**BACKGROUND PAGE**

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The phenotype of a trait in an individual results from a sum of genetic and environmental influences. Phenotypic variation is structured in a hierarchical way and the hierarchical modeling in mixed effect models is great tool to analyze and decompose such variation. Phenotypes vary across species, across populations of the same species, across individuals of the same population, and across repeated observations of the same individual. We focused on the individual level because it represents one of the most important biological levels to both ecological and evolutionary processes. Different sources of variation are at the origin of the phenotype of an individual. Individuals may differ in their phenotypes because they carry different gene variants (i.e. alleles). But individuals also experience different environments during their lifetime. Some environmental influences impose a lasting mark on the phenotype, while others are more ephemerous. The former tend to produce long-lasting, among-individual variation, while the latter causes within-individual variation. However, this depends on the time scale at which the measurements of the phenotypes are done relative that of the environmental influences. Furthermore, individuals differ not only in their average phenotypes but also in how they respond to changes in their environment (i.e. differences in individual phenotypic plasticity). This represents an interaction between the among- and the within-individual levels of variation. The patterns of variation can, thus, be very complex. Selection can act differently on these different components of variance in the phenotypes of a trait, and this is why it is important to quantify their magnitude.

Mixed models are very flexible statistical tools that provide a way to estimate the variation at these different levels, and represent the general statistical framework for evolutionary biology. Because of the progress in computational capacities mixed models have become increasingly popular among ecologists and evolutionary biologists over the last decade. However, fitting mixed model is not a straightforward exercise, and the way data are sampled among and within individuals can have strong implications on the outcome of the model. This is why we created the squid simulation tool that could help new users interested in decomposing phenotypic variance to get more familiar with the concept of hierarchical organization of traits, with mixed models and to avoid pitfalls caused by inappropriate sampling.

**SQuID biological goals**

SQuID seeks to understand patterns of phenotypic variance, which is the material on which natural selection is acting, and thus is a most essential feature of biological investigation. Different sources of variations are at the origin of the phenotype of an individual. Individuals differ in their phenotypes because they have different genes. They also experience different types of environmental effects during their lifetime. Some are imposing a very permanent mark on the phenotype over the whole lifetime. For example, by their parental behaviour individuals can affect their offspring phenotypes permanently, causing among-individual variation. Other environmental sources play more short-term effects on the phenotype, as individuals react in the plastic way to these sources, causing within-individual variation. The patterns of variation can be very complex. For instance individuals differ not only in their average phenotypes but also in how they can change their phenotype according to changes in the environment, which represents an interaction between the among- and the within-individual levels. Selection can act differently on these different components of variance in the phenotypes of a trait, and this is why it is important to estimate them. Mixed models are very flexible statistical tools that provide a way to estimate the variation at these different levels, and represent the general statistical framework for evolutionary biology. Because of the progress in computational capacities mixed models have become increasingly popular among ecologists and evolutionary biologists over the last decade. However, running mixed model is not a straightforward exercise, and the way data are sampled among and within individuals can have strong implications on the outcome of the model. This is why we considered it was necessary to produce a simulation tool that could help new users interested in decomposing phenotypic variance to get more familiar with the concept of hierarchical organization of traits, with mixed models and to avoid pitfalls caused by inappropriate sampling.