Predicting the global response of the glacier-fed streams and their bacterial microbiome to climate change

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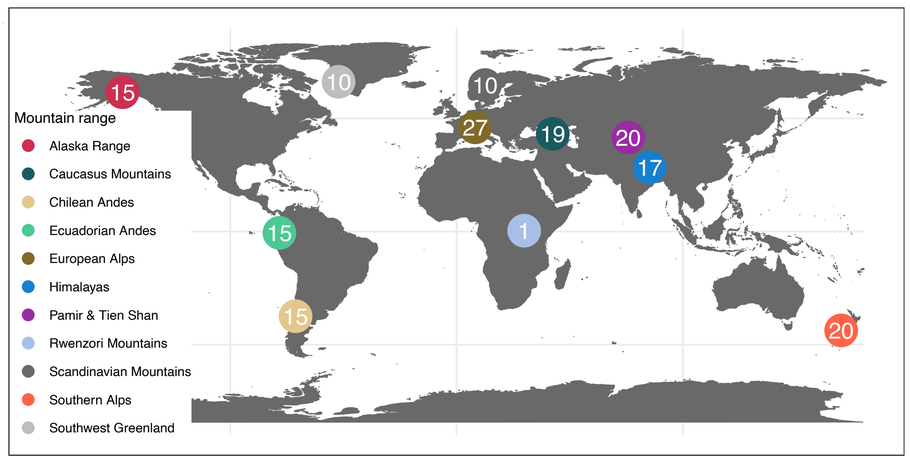
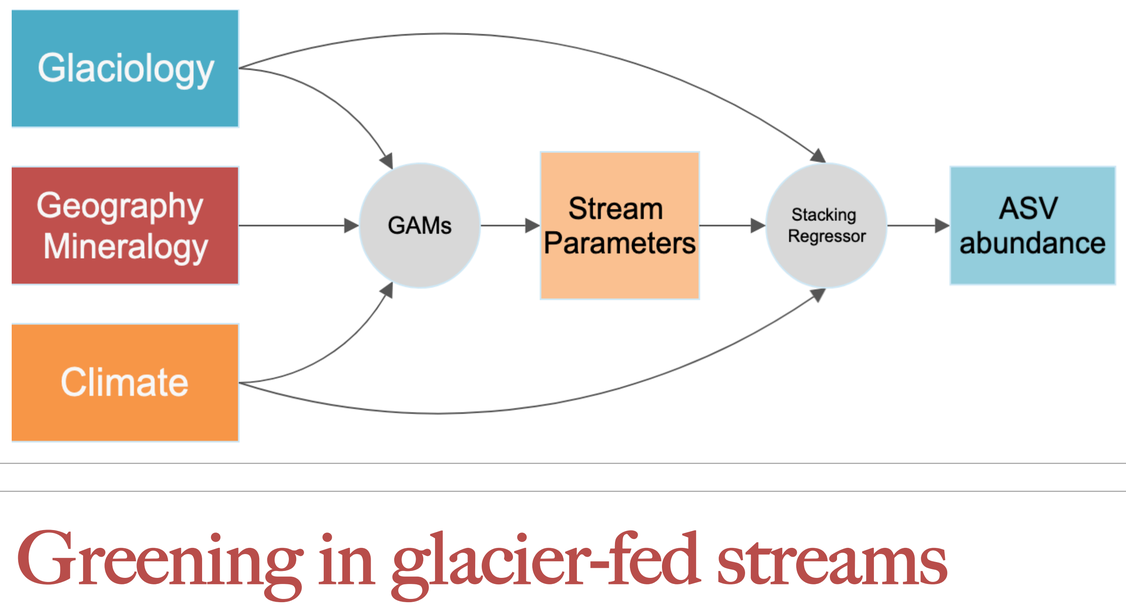
The vanishing glaciers project

Glaciers are melting worldwide owing to climate change. What is the impact on glacier-fed streams biofilms?



- **170 Glacier-fed streams** distributed **globally** (149 metagenomes)
- Metagenome-assembled genomes, **2333 bacterial strains**

Time-for-space substitution: predictions/projections of stream parameters and bacterial strains abundance onto future scenarios of climate change (2070-2100).



