**File:**

Pond\_Dist.csv

**Description:**

Distance between sampled ponds, measured in meters

**Variables:**

PNTID1 = Starting pond location

PNTID2 = Ending pond location

DISTANCE = Euclidean distance measured in meters

**Use:**

This file is used for isolation-by-distance analyses in code files ‘IBD\_Tests.R’, ‘MixedSample\_Analysis.R’, and ‘RatioMixed.R’

**File:**

AMAC\_NoSibs.dat

**Description:**

FSTAT-formatted file containing all the adult, larval, and embryo genotypes at each of five sampled ponds. All life stages are pooled together in this data file and all siblings sampled from within the same pond have been removed using COLONY.

**Use:**

This file is used with the ‘MixedSample\_Analysis.R’ code file.

**File:**

AMAC\_Sibs.dat

**Description:**

FSTAT-formatted file containing all the adult, larval, and embryo genotypes at each of five sampled ponds. All life stages are pooled together in this data. No siblings have been removed.

**Use:**

This file is used with the ‘MixedSample\_Analysis.R’ code file.

**File:**

amac\_data.csv

**Description:**

A comma separated file containing population genetic summary statistics at each pond for each life stage. All siblings were removed using COLONY prior to calculating the values presented in this data file.

**Variables:**

pond = The pond (or pond-pair) that a statistic was calculated for

measure = The genetic measure used

* a.rich = rarefied allelic richness
* private = frequency of private alleles
* samples.removed = proportion of tissue samples removed following COLONY analysis to identify full siblings
* Ne = Effective population size as measured using the linkage disequilibrium approach in COLONY
* He = Expected heterozygosity
* Fst = genetic differentiation for all pairwise comparisons
* Dc = chord distance for all pairwise comparisons

adult = Adult life stage

embryo = Embryo life stage

larvae = Larval life stage

**Use:**

This file is used with the ‘AMAC\_Analysis.R’, ‘IBD\_Tests.R’, and ‘RatioMixed.R’ code files

**File:**

amac\_data\_all.csv

**Description:**

A comma separated file containing population genetic summary statistics at each pond for each life stage. No siblings were removed using COLONY prior to calculating the values presented in this data file.

**Variables:**

pond = The pond (or pond-pair) that a statistic was calculated for

measure = The genetic measure used

* a.rich = rarefied allelic richness
* private = frequency of private alleles
* samples.removed = proportion of tissue samples removed following COLONY analysis to identify full siblings
* Ne = Effective population size as measured using the linkage disequilibrium approach in COLONY
* He = Expected heterozygosity
* Fst = genetic differentiation for all pairwise comparisons
* Dc = chord distance for all pairwise comparisons

adult = Adult life stage

embryo = Embryo life stage

larvae = Larval life stage

**Use:**

This file is used with the ‘AMAC\_Analysis.R’, ‘IBD\_Tests.R’, and ‘RatioMixed.R’ code files

**File:**

adult.gen

**Description:**

GenePop-formatted file containing all the adult genotypes at each of five sampled ponds. No siblings have been removed. This file was used to calculate population genetic summary statistics.

**File:**

adult\_nosibs.gen

**Description:**

GenePop-formatted file containing adult genotypes at each of five sampled ponds. Siblings have been removed. This file was used to calculate population genetic summary statistics.

**File:**

embryo.gen

**Description:**

GenePop-formatted file containing all the embryo genotypes at each of five sampled ponds. No siblings have been removed. This file was used to calculate population genetic summary statistics.

**File:**

embryo\_nosibs.gen

**Description:**

GenePop-formatted file containing embryo genotypes at each of five sampled ponds. Siblings have been removed. This file was used to calculate population genetic summary statistics.

**File:**

larvae.gen

**Description:**

GenePop-formatted file containing all the larval genotypes at each of five sampled ponds. No siblings have been removed. This file was used to calculate population genetic summary statistics.

**File:**

larvae\_nosibs.gen

**Description:**

GenePop-formatted file containing larval genotypes at each of five sampled ponds. Siblings have been removed. This file was used to calculate population genetic summary statistics.

**File:**

AMAC\_analysis.R

**Description:**

R code file to conduct bootstrap ANOVA and permutation t-tests to assess difference in population genetic parameters between life stages, with and without siblings.

**File:**

MixedSample\_Analysis.R

**Description:**

R code file to conduct mixed tissue analysis to determine the effects of pooling adult, larval, and embryonic samples together.

**File:**

IBD\_Tests.R

**Description:**

R code file to calculate the Mantel correlation and P-value for each life stage, with and without siblings.

**File:**

RatioMixed\_v2.R

**Description:**

R code file to assess how Mantel *r* and P-values change as the proportion of larvae and embryos included with adult tissue samples increases. Also assess the effect of sub-sampling the microsatellite data from 15 to 10 and 5.