1172-62-269      **Paul Bastide\***, IMAG – UMR 5149, Université de Montpellier, CC51, Place Eugène Bataillon, 34000 Montpellier, France, and **Claudia Solís-Lemus**, **Ricardo Kriebel**, **K William Sparks** and **Cécile Ané**. *Phylogenetic Comparative Methods on Species Networks.*

The goal of Phylogenetic Comparative Methods (PCMs) is to study the distribution of quantitative traits among related species. The observed traits are often seen as the result of a Brownian Motion (BM) running along a phylogenetic tree. Reticulation events such as hybridization can affect a species' traits, and are modeled using a phylogenetic network instead of a tree. New models of trait evolution are needed, applicable to networks.

One natural extension of the BM is to use a weighted average for a hybrid's trait. This model induces a new variance structure among observed traits, which we show how to compute efficiently. This allows us to extend some standard PCM tools to this new framework, including phylogenetic regression.

The network structure also introduces some new effects, which cannot be studied using a tree. Here, we show how transgressive evolution (TE) events, that see a hybrid trait outside of the range of its two parents, can be modeled using a linear regression with fixed effects.

We assess the behavior of this framework through simulations and a theoretical power study of TE detection. Applied to a dataset of Xiphophorus fishes, these methods confirm and extend previous analyses. These tools are available in the Julia package PhyloNetworks. (Received August 30, 2021)