Supplementary material 1

Texte S1

The described methods can be found with details and demonstration in Satelli et al. (2008)

Outcomes of the individual based model can be represented as a function of physical and biological parameters:

$$Y = (y_i, y_{k,l}) = f(X) = f(\theta_{phys}, \theta_{bio})$$

with:

y_i : recruitment predicted in nursery i

$y_{k,l}$: percentage of larvae originating from spawning ground k into nursery l predicted by the model

$X = (X_1, \dots, X_n)$ a set of model parameters which can be subdivided into two categories:

θ_{bio} : biological parameters (such as spawning date, PLD, behaviour …)

θ_{phys} : physical parameters (such as wind, temperature, tide …)

Variance of Y can be decomposed into

$$\mathbb{Var}(Y) = V_1 + \cdots + V_n + V_{1,2} + V_{n-1,n} + \cdots + \cdots + V_{1,\dots,n}$$

Where V_i is the part of variance from the principal effect of X_i and where each $V_{k,\dots,l}$ is the part of variance from interaction among parameters $X_k, \dots, X_l$.

Sensitivity indices are defined from this decomposition: $\mathrm{SI}_U = \dfrac{V_U}{\mathbb{Var}(Y)}$

with U factorial terms which represent principal effect or interactions.

In practice, **first order sensitivity indices** will be computed with the equation:

$$SI_j = Var\,(E(Y\,|Xj))/Var(Y)$$

Where $Var\,(E(Y\,|X_j)\,)$ assess the mean variability over the domain X_j $\left(\text{i. e estimation of the importance of } X_j\right)$

Similarly, the sensitivity index of interaction among k factors (i,…,k) is computed with the equation:

$$SI_{i,\dots,k} = Var\,(E(Y\,|X_i, \dots, X_k))/Var(Y)$$

Total Effect Sensitivity Indices are computed with the equation:

$$STI_j = \sum_{k \in \#j} S_k = 1 - \sum_{k \in \sim j} S_k$$

with #*j* all the combination of indices including *j*

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These indices help to assess to what degree parameters are influential (i.e. how variation in the parameters impact model prediction). The more the sensitivity index approaches 0, the less the factor is influential; the more the index is close to 1, the more the factor is influential. A specific value of a parameter is hereafter called **modality**.

An **experience** is a set of modalities (one for each parameter which varies).

An **experimental plan** is a collection of different experiences.

An experimental plan which includes all the possible combinations is called a **full factorial design.** The number of experiences in a full factorial design is the number of modalities of each parameter which multiply among themselves and can quickly become important.

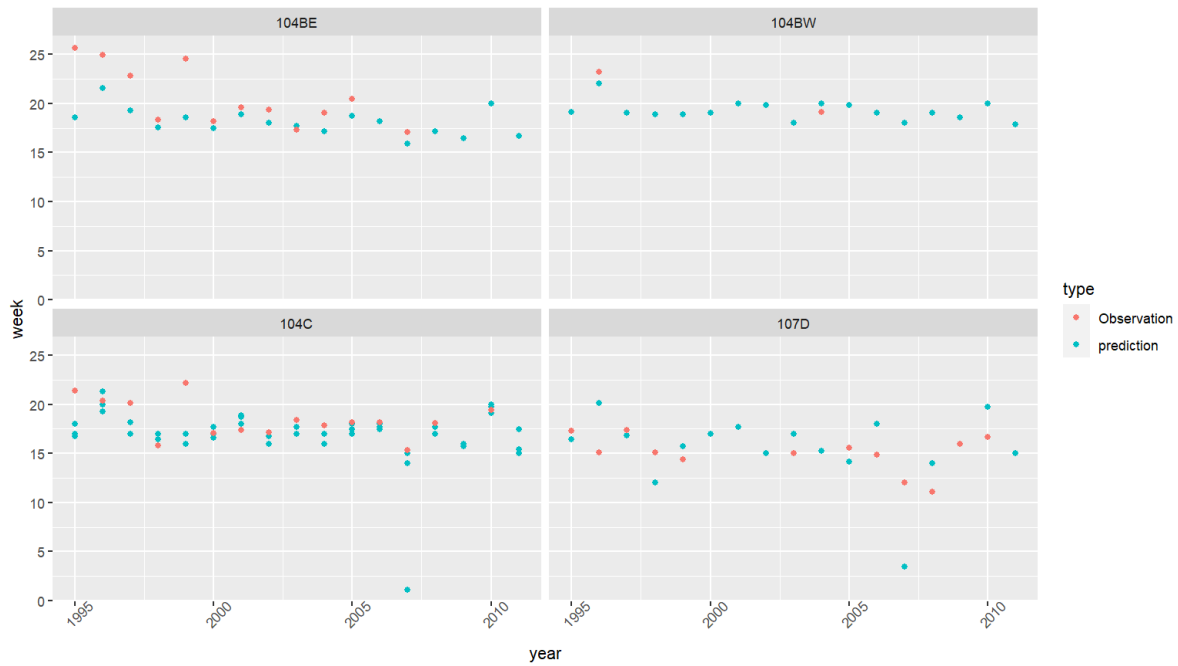## *Figure S1 Spawning period of common sole in the North Sea*

