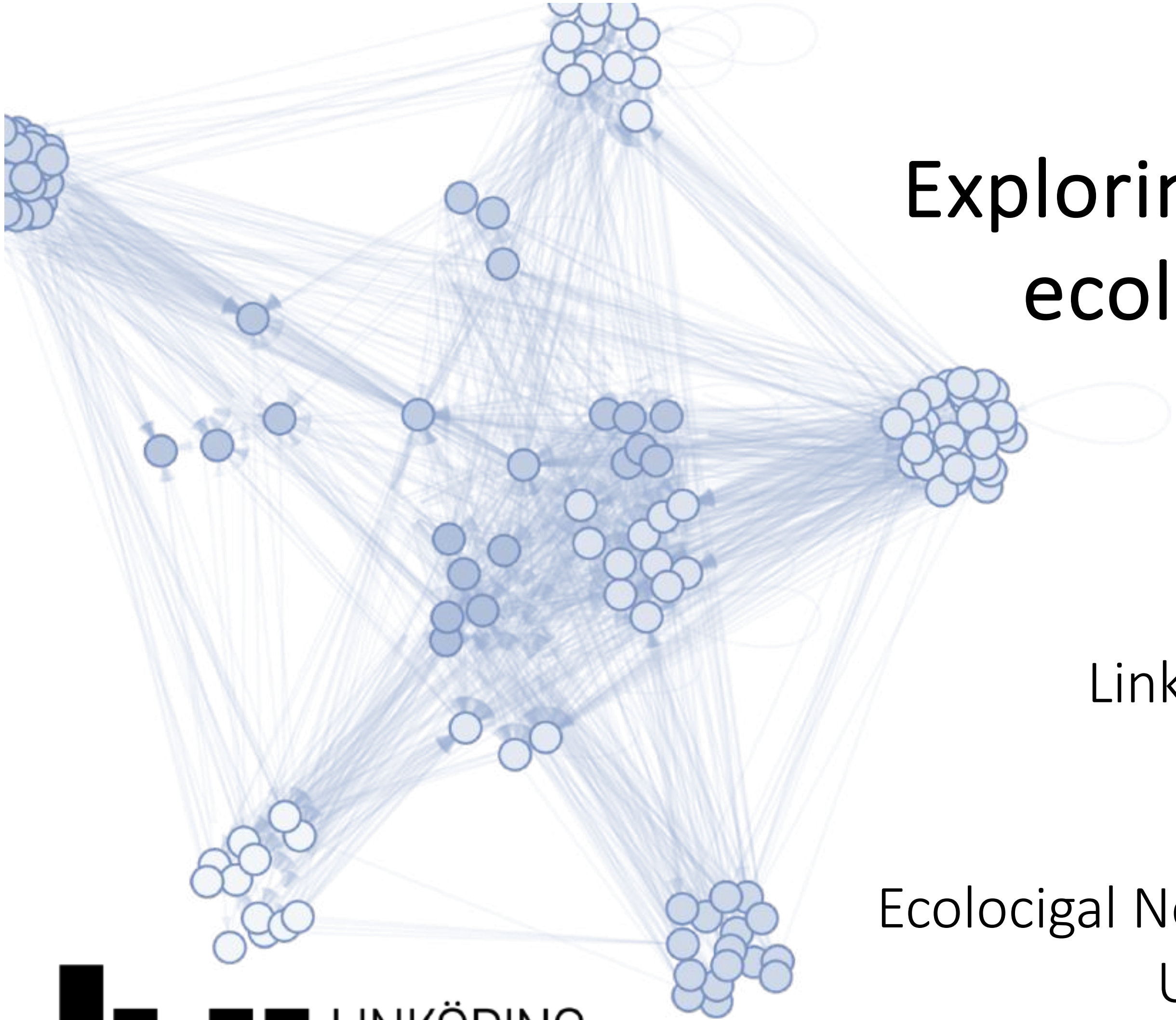

Exploring the role of groups in ecological communities

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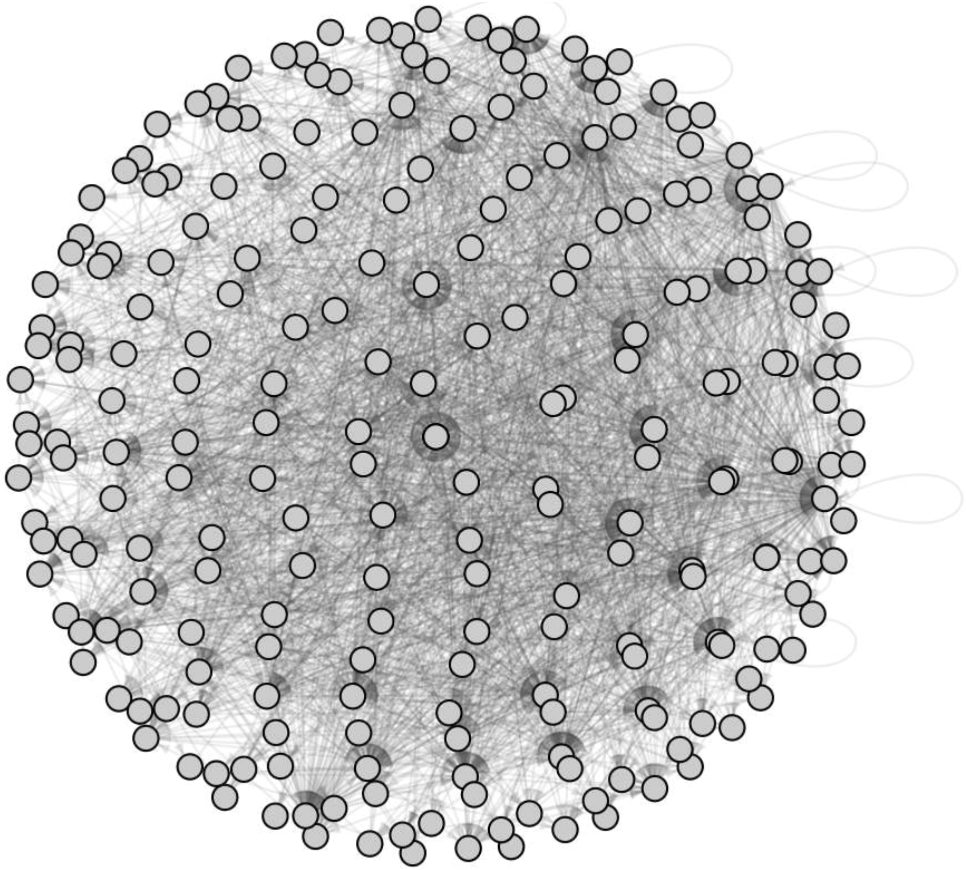
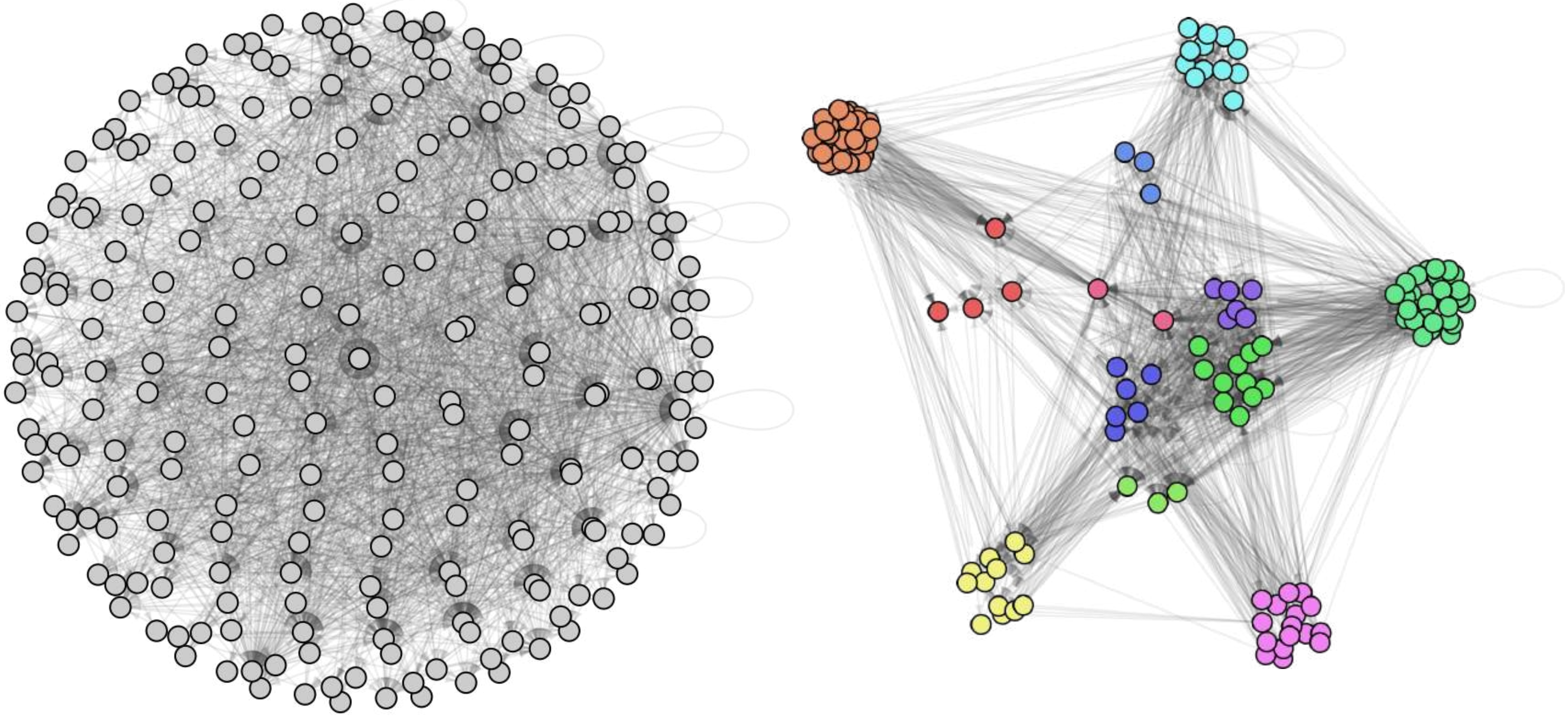
Ecolocigal Networks, complex systems, stability
Université Gustave Eiffel
October 28th - 29th 2024

