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<http://lib.stat.cmu.edu/R/CRAN/web/views/Genetics.html>

<https://cran.r-project.org/web/packages/GameTheory/vignettes/GameTheory.pdf>

<https://cran.r-project.org/web/packages/GA/index.html>

<https://cran.r-project.org/web/packages/DEoptim/index.html>

<http://www.epimodel.org/>

Quantitative genetics deals with the evolution and inheritance of continuous traits, like body size, bone lengths, gene expressions or any other inheritable characteristic that can be measured on a continuous scale, or which can be transformed to a continuous scale. This framework has been used in selective breeding and in describing the different sources of variation in natural populations, as well as understanding the interaction of evolutionary processes with this variation[32](https://f1000research.com/articles/4-925/v3#ref-32).

Evolutionary theory shows that evolution depends critically on the available variation in a given population. When dealing with many quantitative traits this variation is expressed in the form of a covariance matrix, particularly the additive genetic covariance matrix or sometimes the phenotypic matrix, when the genetic matrix is unavailable and there is evidence the phenotypic matrix is sufficiently similar to the genetic matrix. Given this mathematical representation of available variation, the EvolQG package provides functions for calculation of relevant evolutionary statistics; estimation of sampling error; corrections for this error; matrix comparison via correlations, distances and matrix decomposition; analysis of modularity patterns; and functions for testing evolutionary hypotheses on taxa diversification.

Melo D, Garcia G, Hubbe A et al. EvolQG - An R package for evolutionary quantitative genetics [version 3; referees: 2 approved, 1 approved with reservations]. *F1000Research* 2016, 4:925 (doi: [10.12688/f1000research.7082.3](http://dx.doi.org/10.12688/f1000research.7082.3))

qgtools