egssimtools: an R package for the analysis of a model of speciation

This package comes with the ExplicitGenomeSpeciation program, an individual-based simulation of a speciation event with explicitly modelled diploid genomes and a flexible genotype-phenotype map. This package includes tools to facilitate the extraction and processing of the data generated by the simulation model. Throughout we will use example simulations from the `inst/extdata` folder.

Installation

To install the package, click on the RStudio project `egssimtools.Rproj` to open it in RStudio, then in the "Build" tab, click "Install and Restart". The package should be installed on your machine.

Let us now load the package.

```
library(egssimtools)
library(tidyverse)
library(cowplot)
```

Each simulation is stored in a simulation folder. The content of a simulation folder depends on the settings used when running the program (see detailed description). This package introduces functions to retrieve data, but also parameters and genetic architectures saved during the simulations.