The Mode of Toxicant Sensitivity Evolution

What the past can tell us about present day species' responses to toxicants

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Background

Chemical toxicants introducted to aquatic environments have caused substantial biodiversity loss and the degredation of entire ecosystems. Ecotoxicology seeks to identify "acceptable" levels of toxicants in environments, derived from standardised testing single species responses to toxicants. To do this, individual species' responses are combined into mulit-species meta-analytic models (Fig. 1) based on assumed cumulative distributions. However, the assumed distributions of species' responses in these models lacks conceptual motivation, and often real data fits assumptions poorly, directly affecting policy decisions. To address such issues, we first need to understand what has shaped variation in species responses. By treating ecotoxicology data as species level trait data, and combining it with time-calibrated phylogenies, we can fit models of trait evolution to better understand the processes that have given rise to the patterns we see today.

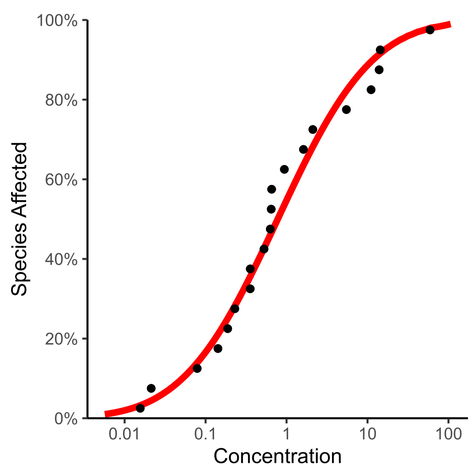

Figure 1: Example of a species sensitivity distribution.

Methods

A

B

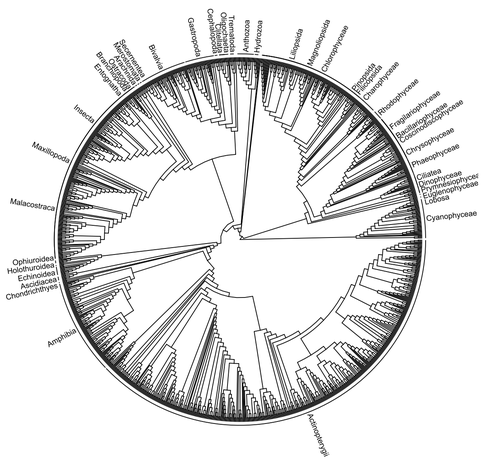

Figure 2: A) Species level response data from US EPA ECOTOX Knowledgebase, B) Time-calibrated phylogeny ($N_{\text{taxa}} = 1278$) from TimeTree5.

- Fit simple models of character evolution with `geiger`
- Explore heterogeneity in optimums across branches with `bayou`

