

Quantifying the diet of the freshwater pearl mussel using stable isotopes ($\delta^{13}C$, $\delta^{15}N$)

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Feeding ecology

- Classified as filter feeder
- Prefers organic particles < 30µm
- Diet composed of algae
- Detrital sources from terrestrial wetlands
- Paddle feeding?
- Most information from captive-held individuals
- Field observation rare



Aims

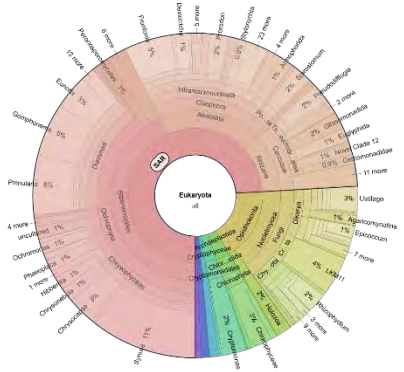
- Quantify resource use of two field populations
- Assess sources of variation determining diets
- Match of gut content with stable isotope analysis
- Preferential assimilation of autochthonous resources

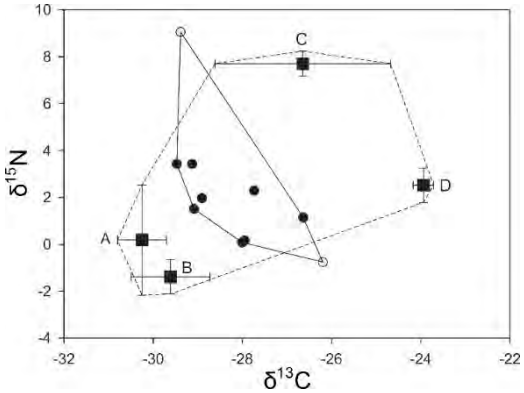


Methods to determine resource use

- Gut content analysis
  - microscopy
  - metabarcoding
- Stabile isotopes
- *Literature or data bases*

