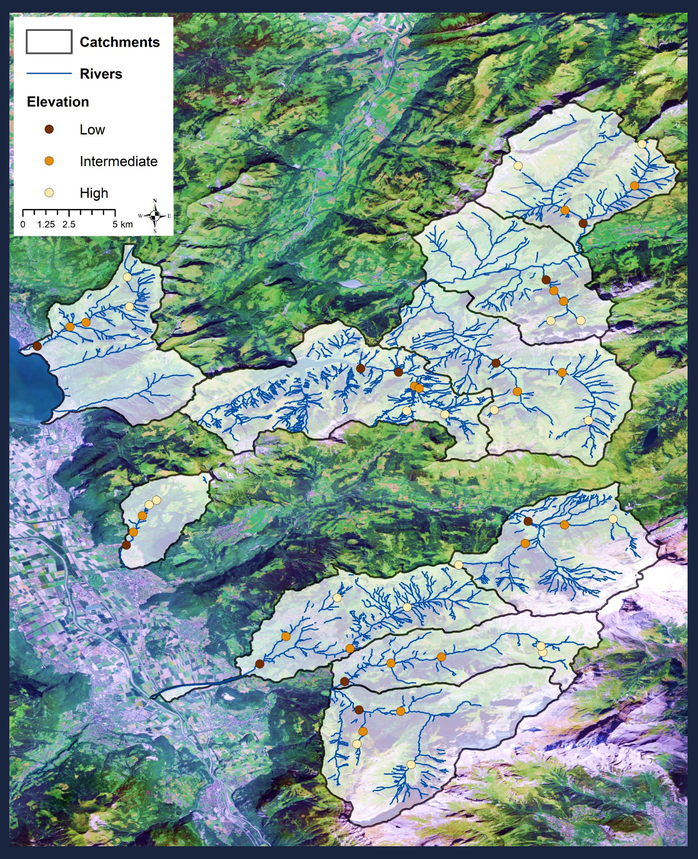


Catchment-based sampling of river eDNA integrates terrestrial and aquatic biodiversity of alpine landscapes

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Background

- environmental DNA (**eDNA**) based large-scale biomonitoring approaches are relatively **fast** and **cheap**[1]
- eDNA shows **rivers integrate terrestrial and aquatic diversity** at the **catchment scale**[2,3]
- **how many filter replicates are needed** to capture regional biodiversity?
- **how does biological information travel** through ecosystems?