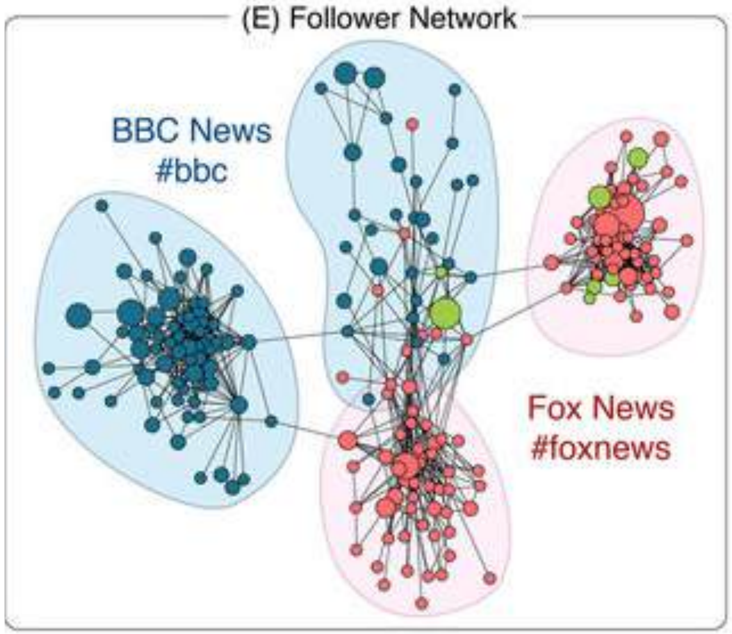
Community detection



Community detection

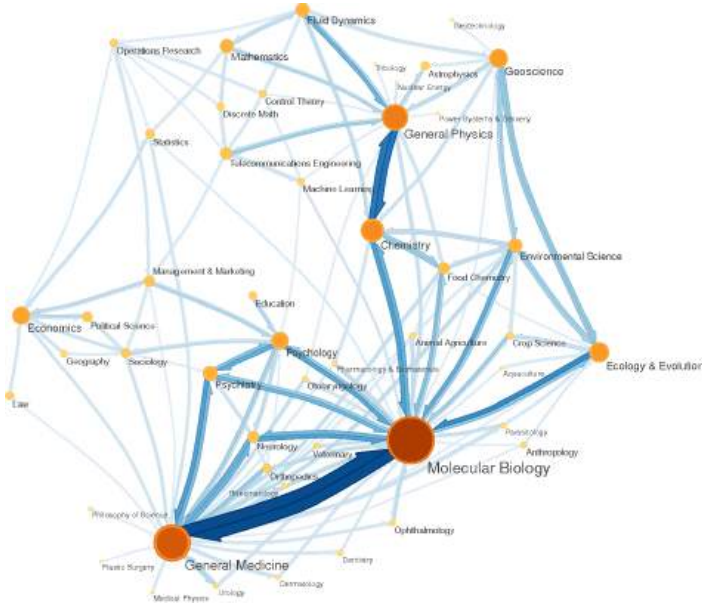


Social networks



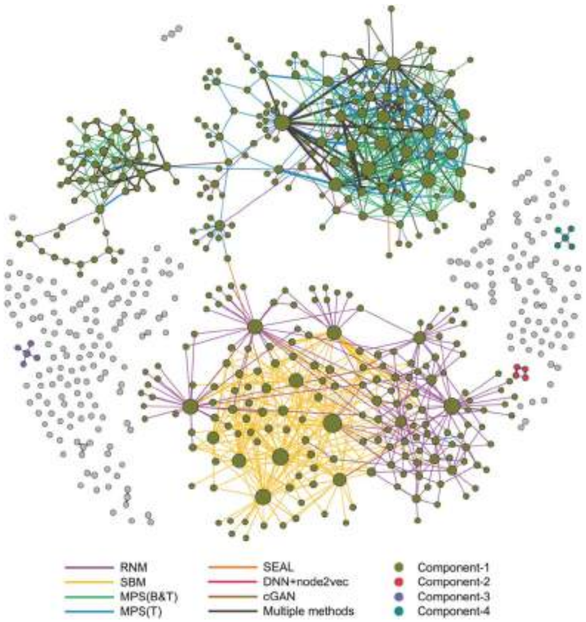
Weng et al, 2013, Scientific Reports

Citation networks

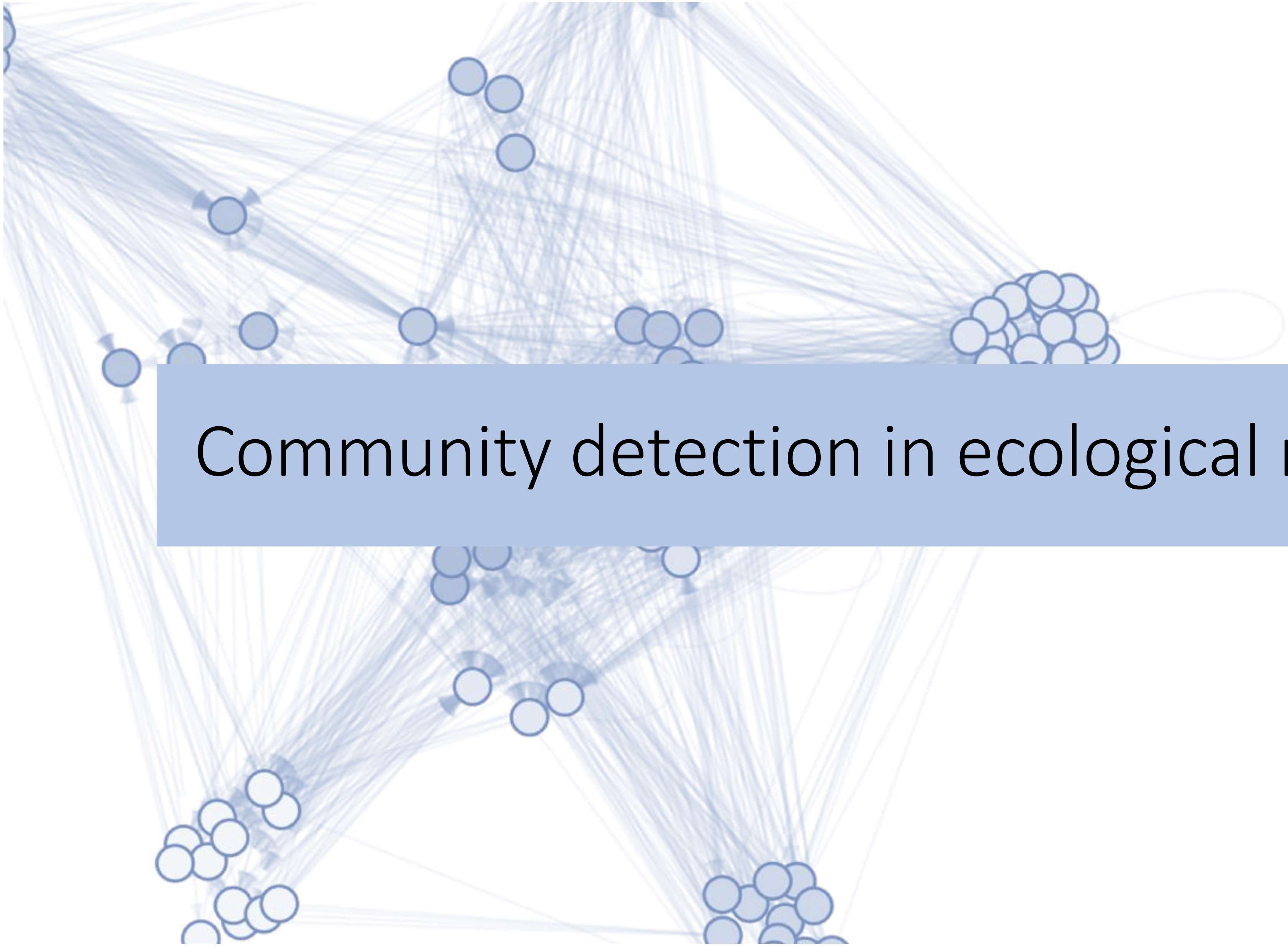


Rosvall & Bergstom, 2008, PNAS

Protein networks

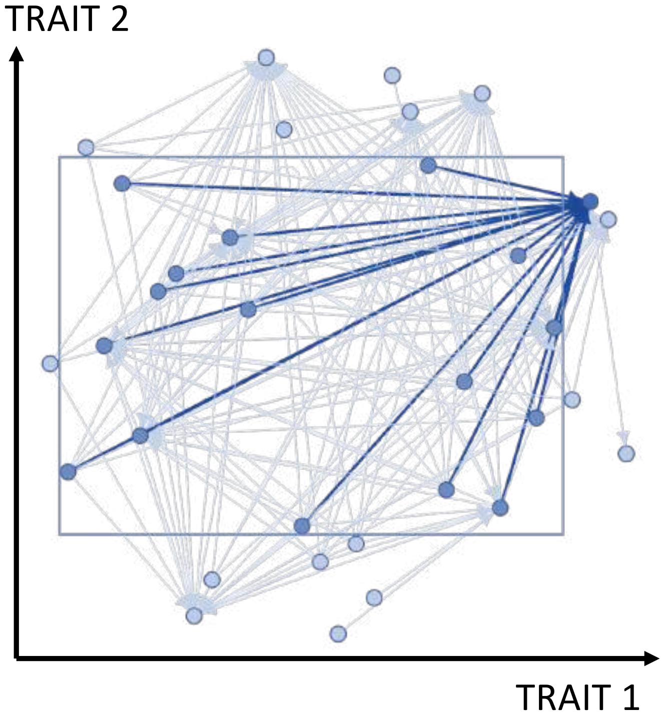


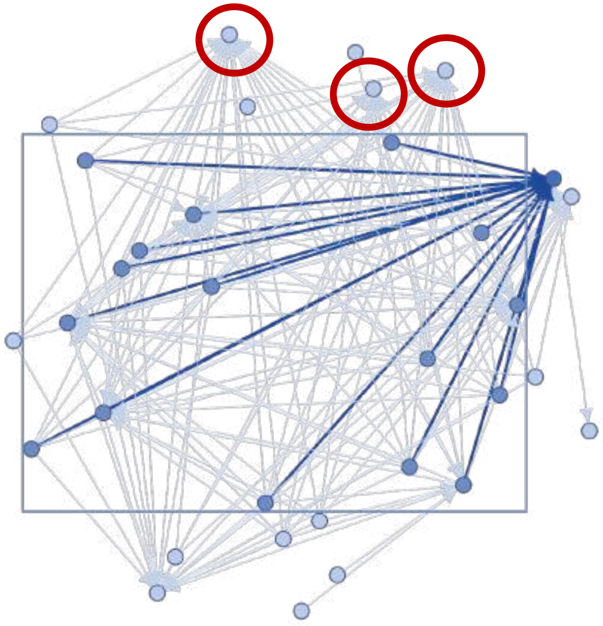
Weng et al, 2021, BioRxiv



Community detection in ecological networks

Community detection – why?





Traits

Interactions

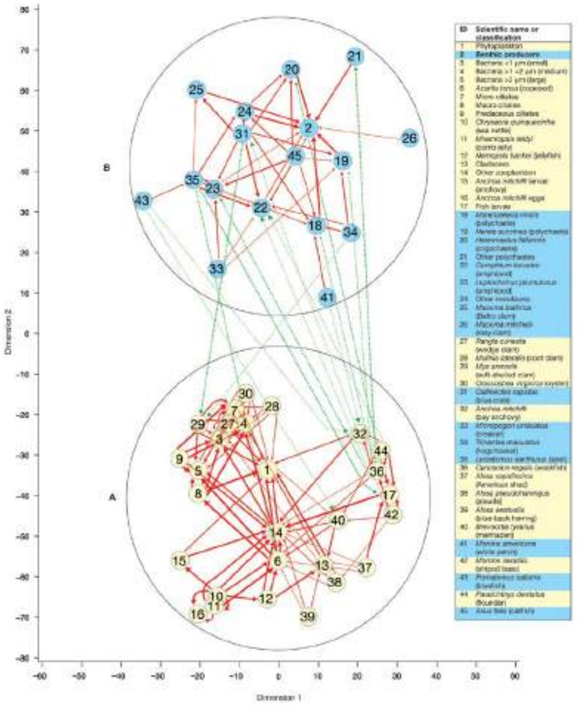
Ecological functions

Outline

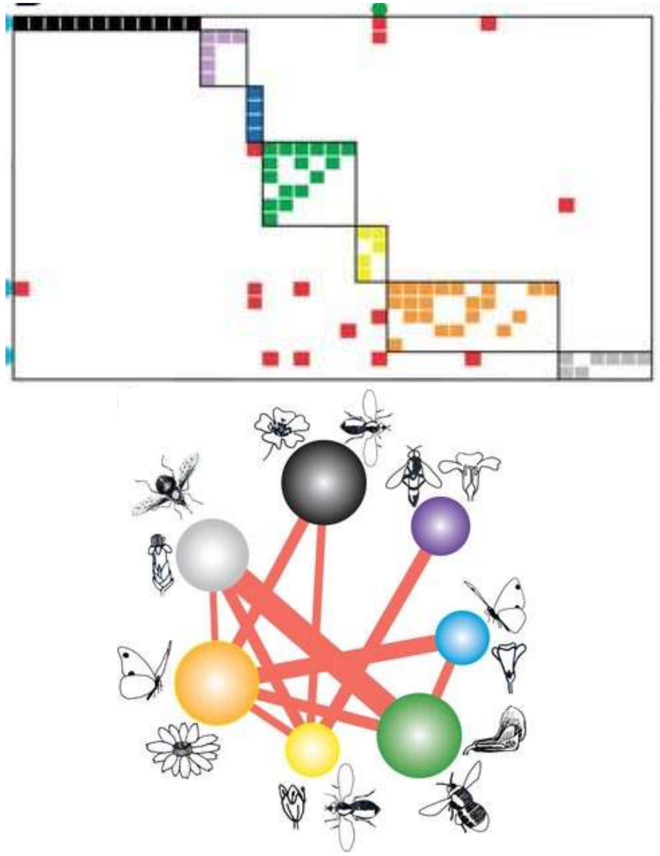
1. Community detection and ecological networks
2. The group model – a (very) brief overview
3. Three recent projects
    - Spatial resolution and impact on food web group structure
    - Evaluating the solution landscape of the identified food web group structure
    - How do disturbances affect food web group structure

Community detection in ecological networks

Modularity



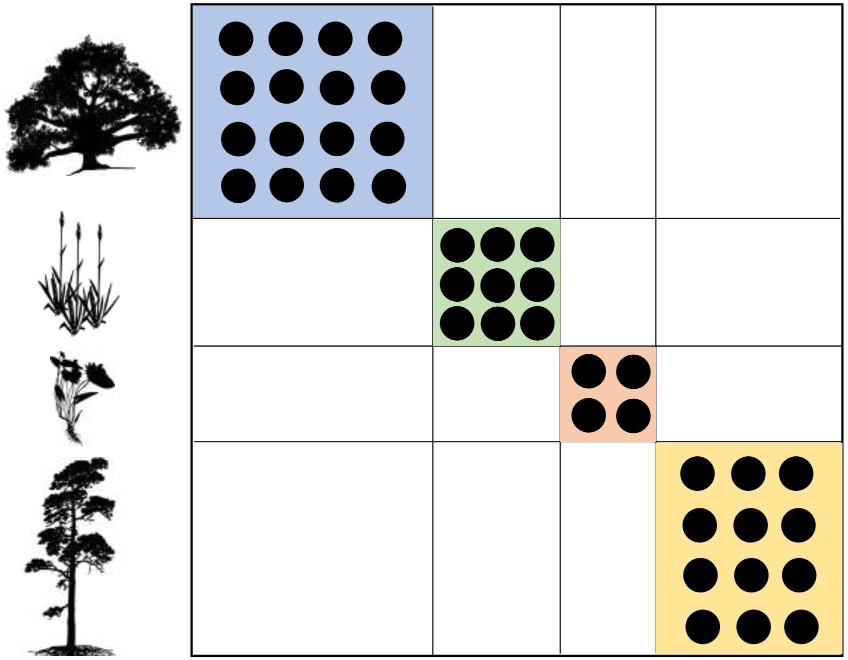
Krause et al, 2003, *Nature*



Olsen et al, 2007, *PNAS*

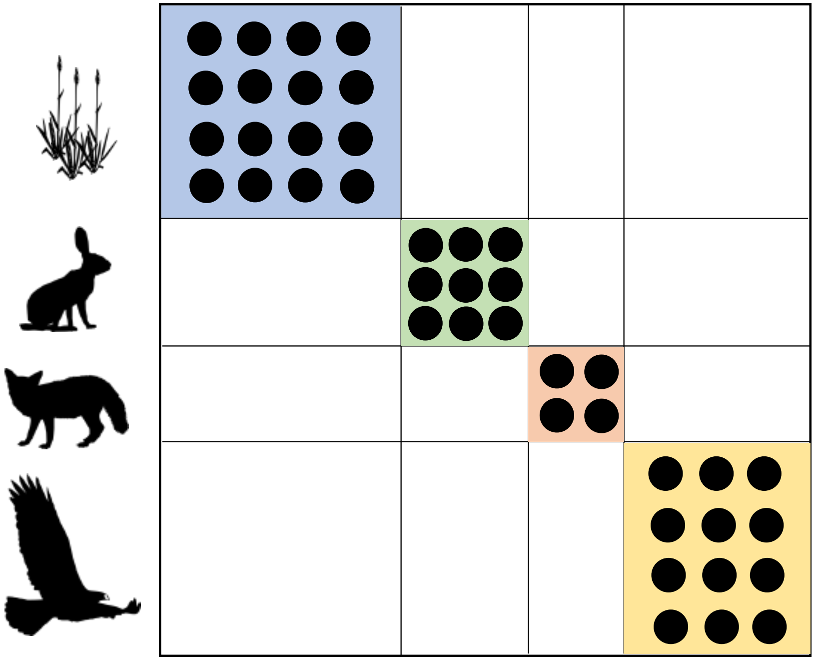
Community detection in ecological networks

Modularity

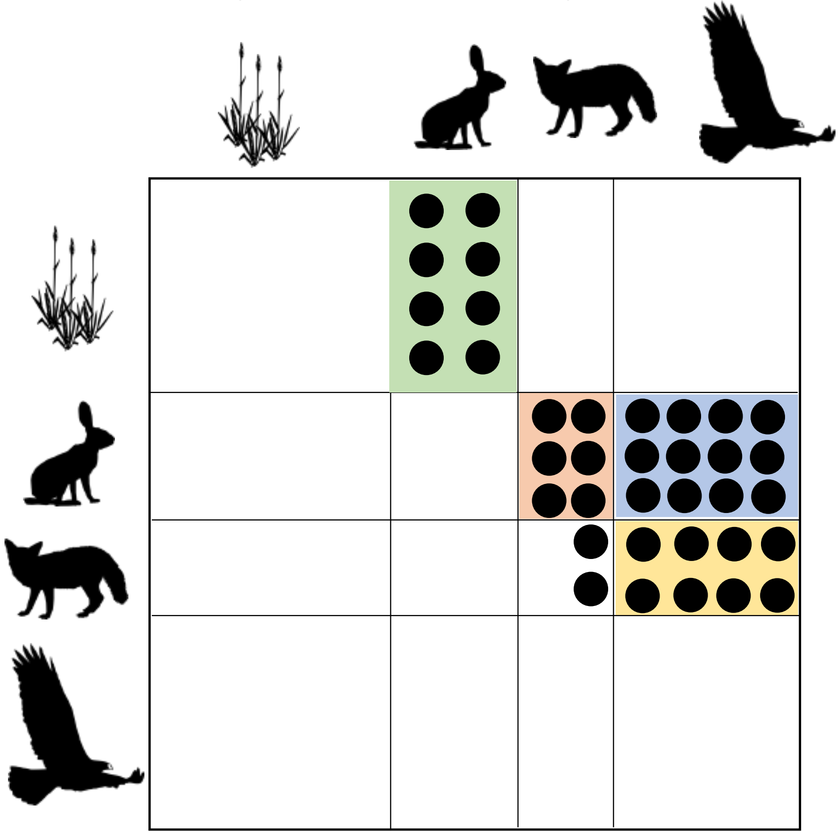


Community detection in ecological networks

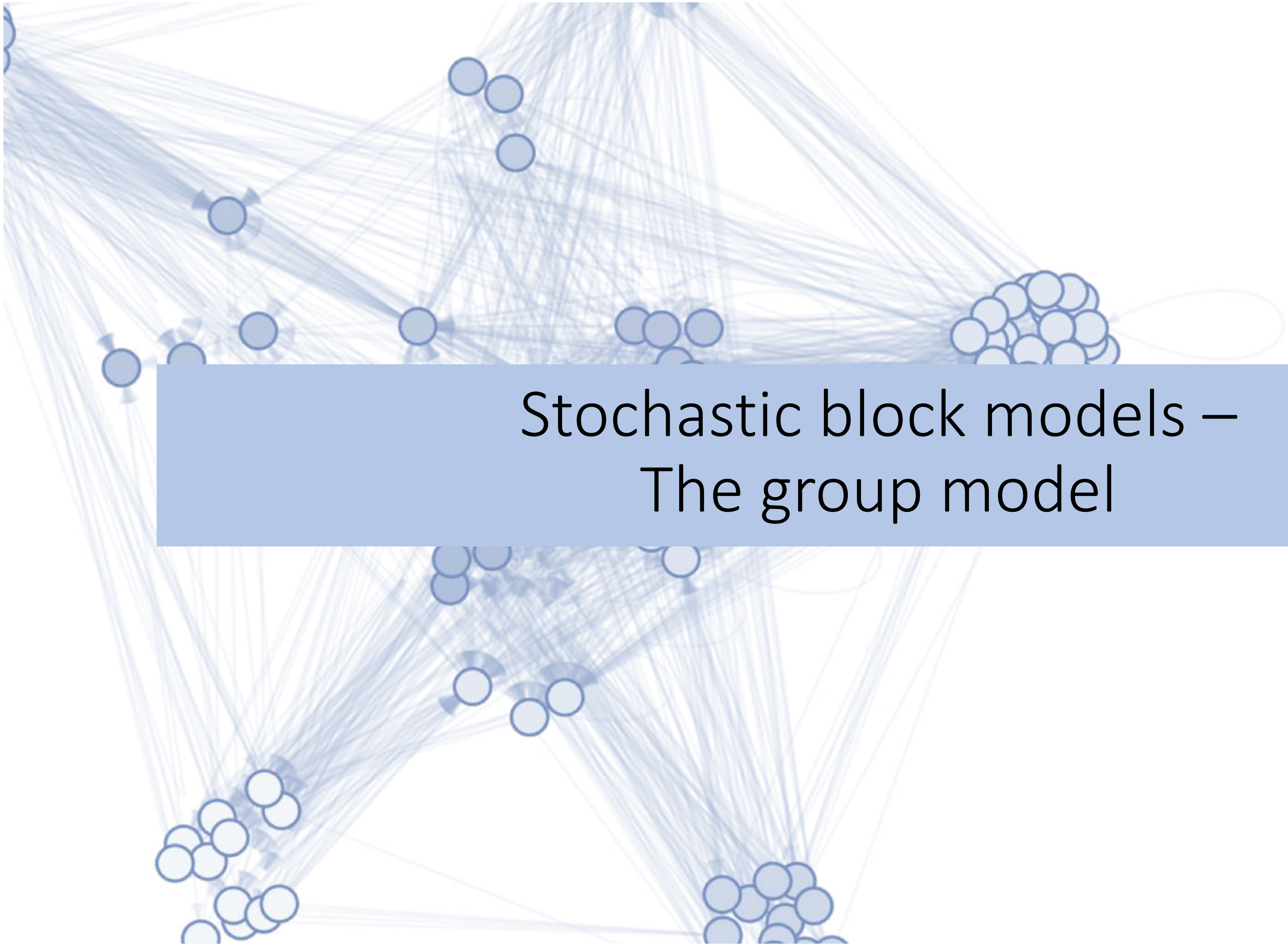
Modularity



Trophic similarity



Stochastic block models –
The group model

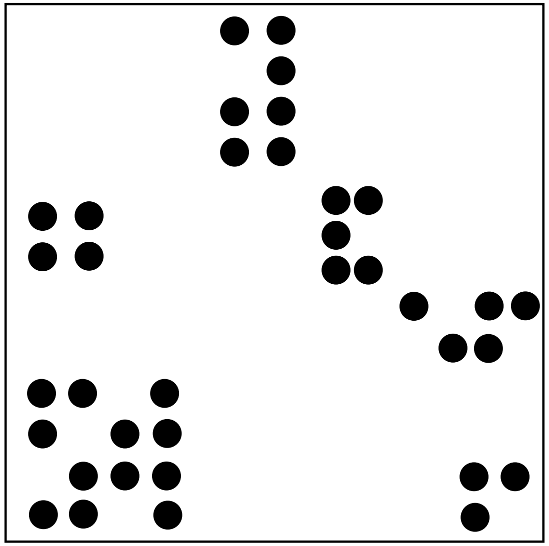


Group model

We can reproduce the empirical network *A* having *S* nodes and *L* interactions using a directed random graph, where the probability of connecting any two nodes is *p*.

The likelihood of obtaining A is then given by:

$$P(A(S,L)|p) = p^L(1-p)^{S^2-L}$$



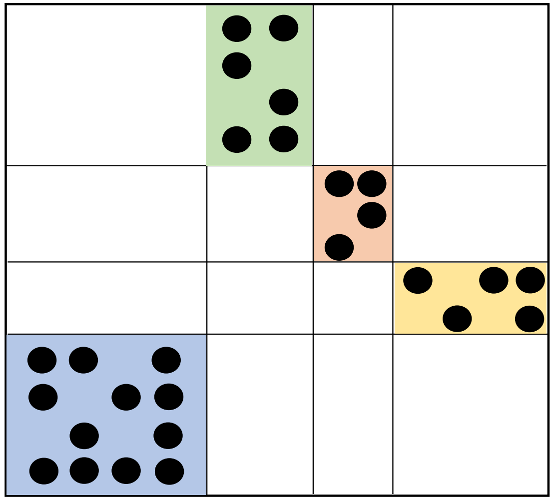
Group model

The group model expands this by looking at the likelihood of randomly generating A after assigning the nodes into *k* groups.

