

The R-Package 'synbreed'

note: vignette is obsolete and will be changed soon

Valentin Wimmer*

March 10, 2011

Abstract

This document gives an introduction to the R-package **synbreed**. This package implements statistical and genetic methods for plant and animal breeding. The goal is to create an analysis pipeline for genomic selection. This comprises tools for genotypic, phenotypic and pedigree data. The steps of a typical analysis are presented in this document. This starts with the coding of the marker data, followed by the estimation of relatedness according to pedigree or molecular marker data, e.g. according to ?). Finally the estimation of breeding values and estimation of variance components using mixed models is described. All steps are illustrated using simulated data for maize.

Keywords: synergistic plant and animal breeding, simulation, pedigree, genomic marker data, mixed models, genomic selection

1 Acknowledgements

This research was funded by the German Federal Ministry of Education and Research (BMBF) within the AgroClustEr *Synbreed – Synergistic plant and animal breeding*.

*Author of correspondence. Contact: Institute for plant breeding, Technische Universität München, Emil-Ramann-Str. 4, 85354 Freising, Germany, Email: Valentin.Wimmer@wzw.tum.de