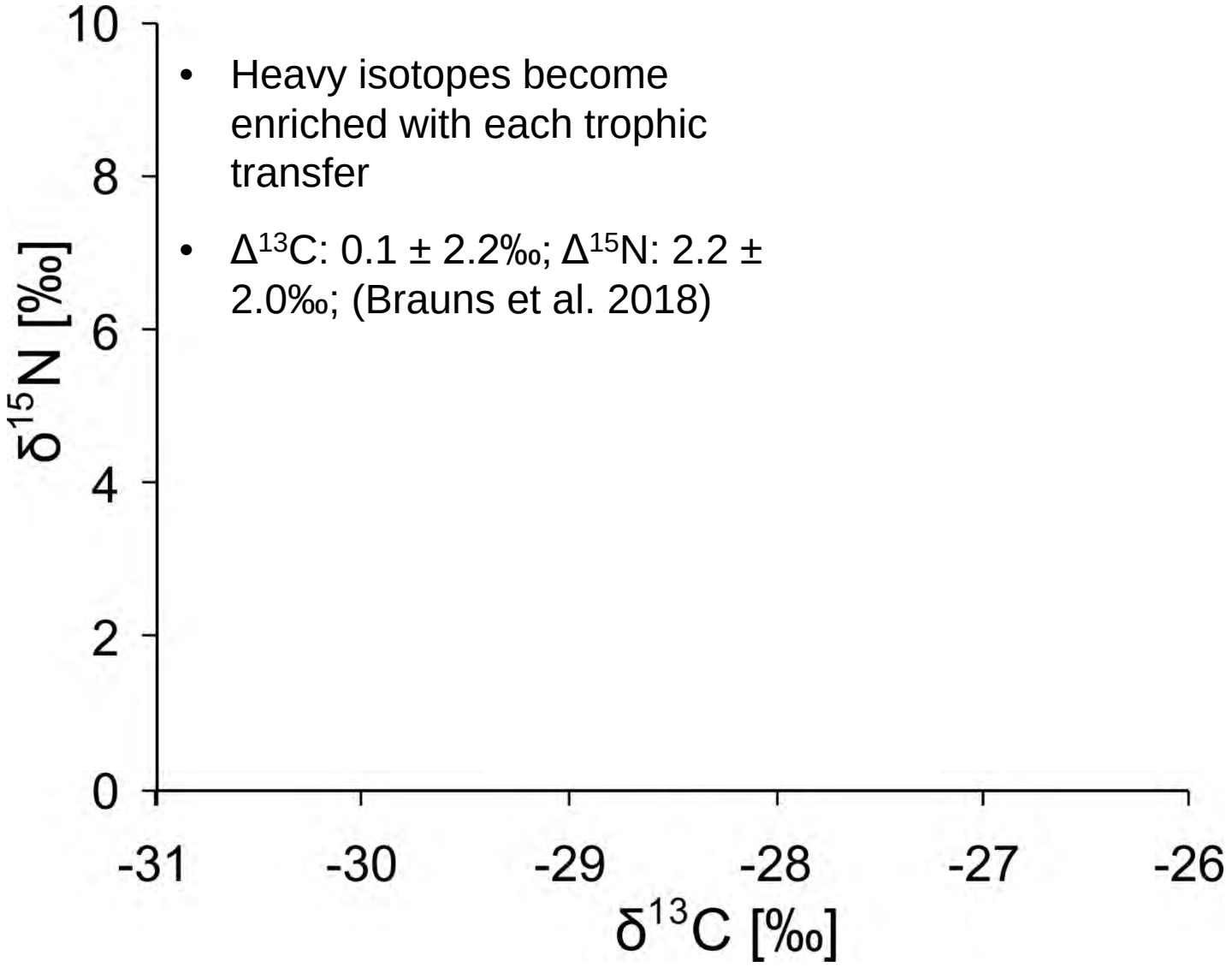




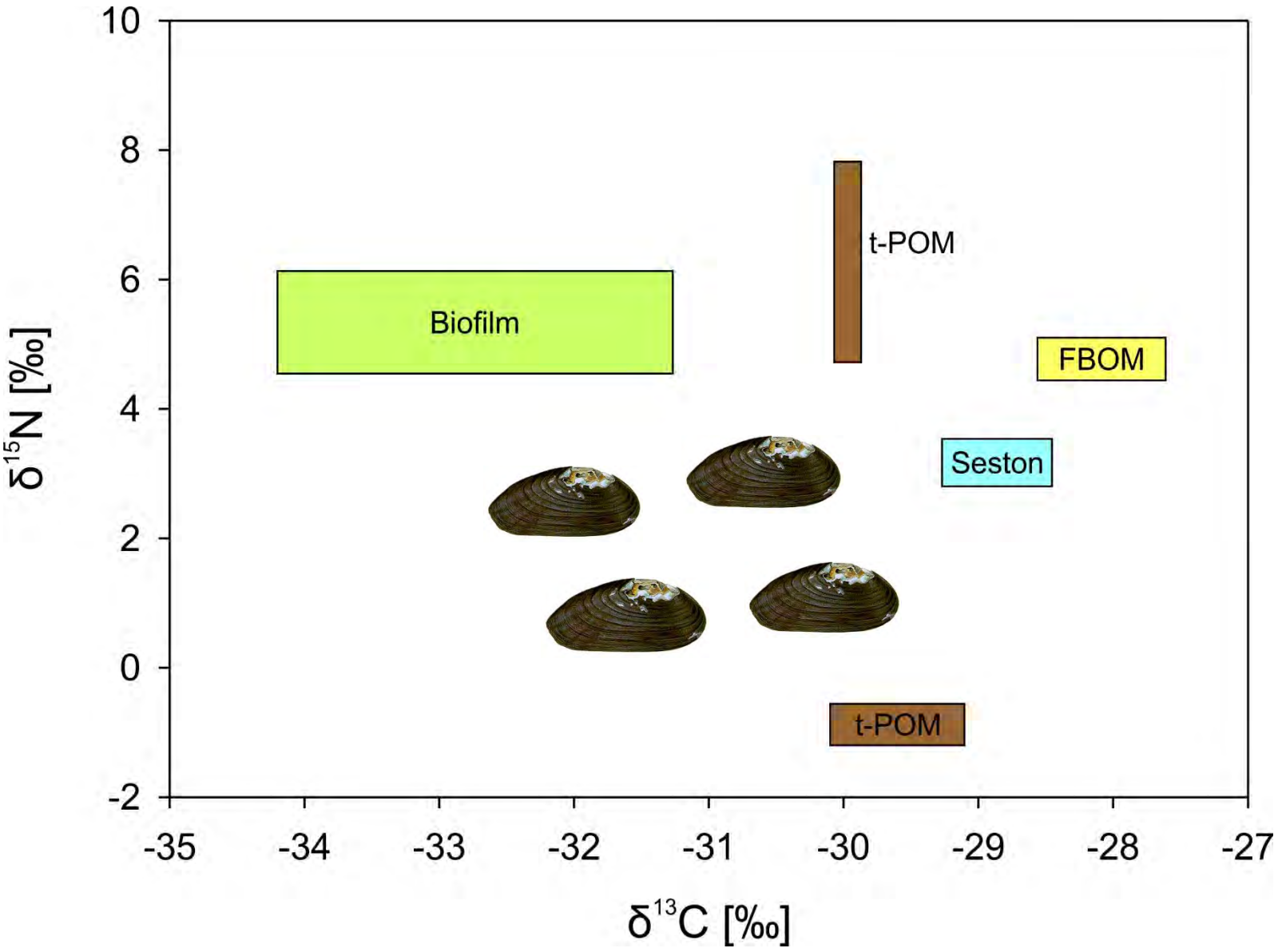


Stable isotopes as dietary tracers

- Heavy isotopes become enriched with each trophic transfer
- $\Delta^{13}C$: 0.1 ± 2.2‰; $\Delta^{15}N$: 2.2 ± 2.0‰; (Brauns et al. 2018)

