

Co-occurrence networks show response of microbial communities to warming in tundra soils

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ITEX-network



Directional changes in vegetation due to warming

- no impact on microbial communities and on nitrogen-cycling
- strong environmental filtering
- very high phylogenetic diversity of the microorganisms

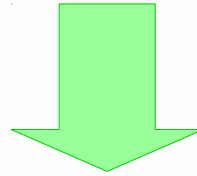
High diversity of interactions ?

Are the interacting species structured by the environment and by the warming treatment ?

- 13 sites (19 experiments)
- 4 control / 4 OTC plots per site
- Humus layer
- C, N, pH and N C isotopes
- Plant abundances classified by functional groups and mycorrhizal type
- Metabarcoding of the 16S rRNA gene and of the ITS2 gene
- Quantification of nitrogen-cycling genes

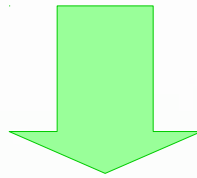


- Prokaryotic species not randomly distributed
- Fungal species present in more than 5 sites

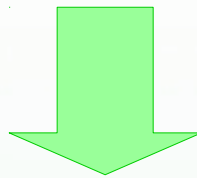


- Highly significant Spearman correlations ($p < 0.001$)
- Non arbitrary cutoffs (RMT– based method) : 0.6 for fungi and 0.81 for prokaryotes

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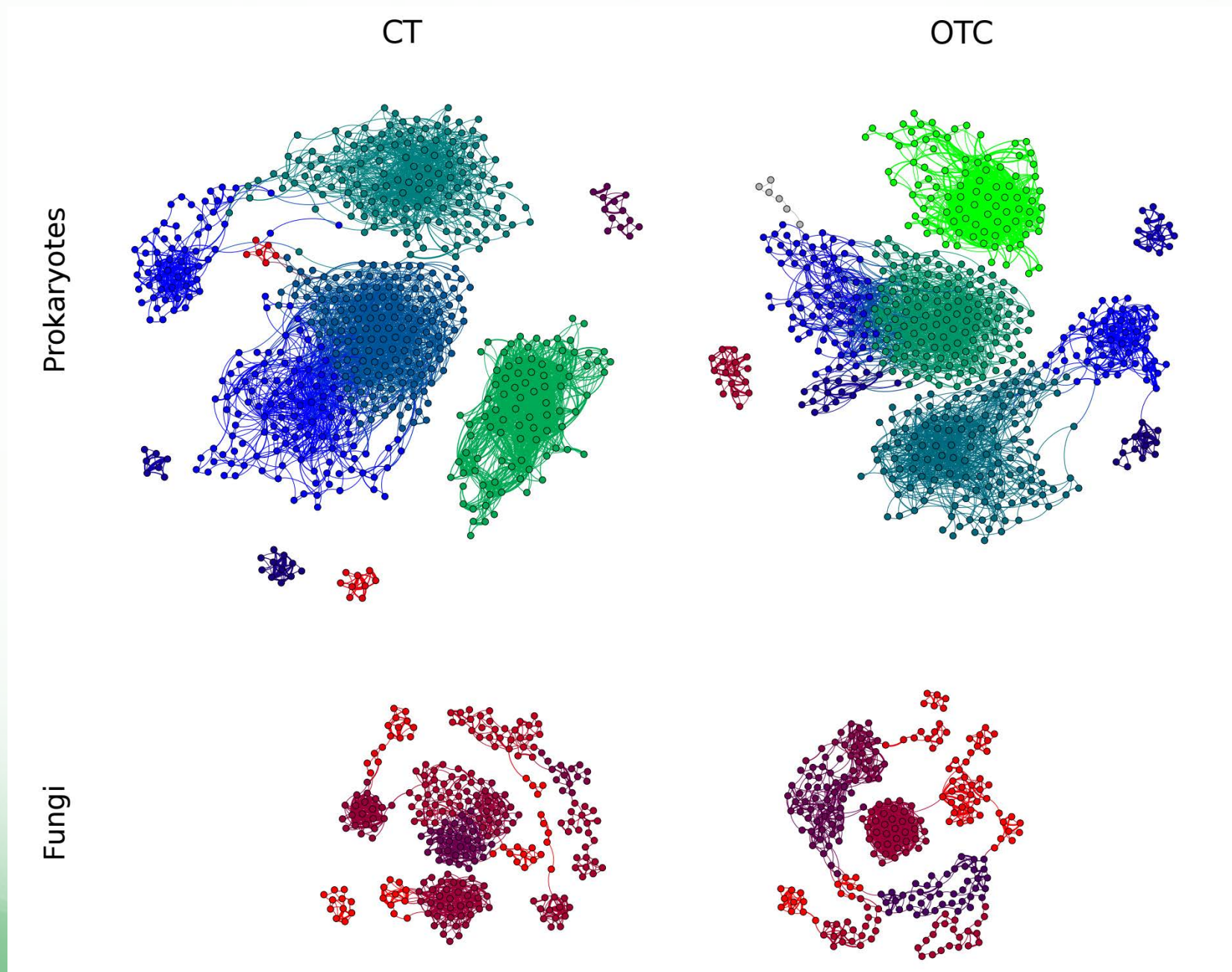