The likelihood of generating network *A* will depend on both the number of groups and the arrangement of the nodes in them according to:

$$P(A(S,L)|\vec{p}) = \prod_{i=1}^{k}\prod_{j=1}^{k} p_{ij}^{L^{ij}}(1-p_{ij})^{S_iS_j-L_{ij}}$$

$\vec{p}$ is a vector with all the probabilities that links occur between all combinations of groups



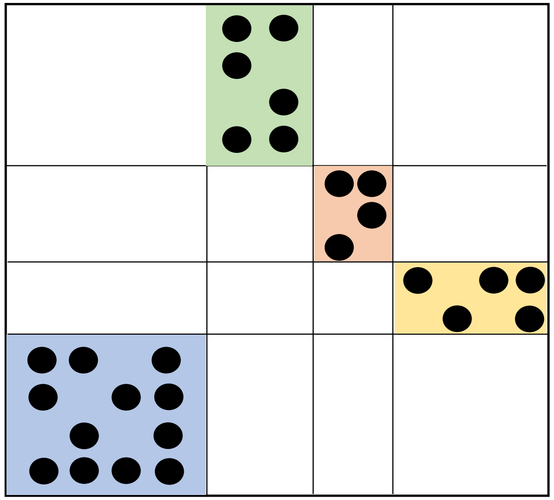
Group model

By testing different partitionings of the nodes into groups we want to find the partitioning with the highest probability of reproducing *A*.

Partitionings differ in their number of parameters and therefore model selection is needed.

The marginal likelihood for partitioning *G* is

$$P(A(G)|\vec{p}) = \prod_{i=1}^{k} \prod_{j=1}^{k} \frac{L_{ij}!(S_i S_j - L_{ij})!}{(1 + L_{ij})(1 + S_i S_j)}$$



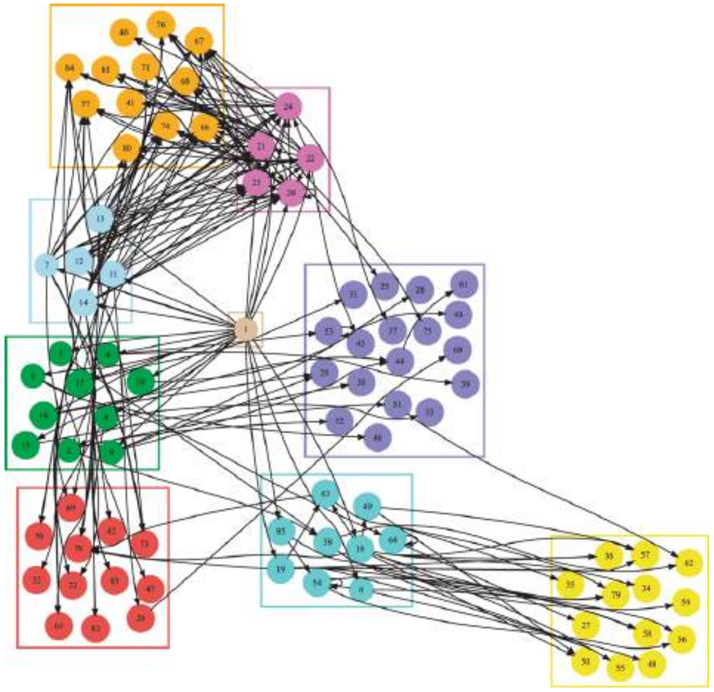
Group model

The model builds on the idea of ecological equivalence

Species roles defined by the group model can be considered functional groups –
species within a group tend to interact with the same sets of species in the same way.

Species have a recursive relationship with each other, meaning that distant speciesstill affect each other's group memberships

Ecologic equivalent groups

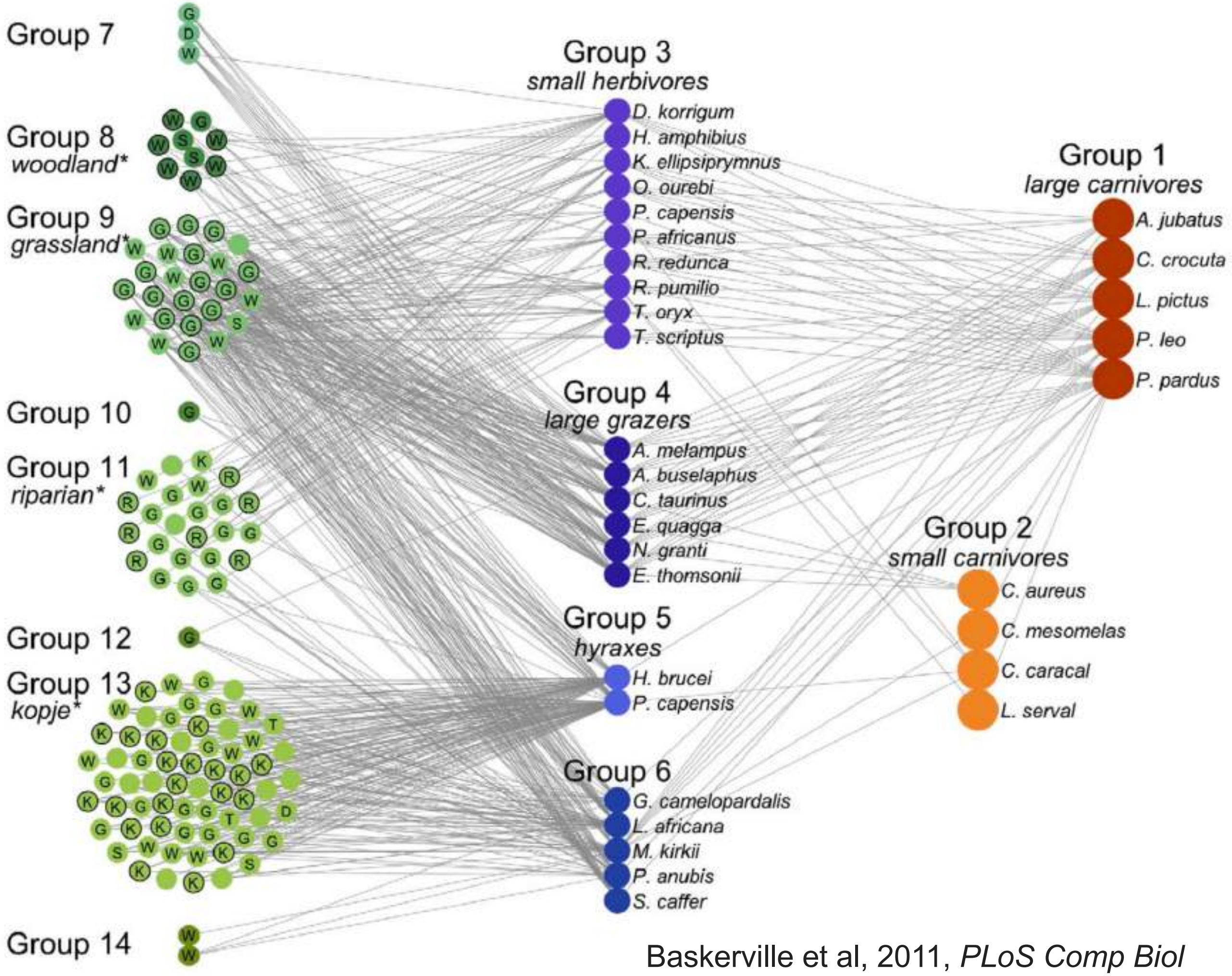


Allesina & Pacual, 2009, *Ecology Letters*

Bayesian modeling approach

- Both data and model parameters are treated probabilistically. Here different priors for partitions and links were used

- The identified plant groups remarkably well resembles habitat types

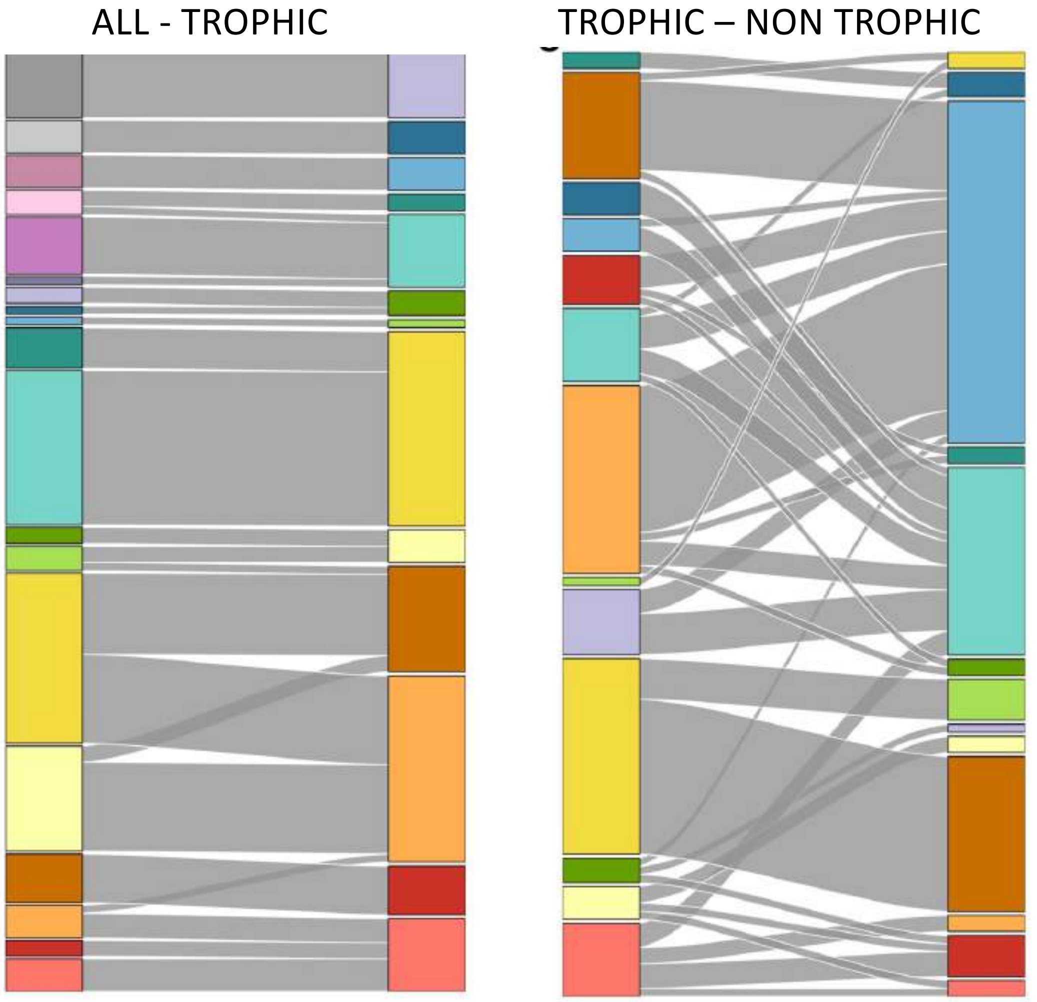


Baskerville et al, 2011, *PLoS Comp Biol*

Multiple interaction types

Extends the group model to include multiple types of interactions

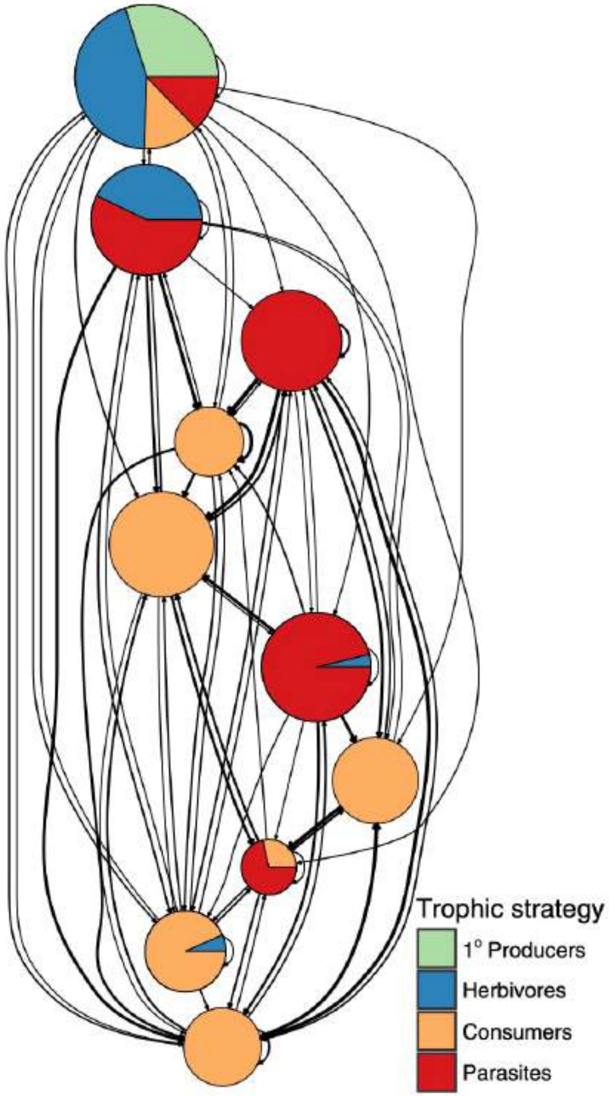
Examine the effects of including or excluding specific interaction types on group structure



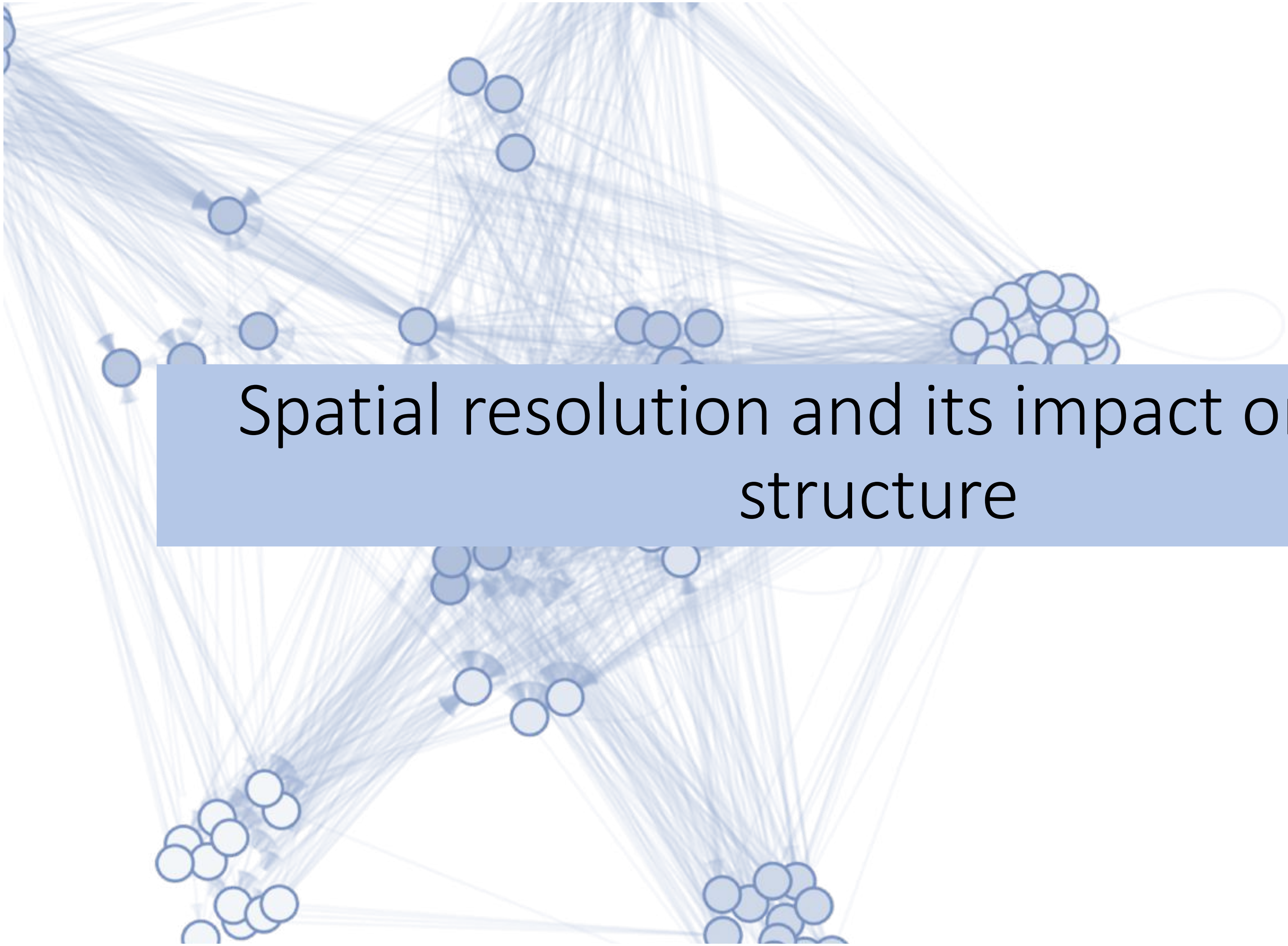
Sander et al, 2015, *PLoS Comp Biol*

More interaction types

- Extends the group model to include parasites
- Analyze if parasites play structurally unique roles in ecological networks
- Concomitant predation improves the group model's ability to distinguish parasites from non-parasites.



