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

J. Clavel [a] , **G. Escarguel**[a] and **G. Merceron** [b]

[a] Laboratoire de Géologie de Lyon : Terre, Planètes, Environnements
UMR 5276 CNRS, ENS Lyon & Université Lyon 1
Campus de la Doua, 2 rue Raphaël Dubois, 69622 Villeurbanne
Julien.clavel@univ-lyon1.fr, gilles.escarguel@univ-lyon1.fr

[b] Institut International de Paléoprimatologie, Paléontologie Humaine, Evolution et Paléoenvironnements
UMR 7262 CNRS & Université de Poitiers
Bat. 8, 5 rue Albert Turpain, 86022
Gildas.merceron@univ-poitiers.fr

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Maximum likelihood comparative methods for fitting evolutionary models to continuous data are becoming increasingly popular. They provide a multiple hypothesis framework to assess evolutionary patterns and processes. However, while phenotypic diversity is often described through multidimensional spaces, most phylogenetic comparative studies still remain limited to univariate analysis. This is basically due to the availability of unified computational environments for fitting various evolutionary models, which are mainly dedicated to univariate data, as for instance in the R “ape”, “geiger”, “phytools”, and “OUwie” packages [1-4].

We present mvMORPH, a new package dedicated to multivariate phylogenetic comparative methods [5]. This new package provides a unified environment for fitting various multivariate evolutionary models under a maximum likelihood criterion, based on the multivariate extension of recently described univariate models. Multivariate models allow studying correlated evolution and selection, comparing evolutionary rates, and generally provide an increased statistical power.

Initially developed in the context of phylogenetic analysis of multiple morphometric traits, use of mvMORPH can be extended to any biological dataset with multiple covarying continuous traits. The fitting models all include the possibility to use SIMMAP-like mapping of discrete traits [6], which may be useful for fitting changes along lineages at a given point in time. All models provide diagnostic metrics for convergence and reliability of estimates, as well as the possibility to include trait measurement errors in model estimates, and to conduct simulations based on estimated parameters.

New features provided by the mvMORPH package also include the possibility of fitting models with changes in the mode of evolution along the phylogeny, which will be particularly meaningful in comparative analyses that include extinct taxa, e.g., when testing changes in evolutionary mode associated with global biotic/abiotic events. Such multivariate models are based on additive, non-ultrametric trees which are not easily handled by current packages that implement fast algorithms for fitting evolutionary models (e.g., [7-8]). mvMORPH uses fast C codes to compute the evolutionary variance-covariance matrix involved in the likelihood calculation.

Models currently available in mvMORPH represent 14 different parameterizations of multivariate Brownian Motion, Ornstein-Uhlenbeck process, ACDC and Early Burst models of evolution, as well as models of shift in modes of evolution. These different parameterizations allow assessing the importance of estimated parameters on each model (e.g., models constrained to equal variance for each trait, different variances and covariances depending on the selective regimes, independent drift, etc).

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