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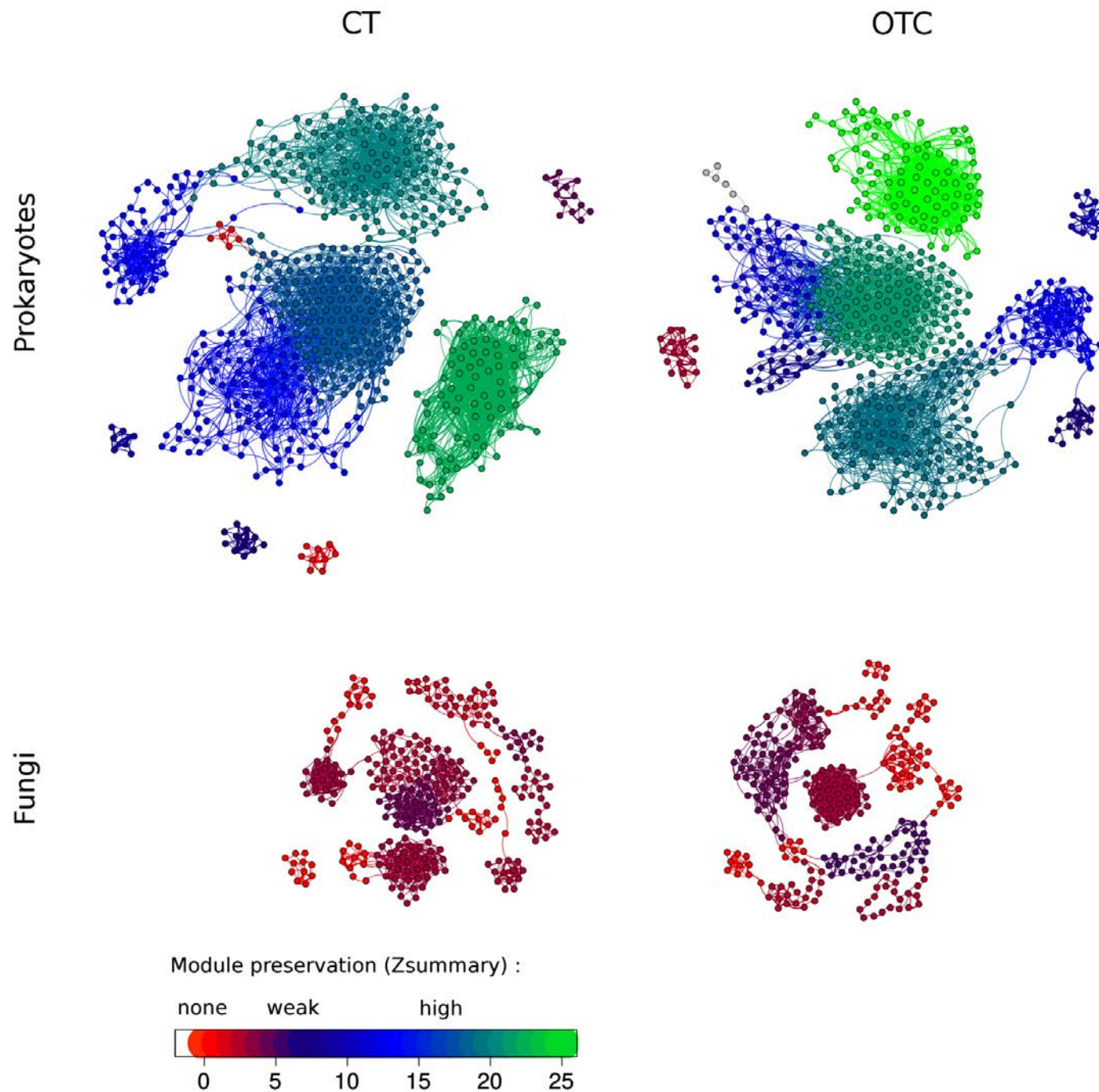


- Highly structured networks (significantly different from random)
- “Small-world” properties
- Modular structure (modules = putative ecological niches)