Michalska-Smith et al, 2017, *JAE*



Spatial resolution and its impact on group structure

Spatial resolution and impact on group structure

Food webs are often assembled over

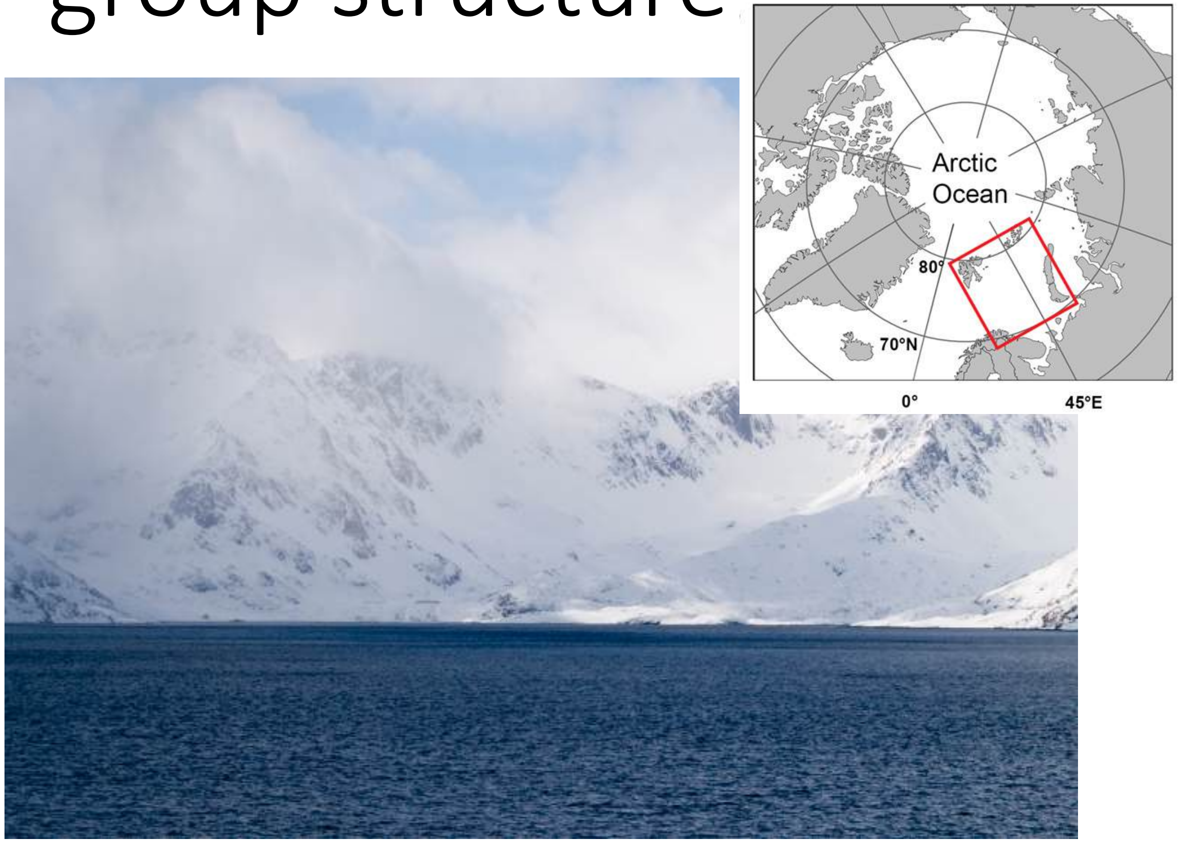
- large or several different spatial areas
- several different time periods

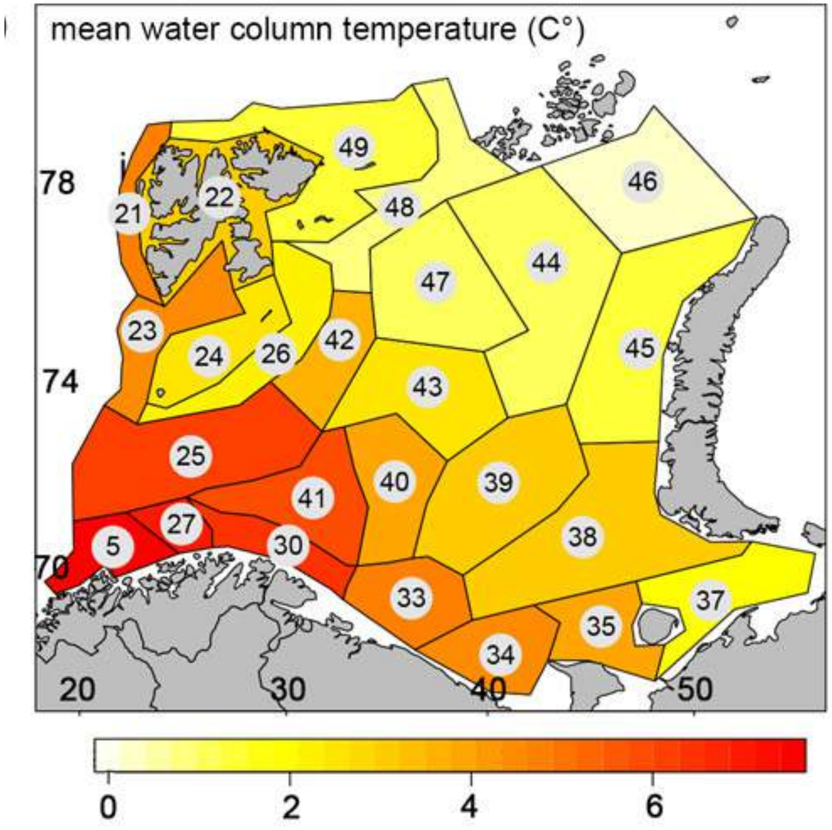
Questions

How does the spatial resolution affect the group structure?

And are some structures more stable across spatial areas?

Spatial resolution and impact on group structure



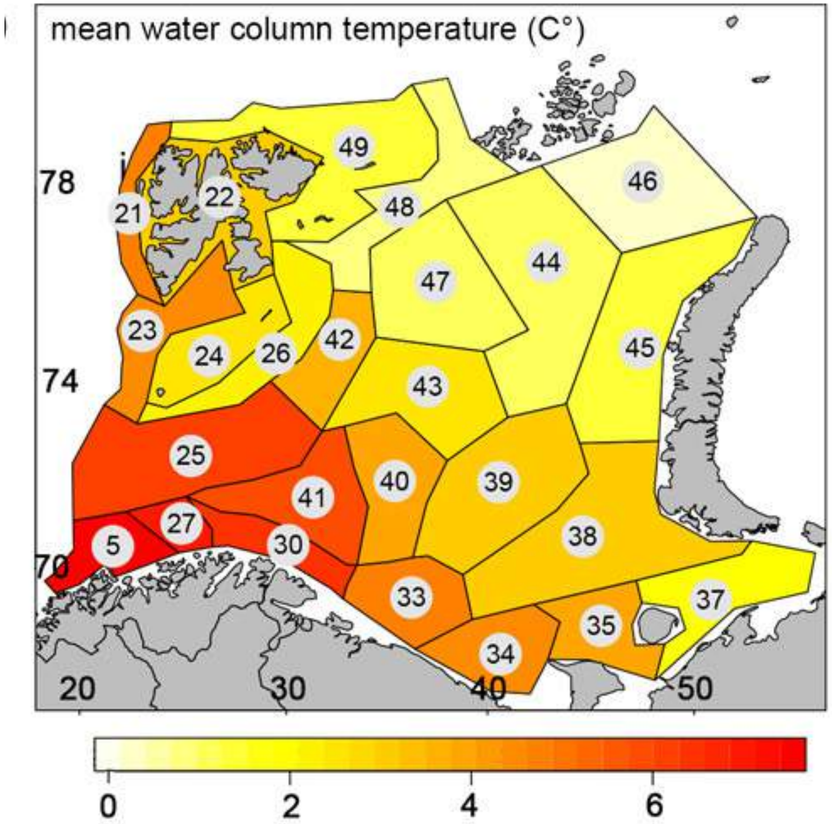


Spatial resolution and impact on group structure

Food web data from Barent Sea

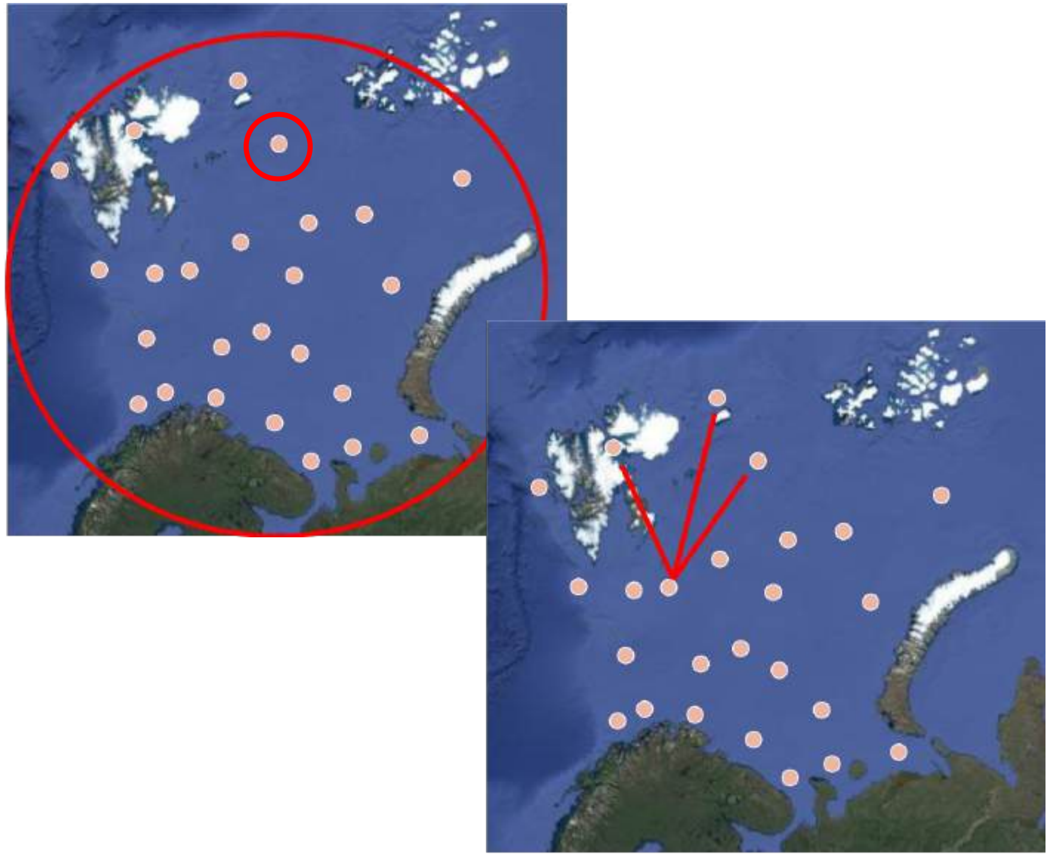
233 species and >2000 feeding interactions in the meta food web

Divided into subregions based on environmental factors



Kortsch, S et al (2019). *Ecography*, *42*(2), 295-308.

Spatial resolution and impact on group structure



Does group structure differ

- between a meta (regional) network and local networks (subregions)?
- between different subregions?

Are certain species more variable in their group membership?

Partition similarity

- Measure to what extend group *k* from partition *A* is resembled in any group of partition B
- Exploring this for every group in partition *A* will give a measure of how well these groups are resembled in partition *B*
- Measured using the complement of the Jaccard index of dissimilarity

$$d_J(C^A, C^B) = \frac{1}{n} \sum_{k=1}^{n} \min_l \left(1 - \frac{|C_k^A \cap C_l^B|}{|C_k^A \cup C_l^B|} \right)$$

where C_k^A is group *k* in partition *A*.

The Jaccard distance takes the value of 0 when partition C^A and C^B are identical and approaches 1 as they become increasingly dissimilar.

Partition similarity

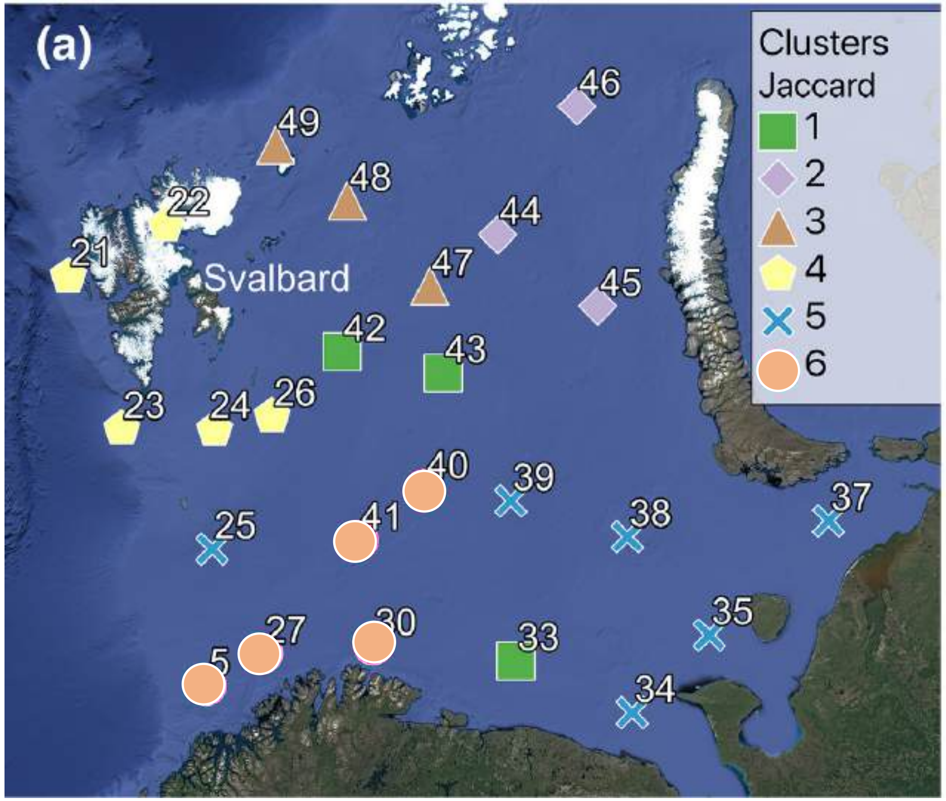
$$d_J(C^A, C^B) = \frac{1}{n} \sum_{k=1}^{n} \min_l \left(1 - \frac{|C_k^A \cap C_l^B|}{|C_k^A \cup C_l^B|}\right)$$

The index differs depending on the direction of the comparison. Jaccard distance both ways for each network pair and calculated the average distance

$$\overline{d}_J(C^A, C^B) = \frac{d_J(C^A, C^B) + d_J(C^B, C^A)}{2}$$

We used UMAP clustering algorithm to cluster food webs with a more similar group structure.

Spatial resolution impact group structure



Ohlsson & Eklöf, 2020, *Ecol. Lett.*

Species overlap:

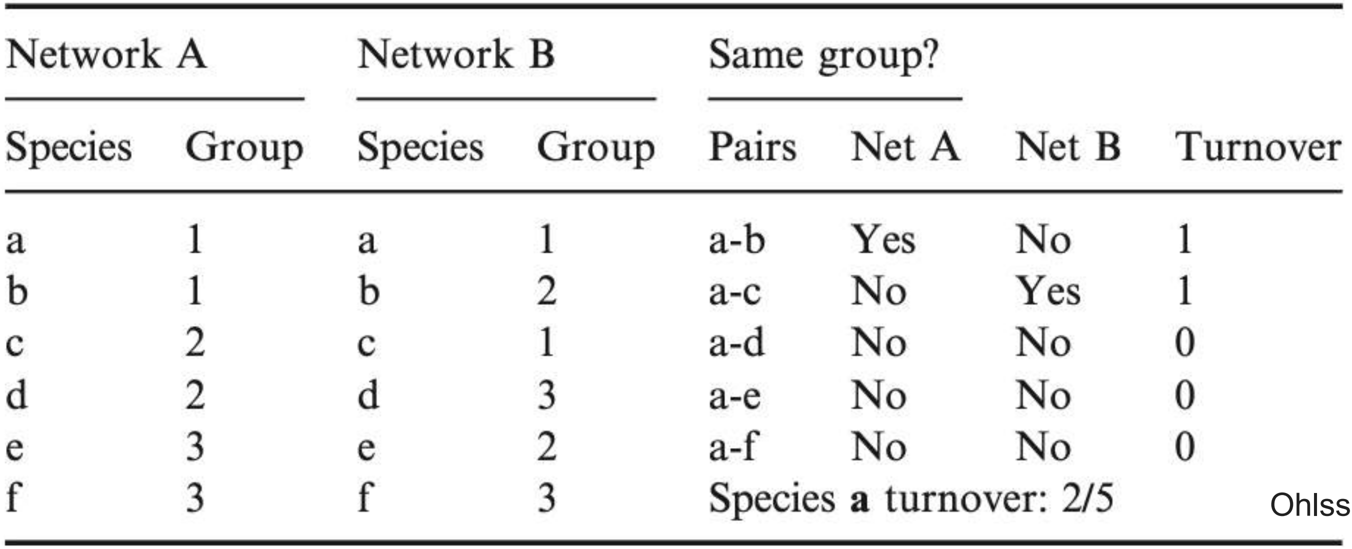
- 38–87% between subregions
- 49% - 76% between subregions and metaweb.

Clusters based on species overlap diverged from the group structure clusters.

Subwebs that shared a large proportion of the species could differ in group structure.

Species-wise group turnover

- If the relationship for a species pair changed between two webs, there was turnover.
- To obtain the mean species pairwise group turnover we calculated the proportion of pairs for each species which experienced turnover.



