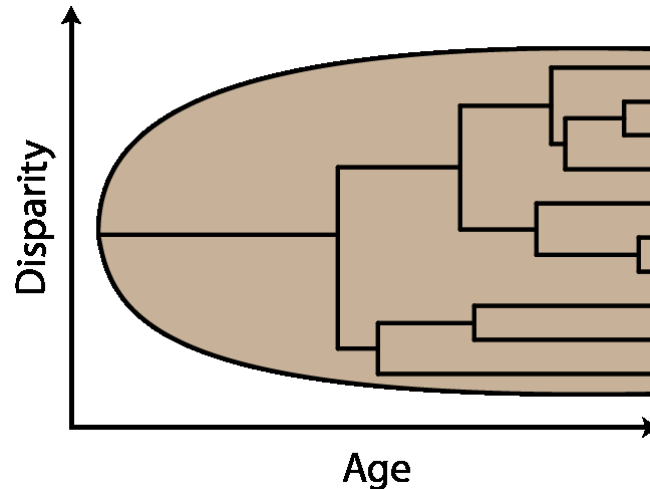


mvMORPH: an R package for the fitting of multivariate evolutionary models to morphometric data



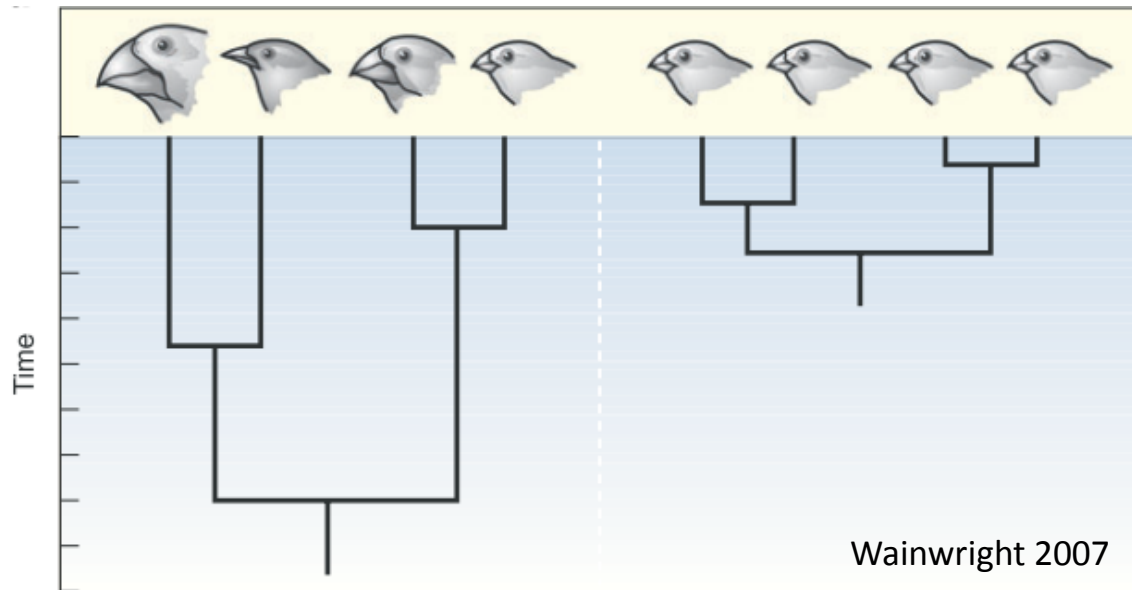
Phylogeny as a modeling framework

*Using phylogeny to describe evolutionary
dynamic:*

tempo of phenotypic evolution

Modelling approach: univariate models

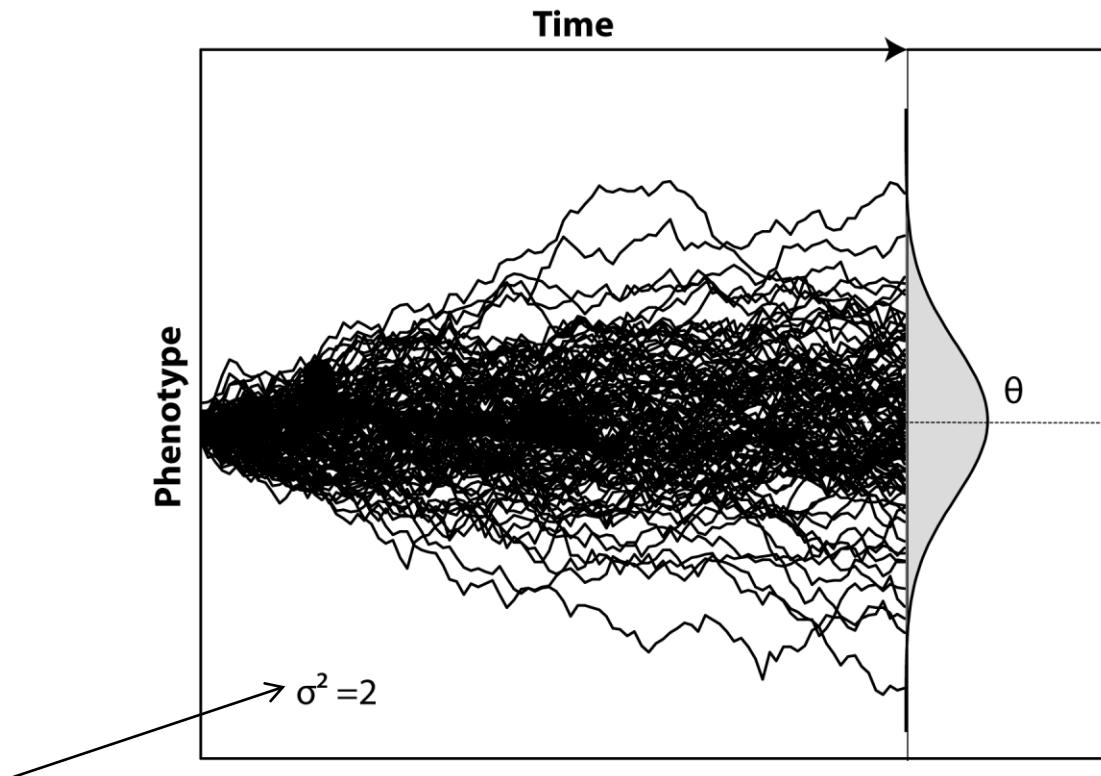
We can use Maximum Likelihood to estimate phenotypic rate of evolution



