

IN / OUT

SUB-PROGRAM

Genotypes.raw

Lifehistories.txt

<Parameter values>

Genotypes.txt

AgePriors.txt

SequoiaSpecs.txt

DuplicatesFound.txt

Parents_assigned.txt

Unassigned_relatives_par.txt

PedSeq.txt

Unassigned_relatives_sib.txt

DummyParents.txt

Prep

Convert genotype file
Create flat age prior
Store parameter values

CheckDup

Parentage

Find likely PO pairs
Assign parents

Sibships

Find likely FS & HS pairs
Cluster sibling pairs
Merge sibships
Add siblings to sibships

Assign:

Parents to sibships
Parents to singletons
Grandparents to sibships *
Grandparents to singletons

iterate

*: real + dummy