)<br>Chapter in EG report |

**Summary of the Work Plan**

| | |
|---|---|
| Year 1 | Address terms of reference through work by correspondence in 2023 |
| Year 2 | Organise a physical meeting for SIMWG for summer 2024 |
| Year 3 | Address terms of reference through work by correspondence in 2025 |

**Supporting information**

| | |
|---|---|
| Priority | Understanding stock structure is a fundamental requirement before any assessment or modelling on a stock level can be contemplated. SIMWG liaises with ICES expert groups and working groups on stock identification issues and continues to review new methods as they develop. |
| Resource requirements | SharePoint website and clear feedback from expert groups. |
| Participants | The Group is normally attended by some 15–20 members and guests. |
| Secretariat facilities | Standard EG support. |
| Financial | None |
| Linkages to ACOM and groups under ACOM | ACOM |
| Linkages to other committees or groups | SIMWG has recently worked closely with a range of ICES working groups including HAWG, WGBIE and WGHANSA; benchmark workshops including WKELASMO, workshops on cod stock structure (WKNSCodID, WK6aCodID). In previous years, SIWMG connected with many more ICES groups to fulfill requests. |
| Linkages to other organizations | There are no obvious direct linkages, beyond the SIMWG members' affiliation and commitment to their own employers. Depending on the request, SIMWG's scope might expand beyond the ICES area to address straddling stocks e.g. in the NAFO, NEAFC, CECAF and other RFMO areas. |

# Annex 3: Review recent advances in stock identification methods (ToR a)

## Advances in Stock Identification Methods in 2024

In 2024 (review period mid-2023 to mid-2024), there were several notable advances in stock identification methods and a proliferation of applications, with many results relevant to ICES science and advice. Here, we summarize advances and results accounting for research in genetics, life history parameters, growth marks in calcified structures, morphometrics, tagging, otoliths, parasites, simulation approaches, and interdisciplinary approaches.

### Genetics (Contributors: Rita Castilho, Florian Berg, Christophe Pampoulie, David Murray, Naiara Rodríguez-Ezpeleta)

Over the past two decades, there has been a significant shift in the genetic markers and approaches used in fisheries research, reflecting technological advancements and research priorities. Beginning in the early 2000s, microsatellites (micros) were the predominant markers used due to their high polymorphism and informativeness for population studies. However, the number of papers employing microsatellites began to decline after peaking around 2009, as Single Nucleotide Polymorphisms (SNPs) started gaining prominence.

In particular, microsatellite papers suffered a noticeable upward trend between 2000 and 2015, peaking at 166 papers in 2018. Following that peak, the numbers fluctuated with a notable decline in recent years, particularly in 2024 when the number dropped to 58 papers. On the other hand, at the beginning of the millennium, the number of papers focusing on SNPs was almost negligible. However, there has been a substantial increase in the number of SNP-related papers since 2011, with a peak in 2022 at 107 papers. This indicates a growing academic interest and likely advancements in SNP-related methodologies and applications. Papers using emerging markers such as structural variants (e.g., copy number variants; CNVs) started from single counts in 2001 but numbers are still low compared to the two other marker types and not common. Yet, it is expected that with the raise of available genomes (see section below), these markers will become easier to identify and to incorporate into future studies. The shift towards genomics since 2018 marks a significant milestone, as depicted in the increasing number of publications from this period, illustrating the field's adaptation to cutting-edge genetic technologies. This evolution of genetic markers not only mirrors technological advancements but also the growing complexity of questions addressed in fisheries science.

In summary, while microsatellite-based research publications saw a rise and then began to taper off in the recent years, SNP-related research has been gaining traction, especially in the past decade. The advent of reference genomes and the decrease of cost for obtaining genomic sequences anticipates a future increase in the use of alternative markers such as copy number variations and other structural variant types. The data paints a picture of the evolving landscape of the use of different genetic marker types for population structure analyses for stock identification.

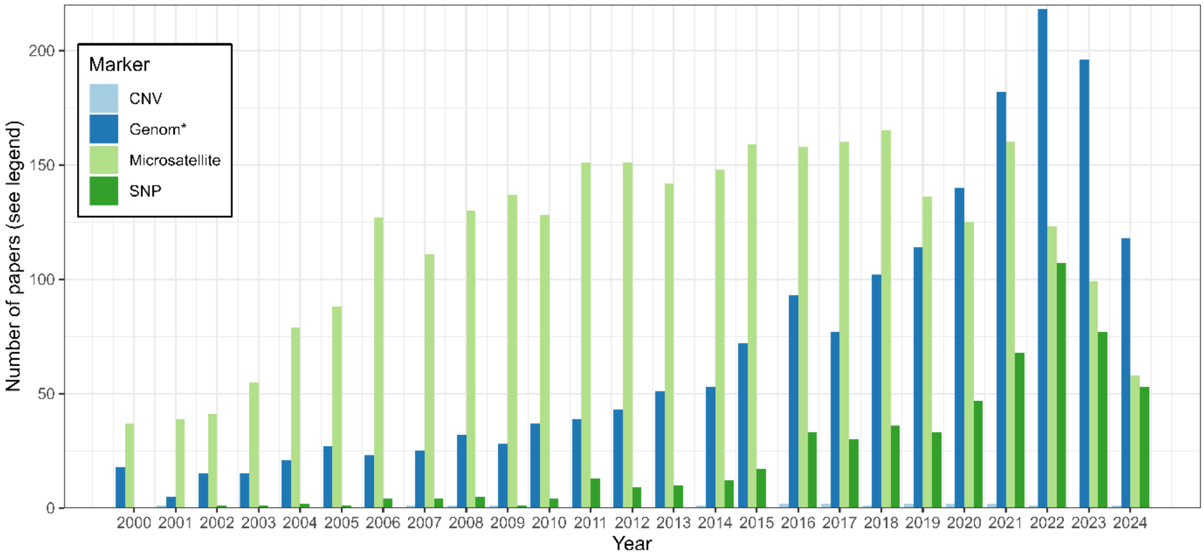

**Figure 1. Scientific publishing trend since 2000, comparing outputs of studies using microsatellite, SNPs and CNVs, as listed in the Clarivate Analytics Web-of-Science. The search criteria were: "fish* AND gene* AND (population OR stock) AND 'molecular marker*', where 'molecular marker*' means "Microsatellite*", "SNP*", "CNV*" or "Genom*". Search link for microsatellite (https://www.webofscience.com/wos/woscc/summary/b5c80b49-662b-4525-b4c1-865c22f99b20-a52e48cd/relevance/1); SNP (https://www.webofscience.com/wos/woscc/summary/c4da2151-03b7-4ed7-b153-12deb40c9041-a52f4b87/relevance/1); CNV (https://www.webofscience.com/wos/woscc/summary/7ee22b70-0976-4fe3-9098-4da0373aa33b-a52f88dd/relevance/1); Genom (https://www.webofscience.com/wos/woscc/summary/bed1f912-d011-44e4-a5f4-bb564cfe4b06-a236a758/relevance/1). Only papers in the following Web of Science categories were considered: 'Fisheries', 'Environmental Sciences', 'Ecology', 'Biodiversity Conservation', 'Marine & Freshwater Biology' and 'Oceanography'. Data for 2024 only represent papers published through to the present date (August 2024). Note: There is the caveat that some of the as genom* identified papers may also be considered as SNP papers and may be counted twice.**

## Comprehensive review papers

The selection of the 2023–2024 papers as examples of advances in genomics for fish stock discrimination reflects the subjective choice of the contributors. While they highlight significant progress and innovation, other important studies may also exist. The choice is influenced by the contributors' perspectives on what constitutes genuine advancement in this field, making the selection inherently subjective.

A comprehensive roadmap for using population genomics to promote sustainable fisheries was published by Andersson *et al.* (2024). This work emphasizes the importance of developing reference genomes and whole genome sequencing due to low genetic differentiation at neutral loci in large populations. The authors discuss using SNP-chip analysis to establish baseline allele frequencies, which can then be used to determine the composition of mixed fish samples, aiding in demographic analyses and sustainable fish quota setting. This study is relevant for its potential to transform stock identification and management through cost-effective genetic marker analysis.

## Examples of genetic stock identification (GSI)

An example of genetic stock identification (GSI) method that integrates regional genetic baselines to analyze fish mixtures from broad geographic ranges was produced by Hsu & Habicht (2023). The multistage framework allows for using disparate baselines in a single integrated process, which is more cost-effective and efficient than developing large-scale genetic baselines. This method significantly improves the accuracy of stock identification across wide geographic areas without requiring extensive updates to regional markers (Hsu & Habicht, 2023).

Manuzzi *et al.* (2024) sequenced and annotated a high-quality genome of Atlantic mackerel (*Scomber scombrus*) which was used to map RAD-seq read for SNP discovery and genotyped more than 500 individuals within their distribution range. The assembly of the reference genome for Atlantic mackerel resulted in a high-quality genome of 741 Mb. Their population genetic results showed that the Atlantic mackerel consist of three previously known genetically isolated units (Northwest Atlantic, Northeast Atlantic, Mediterranean), and provide no evidence for genetically distinct spawning components within the Northwest or Northeast Atlantic. Therefore, previous uncertainties were resolved by confirming the absence of genetically isolated spawning components in each side of the northern Atlantic, thus rejecting homing behaviour and the need to redefine management boundaries in this species.

Pampoulie *et al.* (2024) evaluated if a panel of 120 SNPs associated with spawning characteristics and salinity preferences would be an effective discrimination tool for herring populations in the Norwegian Sea. They observed overall high levels of genetic differentiation and were able to separate individuals from stocks under current management (Norwegian spring-spawning herring (NSSH), North Sea autumn-spawning herring, and Icelandic summer-spawning herring (ISSH)). However, they were not able to separate putative populations of Norwegian autumn spawners, Faroese autumn or spring spawners with the established SNP-panel. When the SNP-panel was tested on commercial fishery samples of NSSH east of Iceland, up to 16% were assigned to ISSH. This implies that catch data are seriously biased and demonstrates the potential of SNP panels as a tool to solve the problem.

Da Fonseca *et al.* (2023) demonstrate that European sardine (*Sardina pilchardus*) consist of at least three genetic clusters using whole genome data from 108 individuals from 16 sampling areas across 5000 km of the species' distribution range (from the Eastern Mediterranean to the archipelago of Azores). The three clusters are found 1) at the Azores and Madeira, 2) broadly corresponds to the center of the distribution, including the sampling sites around Iberia, separated by the Almeria–Oran front from the 3) in the Mediterranean samples, except those from the Alboran Sea. Their results provide a baseline for further characterization of physical and genetic barriers that divide European sardine populations, and information for transnational stock management of this highly exploited species towards sustainable fisheries.

Using genotyping-by-sequencing (GBS), it was possible to uncover a previously unidentified genetic cluster of blackspot seabream (*Pagellus bogaraveo*) in the Gulf of Cádiz, highlighting the impact of ocean circulation patterns and local upwelling on the genetic differentiation of blackspot seabream populations in the Northeast Atlantic (Cunha *et al.* 2024). These findings underscore the significance of fine-scale genetic analysis for defining stock boundaries along the Atlantic Iberian coasts.

### Fully annotated and assembled genomes to support fisheries management

From a fisheries management perspective, having a fully annotated and assembled genome provides substantial resolution for selecting population markers and therefore, assisting with determining biologically relevant stock units (Andersson *et al.*, 2024). For example, cod, herring and horse mackerel genomes have provided greater insight into the biological connectivity, and boundaries, of populations throughout the northeast Atlantic, see the following for examples: Bekkevold *et al.* (2023), Fuentes ‐ Pardo *et al.* (2023), Pampoulie *et al.* (2023), Manuzzi *et al.* (2024) and Cunha *et al.* (2024). Furthermore, the availability of an organism's entire genome can highlight potential responses of populations to environmental impacts, such as heatwaves and climate change (Benestan *et al.*, 2016). However, despite the importance of these tools to fisheries management questions, the majority of species are without a fully annotated and assembled genome.

Recently, collaborative networks have formed to assist with using genomic data to understand and explore the biology of organisms, their place within ecosystems and develop tools to assist in their management and conservation. The Darwin Tree of Life (DToL, https://www.darwintreeoflife.org) and European Reference Genome Atlas (ERGA, https://www.erga-biodiversity.eu) are part of a global initiative, known as the Earth BioGenome Project (https://www.earthbiogenome.org), that are working together to sequence the genome of every species on earth. Relative to terrestrial organisms, there is an inherent difficulty in collecting tissue samples from marine species and as such there is an under representation of genomes for aquatic organisms.

The Centre of Environmental, Fisheries and Aquaculture Science (Cefas) in England/UK signed a memorandum of understanding with DToL to assist with collecting marine species. By tying 'blue sky science' with fisheries management issues, this collaboration hopes to assist DToL with sequencing UK marine species by providing hard to obtain samples for sequencing. Concurrently, the resulting open access assembled and annotated genomes can be used by academia, governmental research institutes and stakeholders to determine biologically relevant populations for species such as sole (*Solea solea*), plaice (*Pleuronectes platessa*) and pollack (*Pollachius pollachius*). DToL provides a variety of services, such as sampling equipment, postage of samples and sequencing the genome free of charge.

Future fisheries management related research projects seeking to utilize genomes should contact ERGA and DToL (or other local initiatives) as early as possible to explore mutually beneficial collaboration between applied and pure science.

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## Growth marks in calcified structures (Contributors: Florian Berg, Kirsteen MacKenzie)

Calcified structures in fish, particularly the ear bones (otoliths), but also scales, spines, and fish rays, are used for identifying stock structure as well as for a variety of research applications (Brophy, 2014, Barrios *et al.*, 2017). Notably, for well over a century, they have been used to age fish when interpreting daily and annual rings (annuli). The utilization of growth marks in calcified structures for stock identification has decreased during the last years and where mainly replaced studies involving their shape or chemical composition.

During the review period (mid-2023 to mid-2024) very few studies were published using growth marks in calcified structures for stock identification.

A study by Malca *et al.* (2023), however, investigated daily growth increments in larval Atlantic bluefin tuna (*Thunnus thynnus*) from the Gulf of Mexico and from the Mediterranean Sea, both sampled in the spawning season of 2014. Their results showed that otolith growth increments were significantly wider for the Gulf of Mexico than for the Mediterranean population, suggesting that the reduced daily growth is likely due to a comparatively lower abundance of mesozooplankton in Mediterranean waters. This is one of the first papers to determine and compare larval growth of Atlantic Bluefin tuna from a temporally consistent sampling regime, and provides a potential mechanism to discriminate between origins in older tuna.

Li *et al.* (2023) published a study where they used otolith microstructure analysis on chub mackerel (*Scomber japonicus*) to determine the hatch dates and growth rates of young-of-the-year individuals. Their results showed that the ages of young chub mackerel ranged between 120 and 180 d, and the estimated hatch date lasted from mid-January to late May with a peak from mid-March to mid-April. Average otolith daily increment width during the early life stages showed an increasing trend. They identified three groups with dissimilar growth histories and migration routes using unsupervised random forest clustering analysis, but all eventually converge on the same nursery ground. However, the faster growth led to better recruitment due to the hypothesis of growth-dependent mortality. Most chub mackerels hatched in March and April, the spawning period is longer and earlier, which could lead to strong year classes.

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## Life history parameters (Contributor: Florian Berg)

From May 2023 to August 2024, there were five papers investigating population or stock structure and their dynamics based on life history parameters. In all studies, life history parameters were estimated to demonstrate differences between groups, however, none used the estimated parameters for direct identification of individuals.

Lundgreen *et al.* (2023) investigated the stock structure of Atlantic cod (*Gadus morhua*) in the western Baltic Sea mainly using tagging data. They demonstrated considerable ecological connectivity between the Sound and Kattegat, primarily during the spawning season. Furthermore, cod tagged in the northern Sound were most likely to be recaptured in Kattegat while cod tagged in the southern part of the Sound were mainly recaptured in the Sound. In addition, they have used length-at-age data to estimate population specific growth parameters. To test for growth differences between areas, a global model assuming no differences in growth was first set up using the von Bertalanffy growth function, and subsequently, another model was created that estimated area-specific parameters. The von Bertalanffy growth curves showed higher growth rates in Kattegat and the Sound while the Belt Sea and Arkona Sea were characterized by lower sizes-at-age.

Úbeda *et al.* (2023) used Multivariate Autoregressive State-Space (MARSS) models to assess population structure by means of abundance and biomass trends of Greenland halibut (*Reinhardtius hippoglossoides*) in four regions (Norwegian Sea, Iceland, Southeast Greenland, and Northwest Atlantic) where three offshore stocks are recognized: (1) Baffin Bay–Davis Strait (Northwest Atlantic stock), (2) Southeast Greenland and Iceland (West Nordic stock (WNS)), and (3) the Barents and Norwegian Seas (Northeast Arctic stock). Abundance and biomass observations from each region were linked to growth rate parameters in MARSS models. Top models, including different growth rate parameters between regions, identified the Northwest Atlantic as an independent population. Best-fit models treated Greenland halibut in the WNS as two independent populations (east and west), with potential connections between eastern Iceland and the western Barents Sea. These results suggest a mismatch between current stock perception and management boundaries in the Northeast Atlantic.

Smith *et al.* (2024) compared life-history traits of *Nematalosa vlaminghi*, a long-lived (20 years), semi-anadromous fish endemic to south-western Australia, in exploited and unexploited populations living in similar environments. Maturation age and length was estimated by logistic regression analysis. Growth curves were fitted to length-at-age data. Compared to the unexploited population, juvenile growth was more than twice as fast, and maturity was attained at least 3 years earlier in the unexploited population. Results supported the hypothesis of faster growth in exploited populations because of density-dependent processes. Environmental factors may also have contributed to trait differences between populations.

Abdussamad *et al.* (2024) demonstrated that yellowfin tuna (*Thunnus albacares*) caught from seas surrounding the Indian mainland and its island territories consist of biologically distinct stocks in the region. Those caught around the submerged mounts of Chagos-Laccadive Ridge in the Lakshadweep Sea, off Kerala-Karnataka coast exhibit early maturity, small size at maturity, short lifespan and a close association with sea mounts. In contrast, those caught off other coasts of the mainland, including Andaman waters, exhibit late maturity and larger sizes at maturity indicating a fishery dominated by larger-sized individuals. These findings suggest that the yellowfin tuna associated with the Lakshadweep Sea mounts constitutes a distinct stock, highlighting the necessity for comprehensive genetic, morphometric and population investigations to confirm their stock status

Hansen *et al.* (2024) quantified the life-history variation among four lake trout (*Salvelinus namaycush*) morphs at six geographically distant locations in Lake Superior. Life-history traits were estimated using length-age analysis of back-calculated growth from sagittal otolith increments. Morphs, assigned using statistical and visual assignment rules, included 122 humpers, 646 leans, 86 redfins, and 1154 siscowets. Density (CPUE) varied 11-fold among morphs, 7-fold among locations, and 3-fold among depths. Morphs seemed to fill the same ecological niche at all locations, because life-history traits related to weight (body condition, buoyancy, mean weight), age, and growth rate varied more among morphs than locations. However, abiotic and biotic variation among locations also seemed to exert control over life-history variation, because life-history traits related to length, maturity, and early life history varied more among locations than morphs.

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## Morphometrics/meristics (Contributors: Eglė Jakubavičiūtė, Steven Cadrin, Emma White)

Morphometric and meristic traits still serve as a cost-effective strategy for phenotypic stock identification, often complementing other approaches. Although there are few recent applications in ICES areas, morphometric stock identification is being widely applied for data-limited fisheries in South Asia. There have also been recent advances in morphometrics for broader applications.

Conventional multivariate morphometrics of digitized measures proved to be a reliable method for several case studies. For example, cleftbelly trevally, *Atropus atropus,* in the South Konkan area was discriminated into three separate stocks (Lanjewar *et al.*, 2024). Kawakawa, *Euthynnus affinis*, another significant but undermanaged species in the Indo-Pacific area, was differentiated into eight populations based on 12 traditional morphometric distances (Binashikhbubkr *et al.*, 2024). Five meristics, six conventional and twelve truss-based morphometric characters were explored for stock identification of Congaturi halfbeak (*Hyporhamphus limbatus*) in Southwestern Bangladesh (Mahfuj *et al.*, 2023).

Many morphometric case studies applied geometric landmark methods for stock identification. For example, Hernandez *et al.* (2023) focused on the species *Plagioscion magdalenae*, an important fishery resource in Colombia. They used 17 landmarks and found morphological differences between individuals from different locations sampled using geometric analysis. The authors relate the differences in morphology to artisanal fishing (e.g., smaller body size in response to fishing). The population structure of the tub gurnard (*Chelidonichthys lucerna*) in the Northeast Atlantic was analysed using geometric morphometric based on a landmark truss network. High differentiation (95%) was detected between tub gurnards sampled from three locations (Ferreira *et al.*, 2023). Geometric morphometric analysis using landmarks was applied to differentiate between three populations of Indian mackerel (*Rastrelliger kanagurta*) from the eastern Indian Ocean where there are conflicting population boundaries. The variations in body shape confirmed three distinct populations of Indian mackerel and this work will inform fisheries management in the area for this species (Kasinath *et al.*, 2024). Asadujjaman *et al.* (2024) used truss-based morphometric characteristics to distinguish grey mullet (*Liza parsia*) stocks in different rivers in the Sundarbans estuary, Bangladesh. Morphometrics for body shape (box-truss and geometric shape indices), and Fourier analysis for otolith shape have revealed three separate stocks of Mediterranean horse mackerel (*Trachurus mediterraneus*) in the Eastern Black Sea, Middle Black Sea, and Sea of Marmara (Dürrani and Seyhan, 2024).

Geometric morphometrics is also proposed to be useful for species identification from scales (Traverso *et al.*, 2024). Once large datasets are available, outline-based geometric morphometry is very promising for future automatization in species identification. Dechsupa *et al.* (2023) developed an approach to classify bivalve morphology based on neural network analysis of size, outline shape, tooth, scars, and texture. The approach adopts some aspects of geometric morphometrics for landmarks and outlines with machine learning classification.

These studies illustrate that morphometrics provide valuable information for better management and conservation. However, since morphometric data cannot provide all the answers, authors strongly recommend inclusion of other methods to get the full picture of the stock structure.

For example, various morphometric methods (traditional morphometrics, truss network system and geometric morphometrics) are now used in association with molecular markers for fish diversity assessment (Dwivedi and De, 2024). De and Dwivedi (2023) offer guidance on free and open source software for morphometric image processing and statistical analyses, ironically in a paper that is behind a pay wall and not open access.

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## Tagging (Contributors: Steve Cadrin, Ann-Britt Florin, Douglas Zemeckis)

There have been several recent case studies that used conventional or electronic tags for stock identification in ICES areas and other regions. Tagging data was often analyzed in combination with other sources of information. New tag technologies continue to be developed as well as advances in analytical techniques.

Several recent studies applied multiple tagging technologies to study movement patterns of European seabass, *Dicentrarchus labrax*. Goosens *et al.* (2024) re-analyzed the data reported by de Pontual *et al.* (2023, reviewed by SIMEG in 2023) as well as other tags released off Belgium (5,598 conventional disc tags released 2006–2021, 150 archival tags released 2006–2021, and 131 newly developed acoustic data storage tags, Goossens *et al.* 2023). Results from the multiple tagging studies confirmed the previously published movement patterns (i.e., connectivity among ICES advisory units), with some residents in the North Sea as well as seasonal migrants among the eastern and western English Channel, the Celtic Sea and the Bay of Biscay. The authors conclude that fine-scaled population structure should be considered for stock assessment and seasonal fisheries closures.

Two recent studies applied Pop-up satellite archival tags (PSATs) to Canadian stocks of Atlantic halibut (*Hippoglossus hippoglossus*) to describe movement patterns. Ransier *et al.* (2024) deployed 71 PSATs, geolocated migration tracks for 41, and found high migratory diversity and complex spatial structure on the Scotian Shelf and southern Grand Banks. Migratory behaviors included shelf residency, slope residency, shelf-channel migration, shelf-slope migration, and dispersal. The high migratory diversity suggests multiple resident and migratory contingents with no apparent genetic structure. Marshall *et al.* (2023) characterized migrations of Atlantic halibut in the Gulf of St. Lawrence using PSATs. Their primary objective was to identify potential industry impacts (e.g., bycatch fleets) using fish harvesters' knowledge, but seasonal migration routes and spawning grounds were described and the potential for inshore and offshore subpopulations were discussed.

Lundgreen *et al.* (2023) evaluated connectivity of Atlantic cod (*Gadus morhua*) in western Baltic Sea and adjacent areas using conventional tagging data in the western Baltic from 1957 to 1987, tagging data from other areas 1960–2018, and recent growth data from 2007–2021 trawl surveys. They found considerable connectivity with the Kattegat, primarily during the spawning season.

Jensen *et al.* (2023) integrated coded-wire tags and genetic identification of Chinook salmon (*Oncorhynchus tshawytscha*) stocks in the northeast Pacific Ocean. They estimated spatial distribution and relative abundance of four stocks to support management of mixed-stock fisheries. They also developed recommendations for routine stock composition sampling and analysis.

Frawley *et al.* (2023) used information from archival tags and fishery monitoring of North Pacific albacore tuna (*Thunnus alalunga*) to quantify seasonal distributions and movement patterns to inform how stock assessment can account for spatial structure. Arostegui *et al.* (2024) demonstrated that this general approach could also be applied to the data-limited shortbill spearfish (*Tetrapturus angustirostris*) by spatially integrating information from conventional tags, satellite telemetry, and fishery data to propose a boundary between North Pacific and South Pacific stocks.

Cramer *et al.* (2023) offered a framework for inferring population connectivity from telemetry. They distinguish connectivity within a generation (i.e., movement of individuals), connectivity from parents to offspring (e.g., larval dispersal), and generational connectivity (e.g., gene flow). All three forms of connectivity can inform a complementary perspective on stock identity.

The reliability of tagging studies can be affected by methods used. In a recent review by Anjarsari *et al.* (2024), different tagging methods are described and pros and cons discussed. Furthermore, Clemens *et al.* (2023) highlights the need for researchers to report the conditions for tagging and holding fish surgically implanted with tags since the conditions might affect the results of the study. For example, in Deters *et al.* (2023) methods for tagging the sensitive American shad (*Alosa sapidissima*) are developed, increasing 24h survival from 78% to 99%. Additionally, Londono *et al.* (2024) provided a promising tagging method for small, soft, and fragile marine animals through the use of a bioadhesive. These advances in tagging methods will open up future research opportunities and stock ID investigations into an even wider range of species

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## Otolith shape (Contributors: Florian Berg, Kélig Mahé, Christoph Stransky)

From June 2023 to June 2024, there were 17 papers dedicated to the otolith shape. For marine organisms, especially for fish, the otolith is the main calcified structure used to identify the stock structure.

### Otolith shape as tool for stock identification

Species/stocks in the ICES area

Vaz *et al.* (2023) studied the structure of the blackbelly rosefish, *Helicolenus dactylopterus*, and European hake, *Merluccius merluccius*, which are two economically important marine fishes, but there are still gaps in knowledge regarding their present stock structure. The objective was to assess the ability of otolith shape to define stock structure for the two species along the Northeastern Atlantic Ocean and the Mediterranean Sea, based on samples from eight and seven areas, for blackbelly rosefish and European hake, respectively. Shape analysis was obtained through Wavelet analysis. Canonical analysis of principal coordinates provided significant evidence for different population units with a clear separation between the Atlantic and Mediterranean populations for both species. However, random forest procedures indicated that the discrimination power varied with species and locations. For blackbelly rosefish, various Atlantic populations were more evident than for European hake. Overall, the usefulness of otolith shape to delineate stock structure of two species with distinct life history traits across a broad spatial region from the mid-Atlantic isles to the polar region, as well as the Mediterranean was demonstrated. Moving forward, it will be key to align our growing understanding of population structure with our increasing knowledge on species' biological traits to ensure management units reflect population structure.

Species/stocks outside the ICES area

Andrialovanirina *et al.* (2023a) analysed sagittal otolith shape was used to understand the stock structures of populations of the main commercial species caught around La Réunion Island. A total of 1091 individuals, belonging to nine species of bentho-pelagic bony fishes (*Aphareus rutilans, Cephalopholis aurantia, Epinephelus fasciatus, Etelis carbunculus, Lutjanus kasmira, Lutjanus notatus, Pristipomoides argyrogrammicus, Pristipomoides filamentosus, Variola albimarginata*), were analyzed and compared between 10 areas around La Réunion. To describe the external shape of the otolith, normalized Fourier elliptical descriptors were extracted. For each species, the analysis of shape data was performed in two steps. The first step was investigating the potential effects of confounding factors such as fish size, symmetry between right and left otoliths, sexual dimorphism and spatial distribution. When location showed a significant effect on otolith shape, a second step coupling two complementary analyses was performed with hierarchical clustering (unsupervised machine learning) and linear discriminant analysis with jackknifed prediction (supervised machine learning), allowing characterization of the potential stock limits for each of the treated species. The results show that, for the nine species treated, only two species (*Etelis carbunculus and Pristipomoides filamentosus*) show spatial structuring around Reunion Island with, for each of them, two stocks potentially separated along a northwest/southeast axis. These results show that some species around La Réunion Island may have local subpopulations.

Adjibayo Houeto *et al.* (2023) investigated the variations in sagittal otolith shape and morphometry, including length (Lo), width (Wo), area (Ao), and perimeter (Po) from two populations of *Chelon ramada* collected from the Boughrara and El Bibane lagoons located in southeastern Tunisia. The objective was to assess the geographic variation in the sagittal otoliths' shape and morphometry and the effect of potential fluctuating asymmetry (FA) in morphometry on the stock structure of C. ramada in the two lagoons to inform on appropriate management procedures. At the interpopulation level, analysis of sagittal otolith shape showed a statistically significant difference ($P = 0.0001$), i.e. there was a bilateral asymmetry, in the shape of left and right otoliths between individuals of the two populations. In addition, significant FA was found only in Lo between the left and right otoliths. At the intrapopulation level, a significant shape difference ($P < 0.0001$), particularly asymmetry, was observed in both left and right otoliths between males and females, indicating sexual dimorphism in shape within the Boughrara lagoon. However, significant shape similarity, i.e. symmetry, was observed in the left and right otoliths among individuals of the El Bibane lagoon. Moreover, a significant FA was detected in Lo between the left and right otoliths only among males, as well as between males and females of the Boughrara lagoon. However, a significant FA between the left and right otoliths was found only in Wo among males and in all morphometric dimensions among females and Wo between males and females of the El Bibane lagoon. Discriminant function analysis of the otolith contour shape confirmed the presence of two separate C. ramada stocks, one corresponding to the Boughrara lagoon and the other representing the El Bibane lagoon, which should be managed separately. The possible cause of morphological variation in the sagittal otoliths' shape and morphometry due to FA between individuals of the two populations was discussed in relation to the biotic and abiotic factors.

Saygin (2024) investigated the sagittal otolith morphometry of the red mullet *Mullus barbatus* inhabiting the Aegean, Black Sea and Mediterranean coastal waters of Türkiye. In the comparison of otolith shape of *M. barbatus*, elliptic Fourier and Wavelet analyses were used as well as otolith shape indices with multivariate statistical techniques. In total, 180 specimens were examined for otolith shape analyses. Otolith shape indices, including form factor, aspect ratio, circularity, roundness, and rectangularity, have been determined. A principal component analysis and canonical discriminant analysis were carried out for the discrimination of the three M. barbatus populations. The PERMANOVA test was used to evaluate differences between populations. The overall classification success for the canonical discriminant analysis in separating red mullet in these three seas was 53.9% in elliptic Fourier analysis and 57.8% in wavelet analysis. The Aegean and Mediterranean Seas have the highest classification success rates, at 65%. Elliptic Fourier analyses (68.6%) separated the Black Sea from the Mediterranean and Aegean Seas while Wavelet analyses (69.3%) separated the Aegean Sea from the Mediterranean and Black Seas.

Yedier *et al.* (2023) extracted 16 morphometric variables of the sagittal otolith of *Pargellus acarne* stocks collected from the Aegean and Marmara Seas coasts of Turkey, including six morphometric characters, six shape indices, and four ecomorphological indexes. Statistically significant differences were found between the right and left otolith variables of *P. acarne* individuals in both stocks ($p < 0.05$). Similarly, significant differences were observed on the same side between stocks ($p < 0.05$). The right otoliths exhibited higher discrimination power than the left within the two stocks. The PCA showed that only five (31.25%) (otolith area, otolith perimeter, form factor, roundness, and edge complexity index) out of the sixteen variables were quite important characters in the differentiation between stocks. These otolith characters demonstrated a very high rate of accurate discrimination (99.0%) between stocks. The results indicated otolith morphometric characters, shape indices, and ecomorphological indexes can be used as suitable tools to discriminate *P. acarne* stocks. This is the first study to include all otolith characters such as morphometrics, shape, and ecomorphological indices that discriminate between *P. acarne* stocks from these localities.

Ben Mohamed *et al.* (2023) analysed the geographic variation in otoliths' shape and size and the effect of potential fluctuating asymmetry (FA) in otolith size on the stock structure of *Mullus barbatus* collected from the Bizerte and Ghar El Melh lagoons located in northeastern Tunisia and to evaluate the relationship between the otolith mass asymmetry (OMA) and total length (TL). Analysis of the otolith shape showed a statistically significant intersexual shape difference, i.e. asymmetry, in the left and right and left-left and right-right otoliths between populations of the two lagoons. In addition, significant intersexual differences were detected in Lo, Wo, and Mo, as well as in FA, between the left and right otoliths among the two populations. Moreover, no statistically significant relationship ($P > 0.05$) was found between OMA and TL between and within the two populations. At the intrapopulation level, a significant intrasexual asymmetry was observed in the left and right, as well as on left-left and right-right sides, otoliths' shape and size only within the Ghar El Melh lagoon. Discriminant function analysis of the otoliths' contour shape confirmed the presence of two separate stocks representing the Bizerte and Ghar El Melh lagoons, which should be managed separately. This significant inter and intrapopulation asymmetry detected in otolith shape and size due to FA can be attributed to the instability of larval development caused either by environmental stress associated with variation in water temperature, salinity, feeding conditions and pollutants or due to poor living conditions of larvae resulting from unfavourable environments.

De Carvalho *et al.* (2024) analysed *Larimus breviceps* which has an important role in the marine food chain, as it is one of the most abundant and frequent species in the bycatch of coastal shrimp fisheries in Brazil. This study aimed at comparing the otolith shape of specimens collected in three different Brazilian coastal areas: Sergipe (SE), northeastern region; São Paulo (SP), southeastern region; and Paraná (PR), southern region. In a laboratory, 88 otoliths were extracted, photographed, and the contour was analyzed by the wavelet method (32 from SE, 28 from SP, and 28 from PR). The otolith contours varied between sampling sites. Linear discriminant analysis correctly reclassified 60.23% otoliths by the sampled sites, with the best reclassifications occurring in SE (62.5%), followed by PR (60.71%) and SP (57.14%). Multivariate analysis of variance also evidenced significant differences in contours among the sampling sites ($F = 2.3$; $P < 0.005$). Thus, two morphotypes of otoliths were found for *L. breviceps*: one from Sergipe (northeastern Brazil) and the second one from southeastern–southern Brazil, indicating connectivity between the populations off São Paulo and Paraná, to be confirmed by future genetic studies.

Zhou *et al.* (2023) want to differentiate different stocks of *Schizothorax grahami* (Regan, 1904) in the Chishui River, an upper reach of the Yangtze River, by otolith morphology. The otolith morphology of *S. grahami* from three different river sections was analyzed using the Shape Index, Fourier coefficients, and wavelet coefficients. The composite discrimination success rate of the Shape Index was 59.7%, and it was difficult to distinguish in the scatter plots. In contrast, canonical principal coordinate scatter plots clearly showed three distinguished stocks. The above results indicate that otolith morphology can discriminate between stocks in plateau endemic fish, and several *S. grahami* stocks may be separately managed in the Chishui River.

Sbida *et al.* (2024) studied *Scomber colias* which is a commercial species in the northwest coasts of Africa (NWA). However, relevant data on the stock structure and connectivity of *S. colias* along the NWA is scarce. The Eastern Central Atlantic Fisheries Committee (CECAF) assumes the existence of two stocks (a northern and a southern stock) between Morocco and Senegal, separated by Cap Boujdour. However, given the absence of relevant biological information on the migration and connectivity of the species, CECAF suggests a joint assessment of the two stocks. Otoliths can be used as natural tracers to study the population structure, fish movements, and habitat connectivity of fish. Otolith morphology, for instance, is a phenotypic trait with a genetic background that usually responds to environmental variables. This study used otolith shape analysis (wavelets) to investigate *S. colias* stock structure along the NWA, from Morocco to Senegal. Fish were collected between September and December of 2019 by a scientific survey in ten sites (Larache, Casablanca, Safi, Agadir, Tantan, Tarfaya, South of Boujdour, North of Cape Barbas, south Mauritania and Senegal) using a purse seine. The hereby results showed a highly significant regional differentiation among the sites, suggesting the existence of two population-units, with an overall correct re-classification of 91% to the two clusters. This dataset indicates the existence of an oceanographic barrier at the level of 28°N (Tarfaya), which limits the connectivity between the two stocks. Moreover, the mean otolith shape based on wavelet reconstruction for the two population-units revealed high phenotypic plasticity for *S. colias* otoliths. The broad variance between the two morphotypes highlights the environmental heterogeneity of the Atlantic Northwest African waters. The variation in the rostrum and anti-rostrum of *S. colias* otoliths is most likely due to genetic diversity or long-term isolation of the two population-units. The hereby data support the hypothesis that *S. colias* in the NWA is divided into two stocks with limited connectivity. In terms of fisheries management, this study recommends a fine-scale stock assessment.

### Otolith 3D shape as tool for stock identification

Andrialovanirina *et al.* (2024) studied innovative automated analysis of the three-dimensional (3D) shape of red mullet otoliths from the Mediterranean Sea, which was compared to conventional two-dimensional (2D) analysis. This new three-dimensional shape technique was found to be more accurate in delineating the stock, whether using unsupervised or supervised classification.

### Otolith shape combined with other descriptors for stock identification

Ankita *et al.* (2023) worked on the possible stock structure of catfish (*Rita rita*) in India. Independent analyses of landmark-based truss morphometry, otolith elemental analysis and otolith shape were conducted from the Ganga River and its tributaries Yamuna and Ramganga. Each of the stock-delineation approaches, namely, truss morphometrics, otolith elemental composition and otolith shape, showed significant differences among the fish groups from three sampling locations ($P \leq 0.003$). Despite these differences, reclassification analyses showed variable (although all greater than random) reclassification rates (truss morphometry: 78%, otoliths elemental data: 98%, otolith shape: 50%). An integrated view of the three analyses suggested spatial structuring and that there may be multiple stocks of *Rita rita* in the Ganges Basin.

Geladakis *et al.* (2023) examined the spatial variation in otolith morphology (shape and asymmetry) and genetic composition of 395 wild-caught Gilthead seabream (*Sparus aurata*) specimens, collected from the Aegean and Ionian Seas (eastern Mediterranean) between 2014–2018. The degree of scale regeneration (SRD, % of regenerated scales) was used as an indicator to assess the potential presence of aquaculture escapees in the wild-caught samples. Otolith shape and asymmetry analyses showed a phenotypic discrimination between northwestern Aegean and Ionian Gilthead seabream populations. Genetic analyses of nine microsatellite markers revealed higher levels of genetic variation in the wild compared with samples obtained from aquaculture farms. Despite the absence of genetic structure among the wild-caught seabream populations, a low but statistically significant genetic differentiation was found between reared fish and fish collected in the field. The SRD was considered effective in detecting the presence of aquaculture escapees that may have escaped in either early or late rearing phases.

Dürrani & Seyhan (2024) used geometric morphometrics for body shape, shape indices, and elliptical Fourier analysis for otolith shape to explore the morphological differences of the

Mediterranean horse mackerel (*Trachurus mediterraneus*) in the Eastern Black Sea, Middle Black Sea, and Sea of Marmara. The findings revealed considerable differences in body and otolith shapes across the examined regions, suggesting the existence of three separate stocks. The geometric morphometrics revealed evident differences in the snout, followed by the caudal peduncle and body depths. Both otolith shape indices and elliptic Fourier analysis revealed significant directional bilateral asymmetry between the left- and right-sided otoliths. The elliptic Fourier analysis revealed a non-overlapping surface difference of 2.12% between the reconstructed left and right otolith outline shapes. However, no significant differences in otolith shape were observed between males and females using either otolith side. In addition, otolith shape analysis using shape indices and elliptic Fourier analysis reliably supported the presence of three distinct stocks of *T. mediterraneus*. This study provides evidence supporting the recognition of multiple phenotypic stocks of *T. mediterraneus.*

De Almeida *et al.* (2023) intended to understand the population dynamics of The Brazilian mojarra, *Eugerres brasilianus* in three costal lagoons located in Rio de Janeiro, Brazil. A total of 90 individuals were collected in the lagoon systems of Itaipu, Saquarema and Araruama, between December 2019 and March 2020. A pre-selection of 30 individuals per location from the same age group (2 years old), following age estimation by counting the annual growth increments, were used. The contour of the sagittal otoliths was evaluated using elliptical Fourier descriptors (EFD), and the multi-elemental signatures (MES) of the whole otoliths were obtained using solution-based inductively coupled plasma mass spectrometry. Data were analyzed using univariate and multivariate statistics to assess the degree of separation between individuals from different lagoons. EFD revealed significant differences among individuals from the different sampling regions. MES exhibited distinct regional patterns, mainly driven by differences in Cu/Ca, Li/Ca, Mg/Ca, Mn/Ca, and Sr/Ca ratios. Reclassification accuracy rates obtained from linear discriminant function analyses using both EFD and MES of otoliths were 100% (Itaipu), 97% (Araruama) and 90% (Saquarema). Therefore, a clear distinction was observed among these groups, which was related to the inherent characteristics of each lagoon system, their semi-restricted connectivity with the adjacent coastal zone, as well as the estuarine-opportunistic behavior of the species. Thus, the results suggest that these fisheries should be managed as different subpopulation-units. However, more studies should be carried out about the fish movements and life history events of this species in southeastern Brazil.

Corti *et al.* (2024) delineated the population structure of common sole (*Solea solea*) in the Mediterranean Sea using genomic and otolith data, based on single nucleotide polymorphism (SNPs) markers, otolith shape and otolith trace element composition data. SNPs were correlated with environmental and spatial variables to evaluate the impact of the selected features on the actual population structure. Specifically, we used a seascape genetics approach with redundancy (RDA) and genetic-environmental association (GEA) analysis to identify loci potentially involved in local adaptation. Finally, putative functional annotation was investigated to detect genes associated with the detected patterns of neutral and adaptive genetic variation. Results from both genetic and otolith data suggested significant divergence among putative populations of common sole, confirming a clear separation between the Western and Eastern Mediterranean Sea, as well as a distinct genetic cluster corresponding to the Adriatic Sea. Evidence of fine-scale population structure in the Western Mediterranean Sea was observed at outlier loci level and further differentiation in the Adriatic. Longitude and salinity variation accounted for most of the wide and fine spatial structure. The GEA detected significant associated outlier loci potentially involved in local adaptation processes under highly structured differentiation. In the RDA both spatial distribution and environmental features could partially explain the genetic structure. Our study not only indicates that separation among Mediterranean sole population is led primarily by neutral processes because of low connectivity due to spatial segregation and limited dispersal, but it also suggests the presence of local adaptation. These results should be taken into account to support and optimize the assessment of stock units, including a review and possible redefinition of fishery management units.

Shahana *et al.* (2024) worked on the Crescent Perch, *Terapon jarbua*, which is one of the important food cum marine ornamental fish in India. The present study deals with the delineation of *T. jarbua* stocks along the Indian coast using the morphology of fish and otolith shape analysis. A total of 609 fish samples were collected from six major fishing harbors representing the Indian coast from February to May 2022. The conventional morphometry, truss network analysis and otolith shape indices revealed the morphological divergence for the fish among the stocks. However, meristic traits could not show the variations among the different stocks. The morphometric and otolith shape variability for the species revealed the existence of different phenotypic stocks along the Indian coast, which might be due to the ability of the *T. jarbua* to adapt to different environmental conditions. The study highlights the need for separate biological and stock assessment studies for developing effective management strategies.

### Otolith shape as tool for species identification

Quigley *et al.* (2023) assembled a species-specific image library of sagittal otoliths from 70 mesopelagic fishes belonging to 29 families collected in the western North Atlantic Ocean. Images of adult sagittal otoliths from 12 species were documented and photographed for the first time. The fish were identified to species with a combination of morphological characters and DNA barcoding. This otolith image library, coupled with otolith-length and width-to-fish-length relationships, can be used for prey identification and back-calculation of fish size, making it a valuable tool for studies relating to food webs in the important yet poorly understood mesopelagic zone.

### Automatic Method to extract the otolith shape

Andrialovanirina *et al.* (2023b) using the routinely measured otolith data of plaice (*Pleuronectes platessa* Linnaeus, 1758) and striped red mullet (*Mullus surmuletus* Linnaeus, 1758) in the eastern English Channel and north-east Arctic cod (*Gadus morhua* Linnaeus, 1758), they generated a greyscale images matrix from the raw images in different formats. Contour detection was then applied to identify broken otoliths, the orientation of each otolith, and the number of otoliths per image. To finalize this standardization process, all images were resized and binarized. Several mathematical morphology tools were developed from these new images to align and to orient the images, placing the otoliths in the same layout for each image. For this study, we used three databases from two different laboratories using three species (cod, plaice and striped red mullet). This method was approved for these three species and could be applied to other species for stock identification.

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## Otolith chemistry (Contributors: Patrick Reis-Santos, Susanne Tanner, Lisa Kerr, Kirsteen Mackenzie)

In the past year, otolith chemistry has been applied as a stock identification tool to discern stock structure of fish species around the world. Below is a summary of recent applications of otolith chemistry to fish stock identification of ICES species of interest, as well as an update on recent advances in the field.

Several studies used otolith chemistry to investigate stock structure and connectivity in Thunnus species, namely *Thunnus thynnus* and *Thunnus albacares*. **Artexte-Arrate *et al.* (2023)** used otolith δ13C and δ18O to assess the contribution of eastern and western populations of Atlantic bluefin tuna (*Thunnus thynnus*) to different mixing areas in the North Atlantic Ocean over 12 years (2009-2021). The stable isotope signatures of 2588 individuals sampled from different areas in the North Atlantic Ocean were compared to the reference baseline obtained from mature adults sampled in spawning grounds in the Gulf of Mexico and the Mediterranean Sea. Results provided strong evidence of longitudinal population structuring, with mixing of the eastern and western stocks occurring on foraging grounds on both sides of the 45ºW management boundary. The proportion of Mediterranean origin fish crossing to the west was higher than those originating from the Gulf of Mexico and crossing to the east. For all regions analysed, mixing rates appear to be non-constant and vary considerably from year to year.

In another study, **Artexte-Arrate *et al.* (2024)**, aimed to reconstruct early life history (<3.5 months) temperatures experienced by Atlantic bluefin tuna using an innovative geothermometer for carbonates to decipher whether the Mediterranean Sea is composed of different subpopulations or contingents. The study found that clumped isotope derived temperatures were not significantly different from satellite derived and otolith oxygen stable isotopic ratios derived temperatures, except in one of the three regions (central Mediterranean Sea). However, the sensitivity of the clumped isotope thermometer was found to be lower than that based on oxygen fractionation equation. Overall, large variations in temperatures from clumped isotopes resulted in a relatively weak thermometer, preventing reliable life history information to be extracted for Atlantic bluefin tuna. Nevertheless, authors caution the study is limited by sample size and that their study may not be representative of all Atlantic bluefin tuna cohorts in the Mediterranean Sea.

Still focusing on Atlantic bluefin tuna, **Logan *et al.* (2023)** investigated pre-spawning habitat use via stable isotope analysis. While spawning ground origin can be readily identified using otolith oxygen isotope analysis of fish caught in both foraging and spawning areas, the understanding of shorter seasonal movements remains incomplete. Authors used nitrogen isoscapes in the North Atlantic (distinct signatures between productive, nearshore and more oligotrophic open ocean foraging habitats) in combination with linear discriminant analysis of bulk nitrogen isotope data to estimate the percent of Atlantic bluefin tuna that occupied shelf or open ocean foraging habitats prior to capture on spawning grounds. Fish from the western spawning area (Gulf of Mexico) were classified as previous shelf foragers (91%), while ABFT associated with eastern Atlantic spawning grounds primarily had an open ocean/Mediterranean Sea classification (96%

Morocco, 79% Strait of Gibraltar, 91% Balearic Sea, 100% Adriatic Sea). Observed bulk nitrogen isotope differences were confirmed to be due to baseline rather than trophic variability based on amino acid nitrogen isotope data. Results obtained provide insights into the foraging habitats of spawning assemblages of Atlantic bluefin tuna on both sides of the Atlantic.

**Rooker *et al.* (2023)** used otolith chemical markers (trace elements, stable isotopes) of yellowfin tuna (*Thunnus albacares*) to i) establish nursery-specific signatures of age-0 fish collected in four nursery areas (Gulf of Mexico, Caribbean Sea, Cape Verde, and Gulf of Guinea), and ii) investigate the origin of sub-adult and adult fish captured in the western Atlantic Ocean (Gulf of Mexico, Mid Atlantic Bight). Mixture and individual assignment methods were used to relate adult core signatures to baseline signatures of age-0 fish from each nursery area. Results showed high levels of mixing by yellowfin tuna from the different nursery areas and pronounced interannual variability in nursery-specific contribution rates in the western Atlantic Ocean. This study provides evidence of the complex and dynamic nature of this species' stock structure and population connectivity and highlights the need for temporally resolved estimates of nursery origin to refine assessment models and promote the species' sustainable harvest.

**Bassi *et al.* (2023)** used otolith chemistry to assess the population structure and connectivity of Greenland halibut across the Gulf St Lawrence and adjacent areas. While previous studies indicated genetic differentiation between the Gulf of St. Lawrence and other Northwest Atlantic regions, otolith chemistry revealed a pronounced connectivity throughout the Gulf of St. Lawrence, including adjacent areas of the Saguenay Fjord. Analysis of the otolith core chemistry indicated three distinct juvenile sources, with fish from multiple sources contributing to the overall population. However, one of the sources had smaller contributions to the overall population and had no clear correspondence to the element composition of the otolith margin of adults collected in the different estuarine areas. The authors suggest that this source might be located outside the Estuary and Gulf of Saint Lawrence, potentially along the Labrador coast, due to its high barium concentration.

Diving deeper into migration patterns of Greenland halibut, **Bassi *et al.* (2024a)** investigated source-sink dynamics and movement between nurseries within the Gulf of St Lawrence. Otolith elemental composition was analysed along core to edge transects, with edge signatures used to infer variations in migratory patterns between the two studied sites. Overall classification of collection sites was good, with 77% overall classification success. Results suggested that most juvenile Greenland halibut originated from the estuarine site, but some migrated to the North Anticosti area at a smaller size than expected. The study found no difference in migration behavior or timing based on sex.

Following their work in the Gulf St Lawrence, **Bassi *et al.* (2024b)** investigated the origin, movement and population structure of Greenland halibut along coastal Greenland and Canada. The aim was to characterize the contribution of seventeen different sampling areas to coastal stocks found in the Northwest Atlantic. Overall, four distinct regions were defined based on pools of adjacent sites with similar chemical signatures. While classification accuracy based on otolith edge chemistry was moderate (53% to 73% correctly classified individuals), unsupervised models of otolith core chemistry suggested the existence of three distinct natal source. From the results authors highlight the high connectivity in the region, but also the existence of a nursery that contributed proportionally more to all collection regions, which is suggested to be around the Disko Bay–Hellefiske Bank. Protection of this area is indicated as key to ensure the sustainability of the fishery.

From the same group, **Gauthier *et al.* (2024)** used otolith chemistry to analyse habitat use and mixing patterns of the Atlantic halibut (*Hippoglossus hippoglossus*) stock in the Gulf of St Lawrence. Signatures in otolith edges were used to two distinct groups, one for shallow and other for deeper waters. Results showed that Atlantic halibut displayed different migration strategies throughout its life that could be grouped into three contingents: resident, annual migrant, and irregular migrant. Most halibut were found to migrate from deep to shallow water in the first three years of life. But after reaching maturity, some became residents in deep areas whilst continued to migrate between shallow and deep waters throughout their lives on an annual or irregular basis.

Still in the Estuary and Gulf of St. Lawrence, **Coussau *et al.* (2023)** determined the origins and movement of deepwater redfish. A similar approach as the other studies was undertaken, analysing core and edge chemical signatures for the 2011 and 2013 cohorts. While an East to West gradient in multi-element edge signatures was found, evidence of temporal variation across the two years was suggested to be more likely due to factors like age or growth rather than changes in environmental conditions. Overall, two possible natal sources were suggested to supply the entire population in the gulf but contributing in different proportions. Authors indicate these findings provide valuable information at an ecologically relevant scale to support the assessment and management of the recovering redfish fishery.

**Fortin *et al.* (2024)** examined the relationship between water chemistry and otoliths in the St. Lawrence River and its tributaries. They found a strong spatial variability and concordance between environmental and otolith concentrations from 930 fish of 21 different species, especially for strontium (Sr) and barium (Ba). Reclassification using these two elements was accurate to overall correctly assign 84% of fish to one of 6 collection clusters, though authors note that some geographically scattered rivers were found within a cluster. Overall, this information can be applied to potentially predict fish origins movements between different habitats, valuable for fisheries but also, for instance, to infer regions used by an invasive species to identify potential introduction pathways and target management efforts.

A little bit further south and motivated by a recent expansion of the northern stock of Black Sea Bass (*Centropristis striata*) into the northern Gulf of Maine, **Koob *et al.* (2023)** used otolith core signatures (stable isotopes and trace elements) assess the natal origin of Black Sea Bass captured off the coast of Maine. Knowledge on fish origin is key as dramatic changes in movement patterns and population dynamics could profoundly impact stock assessment estimates and subsequent management regulations. Spawning condition adults from southern New England (SNE) and the mid-Atlantic Bight (MAB) were used to characterize the chemical fingerprint of known spawning regions with high reclassification success using random forest analysis (16% error rate). Otolith chemical signatures of the Black Sea Bass captured in Maine waters were classified as SNE (85%) and MAB (13%), with one sample remaining unclassified. Results support the current management population separation of the northern stock of Black Sea Bass between SNE and the MAB and highlights the importance of sound knowledge on fish natal origin to ensure long-term sustainable management, particularly as fish stocks continue to shift into new regions due to climate change.

### Combined use of otolith chemistry with other markers

Otolith chemistry has also been applied in combination with other techniques (e.g. genetics, otolith shape) to address population connectivity questions. **Källo *et al.* (2024)** combined otolith chemistry and genetics to investigate patterns of straying over ecological and evolutionary time, respectively, between neighbouring rivers flowing into Mariager fjord, Denmark. Otolith chemistry was used to determine the river of origin for sea trout (*Salmo trutta*) upon their return to freshwater and SNP markers were used to determine genetic structure among the rivers in the fjord. Otolith chemistry achieved 80% assignment accuracy of juvenile brown trout to their natal river, which allowed to determine that approximately 43% of adult sea trout had returned to non-natal rivers to spawn, with a similar proportion of strayers and natal homers in all the rivers.

Genetic analysis further supported that there was substantial gene flow among individuals originating from different rivers. Results obtained by the two methods are complementary and provide further evidence of high connectivity within this system, which consequently affects the genetic structure of the population.

By combining otolith chemistry, otolith shape and genomic markers (SNP - single nucleotide polymorphism), **Corti *et al.* 2024** characterised the population structure of common sole *Solea solea* in the Mediterranean Sea. They confirmed the occurrence of distinct populations in the Western and Eastern Mediterranean, as well as a separate genetic cluster in Adriatic Sea.

Other useful applications of otolith chemistry for fisheries science

Although not strictly related to stock identification and population structure, otolith chemistry has been also applied to enhance and validate age estimation in white hake (*Urophycis tenuis*) (LeFreniere *et al.* 2024), to advance our understanding on how both external and internal factors impact ion uptake, transport and incorporation by combining archival data storage tag derived information with otolith chemistry in cod (*Gadus morhua*) (Hüssy *et al.* 2024), and to reconstruct and quantify larval dispersal portfolio of European sea bass (*Dicentrarchus labrax*) in estuarine nursery areas of the northeast Atlantic Ocean (Teichert *et al.* 2024).

**LeFreniere *et al.* (2024)** compared the consistency of aging with counts of visual annuli to that of aging with cycles of otolith elemental concentrations by testing the hypothesis that oscillations in both environmental conditions and internal physiology through time influence uptake of elements during otolith mineralization. Manganese showed the most promising correlation with visual growth increments, offering an additional tool to enhance increment identification. Results of this study demonstrate that otolith chemistry can be used to improve the accuracy and precision of the estimation of fish age and maturity, even for challenging species.

**Hüssy *et al.* (2024)** investigated factors influencing otolith chemistry, using Baltic cod *Gadus morhua* as a model. By combining otolith data with archival tag records, they analysed the effects of internal (e.g., sex, size, age, growth) and external (e.g., temperature, depth, salinity) conditions on the elemental composition of a mix of elements in otoliths generally accepted to be more strongly under physiological (e.g., P, Mg, Zn) and environmental control (Sr, Ba). The results showed that elements primarily under physiological control exhibited distinct seasonal patterns and were influenced by water temperature and reproductive status. Elements expected to be predominantly under environmental control displayed geographic and depth-related trends. However, unexpectedly, Sr was unrelated to salinity. Additionally, all three elements showed seasonal patterns that were out of phase with each other but appeared to be linked to spawning and feeding migrations. While archival tag data provided insights into fine-scale movement patterns, the study emphasises the importance of understanding how water chemistry and physiology may impact elemental chemistry and its implication for stock identification, mixing patterns and reconstruction of spawning or feeding migrations, among other key life history events.

Dynamic time warping analysis was use by **Teichert *et al.* (2024)** to compare larval trajectories of European sea *Dicentrarchus labrax* bass based on otolith chemistry. This is a flexible, underutilized approach that can compare and align temporal sequences, allowing for variations in length. By applying dynamic time warping to otolith chemistry this study compared and classified similarities between larval trajectories and dispersal patterns of *D. labrax* from six estuarine nursery areas of the northeast Atlantic. The results showed that larvae hatched in distinct environments and dispersed in water masses with contrasting chemical signatures.

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## Parasites (Contributor: Ken Mackenzie)

Seven publications describing the actual or potential application of parasites as biological tags in population studies of marine fish and squid were published in the year from June 2023 to July 2024. Study areas were in the Northeast and Southwest Atlantic and the Northeast and Northwest Pacific. Three of the seven articles are in Russian and one is in Spanish, while two are additions to the already impressive list of publications on this topic from the group led by Timi in Argentina.

Bakay *et al.* (2023) reviewed and analysed the results of long-term studies (1981-2021) of the population biology of beaked redfish *Sebastes mentella* in the pelagic zone of the Irminger Sea and the adjacent bathyal zone of Greenland and Iceland. This fish colonizes a range of depths in the oceanic pelagial and the near-bottom layer of the bathyal zone. The parasitological data support the unity of the pelagic grouping of redfish in this vast study area and throughout its depth distribution.

Frolov *et al.* (2023) Investigated the possibility of using larvae of the nematode *Anisakis simplex* and plerocercoids of the cestode *Dibothriocephalus nihonkaiensis* to differentiate between local stocks of pink salmon *Oncorhynchus gorbuscha* in southern Sakhalin. Data on these two parasite taxa collected from a total of 7457 salmon caught from 1992 to 2022 revealed significant differences in abundance of both parasites between samples collected from the west coast of Sakhalin (Japanese Sea) and the eastern coast (Pacific Ocean). The results suggest that these parasites may be useful biological tags to distinguish between pink salmon stocks in the study area.

Frolov *et al.* (2024) Investigated the possibility of using three parasite taxa as biological tags to identify the source of catches of the saffron cod *Eleginus gracilis* caught around Sakhalin Island. A total of 3760 cod from two positions off the southeast coast and one off the northwest coast of Sakhalin were examined in the period from 1989 to 2016. The parasites selected as possible tags were plerocercoids of the cestodes *Pyramicocephalus phocarum* and *Nybelinia surmenicola* and the adult acanthocephalan *Echinorhynchus gadi.* The long-lived *N. surmenicola* plerocercoids were selected as the best tags and the authors recommended that samples of at least 100 cod should be examined to determine capture locations.

Gutiérrez *et al.* (2023) analysed the variability of parasite loads in the squid *Illex argentinus* caught on the continental shelf of central Patagonia in order to assess their potential value as indicators of stock structure. Four samples of squid, totalling 318 specimens from three successive cohorts caught from 2020 to 2022, were examined for parasites. Twelve parasite taxa were found, most of them larval stages. The results showed heterogeneity of parasite assemblage structure with a strong influence of host size. These changes are related to changes in host habitats and diets during this host's short life span of only one year, which cloud any interpretation of patterns when samples spatially or temporally separated are compared. As many squid species share these characteristics, the authors recommend that the use of parasites as biological tags for squid should be restricted to simultaneous sampling, with host size and age being taken into account.

Lanfranchi *et al.* (2024) evaluated changes in the structure of the northern stock of the striped weakfish *Cynoscion guatucupa* in the Argentine Sea over a period of 25 years by comparing parasite assemblages. Fish from the same three three sampling positions, totalling 85 specimens, were examined in 1993/1994 and again in 2018/2019, during which period the study area experienced significant warming due to climate change. Significant differences in parasite assemblages were found between sampling dates, but not between regions, indicating that the stock structure has remained stable even under a warming process that seems to have affected the parasite assemblages. The results suggest that the changes in parasite burdens are not related to population density or geographic distribution of the fish host, but to changes in temperature, salinity or density of top predators. The parasites appear to have been affected by climate change before the fish host and so can be considered sentinels for monitoring the stability and distribution of this fishery resource.

Morales-Serna *et al.* (2024). The aim of this study was to gain insights into the population structure of a small pelagic fish, the shortjaw leatherjacket *Oligoplites refulgens*, along the east coast of the Gulf of California, using parasites as biological tags. Samples totalling 119 fish were collected at four localities in May 2023 and examined for metazoan parasites. Twelve parasite taxa were found and their infracommunities at each of the four localities were compared. The analyses showed a clear separation between fish from the two northern and the two southern localities sampled, supporting earlier results from host morphometric data suggesting limited connectivity between fish from the northern and southern populations. The authors suggest that the use of parasites should be further explored to determine stock patterns of small pelagic fishes in the Gulf of California.

Morales-Serna *et al.* (2024). This short note briefly describes the use of parasites as biological tags for fish stock identification and introduces a new research project recently started with the aim of identifying possible stocks of Pacific thread herring *Opisthonema libertate* in the Gulf of California using this method. Preliminary results suggest the existence of two separate stocks from the northern and southern coast of Sinaloa.

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## Interdisciplinary approaches (Contributors: Manuel Hidalgo, Steve Cadrin and Lisa Kerr)

The application of interdisciplinary analyses (i.e., the integration of two or more stock identification techniques) had been increasing in the last decade becoming a regular approach. However, while the number of publications under the multidisciplinary category has slightly decreased compared to the last year, the diversity of combinations of methodologies has increased. This includes the combination of classic stock identification methods as well as the use of additional sources of data to support the delineation of stock structure. It is also worth noticing the increasing number of studies combining a high number of techniques (i.e. four, five or more). We here summarize some reviews, integrated approaches and methods development published in the second semester of 2023 and first semester of 2024 that were not included in the review published by SIMWG last year (ICES, SIMWG, 2023).

Integration of genetics and otoliths data is still one of the most recurrent combinations currently found in the literature. **Corti *et al.* (2024)** investigated the population structure of common sole (*Solea solea*) in the Mediterranean Sea using genomic and otolith data, based on single nucleotide polymorphism (SNPs) markers, otolith shape and otolith trace element composition. This study takes a seascape genetics approach combining redundancy and genetic-environmental association analysis to identify loci potentially involved in local adaptation. Results from both genetic and otolith data suggested significant divergence among putative populations of common sole with a clear separation between the Western and Eastern Mediterranean Sea, influenced primarily by neutral processes due to spatial segregation and limited dispersal. In addition, the study also suggests the presence of local adaptation associated to local environmental variability. The same three-technique approach was used by **Franco *et al.* (2023)** to discern fine-scale population structure of whitemouth croaker (*Micropogonias furnieri*) in three localities in Rio de Janeiro State (Brazil). Through the combined use of genetic markers (nuclear microsatellites) and otolith signatures (morphometry and chemistry), two genotypic (north and center/south) and three phenotypic (north, center and south) populations were found, the later in response to local oceanographic conditions, such as upwelling, and local processes in the great bays with different degree of anthropogenic influences.

Genetics information is still found combined with many other classic stock identification methods, but also with contemporary demographic and distribution information. **Zamroni *et al.* (2024**) combines several body morphometric characters and genetics information (COI, cytochrome oxidase I, and Rhodopsin markers) of the squid (*Uroteuthis chinensis*) in the waters of western Kalimantan and northern Java (Indonesia). The results of these two techniques show a lack of significant differences suggesting that the regional *U. chinensis* connectivity and the close kinship should advocate to a single stock approach, which would require collaborative fisheries management across areas (western Kalimantan and northern Java). **Verba *et al.* (2023)** modeled the contemporary and historical distribution of the dog snapper (*Lutjanus jocu*) in Brazil. They described patterns of genomic diversity to better understand how climatic cycles might correlate with the species demographic history and current genetic structure. While the study showed that during the Last Glacial Maximum there were ecological barriers that are absent today, possibly dividing the range of the species into three geographically separated areas of suitable habitat, the results suggest that habitat availability changes have not influenced contemporary levels of genetic divergence between populations. The demographic analyses also show homogeneous sensitivity to environmental variations across the population's distribution . The study concludes that the general low levels of genetic structure and gene flow support a single stock of this species in Brazilian waters, requiring a coordinated legislation and management across its distribution.

The combination of genetics and biophysical modeling represents an integration of methods that has emerged strongly during recent years according to our last reviews (e.g., ICES, SIMWG, 2023). **Abecasis *et al.* (2024)** combined genomics, biophysical modelling, and also biotelemetry to infer the population structure and connectivity of Atlantic meagre (*Argyrosomus regius*) in the south European and north African Atlantic coast, including genetic samples from previously identified Atlantic spawning locations (Gironde, Tejo, Guadalquivir, Banc d'Arguin) and two additional regions (Algarve and Senegal). Nuclear SNP-genotyping showed a clear differences between the European and African populations, with isolation of the few known Atlantic spawning sites. Limited connectivity between subpopulations is potentially associated with restricted adult movement. This study reports evidence of population structure, mainly between Africa and Europe but also within Europe, supporting the management of meagre as separate stocks. **Lima *et al.* (2023)** add ecological niche modeling to the combination of genetics analysis and dispersal models to assess the long-distance connectivity between South America and western Africa of the Brazilian reef octopus (*Octopus insularis*); a species classically distributed in the west Atlantic. The study performed molecular analyses using fragments of the mitochondrial gene from samples collected in Sao Tome Island (west coast of central Africa). A Bayesian phylogenetic reconstruction showed that two of the three octopus sequences from Sao Tome island belong to a monophyletic *O. insularis* clade. The dispersal models pointed out that paralarvae could potentially reach the seamounts region along Africa's coast via oceanic currents from Sao Pedro and Sao Paulo archipelago (central-western Atlantic) in a period ranging 30-60 days. Also, ecological niche modeling showed suitable habitats for octopus settlement from Guinea-Bissau down to Equatorial Guinea and Gabon, and African Islands, suggesting a potential habitat expansion in the future.

Multi shape-based analyses combining body and otolith shape were used by **Durrani and Seyhan (2024)** to assess the stock structure of Mediterranean horse mackerel (*Trachurus mediterraneus*) in the transition between the Mediterranean and the Black Sea, including: Eastern Black Sea, Middle Black Sea, and Sea of Marmara. The geometric morphometrics revealed evident differences in the snout, followed by the caudal peduncle and body depths. Otolith shape analysis using shape indices and elliptic Fourier analysis also supported the presence of three distinct stocks of Mediterranean horse mackerel. The findings revealed considerable differences in both body and otolith shapes across the examined regions, suggesting the existence of at least three separate phenotypic stocks in the region.

Seminal and classical integration of otolith-based methods, shape and microchemistry, are still used in many studies. **De Almeida *et al.* (2023)** combined the contour of the sagittal otoliths evaluated using elliptical Fourier descriptors, and the multi-elemental signatures of the whole otoliths of the Brazilian mojarra (*Eugerres brasilianus*) collected in three costal lagoons located in Rio de Janeiro, Brasil. A pre-selection of 30 individuals per location from the same age group (2 years old). A high classification accuracy rates was obtained combining results from both otoliths-based techniques. The clear distinction observed among groups is related to the inherent characteristics of each lagoon system, their semi-restricted connectivity with the adjacent coastal zone, as well as the estuarine-opportunistic behavior of the species.

Stable isotopes as stock identification technique is historically associated to calcified structures, but is increasingly used with other biological tissues and in combination with other stock identification techniques. **Binstock *et al.* (2023)** assessed the ecological connectivity of blacktip sharks (*Carcharhinus limbatus*) among the western, central, and eastern US coast of the Gulf of Mexico using stable isotope analysis of muscle and vertebral tissues. The study shows that individuals from western and central regions exhibited isotope values and food web niches that were significantly smaller compared to eastern sharks, which were enriched in delta 13C and depleted in delta 15N in the westernmost region. Ontogenetic shifts were identified in most regions with no overlap in average isotope values from early to recent life between regions. These spatiotemporal patterns suggest that in the year following birth and prior to the time of capture, blacktip sharks on the central and western shelves have separated ecologically from blacktips on the eastern closer to the Florida shelf. **Alburquerque *et al.* (2024)** combined muscle stable isotope and otolith chemistry analyses to examine the population structure of dusky groupers (*Epinephelus marginatus*) and its association with the two upwelling systems (Cabo Frio Cabo Santa Marta) in the Brazilian coast. The results show three separate population groups along the coast: north (north of Cabo Frio), center (between upwelling regions); and couth (south of the Cabo Santa Marta system). The study suggests the important role of the upwelling systems in the distribution of groupers stocks along the Brazilian south-western coast, while a causal effect still requires further research. This combined approach, leveraging information from distinct natural tags, reflects the variability of water chemistry and food webs with latitude.

Oceanographic connectivity estimates from biophysical modeling are increasingly used to support population dynamics models in addition to spatial management and the design of spatio-temporal closures. **Allgayer *et al.* (2023)** combined a biophysical model of dispersal with spatial population demography, with the aim of predicting within-stock patterns of connectivity of sandeels (*Ammodytes marinus*) in the North Sea. The approach also uses network topology metrics, particularly several types of centrality to quantify the contribution of immigrants to many other sites and also to identify patches that are particularly isolated, and therefore unlikely to receive immigrants from elsewhere. This study highlights how connectivity characteristics of the stock may influence population recovery to major harvesting events, which often lead to localized patches depletion, providing additional scientific support to spatially-explicit management of commercial marine species. **Lincoln *et al.* (2024)** combined an inverse-parameterized three-dimensional hydrodynamic and Lagrangian particle tracking models (i.e. back-tracking) with otolith daily growth increment counts conducted on 0-group sea bass (*Dicentrarchus labrax*) from seven settlement estuaries in the Irish and Celtic seas to identify probable spawning locations. The study shows two broad spawning areas: the central Irish Sea leading to post-larval recruitment in north Wales and northwest England, and the southern Irish Sea/ Celtic Sea leading to post-larval recruitment in south Wales. This study concludes that the current seasonal closure for northern stock bass may not protect spawning events that drive recruitment into settlement sites in Wales and northwest England.

Fisheries-independent spatial data such as scientific bottom trawl surveys have long supported stock identification research and continue to do so. **Lundgreen *et al.* (2023)** combined contemporary growth data of cod (*Gadus morhua*) from trawl surveys with historical tagging data to assess the ecological connectivity of the Sound area of the western Baltic Sea with the neighboring stock in Kattegat. The study shows high ecological connectivity between the Sound and Kattegat, mainly during the spawning season, but exchange between the regions was asymmetric. While cod tagged in the northern Sound were most likely to be recaptured in Kattegat, cod tagged in the southern part of the Sound were mainly recaptured in the Sound, suggesting further research is needed.

The incorporation of the spatial population structure in stock assessment models will benefit from disentangling the temporal from the spatial dynamics in complex populations; a difficult task as they are both closely interlinked. Recent studies used various sources of data and often different models to shed new light on complex population structures. **Kerametidis *et al.* (2024)**

combined fisheries-dependent and fisheries independent data using different statistical techniques (a generalized empirical orthogonal function and dynamic factor analysis) to reveal whether spatially structured environmental processes across multiple spatiotemporal scales in the western Mediterranean influenced the spatiotemporal dynamics of metapopulation subunits of red mullet (*Mullus barbatus*). Two types of sub-populations were detected, some were persistent but also dynamic aggregations were found with a heterogeneous influence of both local open-ocean convection and large scale climatic modes. **Úbeda *et al.* (2023)** used a similar approach applying multivariate autoregressive state-space models to examine stock structure of Greenland halibut (*Reinhardtius hippoglossoides*) in the North Atlantic. Abundance and biomass observations from four regions (Norwegian Sea, Iceland, Southeast Greenland, and Northwest Atlantic) were combined with growth rate parameters in the models along with the impact of climate (North Atlantic Oscillation Index) and fishing (commercial catches) on the stock dynamics investigated. This approach identified Northwest Atlantic individuals as an independent population, with Greenland halibut in the West Nordic stock (Southeast Greenland and Iceland) as two independent populations (east and west) displaying potential connections between eastern Iceland and the western Barents Sea. **Baltazar-Soares *et al.* (2023)** proposed a method combining temporal projections of species distribution modelling with genomic information of next-generation sequencing. The method introduced genomic information as the basis for a joint-species distribution model designed to explore the range of suitable habitats where stocks could thrive in the future as a function of their current evolutionary potential. This method builds on the limitation of species distribution models, which assumes that the whole population respond homogenously to the range of environmental conditions. It provides a tool to assess how the spatial delineation of fish stocks could evolve over moderate and long terms. **Charsley *et al.* (2023**) also developed a spatio-temporal modelling framework applied to stream ecosystems combining two case studies: a diadromous fish species, the endemic New Zealand longfin eel (*Anguilla dieffenbachii*) in the Waitaki region attending to the probability of encounter, and a simulation experiment over a wider region. The study develops a modelling framework known as the 'VAST stream network modelling framework', evolving from the widely-employed vector autoregressive spatio-temporal modelling, which here better represents the relatedness of points based on physical connectivity. These two applications demonstrate how stream network spatio-temporal models can usefully inform freshwater resource managers, providing insights into changes in fish encounter probability and density for different fish length classes and estimates of effective river length occupied. The simulation experiment using the Waikato model as an operating model was successful at assessing a diversity of sampling scenarios for accuracy, precision and coverage needed.

Studies and/or research projects integrating a high number of stock identification techniques (i.e., four, five or more) are also increasingly observed. **Schroeder *et al.* (2023)** combined meristic information, body shape, otolith morphometry and otolith microchemical tracers to assess the stock structure of mullet (*Mugil liza*) across Brazilian and Argentinian waters. Meristics show two morphotypes in Brazil, which could represent distinct subpopulation-units, potentially segregated from the Argentinian subpopulation. Otolith shape analyses and multi-elemental otolith core analyses showed similarities between one of the morphotypes in Brazil and the one in Argentina. The study suggests that morpho-meristic data and univariate elemental fingerprints reveal distinct environments inhabited by fish along the western coast of South America. Indeed, the multi-elemental otolith core results suggested the existence of more than one nursery area for the species, and support the future consideration of two sub-populations for fisheries management purposes within the current southern stock of mullets. Finally, **Hidalgo *et al.* (2024)** summarize main findings of a research project aimed at revealing the transboundary population structure of sardine (*Sardina pilchardus*), European hake (*Merluccius merluccius*) and blackspot seabream (*Pagellus bogaraveo*) in the Alboran Sea and adjacent waters (TRANSBORAN project). A multidisciplinary set of techniques (genetics, otolith microchemistry, otolith shape, parasite composition, body morphometry, meristic descriptors, numerical hydrodynamic modelling, fishery data analysis, and data obtained through a dedicated ichthyoplankton survey) were analyzed independently and collectively using multivariate analyses and a semi-quantitative stock differentiation index. Considering the results of all disciplines in an integrative manner, the project did not find scientific support for homogenous populations and joint stock management for Aboran Sea European hake and sardine, concluding the existence of two stocks for these two species: north and south stock in the Alboran Sea.

Finally, it is worth highlighting that along the increasing diversity and number of integrated approaches used in stock identification, there is increasingly a need to transfer this information to operational spatial stock assessment. Seminal studies towards this goal have been published this year. **Berger *et al.* (2024)** reviewed the spatial capabilities and functionality across stock assessment platforms to identify future needs for next generation assessment software packages. The review highlights that despite commonalities across platforms (e.g., most models allow for a single population with spatial heterogeneity, apportionment of recruitment, and age-varying connectivity), no single platform is flexible enough to address the full breadth of spatial dynamics complexities observed in empirical and modeling studies as those reviewed in the current report. This review highlighted the need for more generalizable and modular next-generation assessment platforms that can account for the spatiotemporal complexity of marine resources, including natal homing and spawning migrations, ontogenetic movement patterns, metapopulation structure, and complex fleet dynamics. **Goethel *et al.* (2024)** also reviewed all the types of spatial assessment models available and summarized the options to parameterize population structure to offer guidance to promote the development of candidate spatial assessment models for application in management procedures. They also provided pragmatic guidelines for selecting the most appropriated spatial assessment model attending to the observed spatial structure, data limitations, and management concerns.

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# Annex 4: Responses to requests from ICES working groups (ToR b)

## SIMWG review of WGDEEP 2023 WD08 “Refining stock distribution of the current bli.27.nea ICES assessment unit, based on new evidence of genetic and demographic population structure” (WGDEEP request on blue ling)

### Background

The working document (WD) provided by Hege Øverbø Hansen, Pascal Lorance and Rui Vieira examines blue ling (*Molva dypterygia*) stock structure and distribution in the Northeast Atlantic. Current ICES advice is provided for three blue ling stocks: 1) “bli.27.nea” in Subareas 1, 2, 8, 9, 12 and Divisions 3a and 4.a, 2) “bli.5a14” in Subarea 14 and Division 5a, and 3) “bli.5b67” in Subarea 6-7 and Division 5b. The authors have provided biological, ecological, and genetic evidence to suggest that blue ling from the Norwegian Sea, coastal Norway (Subareas 1-2), the northern North Sea (Division 4a) and Skagerrak (Division 3a) should not be assessed with blue ling from Subarea 12 as well as that blue ling do not exist in Subareas 8-9.

### SIMWG review

Recent genetic analysis (McGill *et al.* 2023) showed that blue ling from NW of Scotland and off South Greenland are clearly distinct from blue ling along the Norwegian coast. There were no samples from area 12, however, which the WD refers to in terms of stock allocation. According to the WD, bathymetric and hydrological features south of Iceland suggest that deeper waters (<1500m) are separating blue ling in the west and east and “western” blue ling should be included in bli.5a14, whereas “eastern” blue ling (from area 12b) should be included in bli.5b67. Assessment and survey results demonstrate that blue ling from Iceland and East Greenland (bli.5a14) and around the Faroes and West of the British Isles (bli.5b67) follow distinct stock dynamics and should thus not be combined. The WD notes the clear separation between “Norwegian” and “Rockall” types, but it also makes considerations about areas 1 and 12, which cannot be robustly supported by the data, as:

1) the “Norwegian” samples are really only coming from areas 2 and 4a, so nothing can be said about area 1;
2) the genetic study did not have fish from area 12, so it is speculative to argue about the identity of fish from this area and assume that they would form some sort of continuum between East Greenland (area 14) and area 6 around Rockall. Although this would appear logical, a firm conclusion would require at least some genotypes from area 12. No speculations around demersal movements from area 12b can justify the merging;
3) there is no doubt that the “Norwegian” fish from areas 2 and 4 are distinct from area 6 (and possibly 5), so there are certainly at least two independent stocks in blue ling and thus, the separation between these two genetically identifiable stocks would represent an improvement to the assessment. The question remains whether it is appropriate to arbitrarily “expand” the reach of each of these two stocks to adjacent areas (i.e. area 1 for the Norwegian stock and area 12 for the Rockall stock) for which no genetic information is available. Although it is not formally appropriate, assessing the stocks in this way would likely offer a more refined delivery than in the past.

Blue ling from areas 8-9 appear to be Spanish ling (*Molva macrophthalma*), so that these areas should be excluded from bli.27.nea.

## SIMWG conclusions

The provided evidence for allocating blue ling from area 12 is weak, since no samples from area 12 were included in the genetic analysis. However, we support the consideration that it is unlikely that blue ling from area 12 are the same population as blue ling in areas 1,2,4a, and 3a. Although a separation of blue ling in “western” and “eastern” part of area 12 would formally not be appropriate, it would appear logical and could be considered in stock simulations to improve the assessment. In any case, blue ling from areas 2 and 4 should not be assessed together with blue ling from areas 5-7 and areas 8-9 should be excluded.

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## SIMWG response to a request from the Data Evaluation Workshop (DEWK) for the Benchmark Workshop on Horse Mackerel and Boarfish stocks (WKBHMB) to review a working document (WD) on changing stock boundaries for two horse mackerel stocks

### Background

The specific request was to review WD02 (see below) and to confirm if SIMWG supported:

1. the proposed reallocation of the catches in Divisions 3.a and 4.a in quarters 1 and 2 to the Western stock;
2. the undertaking of sensitivity analysis of the North Sea assessment to the assignment results from Divisions 7.d and 7.e.

The request was accompanied by:

1) WD02 (*"A summary working document on the genetic stock identification and assignment of Western and North Sea horse mackerel, Trachurus trachurus. ICES Data Evaluation Workshop (DEWK) for the Benchmark workshop on horse mackerel and boarfish stocks (WKBHMB)"* by E. Farrell);

2) WD01 (*"A working document on the genetic Stock Identification of horse mackerel, Trachurus trachurus for the ICES Benchmark workshop on horse mackerel and boarfish stocks (WKBHMB) Version 4.0, 25th January 2024"* by Farrell *et al.*);

3) WD05 (*"WKBHMB – Predicting proportion North Sea horse mackerel by ICES rectangle"* by N. Hintzen and E. Farrell).

SIMWG is expected to provide an expert opinion on the proposed changes and approach before the final benchmark meeting, 8-12 April 2024.

### SIMWG review

### 1. Review of the historical stock delineation of horse mackerel

The current delineation of the three horse mackerel stocks is as follows (Figure A.4.1):

- Western stock (Subarea 8 and Divisions 2.a, 5.b, 6.a, 7.a–c, and 7.e–k and 3.a & 4.a in quarters 3 and 4)
- North Sea stock (Divisions 4.b–c, 7.d and 3.a & 4.a in quarters 1 and 2)
- Southern stock (Division 9.a)

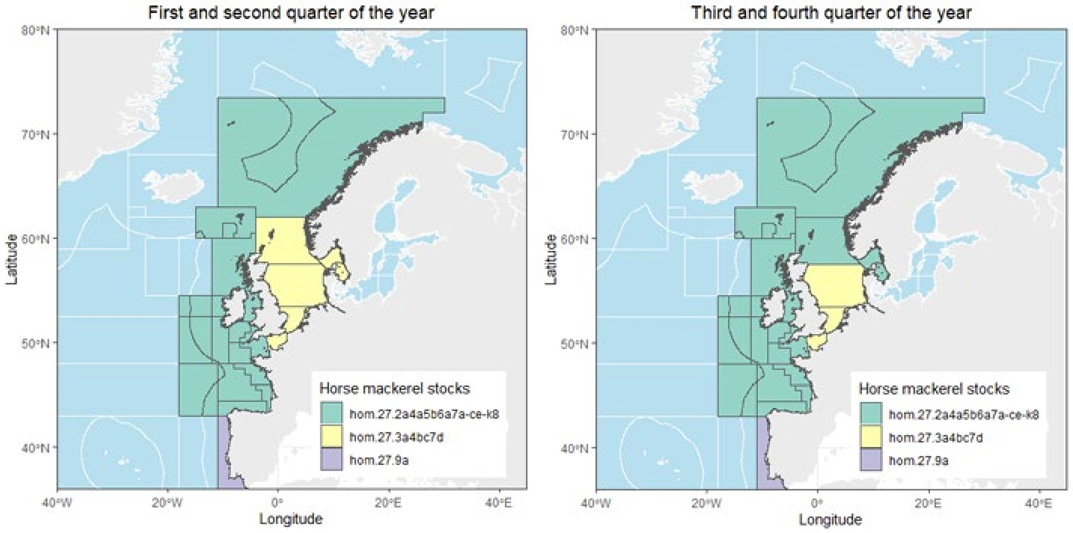

**Figure A.4.1. Current stock delimitation of horse mackerel stocks for the 1st and 2nd (left) and 3rd and 4th (right) quarters.**

The review of the history of the stock identification of horse mackerel revealed that there are significant uncertainties concerning the delineation of the stocks and many of the decisions, which led to the current delineation, were not supported by robust scientific evidence.

The most comprehensive work before the one reviewed here was that derived from the HOMSIR project which concluded presence of three genetically distinct population: one located in the ICES Division 9.a, another located in the North Sea and a western stock spanning from the Bay of Biscay to the Norwegian sea. Yet, mixing between populations was also detected. In this review, it is claimed that this work needed to be updated considering that it was based on a limited number of samples covering a few years collected opportunistically and on methods that are now obsolete and considering that the results are >20 years old and that stock abundances as well as environmental conditions have changed since then.

*SIMWG supports the need to update the information on the population structure of the horse mackerel in view of the high-resolution genetic methods currently available can provide.*

## 2. Research programme to develop and apply a genetic-based stock identification method

### 2.1 Summary of work by Fuentes-Pardo *et al.* (2023)

A recent study based on genome-wide markers has been performed (Fuentes-Pardo *et al.* 2023). The potential for resolution of this study is high due to the large number of genetic markers analyzed (about 13 million single-nucleotide polymorphism = SNPs). The study finds low population structure, yet a PCA based on ~60K neutral markers solidly supports the genetic isolation between the Mediterranean and Atlantic locations and within the Atlantic, between locations north and south of mid-Portugal and between the later and north Africa. Using ~800 outlier markers, differentiation between Mediterranean and north Atlantic locations is not appreciated, whereas North African samples differ more; additionally, outlier markers find significant differentiation between samples from North Sea and the rest of the Atlantic. A reduced panel of 17 SNPs was shown to be highly discriminant between populations (9 outlier and 8 neutral) and could differentiate the North Sea and North Africa between themselves and from the rest of the locations although admixed individuals were also found. Mediterranean locations were not included in these analyses.

*SIMWG considers that the main conclusions of the study of Fuentes-Pardo et al. (2023) are solid in terms of understanding population structure of the horse mackerel using neutral markers (which reflect demographic history) and potentially adaptive markers (which reflect selection and adaptation). SIMWG, however, also considers that further work is needed to investigate the effect of using pooled samples and selecting the most highly discriminant SNPs on deriving stock boundaries and connectivity.*

## 2.2 Summary of work by Farrell *et al.* (2024)

From the ~13 million SNPs identified through pool-seq by Fuentes-Pardo *et al.* (2023), Farrell *et al.* (2024) selected 4,242 highly discriminant SNPs to be included into an Axiom SNP array. Analyses based on the neutral markers did not reveal any genetic population structure in the NEA horse mackerel; however, outlier SNPs revealed a tree cluster pattern compatible with a chromosomal inversion (already identified in Fuentes-Pardo *et al.* 2023) and an additional separation between the North Sea and the rest of the locations. Additionally, based on $F_{ST}$ values, locations cluster in North Sea, southern Portugal, North Africa, and the rest of the locations (in an isolation-by-distance-like grouping pattern).

From these results, assignment panels were developed based on alternative approaches. The panels were built to assign samples to North Sea or Western population and several values to assess confidence of the panels are provided. The panel and assignment confidence was thoroughly tested. The panels have been developed using reference samples (spawning individuals) and applied to assign mixed samples.

*SIMWG considers that the lack of neutral genetic structure in reference samples indicates lack of or very limited homing behavior in horse mackerel, questioning the existence of non-mixed (spawners returning to origin) and mixed (feeding aggregates) samples. Here, the situation seems to be presence of locally adapted groups (e.g. North Sea) which are not completely isolated from adjacent populations, but which could be in the future. These locally adapted units are biologically relevant for the purposes of stock assessment and as such a tool to assign individuals to their unit of origin is required to improve assessment input data.*

*SIMWG observes, however, that the results clearly show that samples from Division 3.a and 4.a are primarily from the western population and not from the North Sea population. Moreover, due to the observed stock mixing in the Channel, the assignment results from Divisions 7.d and 7.e should undergo a sensitivity analysis of the North Sea assessment.*

*SIMWG considers that further work should be conducted to investigate the temporal stability of the North Sea stock boundaries, also taking into account that some separation from the Western stock is visible in Division 4.b at approximately 55°N.*

**SIMWG conclusions**

- SIMWG supports the view of three genetically distinguishable populations of horse mackerel within the ICES areas, being the difference between southern Portugal and the rest of the locations clear and supported by neutral markers (demographic isolation) and that between the North Sea and the western locations supported by outlier markers (local adaptation or selection);
- SIMWG supports the view that samples from Division 3.a and 4.a are primarily from the western population and not from the North Sea population;

**=> Thus, SIMWG recommends revisiting the stock delineation in the light of these conclusions.**

- SIMWG supports the need for a sensitivity analysis of the North Sea assessment to the assignment results from Divisions 7.d and 7.e, to be undertaken as part of the benchmark;
- SIMWG considers that more work is needed to investigate the North Sea stock boundaries and its temporal stability, as well as the effect of pooling samples and selecting the most highly discriminant SNPs on deriving stock boundaries and connectivity.

### References

Farrell, E.D. Fuentes-Pardo, A.P., Murray, D.S. Andersson, L. (2024). A working document on the genetic Stock Identification of horse mackerel, *Trachurus trachurus* for the ICES Benchmark workshop on horse mackerel and boarfish stocks (WKBHMB), Version 4.0, 25th January 2024, 95 pp.

Fuentes-Pardo, A.P., Farrell, E.D., Pettersson, M.E., Sprehn, C.G., Andersson, L. (2023). The genomic basis and environmental correlates of local adaptation in the Atlantic horse mackerel (*Trachurus trachurus*). Evolutionary Applications, 16, 1201–1219. https://doi.org/10.1111/eva.13559

## SIMWG response to a request from WGHANSA on stock structure of European anchovy (*Engraulis encrasicolus*) in the ICES Division 9.a

### Request

The Working Group on Southern Horse Mackerel, Anchovy and Sardine (WGHANSA), in preparation of the Benchmark Workshop on Anchoy Stocks (WKBANSP), is requesting SIMWG to review the information provided as a Working Document (Garrido *et al.*, 2024) on the connectivity between the 9.a west and south components of the European anchovy. WGHANSA and WKBANSP seek feedback from SIMWG to ascertain whether there is agreement or disagreement with the proposal to separate the two components within the 9.a stock.

### Background

In 2014, SIMWG was requested to review a working document provided by WGHANSA regarding the stock identity of European anchovies in ICES Division 9.a. WGHANSA proposed exploring a two-stock distinction for anchovies within this division: Subdivision 9.a South and Subdivisions 9.a North, North Central, and South Central. However, the SIMWG's findings, published in their 2015 report, concluded that insufficient scientific evidence supported redefining the anchovy stock unit in ICES Division 9.a.

The European anchovy (*Engraulis encrasicolus*) in ICES Division 9.a has been a subject of ongoing study due to its economic importance and the complexities surrounding its population dynamics and management. ICES Division 9.a encompasses the coastal waters of Portugal and parts of Spain, a region characterized by diverse ecological conditions influencing marine life. Historically, the European anchovy in this area has been treated as a single stock unit for management purposes. However, recent advances in genetic, ecological, and fisheries research have prompted a re-evaluation of this assumption. Understanding whether the anchovy population should be treated as one or more distinct stocks is crucial for implementing effective conservation and management strategies, which can impact fisheries' sustainability and marine ecosystems' health.

### European Anchovy Stocks in ICES Division 9.a

ICES consider the European anchovy in ICES Division 9.a (Figure A.4.2) as a single stock. The request by WGHANSA in 2014 proposed a revision of stock units to two: (1) 9.a West (9.a N, 9.a C-N, 9.a C-S) and (2) 9.a South. Since the WKPELA benchmark in 2018, the stock has been assessed as two separate components: the western component comprising 9.a N, 9.a C-N, 9.a C-S and the southern component comprising 9.a S (Portugal) and 9.a S (Spain). Since then, WGHANSA has conducted separate assessments, and ICES has provided separate advice and catch options for the two components on the single 9.a Anchovy advice sheet. The 2024 advice sheet noted "*The use of a combined TAC for the western and southern components of the stock prevents effective control of single component exploitation rates and could lead to the overexploitation of either component. ICES recommend that management should be implemented at the stock component area level*".

In 2024, WGHANSA presented another report, proposing that the western and southern components be separated into two stocks. Such a change would not affect the current assessments of the components or the provision of separate advice and catch options. The substantive change would be the provision of advice and catch options in two separate advice sheets.

**Figure A.4.2. ICES Statistical Divisions and Subdivisions around the Iberian Peninsula. The western component of anchovy stock is distributed in Subdivision 9.a West, which comprises Subdivisions 9.a N, 9.a C-N, 9.a C-S. The southern component of anchovy stock is distributed in area 9.a. South, comprising subdivisions 9.a.S (Portugal) and 9.a.S (Spain). From Garrido *et al.* (2024).**

### Survey Trends

Survey trends for European anchovy in Division 9.a highlight significant spatial and temporal variations in abundance. Acoustic and trawl surveys conducted over the past decade reveal that while some sub-areas exhibit consistent anchovy presence, others show episodic peaks in biomass, often associated with favourable environmental conditions such as upwelling events or changes in sea surface temperature. Except for a single year's concentrated spawning on either side of Cabo de Sao Vincente (2020), these trends suggest the possibility of sub-stock structures with distinct ecological niches within the broader 9.a area. In analysing the spatial distribution of European anchovy catches, we observe significant concentration in specific coastal regions within Division 9.a, indicating potential localised populations. Furthermore, seasonal variability in biomass highlights distinct temporal patterns in anchovy abundance, suggesting differential use of habitats across seasons. These observations are consistent with the hypothesis of sub-stock structures within Division 9.a, which has critical implications for the management and conservation of the species. However, they are insufficient evidence in their own right to support a re-delineation of the stocks.

### Life History Parameters

Regarding the life history parameters, we note that according to the WD, length- and weight-at-age (growth) in acoustic surveys showed marked differences between the 9.a South and 9.a West subdivisions. Indeed, for most survey years, weight at ages 1-3 in the Gulf of Cadiz were <50% of that in the 9.a West subdivision. This difference in growth rate may have large consequences for potential production and possibly maturation rates, affecting yield and sustainable biological reference points from the Gulf of the Cadiz. Moreover, morphometric analyses show larger heads and smaller body dimensions for the Sea of Cadiz compared to the Bay of Biscay samples. This could relate to the large growth differences observed in the acoustic surveys. However, otolith shape analysis (Bacha *et al.* 2014) has not been conducted specifically on samples from Subdivision 9.a South and was uninformative in discriminating groups within the 9.a subdivisions. Finally, cohort tracking suggested a lack of covariance in recruitment and age structure between subdivision 9.a South and 9.a West while showing the existence of covariance between western-northern 9 areas (Subdivisions 9.a N, 9.a C-N) and the Cantabrian Sea (Division 8.c), suggesting connectivity between these Atlantic regions. Still, it would have been useful for cohorts to be tracked within specific 9.a subdivisions (including assessment considering west-to-south movement/link) to confirm that precision in surveys and ageing can support this approach.

**Stable isotope composition**

The eye lens stable isotope (SI) composition was utilised as a natal marker (juvenile, age-0) to determine sea surface temperature (SST) through carbon-13 (13C) and primary production/nutrient levels via nitrogen-15 (15N). Generally, 13C is expected to show positive associations with SST, mediated by phytoplankton, while 15N should be inversely related to ocean nutrients and productivity. However, neither of these markers has been fully calibrated in eye lens applications, and their uptake mechanism, particularly for *E. encrasicolus*, remains unknown. A partial calibration revealed that age-0 eye lens 13C showed expected patterns linked to SST, with southern areas such as the Sea of Cadiz, Morocco Atlantic, and the Alboran Sea displaying elevated 13C levels compared to the Bay of Biscay and areas off western Portugal. The 15N levels were anomalously high in the Sea of Cadiz, likely due to lower nutrient availability compared to other sampled regions. In contrast, low 15N levels in age-0 eye lenses from the Alboran Sea were attributed to nitrogen fixation despite limited nutrient availability in the region. However, no supporting literature was provided for these cases.

Significant differences in age-0 SI markers persisted for the Sea of Cadiz in inter-regional comparisons despite interannual differences among four sampled years, indicating the approach's potential. However, the authors suggest a possible northward migration from the African coast to the southern Iberian coast based on age-0 and age-1 SI values in the eye lenses of fish sampled in ALG and MOR. This comparison between samples collected in 2022 and 2017 might reflect interannual variation rather than spatial variation. Age-1 and older samples were examined to evaluate whether regional mixing among natal markers occurred. The Sea of Cadiz showed less discrete separation than age-0 samples, suggesting possible mixing. The 13C values broadly overlapped between regions, and although elevated, the 15N levels for the Sea of Cadiz showed greater overlap with areas off western Portugal and even the Bay of Biscay.

The report's conclusion that "*These results support the hypothesis that connectivity between the western and southern Iberian coast is limited*" does not seem fully supported by the presented findings. The findings support this, but the WG notes that some degree of connectivity is supported. While this marker shows promise, the current data does not support separating the two areas alone. Further studies developing baseline data and cohort-matched analysis of eye lens SI are necessary to clarify the degree of connectivity between western and southern areas and other regions (e.g. Morocco and Alboran). The stable isotope composition of eye lenses could be an important research tool for evaluating ecosystem dependencies and key nursery habitats. It merits additional development, calibration, and application for *E. encrasicolus*. For instance, the role of estuarine production on the two SI tracers deserves further research, as estuaries likely yield unique SIs. Estuarine/coastal ecotypes could play a significant role in stock production within certain regions (see Section 6.3.1).

**Larval dispersal**

The modelling of larval dispersal yielded intriguing results, indicating dispersal from Division 8.c into Subdivision 9.a North and primarily recirculation within the Gulf of Cadiz. These findings may partly explain the observed patterns of structure identified through other methods. There is notable inter-annual variation in the extent of larval dispersal, with one of the eight simulation years, 2020, predicting connectivity between areas 9.a S and 9.a C-N. However, a significant gap exists in the spawning in areas 9.a N and 9.a C-N and the potential larval dispersal from these regions have not been considered. Survey data indicates spawning in these areas, raising key questions about whether larval recirculation occurs or if larvae are advected north or south. The analyses suggest that anchovies in 9.a N and 9.a C-N may originate from the north (area 8), prompting further stock identification questions, such as the appropriateness of splitting Division 9.a into two assessments without considering connectivity with area 8 and beyond. Expanding the analysis to address these considerations would be highly informative.

### Genetics

Whilst the recent genetic analyses appear informative about stock identification and delineation for assessment, there was insufficient information in the working document submitted to SIMWG to review the methodology or assess the validity of the results or conclusions. It became apparent in plenary and during the discussions that more information was needed, particularly on the date of sample collection, number of individuals, length/age composition, number genotyped, the number included in analyses and details on the genotyping of the individuals.

Following SIMWG and in response to the queries raised above, an additional genetic report was submitted to the review group, which contained more details of the genetic analyses undertaken. On further request, the sample details were also provided. A review of the samples included in the study, with particular reference to the core study area in Division 9.a and area 8, indicated that only a very small number of individuals were collected and analysed in this area. In Division 9.a all individuals were collected in a single year apart from one sample in 9.a S, which comprised 6 individuals. Further, the samples collected in the core study area were all collected outside of the spawning season noted in the main working document, which questions their reliability as baseline samples for delineating biological units. There was also a notable gap in the genetic samples between the samples collected at the northern border of 9.a C-S and 9.a S. Whilst it can be argued that there is a hiatus in the distribution of the species in the area, the egg and bottom trawl data does show that in some years they are present in this area. Further, the catch data also shows catches of similar magnitude in this area to that in the southern component area. The updated genetic report also proposed that the results supported a redefinition of the delineation of the stock, with a new limit being located at the south of Lisbon. This proposed limit does not align with the delineation of the current stock assessment components. However, it is not supported by samples due to the sampling gap in this area.

In summary, the genetic analyses indicated population structure between samples collected in the western component and southern component areas. However, the temporal stability was not robustly tested and there were insufficient samples to assess connectivity or to make a conclusive decision on stock delineation. The genetic analyses also indicated that the western component is genetically undifferentiated from the anchovy in area 8.

Concerning the genetic analyses, there is no unanimous opinion on the following points:

- The lack of reliability of using non-spawning samples to delineate biological units. The opposing view argues that finding population differentiation, even with non-spawning samples, indicates that southern and western anchovy populations do not mix at any stage, suggesting the presence of a barrier preventing interaction between these components. Thus, identifying structure with non-spawning samples reinforces, rather than questions, the observed population differentiation.
- That temporal stability was not robustly tested. The opposing view argues that the observed population differentiation results from accumulated genetic differences between

populations through time; that is, which have developed over generations of reproductive isolation. Thus, temporal stability is implicit in the results obtained.

- The fact that the number of samples was insufficient to assess connectivity. The opposing view argues that between 35 and 38 genotypes were analyzed per component, which exceeds the typical sample size in this kind of analyses. The clear results obtained and lack of unresolved or ambiguous findings suggest that sample size is not a limiting factor.

Given the disagreement on the points above, the opposing view does not support the conclusion that the analyses do not enable an assessment of connectivity to be conducted [in the case of 9a] and to do so more intensive catch and survey sampling and analyses are required. The opposing view argues that the genetic results show strong evidence of population differentiation within 9a and that additional catch and survey sampling and analyses would not provide additional information regarding this particular question.

**Conclusions and recommendations**

SIMWG compliments the extensive evaluation of multidisciplinary information provided by Garrido *et al.* (2024) in the Working Document. During the review process by SIMWG, additional information was requested and supplied including unpublished studies. The lack of complete documentation in the Working Document, particularly the inclusion of unpublished data curtailed a comprehensive evaluation of population structure by the SIMWG.

The analyses presented to SIMWG indicated that there is likely population structure within the Division 9.a anchovy stock area, that aligns to some degree with the current components (western and southern) of the two assessments conducted on this stock. However, the analyses do not enable an assessment of connectivity to be conducted and to do so, more intensive catch and survey data analyses are required. This should also include further assessment of the connectivity of the southern unit to units to the south of the assessment area and also of the western unit to stocks to the north. The evidence presented indicated that there is equal support for combining the western component with the Subarea 8 anchovy stock, however this was not proposed by WGHANSA.

Given the evidence presented it would not be appropriate to establish a separate stock for the western component in the knowledge that it does not represent a biological unit and is likely part of the area 8 stock. A more comprehensive and holistic approach should be used to assess the stock structure of anchovy across its distribution in order to robustly assess the validity of the current delineation.

Splitting the Division 9.a components into two separate stocks, as requested by WGHANSA, will have no impact on the current assessments or development of catch options for the components. It would result in two advice sheets instead of a single combined advice sheet with separate catch options for the two components as is currently the case. This combined advice sheet already states that *"management should be implemented at the stock component area level"*. This is a key point as currently the landings from Subdivision 9.a S are in excess of the advised catch for this component. SIMWG agrees that management should be aligned with the current advice provided by ICES.

Whilst the current misalignment of management and advice provides an argument for the need to change the management area, this is not sufficient reason to change the current stock definitions. Further SIMWG can only consider the evidence provided for redefining the stock definition and not the implications for management.

SIMWG suggests that a more comprehensive and holistic stock identification programme is introduced that addresses the issues identified in this review, including the connectivity to anchovy in Subarea 8. Once sufficient temporal and spatial evidence is available to redefine the assessment areas then a specific workshop should be convened with all relevant stakeholders to review the data and to also consider the implications for management. In the interim SIMWG considers that the separate assessment of the two components should be continued with separate catch advice and the recommendations that *"management should be implemented at the stock component area level"*.

Given the disagreement on the points above regarding the genetic analyses, however, there is no unanimous opinion on the conclusions. The opposing view does not support the conclusion that the analyses do not enable an assessment of connectivity to be conducted (in the case of Div. 9a) and to do so, more intensive catch and survey sampling and analyses are required. The opposing view argues that the genetic results show strong evidence of population differentiation within Div. 9a and that additional catch and survey sampling and analyses would not provide additional information regarding this particular question.

