**Supporting Information**

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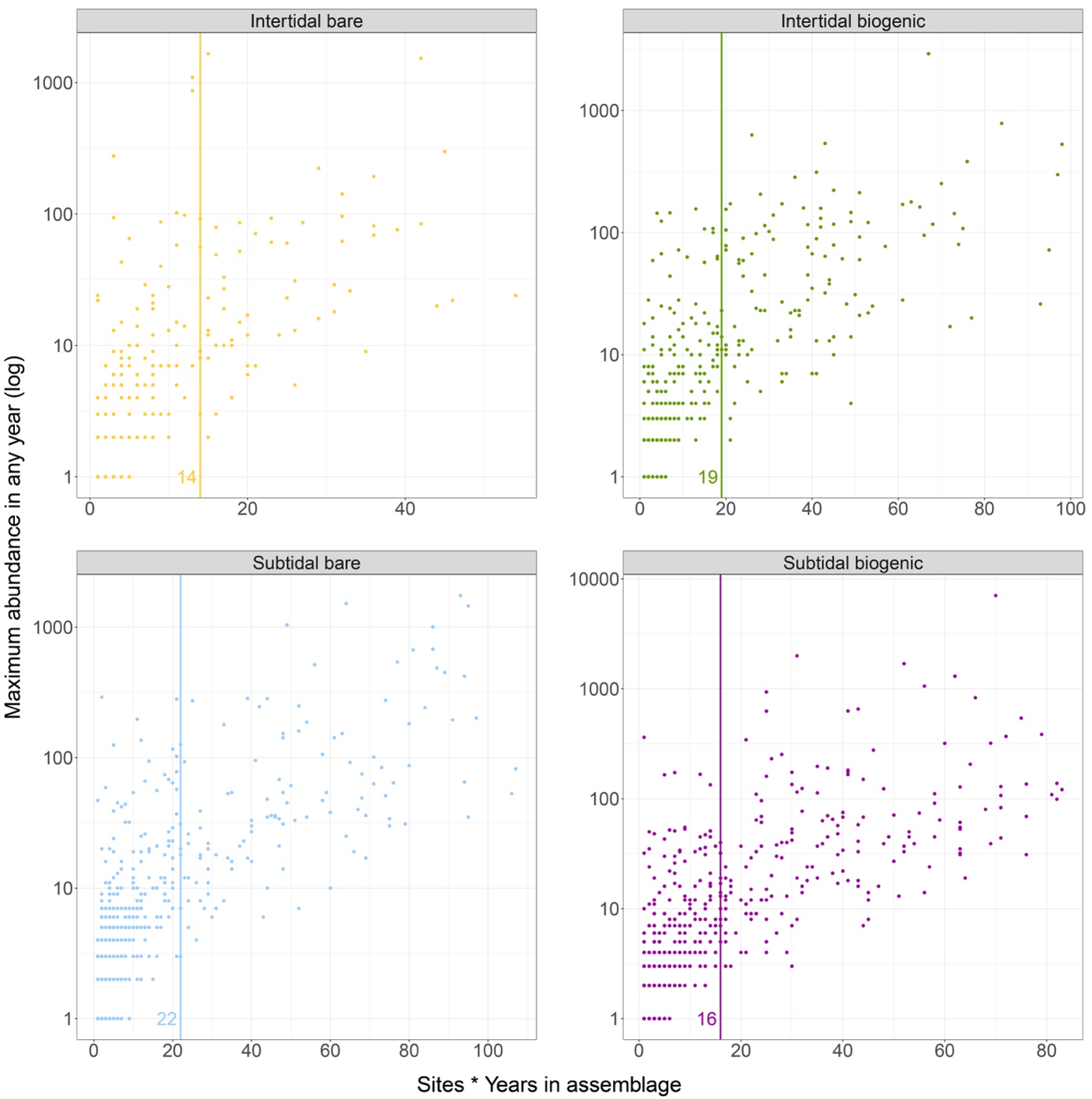
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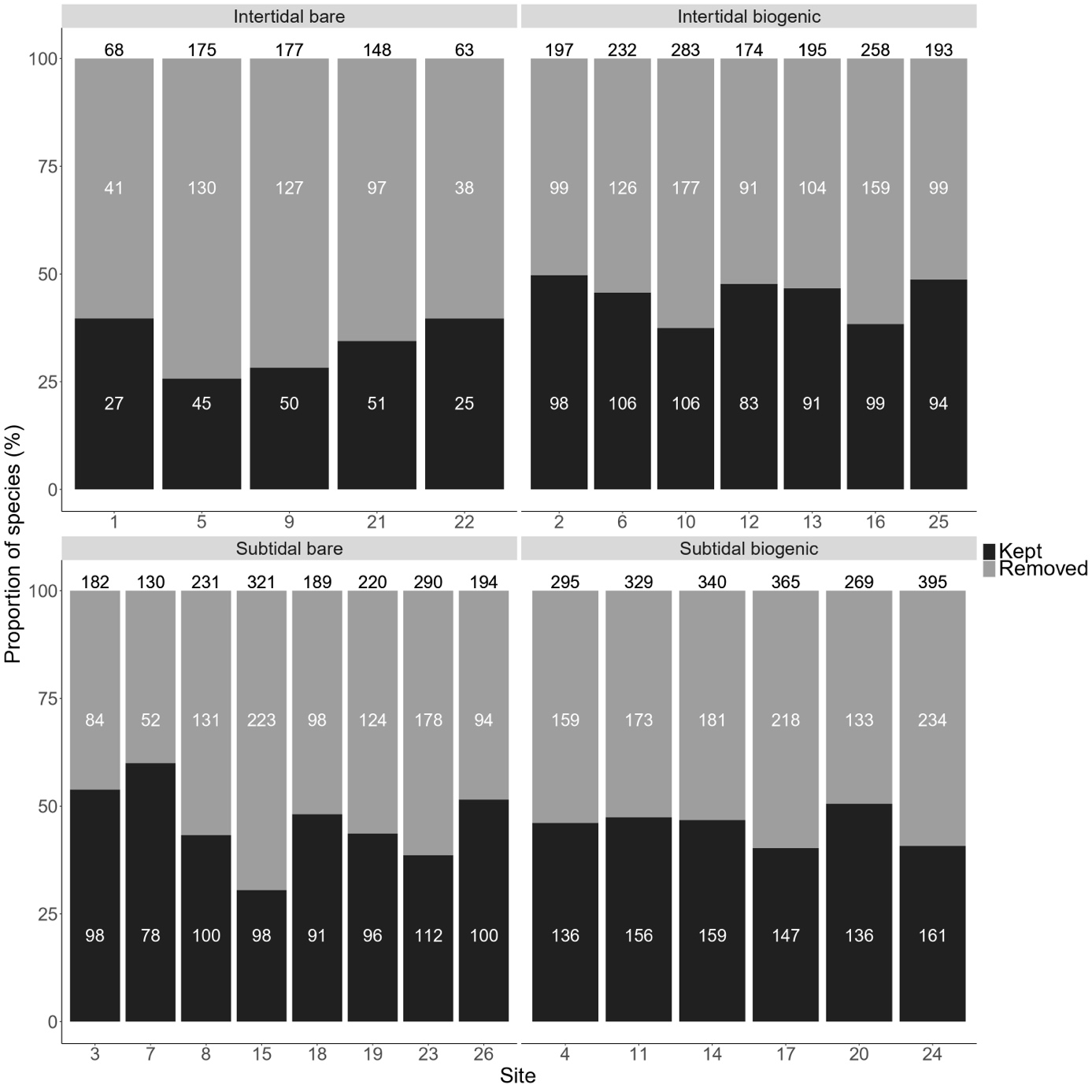
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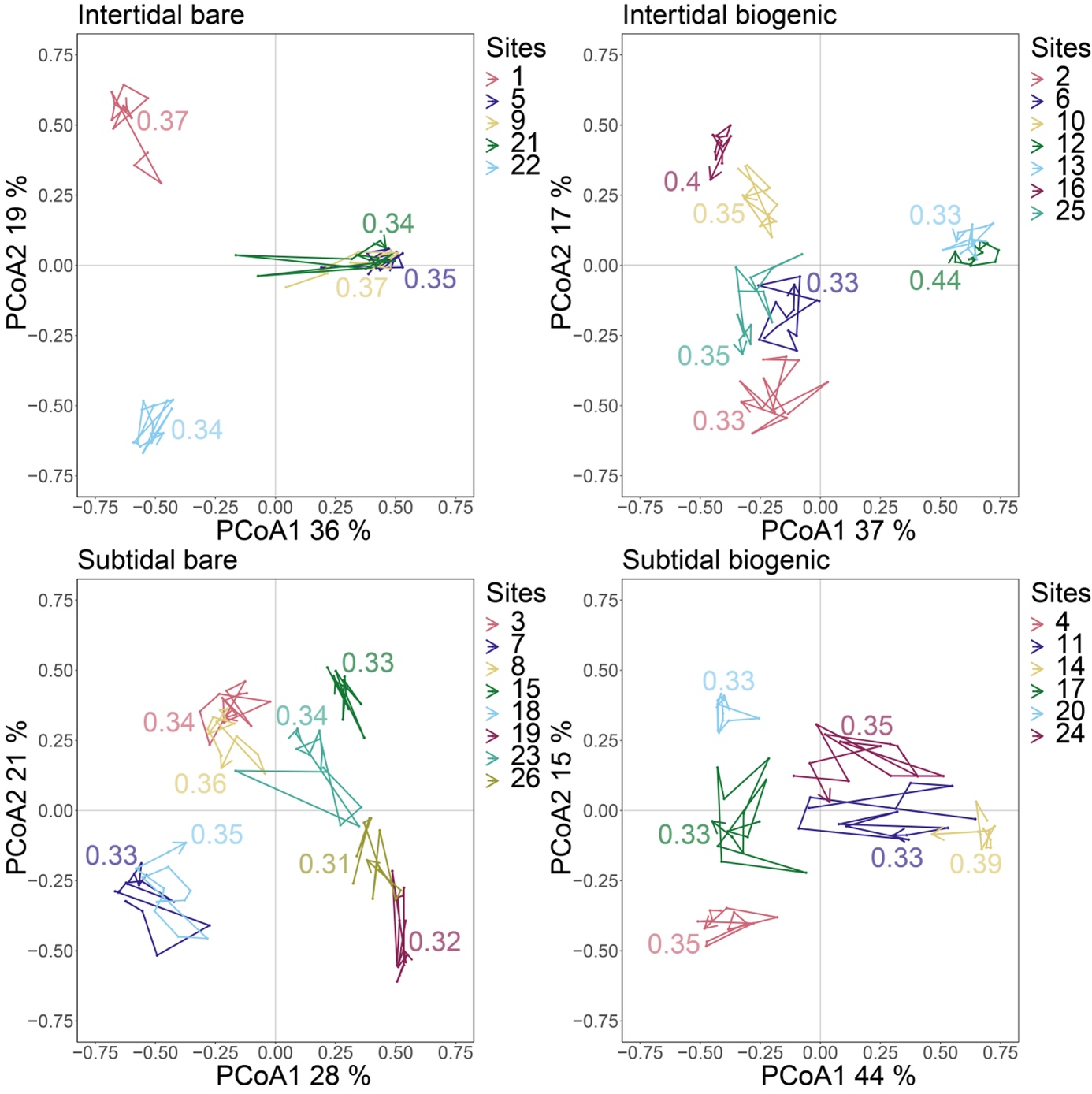
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**Supporting Information**: Simulation procedure of the non-directional null model.

For each habitat, steps of the simulation were as follows:

1. At *,* the community is generated by sampling species from the species pool with their occurrence frequency as weights, where is a number of species sampled from the empirical distribution of observed values of species richness.
2. For each species of the generated community, a value of abundance is sampled from the empirical distribution of observed abundances of the corresponding species.
3. The abundances are then rescaled to match a value of total abundance also sampled from the empirical distribution of total observed abundances, keeping relative abundances constant.
4. For each following time step, a new value of species richness is sampled with the following constraints:
   * Limiting species loss: the new species richness should not have a value to maintain the fixed extinction rate.
   * Limiting species gain: should not have a value greater than the maximum difference of species richness observed at any site between two consecutive years in the habitat.