- ✓ ***Is disparity related to the age of the clade?***
- ✓ ***We need a model of trait evolution***

Phenotypic Evolution on Phylogeny

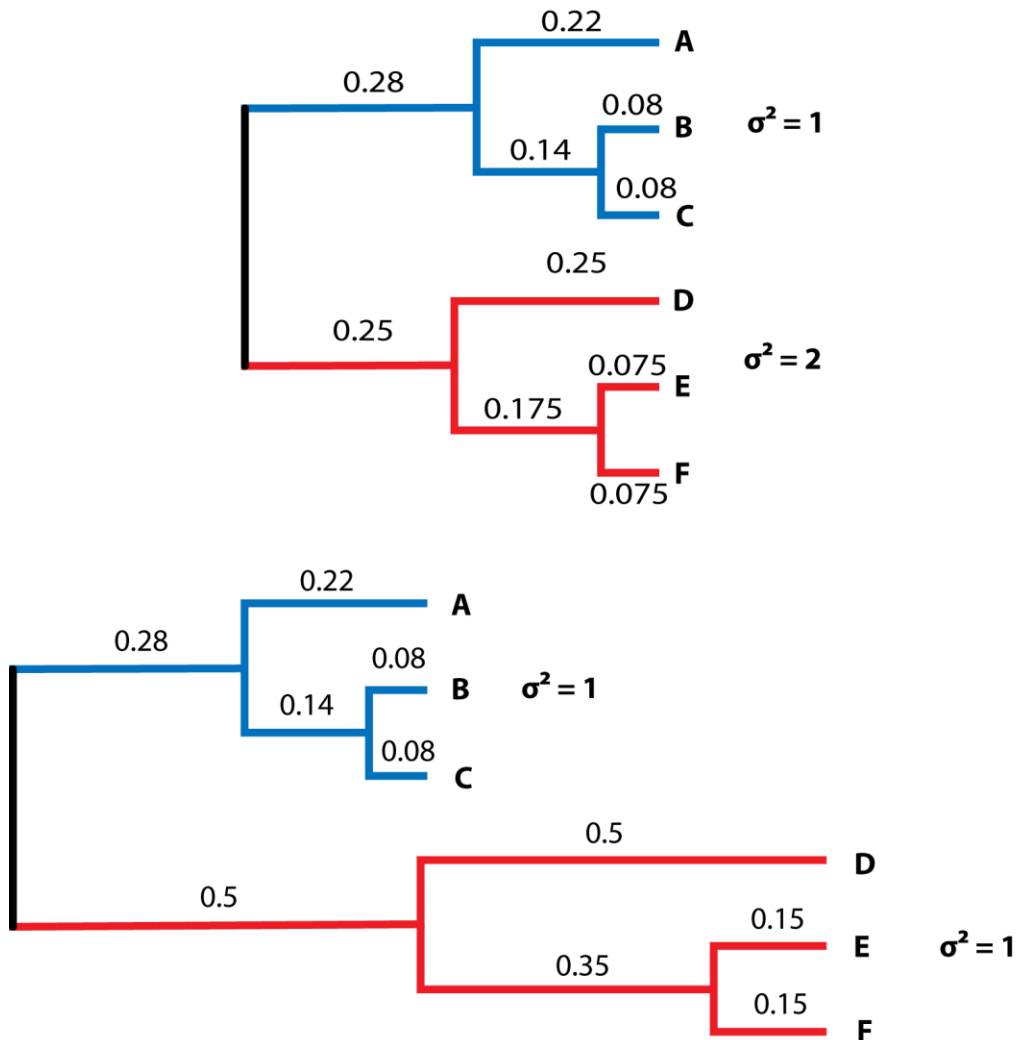
- ✓ *Evolution of the phenotypic variance between species*
- ✓ *e.g. Brownian motion (BM)*



Brownian rate: rate of variance accumulation through time

Modelling approach: univariate models

✓ Filling the VCV matrix/ or transforming the tree

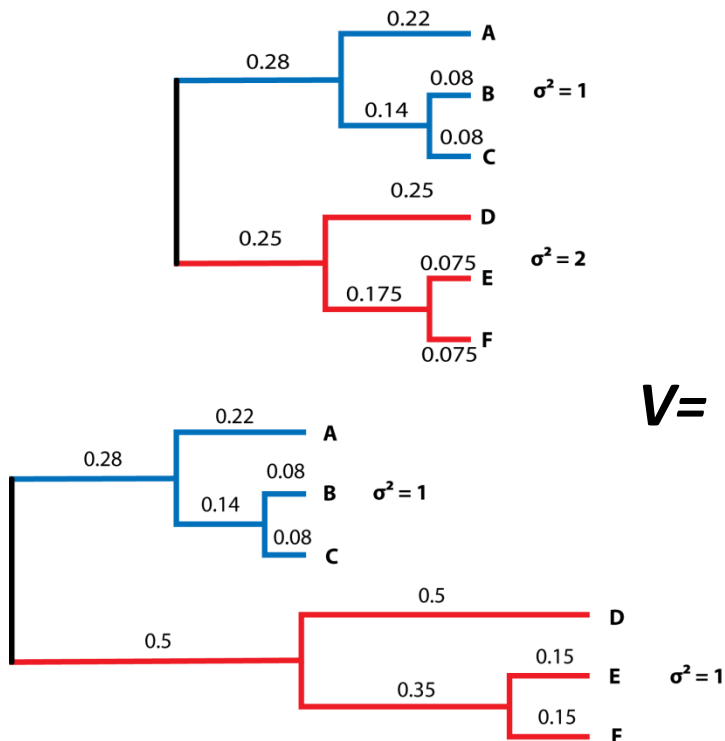


Different evolutionary rates between clades

| | A | B | C | D | E | F |
|---|------|------|------|-----|------|------|
| A | 1 | 0.28 | 0.28 | 0 | 0 | 0 |
| B | 0.28 | 1 | 0.42 | 0 | 0 | 0 |
| C | 0.28 | 0.42 | 1 | 0 | 0 | 0 |
| D | 0 | 0 | 0 | 2 | 0.5 | 0.5 |
| E | 0 | 0 | 0 | 0.5 | 2 | 0.85 |
| F | 0 | 0 | 0 | 0.5 | 0.85 | 2 |