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## SIMWG response to a request from WGBFAS on stock definition of Baltic Sea dab (dab.27.22-32) and North Sea dab (dab.27.3a4)

### Background

The working document (WD) produced by Sven Stötera from the Thünen Institute (Annex 5) examines dab stock identification for dab27.3a4 (North Sea, Skagerrak and Kattegat) and dab 27.22-32 (encompasses the Baltic Sea) and is an update on a previous working document reviewed by SIMWG in 2023. The authors have provided a SPCiT assessment model, spatio-temporal distribution (survey and fishery data) and biological (maturity and length-weight data) evidence to suggest that dab from the Kattegat area (27.3a.21) should be included within the ICES dab 27.22-32 and not ICES dab27.3a4.

### SIMWG review

#### Evidence from assessment working groups WGBFAS and WGNSSK

During WKBMSYSPiCT and WGBFAS, a SPiCT (stochastic surplus production model in continuous time) assessment was used on the author's proposed stock units (dab27.21-32 and dab27.3a20 and 4). The model converged and performed well in sensitivity tests. While SIMWG appreciates the effort of both WKBMSYSPiCT and WGBFAS regarding this work, stock assessment models are not a recognised stock identification method and cannot be used to infer biological or ecological connectivity or boundaries.

The data used for the model originated from two international surveys:

- The International Bottom Trawl Survey (IBTS) covers the North Sea (Subarea 4) and the transition areas of Skagerrak (3a.20) and Kattegat (3a.21) and is conducted twice per year in Quarter 1 and 3.
- The Baltic International Trawl Survey (BITS) covers the entire Baltic Sea, as well as Kattegat (3a.21) in Q1 and Q4.

Figure 5 of the WD shows the "Overall biomass distribution in Kattegat (SD21) and Baltic Sea, derived from IBTS and BITS survey data" and suggests no differentiation between Kattegat dab and those found in the adjoining areas 3a22-24. The three main issues with this inference are that

1) Despite the figure heading stating that this data originated from the IBTS, there is no information regarding the biomass distribution among Skagerrak and North Sea.

2) The gear type is size-selective for adult and sub-adult dab and does not sample juvenile dab properly and therefore can not provide an accurate representation of their distribution.

3) While the proposal calls for a dab27.21-32 stock unit, there is no evidence of biomass connectivity beyond area 27.24. The second point is also pertinent for Figure 6 of the WD, where potential linkages among abundance distributions are not seen beyond area 27.24.

#### Spatio-temporal distribution

The author has provided a selected time series of CPUEs of 15 cm+ dab from both the IBTS and BITS (Figures 12-15) and, within Annex 1.1 and 1.2, a larger time series of combined IBTS/BITS Quarter 1 and 4 Survey Index CPUEs. This information provides spatio-temporal distribution patterns of adult dab as well as changes in these patterns over time. There is inter- and intra-annual variation in the spatial distribution of the highest CPUEs of adult dab. In some surveys, a high CPUE was observed on the border between the Skagerrak (Division 3a) and Kattegat (SD21), e.g. in Q4 2004, suggesting that this may not represent a border.

The majority of adult dab appear to mix within SD 21-23, but there is also evidence of mixing between the Skagerrak and Kattegat (e.g. Q4 2022, Annex 1.2). Unfortunately, there was no evidence presented to support the author's proposal that 3a21 dab are connected to any dab beyond 3a24.

In general, it should be noted that whilst spatial distribution data can provide support for further testing stock definition assumptions, it is not suitable as the primary basis for delineating stocks for assessment.

### Fishery

In general, the main landings (tonnes) show the highest amount of dab landings occurring in 27.3.c.22 (Belt Sea, part of the Baltic Sea dab stock) with few landings being registered within the Kattegat region (4-6 tonnes). The authors point out that there is potential misreporting of dab landing data, either dab being caught and landed in different areas or dab being assigned as 'mixed flatfish' limiting the inferences that can be made regarding stock identification. It should also be noted that the majority of dab are discarded due to low commercial value e.g. in dab.27.3a4, the annual landings are approx. 3000 t and the annual discards approx. 33,000 t. The distribution of discards is unclear and may be more informative than landings, given the difference in scale.

### Life history parameters

The final evidence provided is life history parameters, including maturity, growth, and length-weight relationships (see Table 2 and Figure 17). As no age reading data are derived from IBTS samples, North Sea dab maturity at age data was replaced by analyses of southern North Sea dab (Rijnsdorp *et al.*, 1992). It should be noted that Rijnsdorp reported $L_{mat}$ values of 11 cm (2 years old) for males and 14 cm (2-3 years old) for females is based on information from Bohl (1957), see General Biology - Maturation and Spawning, Rijnsdorp *et al.* (1992). Despite information that dab in the southern North Sea mature at a much older age and differ in length at maturity compared dab from the Baltic Sea and Kattegat, which have similar values (see Table 2), this biological information is nearly seven decades old. Finally, Figure 17 shows the length-weight relationship among Baltic Sea, Kattegat and North Sea dab from the Q1 surveys (IBTS and BITS) from 2022. Baltic and Kattegat dab have a similar length-weight relationship compared to North Sea dab. We assume that this is mean values and as such confidence intervals would provide insight on whether there are significantly different trends among dab from these specified regions. Note: It would also be helpful to add length-weight relationships for dab from Skagerrak, as the spatio-temporal evidence presented within the WD suggests connectivity with Kattegat dab

### Conclusions

Since the last submission, the author provides additional biomass and abundance distribution data, including information on exploratory assessment models under different assumptions of stock delineation. Stock assessment model convergence, improved residual patterns and better assessment model outputs were suggested to be additional evidence for realignment of the stock areas however it should be clarified that this is not an appropriate stock identification method.

The additional evidence provided was not sufficient to change the review that SIMWG provided in 2023 and still does not provide the evidence to conclude that the dab in the Kattegat (SD21) are the same biological unit as the dab in SD 22-23. As such, there is no biological support for the proposed revision of the stock assessment units, i.e. of dab27.21-32 and dab27.3a20 and 4. Further it should be noted that the review of stock delineation is solely concerned with the definition of the stocks for the purpose of data collection and collation for stock assessment. The definition of management areas is beyond of the remit of SIMWG and ICES.

If anything, the evidence provided in this Working Document and last year's submission raises more questions regarding the connectivity between 3a.20 and 3a.21 as well as the lack of evidence that dab within 3a.21 is connected, in any way, to dab beyond 3a.24. The questions arising from this document pertains to the complexity of biological populations and the need for additional biological studies, as stated in the previous review provided by SIMWG. While SIMWG understands that certain stocks and species of low commercial value suffer from a lack of resources for dedicated scientific research programmes, attempting to delineate new stock units with limited biological evidence that does not capture the complex biological interactions among populations (and thus stocks) should be avoided.

Although there is a drive within ICES to align stocks to biological units, there must be a threshold of evidence to do so. This point has been discussed in recent ICES Stock Identification Benchmarks for sea bass (ICES, 2023), as well as North Sea and West of Scotland cod (ICES, 2020, 2022).

If ICES chooses to realign the stock delineation of the dab stocks, based on the currently proposed analyses, then the limited evidence based and associated uncertainties should be communicated clearly in the benchmark report and associated advice sheets.

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## SIMWG response to a request from WGBFAS on stock definition of flounder in the Belt Seas and the Sound (fle.27.22-23) and North Sea flounder (fle.27.3a4)

### Background

The working document produced by Sven Stötera from the Thünen Institute (Annex 6) examines flounder stock identification in the North Sea, Skagerrak, Kattegat and the Baltic Sea. Current ICES advice is provided for fle.27.3a4 (North Sea, Skagerrak and Kattegat) and fle.27.22-23 (southern Baltic Sea). This is an update on a previous working document reviewed by SIMWG in 2023, with the author adding SPiCT assessment model and biomass distribution data to previously provided spatio-temporal distribution (survey and fishery data), biological (maturity and length-weight data) and genetic evidence. Using the evidence provided, the author proposes changing the current stock units fle27.22-23 (Belt Seas and the Sound) and fle27.3a4 (North Sea, Skagerrak and Kattegat) to the following:

- fle.27.21-23 (Kattegat, Belt Sea and Sound)
- fle.27.3a20.4 (Skagerrak, North Sea)

### SIMWG review

#### Evidence from assessment working groups/workshops (WKBMSYSPiCT3, WGBFAS and WGNSSK)

During WKBMSYSPiCT3, WGNSSK and WGBFAS, a SPiCT (stochastic surplus production model in continuous time) assessment was used on stock unit fle.27.22-23, during the benchmark the group conducted additional sensitivity analyses using Kattegat flounder data. The additional data improved SPiCT model performance by reducing uncertainty. While SIMWG appreciates the effort of WKBMSYSPiCT3, WGBFAS and WGNSSK regarding their work, stock assessment models are not a recognised stock identification method and cannot be used to infer biological or ecological connectivity or boundaries.

The data used for the model originated from two international surveys;

- The International Bottom Trawl Survey (IBTS) covers the North Sea (Subarea 4) and the transition areas of Skagerrak (3a.20) and Kattegat (3a.21) and is conducted twice per year in Q1 and Q3.
- The Baltic International Trawl Survey (BITS) covers the entire Baltic Sea, as well as Kattegat (3a.21) in Q1 and Q4.

Figure 5 of the Working Document shows the “Overall biomass distribution of flounder in Kattegat and Baltic Sea, derived from IBTS and BITS survey data” and suggests no differentiation between Kattegat flounder and those found in the adjoining areas 3a22-24. The two main issues with this inference is that:

1) Despite the figure heading stating that this data originated from the IBTS, there is no biomass distribution information among Skagerrak and North Sea flounder.
2) Neither survey can sample juvenile flounder properly, so does not represent the true distribution of biomass. If this metric is used as the basis for delineating stocks, the gap in juvenile distribution needs to be clearly identified.

The author presents Figure 6, recent abundance distributions of juveniles (<20cm, TL) and adults (>20cm, TL) and shows temporal variation in juvenile and adult flounder within the Baltic Sea and surrounding areas. As bottom trawls underestimate juvenile catch, for the reasons stated by the author, this does not clarify point 2) stated above. The lack of flounder abundance distributions within the Kattegat highlights the minor importance of this component of the stock to the wider area but this is not a significant biological reason for delineating stock units. Finally, the stock unit of interest are fle3a22-24 and fle3a20-21.4, but there is no information on the adult or juvenile distributions within ICES Subarea 4 or SD 3a20 for comparison.

### Spatio-Temporal Distribution

The author has provided a modelled biomass distribution chart of flounder in the Baltic Sea (SDs 22-25, BITS) in Q1 courtesy of Berg *et al.*, 2014 (Figure 12). Biomass data shows concentrations of flounder in eastern Kattegat and a more substantial biomass within 3a23-24 (specific areas of flounder concentrations vary temporally). There is no information on Figure 12 on biomass distributions within the North Sea or Skagerrak. However, the author states within the text that "flounder are rare in the Skagerrak and the North Sea with a CPUE of 0 in central Skagerrak". Again, this could be due to trawl gear selectivity underestimating biomass and distribution.

There appears to be a mistake with Figure 14, the caption states that the North Sea IBTS, as well as Baltic Sea BITS CPUE data, is shown but the figure shows no information on North Sea flounder CPUE distributions. It may be the authors only included Kattegat flounder data from the IBTS survey, in which case the caption for Figure 14 is confusing. Otherwise, Figure 14 shows low flounder abundances within 3a21 but higher abundances from the Belt Sea and Sound in Q4.

The author has provided a selected time series of CPUEs of 15cm + flounder from both the IBTS and BITS (Figures 13, 15 and 16) and, within Annex 1.1 and 1.2, a larger time series of combined IBTS/BITS Quarter 1 and 4 Survey Index CPUEs. The CPUEs highlight Kattegat flounder linkages between both the Belt Sea and Sound, as well as Skagerrak. Specifically, in Q1 and Q3, there is CPUE connectivity between the northern Kattegat and southern Skagerrak (e.g. flounder Q3 2022, Figure 15), but there is also a semi-continuous CPUE distribution between the southern Kattegat and Belt Sea/Sound (e.g. flounder Q1 2023, Figure 13). In general, it should be noted that whilst spatial distribution data can provide support for further testing stock definition assumptions, it is not suitable as the primary basis for delineating stocks for assessment. There is also a size-selectivity issue, with juvenile flounder unlikely to be captured using current gear types.

### Fishery

The fishing pattern revealed by averaged landings data from 2019 until 2022 show that most landings in Kattegat are taken close the border of SD 22 & SD 23, while many landings in Skagerrak occur in the western region. The authors view the fishery data as supporting conclusions from the trawl surveys i.e., that there is little connection between Kattegat and the North Sea via Skagerrak but a more substantial landing connection between Kattegat and the southern Baltic Sea. It is also mentioned in the background data that > 90 % of flounder landings in the fle27.3a4 is from Subarea 4, i.e less than 10% is from the Skagerrak/Kattegat area. Flounder are likely to be discarded, but no data has been provided to examine if this changes distribution inferences. In general, landings data is not indicative of distribution and – while interesting for assessment purposes – is not an informative metric for stock delineation.

### Life History Parameters

Analyses of life-history parameters from IBTS and BITS Q1 surveys in 2022 (length at maturity, growth, and $L_{inf}$) show differences between samples from North Sea, Kattegat and Baltic Sea but gives no statistical analysis (despite seemingly high sample numbers (N)) if differences are statistically significant and only one year (2022) is provided as evidence. SIMWG assumes that Figure 18 contains mean values and as such confidence intervals would provide insight on whether there are significantly different trends among flounder from these specified regions. Note: It would also be helpful to add length-weight relationships for flounder from the Skagerrak as the spatio-temporal evidence presented within the WD suggests connectivity with Kattegat flounder.

## <u>Genetics</u>

Peer review literature suggests a recent taxonomic split in European flounder within the Baltic Sea into pelagic spawning European flounder (*Plathichthys flesus*) and demersal spawning Baltic Sea flounder (*Platichthys solemdali*) (Momigliano *et al.*, 2017). There are evidence for the existence of these two different ecotypes (ICES 2010; Orio *et al.*, 2017) which probably have different population dynamics and might be better managed separately. However for the moment, this splitting of taxon appears to be an academic determination based on genetic evidence. From an assessment perspective, both putative species are, for now at least, aggregated. However, ICES needs to be aware of the complexity and consequences of what taxonomist refer to the 'lumping and splitting' of species. For example, the results reported within Momigliano *et al.* (2017), and thus used to split European flounder into two species, are not dissimilar to the genetic heterogeneity observed among North Sea and Baltic Sea herring spawning ecotypes (Farrell *et al.*, 2022; Bekkevold *et al.*, 2023; Mueller *et al.*, 2023). Consequently, the same analyses used to split flounder into two species, could theoretically be used to create 8-9 different species of herring in the North Sea and Baltic Sea. In future, any consensus to disaggregate the two putative species for assessment purposes should be carefully considered by ICES before being implemented.

Current genetic information on flounder from the areas of interest lack, what is currently agreed to be, a robust experimental design (Andersson *et al.*, 2023). For example, many studies utilise previous generations of genetic analysis (e.g. microsatellite markers), which are less sensitive to detecting population structure due to reduced marker availability. Studies which do utilise current genetic techniques, such as genotype by sequencing, have not collected baseline and mixed samples, as well as having no assignment models to infer population structure.

Unfortunately, no study managed to collect genetic samples from all areas of interest, so that a robust comparison between stocks could be undertaken. For example, Hemmer-Hansen *et al.* (2007) collected samples from the North Sea but not Kattegat or Skagerrak. Alternatively, Momigliano *et al.* (2017, 2018, 2019) obtained genetic samples from both Kattegat and Skagerrak but not the North Sea.

SIMWG is aware that obtaining funding for robust population genetic studies on low commercial value species is difficult, especially when existing genetic studies have been published. The lack of key design elements (e.g. comprehensive geographical and temporal sample collection from baseline and mixed stock samples) limits interpretation. However, we provide feedback using the evidence provided.

The author states that none of the genetic studies so far conducted show any differentiation between Kattegat and Belt Sea, hence supporting the conclusion of a large homogenous flounder population in the Kattegat and western Baltic Sea (Hemmer-Hansen *et al.*, 2007; Florin and Höglund, 2008; Momigliano *et al.*, 2017; Jokinen *et al.*, 2019; Kuciński *et al.*, 2023). Using a genotype-by-sequencing approach, Momigliano *et al.* (2017) found evidence supporting three populations in this region, with a putative 'North Sea' (3a20, 21 and 23) population emerging from Skagerrak, Kattegat and Sound samples. STRUCTURE analysis on samples collected highlighted that flounder collected in ICES SD 3a.23 contained a mix of the 'North Sea' and 'Pelagic' genotypes, with the putative Pelagic type being identified further east (i.e. ICES subareas 3a.23-28). However, as stated above, no flounder samples were collected from ICES Divsions 4a-c for comparison. Momigliano *et al.* (2018, 2019) and Jokinen *et al.* (2019) utilised and/or reported on a substantially reduced marker selection, used to target genetic differences between their two putative species. While results also highlighted no structure among Skagerrak, Kattegat or Sound flounder, the reduced marker panel substantially limits inferences regarding population differentiation. Kuciński *et al.* (2023), only sampled flounder from ICES SD 3a26 which isn't part of the stock units being investigated. Florin and Höglund (2008) utilised microsatellite markers and sampled flounder from the Skagerrak, Kattegat and Sound, observing no significant genetic differentiation between ICES SD 3a20 flounder compared to those collected from ICES SD 3a23 and 3a24.

## Conclusions

Since the last submission, the authors provided additional biomass and abundance distribution data, including information on exploratory assessment models under different assumptions of stock delineation. Stock assessment model convergence, improved residual patterns and better assessment model outputs were suggested to be additional evidence for realignment of the stock areas. However, it should be clarified that this is not an appropriate stock identification method.

The additional evidence provided was not sufficient to change the conclusion of the review SIMWG provided in 2023, that the flounder in the Kattegat (3a.21) are the same biological unit as the flounder in 3a.22-23, nor does it provide sufficient biological evidence to suggest a split in stock units between Skagerrak and Kattegat flounder to support the proposed new stock units (fle.27.21-23 and fle.27.3a20.4).

The available genetic data, as well as the CPUE and newly added abundance data, suggests linkages between Skagerrak and Kattegat (and Belt) flounder. However, SIMWG notes that Skagerrak was not part of the proposed changes to the stock unit.

Although there is a drive within ICES to align stocks to biological units, there must be a threshold of evidence to do so. This point has been discussed in recent ICES Stock Identification Benchmarks for sea bass (ICES, 2023), as well as North Sea and West of Scotland Cod (ICES, 2020, 2022). If ICES chooses to realign the stock delineation of the flounder stocks, based on the currently proposed analyses, then the limited evidence base and associated uncertainties should be communicated clearly in the benchmark report and associated advice sheets.

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## SIMWG response to a request from WGBFAS and WGNSSK on stock definition of plaice in the Baltic Sea

### Background

The working document (WD) "Evidence for a single plaice stock in the Baltic Sea" by Uwe Krumme, Sven Stötera, and Elliot Brown (Annex 7) proposes merging of the two currently used stock units "ple.27.21-23" (Kattegat, Belt Sea and the Sound) and "ple.27.24-32" (Baltic Sea, excluding the Sound and Belt Sea) into a single stock "ple.27.21-32" (Baltic Sea and Kattegat). The authors provide evidence from recent genetic studies, historical and contemporary mark-recapture experiments, biological information and stock assessment trends to support their proposition.

### SIMWG review

The current stock definition – two separate Baltic Sea plaice stocks – is based on a recommendation by WKPESTO (ICES 2012b). The main argument in the present WD is that the WKPESTO recommendation suffers from a lack of data and that the focus of the working group was on the connection between plaice stocks of Skagerrak and North Sea. According to the authors of the WD, genetic studies published since WKPESTO, stock assessments, survey indices and mark-recapture data provide evidence for merging the Baltic Sea plaice stocks into one.

The authors claim that the recent genetic studies (Ulrich *et al.* 2017; Le Moan *et al.* 2019, 2021; Weist *et al.* 2022) support the assumption that plaice in the Baltic Sea is a single stock. However, the authors also note that all the genetic studies provide evidence for genomic heterogeneity of the Baltic Sea plaice. There are two levels of genetic differentiation that need to be considered here – neutral genetic differentiation and differentiation in genes underlying adaptive traits. Neutral genetic differentiation reflects population history and current gene flow, while differentiation in genes underlying adaptive traits reflects differences in adaption to different environments and selective regimes (Lewontin & Krakauer 1973; Beaumont *et al.* 2005). Because the aim of identifying and assessing fish stocks is to ensure their persistence and sustainable harvest, it is important to consider both types of genetic differentiation when making decisions on stock delineation. In the WD, only neutral genetic differentiation is discussed and considered as evidence for a single Baltic Sea plaice stock.

Weist *et al.* (2022) show that despite the high gene flow and the associated low neutral genetic differentiation, there is population sub-structuring between the plaice from the North Sea to the Baltic Sea, as indicated by structural variants (SVs) that are linked to adaptation to differences in salinity. Le Moan *et al.* (2019 and 2021) also find genomic heterogeneity in structural variants and attribute it to adaptive differences among plaice from different sampling sites. Le Moan *et al.* (2019) find outlier loci that are linked to differences in the environment, and Le Moan *et al.* (2021) show that there are genetic differences in SVs from chromosome 19 between plaice from SD 21-23 and the Baltic Sea. Both studies by Le Moan *et al.* (2019 and 2021) concur with Weist *et al.* (2022) that neutral genetic differentiation is low among the Baltic Sea plaice. Ulrich *et al.* (2017) concentrate on plaice from the North Sea and Skagerrak. Ulrich *et al.* (2017) only consider neutral genetic differentiation, but by combining the genetic data and growth trajectories conclude that there is a more significant differentiation between the Baltic Sea and Kattegat – Belt Sea area (SD 21-23) plaice than within the Baltic Sea (SD 24-25) plaice. Ulrich *et al.* (2017) also note that the pattern is consistent with tagging data.

Similar patterns – adaptive differentiation despite high gene flow – have been found also in other Baltic Sea fish species (e.g. DeFaveri *et al.* 2013; Berg *et al.* 2015; Guo & Merilä 2016). As Ulrich *et* *al.* (2017) note, this complicates stock assessment and management not only in plaice, but other North Sea - Baltic Sea fish species. Ulrich *et al.* (2017) discuss options of splitting or lumping together the North Sea and Skagerrak stocks and raise a valid point that both choices have upsides and downsides and depending on the goal. Splitting the stocks would be better for the protection of the local populations, while lumping the stocks together would benefit the feasibility of stock assessment and fisheries management. The same reasoning should be true for the plaice in SD 21-32.

The tagging data presented in the WD show that different spawning populations mix during feeding migration. The results from BITS show that during spawning time, plaice are continuously distributed between SD 22-24. Together, these data support a joint stock in SD 22-24. However, the implications of mixing during certain life stages to management are not unlike those in mixed stock fisheries. Despite mixing during feeding migration, the plaice might be adapted to spawn at different salinities. Some of the presented genetic data – population structure following adaptation to different salinities (Weist *et al.* 2022) – support this. The effect of salinity on plaice spawning has been studied by Nissling *et al.* (2002), who found that there are no plaice spawning east of Bornholm, at least at present, which might indicate that the unique plaice stock in SD 25 might be already lost.

It must be also noted that with a couple of exceptions, the tagging data come from SD 22 and 24. According to the surveys, there are very little plaice in SD 21 and 25. It would be valuable to see, whether historical maps show the same, or has there been a loss of plaice populations in these areas. There is also no reflection on the arguments put forward in WKFLABA (ICES 2010, 2012a). Poulsen (1932) found differences in the number of anal fin rays between SD22 and the western SD24 on one hand, and eastern SD24 vs. SD25 on the other, suggesting two stocks, a western and an eastern Baltic Sea stock.

### SIMWG conclusions

Based on neutral genetic data only, the presented data support a joint Baltic stock including SD 22-32, but there is no evidence on where to merge SD21. It is also unclear whether the low number of plaice in SD 25 and SD21 is reflecting the natural state. If so, merging SD 21 with the Baltic Sea will probably not have any drastic negative effect on the plaice stocks. On the other hand, if the low number of plaice in Kattegat nowadays is a small remnant of the original populations, care should be taking not to merge it with other stocks. When considering ecologically important adaptive traits, the picture becomes more complex – there is some evidence, also at the genetic level, of adaptive differences along the continuum of plaice distribution from Kattegat to the Baltic Sea. There is a need for additional data on adaptive traits to make sure that the possible merging of plaice stocks will not result in a loss of adaptive variation.

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# Annex 5: Working Document on stock structure of dab

# Review and update of the stock definition of Baltic Sea dab (dab.27.22-32) and North Sea dab (dab.27.3a4)

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## Summary

European dab is a marine flatfish species that usually inhabits the deeper parts of sea basins. Presently, dab in the Kattegat is considered a part of the North Sea stock. The adjacent Baltic Sea dab stock covers the areas of the Belt Sea and the Sound (SD 22-23), Arkona Sea (SD24) and parts of the Bornholm Sea (SD25). Only occasional catches of dab occur in the more eastern parts of the Baltic Sea.

We provide evidence that the management areas may require a change. Distribution maps from scientific surveys strongly suggest that there is no spatio-temporal separation between dab in the Kattegat and the western Baltic (Belt Sea and the Sound) and that dab in the Kattegat have negligible links to dab in the North Sea. The Danish Straits are highly dynamic connecting channels between the southern Kattegat and Kiel and Mecklenburg Bight south of Denmark that make a stock separation between the Belt Sea and Kattegat highly unlikely. No distinct differences were found in biological life history parameters (i.e., maturity and growth) between dab from SD 21 and SDs 22-23, whereas the growth and maturation pattern of dab in the North Sea is different from the pattern displayed by dab in SD 21 and SD22-32. There is no new genetic study available and, given the low commercial importance of dab in the area, it is unlikely that a genetic study will be conducted in the near future.

After the last review of the stock-merging document in 2023, additional SPiCT assessments have been conducted during the benchmark in 2024, using an improved and extended biomass index and commercial landings from Kattegat. Sensitivity runs show that the perception of the stock development (e.g., trends in SSB or F) does not change when including Kattegat. Quite the contrary, the uncertainty in the model decreased and retrospective analyses (retros and MASE indices) improved. The results have been presented and discussed during the assessment working groups of the Baltic Sea (WGBFAS) and North Sea – North Atlantic (WGNSSK) and both groups support the change in stock boundaries and forwarded this by a joint recommendation to ICES.

Thus, a stock comprising dab from the management areas SD 21-32 would realistically reflect the dab population in the Baltic Sea.

## Proposal

We propose to update the stock definition and boundaries of the dab stocks in the North Sea and Baltic Sea by removing Kattegat (Area 9, Subdivision SD 21) from the North Sea stock and adding it to the dab stock of the Baltic Sea to realistically reflect the dab population in the Baltic Sea. Similar analyses in other flatfish species already resulted in the inclusion of Kattegat to the western Baltic plaice stock (ple.27.21-23) and of Kattegat and Skagerrak to the Baltic sole stock (sol.27.20-24), making a similar scenario for other flatfishes very likely.

The updated dab stocks *„dab.27.21-32"* (Baltic Sea) and *„dab.27.3an4*" (North Sea) would be part of the benchmark "WKMSYSPICT4" by ICES in late 2024/early 2025 where the settings of the SPiCT model (priors, CVS, etc.) would be checked and approved again by the reviewers.

## Progress since last review

The initial working document was submitted and reviewed in September to October 2023. The reviewer did not see enough evidence to support the proposal of merging the stock component in Kattegat and the Baltic Sea. In early 2024, the Baltic dab stock was part of the WKMSYSPICT3 benchmark and explorative runs with updated stock boundaries (dab21-32) were conducted that actually gave better results than the current stock boundary (SD 2232). The assessment model and biomass index calculation were changed during WKMSYSPICT3.

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### Summary of the benchmark WKMSYSPICT3

The dab stock *dab.27.22-32* was benchmarked in December 2023 (data compilation) and January 2024 by WKMSYSPICT3 (ICES 2024a). The assessment method changed from category 3 to category 2. The stock assessment method was changed from Length-based-Indicators (LBI) to a surplus production model (SPiCT), using a model-based approach to calculate an exploitable biomass index (Berg et al. 2013). The same calculation method is also used for the biomass index of plaice in the Western Baltic and Kattegat (*ple.27.21-23*) and Kattegat cod (*cod.27.21*).
The calculation of the survey index changed from a biomass index to a delta GAM model-based approach after the benchmark in 2024. This was done to account for reduced spatial coverage in earlier years (before 2000). Before 2000, the BITS survey was not standardized, different survey gears were used, and spatial coverage was incomplete. The model-based approach accounts for different catchability between gears, unsampled areas, and quantifies the increased index uncertainty due to these issues and also combines the index values of the IBTS and BITS surveys in the Kattegat (SD21).

The new index calculation also accounts for a substantial decreasing trend in the body condition of dab since the mid 1990 by using annual length-weight relationships instead of a fixed one.

After reviewing the available data during the data compilation, the benchmark group decided to conduct additional sensitivity analyses using an extended biomass survey (including Kattegat) and additional fisheries data (landings in Kattegat, provided by WGNSSK). Other settings (CVs, catch uncertainty, priors, etc.) were kept identical to the final settings of *dab.27.22-32*.

The two additional SPiCT runs including Kattegat improved the model performance by decreasing uncertainties, and resulting in lower CVs and lower MASE values in the index time series (all details given in the next chapter and Annex 1.4).

Since the ToR of WKMSYSPICT3 did not include stock identity and stock boundary issues, the group forwarded a recommendation to ICES and the relevant stock identification group to consider the inclusion of Kattegat into the Baltic Sea dab stock.

## SPiCT sensitivity runs

Three different datasets were tested during WKMSYPICT and during the assessment working group WGBFAS (including the latest 2023 data, Table 1). Dataset 1 included only Baltic Sea data, whereas Dataset 2 used the combined index of IBTS/BITS of areas SD21-32. Dataset 3 used the combined areas index and landings of areas SD21-32 (Kattegat and Baltic Sea. The sensitivity analyses were performed to determine the influence of the inclusion of Kattegat to the overall performance of the model.

**Table 1:** Dataset and overview of SPiCT settings of the sensitivity analyses

| **Setting/Data** | **Dataset 1: Baltic Sea** | **Dataset 2: Baltic Sea & Kattegat-Baltic index** | **Dataset 3: combined Baltic Sea & Kattegat** |
|---|---|---|---|
| **Catch time series** | Baltic Sea<br>(Areas SD22-SD32)<br>landings data 1991–2023 | Baltic Sea<br>(Areas SD22-SD32)<br>landings data 1991–2023 | Baltic and Kattegat<br>(Areas SD21-SD32)<br>landings data 1991–2023 |
| **BITS biomass Index quarter 1, "Bergdex"** | Baltic Sea<br>(Areas SD22-32)<br>1991-2023, ≥ 15 cm | Baltic and Kattegat<br>(Areas SD21-SD32),<br>1991-2023, ≥ 15 cm | Baltic and Kattegat<br>(Areas SD21-SD32),<br>1991-2023, ≥ 15 cm |
| **BITS biomass Index quarter 4, "Bergdex"** | Baltic Sea<br>(Areas SD22-32)<br>1991-2023, ≥ 15 cm | Baltic and Kattegat<br>(Areas SD21-SD32),<br>1991-2023, ≥ 15 cm | Baltic and Kattegat<br>(Areas SD21-SD32),<br>1991-2023, ≥ 15 cm |
| | | | |
| **SPiCT settings** | | | |
| - Standard deviation on the indices (sdi) | Log(sdi1)~N(log(index_CV),0.3^2)<br>Log(sdi2)~N(log(index_CV), 0.3^2) | | |
| - Standard deviation on the indices (observation) (stdevfacI) | indexQ1_CV/mean(indexQ1_CV),<br>indexQ4_CV /mean(indexQ4_CV) | | |
| - Standard deviation on the catch (observation) (stdevfacC) | For >2021 stdevfacC = 2; | | |

| | |
|---|---|
| - Biomass process noise (logsdb) | Log(0.15)-0.5*0.5^2, 0.5 |
| - Catch observation error (logsdc) | Log(0.1)-0.5*0.5^2, 0.5 |
| - Uncertainty ratio of index (observation) to biomass process (alpha) | Deactivated |
| - Uncertainty ratio of catch (observation) to fishing mortality process (beta) | Deactivated |
| - Shape parameter (n) | Thorson model, Log(n)~N(log(1.353),0.55) |
| - Intrinsic growth rate (r) | Log(r)~N(log(0.71*0.6765), -0.5*0.5^2,0.5) |
| - Initial depletion (bkfrac) | None (default) |
| - Discretion time step (dteuler) | 1/16 year (default) |

All three models converged and performed well in sensitivity tests. The general trends in the different parameters (biomass, fishing mortality and catch trends) did not change between the three datasets, i.e., including the Kattegat did not change the perception of the stock development (Fig. 1). Datasets 1 and 2 (Baltic Sea only and Baltic landings using an extended SD21-32 index) displayed nearly similar outcomes. Dataset 3 displayed higher biomass estimates.

Naturally, dataset 3 (including landings and index data from Kattegat) displayed the highest biomass and catches, resulting in a higher production curve estimate.

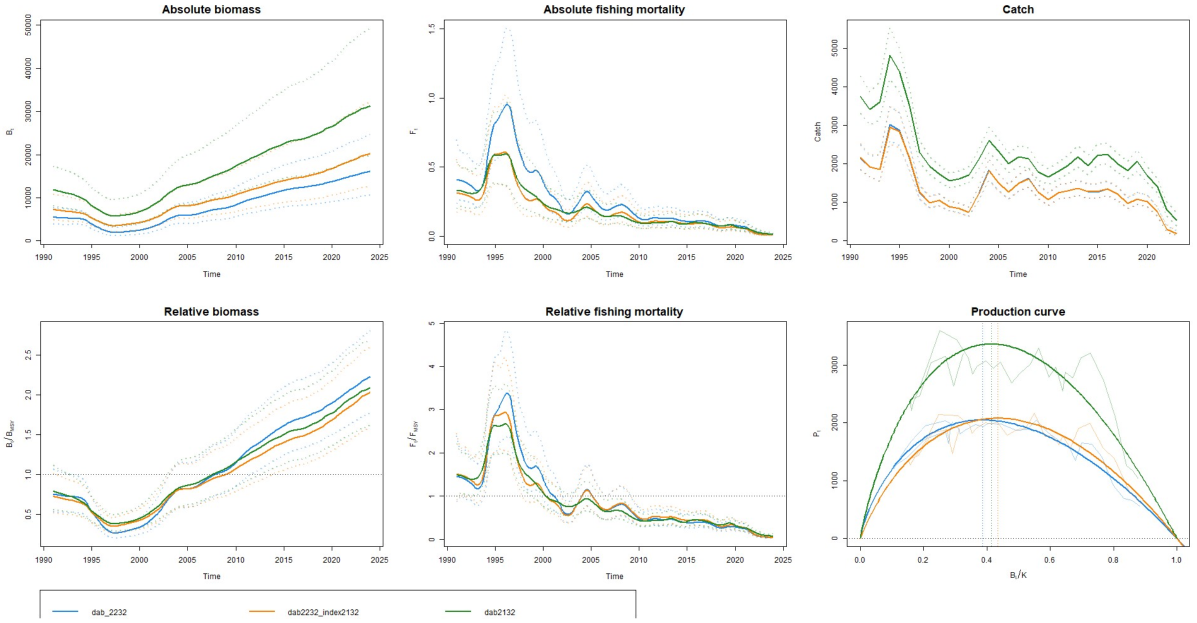

**Figure 1**: Comparison of SPiCT outputs for the sensitivity runs of Baltic dab (blue line), Baltic dab landings and extended survey index (SD21-32, green line) and the extended dab stock 21-32 (red line).

Adding Kattegat data seems to overall stabilize the model estimates and to decrease uncertainties in the estimates (Fig. 1). It is likely that adding Kattegat is explaining changes in biomass in the Baltic Sea (as larger parts of the stock are found at the border between Kattegat and Belt Sea and thus migration across the area border is causing artificial biomass loss, if only looking at the Baltic Sea).

All three models showed good diagnostics. Empirical autocorrelation of the residuals and process residuals for the biomass and fishing mortality were checked in all three datasets. Residuals showed no violations of the model assumptions and improved slightly when Kattegat data were added to the SPiCT model (Annex 1.3).

Retrospective pattern did not change much between datasets, however the Mohn's Rho values improved when adding Kattegat into the datasets (Fig. 2).

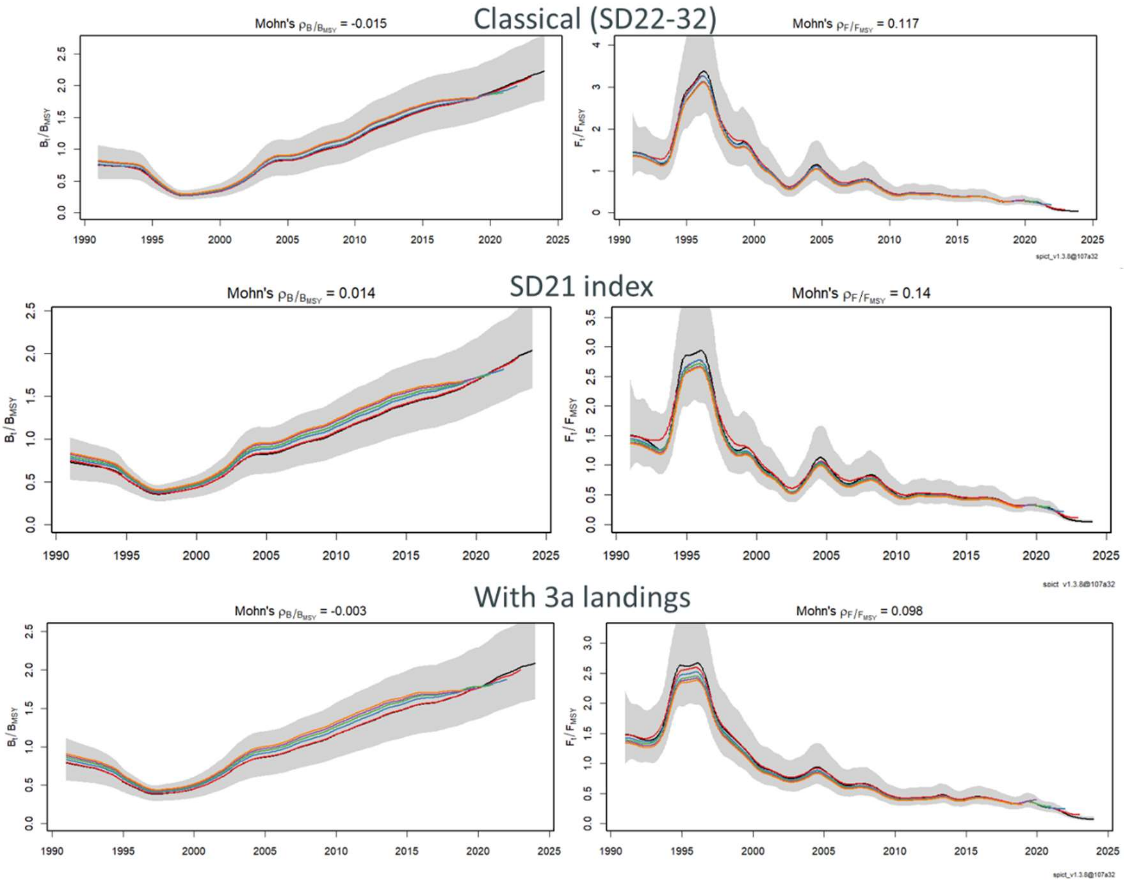

**Figure 2**: *Comparison of the three SPiCT datasets used in the sensitivity runs of dab. Upper graphs: Dataset 1, using only Balti Sea data. Middle graph: Dataset 2, using Baltic Sea catches and biomass index covering Kattegat and Baltic Sea. Lower graphs: Dataset 3, using combined catches and index covering Kattegat and Baltic Sea.*

A hindcast cross validation analysis ("MASE") was performed on each of the datasets, which indicates if the final assessment model can predict the abundance index more accurately than the naïve predictor. The MASE scores from the hindcast analysis in Dataset 1 were 1.04 and 0.686 for the Q1 and Q4 indices, respectively, and no retrospective patterns were found. The scores for both indices did not change significantly when adding Kattegat data (Figure 3), but also did not change the perception of the hindcast patterns, thus validating all model runs.

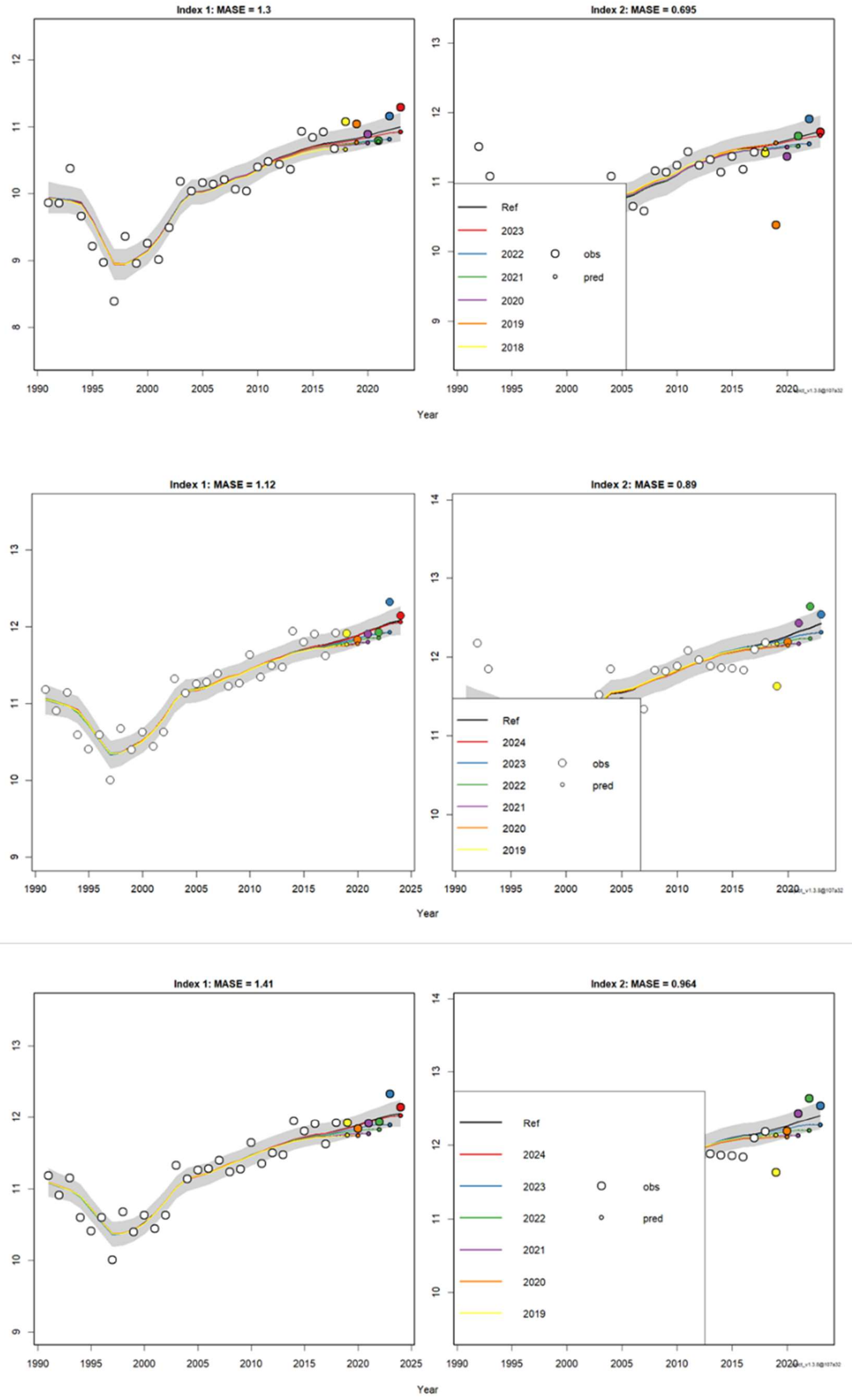

**Figure 3**: *MASE indices of the three sensitivity runs of dab. Upper graphs: Dataset 1, using only Baltic Sea data. Middle graph: Dataset 2, using Baltic Sea catches and biomass index covering Kattegat and Baltic Sea. Lower graphs: Dataset 3, using combined catches and index covering Kattegat and Baltic Sea.*

The final SPiCT run was performed on landings only, so the sensitivity runs also only included landings. Discards are known to be substantial in SD21, but are also quite high in SD22 (>40%). SPiCT is yet not able to use time series that include a mix of landings and catches.

Overall, the uncertainty in the model parameter estimates decreased (for biomass, fishing mortality, index 1 and index 2, respectively) in both the average and the upper and lower limits (Fig. 4). Only the SD of the catch estimates displayed a slightly higher value when adding the index and catch data of Kattegat dab.

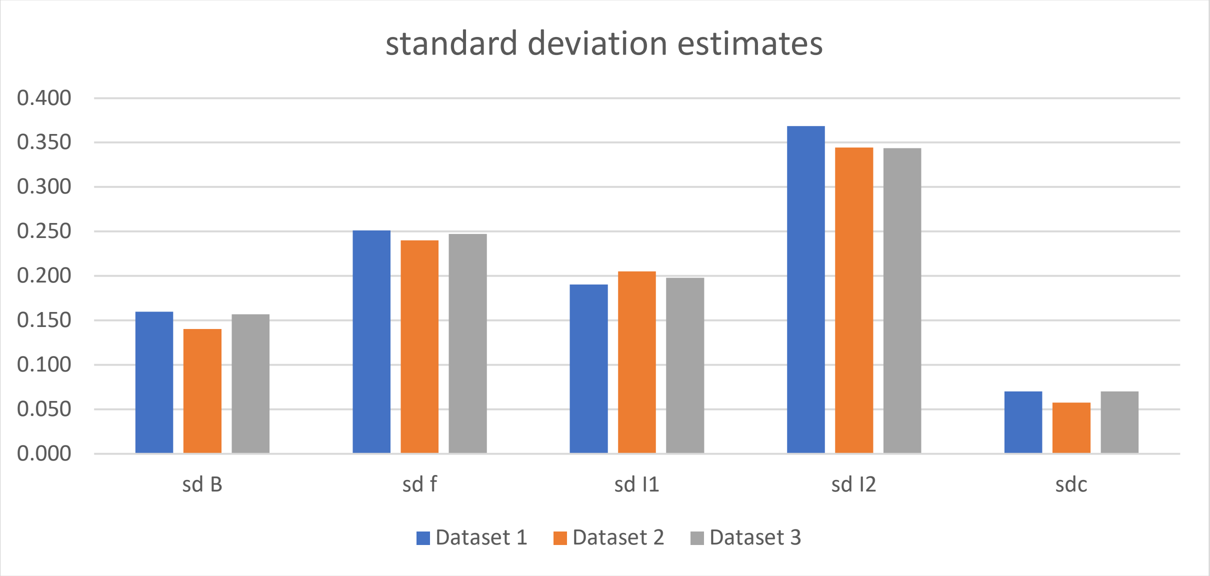

***Figure 4:*** *standard deviation of the estimated parameters for biomass (sd B), fishing mortality (sd F), the two survey indices (sd I1, sd I2) and the catch data (sdc) in the three different SPiCT runs (Dataset 1: Baltic Sea only, Dataset 2: including Kattegat index, Dataset 3: including Kattegat landings and index)*

The uncertainty of estimated parameter might change if the priors and settings of SPiCT are adjusted accordingly to the included Kattegat stock components and further decrease.

All details on the model estimates, variables and priors are given in Annex 1.4

The final SPiCT run was performed on landings only, so the sensitivity runs also only included landings. Discards are known to be substantial in SD21, but are also quite high in SD22 (>40%). SPiCT is yet not able to use datasets that contain landings and catches.

## Assessment working groups WGBFAS and WGNSSK

The results of the benchmark were presented to both relevant working groups for the Baltic Sea (WGBFAS) and North Sea/North Atlantic (WGNSSK).

WGBFAS reviewed the updated SPiCT assessment and the new GAM model biomass index. The index displayed very similar distributions of dab as seen in the biomass index that was used prior to the benchmark (ICES 2024a). The overall distribution of dab in Kattegat and Baltic Sea (Figure 5) indicated no spatial differentiation between the areas. The major part of the stock is aggregated in the Belt Sea and southern Kattegat, only low numbers are found in the eastern Arkona Sea and Bornholm Sea.

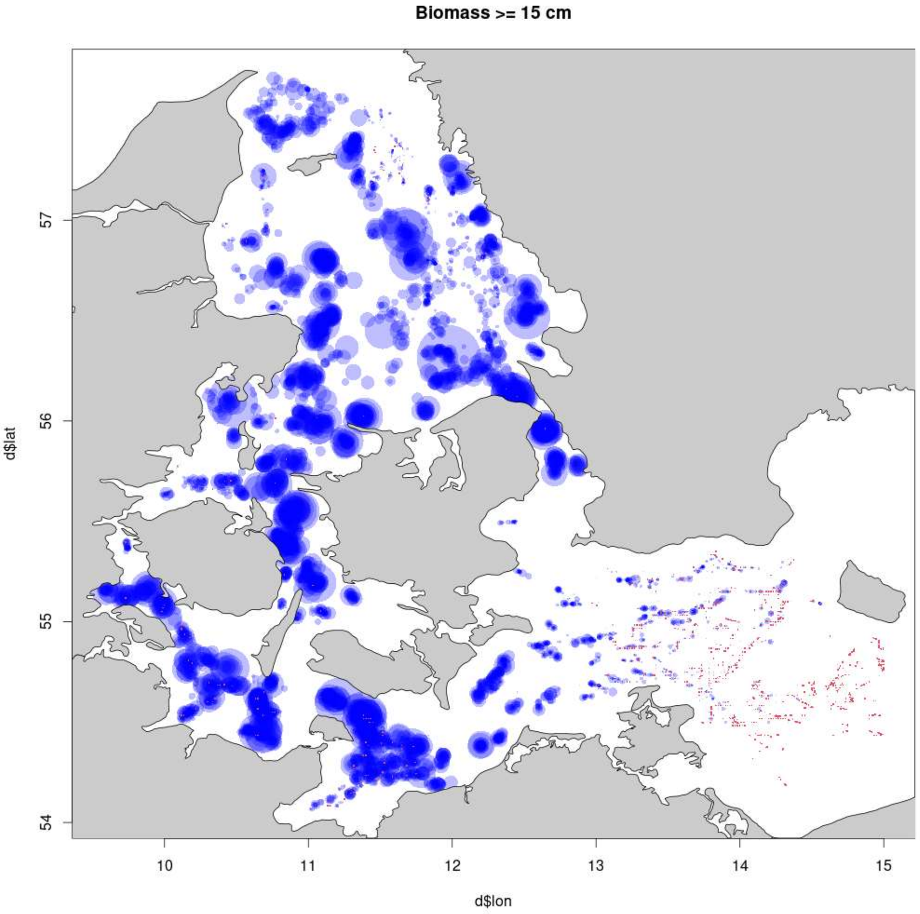

*Figure 5: Overall biomass distribution in Kattegat and Baltic Sea, derived from IBTS and BITS survey data*

WGBFAS also checked the stock distribution in the two latest surveys in Q4 of 2023 and the (preliminary) Q1 2024 (Figure 6). Small dab are not representatively sampled by the bottom trawl surveys because juvenile dab usually are distributed in areas shallower than those covered by the surveys. However, dab were mainly found in the northern part of the Belt Sea and southern Kattegat in both quarters. Adult dab displayed slightly different abundances between quarters, with higher numbers in Q4 2023 along the German coast in the southern Belt Sea, the Sound and west of Sjælland. Lower abundances were found in Q1 2024 in general, with highest abundances west of Sjælland and the northern part of the Sound.

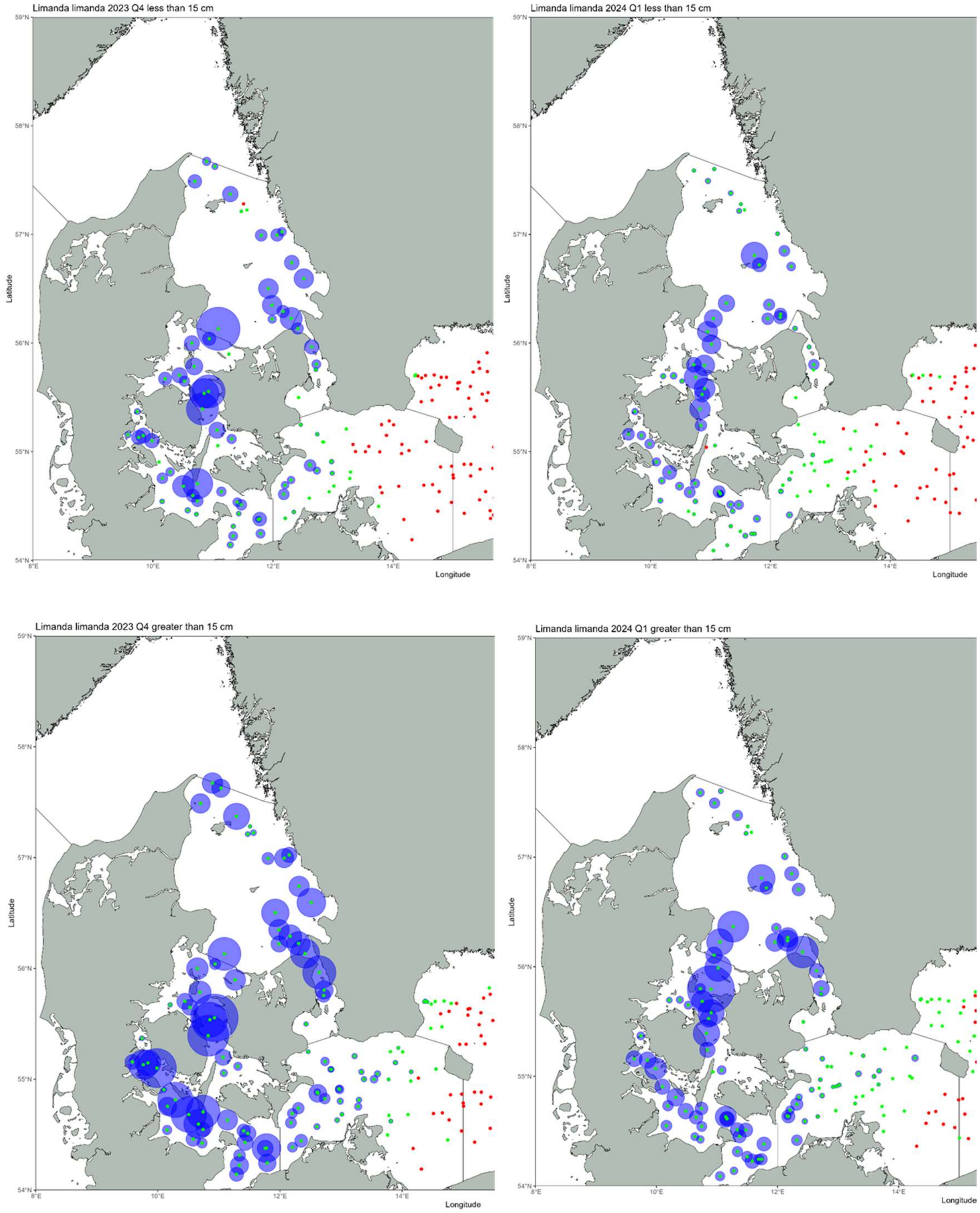

*Figure 6: Most recent abundance distribution of dab in scientific surveys. Upper graphs: Abundance of dab <15cm TL in surveys of Q4 2023 (left) and Q1 2024 (preliminary, right). Lower graphs: Abundance of adult dab >15cm TL in scientific surveys in surveys of Q4 2023 (left) and Q1 2024 (preliminary, right).*

In a joint meeting, WGBFAS and WGNSSK discussed the merging of Kattegat into the Baltic Sea stock after reviewing the latest biomass indices, survey distributions and the SPiCT sensitivity runs.

WGNSSK agrees that dab in the Kattegat is most likely part of the Baltic Sea stock and strongly supports adding the stock component to the Baltic Sea stock. Furthermore, WGNSSK confirmed that the stock component of dab in Kattegat is of such minor importance compared to the North Sea stock, that commercial sampling data and survey indices from that area are usually not even used in the assessment. Instead, settings and data extrapolations from the North Sea stock are used in the process. Thus, adding Kattegat dab to the Baltic Sea would also will increase the data quality of that area, as extrapolations and estimation will come from the well-sampled Belt Sea, which is much more accurate than using North Sea data.

The Baltic assessment working group WGBFAS is willing to take up the area and update the respective assessments and get it reviewed at the earliest possibility.

Both assessment working groups agreed on a joint recommendation to merge SD21 into the Baltic Sea stock, which will be part of the 2024 meeting reports (ICES 2024b).

Furthermore, WKMSYSPICT already signalled the willingness to review and approve an updated SPiCT assessment for next year's assessment working groups and also contributed a recommendation in their 2024 report to support the change in stock boundaries.

## Current status

The current status section has only slightly been updated compared to the first WD of 2023. The stock assessment description was updated and the maps were slightly changed.

### North Sea

Dab and flounder in the North Sea have been assessed under a shared TAC until 2017. Since 2018, dab in the North Sea is assessed as one stock (*dab.27.3a4*), covering Subarea 4 (North Sea) and Division 3.a. (Skagerrak and Kattegat) and is no longer subject to a TAC. Instead, a catch advice is given as long as dab and flounder remain largely bycatch species, with the main fleets catching dab and flounder continuing to fish the target species (plaice and sole) sustainably within the $F_{MSY}$ ranges provided by ICES. If this situation changes, or dab is no longer within safe biological limits, this advice would need to be reconsidered (ICES 2023a).

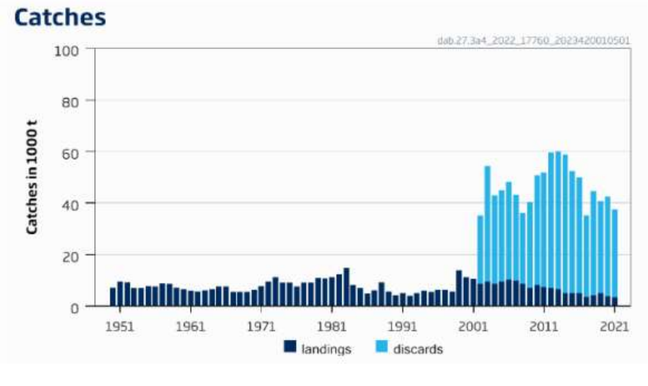

**Figure 7:** Official landings (1950–2001) and ICES estimates of landings and discards (2002–2021).

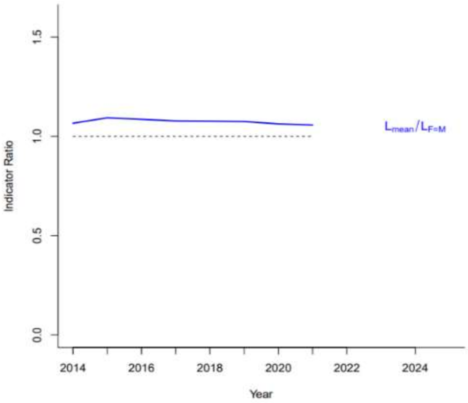

**Figure 8:** Index ratio $L_{mean}/L_{F=M}$ from the length-based indicator method (LBI; ICES, 2023a). The exploitation status is below the $F_{MSY}$ proxy (dotted line) when the index ratio value is above one.

Catch advice is given for three years and was last given in 2022 (for 2023, 2024 and 2025, updated advice in May 2023). Dab is mainly a bycatch species in the mixed demersal fisheries for North Sea plaice and sole, with a high discard rate (>90% on average, included in the assessment since 2002). Division 3.a. contributes <10% of total landings.

The stock is categorized as "data limited", following the ICES framework for category 3 stocks (ICES, 2023a). The most recent advice is based on the *chr* rule to provide MSY advice (ICES, 2023b). A survey combined biomass index is used as an indicator of stock development. An additional index ratio $L_{mean}$ /$L_{F=M}$ from the length-based indicator (LBI; ICES, 2022a) method is used for the evaluation of the exploitation status. In former years, a SPiCT assessment has been performed to evalaute the stock and give advice (ICES 2023b)

## Baltic Sea

Dab in the Baltic Sea is assessed as one stock (*dab.27.22-32*) covering Divisions 3.b., 3.c. and 3.d. (ICES Subdivisions 27.3.c.22-27.3.d.32). Catch advice was given between 2016 and 2018. Since 2019, ICES has not been requested to provide advice on fishing opportunities (ICES, 2023c). Instead, a stock status update is given every three years. The last “advice” was given in 2023 for 2024, 2025 and 2026 (ICES 2023c). Dab is mainly caught in a mixed flatfish fishery and was as a bycatch species in the mixed demersal fisheries for Baltic Sea plaice and cod, with a high discard rate (>40% on average, included in the assessment since 2012).

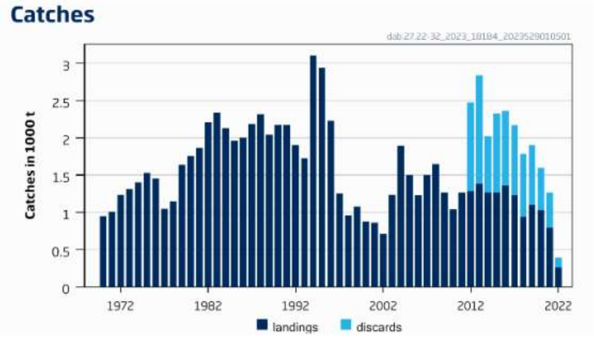

**Figure 9:** Official landings (1971–2001) and ICES estimates of landings and discards (2012–2022).

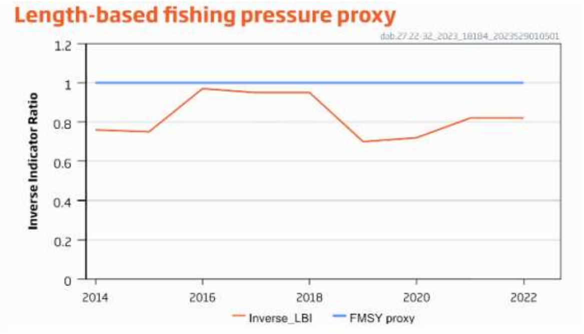

**Figure 10:** inversed Indicator ratio from the length-based indicator method (LBI; ICES, 2023c). The exploitation status is below the $F_{MSY}$ proxy (dotted line) when the inverted index ratio value is lower than one.

The stock was categorized as “data limited”, following the ICES framework for category 3 stocks (ICES, 2023c) and upgraded to a category 2 SPICT model after the benchmark in 2024 (ICES, 2024a). Dab catches in the Baltic Sea are not currently regulated by a TAC.

The stochastic production model in continuous time (SPiCT) was applied to the dab stock dab.27.22-32. Input data are commercial landings from 1991 to present and the BITS delta-GAM model index Q1 and Q4 (Fig. 11). No reference points are defined for this stock in terms of absolute values. The SPiCT-estimated values of the ratios $F/F_{MSY}$ and $B/B_{MSY}$ are used to estimate stock status relative to the MSY reference points and are used to estimate catch advice and catch scenarios.

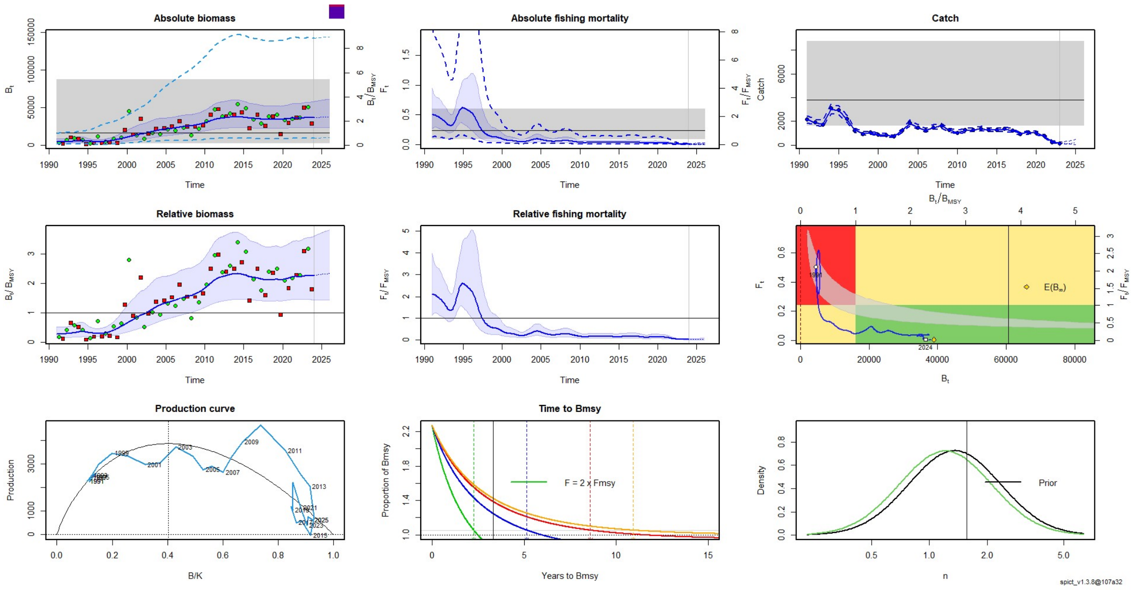

*Figure 11: current SPiCT assessment results for dab in SD22-32 (ICES 2024b).*

A short-term forecast was conducted assuming $F_{sq}$. The current time-series of commercial and survey data combined with continuously increasing data quality (in terms of spatiotemporal sampling coverage, number of samples and error/consistency checks) justifies the use of this model as basis for the advice and to give stock status updates. In addition, trends by SPiCT align with those of the previous LBI and survey (BITS) biomass indices.

# Spatio-temporal distribution

## Surveys

The data of scientific trawl surveys were used to generate distribution maps and overviews for dab in the north-eastern North Sea, Skagerrak and Kattegat, as well as the western Baltic Sea. The aim was to investigate spatio-temporal distribution patterns and changes since the start of the time series and between seasons.

The International Bottom Trawl Survey (IBTS) covers the North Sea (Subarea 4) and the Transition area (Division 3.a. including the Skagerrak 3.a.20 and Kattegat 3.a.21) and is conducted two times per year in Quarter 1 and 3 (Q1, Q3). The Baltic International Trawl Survey (BITS) covering the entire Baltic Sea and Kattegat (3.a.21) and is conducted also twice per year, in Q1 and Q4. Both surveys are conducted using the same sampling protocols and data are publicly available at the International Survey database DATRAS, hosted by ICES (https://datras.ices.dk).

Survey indices of exploitable stock biomass (15 cm+) are calculated using the methodology similar to what is described in Berg and Kristensen (2014), that is a Delta-Lognormal model which consists of a binomial presence/absence model and a lognormal model for strictly positive responses. Once the parameters in the model are estimated, a standardized survey index is obtained by predicting and adding up the abundances in a fine meshed grid of points that is the same in all years. This can be thought of as performing a virtual experiment where the experimental conditions such as the haul positions, gear type etc. are exactly the same in each year.

The observed exploitable stock biomass is calculated from observed numbers-at-length and a length-weight model with time-varying coefficients (because there have been significant changes in the LW relationship over time for dab).

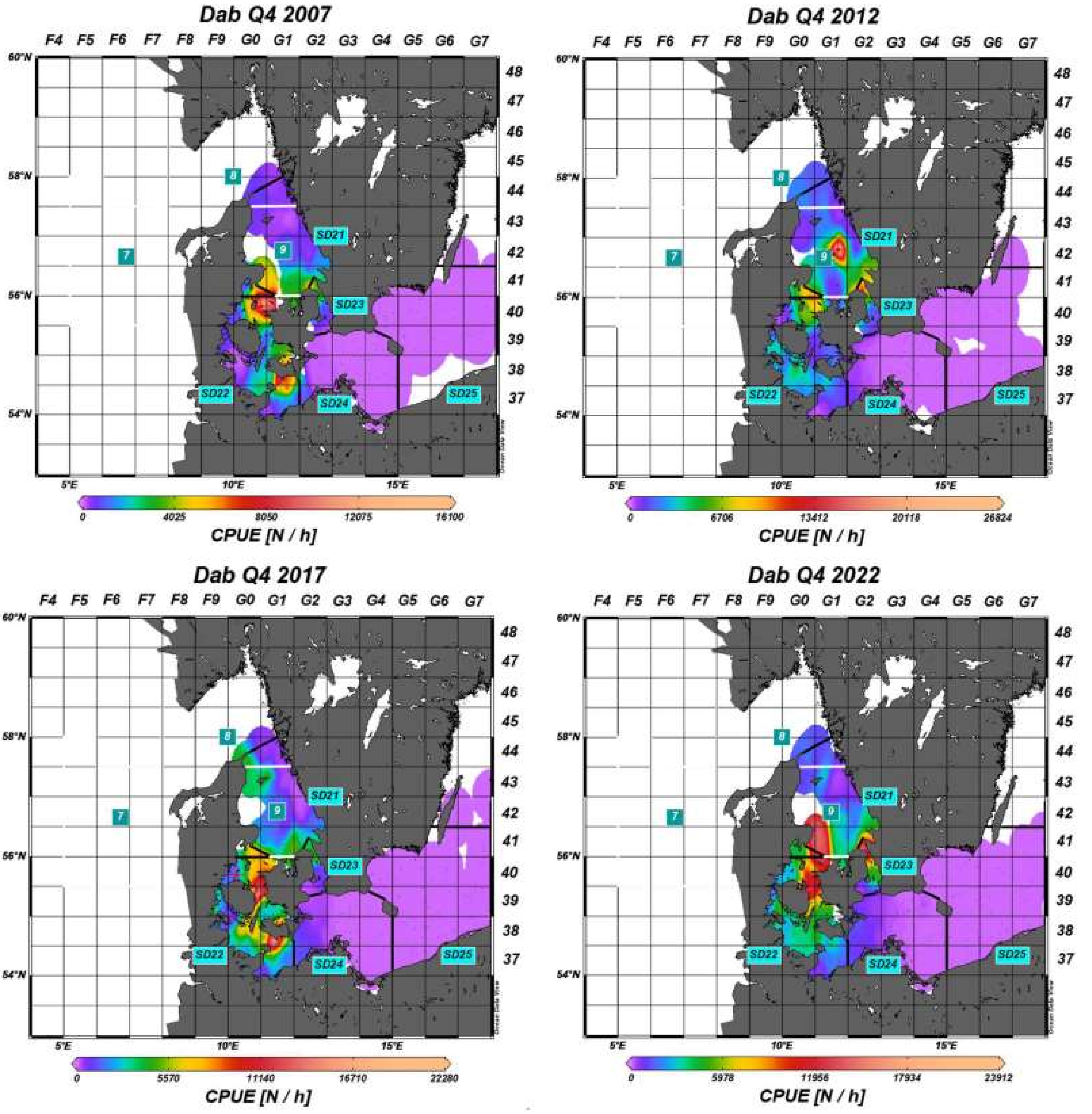

**Figure 12:** Distribution area of dab in the Baltic Sea and Kattegat (Q1 BITS survey index) including SDs 24 and 25 (Arkona and Bornholm Sea.

Although the Baltic Sea dab stock virtually covers the entire Baltic Sea, the focal point of its distribution is the western part of the Baltic Sea. Only very few dab are found east of the Arkona basin (SD 24) and almost no dab are found east of Bornholm (Figure 12). These areas were therefore excluded for the survey overviews.

Combined survey indices of quarter 1 (Q1) surveys from 1992-2023 in IBTS areas 7, 8, and 9 and the Western Baltic Sea (SDs 22, 23) showed that the main distribution area of dab in Division 3.a. and the Baltic Sea was found in the northern part of the Belt Sea and southern Kattegat around Sjælland (Figure 13, Annex 1.1). That is, the Danish archipelago is the centre of distribution of dab in the region.

In the northern Kattegat, a smaller aggregation of dab around Læsø was present in the early 2000's and some years in the 2010's. In most years, a clear connectivity between all three areas (SD 21, 22 and 23) through the Danish straits was displayed, whereas the link to Skagerrak and the North Sea is negligible with a CPUE of 0 in central Skagerrak. Only very few dab were found in the region between Skagerrak and Kattegat (Figure 13, Annex 1.1).

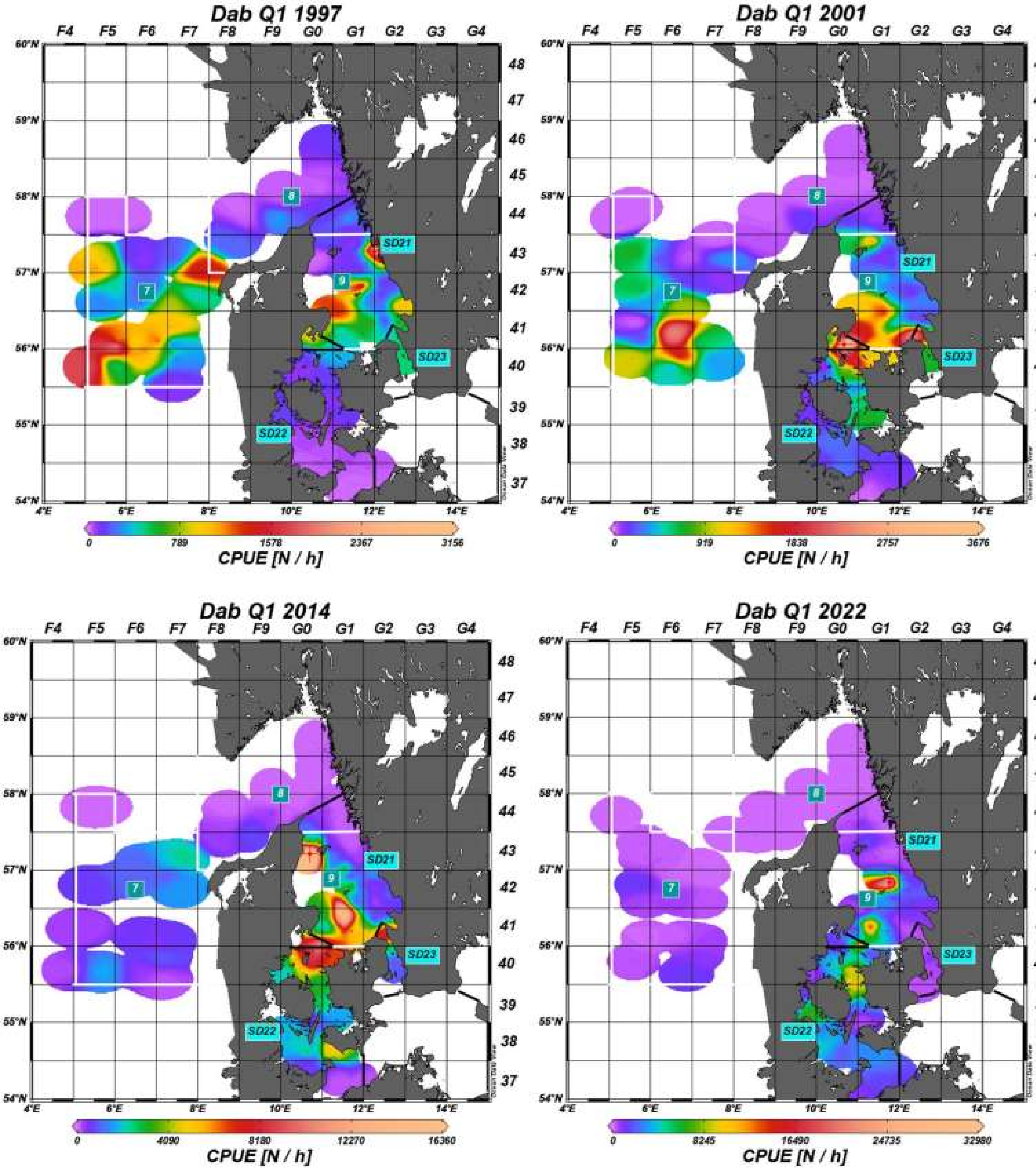

**Figure 13:** Survey-based CPUE distribution of dab in North Sea (Areas 7,8,9, IBTS) and Baltic Sea (SDs 22-23, BITS)

The Q4 BITS and IBTS Survey showed a similar distribution with high accumulations of dab around Sjælland, connecting all three areas (SDs 21, 22 and 23) with each other (Figure 14, Annex 1.2). The IBTS indicated a very high CPUE of dab in the Subareas 7 and 8 until 1994. In 1995 and 1996, the spatial distribution was similar to the Q1 distribution pattern. However, IBTS has only been conducted in Q4 until 1996.

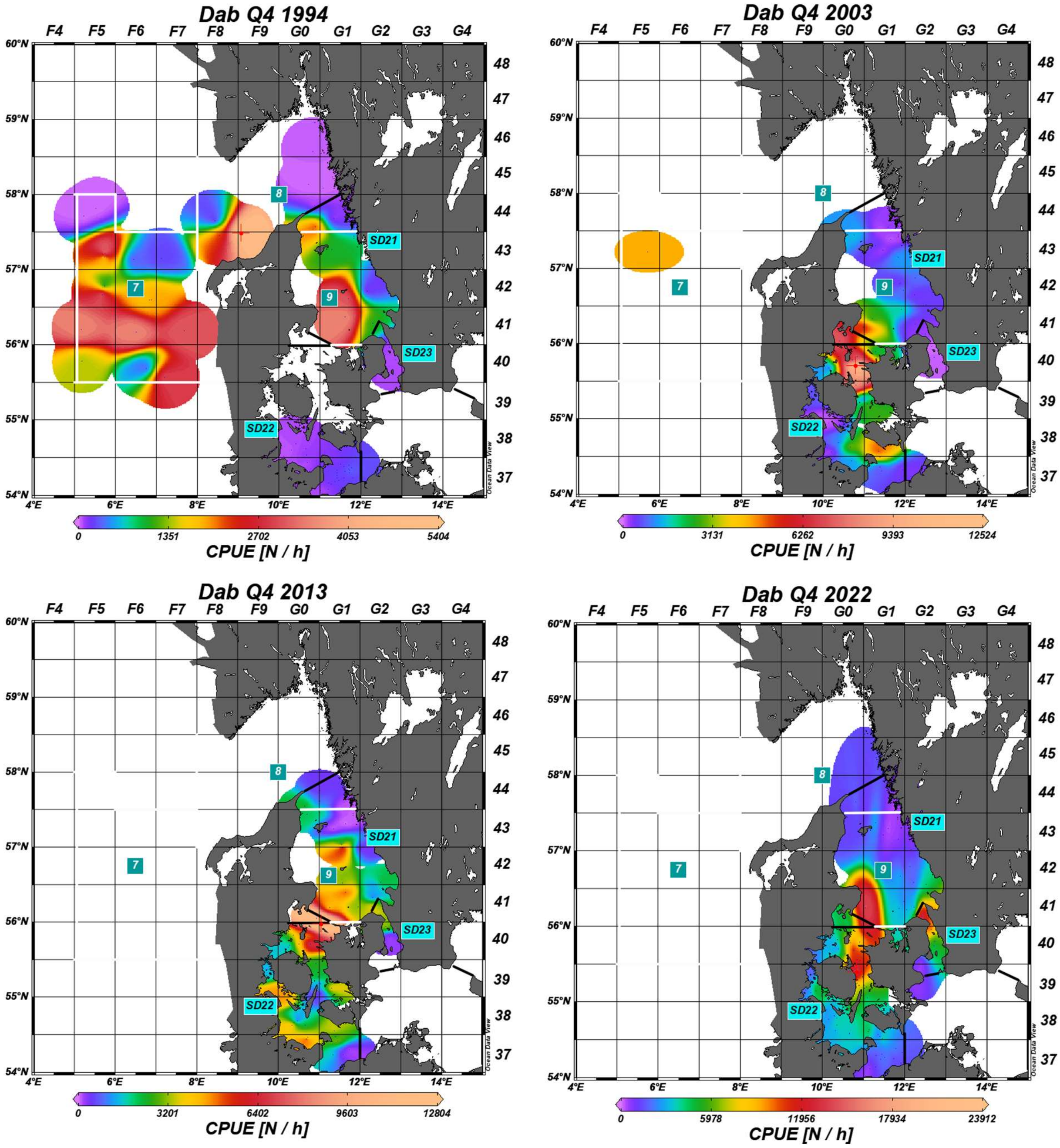

**Figure 14:** Survey-based CPUE distribution of dab in North Sea (Areas 7,8,9, IBTS) and Baltic Sea (SDs 22-32, BITS)

Additionally, the Q3 IBTS index of dab displayed a similar distribution pattern (Figure 15) with high abundances of dab in the North Sea (Area 7,) and southern Kattegat, exceeding the border to SD 22 and reaching into the Baltic Sea. There is no connection of the high abundances in North Sea and Kattegat via the Skagerrak where the abundance of dab was as low as seen in Q1 and Q4 surveys. Only a small aggregation of dab was present along the northern Danish coast.

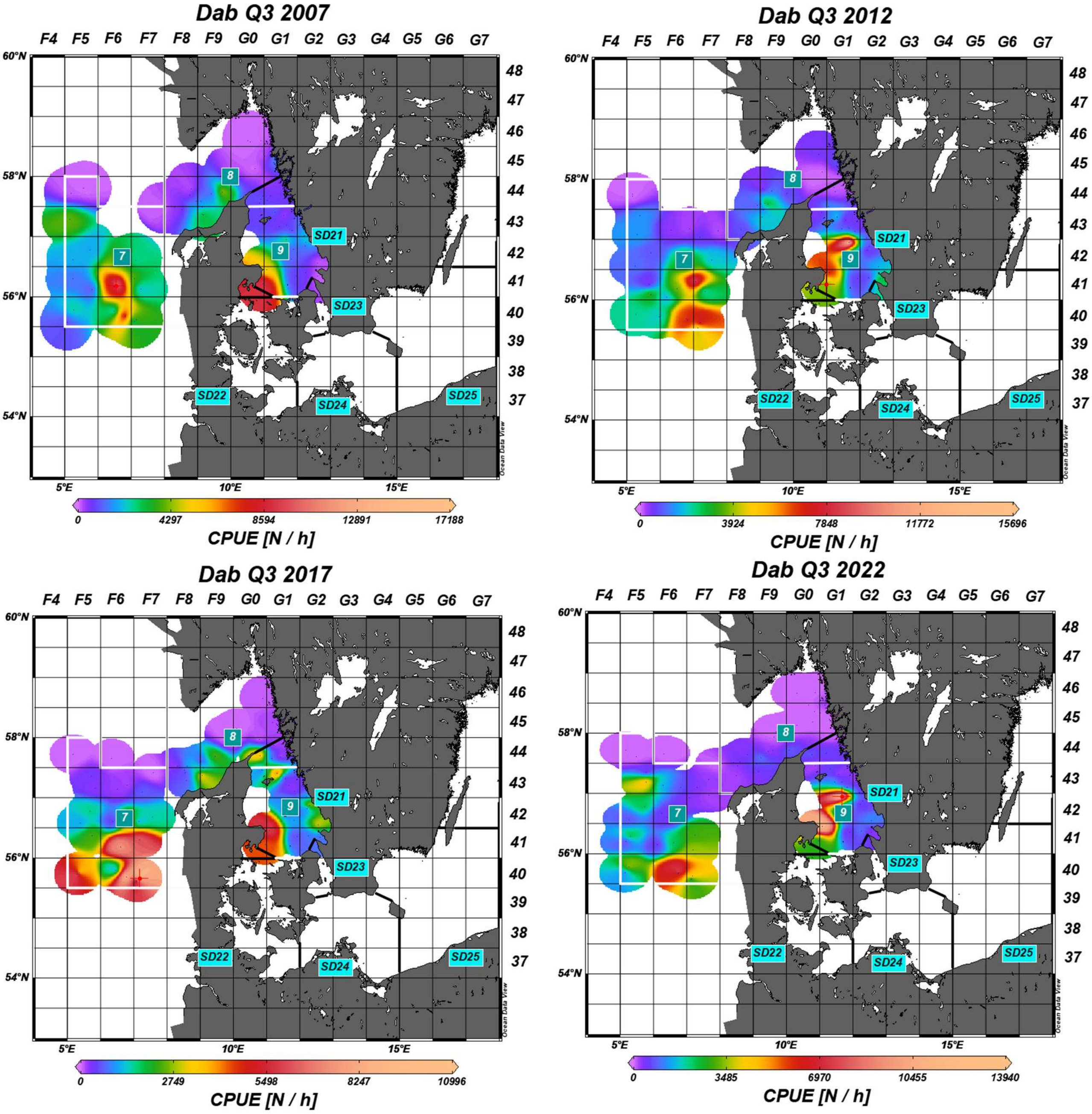

**Figure 15:** Survey-based CPUE distribution of dab in North Sea (Areas 7,8,9) during the Q3 IBTS survey

## Fishery

The fishing pattern in Division 3.a. showed a similar species distribution as seen in the survey indices, with the major part of dab landings originating from the southern Kattegat and western Skagerrak (Figure 16, Annex 1.3). However, dab is also caught and landed close to the two major harbours in northern Denmark, Hirtshals and Skagen, where the survey index indicates low abundances.

Aside these two hotspots close to the harbours, only occasional and very low (<1t/year) landings were registered in the central part of Division 3.a., indicating a low link between the stock components, presently considered to be part of one North Sea stock.

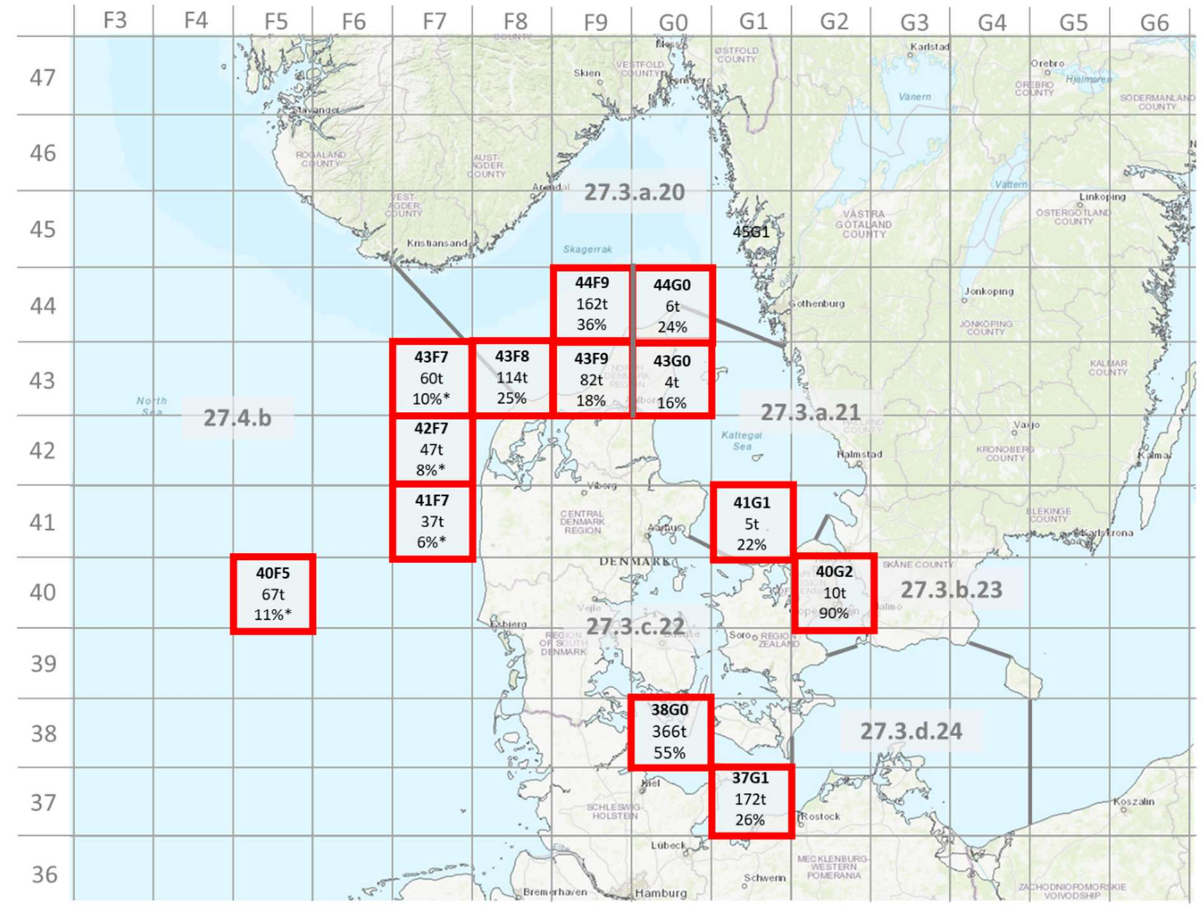

**Figure 16:** Landings of dab in the North Sea (27.4.b), Transition area (27.3.a) and the Baltic Sea. Averaged (2019-2022) contribution of ICES statistical rectangles that provide >75% of landings per Area.

* 2% (~10t) of Dab landings in the North Sea are not allocated to a statistical rectangle and were not used for the calculation

Generally, Kattegat has very low landings of dab (around 17-25t/year), where the species is mainly caught as bycatch in Nephrops-directed fisheries and thus usually discarded. Landings are registered mainly in the southern part of the Kattegat (ICES rectangles 41G0, 41G1 and 42G1) and between Læsø island and Skagen in northern Kattegat (44G0 and 43G8).

Dab landings in Skagerrak were higher, with around 400t/year, mostly along the northern Danish coastline of western Skagerrak, with 44F9 and 43G8 contributing most (>60%) of these landings. However, given the low abundance in the IBTS surveys in Q1, Q3 and Q4 it is likely that these dab landings were taken in the North Sea and rectangles were assigned afterwards, using the landings harbours in Skagerrak. WGNSSK also stated that species misreporting has been an issue in dab fisheries in former times as it was caught as “mixed flatfish” along with flounder (ICES 2023a).

Regionally estimated discards are not available for Kattegat nor Skagerrak, as these are estimated along with Division 4 (North Sea).

The fishery on dab in the Baltic Sea is concentrated on the Belt Sea (SD 22). On average, >90% of the annual landings originate from the Belt Sea, mainly by Germany and Denmark. Average landings have been around 1000t/year, except for 2022 where a strong decline in fishing activity (caused by Western Baltic cod TAC restrictions and limited fishing opportunities) also decreased landings to around 250t (Figure 10). The major part of the landings is taken in two ICES statistical rectangles (38G0 and 37G1, Figure 15).

## Life history parameters

Different life history parameters were obtained from Q1 surveys (IBTS, covering North Sea) and BITS (covering Kattegat and Baltic Sea.). The maturation is very similar between dab in Kattegat and Baltic Sea, where females mature at 12cm total length.

Dab in the North Sea displayed a slower growth than dab caught in Kattegat and the Baltic Sea (Figure 16, Table 2), the latter two being very similar in length-weight relationship. This also suggests a close link of dab in the Kattegat to the western Baltic Sea rather than to the North Sea.

**Table 2:** life history parameter of dab caught in Q1 Surveys in 2022 in the North Sea (IBTS), Kattegat (BITS) and Baltic Sea (BITS)

| | **North Sea** | **Kattegat** | **Baltic Sea** |
|---|---|---|---|
| Maturity age<br>(Lmat) length | 2-3 years*<br>10cm (F), 11cm (M) | 1 year<br>12 cm (F), 11cm (M) | 1 year<br>12cm (F), 11cm (M) |
| Growth intercept<br>slope | 0.004<br>3.262 | 0.0089<br>3.148 | 0.0084<br>3.155 |
| N | 1133 | 125 | 978 |

** No age reading conducted on IBTS for dab; From Rijnsdorp et al. (1992) for the Southern North Sea*

**Figure 17:** Length-weight correlation of dab in the North Sea (blue line), Kattegat (red line) and Baltic Sea (green line). Data obtained from Q1 Surveys (IBTS and BITS)

## Genetics

No genetic studies were found that investigate stock boundaries of dab in the Baltic Sea and North Sea.

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ICES (2023a). ICES Advice 2023 – dab.27.3a4 – https://doi.org/10.17895/ices.advice.22793633

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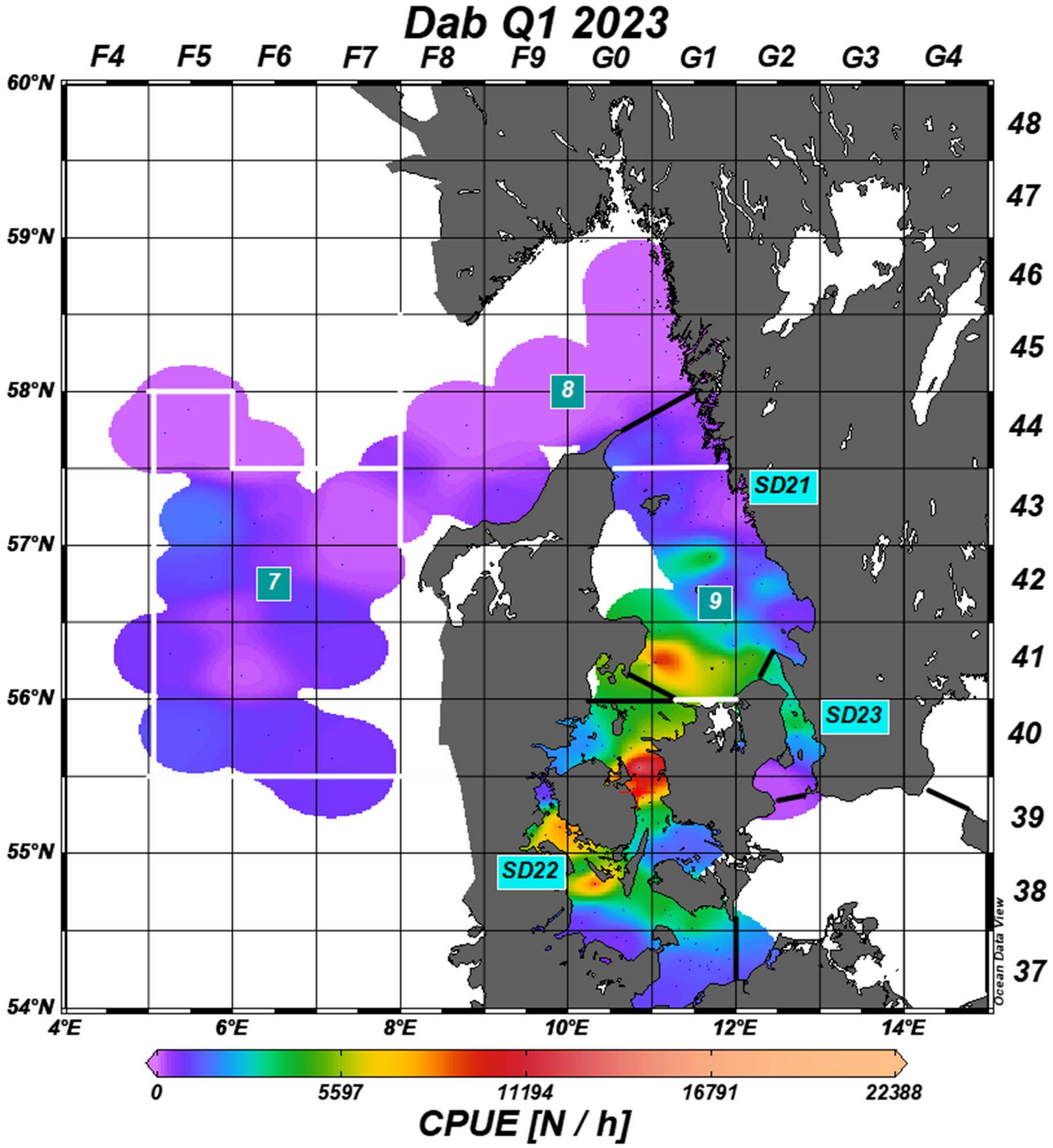
ICES (2024b) Baltic Fisheries Assessment Working Group (WGBFAS). ICES Scientific Reports. 6:53. 584 pp. https://doi.org/10.17895/ices.pub.25764978

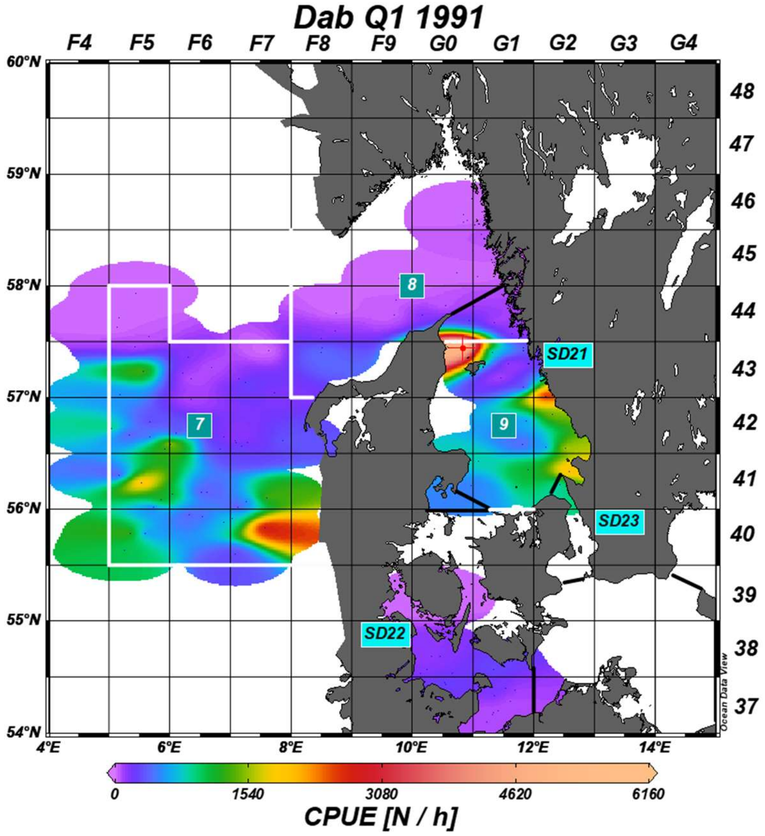
Rijnsdorp, A.D., Vethaak, A.D., van Leeuwen, P.I. (1992). Population biology of dab *Limanda limanda* in the south-eastern North Sea. Mar. Ecol. Prog. Ser. 91, 19-35

# ANNEX 1.1

Combined **Quarter 1 Survey Index** CPUE (no/hour) of IBTS, covering Areas 7, 8 and 9 and BITS, covering Areas SD21, 22 and 23.

The colour scheme is adjusted to the maximum value of each year to make maps easier to read.