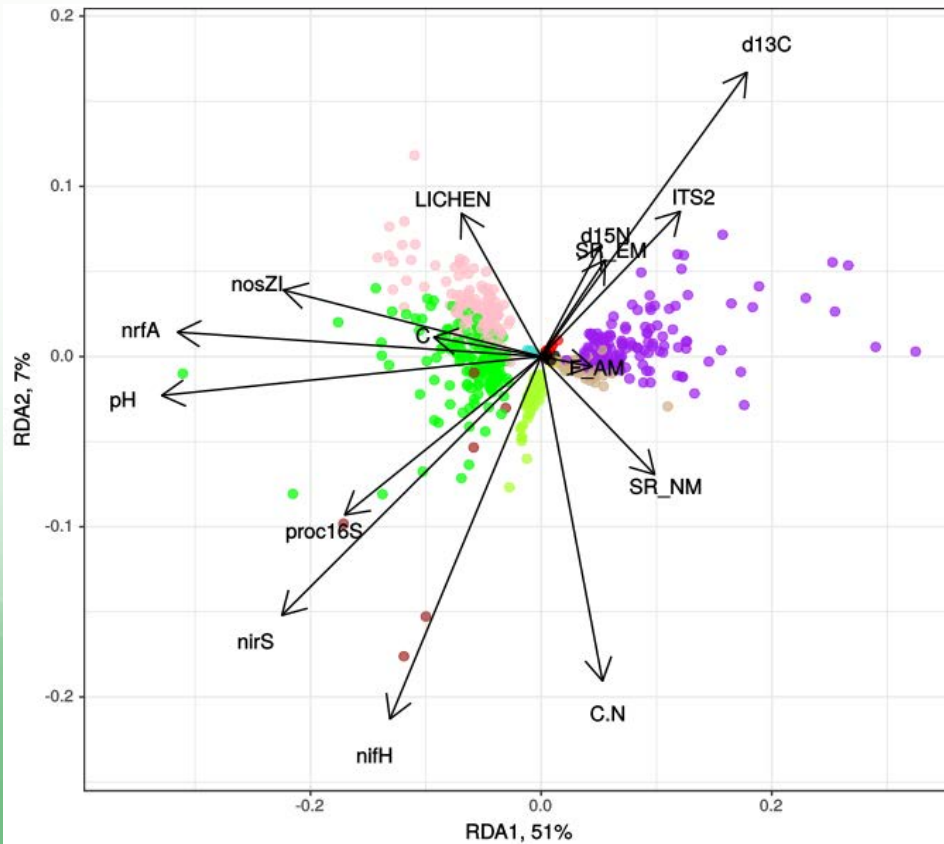
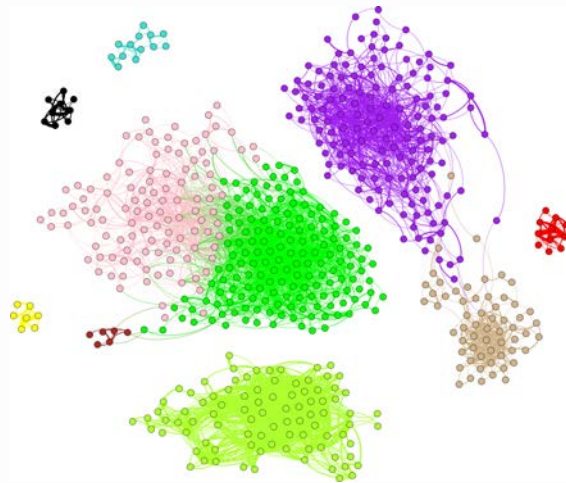
Network comparison between treatments



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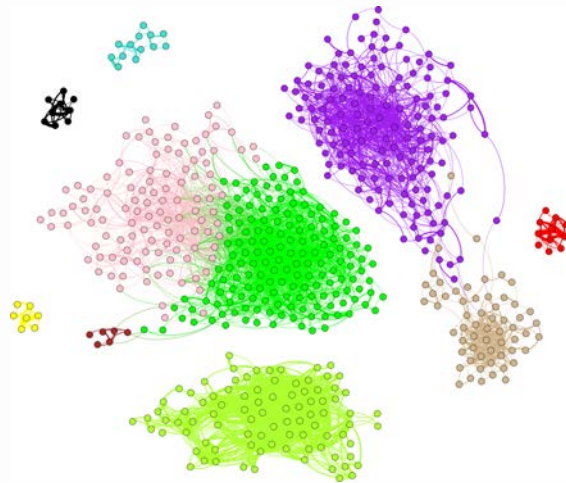