5. If , a proportion of species equal to the value of the set extinction rate is removed from the community present at . The lower the abundance of species the more likely they are to be removed.
6. If , a proportion of species equal to the value of the set extinction rate is removed from the community present at . The lower the abundance of species the more likely they are to be removed. Species from the species pool are sampled (with their frequency of occurrence as weights) until the value is reached. Only species that have not been removed between and and species that are not already in the community can be sampled from the species pool and added to the community.
7. The abundances of each species are then sampled and rescaled as in steps 2 and 3.

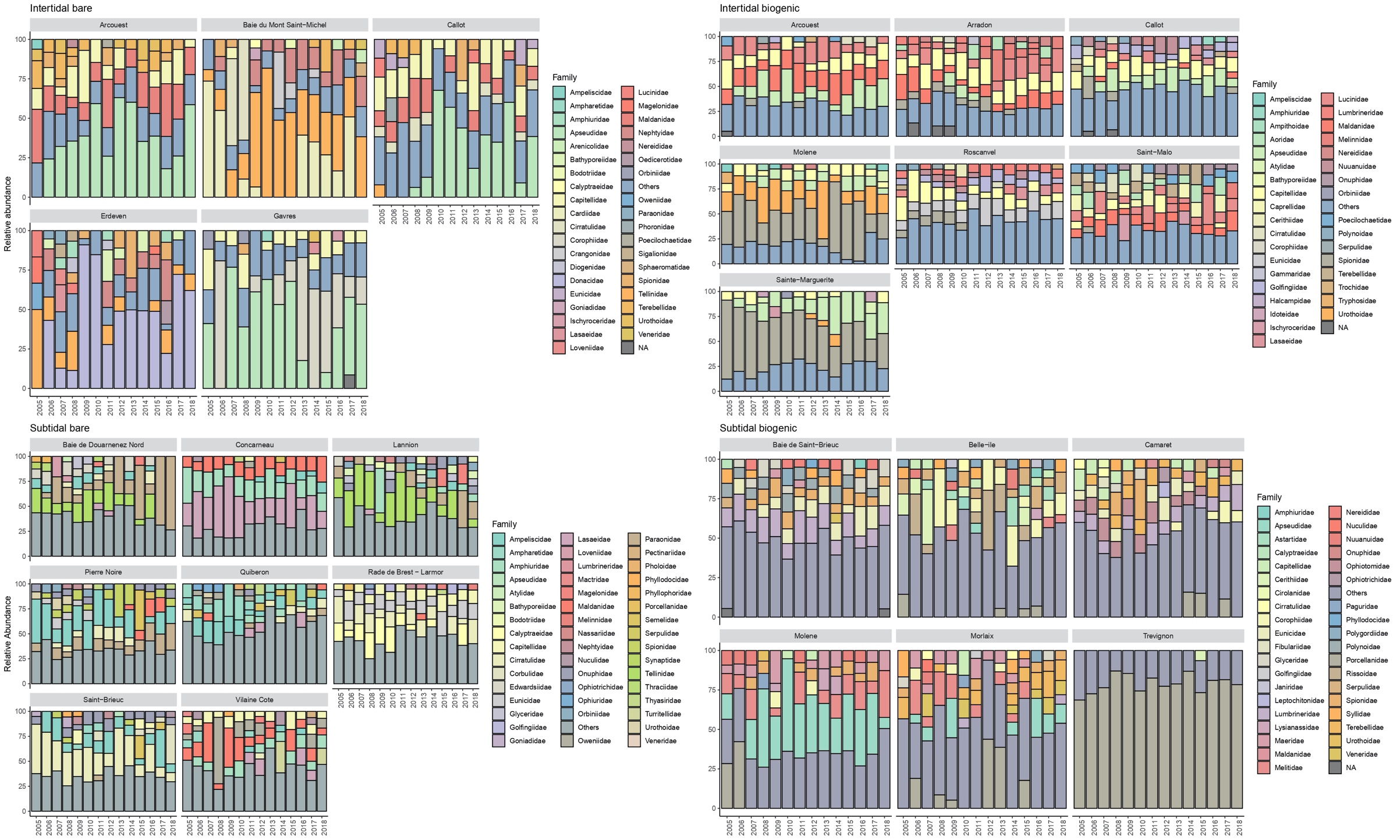
We generated 15 years of community dynamics 100 times (i.e., in 100 virtual sites) for each habitat. The communities at t=0 were removed because the initial set of species is not generated in the exact same way as the communities in the other time steps. CTA metrics were then computed on the trajectories of the simulated communities with a 14 years dynamic to have the same number of surveys as the observed communities.