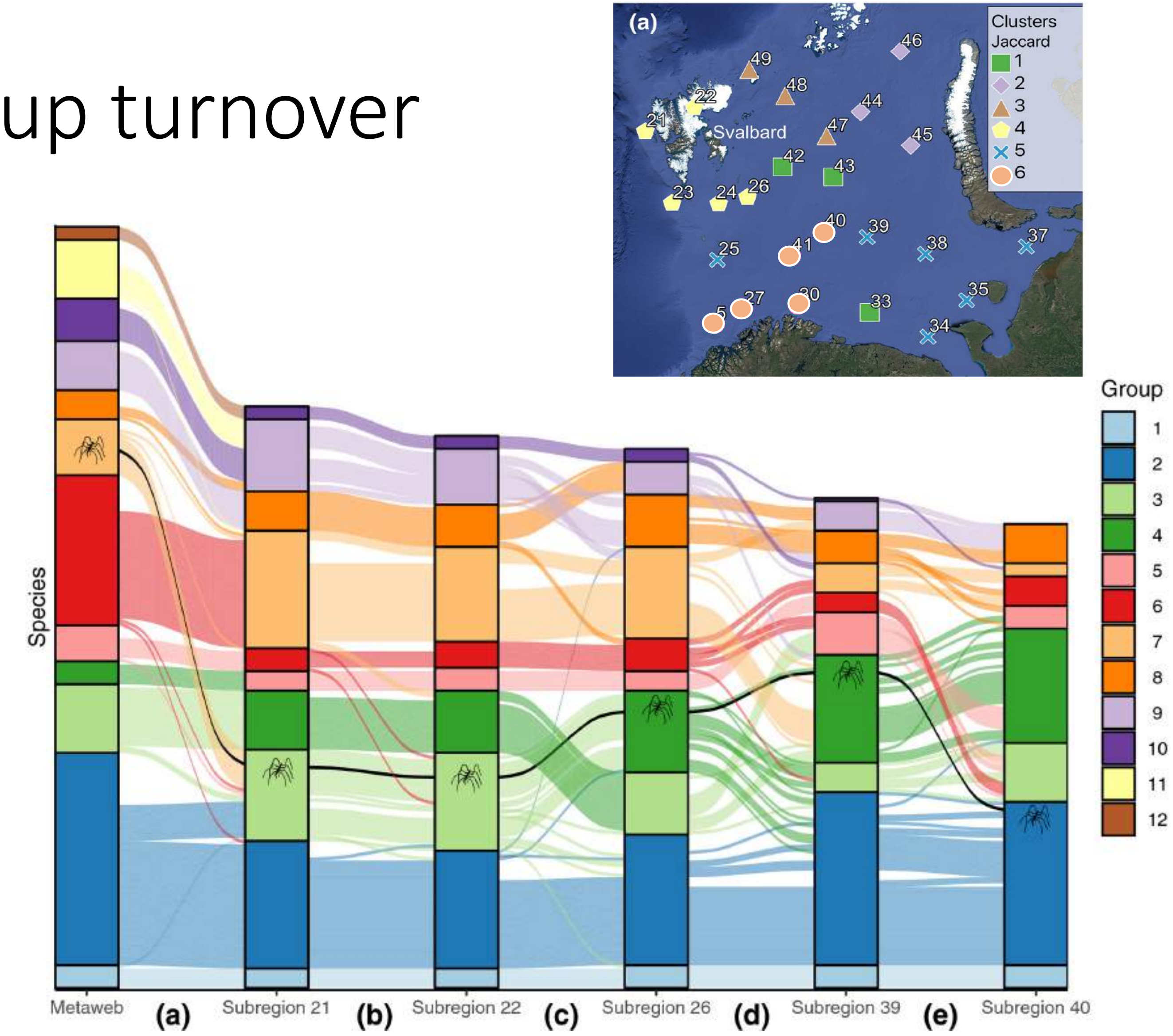
Network A		Network B		Same group?			
Species	Group	Species	Group	Pairs	Net A	Net B	Turnover
a	1	a	1	a-b	Yes	No	1
b	1	b	2	a-c	No	Yes	1
c	2	c	1	a-d	No	No	0
d	2	d	3	a-e	No	No	0
e	3	e	2	a-f	No	No	0
f	3	f	3	Species **a** turnover: 2/5			

Ohlsson & Eklöf, 2020, *Ecol. Lett.*

Species-wise group turnover

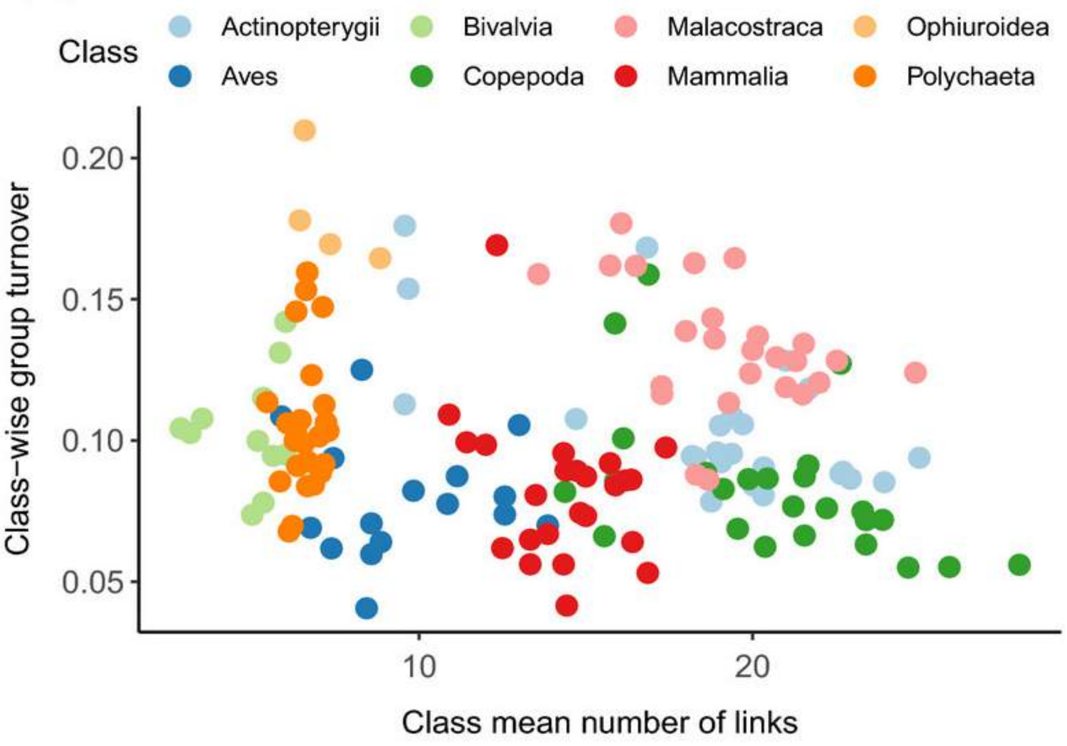
Example of how *Pycnogonida spp* changes group membership in different sub regions.

Species group turnover connected to traits: e.g. more mobile species change groups less than sessile species



Species-wise group turnover

- Species with more links experienced less turnover.
- The eight most species-rich taxonomic classes showed a clear pattern of how class identity held additional importance to the turnover rate
- Some connection to traits such as mobility



Examples

Common ling (*Molva molva*): strictly piscivorous in subregion 5, mixed diet in subregion 25.

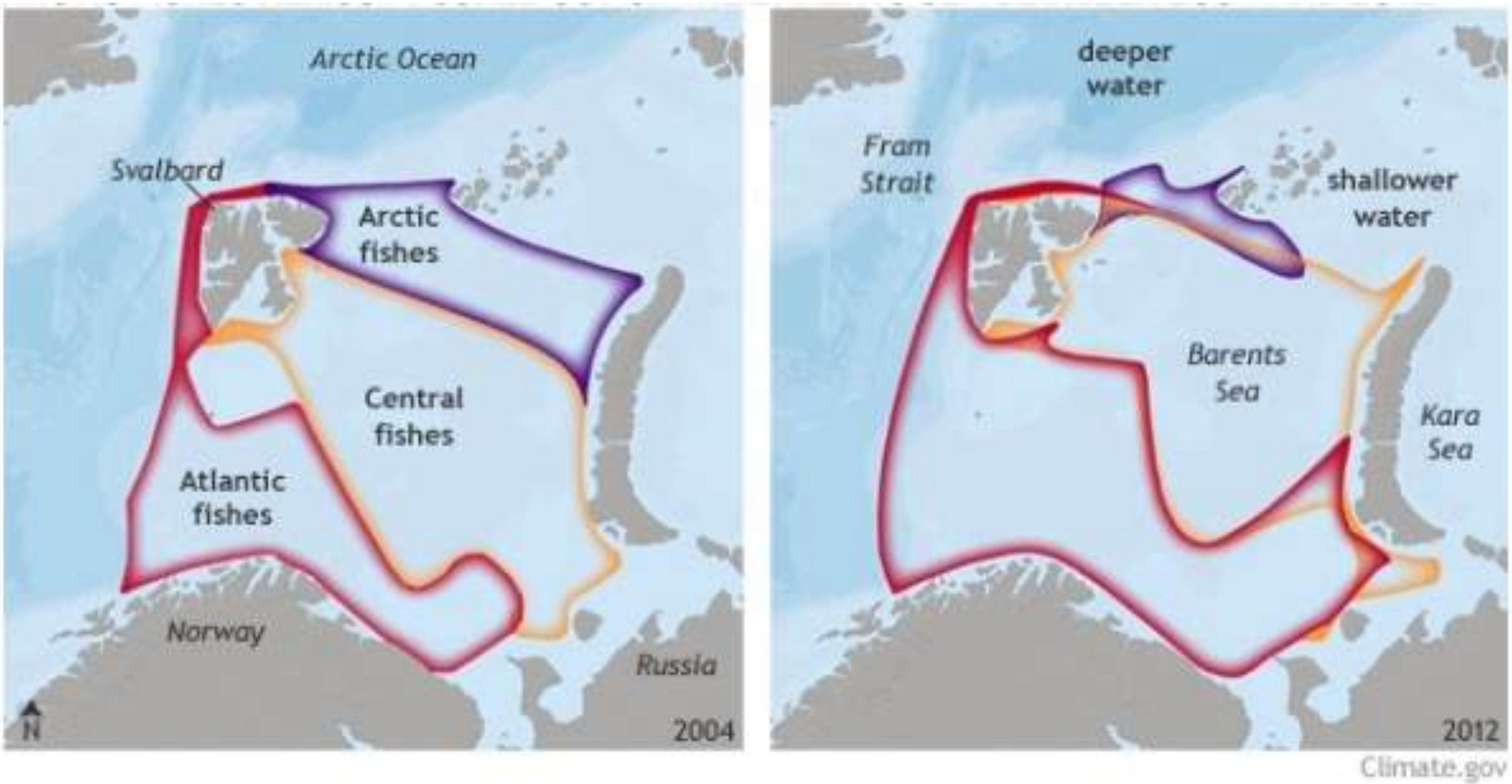
Benthic (e.g. Ophiuroidea) vs more mobile species, e.g. mammals and birds

Spatial resolution impacts group structure

SUMMARY

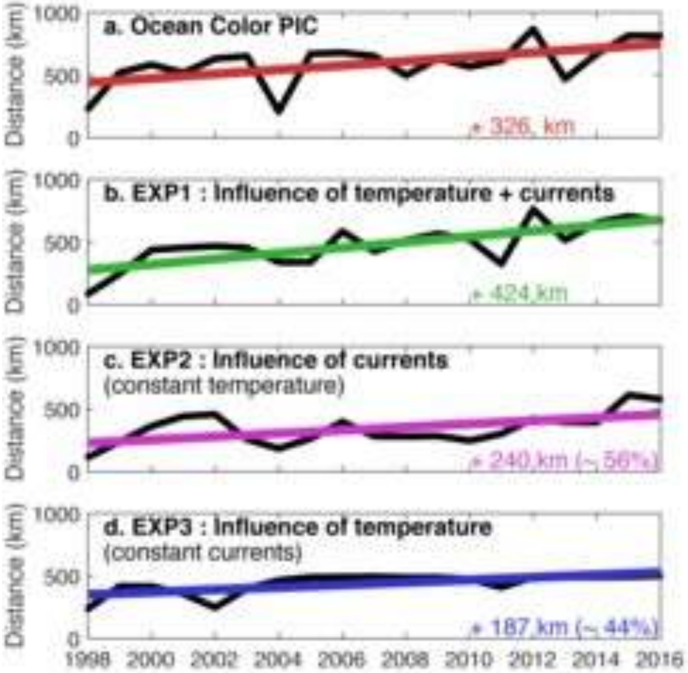
- Identifying how a network's group structure change between spatial scales and regions can provide important information on species ecological roles.
- Subregions had group structures which differed substantially, both between each other and compared to the metaweb.
- Functionality of species potentially changing between sub-regions.
- Group structure from the metaweb can be misleading.

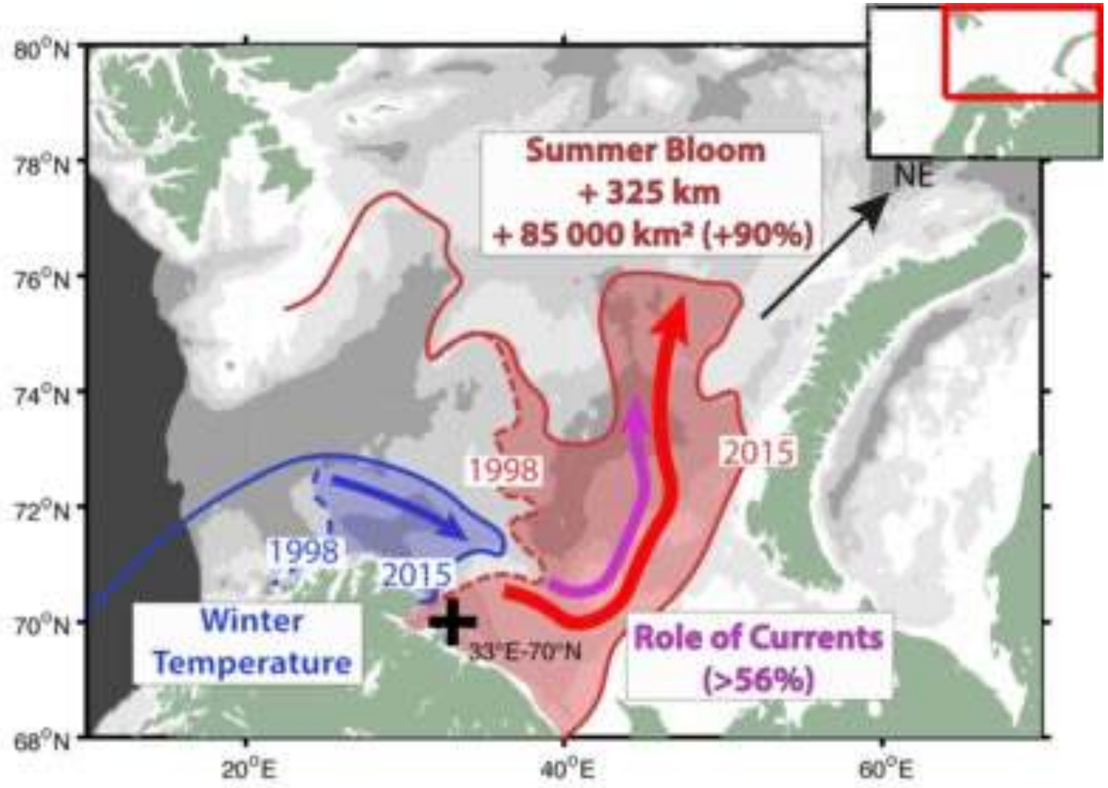
Arctic fishes almost pushed out in Barents sea between 2004 and 2012.



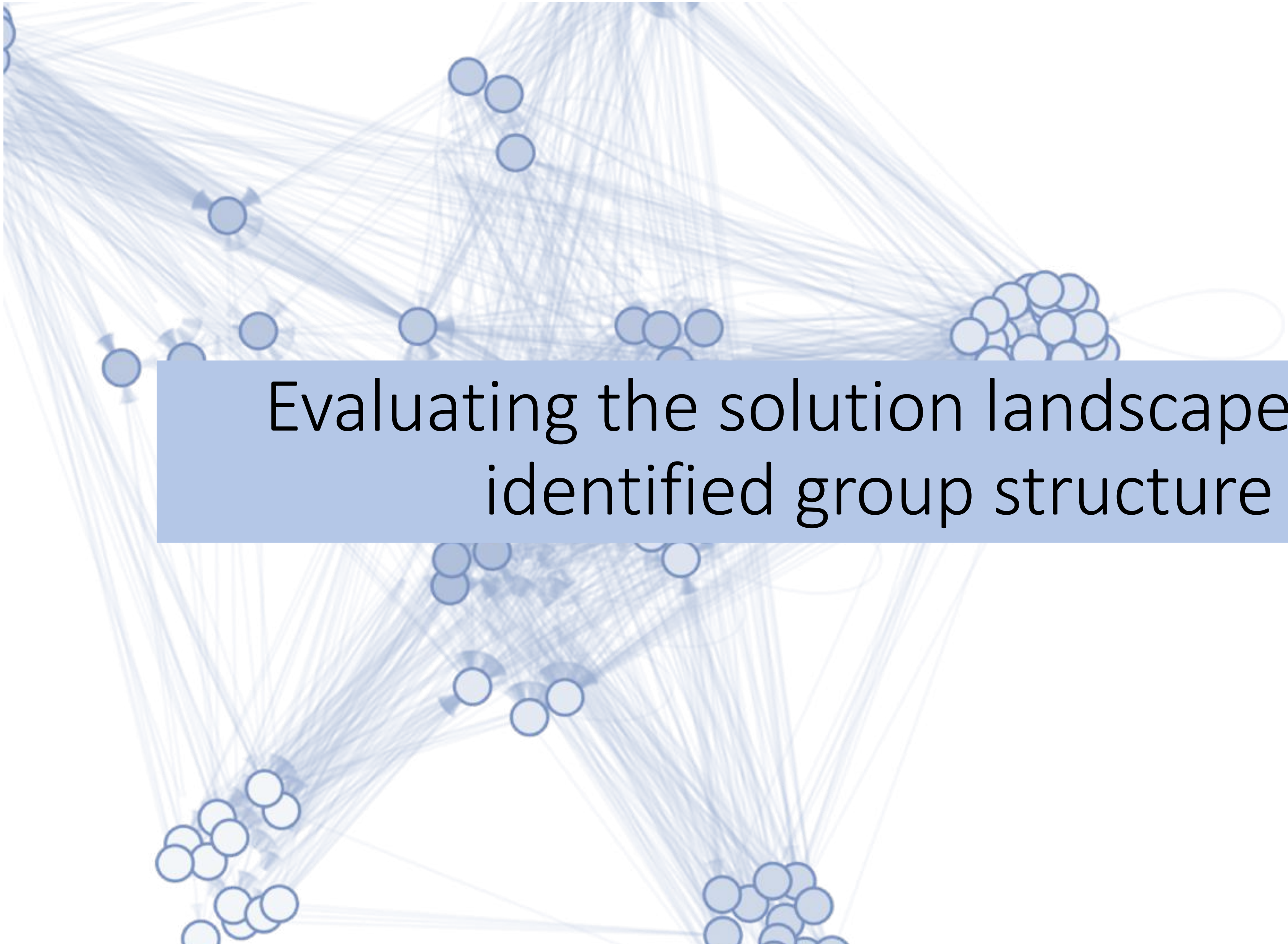
Fossheim et al., 2015, *Nature climate change*

Changes in currents and temperature lead to altered plankton communities in the Arctic





Oziel et al., 2020, *Nature climate change*



Evaluating the solution landscape of the identified group structure

Evaluation of the solution landscape

- The identified ’best’ solution is not guaranteed to be the actual best solution.

