BGmisc: An R Package for Extended Behavior Genetics Analysis

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Summary

Behavior genetics focuses on understanding genetic and environmental influences on individual differences, traditionally through twin studies. With the expansion of research to more complex data structures like extended family data, there arises a need for specialized software tools. The BGmisc package fills this gap by offering a suite of functions specifically tailored for modeling such data.

Statement of need

As behavior genetics delves into more complex data structures like pedigrees, the limitations of current tools become evident. The BGmisc R package is designed specifically to address these challenges, going beyond what is available in tools like OpenMx and EasyMx that mainly focus on classical twin models.

Two widely used R packages in genetics modeling are OpenMx (Neale et al., 2016) and kinship2 (J. P. Sinnwell et al., 2014; J. Sinnwell & Therneau, 2022). The OpenMx (Neale et al., 2016) package is a workhorse in behavior genetic research. Not only is it a general purpose software for structural equation modeling that is popular among behavior geneticists (Garrison, 2018), but also for its unique features – the mxCheckIdentification() function. This function checks whether a model is identified, which means determining if there is a unique solution to estimate the model's parameters based on the observed data. In addition, EasyMx (Hunter, 2023) is a more user-friendly package that streamlines the process of building and estimating structural equation models. It seamlessly integrates with OpenMx's infrastructure. Its functionalities range from foundational matrix builders like emxCholeskyVariance and emxGeneticFactorVariance to more specialized functions like emxTwinModel designed for classical twin models.

Although not a staple in behavior genetics, the kinship2 (J. P. Sinnwell et al., 2014) package provides core feature to the broader statistical genetics scientific community, such as computing genetic relatedness matrices and plotting pedigrees. It uses the Lange algorithm to compute relatedness, which BGmisc package extends the capabilities of kinship2 by introducing an alternative algorithm to calculate the relatedness coefficient, based on network models. This alternative algorithm harnesses networks to trace paths, applying traditional path tracing rules to the entirety of the network.

Despite their strengths, kinship2, EasyMx and OpenMx have limitations when it comes to handling extended family data. Notably, they lack functions for handling modern molecular designs (Kirkpatrick et al., 2021), modeling genetic complex relationships, inferring relatedness, or simulating pedigrees. Additionally, they can be computationally inefficient when dealing with large pedigrees.

Features

The `BGmisc` package offers an array of features tailored for in-depth behavior genetics analysis, organized under two headings for clarity:

Pedigree Analysis and Simulation:

- Relatedness Coefficient Calculation: Using path tracing rules first described in (Wright, 1922), `BGmisc` calculates the relatedness coefficient between all pairs of individuals based on mother and father identifiers. Building upon established packages such as `kinship2`, `BGmisc` introduces an alternative algorithm for calculating the relatedness coefficient. Leveraging the power of network analysis, this new method traces paths using classic path tracing rules applied to the entire network, bypassing the need for a multi-step recursive approach.

- Pedigree Conversion: `BGmisc` converts pedigrees into various relatedness matrices, including additive genetics, mitochondrial, common nuclear, and extended environmental relatedness matrices.

- Pedigree Simulation: `BGmisc` simulates pedigrees based on parameters including the number of children per mate, generations, sex ratio of newborns, and mating rate.

Modeling and Relatedness:

- Relatedness Inference: `BGmisc` infers the relatedness between two groups based on their observed total correlation, given additive genetic and shared environmental parameters.

- Model Identification: `BGmisc` evaluates whether a variance components model is identified and fits the model's estimated variance components to observed covariance data. The technical aspects related to model identification have been described in Hunter et al. (2021).

These tools collectively provide a valuable resource for behavior geneticists and others working with extended family data. Developed as part of a grant, it has been used in several ongoing projects (Burt, 2023; Garrison et al., 2023; Hunter et al., 2023; Lyu et al., 2023) and theses (Lyu, 2023).

Availability

The `BGmisc` package is open-source and available on both GitHub at https://github.com/R-Computing-Lab/BGmisc and the Comprehensive R Archive Network (CRAN) at https://cran.r-project.org/package=BGmisc. It is licensed under the GNU General Public License

Acknowledgements

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