Non-independence of observations

Examples of non-independence of observations in meta-analysis

a Shared study identity
b Shared measurements within study
c Shared control group within study
d Shared taxa (species) and phylogeny across studies
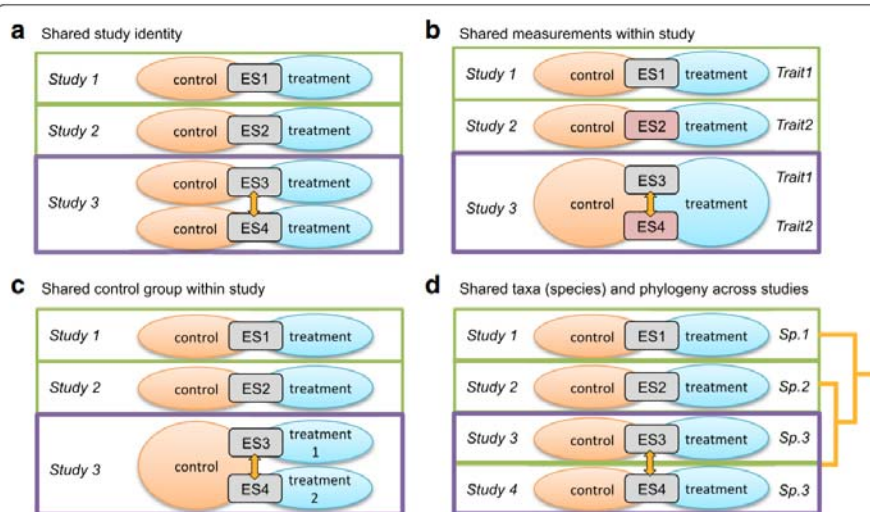
From Nakagawa et al. BMC Biology (2017) 15:18

Broad strategies for handling non-independence in meta-analysis

- Sensitivity analysis
- Select a single measurement per study
- Combine multiple measurements into a single effect measure
- Sub-classify/conduct hierarchical analysis
- Model non-independence (e.g. by using multivariate meta-analysis, including study as a random effect in the model, or by deriving new formulas for variance)

Dealing with within-study non-independence

- Multiple treatments with common control

Ecology, 92(11), 2011, pp. 2049–2055
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On the meta-analysis of response ratios for studies with correlated and multi-group designs

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✓ Variances are derived for several common experimental designs, e.g. multiple treatments with common control, repeated measures, multivariate or correlated factorial designs

Dealing with within-study non-independence (cont.)

- Repeated measures
  - ✓ Use a single time point (e.g. final measure)
  - ✓ Use effect metric which assesses change in effect over time (e.g. correlation with time or standardized mean difference between 2 time points) and then combine these in a meta-analysis
  - ✓ Treat repeated measures as a multivariate outcome (autoregression or other covariance structure)
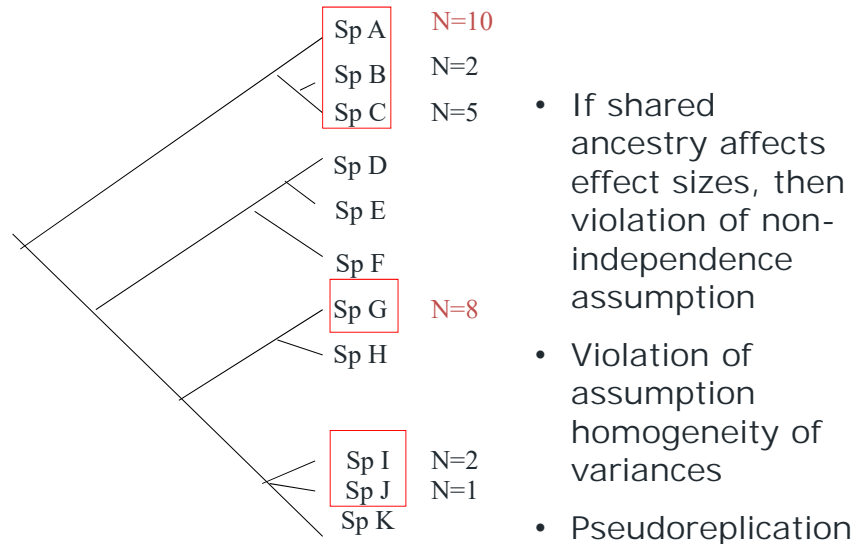
Software for MA with non-independent effects

metafor: function rma.mv

String struct specifies the variance structure of the data.

Options include "AR" for an AR(1) autoregressive structure, or "HAR" for a heteroscedastic AR(1) autoregressive structure.

Issues with phylogenetic dependencies and research bias

Sp A	N=10
Sp B	N=2
Sp C	N=5

Sp D	
Sp E	
Sp F	
Sp G	N=8
Sp H	

Sp I	N=2
Sp J	N=1
Sp K	

- If shared ancestry affects effect sizes, then violation of non-independence assumption
- Violation of assumption homogeneity of variances
- Pseudoreplication

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Meta-Analysis and the Comparative Phylogenetic Method

Marc J. Lajeunesse[*]

- In traditional meta-analysis, effect sizes with large sampling variances are weighted less heavily because they may represent inaccurate estimates of the "true" population
- In phylogenetically-controlled meta-analysis, an additional weighting is used to account for the correlated evolution history of taxa
- The strengths of correlations among effect sizes due to the shared phylogenetic history of taxa are defined as the phylogenetic branch length distance between taxa
- Less weight is given to taxa that are more closely related to other taxa

Phylogenetic meta-analysis

- *metafor* package in R

    - rma.mv () function

    - argument R is used to specify the phylogenetic correlation matrix of the species studied in the meta-analysis

    - See Nakagawa and Santos (2012, Evolutionary Ecology, 26, 1253–1274) for more details

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REVIEW AND SYNTHESES

Does phylogeny matter? Assessing the impact of phylogenetic information in ecological meta-analysis

Scott A. Chamberlain,[1]* Stephen M. Hovick,[1] Christopher J. Dibble,[1] Nick L. Rasmussen,[1] Benjamin G. Van Allen,[1] Brian S. Maitner,[1] Jeffrey R. Ahern,[1] Lukas P. Bell-Dereske,[1] Christopher L. Roy,[1] Maria Meza-Lopez,[1] Juli Carrillo,[1] Evan Siemann,[1] Marc J. Lajeunesse[2] and Kenneth D. Whitney[1]

- Re-analyzed 30 published meta-analyses

- Accounting for phylogeny significantly changed estimates of mean effect in 47% of datasets for FEM and 7% of datasets for REM

- Accounting for phylogeny also changed whether those effect sizes were significantly different from 0 in 23% (FEM) and 40% (REM) of the datasets

Confounded moderators

- Example:
  - ✓ Moderator 1: plant type (woody vs herbaceous)
  - ✓ Moderator 2: study type (field vs lab)

	Woody	Herbs
Field	35	15
Lab	1	40

- Effect of study type can be properly tested only within herbaceous plants
- Comparison of plant types might be confounded by differences between study types (most studies on woody plants are field studies whereas for herbs it is a mixture of field and lab studies)

Dealing with confounded moderators

- ✓ Always aim to include all moderators into the model instead of testing them one by one, but also check whether there are enough studies to test for interactions between moderators.
- ✓ Always consider and test for potential dependencies between moderators
- ✓ If dependencies are extreme (as in the example above), use hierarchical approach (e.g. test for study type for herbs only) or use 3 categories in 1-way analysis (woody-field, herbs-field, herbs-lab)