Aims

- Compare the solution landscapes between food webs
- Analyze explanatory factors for differences between solutions between food webs
- Analyze explanatory factors for differences between food webs

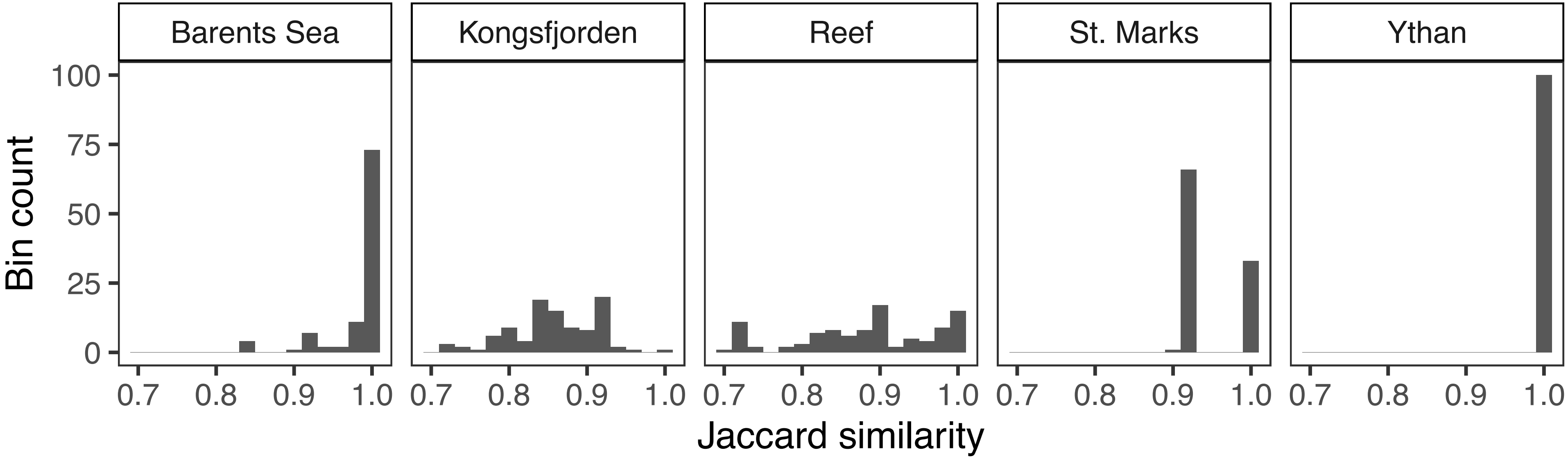
Evaluation of the solution landscape

Comparing solution landscapes for five marine food webs

100 iterations (searches) for identification of ‘best’ partitioning of each food web

Measuring partition similarity with the Jaccard distance

Evaluation of the solution landscape



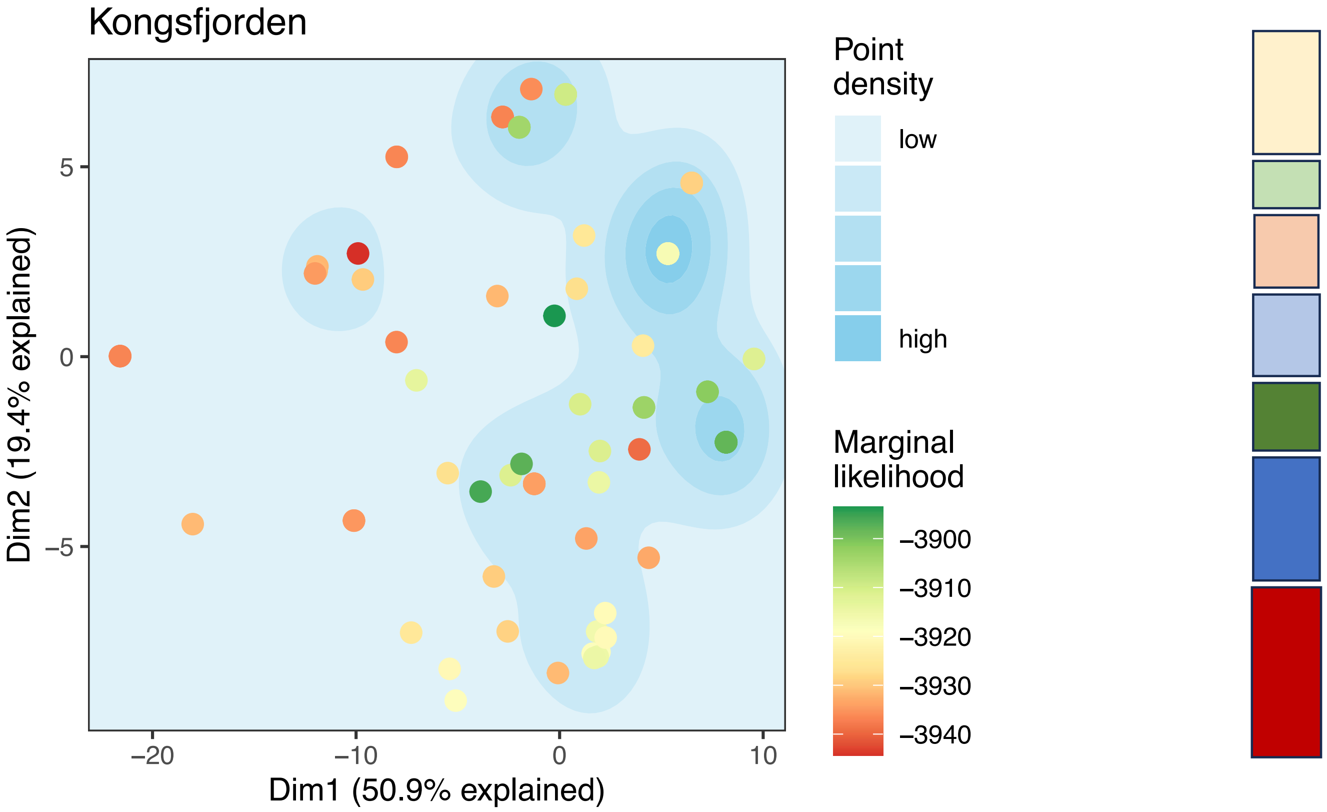
From the 100 iterations, St. Marks converged to a total of 4 solutions, Barents Sea 10 solutions, Kongsfjorden 50 solutions, and Reef 70 solutions.

Evaluation of the solution landscape

- The Jaccard index (the number of intersecting species divided by the total number of unique species in the two groups) was calculated for the best-matching group pair

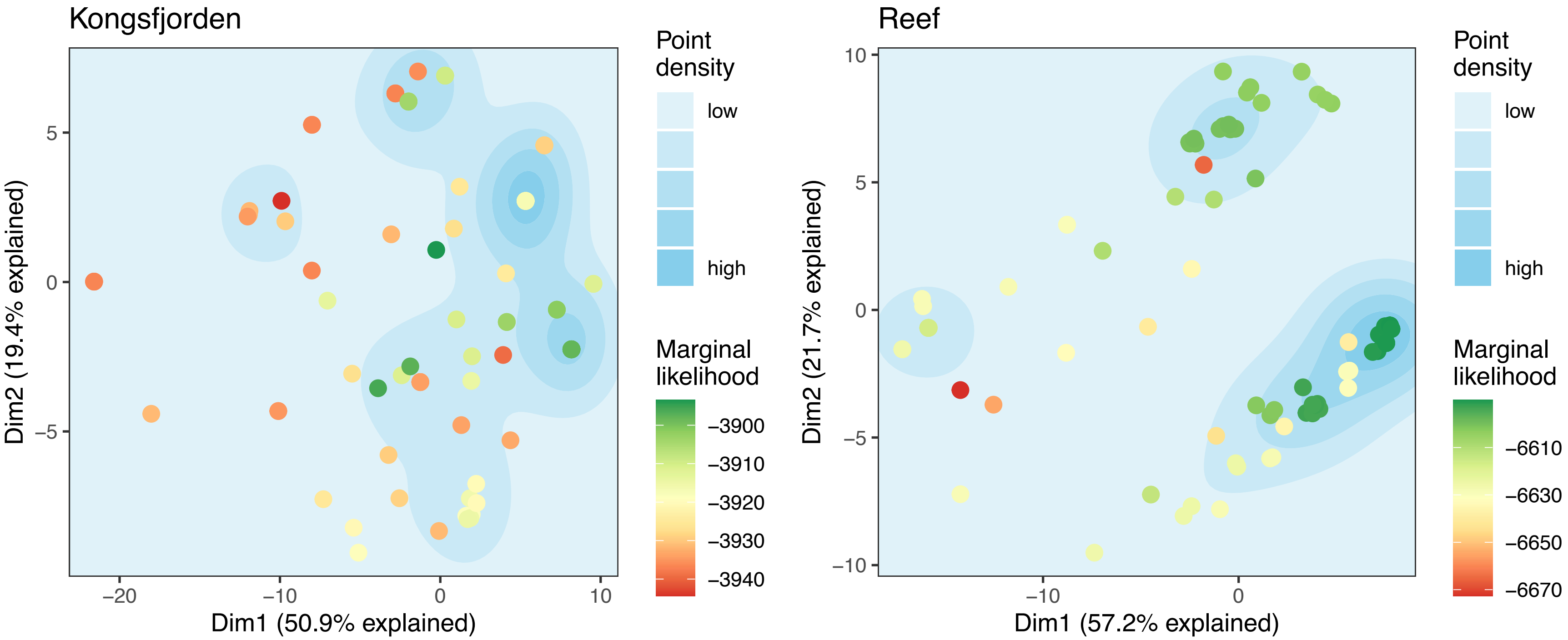
$$J\left(C_k^A, C_l^B\right) = \max_l \left(\frac{\left|C_k^A \cap C^B\right|}{\left|C_k^A \cup C^B\right|} \right)$$

Evaluation of the solution landscape

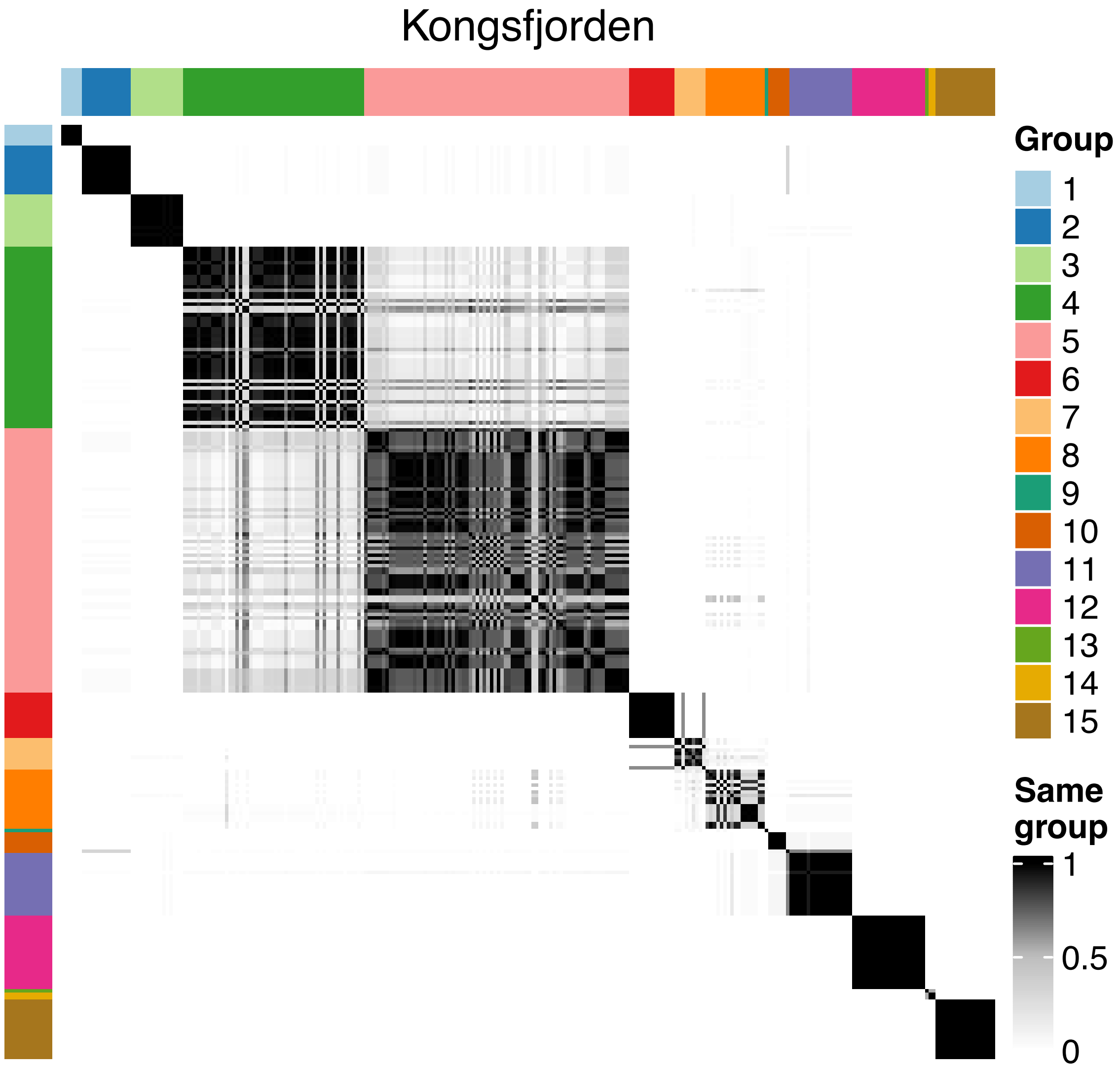


Evaluation of the solution landscape

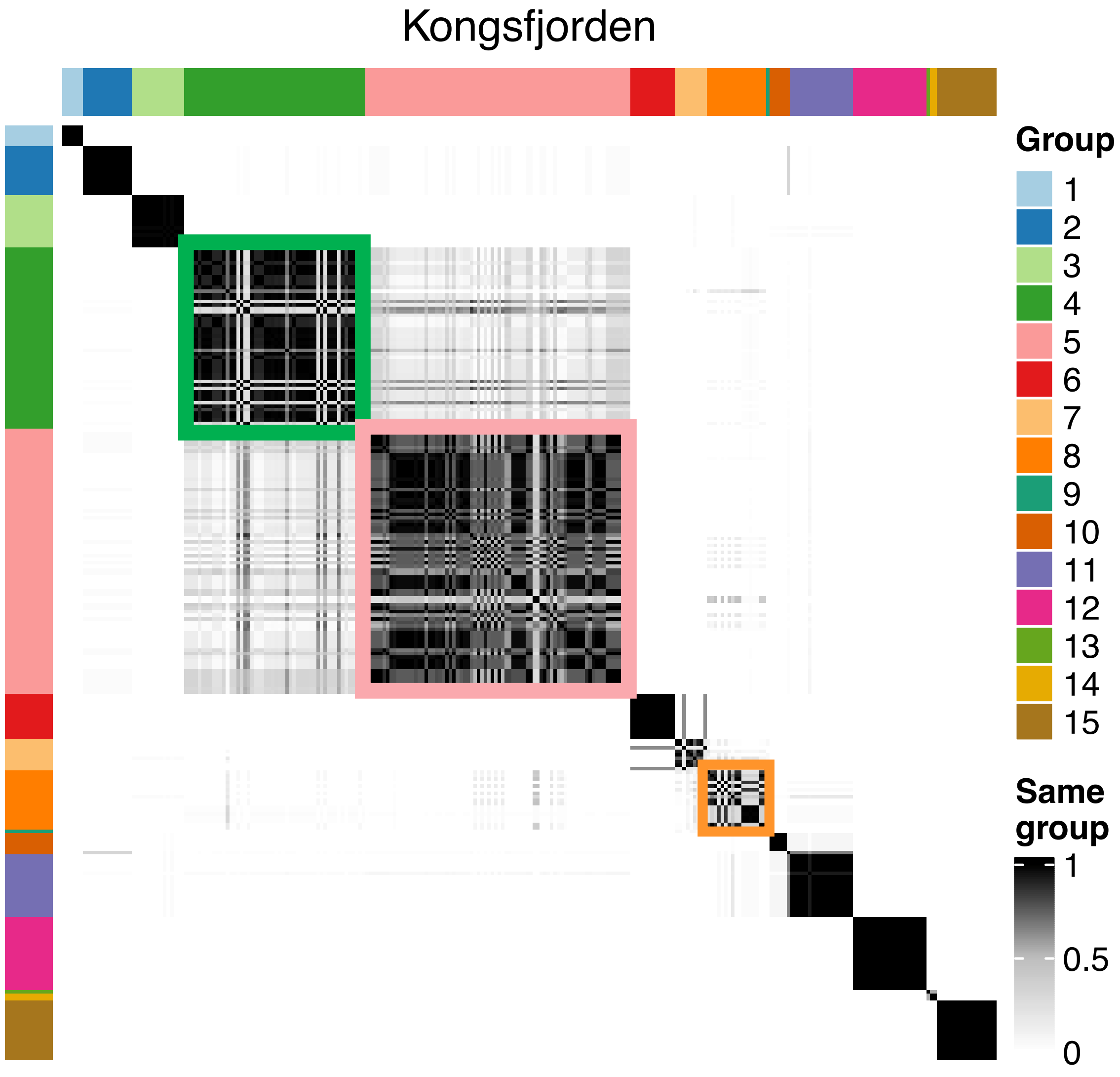
Each point represents the best solution in one iteration