Figure S1: Comparison between the peak of the spawning period, estimated based on gonad analysis from Fincham et al. 2013 (represented by pink dots), and the estimation based on sea surface temperature from this study (represented by blue dots), is presented for different areas. The areas are labelled as follows: 104BE corresponds to the German Bight; 104BW to Norfolk; 104C to the Belgium, Thames, and Texel spawning grounds; and 107D to the English eastern channel spawning ground. The values are not directly comparable due to differences in the areas considered. However, incorporating a two-week uncertainty range around the predictions seems to be a reasonable estimation of the uncertainties associated with this parameter.

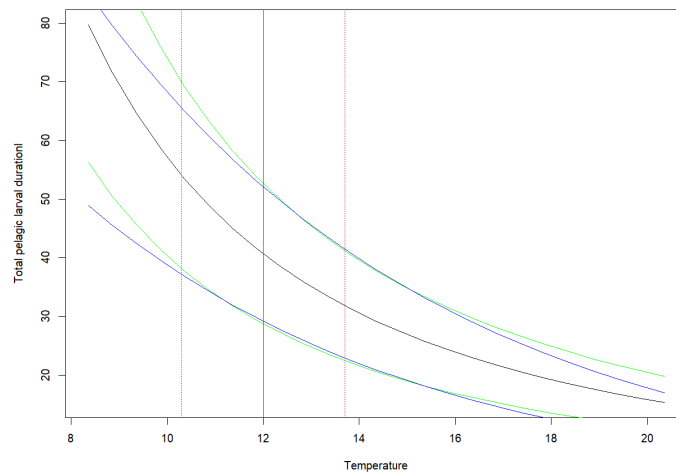## *Figure S2 Range of PLD*

Figure S2: Comparison of the total pelagic larval duration and the interval found in literature. The black line represents the standard parameterization, while the green lines represent the short and long durations. The blue lines represent the minimum and maximum durations found in literature, as summarized in Bolle et al. 2005, table 4.3.2. To assess the larger uncertainties possible, we assume that the interval found in literature is derived by considering the shortest case for each stage and the longest case for each stage. Red lines represent the mean and standard deviation of temperature encountered by sole larvae in the model.