Modelling approach: univariate models

✓ Filling the VCV matrix/ or transforming the tree



$V =$

Different evolutionary rates between clades

| | A | B | C | D | E | F |
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| D | 0 | 0 | 0 | 2 | 0.5 | 0.5 |
| E | 0 | 0 | 0 | 0.5 | 2 | 0.85 |
| F | 0 | 0 | 0 | 0.5 | 0.85 | 2 |

Expectation

Phenotypic trait vector

$$\log(L) = \log \left[\frac{\exp\left\{-\frac{1}{2}[X-E(X)]'(V)^{-1}[X-E(X)]\right\}}{\sqrt{2\pi^N \times |V|}} \right]$$

Evolutionary vcv matrix

Macroevolution

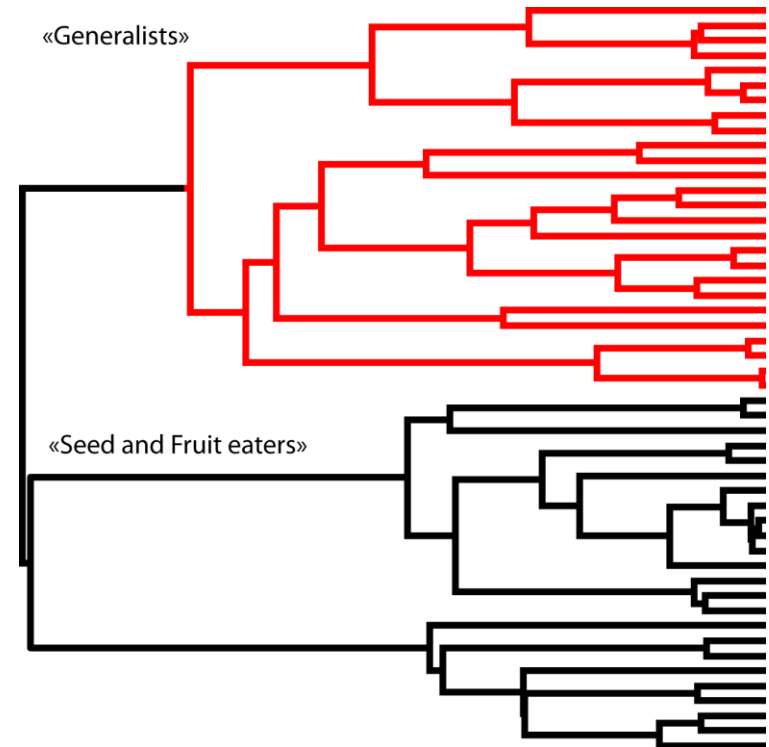
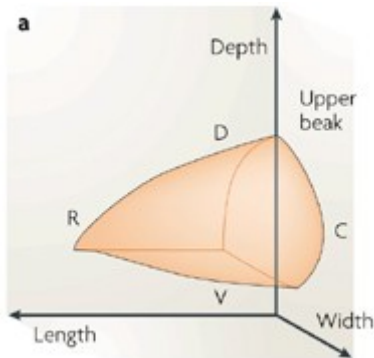
Multivariate evolution?

Multivariate models

Dealing with multivariate data: phenotypic disparity and integration

Traits interactions in a hypothesis testing framework

Evolutionary rates are expressed in $n \times n$ dimensions matrices



Multivariate models

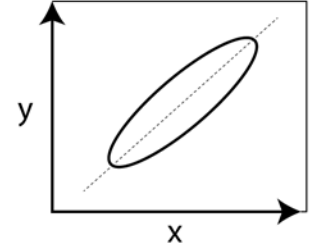
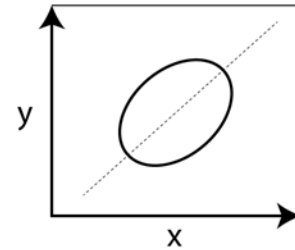
Dealing with multivariate data: phenotypic disparity and integration

Selection on multiple traits allows making predictive assumptions on the way the traits may covary through time. Evolutionary rates are expressed in $n \times n$ dimensions matrices

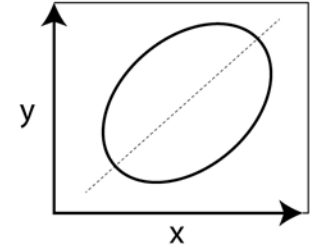
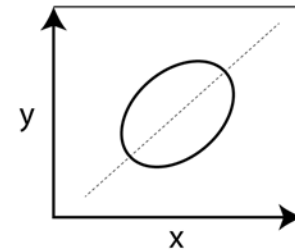
Evolutionary rates matrix describe at least three aspects:

- ✓ The size: the total amount of phenotypic variance in traits (evolutionary rates)
- ✓ Phenotypic covariances/correlations (describe the phenotypic integration)
- ✓ Orientation of covariances (Does the evolutionary rates matrix for different clades share the same eigen-structure?)

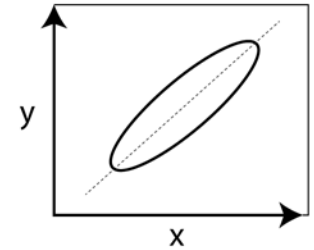
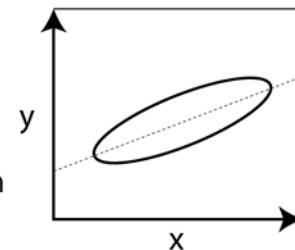
Change in shape



Change in size



Change in orientation



Multivariate models

Dealing with multivariate data: kroenecker product of rate and vcv matrix

$$R_2 = \begin{bmatrix} 2 & 0 \\ 0 & 2 \end{bmatrix}$$

\otimes

$$C_1 = \begin{matrix} & \begin{matrix} A & B & C & D & E & F \end{matrix} \\ \begin{matrix} A \\ B \\ C \\ D \\ E \\ F \end{matrix} & \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 2 & 0.5 & 0.5 \\ 0 & 0 & 0 & 0.5 & 2 & 0.85 \\ 0 & 0 & 0 & 0.5 & 0.85 & 2 \end{bmatrix} \end{matrix}$$

