

Evanno et al., 2005. Molecular Ecology 14 , 2611–2620

**Can Structure detect the true (K) in when patterns of dispersal are not the same or when population structure is complex?**

**OBJECTIVE – To simulate a population that has a more complex population structure, then use this data to test if STRUCTURE detects K – Specifically we will create a data set that simulates a hierarchical structure**

**FIRST STEP – Simulate data. Prompts from EASYPOP are in normal text below. The responses to the prompts are given below each prompt in bold. My comments are italicized next to the response.**

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EASYPOP (v. 2.0.1)  
Author: F. Balloux  
Available at: <http://www.unil.ch/izea/software/easypop.html>  
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Ploidy level ? (0=haplo-diploid; 1=haploid; 2=diploid)

**2 – *assume we are working with a diploid organism***

Two sexes?:y/n

**N – *Assume we are working with plants or hermaphrodites***

Random mating?:y/n

**Y**

Number of populations ?

**6 – *Pick a number for the total number of pops -***

Same number of individuals in each populations?:y/n

**Y – *Just to make this easy on us***

Number of individuals ?

**50 – *Sounds like a good number***

Same migration scheme over all simulation? (y/n)

**y**

migration model?

1 = 1-dimension stepping stone;

2 = 2-dimension stepping stone (only with a square number of populations, e.g. 9, 16,..144..);

3 = island model;

4 = hierarchical stepping stone ('contact zone');

5 = hierarchical island ;

6 = spatial models;

**5 – *We want to simulate a hierarchical model to test STRUCTURE***

Number of archipelagos?

**2 – Make this less than total number of pops and less than 5. Uppermost layer of population structure that we want to detect. For the purposes of our demonstration, do not make this number**

Same number of populations in each archipelago:y/n

**N – Your choice here – if you select N, decide how you will divide your pops, if you enter Y, populations are divided equally amongst archipelagos**

enter number of populations of archipelago 1

2

enter number of populations of archipelago 2

4

proportion of migration within groups?(between 0 and 1)

**.01 – levels of migration within an archipelago – you want this number to be smaller than the next input, proportion of migration between groups so that there is a chance for population structure to develop**

proportion of migration between groups?(between 0 and 1)

**.005 – Smaller than the previous so that migration does not wash out the structure**

Number of loci ?

**10 – Put your favorite number here – just keep track of this for subsequent analysis**

Free recombination between loci?:y/n

**Y – Assuming no linkage between markers – a common SSR assumption**

Do all loci have the same mutation scheme?:y/n

**Y - yes**

Mutation rate?(between 0 and 1, e.g. 0.0001)

**.0001 – keep it small so that mutation does not wash out our structure**

Mutation model

1= Kam,(same probability to mutate to any allelic state)

2= Ssm, (single step mutation model)

3= Mixed model of Ssm with a proportion of Kam mutation events)

4= Mixed model of Ssm with a proportion of double step mutation events)

**2 – This is the common SSR model used (perhaps incorrectly, but...)**

Number of possible allelic states?(below 1000)

**10 – number of alleles per locus**

Variability of the initial population

1= Maximal, (randomly assigned alleles)

2= Minimal, (all individuals start with the same allele)

1

Number of generations ?

**10000 – Choose enough to get some separation.**

Do you want the complete dataset in the '.dat' and '.gen' result files?:y/n

y

Do you want a file giving the complete pedigree of the simulation?:y/n

(Please notice that this file can be very huge and will slow down simulations)

n

Name of the file?

**testpop1 – Name it something you will remember.**

Number of replicates? (between 1 and 999)

**1 – Just one for class purposes**

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**STEP 2:** Convert data into .str format.

OPEN CONVERT

- ➔ Load data – choose GENPOP File.
- ➔ Find your file that you just created with the .gen
- ➔ Rewrite the pop names – I don't know why it helps, but it does.
- ➔ Choose . str output.

**STEP 3:** Run STRUCTURE as we did in previous exercise – except for 1 changes. 5 iterations - of K 1 to 6.

SAVE Summary of Analysis as a txt file.

**STEP 4:** Generate ad hoc statistic of delta K – 2<sup>nd</sup> rate order change

Open in Excel. Open XXX -

Open text file – delimited by spaces.

Generate delta K statistic for second rate order change:

Delta K = mean(second order rate change of log probability)/ s.d. log probability

I've created a spreadsheet that does the dirty work for you. Open “excel for delta K”.

Copy the ln (P) statistic and paste it into column D.