

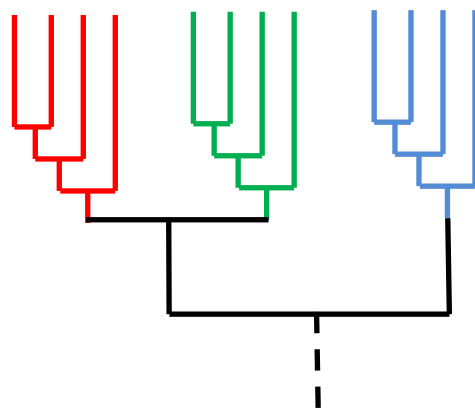
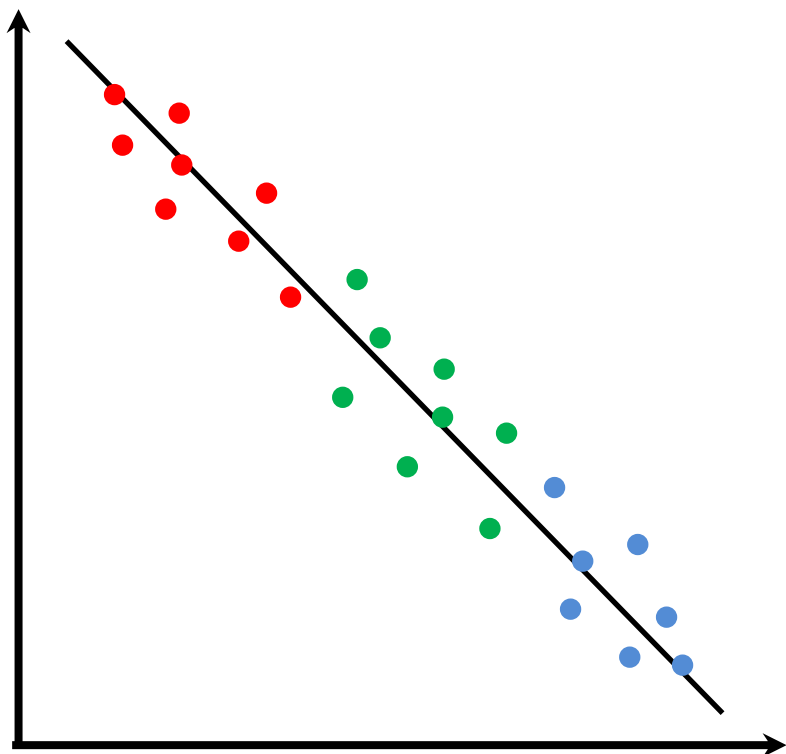
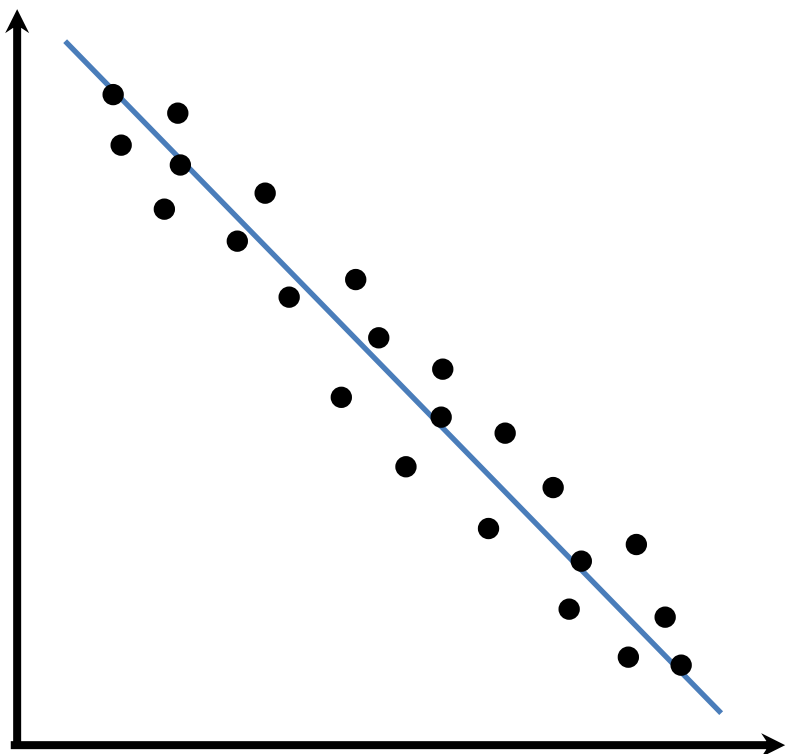