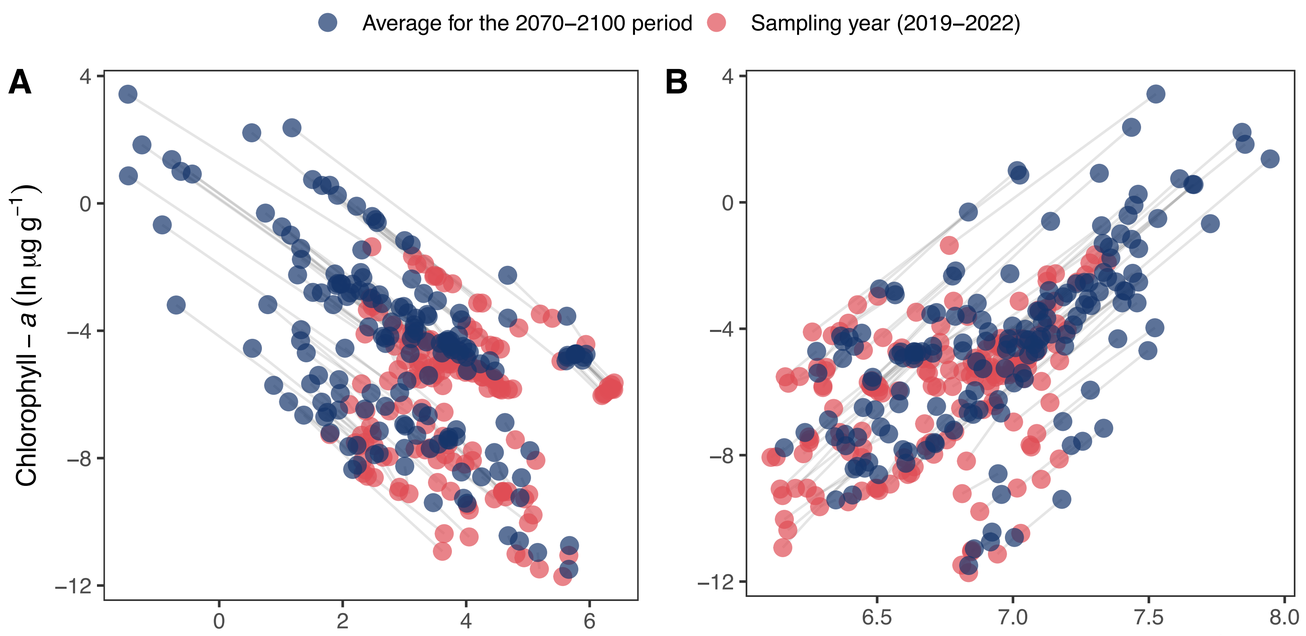
The modelling approach

- **Generalised additive models** (GAMs), leave-one-out **cross-validation**, for the prediction of stream **physico-chemical parameters changes in the future**.
- **Bacterial strains abundance models** based on all parameters. Approach includes a **variable selection** procedure, **cross-validation**, and **stacked GAMs**.

