**PORTAL PAGE**

**SQuID goal**

**SQuID** stands for **S**tatistical **Qu**antification of **I**ndividual **D**ifferences and is the product of the SQuID working group. The package aims to help scholars who, like us, are interested in understanding patterns of phenotypic variance. Individual differences are the raw material for natural selection to act on and hence the basis of evolutionary adaptation. Understanding the sources of phenotypic variance is thus a most essential feature of biological investigation and mixed effects models offer a great, albeit challenging tool. Disseminating the properties, potentials and interpretational challenges in the research community is thus a foremost goal of SQuID.

The squid package has two main objectives: First, it provides an educational tool useful for students, teachers and researchers who want to learn to use mixed-effects models. Users can experience how the mixed-effects model framework can be used to understand distinct biological phenomena by interactively exploring simulated multilevel data. Second, squid offers research opportunities to those who are already familiar with mixed-effects models, as squid enables the generation of datasets that users may download and use for a range of simulation-based statistical analyses such as power and sensitivity analysis of multilevel and multivariate data.

**Guidance for users**

*For beginners:* The SQuID modules are designed for users who have some but not a lot of statistical background, particularly with linear mixed models. We strongly recommend that if you are in this category, you begin with the module “Basic Lessons”. That should be followed by the module “Non-stochastic environments”. You will need to be very comfortable with the ideas here before moving on. Which module you choose next depends on your interests but Step 1 in module “Multidimensional Plasticity” introduces multiple regression. The module “Random regression” may also be good to do after module “Non- stochastic environments”.

*For teachers:* The SQuID modules can be very useful for teaching statistical concepts, especially ones related to linear mixed models. Which module to use depends on your students and what you want them to learn. Brief descriptors of each module are available on this page (instructions to see them). We also recommend that you skim some of the modules or visit the full equation step-by-step page to better understand how SQuID works.

*For Experts:* SQuID was designed to provide a user-friendly and web-based program to simulate data for testing a variety of ideas about sampling and bias in hierarchical mixed modeling. For those very familiar with these approaches and curious about SQuID, we recommend initially using the module “Full model” and the option “Step-by-step”. Once you understand how SQuID works, the “Express model” version will work best. Finally, we have SQuID available as an R function “runSQUIDfct()” for those interested in doing efficient simulations.

**Brief description of modules**

**SQuID** is made to help researchers to become familiar with multilevel variation, and to build up sampling designs for their study. SQuID is built up as a series of modules thatguide the user into situations of increasing complexity to explore the dynamics between the way records are collected and estimates of parameters of specific interest; The last module (Module 11) is the ***full model simulation package*** thatallows the user to generate data sets that can then be used to run analyses in the statistical package of their choice for specific research questions.

**SQuID** is based on a mathematical model that creates a group of individuals (i.e. study population) repeatedly expressing phenotypes, for one or different traits, in uniform time. Phenotypic values of traits are generated following the general principle of the phenotypic equation (Dingemanse & Dochtermann 2013, Journal of Animal Ecology): phenotypic variance (*Vp*) is assumed to be the sum of a series of components (see the full model). The user has thus the flexibility to add different variance components that will form the phenotype of the individual at each time step, and to set up the relative importance of each component. SQuID then allows the user to collect a subsample of phenotypes for each simulated individual (i.e. operational data set), according to a specific sampling design. For most of the modules, the operational data set generated is automatically fed into a statistical model in R and the main results of the analysis shown in an output. For module 11 (full model) the user has the opportunity to download the operational data set for further analyses.

**References**

Allegue, H., Araya-Ajoy, Y.G., Dingemanse, N.J., Dochtermann N.A., Garamszegi, L.Z., Nakagawa, S., Réale, D., Schielzeth, H. and Westneat, D.F. (2016). SQuID - Statistical Quantification of Individual Differences: an educational and statistical tool for understanding multi-level phenotypic data in the mixed modelling framework. Methods in Ecology and Evolution, submitted manuscript.  
  
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