Incorporating phylogeny into linear regression

Sergey Rosbakh
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Why phylogenetic relatedness matters?

- 1) To carry out statistical analysis correctly: independence of data points in a data set is one of assumptions for linear models
- 1) To disentangle evolution history from ecological processes: closely related species (e.g. genus and family levels) tend to occur in a community together, because they have similar ecological niches
- 1) To understand evolution of taxon/taxonomic group better: presence of phylogenetic signal in the group might indicate a common ancestor



What do I need for an analysis?

1) Species list with actual taxonomic status:

- The Plant List: <http://www.theplantlist.org/>
- The National Center for Biotechnology: <https://www.ncbi.nlm.nih.gov/taxonomy>

2) Phylogeny:

- Make your own tree: package *V.Phylomaker* in R
- Prune available 'mega-tree' (e.g Durka and Michalski, 2012 or Qian and Jin, 2016)

3) Traits:

- Own data
- Literature
- Data bases: TRY (<https://www.try-db.org/TryWeb/Home.php>), BROT (<https://www.uv.es/jgpausas/brot.htm>), etc.

Available phylogenies

LETTER

doi:10.1038/nature12872

Three keys to the radiation of angiosperms into freezing environments

Amy E. Zanne^{1,2}, David C. Tank^{3,4}, William K. Cornwell^{5,6}, Jonathan M. Eastman^{3,4}, Stephen A. Smith⁷, Richard G. FitzJohn^{8,9}, Daniel J. McGlinn¹⁰, Brian C. O'Meara¹¹, Angela T. Moles⁶, Peter B. Reich^{12,13}, Dana L. Royer¹⁴, Douglas E. Soltis^{15,16,17}, Peter F. Stevens¹⁸, Mark Westoby⁹, Ian J. Wright⁹, Lonnie Aarssen¹⁹, Robert I. Bertin²⁰, Andre Calaminus¹³, Rafaël Govaerts²¹, Frank Hemmings⁶, Michelle R. Leishman⁹, Jacek Oleksyn^{12,22}, Pamela S. Soltis^{16,17}, Nathan G. Swenson²³, Laura Warman^{6,24} & Jeremy M. Beaulieu²⁵



Received: August 19, 2016
Accepted: March 3, 2017

Data Papers

Ecology, 93(10), 2012, p. 2297
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Daphne: a dated phylogeny of a large European flora for phylogenetically informed ecological analyses

Ecological Archives E093-214

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Software note

V.PhylMaker: an R package that can generate very large phylogenies for vascular plants

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Journal of
Plant Ecology

VOLUME 9, NUMBER 2,
PAGES 233–239

APRIL 2016

doi:10.1093/jpe/rv047

Advance Access publication
15 June 2015

available online at
www.jpe.oxfordjournals.org

An updated megaphylogeny of plants, a tool for generating plant phylogenies and an analysis of phylogenetic community structure

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INVITED SPECIAL ARTICLE

For the Special Issue: Using and Navigating the Plant Tree of Life

Constructing a broadly inclusive seed plant phylogeny

Stephen A. Smith^{1,2} and Joseph W. Brown¹

Phylogenetic generalized least squares (PGLS)

Useful links:

https://lukejharmon.github.io/pcm/chapter3_bmintro/

<https://lukejharmon.github.io/ilhabela/instruction/2015/07/03/PGLS/>

<http://www.phytools.org/Cordoba2017/ex/4/PGLS.html>

<https://www.r-phylo.org/wiki/HowTo/PGLS>