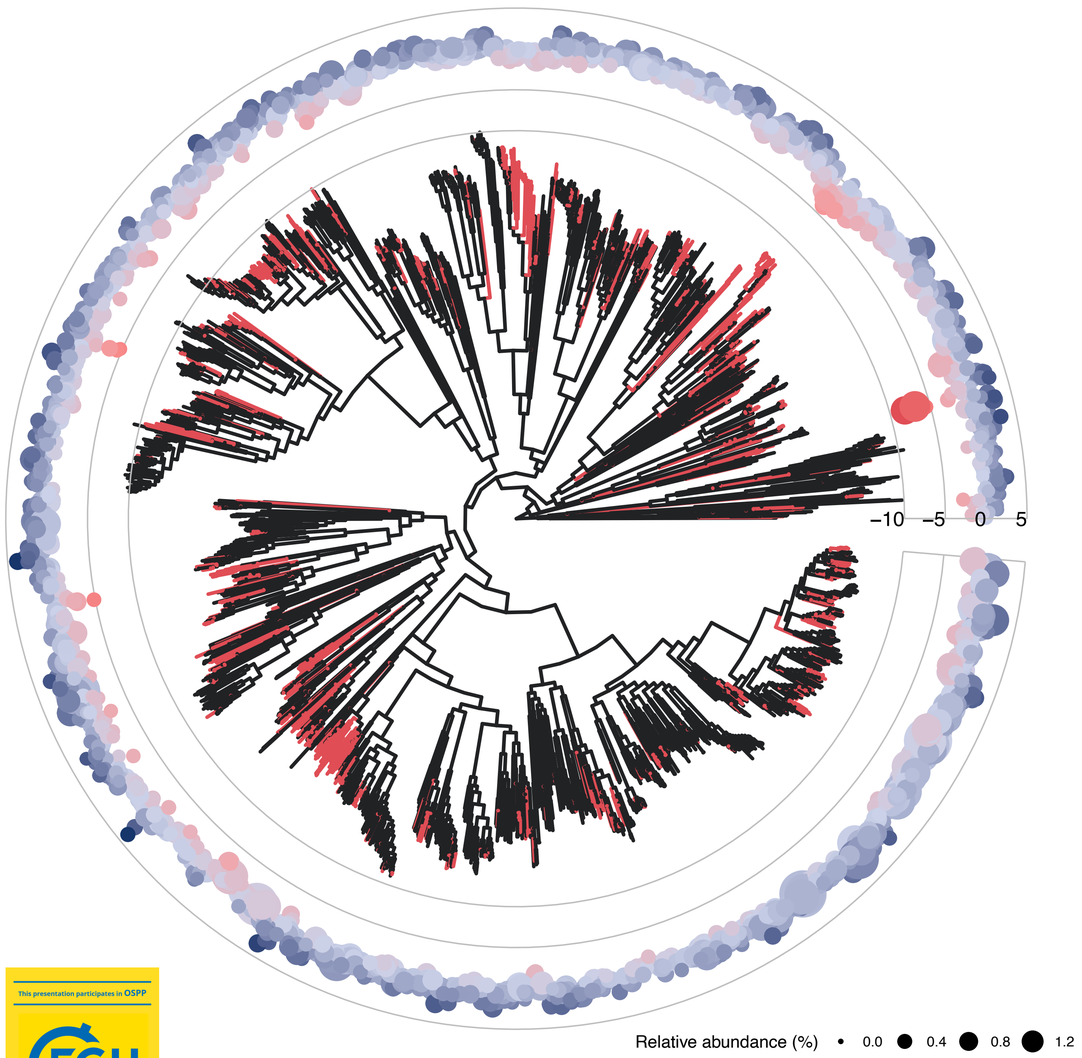
Greening in glacier-fed streams

- Increased water temperature and reduced turbidity associated with increases in chlorophyll-a (**A**, *+2.294 median relative change for RCP 4.5*) and bacterial abundance (**B**, *+0.467 median relative change for RCP 4.5*)
- Significant changes in **pH** (-), **conductivity** (+), **dissolved inorganic nitrogen** (-), and **soluble reactive phosphate** (*+/- depending on scenarios*)

We forecast larger biofilms (more chlorophyll-a and bacteria) in the future owing to climate change.



Phylogeny-associated ecological shifts



- Increase in abundance of most bacterial strains under future scenarios of climate change
  - *54.6% increasing, 29.6% decreasing*
- Changes in abundance highly correlated with phylogeny
  - Several large and deep-branching monophyletic clades decreasing in abundance consistently (**Tree, in red**)
- **Main drivers of bacterial strains' abundance** are: bioclimatic parameters, pH, and dissolved inorganic nitrogen
  - Also associated with phylogeny
- **Ecological shifts with potential effects on ecosystem functioning**:
  - Clades decreasing in abundance harbour alternative genes involved in glycolysis/gluconeogenesis, pyruvate and butanoate metabolism, and carbon fixation.

Increase in abundance of most strains is consistent with the predicted increase in bacterial abundance. Nevertheless, phylogenetic signal may indicate potential biodiversity losses.