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# Multivariate comparative analysis

The need for taking into account phylogenetic dependencies between trait measurements in comparative analysis is something which has become obvious. One approach to capture this dependency is to assume that the trait(s) evolve as a time dependent branching stochastic differential equation along the phylogenentic tree. The development of this branch of comparative analysis started with [1] and was continued in [2],[3],[4],[5]. However all these proposed methods lacked a fully multivariate implementation of the proposed models. We have developed a generalization of these models into the fully multivariate setting and implemented an estimation package in `R` to analyze comparative data under these models. The multivariate setting gives us much more flexibility and allows to e.g. model codevelopment of allometry, indications of a trade-off and gain understanding of trait coevolution. In the talk we will discuss the multivariate model, possible hypothesis (allometry, trade-off) one can study with it and go through an example study of how sexual selection acts on the development of male canine and body sizes in Primates.

## REFERENCES

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