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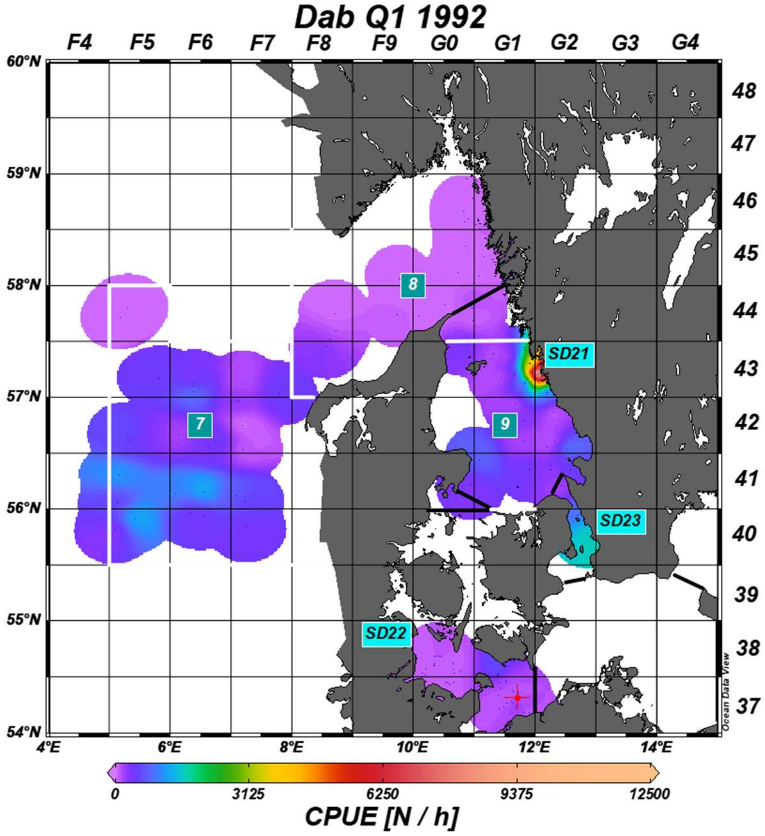
48 47 46 45 44 43 42 41 40 39 38 37
4°E 6°E 8°E 10°E 12°E 14°E
8
7
9
SD21
SD22
SD23
Ocean Data View
0 1540 3080 4620 6160
CPUE [N / h]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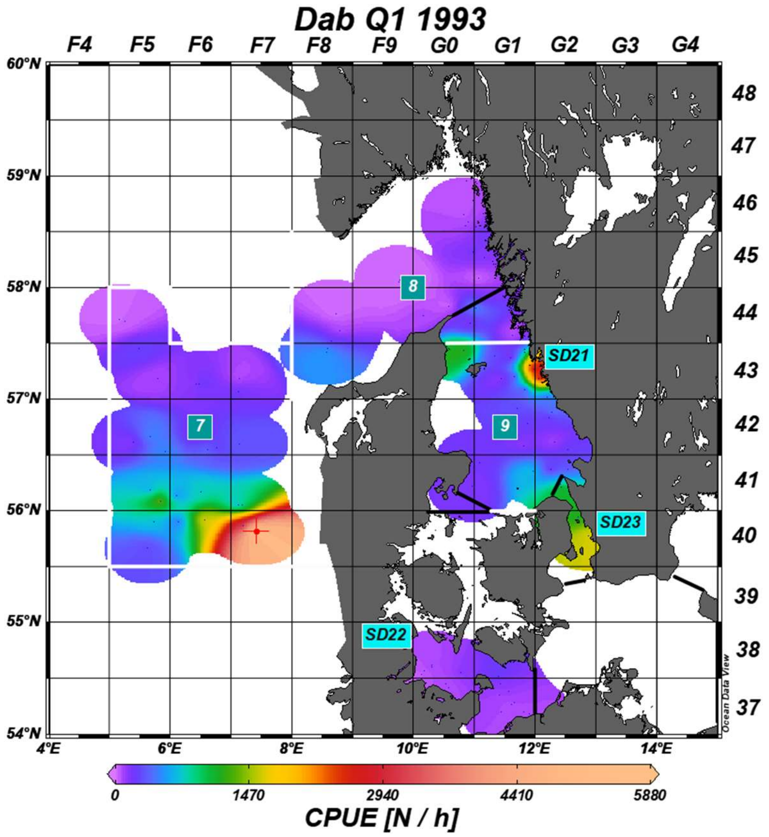
60°N 59°N 58°N 57°N 56°N 55°N 54°N
48 47 46 45 44 43 42 41 40 39 38 37
4°E 6°E 8°E 10°E 12°E 14°E
8
7
9
SD21
SD22
SD23
Ocean Data View
0 3125 6250 9375 12500
CPUE [N / h]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F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
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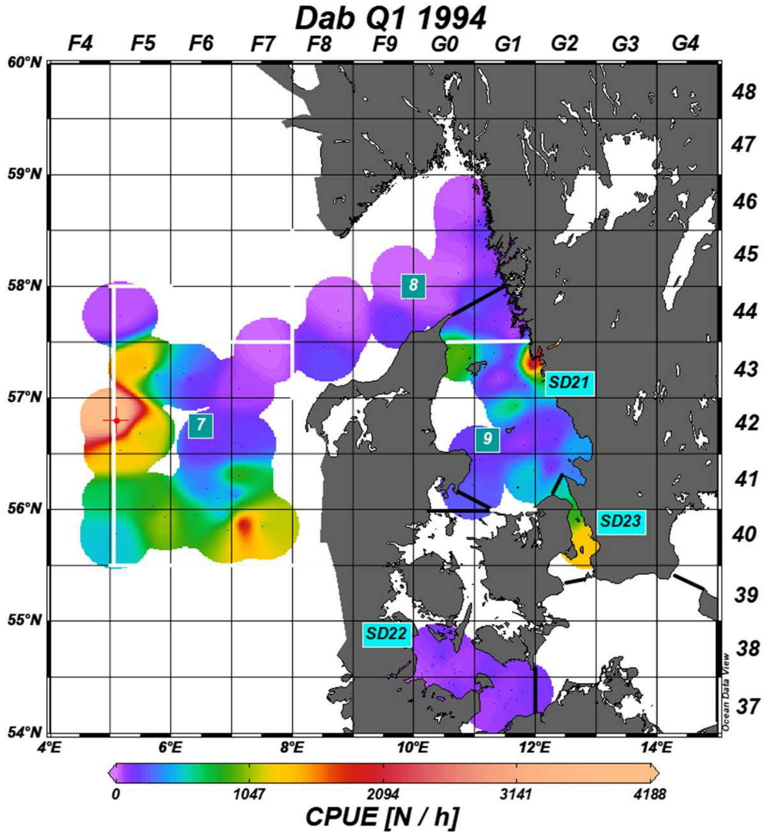
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD22
SD23
Ocean Data View
0
1470
2940
4410
5880
CPUE [N / h]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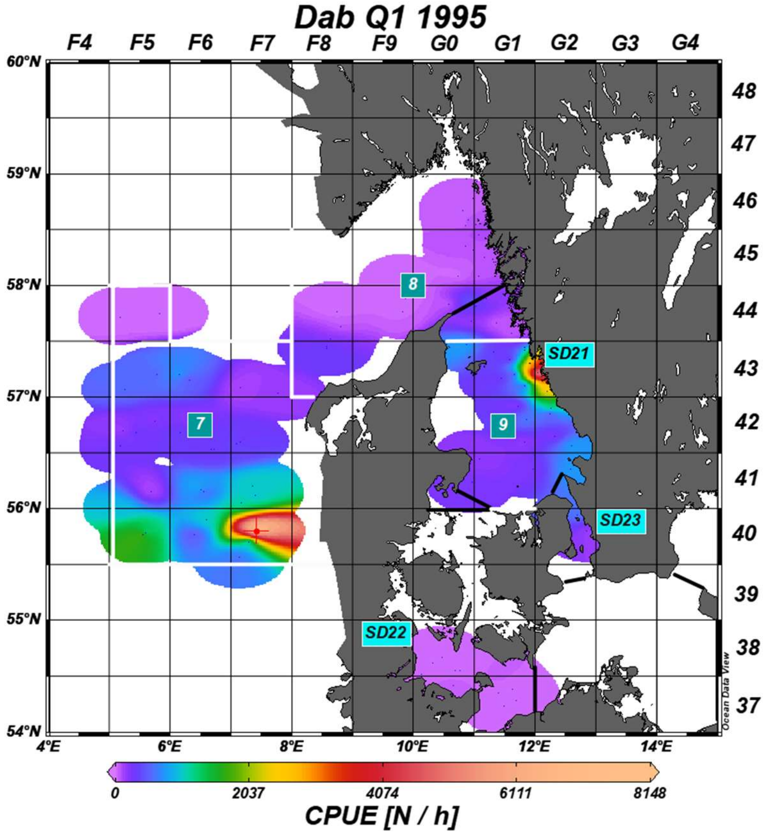
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD22
SD23
Ocean Data View
0
1047
2094
3141
4188
CPUE [N / h]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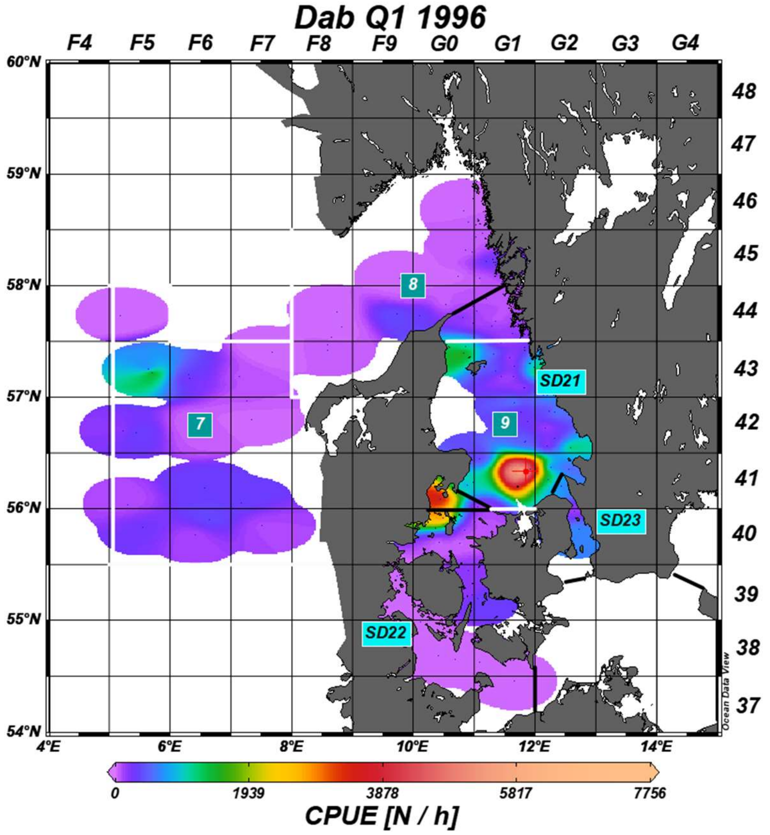
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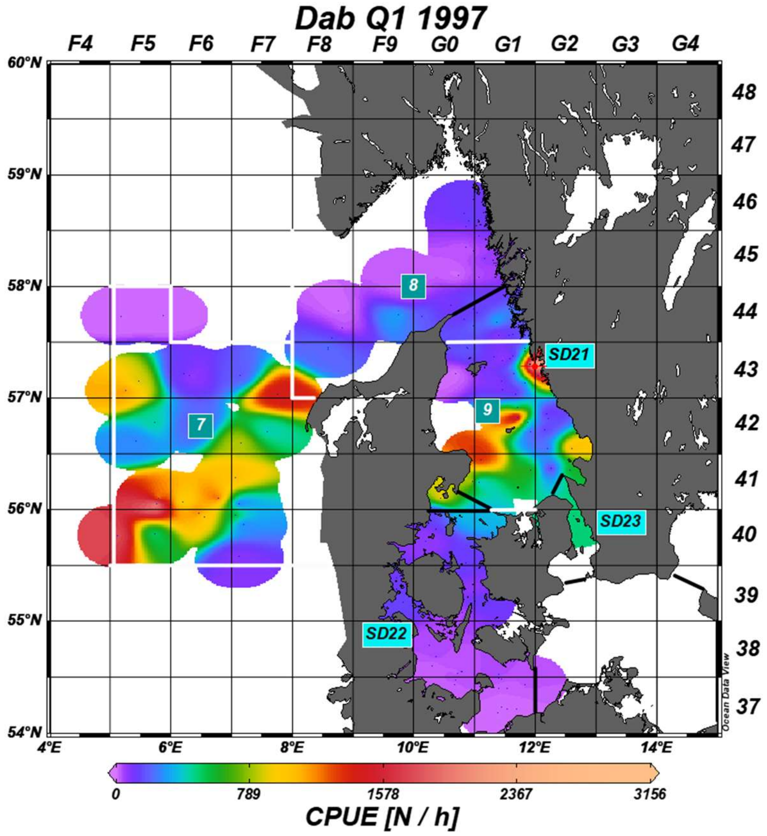
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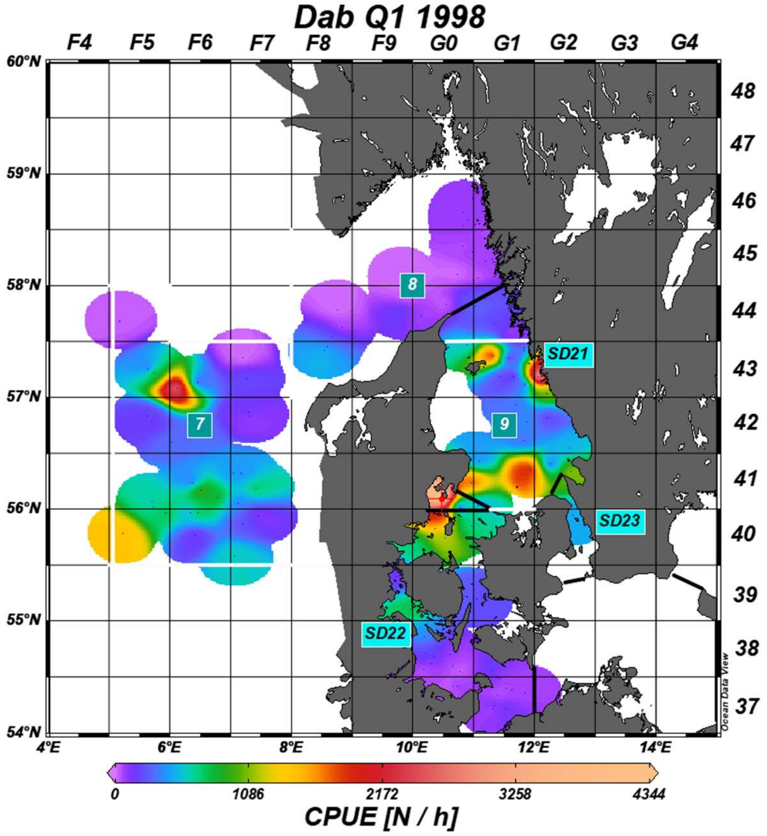
59°N
58°N
57°N
56°N
55°N
54°N
48 47 46 45 44 43 42 41 40 39 38 37
4°E 6°E 8°E 10°E 12°E 14°E
8
7
9
SD21
SD22
SD23
Ocean Data View
0 789 1578 2367 3156
CPUE [N / h]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58°N
57°N
56°N
55°N
54°N
48 47 46 45 44 43 42 41 40 39 38 37
4°E 6°E 8°E 10°E 12°E 14°E
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7
9
SD21
SD22
SD23
Ocean Data View
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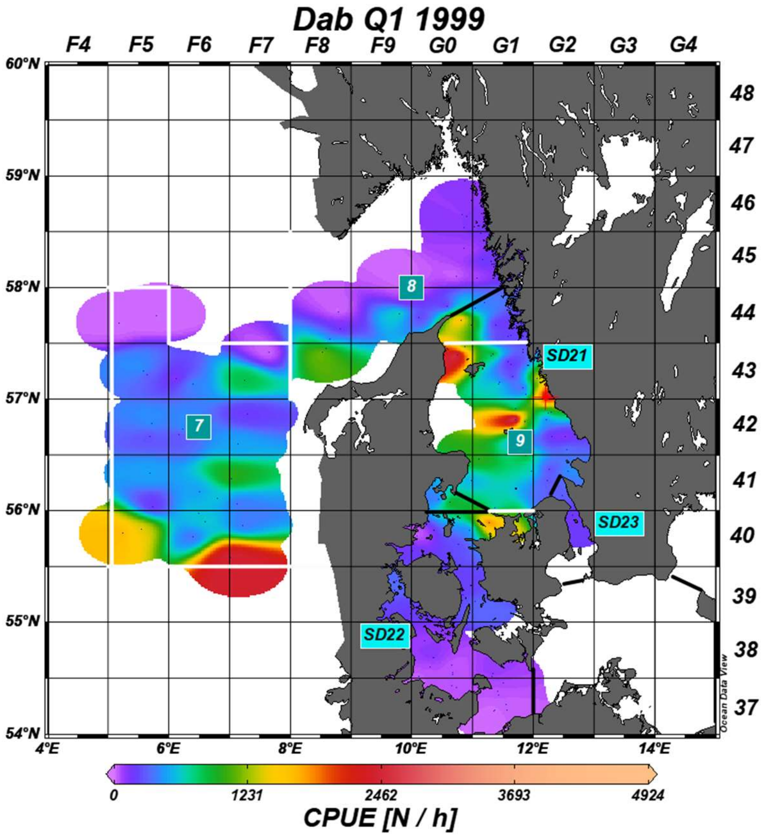
CPUE [N / h]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F8
F9
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G2
G3
G4
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58°N
57°N
56°N
55°N
54°N
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42
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4°E
6°E
8°E
10°E
12°E
14°E
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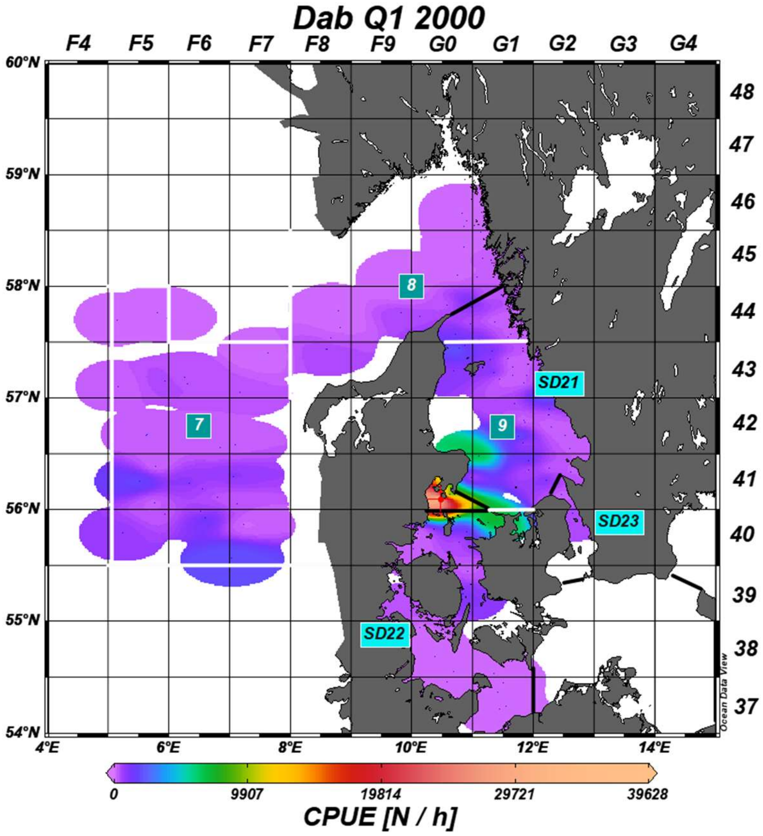
8
9
SD21
SD22
SD23
Ocean Data View
0
1231
2462
3693
4924
CPUE [N / h]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G0
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G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
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42
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38
37
4°E
6°E
8°E
10°E
12°E
14°E
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8
9
SD21
SD22
SD23
Ocean Data View
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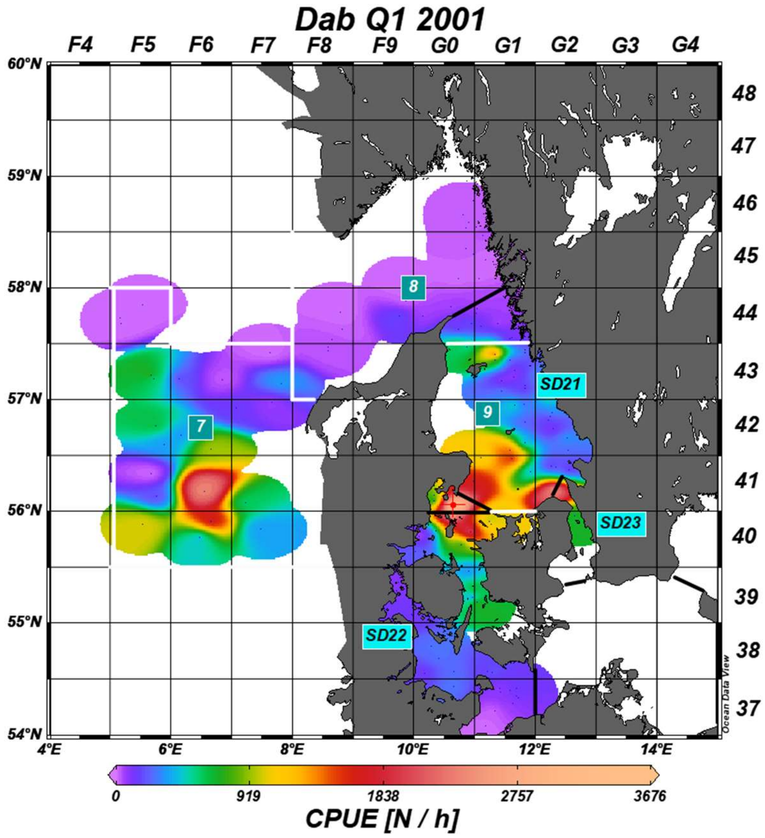
9907
19814
29721
39628
CPUE [N / h]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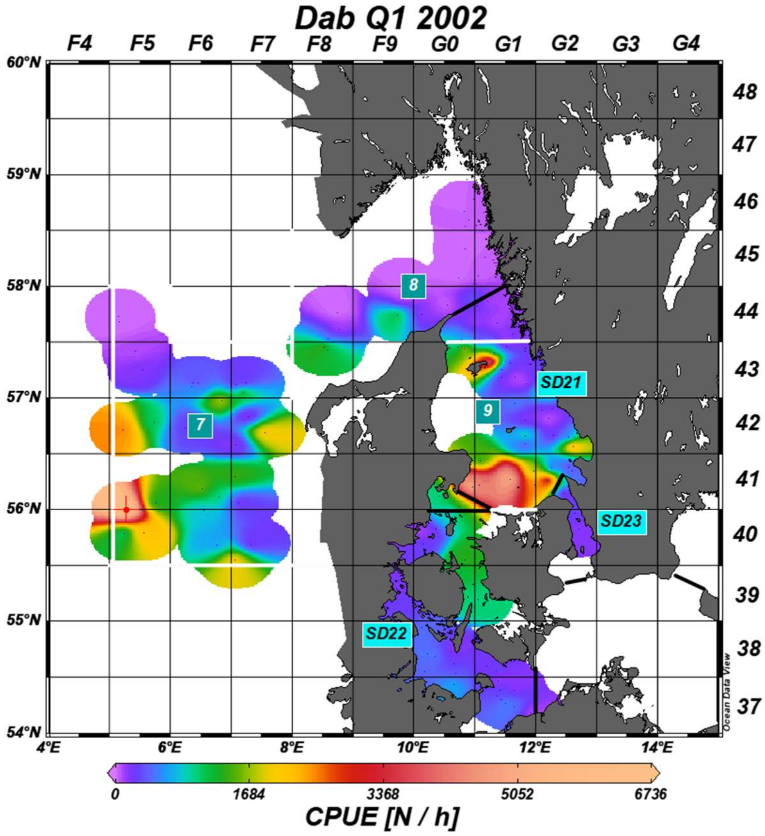
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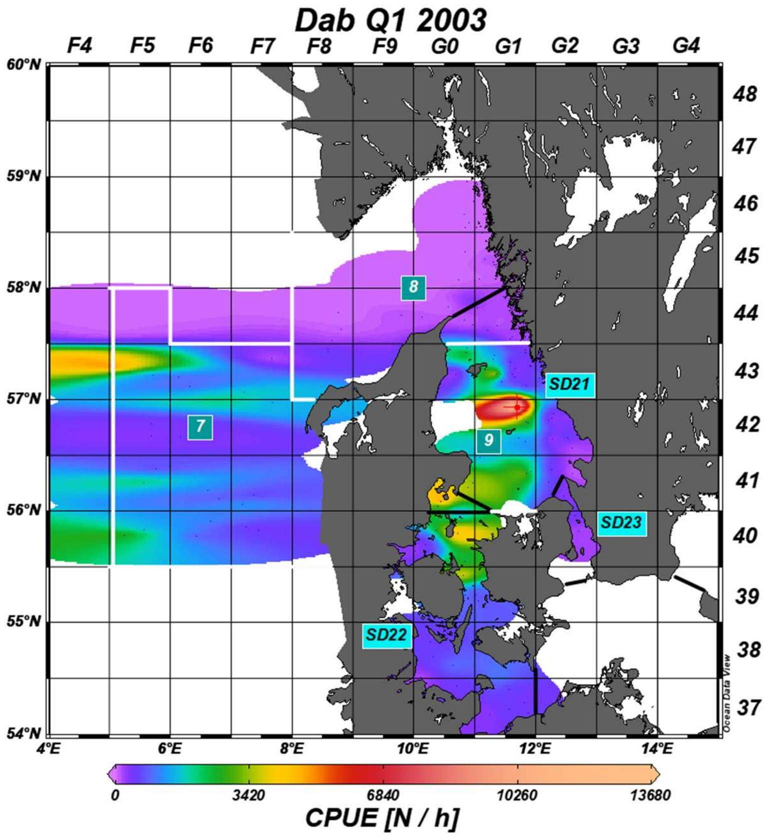
Dab Q1 2003
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
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58°N
57°N
56°N
55°N
54°N
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6°E
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10°E
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SD21
SD22
SD23
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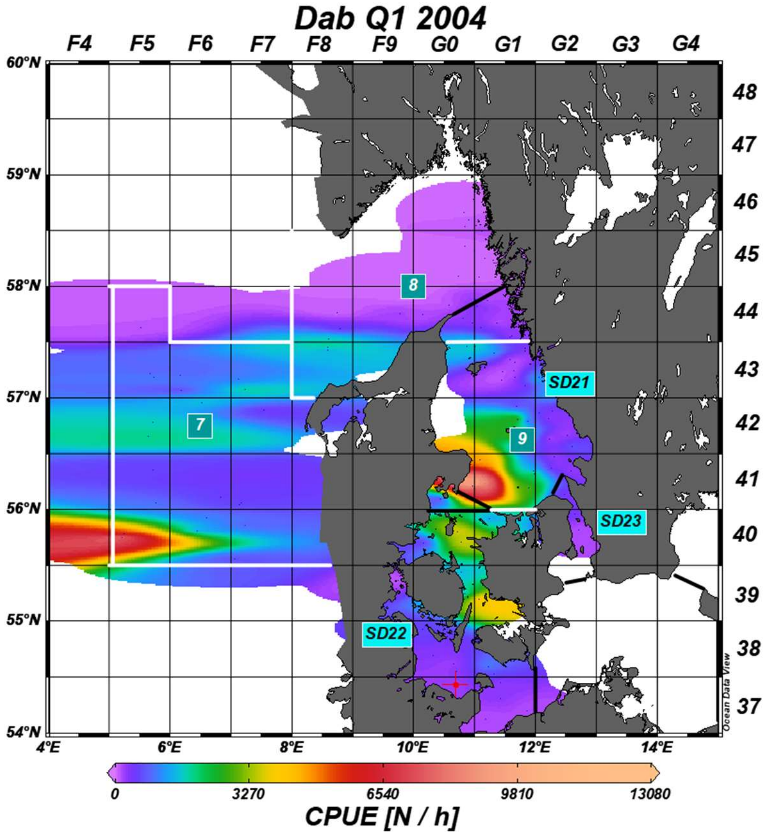
CPUE [N / h]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F9
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SD21
SD22
SD23
Ocean Data View
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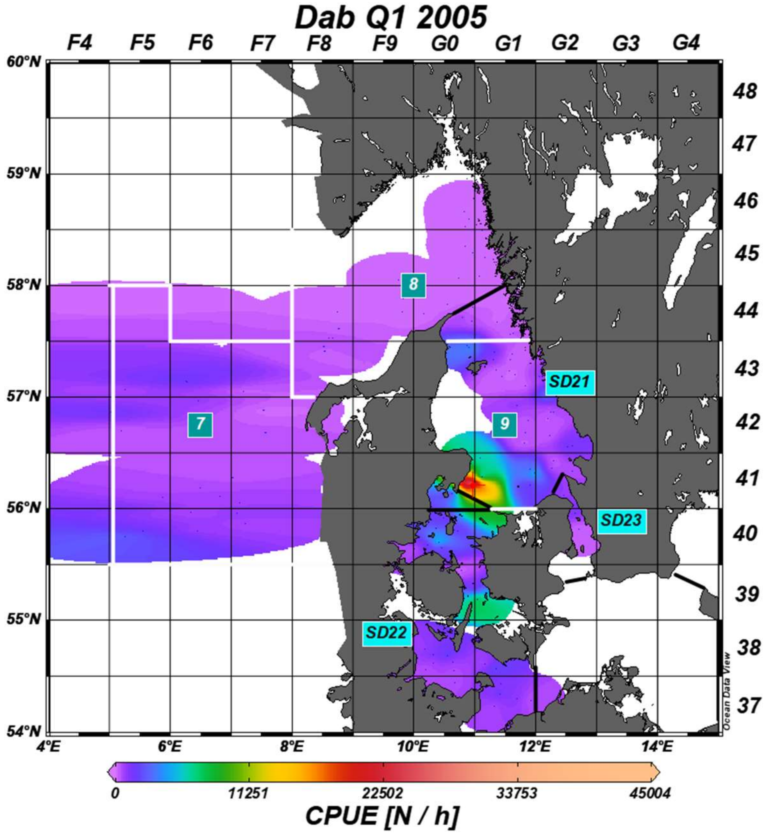
CPUE [N / h]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F7
F8
F9
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G1
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G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
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38
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4°E
6°E
8°E
10°E
12°E
14°E
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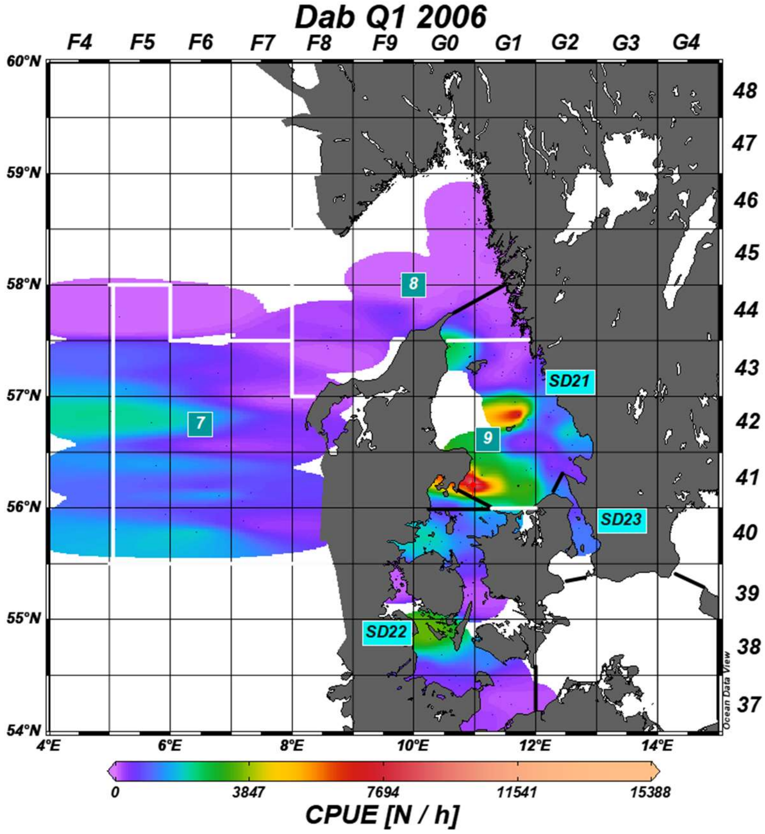
SD21
SD23
SD22
Ocean Data View
0
11251
22502
33753
45004
CPUE [N / h]


Dab Q1 2006
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
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39
38
37
4°E
6°E
8°E
10°E
12°E
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7
9
SD21
SD23
SD22
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7694
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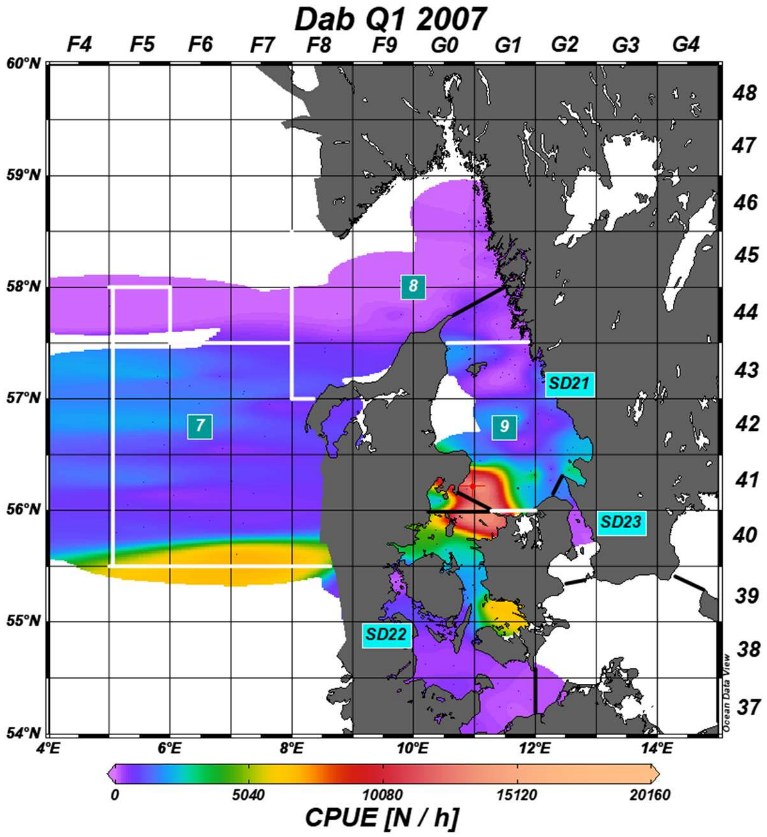
CPUE [N / h]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G4
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14°E
48
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SD21
SD22
SD23
Ocean Data View
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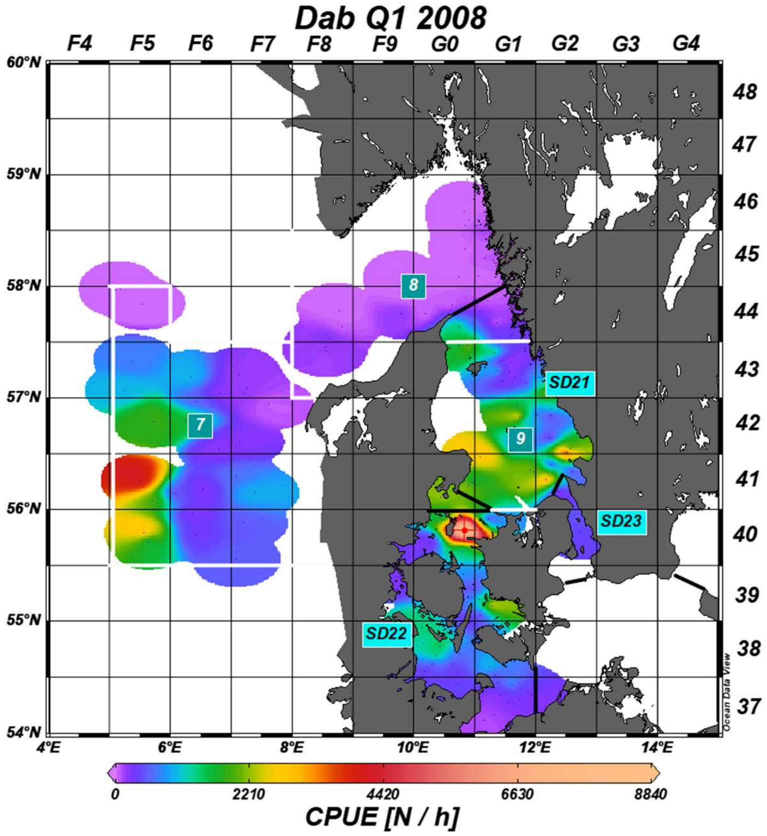
5040
10080
15120
20160
CPUE [N / h]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F5
F6
F7
F8
F9
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G1
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G3
G4
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14°E
48
47
46
45
44
43
42
41
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39
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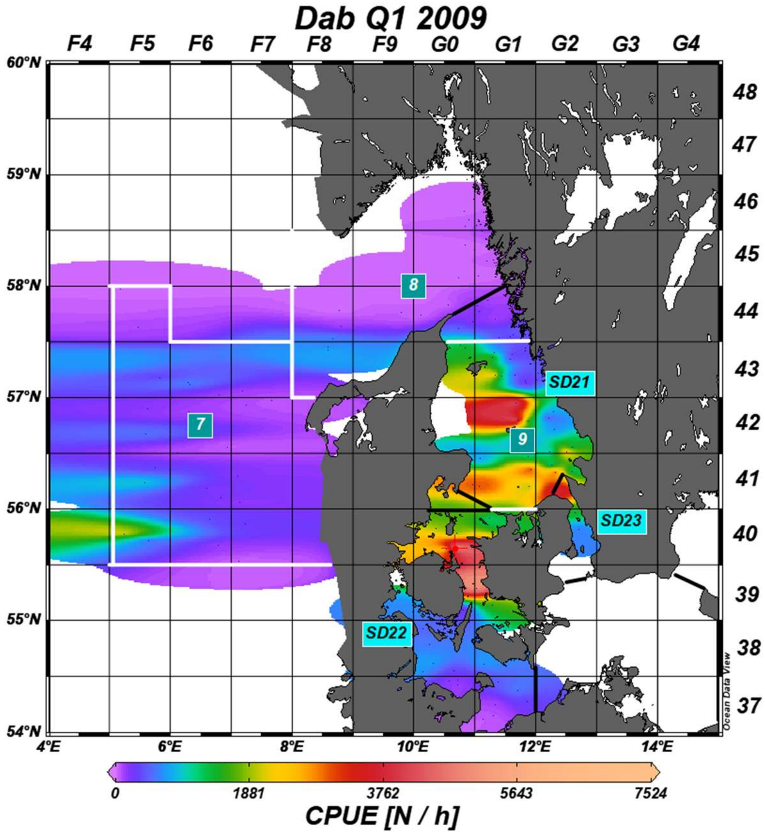
SD21
SD22
SD23
Ocean Data View
0
2210
4420
6630
8840
CPUE [N / h]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F4
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F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
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44
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42
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40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
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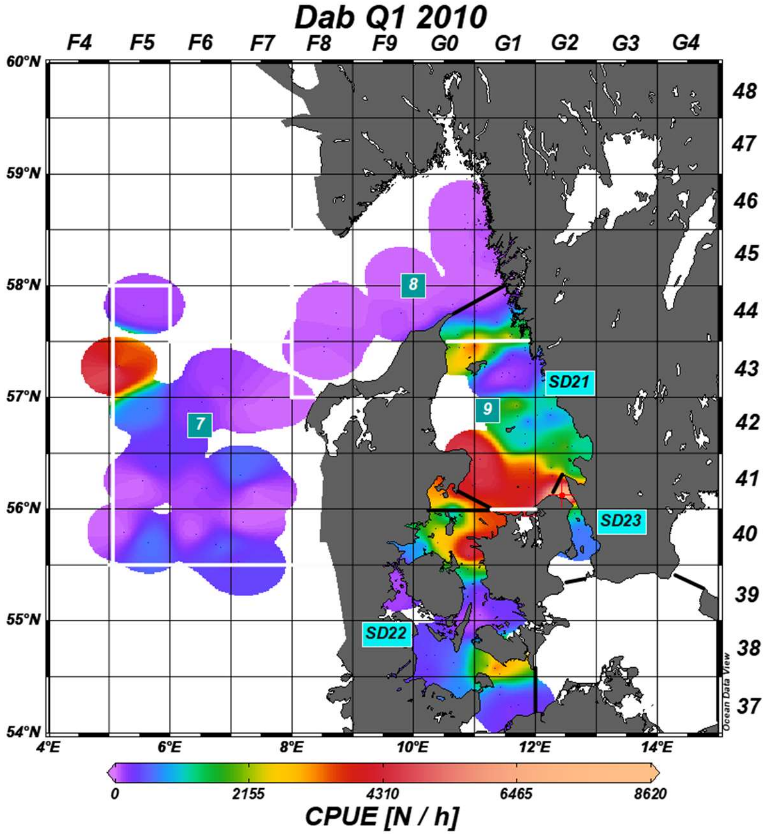
SD21
SD22
SD23
Ocean Data View
0
1881
3762
5643
7524
CPUE [N / h]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F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
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37
4°E
6°E
8°E
10°E
12°E
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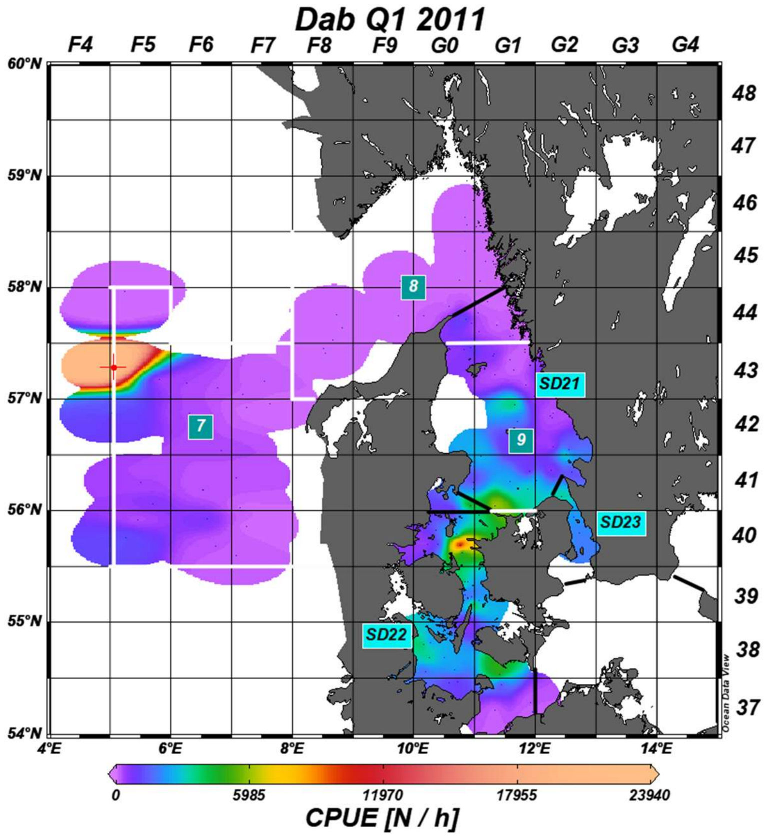
SD21
SD22
SD23
Ocean Data View
0
2155
4310
6465
8620
CPUE [N / h]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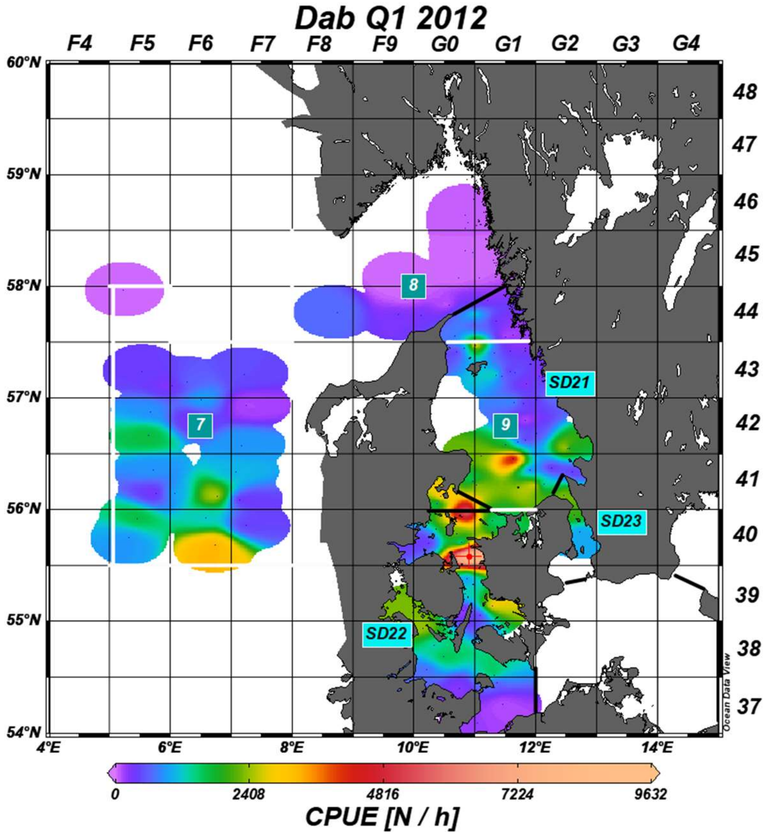
4°E 6°E 8°E 10°E 12°E 14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0 5985 11970 17955 23940
CPUE [N / h]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4°E 6°E 8°E 10°E 12°E 14°E
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7
9
SD21
SD23
SD22
Ocean Data View
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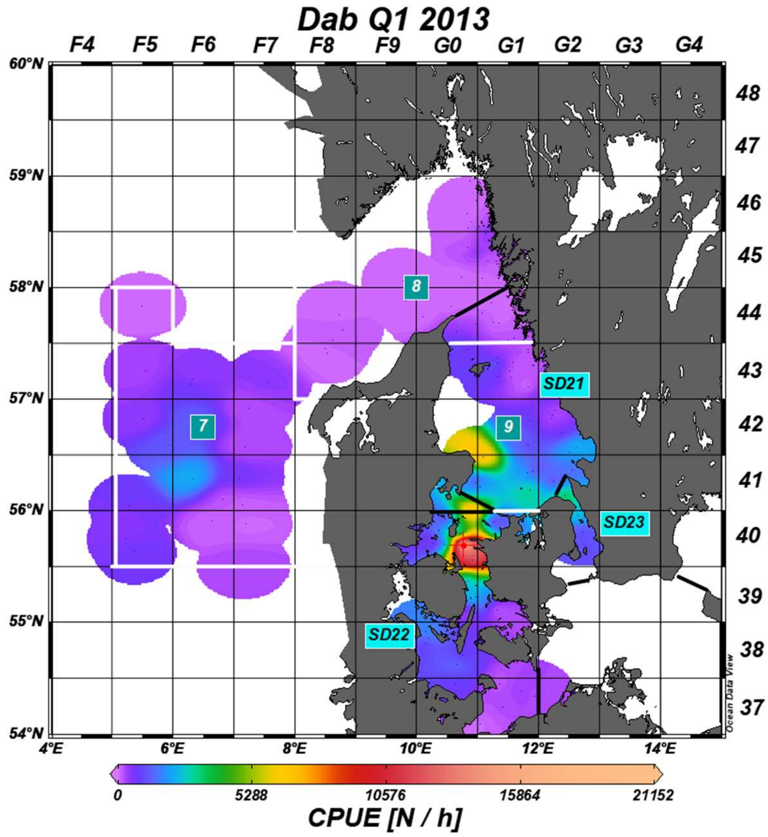
CPUE [N / h]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4°E 6°E 8°E 10°E 12°E 14°E
8
7
9
SD21
SD22
SD23
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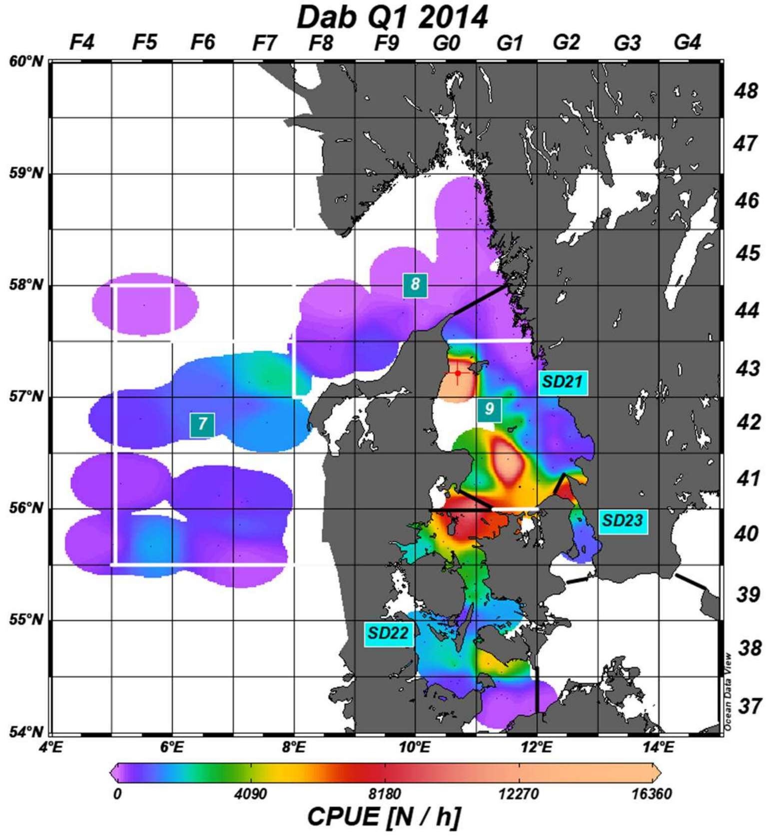
CPUE [N / h]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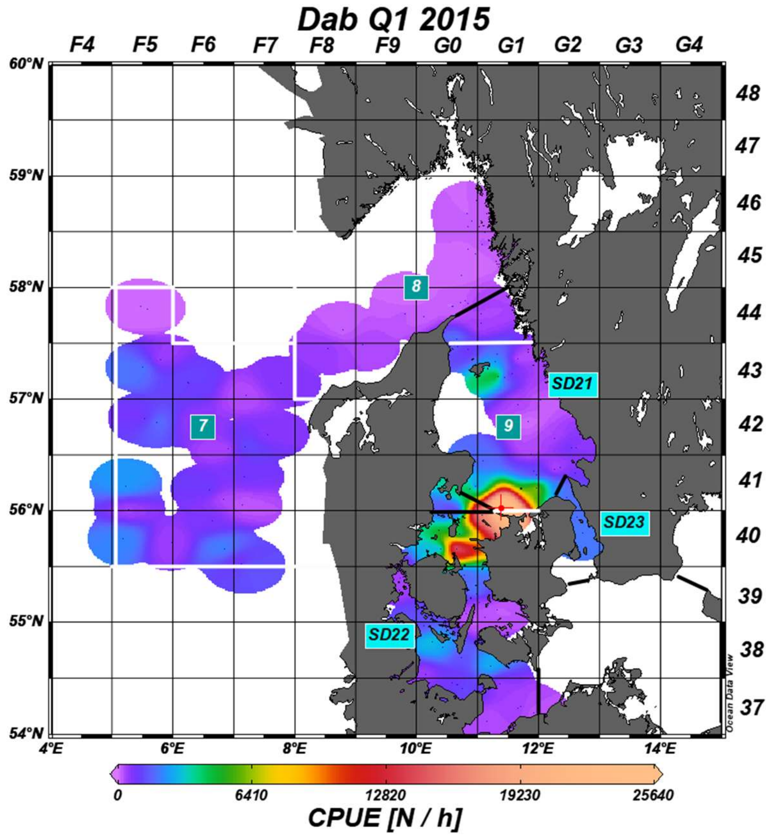
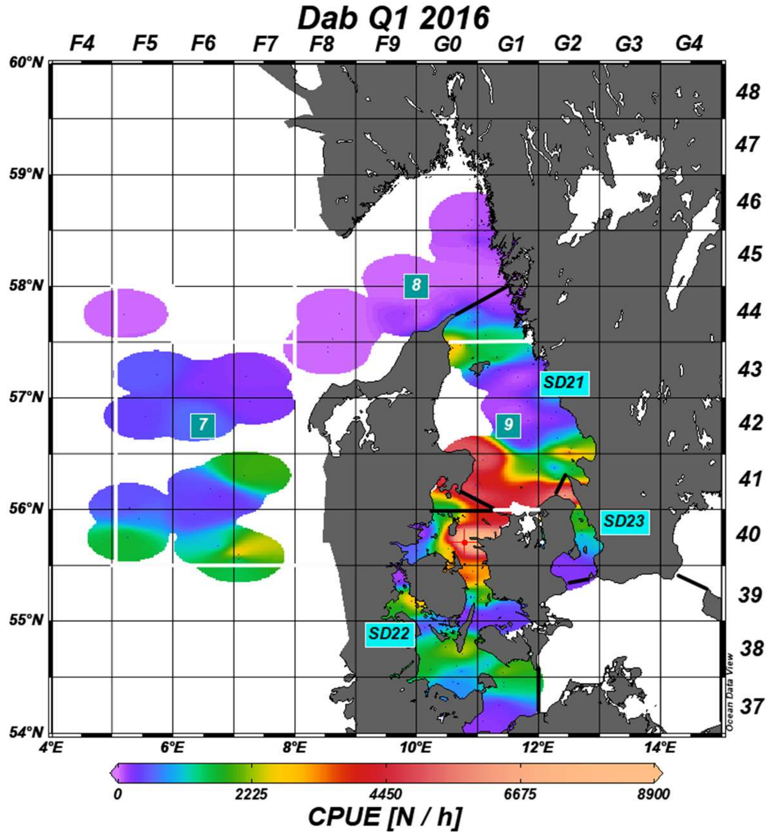
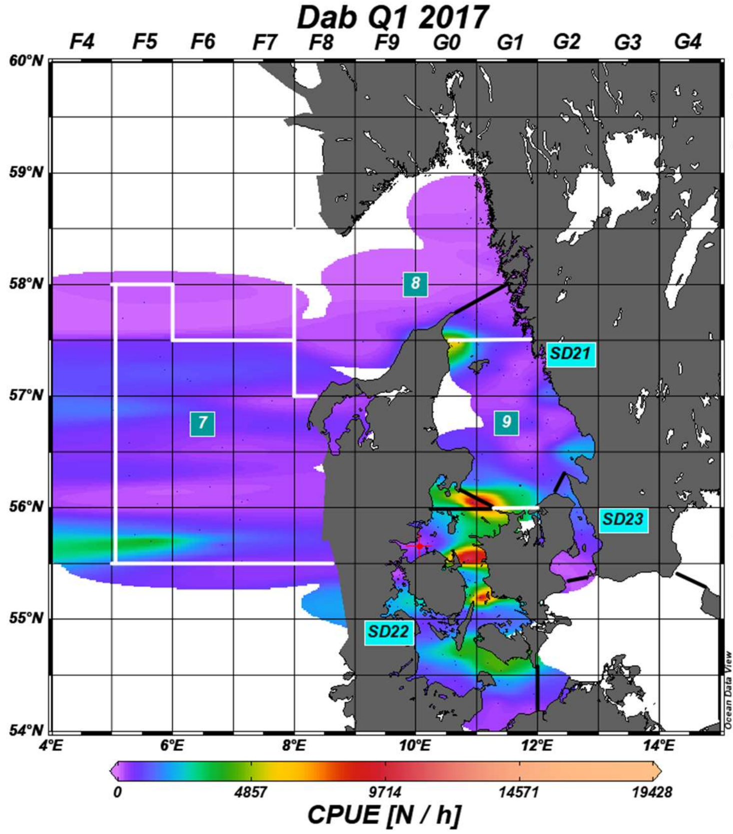
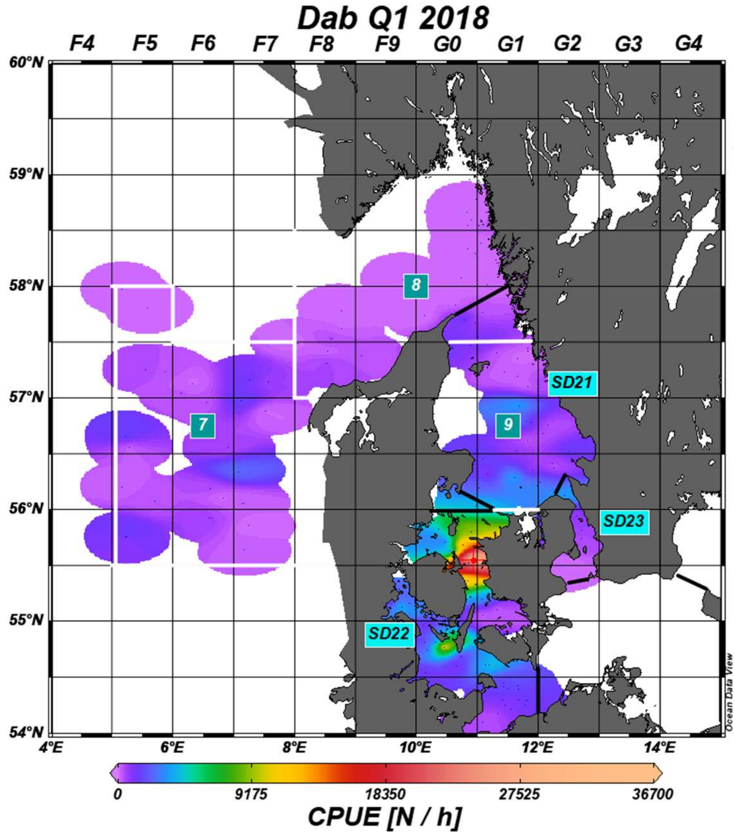
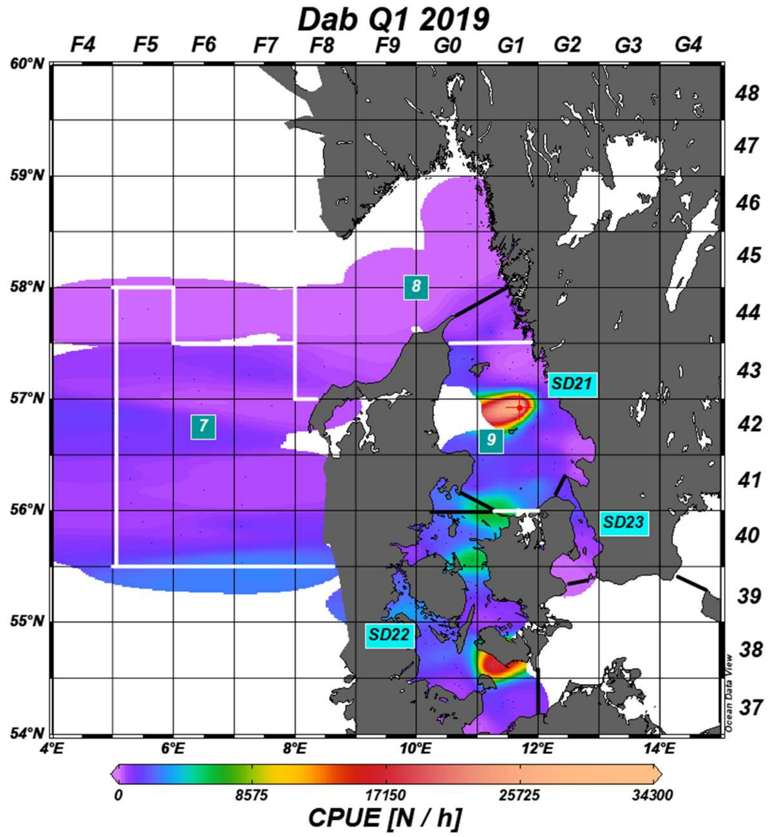
4°E 6°E 8°E 10°E 12°E 14°E
8
7
9
SD21
SD22
SD23
Ocean Data View
0 4090 8180 12270 16360
CPUE [N / h]

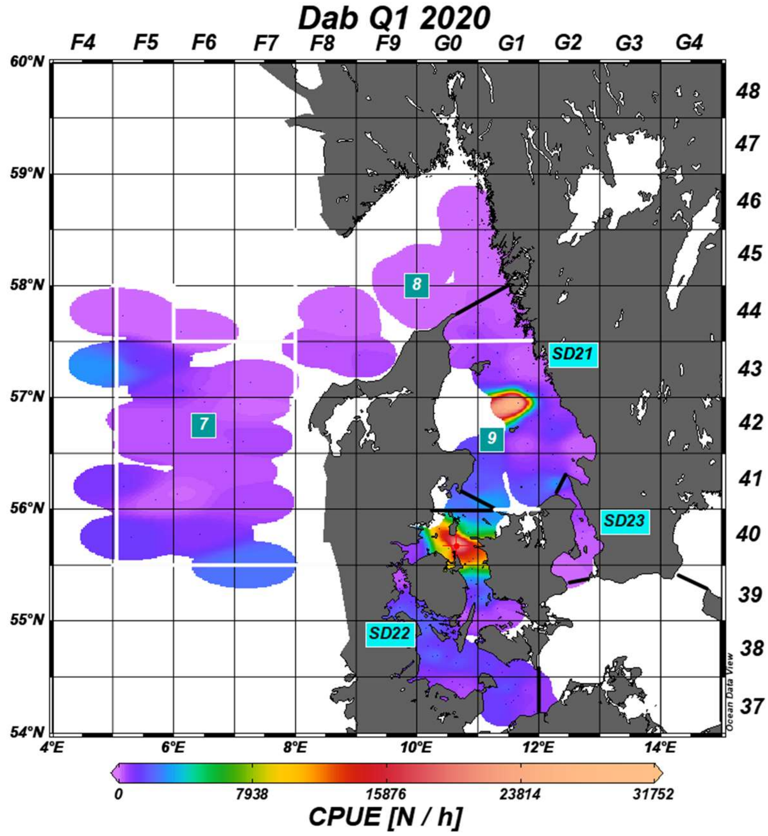

Dab Q1 2015
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD22
SD23
Ocean Data View
0
6410
12820
19230
25640
CPUE [N / h]

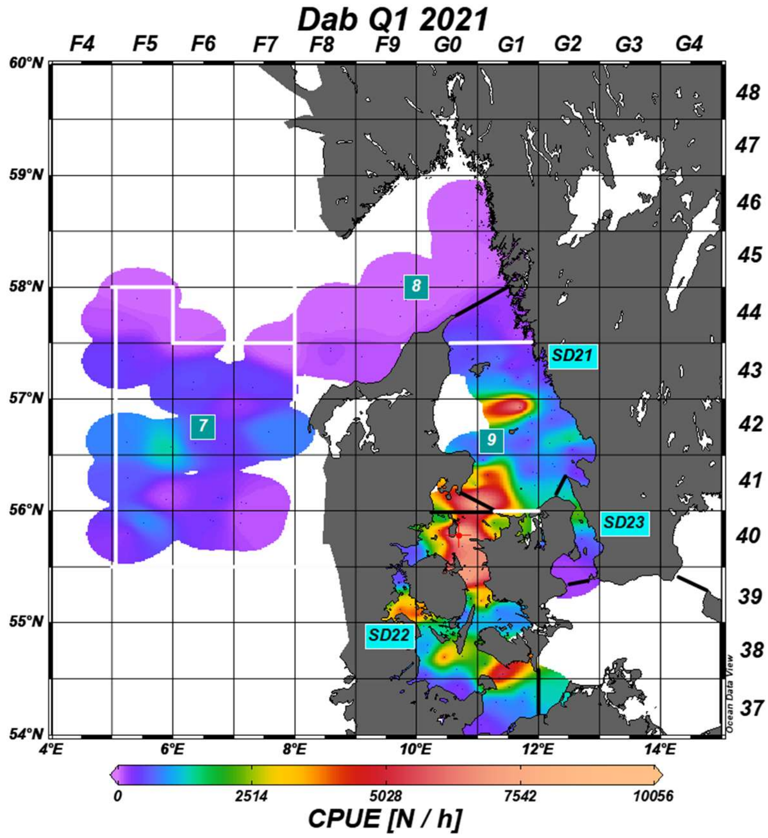

Dab Q1 2016
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD22
SD23
Ocean Data View
0
2225
4450
6675
8900
CPUE [N / h]

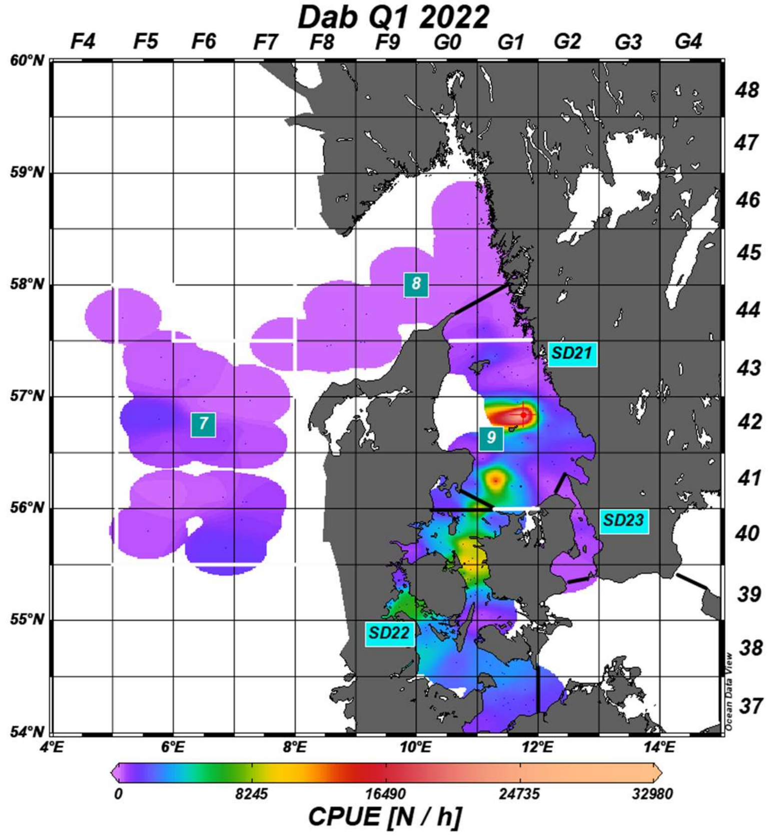

Dab Q1 2017
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
4857
9714
14571
19428
CPUE [N / h]


Dab Q1 2018
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
9175
18350
27525
36700
CPUE [N / h]


Dab Q1 2019
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
Ocean Data View
0
8575
17150
25725
34300
CPUE [N / h]


Dab Q1 2020
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
Ocean Data View
0
7938
15876
23814
31752
CPUE [N / h]

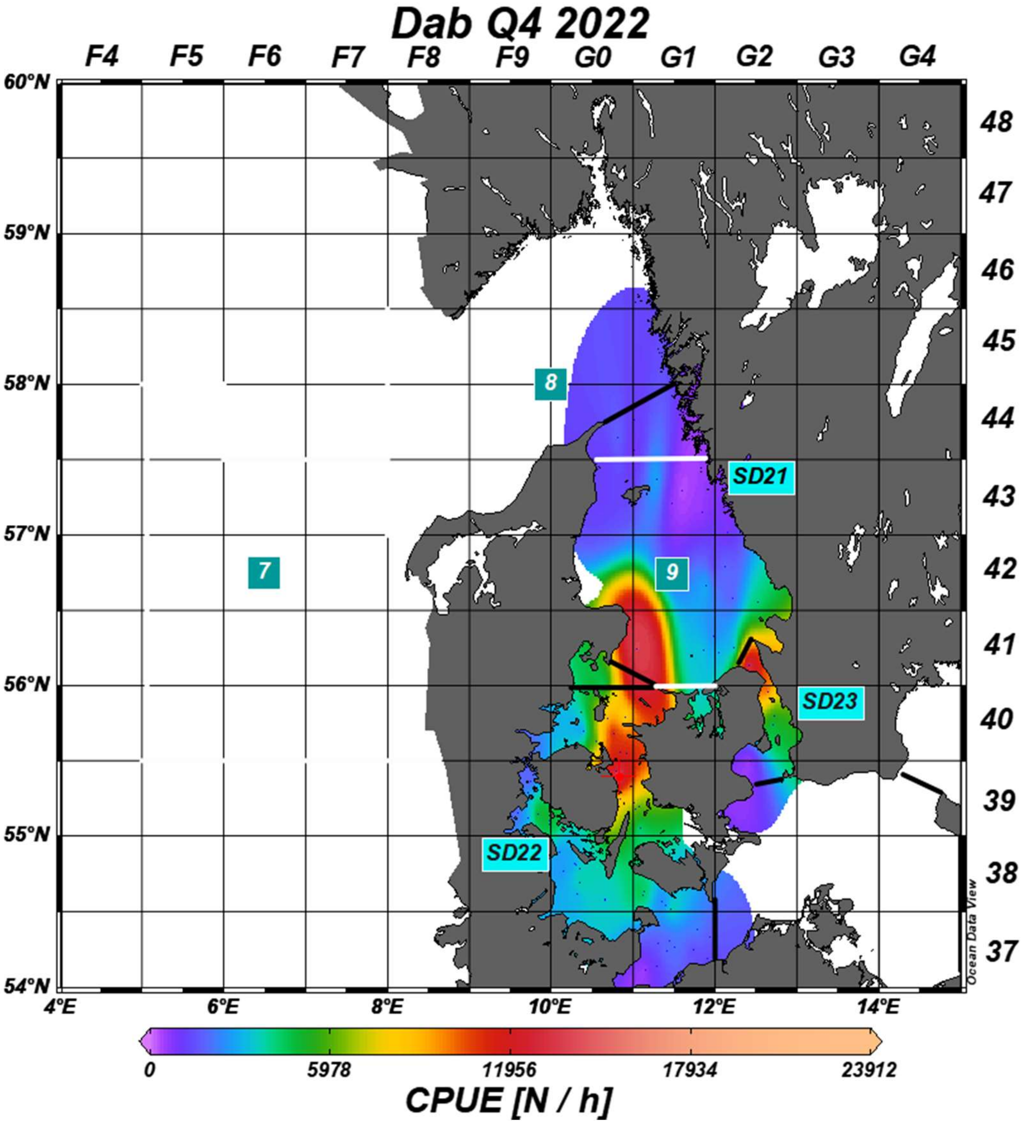

Dab Q1 2021
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD23
SD22
Ocean Data View
0
2514
5028
7542
10056
CPUE [N / h]

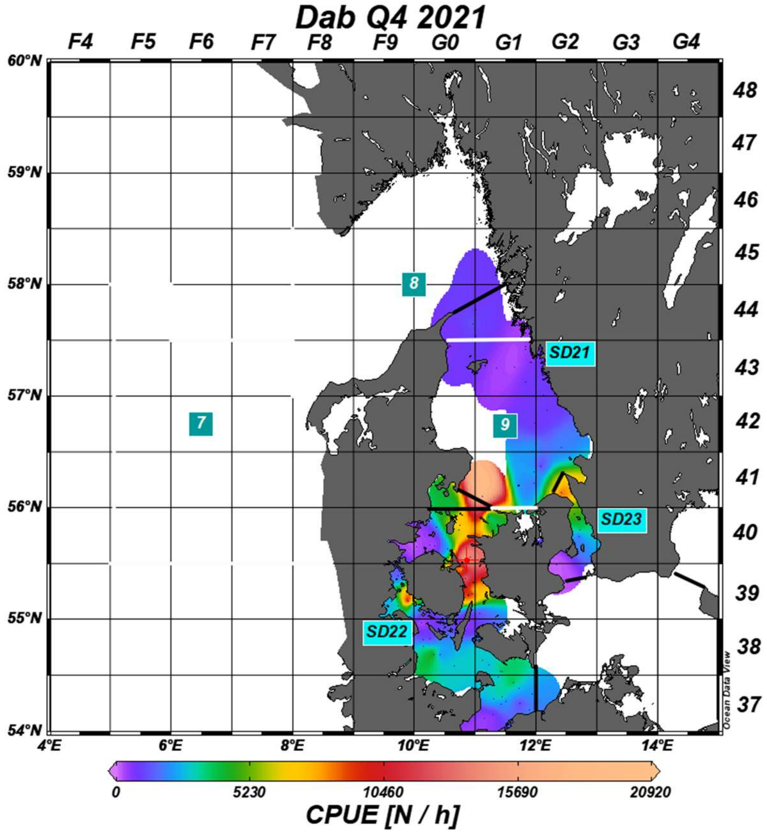

Dab Q1 2022
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD23
SD22
Ocean Data View
0
8245
16490
24735
32980
CPUE [N / h]

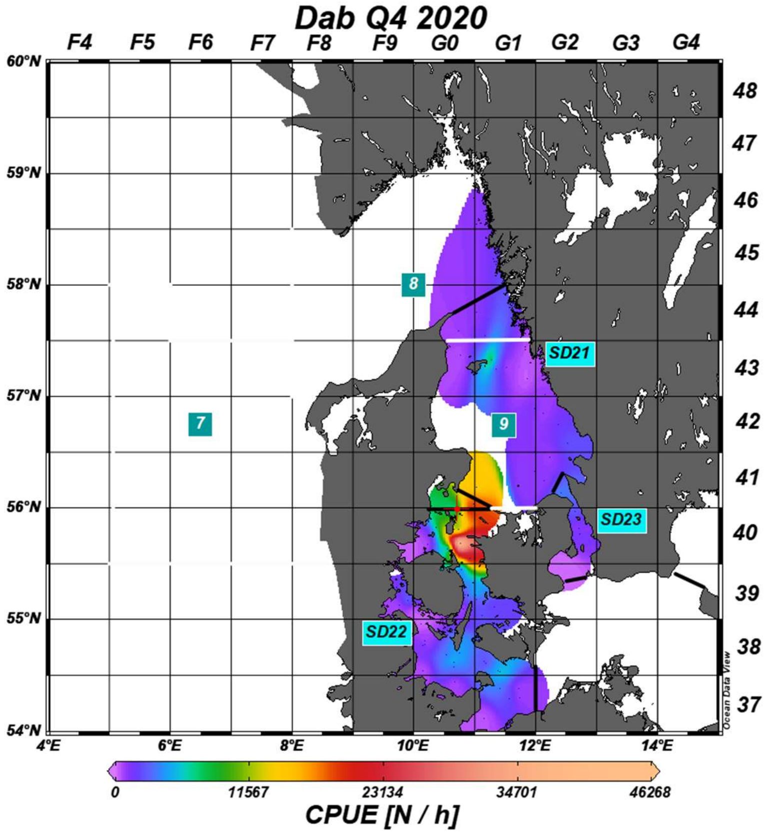
# ANNEX 1.2

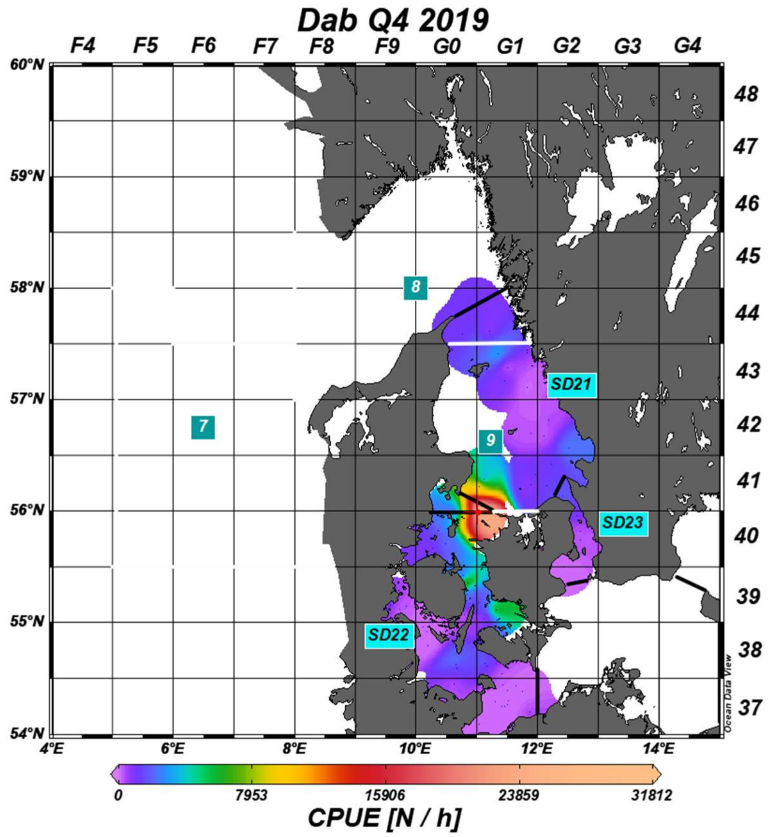
Combined **Quarter 4 Survey Index** CPUE (no/hour) of IBTS, covering Areas 7, 8 and 9 and BITS, covering Areas SD21, 22 and 23. IBTS has not been conducted in Q4 since 1996.

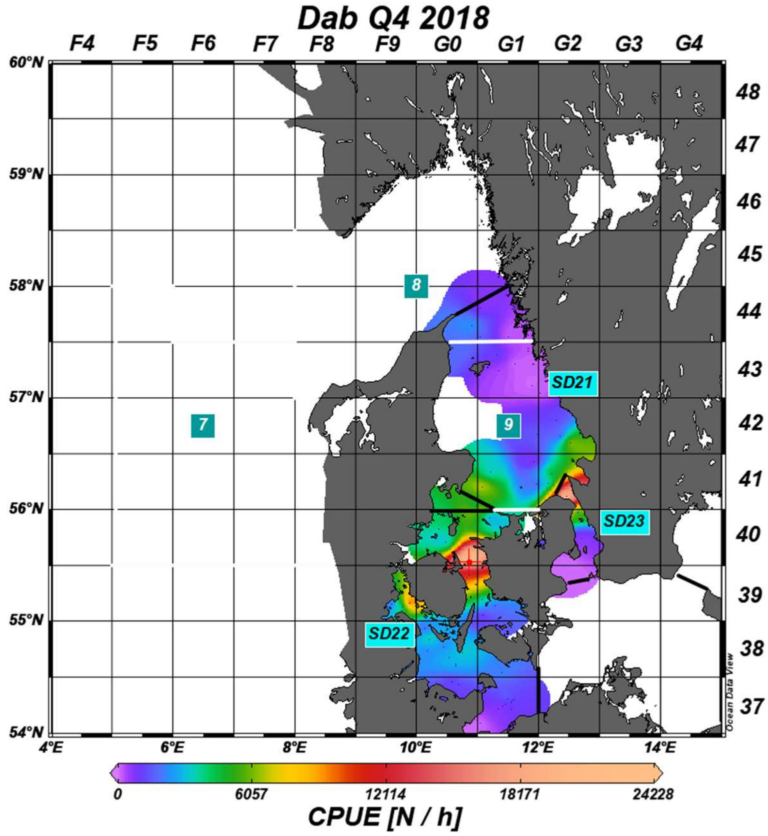
The colour scheme is adjusted to the maximum value of each year to make maps easier to read.

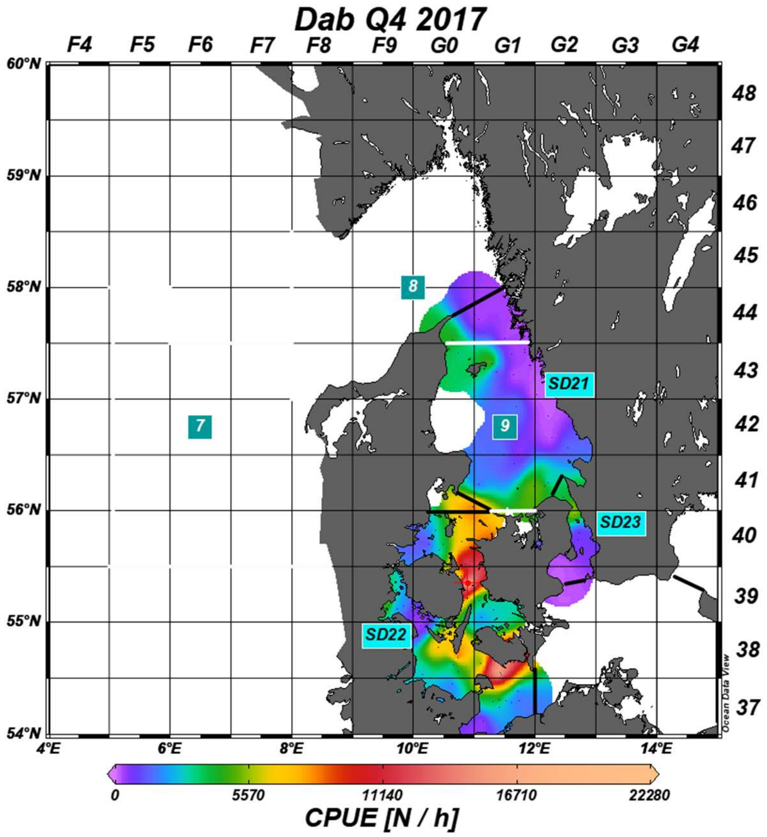


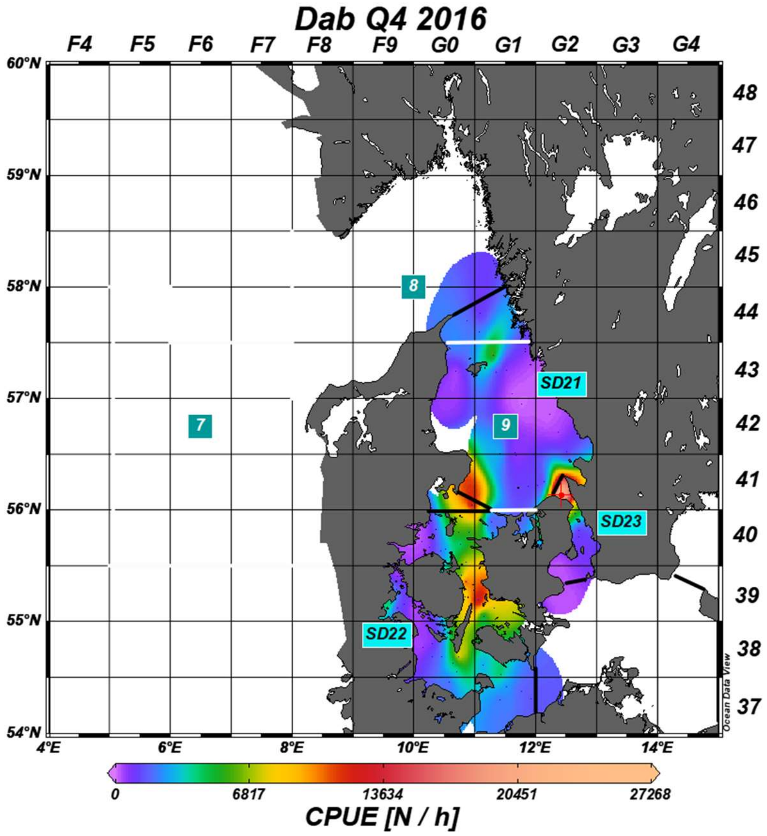

Dab Q4 2021
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48 47 46 45 44 43 42 41 40 39 38 37
8
7
9
SD21
SD23
SD22
4°E 6°E 8°E 10°E 12°E 14°E
Ocean Data View
0 5230 10460 15690 20920
CPUE [N / h]

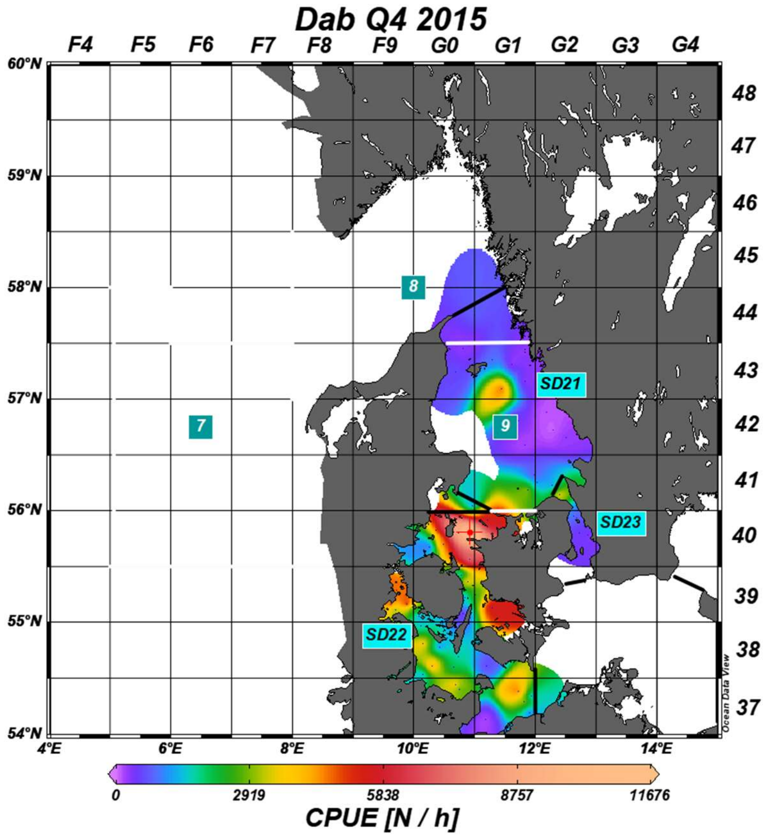

Dab Q4 2020
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48 47 46 45 44 43 42 41 40 39 38 37
8
7
9
SD21
SD23
SD22
4°E 6°E 8°E 10°E 12°E 14°E
Ocean Data View
0 11567 23134 34701 46268
CPUE [N / h]

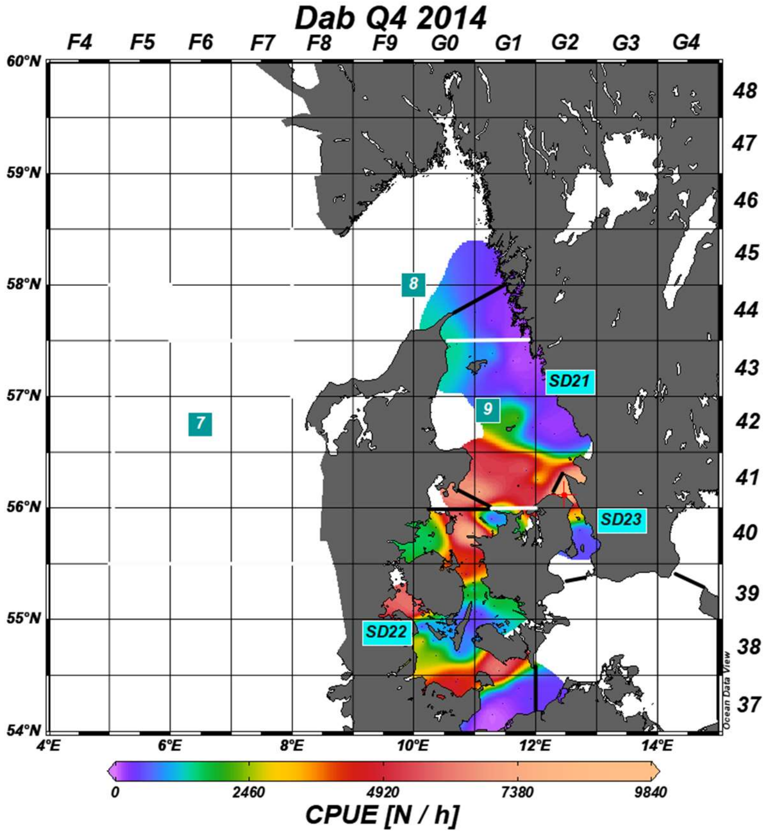

Dab Q4 2019
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
Ocean Data View
0
7953
15906
23859
31812
CPUE [N / h]

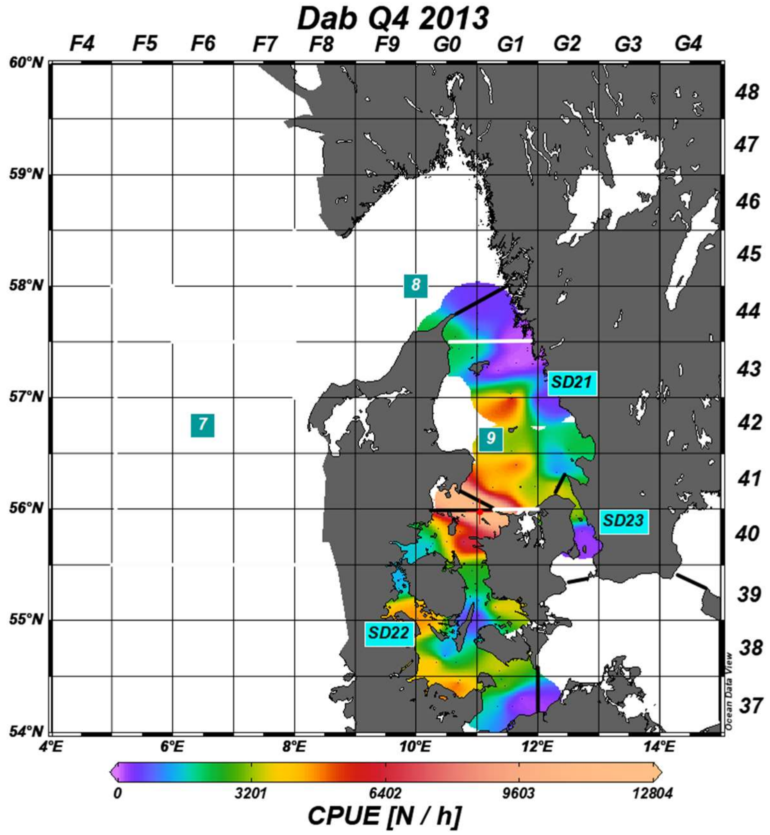

Dab Q4 2018
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
Ocean Data View
0
6057
12114
18171
24228
CPUE [N / h]

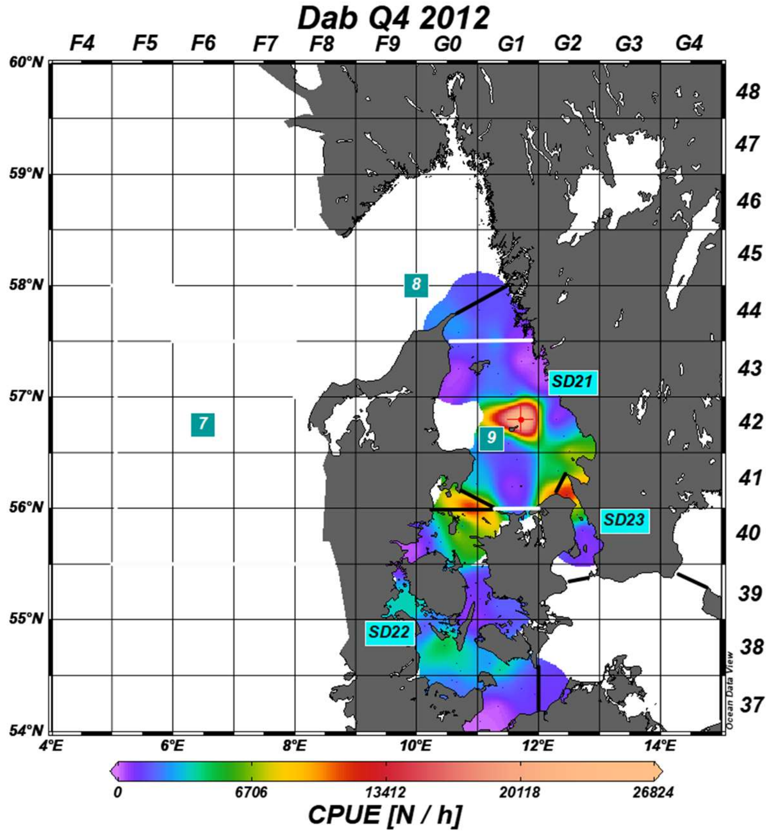

Dab Q4 2017
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
5570
11140
16710
22280
CPUE [N / h]


Dab Q4 2016
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
6817
13634
20451
27268
CPUE [N / h]


Dab Q4 2015
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD23
SD22
Ocean Data View
4°E
6°E
8°E
10°E
12°E
14°E
0
2919
5838
8757
11676
CPUE [N / h]


Dab Q4 2014
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD23
SD22
Ocean Data View
4°E
6°E
8°E
10°E
12°E
14°E
0
2460
4920
7380
9840
CPUE [N / h]


Dab Q4 2013
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD23
SD22
Ocean Data View
0
3201
6402
9603
12804
CPUE [N / h]


Dab Q4 2012
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
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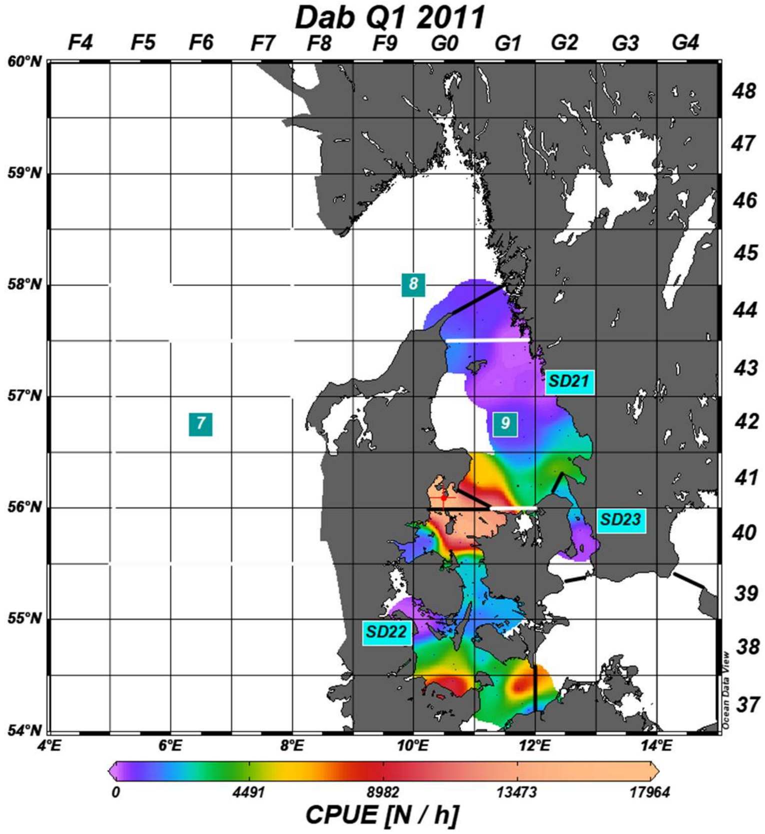
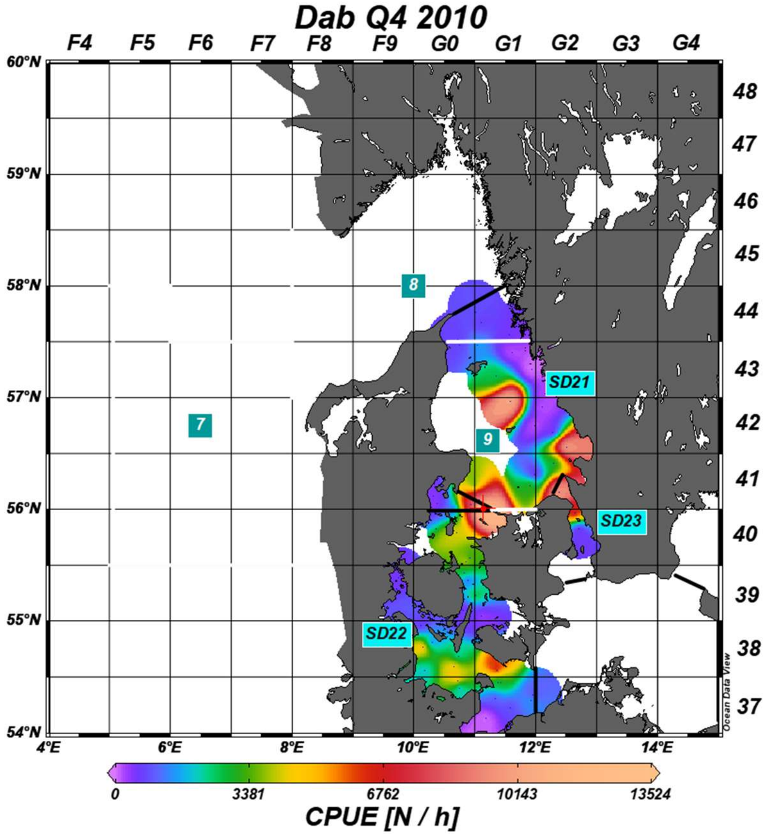
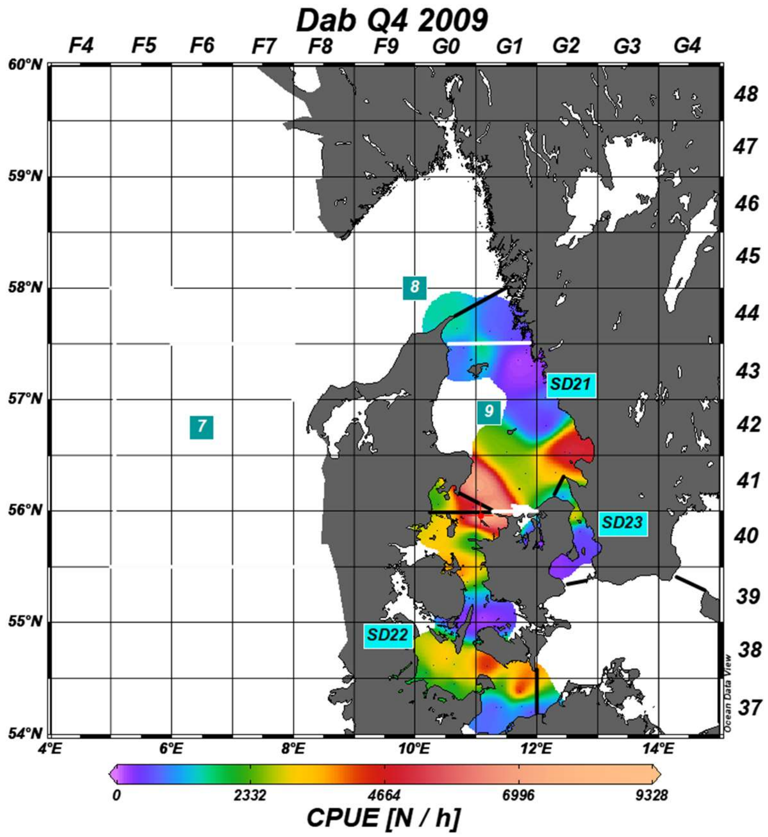
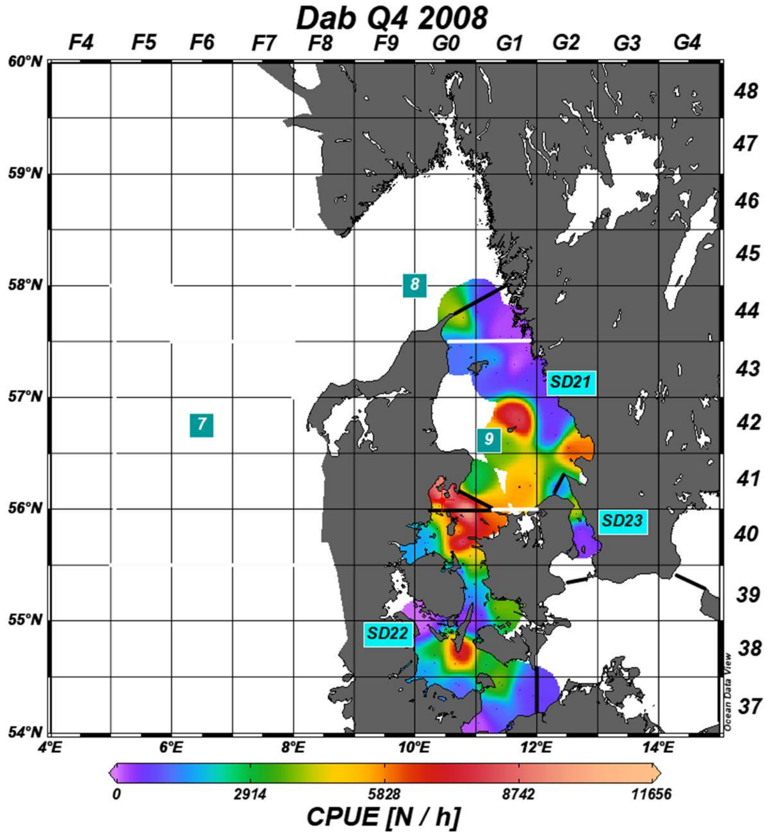
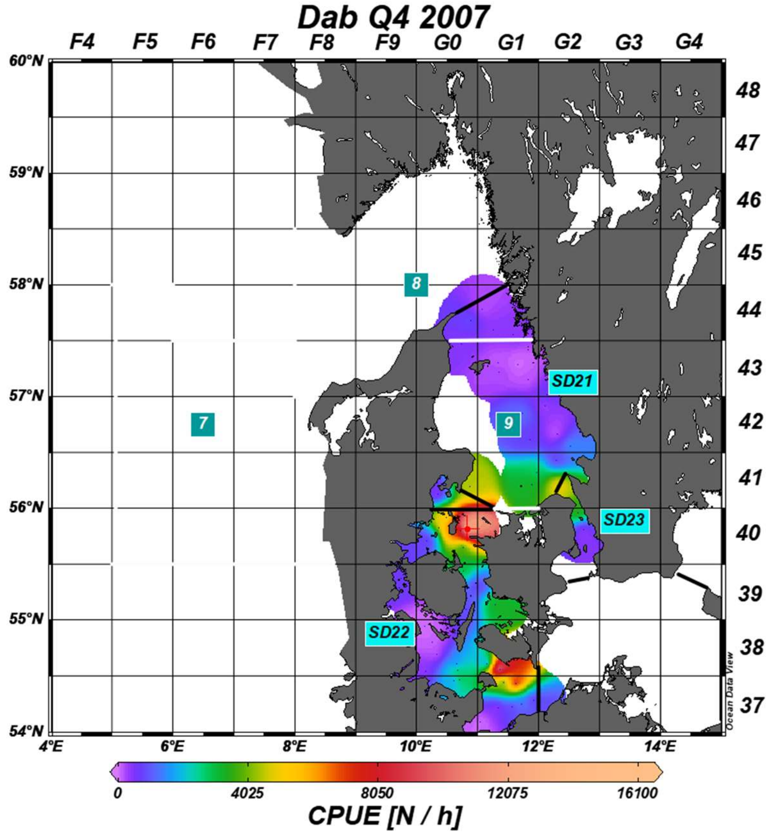
9
SD21
SD23
SD22
Ocean Data View
0
6706
13412
20118
26824
CPUE [N / h]

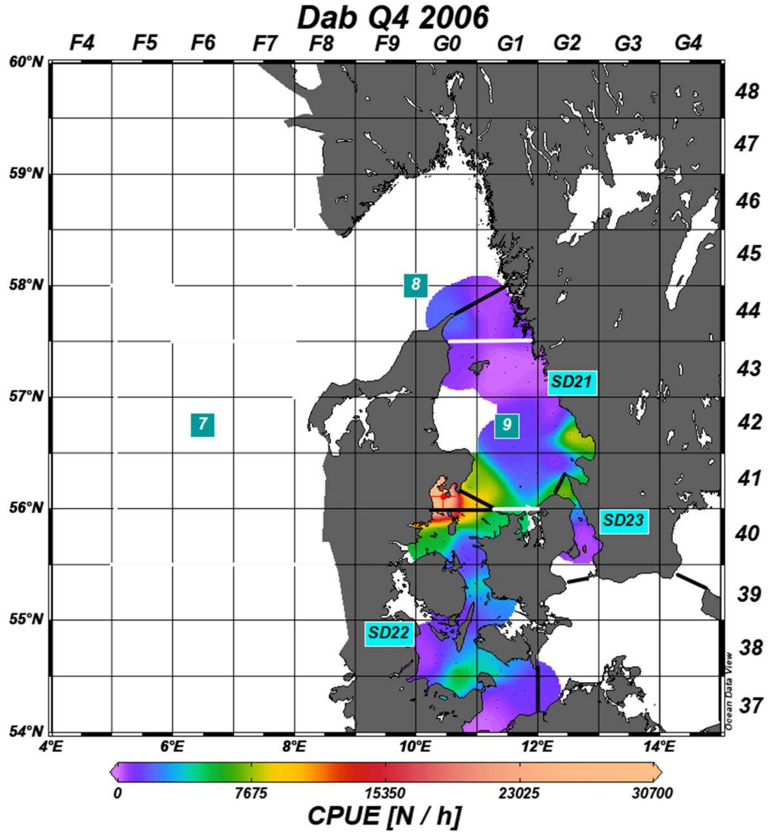

Dab Q1 2011
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
7
8
9
SD21
SD22
SD23
Ocean Data View
0
4491
8982
13473
17964
CPUE [N / h]

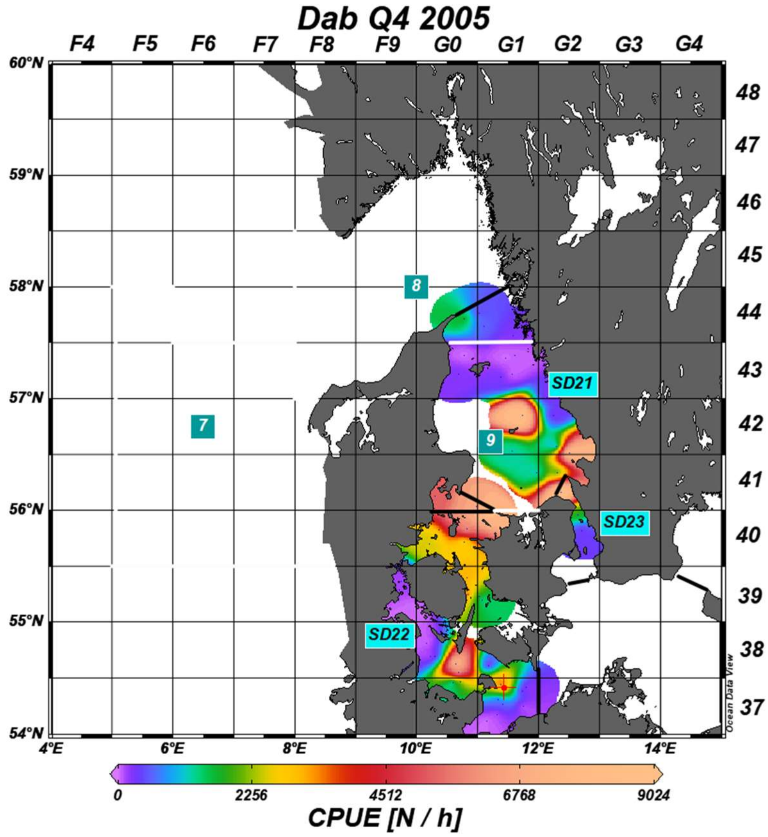

Dab Q4 2010
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
7
8
9
SD21
SD22
SD23
Ocean Data View
0
3381
6762
10143
13524
CPUE [N / h]


Dab Q4 2009
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N 59°N 58°N 57°N 56°N 55°N 54°N
48 47 46 45 44 43 42 41 40 39 38 37
4°E 6°E 8°E 10°E 12°E 14°E
7
8
9
SD21
SD22
SD23
Ocean Data View
0 2332 4664 6996 9328
CPUE [N / h]


Dab Q4 2008
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N 59°N 58°N 57°N 56°N 55°N 54°N
48 47 46 45 44 43 42 41 40 39 38 37
4°E 6°E 8°E 10°E 12°E 14°E
7
8
9
SD21
SD22
SD23
Ocean Data View
0 2914 5828 8742 11656
CPUE [N / h]


Dab Q4 2007
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N 59°N 58°N 57°N 56°N 55°N 54°N
48 47 46 45 44 43 42 41 40 39 38 37
4°E 6°E 8°E 10°E 12°E 14°E
7
8
9
SD21
SD22
SD23
Ocean Data View
0 4025 8050 12075 16100
CPUE [N / h]


Dab Q4 2006
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N 59°N 58°N 57°N 56°N 55°N 54°N
48 47 46 45 44 43 42 41 40 39 38 37
4°E 6°E 8°E 10°E 12°E 14°E
7
8
9
SD21
SD22
SD23
Ocean Data View
0 7675 15350 23025 30700
CPUE [N / h]


Dab Q4 2005
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
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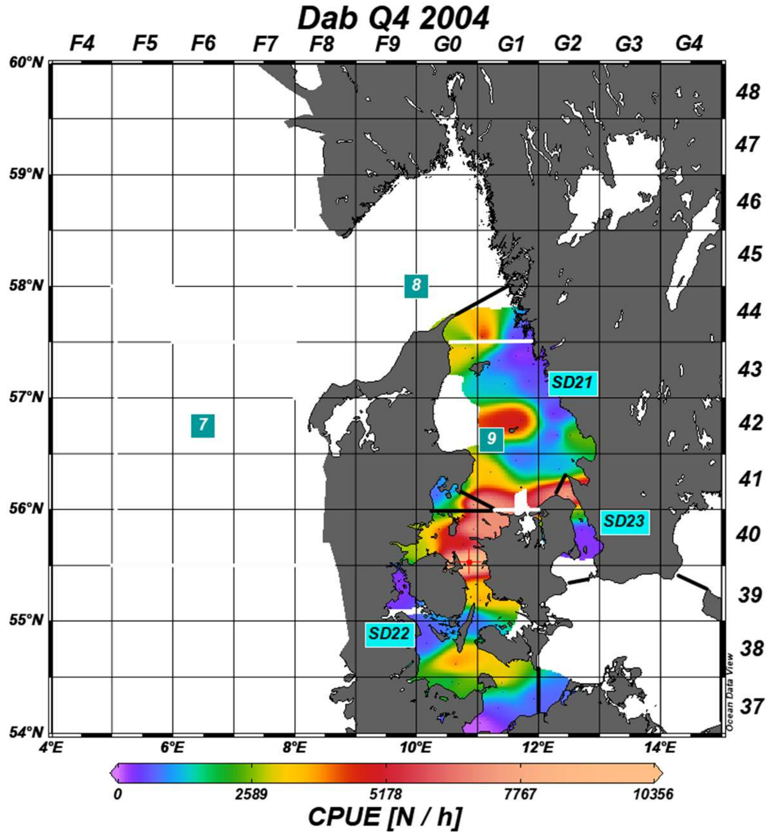
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
7
8
9
SD21
SD22
SD23
Ocean Data View
0
2256
4512
6768
9024
CPUE [N / h]