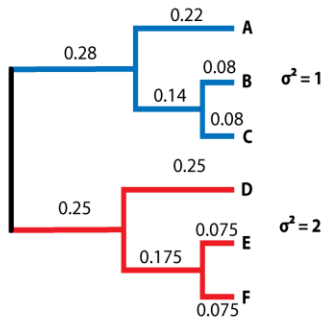
=

$$C_2 = \begin{matrix} & \begin{matrix} \text{Trait 1} & & & & & & \text{Trait 2} & & & & & & \end{matrix} \\ \begin{matrix} A \\ B \\ C \\ D \\ E \\ F \end{matrix} & \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 2 & 0.5 & 0.5 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0.5 & 2 & 0.85 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0.5 & 0.85 & 2 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 2 & 0.5 & 0.5 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0.5 & 2 & 0.85 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0.5 & 0.85 & 2 \end{bmatrix} \end{matrix}$$

A B C D E F

Multivariate models

Dealing with multivariate data: kroenecker product of rate and vcv matrix



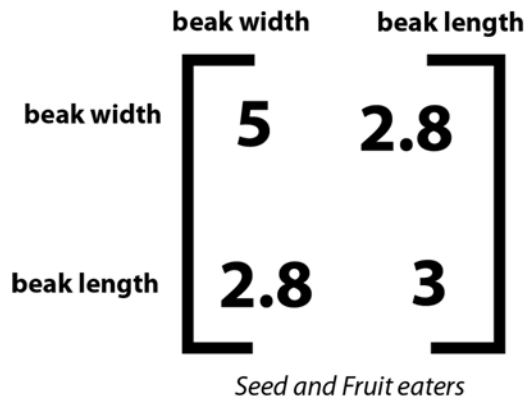
$$V = C_1 + C_2 =$$

| | Trait 1 | | | | | | Trait 2 | | | | | | |
|---|---------|------|------|-----|------|------|---------|------|------|-----|------|------|---|
| | A | B | C | D | E | F | | | | | | | |
| A | 1 | 0.28 | 0.28 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| B | 0.28 | 1 | 0.42 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| C | 0.28 | 0.42 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| D | 0 | 0 | 0 | 2 | 0.5 | 0.5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| E | 0 | 0 | 0 | 0.5 | 2 | 0.85 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| F | 0 | 0 | 0 | 0.5 | 0.85 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0.28 | 0.28 | 0 | 0 | 0 | 0 |
| | 0 | 0 | 0 | 0 | 0 | 0 | 0.28 | 1 | 0.42 | 0 | 0 | 0 | 0 |
| | 0 | 0 | 0 | 0 | 0 | 0 | 0.28 | 0.42 | 1 | 0 | 0 | 0 | 0 |
| | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 2 | 0.5 | 0.5 | 0 |
| | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.5 | 2 | 0.85 | 0 |
| | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.5 | 0.85 | 2 | 0 |
| | | A | B | C | D | E | F | | | | | | |

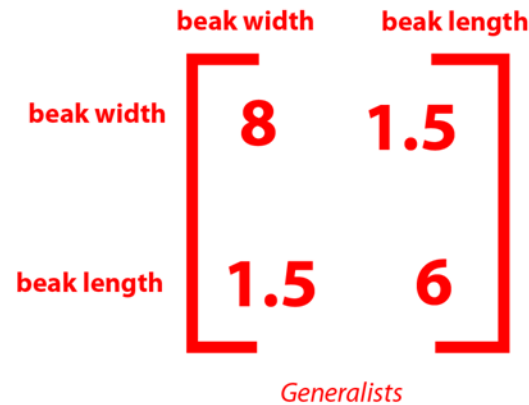
Multivariate models

Dealing with multivariate data: phenotypic disparity and integration

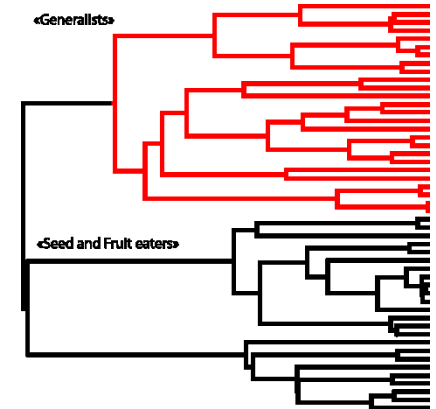
Evolutionary traits interactions in a hypothesis testing framework