Control

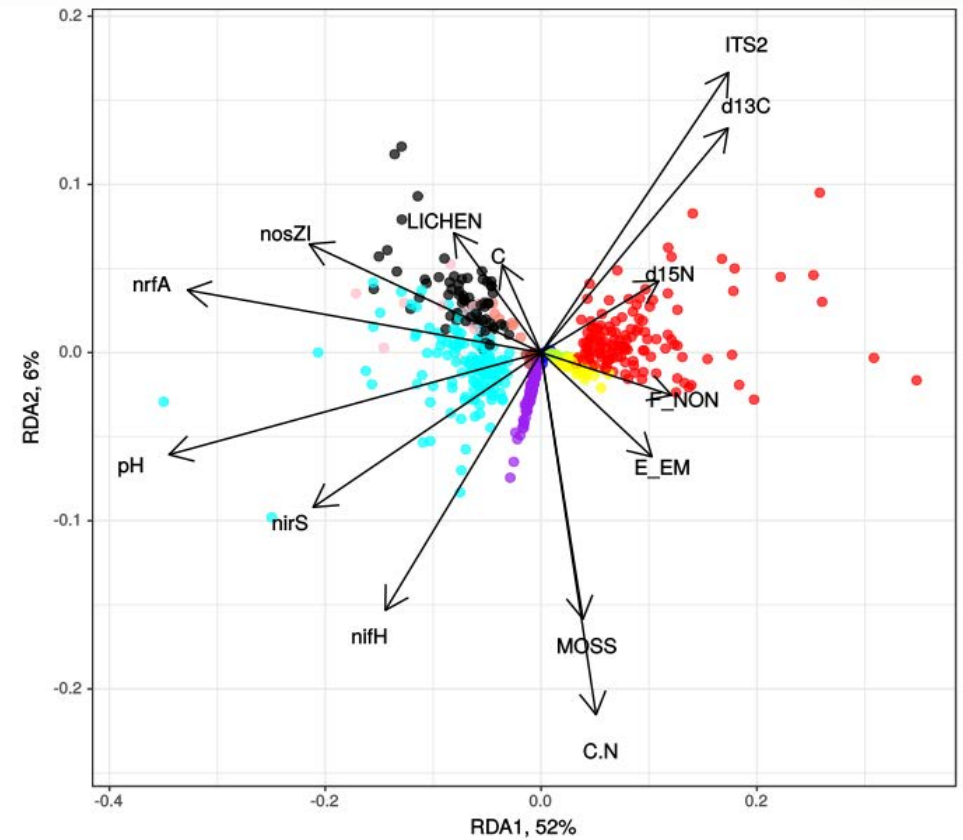
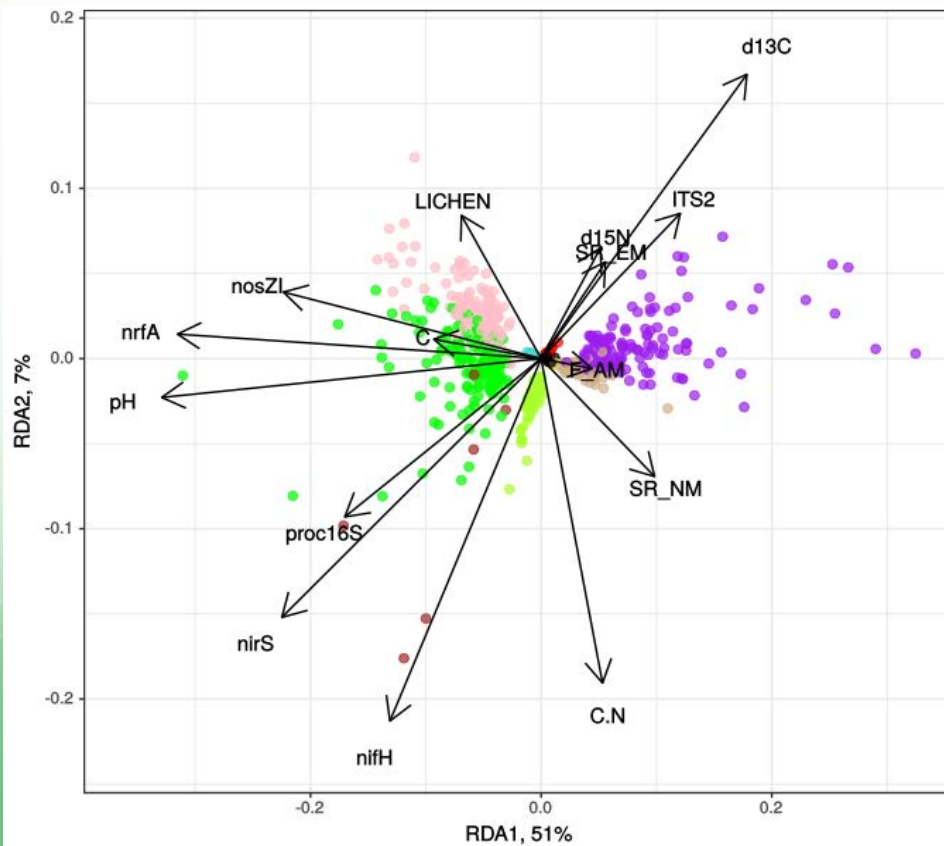
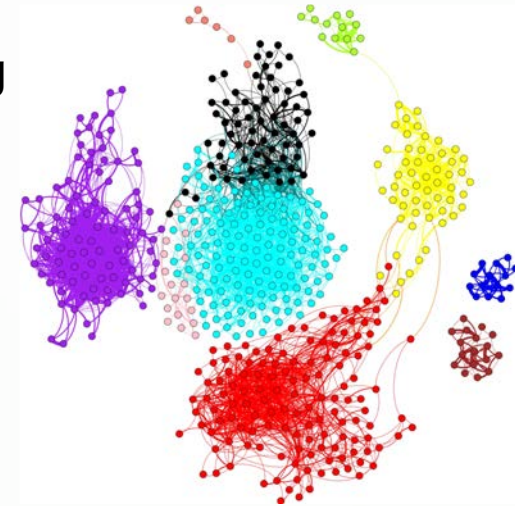