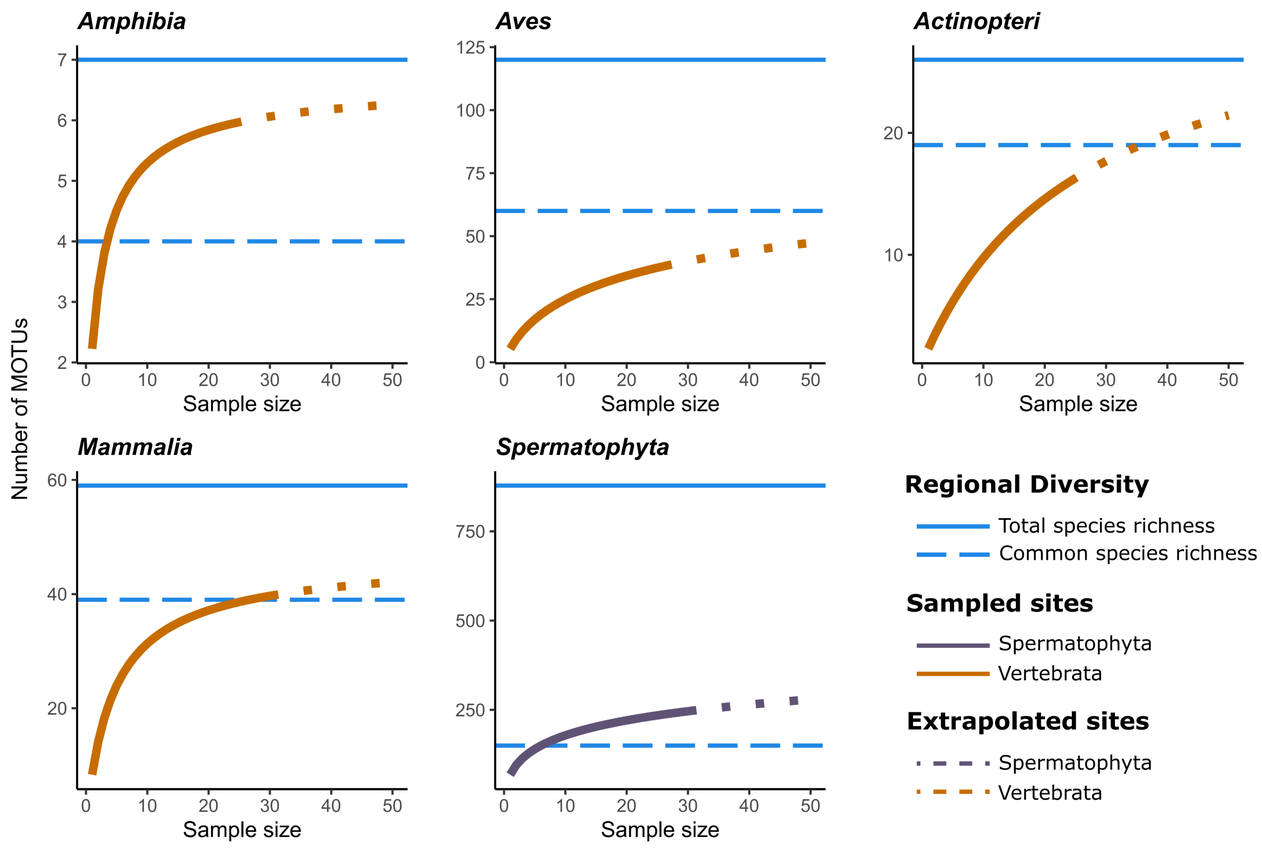
Methods

- **1 800 L of river water** filtered across 10 catchments **over 5 days** in Vaud, 2020 over relative elevation gradient
- broad **vertebrate and spermatophyte** primers
- **species accumulation curves** across filters for all and only common species
- **distance-based redundancy analysis** to compare spermatophyte and vertebrate assemblages

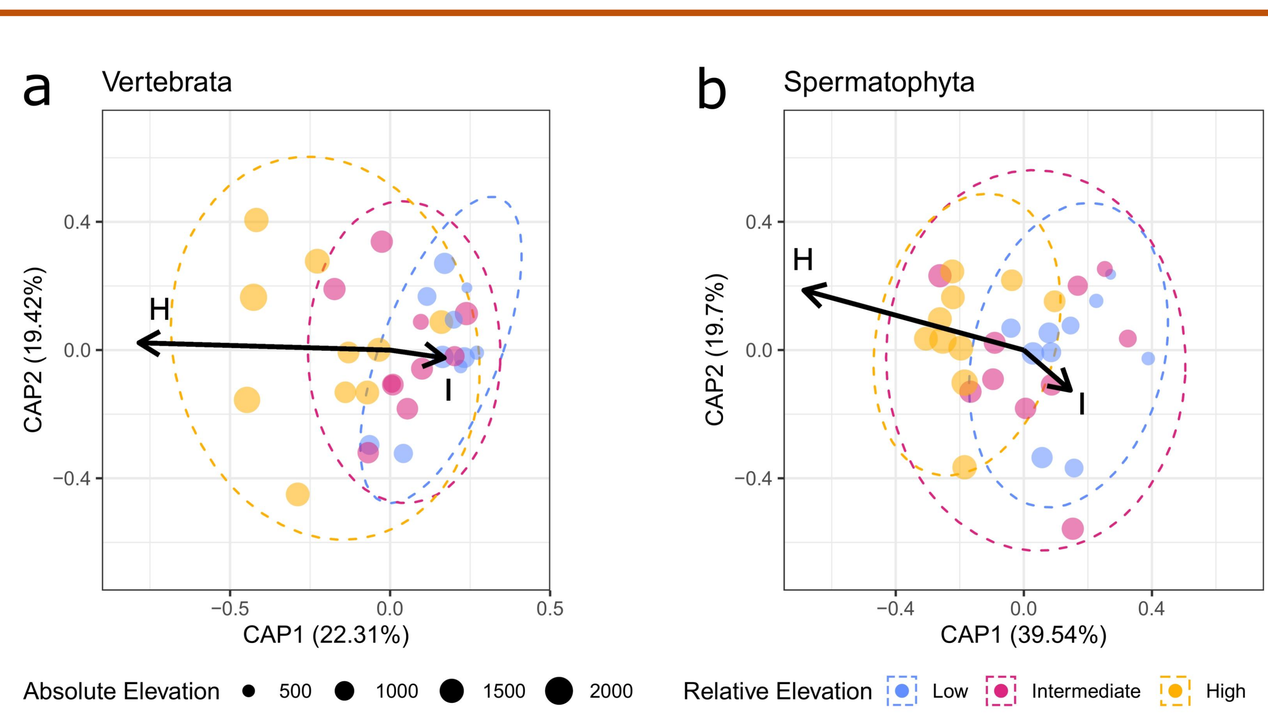
Outlook

- historical records covered by 5 day sampling for some groups but we miss rare species
- **water at low elevation sites does not aggregate information on high elevation species**
- eDNA approach shows promise in **large-scale biodiversity mapping of multiple taxonomic groups**

Results



Common **regional species richness** is captured within **30 filters** for amphibians, mammals and seed-bearing plants



Plant and vertebrate **composition explained by relative elevation and catchment identity**

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References

[1]Fediajevaite, J, Priestley, V, Arnold, R, Savolainen, V. Meta-analysis shows that environmental DNA outperforms traditional surveys, but warrants better reporting standards. *Ecol Evol*. 2021; 11: 4803– 4815. https://doi.org/10.1002/ece3.7382

[2]Altermatt, F., Little, C. J., Mächler, E., Wang, S., Zhang, X., & Blackman, R. C. (2020). Uncovering the complete biodiversity structure in spatial networks: the example of riverine systems. *Oikos*, *129*(5), 607–618. https://doi.org/10.1111/oik.06806

[3]Deiner, K., Fronhofer, E. A., Mächler, E., Walser, J. C., & Altermatt, F. (2016). Environmental DNA reveals that rivers are conveyer belts of biodiversity information. *Nature Communications*, *7*(1), 1–9. https://doi.org/10.1038/ncomms12544



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