≈ correlation: 0.72



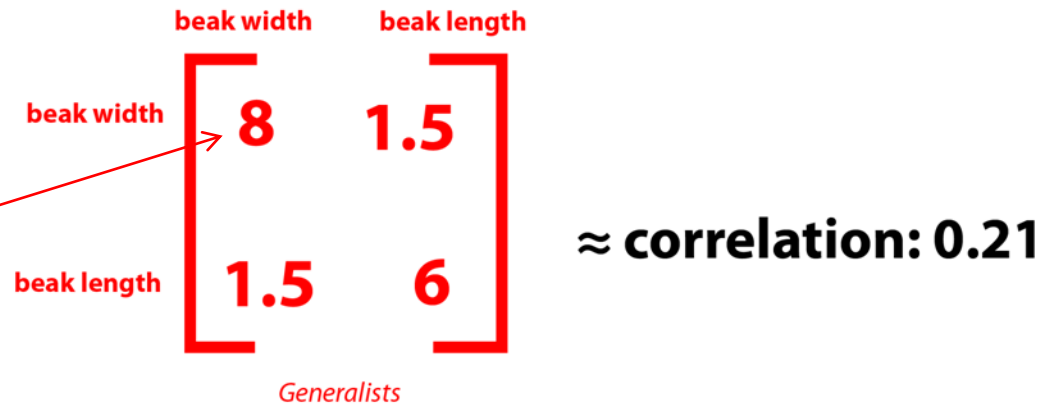
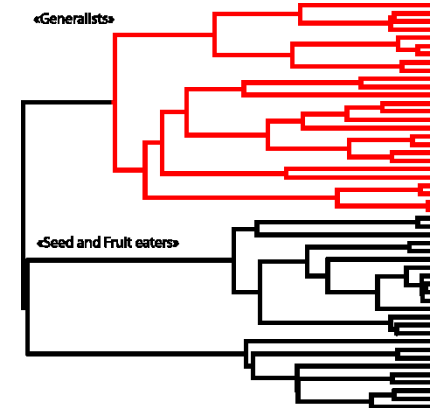
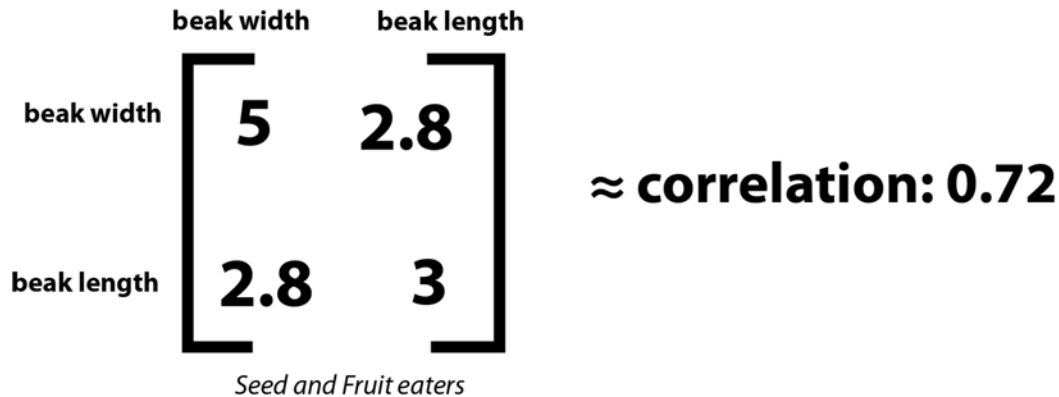
≈ correlation: 0.21



Multivariate models

Dealing with multivariate data: phenotypic disparity and integration

Evolutionary traits interactions in a hypothesis testing framework

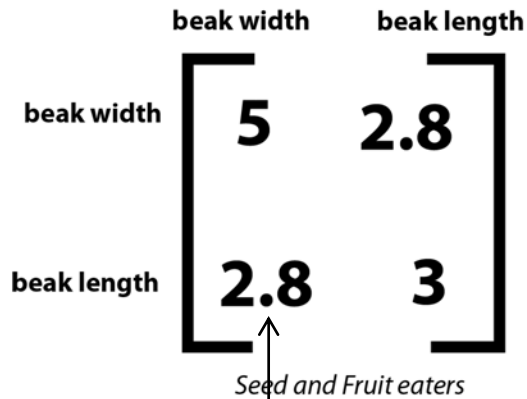


More variance on traits for generalists species
And lower evolutionary correlations:
disparate clade

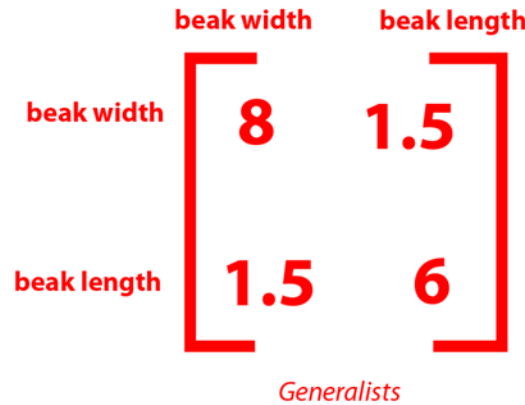
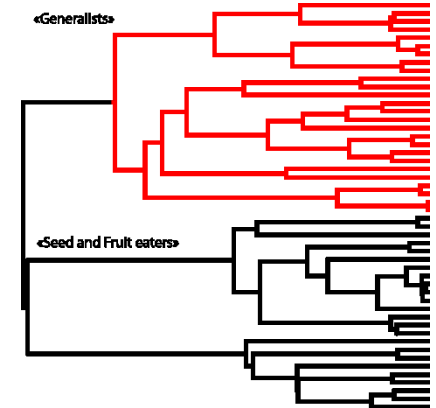
Multivariate models

Dealing with multivariate data: phenotypic disparity and integration

Evolutionary traits interactions in a hypothesis testing framework



≈ correlation: 0.72



≈ correlation: 0.21

Higher evolutionary covariance between traits: correlative selection? Functional constraints?