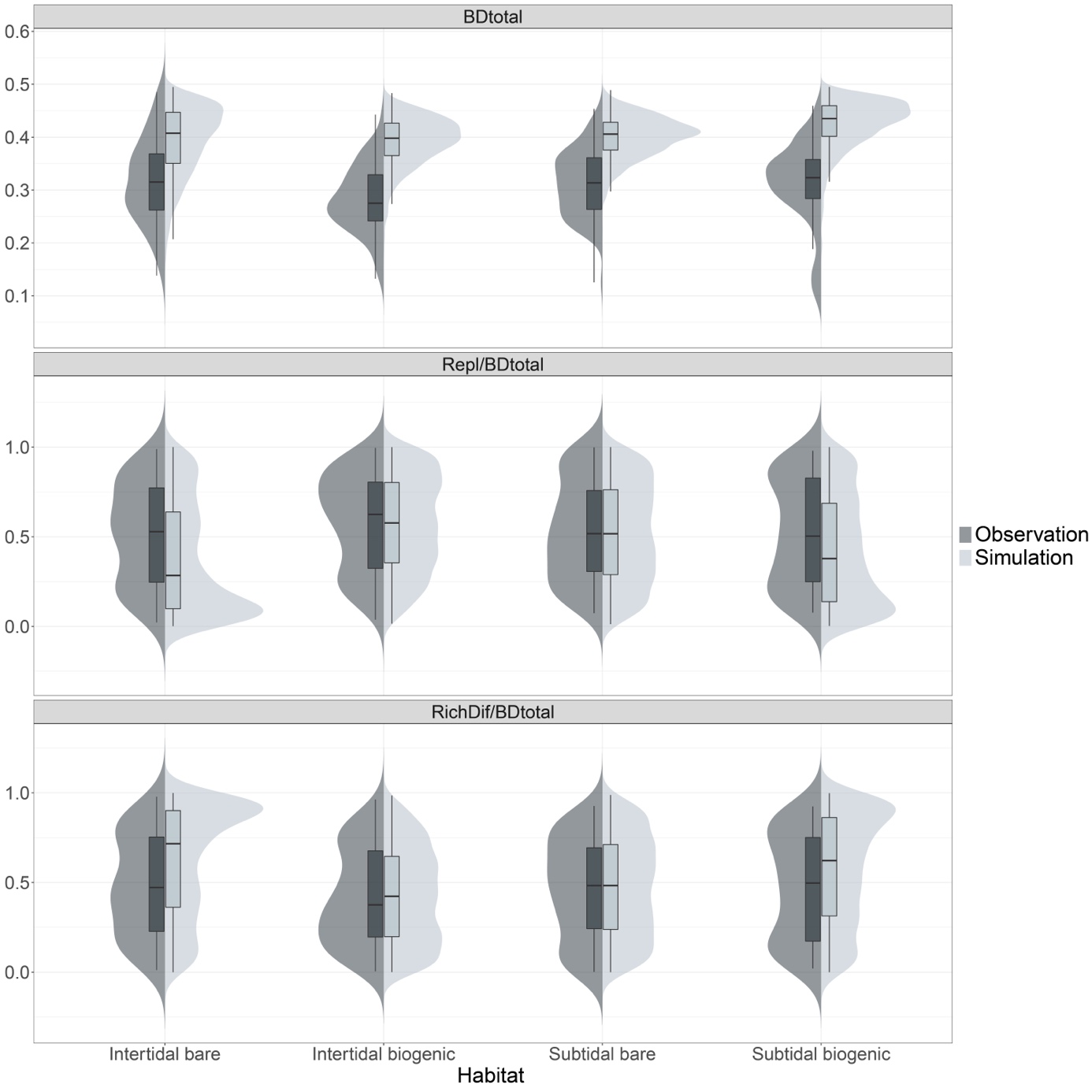
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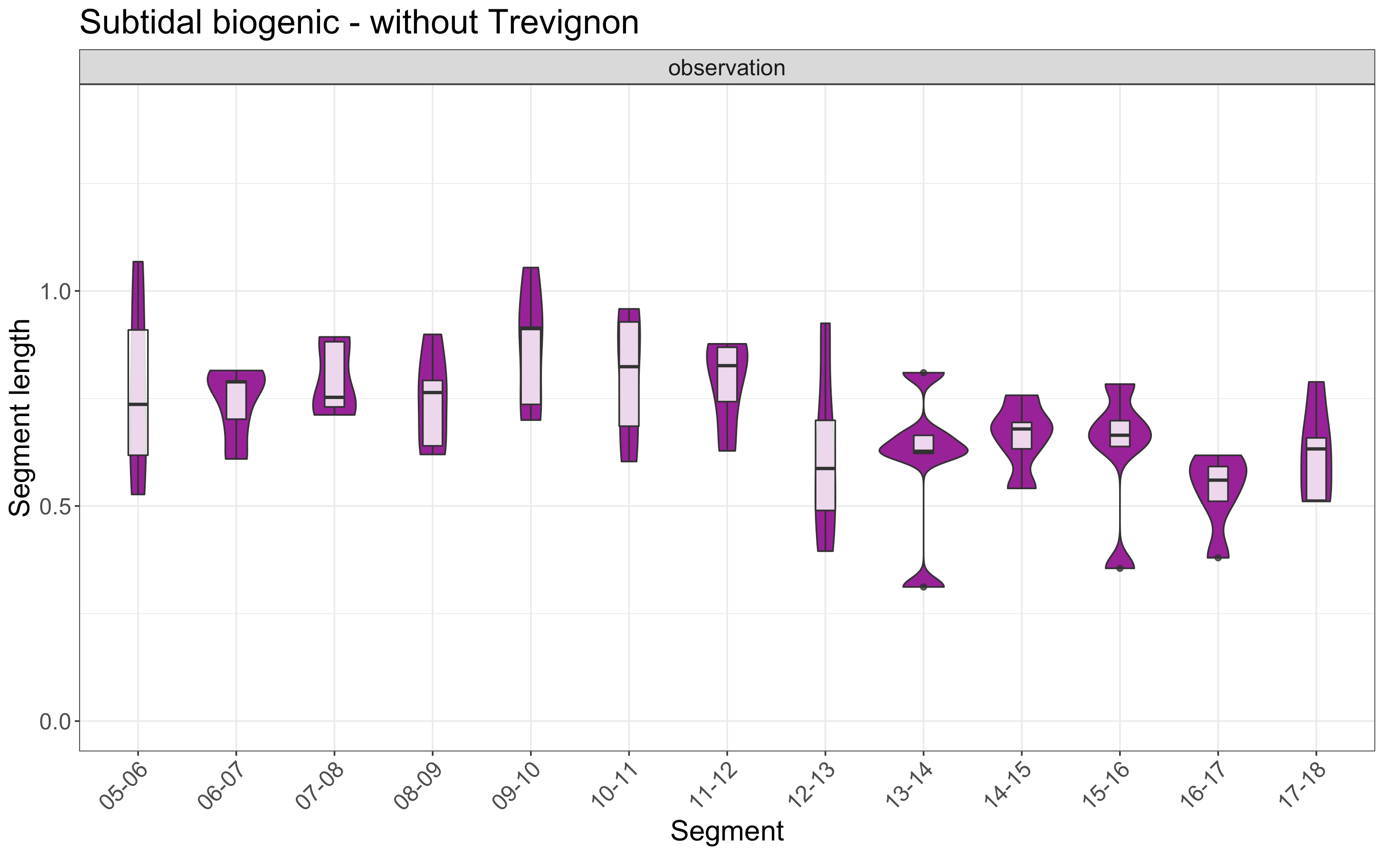
|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Global community | | | | Without LOLAS | | | |