Dab Q4 2004
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
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46
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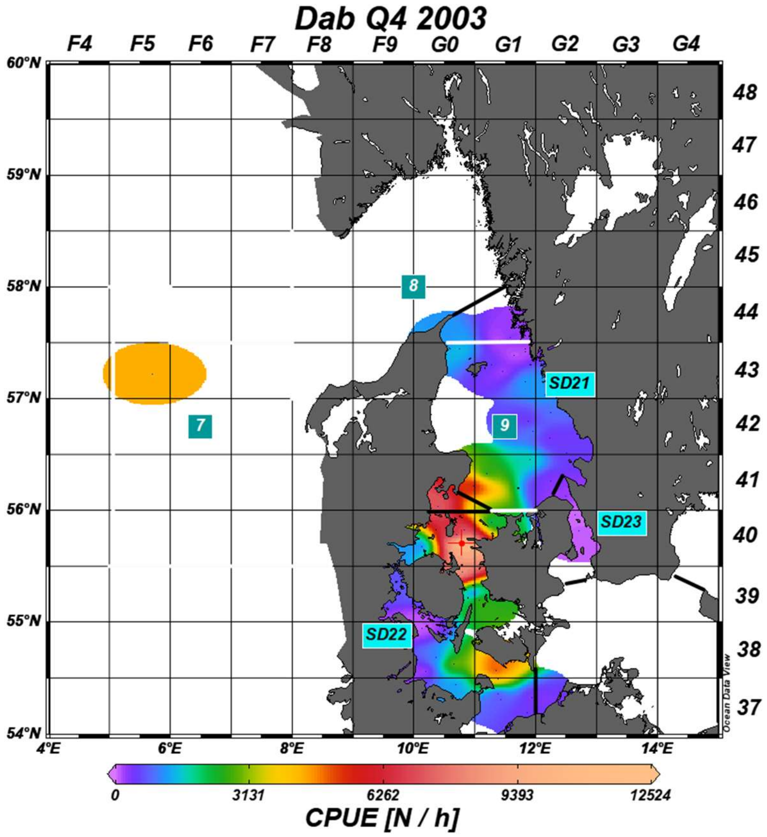
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
7
8
9
SD21
SD22
SD23
Ocean Data View
0
2589
5178
7767
10356
CPUE [N / h]


Dab Q4 2003
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
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55°N
54°N
48
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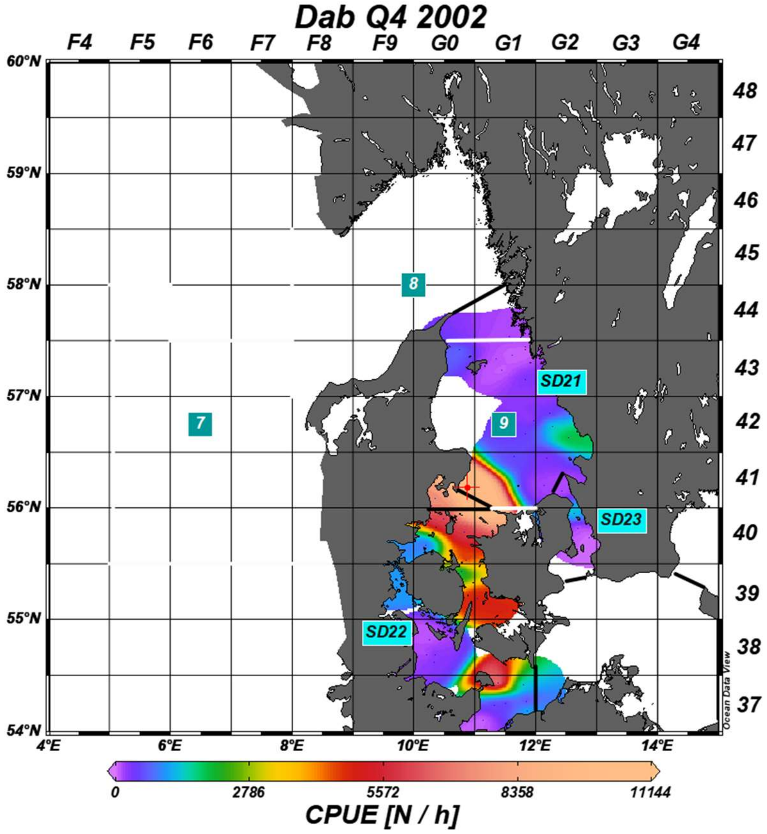
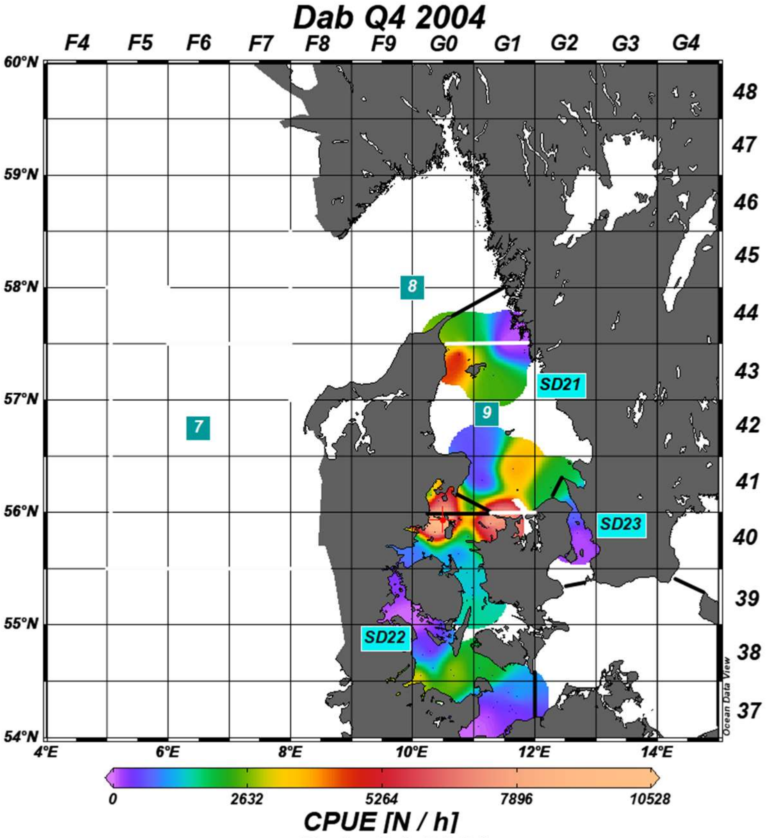
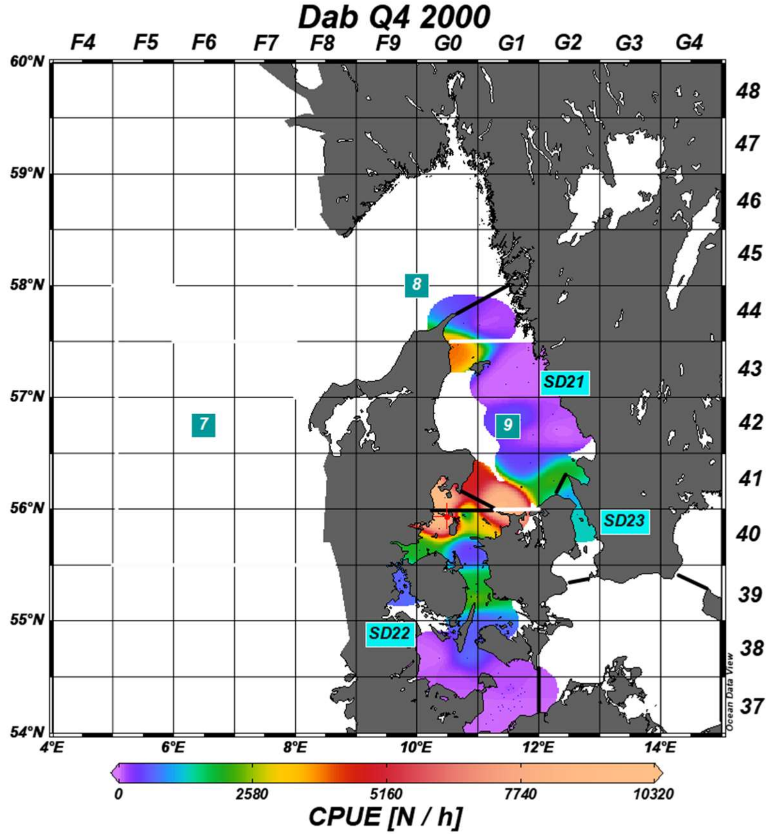
39
38
37
8
7
9
SD21
SD22
SD23
4°E
6°E
8°E
10°E
12°E
14°E
0
3131
6262
9393
12524
CPUE [N / h]
Ocean Data View


Dab Q4 2002
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
4°E
6°E
8°E
10°E
12°E
14°E
0
2786
5572
8358
11144
CPUE [N / h]
Ocean Data View


Dab Q4 2004
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
7
8
9
SD21
SD22
SD23
Ocean Data View
0
2632
5264
7896
10528
CPUE [N / h]


Dab Q4 2000
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
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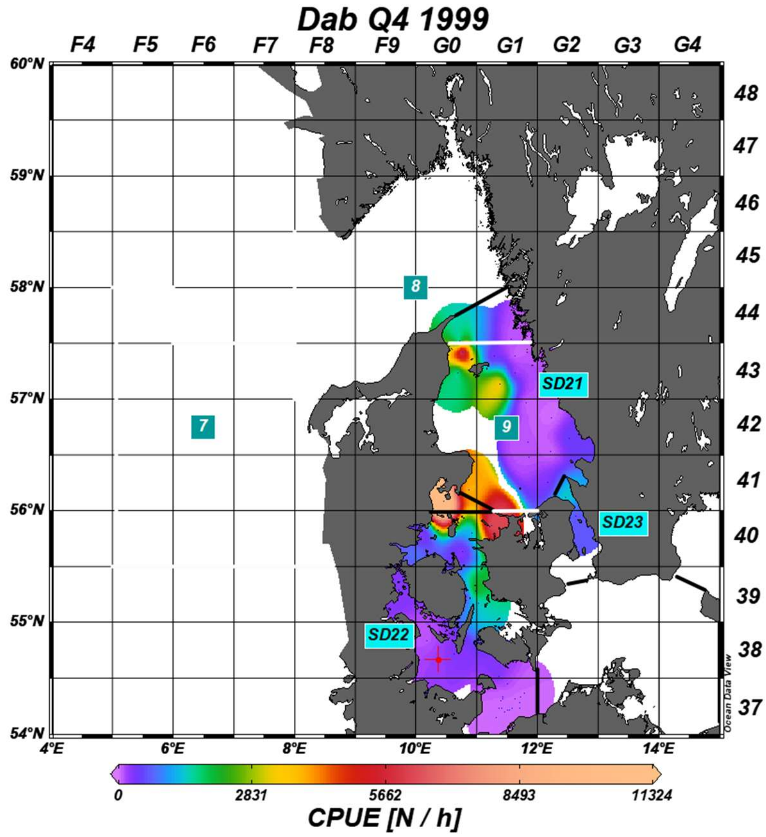
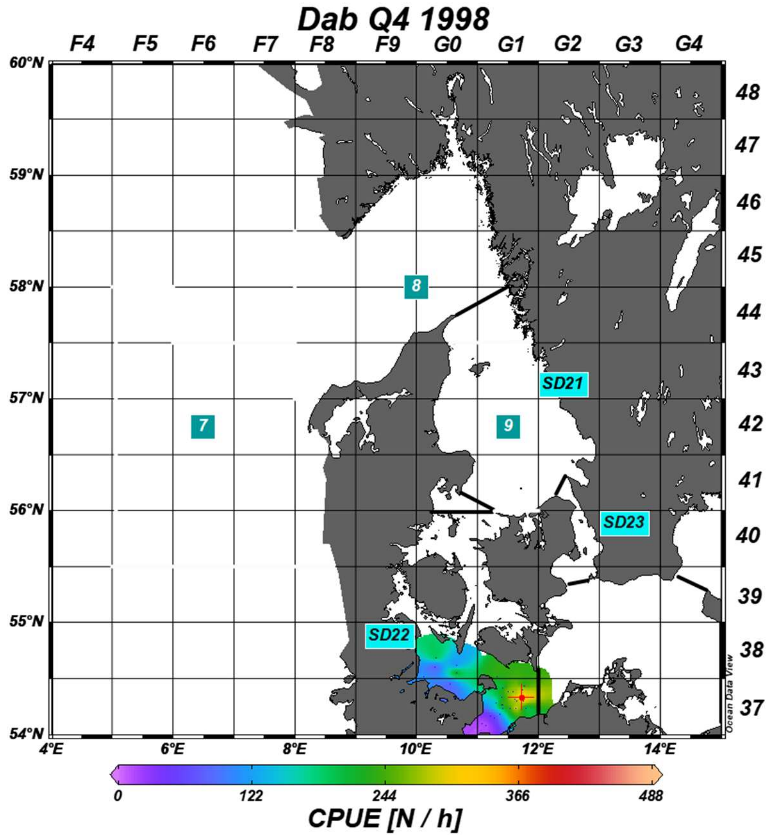
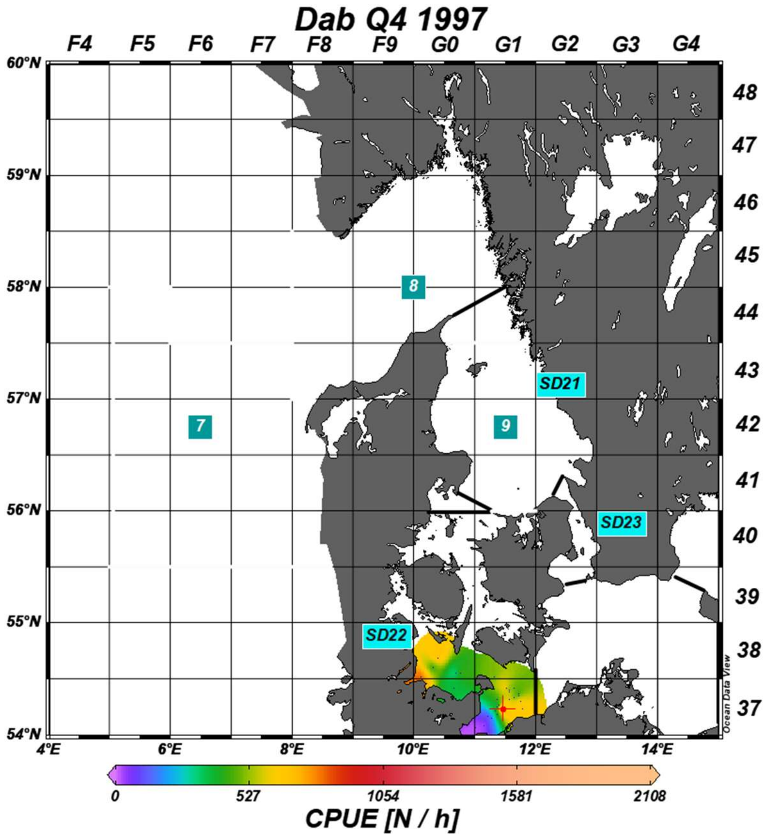
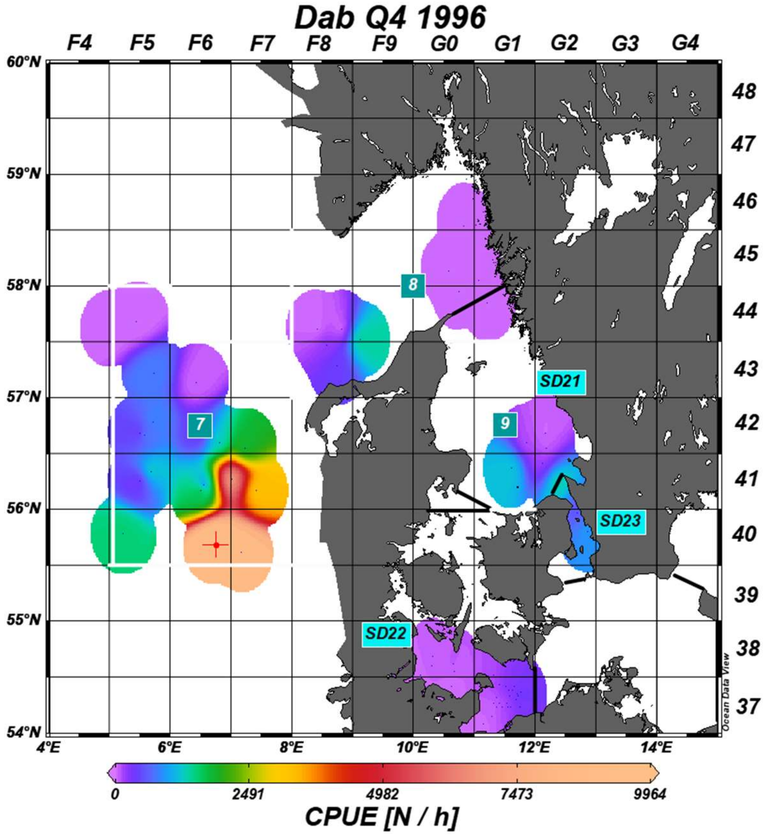
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
7
8
9
SD21
SD22
SD23
Ocean Data View
0
2580
5160
7740
10320
CPUE [N / h]


Dab Q4 1999
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N 59°N 58°N 57°N 56°N 55°N 54°N
48 47 46 45 44 43 42 41 40 39 38 37
4°E 6°E 8°E 10°E 12°E 14°E
8
7
9
SD21
SD22
SD23
Ocean Data View
0 2831 5662 8493 11324
CPUE [N / h]

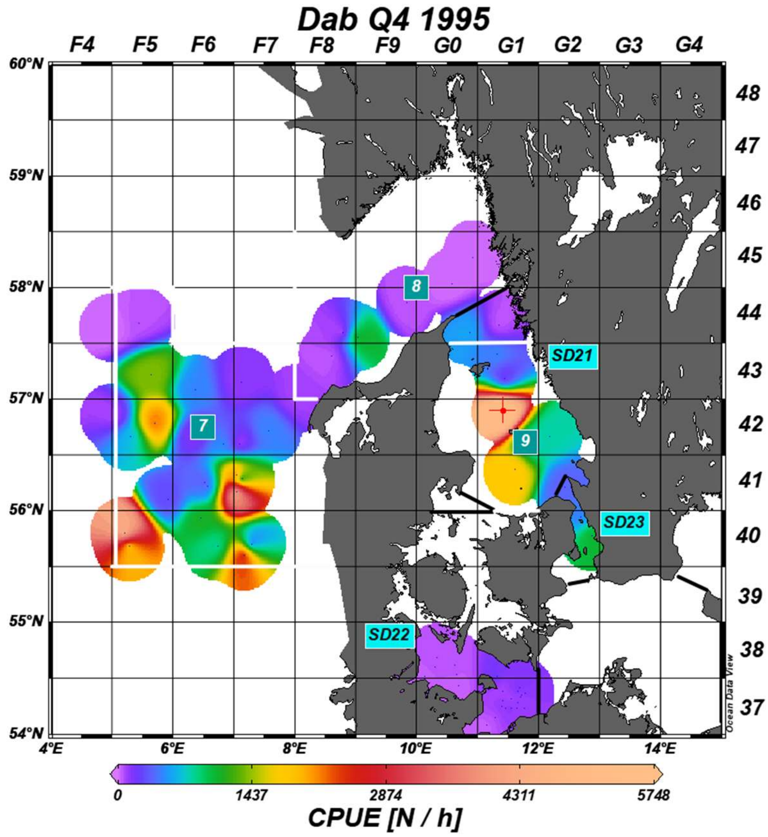

Dab Q4 1998
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N 59°N 58°N 57°N 56°N 55°N 54°N
48 47 46 45 44 43 42 41 40 39 38 37
4°E 6°E 8°E 10°E 12°E 14°E
8
7
9
SD21
SD22
SD23
Ocean Data View
0 122 244 366 488
CPUE [N / h]



Dab Q4 1997



Dab Q4 1996


Dab Q4 1995
F4
F5
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F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
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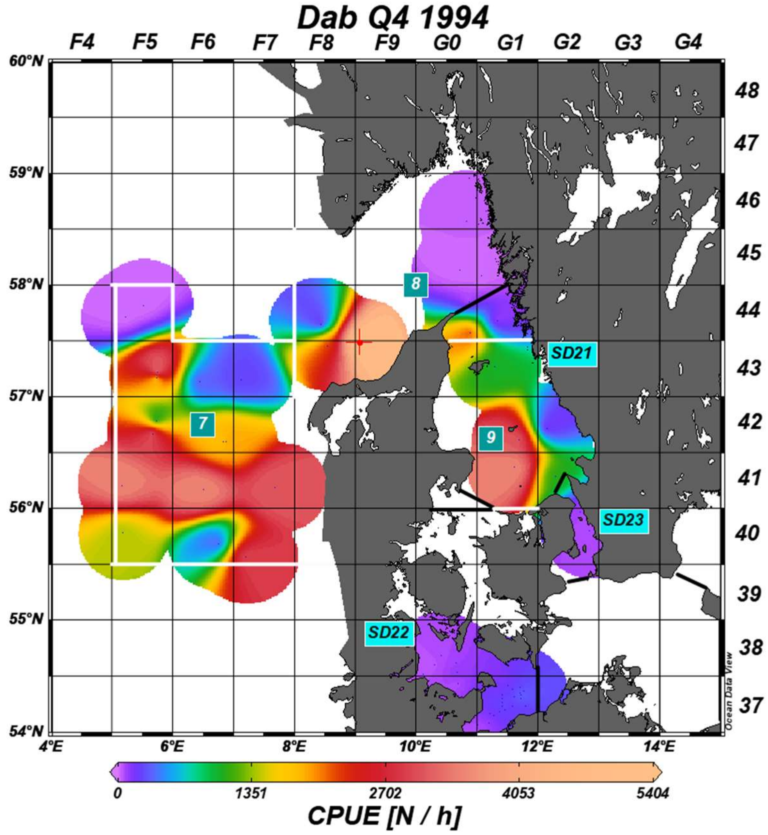
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
1437
2874
4311
5748
CPUE [N / h]


Dab Q4 1994
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
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42
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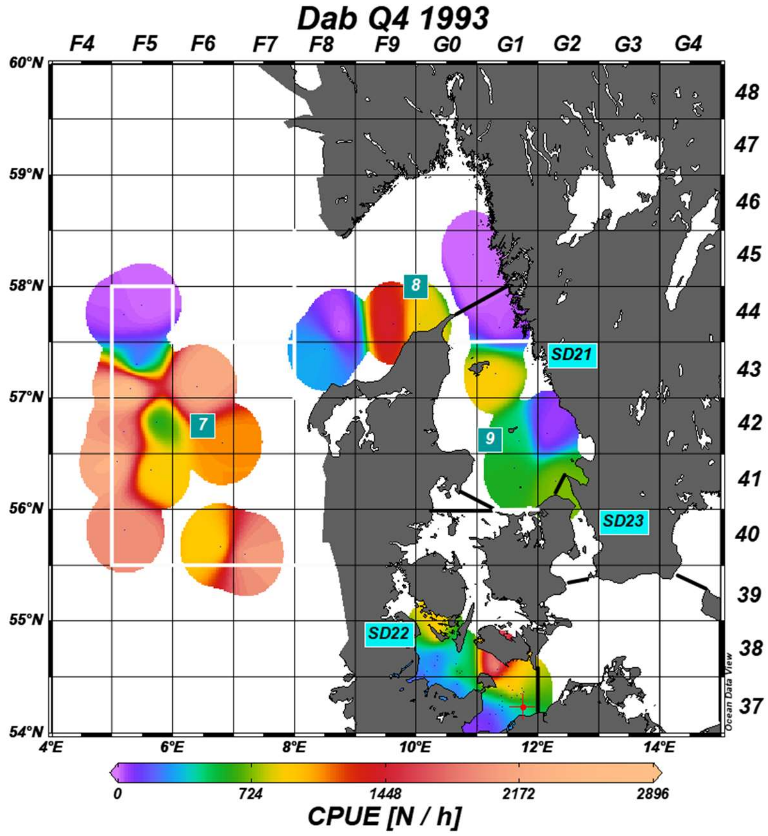
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
1351
2702
4053
5404
CPUE [N / h]


Dab Q4 1993
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
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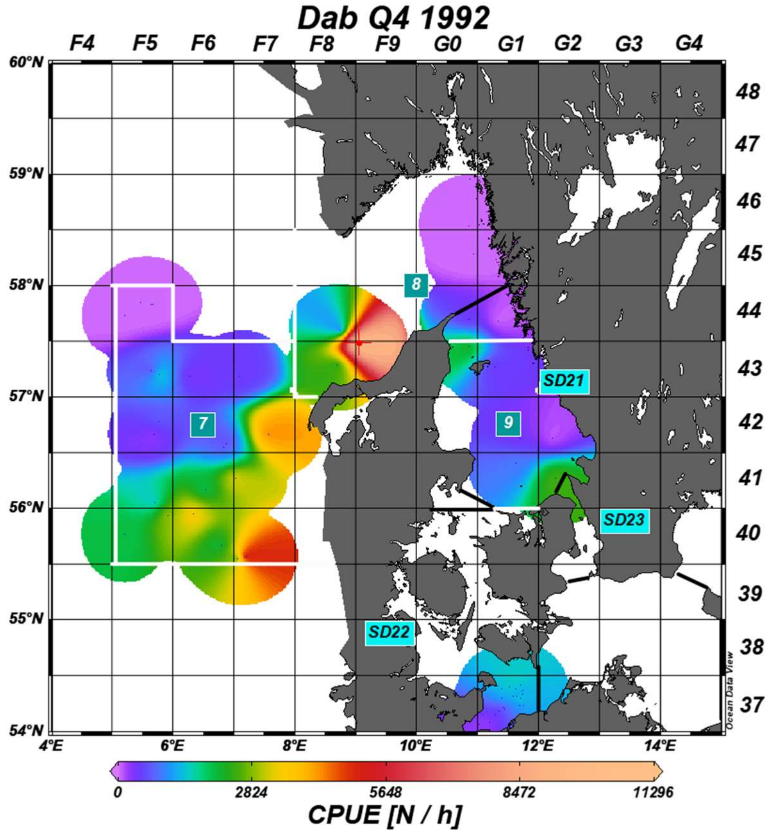
38
37
8
7
9
SD21
SD22
SD23
Ocean Data View
0
724
1448
2172
2896
CPUE [N / h]


Dab Q4 1992
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
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44
43
42
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37
8
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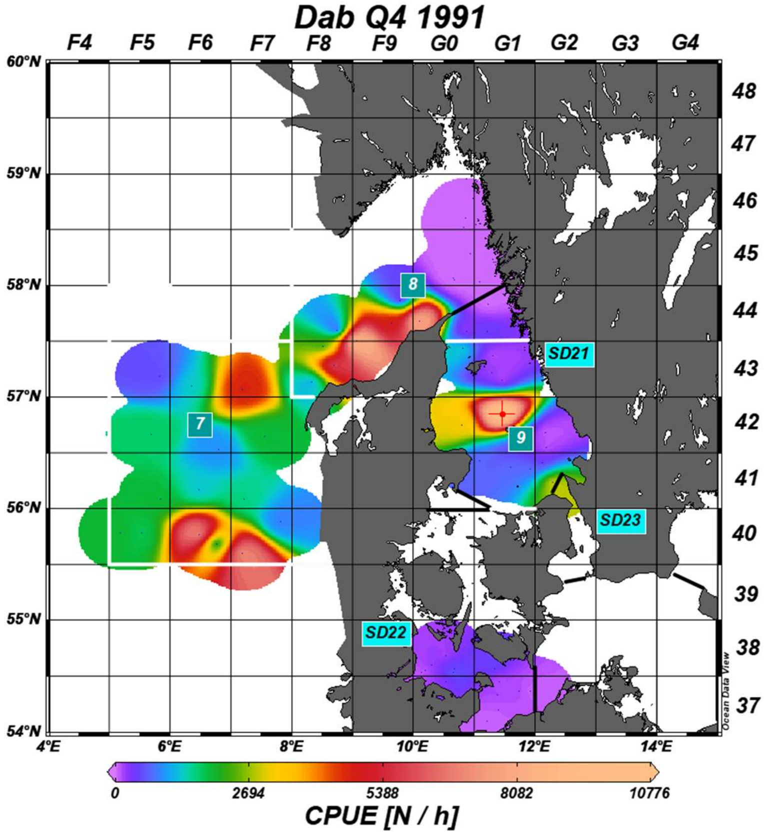
SD21
SD22
SD23
Ocean Data View
0
2824
5648
8472
11296
CPUE [N / h]


Dab Q4 1991
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
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37
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8
9
SD21
SD22
SD23
0
2694
5388
8082
10776
CPUE [N / h]
Ocean Data View

# ANNEX 1.3

## Annual landings of Dab in tons per ICES Subdivision and statistical rectangle

All data are taken from the Regional Database (RDB) hosted by ICES (ICES 2023a). Aggregation of data is following the ICES Data Guidelines (ICES 2023b)

ICES. 2023b. Regional Database (RDB) and Regional Database and Estimation System (RDBES). ICES Data Portal: https://www.rdb-fishframe.org/

ICES. 2023b. Data policy for the Regional Database (RDB) and Regional Database and Estimation System (RDBES). ICES Data Guidelines. 7 pp. https://doi.org/10.17895/ices.pub.22188157

| Area | 2019 | 2020 | 2021 | 2022 | average | % |
|---|---|---|---|---|---|---|
| **27.3.a.20** | **590.095** | **376.283** | **425.817** | **417.406** | | |
| **43F7** | 0.095 | 0.024 | 0.203 | 0.051 | 0.093 | 0.02% |
| **43F8** | 138.554 | 109.155 | 130.193 | 77.140 | 113.761 | 25.15% |
| **43F9** | 114.922 | 87.528 | 70.113 | 56.228 | 82.198 | 18.17% |
| **43G0** | 0.000 | 0.000 | 0.011 | 0.000 | 0.003 | 0.00% |
| **43G1** | 0.000 | 0.003 | 0.004 | 0.000 | 0.002 | 0.00% |
| **44F7** | 1.744 | 0.030 | 0.180 | 0.092 | 0.512 | 0.11% |
| **44F8** | 57.612 | 37.211 | 35.616 | 25.892 | 39.083 | 8.64% |
| **44F9** | 224.096 | 108.804 | 144.762 | 169.917 | 161.895 | 35.79% |
| **44G0** | 50.367 | 29.823 | 42.105 | 84.585 | 51.720 | 11.43% |
| **44G1** | 2.067 | 1.915 | 1.655 | 2.630 | 2.067 | 0.46% |
| **45F9** | 0.040 | 0.050 | 0.083 | 0.026 | 0.050 | 0.01% |
| **45G0** | 0.327 | 1.358 | 0.518 | 0.364 | 0.642 | 0.14% |
| **45G1** | 0.232 | 0.363 | 0.228 | 0.480 | 0.326 | 0.07% |
| **46G0** | 0.039 | 0.009 | 0.146 | 0.001 | 0.049 | 0.01% |
| **46G1** | 0.000 | 0.010 | 0.000 | 0.000 | 0.003 | 0.00% |

| Area | 2019 | 2020 | 2021 | 2022 | average | % |
|---|---|---|---|---|---|---|
| **27.3.a.21** | **22.688** | **17.887** | **25.553** | **32.087** | | |
| **40F7** | 0.000 | 0.000 | 0.064 | 0.000 | 0.016 | 0.07% |
| **40G1** | 0.023 | 0.022 | 0.074 | 0.525 | 0.161 | 0.66% |
| **40G2** | 0.009 | 0.022 | 0.000 | 0.017 | 0.012 | 0.05% |
| **41G0** | 0.672 | 0.573 | 0.420 | 0.131 | 0.449 | 1.83% |
| **41G1** | 2.612 | 2.166 | 8.156 | 8.781 | 5.429 | 22.11% |
| **41G2** | 2.200 | 1.490 | 1.901 | 1.293 | 1.721 | 7.01% |
| **42G0** | 0.749 | 0.118 | 0.692 | 0.385 | 0.486 | 1.98% |
| **42G1** | 1.089 | 1.118 | 1.663 | 1.328 | 1.300 | 5.29% |
| **42G2** | 1.652 | 0.752 | 1.009 | 1.062 | 1.119 | 4.56% |

| | | | | | | |
|---|---|---|---|---|---|---|
| **43F9** | 0.000 | 0.000 | 0.027 | 0.000 | 0.007 | 0.03% |
| **43G0** | 3.863 | 3.229 | 2.329 | 5.933 | 3.839 | 15.63% |
| **43G1** | 1.552 | 1.821 | 2.229 | 3.019 | 2.155 | 8.78% |
| **43G2** | 0.067 | 0.023 | 0.016 | 0.002 | 0.027 | 0.11% |
| **44F9** | 0.000 | 0.000 | 0.123 | 0.000 | 0.031 | 0.13% |
| **44G0** | 6.073 | 4.292 | 5.870 | 7.669 | 5.976 | 24.34% |
| **44G1** | 2.127 | 2.261 | 0.980 | 1.942 | 1.828 | 7.44% |

| **Area** | **2019** | **2020** | **2021** | **2022** | **average** | **%** |
|---|---|---|---|---|---|---|
| **27.3.b.23** | **16.072** | **13.002** | **8.131** | **7.320** | | |
| **39G2** | 0.059 | 0.030 | 0.003 | 0.006 | 0.025 | 0.22% |
| **40G2** | 13.996 | 11.805 | 7.659 | 6.500 | 9.990 | 89.75% |
| **40G3** | 0.000 | 0.079 | 0.055 | 0.020 | 0.039 | 0.35% |
| **41G2** | 2.017 | 1.088 | 0.414 | 0.794 | 1.078 | 9.69% |

| **Area** | **2019** | **2020** | **2021** | **2022** | **average** | **%** |
|---|---|---|---|---|---|---|
| **27.3.c.22** | **955.6** | **854.0** | **654.5** | **211.9** | | |
| **37F0** | 0.0 | 0.0 | 0.0 | 0.0 | 0.005 | 0.00% |
| **37F9** | 0.1 | 0.0 | 0.0 | 0.0 | 0.019 | 0.00% |
| **37G0** | 53.1 | 62.0 | 93.5 | 34.0 | 60.663 | 9.07% |
| **37G1** | 212.2 | 288.4 | 147.5 | 39.2 | 171.815 | 25.68% |
| **37G2** | 0.0 | 0.0 | 0.2 | 0.0 | 0.044 | 0.01% |
| **38F9** | 4.7 | 3.3 | 1.8 | 0.8 | 2.685 | 0.40% |
| **38G0** | 611.2 | 424.2 | 302.2 | 126.7 | 366.097 | 54.72% |
| **38G1** | 29.9 | 49.8 | 91.6 | 3.5 | 43.692 | 6.53% |
| **38G2** | 0.0 | 0.3 | 0.0 | 0.0 | 0.066 | 0.01% |
| **38H0** | 0.4 | 0.0 | 0.0 | 0.0 | 0.100 | 0.01% |
| **39F9** | 1.1 | 2.2 | 1.3 | 0.9 | 1.398 | 0.21% |
| **39G0** | 16.6 | 10.0 | 9.3 | 3.4 | 9.820 | 1.47% |
| **39G1** | 21.3 | 12.3 | 5.7 | 1.8 | 10.277 | 1.54% |
| **40G0** | 2.5 | 0.8 | 0.2 | 0.1 | 0.914 | 0.14% |
| **40G1** | 2.0 | 0.6 | 1.0 | 1.4 | 1.252 | 0.19% |
| **41G0** | 0.0 | 0.0 | 0.0 | 0.0 | 0.013 | 0.00% |
| **41G1** | 0.4 | 0.0 | 0.1 | 0.0 | 0.137 | 0.02% |

| **Area** | **2019** | **2020** | **2021** | **2022** | **average** | **%** |
|---|---|---|---|---|---|---|
| **27.4.b** | **914.036** | **650.239** | **498.149** | **342.666** | | |
| **36F2** | 3.887 | 2.358 | 2.386 | 0.364 | 2.249 | 0.37% |
| **36F3** | 4.645 | 4.476 | 3.366 | 0.46 | 3.237 | 0.54% |
| **36F4** | 8.773 | 19.714 | 8.241 | 3.483 | 10.053 | 1.67% |

| | | | | | | |
|---|---|---|---|---|---|---|
| **36F5** | 1.079 | 4.798 | 10.877 | 1.218 | 4.493 | 0.74% |
| **36F6** | 0.144 | 0.311 | 2.417 | | 0.957 | 0.16% |
| **36F7** | 0.353 | 1.287 | 0.282 | 0.076 | 0.500 | 0.08% |
| **36F8** | 0.015 | | 0.057 | 0.048 | 0.040 | 0.01% |
| **37F0** | 1.625 | 1.527 | 0.053 | 0.822 | 1.007 | 0.17% |
| **37F1** | 1.889 | 0.105 | 0.197 | 0.033 | 0.556 | 0.09% |
| **37F2** | 4.777 | 2.561 | 1.25 | 0.199 | 2.197 | 0.36% |
| **37F3** | 7.214 | 7.482 | 0.494 | 0.076 | 3.817 | 0.63% |
| **37F4** | 4.781 | 3.856 | 3.491 | 2.849 | 3.744 | 0.62% |
| **37F5** | 14.68 | 15.017 | 9.911 | 6.604 | 11.553 | 1.91% |
| **37F6** | 6.004 | 10.174 | 7.865 | 1.18 | 6.306 | 1.04% |
| **37F7** | 2.476 | 12.539 | 3.735 | 2.062 | 5.203 | 0.86% |
| **37F8** | 0.478 | 3.949 | 0.247 | 0.106 | 1.195 | 0.20% |
| **38F1** | 1.328 | 1.561 | 0.941 | 0.649 | 1.120 | 0.19% |
| **38F2** | 0.154 | 0.452 | 0.01 | | 0.205 | 0.03% |
| **38F3** | 6.929 | 5.125 | 9.023 | 0.04 | 5.279 | 0.87% |
| **38F4** | 6.24 | 19.29 | 12.718 | 2.954 | 10.301 | 1.71% |
| **38F5** | 5.74 | 7.246 | 4.552 | 2.453 | 4.998 | 0.83% |
| **38F6** | 5.19 | 8.728 | 6.185 | 6.721 | 6.706 | 1.11% |
| **38F7** | 0.023 | | 0.01 | | 0.017 | 0.00% |
| **38F8** | 0.003 | 0.275 | | | 0.139 | 0.02% |
| **38F9** | | 0.588 | | | 0.588 | 0.10% |
| **39F0** | 0.154 | | | | 0.154 | 0.03% |
| **39F1** | 14.647 | 1.164 | 0.04 | | 5.284 | 0.88% |
| **39F2** | 0.58 | 0.273 | 0.051 | | 0.301 | 0.05% |
| **39F3** | 2.477 | 1.802 | 2.12 | 3.301 | 2.425 | 0.40% |
| **39F4** | 8.091 | 5.309 | 3.763 | 0.63 | 4.448 | 0.74% |
| **39F5** | 70.367 | 18.311 | 3.66 | 10.004 | 25.586 | 4.24% |
| **39F6** | 31.103 | 5.045 | 12.946 | 11.605 | 15.175 | 2.51% |
| **39F7** | 0.791 | 0.145 | 0.089 | | 0.342 | 0.06% |
| **39F8** | | 0.138 | 0.037 | 0.633 | 0.269 | 0.04% |
| **40F0** | 0.003 | | | 0.079 | 0.041 | 0.01% |
| **40F1** | 2.464 | 0.004 | | | 1.234 | 0.20% |
| **40F2** | 0.012 | 0.262 | | | 0.137 | 0.02% |
| **40F3** | 0.374 | 0.141 | 0.714 | 0.17 | 0.350 | 0.06% |
| **40F4** | 3.526 | 2.56 | 3.641 | 5.317 | 3.761 | 0.62% |
| **40F5** | 155.894 | 82.815 | 8.774 | 19.519 | 66.751 | 11.06% |
| **40F6** | 20.142 | 12.368 | 25.332 | 8.596 | 16.610 | 2.75% |
| **40F7** | 7.634 | 2.758 | 2.799 | 2.545 | 3.934 | 0.65% |
| **40F8** | 0.56 | 0.098 | 0.265 | 1.357 | 0.570 | 0.09% |
| **41F0** | | | 0.002 | | 0.002 | 0.00% |
| **41F2** | 0.073 | 0.01 | | | 0.042 | 0.01% |
| **41F3** | 1.049 | 1.191 | 0.538 | 0.091 | 0.717 | 0.12% |
| **41F4** | 0.723 | 0.594 | 0.319 | 0.41 | 0.512 | 0.08% |
| **41F5** | 66.086 | 24.616 | 13.037 | 9.87 | 28.402 | 4.71% |
| **41F6** | 24.901 | 31.033 | 21.579 | 16.864 | 23.594 | 3.91% |

| | | | | | | |
|---|---|---|---|---|---|---|
| **41F7** | 39.481 | 37.942 | 40.743 | 30.816 | 37.246 | 6.17% |
| **41F8** | 8.397 | 7.172 | 15.373 | 13.211 | 11.038 | 1.83% |
| **42F2** | 0.185 | 0.117 | 0.056 | 0.039 | 0.099 | 0.02% |
| **42F3** | 1.482 | 2.431 | 0.592 | 0.74 | 1.311 | 0.22% |
| **42F4** | 6.767 | 5.078 | 2.61 | 1.089 | 3.886 | 0.64% |
| **42F5** | 10.95 | 6.162 | 9.948 | 7.17 | 8.558 | 1.42% |
| **42F6** | 37.526 | 30.162 | 30.585 | 15.366 | 28.410 | 4.71% |
| **42F7** | 55.571 | 44.097 | 47.905 | 40.79 | 47.091 | 7.80% |
| **42F8** | 10.004 | 11.879 | 16.123 | 6.029 | 11.009 | 1.82% |
| **43F0** | 0.027 | | 0.01 | | 0.019 | 0.00% |
| **43F2** | 0.166 | 0.516 | 0.047 | 0.051 | 0.195 | 0.03% |
| **43F3** | 1.31 | 0.71 | 0.455 | 0.885 | 0.840 | 0.14% |
| **43F4** | 10.943 | 9.98 | 4.045 | 3.223 | 7.048 | 1.17% |
| **43F5** | 38.788 | 30.772 | 28.941 | 34.51 | 33.253 | 5.51% |
| **43F6** | 53.589 | 21.377 | 23.541 | 13.498 | 28.001 | 4.64% |
| **43F7** | 92.034 | 72.475 | 52.397 | 23.395 | 60.075 | 9.95% |
| **43F8** | 28.076 | 25.385 | 33.523 | 27.594 | 28.645 | 4.75% |
| **43F9** | | | 0.006 | | 0.006 | 0.00% |
| **44F3** | | | 0.017 | 0.006 | 0.012 | 0.00% |
| **44F4** | | 0.08 | 0.083 | 0.02 | 0.061 | 0.01% |
| **44F6** | | | 0.081 | 0.009 | 0.045 | 0.01% |
| **44F7** | | | 0.014 | | 0.014 | 0.00% |
| **(NA)** | 18.277 | 19.371 | 0.701 | 0.103 | 9.613 | 1.59% |

# ANNEX 1.4

## Results of the SPiCT sensitivity runs

All data are taken from the Regional Database (RDB) hosted by ICES (ICES 2023a). Aggregation of data is following the ICES Data Guidelines (ICES 2023b)

Three different datasets were tested during WKMSYPICT and during the assessment working group WGBFAS (including the latest 2023 data, Table 1). Dataset 1 included only Baltic Sea data, whereas Dataset 2 used the combined index of IBTS/BITS of areas SD21-32. Dataset 3 used the combined areas index and landings of areas SD21-32 (Kattegat and Baltic Sea. The sensitivity analyses were performed to determine the influence of the inclusion of Kattegat to the overall performance of the model.

The SPiCT settings (CVs, catch uncertainty, priors, etc.) were kept identical to the final settings of *dab.27.22-32.*

**Table 1:** Dataset and overview of SPiCT settings of the sensitivity analyses

| **Setting/Data** | **Dataset 1: Baltic Sea** | **Dataset 2: Baltic Sea & Kattegat-Baltic index** | **Dataset 3: combined Baltic Sea & Kattegat** |
|---|---|---|---|
| **Catch time series** | Baltic Sea<br>(Areas SD22-SD32)<br>landings data 1991–2023 | Baltic Sea<br>(Areas SD22-SD32)<br>landings data 1991–2023 | Baltic and Kattegat<br>(Areas SD21-SD32)<br>landings data 1991–2023 |
| **BITS biomass Index quarter 1, “Bergdex”** | Baltic Sea<br>(Areas SD22-32)<br>1991-2023, ≥ 15 cm | Baltic and Kattegat<br>(Areas SD21-SD32),<br>1991-2023, ≥ 15 cm | Baltic and Kattegat<br>(Areas SD21-SD32),<br>1991-2023, ≥ 15 cm |
| **BITS biomass Index quarter 4, “Bergdex”** | Baltic Sea<br>(Areas SD22-32)<br>1991-2023, ≥ 15 cm | Baltic and Kattegat<br>(Areas SD21-SD32),<br>1991-2023, ≥ 15 cm | Baltic and Kattegat<br>(Areas SD21-SD32),<br>1991-2023, ≥ 15 cm |
| | | | |
| **SPiCT settings** | | | |
| - Standard deviation on the indices (sdi) | Log(sdi1)~N(log(index_CV),0.3^2)<br>Log(sdi2)~N(log(index_CV), 0.3^2) | | |
| - Standard deviation on the indices (observation) (stdevfacI) | indexQ1_CV/mean(indexQ1_CV),<br>indexQ4_CV /mean(indexQ4_CV) | | |
| - Standard deviation on the catch (observation) (stdevfacC) | For >2021 stdevfacC = 2; | | |
| - Biomass process noise (logsdb) | Log(0.15)-0.5*0.5^2, 0.5 | | |
| - Catch observation error (logsdc) | Log(0.1)-0.5*0.5^2, 0.5 | | |

| | |
|---|---|
| - Uncertainty ratio of index (observation) to biomass process (alpha) | Deactivated |
| - Uncertainty ratio of catch (observation) to fishing mortality process (beta) | Deactivated |
| - Shape parameter (n) | Thorson model, Log(n)~N(log(1.353),0.55) |
| - Intrinsic growth rate (r) | Log(r)~N(log(0.71*0.6765), -0.5*0.5^2,0.5) |
| - Initial depletion (bkfrac) | None (default) |
| - Discretion time step (dteuler) | 1/16 year (default) |

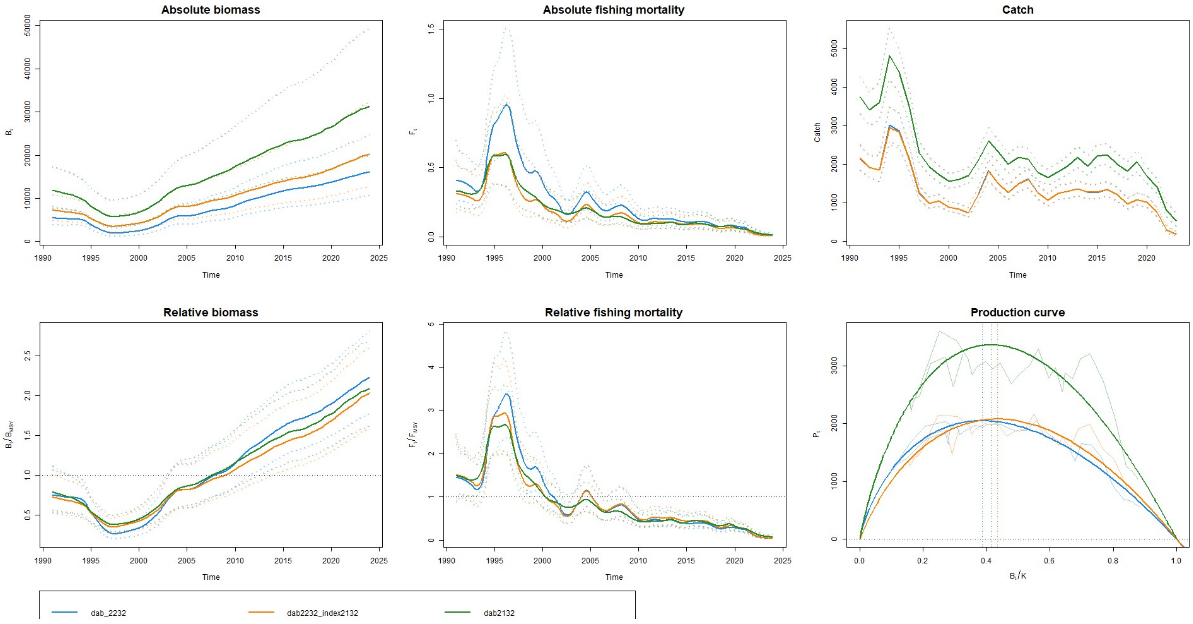


*Figure 1: Comparison of the model estimates of biomass, fishing mortality, production curve and catch of all three sensitivity runs*

## Dataset 1

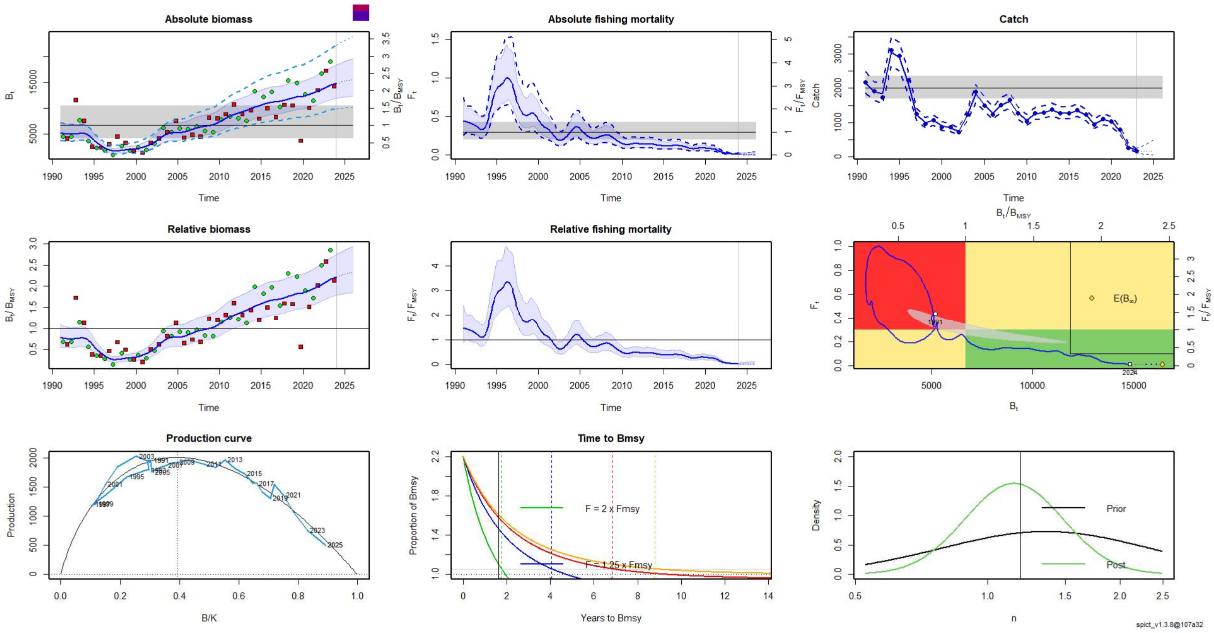


*Figure 2: Overview of the SPiCT results for Dataset 1*

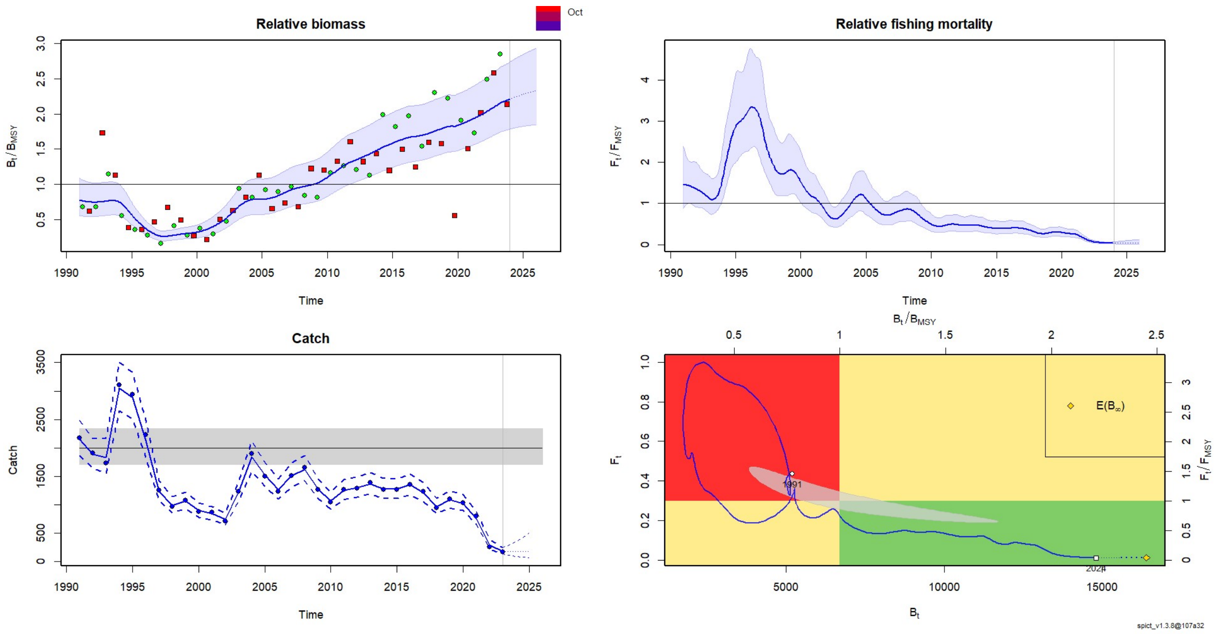


*Figure 3: Overview of the relative estimates of the SPiCT output for Dataset 1*

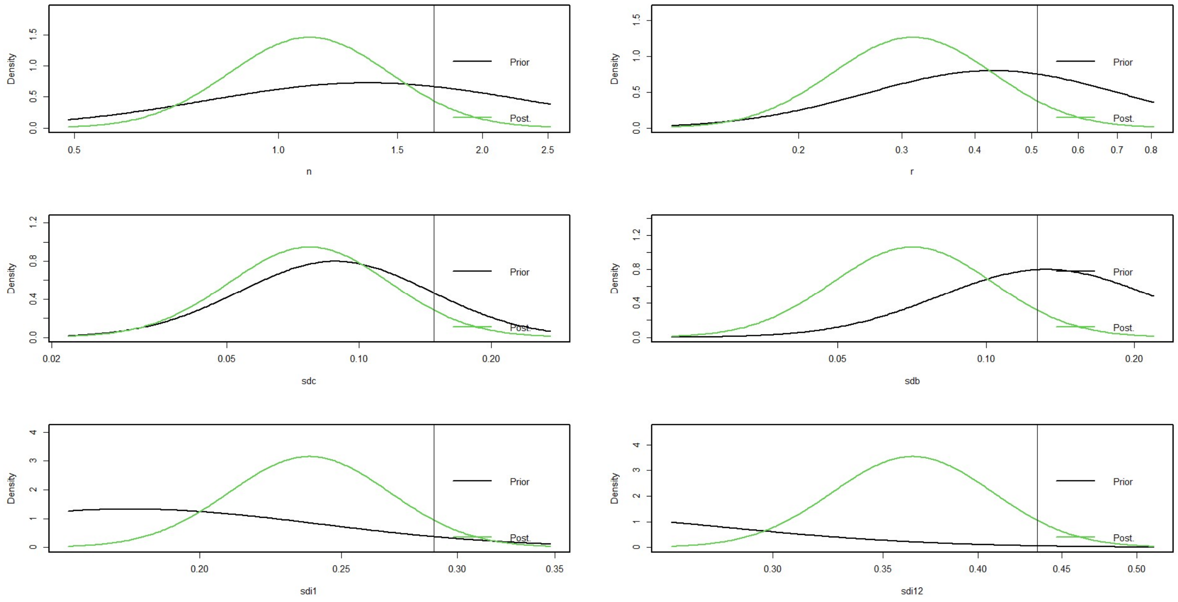


*Figure 4: Prior and posterior distributions of the set priors in Dataset 1*

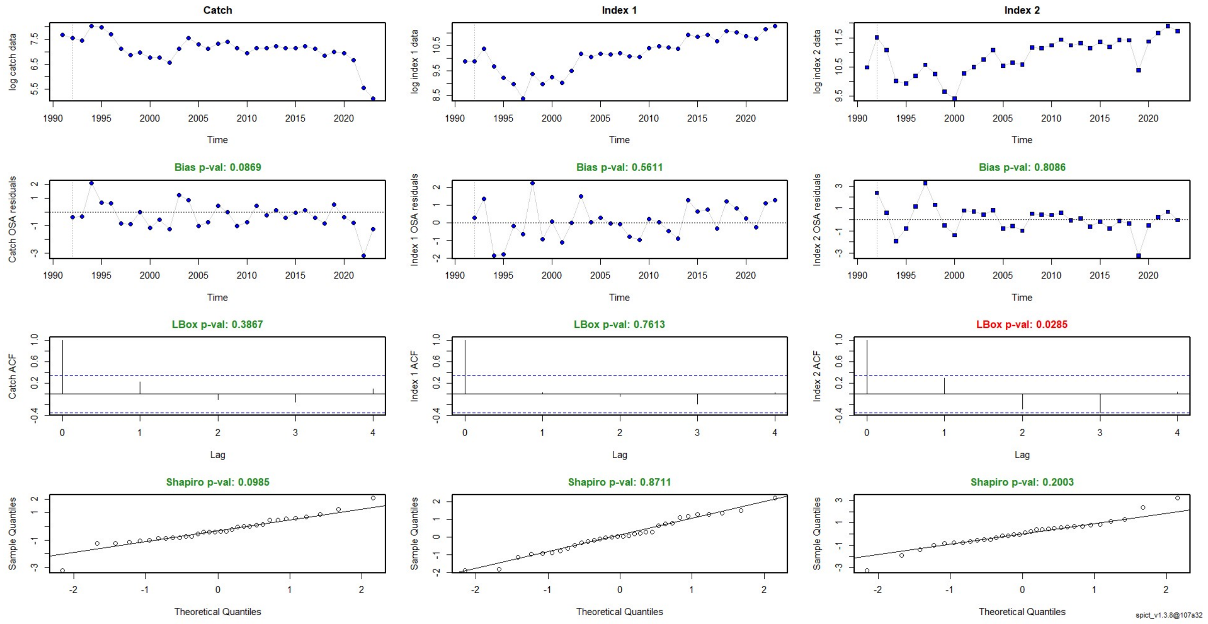


*Figure 5: One-Step-Ahead residuals for observations of Dataset 1*

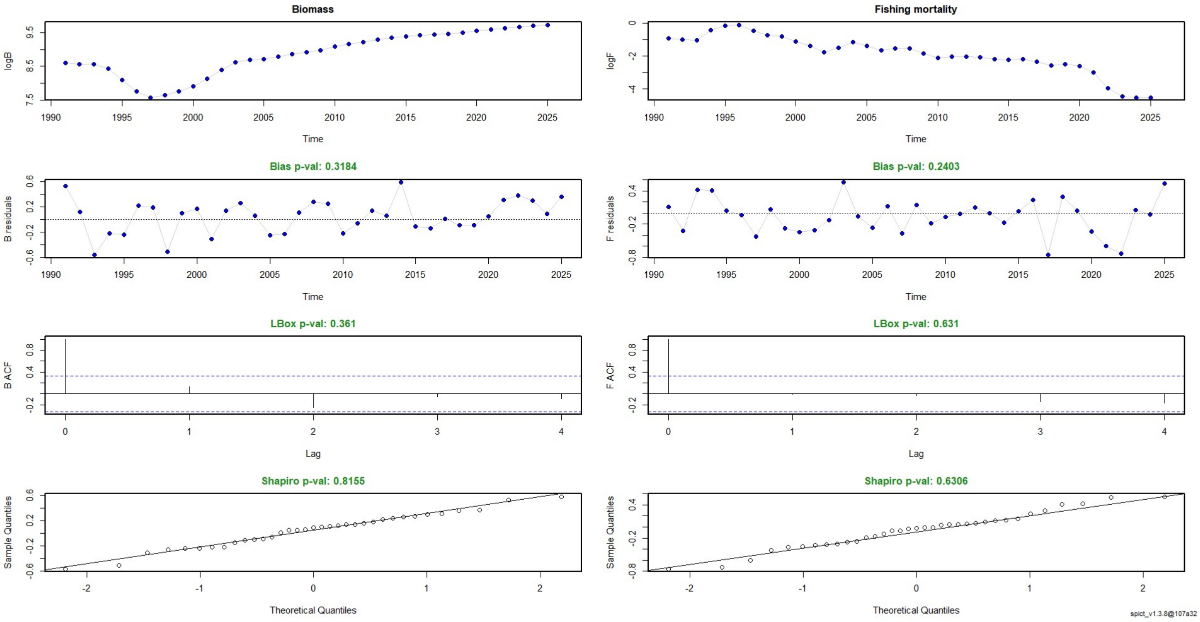


*Figure 6: Process residuals of Dataset 1*

*Table 2: model and parameter estimate of Dataset 1 (estimate, lower limit, upper limit and log-transformed estimate)*

| Dataset1 | estimate | cilow | ciupp | log.est |
|---|---:|---:|---:|---:|
| **alpha1** | 3.351 | 1.525 | 7.365 | 1.209 |
| **alpha2** | 5.145 | 2.366 | 11.187 | 1.638 |
| **beta** | 0.205 | 0.079 | 0.530 | -1.585 |
| **r** | 0.313 | 0.169 | 0.582 | -1.161 |
| **rc** | 0.564 | 0.385 | 0.825 | -0.574 |
| **rold** | 2.803 | 0.022 | 357.757 | 1.031 |
| **m** | 2049.544 | 1721.934 | 2439.486 | 7.625 |
| **K** | 18770.330 | 11762.480 | 29953.300 | 9.840 |
| **q1** | 3.835 | 2.642 | 5.566 | 1.344 |
| **q2** | 7.964 | 5.422 | 11.696 | 2.075 |
| **n** | 1.112 | 0.651 | 1.899 | 0.106 |
| **sdb** | 0.071 | 0.034 | 0.148 | -2.646 |
| **sdf** | 0.376 | 0.280 | 0.506 | -0.977 |
| **sdi1** | 0.238 | 0.185 | 0.305 | -1.437 |
| **sdi2** | 0.365 | 0.293 | 0.455 | -1.008 |
| **sdc** | 0.077 | 0.034 | 0.176 | -2.562 |

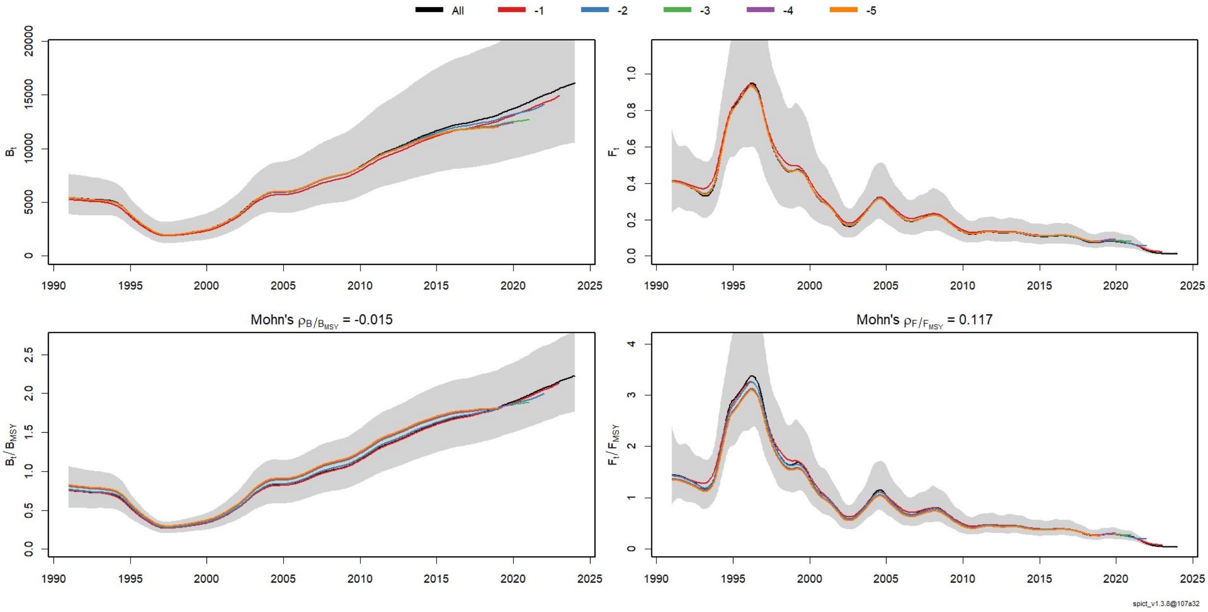


*Figure 7: Retrospective analysis of Dataset 1*

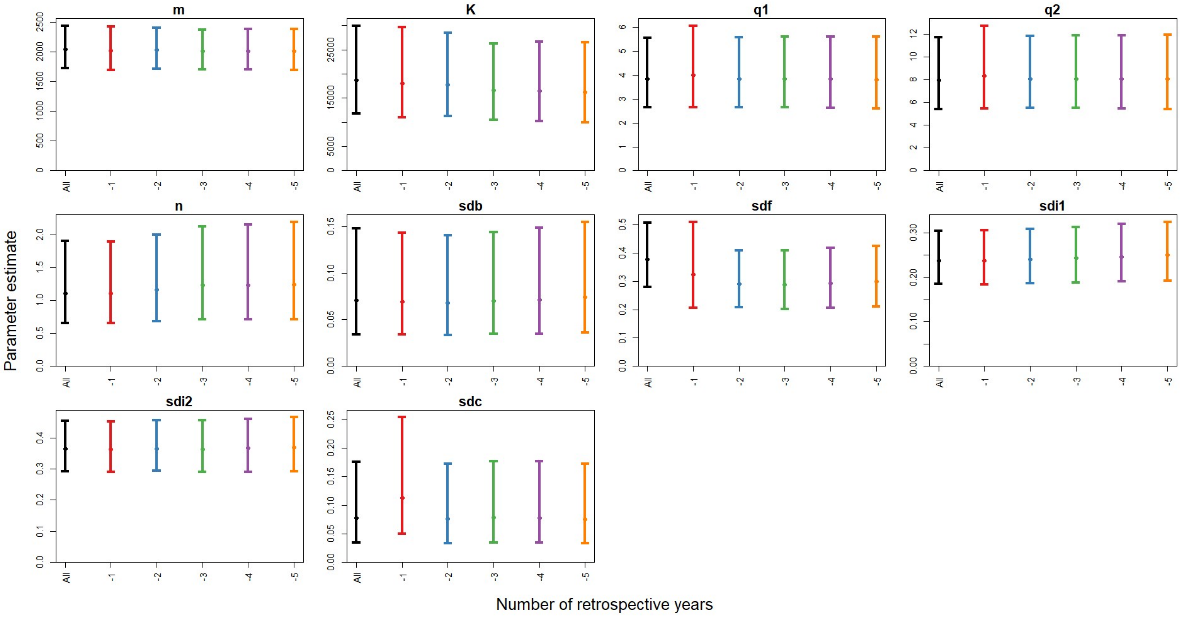


*Figure 8: Retrospective analysis of the model parameter of Dataset 1*

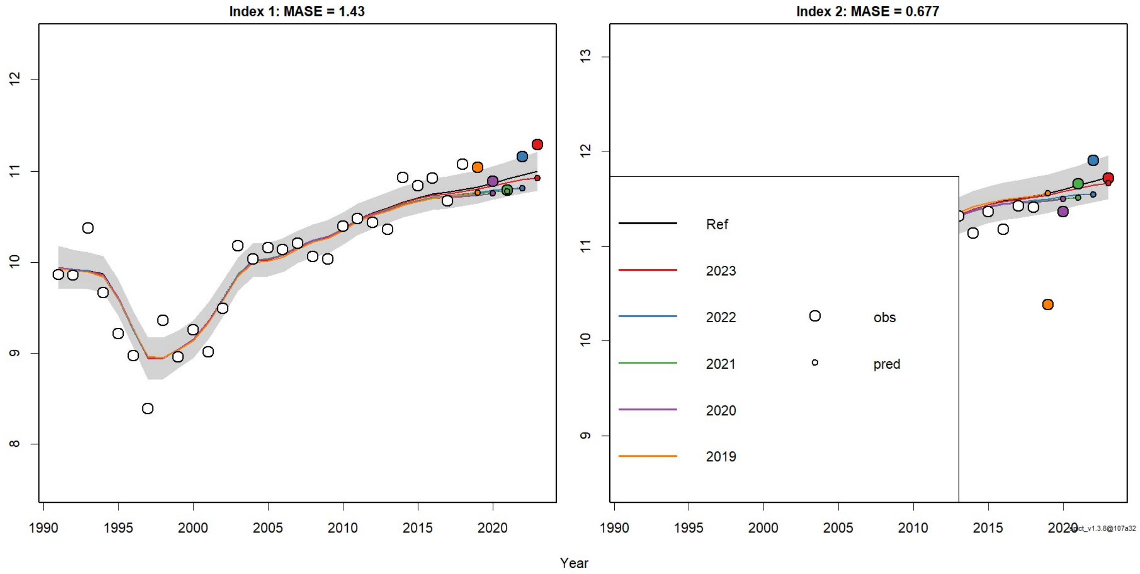


*Figure 9: Hindcast analysis of Dataset 1 ("MASE")*

## Dataset 2:

### Landings of Dab in the Baltic (27.3.c.22 to 27.3.d.32) and Survey index data from Kattegat and Baltic Sea combined

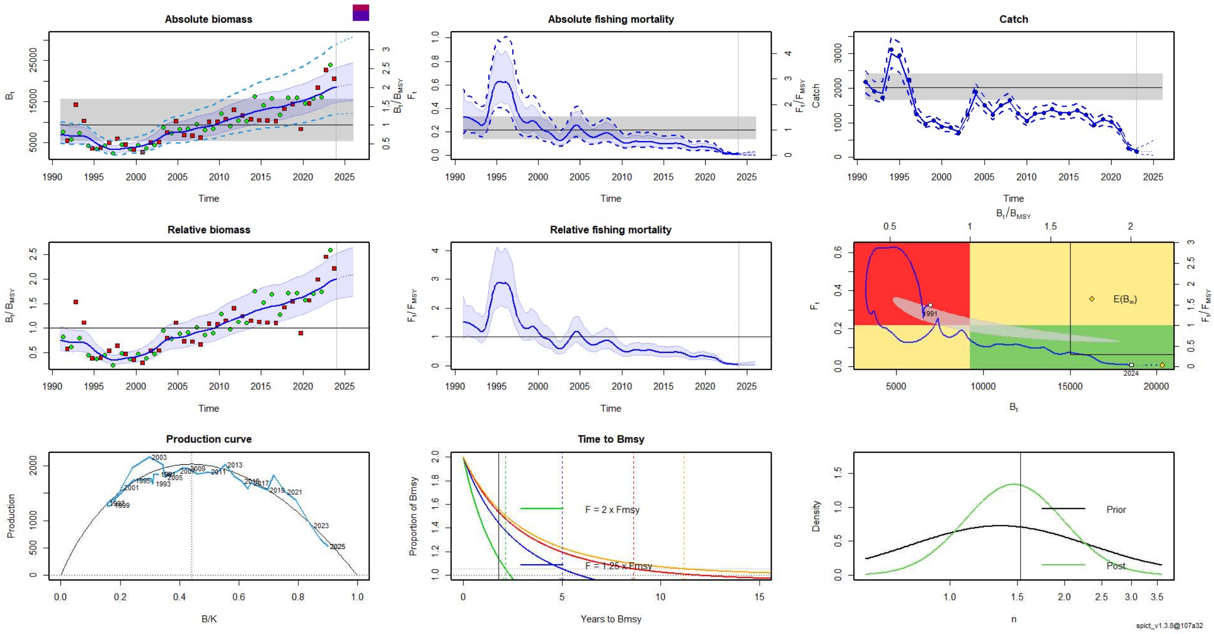


*Figure 10: Overview of the SPiCT results for Dataset 2*

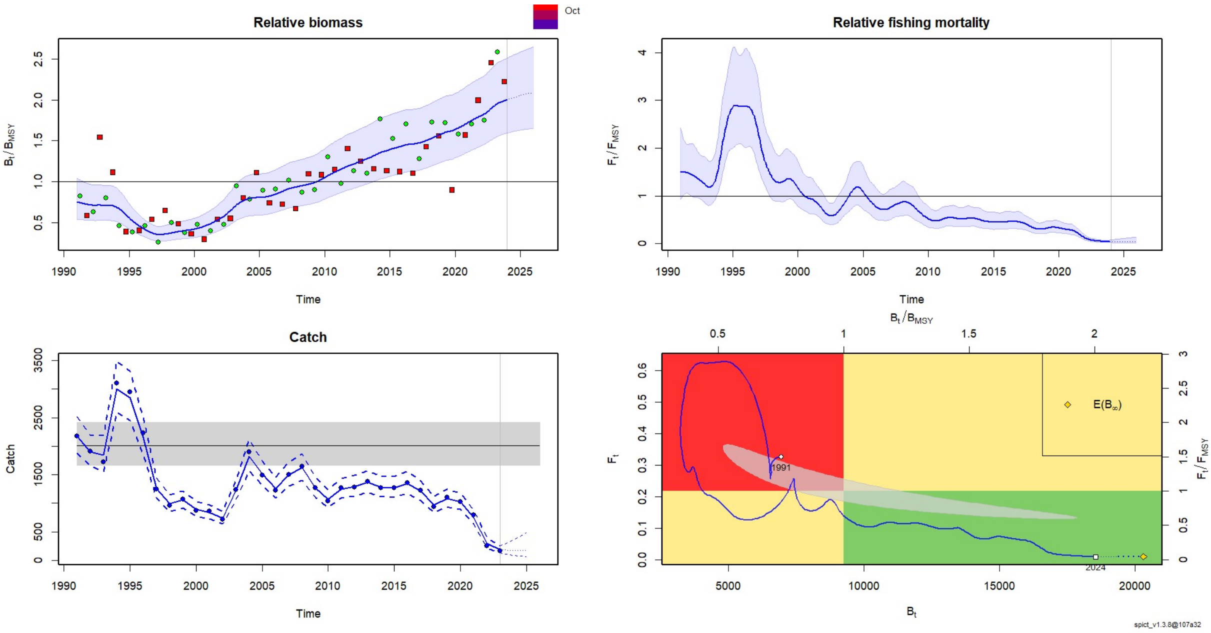


*Figure 11: Overview of the relative estimates of the SPiCT output for Dataset 2*

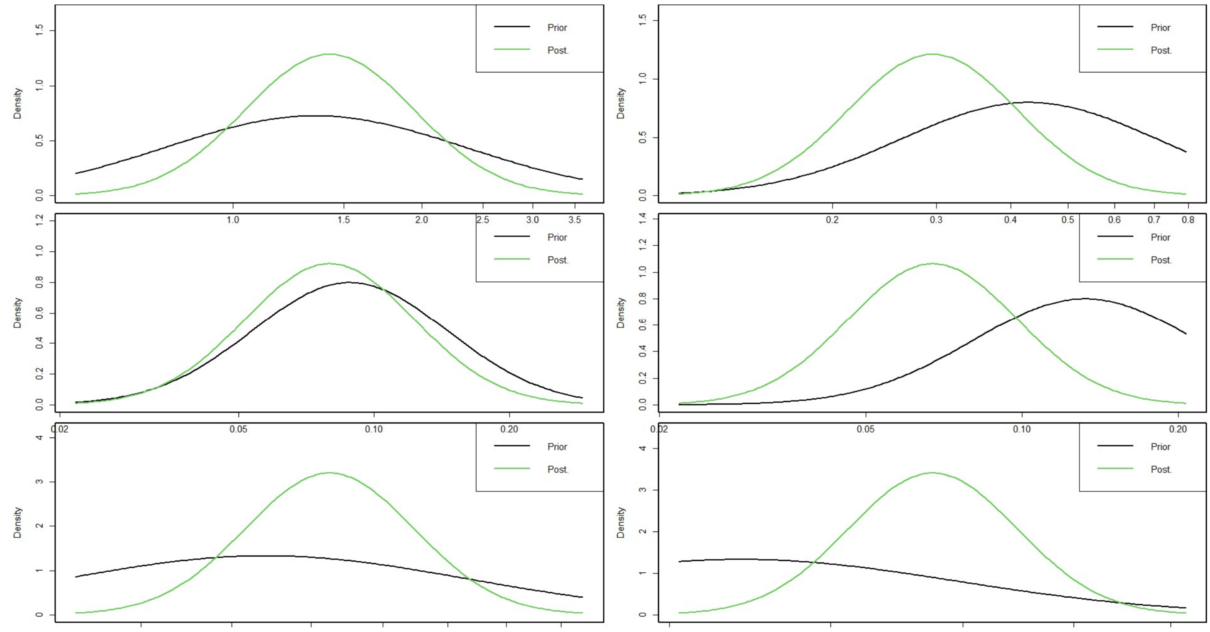


*Figure 12: Prior and posterior distributions of the set priors in Dataset 2*

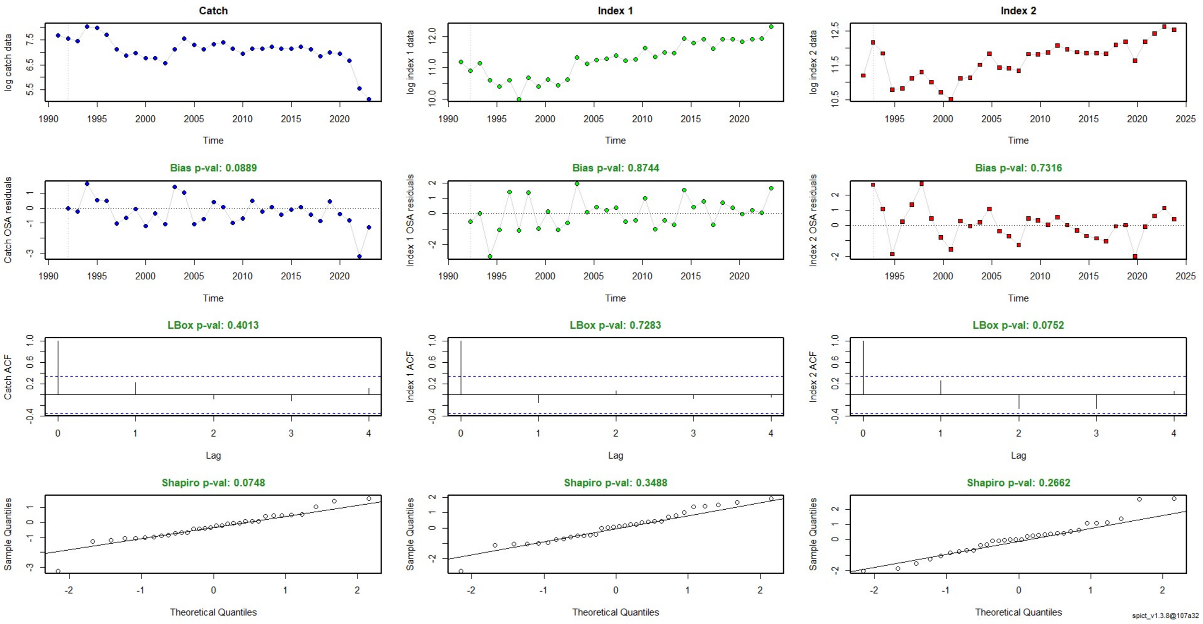


*Figure 13: One-Step-Ahead residuals for observations of Dataset 2*

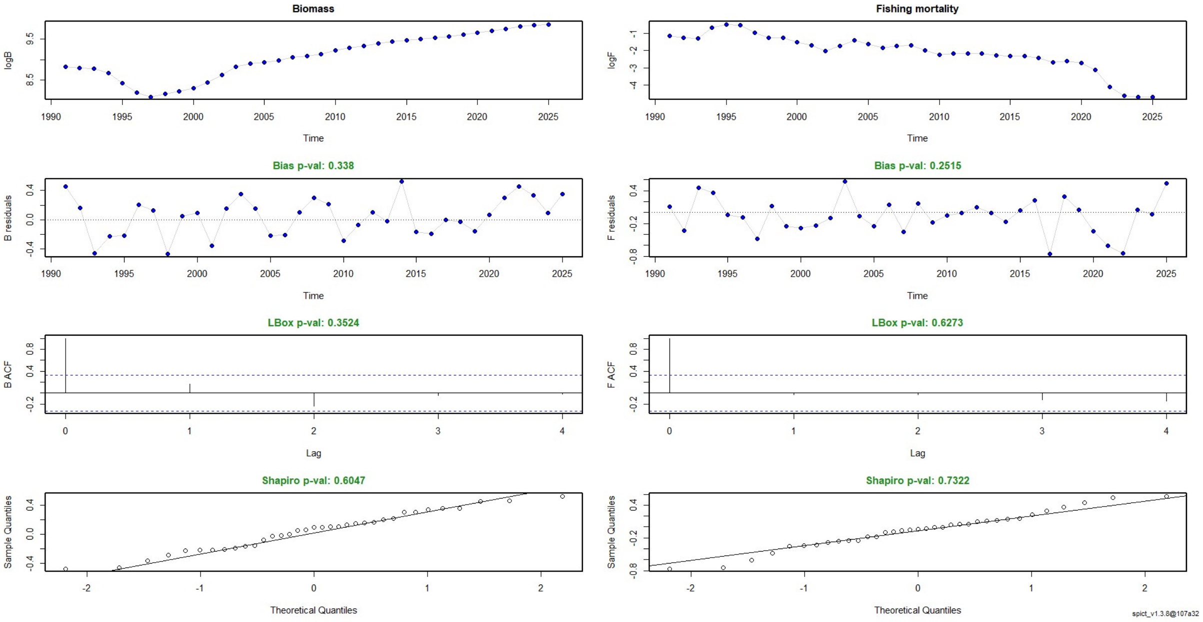


*Figure 14: Process residuals of Dataset 2*

*Table 3: model and parameter estimate of Dataset 2 (estimate, lower limit, upper limit and log-transformed estimate)*

| Dataset2 | **estimate** | **cilow** | **ciupp** | **log.est** |
|---|---|---|---|---|
| **alpha1** | 2.833 | 1.290 | 6.221 | 1.041 |
| **alpha2** | 4.367 | 1.993 | 9.569 | 1.474 |
| **beta** | 0.204 | 0.079 | 0.530 | -1.589 |
| **r** | 0.320 | 0.166 | 0.618 | -1.139 |
| **rc** | 0.436 | 0.288 | 0.659 | -0.831 |
| **rold** | 0.680 | 0.172 | 2.697 | -0.385 |
| **m** | 2026.364 | 1675.211 | 2451.125 | 7.614 |
| **K** | 21117.880 | 12800.780 | 34838.900 | 9.958 |
| **q1** | 9.396 | 6.230 | 14.170 | 2.240 |
| **q2** | 13.517 | 8.893 | 20.545 | 2.604 |
| **n** | 1.471 | 0.819 | 2.642 | 0.386 |
| **sdb** | 0.065 | 0.032 | 0.136 | -2.726 |
| **sdf** | 0.374 | 0.278 | 0.503 | -0.984 |
| **sdi1** | 0.185 | 0.145 | 0.238 | -1.685 |
| **sdi2** | 0.286 | 0.227 | 0.360 | -1.252 |
| **sdc** | 0.076 | 0.033 | 0.174 | -2.573 |

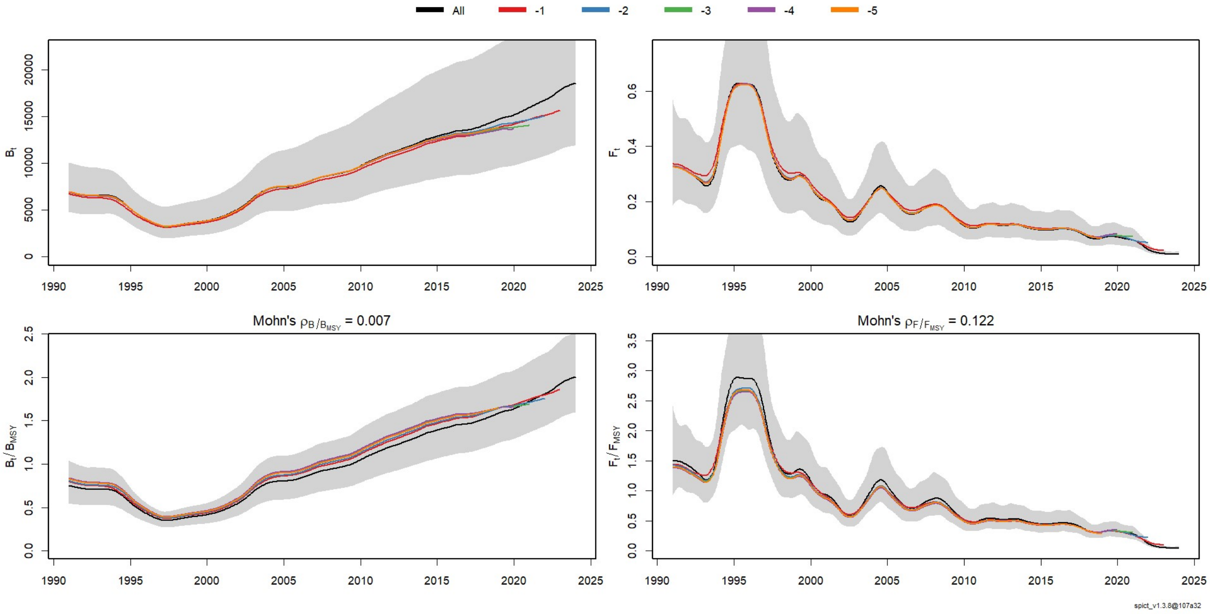


*Figure 15: Retrospective analysis of Dataset 2*

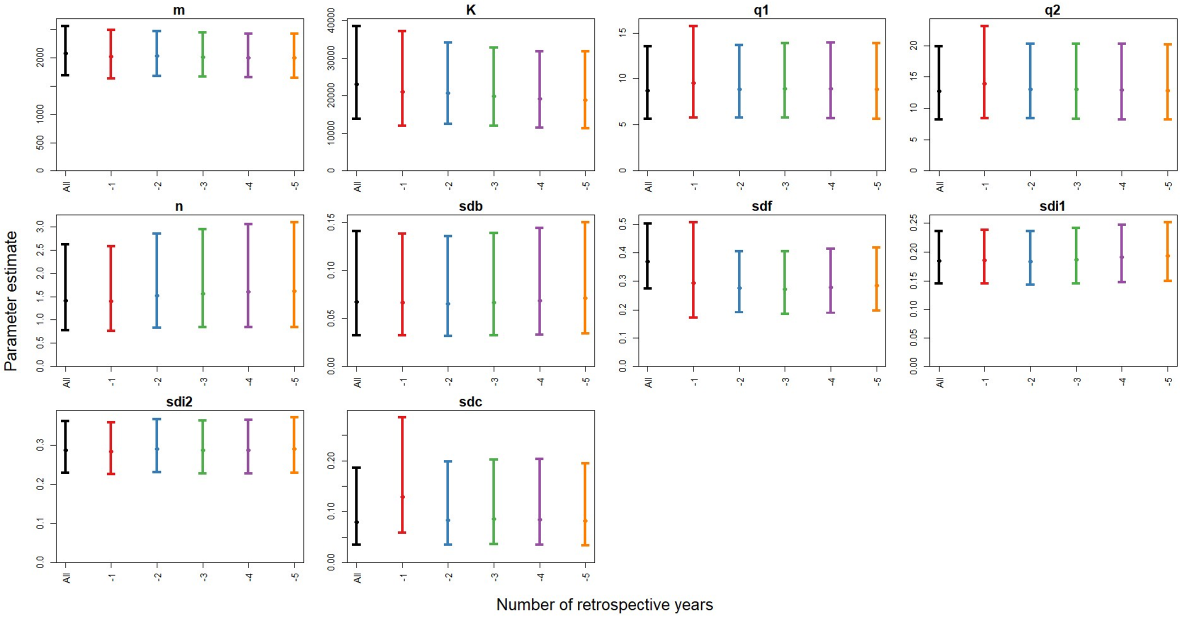


*Figure 16: Retrospective analysis of the model parameter of Dataset 2*

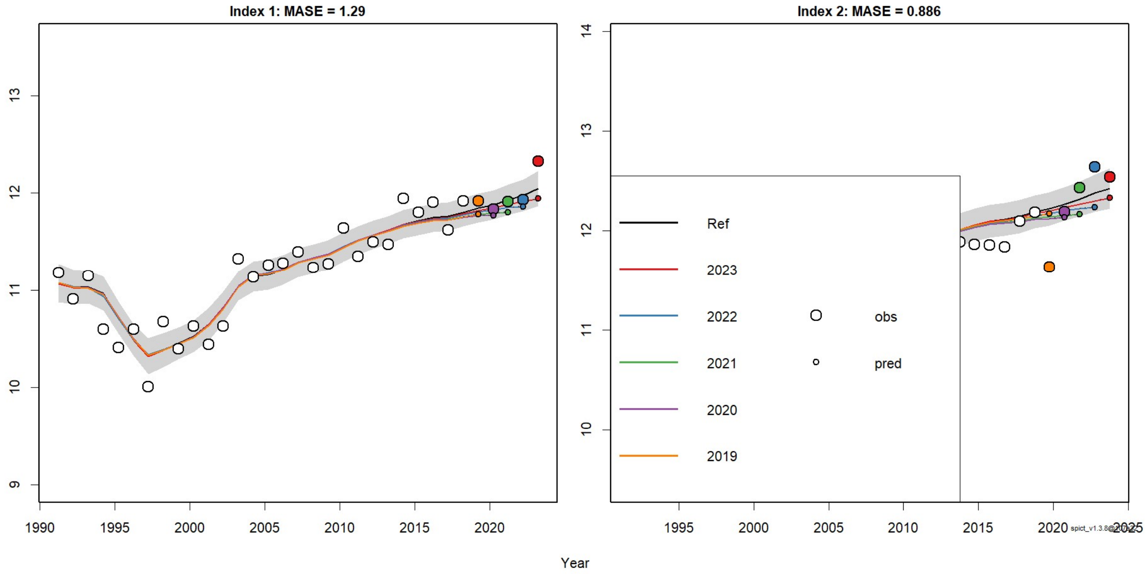


*Figure 17: Hindcast analysis of Dataset 2 (“MASE”)*

# Dataset 3:

## Landings and Survey index data of Dab in the Baltic and Kattegat combined

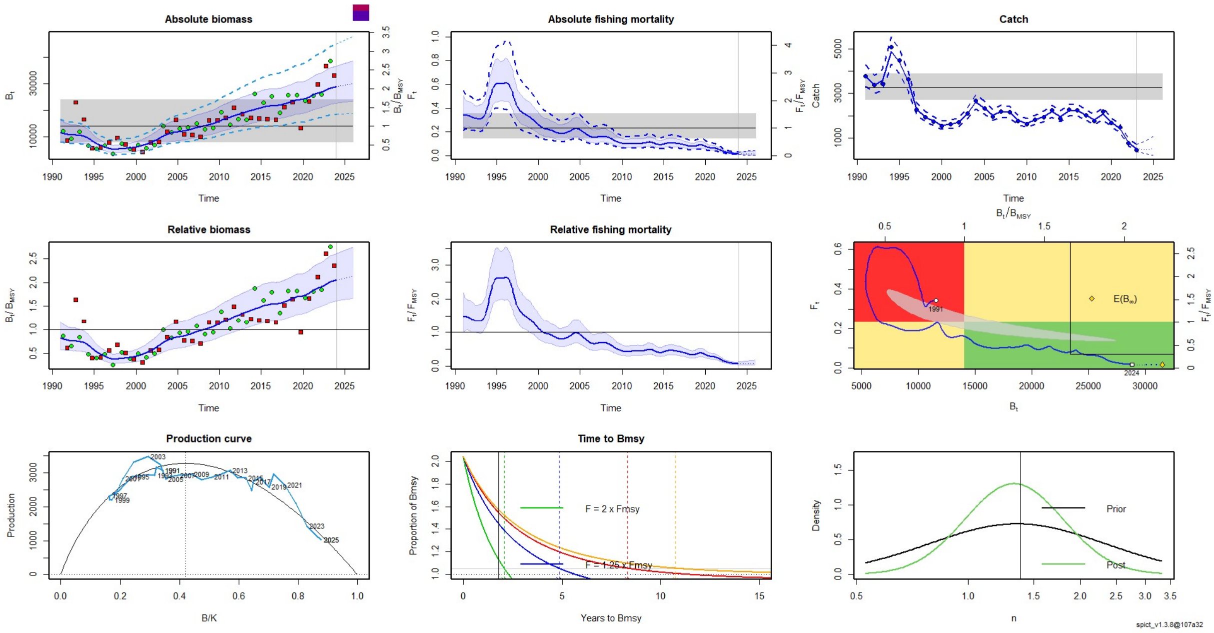


*Figure 18: Overview of the SPiCT results for Dataset 2*

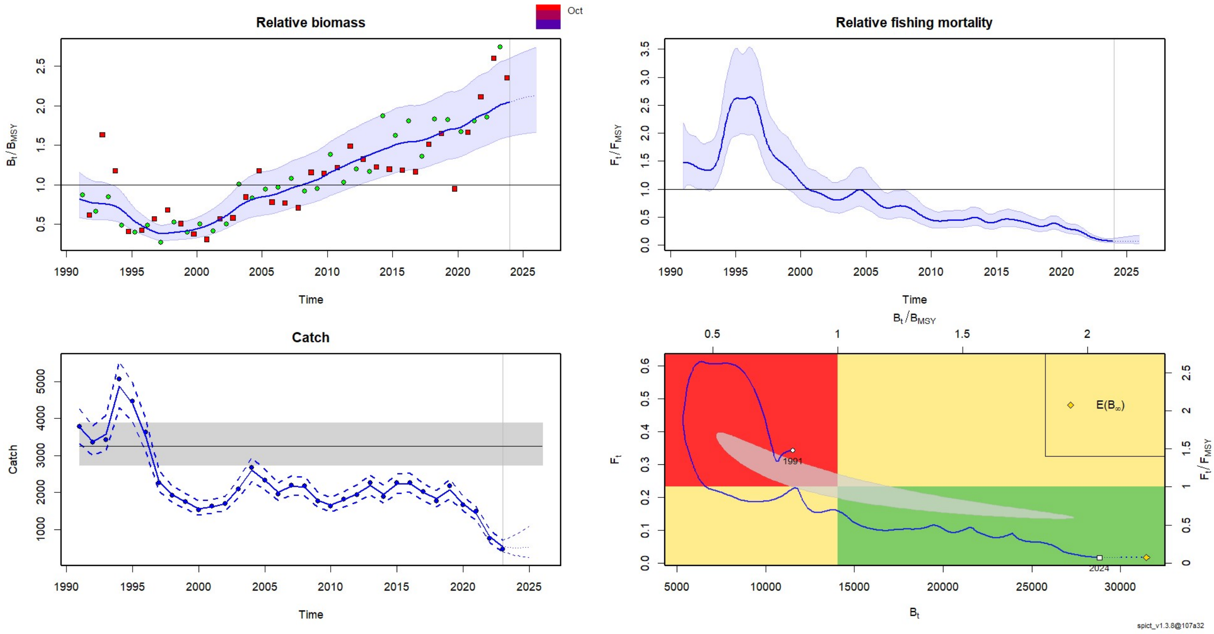


*Figure 19: Overview of the relative estimates of the SPiCT output for Dataset 3*

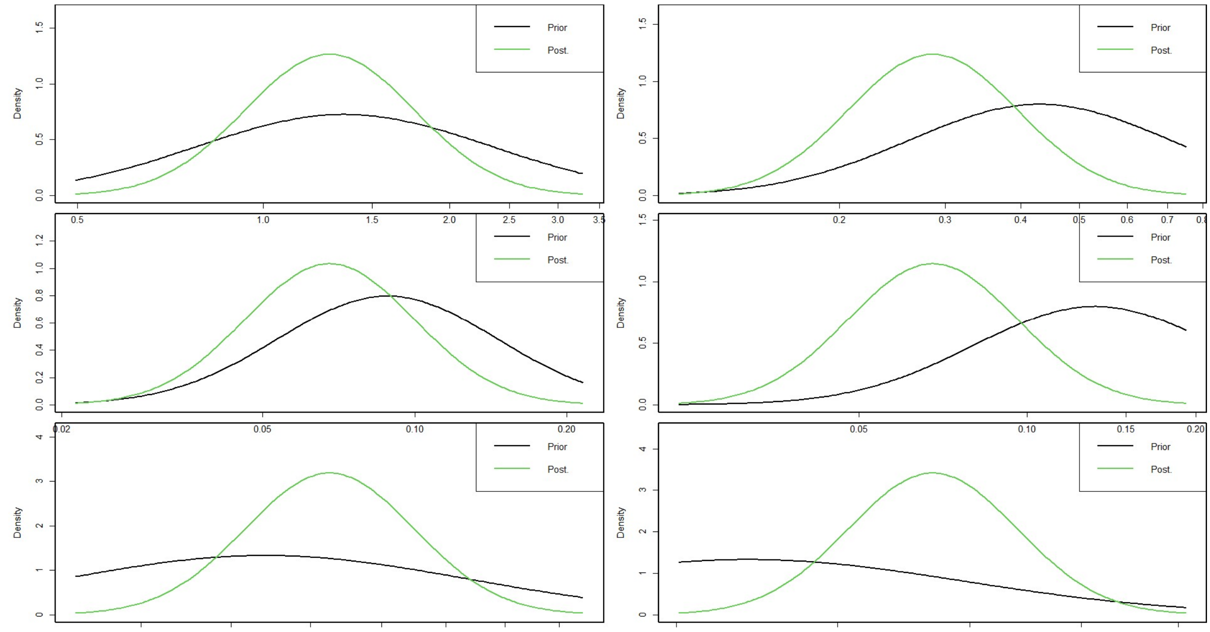


*Figure 20: Prior and posterior distributions of the set priors in Dataset 3*

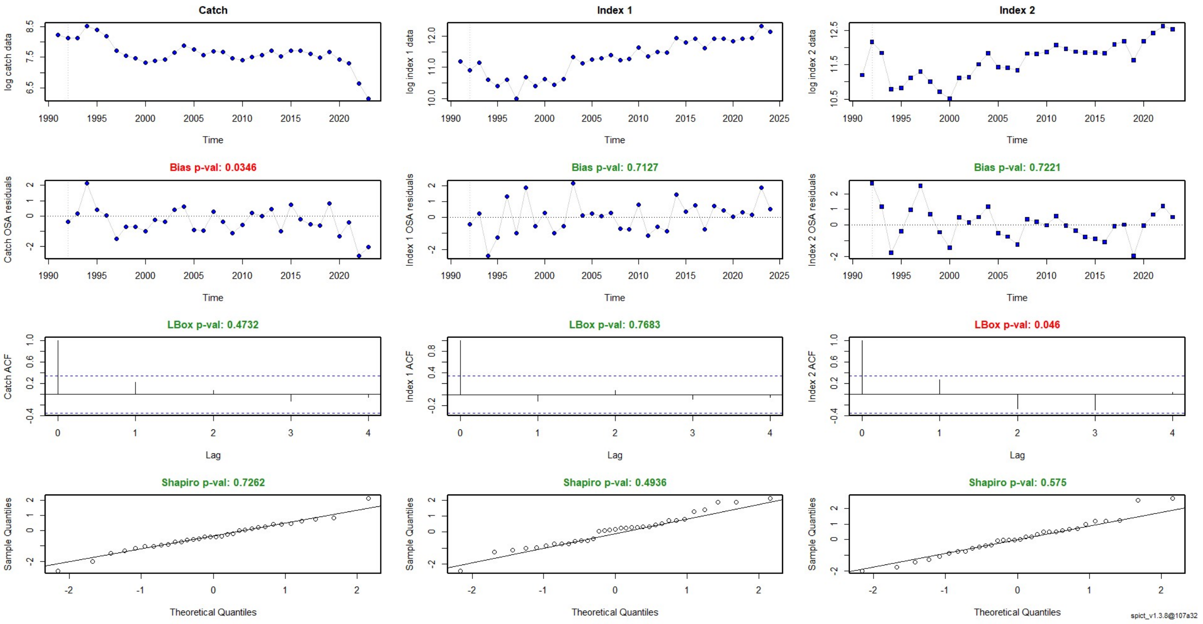


*Figure 21: One-Step-Ahead residuals for observations of Dataset 3*

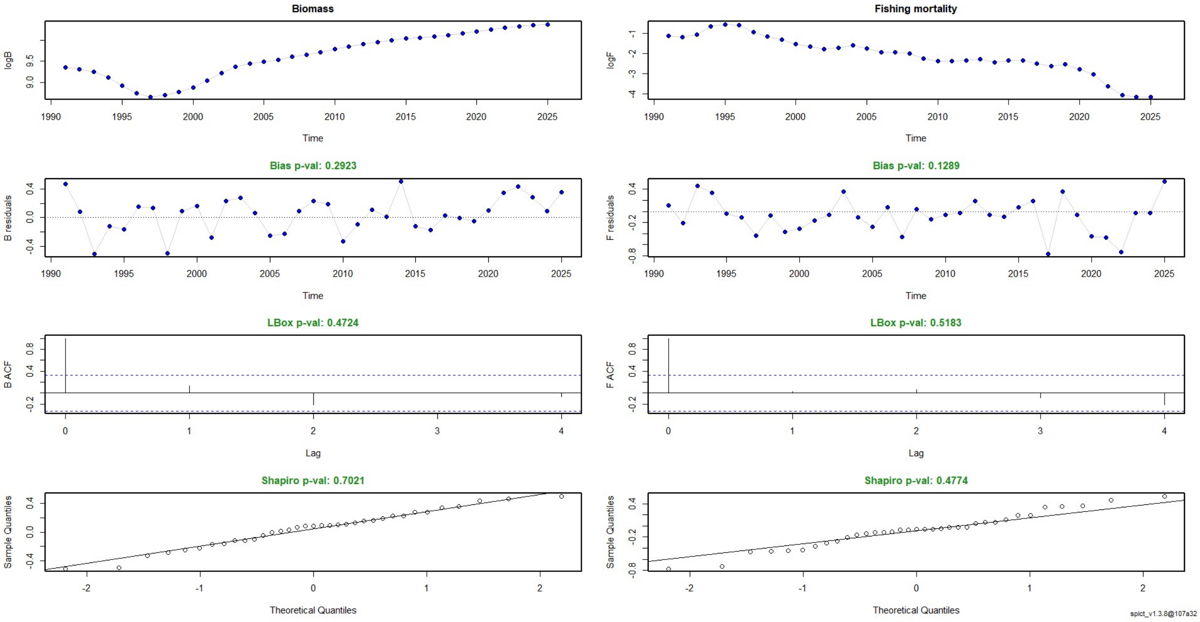


*Figure 22: Process residuals of Dataset 3*

*Table 4: model and parameter estimate of Dataset 3 (estimate, lower limit, upper limit and log-transformed estimate)*

| Dataset3 | **estimate** | **cilow** | **ciupp** | **log.est** |
|---|---|---|---|---|
| **alpha1** | 2.809 | 1.323 | 5.965 | 1.033 |
| **alpha2** | 4.273 | 2.029 | 9.000 | 1.452 |
| **beta** | 0.243 | 0.100 | 0.591 | -1.413 |
| **r** | 0.308 | 0.162 | 0.585 | -1.179 |
| **rc** | 0.464 | 0.302 | 0.712 | -0.768 |
| **rold** | 0.943 | 0.129 | 6.908 | -0.059 |
| **m** | 3281.719 | 2742.341 | 3927.185 | 8.096 |
| **K** | 33614.240 | 20612.220 | 54817.810 | 10.423 |
| **q1** | 5.836 | 3.894 | 8.746 | 1.764 |
| **q2** | 8.405 | 5.564 | 12.696 | 2.129 |
| **n** | 1.326 | 0.728 | 2.417 | 0.282 |
| **sdb** | 0.066 | 0.033 | 0.133 | -2.711 |
| **sdf** | 0.268 | 0.196 | 0.366 | -1.317 |
| **sdi1** | 0.187 | 0.145 | 0.240 | -1.678 |
| **sdi2** | 0.284 | 0.225 | 0.358 | -1.259 |
| **sdc** | 0.065 | 0.031 | 0.137 | -2.730 |

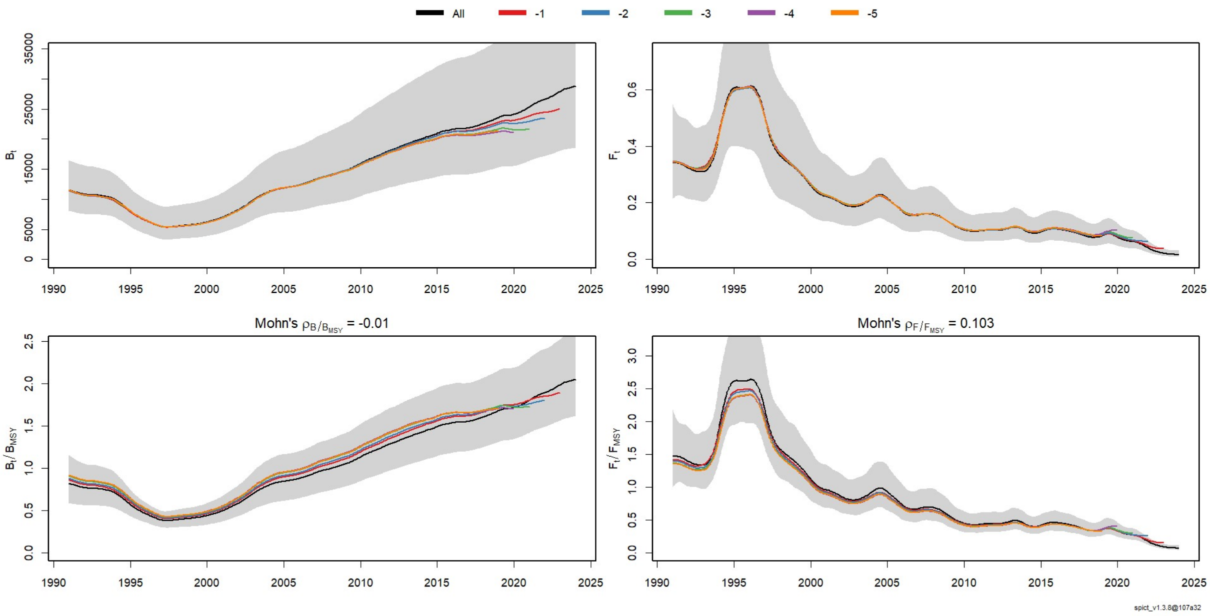


*Figure 23: Retrospective analysis of Dataset 3*

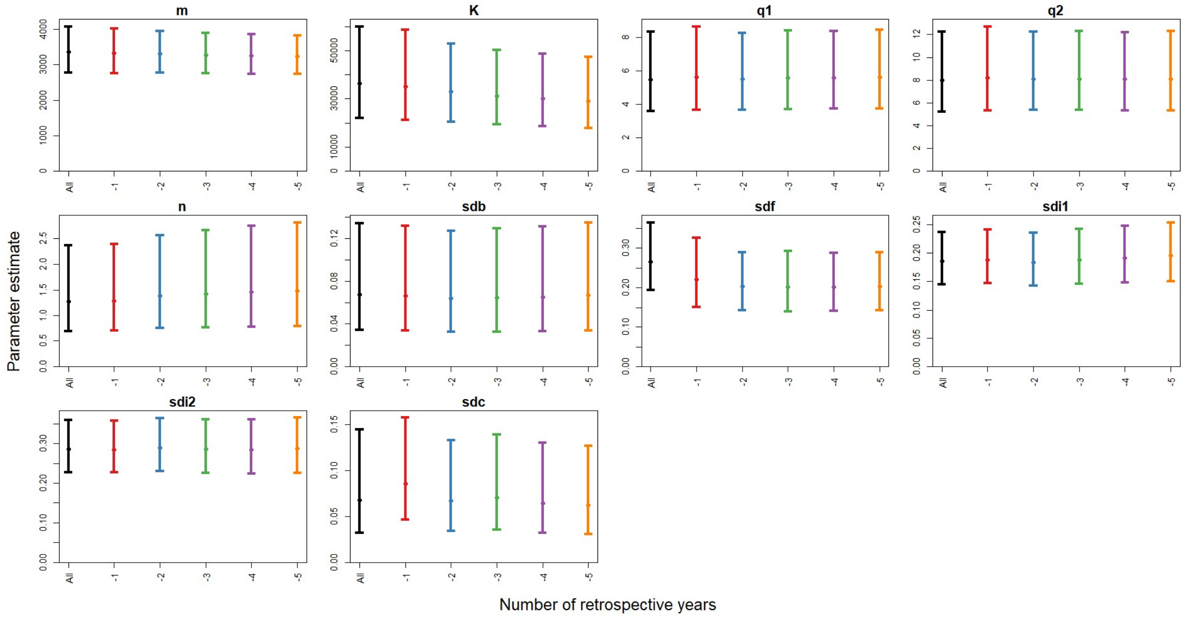


*Figure 24: Retrospective analysis of the model parameter of Dataset 1*

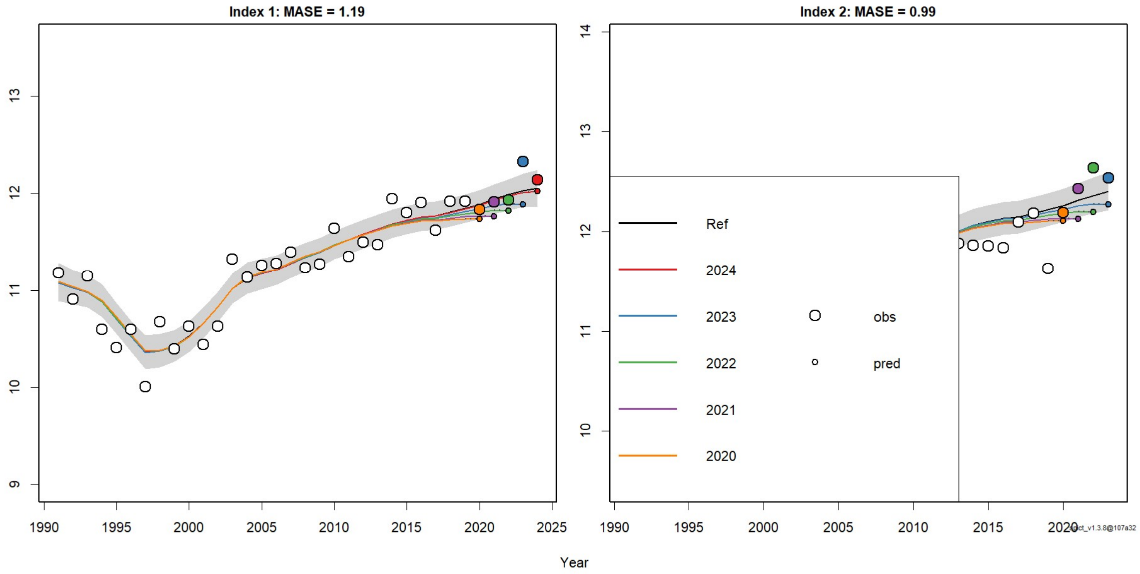
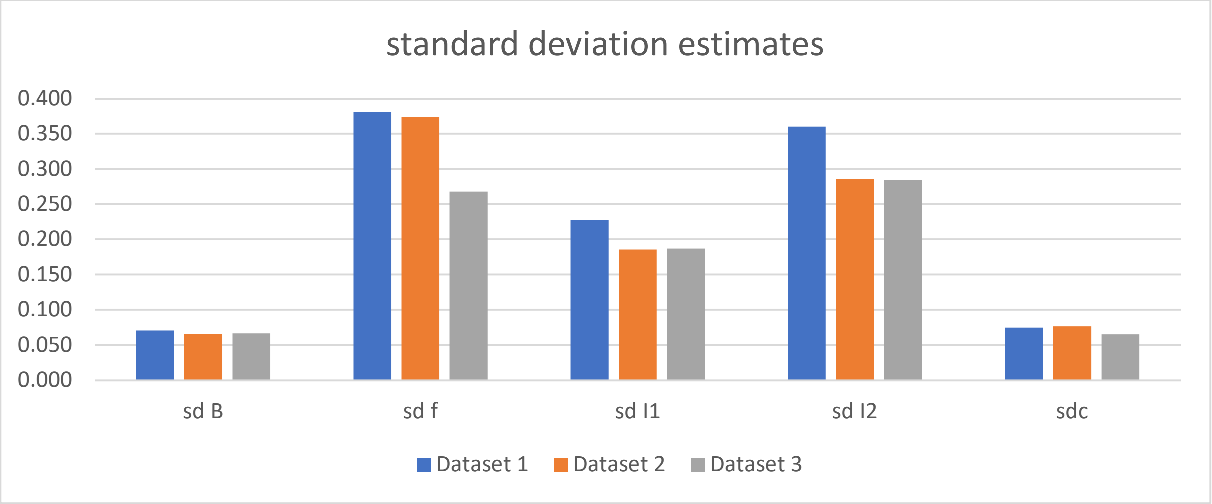
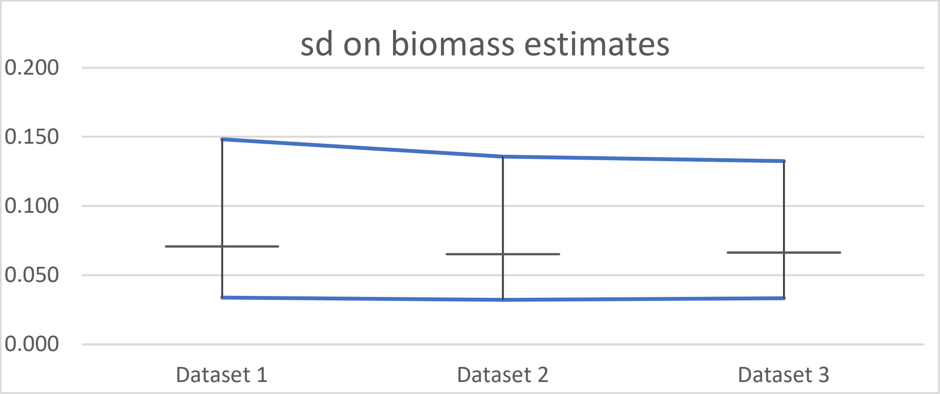
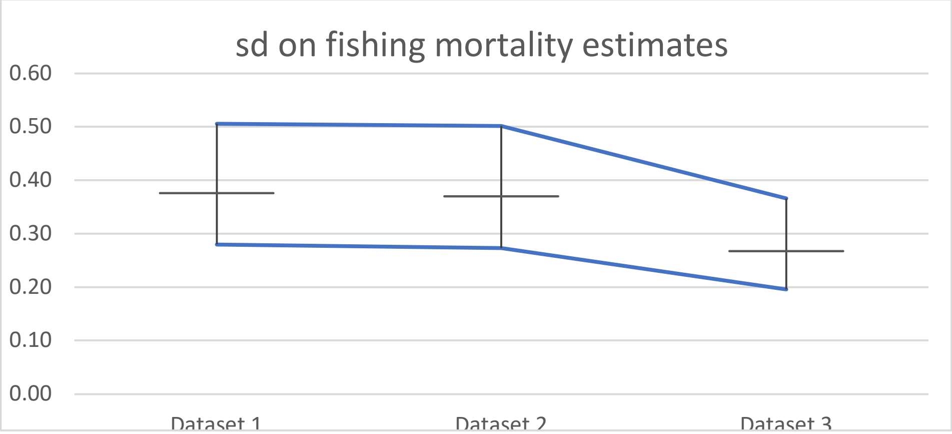


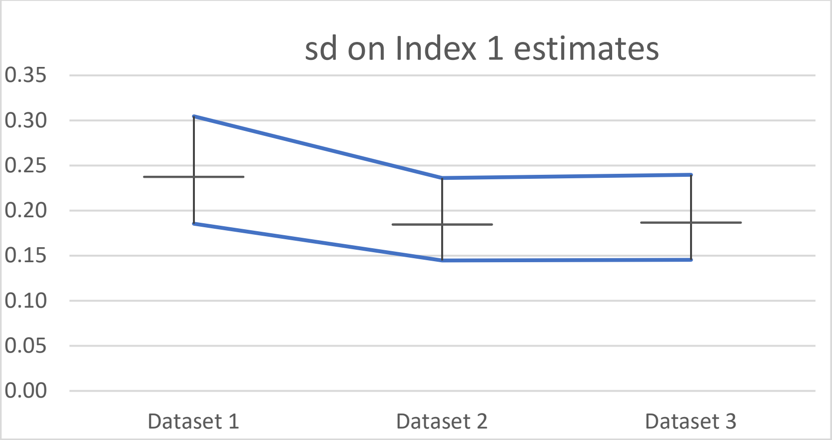
*Figure 25: Hindcast analysis of Dataset 3 ("MASE")*

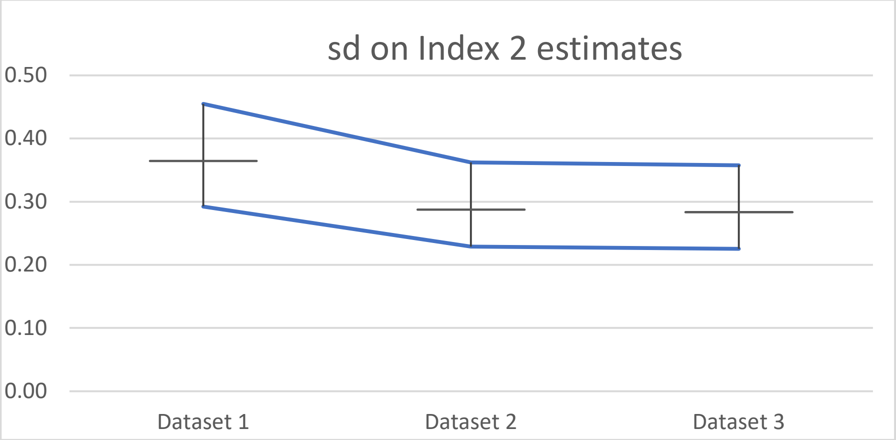
## Model estimates comparisons (data in tables 2, 3 and 4)

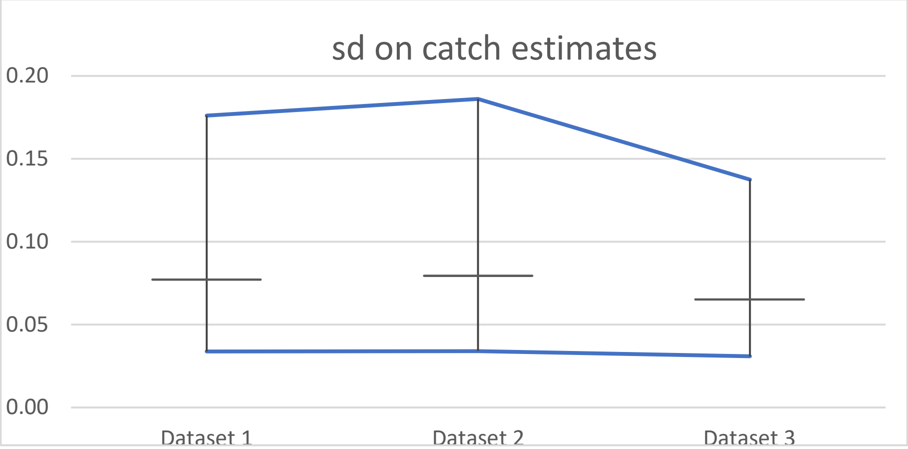







sd on Index 1 estimates
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Dataset 1
Dataset 2
Dataset 3


sd on Index 2 estimates
0.50
0.40
0.30
0.20
0.10
0.00
Dataset 1
Dataset 2
Dataset 3


sd on catch estimates
0.20
0.15
0.10
0.05
0.00
Dataset 1
Dataset 2
Dataset 3

# ANNEX 1.5

## Connectivity of dab stock components in Skagerrak (SD20) and Kattegat (SD21)

### Background

After the re-submission of the working documents on merging the stock components of dab in Kattegat (SD21) into the Baltic Sea stock (SDs 22-32) to SIMWG in June 2024, an additional analysis was requested to confirm whether or not to include Skagerrak (SD20) in the respective stock merging as well.

