

# BGmisc: An R Package for Extended Behavior Genetics Analysis

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## Summary

The field of behavior genetics focuses on illuminating genetic and environmental influences on individual differences. Traditionally, twin studies have been at the forefront of this discipline. However, research has moved beyond the classical twin design to embrace more complex family structures such as children of twins (CoT) (D'Onofrio et al., 2003), mother-daughter-aunt-niece (MDAN) (Rodgers, Bard, Johnson, D'Onofrio, & Miller, 2008), and other extended family designs. These expansions allow for a deeper, more nuanced exploration of genetic and environmental influences, but it also introduces challenges, particularly in data structuring and modeling. In particular, the data structures inherent in these more complicated family designs are orders of magnitude larger than traditional designs. In the classical twin study, for example, a family will consist of a single pair of twins (i.e., two people), whereas in the MDAN design, a family consists of two mother-daughter pairs (i.e., four people). This problem quickly becomes intractable when applied to very extended family pedigrees, where a single family can be of any size. The BGmisc package addresses this gap by offering a comprehensive suite of functions for structuring and modeling extended family pedigree data.

## Statement of need

As behavior genetics delves into more complex data structures like extended pedigrees, the limitations of current tools become evident. Understandably, packages like OpenMx (Neale et al., 2016), EasyMx (Hunter, 2023), and kinship2 (J. P. Sinnwell, Therneau, & Schaid, 2014; J. Sinnwell & Therneau, 2022) were built for smaller families and classical designs. In contrast, the BGmisc R package was specifically developed to structure and model extended family pedigree data.

Two widely-used R packages in genetic 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 general-purpose software for structural equation modeling that is popular among behavior geneticists (Garrison, 2018) for its unique features, like the `mxCheckIdentification()` function. This function checks whether a model is identified, 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. Despite their strengths, EasyMx and OpenMx have limitations when

43 handling extended family data. Notably, they lack functions for handling modern molecular  
44 designs (Kirkpatrick, Pritikin, Hunter, & Neale, 2021), modeling complex genetic relationships,  
45 inferring relatedness, and simulating pedigrees.

46 Although not a staple in behavior genetics, the kinship2 (J. P. Sinnwell et al., 2014) package  
47 provides core features to the broader statistical genetics scientific community, such as plotting  
48 pedigrees and computing genetic relatedness matrices. It uses the Lange algorithm (Lange,  
49 2002) to compute relatedness coefficients. This recursive algorithm is discussed in great detail  
50 elsewhere, laying out several boundary conditions and recurrence rules. The BGmisc package  
51 extends the capabilities of kinship2 by introducing an alternative algorithm to calculate the  
52 relatedness coefficient based on network models. By applying classic path-tracing rules to the  
53 entire network, this new method is computationally more efficient by eliminating the need for  
54 a multi-step recursive approach.

## 55 Features

56 The BGmisc package offers features tailored for extended behavior genetics analysis. These  
57 features are grouped under two main categories, mirroring the structure presented in our  
58 vignettes.

### 59 Modeling and Relatedness:

- 60 ■ Model Identification: BGmisc evaluates whether a variance components model is identified  
61 and fits the model's estimated variance components to observed covariance data. The  
62 technical aspects related to model identification have been described by Hunter, Garrison,  
63 Burt, & Rodgers (2021).
- 64 ■ Relatedness Coefficient Calculation: Using path tracing rules first described by Wright  
65 (1922) and formalized by McArdle & McDonald (1984), BGmisc calculates the (sparse)  
66 relatedness coefficients between all pairs of individuals in extended pedigrees based solely  
67 on mother and father identifiers.
- 68 ■ Relatedness Inference: BGmisc infers the relatedness between two groups based on their  
69 observed total correlation, given additive genetic and shared environmental parameters.

### 70 Pedigree Analysis and Simulation:

- 71 ■ Pedigree Conversion: BGmisc converts pedigrees into various relatedness matrices, in-  
72 cluding additive genetics, mitochondrial, common nuclear, and extended environmental  
73 relatedness matrices.
- 74 ■ Pedigree Simulation: BGmisc simulates pedigrees based on parameters including the  
75 number of children per mate, generations, sex ratio of newborns, and mating rate.

76 Collectively, these tools provide a valuable resource for behavior geneticists and others who  
77 work with extended family data. They were developed as part of a grant and have been used  
78 in several ongoing projects (Burt, 2023; Garrison et al., 2023; Hunter et al., 2023; Lyu et al.,  
79 2023) and theses (Lyu, 2023).

## 80 Availability

81 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.

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