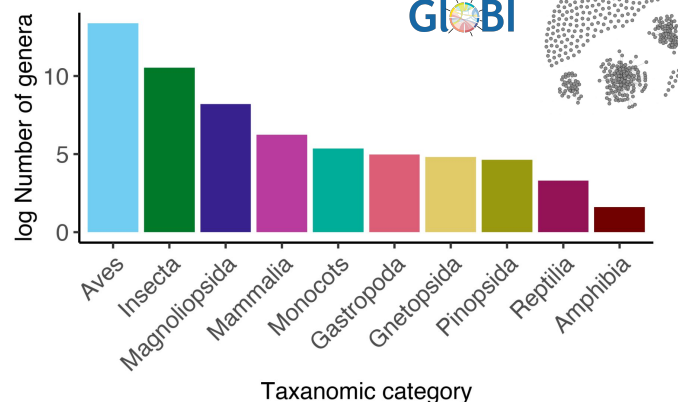
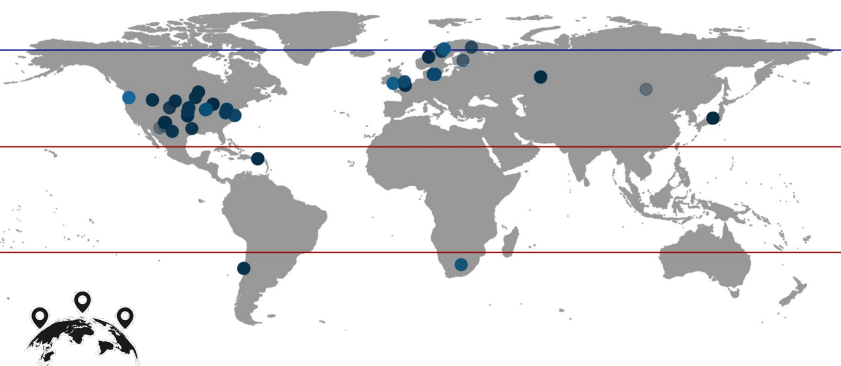
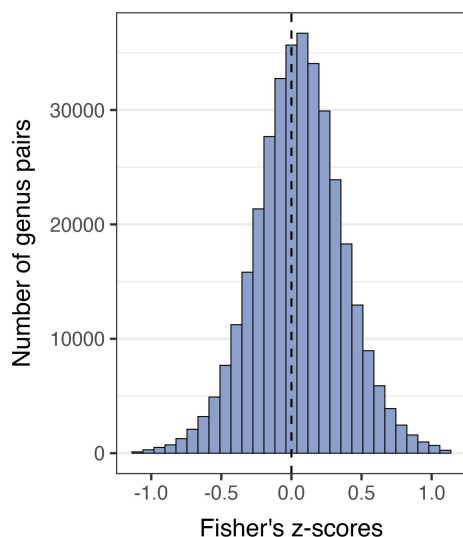


1. Obtain and clean BioTIME data



- I. Download BioTIME version 1.0
- II. Exclude biomass, marine, aquatic surveys
- III. Aggregate abundance to genus level 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. Subset data to relatively strong correlations ($-0.8 < r < 0.8$) and to time series where there are less than $\Delta 1000$ individuals and $\Delta 30$ species between genera pairs
- III. Transform pearson correlations into z-scores
$$z = \frac{1}{2} \log \frac{1+r}{1-r}$$
- IV. Calculate the standard error for each z-score based on the cumulative number of species recorded across both time series
- V. Final $N = 345860$ genus pairs across time

3. Run meta-regression

Can long-term global abundance time-series data be used to identify correlated abundance changes between geographically proximal organisms (aggregated at the genus level)? 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 and the standard error of the sum of genera across which those z-scores are calculated