### Summary

Data from commercial fisheries and surveys from Skagerrak (SD20) confirm that dab is almost exclusively caught in Western Skagerrak (Jammerbay) and to a small amount at the border between Skagerrak and Kattegat. Virtually no dab is present in the central area of Skagerrak. Higher abundances in the surveys are only recognized at the border to Kattegat and to the North Sea around Jammerbay. High numbers of “zero-catches” in both IBTS and BITS hauls indicate low abundance in the covered quarters. The distribution of dab in the Skagerrak indicates only rare, unregular exchange with Kattegat.

Considering the very low index values, no extended GAM model was conducted and no new survey index was calculated. The high number of “zero-catches” would result in an overall lower survey index and increase the uncertainty in the annual average values, which in turn will mask the development of the stock in Kattegat and the Baltic Sea.

In terms of stock boundaries and distribution, the area North of Skagen, the tip of Grenen, acts as a natural barrier between North Sea and Baltic Sea. Therefore, it seems reasonable to keep Skagerrak as part of the North Sea dab stock.

### Connectivity of Skagerrak and Kattegat

*Fishery*

Commercial landings of dab landings can reach several hundred tons per year, originating almost completely (>80% on average, see also Fig. 16 and fisheries text in the dab WD) from the coastal areas west of Skagen and Jammerbay (Table 1).

Some countries are not reporting landings by subdivision, as their fishery does not separate commercially low-valued and non-TAC regulated species in the harbour. No directed fisheries on dab were reported for Skagerrak, misreporting is known to occur (as they are often caught at the border to the North Sea or Kattegat and only landed in SD20, ICES 2023).

*Table 1: overview of official landings of dab in tons from Intercatch.*

| Year | Division 3.a* | Skagerrak (SD20) | Kattegat (SD21) | Baltic Sea |
|---|---|---|---|---|
| **2002** | 0 | 784 | 225 | 715 |
| **2003** | 161 | 552 | 349 | 1233 |
| **2004** | 125 | 491 | 212 | 1894 |
| **2005** | 87 | 585 | 230 | 1495 |
| **2006** | 109 | 489 | 192 | 1228 |
| **2007** | 127 | 436 | 188 | 1504 |
| **2008** | 25 | 380 | 124 | 1648 |
| **2009** | 3 | 407 | 91 | 1268 |
| **2010** | 120 | 388 | 71 | 1041 |
| **2011** | 0 | 508 | 63 | 1268 |
| **2012** | 1 | 632 | 220 | 1285 |
| **2013** | 173 | 852 | 75 | 1384 |
| **2014** | 74 | 538 | 60 | 1269 |
| **2015** | 220 | 717 | 98 | 1268 |
| **2016** | 239 | 659 | 58 | 1358 |
| **2017** | 156 | 572 | 58 | 1227 |
| **2018** | 253 | 539 | 56 | 941 |
| **2019** | 468 | 639 | 45 | 1102 |
| **2020** | 210 | 428 | 35 | 1026 |
| **2021** | 260 | 429 | 26 | 793 |
| **2022** | 65 | 419 | 32 | 256 |
| **2023** |  | 475 | 20 | 169 |

* data were not split into subdivisions and only allocated to the division

The majority of discards are caught in the beam trawl fishery on plaice, on sole, and the otter trawl fishery on plaice and nephrops. The Fishing pattern in terms of gears and target species is more similar to the North Sea, making allocations and extrapolations of fishing activities rather inaccurate.

### *Survey Indices*

Combined cpue data of the North Sea Trawl survey (IBTS) and the Baltic Sea trawl survey (BITS) display low numbers of dab in all covered quarters (Fig. 1 and Fig. 2). While in some years and quarters dab are present in Skagerrak, others show virtually no fish. The largest abundances were registered at the subdivision borders to the North Sea and the Kattegat. However, the majority of hauls conducted during the surveys are usually “zero-hauls”. Adding these into the calculation of the index of the SPiCT assessment (i.e., the “Bergdex”, a GAM modelled survey index after Berg et al. 2014, ICES 2024) will add no supporting information and decrease the index, while possibly adding more uncertainty around the average per year.

Additionally, the area north of Skagen and the tip of Grenen (central Skagerrak) is especially void of dab. The area where the water bodies of North Sea and Baltic Sea are meeting seems to act as a natural border between the stock components. Highest abundances of dab are found in Jammerbay, west of Skagen, yet these accumulations barely reach further than Grenen. Quite the contrary, they regularly connect to the North Sea (see survey maps in Annex folder).

No annual GAM index was calculated for Skagerrak. For comparison, the simple cpue (as individuals caught per hour trawling) from DATRAS was displayed (all maps are included in the respective maps folder on the SIMWG sharepoint.

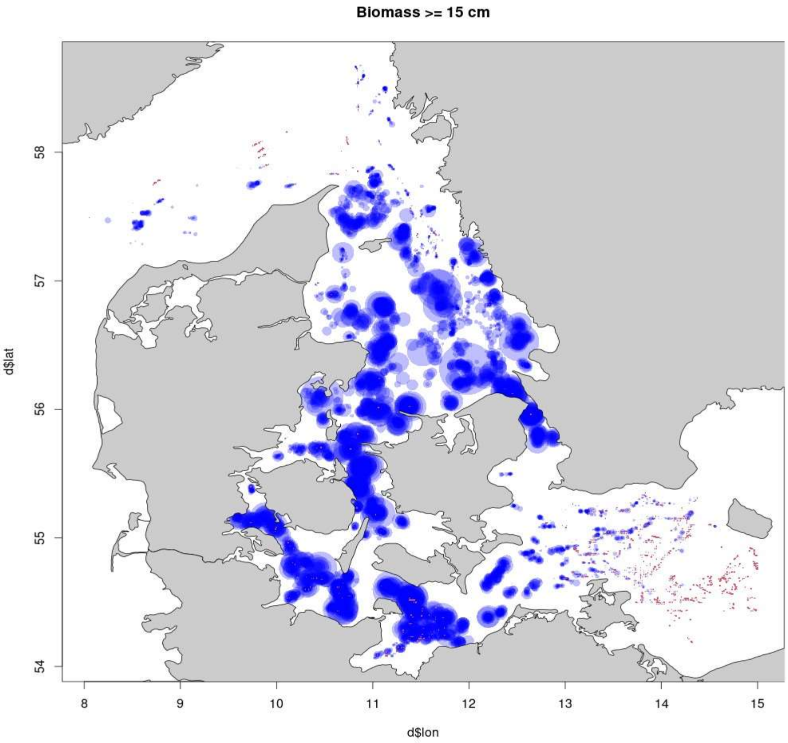


***Figure 1:** average distribution of dab in the Western Baltic (SDs 22-25) and Division 3a (Skagerrak SD20 and Kattegat SD21) derived from a GAM-model approach after Berg et al. 2014) based on survey data (BITS and IBTS).*

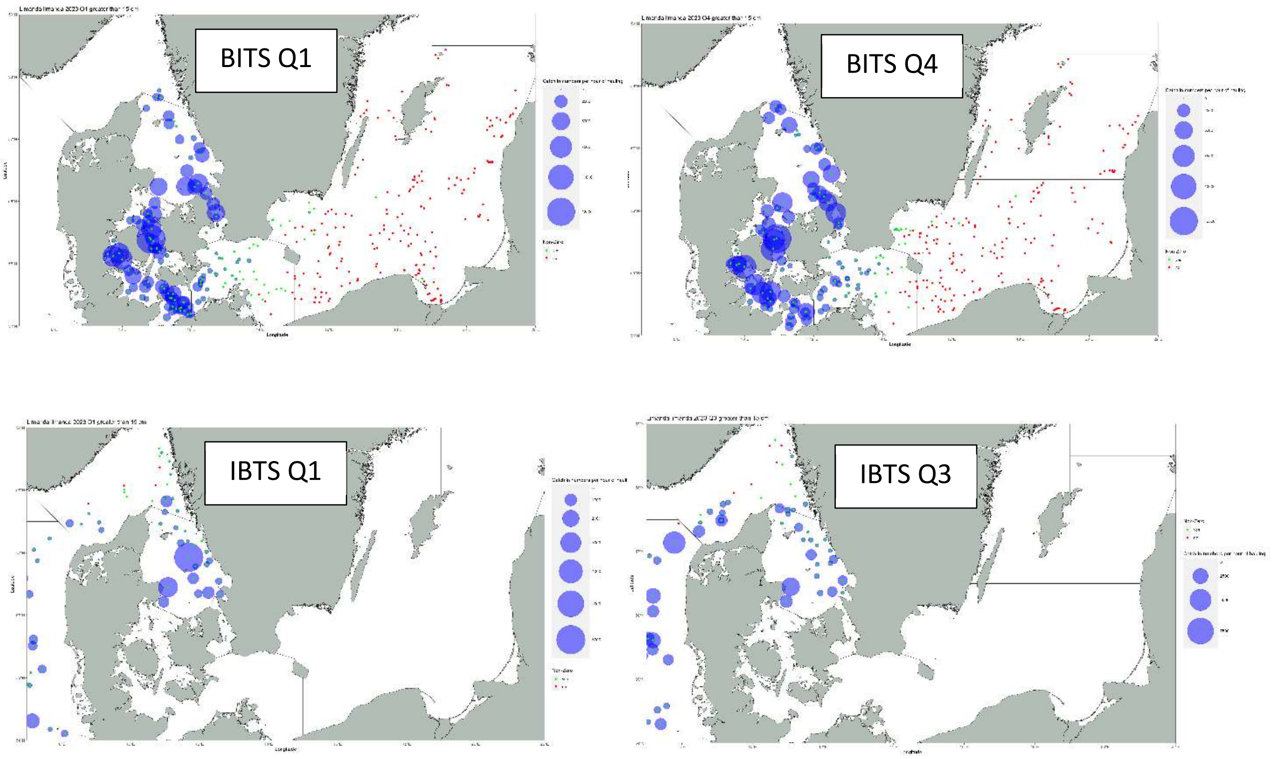


***Figure 2**: average CPUE distribution of dab >15cm in the Baltic Sea (SDs 22-32) and Division 3a (Skagerrak SD20 and Kattegat SD21) in the latest survey year 2023. All other years given in the maps annex.*

*Upper figures: BITS, lower figure: IBTS. Bubble size is calculated per map, based on the maximum cpue. Red dots: zero-catches. Green dots: catches below threshold for bubble plots*

## SPiCT comparisons

Two additional SPICT runs were performed for dab. No new index values were calculated, as the high number of zero-catch hauls would increase uncertainty in the averaged annual index values in both, the Q1 and Q4 index.

The additional runs were performed using landings only, priors and setting were kept identical with the final run of the WDs and the agreed settings used for the assessment (ICES 2024). The base run includes landings of the Baltic Sea and Kattegat, while the second run also included landings from Skagerrak. The third run included all landings of Division 3.a. (i.e., including those, that were submitted without information on the respective subdivision, see Table 1).

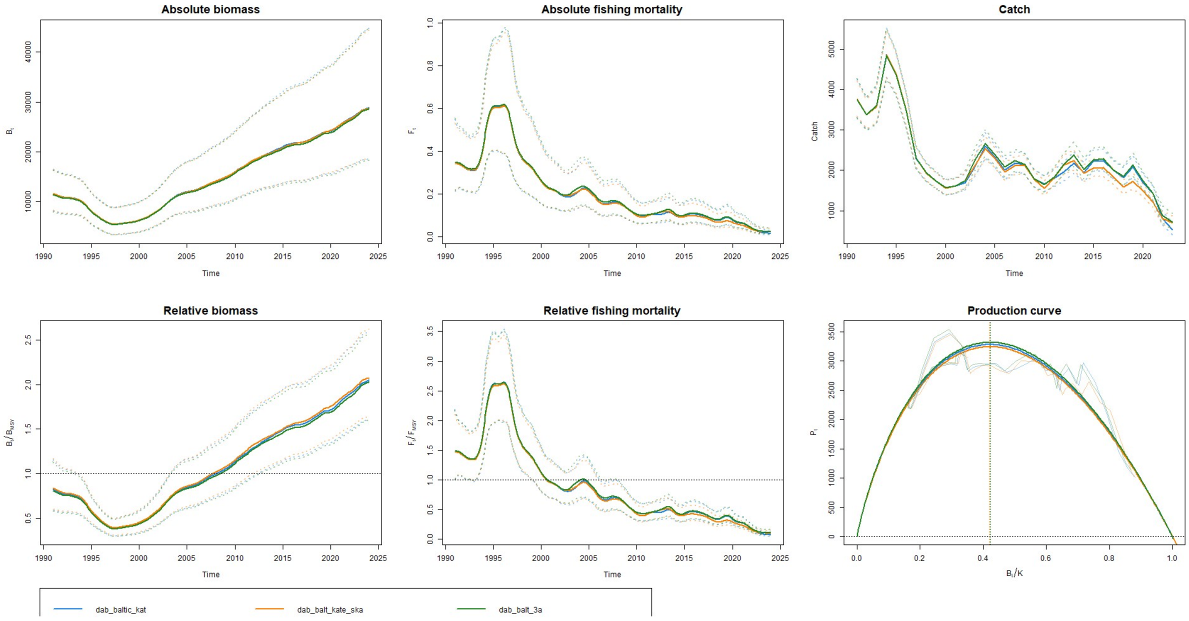


*__Figure 3:__ comparison of the additional SPiCT runs using landings information of SD20. Blue line: landings of Baltic Sea and Kattegat. Green line: landings of Baltic Sea, Kattegat and Skagerrak. Red line: Landings of Baltic Sea and Division 3.a*

Including landings of Skagerrak and Division 3.a did not change the perception of the stock development, both the biomass and fishing mortality did not change.

## References

Berg, C.W., Nielsen, A., Kristensen, K. (2013) Evaluation of alternative age-based methods for estimating relative abundance from survey data in relation to assessment models. Fisheries Research 151, pp. 91-99. https://doi.org/10.1016/j.fishres.2013.10.005

ICES (2023). Working Group on the Assessment of Demersal Stocks in the North Sea and Skagerrak (WGNSSK). ICES Scientific Reports. 5:39. 1072pp.https://doi.org/10.17895/ices.pub.22643143

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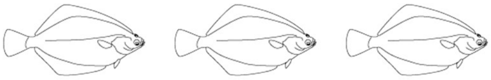
# Annex 6: Working Document on stock structure of flounder

# Review and update of the stock definition of flounder in the Belt Seas and the Sound (fle.27.22-23) and North Sea flounder (fle.27.3a4)



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(Stock coordinator and stock assessor of Western Baltic flounder)

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## Summary

European flounder is an estuarine flatfish species, migrating to higher salinity waters only during the spawning time. Presently, flounder in the Kattegat are considered as part of the North Sea stock. The adjacent flounder stock in the western part of the Baltic Sea covers the areas of the Belt Seas and the Sound (SDs 22-23) and is one of four flounder stocks in the Baltic Sea.

We provide evidence that the management areas may require a change. Distribution maps from scientific surveys strongly suggest that there is no spatio-temporal separation between flounder in Kattegat and the Western Baltic (Belt Seas and the Sound) and that flounder in the Kattegat have negligible links to flounder in the North Sea. The Danish Straits are highly dynamic connecting channels between the southern Kattegat and Kiel and Mecklenburg Bight south of Denmark that make a stock separation between SDs 22-23 and SD21 highly unlikely. Furthermore, no distinct differences were found in biological life history parameters (i.e. maturity and growth) between flounder from SD21 and SDs 22-23. There is no new genetic study available and, given the low commercial importance of flounder in the area, it is unlikely that a genetic study will be conducted in the near future. However,

available genetic studies confirm that all flounder found in Kattegat and the Western Baltic are in fact European flounder *Platichthys flesus*, whereas the Baltic flounder *P. solemdali* only occurs further east. Thus, a stock comprising flounder from the management areas SD 21-23 would realistically reflect the flounder population around the Danish archipelago.

After the last review of the stock-merging document in 2023, additional SPiCT assessment runs have been conducted during the benchmark in 2024, using an improved and extended biomass index and commercial landings from Kattegat. Sensitivity runs showed that the perception of the stock development (e.g., trends in SSB or F) does not change when including Kattegat. Instead, the uncertainty in the model decreased and retrospective analyses (retros and MASE indices) even improved. The results have been presented and discussed during the assessment working groups of the Baltic Sea (WGBFAS) and North Sea – North Atlantic (WGNSSK) and both groups support the change in stock boundaries and forwarded this by a joint recommendation to ICES.

# Proposal

We propose to update the stock definition and boundaries of the flounder stocks in the North Sea and the Belt Seas and the Sound (Western Baltic Sea) by removing Kattegat (Area 9, Subdivision SD 21) from the North Sea stock and adding it to the flounder stock of the Belt Seas and the Sound (SDs 22-23) to realistically reflect the flounder population around the Danish archipelago.

Similar analyses in other flatfish species already resulted in the inclusion of Kattegat to the Western Baltic plaice stock (ple.27.21-23) and of Kattegat and Skagerrak to the Baltic sole stock (sol.27.20-24), making a similar scenario for other flatfishes very likely.

The updated flounder stocks *„fle.27.21-23“* (Western Baltic Sea) and *„fle.27.3an4”* (North Sea) could be part of the benchmark “WKMSYSPICT4” by ICES in late 2024/early 2025 where the settings of the SPiCT model (priors, CVS, etc.) would be checked and approved again by the reviewers.

# Progress since last review

The initial working document was submitted and reviewed in September to October 2023. The reviewer did not see enough evidence to support the proposal of merging the stock component in Kattegat and the Baltic Sea. In early 2024, Western Baltic flounder was part of the WKMSYSPICT3 benchmark and explorative runs with updated stock boundaries (fle21-23) were conducted that actually gave better results than the current stock boundary (SD 2223). The assessment model and biomass index calculation were changed during WKMSYSPICT3.

## Summary of the benchmark WKMSYSPICT3

The flounder stock *fle.27.22-23* was benchmarked in December 2023 (data compilation) and January 2024 by WKMSYSPICT3 (ICES 2024a). The assessment method changed from category 3 to category 2. The stock assessment method was changed from Length-based-Indicators (LBI) to a surplus production model (SPiCT), using a model-based approach to calculate an exploitable biomass index (Berg et al. 2013). The same calculation method is also used for the biomass index of plaice in the Western Baltic and Kattegat (*ple.27.21-23*) and Kattegat cod (*cod.27.21*).
The calculation of the survey index changed from a biomass index to a delta GAM model-based approach after the benchmark in 2024. This was done to account for reduced spatial coverage in earlier

years (before 2000). Before 2000, the BITS survey was not standardized, different survey gears were used, and spatial coverage was incomplete. The model-based approach accounts for different catchability between gears, unsampled areas, and quantifies the increased index uncertainty due to these issues and also combines the index values of the IBTS and BITS surveys in the Kattegat (SD21). The new index calculation also accounts for a substantially decreasing trend in the body condition of flounder since the mid 1990s by using annual length-weight relationships instead of a fixed one.

After reviewing the available data during the data compilation, the benchmark group decided to conduct additional sensitivity analyses using an extended biomass survey (including Kattegat) and additional fisheries data (landings in Kattegat, provided by WGNSSK). Other settings (CVs, catch uncertainty, priors, etc.) were kept identical to the final settings of *fle.27.22-23*.

The two additional SPiCT runs including Kattegat improved the model performance by decreasing uncertainties, and resulted in lower CVs and lower MASE values in the index time series (all details given in the next chapter and Annex 1.3).

Since the ToR of WKMSYSPICT3 did not include stock identity and stock boundary issues, the group forwarded a recommendation to ICES and the relevant stock identification group to consider the inclusion of Kattegat into the Baltic Sea flounder stock covering SDs 22-23.

## SPiCT sensitivity runs

Three different datasets were tested during WKMSYPICT and during the assessment working group WGBFAS (including the latest 2023 data, Table 1). Dataset 1 included only Western Baltic Sea data, whereas Dataset 2 used the combined index of IBTS/BITS of areas SD21-32. Dataset 3 used the combined area index and landings of areas SD21-23 (Kattegat and Western Baltic Sea. The sensitivity analyses were performed to determine the influence of the inclusion of Kattegat to the overall performance of the model.

Table 1. Dataset and overview of SPiCT settings of the sensitivity analyses

| **Setting/Data** | **Dataset 1: Baltic Sea** | **Dataset 2: Baltic Sea & Kattegat-Baltic index** | **Dataset 3: combined Baltic Sea & Kattegat** |
|---|---|---|---|
| **Catch time series** | Baltic Sea<br>(Areas SD22-SD23)<br>landings data 1973–2023 | Baltic Sea<br>(Areas SD22-SD23)<br>landings data 1973–2023 | Baltic and Kattegat<br>(Areas SD21-SD23)<br>landings data 193–2023 |
| **BITS biomass Index quarter 1, "Bergdex"** | Baltic Sea<br>(Areas SD22-23)<br>1991-2023, ≥ 20 cm | Baltic and Kattegat<br>(Areas SD21-SD23),<br>1991-2023, ≥ 20 cm | Baltic and Kattegat<br>(Areas SD21-SD23),<br>1991-2023, ≥ 20 cm |
| **BITS biomass Index quarter 4, "Bergdex"** | Baltic Sea<br>(Areas SD22-23)<br>1991-2023, ≥ 20 cm | Baltic and Kattegat<br>(Areas SD21-SD23),<br>1991-2023, ≥ 20 cm | Baltic and Kattegat<br>(Areas SD21-SD23),<br>1991-2023, ≥ 20 cm |
| | | | |
| **SPiCT settings** | | | |
| - Standard deviation on the indices (sdi) | Log(sdi1)~N(log(index_CV),0.3^2)<br>Log(sdi2)~N(log(index_CV), 0.3^2) | | |

| | |
|---|---|
| - Standard deviation on the indices (observation) (stdevfacI) | indexQ1_CV/mean(indexQ1_CV),<br>indexQ4_CV /mean(indexQ4_CV) |
| - Standard deviation on the catch (observation) (stdevfacC) | For >2021 stdevfacC = 2; |
| - Biomass process noise (logsdb) | Log(0.15)-0.5*0.5^2, 0.5 |
| - Catch observation error (logsdc) | Log(0.1)-0.5*0.5^2, 0.5 |
| - Uncertainty ratio of index (observation) to biomass process (alpha) | Deactivated |
| - Uncertainty ratio of catch (observation) to fishing mortality process (beta) | Deactivated |
| - Shape parameter (n) | Schaefer model, Log(n)~N(log(2),0.001) |
| - Intrinsic growth rate (r) | Log(r)~N(log(0.56), 0.2) |
| - Initial depletion (bkfrac) | None (default) |
| - Discretion time step (dteuler) | 1/16 year (default) |

All three models converged and performed well in sensitivity tests. The general trends in the different parameters (biomass, fishing mortality and catch trends) did not change between the three datasets, i.e., including Kattegat did not change the perception of the stock development (Fig. 1). Datasets 1 and 2 (Western Baltic Sea only and Baltic landings using an extended SD21-23 index) displayed nearly similar outcomes. Dataset 1 displayed higher fishing mortality. Naturally, dataset 3 (including landings form Kattegat) displayed the highest estimated biomass and catches, resulting in a higher production curve estimate.

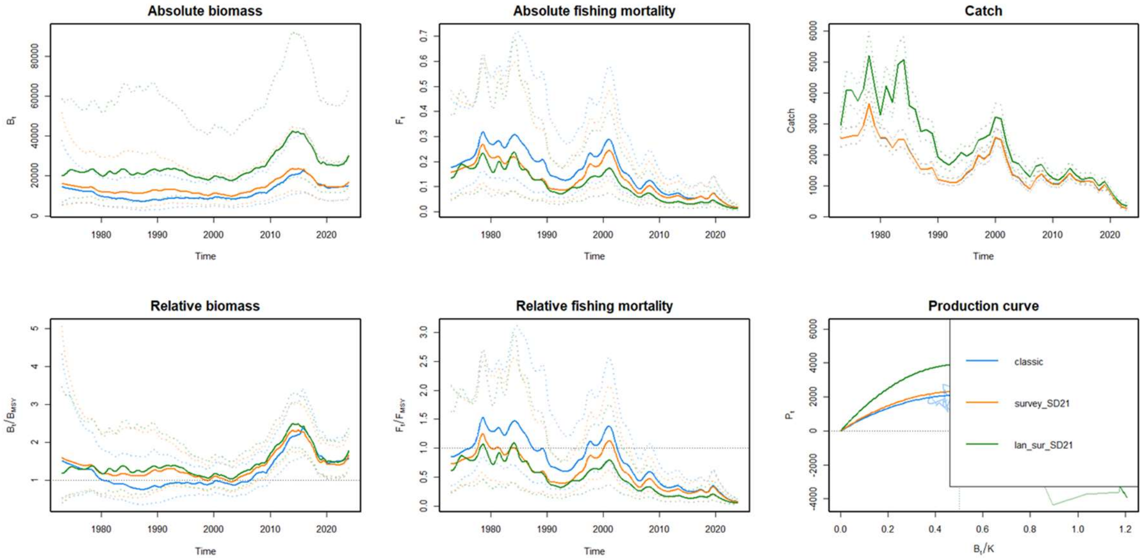
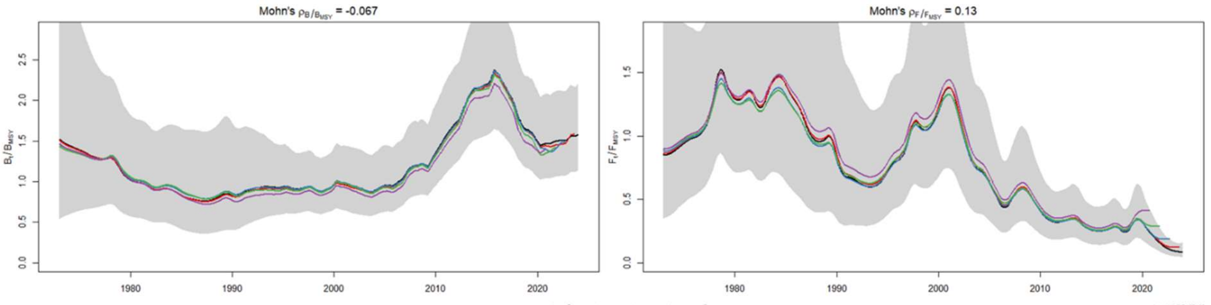


**Figure 1**: Comparison of SPiCT outputs for the sensitivity runs of flounder in SD22-23 (blue line), flounder landings and extended survey index (SD21-23, green line) and the extended flounder stock 21-23 (red line).

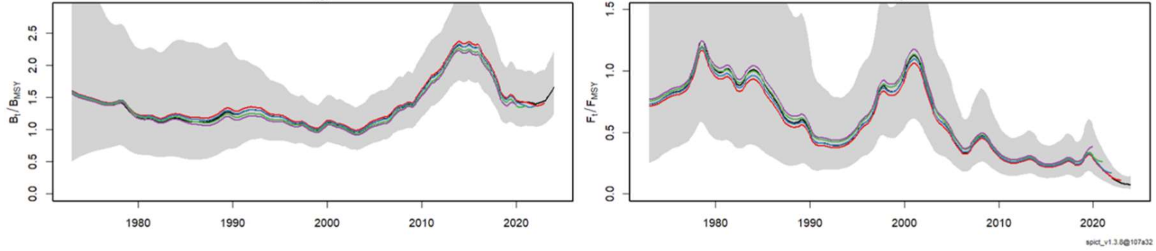
Adding Kattegat data seems to overall stabilize the model estimates and to decrease uncertainties in the estimates (Fig. 2). It is likely that adding Kattegat is explaining changes in biomass in the Western Baltic Sea as larger parts of the stock are found at the border between Kattegat and Belt Sea and thus, migration across the area border is causing artificial biomass loss, if only looking at the Baltic Sea SDs 22-23 alone.

All three models showed good diagnostics. Empirical autocorrelation of the residuals and process residuals for the biomass and fishing mortality were checked in all three datasets. Residuals showed no violations of the model assumptions and improved slightly when Kattegat data were added to the SPiCT model (Annex III).

Retrospective pattern did not change much between datasets, however, the Mohn's Rho values improved (Figure 2).



With SD21 index



With 3a landings

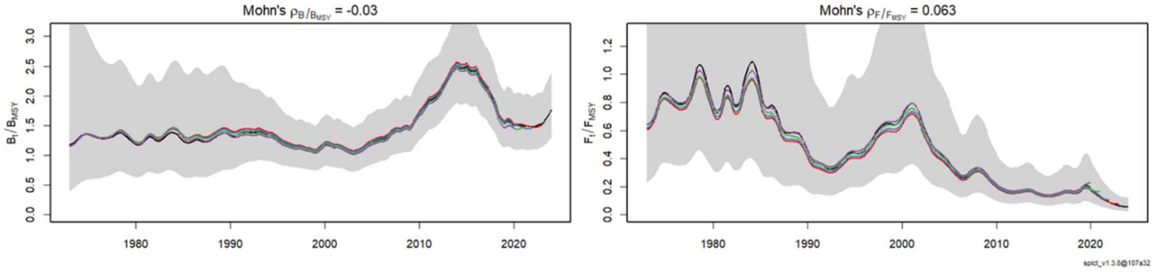
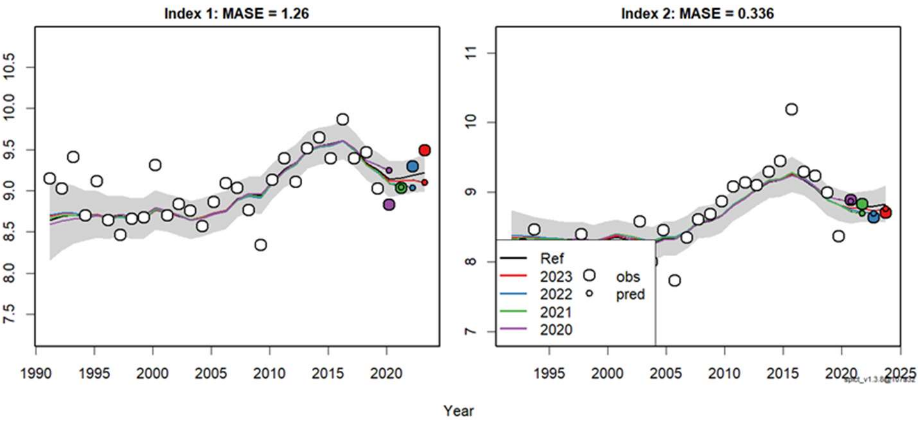
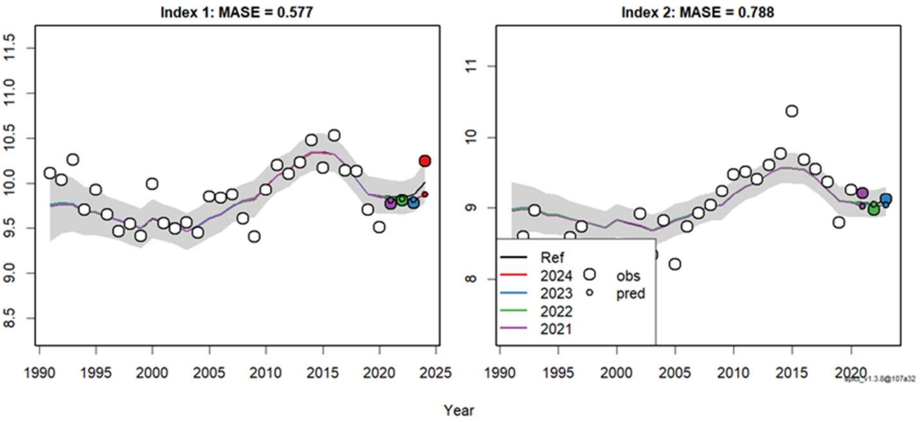


*Figure 2. Comparison of the three SPiCT datasets used in the sensitivity runs of flounder. Upper graphs: Dataset 1, using only Baltic Sea data. Middle graph: Dataset 2, using Western Baltic Sea catches and biomass index covering Kattegat and Baltic Sea. Lower graphs: Dataset 3, using combined catches and index covering Kattegat and Western Baltic Sea.*

A hindcast cross validation analysis ("MASE") was performed on each of the datasets, which indicates if the final assessment model can predict the abundance index more accurately than the naïve predictor. The MASE scores from the hindcast analysis in Dataset 1 were 1.26 and 0.336 for the Q1 and Q4 indices, respectively. There was no retrospective pattern. The scores for the Q1 index improved significantly when adding Kattegat data (Figure 3), decreasing from 1.26 to 0.544. The score in the Q4 index increased, but remained below 1 and was still considered a reliable value with no indication of retrospective patterns.



With SD21 index



With 3a landings

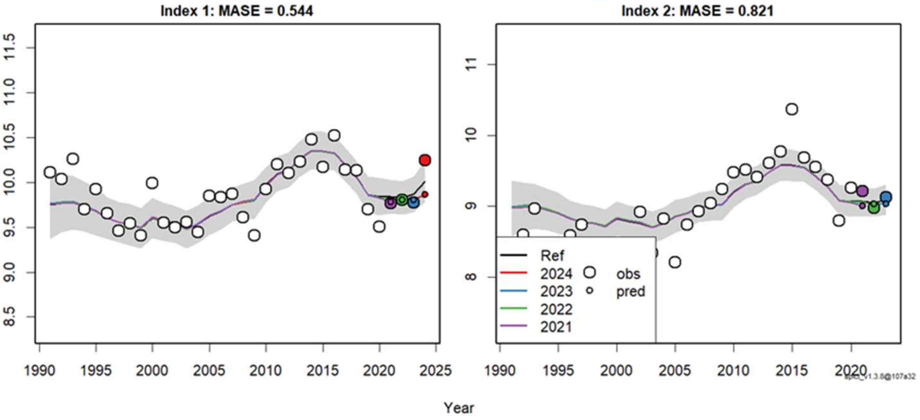


*Figure 3: Hindcast plot of the SPiCT assessments for flounder with MASE predictor. Upper graphs: Dataset 1, using only Baltic Sea data. Middle graphs: Dataset 2, using Western Baltic Sea catches and biomass index covering Kattegat and Baltic Sea. Lower graphs: Dataset 3, using combined catches and index covering Kattegat and Western Baltic Sea*

Overall, the uncertainty in the model parameter estimates decreased (for biomass, fishing mortality, index 2 and catch, respectively) in both the average and the upper and lower limits (Fig. 4). Only the SD of index 2 displayed a slightly higher value when adding the index and catch data of Kattegat flounder.

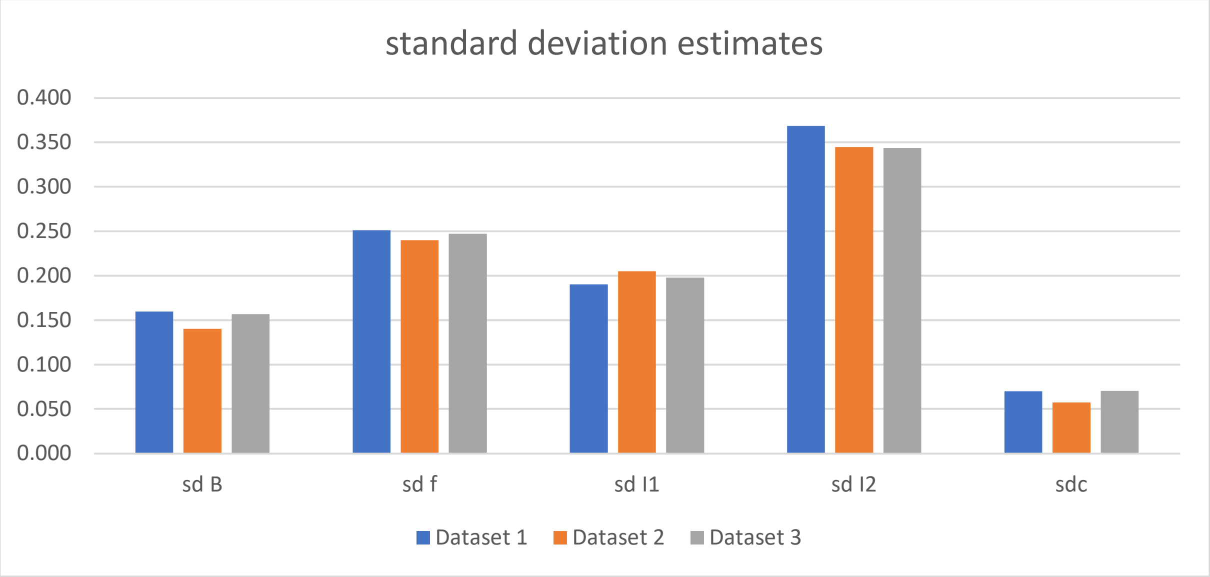


***Figure 4:*** *standard deviation of the estimated parameters for biomass (sd B), fishing mortality(sd F), the two survey indices (sd I1, sd I2) and the catch data (sdc) in the three different SPiCT runs (Dataset 1: Baltic Sea only, Dataset 2: including Kattegat index, Dataset 3: including Kattegat landings and index)*

The uncertainty of estimated parameter might change if the priors and settings of SPiCT are adjusted accordingly to the included Kattegat stock components and further decrease.

All details on the model estimates, variables and priors are given in Annex 1.4

The final SPiCT run was performed on landings only, so the sensitivity runs also only included landings. Discards are known to be substantial in SD21, but are also quite high in SD22 (>40%). SPiCT is yet not able to use datasets that contain landings and catches.

## Assessment working groups WGBFAS and WGNSSK

The results of the benchmark were presented to both relevant working groups for the Baltic Sea (WGBFAS) and North Sea/North Atlantic (WGNSSK).

WGBFAS reviewed the updated SPiCT assessment and the new GAM model biomass index. The index displayed very similar distributions of flounder as seen in the biomass index that was used prior to the benchmark (Annex I). The overall distribution of flounder in Kattegat and Baltic Sea (Figure 5) indicates no spatial differentiation between the areas. The major part of the stock is aggregated in the Belt Sea and Southeastern Kattegat. High abundances of flounder (presumably involving also Baltic Sea flounder *P. solemdali*, see chapters on genetics below) are found in the Eastern Arkona and Bornholm Sea, where some mixing with the flounder stock in SD22-23 may occur.

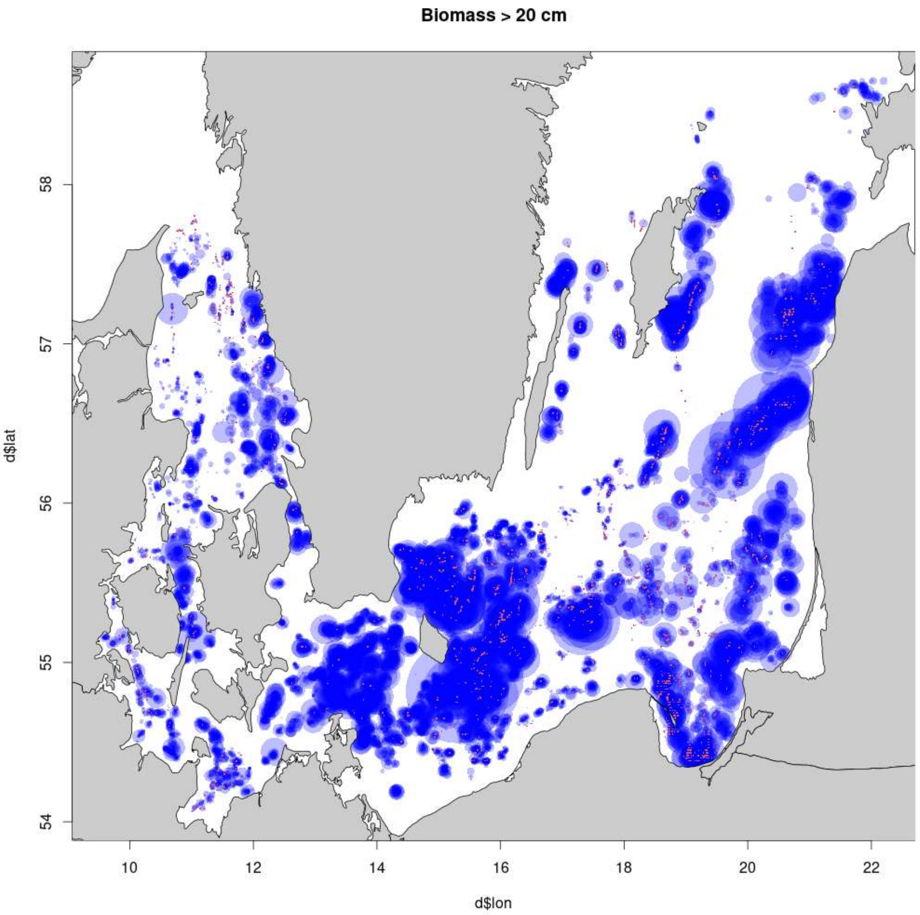


*Figure 5: Overall biomass distribution of flounder in Kattegat and Baltic Sea, derived from IBTS and BITS survey data*

WGBFAS also checked the stock distribution in the two latest surveys in Q4 of 2023 and the (preliminary) Q1 2024 (Figure 6). Small flounder are not representatively sampled by the bottom trawl surveys because juvenile flounder usually are distributed in areas shallower than those covered by the surveys. However, flounder were mainly found in the northern part of the Belt Sea and southern Kattegat in both quarters, however in very low abundances. Adult flounder displayed slightly different abundances between quarters, with higher numbers in Q4 2023 along the German coast in the southern Belt Sea, the Sound and West of Sjælland. Lower abundances were found in Q1 2024 in general, with highest abundances West of Sjælland and the northern part of the Sound.

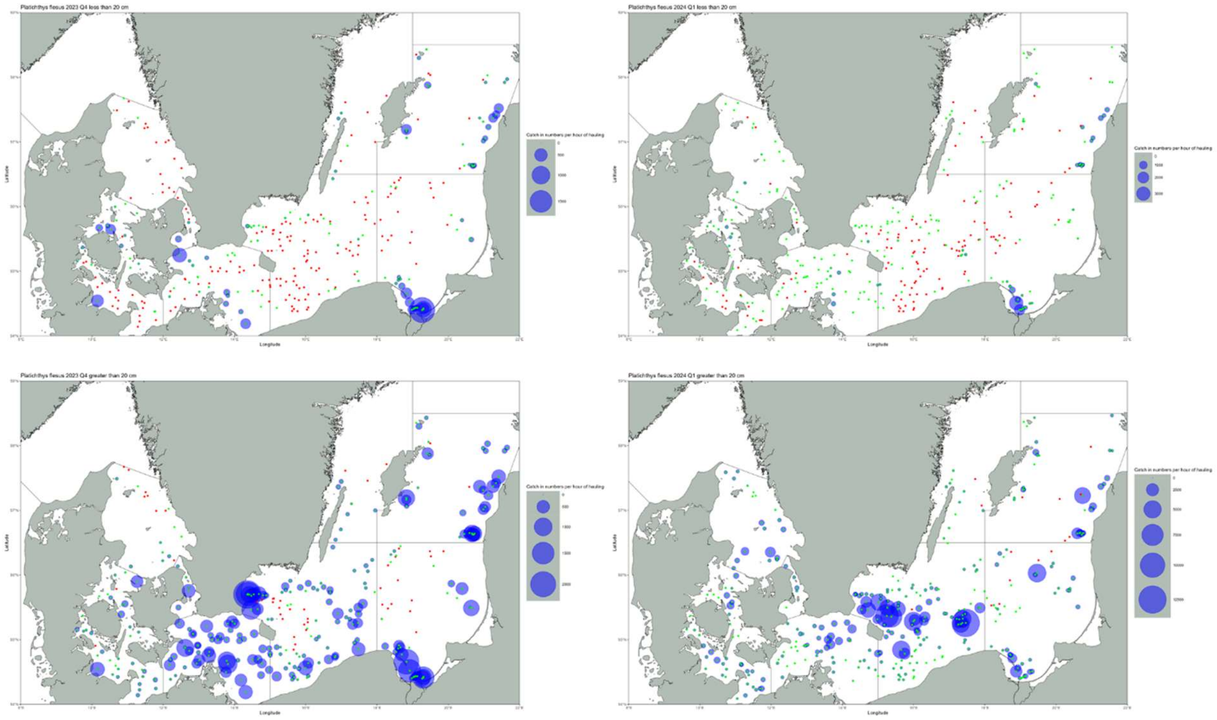


***Figure 6:*** *Most recent abundance distribution of flounder in scientific trawl surveys. Upper graphs: Abundance of flounder <20cm TL in surveys of Q4 2023 (left) and Q1 2024 (preliminary, right). Lower graphs: Abundance of adult flounder >20cm TL in scientific surveys in surveys of Q4 2023 (left) and Q1 2024 (preliminary, right).*

In a joint meeting, WGBFAS and WGNSSK discussed the merging of Kattegat into the Baltic Sea stock after reviewing the latest biomass indices, survey distributions and the SPiCT sensitivity runs.

WGNSSK agrees that flounder in the Kattegat is most likely part of the Western Baltic Sea stock and strongly supports adding the stock component to the Western Baltic Sea stock. Furthermore, WGNSSK confirmed that the stock component of flounder in Kattegat is of such minor importance compared to the North Sea stock, that commercial sampling data and survey indices from that area are usually not even used in the assessment. Instead, settings and data extrapolations from the North Sea stock are used in the process. Thus, adding Kattegat flounder to the Baltic Sea would also increase the data quality of that area, as extrapolations and estimation will come from the well-sampled Belt Sea, which is much more accurate than using North Sea data.

The Baltic assessment working group WGBFAS is willing to take up the area and update the respective assessments and get it reviewed at the earliest possibility.

Both assessment working groups agreed on a joint recommendation to merge SD21 into the Baltic Sea stock, which will be part of the 2024 meeting reports (ICES 2024b).

Furthermore, WKMSYSPICT already signalled the willingness to review and approve an updated SPiCT assessment for next year's assessment working groups and also contributed a recommendation in their 2024 report to support the change in stock boundaries.

# Current Status

The current status section has only slightly been updated compared to the first WD of 2023. The stock assessment description was updated and the maps slightly changed.

## North Sea

Flounder and dab in the North Sea have been assessed under a shared TAC until 2017. Since 2018 flounder in the North Sea is assessed as one stock (*fle.27.3a4*), covering Subarea 4 (North Sea) and Division 3.a. (Skagerrak and Kattegat) and is no longer subject to a TAC. Instead, a catch advice is given as long as dab and flounder remain largely bycatch species, with the main fleets catching dab and flounder continuing to fish the target species (plaice and sole) sustainably within the $F_{MSY}$ ranges provided by ICES. If this situation changes, or flounder is no longer within safe biological limits, this advice would need to be reconsidered (ICES 2023a).

Catch advice is given for two years and was last given in 2023 (for 2024 and 2025, ICES 2023a). Flounder is mainly a bycatch species in the mixed demersal fisheries targeting North Sea plaice and sole, with a variable medium discard rate (12-49% on average, included in the assessment since 2002). Flounder is of relatively little commercial importance in the North Sea and the Skagerrak/Kattegat. Therefore, there are uncertainties in the landings data with misreporting in previous years. Discard estimations are uncertain due to the high variability between years and low priority in former catch sampling programs. Landings have decreased in the 2010s from around 3-4000t/year to around 1500t/year. Subarea 4 provides >90% of landings (ICES 2023a).

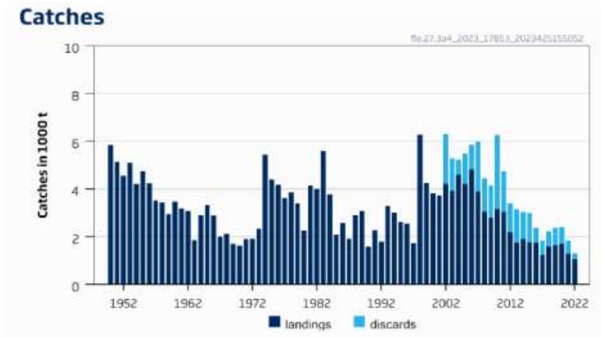


**Figure 7:** Official landings (1950–2001) and ICES estimates of landings and discards (2002–2021).

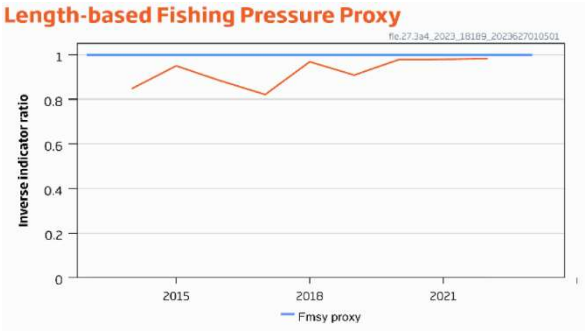


**Figure 8:** Index ratio $L_{mean}$ /$L_{F=M}$ from the length-based indicator method (LBI; ICES, 2023b). The exploitation status is below the $F_{MSY}$ proxy (dotted line) when the inverted index ratio value is lower than one.

The stock is categorized as "data limited", following the ICES framework for category 3 stocks (ICES, 2023a). The most recent advice is based on the *chr* rule to provide MSY advice (ICES, 2023b). A survey combined biomass index is used as an indicator of stock development. An additional index ratio $L_{mean}$ /$L_{F=M}$ from the length-based indicator method (LBI; ICES, 2023a) is used for the evaluation of the exploitation status.

## Baltic Sea

Flounder is the most widely distributed among all flatfish species in the Baltic Sea, occurring virtually in the entire Baltic Sea. The flounder stocks in the Baltic were benchmarked in 2014. As a result, four different stocks of flounder were identified (WKBALFLAT, ICES 2014). Recently, a new flounder species was identified (Momigliano et al. 2018, Jokinen et al., 2019), characterised by demersal spawning, which is an adaptation to the low salinities in the north-eastern Baltic Sea. The two described flounder species (pelagic spawning European flounder *Platichthys flesus* and demersal spawning Baltic flounder *Platichthys solemdali*) are sympatric and are considered to mix in SDs 24-32 with an increasing share of *P. solemdali* east- and northwards (Kuciński et al., 2022, Table 2).

Currently these two Baltic flounder species can be separated only through genetic analysis, therefore at present there is no easy and inexpensive way to separate these species in commercial catches or in BITS survey trawls. Therefore, it is acknowledged that there are two different flounder species in the Baltic, and in all management units, except for SDs 22 and 23 (Table 2), there is a mix of these two species, however, no separation between species is attempted during the assessment process.

The flounder stock in the Belt Sea and the Sounds (SDs 22 and 23) consists only of European flounder (*P. flesus*) and even though there is no physical connection between SD22 and SD23, flounder in these areas are assumed to be connected through the western part of SD24 (i.e., 12°-13°E of SD24, west of Darss Sill and Hanö Bight). This connection and the presence of flounder from SDs 22 and 23 in western SD24 is, however, masked by the presence of the much larger flounder stock in SD24-25. Additionally, survey data suggest a high connectivity with Kattegat, assuming it to be part of the stock (ICES 2023b). As the Darss sill in the western part of the Arkona Sea is the only physical barrier that would restrict flounder movements in SD24, it is likely that a large part of flounder in area SD24.1 (i.e., the western part of the Arkona basin between 12° and 13°E) is also part of the stock fle.27.22-23. An inclusion of this area into the Western Baltic flounder stock could be considered. A similar approach has been taken in the separation between Western Baltic cod and Eastern Baltic cod in SD 24 (ICES 2015, 2019).

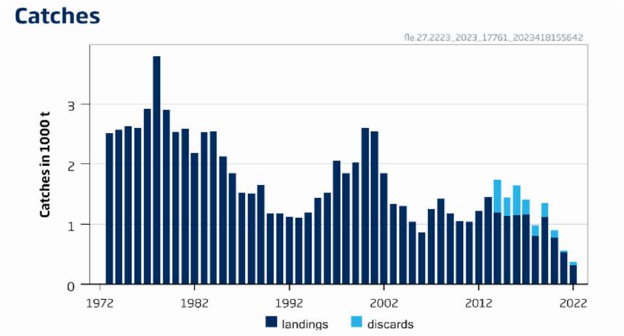


**Figure 9:** Official landings (1972–2001) and ICES estimates of landings and discards (2006–2022).

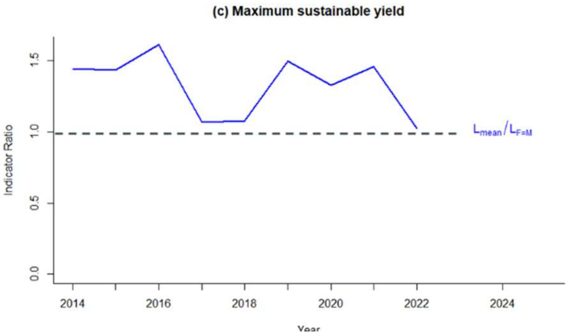


**Figure 10:** Index ratio $L_{mean}$ /$L_{F=M}$ ratio from the length-based indicator method (LBI; ICES, 2023c) The exploitation status is below the $F_{MSY}$ proxy (dotted line) when the index ratio value is higher than one.

The largest and most productive flounder stock of Europe is found in the southern Baltic (SD24-25). Fle.27.22-23 is the second largest flounder stock in the Baltic Sea. Flounder is mainly caught in the area of the Belt Sea (SD 22). The Sound (SD 23) is of minor importance for the contribution to the total landings. Commercial landings have been around 2000 tons/year since 1972. However, landings decreased to below 1000 tons in the early 1990s and again in the early 2000s and remained at around 1000 tons/year since then. Discards of flounder are recorded since 2014 and vary greatly with ratios around 20–50% of the total catch of vessels using active gears (e.g., otter trawls). Passive fishing gears have lower discards, varying between 10 to 20% of the total catch (ICES 2023d).

The flounder stock in SD 22–23 is categorized as a data-limited-stock (DLS). Especially sampling data from the beginning of the time-period (2000–2006) are considered poor with a low sampling coverage in time and space. More than half of the strata (landings and discards) from that period had to be filled with borrowed data (extrapolated length-distributions and mean weights per length-class). It is assumed that an analytical assessment using this data matrix prior to 2007 can only have the level of an exploratory assessment, but is recommended for a reasonable advice.

The update on the stock status is based on the data-limited approach of ICES. Catch advice is given since 2016. Recently, ICES is only requested to give stock status updates every three years. The last stock update was given in 2022 (for 2023 and 2024, ICES, 2022c).

The stock was reviewed and upgraded to a category 2 SPICT model after the benchmark in 2024 (ICES, 2024a). Flounder catches in the Baltic Sea are not currently regulated by a TAC.

The stochastic production model in continuous time (SPiCT) was applied to the flounder stock fle.27.22-23. Input data are commercial landings from 1973 to present and the BITS delta-GAM model index Q1 and Q4 (Fig. 11). No reference points are defined for this stock in terms of absolute values. The SPiCT-estimated values of the ratios F/$F_{MSY}$ and B/$B_{MSY}$ are used to estimate stock status relative to the MSY reference points and are used to estimate catch advice and catch scenarios.

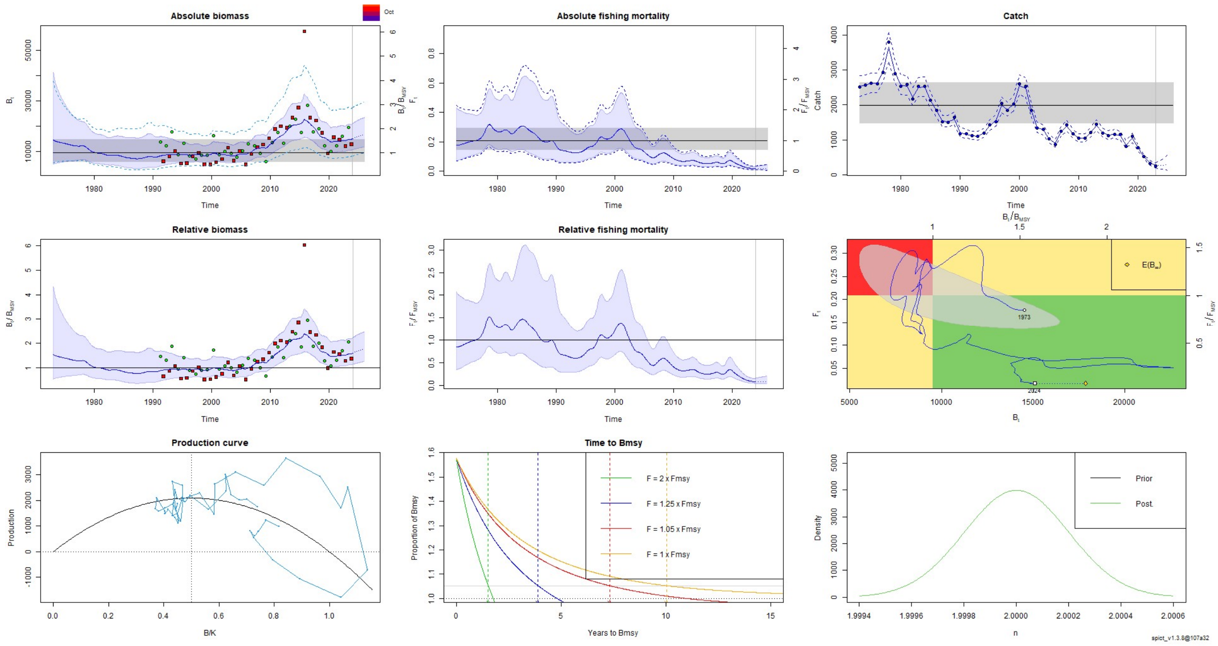


*Figure 11: Current SPiCT assessment results for fle in SD22-23 (ICES 2024b).*

A short-term forecast was conducted assuming Fsq. The current time-series of commercial and survey data combined with continuously increasing data quality (in terms of spatio-temporal sampling coverage, number of samples and error/consistency checks) justifies the use of this model as basis for the advice and to give stock status updates. In addition, trends by SPiCT align with those of the previous LBI and survey (BITS) biomass indices.

## Spatio-temporal distribution

### Surveys

The data of scientific trawl surveys were used to generate distribution maps and overviews for flounder in the north-eastern North Sea, Skagerrak and Kattegat, as well as the western Baltic Sea. The aim was to investigate spatio-temporal distribution patterns and changes since the start of the time series and between seasons.

The International Bottom Trawl Survey (IBTS) covers the North Sea (Subarea 4) and the Transition area (Division 3.a. including the Skagerrak 3.a.20 and Kattegat 3.a.21) and is conducted two times per year in Quarter 1 and 3 (Q1, Q3). The Baltic International Trawl Survey (BITS) covering the entire Baltic Sea and Kattegat (3.a.21) and is conducted also twice per year, in Q1 and Q4. Both surveys are conducted using the same sampling protocols and data are publicly available at the International Survey database DATRAS, hosted by ICES (https://datras.ices.dk).

Survey indices of exploitable stock biomass (20 cm+) are calculated using the methodology similar to what is described in Berg and Kristensen (2014), that is, a Delta-Lognormal model which consists of a binomial presence/absence model and a lognormal model for strictly positive responses. Once the parameters in the model are estimated, a standardized survey index is obtained by predicting and adding up the abundances in a fine meshed grid of points that is the same in all years. This can be thought of as performing a virtual experiment where the experimental conditions such as the haul positions, gear type etc. are exactly the same in each year.

The observed exploitable stock biomass is calculated from observed numbers-at-length and a length-weight model with time-varying coefficients (because there have been significant changes in the LW relationship over time for flounder).

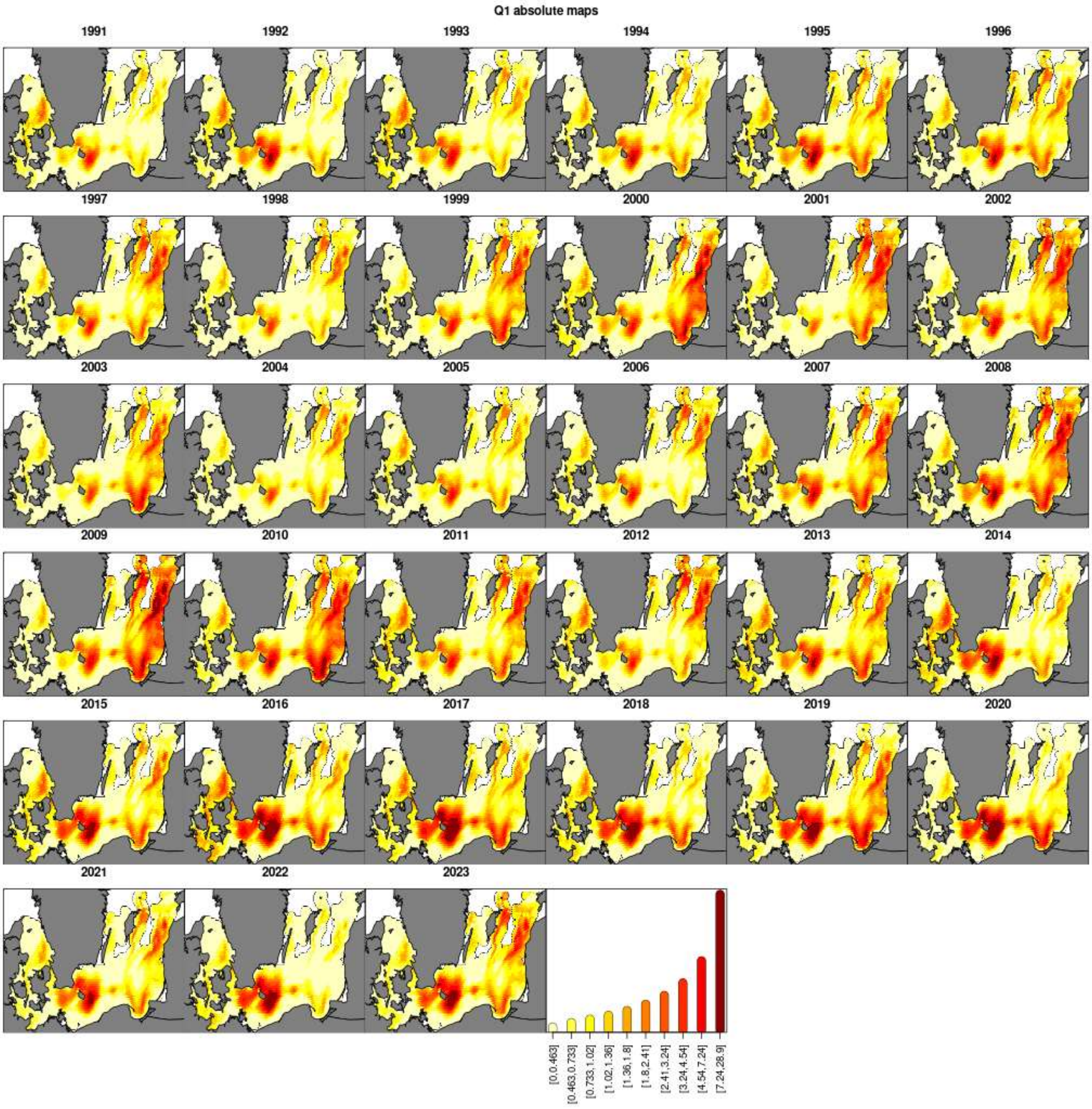


**Figure 12:** Survey-based biomass distribution of flounder in the Baltic Sea (SDs 22-25, BITS) in Q1, based on a GAM model approach (Berg et al. 2014)

When only considering the western Baltic flounder stock in SDs 22 and 23, the main distribution of flounder is located in the northern part of the Belt Sea and the southern Kattegat around Sjælland (Figure 12, Annex 1.1). In most years, a clear link with continuous higher densities in SDs 21, 22 and 23 is apparent, whereas flounder are rare in the Skagerrak and the North Sea with a CPUE of 0 in central Skagerrak. The distribution shifts between years, moving from central to Southern Kattegat in the mid 1990’s and in the mid 2000’s. Only very few flounder were found in the region between Skagerrak and Kattegat (Figure 12, Annex 1.1). Hence, while flounder densities are low in the North Sea and Skagerrak, higher densities characterize the Danish archipelago, ranging from the Kattegat to the southern Belt Sea.

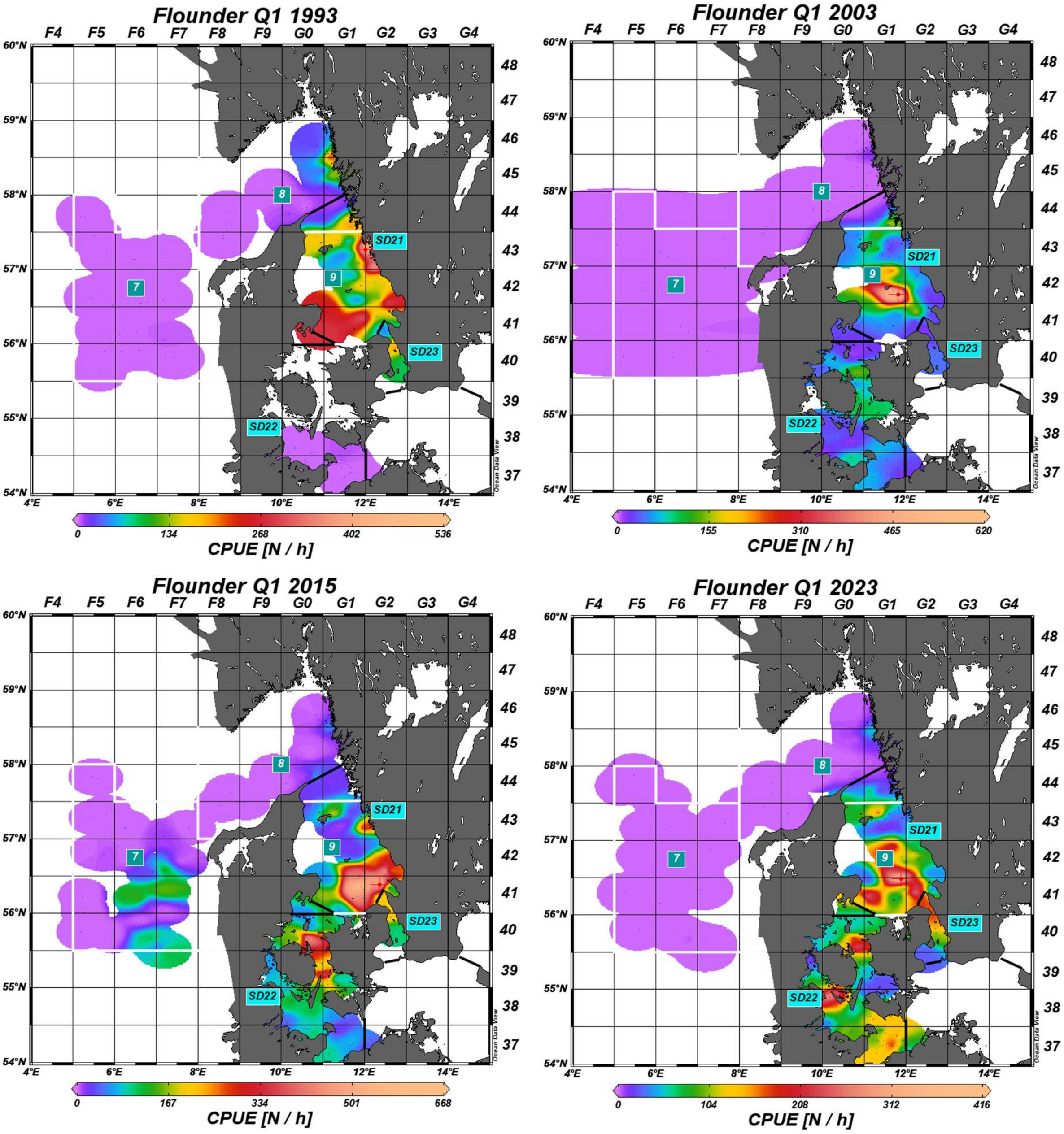


**Figure 13:** Survey-based CPUE distribution of flounder in North Sea (Areas 7,8,9, IBTS) and western Baltic Sea (SDs 22-23, BITS) in Q1 surveys of selected years. Maps from all years are shown in Annex 1.1.

The Q4 BITS and IBTS surveys showed a similar distribution with high accumulations of flounder around Sjælland, connecting all three areas (SD21, 22 and 23) with each other (Figure 14, Annex 1.2). IBTS has only been conducted in Q4 until 1996, but also displayed similarly low abundances of flounder in Skagerrak as seen in Q1. The modelled distribution is assuming large quantities of flounder along the coast of Latvia and Lithuania which is weakening the signals from the Western and Central Baltic.

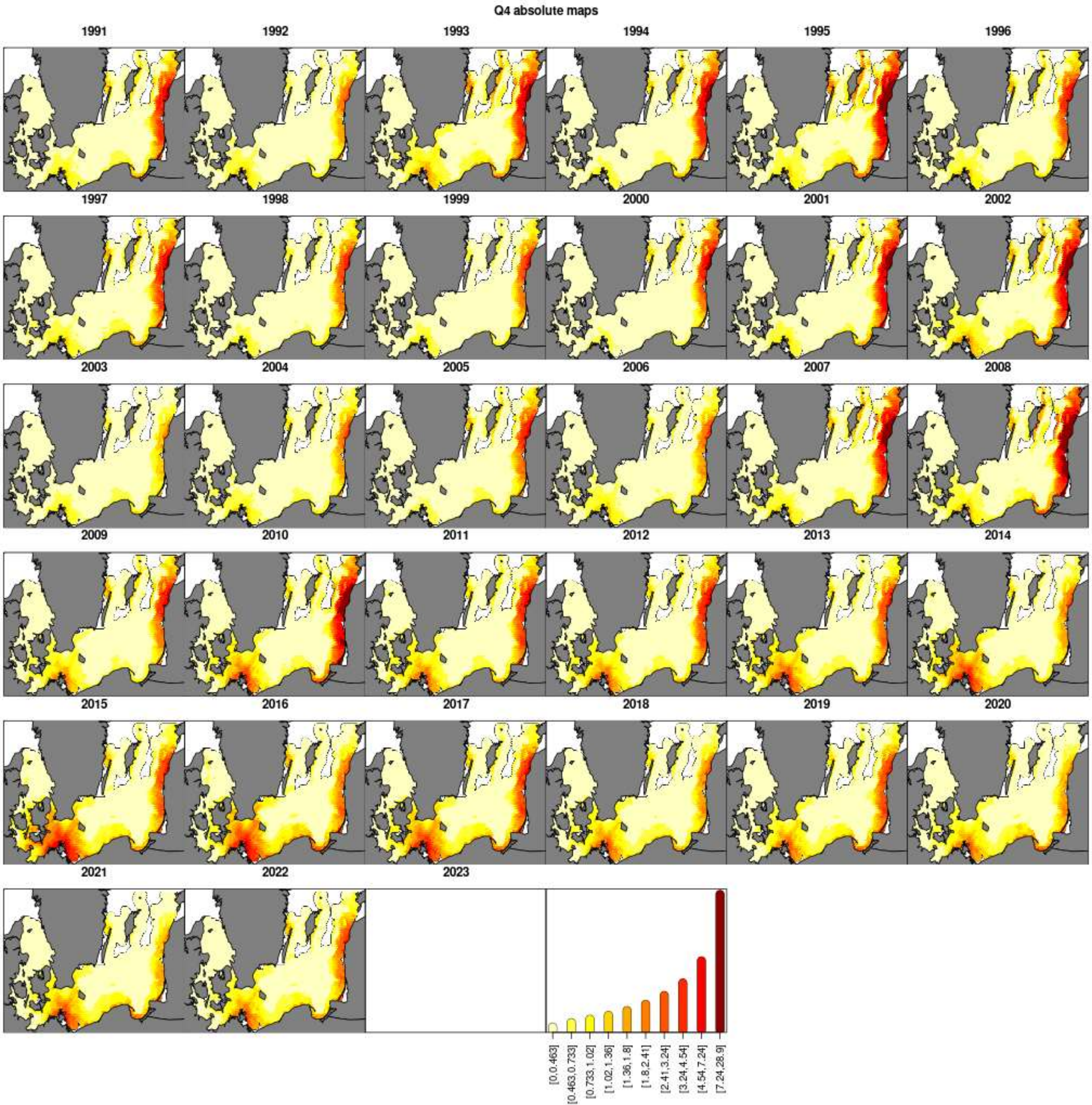


**Figure 14:** Survey-based CPUE distribution of flounder in North Sea (Areas 7,8,9, IBTS) and Baltic Sea (SDs 22-23, BITS) in Q4 surveys from a GAM-modelled approach (Berg aet al. 2014). Maps from all years are shown in Annex 1.2.

Likewise, the Q3 IBTS index of flounder displayed a similar distribution pattern (Figure 14) with high abundances of flounder in the southern Kattegat. The spatial connectivity between North Sea and Kattegat via the Skagerrak is as low as seen in Q1 and Q4 surveys. Only a small aggregation of flounder was present along the northern Danish coast. This aggregation was fished and landed by commercial fisheries, whereas almost no landings (<1t/year per ICES statistical rectangle) were reported from the rest of the Skagerrak area.

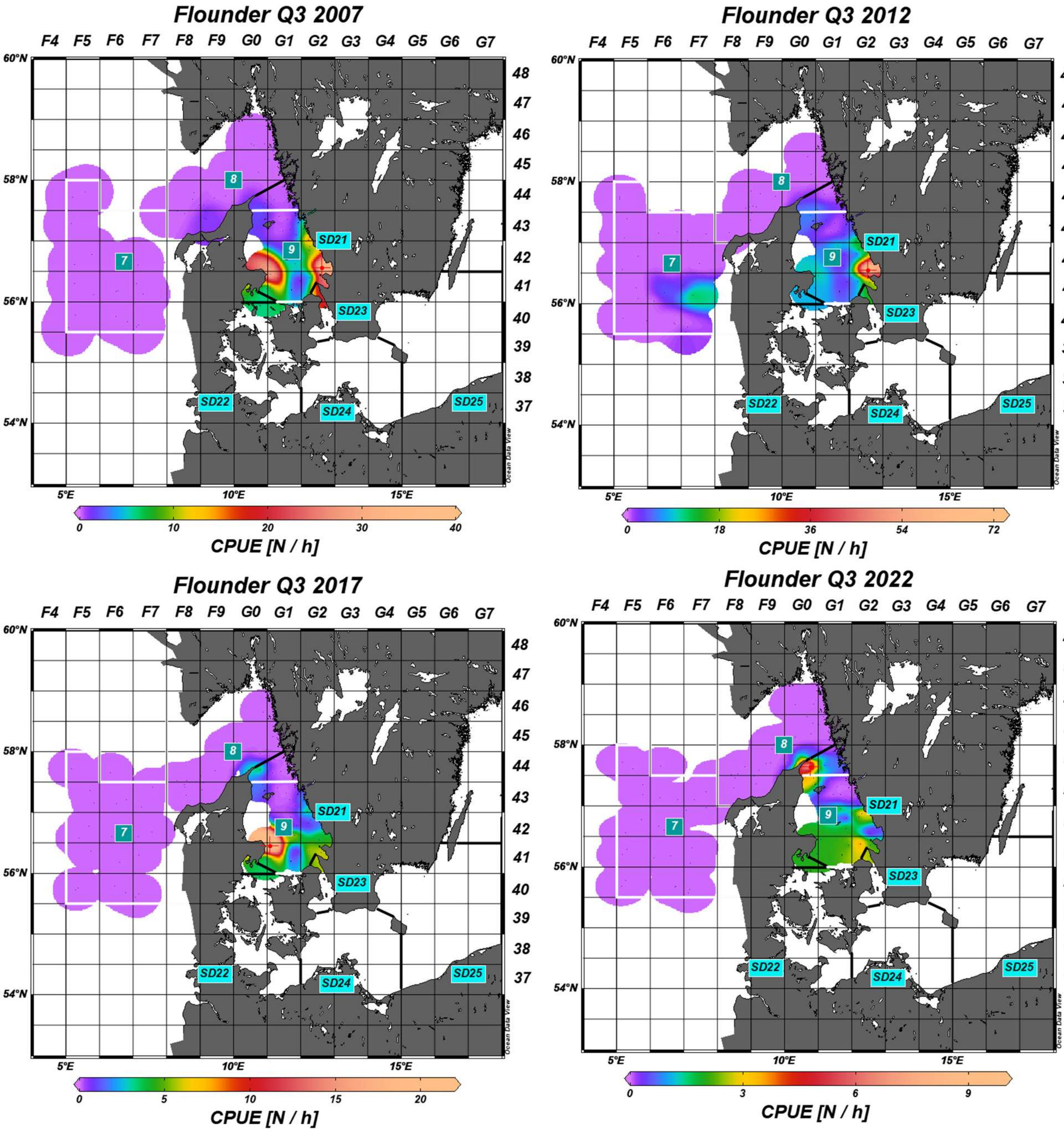
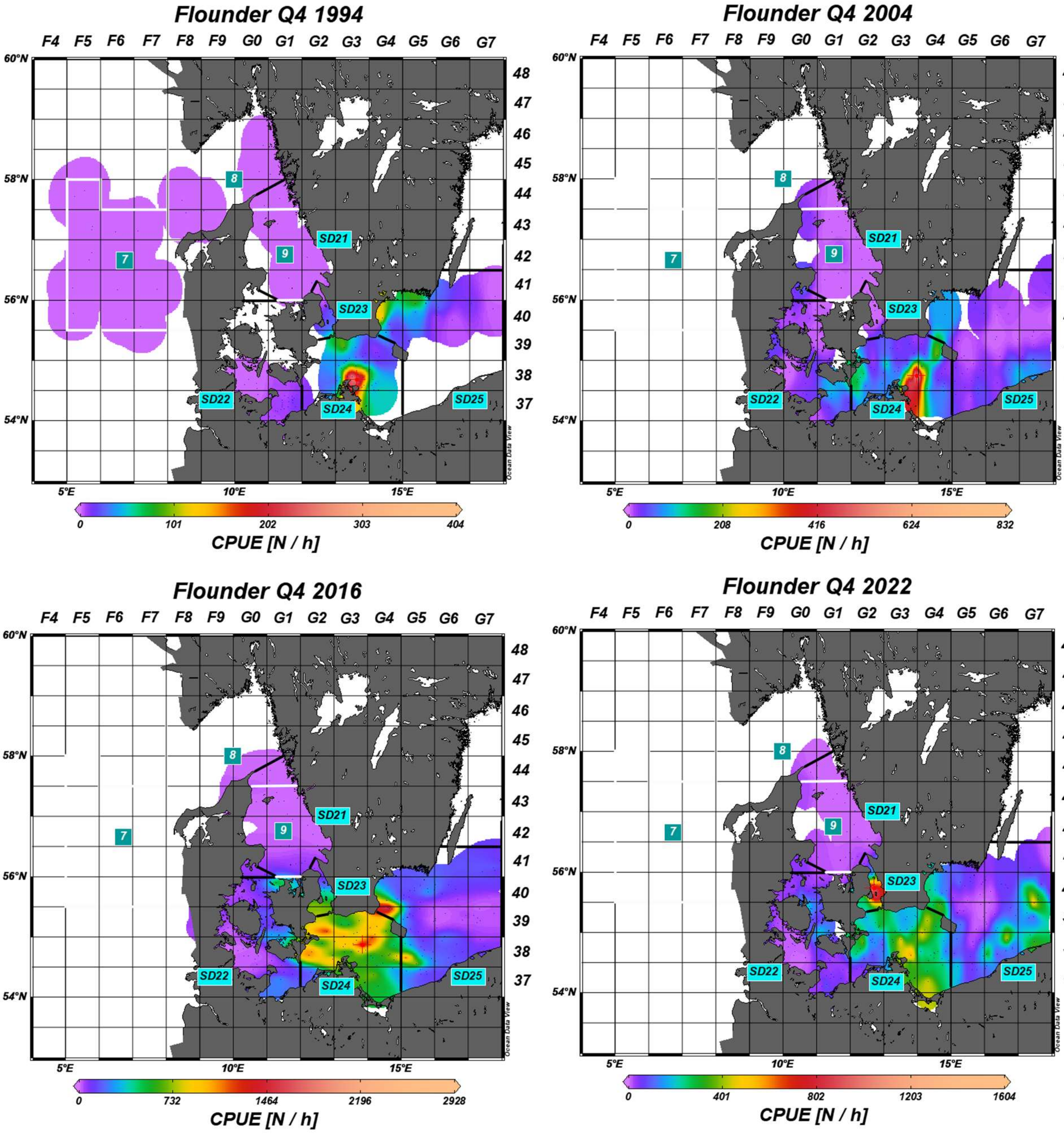


**Figure 15:** Survey-based CPUE distribution of flounder in the North Sea (Areas 7,8,9) during the Q3 IBTS survey.

The lack of flounder between the North Sea and the Kattegat area derived from the IBTS data suggest that there is limited connectivity, and at least two separate stocks might exist (Jokinen et al., 2019, ICES 2023a). However, a robust understanding of the population structure would require a thorough analysis of biological data and genetic analyses. WGNSSK stated that there is no information about stock identity and possible stock assessment areas in the North Sea, Skagerrak and Kattegat. Within the North Sea there may exist a number of sub-populations (ICES 2023a), given that flounder spend the feeding period mainly in or near estuaries and only migrate to more saline waters during the spawning period.

Additional analysis of the CPUE distribution of flounder in Q4 from surveys in the areas of Arkona Sea (SD 24) and Bornholm Sea (SD 25) displayed high densities of flounder in the coastal and estuarine feeding grounds (Figure 16). The high CPUE of flounder from the southern Baltic stock in SD24-25 is masking possible connections between flounder from the Belt Seas and the Sound via SD24. Given that the Danish straits do not provide large physical barriers and hydrographical conditions do not vary much, it is likely, that flounder from SDs 22 and 23 are also migrating through the western parts of



Flounder Q4 1994

Flounder Q4 2004

Flounder Q4 2016

Flounder Q4 2022

**Figure 16:** Survey-based CPUE distribution of flounder in the Baltic Sea (SDs 22-25) and Kattegat (SD 21) during the Q4 BITS survey in selected years, indicating a spatiotemporal connectivity of the areas SD 22 and 23 via SD 24.

SD24. And while several genetic studies confirmed that the major part of flounder in SD 24 is in fact European flounder (*P. flesus*, see chapter "genetics", e.g., Momigliano et al., 2018, 2019, Kuciński et al., 2023, Jokinen et al., 2019), it is so far not possible to distinguish stocks from each other to estimate the number of flounder from the fle.27.22-23 stock in SD24.

## Fishery

The fishing pattern in Division 3.a. (i.e., SDs 20 and 21) basically reflects the distribution of flounder from the survey indices, with the major parts of flounder landings originating from the southern Kattegat and western Skagerrak close to the two major harbours in northern Denmark, Hirtshals and Skagen.

Only occasional and very low (<1t/year) landings were registered from other areas of Skagerrak and Kattegat, confirming the low abundance of flounder in this area (Figure 17, Annex 1.3).

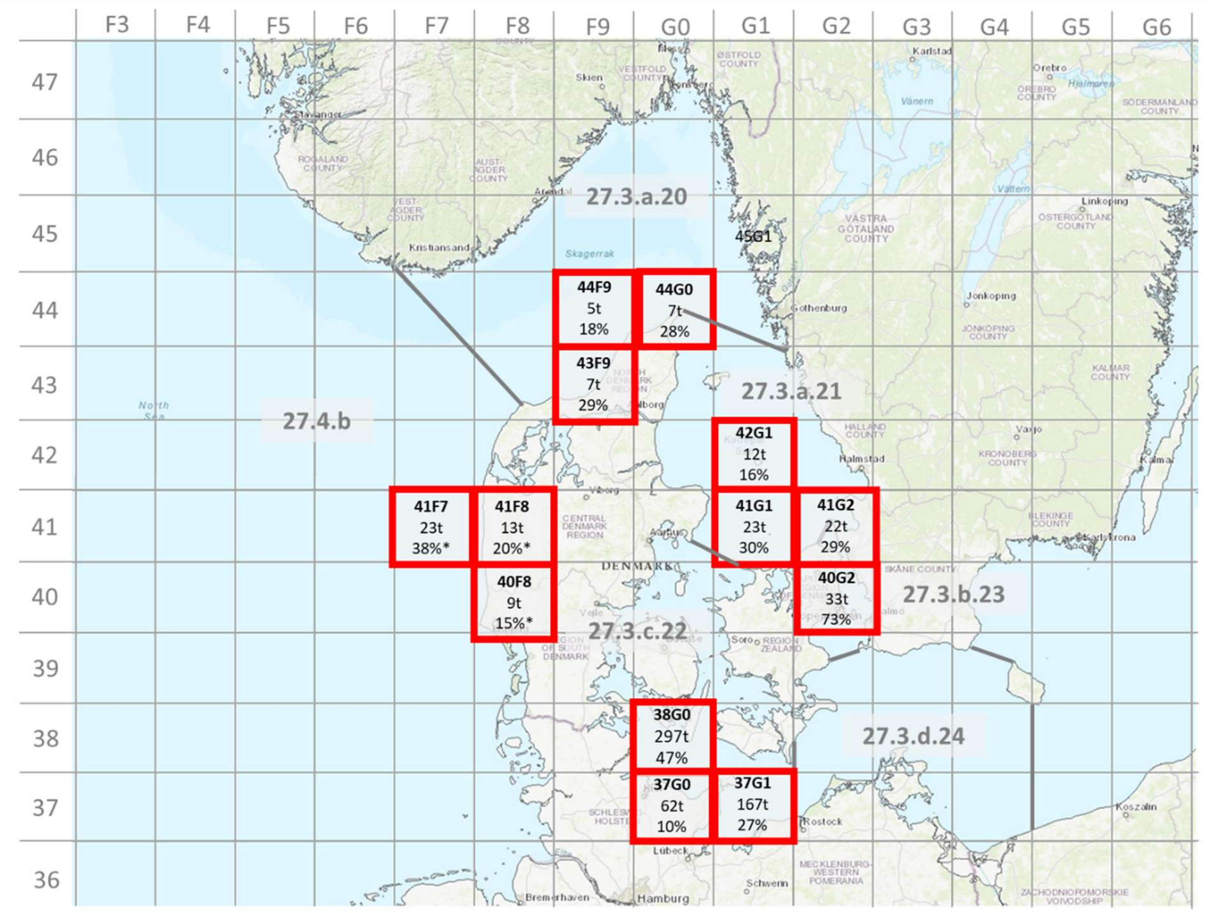


**Figure 17:** Landings of flounder in the North Sea (27.4.b), transition area (27.3.a) and the western Baltic Sea. Averaged (2019-2022) contribution of ICES statistical rectangles that provide >75% of landings per Subdivision.

* 60% (~100t) of flounder landings in the North Sea are not allocated to a statistical rectangle and were not used for the calculation

The Kattegat (SD21) had relatively low landings of flounder (around 80t/year), where the species is mainly caught as bycatch in *Nephrops*-directed fisheries and thus usually discarded. The major part (>60%) of the landings is taken in the southern area (ICES statistical rectangles 41G1 and 41G2) at the border to SD 22 and SD 23.

Landings in Skagerrak (SD20) were usually low at around 20t/year and were taken mostly along the northern Danish coastline of western Skagerrak, with 43F9, 44F9 and 44G0 contributing most (>75%) of the landings. Discards were estimated for Kattegat and Skagerrak together (as Division 3.a) and range from 27% to 87% of the total flounder catch and were usually higher than in the North Sea or western Baltic Sea (ICES 2023a, 2023b).

The fishery on flounder in the western Baltic Sea was concentrated in the Belt Sea. On average, >95% of the annual landings originated from the Belt Sea, mainly by Germany and Denmark. Average landings have been >1000t/year, decreasing to around 700t/year in 2020/2021. A strong decline in fishing activity (caused by low TACs of western Baltic cod and decreased fishing opportunities) in 2022 also decreased landings of flounder to around 320t (Figure 9). Discards have been stable in the last few years at around 18% of the total catch (ICES 2023d).

## Life history parameters

Different life history parameters were obtained from Q1 surveys (IBTS for the North Sea) and from BITS, covering Kattegat and the western Baltic Sea. Maturation and growth in North Sea, Kattegat and western Baltic Sea were very similar (Figure 18, Table 2), with an average maturation at around 20cm total length and similar growth patterns in the current data year. Flounder in Kattegat was only occasionally sampled for detailed biological data so that life history parameters for the comparison could only be obtained for 2010.

Flounder in the North Sea displayed a very similar growth pattern like flounder caught in Kattegat and the western Baltic and were very similar in length-weight relationships.

**Table 2:** Life history parameter of flounder caught in Q1 Surveys in 2022 in the North Sea (IBTS), Kattegat (BITS) and Baltic Sea (BITS)

| | **North Sea*** | **Kattegat** | **Baltic Sea** |
|---|---|---|---|
| Maturity-at-length | 21cm | 20cm** | 20.5cm |
| Growth intercept | 0.004 | 0.0122** | 0.0166 |
| slope | 3.262 | 2.948* | 2.872 |
| $L_{inf}$ | 41.3cm | -*** | 44.3cm |
| N | 318 | 78 | 362 |

* Flounder is only sampled occasionally during IBTS, data are averaged from 2012, 2013 and 2022 Q1 surveys

**only Q1 2010 data available, only few individuals measured

***no age reading conducted in SD21

**Figure 18:** Length-weight correlation of flounder in the North Sea (blue line), Kattegat (red line) and western Baltic Sea (green line). Data obtained from Q1 surveys (IBTS and BITS).

## Genetics

It has been long believed that in the Baltic Sea European flounder has two distinctively different ecotypes (sometimes also considered as two sympatric flounder populations) – the pelagic and demersal spawning flounder. In 2018, Momigliano and co-athors revealed that these two ecotypes are in fact two different species - European flounder *Platichthys flesus* (pelagic spawners) and Baltic flounder *Platichthys solemdali* (demersal spawners).

Despite having a parapatric distribution, *P. flesus* and *P. solemdali* in the Baltic Sea show strongly bimodal genotypic clustering based on genome-wide single nucleotide polymorphism (SNP) markers and strong reproductive isolation (Momigliano et al., 2017). Genetic studies carried out over the past decade demonstrated that these morphological, physiological, and life-history differences are linked to stable and distinct genetic populations. Hemmer-Hansen et al. (2007) and Florin and Höglund (2008) investigated *P. flesus* population genetics using microsatellite markers, and discovered significant (albeit very weak, $F_{ST}$ 0.01–0.03) genetic differentiation associated with spawning behaviour. Using a combination of genome-wide SNP genotyping and approximate Bayesian computation modelling, Momigliano et al., 2017 demonstrated that the two flounder types originated via two distinct colonisations of the Baltic Sea from the same ancestral population.

