Sambar workflow

Load SambaR into R

source('C:/path/to/dir/SAMBAR.txt')

SambaR can be downloaded from Github: https://github.com/mennodejong1986/SambaR

Install and load dependencies

getpackages(mylib=NULL)

Import data (binary PED/MAP) into R

setwd('C:/path/to/workdir/')

importdata(inputprefix='prefix',samplefile=NULL, sumstatsfile=NULL,depthfile=FALSE)

Or instead convert from an existing genlight object:

genlight2sambar(genlight_object=NULL)

Filter data

filterdata(indmiss=0.25,snpmiss=0.1,min_mac=2 ,dohefilter=TRUE,snpdepthfilter=TRUE, min_spacing=500,nchroms=NULL,silent=TRUE)

Included: quality control, F, HWE, relatedness

Analyze data

population structure

findstructure(Kmax=6,add_legend=TRUE, legend_pos='bottomright',legend_cex=3, symbol_size=3)

Included: PCoA, PCA, DAPC, CA, MDS, admixture analyses (LEA), Tess3r

population differentiation

calcdistance(nchroms=NULL)

Included: Nei's D, (sliding window) Wright's Fst, Nei's Fst, Weir & Cockerham Fst, ABBA-BABA

genetic diversity

calcdiversity(nrsites=NULL,legend_cex=2.5)

Included: SFS, heterozygosity, nucleotide diversity, Watterson's theta, Tajima's D, private alleles, proportion segregating sites

selection analyses

selectionanalyses(do_pcadapt=TRUE,do_outflank =TRUE,do_fsthet=TRUE,export='pdf')

Included: GWDS, FstHet, OutFLANK, PCadapt

Sambar output