**ComGenR: A package for community genetics analyses**

M.K. Lau

* Community genetics works at the interface between community ecology and ecological genetics.
* As this field is inherently multi-disciplinary, it utilizes analytics from different fields of study in statistics, ecology and genetics.
* Here we present a package that brings together functions for community genetics analyses with the intent of merging and adding new analyses that are available to researchers in this field.
* After presenting the package, we use tools in the package to show that assessing from a PerMANOVA based approach should be preferred to a NMDS ordination approach when quantifying community heritability
* The package is available as a stable release on CRAN and as a development version on GitHub