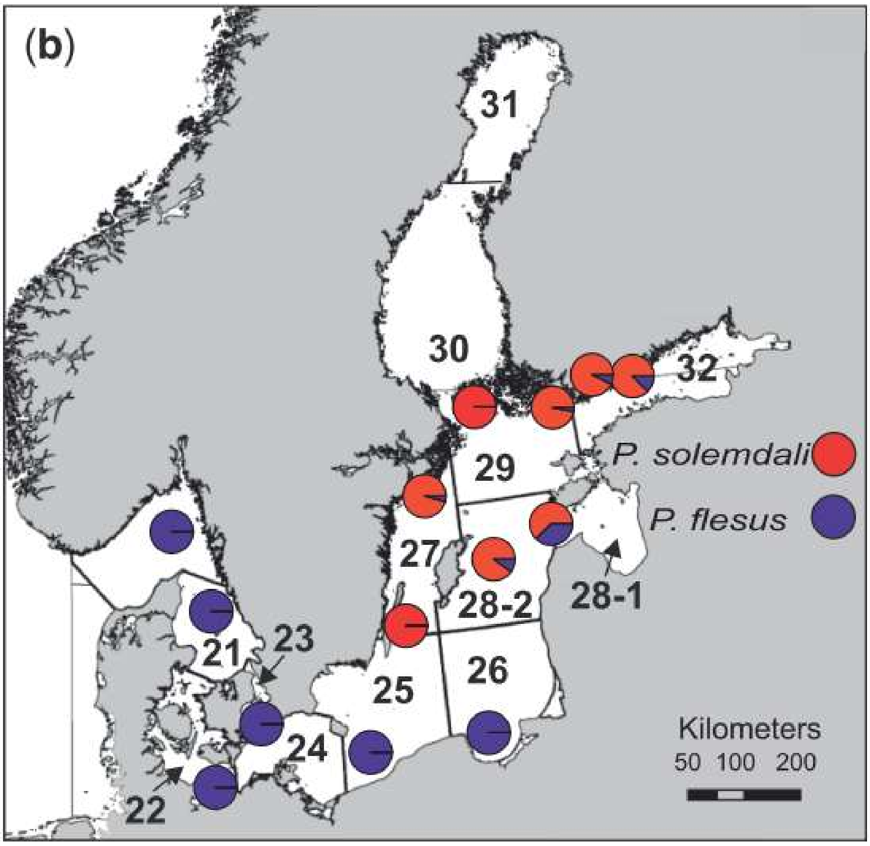


**Figure 18:** Contemporary proportion of the two main flounder lineages (European *P. flesus*, Baltic Sea *P. solemdali*) in different localities and across ICES subdivisions of the Baltic Sea (SD 21–32), based on previously published data (Momigliano et al., 2017, 2018, 2019).

It should be noted that these do not represent accurate and stable proportions in each of the localities, as they are likely affected by sampling strategy (both within and between years, and water depths), but they do provide evidence of mixed stocks in several locations (Jokinen et al. 2019)

However, none of these studies could find differences in genetic population structure between the areas SD 21 (Kattegat) and SD 22 (Belt Sea), where all sampled species were identified as European flounder *P. flesus* (Figure 12). Additionally, about 97% of the sampled individuals in SD 24 (Arkona Sea) were identified as European flounder (Jokinen et al. 2019, Figure 18, Table 3). A recent study investigated flounder sampled along the Polish coast of SD 24 concluded that European flounder (*P. flesus*) from the southern Baltic Sea represent a single and homogenous genetic cluster (Kucinski et al. 2022).

**Table 3.** Proportion of flounder with pelagic eggs (European flounder) per SD in the Baltic Sea (from: Momigliano et al., 2018).

| ICES Subdivision | Proportion |
|---|---|
| **32** | 8% |
| **28** | 24% |
| **26** | 98% |
| **25** | 76% |
| **24** | 97% |

Linking these genetic findings with the distribution from the two surveys suggests that the flounder population in Kattegat (SD21) is rather part of the larger population of European flounder in the western Baltic Sea. European flounder seems to have three areas of occurrence with distinct density levels: Low levels are found in North Sea and Skagerrak, medium densities around the Danish archipelago involving the Kattegat, Belt Seas and Sound (SDs 21-23); and highest density of European flounder in the southern Baltic Sea, populated by the highly productive flounder stock of SD 24-25.

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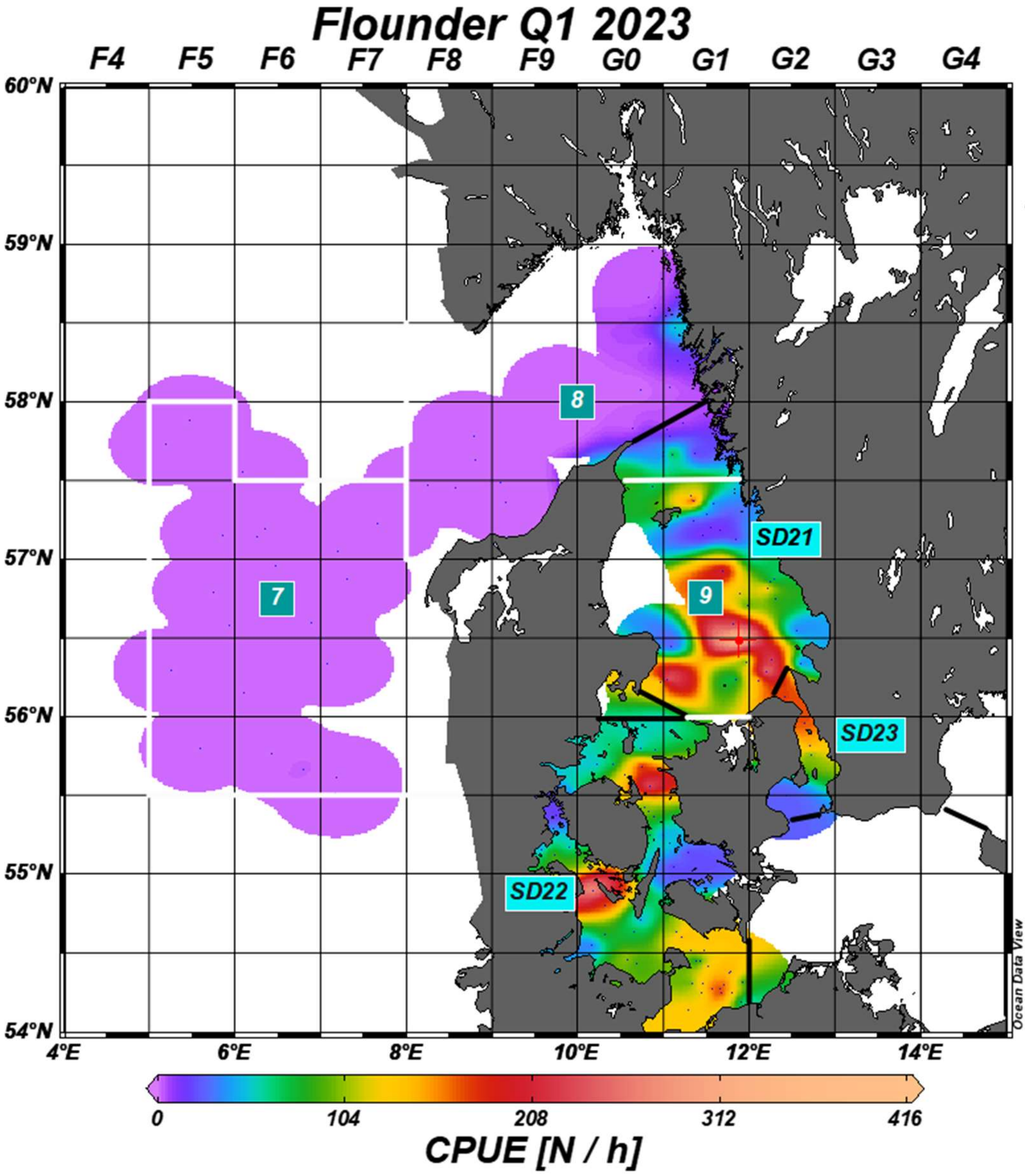
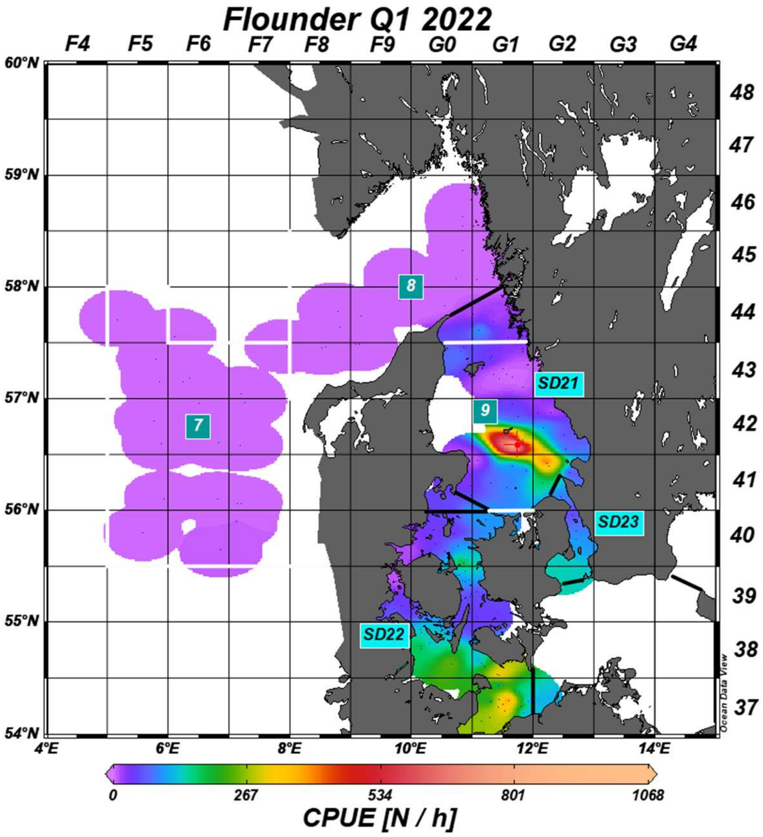
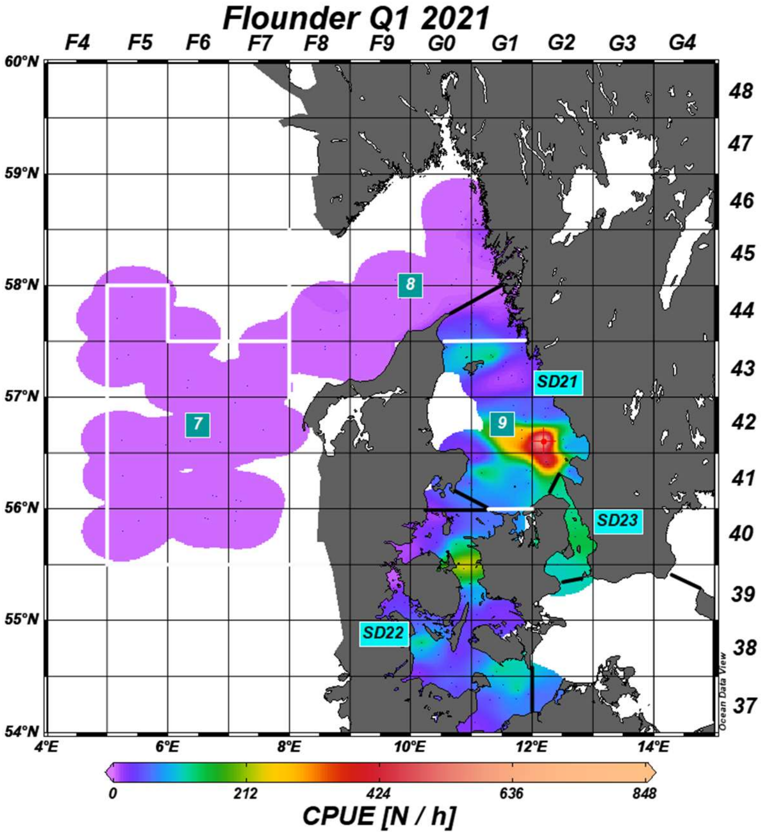
# ANNEX 1.1

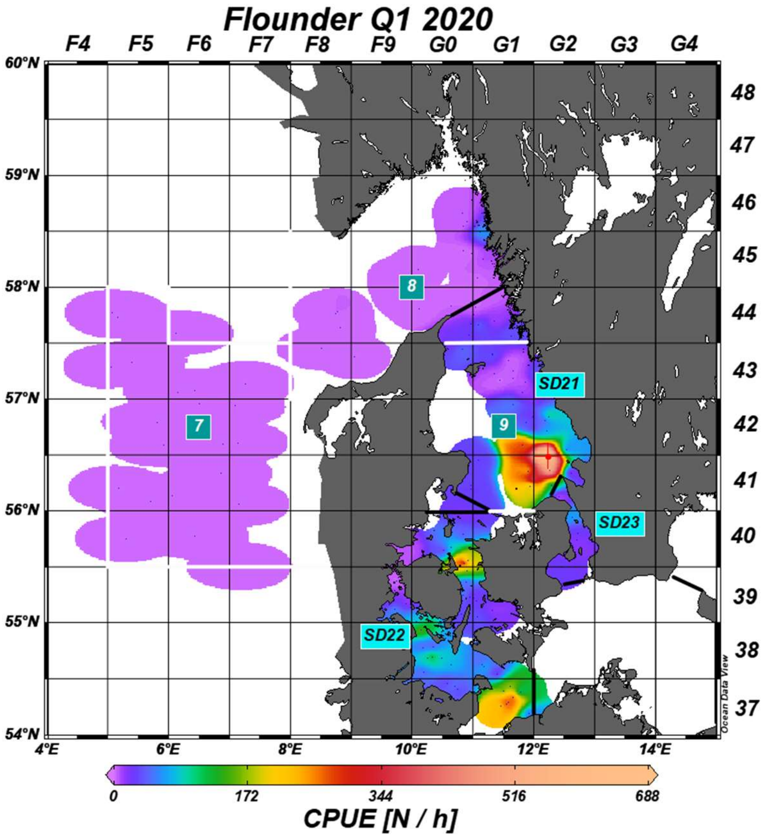
Combined **Quarter 1 Survey Index** CPUE (no/hour) of IBTS, covering Areas 7, 8 and 9 and BITS, covering Areas SD21, 22 and 23.

The colour scheme is adjusted to the maximum value of each year to make maps easier to read.




Flounder Q1 2022
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E 6°E 8°E 10°E 12°E 14°E
48 47 46 45 44 43 42 41 40 39 38 37
8
7
9
SD21
SD22
SD23
Ocean Data View
0 267 534 801 1068
CPUE [N / h]


Flounder Q1 2021
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E 6°E 8°E 10°E 12°E 14°E
48 47 46 45 44 43 42 41 40 39 38 37
8
7
9
SD21
SD22
SD23
Ocean Data View
0 212 424 636 848
CPUE [N / h]


Flounder Q1 2020
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SD21
SD23
SD22
4°E
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Ocean Data View
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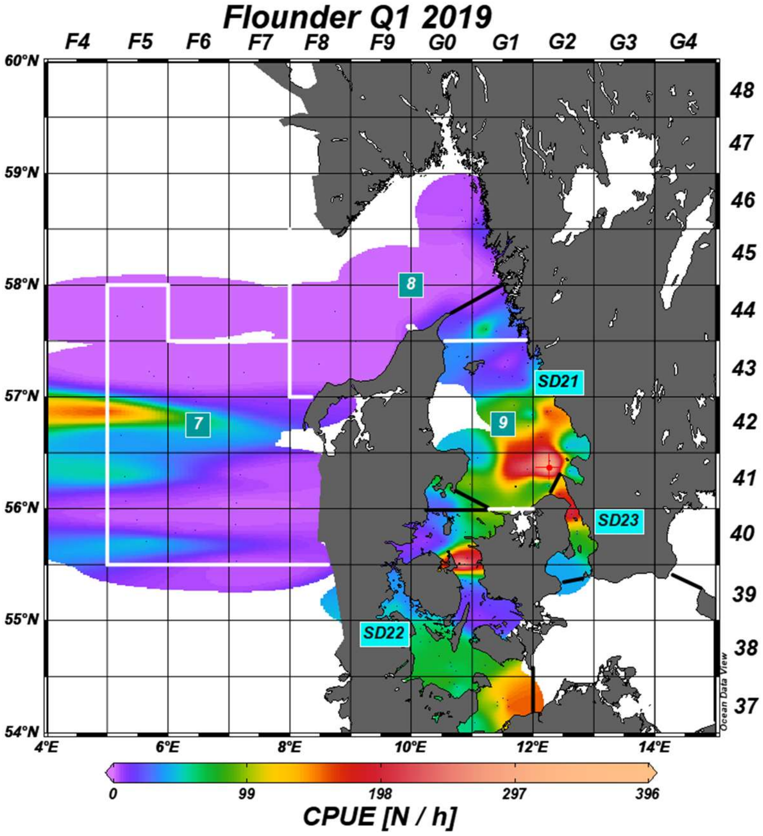
172
344
516
688
CPUE [N / h]


Flounder Q1 2019
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SD21
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Ocean Data View
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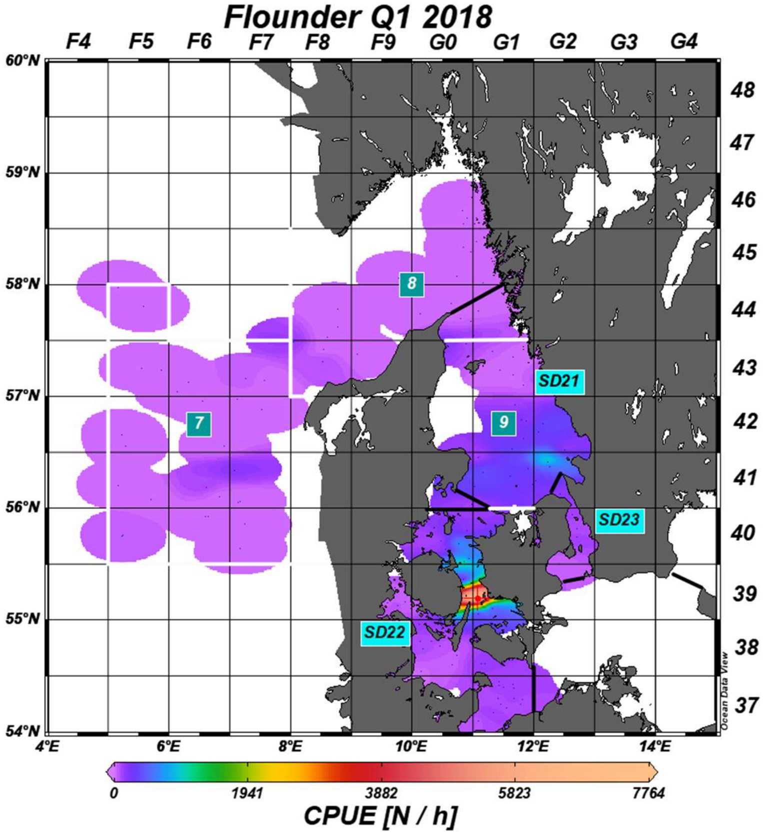
198
297
396
CPUE [N / h]


Flounder Q1 2018
F4
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F6
F7
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G0
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G2
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57°N
56°N
55°N
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8
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9
SD21
SD23
SD22
Ocean Data View
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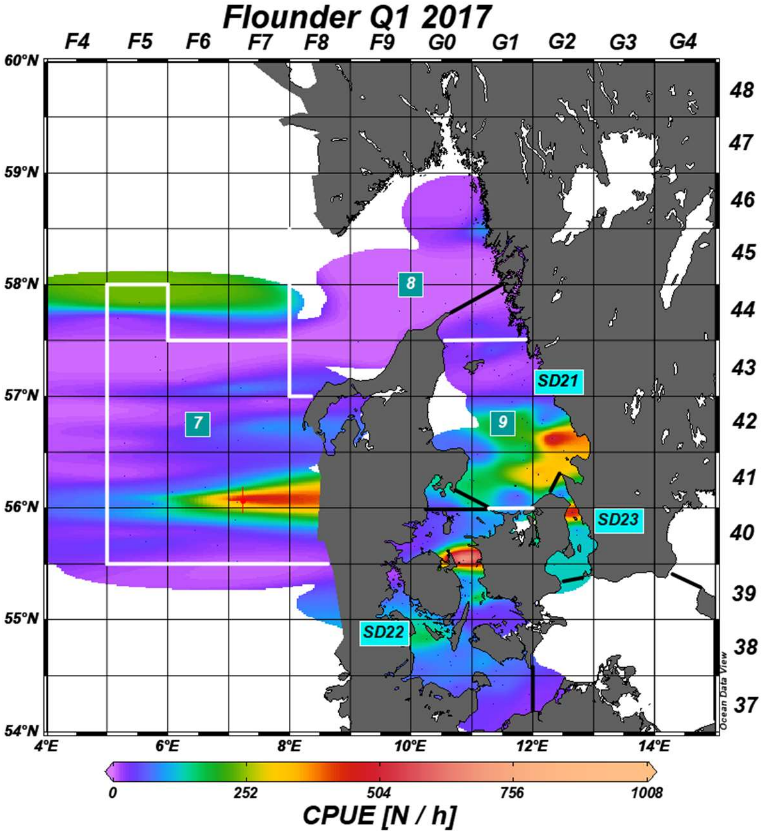
5823
7764
CPUE [N / h]


Flounder Q1 2017
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G3
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SD21
SD23
SD22
Ocean Data View
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10°E
12°E
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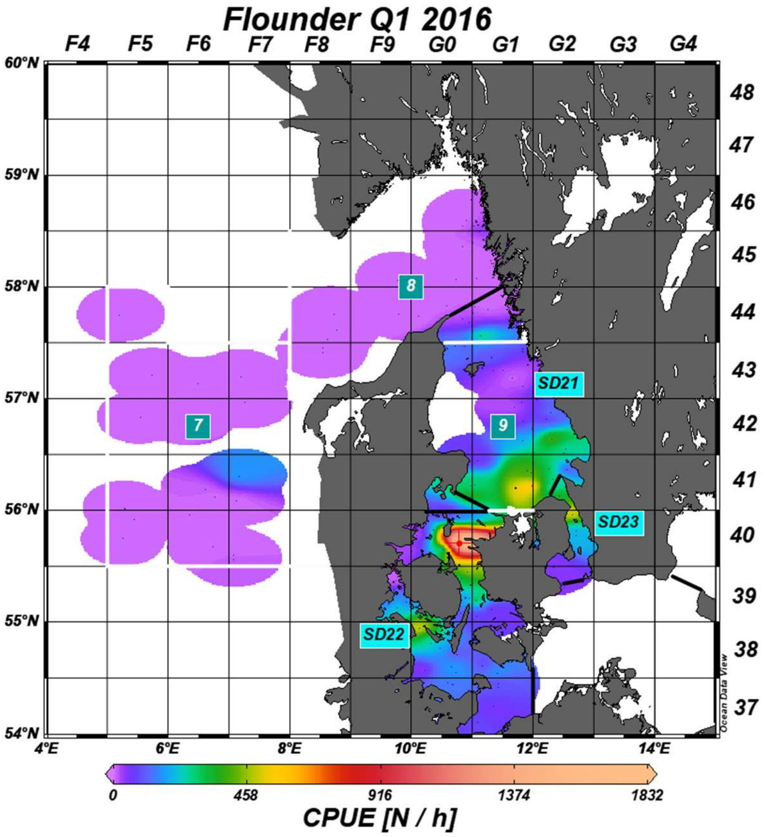
252
504
756
1008
CPUE [N / h]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F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48 47 46 45 44 43 42 41 40 39 38 37
4°E 6°E 8°E 10°E 12°E 14°E
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9
SD21
SD23
SD22
Ocean Data View
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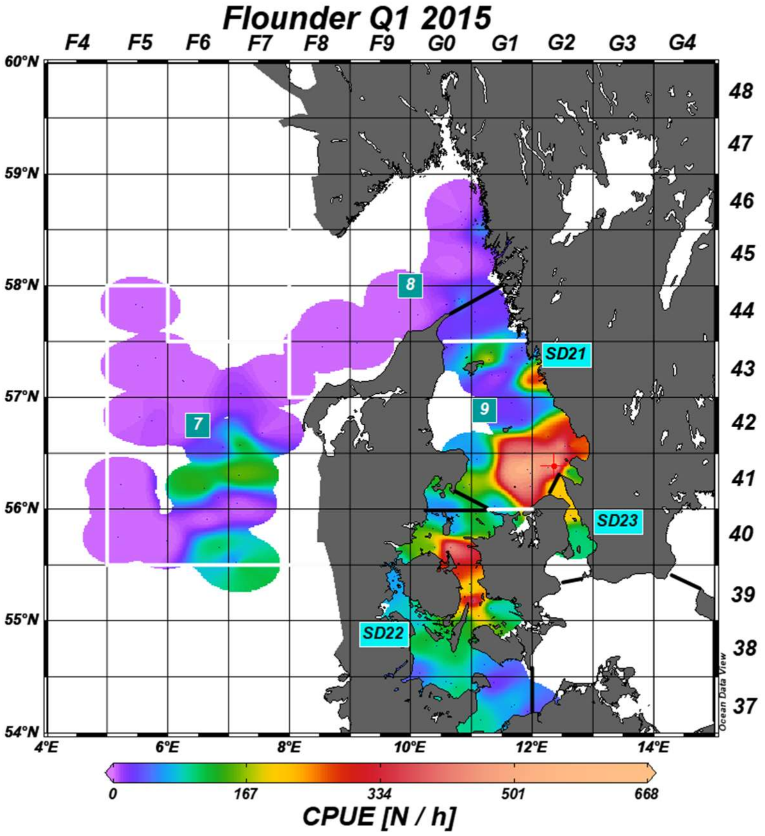
CPUE [N / h]


Flounder Q1 2015
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59°N
58°N
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48 47 46 45 44 43 42 41 40 39 38 37
4°E 6°E 8°E 10°E 12°E 14°E
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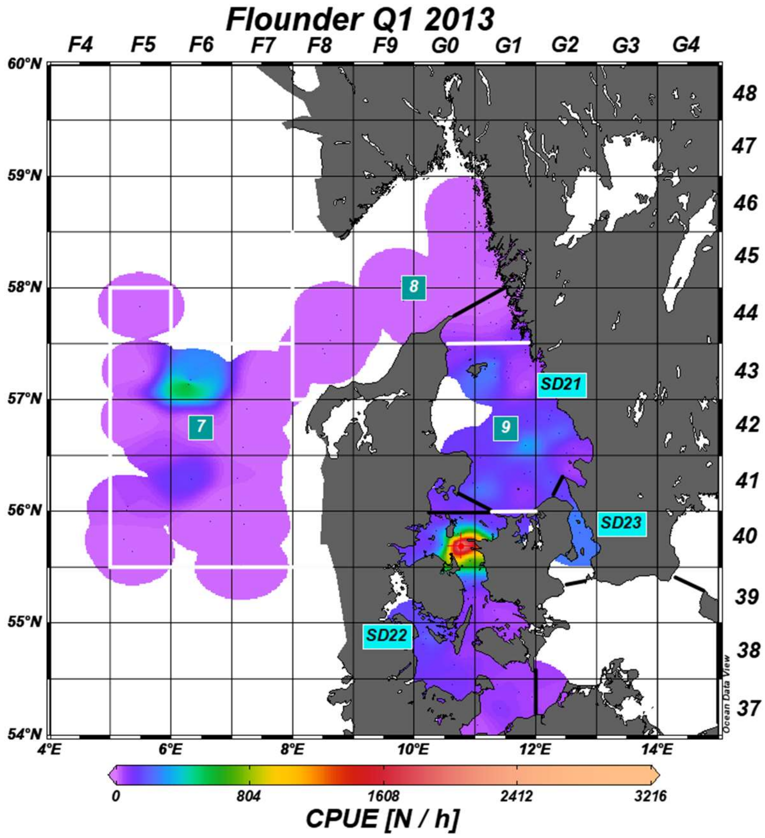
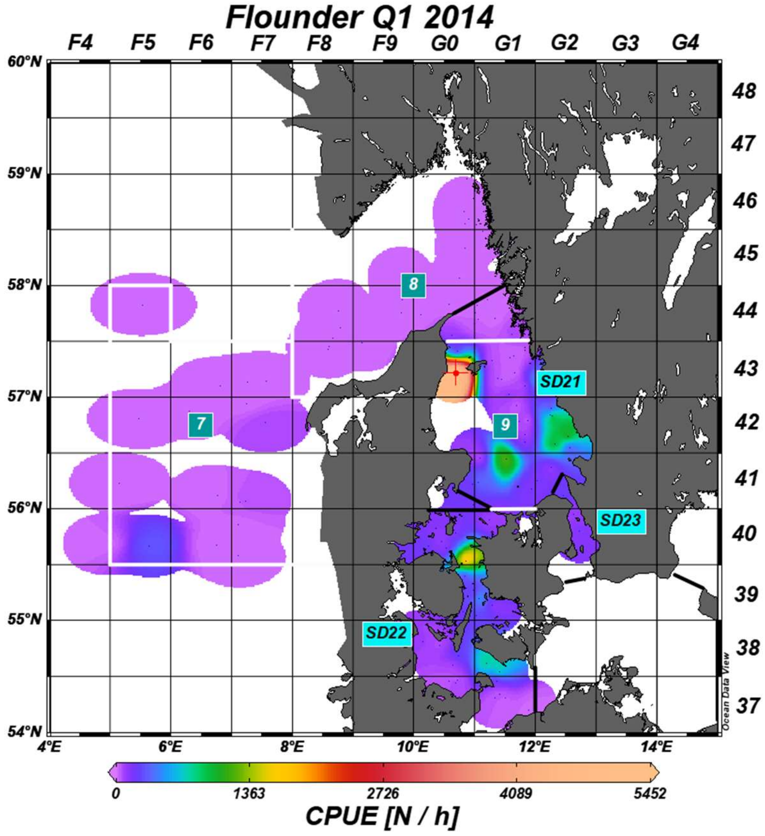
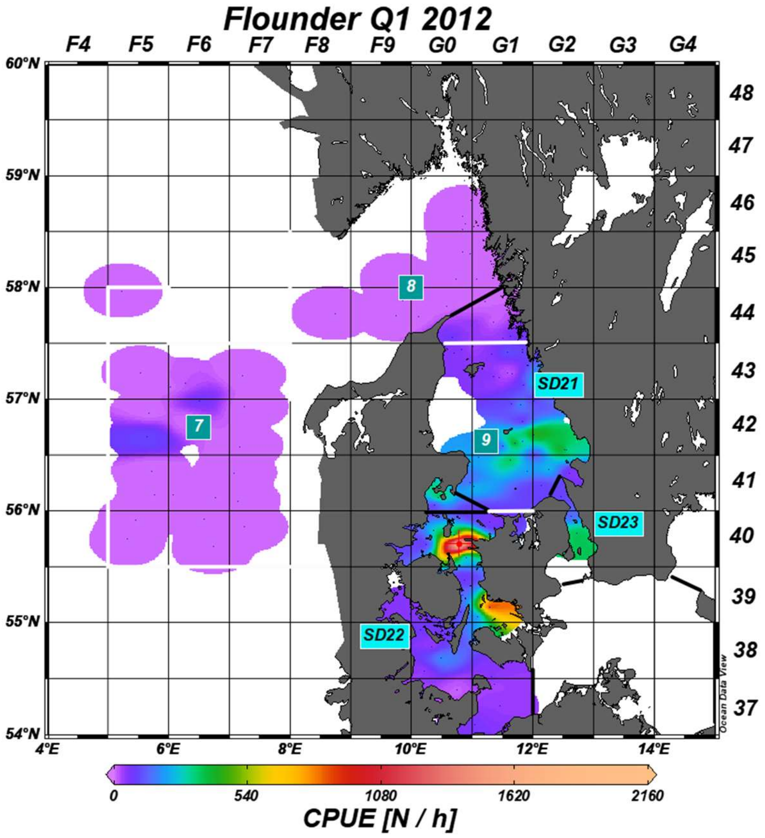
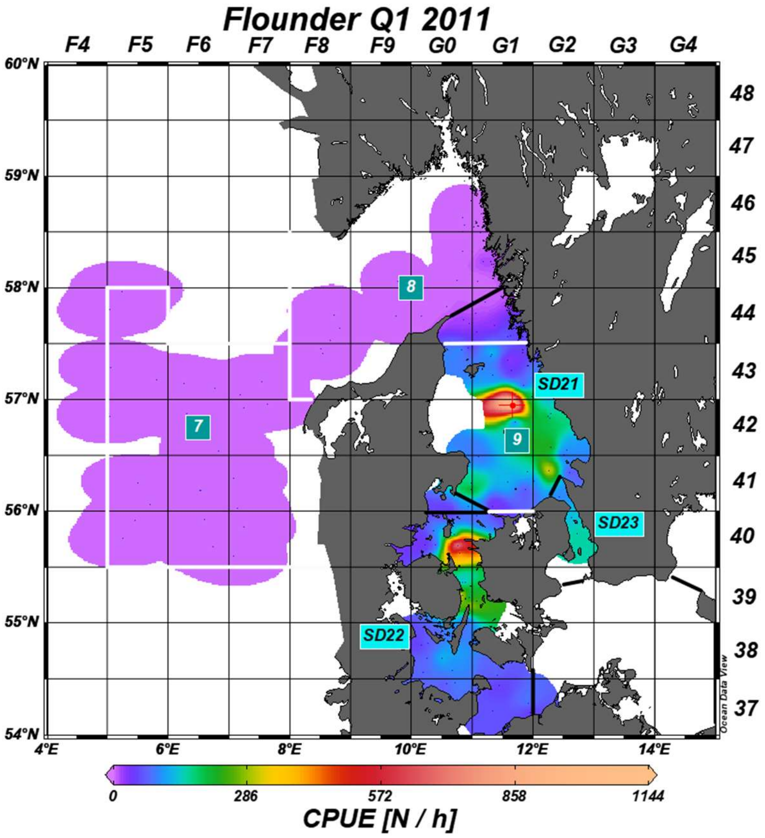
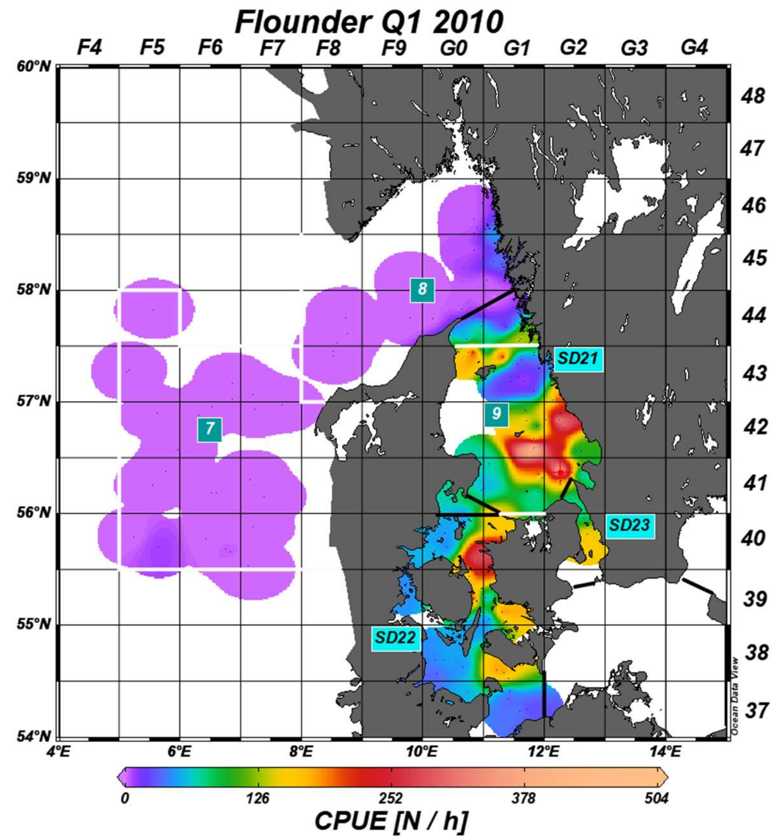
SD21
SD23
SD22
Ocean Data View
0 167 334 501 668
CPUE [N / h]

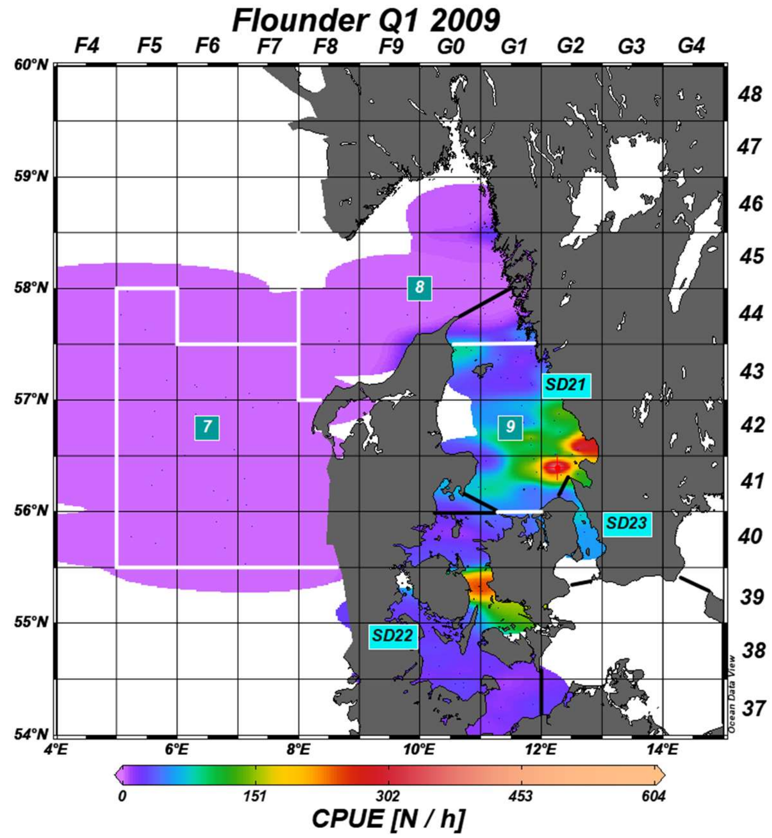

Flounder Q1 2013
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
4°E
6°E
8°E
10°E
12°E
14°E
0
804
1608
2412
3216
CPUE [N / h]
Ocean Data View

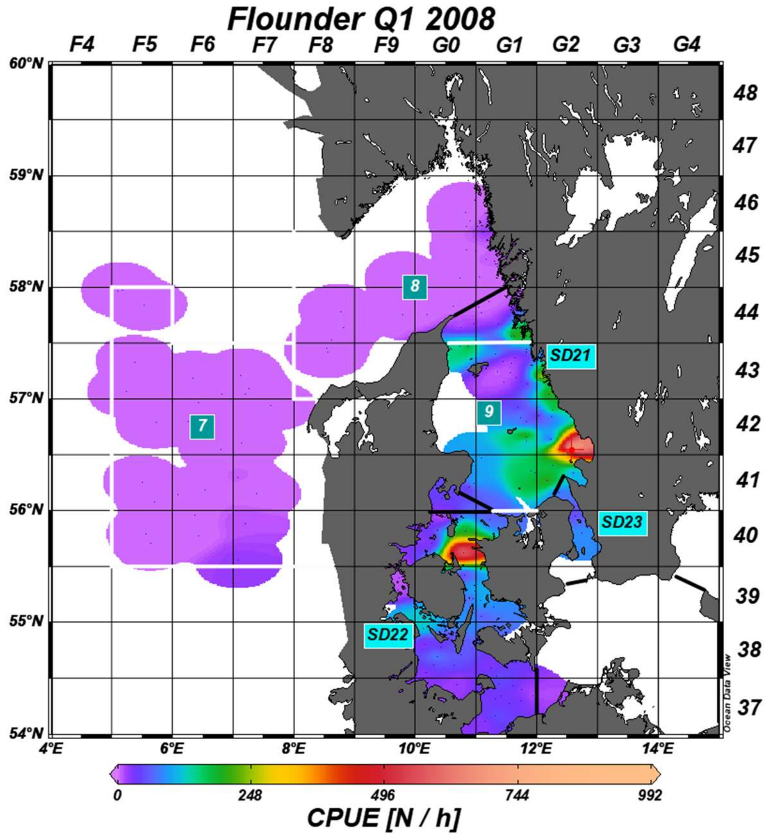

Flounder Q1 2014
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
4°E
6°E
8°E
10°E
12°E
14°E
0
1363
2726
4089
5452
CPUE [N / h]
Ocean Data View

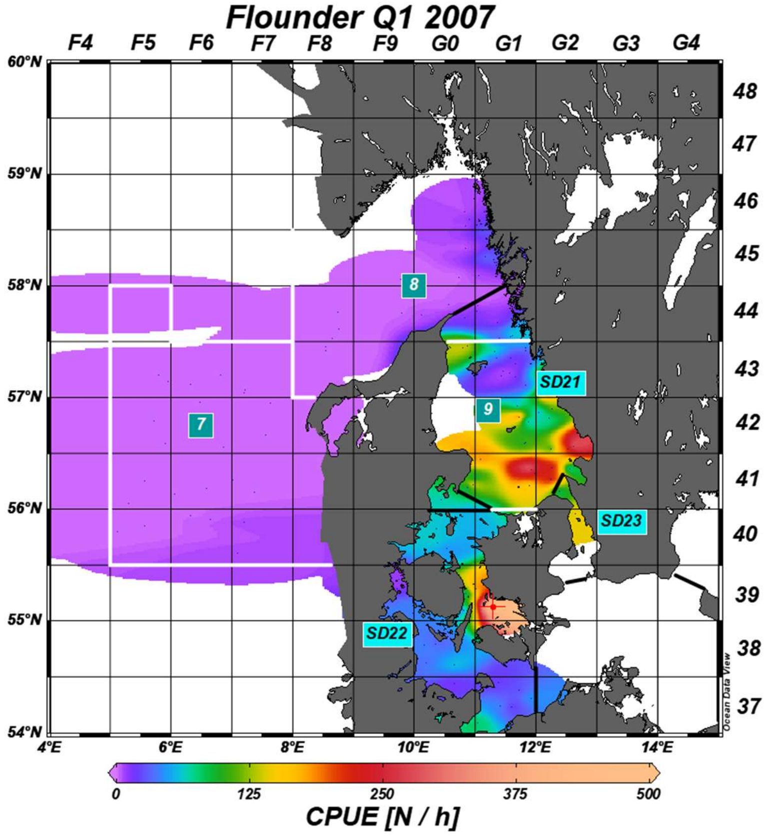

Flounder Q1 2012
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
540
1080
1620
2160
CPUE [N / h]

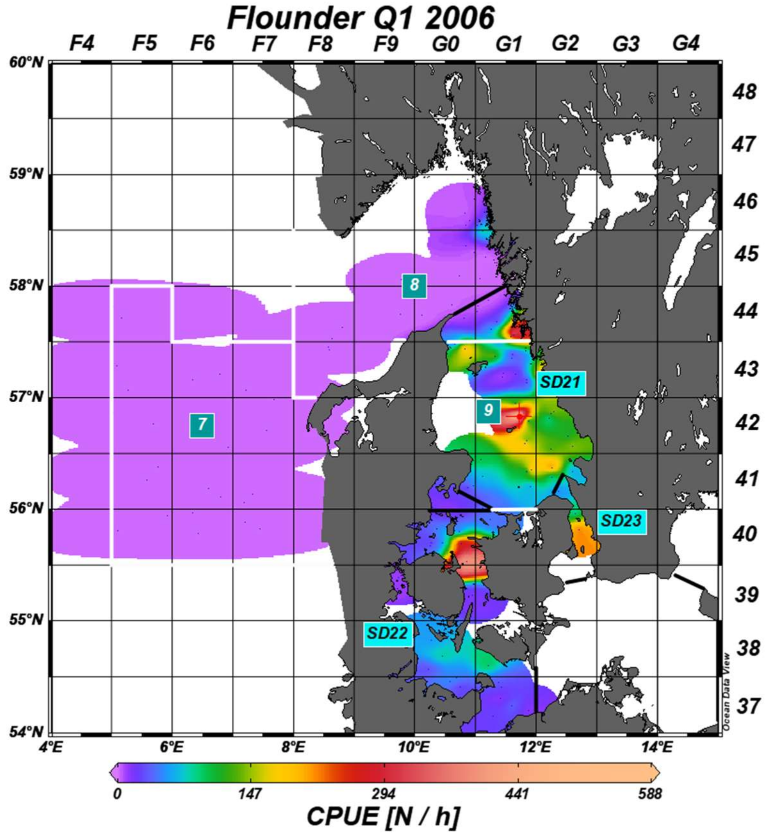

Flounder Q1 2011
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
286
572
858
1144
CPUE [N / h]

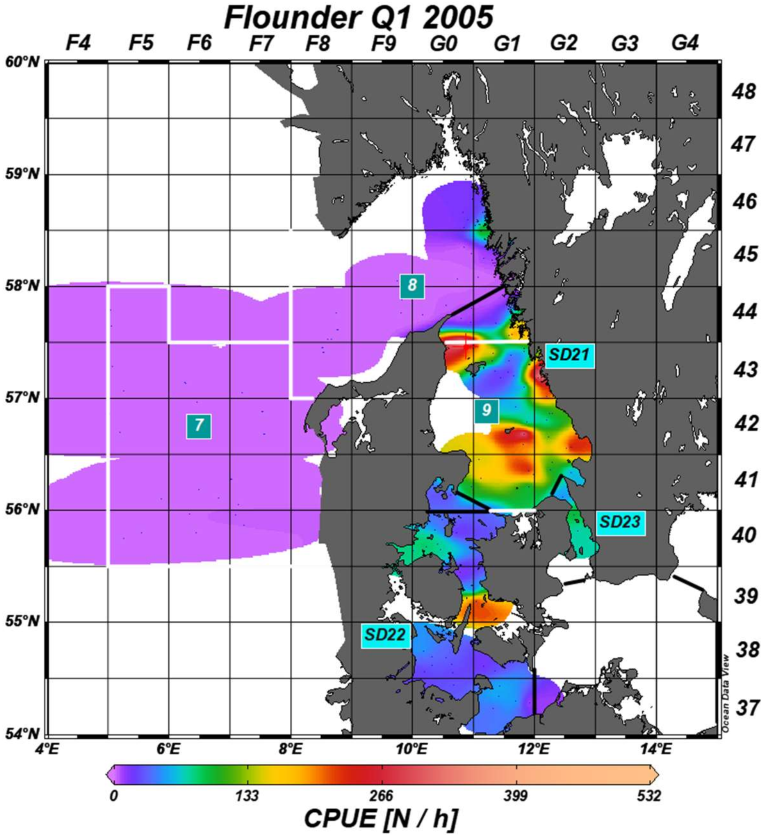

Flounder Q1 2010
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD23
SD22
4°E
6°E
8°E
10°E
12°E
14°E
Ocean Data View
0
126
252
378
504
CPUE [N / h]

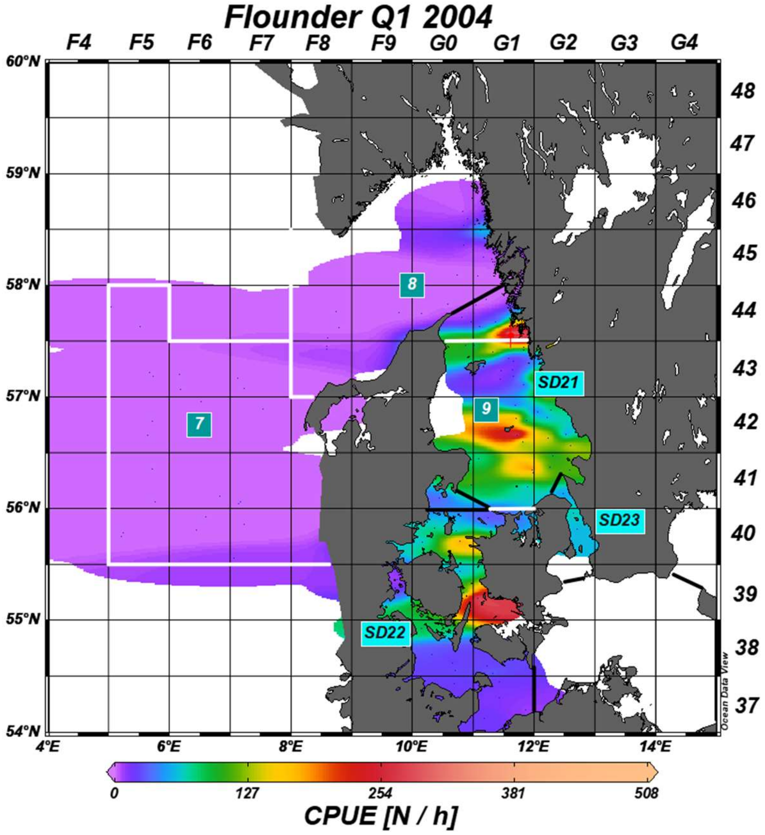

Flounder Q1 2009
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD23
SD22
4°E
6°E
8°E
10°E
12°E
14°E
Ocean Data View
0
151
302
453
604
CPUE [N / h]

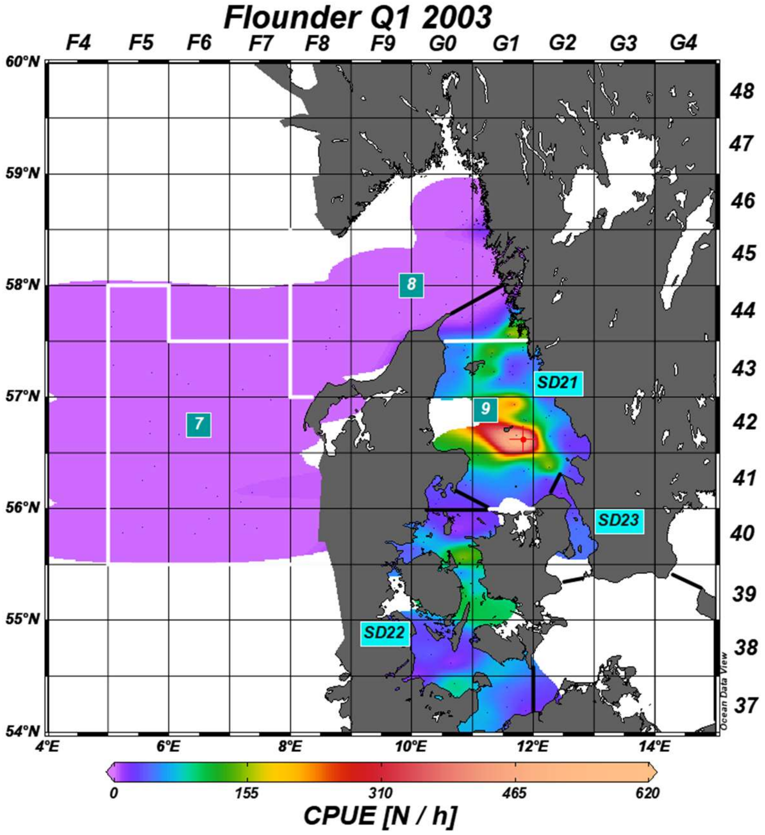

Flounder Q1 2008
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
0
248
496
744
992
CPUE [N / h]
Ocean Data View


Flounder Q1 2007
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
0
125
250
375
500
CPUE [N / h]
Ocean Data View

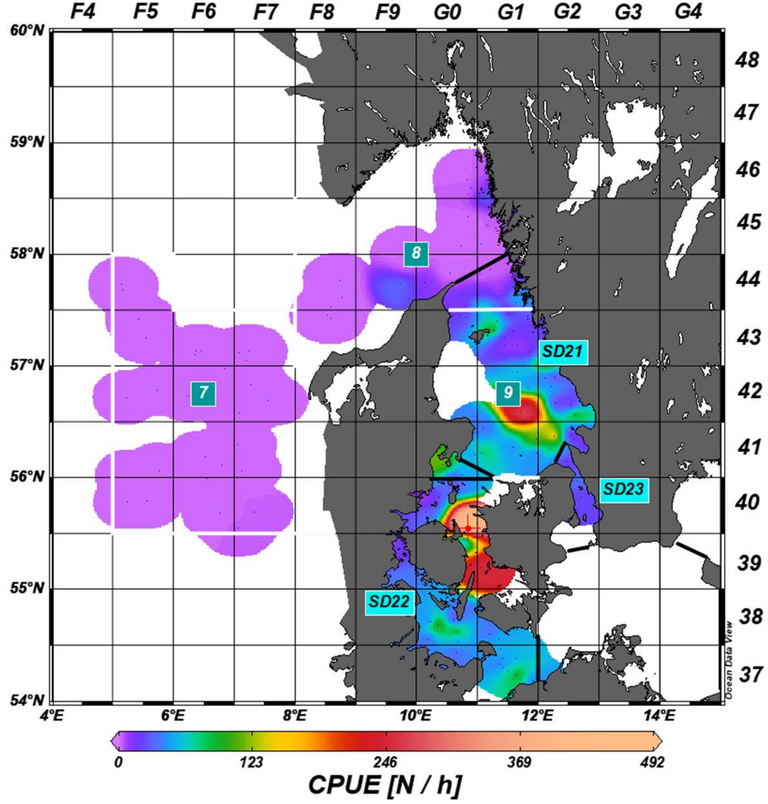

Flounder Q1 2006
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
7
8
9
SD21
SD22
SD23
Ocean Data View
0
147
294
441
588
CPUE [N / h]


Flounder Q1 2005
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
7
8
9
SD21
SD22
SD23
Ocean Data View
0
133
266
399
532
CPUE [N / h]

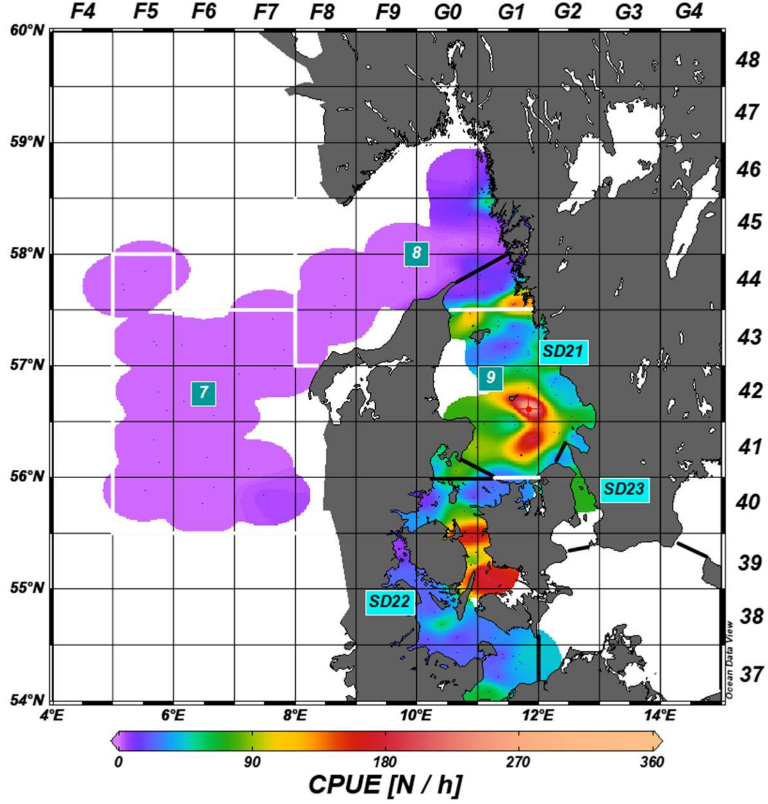

Flounder Q1 2004
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD23
SD22
4°E 6°E 8°E 10°E 12°E 14°E
0 127 254 381 508
CPUE [N / h]
Ocean Data View

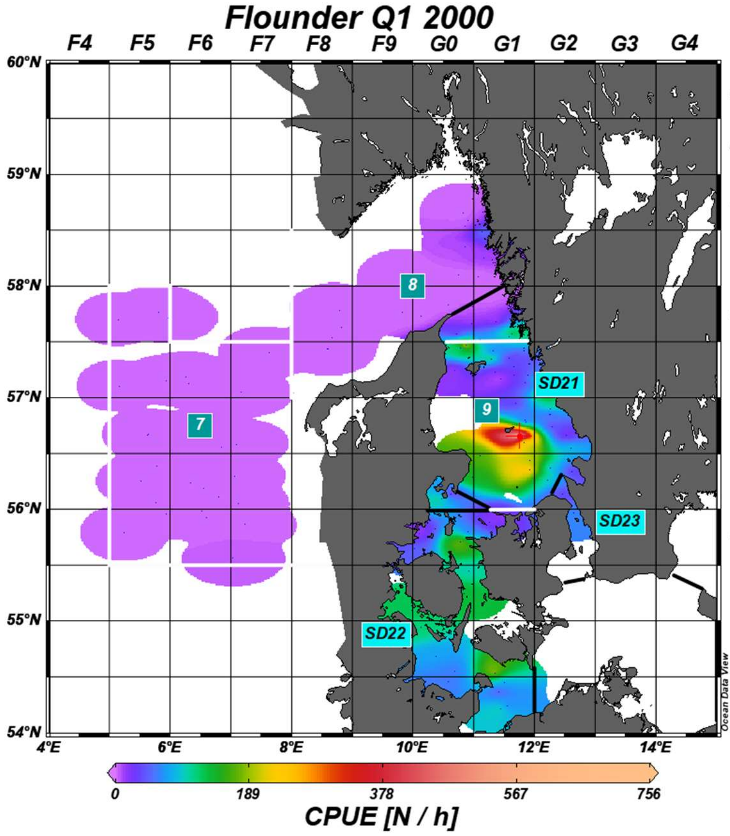

Flounder Q1 2003
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD23
SD22
4°E 6°E 8°E 10°E 12°E 14°E
0 155 310 465 620
CPUE [N / h]
Ocean Data View

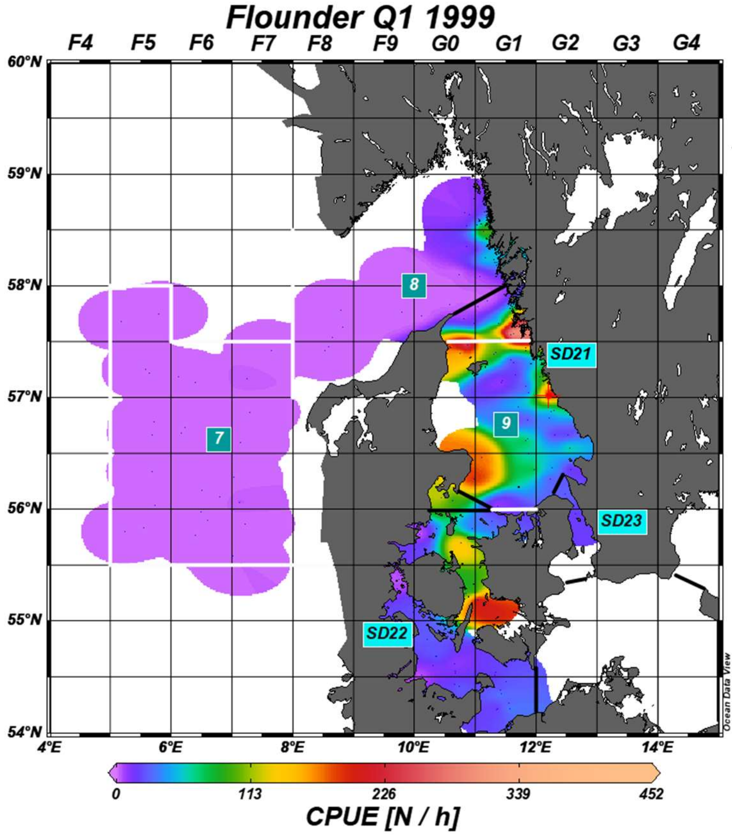
Flounder Q1 2002

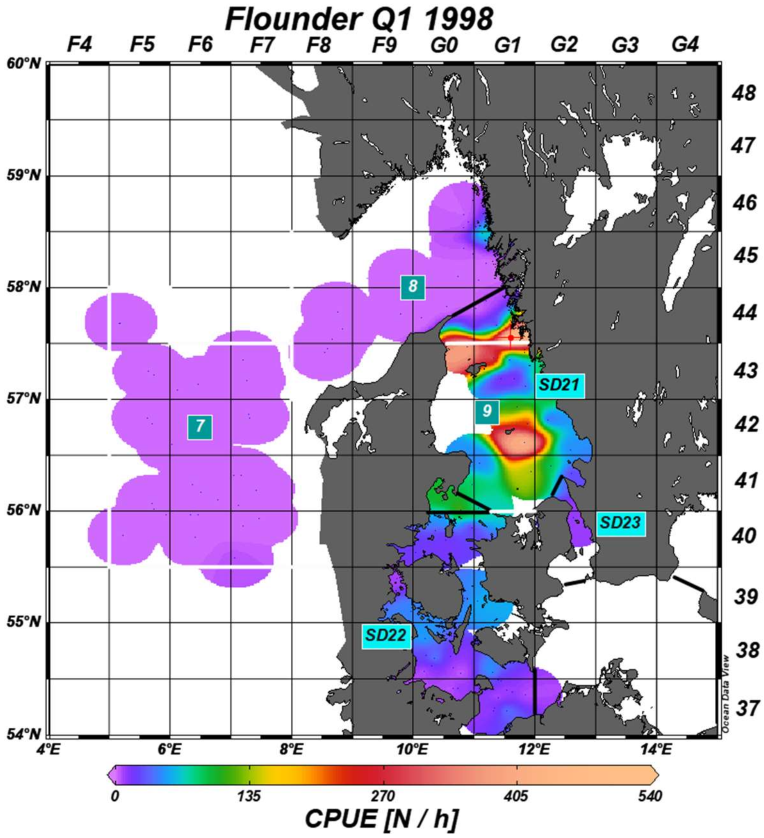


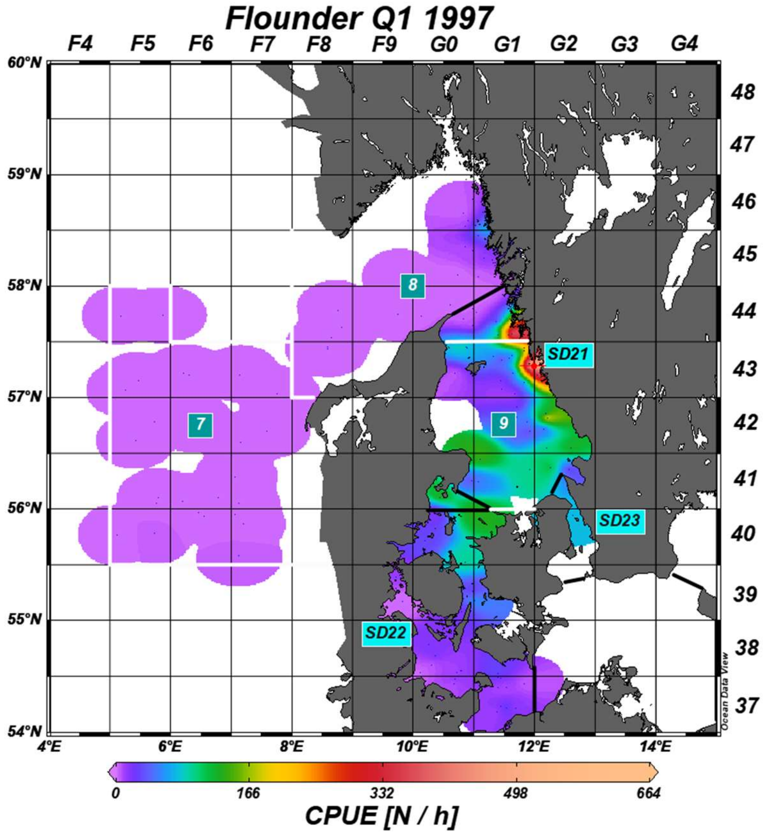
Flounder Q1 2001

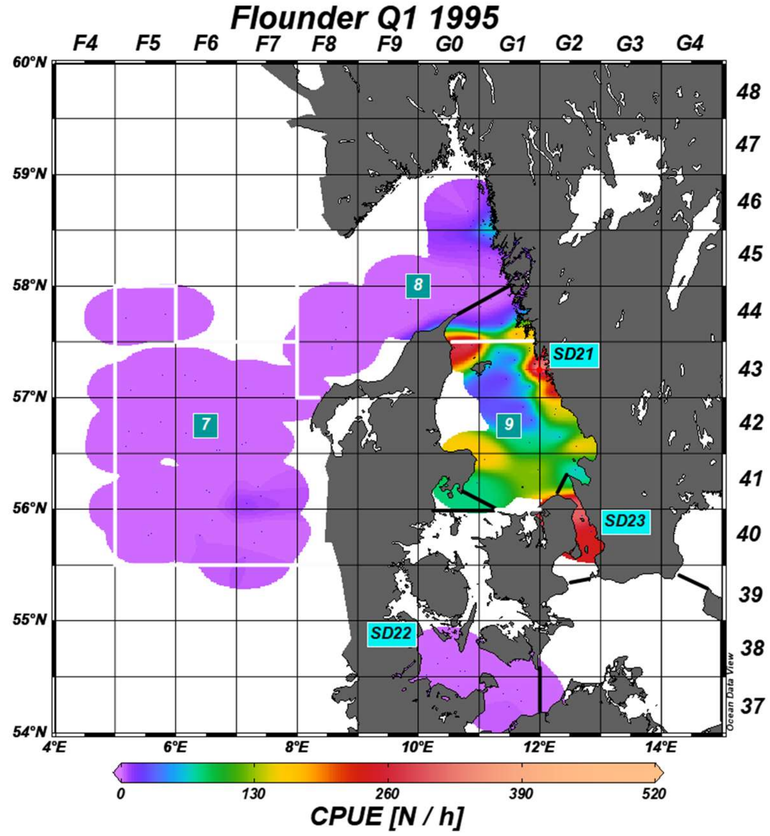


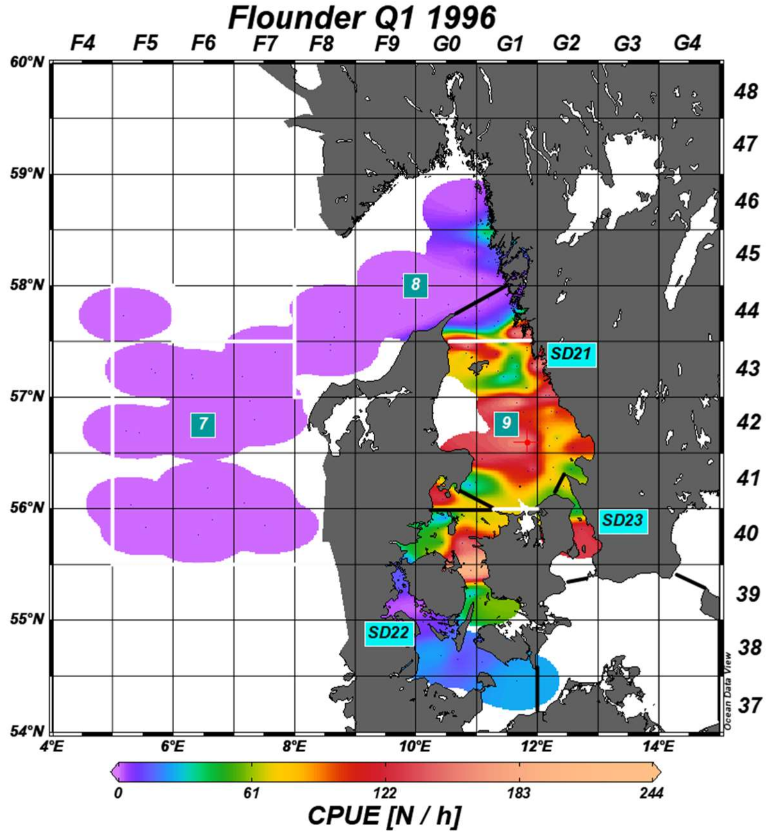

Flounder Q1 2000
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
7
8
9
SD21
SD22
SD23
Ocean Data View
0
189
378
567
756
CPUE [N / h]

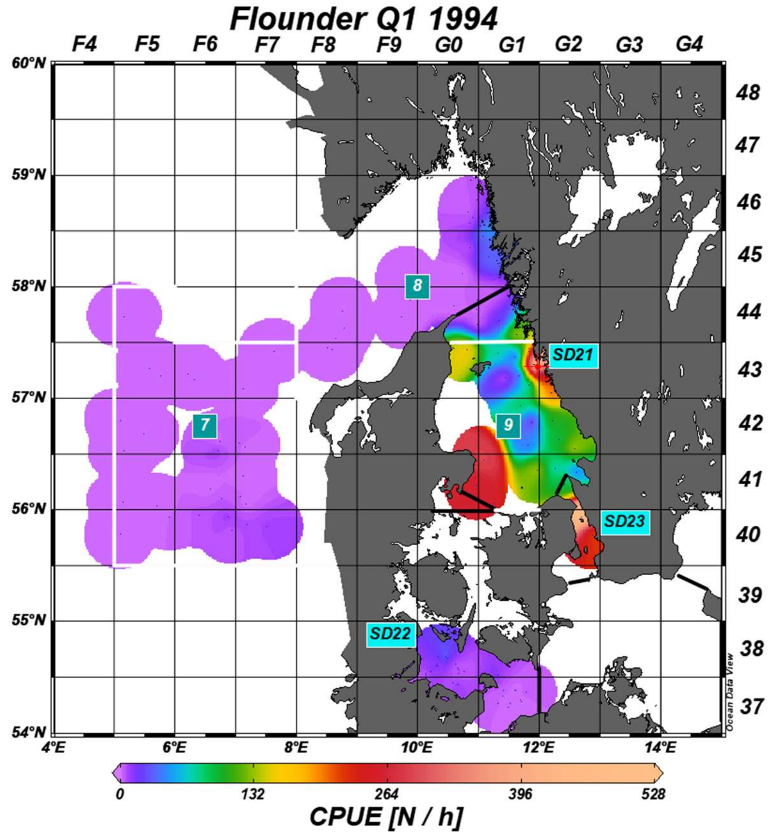

Flounder Q1 1999
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
7
8
9
SD21
SD22
SD23
Ocean Data View
0
113
226
339
452
CPUE [N / h]

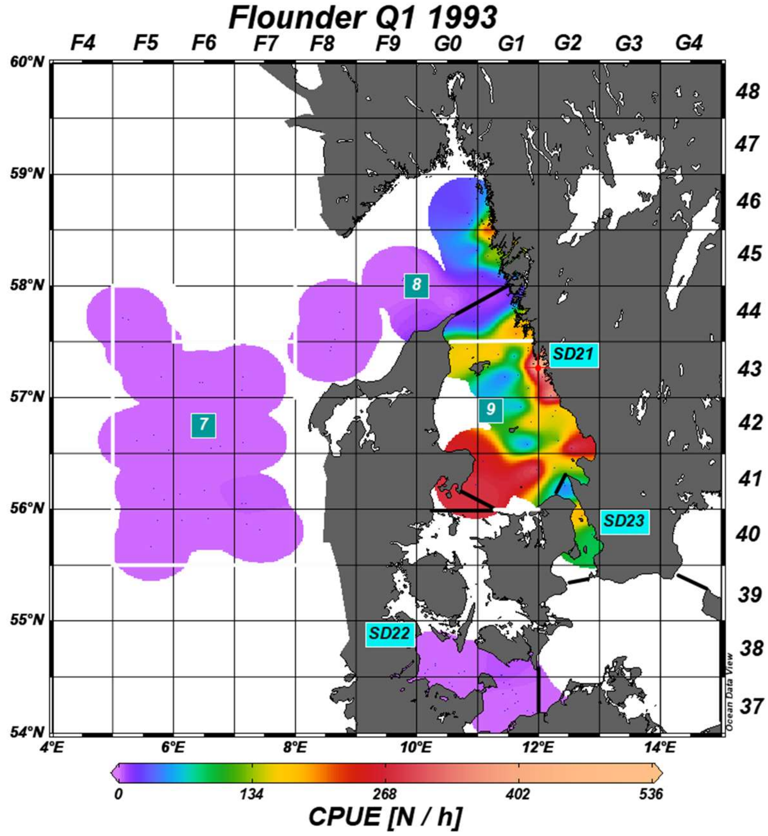

Flounder Q1 1998
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD23
SD22
Ocean Data View
4°E
6°E
8°E
10°E
12°E
14°E
0
135
270
405
540
CPUE [N / h]

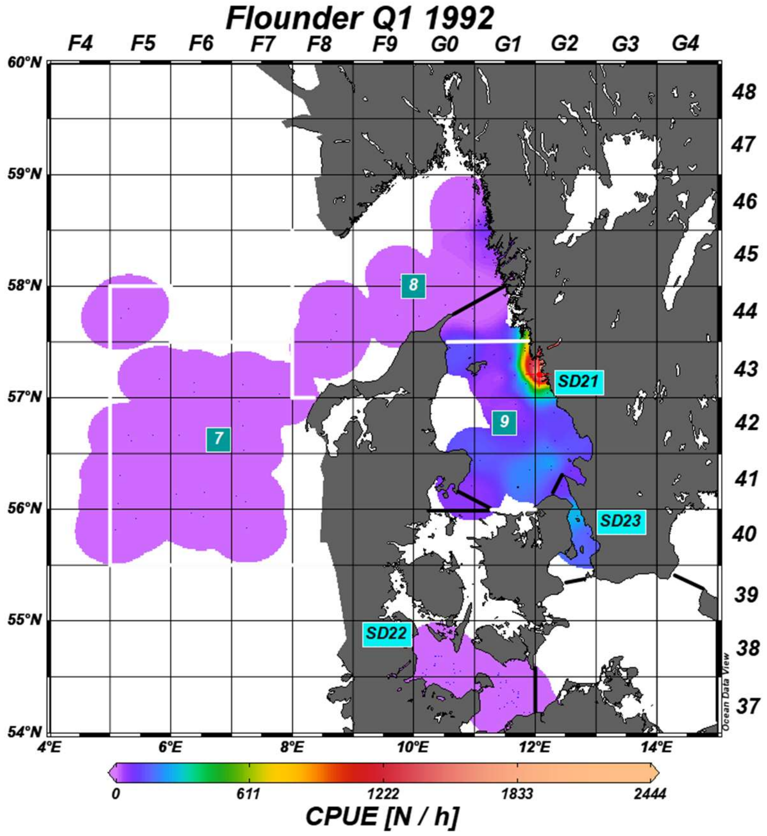

Flounder Q1 1997
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD23
SD22
Ocean Data View
4°E
6°E
8°E
10°E
12°E
14°E
0
166
332
498
664
CPUE [N / h]

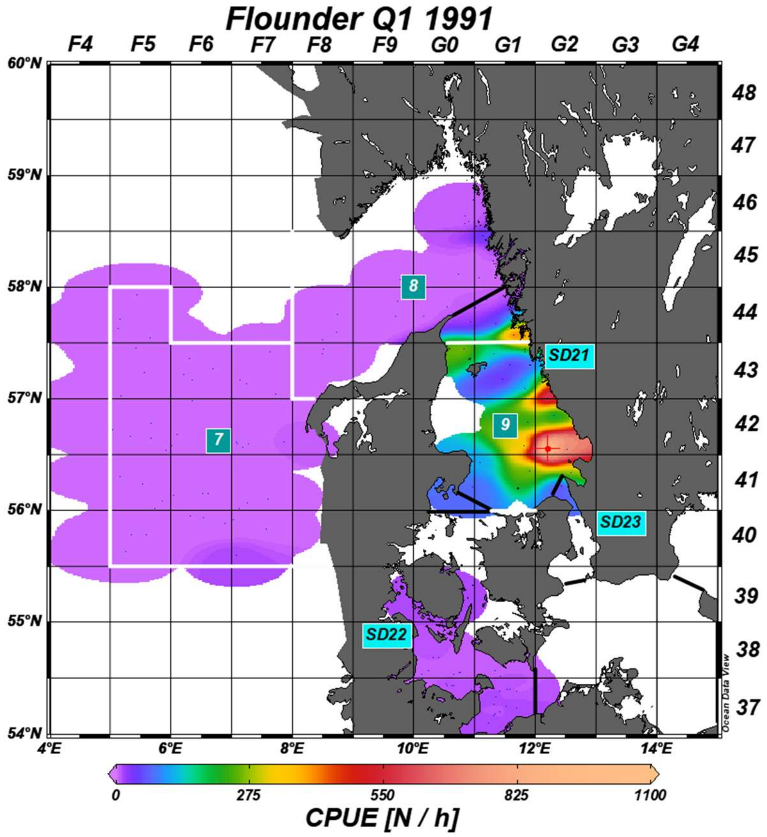

Flounder Q1 1995
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD22
SD23
Ocean Data View
0
130
260
390
520
CPUE [N / h]


Flounder Q1 1996
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD22
SD23
Ocean Data View
0
61
122
183
244
CPUE [N / h]


Flounder Q1 1994
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD23
SD22
4°E
6°E
8°E
10°E
12°E
14°E
0
132
264
396
528
CPUE [N / h]
Ocean Data View


Flounder Q1 1993
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD23
SD22
4°E
6°E
8°E
10°E
12°E
14°E
0
134
268
402
536
CPUE [N / h]
Ocean Data View

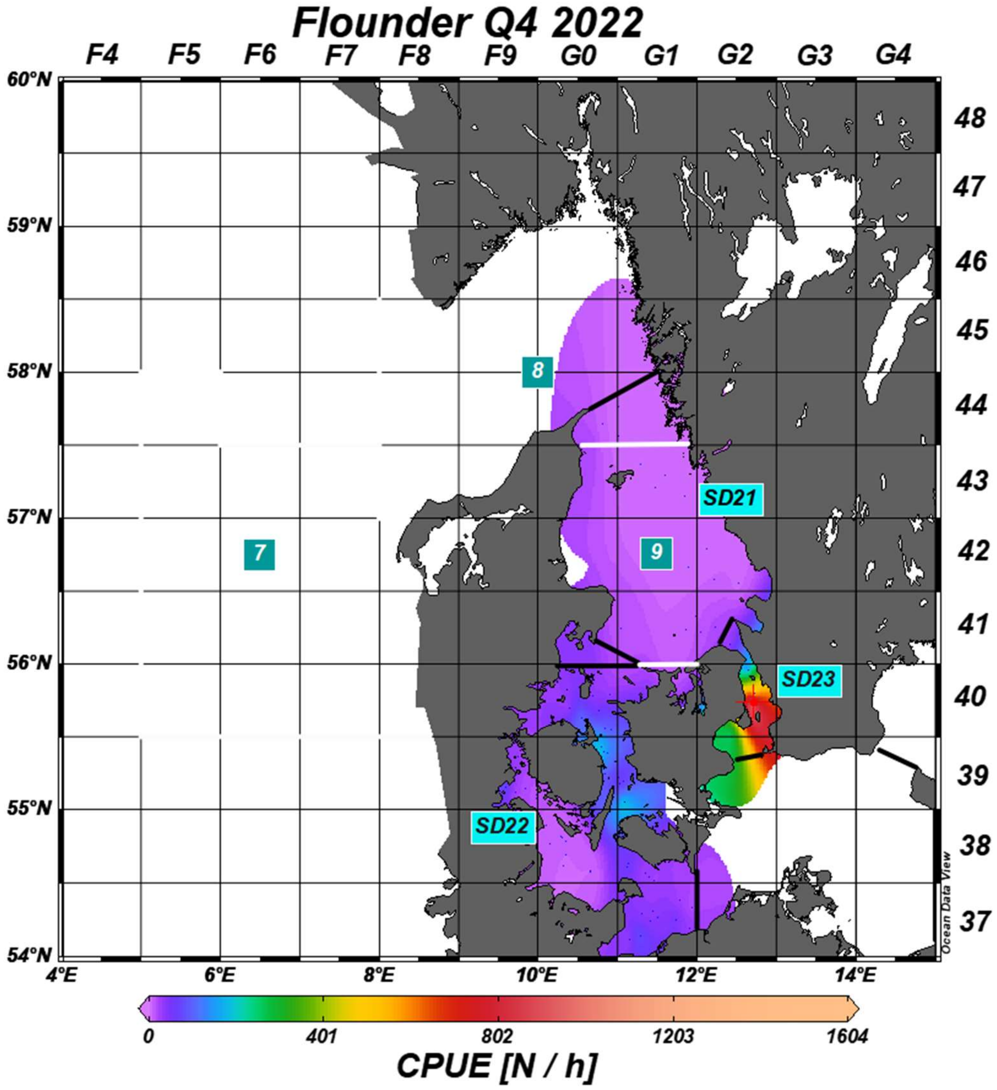

Flounder Q1 1992
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E 6°E 8°E 10°E 12°E 14°E
48 47 46 45 44 43 42 41 40 39 38 37
7
8
9
SD21
SD22
SD23
Ocean Data View
0 611 1222 1833 2444
CPUE [N / h]

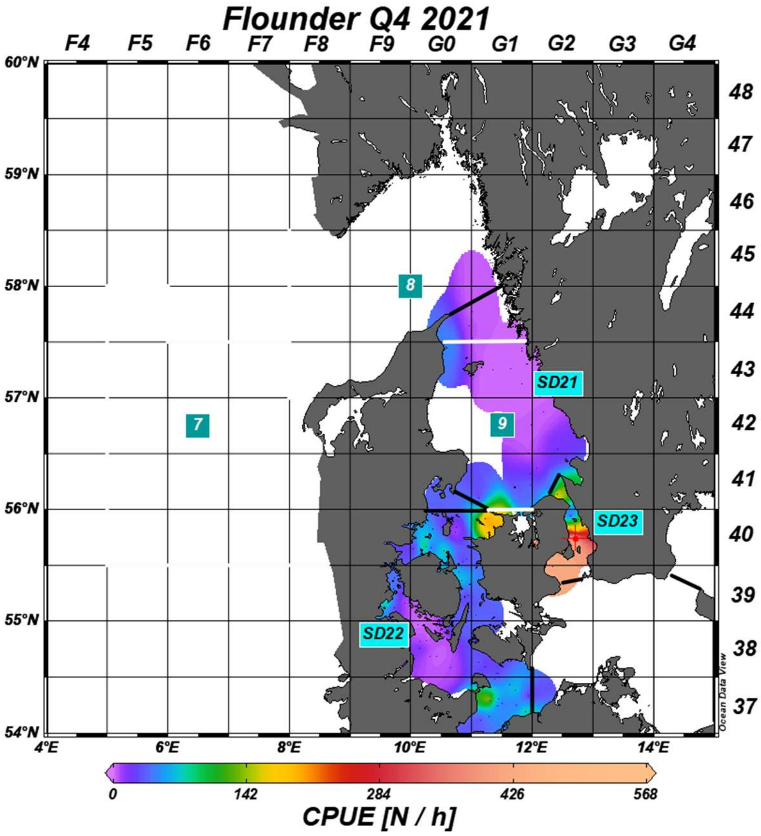

Flounder Q1 1991
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E 6°E 8°E 10°E 12°E 14°E
48 47 46 45 44 43 42 41 40 39 38 37
7
8
9
SD21
SD22
SD23
Ocean Data View
0 275 550 825 1100
CPUE [N / h]

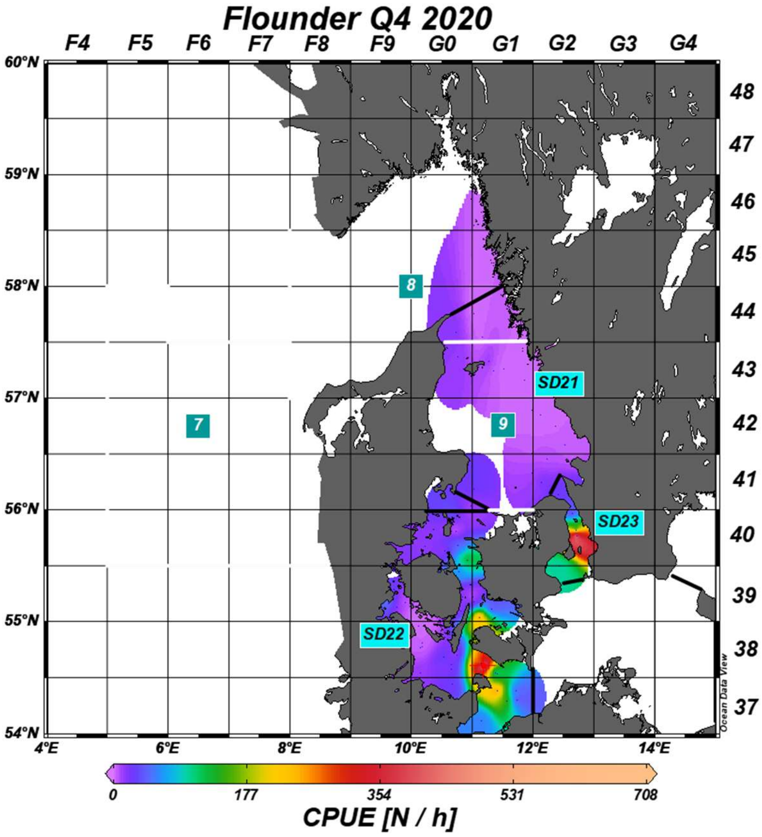
# ANNEX 1.2

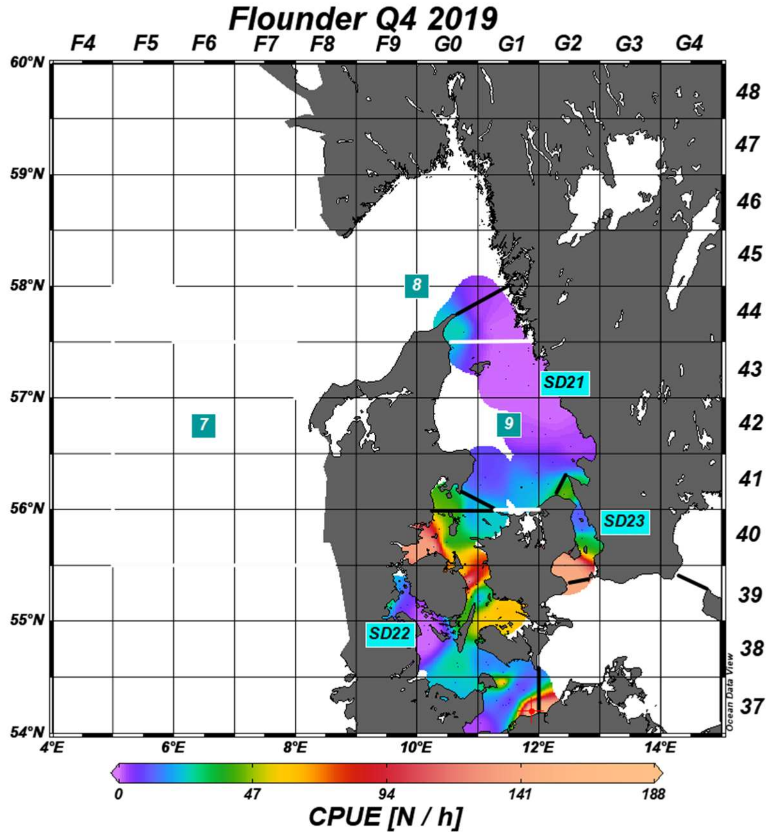
Combined **Quarter 4 Survey Index** CPUE (no/hour) of IBTS, covering Areas 7, 8 and 9 and BITS, covering Areas SD21, 22 and 23. IBTS has not been conducted in Q4 since 1996.

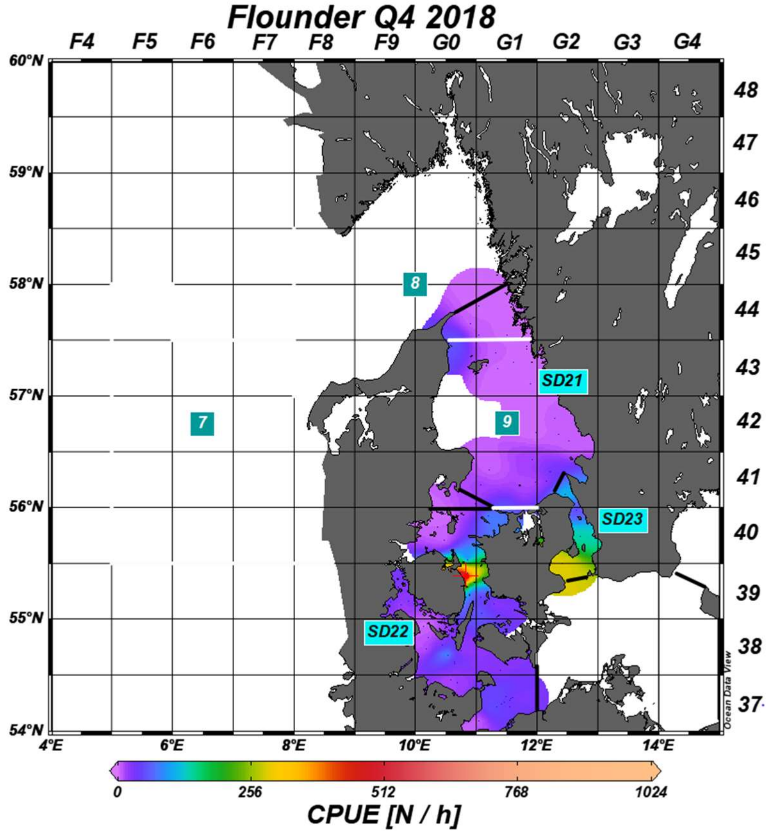
The colour scheme is adjusted to the maximum value of each year to make maps easier to read.

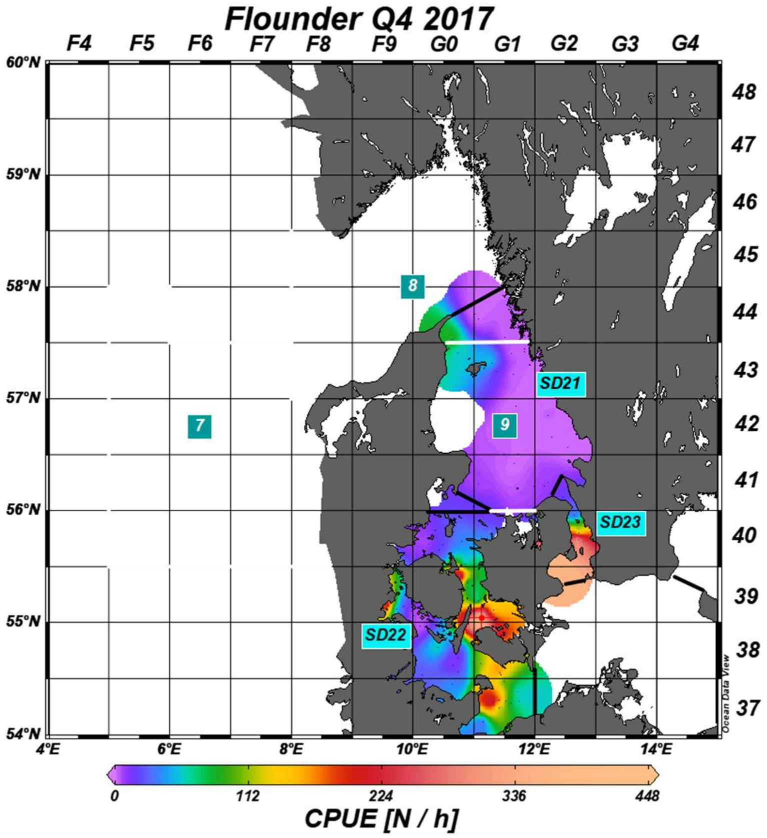


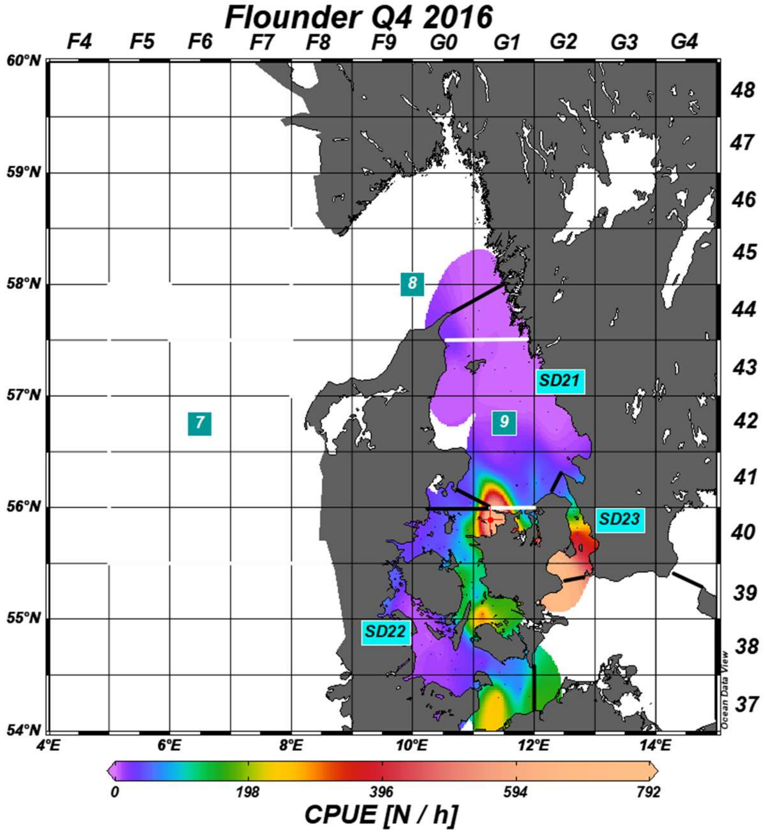

Flounder Q4 2021
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD23
SD22
4°E
6°E
8°E
10°E
12°E
14°E
Ocean Data View
0
142
284
426
568
CPUE [N / h]

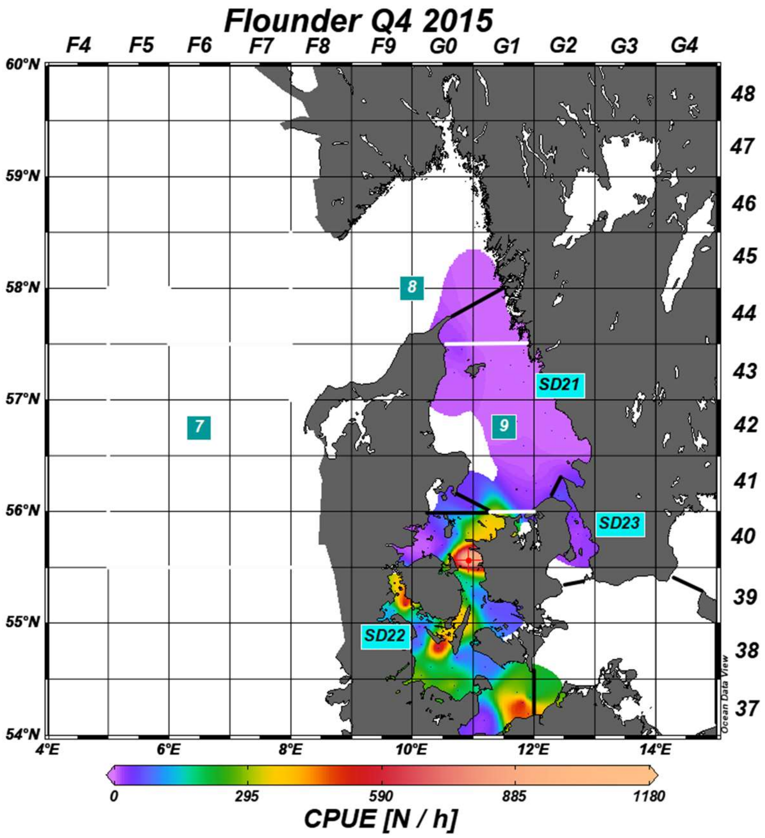

Flounder Q4 2020
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD23
SD22
4°E
6°E
8°E
10°E
12°E
14°E
Ocean Data View
0
177
354
531
708
CPUE [N / h]

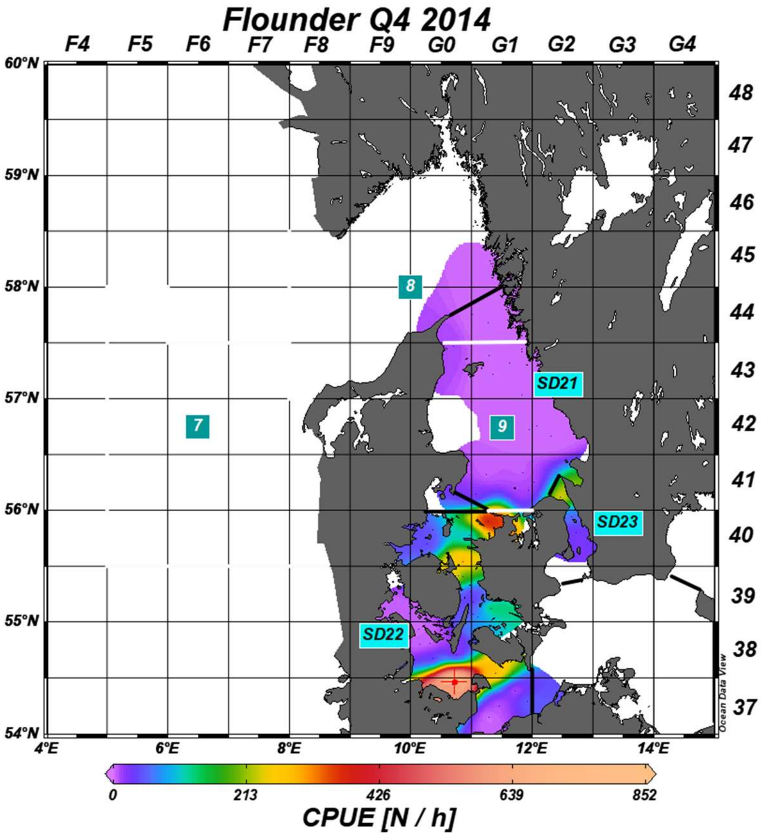

Flounder Q4 2019
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
Ocean Data View
0
47
94
141
188
CPUE [N / h]

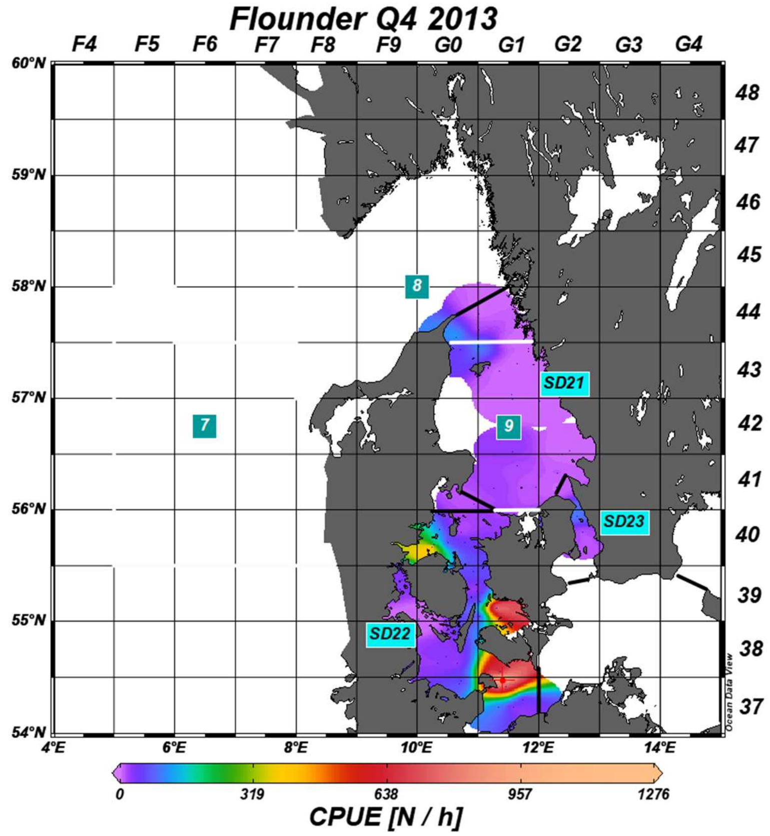

Flounder Q4 2018
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
Ocean Data View
0
256
512
768
1024
CPUE [N / h]

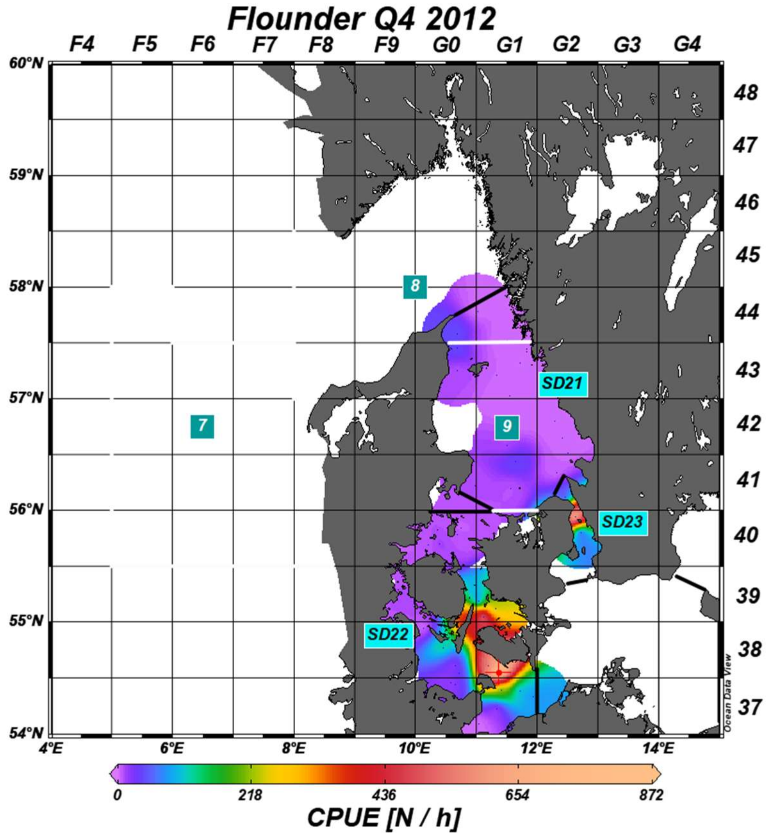

Flounder Q4 2017
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD22
SD23
Ocean Data View
0
112
224
336
448
CPUE [N / h]

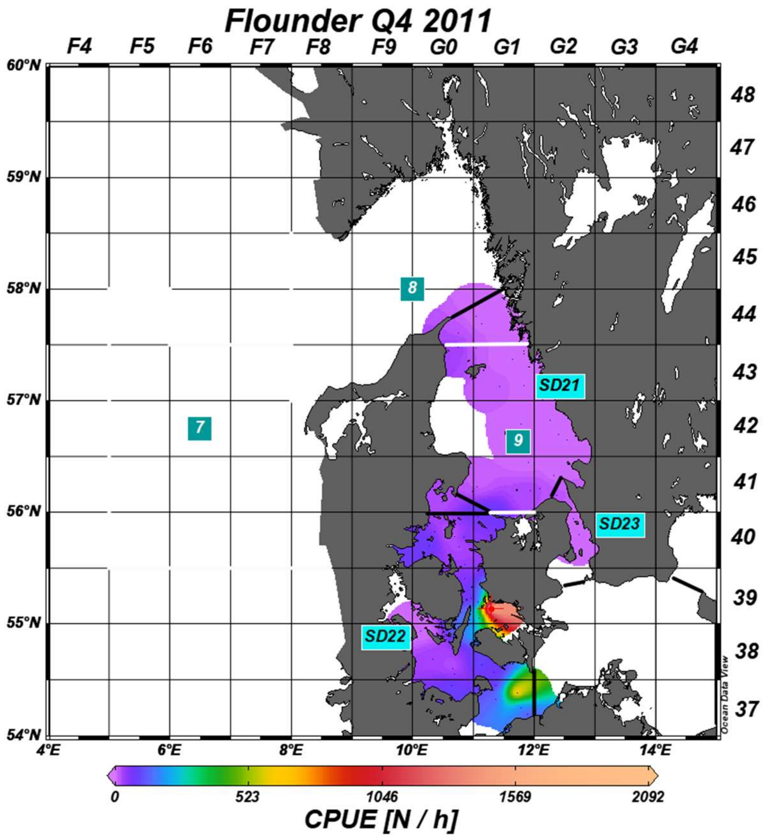

Flounder Q4 2016
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD22
SD23
Ocean Data View
0
198
396
594
792
CPUE [N / h]