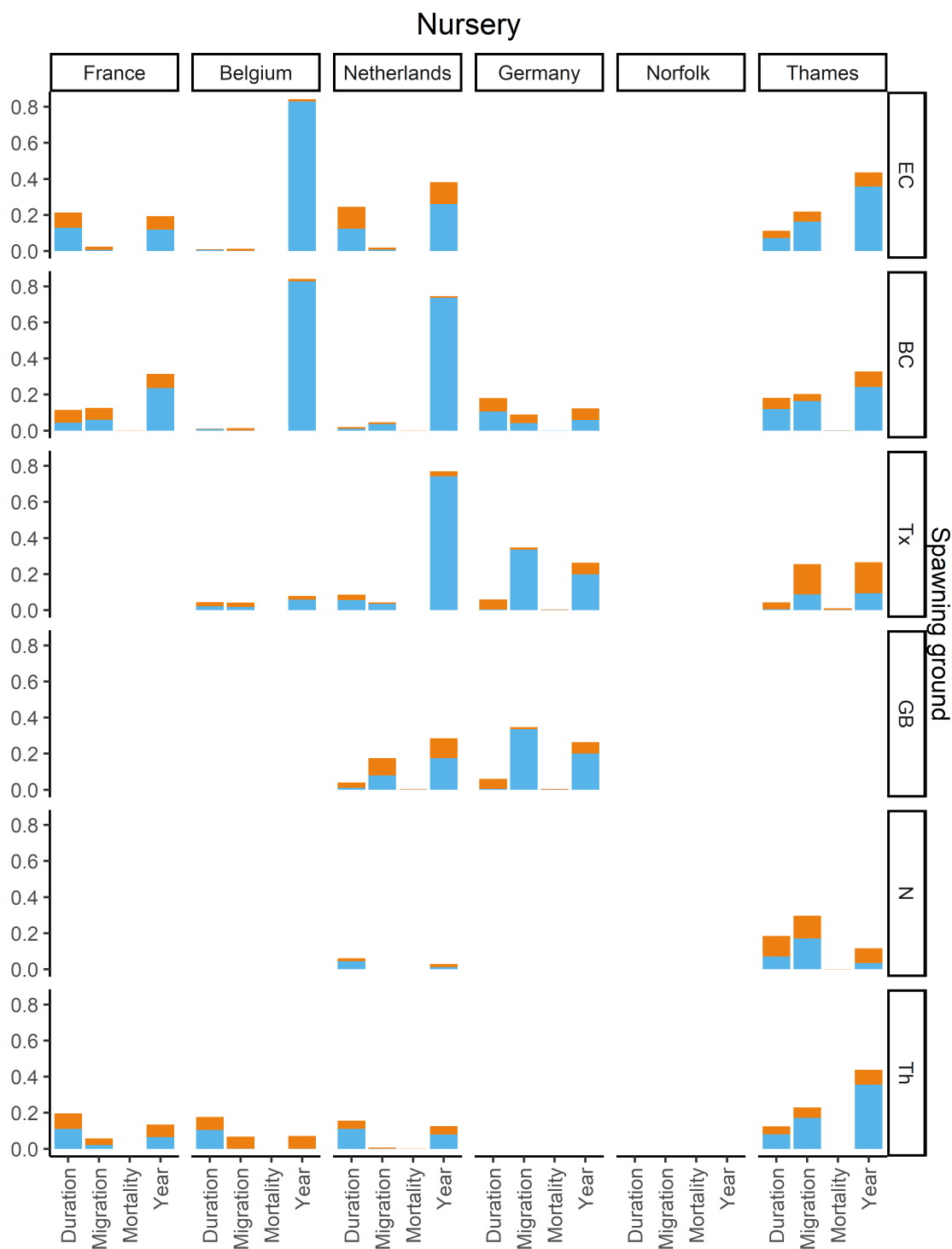### Figure S3 Sensitivity indices on connectivity Step 1

Figure S3: Sensitivity indices compute on connectivity in each nursery for the different parameters tested in Step 1 in the six nurseries from the 6 spawning grounds of common sole in France. Blue: SI, orang: TSI. A zero value in a nursery is attributed to the absence of variation.