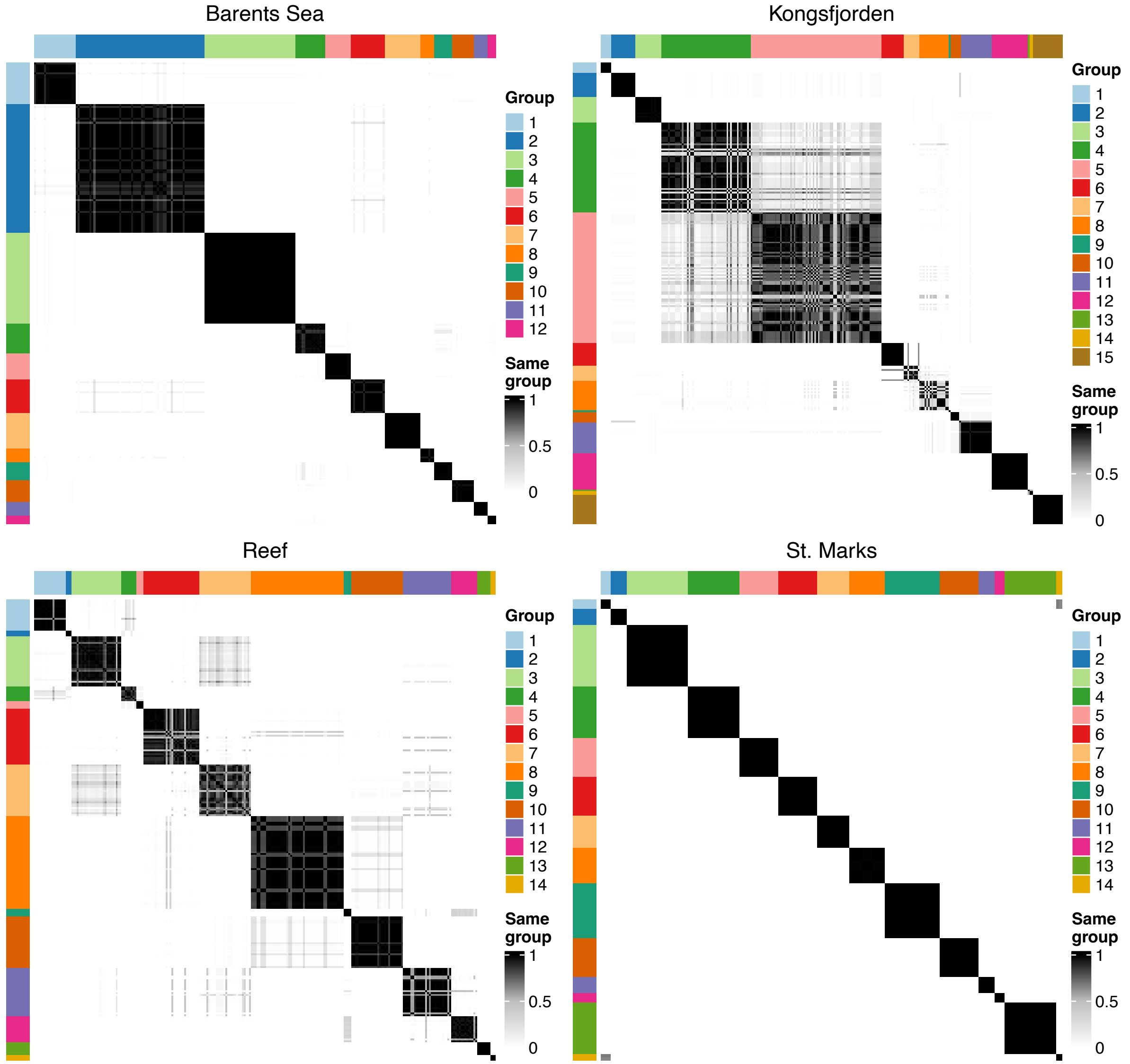
Which groups and species are changing the most?



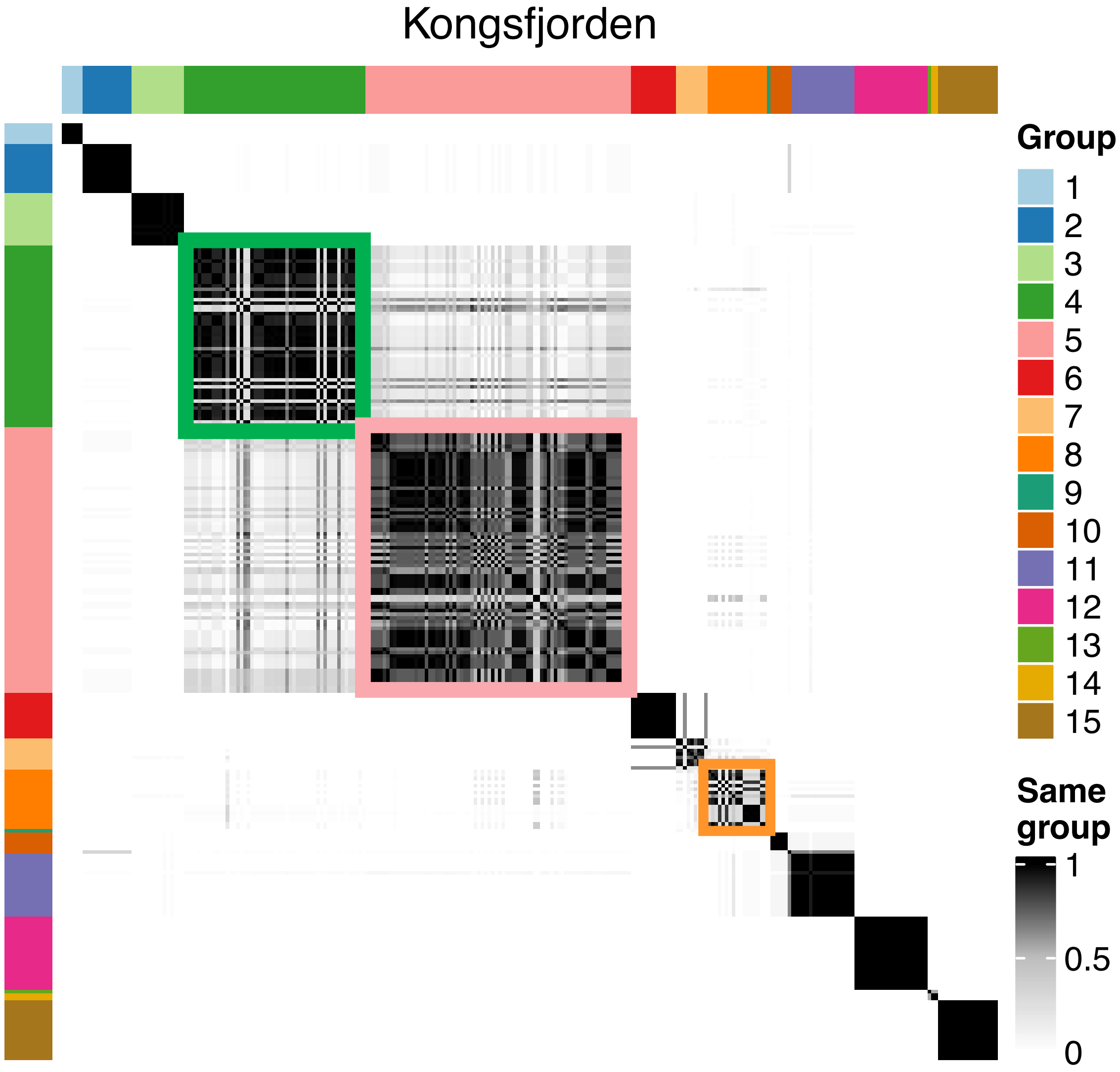
Which groups and species are changing the most?



Which groups and species are changing the most?



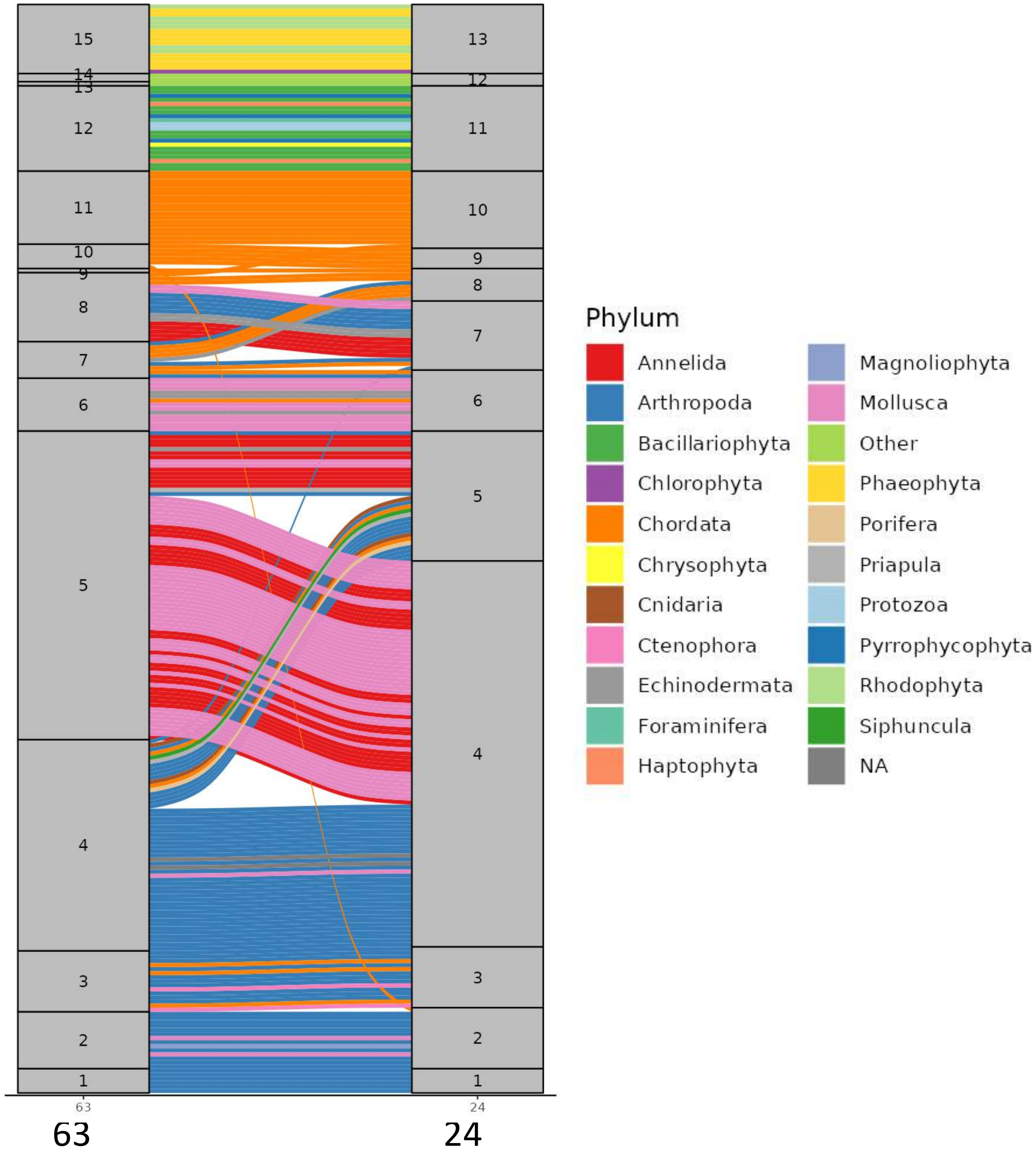
The changes in solutions are driven by a set of species alternating their group membership between two large groups, both of which are comprised of benthic species with similar diets.



Which groups and species are changing the most?

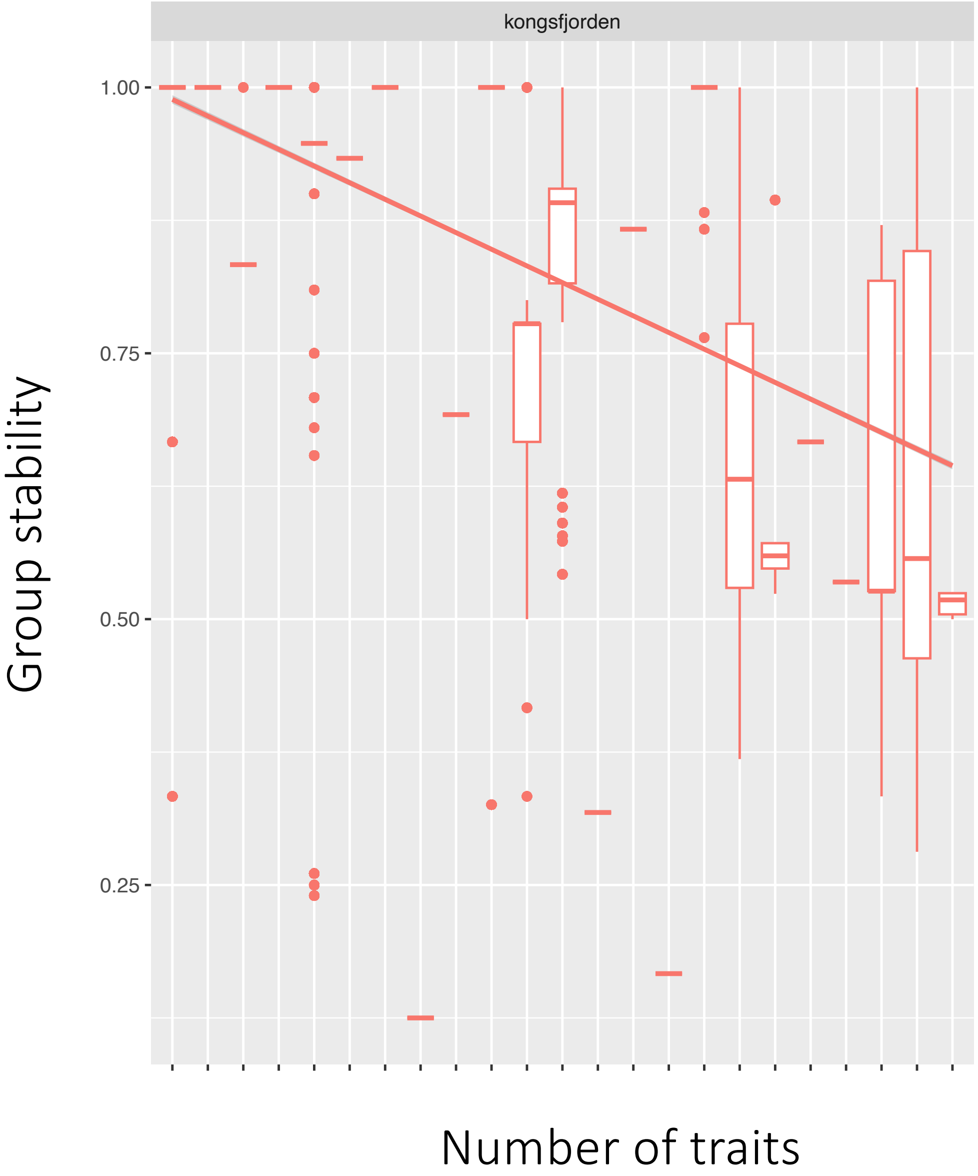
Comparison with iteration 63 ("best" solution) and iteration 24.

Jaccard similarity 0.712



Which groups and species are changing the most?