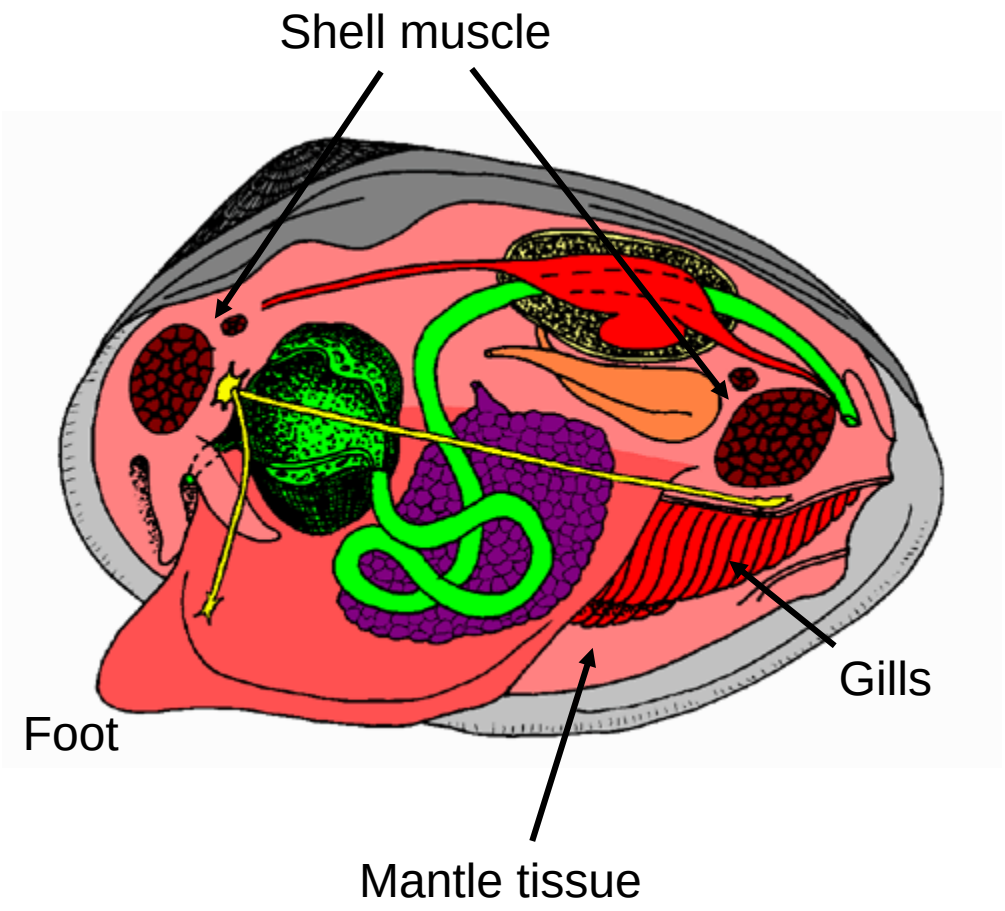


Stable isotopes as dietary tracers



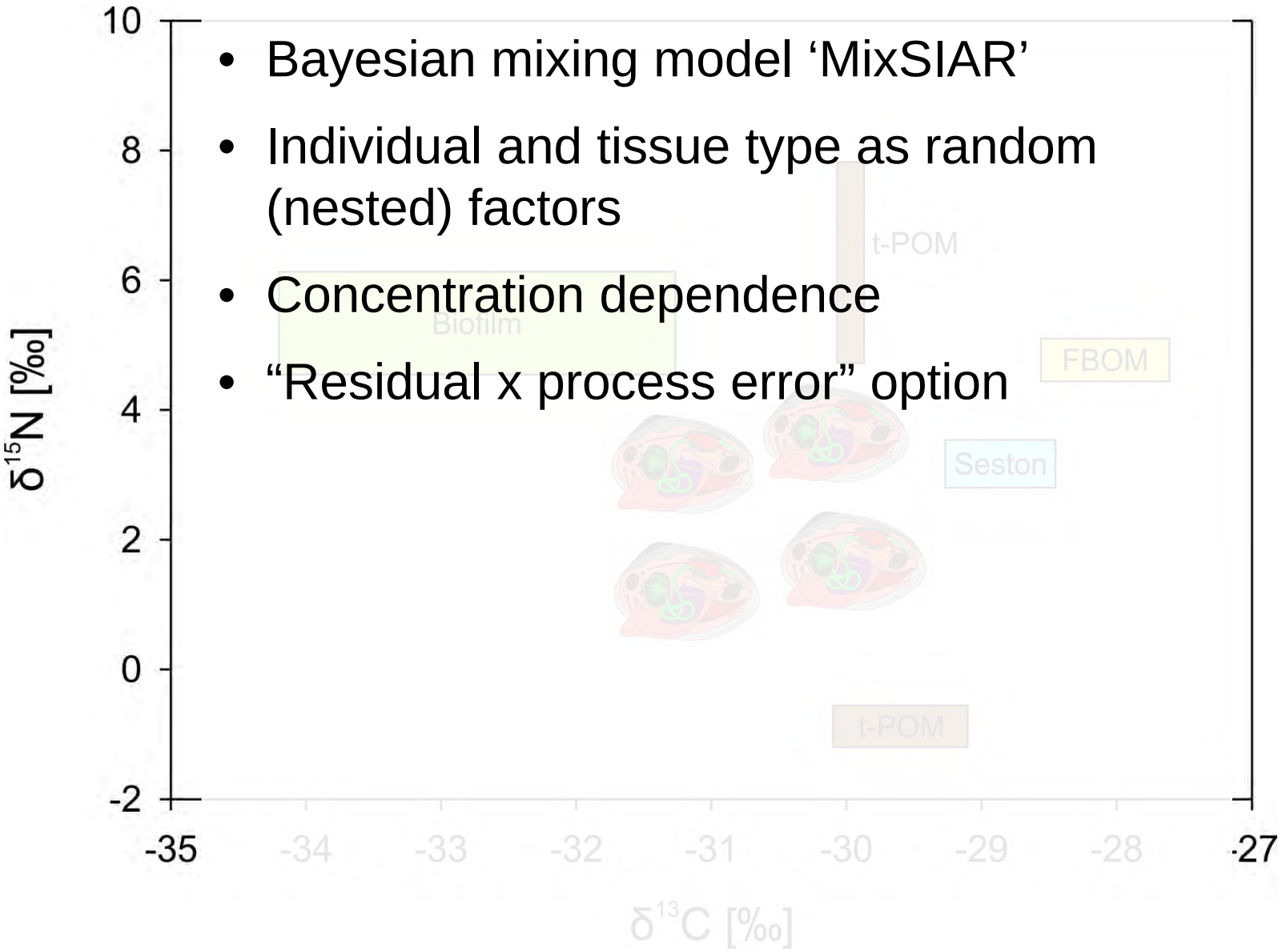
Stable isotopes as dietary tracers

- Tissues differ in physiological activity and biochemical composition
- Activity determines degree of diet-tissue isotopic similarity
- Tissue composition drives where dietary constituents are allocated