Model parameter heterogeneity across clades

A

B

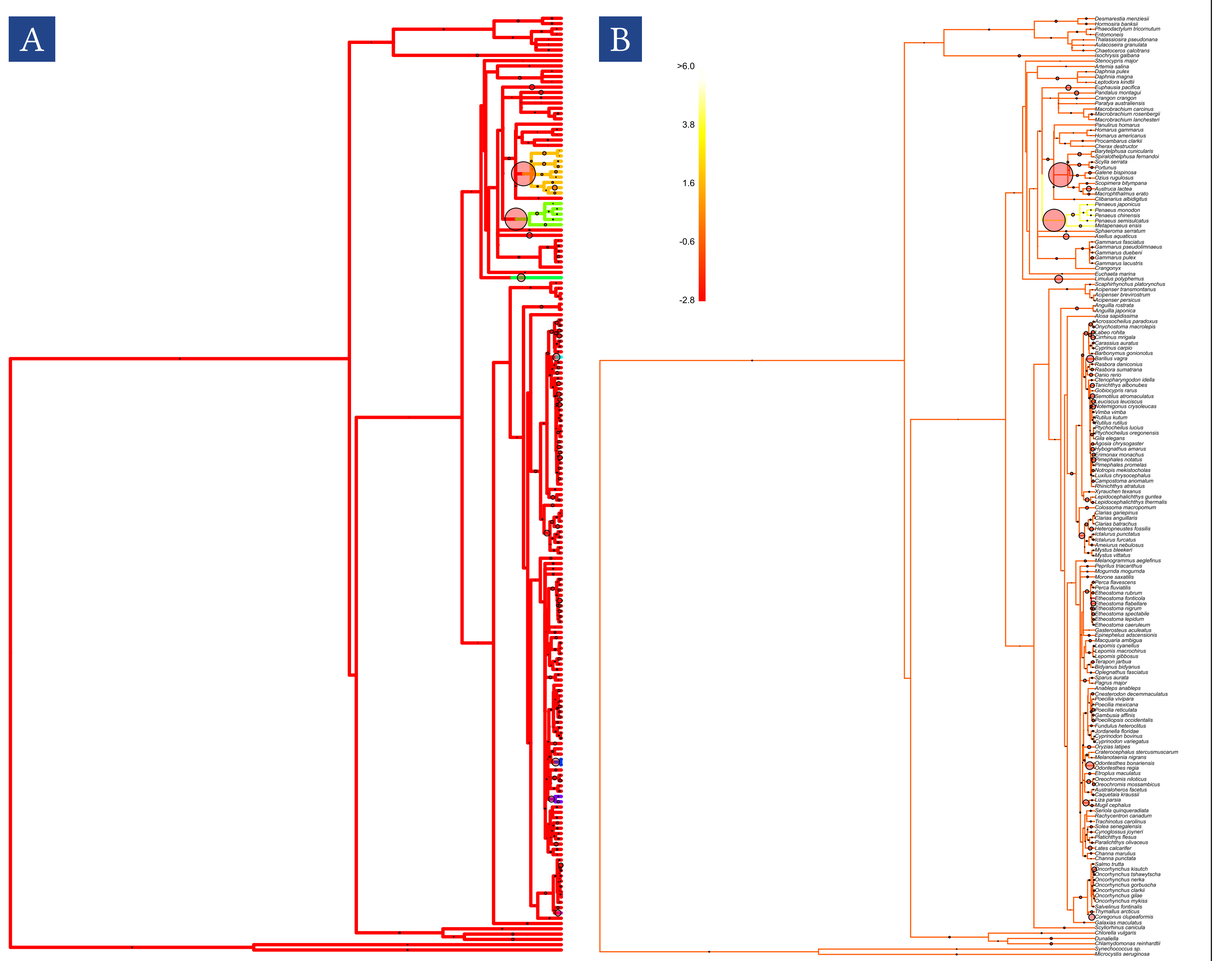

Figure 3: Phylogeny showing the results of rjMCMC analysis of multi-regime OU model fit to median LC_{50} values for Copper sulphate. Circle size indicates posterior probability of shift. (A) Regime changes mapped to different colours. (B) Colours of edges indicate mean θ.

Take-away

- Ecotoxicologists have been measuring standardised trait data for decades, yet it has rarely been explored in an evolutionary context (but see Guénard et al. 2011, 2014).
- Tempo (not shown) and mode (Fig. 4) of evolution differs between toxicants.
- Signatures of shifts in optimum values (example for $CuSO_4$ shown in Fig. 3) are regularly recovered across different toxicants.

Future directions

- Fit dose-response curves to combine different endpoints (e.g. LC_5, LC_{50}, LC_{95}) and fit model parameters (e.g. NEC) as traits.
- Explore correlated evolution of traits and correlated changes in regimes.
- Formally compare different toxicant groups that differ in mode of action.
- Use models to predict unknown tip values, which will be validated with ongoing experiments.

Mode of evolution differs between toxicants

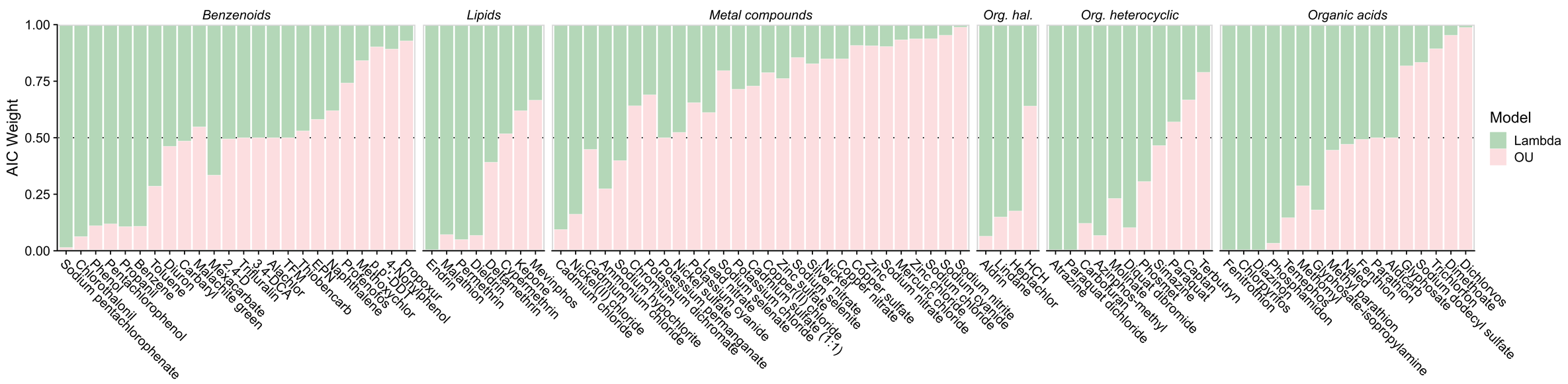

Figure 4: AIC weights of two models of trait evoltion, grouped by chemical class. Lambda (Pagel 1999) fits how well the phylogeny predicts covariance among trait values (assuming Brownian motion) by transforming the tree to be more or less star-like. OU (Butler and King 2004) fits a random walk with a central tendency and an attractor.

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