Prokaryotic networks

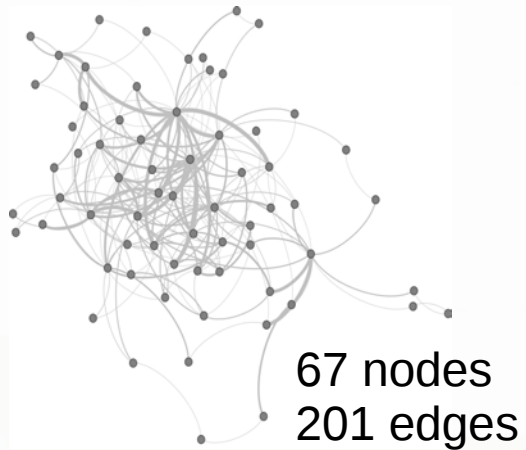
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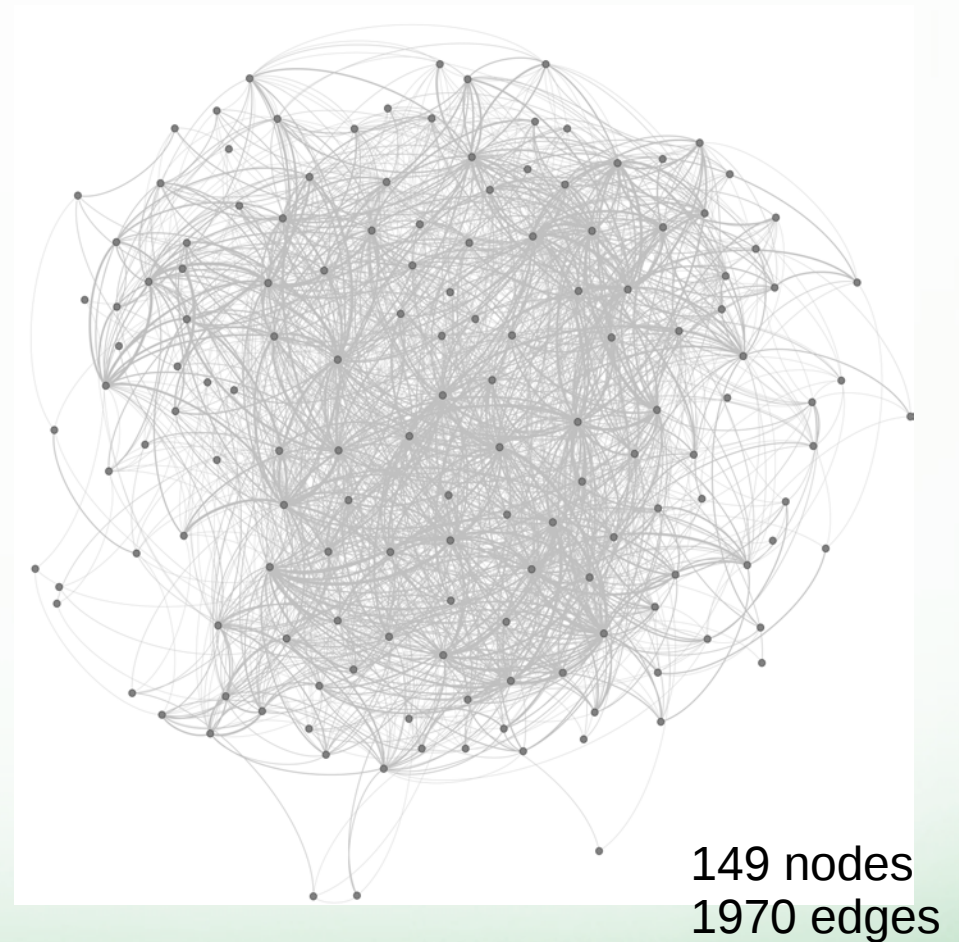
Warming



