

SimBiMarkersinNetwork

Description

Simulate bi-allelic markers in a phylogenetic network with branch lengths, population mutation rates, and inheritance probabilities.

Usage

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SimBiMarkersinNetwork [-pi0 PI0] [-sd seed] [-diploid] [-dominant] -num numMarkers [-cu rate] [-tm taxonMap] -
truenet trueNetwork [-op]
```

| Data related settings | | |
|---|--|--------------------------------------|
| -pi0 <i>PI0</i> | Specify the stationary probability of marker '0'. The default is 0.5. | o p t i o n a l |
| -sd <i>seed</i> | The random seed. The default seed is 12345678. | o p t i o n a l |
| - dipl oid | Specify whether generate sequence from diploids. If this is set without -dominant, the sequence is with 0, 1, 2. | o p t i o n a l |
| - dom inant | Specify whether generate sequence with dominant markers. If this is set, '0' is dominant. | o p t i o n a l |
| - num <i>num Mar kers</i> | Specify the number of markers to be generated. | |
| -tm <i>taxo nMap</i> | Gene tree / species tree taxa association . By default, it is assumed that only one individual is sampled per species in gene trees. This option allows multiple alleles to be sampled. For example, the gene tree is $((a1,a2),(b1,b2)),c$; and the species tree is $((a,b),c)$; the command is <code>-tm <a:a1,a2; b:b1,b2;c:c></code> . Note that the taxa association should cover all species, e.g. <code>-tm <a:a1,a2; b:b1,b2></code> is incorrect because <code>c:c</code> is dropped out. | o p t i o n a l |
| - true net | Specify the true network. If -cu is not set, the input network should contain divergence times in units of expected number of mutations per site, inheritance probabilities and population sizes in units of population mutation rate. If -cu is set, the input network should contain divergence times in units of coalescent units, inheritance probabilities. | |

| | | |
|--------------------|---|--------------------------------------|
| -cu <i>rate</i> | Specify whether the true network uses coalescent units. If set, <i>rate</i> will be the overall population mutation rate. | o p t i o n a l |
| -op | Specify whether the generated sequence contains only polymorphic sites. | |

Examples

#NEXUS

BEGIN PHYLONET;

SimBiMarkersinNetwork -pi0 0.5 -sd 12345678 -num 1000 -cu 0.036 -truenet "((((Q:0.5)I8#H1 :0.5::0.7,(A:0.5)I6#H2:0.5::0.8)I4:1.0,L:2.0) I3:2.0,(I8#H1:1.0::0.3,R:1.5)I7:2.5)I2:1.0,((I6#H2:0.5::0.2,C:1.0)I5:1.0,G:2.0)I1:3.0)I0;"

END;

This command makes Phylonet generate sequence with 1000 sites. The stationary probability of marker '0' is set to 0.5. The seed is set to 12345678. The true network contains divergence times in units of coalescent units, inheritance probabilities, and population mutation rate is set to 0.036.

#NEXUS

BEGIN PHYLONET;

SimBiMarkersinNetwork -diploid -dominant -op -pi0 0.5 -sd 123456 -num 10000 -tm <A:A_0; B:B_0; C:C_0,C_1,C_2,C_3; D:D_0> -truenet "[0.005]((((C:0.005:0.005)I1#H1:0.006:0.005:0.8,D:0.011:0.005):0.009:0.005,(B:0.014:0.005,I1#H1:0.009:0.005:0.2):0.006:0.005):0.005:0.005,A:0.025:0.005);"

END;

This command makes Phylonet generate sequence with 10000 sites with only polymorphic sites. The bi-allelic markers are from diploid and '0' is the dominant marker. The stationary probability of marker '0' is set to 0.5. The seed is set to 12345678. The true network contains divergence times in units of expected number of mutations per site, inheritance probabilities and population sizes in units of population mutation rate.