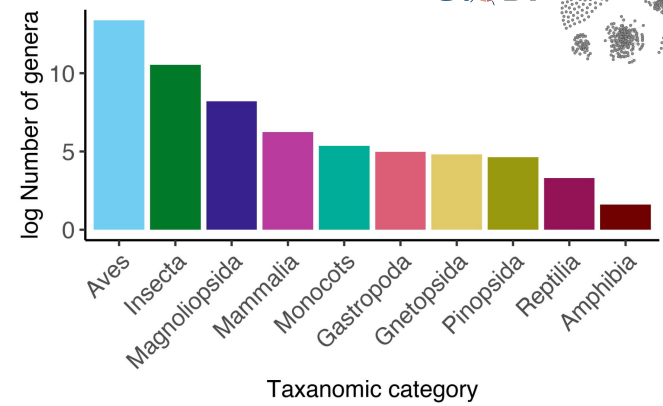
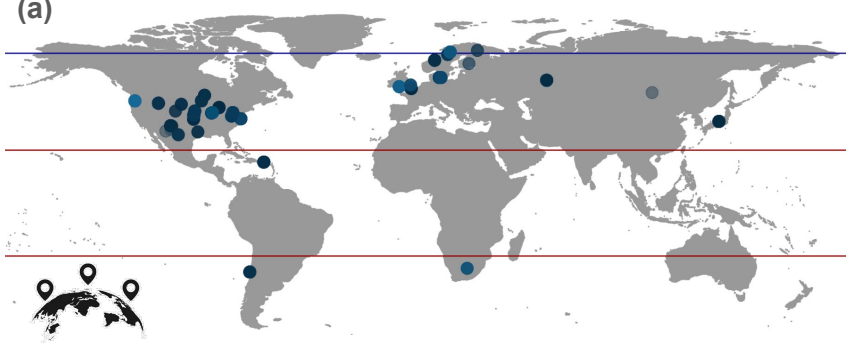


1. Obtain and clean BioTIME data

(b)



(a)



- I. Download BioTIME version 1.0
- II. Exclude biomass, marine, aquatic surveys
- III. Aggregate abundance to genus level per plot to ensure there is a record of observation in each year
- IV. Subset data to include only abundance time series that contain 10+ consecutive overlapping years
- V. For each genus, calculate the log proportional change in abundance for each time step to remove temporal autocorrelation
- VI. For each genus pair correlation, pull the absolute latitude of the study, information on disturbance during the time series, time series length from the BioTIME metadata
- VII. Use `rGlobi` to identify if there are known interactions between each genus pair and assign genus pairs to taxonomic categories with `taxize`, drop taxonomic categories with <5 observations

2. Calculate z-scores

- I. Calculate the Pearson correlation (r) between the log proportional abundance changes across the time series for each pair of genera (genus pair) observed at each plot within each study
- II. Filter unrealistic r values >+/-0.8 and highly uneven sample sizes > Δ1000 individuals or Δ30 species
- III. Transform Pearson correlations into z-scores: $z = \frac{1}{2} \log(1+r)/(1-r)$
- IV. Final N = 345860 genus pairs across time

3. Fit hierarchical regression

Are abundance changes between geographically proximal taxa correlated in long-term data? Is the strength of these relationships moderated by ecological and temporal factors?

- I. Centre and scale continuous predictors
- II. Fit models to estimate how latitude, taxonomic identity, disturbance, and time series length moderate the magnitude of genus pair z-scores
- III. Incorporate group level (i.e. random) intercepts for study identity and taxonomic category

