

Multivariate linear phylogenetic comparative models and adaptation

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Abstract

The need for taking into account evolutionary relationships when analyzing between species data is by now firmly established. However stochastic models allowing for multiple co-evolving traits are extremely limited and essentially do not go beyond a multivariate Brownian motion with a trend. This does not allow one to model adaptation, not even with a definition as weak as convergence in distribution. The linear stochastic differential equation model presented in [3],

$$d\vec{Y}(t) = -\mathbf{A}(\vec{Y}(t) - \vec{\psi}(t))dt + \Sigma d\vec{W}(t),$$

where $\vec{W}(t)$ is a standard Brownian motion, allows for modelling adapting traits with such as notion of adaptation but up till now had only partial multivariate implementations [2, 4]. In the talk a recently developed R package [1] which nearly completely covers the framework from [3] in multiple dimensions will be presented. The properties of the mean and covariance functions will be discussed in terms of the definition of adaptation as weak convergence. With multiple interacting traits the study of adaptation requires one to look at conditional distributions of interest, especially their limiting properties. These will be presented and discussed with an emphasis on their biological interpretation. For example if we consider the multivariate extension of the model from [4],

$$\begin{aligned} d\vec{Y}(t) &= -\mathbf{A}(\vec{Y}(t) - (\vec{\psi}(t) + \mathbf{B}\vec{X}(t)))dt + \Sigma_y d\vec{W}_y(t) \\ d\vec{X}(t) &= \Sigma_x d\vec{W}_x(t), \end{aligned}$$

then if \mathbf{A} has positive real part eigenvalues, the regression coefficient of $\vec{Y}(t)$ on $\vec{X}(t)$ will converge to \mathbf{B} , but if the \vec{X} variables are also adapting,

$$\begin{aligned} d\vec{Y}(t) &= -\mathbf{A}_y(\vec{Y}(t) - (\vec{\psi}_y(t) + \mathbf{B}\vec{X}(t)))dt + \Sigma_y d\vec{W}_y(t) \\ d\vec{X}(t) &= -\mathbf{A}_x(\vec{X}(t) - \vec{\psi}_x(t))dt + \Sigma_x d\vec{W}_x(t), \end{aligned}$$

then this limit will not in general equal \mathbf{B} . This can be interpreted that even if evolution would go on for infinity the \vec{Y} and \vec{X} traits would never evolve to the optimal relationship between them. These concepts will be illustrated by an example re-analysis of the Cervidae dataset [5].

Keywords

Ornstein–Uhlenbeck process, Phylogenetic comparative methods, Multivariate models, Evolution, Adaptation.

References

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