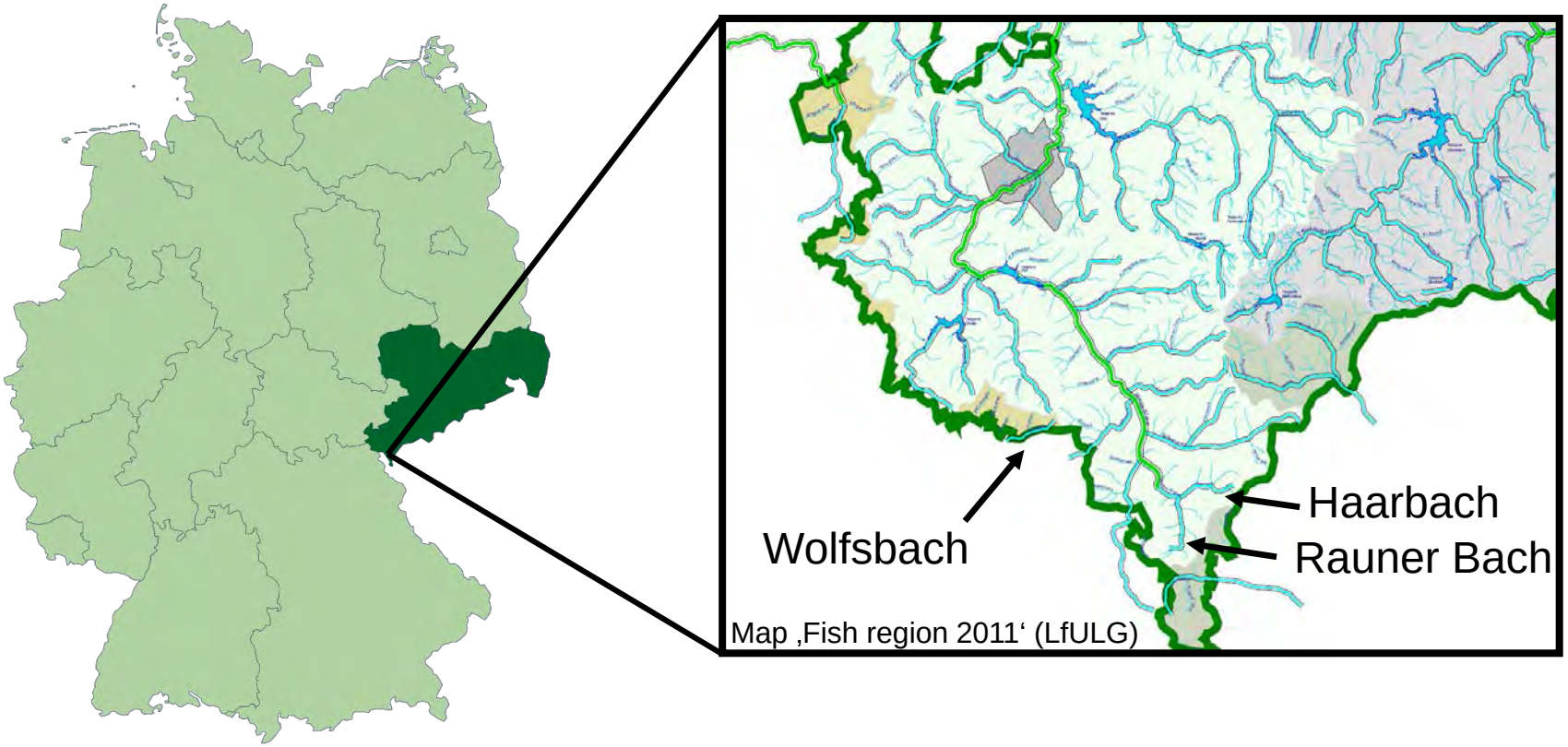
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Stable isotopes as dietary tracers



- Bayesian mixing model ‘MixSIAR’
- Individual and tissue type as random (nested) factors
- Concentration dependence
- “Residual x process error” option

Study area



Sampling

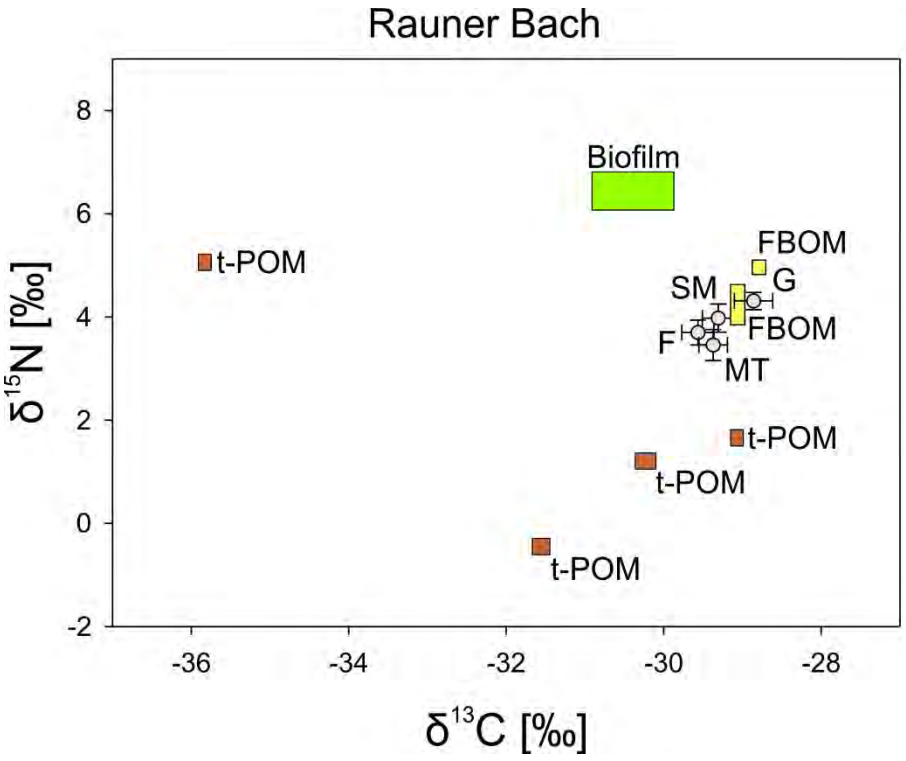
- PM exposed 5 months prior to sampling (4 ind./stream)
- Sampling of PM and potential resources November 2017
- Biofilm, BOM (autochthonous), leaves, herbaceous vegetation, detritus (allochthonous)
- Separation of OM into a < 30µm fraction (Geist et al. 2005)
- Separated into food, shell muscle, gill, mantle
- Metabarcoding (18S rRNA) of gut content from 1 ind. from Haarbach