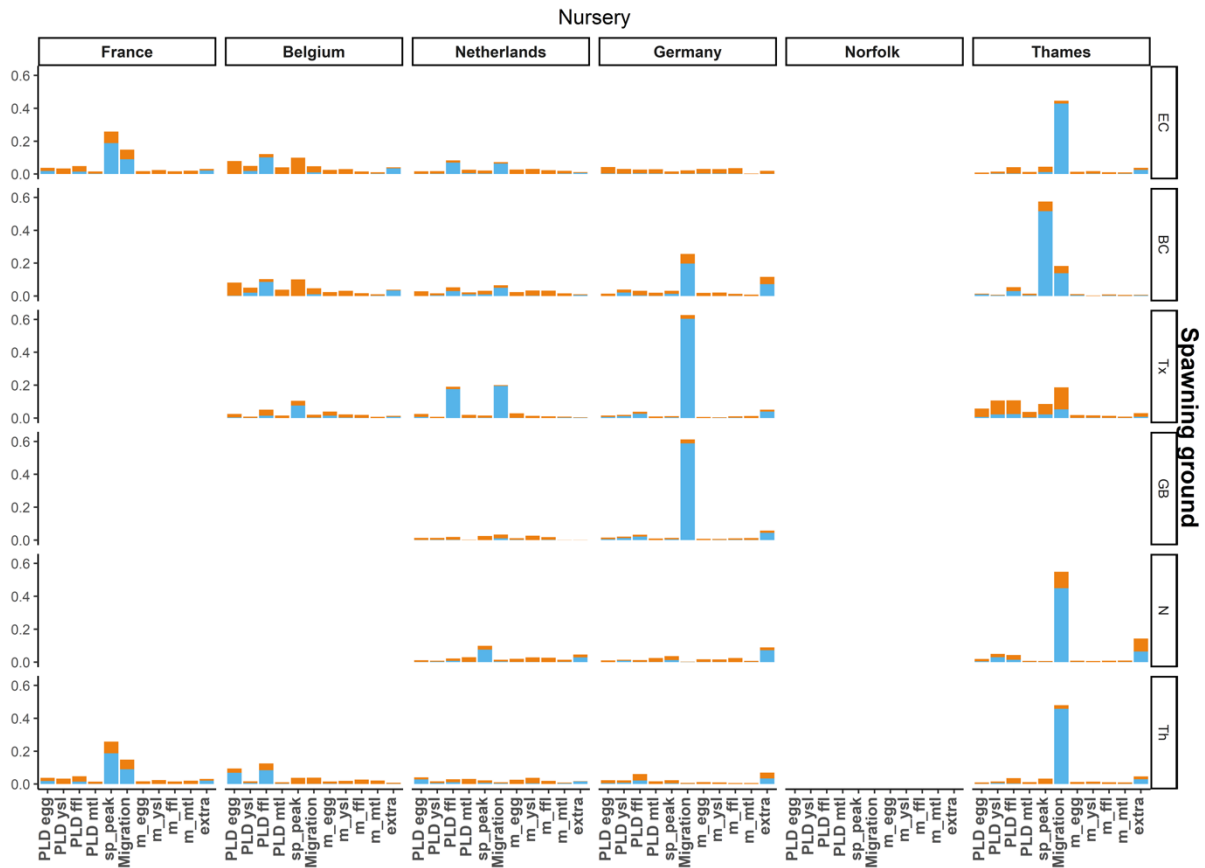***Figure S4 Sensitivity indices on connectivity Step 2***

Figure S4: Sensitivity indices computed by nursery on connectivity of larval common sole for the biological parameters (duration of egg phase: 'd_egg', duration of yolk-sac larvae: 'd_ysl', duration of first-feeding larvae: 'd_ffl', duration of metamorphosis larvae: 'd_mtl', spawning peak date: 'sp_peak', vertical migration type: 'Migration', mortality of the different stages: 'm_egg', 'm_ysl', 'm_ffl' and 'm_mtl' and settlement delay: 'extra') for the six nurseries and from the 6 spawning grounds. Red: SI, orange: TSI. A zero value in a nursery is attributed to the absence of variation.

