

Results file name:-

Q return OK

Basic info, RETURN

Level of Analysis

1 Individuals

2 Categorical

3 Spatial

4 S+C

Statistics

Individual

1 Kinship

2 Kinship

3

4

5

6

7

8

9

10

Population

Pairwise genetic distances b/c alleles (Haplotype)

enter if detectable

Flagging w/ ref. allele freq. (default: freq. 1%)

Computational Population Options

1 Matrix input

2 Regression

3 Perm. tests

4 Jackknife

5 Restricted

6 Ref. allele freqs

Pairwise dist. file name:

or

return

detectable

Minimal

Minimal

Perm. options

1 Pvals

2 # perms

3 RML

Types of Pairwise Comparisons

1

2

3

Output options

1

2

3

4

5

6

7

# perms

Gene Copy

# perms

Individual

hatched seed#

Ref. allele freq.

Spagetti





# Statistics

## Population

- ① F-stat / pair Fst
- ② F-stat / pair Rho
- ③ Gst / pair Gst
- ④ Gst / pair G<sub>ij</sub>
- ⑤ F-stat / pair Ds
- ⑥ R-stat / pair R<sub>ij</sub>
- ⑦ R-stat / pair D<sub>ij</sub>
- ⑧ Gst / pair N<sub>ij</sub>
- ⑨ Nst / pair N<sub>ij</sub>

## Computational Options

- ① Matrix pairwise snp dist
- ② Restricted regression
- ③ Permutation tests
- ④ Jackknife over loci
- ⑤ 
- ⑥ Pairwise Fst (or Rst or Rho) as  $\frac{F_T}{1-F_T}$  ratios

⑦  file: pairwise genetic distances by alleles  
(order of data file)

Permutation  
(1-3) same  
(4) Diff. populations

→ (see below)

#Reps: [40, 20000]

## Output options

- ①
- ②
- ③
- ④
- ⑤
- ⑥
- ⑦

→  $\phi$