| Habitat | dBDtot | Mean length ± se | Mean angle ± se | Mean net ± se | dBDtot | Mean length ± se | Mean angle ± se | Mean net ± se |
| Subtidal biogenic | 0.19 | 8.31±0.91 | 117.23±1.35 | 0.74±0.07 | 0.10 | 6.22±0.6 | 118.3±1.88 | 0.58±0.07 |
| Subtidal biogenic without Trevignon (20) | 0.22 | 9.17±0.38 | 116.98±1.42 | 0.8±0.03 | 0.10 | 6.36±0.71 | 117.87±2.15 | 0.62±0.07 |



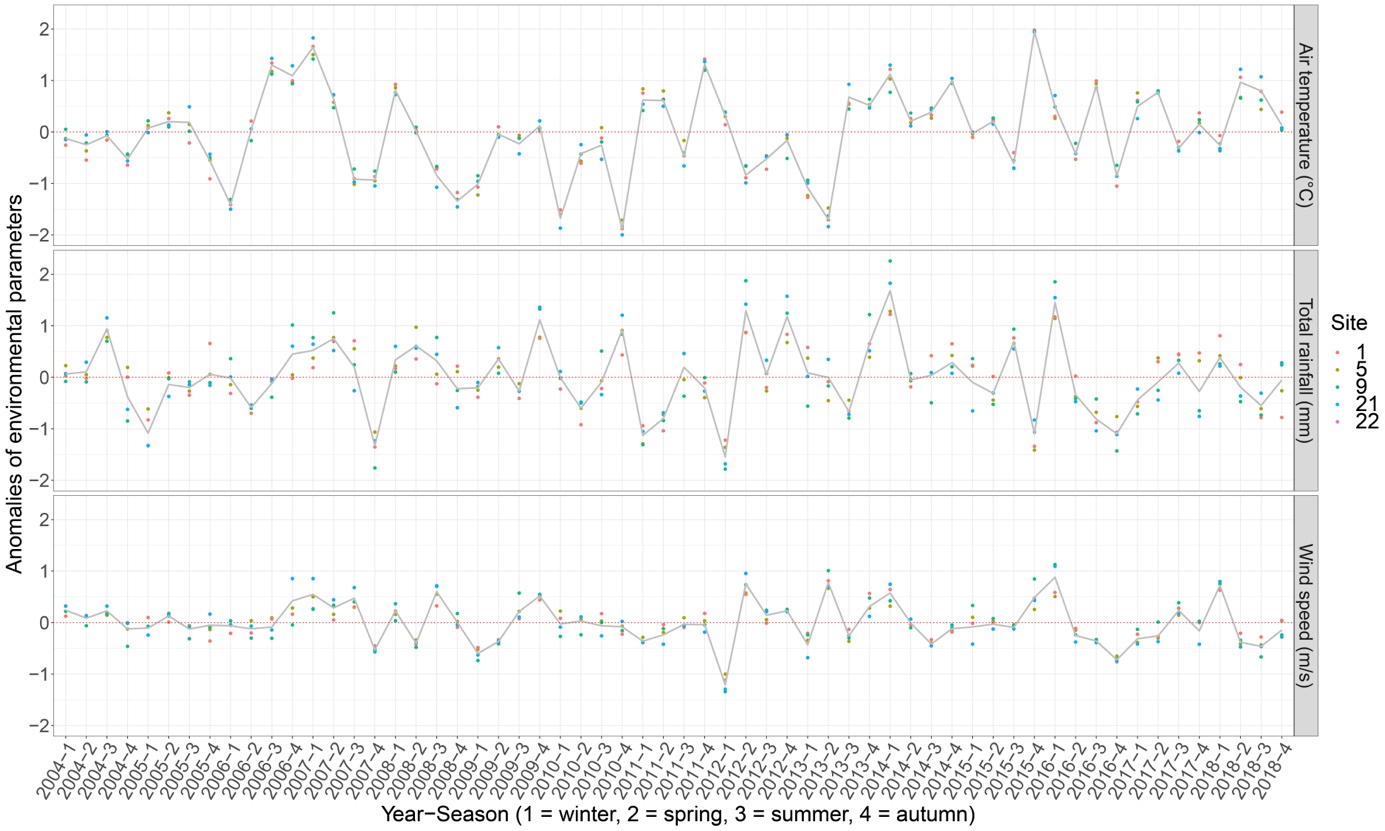
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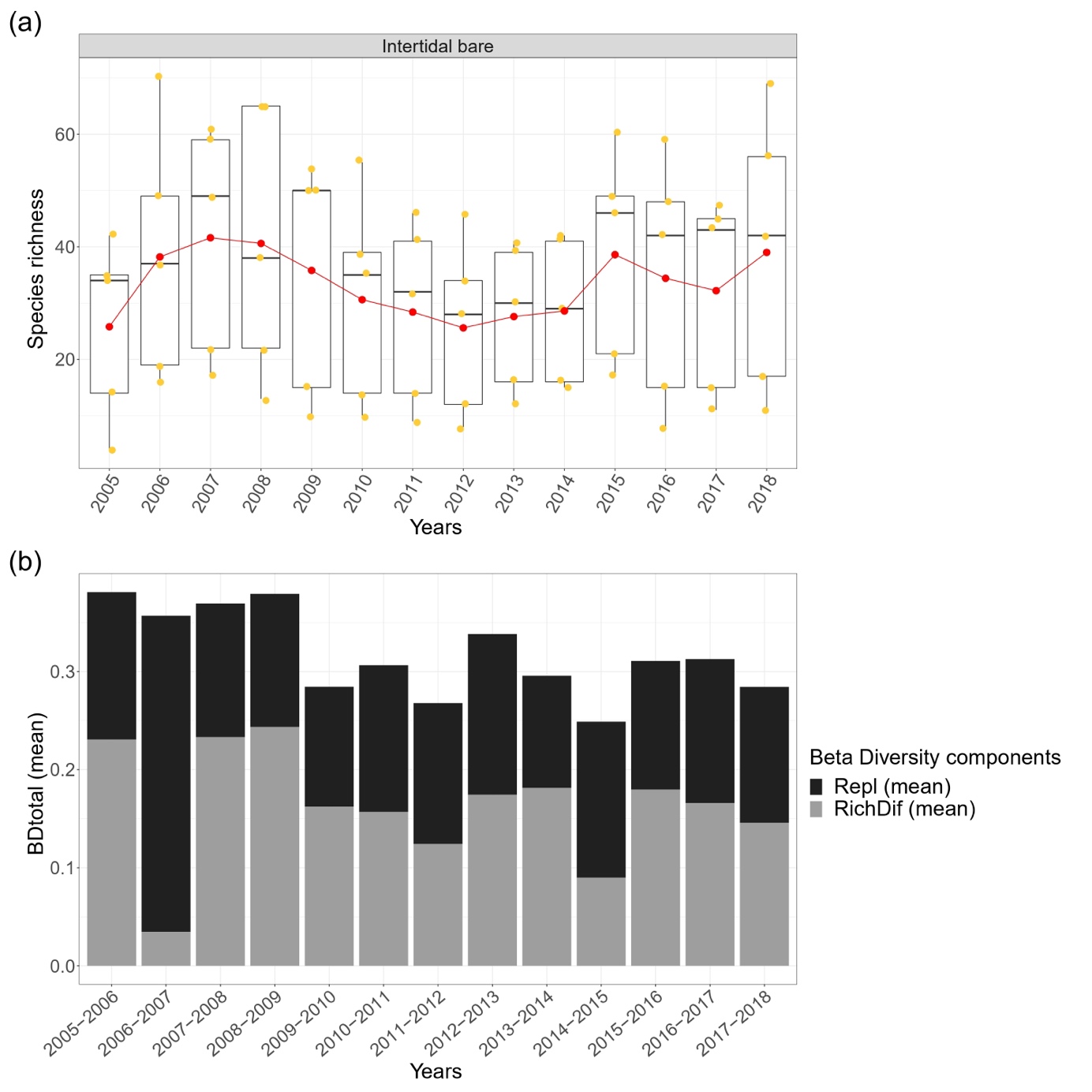
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**References:**

Legendre, P. 2014. Interpreting the replacement and richness difference components of beta diversity: Replacement and richness difference components. - Glob. Ecol. Biogeogr. 23: 1324–1334.

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