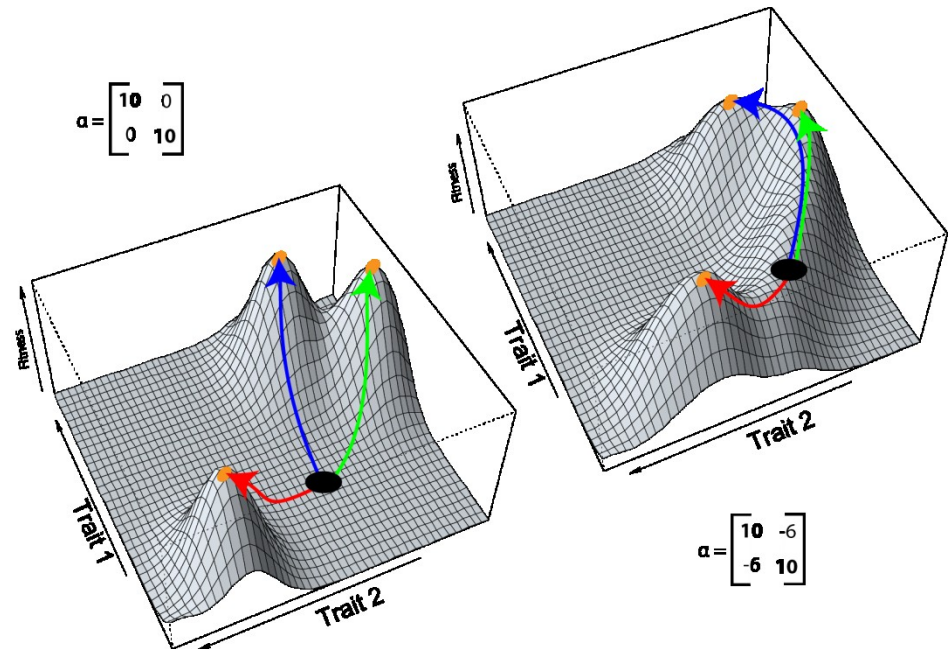
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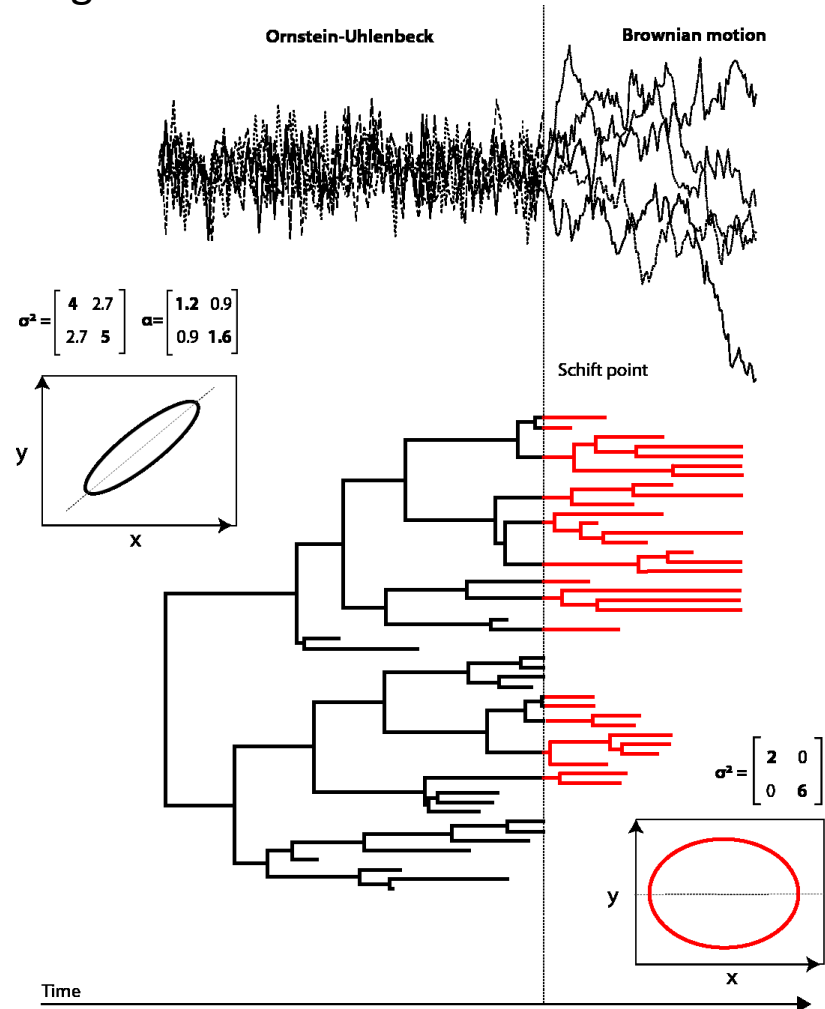
Multivariate models

Dealing with multivariate data: phenotypic disparity and integration

-E.g. we could expect that environmentally driven changes in evolutionary modes is accompanied by a change in phenotypic integration of functional traits.

Exemple: diversification associated to the intrusion of a competitive specie followed by a functional diversification

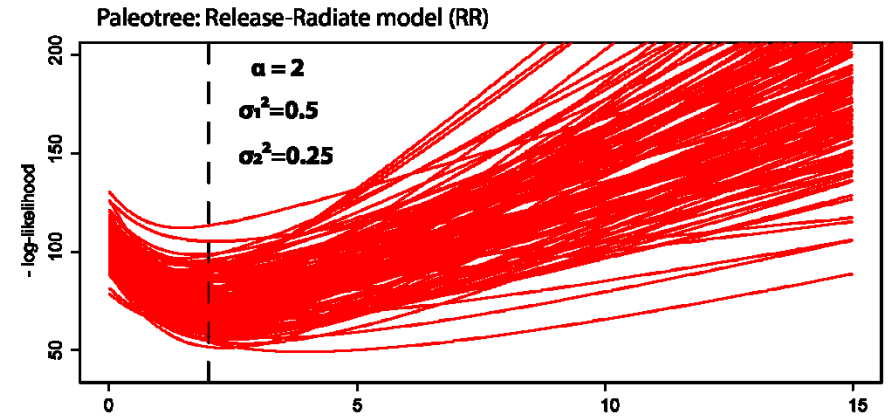
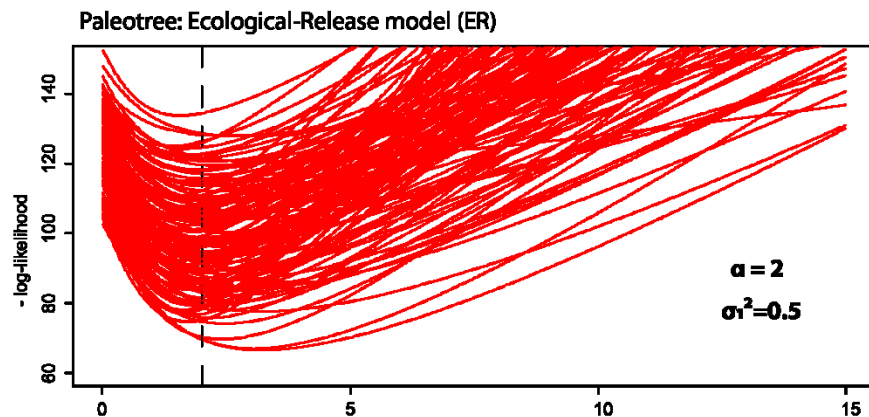
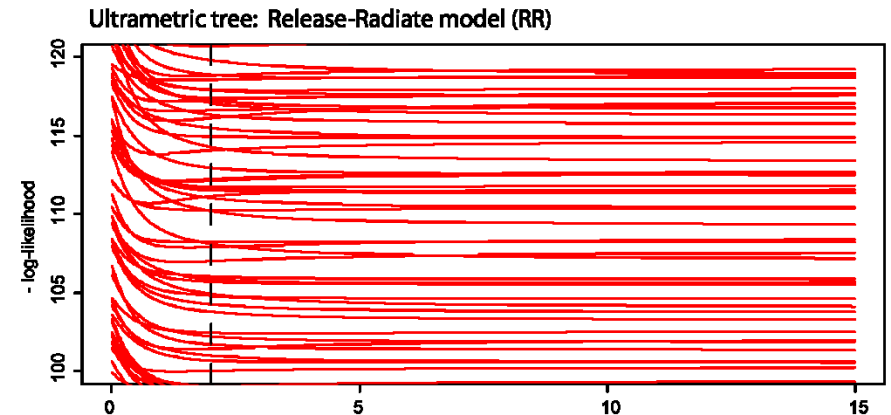
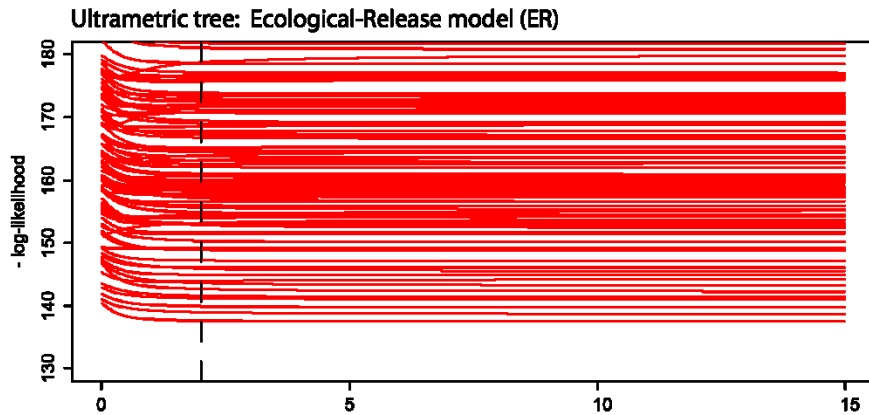
But... few tools allows such a modeling approach



