

Results file name:

① return
② OK

Basic info, RETURN

Level
of
Analysis

- ① Individuals
- ② Categorical
- ③ Spatial
- ④ S+C

Spagedi:

Statistics

Individual

- ① Kinship
- ② Kinship
- ③
- ④
- ⑤
- ⑥
- ⑦
- ⑧
- ⑨

Population

- ①
- ②
- ③
- ④
- ⑤
- ⑥
- ⑦
- ⑧
- ⑨
- ⑩
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A
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Pairwise genetic
distances b/t
alleles (Haplotype)

Computational Permutation Options

- ① Matrix input
- ② Regression
- ③ Perm. tests
- ④ Jackknife
- ⑤ Restricted
- ⑥ Ref. allele freqs.

Filename w/ ref.
allele freqs.
(default: freq.txt)

Types of pairwise comp.

Pairwise
dist. file
name:

or
return
if
detectable
same

minimal
distance

maximal
distance

Perm.
options

- ① Prals
- ② # perms
- ③ RNG

Perms:
[40,20000]

perms
[0,14020000]
LOCATION

perms
(same as
①)

Reference
allele
freq.

- ①
- ②

Ref. allele
freq.

- ①
- ②
- ③

Types of
Pairwise
Comparisons

- ①
- ②
- ③
- ④
- ⑤

1st category

2nd category

Name of category

Output options

- ①
- ②
- ③
- ④
- ⑤
- ⑥
- ⑦

perms
Gene Copy
perms
INDIVIDUAL

Initial
seed#