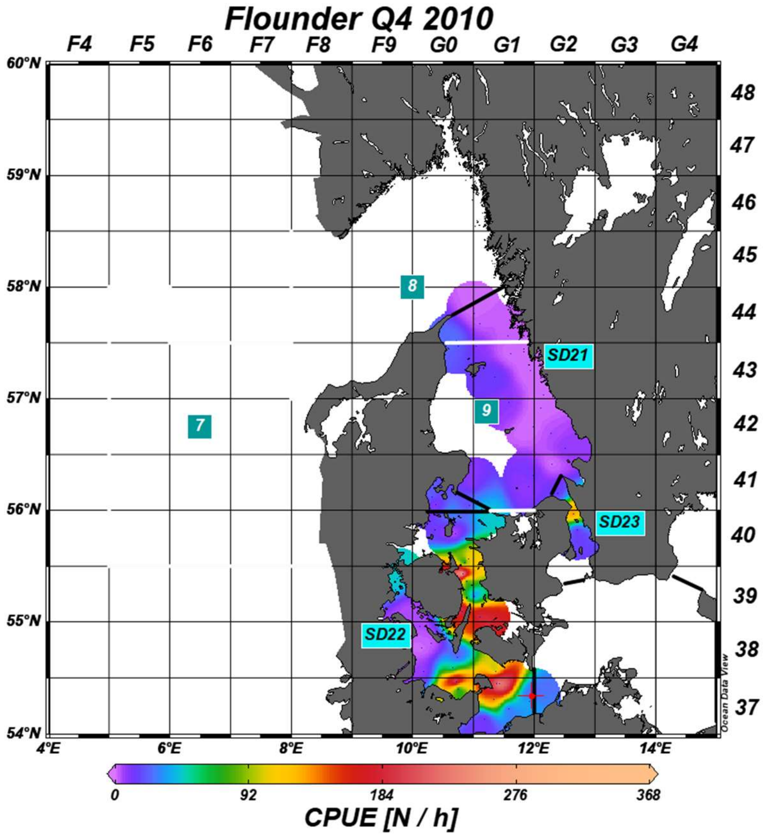

Flounder Q4 2015
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
4°E
6°E
8°E
10°E
12°E
14°E
Ocean Data View
0
295
590
885
1180
CPUE [N / h]

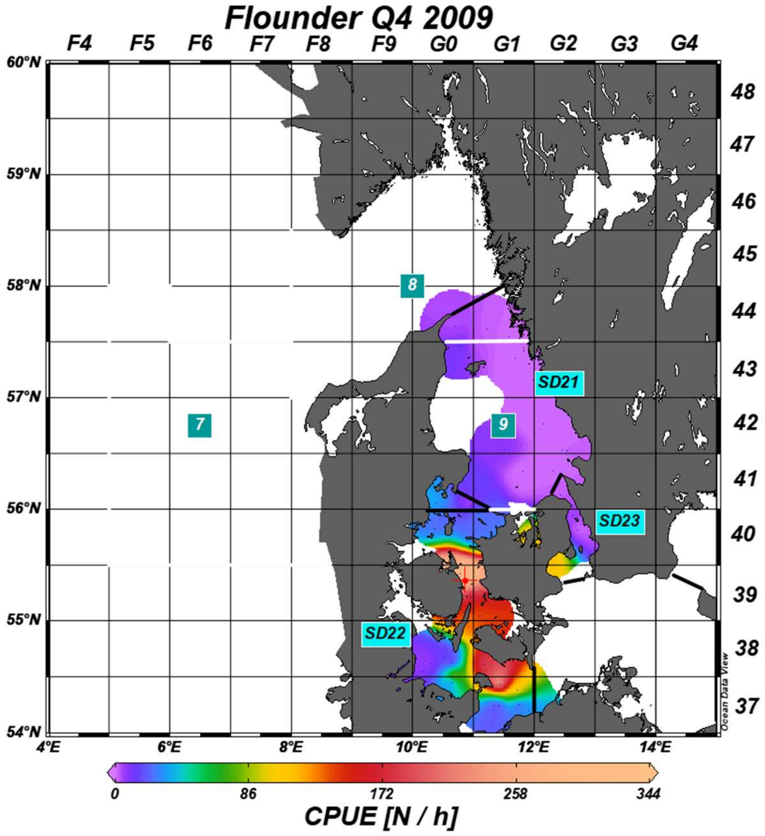

Flounder Q4 2014
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
4°E
6°E
8°E
10°E
12°E
14°E
Ocean Data View
0
213
426
639
852
CPUE [N / h]

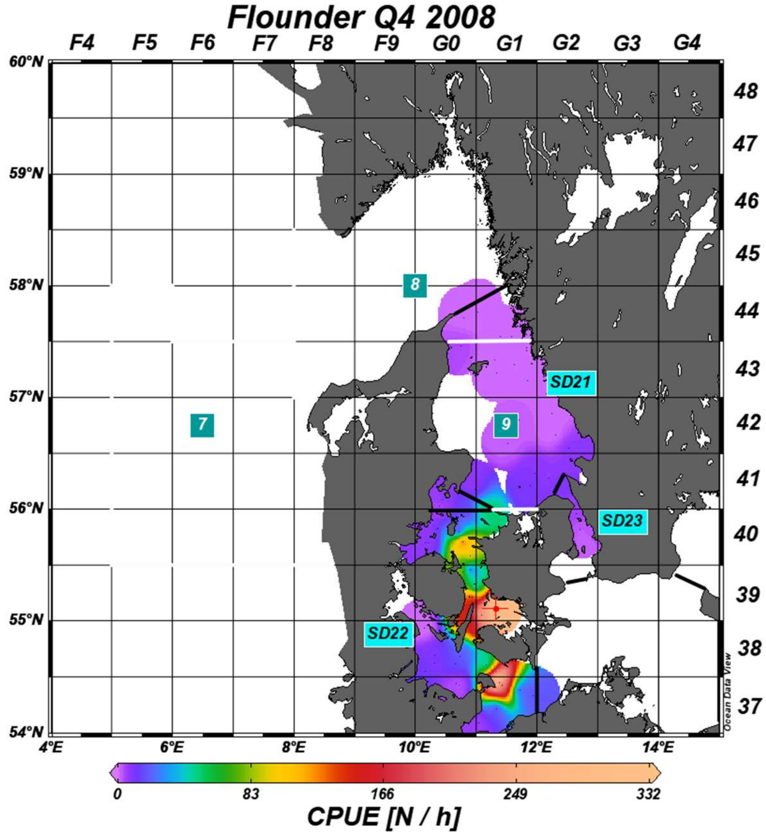

Flounder Q4 2013
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD22
SD23
Ocean Data View
0
319
638
957
1276
CPUE [N / h]

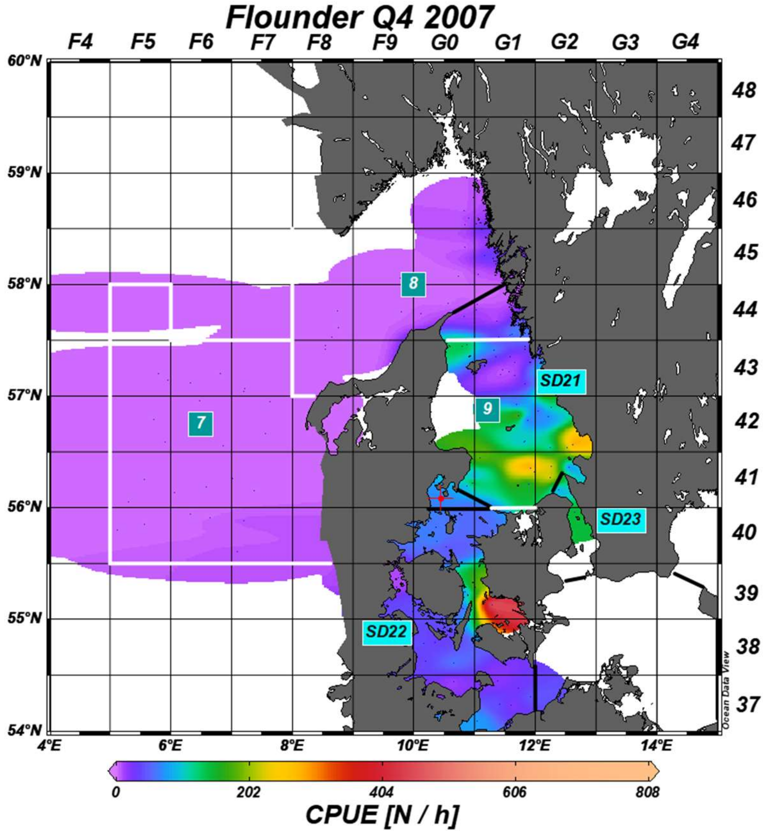

Flounder Q4 2012
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD22
SD23
Ocean Data View
0
218
436
654
872
CPUE [N / h]

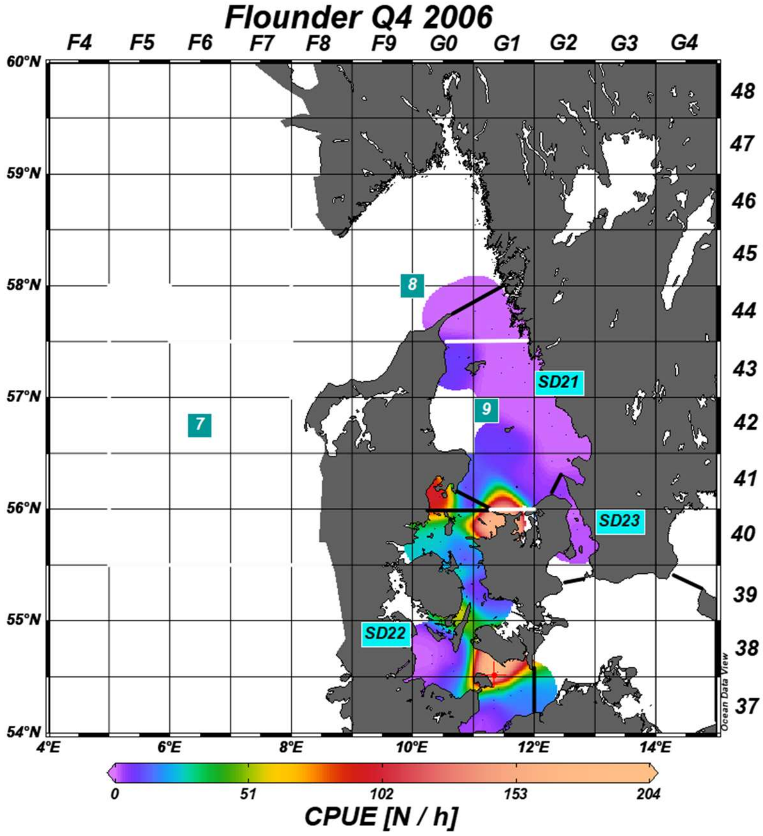

Flounder Q4 2011
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48 47 46 45 44 43 42 41 40 39 38 37
8
7
9
SD21
SD23
SD22
4°E 6°E 8°E 10°E 12°E 14°E
Ocean Data View
0 523 1046 1569 2092
CPUE [N / h]

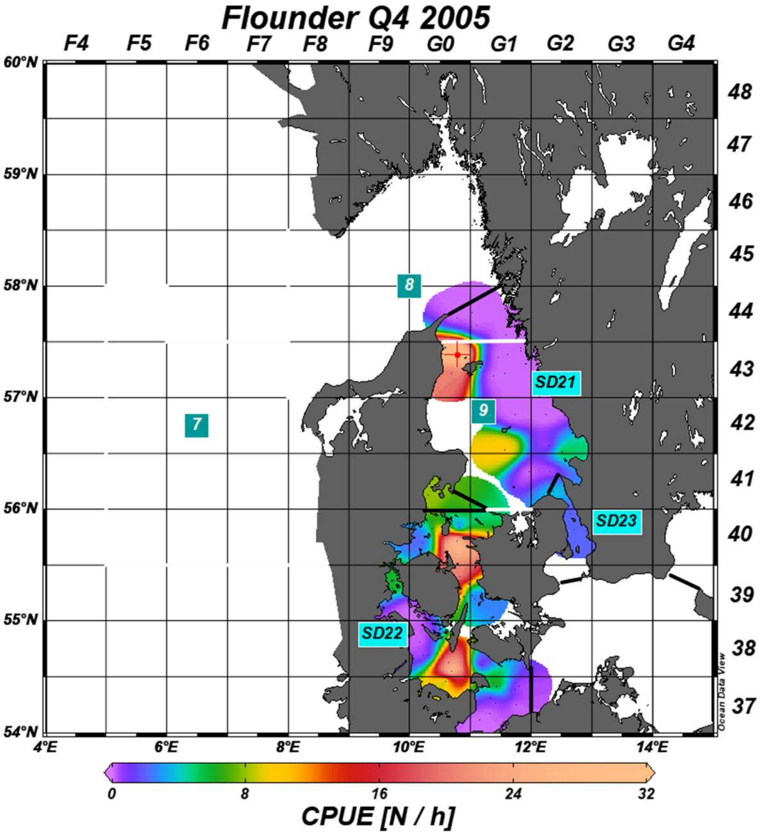

Flounder Q4 2010
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48 47 46 45 44 43 42 41 40 39 38 37
8
7
9
SD21
SD23
SD22
4°E 6°E 8°E 10°E 12°E 14°E
Ocean Data View
0 92 184 276 368
CPUE [N / h]

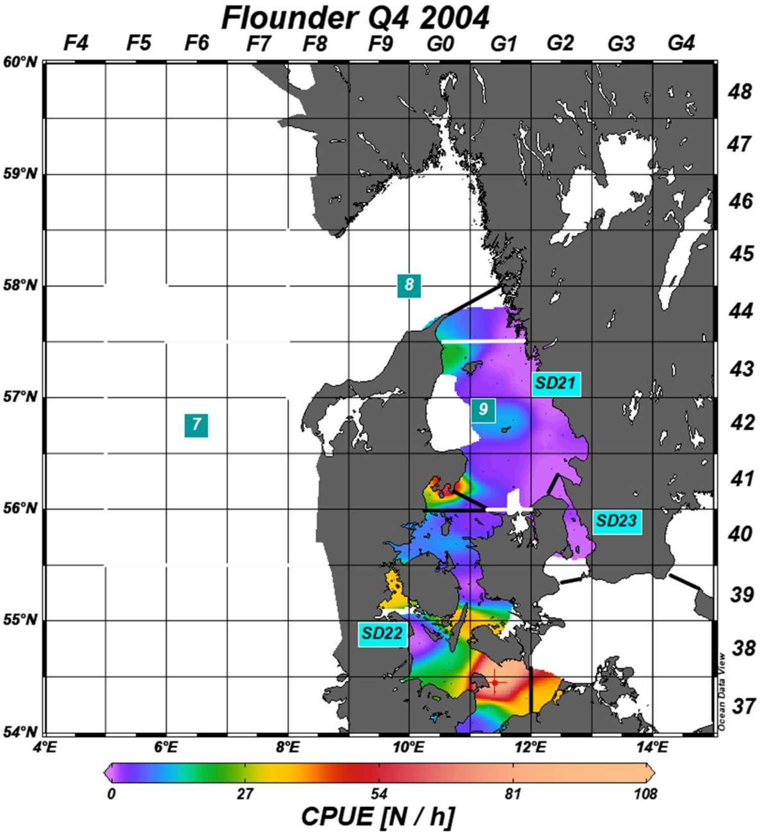

Flounder Q4 2009
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD22
SD23
Ocean Data View
0
86
172
258
344
CPUE [N / h]

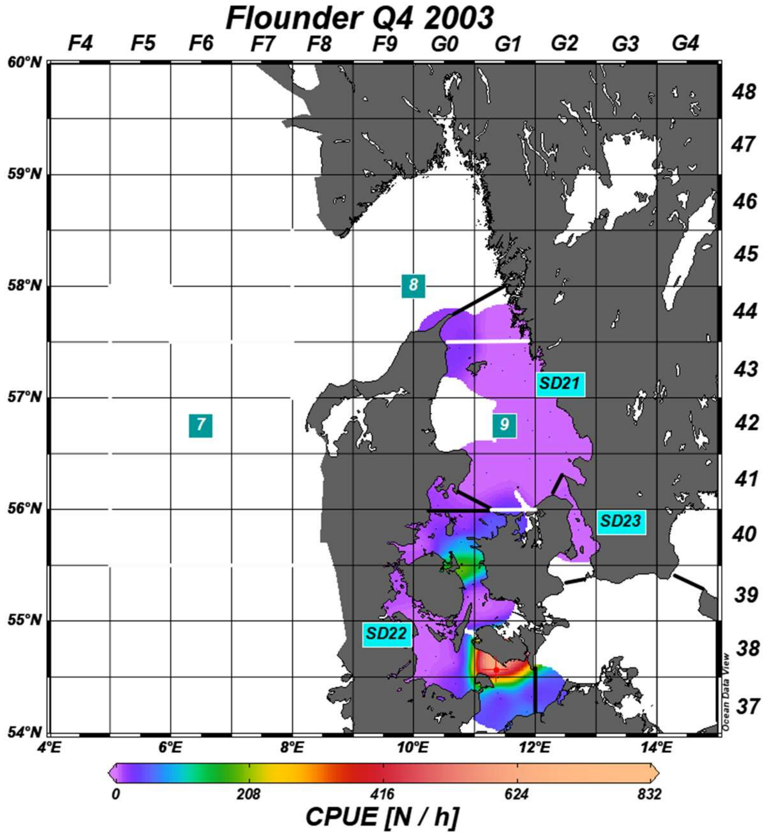

Flounder Q4 2008
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD22
SD23
Ocean Data View
0
83
166
249
332
CPUE [N / h]

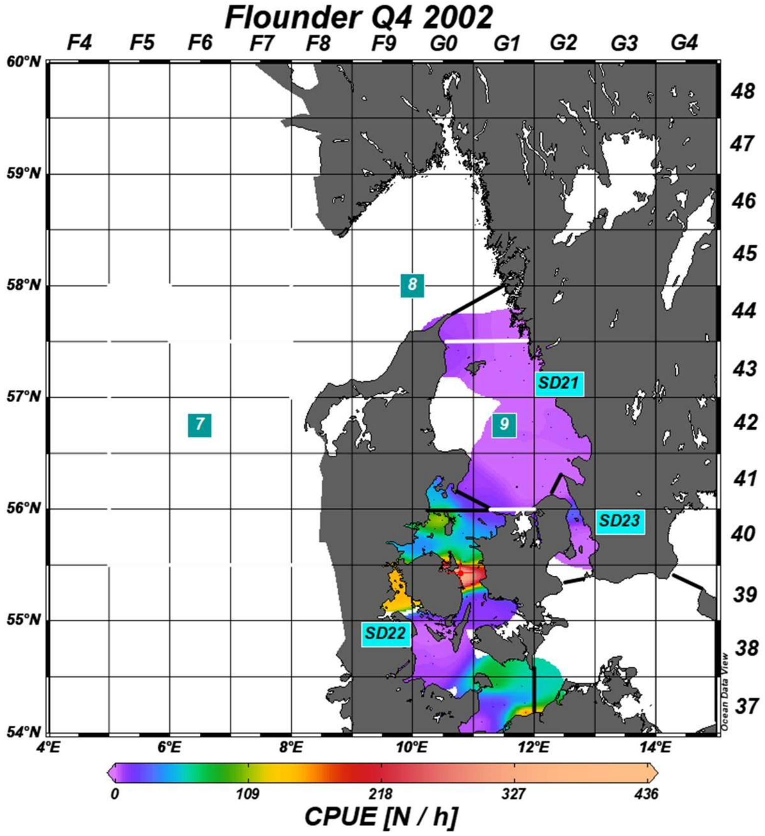

Flounder Q4 2007
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD22
SD23
Ocean Data View
0
202
404
606
808
CPUE [N / h]

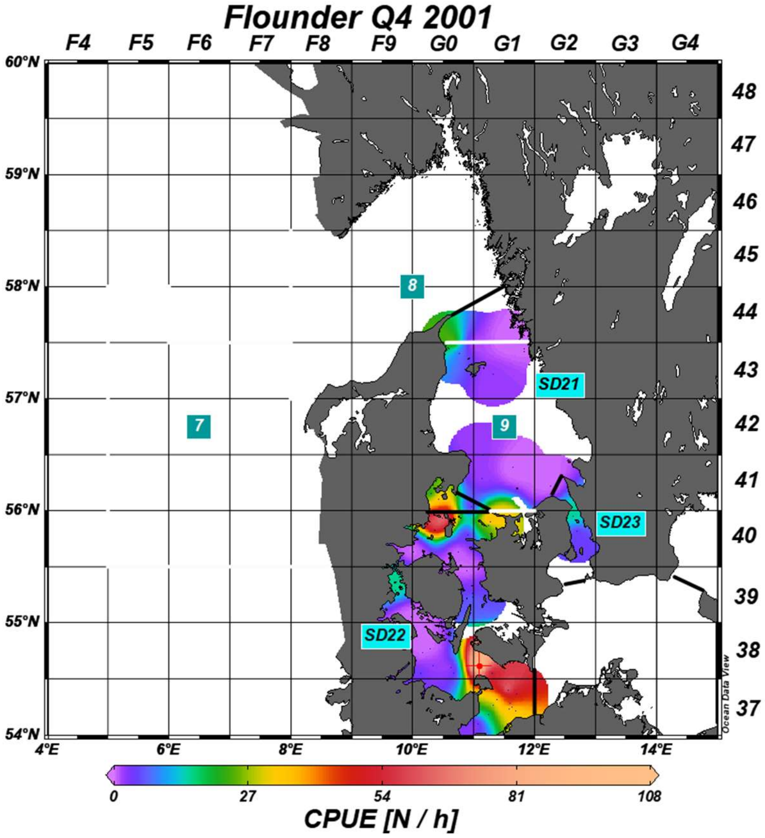

Flounder Q4 2006
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD22
SD23
Ocean Data View
0
51
102
153
204
CPUE [N / h]


Flounder Q4 2005
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
8
16
24
32
CPUE [N / h]

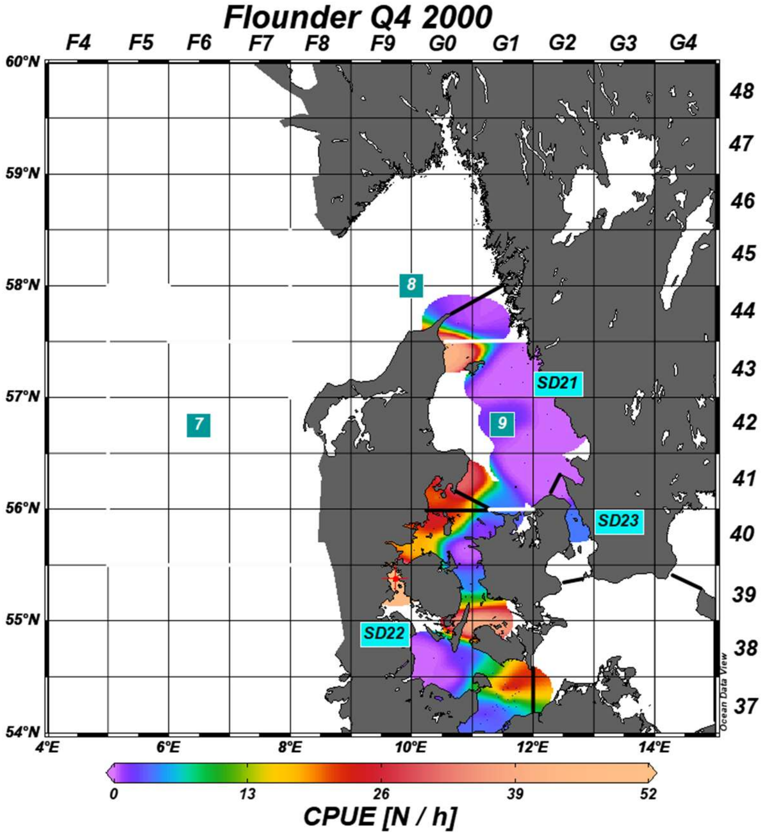

Flounder Q4 2004
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
27
54
81
108
CPUE [N / h]


Flounder Q4 2003
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
208
416
624
832
CPUE [N / h]

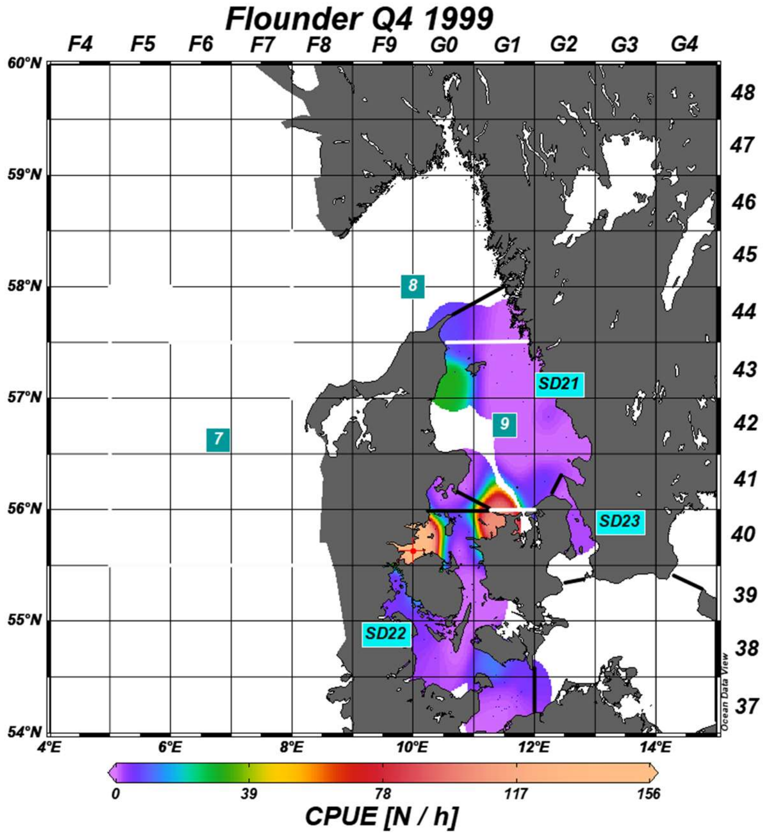

Flounder Q4 2002
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
109
218
327
436
CPUE [N / h]

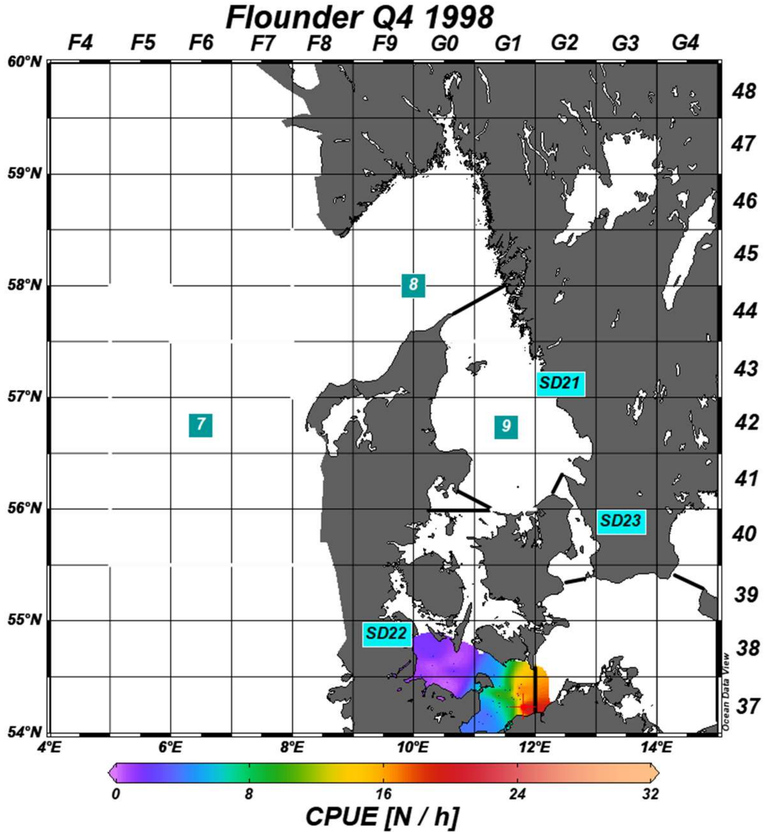


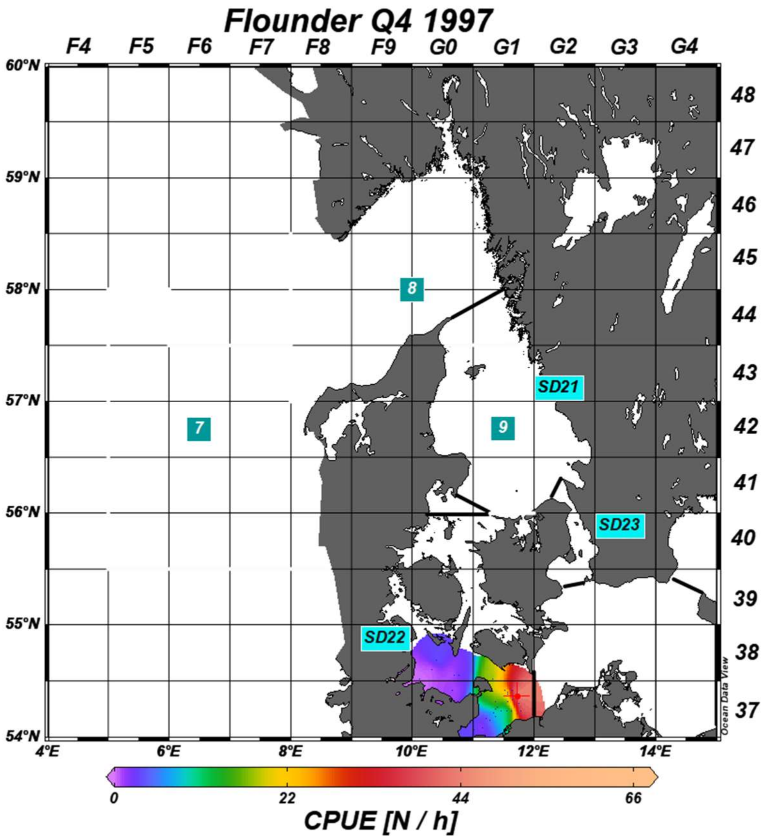
Flounder Q4 2001

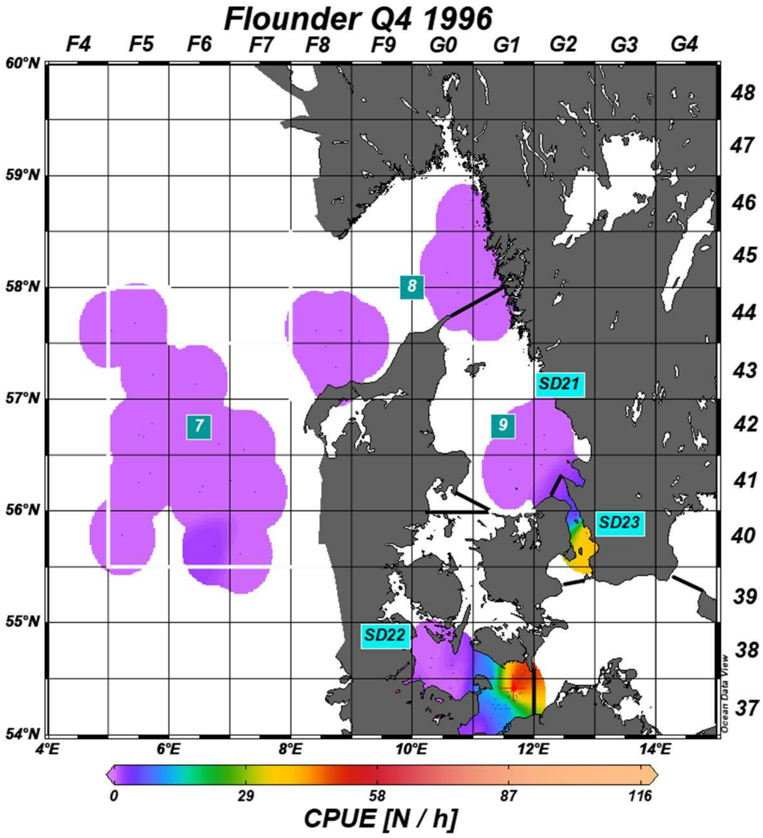


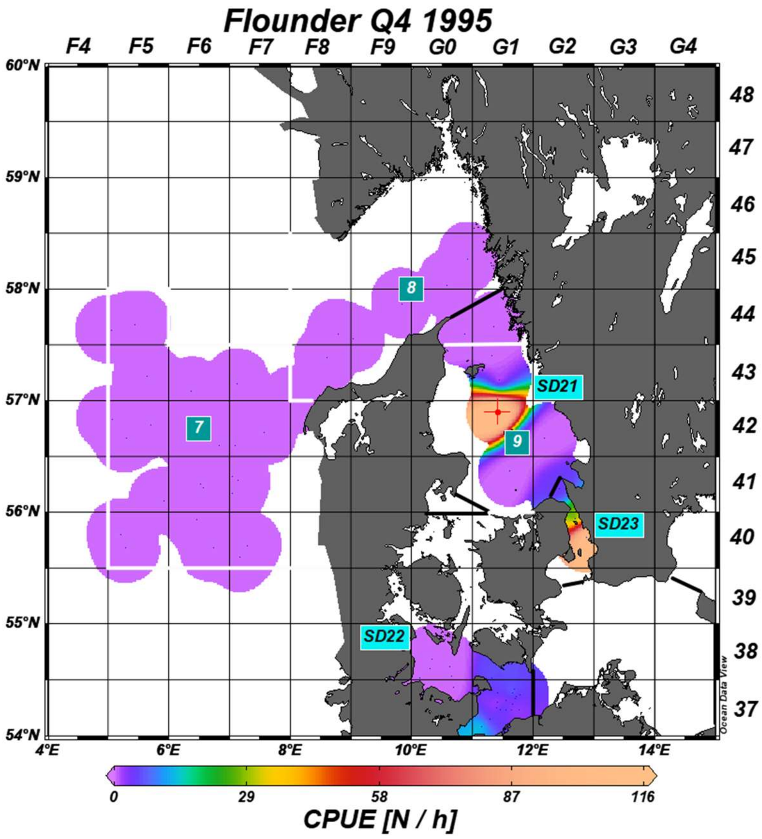
Flounder Q4 2000

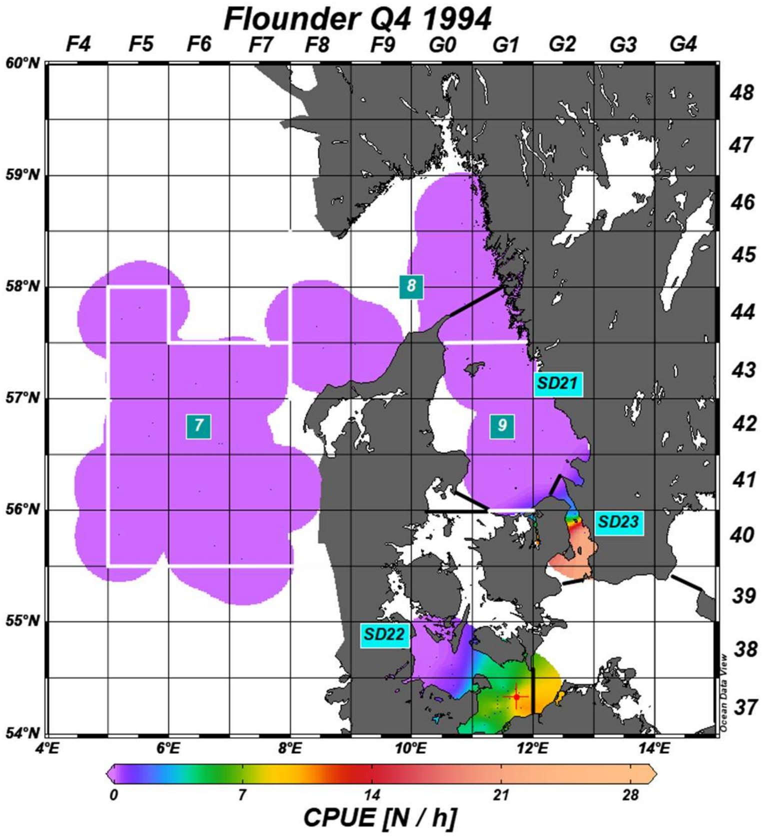

Flounder Q4 1999
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
4°E
6°E
8°E
10°E
12°E
14°E
Ocean Data View
0
39
78
117
156
CPUE [N / h]

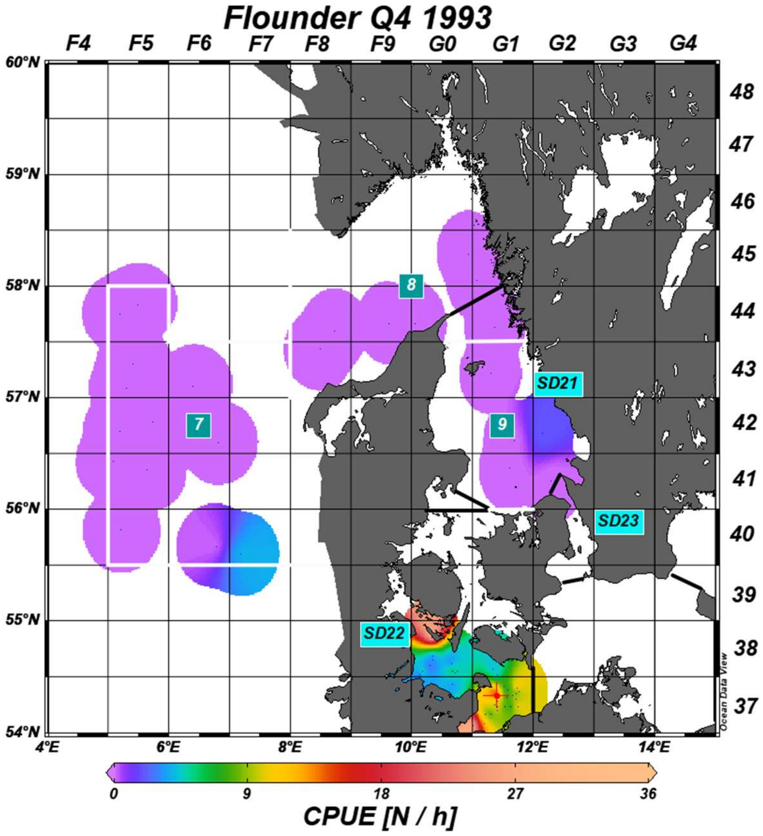

Flounder Q4 1998
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
4°E
6°E
8°E
10°E
12°E
14°E
Ocean Data View
0
8
16
24
32
CPUE [N / h]

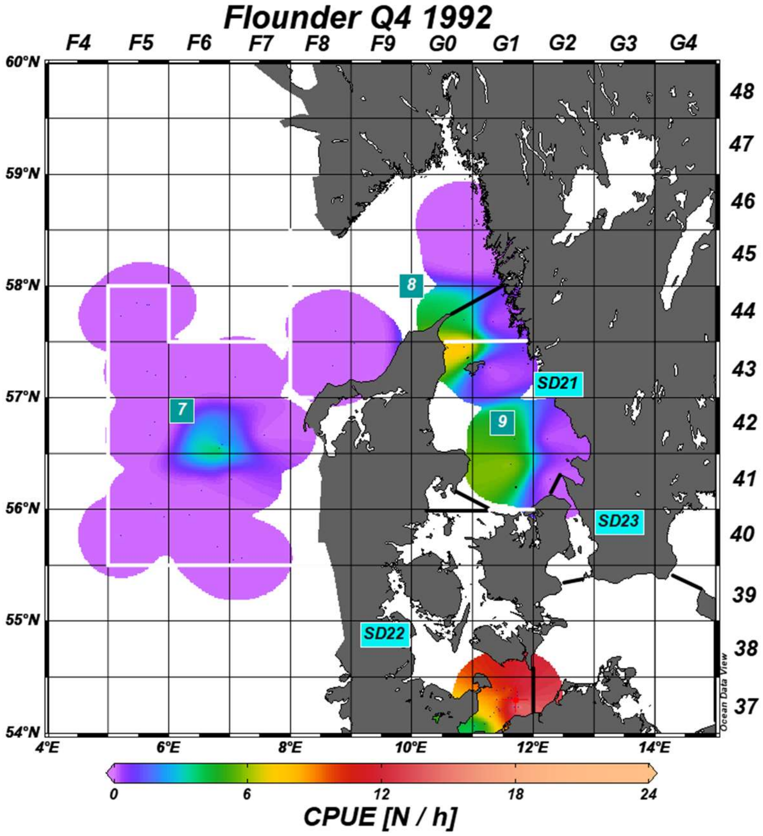

Flounder Q4 1997
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
4°E
6°E
8°E
10°E
12°E
14°E
Ocean Data View
0
22
44
66
CPUE [N / h]

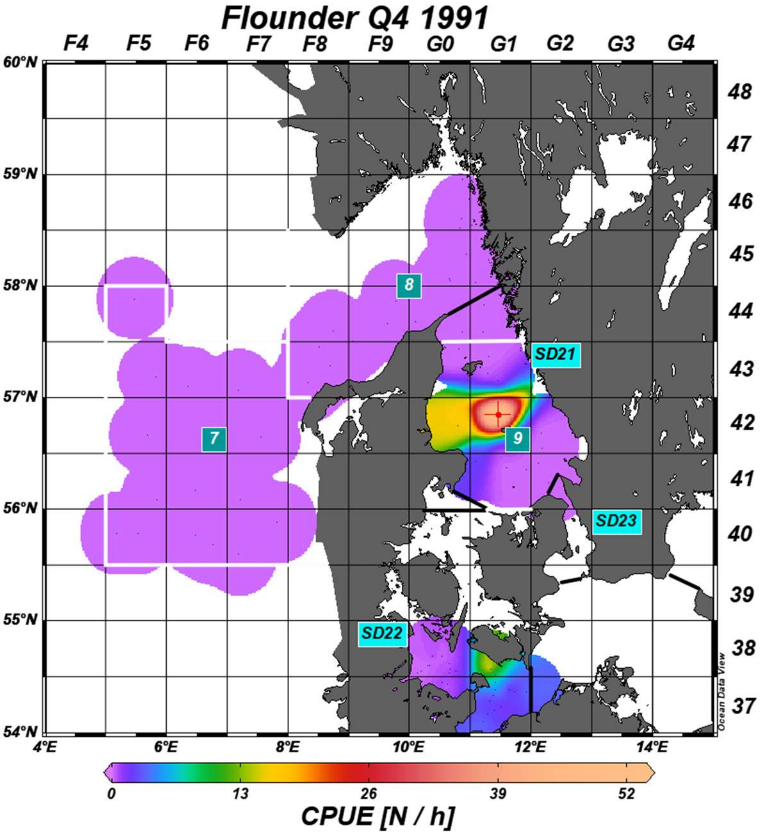

Flounder Q4 1996
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
4°E
6°E
8°E
10°E
12°E
14°E
Ocean Data View
0
29
58
87
116
CPUE [N / h]


Flounder Q4 1995
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
29
58
87
116
CPUE [N / h]


Flounder Q4 1994
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
7
14
21
28
CPUE [N / h]


Flounder Q4 1993
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N 59°N 58°N 57°N 56°N 55°N 54°N
48 47 46 45 44 43 42 41 40 39 38 37
4°E 6°E 8°E 10°E 12°E 14°E
7
8
9
SD21
SD22
SD23
Ocean Data View
0 9 18 27 36
CPUE [N / h]


Flounder Q4 1992
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N 59°N 58°N 57°N 56°N 55°N 54°N
48 47 46 45 44 43 42 41 40 39 38 37
4°E 6°E 8°E 10°E 12°E 14°E
7
8
9
SD21
SD22
SD23
Ocean Data View
0 6 12 18 24
CPUE [N / h]


Flounder Q4 1991
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
7
8
9
SD21
SD22
SD23
Ocean Data View
0
13
26
39
52
CPUE [N / h]

# ANNEX 1.3

## Annual landings of flounder in tons per ICES Subdivision and statistical rectangle

All data are taken from the Regional Database (RDB) hosted by ICES (ICES 2023a). Aggregation of data is following the ICES Data Guidelines (ICES 2023b)

ICES. 2023a. Regional Database (RDB) and Regional Database and Estimation System (RDBES). ICES Data Portal: https://www.rdb-fishframe.org/

ICES. 2023b. Data policy for the Regional Database (RDB) and Regional Database and Estimation System (RDBES). ICES Data Guidelines. 7 pp. https://doi.org/10.17895/ices.pub.22188157

| Area | 2019 | 2020 | 2021 | 2022 | average | % |
|---|---|---|---|---|---|---|
| **27.3.a.20** | **42.37** | **17.015** | **24.958** | **18.913** | | |
| **43F8** | 8.084 | 2.316 | 4.057 | 3.182 | 4.410 | **17.1%** |
| **43F9** | 10.383 | 3.679 | 9.572 | 6.077 | 7.428 | **28.7%** |
| **43G0** | | | 0.002 | | 0.002 | **0.0%** |
| **43G1** | | | 0.033 | | 0.033 | **0.1%** |
| **44F7** | 0.037 | | 0.01 | 0.003 | 0.017 | **0.1%** |
| **44F8** | 0.076 | 0.197 | 0.033 | 0.02 | 0.082 | **0.3%** |
| **44F9** | 7.945 | 1.851 | 6.358 | 2.524 | 4.670 | **18.1%** |
| **44G0** | 15.069 | 3.757 | 3.868 | 5.878 | 7.143 | **27.6%** |
| **44G1** | 0.736 | 4.992 | 0.937 | 1.079 | 1.936 | **7.5%** |
| **45F9** | 0.003 | 0.007 | | 0.002 | 0.004 | **0.0%** |
| **45G0** | 0.013 | 0.027 | 0.028 | 0.071 | 0.035 | **0.1%** |
| **45G1** | 0.015 | 0.181 | 0.04 | 0.048 | 0.071 | **0.3%** |
| **46G0** | 0.009 | 0.008 | 0.02 | 0.008 | 0.011 | **0.0%** |
| **46G1** | | | | 0.015 | 0.015 | **0.1%** |
| **47G0** | | | | 0.006 | 0.006 | **0.0%** |

| Area | 2019 | 2020 | 2021 | 2022 | average | % |
|---|---|---|---|---|---|---|
| **27.3.a.21** | **78.182** | **78.447** | **66.333** | **78.887** | | |
| **40F7** | | | 0.229 | | 0.229 | 0.30% |
| **40G1** | 0.615 | 0.35 | 0.612 | 2.809 | 1.097 | 1.45% |
| **40G2** | 0.591 | 0.017 | 0.36 | 0.77 | 0.435 | 0.57% |
| **41G0** | 0.63 | 1.189 | 0.793 | 0.6 | 0.803 | 1.06% |
| **41G1** | 21.717 | 28.194 | 15.147 | 26.112 | 22.793 | 30.12% |
| **41G2** | 31.091 | 18.456 | 17.032 | 21.471 | 22.013 | 29.09% |
| **42G0** | 0.014 | 0.001 | 0.581 | 1.075 | 0.418 | 0.55% |
| **42G1** | 9.552 | 12.953 | 13.93 | 12.611 | 12.262 | 16.20% |
| **42G2** | 7.386 | 2.415 | 6.03 | 4.587 | 5.105 | 6.74% |

| | | | | | | |
|---|---|---|---|---|---|---|
| **43G0** | 1.59 | 2.89 | 1.549 | 1.793 | 1.956 | 2.58% |
| **43G1** | 1.182 | 2.751 | 2.59 | 1.422 | 1.986 | 2.62% |
| **43G2** | 0.003 | 0.226 | 0.085 | 0.046 | 0.090 | 0.12% |
| **44F9** | | | 0.06 | | 0.060 | 0.08% |
| **44G0** | 2.88 | 4.666 | 6.176 | 4.214 | 4.484 | 5.93% |
| **44G1** | 0.931 | 4.339 | 1.159 | 1.377 | 1.952 | 2.58% |

| Area | 2019 | 2020 | 2021 | 2022 | average | % |
|---|---|---|---|---|---|---|
| **27.3.b.23** | **64.449** | **43.687** | **45.44** | **30.248** | | |
| **39G2** | 5.968 | 3.552 | 4.239 | 2.36 | 4.030 | 8.77% |
| **40G2** | 47.593 | 29.26 | 35.082 | 19.387 | 32.831 | 71.44% |
| **40G3** | 1.293 | 1.633 | 2.177 | 3.61 | 2.178 | 4.74% |
| **41G2** | 9.595 | 9.242 | 3.942 | 4.891 | 6.918 | 15.05% |

| Area | 2019 | 2020 | 2021 | 2022 | average | % |
|---|---|---|---|---|---|---|
| **27.3.c.22** | **1055.812** | **697.052** | **480.367** | **291.322** | | |
| **36G0** | | | | 0.008 | 0.008 | 0.00% |
| **37F0** | | 0.081 | 0.046 | 0.032 | 0.053 | 0.01% |
| **37F9** | 1.377 | 2.489 | 2.181 | 3.311 | 2.340 | 0.37% |
| **37G0** | 66.428 | 73.938 | 57.232 | 50.079 | 61.919 | 9.80% |
| **37G1** | 254.742 | 212.689 | 128.976 | 79.146 | 168.888 | 26.73% |
| **37G2** | | | | 0.297 | 0.297 | 0.05% |
| **38F9** | 11.568 | 13.395 | 14.571 | 16.04 | 13.894 | 2.20% |
| **38G0** | 542.282 | 310.115 | 219.864 | 111.809 | 296.018 | 46.85% |
| **38G1** | 19.791 | 25.52 | 15.932 | 1.55 | 15.698 | 2.48% |
| **38G2** | | 0.327 | 0.005 | | 0.166 | 0.03% |
| **38H0** | 0.25 | | | | 0.250 | 0.04% |
| **39F9** | 6.709 | 3.867 | 9.548 | 7.379 | 6.876 | 1.09% |
| **39G0** | 71.185 | 38.742 | 16.832 | 11.967 | 34.682 | 5.49% |
| **39G1** | 67.183 | 12.444 | 9.222 | 2.721 | 22.893 | 3.62% |
| **40F9** | | | | 0.062 | 0.062 | 0.01% |
| **40G0** | 8.377 | 2.657 | 1.024 | 0.963 | 3.255 | 0.52% |
| **40G1** | 4.798 | 0.788 | 4.592 | 5.64 | 3.955 | 0.63% |
| **41G0** | 0.004 | | 0.187 | 0.303 | 0.165 | 0.03% |
| **41G1** | 1.118 | | 0.155 | 0.015 | 0.429 | 0.07% |

| Area | 2019 | 2020 | 2021 | 2022 | average | % |
|---|---|---|---|---|---|---|
| **27.4.b** | **136.453** | **127.172** | **102.883** | **35.833** | | |
| **36F2** | 0.013 | 0.012 | 0.005 | 0.02 | 0.013 | 0.02% |
| **36F3** | 0.046 | 0.012 | 0.059 | | 0.039 | 0.06% |
| **36F4** | 0.497 | 0.507 | 2.696 | 0.259 | 0.990 | 1.62% |
| **36F5** | 0.003 | 0.138 | 3.753 | 0.01 | 0.976 | 1.59% |
| **36F6** | | 0.024 | | | 0.024 | 0.04% |
| **36F7** | 0.132 | 0.004 | 0.02 | 0.015 | 0.043 | 0.07% |
| **36F8** | 0.081 | | 0.03 | | 0.056 | 0.09% |
| **36F9** | 0.064 | 0.066 | 0.031 | | 0.054 | 0.09% |
| **37F3** | | 0.012 | | | 0.012 | 0.02% |
| **37F4** | 0.014 | 0.002 | 0.126 | 0.001 | 0.036 | 0.06% |
| **37F5** | 0.102 | 0.33 | 1.898 | 0.171 | 0.625 | 1.02% |
| **37F6** | 0.042 | 0.28 | 0.782 | 0.005 | 0.277 | 0.45% |
| **37F7** | 0.36 | 0.178 | 0.087 | | 0.208 | 0.34% |
| **37F8** | 0.204 | 0.034 | 0.01 | | 0.083 | 0.13% |
| **37F9** | | 2.489 | | | 2.489 | 4.06% |
| **38F1** | | 0.033 | | | 0.033 | 0.05% |
| **38F2** | | 0.054 | | | 0.054 | 0.09% |
| **38F5** | 0.026 | 0.001 | 0.002 | | 0.010 | 0.02% |
| **38F6** | 0.028 | 0.032 | 0.13 | | 0.063 | 0.10% |
| **38F7** | 0.03 | | 0.01 | | 0.020 | 0.03% |
| **38F8** | | 0.054 | 0.003 | 0.001 | 0.019 | 0.03% |
| **38F9** | | 6.81 | | | 6.810 | 11.11% |
| **39F1** | | 0.031 | | | 0.031 | 0.05% |
| **39F5** | 0.002 | 0.05 | | | 0.026 | 0.04% |
| **39F6** | 0.001 | | 0.055 | 0.002 | 0.019 | 0.03% |
| **39F7** | 0.045 | 0.006 | | | 0.026 | 0.04% |
| **40F5** | 0.002 | | | 0.084 | 0.043 | 0.07% |
| **40F6** | 0.151 | | 0.777 | 0.024 | 0.317 | 0.52% |
| **40F7** | 2.966 | 0.513 | 0.308 | 0.291 | 1.020 | 1.66% |
| **40F8** | 3.388 | 4.211 | 24.396 | 5.843 | 9.460 | 15.44% |
| **41F4** | | 0.066 | | | 0.066 | 0.11% |
| **41F5** | 0.011 | 0.101 | 0.005 | 0.008 | 0.031 | 0.05% |
| **41F6** | 0.041 | 0.008 | 0.059 | 0.019 | 0.032 | 0.05% |
| **41F7** | 24.315 | 8.94 | 39.016 | 20.41 | 23.170 | 37.81% |
| **41F8** | 8.137 | 6.822 | 27.24 | 7.815 | 12.504 | 20.41% |
| **42F5** | 0.005 | | | | 0.005 | 0.01% |
| **42F6** | 0.022 | | 0.007 | | 0.015 | 0.02% |
| **42F7** | 0.584 | 0.749 | 0.237 | 0.291 | 0.465 | 0.76% |
| **42F8** | 0.305 | 0.063 | 0.533 | 0.373 | 0.319 | 0.52% |
| **43F0** | | | 0.03 | | 0.030 | 0.05% |
| **43F5** | | 0.001 | | | 0.001 | 0.00% |
| **43F6** | 0.008 | 0.005 | 0.14 | 0.002 | 0.039 | 0.06% |
| **43F7** | | 0.332 | 0.004 | 0.008 | 0.115 | 0.19% |

| | | | | | | |
|---|---|---|---|---|---|---|
| **43F8** | 1.408 | 0.455 | 0.389 | 0.181 | 0.608 | 0.99% |
| **(NA)** | 93.42 | 93.747 | | | 93.584 | 60.43% |

# ANNEX 1.4

## Results of the SPiCT sensitivity runs for Flounder

All data are taken from the Regional Database (RDB) hosted by ICES (ICES 2023a). Aggregation of data is following the ICES Data Guidelines (ICES 2023b).

Three different datasets were tested during WKMSYPICT and during the assessment working group WGBFAS (including the latest 2023 data, Table 1). Dataset 1 included only western Baltic Sea data, whereas Dataset 2 used the combined index of IBTS/BITS of areas SD21-23. Dataset 3 used the combined areas index and landings of areas SD21-23 (Kattegat and western Baltic Sea). The sensitivity analyses were performed to determine the influence of the inclusion of Kattegat to the overall performance of the model.

The SPiCT settings (CVs, catch uncertainty, priors, etc.) were kept identical to the final settings of *fle.27.22-23.*

**Table 1:** Dataset and overview of SPiCT settings of the sensitivity analyses

| **Setting/Data** | **Dataset 1: Baltic Sea** | **Dataset 2: Baltic Sea & Kattegat-Baltic index** | **Dataset 3: combined Baltic Sea & Kattegat** |
|---|---|---|---|
| **Catch time series** | Baltic Sea<br>(Areas SD22-SD23)<br>landings data 1973–2023 | Baltic Sea<br>(Areas SD22-SD23)<br>landings data 1973–2023 | Baltic and Kattegat<br>(Areas SD21-SD23)<br>landings data 193–2023 |
| **BITS biomass Index quarter 1, “Bergdex”** | Baltic Sea<br>(Areas SD22-23)<br>1991-2023, ≥ 20 cm | Baltic and Kattegat<br>(Areas SD21-SD23),<br>1991-2023, ≥ 20 cm | Baltic and Kattegat<br>(Areas SD21-SD23),<br>1991-2023, ≥ 20 cm |
| **BITS biomass Index quarter 4, “Bergdex”** | Baltic Sea<br>(Areas SD22-23)<br>1991-2023, ≥ 20 cm | Baltic and Kattegat<br>(Areas SD21-SD23),<br>1991-2023, ≥ 20 cm | Baltic and Kattegat<br>(Areas SD21-SD23),<br>1991-2023, ≥ 20 cm |
| | | | |
| **SPiCT settings** | | | |
| - Standard deviation on the indices (sdi) | Log(sdi1)~N(log(index_CV),0.3^2)<br>Log(sdi2)~N(log(index_CV), 0.3^2) | | |
| - Standard deviation on the indices (observation) (stdevfacI) | indexQ1_CV/mean(indexQ1_CV),<br>indexQ4_CV /mean(indexQ4_CV) | | |
| - Standard deviation on the catch (observation) (stdevfacC) | For >2021 stdevfacC = 2; | | |
| - Biomass process noise (logsdb) | Log(0.15)-0.5*0.5^2, 0.5 | | |
| - Catch observation error (logsdc) | Log(0.1)-0.5*0.5^2, 0.5 | | |

| | |
|---|---|
| - Uncertainty ratio of index (observation) to biomass process (alpha) | Deactivated |
| - Uncertainty ratio of catch (observation) to fishing mortality process (beta) | Deactivated |
| - Shape parameter (n) | Schaefer model, Log(n)~N(log(2),0.001) |
| - Intrinsic growth rate (r) | Log(r)~N(log(0.56), 0.2) |
| - Initial depletion (bkfrac) | None (default) |
| - Discretion time step (dteuler) | 1/16 year (default) |

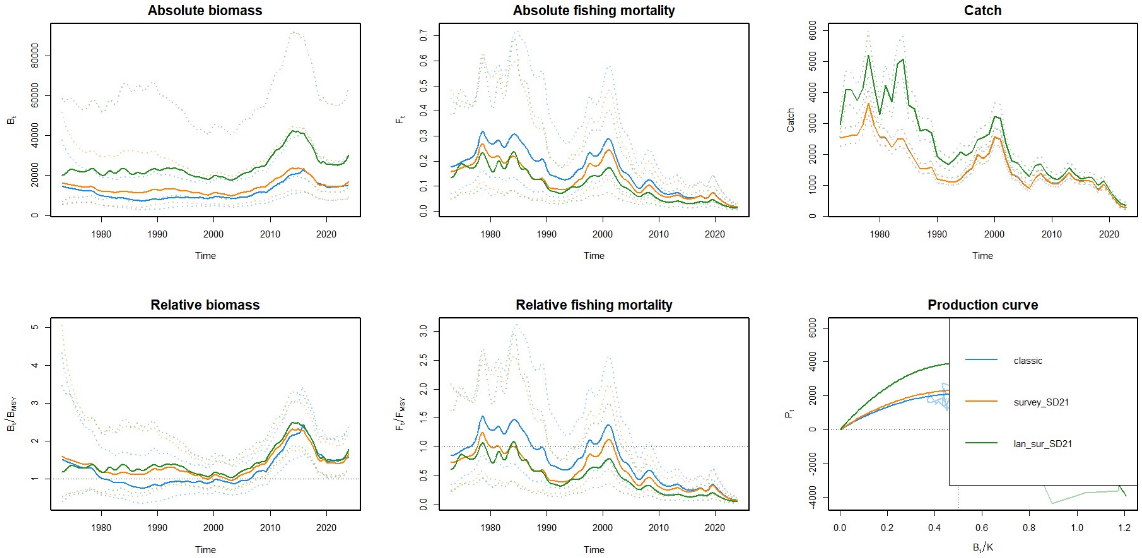


*Figure 1: Comparison of the model estimates of biomass, fishing mortality, production curve and catch of all three sensitivity runs*

## Dataset 1:

## Including Landings and Survey data from the Western Baltic Sea (27.3.c.22 and 27.3.b.23)

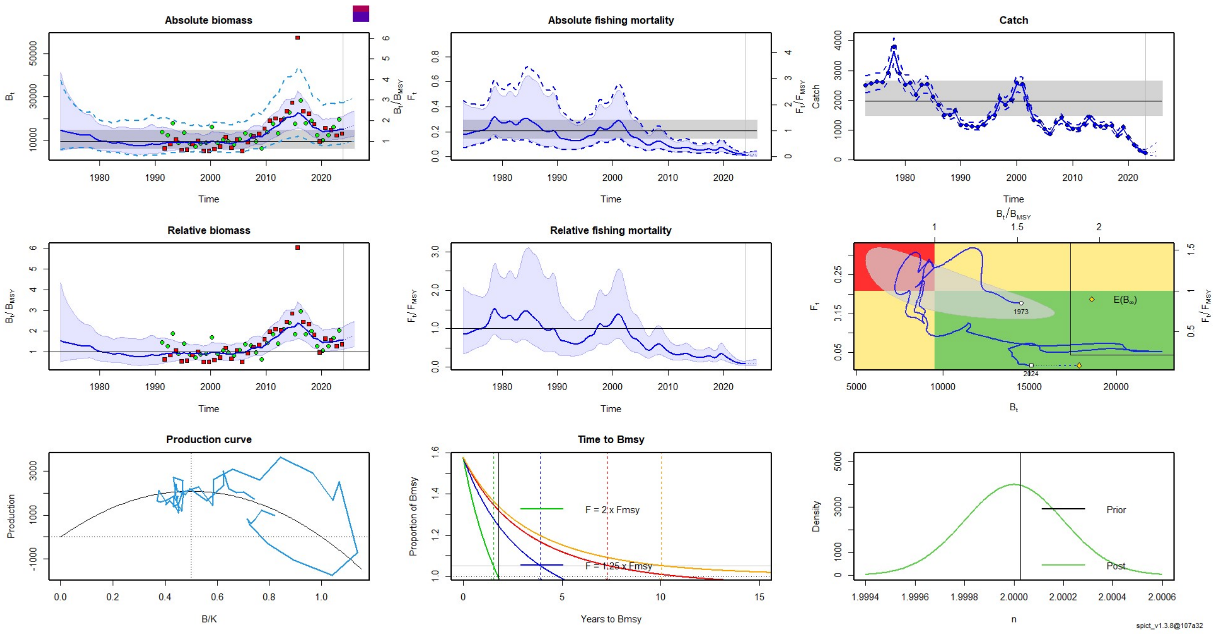


*Figure 2: Overview of the SPiCT results for Dataset 1*

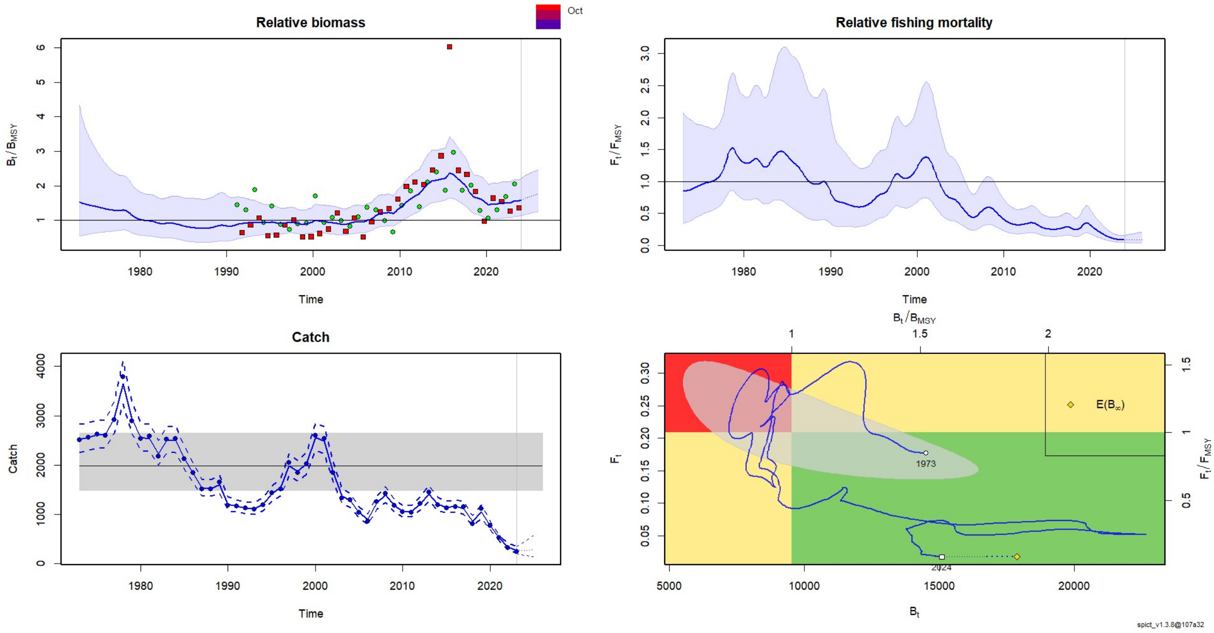


*Figure 3: Overview of the relative estimates of the SPiCT output for Dataset 1*

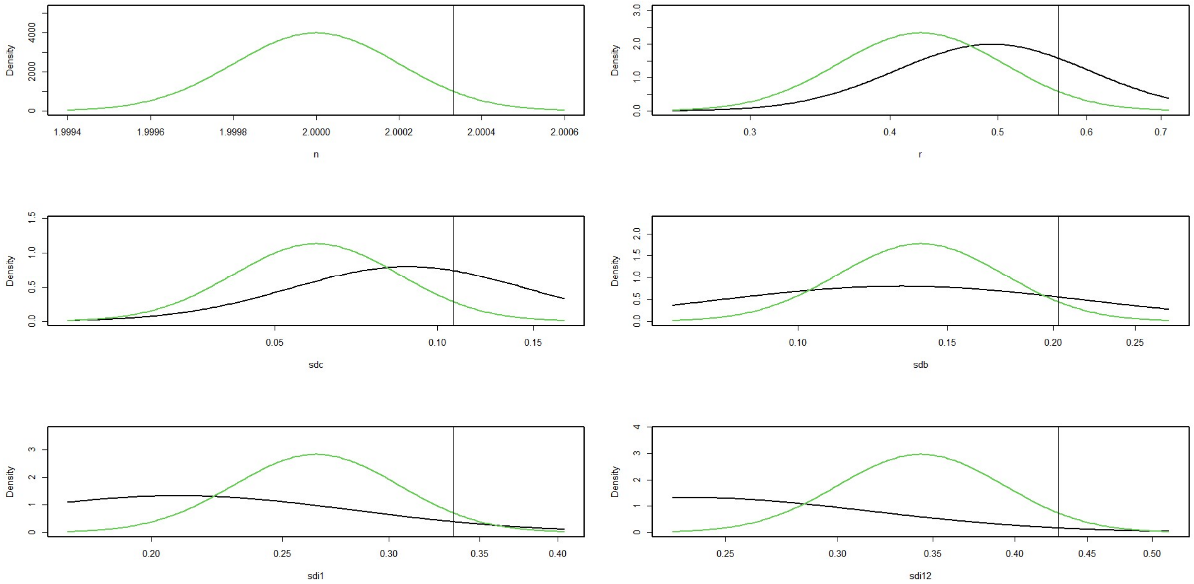


*Figure 4: Prior and posterior distributions of the set priors in Dataset 1*

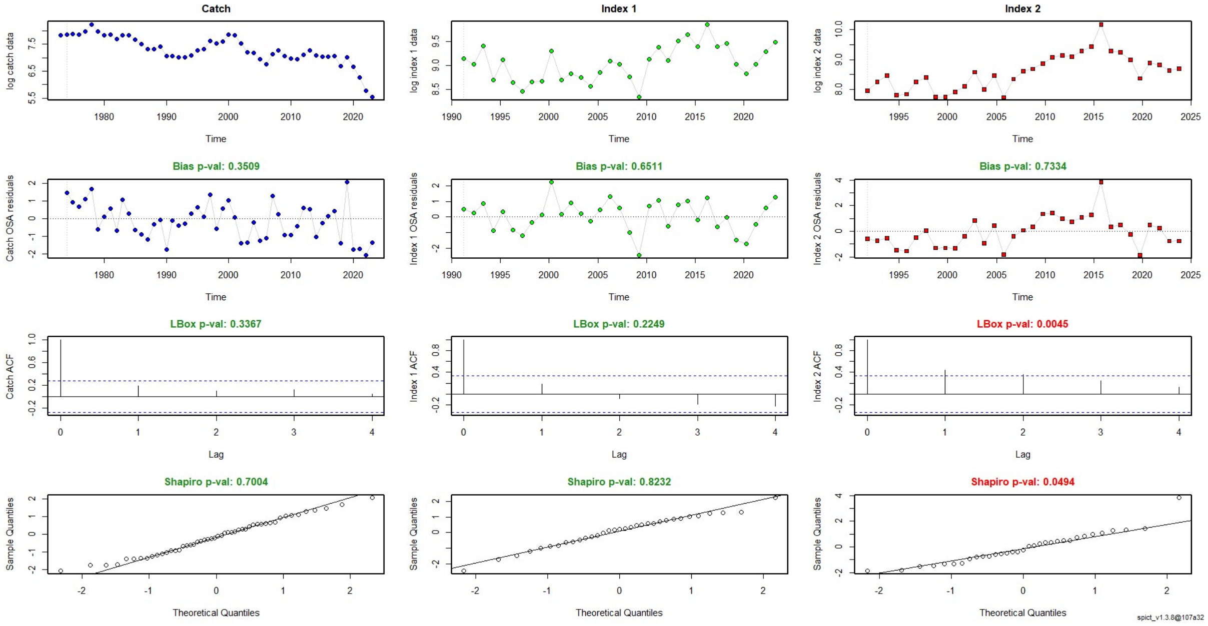


*Figure 5: One-Step-Ahead residuals for observations of Dataset 1*

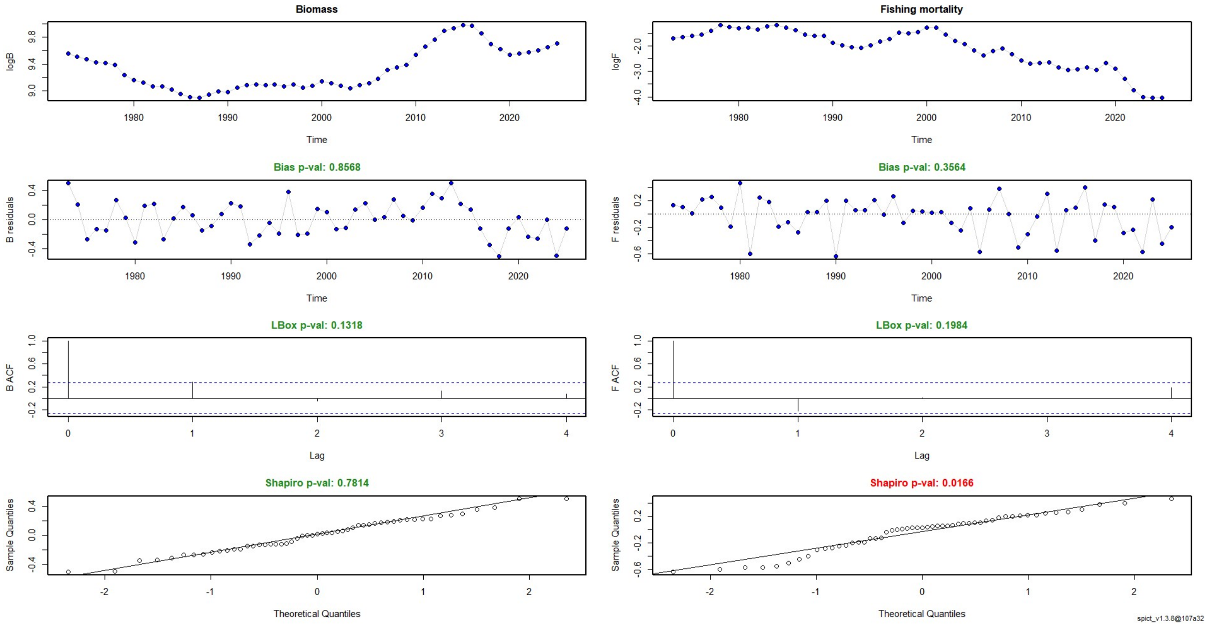


*Figure 6: Process residuals of Dataset 1*

*Table 2: model and parameter estimate of Dataset 1 (estimate, lower limit, upper limit and log-transformed estimate)*

| Dataset1 | estimate | cilow | ciupp | log.est |
|---|---|---|---|---|
| **alpha1** | 1.897 | 1.089 | 3.304 | 0.640 |
| **alpha2** | 2.459 | 1.412 | 4.284 | 0.900 |
| **beta** | 0.253 | 0.111 | 0.578 | -1.373 |
| **r** | 0.427 | 0.305 | 0.596 | -0.852 |
| **rc** | 0.427 | 0.305 | 0.596 | -0.852 |
| **rold** | 0.427 | 0.305 | 0.596 | -0.852 |
| **m** | 2091.460 | 1538.894 | 2842.435 | 7.646 |
| **K** | 19610.570 | 12559.360 | 30620.550 | 9.884 |
| **q1** | 0.677 | 0.360 | 1.274 | -0.390 |
| **q2** | 0.462 | 0.246 | 0.870 | -0.772 |
| **n** | 2.000 | 2.000 | 2.000 | 0.693 |
| **sdb** | 0.140 | 0.090 | 0.217 | -1.969 |
| **sdf** | 0.236 | 0.176 | 0.315 | -1.446 |
| **sdi1** | 0.265 | 0.201 | 0.349 | -1.328 |
| **sdi2** | 0.343 | 0.264 | 0.447 | -1.069 |
| **sdc** | 0.060 | 0.030 | 0.119 | -2.819 |

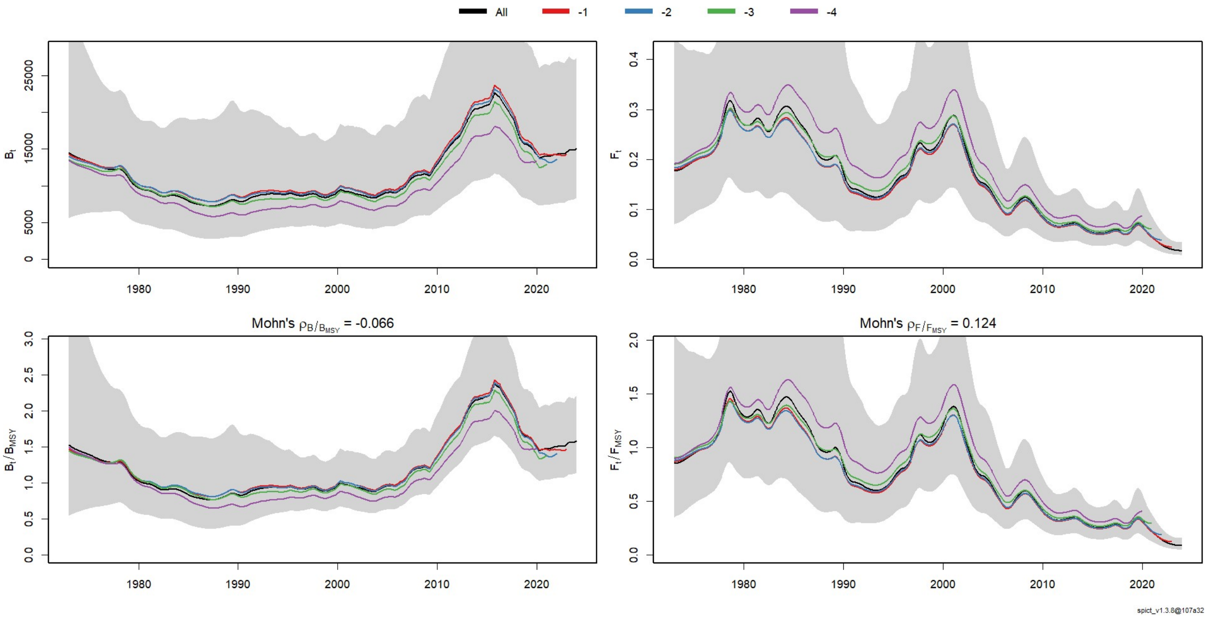


*Figure 7: Retrospective analysis of Dataset 1*

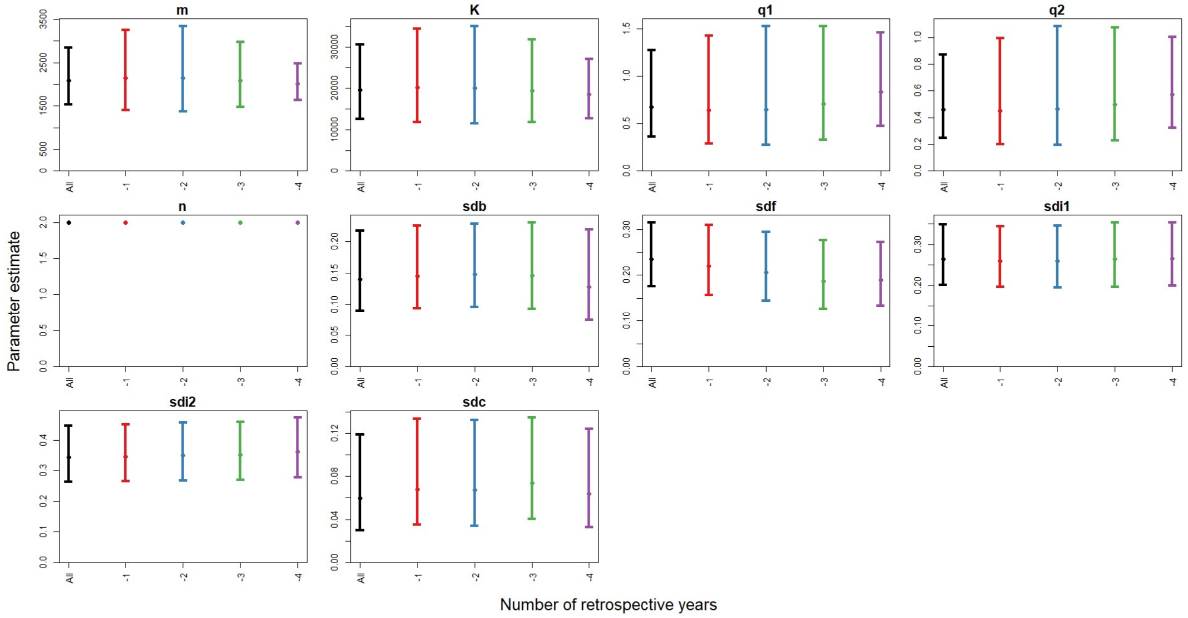


*Figure 8: Retrospective analysis of the model parameter of Dataset 1*

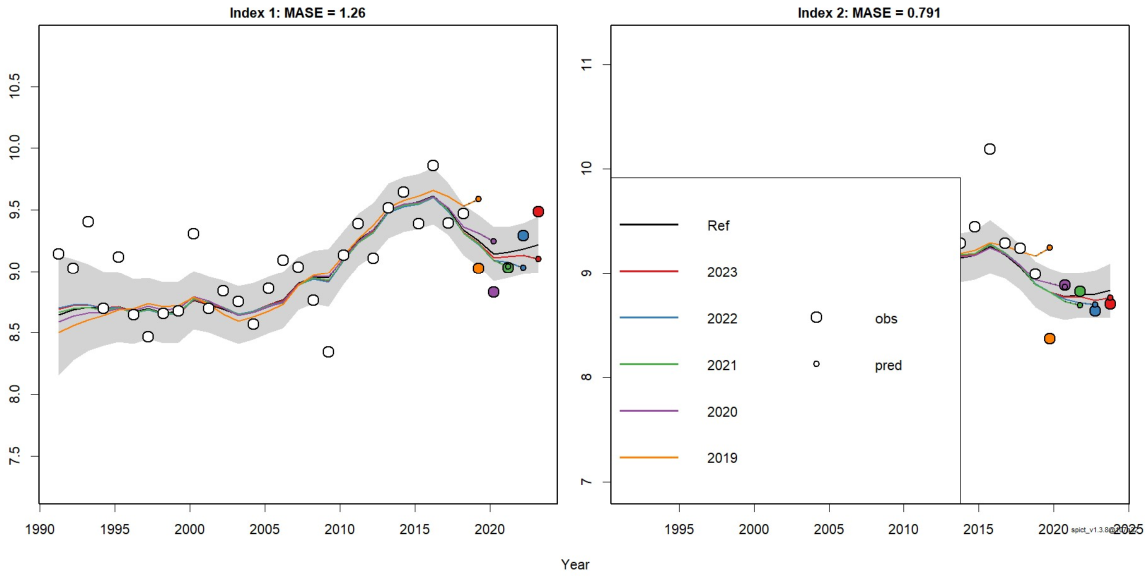


*Figure 9: Hindcast analysis of Dataset 1 (“MASE”)*

## Dataset 2:

## Landings of flounder in the Western Baltic (27.3.c.22 and 27.3.b.23) and Survey index data from Kattegat and Western Baltic Sea combined

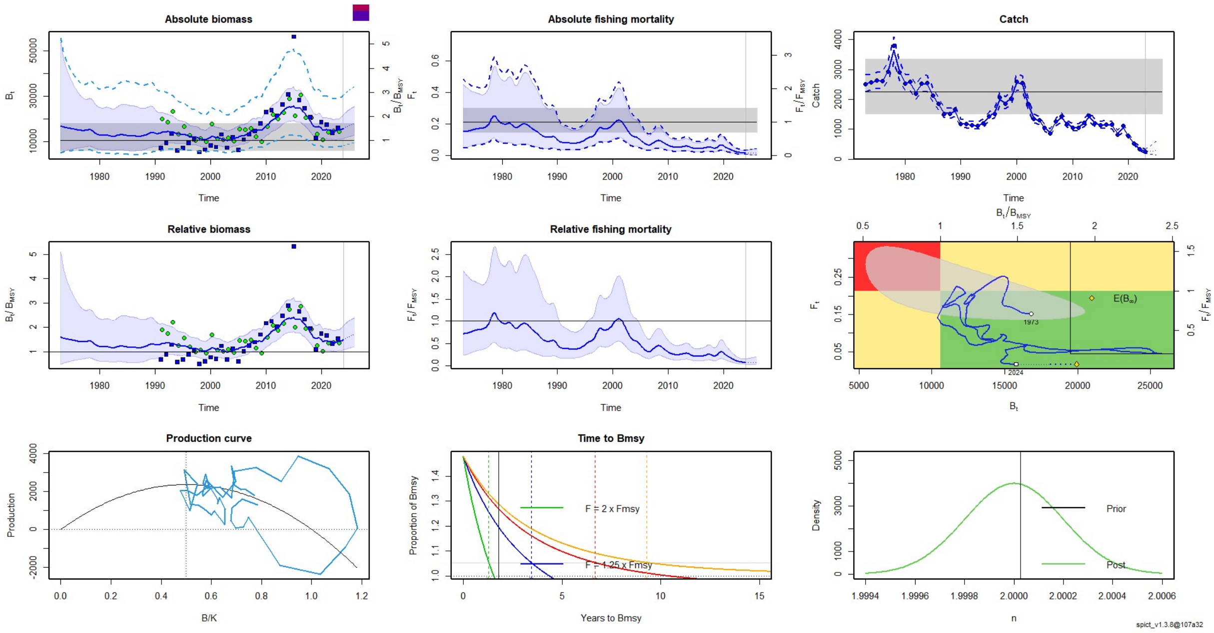


*Figure 10: Overview of the SPiCT results for Dataset 2*

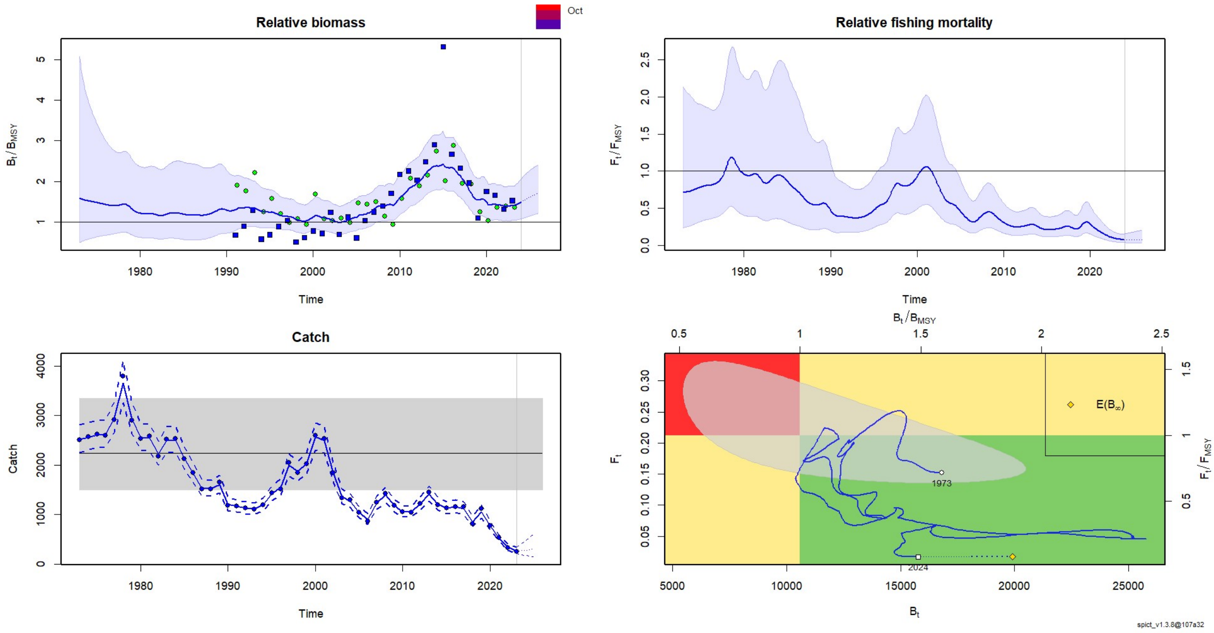


*Figure 11: Overview of the relative estimates of the SPiCT output for Dataset 2*

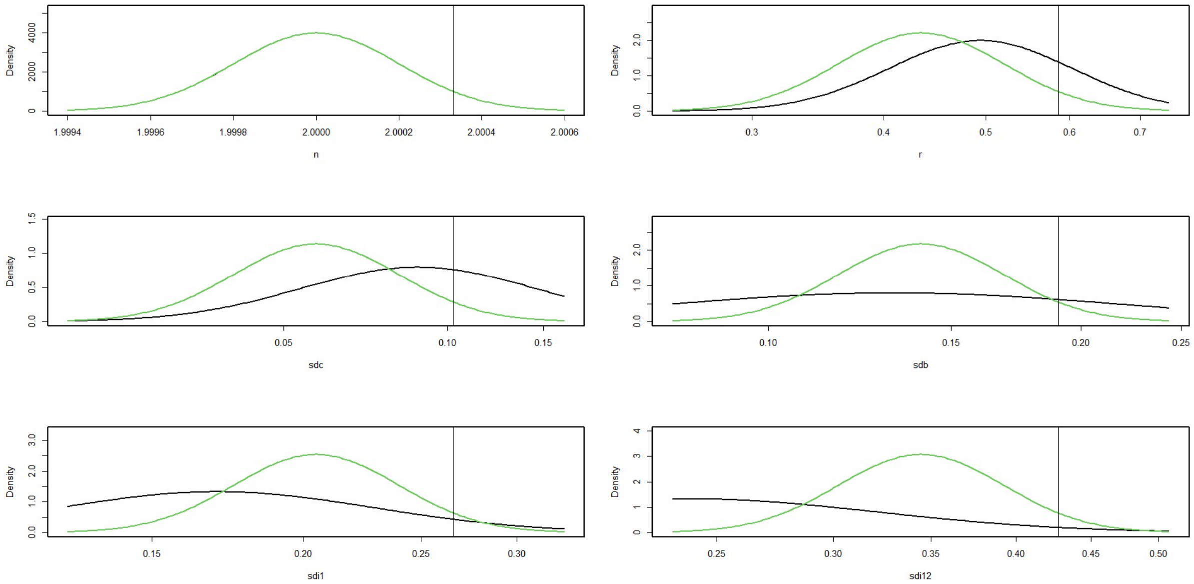


*Figure 12: Prior and posterior distributions of the set priors in Dataset 2*

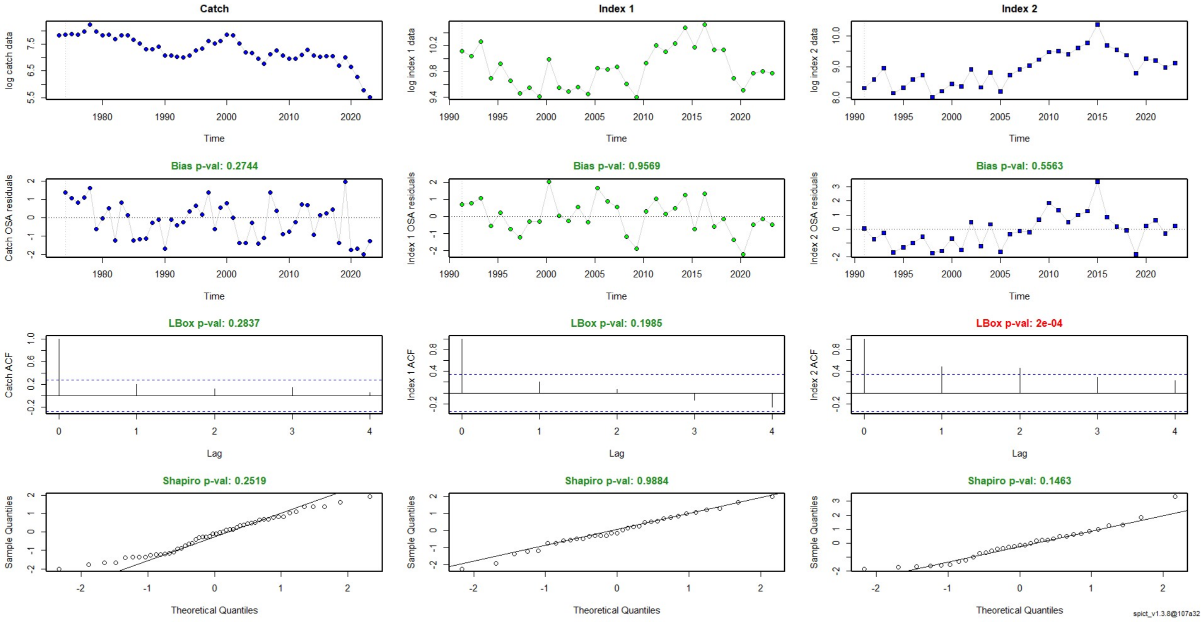


*Figure 13: One-Step-Ahead residuals for observations of Dataset 2*

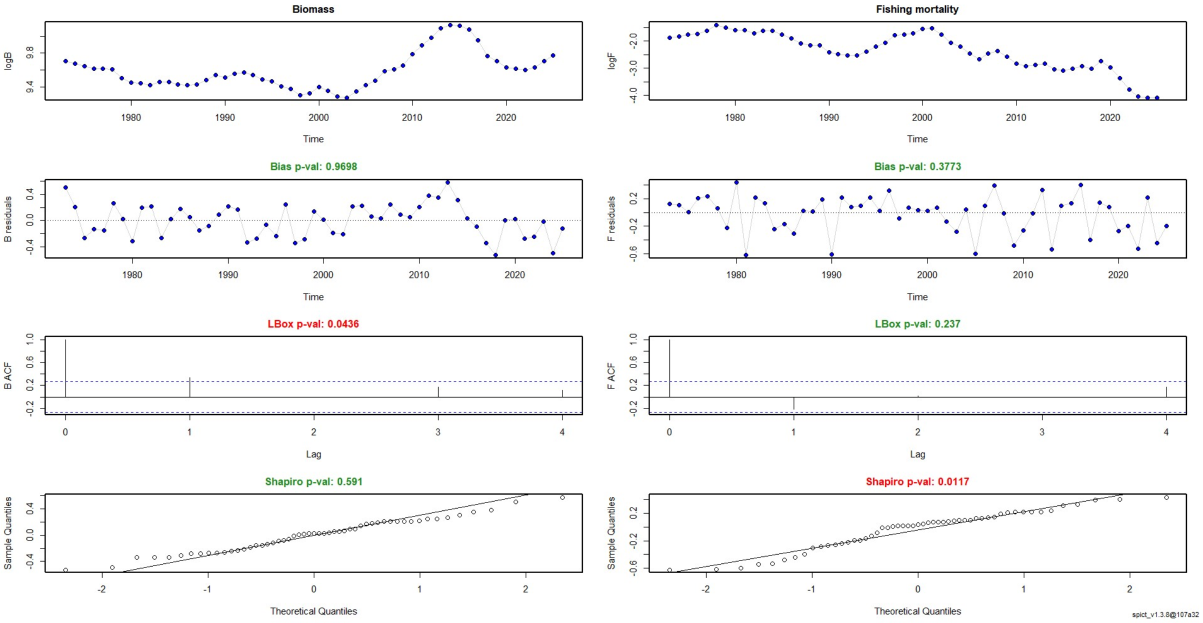


*Figure 14: Process residuals of Dataset 2*

*Table 3: model and parameter estimate of Dataset 2 (estimate, lower limit, upper limit and log-transformed estimate)*

| Dataset2 | estimate | cilow | ciupp | log.est |
|---|---|---|---|---|
| **alpha1** | 1.461 | 0.888 | 2.403 | 0.379 |
| **alpha2** | 2.456 | 1.556 | 3.876 | 0.898 |
| **beta** | 0.239 | 0.107 | 0.534 | -1.431 |
| **r** | 0.434 | 0.304 | 0.619 | -0.835 |
| **rc** | 0.434 | 0.304 | 0.619 | -0.835 |
| **rold** | 0.434 | 0.304 | 0.619 | -0.835 |
| **m** | 2388.103 | 1563.113 | 3648.513 | 7.778 |
| **K** | 22012.030 | 12757.040 | 37981.340 | 9.999 |
| **q1** | 1.206 | 0.607 | 2.394 | 0.187 |
| **q2** | 0.559 | 0.281 | 1.112 | -0.582 |
| **n** | 2.000 | 2.000 | 2.000 | 0.693 |
| **sdb** | 0.140 | 0.098 | 0.201 | -1.964 |
| **sdf** | 0.240 | 0.181 | 0.317 | -1.428 |
| **sdi1** | 0.205 | 0.151 | 0.279 | -1.585 |
| **sdi2** | 0.344 | 0.267 | 0.444 | -1.066 |
| **sdc** | 0.057 | 0.029 | 0.114 | -2.859 |

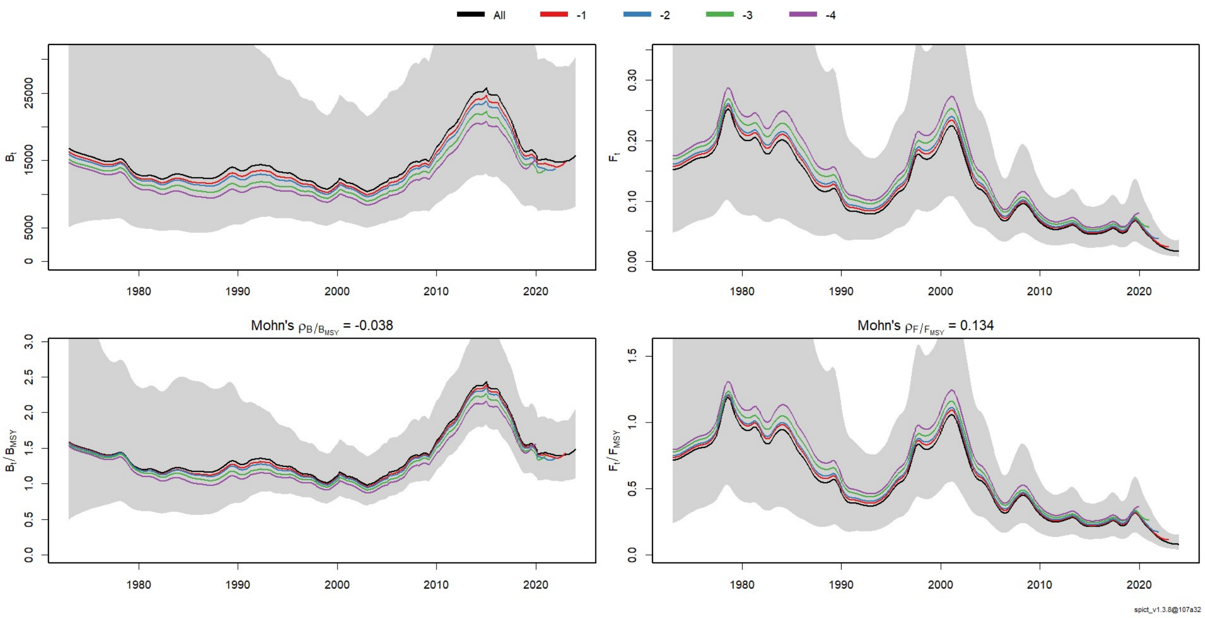


*Figure 15: Retrospective analysis of Dataset 2*

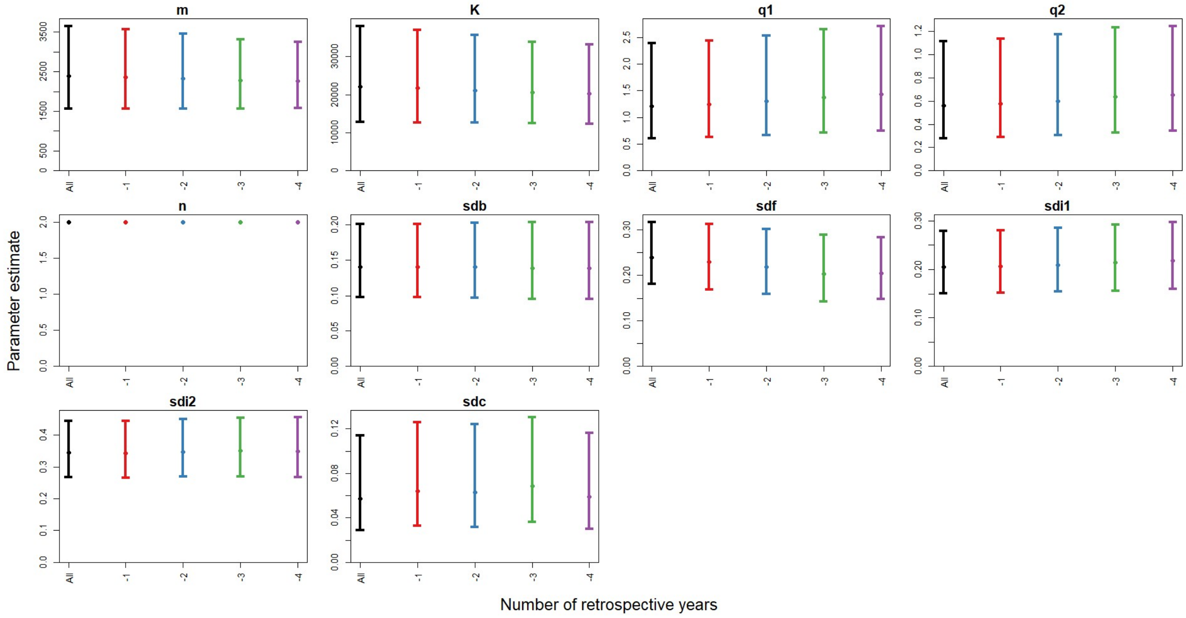


*Figure 16: Retrospective analysis of the model parameter of Dataset 2*

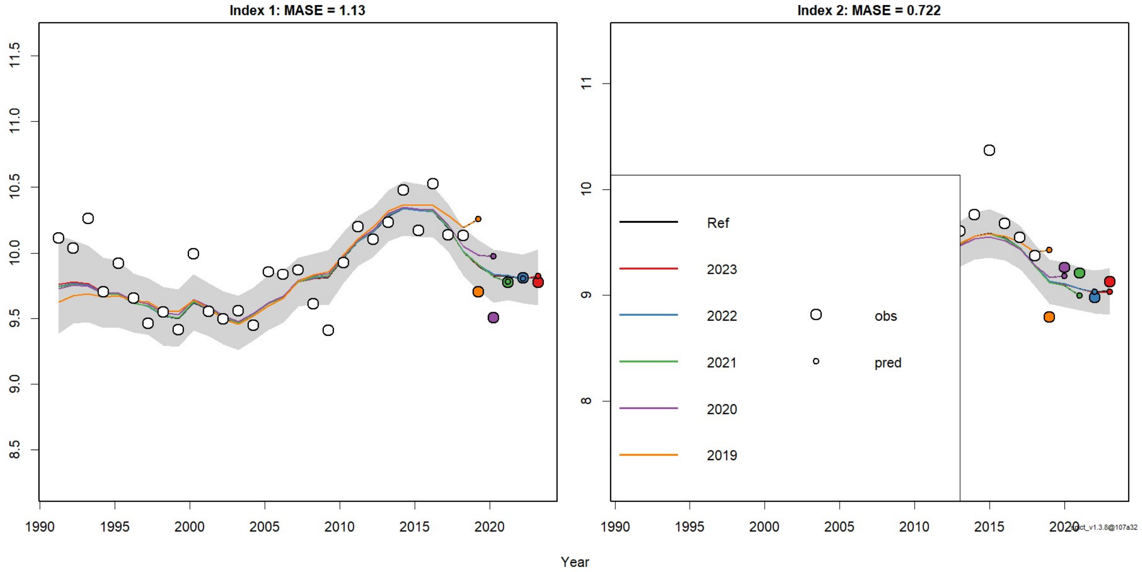


*Figure 17: Hindcast analysis of Dataset 2 ("MASE")*

## Dataset 3:

## Landings and Survey index values from Kattegat and Western Baltic Sea (27.3.c.22 and 27.3.b.23) combined

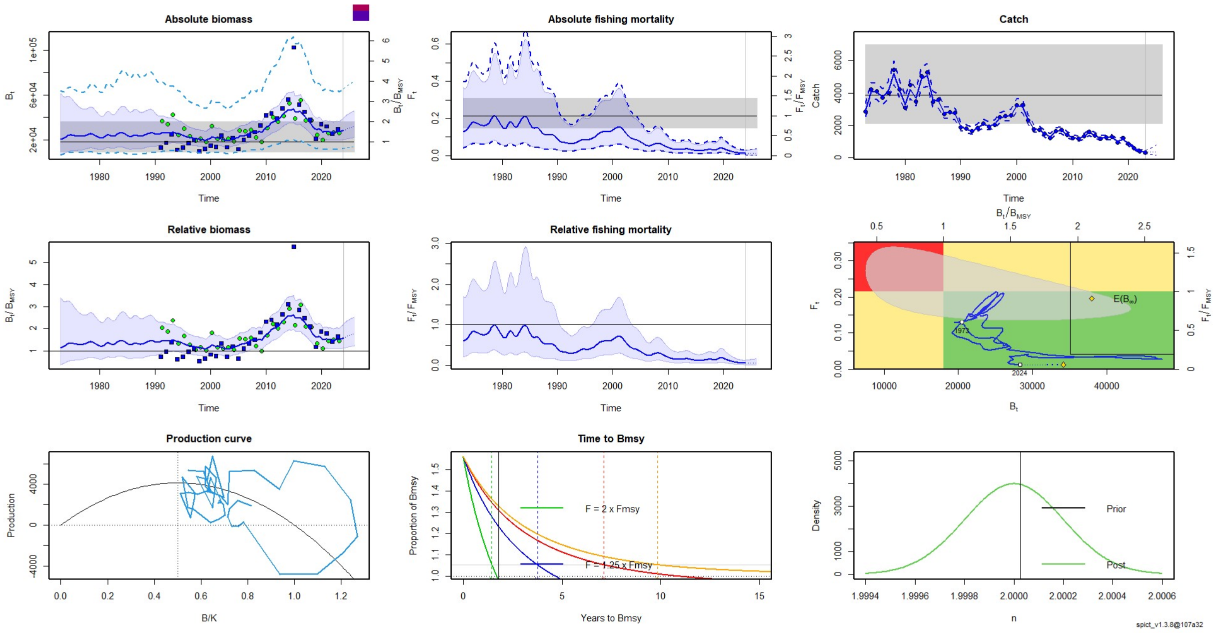


*Figure 18: Overview of the SPiCT results for Dataset 2*

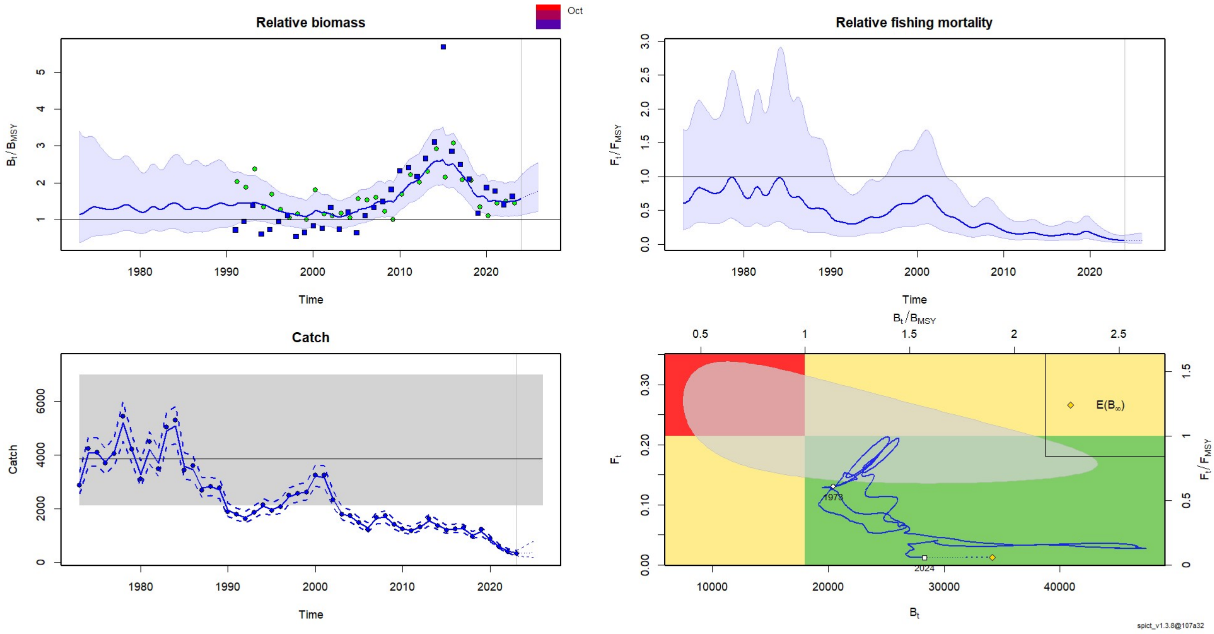


*Figure 19: Overview of the relative estimates of the SPiCT output for Dataset 3*