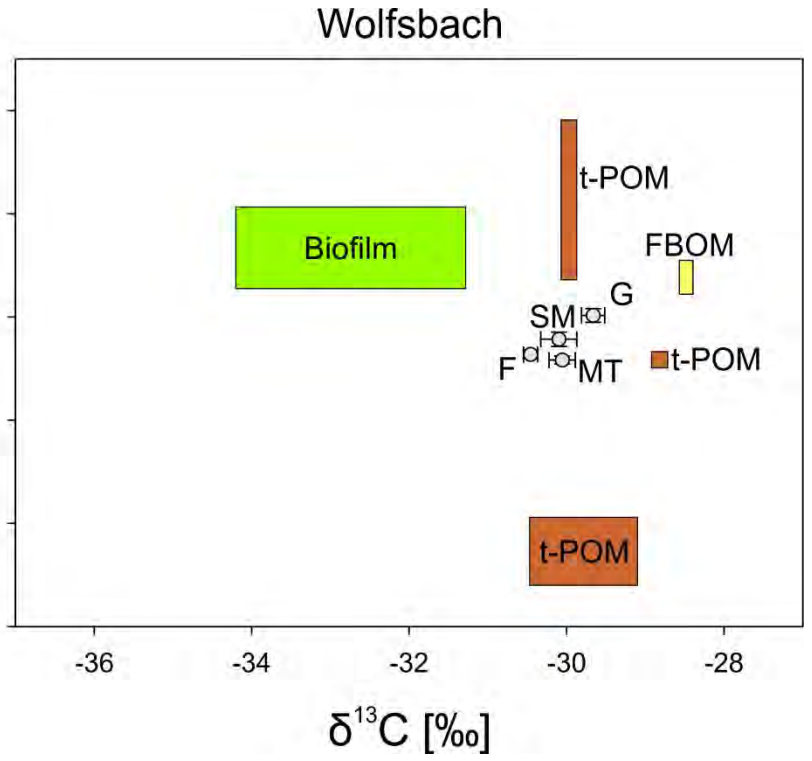




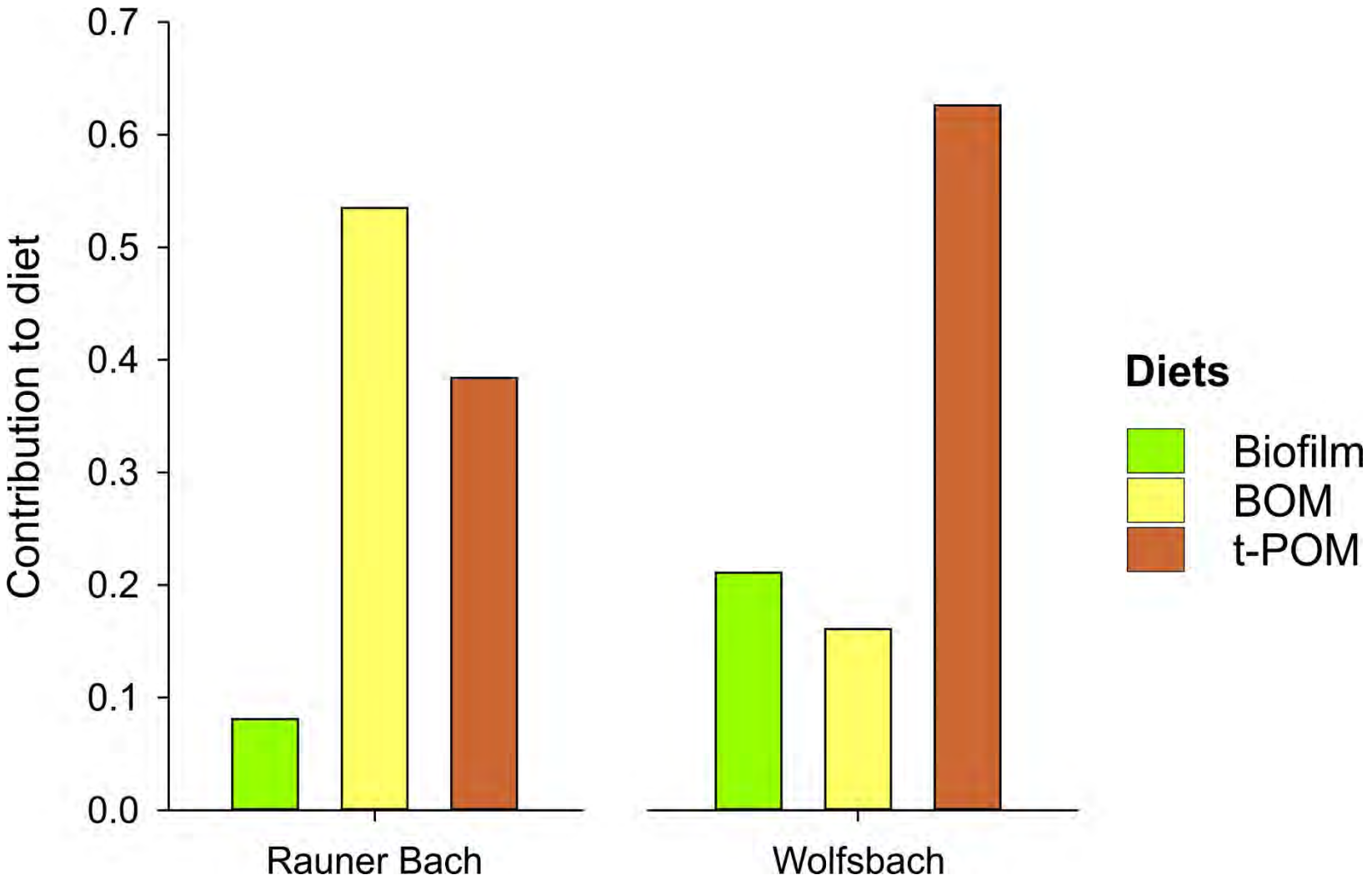


Stable isotope composition

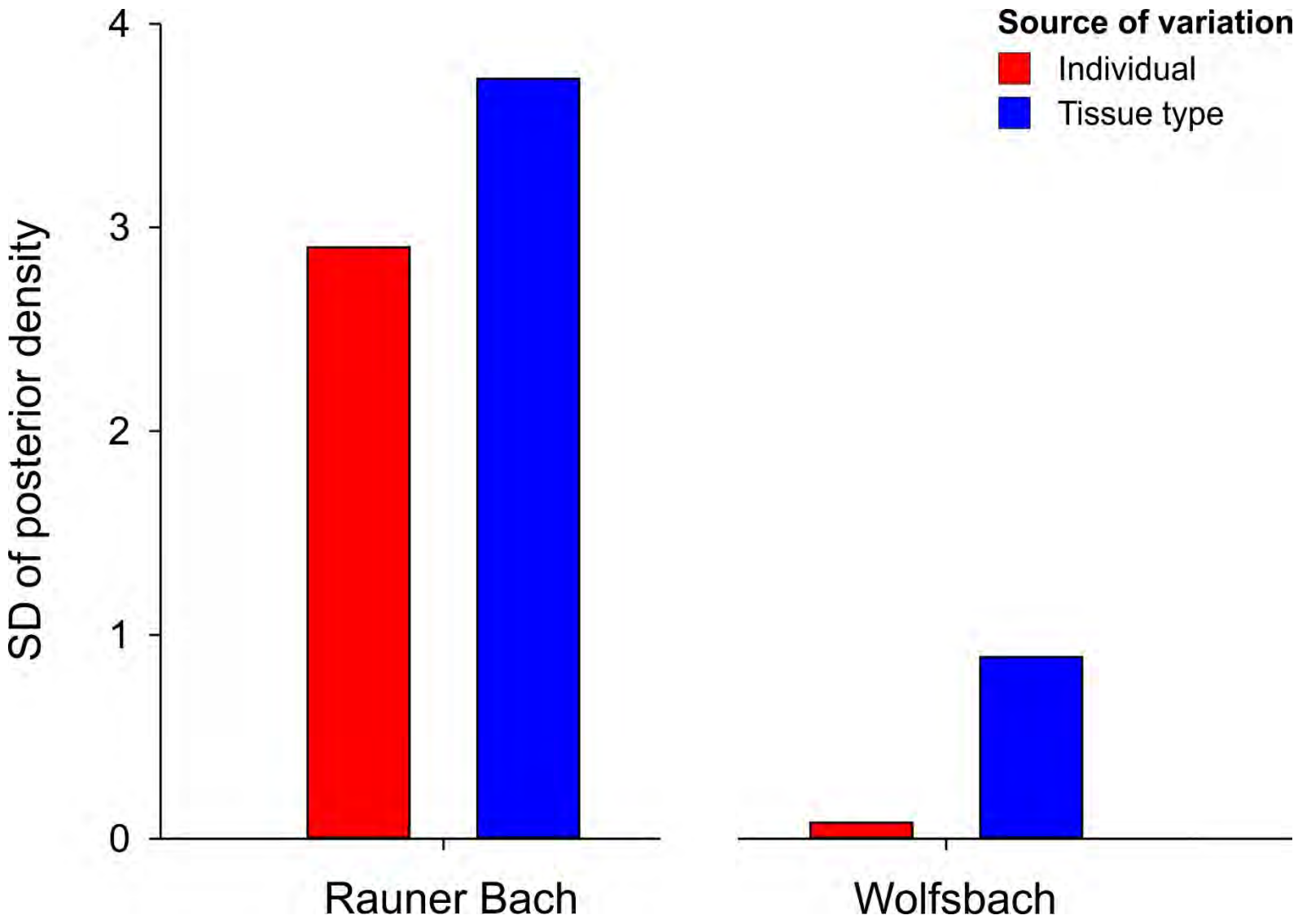




Contribution to pearl mussels diet

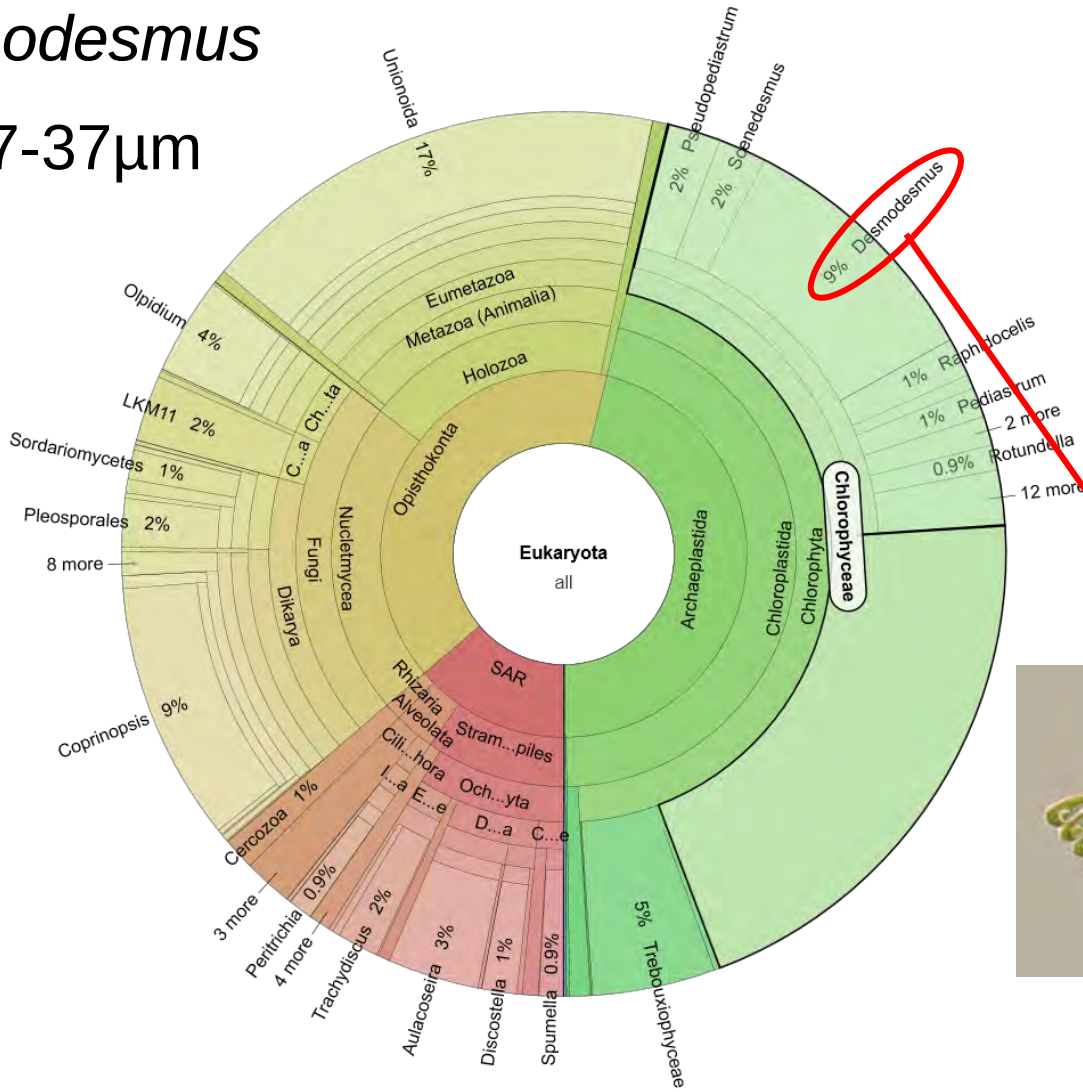


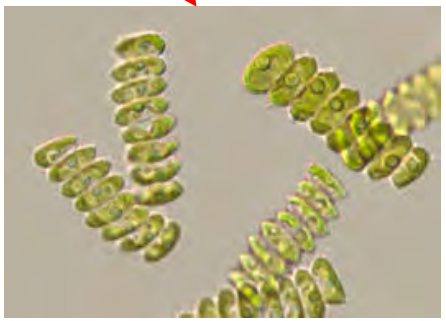