Tempos & Modes of Evolution

Dealing with paleotrees: Development of models of evolutionary shifts

Paleo-trees allows estimating changes in evolutionary rates (tempo), but also changes in modes! No local or global minimum on ultrametric trees



100 simulated trees

mvMORPH

mvMORPH: an R package for the fitting of multivariate evolutionary models and other things...

mvMORPH : an R package motivated by the need for tools to study the evolution of phenotypic traits with fossil data, and to study multivariate evolution of disparity and phenotypic integration in macroevolutionary studies

← cran.r-project.org/web/packages/mvMORPH/index.html

mvMORPH: Multivariate Comparative Tools for Fitting Evolutionary Models to Morphometric Data

Fits multivariate (Brownian Motion, Early Burst, ACDC, Ornstein-Uhlenbeck and Shifts) models of continuous traits evolution on trees

Version: 1.0.2
Depends: R (≥ 2.9.1), [phytools](#), [ape](#), [corpcor](#), [subplex](#)
Published: 2014-04-24
Author: Julien Clavel, with contributions from Aaron King, and Emmanuel Paradis
Maintainer: Julien Clavel <julien.clavel at hotmail.fr>
License: [GPL-2](#) | [GPL-3](#) [expanded from: GPL (≥ 2.0)]
NeedsCompilation: yes
CRAN checks: [mvMORPH results](#)

Downloads :

Reference manual: [mvMORPH.pdf](#)
Package source: [mvMORPH 1.0.2.tar.gz](#)
Windows binaries: r-devel: [mvMORPH 1.0.2.zip](#), r-release: [mvMORPH 1.0.2.zip](#), r-oldrel: [mvMORPH 1.0.2.zip](#)
OS X Snow Leopard binaries: r-release: [mvMORPH 1.0.2.tgz](#), r-oldrel: [mvMORPH 1.0.2.tgz](#)
OS X Mavericks binaries: r-release: [mvMORPH 1.0.2.tgz](#)
Old sources: [mvMORPH archive](#)

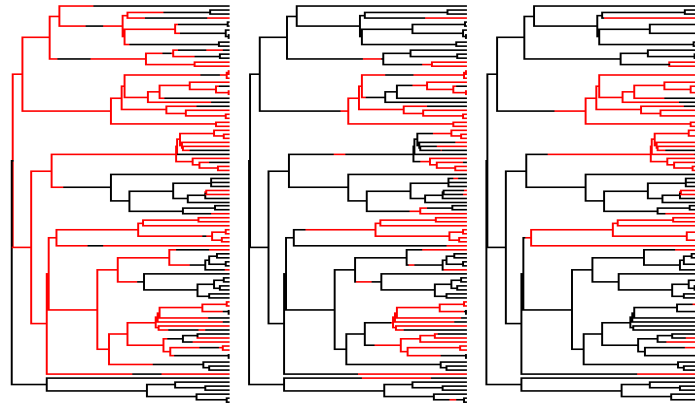


mvMORPH

R packages for dealing with multivariate data

✓ Some packages available on CRAN

| Packages | BM | OU | multiple optimum | changes in mode | Measurement error | stochastic mapping | n-ultrametric trees | Cons. | diagnostics |
|----------------|----|----|------------------|-----------------|-------------------|--------------------|---------------------|-------|-------------|
| OUCH | X | X | X | | | | | | |
| phytools | X | | X | | | X | X | | |
| mvSLOUCH | X | X | X | | X | | X | X | |
| MotMot | X | X | | | X | | | | |
| mvMORPH | X | X | X | X | X | X | X | X | X |



+ multivariate Early-Burst Model, models of changes in evolutionary modes through times, possibility of testing for differences in evolutionary rates between traits...



mvMORPH

mvMORPH: an R package for the fitting of multivariate evolutionary models and other things...