Control



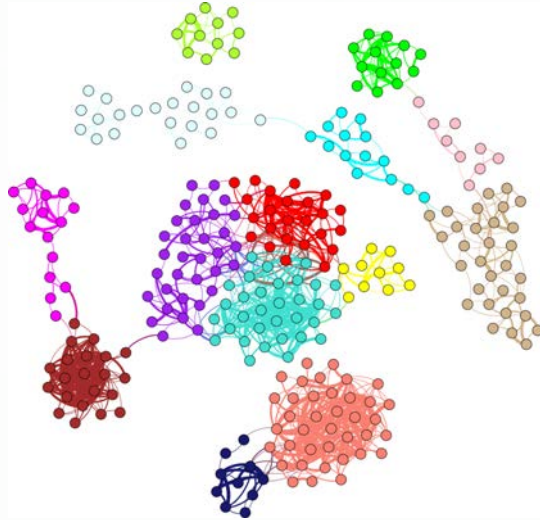
Warming



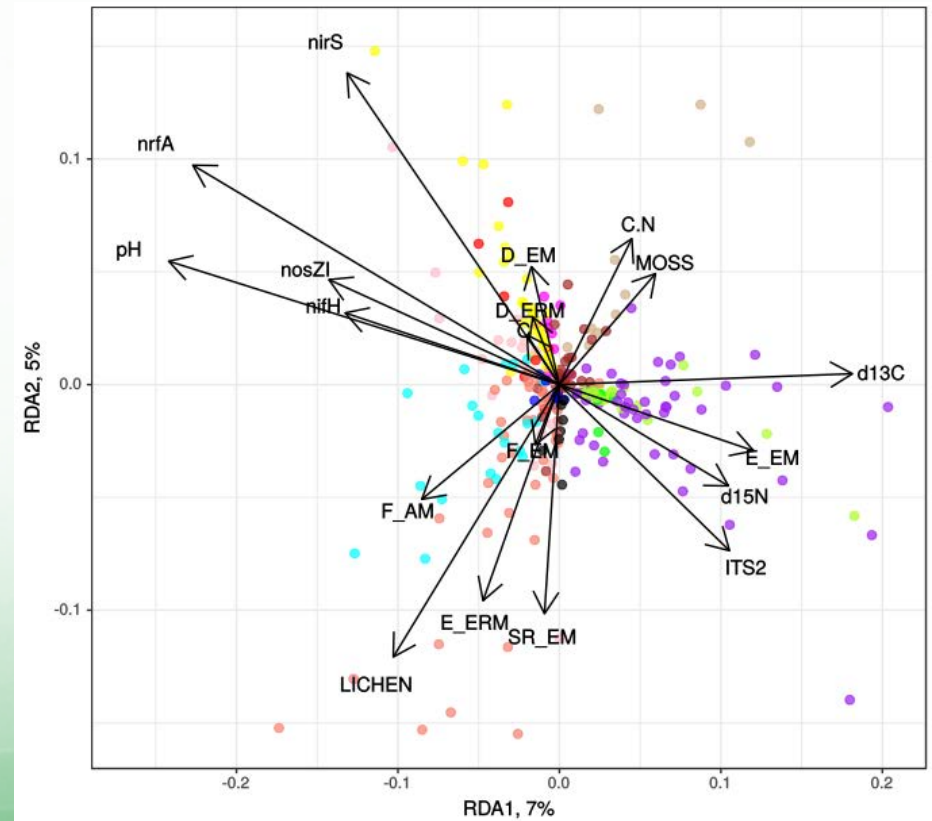
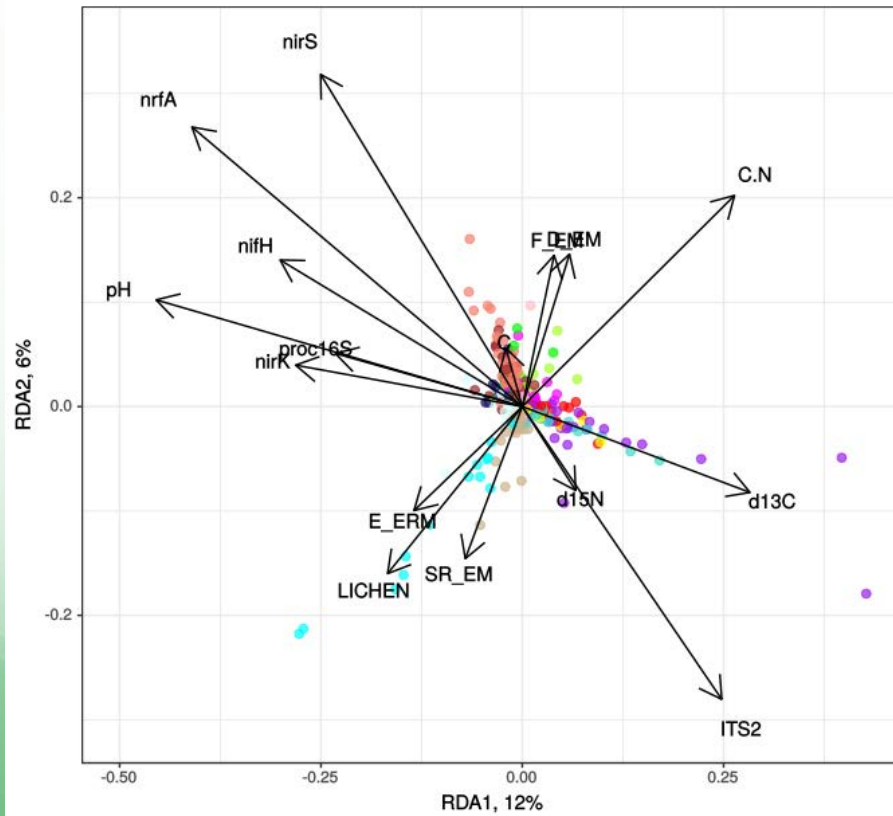
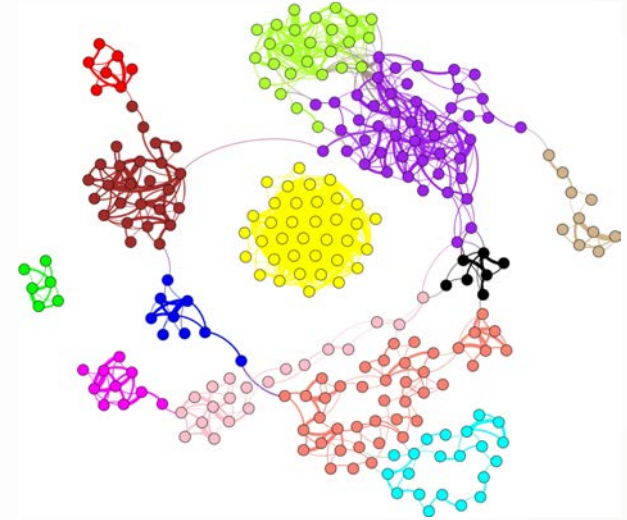
→ Increase of negative links is an indication of perturbation

