

## **AFEchidna is a R package for genetic evaluation of plant and animal breeding datasets**

Weihua Zhang<sup>1,2</sup> Ruiyan Wei<sup>1</sup> Yan Liu<sup>1</sup> Yuanzhen Lin<sup>1</sup>

(1 College of Forestry and Landscape Architecture, South China Agricultural University / Guangdong Key

Laboratory for Innovative Development and Utilization of Forest Plant Germplasm, Guangzhou 510642; 2 Guangdong Academy of Forestry, Guangzhou 510520)

**Abstract:** Progeny tests play important roles in plant and animal breeding programs, and mixed linear models are usually performed to estimate variance components of random effects, estimate the fixed effects (Best Linear Unbiased Estimates, BLUES) and predict the random effects (Best Linear Unbiased Predictions, BLUPs) via restricted maximum likelihood (REML) methods in progeny test datasets. The current pioneer software for genetic assessment is ASReml, but it is commercial and expensive. Although there is free software such as Echidna or the R package sommer, the Echidna syntax is complex and the R package functionality is limited. Therefore, this study aims to develop a R package named AFEchidna based on Echidna software. The mixed linear models are conveniently implemented for users through the AFEchidna package to solve variance components, genetic parameters and the BLUP values of random effects, and the batch analysis of multiple traits, multiple variance structures and multiple genetic parameters can be also performed, as well as comparison between different models and genomic BLUP analysis. The AFEchidna package is free, please email us (yzhlinscau@163.com) to get a copy if one is interested for it. The AFEchidna package is developed to expand free genetic assessment software with the expectation that its efficiency could be close to the commercial software.