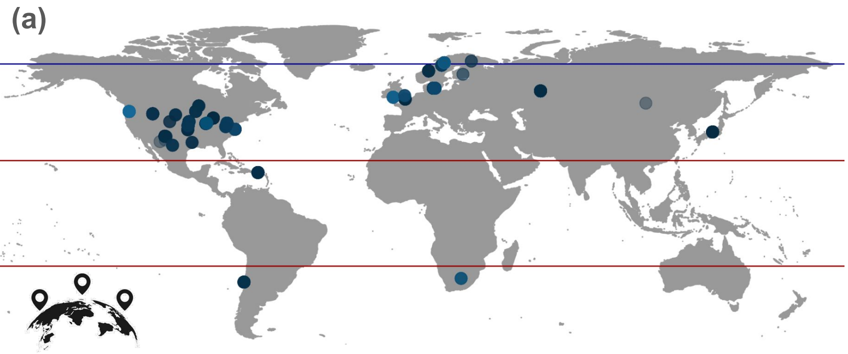
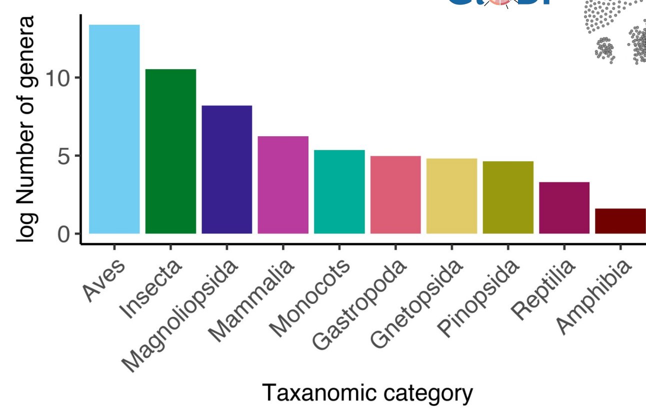
1. Obtain and clean BioTIME data

(a)



(b)

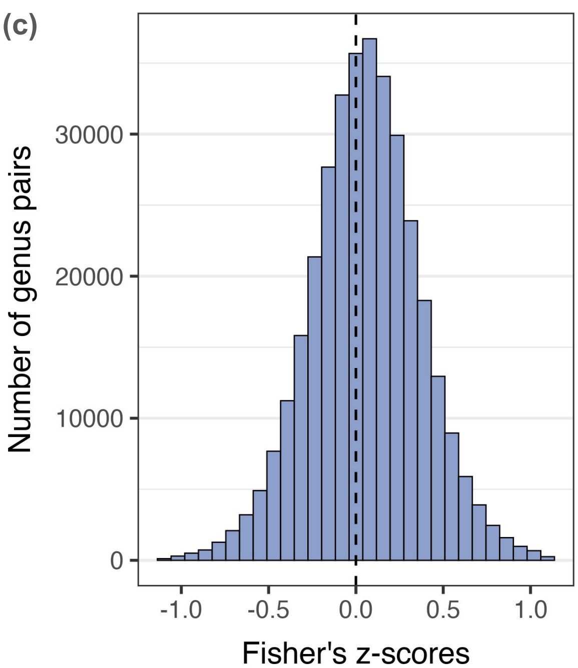


I. Download BioTIME version 1.0
II. Exclude biomass, marine, aquatic surveys
III. Aggregate abundance to genus level per plot to ensure there is a record of observation in each year
IV. Subset data to include only abundance time series that contain 10+ consecutive overlapping years
V. For each genus, 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: $z = ½ \log(1+r)/(1-r)$
IV. Final N = 345860 genus pairs across time

(c)



3. Run 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