Groups where the included species have more traits in total were less stable

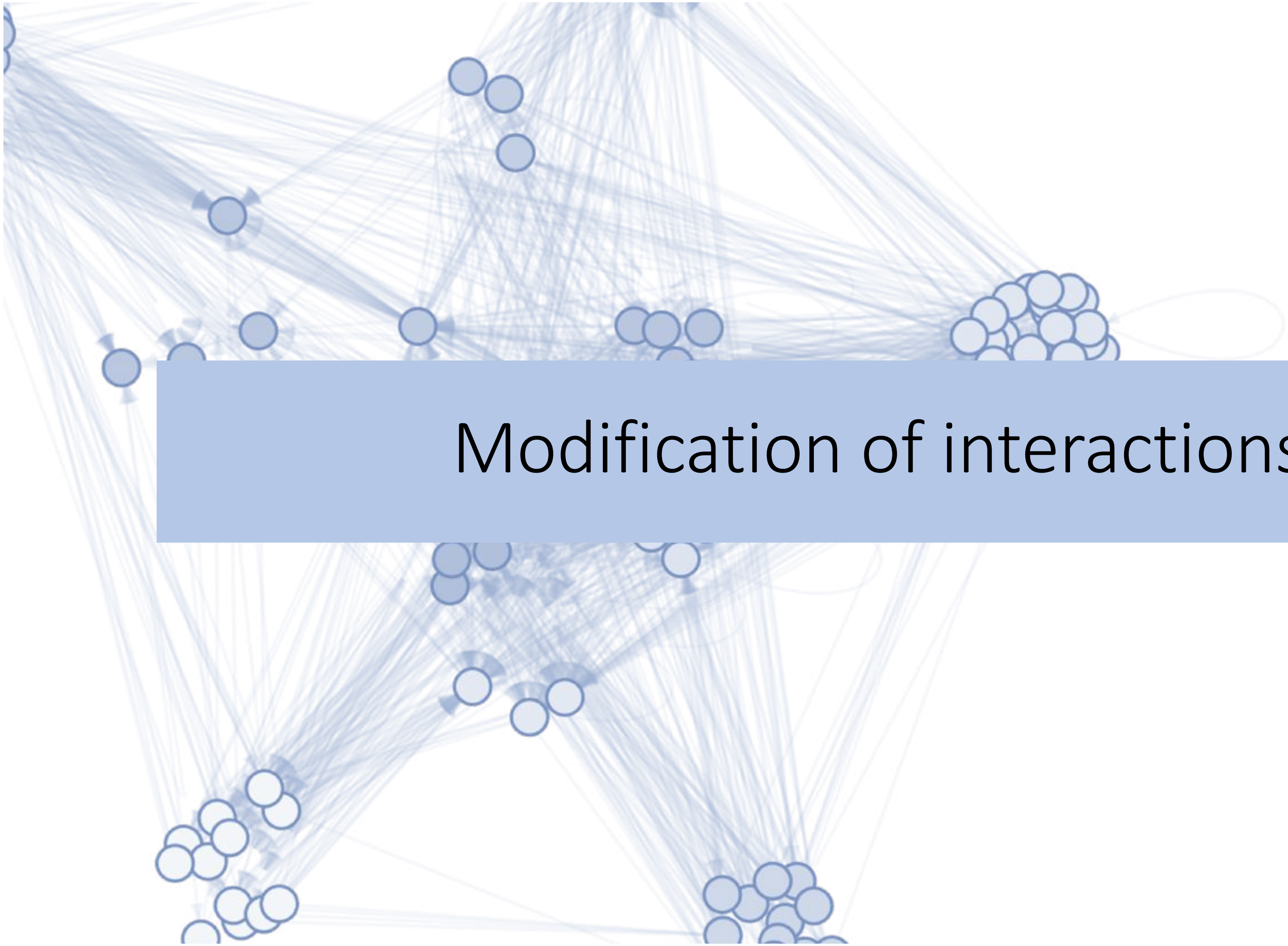


Evaluation of the solution landscape

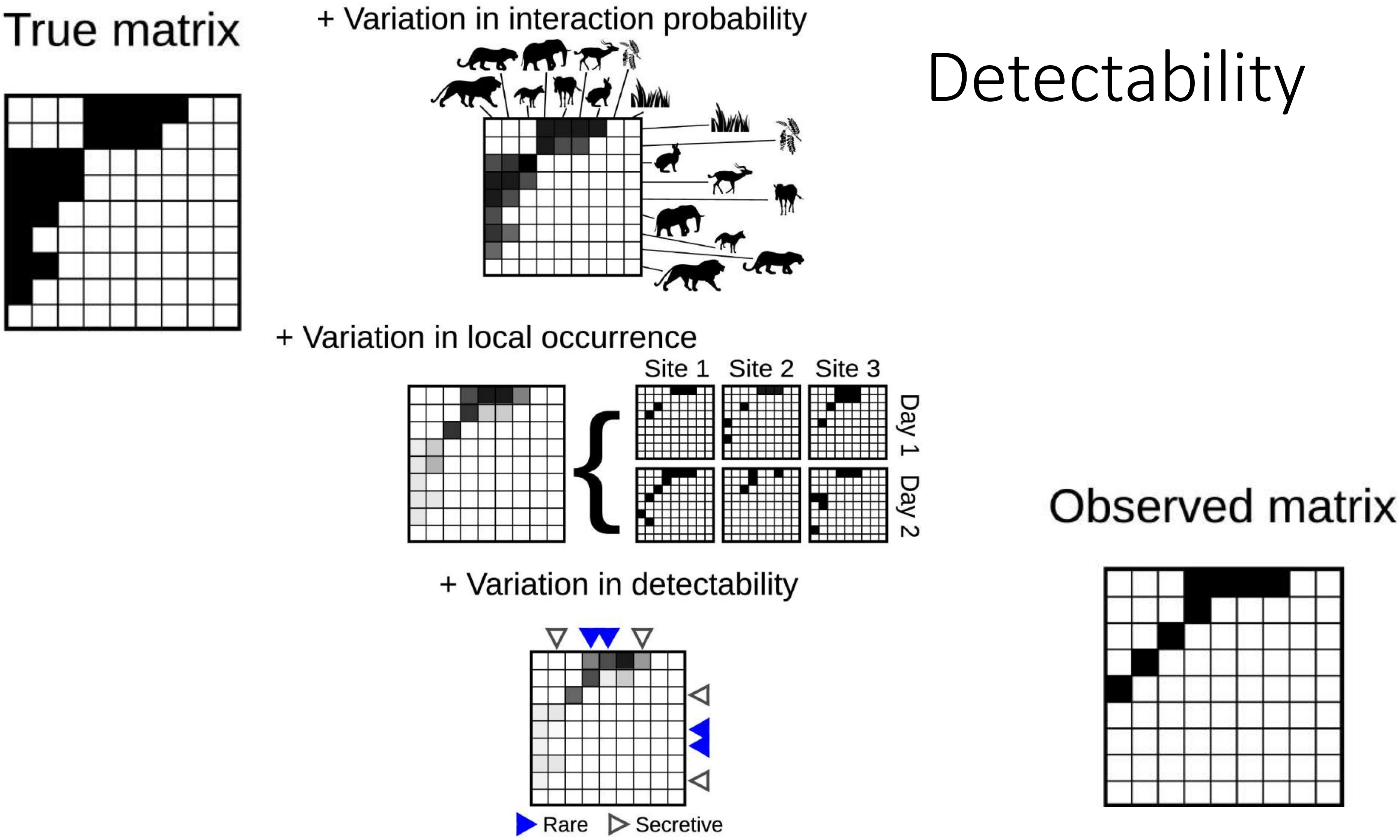
SUMMARY

- The width of the solution landscapes differ between food webs
- In general, the partitioning is relatively similar
- Changes often due to a limited number of specific groups and species
- More variable trait profile gives lower group stability

Modification of interactions

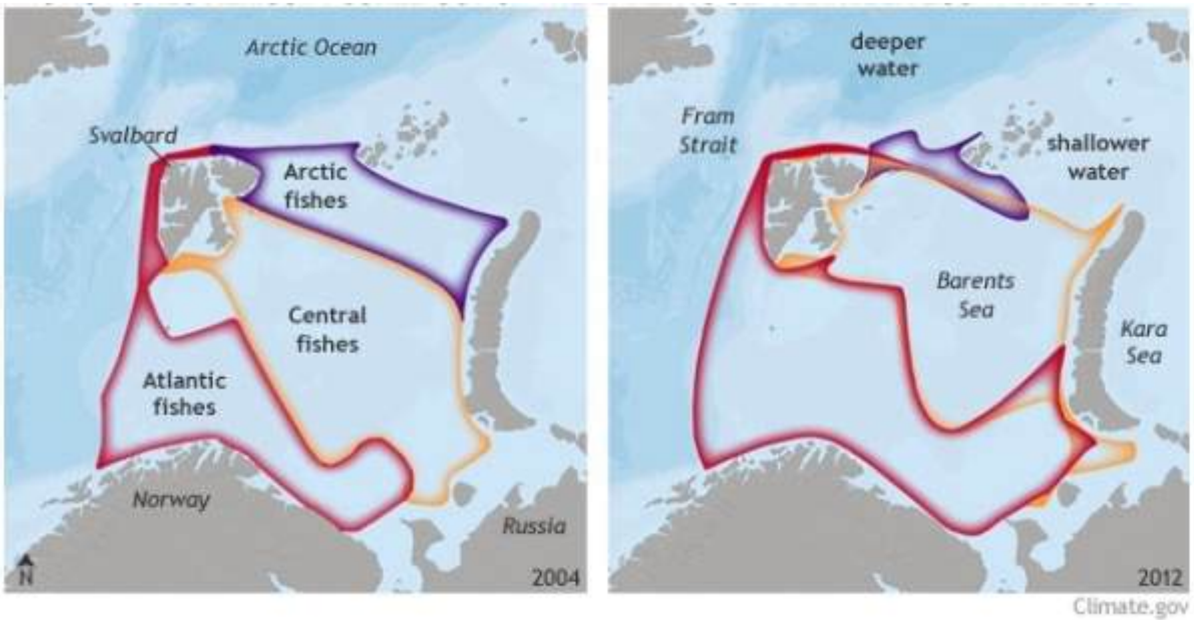


Detectability



Disturbances

- Species extinctions
- Invasive species
- Changes in interactions



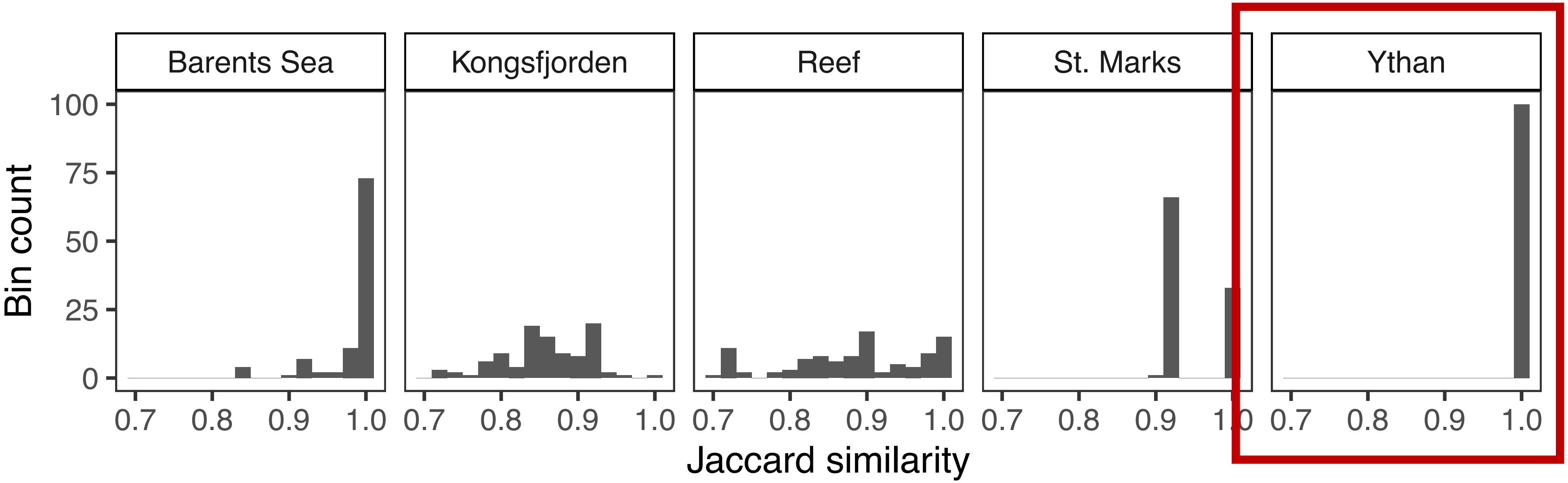
Modifications of interactions and group structure

- Uncertainties in the data collected
- Disturbances can change interactions

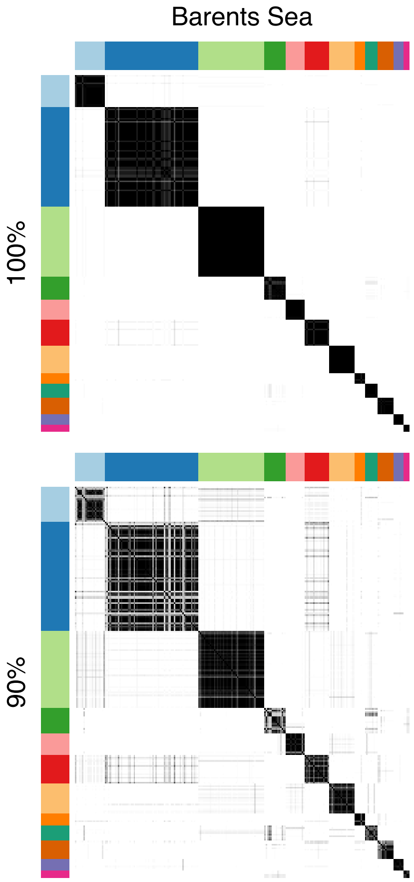
- Disturbance here: simulated as removal of a fraction of the links

Modifications of interactions and group structure

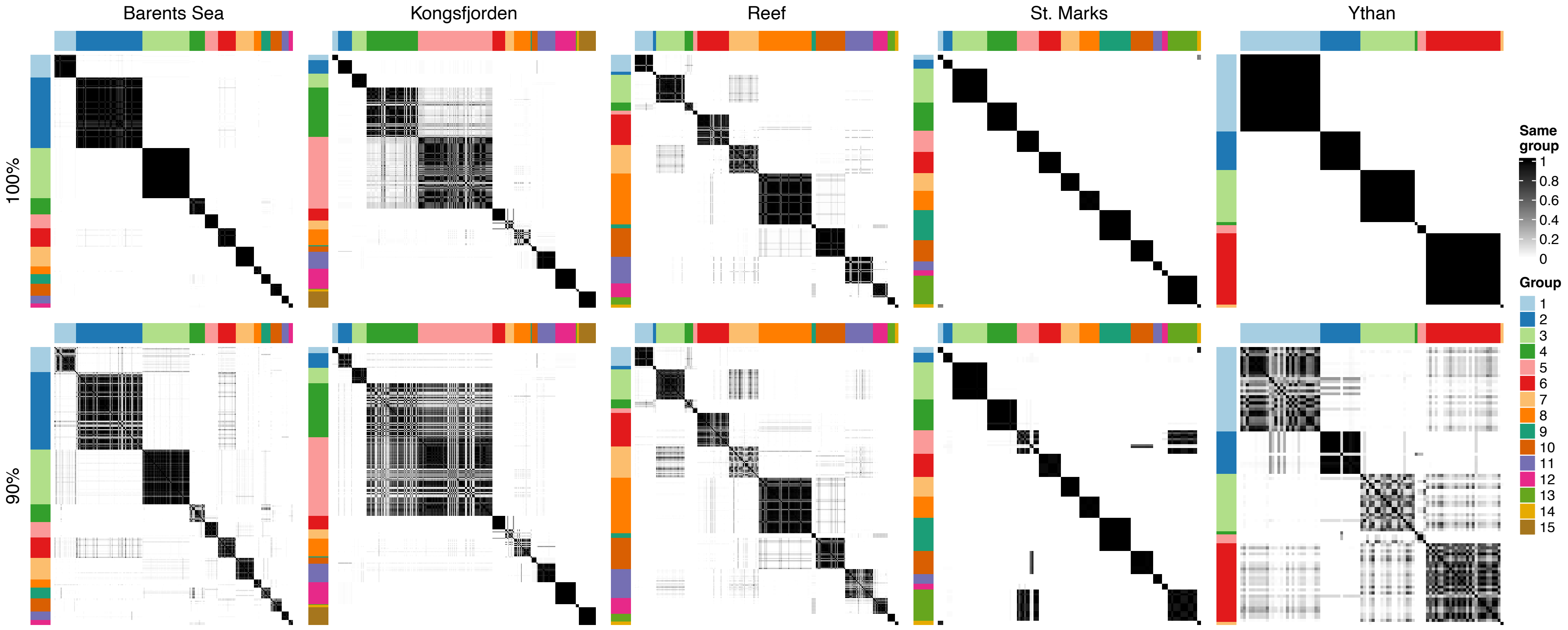
Reminder – Ythan very stable



Modifications of interactions and group structure



Modifications of interactions and group structure



Conclusions

- Identified species groups shows coupling to species ecological roles in networks – relevant for understanding relationships between network structure and functionality

- Althogh there are variations between food webs in how wide the solution landscapes are the identified group structure for a food web is to large extent intact ascross iterations. This points towards presence of a strong group structure.

- Group stability informed by traits/phylogeny. Could assist in identifying 'stable' groups in networks where information on species interactions is limited.

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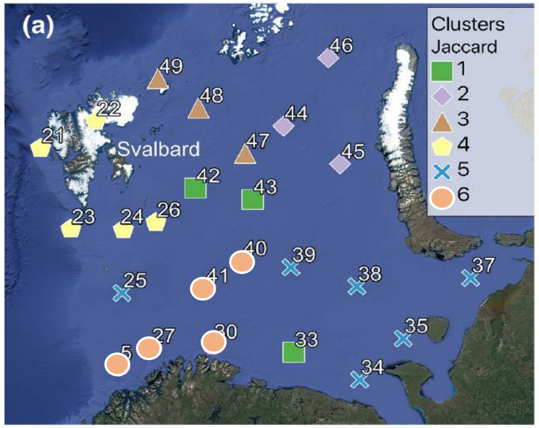
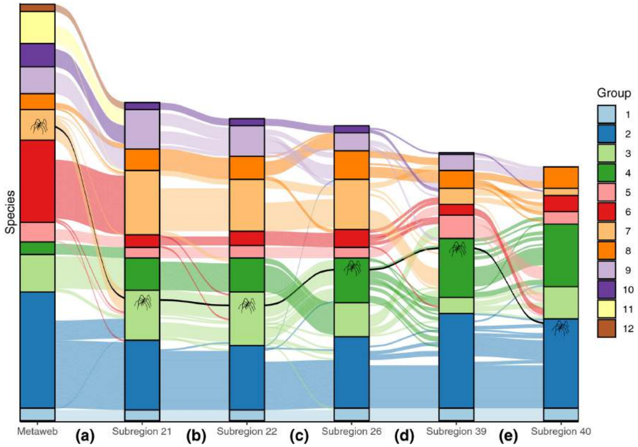
Vetenskapsrådet

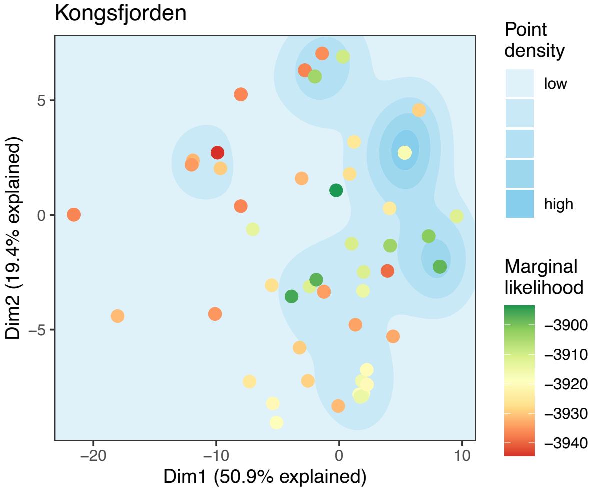
FORMAS

Familjen Kamprads stiftelse
The Kamprad Family Foundation for Entrepreneurship, Research & Charity

Thank you


(a)
Clusters
Jaccard
1
2
3
4
5
6
46
49
48
44
22
21
Svalbard
47
45
42
43
23
24
26
40
39
41
25
38
37
27
30
5
33
35
34


Species
Metaweb
(a)
Subregion 21
(b)
Subregion 22
(c)
Subregion 26
(d)
Subregion 39
(e)
Subregion 40
Group
1
2
3
4
5
6
7
8
9
10
11
12


Kongsfjorden
Dim2 (19.4% explained)
5
0
−5
−20
−10
0
10
Dim1 (50.9% explained)
Point
density
low
high
Marginal
likelihood
−3900
−3910
−3920
−3930
−3940