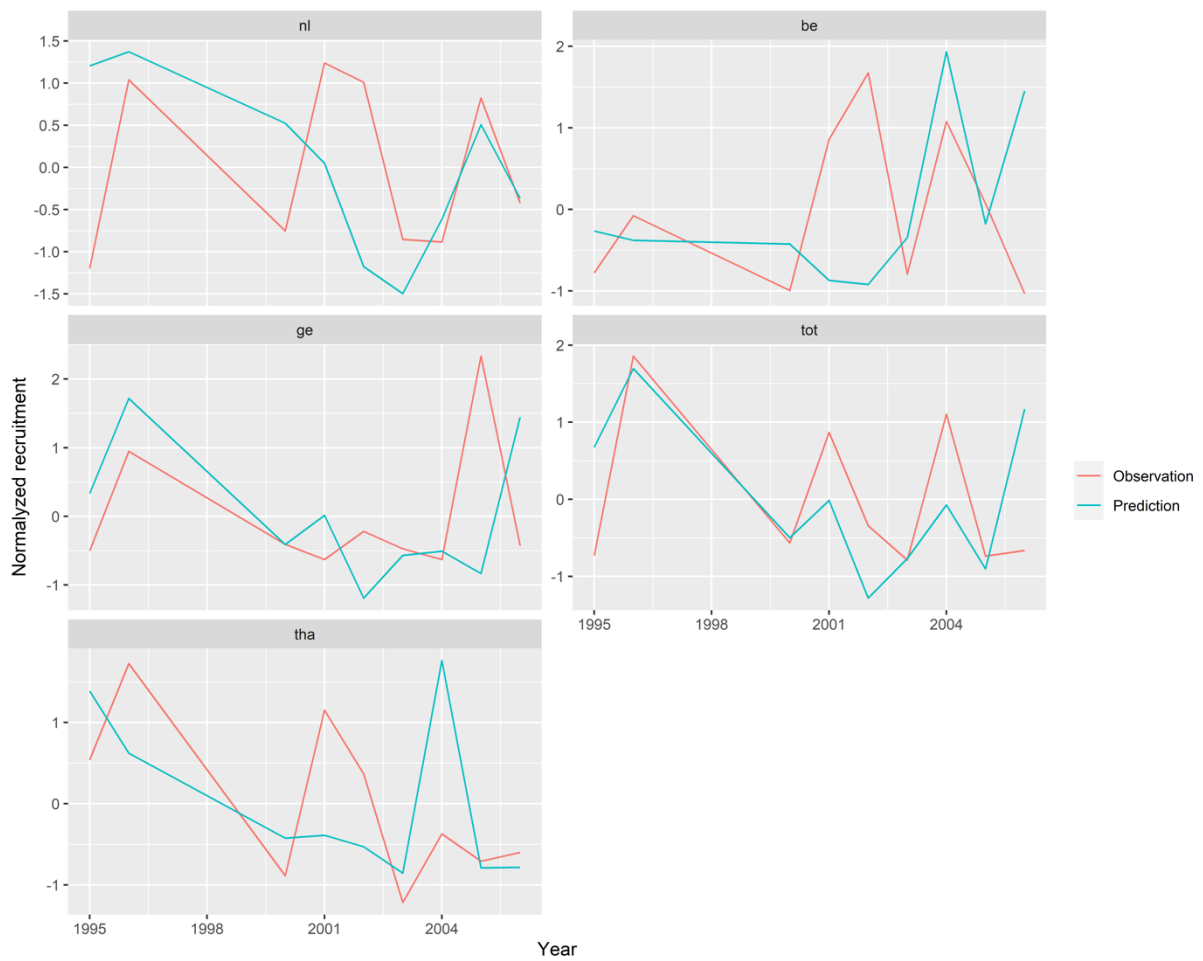### Figure S5 Time series of normalized recruitment

Figure S5: Time series of normalized recruitment in the different nurseries, including observations and predictions from the model with the lowest RMSE (Root Mean Square Error). This model corresponds to low mortality, a long larval duration for eggs and yolk-sac larvae, a baseline spawning peak, and a behaviour involving nycthemeral and tidal migration.