

Kinship and Relatedness

SPAGeDi

Basics

Download: <http://www.ulb.be/sciences/ecoevol/spagedi.html>

Operating system: PC under Windows 9x or later versions, or VirtualPC for Macintosh user's.

File format: SPAGeDi, GENEPOP, FSTAT

Data type: Dominant genotype data (RAPD, AFLP) in diploid organisms, or co-dominant genotype data (microsatellites, RFLP, isozymes, etc.) of any ploidy level

Background

SPAGeDi is designed to characterize the spatial genetic structure of mapped individuals and/or mapped populations using genotype data of any ploidy level

Pros

Multiple ploidy levels, works on the individual or population level, many statistics from which to choose.

Cons

Command line interface, possibly too many options

Getting started

1. Load data file

If using SPAGeDi file

- a. Either drag file onto SPAGeDi icon
- b. Or open program
- c. Enter name of file

If using GENEPOP or FSTAT file

- d. Open program
- e. <Spacebar> <Enter>
- f. Select format:
 - i. 1 = GENEPOP
 - ii. 2 = FSTAT
- g. Enter name of data file
- h. Enter name of desired SPAGeDi file
- i. Enter name of desired results file

When the program is complete it will return basic information on your data file to verify

2. Select analysis level

- a. 1 = individual (kinship coefficients)
- b. 2 = population (F-statistics)

From here there are many options for various calculations. The following is a list of some of the choices, for more information and descriptions of the tests consult the SPAGeDi User Manual.

Statistics

Individual co-dominant markers

1. Kinship coefficient (J. Nason)
 2. Kinship coefficient (Ritland)
 3. Relationship coefficient (Moran's *I* statistic)
 4. Relationship coefficient (Queller and Goodnight)
 5. Relationship coefficient (Lynch and Ritland)
 6. Relationship coefficient (Wang)
 7. Relationship coefficient (Li et al.)
 8. Fraternity coefficient (Lynch and Ritland)
 9. Fraternity coefficient (Wang)
 10. Distant measure (Rousset)
 11. Correlation coefficient for microsatellites (Streiff)
- *4-9 can only be calculated with diploid data. 5, 6, 8, and 9 assume HWE. 10 cannot calculate haploid data*

Individual dominant markers

1. Kinship coefficient (Hardy)
2. Relationship coefficient (Hardy)

Additional Information

k_0 = the probability of two individuals sharing 0 alleles
 k_1 = the probability of two individuals sharing 1 allele
 k_2 = the probability of two individuals sharing 2 alleles

$k_0 + k_1 + k_2 = 1$
 $r = \frac{1}{2} k_1 + k_2$ (r = relationship coefficient)
 $r = 2\theta$ (θ = kinship coefficient)
 $\Delta = k_2$ (Δ = fraternity coefficient)

Therefore we can calculate:

$k_0 = 1 - 3\Delta - 2r$
 $k_1 = 2(r - \Delta)$
 $k_2 = \Delta$

Relationship	k_2	k_1	k_0	$\theta = k_1/4 + k_2/2$
Identical twins	1	0	0	1/2
Full-siblings	1/4	1/2	1/4	1/4
Parent-child	0	1	0	1/4
Double first cousins	1/16	3/8	9/16	1/8
Half-siblings*	0	1/2	1/2	1/8
First cousins	0	1/4	3/4	1/16
Unrelated	0	0	1	0

*Also grandparent-grandchild and avuncular (for example, uncle-niece). The table shows the three identity-by-descent probabilities (k_{0-2}) and the coancestry coefficients (θ) for common relationships. Note that the coancestry coefficient for full-siblings and parent-child is the same (1/4), but that the pattern of allele sharing is different in each case (that is, there is a different set of k values). k_i , the probability of sharing i number of identical-by-descent alleles (where $i = 0-2$; see also BOX 1; FIG. 1; θ , the coancestry coefficient of two individuals (equivalent to the inbreeding coefficient of their offspring).