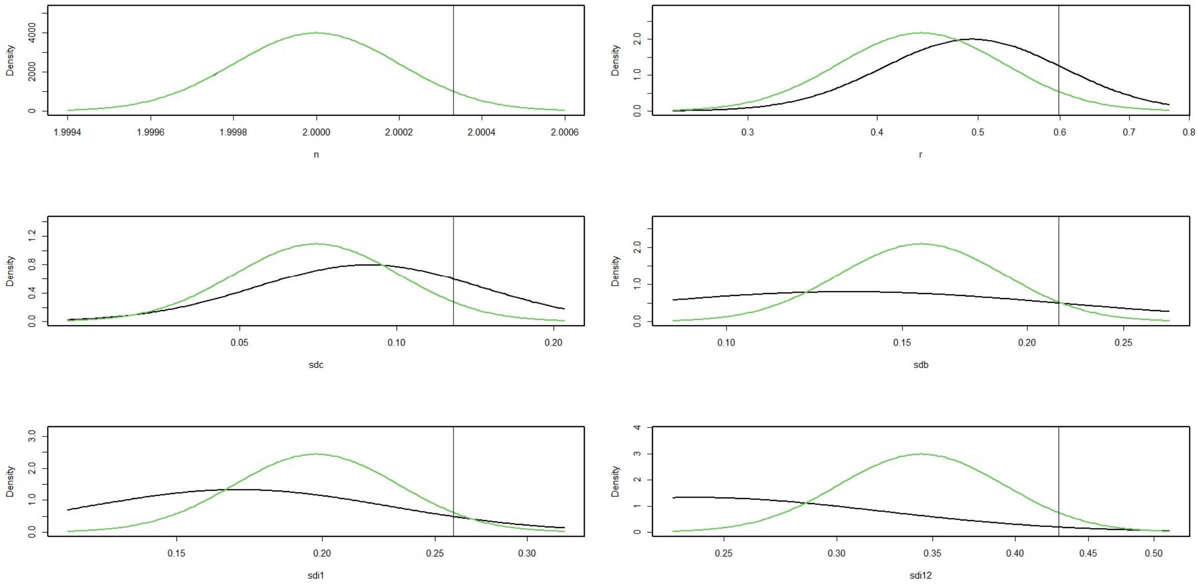


*Figure 20: Prior and posterior distributions of the set priors in Dataset 3*

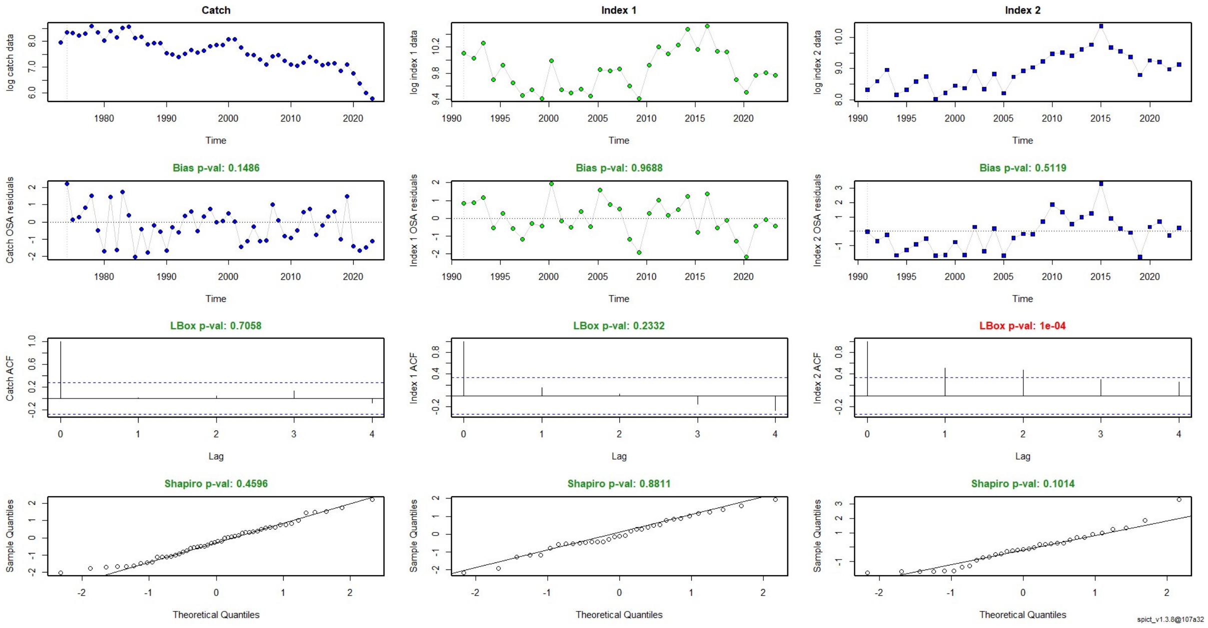


*Figure 21: One-Step-Ahead residuals for observations of Dataset 3*

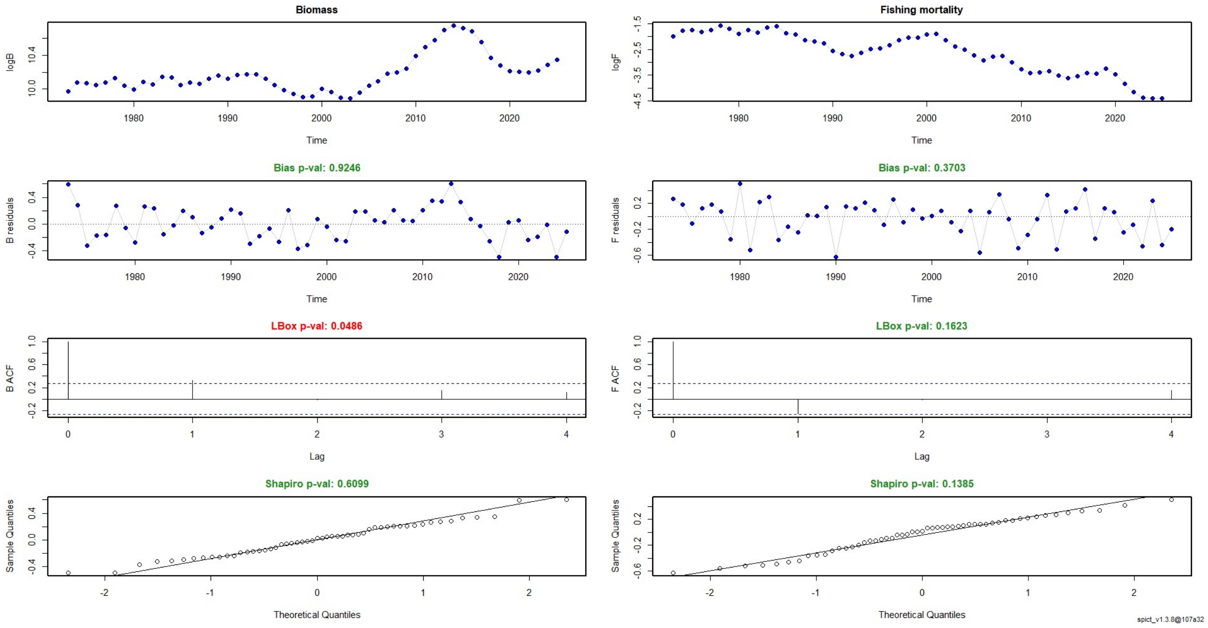


*Figure 22: Process residuals of Dataset 3*

*Table 4: model and parameter estimate of Dataset 3 (estimate, lower limit, upper limit and log-transformed estimate)*

| Dataset3 | estimate | cilow | ciupp | log.est |
|---|---|---|---|---|
| **alpha1** | 1.261 | 0.744 | 2.137 | 0.232 |
| **alpha2** | 2.192 | 1.364 | 3.523 | 0.785 |
| **beta** | 0.284 | 0.115 | 0.700 | -1.259 |
| **r** | 0.441 | 0.308 | 0.633 | -0.818 |
| **rc** | 0.441 | 0.308 | 0.633 | -0.818 |
| **rold** | 0.441 | 0.308 | 0.633 | -0.818 |
| **m** | 4121.579 | 2254.141 | 7536.092 | 8.324 |
| **K** | 37373.980 | 18439.620 | 75750.720 | 10.529 |
| **q1** | 0.673 | 0.286 | 1.584 | -0.397 |
| **q2** | 0.311 | 0.132 | 0.734 | -1.168 |
| **n** | 2.000 | 2.000 | 2.000 | 0.693 |
| **sdb** | 0.157 | 0.108 | 0.228 | -1.853 |
| **sdf** | 0.247 | 0.179 | 0.342 | -1.398 |
| **sdi1** | 0.198 | 0.143 | 0.273 | -1.621 |
| **sdi2** | 0.344 | 0.265 | 0.447 | -1.068 |
| **sdc** | 0.070 | 0.034 | 0.144 | -2.657 |

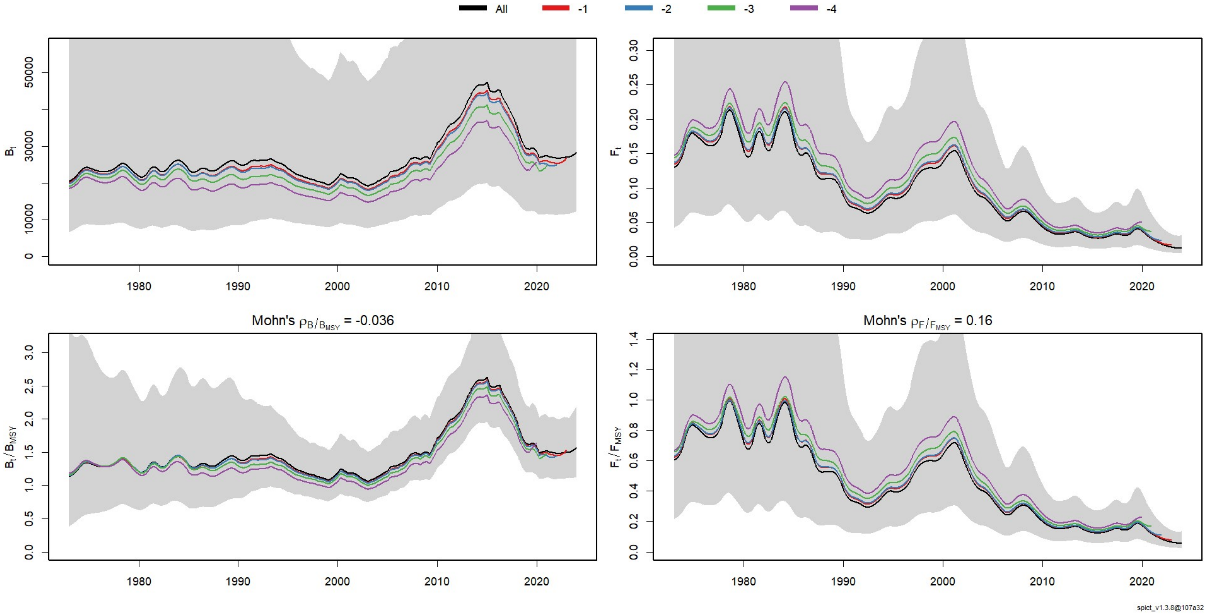


*Figure 23: Retrospective analysis of Dataset 3*

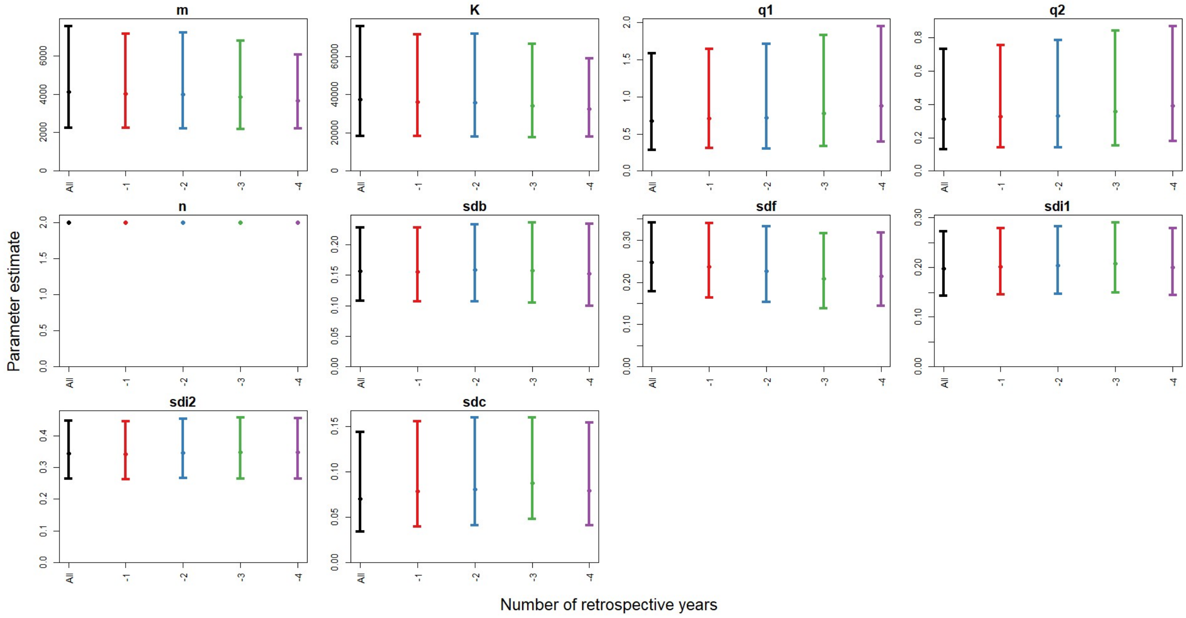


*Figure 24: Retrospective analysis of the model parameter of Dataset 1*

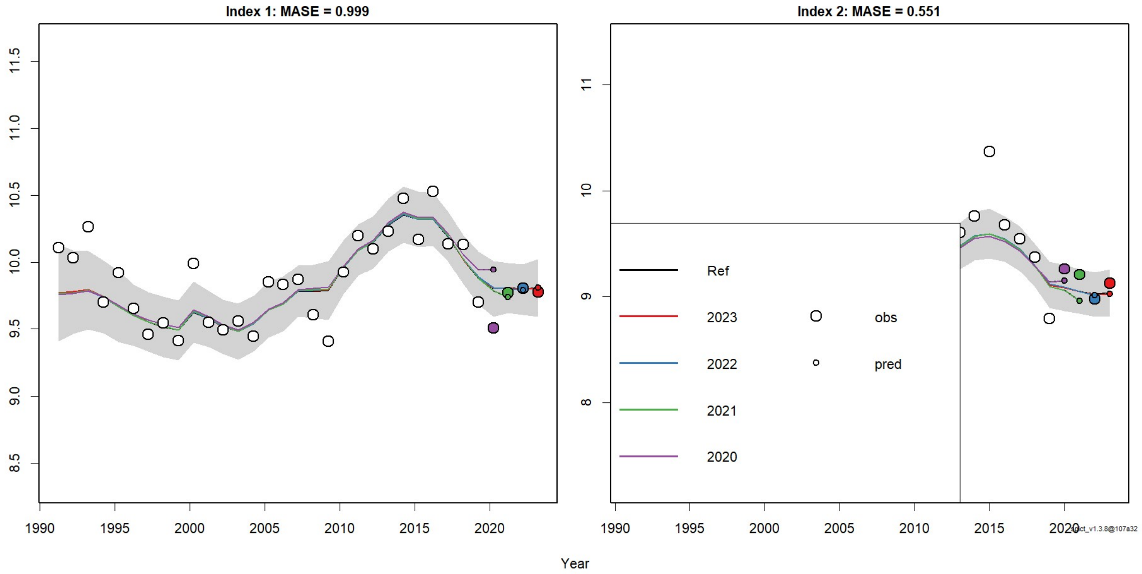
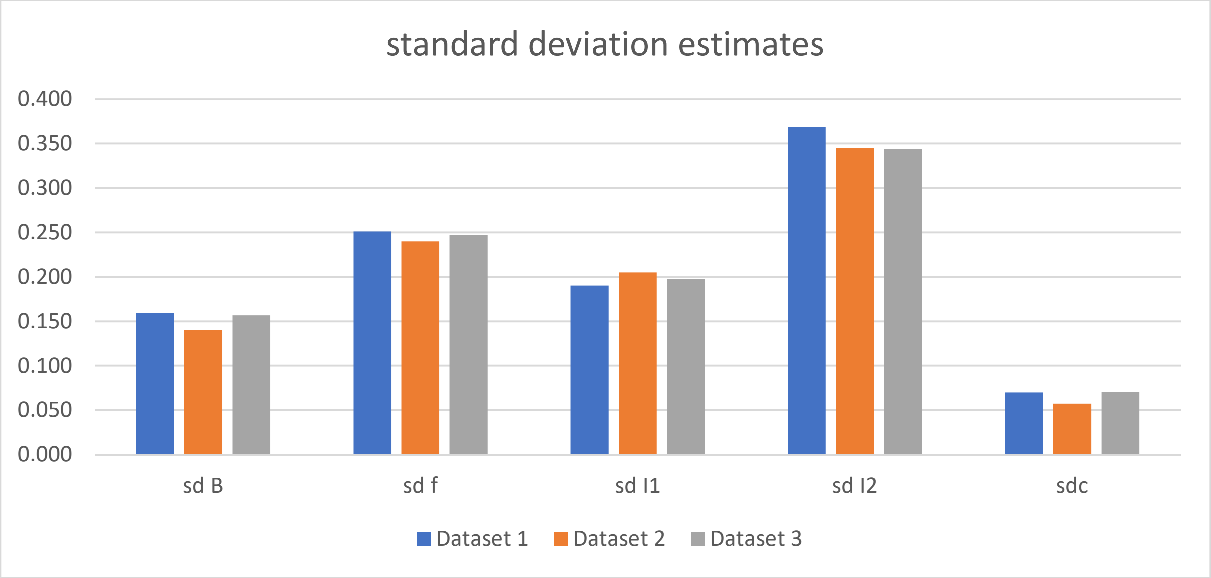
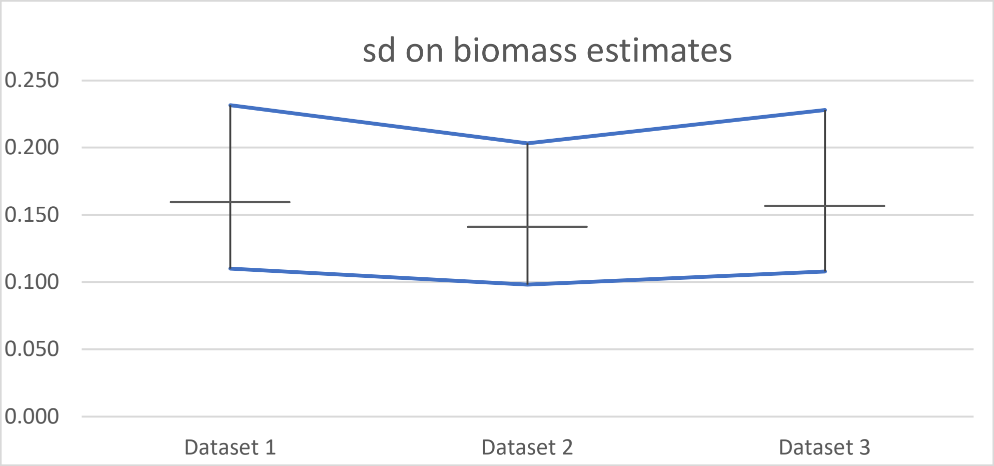
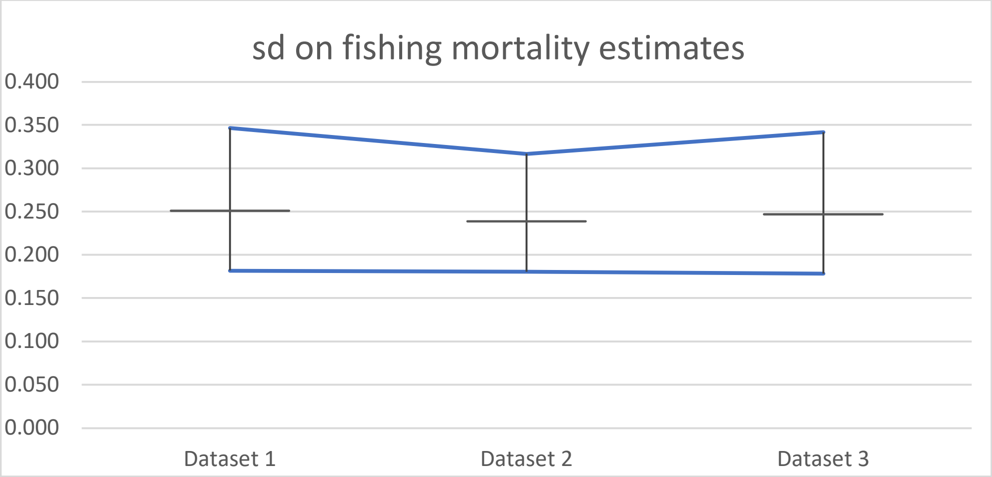


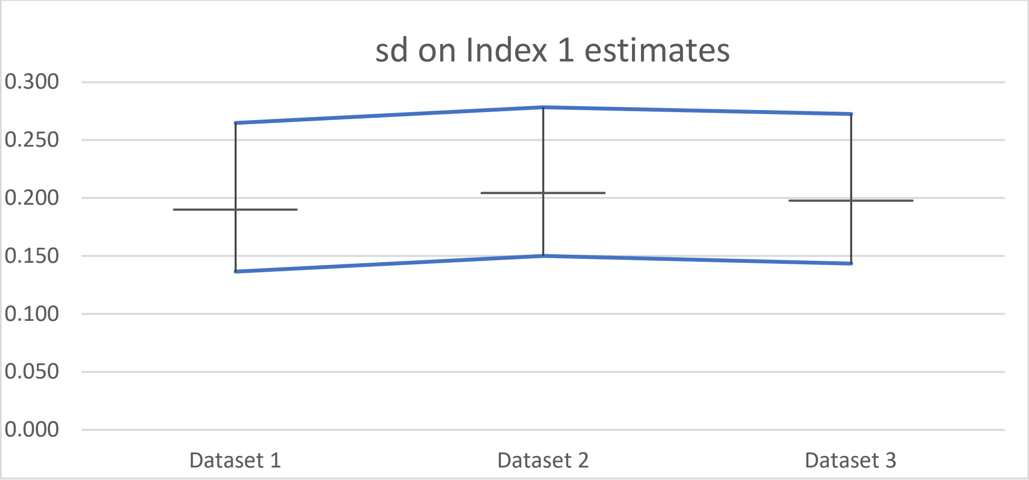
*Figure 25: Hindcast analysis of Dataset 3 ("MASE")*

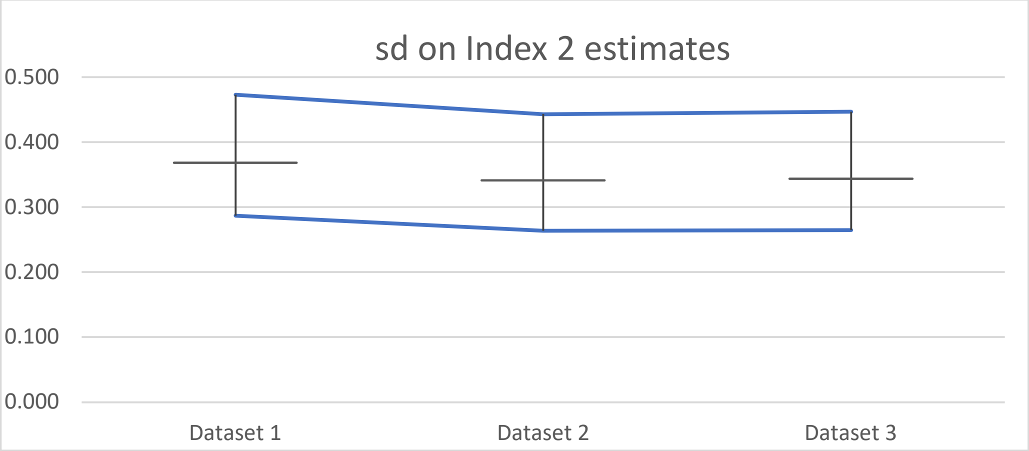
## Model estimates comparisons (data in tables 2, 3 and 4)

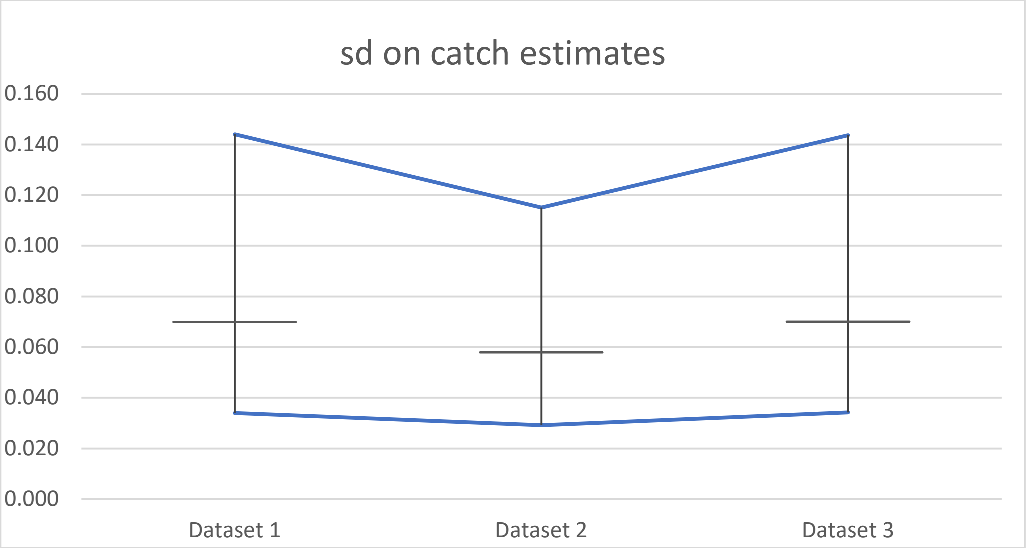







sd on Index 1 estimates
0.300
0.250
0.200
0.150
0.100
0.050
0.000
Dataset 1
Dataset 2
Dataset 3


sd on Index 2 estimates
0.500
0.400
0.300
0.200
0.100
0.000
Dataset 1
Dataset 2
Dataset 3


sd on catch estimates
0.160
0.140
0.120
0.100
0.080
0.060
0.040
0.020
0.000
Dataset 1
Dataset 2
Dataset 3

# ANNEX 1.5

## Connectivity of flounder stock components in Skagerrak (SD20) and Kattegat (SD21)

### Background

After the re-submission of the working documents on merging the stock components of flounder in Kattegat (SD21) into the Western Baltic Sea stock (SDs 22-23) to SIMWG in June 2024, an additional analysis was requested to confirm whether or not to include Skagerrak (SD20) in the respective stock merging as well.

### Summary

Data from commercial fisheries and surveys from Skagerrak (SD20) confirm that virtually no flounder is present in the area. Less than 10% of the flounder landings in division 3.a. are originating from Skagerrak. High numbers of “zero-catches” in both IBTS and BITS hauls indicate low abundance in the covered quarters. The distribution of flounder in Skagerrak shows only very low and unregular exchange with Kattegat.

Considering the low landings and the very low index values, no extended GAM model run was conducted. The high number of “zero-catches” would result in an overall lower survey index and increase the uncertainty in the annual average values, which in turn will mask the development of the stock in Kattegat and the Baltic Sea.

In terms of stock boundaries and distribution, the area North of Skagen, the tip of Grenen, acts as a natural barrier between North Sea and Baltic Sea. It is therefore reasinable to keep Skagerrak as part of the North Sea flounder stock.

### Connectivity of Skagerrak and Kattegat

*Fishery*

Commercial landings are very low for flounder (Table 1), often accounting for less than 10% of the total catches in Division 3.a, rarely being above 20t/year. Landings are mostly originating from the coastal areas west of Skagen.

Some countries are not reporting landings by subdivision, as their fishery does not separate commercially low-valued and non-TAC regulated species in the harbour. No directed fisheries on flounder were reported for Skagerrak, misreporting is known to occur (as they are often caught at the border to the North Sea or Kattegat and only landed in SD20, ICES 2023).

*Table 1: overview of official landings of flounder in tons from Intercatch.*

| Year | Division 3.a* | Skagerrak (SD20) | Kattegat (SD21) | Baltic Sea (SD22-23) |
|---|---|---|---|---|
| **2002** | 0.1 | 45 | 481 | 1849 |
| **2003** | 2.7 | 32 | 441 | 1337 |
| **2004** | 1.7 | 30 | 448 | 1298 |
| **2005** | 2.5 | 40 | 443 | 1041 |
| **2006** | 1.4 | 25 | 365 | 866 |
| **2007** | 3.8 | 19 | 413 | 1250 |
| **2008** | 4.0 | 23 | 314 | 1427 |
| **2009** | 1.7 | 26 | 240 | 1176 |
| **2010** | 0.4 | 22 | 179 | 1053 |
| **2011** | 0.0 | 20 | 122 | 1044 |
| **2012** | 0.1 | 17 | 100 | 1219 |
| **2013** | 0.1 | 13 | 158 | 1454 |
| **2014** | 0.0 | 19 | 174 | 1193 |
| **2015** | 0.0 | 11 | 66 | 1130 |
| **2016** | 0.1 | 18 | 88 | 1153 |
| **2017** | 0.1 | 22 | 131 | 1158 |
| **2018** | 0.1 | 41 | 151 | 809 |
| **2019** | 1.4 | 57 | 102 | 1114 |
| **2020** | 0.0 | 21 | 94 | 775 |
| **2021** | 0.2 | 25 | 66 | 526 |
| **2022** | | 19 | 79 | 322 |
| **2023** | | 17 | 70 | 252 |

* data were not split into subdivisions and only allocated to the division

The majority of discards are caught in the beam trawl fishery on plaice, on sole, and the otter trawl fishery on plaice and nephrops. The Fishing pattern in terms of gears and target species is more similar to the North Sea, making allocations and extrapolations of fishing activities rather inaccurate.

### *Survey Indices*

Combined cpue data of the North Sea Trawl survey (IBTS) and the Baltic Sea trawl survey (BITS) display low numbers of flounder in all covered quarters (Fig. 1 and Fig. 2). While in some years and quarters flounder are present in Skagerrak, others show virtually no fish. The largest abundances were registered at the subdivision borders to Kattegat and in the Kosterhavet area at the Swedish coastline. However, the majority of hauls conducted during the surveys are usually “zero-hauls”. Adding these into the calculation of the index of the SPiCT assessment (i.e., the “Bergdex”, a GAM modelled survey index after Berg et al. 2014, ICES 2024) will add no supporting information and decrease the index, while adding more uncertainty around the average per year.

Additionally, the area north of Skagen and the tip of Grenen (central Skagerrak) is especially void of flounder. The area where the water bodies of North Sea and Baltic Sea are meeting seems to act as a natural border between the stock components. Low abundances of flounder are found in Jammerbay, west of Skagen, yet these accumulations barely reach further than Grenen. Quite the contrary, they regularly connect to the North Sea (see maps in Annex folder).

No GAM index was calculated for Skagerrak. For comparison, the simple cpue (as individuals caught per hour trawling) from DATRAS was displayed (all maps are included in the respective maps folder on the SIMWG sharepoint.

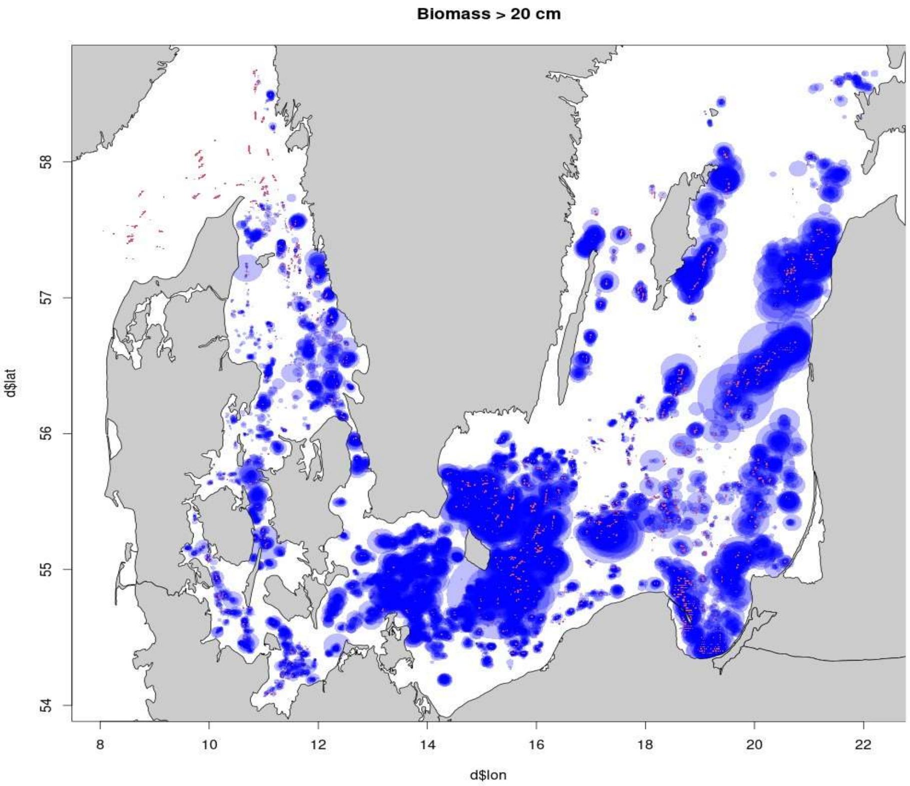


***Figure 1****: average distribution of flounder >20cm in the Baltic Sea (SDs 22-32) and Division 3a (Skagerrak SD20 and Kattegat SD21) derived from a GAM-model approach after Berg et al. 2014) based on survey data (BITS and IBTS).*

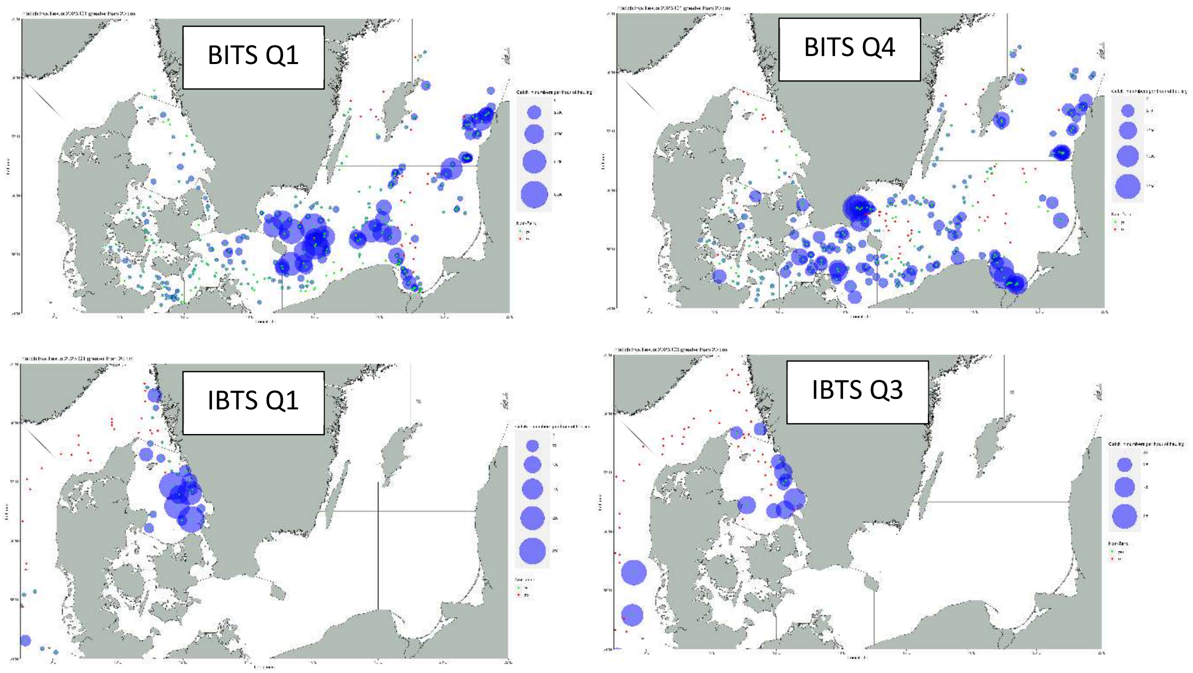


*Figure 2: average CPUE distribution of flounder >20cm in the Baltic Sea (SDs 22-32) and Division 3a (Skagerrak SD20 and Kattegat SD21) in the latest survey year 2023. All other years given in the maps annex.*

*Upper figures: BITS, lower figure: IBTS. Bubble size is calculated per map, based on the maximum cpue. Red dots: zero-catches. Green dots: catches below threshold for bubble plots*

## SPiCT comparisons

Two additional SPICT runs were performed for flounder respectively. No new index values were calculated, as the high number of zero-catch hauls would increase uncertainty in the average annual index values in both, the Q1 and Q4 index.

The additional runs were performed using landings only, priors and setting were kept identical with the final run of the WDs and the agreed settings used for the assessment (ICES 2024). The base run includes landings of the Baltic Sea and Kattegat, while the second run also included landings from Skagerrak. The third run included all landings of Division 3.a. (i.e., including those, that were submitted without information on the respective subdivision, see Table 1).

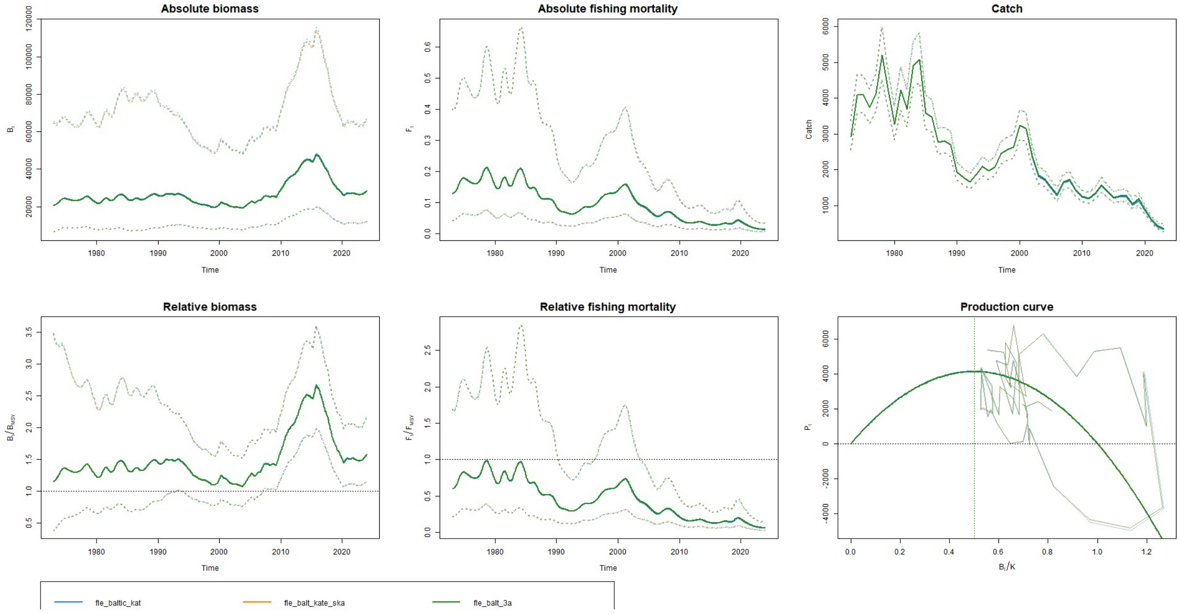


*Figure 3: comparison of the additional SPiCT runs using landings information of SD20. Blue line: landings of Baltic Sea and Kattegat. Green line: landings of Baltic Sea, Kattegat and Skagerrak. Red line: Landings of Baltic Sea and Division 3.a*

Including landings of Skagerrak and Division 3.a did not change the perception of the stock development, both the biomass and fishing mortality did not change.

## References

Berg, C.W., Nielsen, A., Kristensen, K. (2013) Evaluation of alternative age-based methods for estimating relative abundance from survey data in relation to assessment models. Fisheries Research 151, pp. 91-99. https://doi.org/10.1016/j.fishres.2013.10.005

ICES (2023). Working Group on the Assessment of Demersal Stocks in the North Sea and Skagerrak (WGNSSK). ICES Scientific Reports. 5:39. 1072pp.https://doi.org/10.17895/ices.pub.22643143

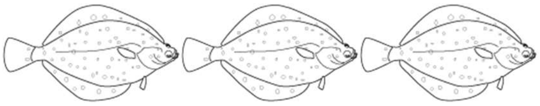
ICES (2024) Benchmark workshop 3 on the development of MSY advice using SPiCT (WKBMSY SPiCT3). ICES Scientific Reports. 6:6. 370 pp. https://doi.org/10.17895/ices.pub.24998858

# Annex 7: Working Document on stock structure of plaice

# Evidence for a single plaice stock in the Baltic Sea

Working Document

Review of current stock boundaries and recent research publication on the stock structure



Contact Persons:
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## Table of content

## What is the proposal for stock merging?

We propose to merge the two currently used stock units “ple.27.21-23” (Kattegat, Belt Seas, and the Sounds) and “ple.27.24-32” (Baltic Sea, excluding the Sound and Belt Sea) into one stock “ple.27.21-32” (Baltic Sea and Kattegat).

Recent genetic studies, historical and contemporary mark-recapture experiments, biological information and stock assessment trends are supporting the assumption that plaice in the Baltic Sea is in fact only stock that is extending into the Kattegat and has only very limited exchange with plaice in Skagerrak and North Sea.

## Summary

Plaice in the Baltic Sea (subdivisions 22 to 32) has been split into two stocks based on a recommendation made by the Workshop on the Evaluation of Plaice Stocks (WKPESTO) in 2012, which was kept by the WKPLE benchmark in 2014. However, the WKPESTO decision was based on very little data, as the focus of the group was to investigate the connection of plaice stocks in the Skagerrak towards the North Sea. The genetic study used at this time included very few samples from the Eastern Baltic Sea as reference material and did not sample the major part of the stock in the Belt Sea.

Additional assumptions on possible spawning grounds also proved to be inaccurate, as shown by later distribution analyses.

A recent genetic study from 2022 (Weist et al. 2022) reported on the generation of an annotated draft plaice genome assembly in combination with population sequencing data—following the salinity gradient from the Baltic Sea into the North Sea. Genome-wide selection analyses (*xp-EHH*) did not display any differentiation between the two plaice stocks in the Baltic Sea, suggesting that there is in fact one Baltic plaice stock.

Additionally, the developments of the two stocks (in terms of survey indices, stock assessment trends, Stock-Recruitment-relationships) are almost identical. Historic and recent tagging studies display regular recaptures of plaice across their assumed stock boundaries, further supporting a merging of the two stock units into one stock, covering the Baltic Sea and Kattegat.

# Background and recent publications on Baltic Sea plaice stock identity

## History of stock ID in Baltic plaice

Presently, sole (*Solea Solea*) and plaice (*Pleuronectes platessa*) are the only flatfish species in the Baltic Sea regulated by catch limits. Plaice in the Baltic Sea was treated as a single stock (plaice in subdivisions 22-32) until WKPESTO (ICES 2012). ICES decided that plaice from Subdivisions 22 (the Belts) and 23 (the Sound), which were previously assumed to be part of the Baltic Sea stock, should be considered a separate stock unit together with Subdivision 21 (Kattegat) (ICES, 2012). Plaice in Subdivisions 24 to 32 was considered to be a different stock. The assessment units were amended to fit these new stock definitions, i.e. ple.27.21-23 and ple.27.24-32. For management purposes, however, the old areas were retained and a TAC is fixed for SD22-32 and Plaice in the Kattegat (SD21) separately.

WKPESTO (2012) was tasked to look at the stock ID of plaice in the Skagerrak (SD 20) and adjacent areas. The group focused almost exclusively on the Kattegat and Skagerrak populations and this was also reflected in the participation and data provided to the workshop (e.g., almost no data was available from the Baltic proper). Apparently, the group thought it should also propose new stocks further to the East even with the serious limitations of data available from that area.

There is very little information available in the WKPESTO (2012) report on the rationale of splitting SD24-32 from the westerly areas (SDs 22-32), among these is: “*5.3.3 BITS Survey: A combined BITS survey index for the area 22-25 was computed by ICESe, including the German Solea survey. This survey was not investigated during the WK, and this time series should be revised in order to include areas 24-25 only*”. WKPESTO also stated that there are “indications that the spawning areas are likely to be located in the southern part of SD 25 and 26, but the exact spawning locations are not known” (ICES 2012), but did not provide further evidence or data on that matter. Historic and recent tagging studies and distribution maps from surveys and fisheries (presented in this working document) are indicating that the spawning grounds are rather located in the Arkona basin in SD24, neighboring the spawning grounds of the Bel Sea in SD22.

Scientific evidence from both areas in question such as genetics, maturity patterns, population dynamic, behavior, tagging or survey data were not analyzed. Nevertheless, WKPESTO (2012) recommended defining a separate stock in SD 24-32 and to adjust the management area to the new stock distribution area.

Overall, the null hypothesis "there is one plaice stock in (21)22-32" has never been rejected based on genetic evidence. ACOM decided to give advice for plaice in SD21-23 (and not split this in even smaller units), and a second stock in SD24-32 separately, but at the same time withdrew the recommendation to amend the management areas until the stock ID issues with Baltic plaice were satisfactorily resolved. WGBFAS repeatedly raised serious concerns about the validity of a separation between the eastern and the western populations.

## Latest genetic evidence

Now, Weist et al. 2022 reported "the generation of an annotated draft plaice genome assembly in combination with population sequencing data—following the salinity gradient from the Baltic Sea into the North Sea together with samples from Icelandic waters—to illuminate genome-wide patterns of divergence." The sampling covered all relevant subdivisions (SDs 21, 22, 24, 25, 26) and at three locations in the North Sea, with plaice from Iceland as an outgroup. Weist et al. 2022 "detected subtle levels of genetic substructure among North Sea samples and between samples from the North Sea and the Baltic Sea (Table 2). Within the Baltic Sea, we observed low levels of genetic differentiation among all four sampling locations (SD 22, 23, 24, 25). And no significant population structure was identified among plaice specimens caught throughout the steep salinity gradient from the Baltic Sea following the shallow straits of the archipelago into the North Sea area based on neutral SNP markers…". More details can be found in Weist et al. 2022.

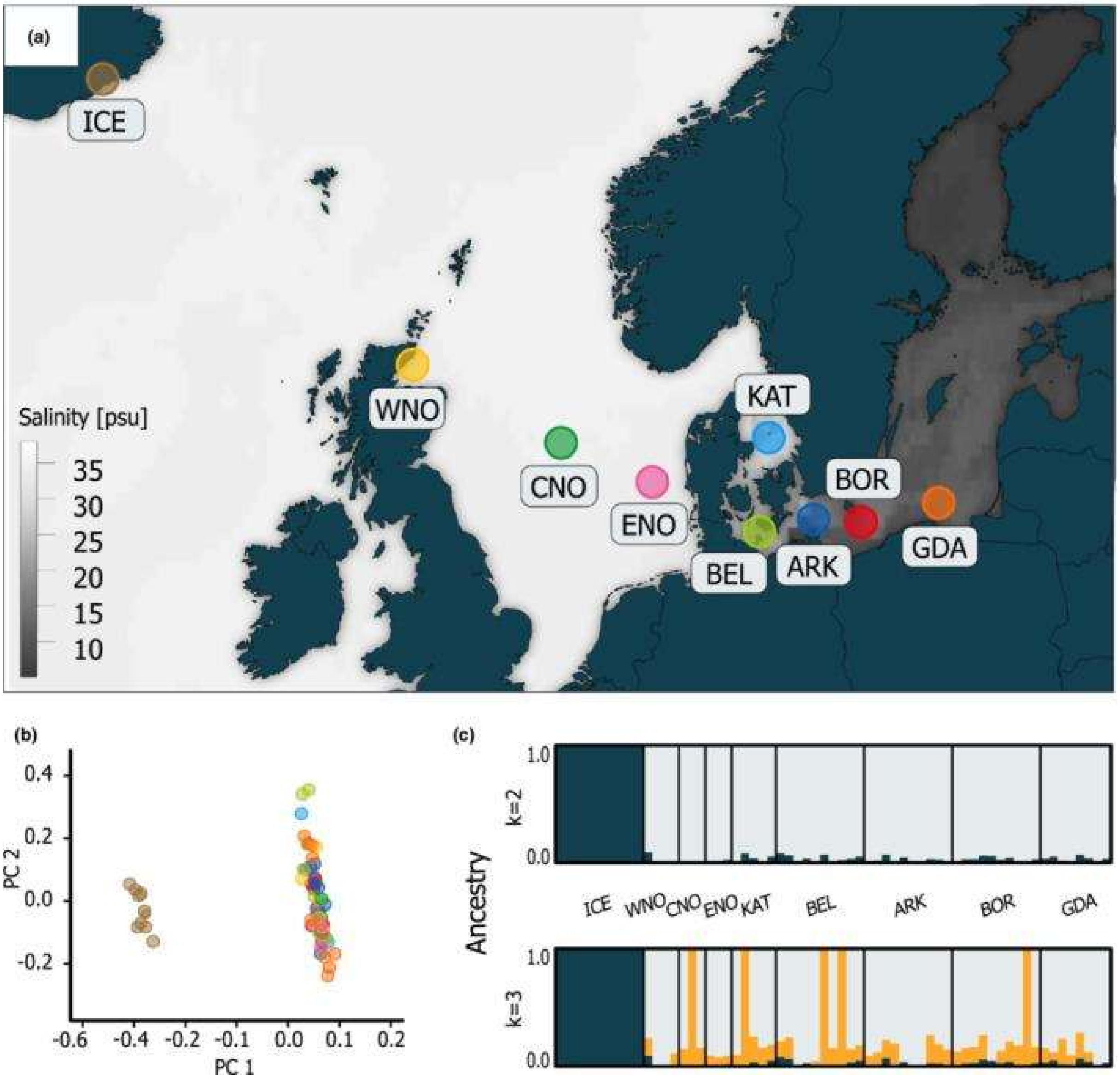


**Fig. 1.** Population structure analysis from a total of 63 European plaice samples based on 83,011 genome-wide distributed single nucleotide polymorphisms (SNPs) (Weist et al. 2022). (a) Map of sampling locations of plaice individuals included in this study (see also Table S1). (b) Principal component analysis (PCA) of population differentiation. Individuals are color-coded corresponding to the sampling locations in (a). (c)

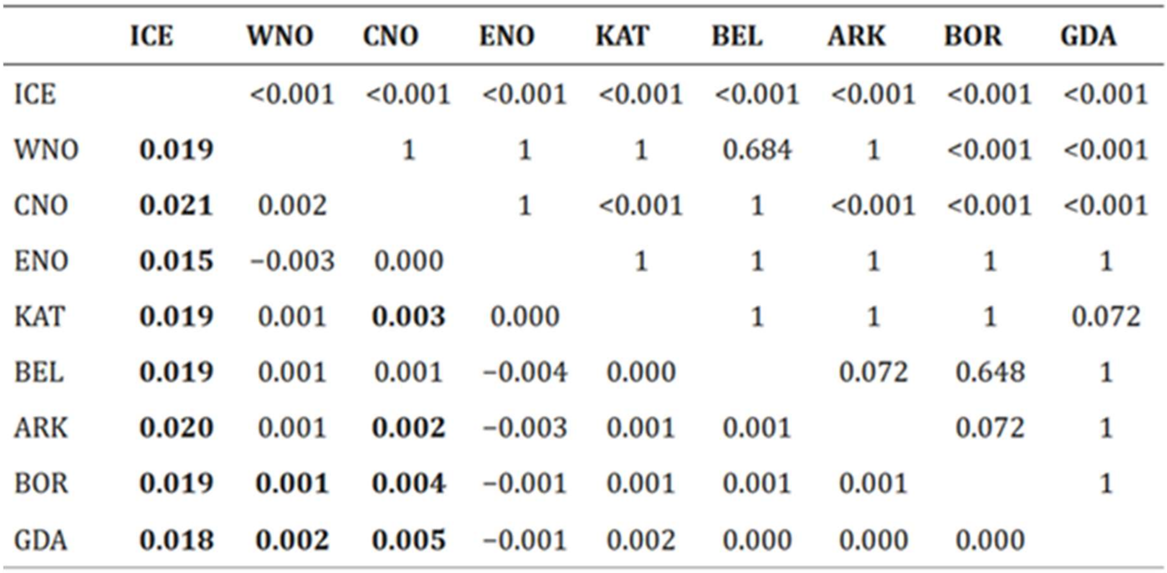
Genetic clustering according to an analysis with admixture for *k* = 2 (above; most likely number of putative ancestral populations) and *k* = 3 (below). Genetic clusters are represented by different colors with vertical bars showing the ancestry proportion for each individual genotype.

The results of Weist et al. (2022) are supporting earlier findings by Le Moan et al. (2019, 2021) who compared genome-wide population structure using sets of RAD-sequencing SNPs with the spatial structure of Structural variant (SV) polymorphisms.

Their data show genomic heterogeneity of the European plaice population structure and discovered two putative SVs displaying allele frequency differentiation following the salinity gradient from the North Sea into the Baltic Sea.

Based on pairwise $F_{ST}$ analyses by Weist et al (2022) on the pruned/neutral marker, subtle differentiation between plaice from Central and Western North Sea (CNO, WNO) versus the eastern Baltic Sea samples (ARK, BOR, GDA) was detected (see Table 1), refining the results of Le Moan et al (2021). No genetic differentiation among Baltic samples was detected.

**Table 1.** Estimates of genome-wide differentiation between samples of European plaice based on 83,011 SNPs (Weist et al. 2022)



| | **ICE** | **WNO** | **CNO** | **ENO** | **KAT** | **BEL** | **ARK** | **BOR** | **GDA** |
|---|---|---|---|---|---|---|---|---|---|
| ICE | | <0.001 | <0.001 | <0.001 | <0.001 | <0.001 | <0.001 | <0.001 | <0.001 |
| WNO | **0.019** | | 1 | 1 | 1 | 0.684 | 1 | <0.001 | <0.001 |
| CNO | **0.021** | 0.002 | | 1 | <0.001 | 1 | <0.001 | <0.001 | <0.001 |
| ENO | **0.015** | −0.003 | 0.000 | | 1 | 1 | 1 | 1 | 1 |
| KAT | **0.019** | 0.001 | **0.003** | 0.000 | | 1 | 1 | 1 | 0.072 |
| BEL | **0.019** | 0.001 | 0.001 | −0.004 | 0.000 | | 0.072 | 0.648 | 1 |
| ARK | **0.020** | 0.001 | **0.002** | −0.003 | 0.001 | 0.001 | | 0.072 | 1 |
| BOR | **0.019** | **0.001** | **0.004** | −0.001 | 0.001 | 0.001 | 0.001 | | 1 |
| GDA | **0.018** | **0.002** | **0.005** | −0.001 | 0.002 | 0.000 | 0.000 | 0.000 | |

**Note*: Pairwise $F_{ST}$ estimates are presented below the diagonal and corresponding *p*-values above the diagonal. Significant estimates are indicated in bold.

These studies were building on an earlier multi-disciplinary study by Ulrich et al. (2017) on plaice from the Eastern North Sea to the Baltic Sea involving genetic and biological analyses. While the focus was on the transition zone (Skagerrak and Kattegat), the Baltic Sea was also covered. Samples from the Western Baltic and Eastern Baltic were available and enhanced findings from a former study (Ulrich et al., 2013), which did not consider comparison within the Baltic Sea. The genetic results of Ulrich et al. (2017) suggested “the existence of different genetic populations in the North Sea, the transition zone and the Baltic Sea. The results from the AMOVA analysis, with samples grouped according to the patterns observed in Fig. 3 (i.e., three groups represented by the samples [North Sea], [Kattegat, West Skagerrak, Skagerrak] and [Western Baltic, Eastern Baltic], respectively, supported this pattern.” However, both studies did not include samples from the Belt Sea, which was also recognized as an issue by WKPLE (ICES 2015), adding uncertainty to the stock splitting that was suggested by WKPESTO in 2012.

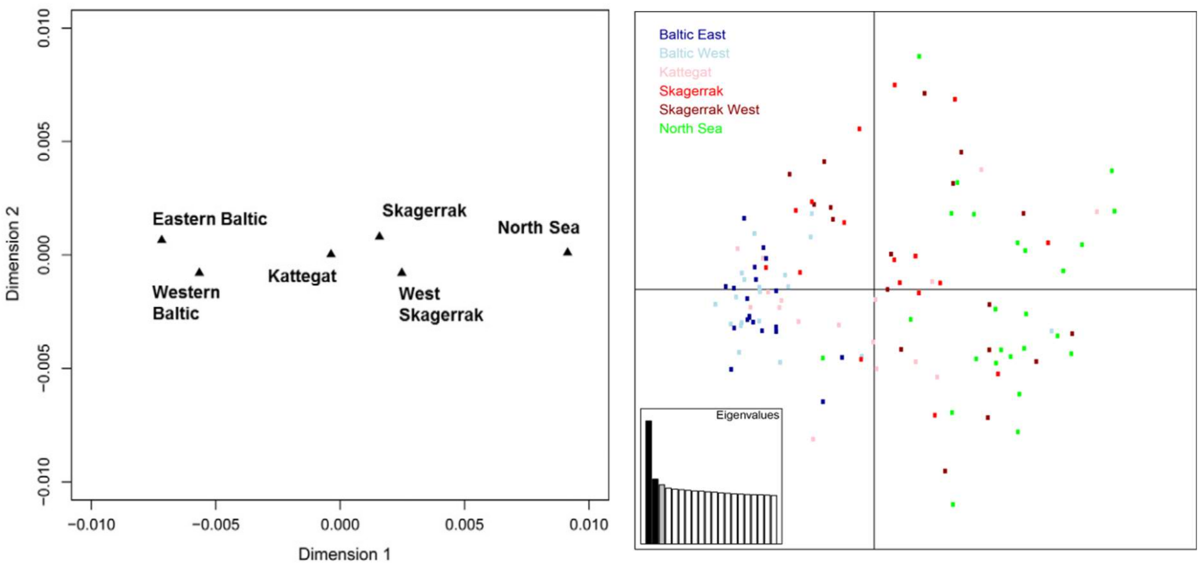
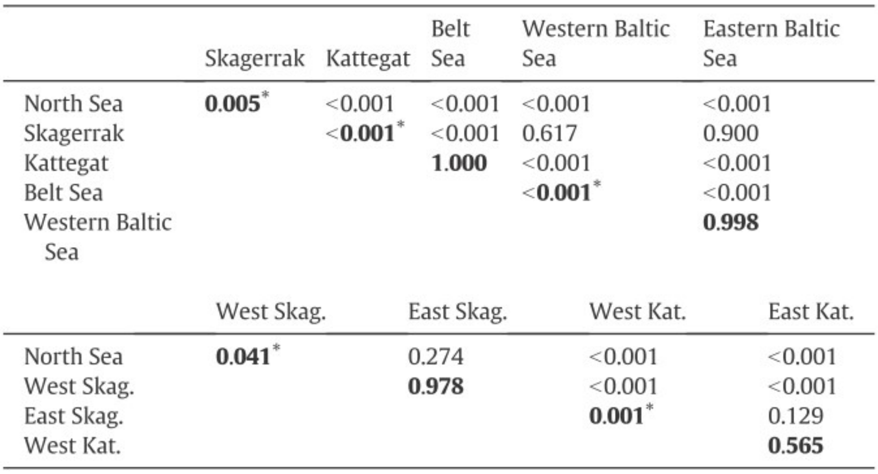


**Fig. 3:** Results of the genetic study conducted by Ulrich et al., 2017 Left Figure: Multidimensional scaling plot of pairwise estimates of genetic population differentiation (FST). Right Figure: Eigenvalue plots of the samples of plaice.

Ulrich et al. (2017) also investigated growth parameters in adult plaice based on otolith growth. The samples also did not indicate any differences in growth of plaice between the Western and Eastern Baltic Sea, but also none between Kattegat and the Belt Sea.

**Table 2:** Results of the pairwise comparison of back calculated growth between areas at two different spatial scales: Top: management areas scale (all fish). Bottom: at the scale of ICES (2012) Eastern and Western areas within Skagerrak and Kattegat (females only): Bold numbers represent geographically adjacent areas. Statistically different areas (p b 0.05) are marked with an asterisk.



| | Skagerrak | Kattegat | Belt Sea | Western Baltic Sea | Eastern Baltic Sea |
|---|---|---|---|---|---|
| North Sea | **0.005**$^*$ | <0.001 | <0.001 | <0.001 | <0.001 |
| Skagerrak | | <**0.001**$^*$ | <0.001 | 0.617 | 0.900 |
| Kattegat | | | **1.000** | <0.001 | <0.001 |
| Belt Sea | | | | <**0.001**$^*$ | <0.001 |
| Western Baltic Sea | | | | | **0.998** |

| | West Skag. | East Skag. | West Kat. | East Kat. |
|---|---|---|---|---|
| North Sea | **0.041**$^*$ | 0.274 | <0.001 | <0.001 |
| West Skag. | | **0.978** | <0.001 | <0.001 |
| East Skag. | | | **0.001**$^*$ | 0.129 |
| West Kat. | | | | **0.565** |

# Stock assessments and survey indices comparisons

## Similar trends in ICES stock assessments

Plaice in SDs 21-23 is assessed by an age-based SAM model, which also has been conducted for plaice in SDs 24-32 (although advice was given on the relative SSB and relative R development). The SAM stock assessments of the two Baltic Sea plaice stocks ple2123 and ple2432 show very similar trends since the beginning of the time series in 2002, indicating similar stock developments. Similar trends can be seen in SSB, F, and R development. Especially the outstanding recruitment peaks in recent years and the rise in SSB are characteristics equally seen in both “stocks” (Figure 4).

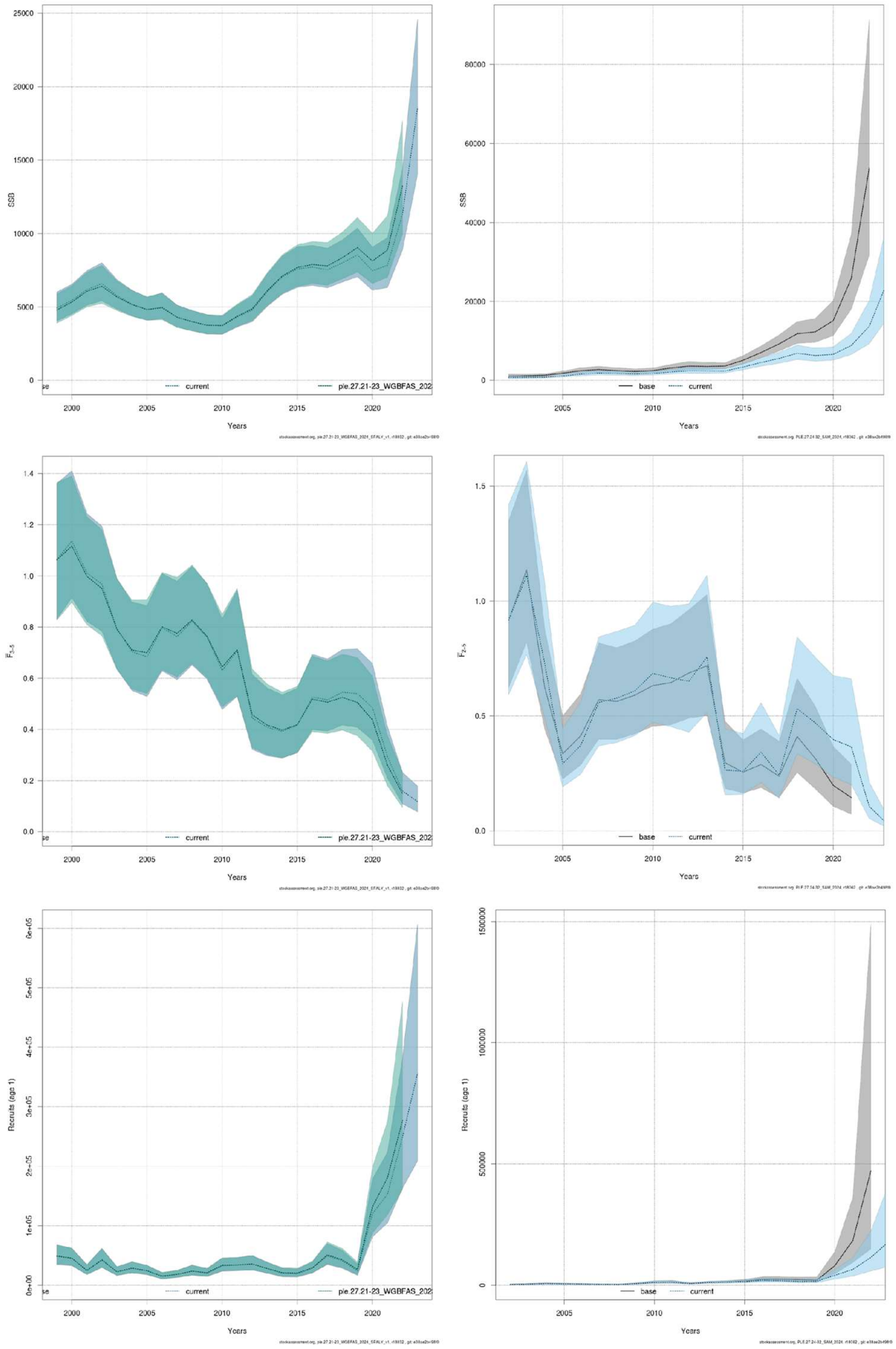


**Fig. 4**. Direct comparison of the most recent SAM outputs (ple21-23 on the left, ple 24-32 on the right). Note that the SAM assessment of ple24-32 has not been approved as an assessment method by ICES and input parameters in 2024 were not checked, as the assessment and advice is based on a SPiCT assessment since 2022.

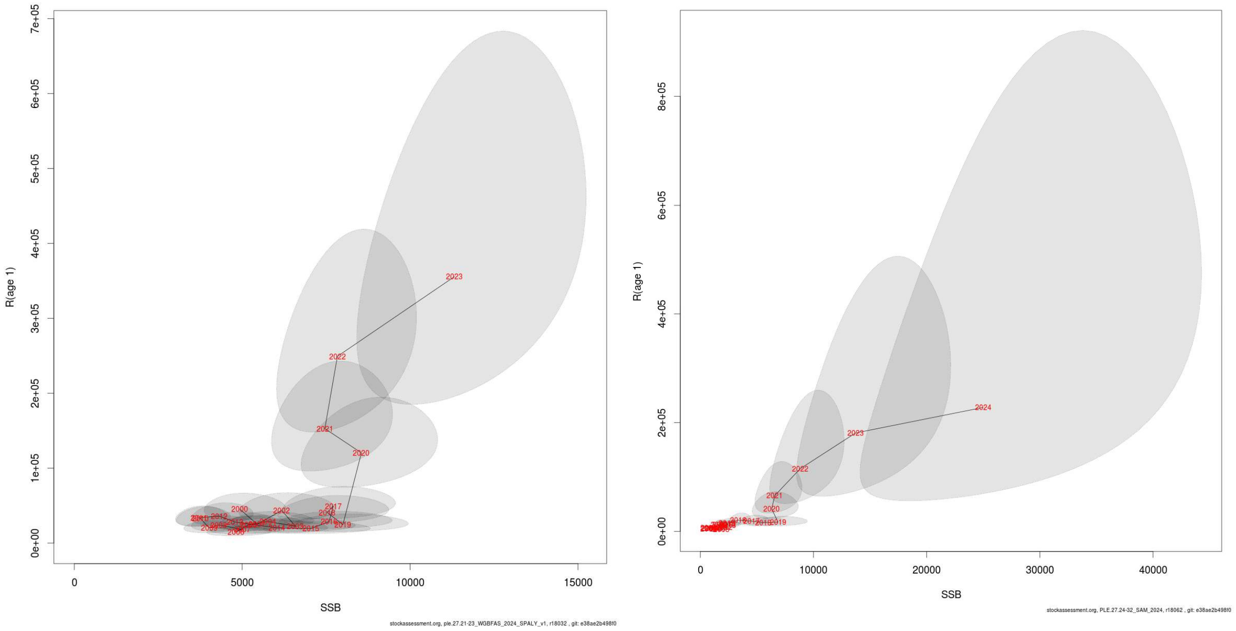


**Fig. 5**. Direct comparison of the most recent SAM outputs (ple21-23 on the left, ple 24-32 on the right). Spawner-recruitment relationships in the two stocks. Note that the SAM assessment of ple24-32 has not been approved as an assessment method by ICES and input parameters in 2024 were not checked, as the assessment and advice was based on a SPiCT assessment since 2022.

## Survey trends

The International Bottom Trawl Survey (IBTS) covers the North Sea (Subarea 4) and the Transition area (Division 3.a. including the Skagerrak 3.a.20 and Kattegat 3.a.21) and is conducted two times per year in Quarter 1 and 3 (Q1, Q3). The Baltic International Trawl Survey (BITS) covers the entire Baltic Sea and Kattegat (3.a.21) and is also conducted twice per year, in Q1 and Q4. Both surveys are conducted using the same sampling protocols and data are publicly available at the International Survey database DATRAS, hosted by ICES (https://datras.ices.dk).

Survey CPUE indices for plaice at length per haul from before 2001 are standardized to the standard TV3 trawl used by all vessels since 2001 by multiplying with a conversion factor. Then the mean age at length per depth stratum and sub-division are calculated and weighted with the surface area (m2) of the stratum. From these means, the mean catch-at-age per sub-division and then the mean catch per index area are calculated.

Calculations:

- CPUE per length (l) and haul (H) are multiplied with the conversion factor (conf) for the gear to give CPUE adjusted for gear performances (conf)

$$confCPUE_{H,l} = CPUE_{H,l} * conf$$

- Age is allocated to the length distribution as described above.

- Number per length (l) (1 cm group) per haul is summed by year, quarter, sub-division and depth stratum (DS) and divided with total hauls in the depth stratum.

The indices are currently compiled for each stock outside of DATRAS, using the CPUE per age per area (subdivision) and combined according to the stock boundaries.

The CPUE survey indices display very similar trends between the two stocks ple21-23 and ple24-32 (Figure 6). Both stocks slowly increased in the early 2000s and rapidly increased in the late 2010s.

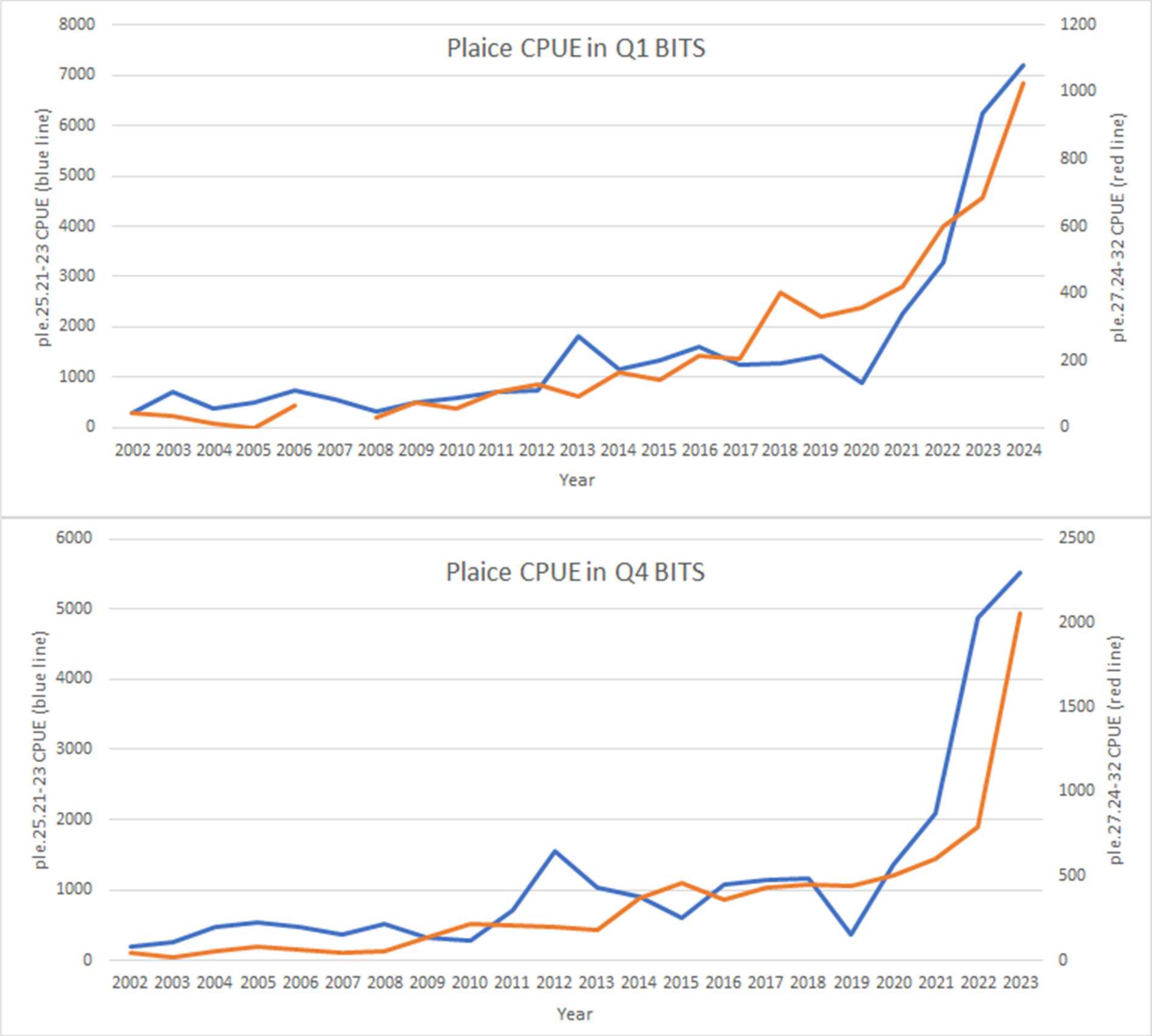


**Fig. 6**. Comparison of the cpue by age indices (age classes 1 to 7) between the two plaice stocks, ple.27.21-23 (blue line, left axis)and ple.27.24-32 (red line, right axis) in the two surveys BITS Q1 (upper graph) and BITS Q4 (lower graph)

Survey distribution maps of the two most recent BITS (Q4 in 2023 and Q1 in 2024) do not display any spatial separation between plaice in the Belt Sea and Sounds and Arkona Sea (Fig. 7). In both quarters, plaice seems to be concentrated in the Belt Sea, extending into southern Kattegat and the Arkona Sea.

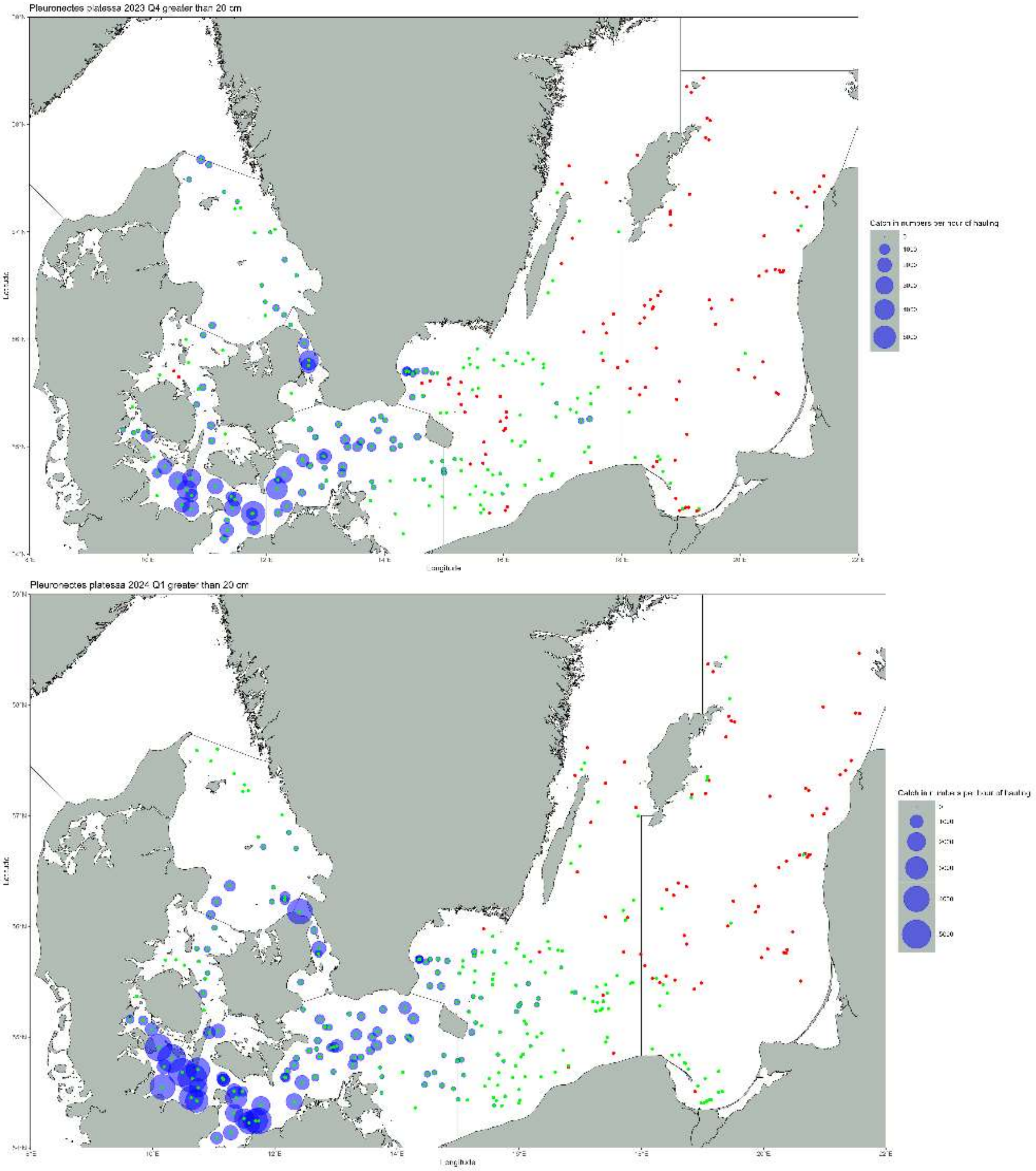


**Fig. 7**. Distribution maps of the most recent surveys (BITS in Q1 2024 and Q4 2023), raised to numbers per hour. Red dots indicate stations with zero plaice catches. Green dots indicate stations with very low numbers caught (threshold <10 individuals) and no raising to CPUE was conducted.

More distribution maps, covering the assessment time series from 2002 to recent (2024 Q1, preliminary), divided by length groups (juveniles <20cm and adult >20cm) and by survey (Q1 and Q4) are given in **Annex 1**.

## Migration and tagging studies

Recaptures from tagging experiments conducted by the Thünen-OF since 2017 in SD22 and SD24 suggest that plaice mainly stay in the same subdivision. However, plaice tagged in the south of SD24 seem to conduct spawning migrations in Q1 towards the deeper areas around Bornholm (Bornholms Gatt and Bornholm basin, i.e., northeast part of SD24 and western part of SD25). Plaice tagged in SD22 and on Darss Sill (western part of SD24) were recaptured in SD22; but there was also one individual that was tagged in Pomeranian Bay (SD24) and recaptured in Lübeck Bay (SD22) while another individual tagged nearby Pomeranian Bay was recaptured in SD25 (Fig. 8). Growth of recaptured adult plaice was generally low, ranging from rarely 4 cm/yr to usually something between 1 and 2 cm/yr.

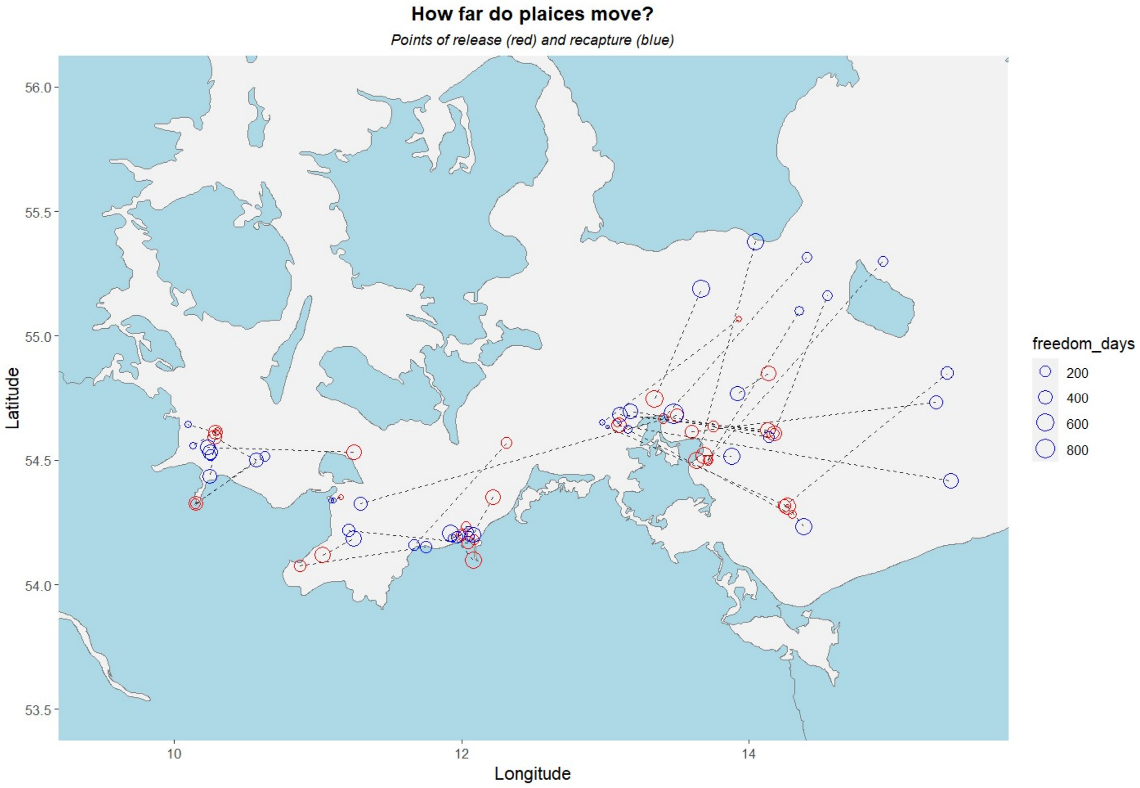


**Fig. 8.** Overview of plaice recaptures since 2017. Circle size indicates the days at liberty. Red dots: release location, blue dots: recapture location. Krumme U, unpublished data.

Historic tagging studies show a similar pattern with plaice displaying seasonal migration between the basins (during spawning time) and the slopes (feeding grounds). However, in almost all tagging studies, some plaice were recaptured in other areas that are not part of their assigned stock boundary, sometimes even more than 20% of the plaice were recaptured outside the subdivision in which they were released (Nielsen et al., 2007, ICES 2007).

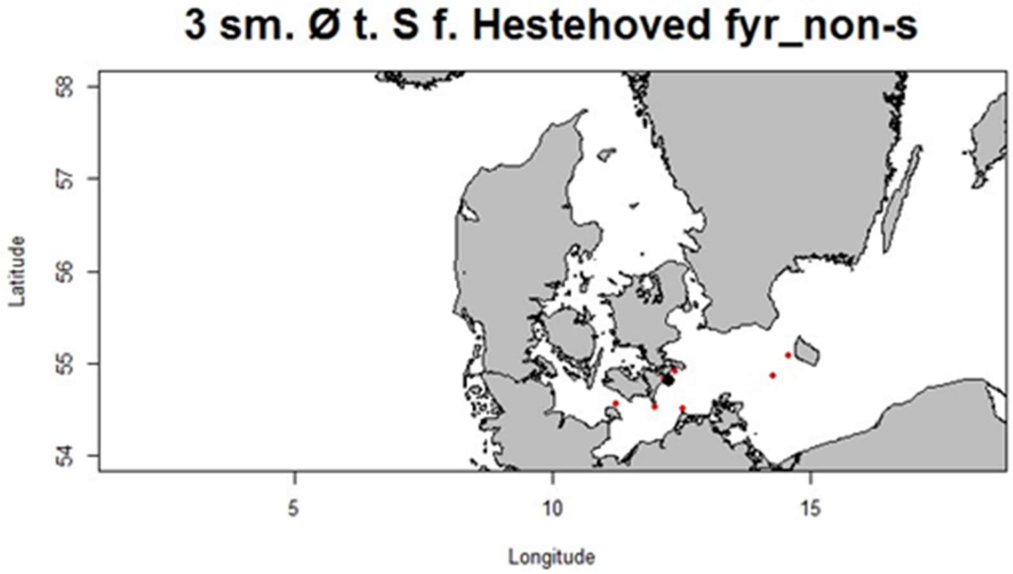
Nielsen and co-authors worked up recapture data from more than 13.000 tagged plaice (of a total of over 40.000 tagged fish) in the North Sea, Skagerrak, Kattegat and Baltic Sea for an extensive working document of WGNSSK in 2006 (ICES 2007). The analyzed recaptures are covering more than 300 releases over a time span of >60 years (1903 to early 1964) and while most of the tagging studies have been conducted in the North Sea and the transition area, several tagging results are presented for the Baltic Sea as well, showing migrations from the Arkona Sea into the Belt Sea (Fig. 9). Most of the tagging studies in the Western Baltic (including SD24) have been conducted in the mid- to end-1950s, while the two tagging studies east of Bornholm (SD25) have been conducted in 1956 and 1957, respectively.

Based on a calibration with fishing effort within the area, these data revealed a stable migration pattern over the years (Table 4). There was in general a high level of resident behavior observed within the various sub-areas, and especially in the Belt and Western Baltic (between SDs 22-24!), in Kattegat and in the North Sea, where up to 90% of the fish were recaptured in the same area in which they were released. However, most of these were recaptured within the tagging year. Residency in the Eastern Baltic (SDs 25-32) proved to be low, because about 39% of recaptures occurred in SDs22-24.

**Table 4:** Migration rates (in column percentage) between management areas, using Danish tagging experiments during the period 1903-1964. Data adjusted for fishing effort. Bold: residency.

| | **Tagging management area** | | | |
|---|---|---|---|---|
| **Recapture management area** | 22-24 | 25-32 | IIIa | IVabc |
| 22-24 | **97** | 39 | 2 | 0 |
| 25-32 | 0 | **61** | 0 | 0 |
| IIIa | 3 | 0 | **95** | 10 |
| IVabc | 0 | 0 | 3 | **90** |

The Baltic Sea was poorly covered by marked releases, only , but even the few recaptures available regularly displayed exchanges across the administrative borders of the two current stocks (Figure 9), with plaice released east of Hestehoved (SD22) being recaptured west of Bornholm Island, in SD24.



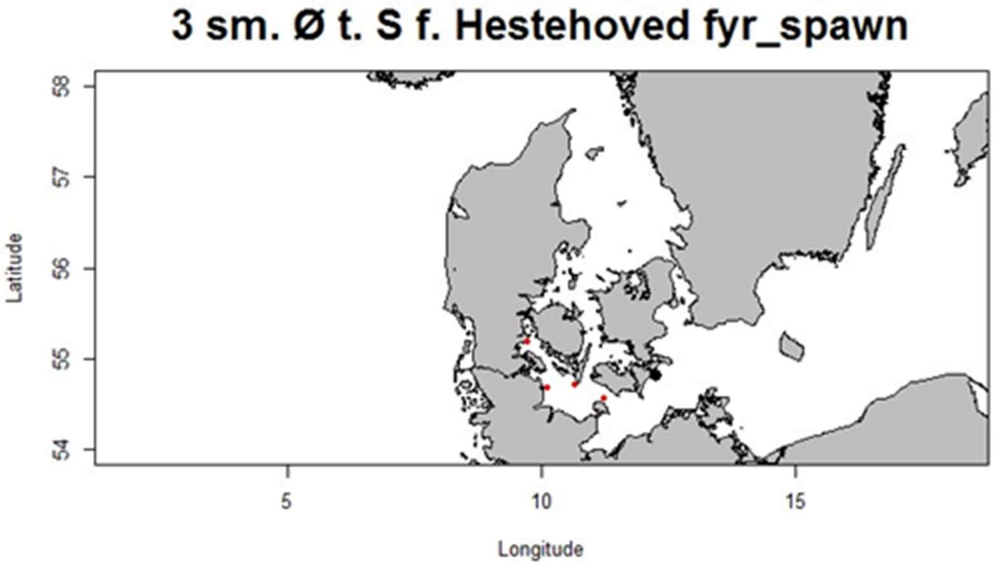


**Figure 9:** Plaice tagging results from Nielsen et al. (2006, as WD for ICES 2006) in the Baltic Sea. Black dot: release station, red dots: recapture location of non-spawning (upper figure) and spawning (lower figure) plaice.

Results from another historic tagging study are available for this report which focused on plaice in the Baltic Sea. Strodtmann (1918) reported recaptures results from tagging experiments with plaice from SD22, SD24 and SD25 from the period 1905 to 1907. These recaptures were neither considered in WKPESTO (2012) nor in Ulrich et al. (2013, 2017). The publication of Strodtmann (1918) is in German and was re-discovered during the data compilation workshop of WKBPLAICE in June 2024. These historic results from almost 120 years ago clearly show that 1) plaice display the same annual movement pattern since decades (use of deeper basins mainly during spawning time in quarter 1, use of shallower slope areas during the rest of the year to feed), 2) there is no evidence suggesting any effective divide between plaice in SD24 and SD22, or between plaice in SD24 and SD 23, neither today nor more than 100 years ago. Or conversely, the historical tagging experiments clearly call into question how WKPESTO (2012) could recommend and ACOM later on accept a stock separation of plaice in the Baltic Sea.

60 S. Strodtmann, Weitere Untersuchungen über Ostseefische.

B. Die Aussetzungsversuche mit Plattfischen.

I. Scholle.

Spezieller Teil.

1. Aussetzungen im nördlichen Teil der Beltsee.

Die Aussetzungsversuche umfassen den zwischen Alsen, Langeland, Laaland, der schleswig-holsteinischen Küste und Fehmarn gelegenen Meeresteil, nach Osten zu bildet die Meerenge zwischen Fehmarn und Laaland die Grenze. Von Reibisch wird dies Gebiet mit Region I und II bezeichnet. Leider ist die Zahl der Versuche nur gering.

Figur 3.

Es gehören hierher Nr. IX, X und XXII. An der schleswig-holsteinischen Küste wurde nur ein Versuch gemacht (XXII). Die Schollen wurden mit einer Zeese durch ein Motorboot in der Nähe von Aerö auf 23 m Schlick gefangen und zwar im September 1907. Unter den 599 Schollen waren, wie stets auf den

**Fig. 10.** Recaptures of plaice released in February 28th, 1906 (Fehmarnsund, south of Langeland) and September 5th, 1907 (Eckernförde Bay, caught by trawl at 23 m water depth on muddy ground). Map from Strodtmann (1918).

In the Belt Sea (SD 22) recaptures showed that plaice moved from the spawning grounds (deeper areas in Fehmarnbelt and south of Langeland) to shallower areas outside the spawning ground (Fig. 11). Recapture rates ranged between 0.4 and 15%. Selected growth rates that were reported are: 2 cm/yr for two recaptures,2 cm in 18 months and 2,5 cm in 6,5 years.

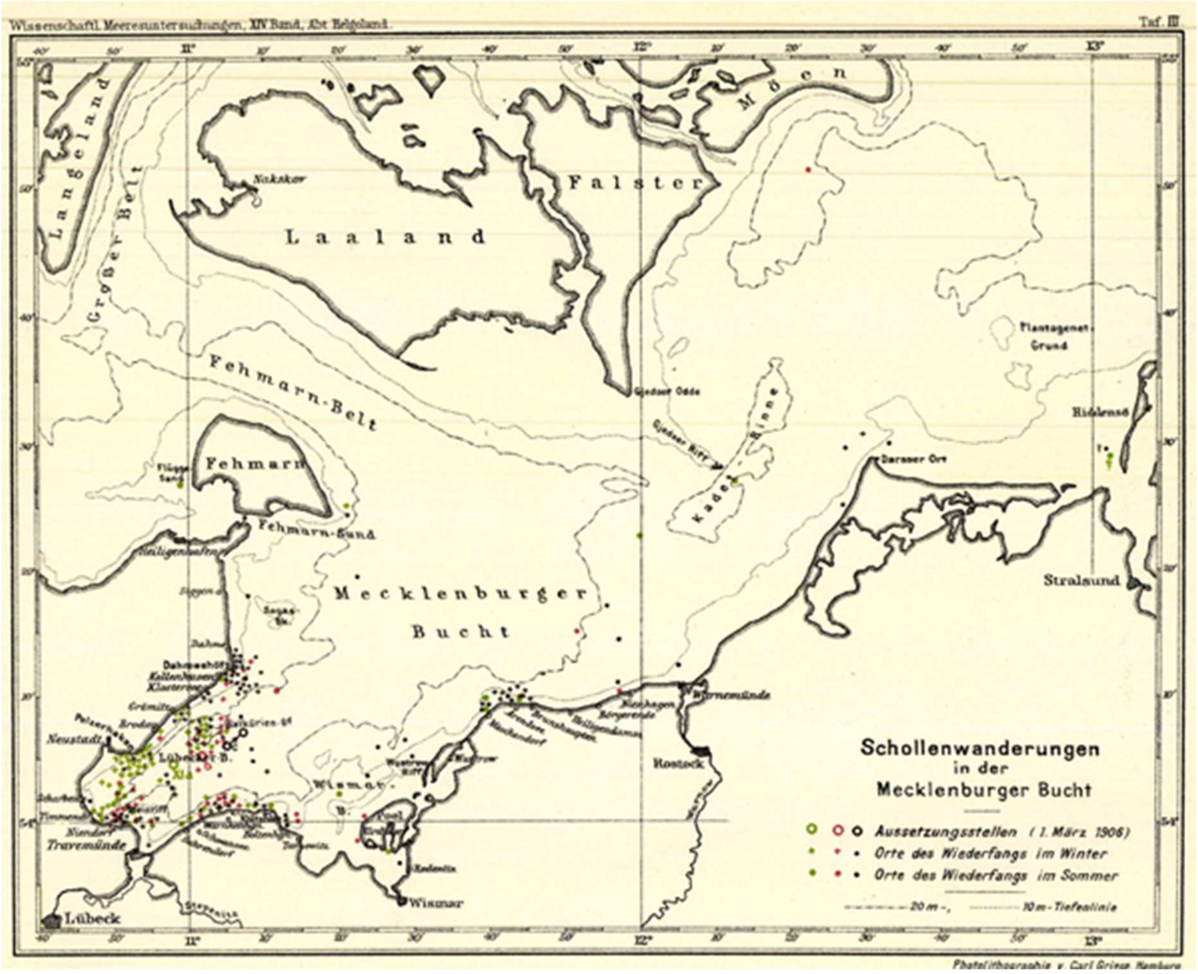
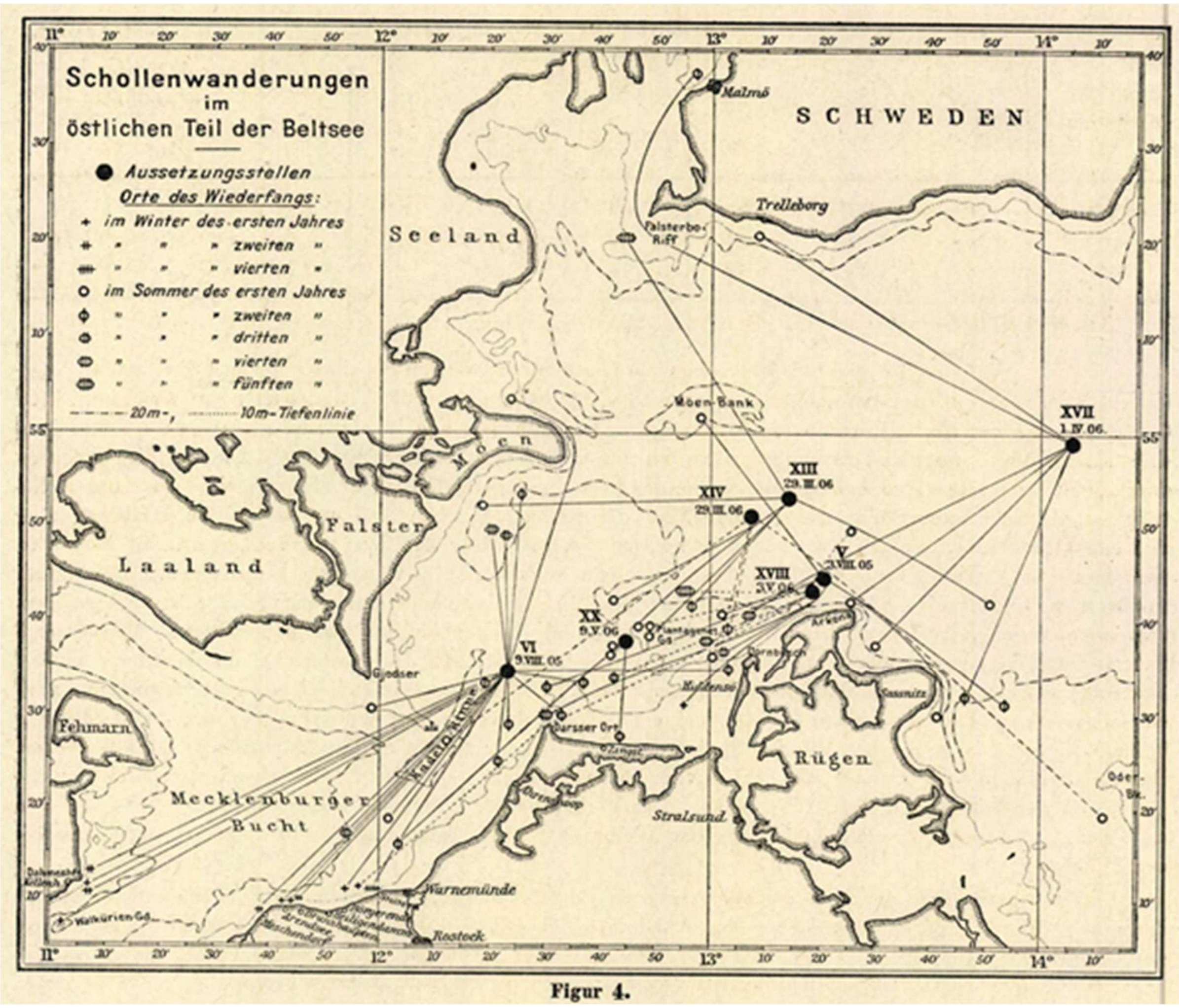


**Fig. 11.** Recaptures of plaice released on March 1st, 1906 (off Pelzerhaken). Map from Strodtmann (1918).

In Mecklenburg Bay marked plaice were released in Neustädter Bucht, close to Pelzerhaken.

Recapture rates within the first winter post-release were high, ranging between 40 and 61%. “This is proof that a very intensive plaice fishery took place the further you go into the bay, the more intensive the fishing” (translated text from Strodtmann 1918).

“Most of the animals were recaptured in the bay itself, but quite a few have made their way to the Mecklenburg coast, and we have recovered animals from almost all the fishing villages. Also, from the Kadettrinne, the area between Gedser and Darsser Ort, some were returned (5). Even lower was the number further east, one from Moen and 2 from Stralsund. Not a single one had migrated into the Baltic proper. The plaice also proved to be a stable fish here, even after years (one after six years) it does not move away from its sea area” (translated text from Strodtmann 1918). These historic recaptures clearly show that there was a regularly link between spawning fish in SD22 (Mecklenburg Bay) and feeding grounds in SD24 (Darss sill).



Figur 4.

**Fig. 12.** Recaptures of plaice released in SD24; east of Kadettrinne on Darss sill at September 9t, 1905, in 1905/06 north off Rügen island, and April 1st 1906 in the Arkona basin. Map from Strodtmann (1918).

Figure 12 "gives an overview of the movements of the plaice released in the eastern part of the Belt Sea beyond the Darsser Ort-Gedser line and in the Rügen Basin. The release at the Kadettrinne, slightly east of it, at a depth of 20 m and on a sandy bottom is remarkable. Initially, all the animals, with one exception, were only recaptured after a longer period of time, after 6 months to 4 years. Nevertheless, 5 were recaptured within a radius of 10 seamiles. Of those that have traveled further, only one went to the east, 27 sm. to Hiddensö, but 13 went to the west to the various sites of the Mecklenburg Bay. 4 were recaptured in a northerly direction near the island of Moen.

The majority (9) of the fish that moved to the west fell victim to winter fishing, while east of the Gedser-Warnemünde line they were all caught in the summer. What is more striking is the high percentage of recovered females - 34 % of the released ones, while only 4% of the males were recaptured" (translated text from Strodtmann 1918).

Maximum reported growth rate of the tagging in this area was 4 cm /yr, but usually growth comprised 1,5-2 cm/yr.

Plaice tagged in the central Arkona basin moved into SD23 and many fish released on Darss sill moved into SD22, thus clearly violating the (untested) assumption of WKPESTO (2012) that SD24 is separated from SD22 and SD23.

"Further to the east, we have only carried out tagging in the Bornholm Basin. In the Gdansk Basin, the plaice is already too sparse to obtain useful results" (translated text from Strodtmann 1918). Unfortunately, no recapture map from the recapture distribution around Bornholm basin is available in Strodtmann (1918). Plaice were released at 95 m depth in the Bornholm basin and "the animals first have to travel 60 or more sea miles until they arrive at areas where fishing occurs. The vast majority were caught" south of the Bornholm basin and had thus moved "in a southerly and south-easterly direction, only one had migrated to Rügen" (translated text from Strodtmann 1918). Plaice released at another location around 60-75m deep spread across a wider area (east, south and west) but most traveled south and west (e.g. Oderbank and off Rügen).

"The theory of Reibisch that there was a lively exchange of plaice between the individual regions in terms of large and regular migrations from west to east take place, is conclusively refuted by the results of our tagging. It is true that within the individual basins there is a regular shift of the plaice populations within the individual regions. In late summer and fall, the animals move to the deeper areas, complete their spawning period in more saline depths, then in the spring move to the shallower, warmer parts of the sea" (translated text from Strodtmann 1918).

Strodtmann (1918) further concluded that "the plaice in the Baltic Sea is to a much greater degree a distinctly resident fish than in the North Sea. The migration of the animals from one region to another is in any case quite insignificant. They stay in the same area for years. Likewise, the Danish investigations have also shown that there is no significant migration of plaice from the southern Kattegat neither through the Belts nor through the Sound" (translated text from Strodtmann 1918).

At that time they even did exchange experiments that pointed to genetically determined difference in growth performance between plaice from the North Sea and the Baltic Sea: "We have moved plaice from the Baltic Sea to the North Sea (see Reichard (23)), but the animals have not grown any more here than in the Baltic, while conversely plaice, which the sea fishing association brought over from the North Sea to the Baltic Sea, exceeded the Baltic Sea plaice in growth despite the unfavorable conditions: the best proof that it is not external circumstances alone that are decisive here, but internal are decisive here, but internal causes play a role. (Translated text from Strodtmann 1918).

## What would be the next steps in relation to WKBPLAICE

If plaice in the Baltic is considered as one stock, the following tasks need to be completed before the benchmark in October 2024:

- Merging survey data and create a combined index with annual length-weight relationships (delta GAM model after Berg et al., 2013)
- Merging commercial data
    - Landings and estimated discards, including BMS landings
    - Biological data and catch composition (numbers-at-age, weight-at-age, etc.)
- Have all other relevant data match the new assessment unit
- Calculating new reference points for the stock
- Determine if the TAC is still fixed for SD22-32 and Plaice in the Kattegat (SD21) separately
- Conducting assessment runs and sensitivity analyses for the merged stock

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