Drivers of assimilated diet



Metabarcoding of gut content

- 40% green algae (Chlorophyceae)
- 9% *Desmodesmus*
- Cell size 7-37µm

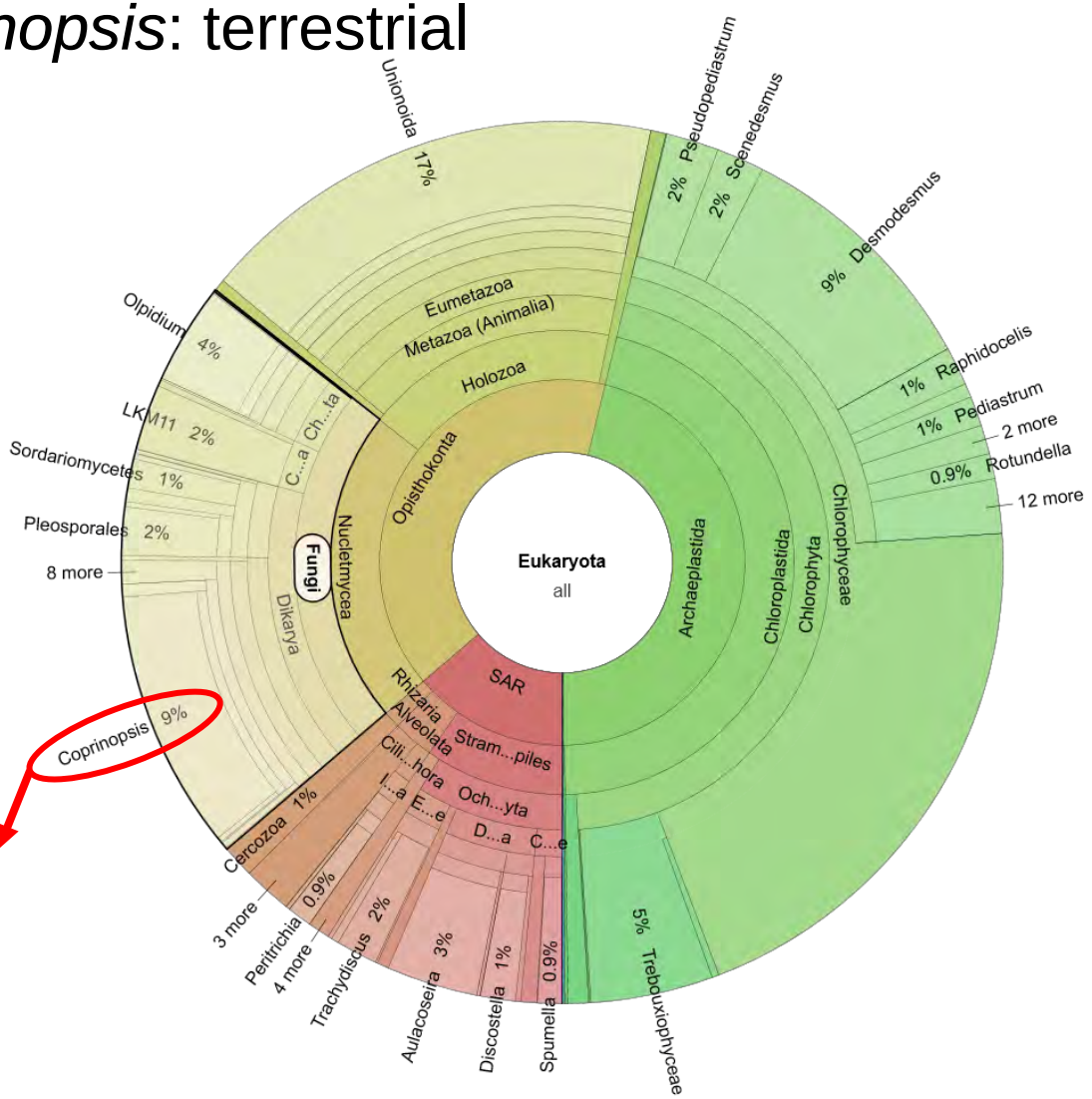


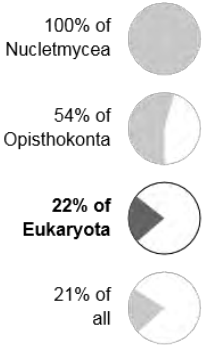


Metabarcoding of gut content

- 22% fungi
- 9% *Coprinopsis*: terrestrial







Discussion

