AutoPoly simulation overview

David Field

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This is an overview of the power testting routine for *AutoPoly* and detailed in Field et al., (in review A) and Field et al., (in review B). This includes: (1) Setting up initial metapopulation and generating the bases genetic data, (2) generating replicate data sets from the base, (3) population assignment power testing over a set (batch) of replicate data sets.

1. Setting up initial metapopulation

Unzip the file: *metaPopSim_autoPoly.zip*

run the code in here to begin the simulation: *build_Metapopulation.R*

Check the metapopulation is at the expected equilibrium value.

2. Generate replicates

To save computation time, in this example lets import a previously generated metapopulation with mean Fst = 0.09 All scripts and project files requires can be found in: *powerSims.zip*

Run the scripts within R project: *Fst0_09.Rproj* and *x6_Fst_0_09makeReps.R*

This will generate a new set of adults and offspring from the metapopulation. In the current example, the script is set to make 10 replicates data sets for each of three different migration rates (0.02,0.1,0.2).

3. Run power testing (batches)

This script will run the population assignment and evaluate the power of batches of individual replicates. Currently, it is set to evaluate 10 replicates data sets for each of three different migration rates (0.02,0.1,0.2), and also do this for phenotype data at 24 loci. For exploring other combinations of parameters you would have to alter the details in the object *batchParameters*

All results will be sent to folder specified in *folder_powerSimRes*:

e.g. ~/SimulationIslandModel/powerSims/Fst0_09/Fst0_09_assign/results

And will appear in a file with the following (depending on ploidy and Fst): e.g. x6_Fst0_09_batchParameters

In these files, you will see an excel file with the first nine columns list the specific parameters for the batch.

The next column headers include:

- Accuracy_WIPOP = accuracy for the crosses within populations
- Accuracy_BWPOP = accuracy for the crosses between populations
- Accuracy_Total = total accuracy across within and between populations
- Efficiency_WIPOP = efficiency of correctly identifying within population crosses
- Efficiency_BWPOP = efficiency of correctly identifying between population crosses
- Efficiency_Total = total effiency across within and between populations

- B-POP Estimate = point estimate of migration rate among populations
- Critical80 = critical values at 80%
- Critical90 = critical values at 90%
- Critical95 = critical values at 95%
- Critical99 = critical values at 99%
- Assign80 = the proportion of individuals that could be assigned with 80% confidence
- Assign90 = the proportion of individuals that could be assigned with 90% confidence
- Assign95 = the proportion of individuals that could be assigned with 95% confidence
- Assign99 = the proportion of individuals that could be assigned with 99% confidence

References

Field DL, Broadhurst LM, Elliot C, Young AG (in review A). Population assignment in autopolyploids.
Field DL, Broadhurst LM, Young AG (in review B). AutoPoly: An R package for population assignment in autopolyploids.