Fungal networks

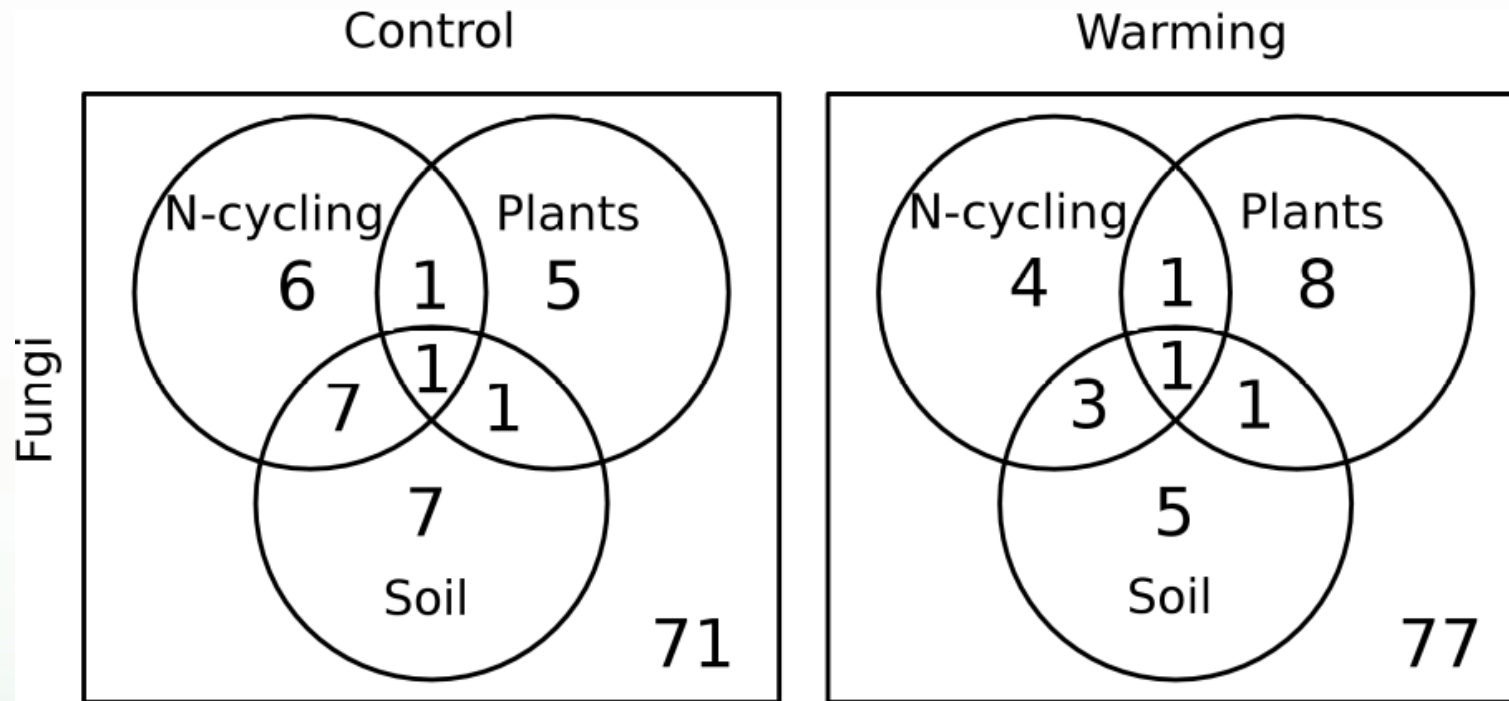
Control



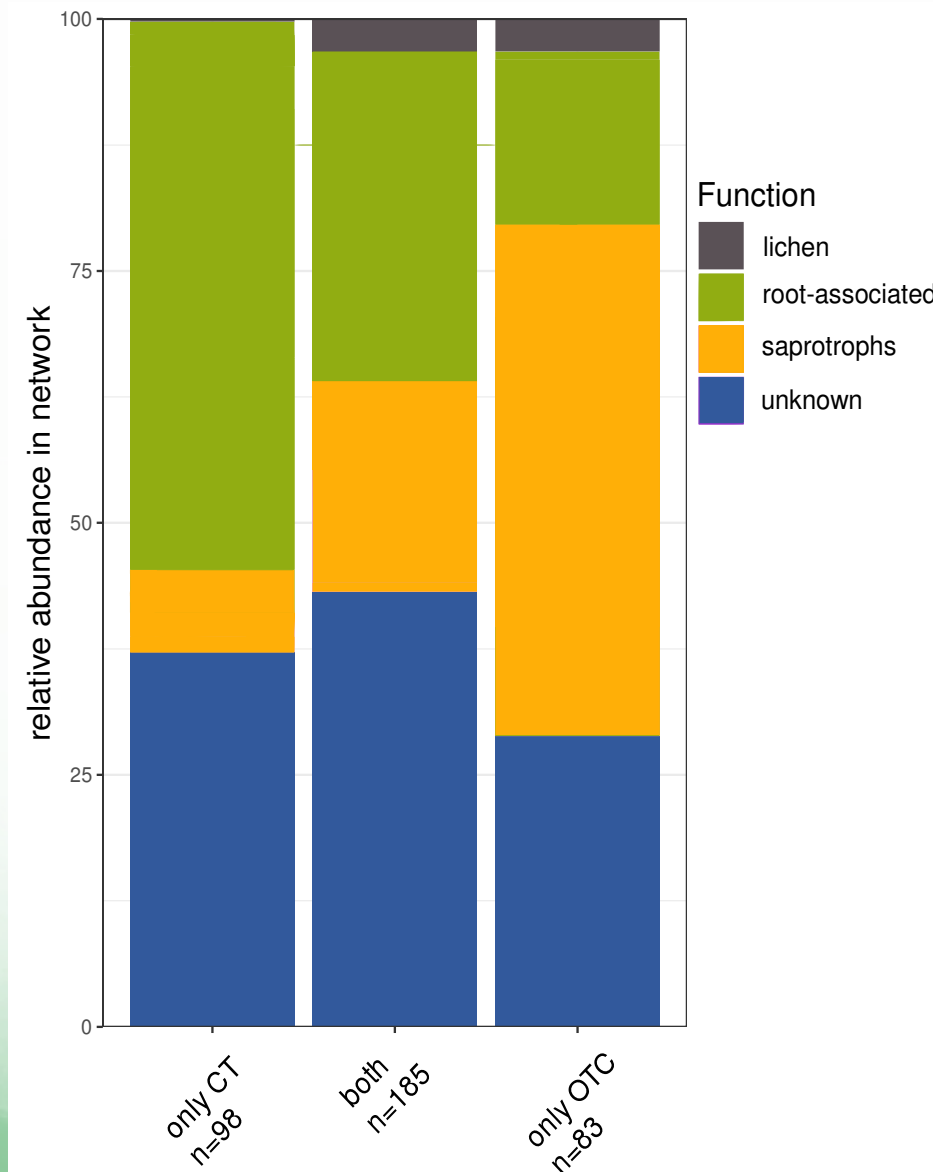
Warming



- Variance partitioning (%) :



- Are those differences reflected in the functional diversity?



- Stability of the prokaryotic network in response to long-term warming
- Sensitivity of the fungal network to long-term warming, driven by changes in the aboveground vegetation
- Potential impacts on the N and C balances

Thank you for your attention !