-Allows the fitting of 14 evolutionary models by maximum likelihood, mostly dedicated to multivariate data, but also on models dedicated to paleo-trees

| Function | Model | Short description of the associated evolutionary model |
|----------|-----------------|--------------------------------------------------------------------------------------|
| mvBM | BM1 | One BM rate per trait |
| | BM1-constrained | Constrained to a unique BM rate common to all traits |
| BMM | BMM | One BM rate per selective regime and per trait |
| | BMM-constrained | Constrained to one BM rate per selective regime common to all traits |
| mvOU | OU1 | OU process with a unique adaptive optimum per trait |
| | OU1-constrained | OU process constrained to evolve independently on each traits |
| | OUM | OU process with multiple adaptive optima per trait |
| | OUM-constrained | OU process constrained to evolve independently on each traits (with multiple optima) |
| mvEB | EB - ACDC | EB model or decelerating model of evolutionary rates. |
| mvSHIFT | ER | OU process that collapses to a BM drift at a given point in time |
| | RR | OU process that switches to an independent BM process at a given point in time |
| | EC | BM process pulled to an OU process at a given point in time |
| | RC | Independent BM process switch to an OU process |
| | SR | Change in BM rates at a given point in time |

Current models in mvMORPH 1.0.2 available on CRAN



mvMORPH

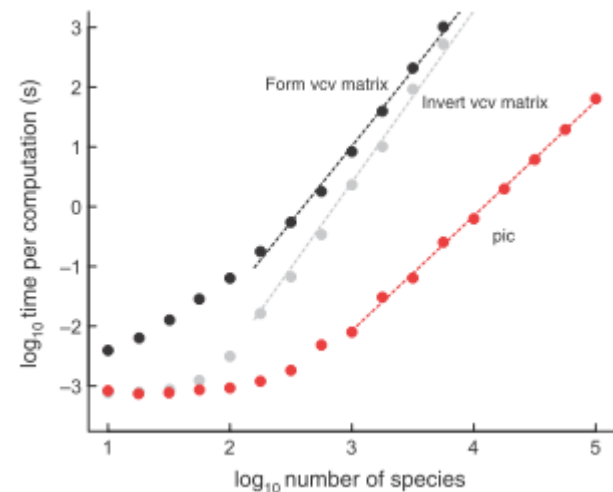
mvMORPH: an R package for the fitting of multivariate evolutionary models and other things...

Main drawback

- ✓ Dealing with huge dataset (uncertainty due to rounding errors, and computational time (number of arithmetic operations (O^3) for matrix inversion)
- ✓ Number of parameters

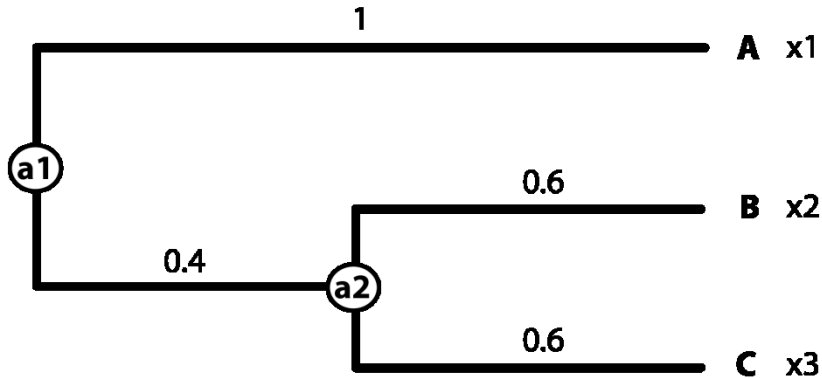
But...

- ✓ Allows SIMMAP mapping, integrating uncertainty, working with paleotrees
- ✓ Building of variances-covariances matrix using faster C-code



Performances

- ✓ *Using Phylogenetic independent contrast (PIC) instead?*



$$a2 = \text{Contraste (B-C)} = (x2 - x3) / 0.6$$

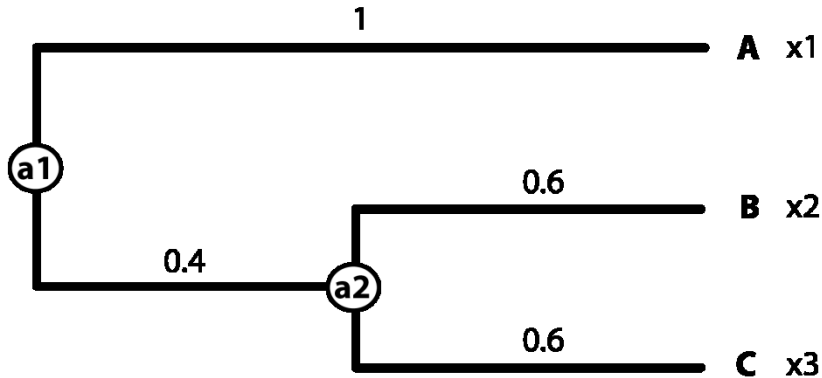
$$a1 = \text{Contraste (A-a2)} = (((x2 + x3) / 2) - x1) / 0.4$$

Main advantage:

- ✓ Does not need the computation (and inversion) of a variance-covariance matrix
- ✓ Time linear algorithm, need a transformed tree.

Performances

- ✓ *Using Phylogenetic independent contrast (PIC) instead?*



$$a2 = \text{Contraste (B-C)} = (x2-x3)/0.6$$

$$a1 = \text{Contraste (A-a2)} = (((x2+x3)/2)-x1)/0.4$$

Main disadvantage:

- ✓ Some tree transformation don't works for paleo-trees
- ✓ Complex models that need a conception matrix are not easily handled

mvMORPH

mvMORPH: an R package for the fitting of multivariate evolutionary models and other things...

Forthcoming: mvMORPH 1.0.3

- ✓ Additional models (multiple optimums in shifts,...)
- ✓ MANOVA parameterizable with the various models of mvMORPH
- ✓ S3 class for various functions of the package (loglik, summary, simulate...)
- ✓ Simulations functions with fitted models parameters
- ✓ Fast likelihood algorithms (three points structure) – Ho & Ané 2014 (*Syst. Biol.*)
- ✓ Combined calculation of the inverse and determinant of phylogenetic evolutionary matrix
Involved in likelihood estimation with a LDL Cholesky factorizations (actually in C but maybe also done in Fortran for performances?)

The goal:

Tools for working with huge paleotrees!! (e.g. Raia et al. (2013) *Proc. Roy. Soc.*, paleotree with 1100 taxa!); and multivariate datasets...

Julien Clavel

Thank you very much for your attention

 cran.r-project.org/web/packages/mvMORPH/index.html

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CRAN checks: [mvMORPH results](#)

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Laboratoire de Géologie de Lyon
Terre Planètes Environnement