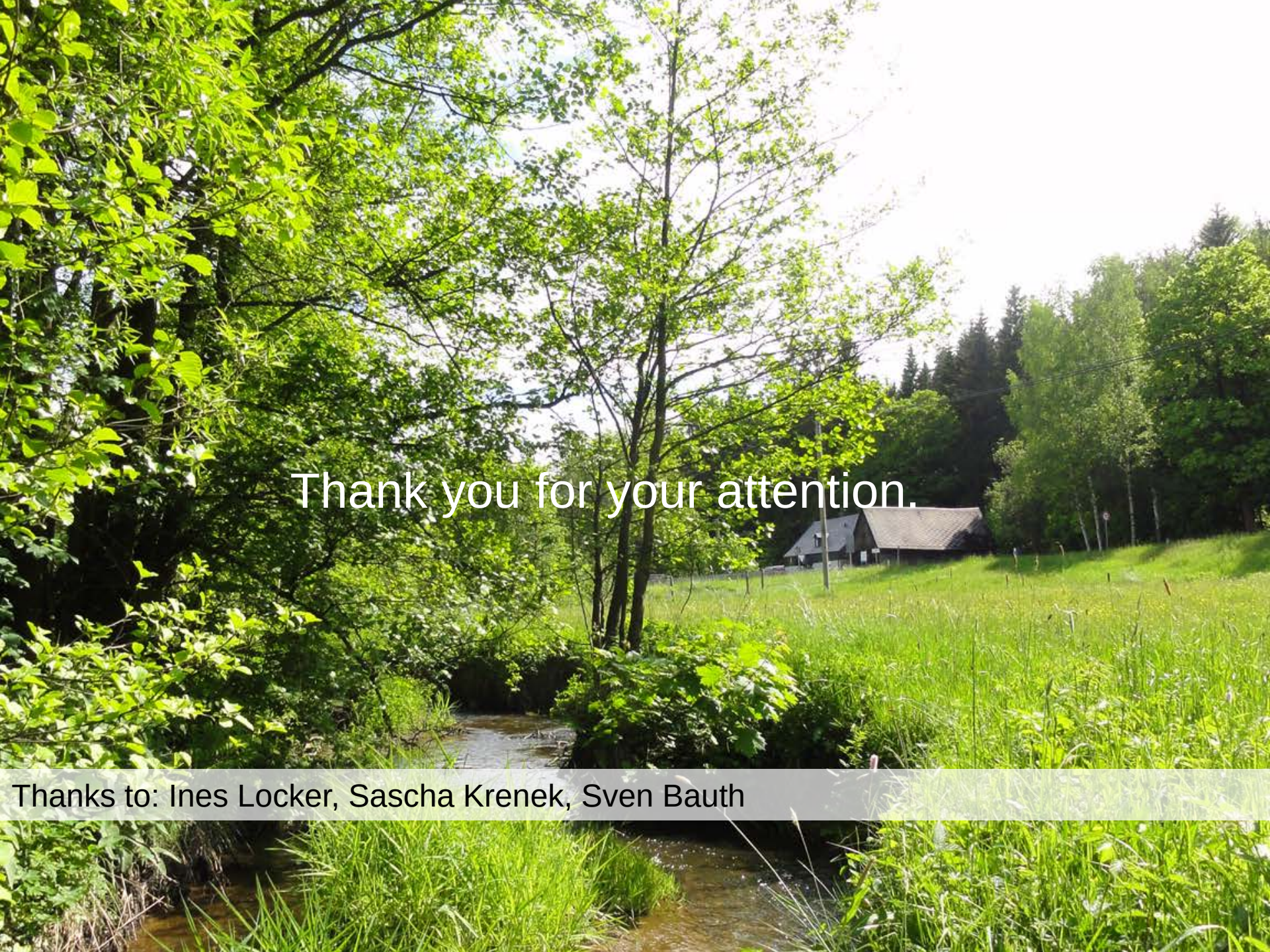
- Low contribution of autochthonous resources → paddle feeding?
- High contribution of t-POM → aquatic terrestrial coupling
- Individual variability rather low
- Importance of tissue type suggests specific discrimination factors
- BUT mismatch between gut content and SIA



Next steps

- Controlled feeding experiments for tissue-specific discrimination factors
- Other tracers such as Ca, Mg
- Relationship between gut content and assimilated diets
- Quantify effects of season, age





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