Metafor Tutorial - <https://www.youtube.com/watch?v=IkduL5iRdqo&t=5048s>

* Metadata is a package of meta-analysis datasets
* Choosing effect size statistic:
  + Measures for 2x2 table data – risk difference, risk ratio, odds ratio
  + Measures for two-group i.e. treatment and control data – standardised mean difference or response ratio
  + Association between 2 variables – raw or Fisher's transformed correlation coefficients
  + Use escalc() function to get effect sizes from each study
* Then use fixed, random, mixed effect (meta-regression), mulitlevel models
  + rma.mv() function is one of the unique features of the metafor package – can do multilevel models
* Plots and figures e.g. forest and funnel plots
* Publication bias – rank correlation test, Egger's regression test, trim and fill
* Perform sensitivity analyses with leave1out() function – see how much results change by leaving out 1 study

Diagram

Description automatically generated

Demo of metafor – see R script 'metafor\_tutorial'

* Phylogenetic MA
  + Species share evolutionary history – so effects for species that are more similar to each other might also correlate more strongly
  + Developed a way to incorporate correlation matrices into rma.mv() – could be phylogenetic (or spatial)
  + Allows you to account for dependencies
  + Without accounting for these things, you will under-estimate SE