

List of PhyloNet Commands

PhyloNet 3.X.X Commands

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("Ref" lists the main reference; clicking on the command takes you to a page that lists all the relevant references.)

| Name | Description | Ref | Since |
|---|--|----------------------|-------|
| Methods for Species Network (and Tree) Inference (all account for ILS) | | | |
| MCMC_SEQ | Bayesian MCMC posterior estimation of phylogenetic networks and gene trees on sequences from multiple independent loci. | here | 3.6.1 |
| MCMC_BiMarkers | Bayesian estimation of the posterior distribution of phylogenetic networks given bi-allelic genetic markers (SNPs, AFLPs, etc). | here | 3.6.1 |
| MCMC_GT | Bayesian MCMC posterior estimation of phylogenetic networks given a list of gene tree topologies. | here | 3.6.0 |
| MLE_BiMarkers | Maximum (pseudo-)likelihood estimation of phylogenetic networks given bi-allelic genetic markers (SNPs, AFLPs, etc). | here | 3.6.4 |
| InferNetwork_MPL | Infers a phylogenetic network from gene trees under maximum pseudo-likelihood. | here | 3.5.5 |
| InferNetwork_ML_Bootstrap | Infers a phylogenetic network from gene trees under maximum likelihood with parametric bootstrap. | here | 3.5.2 |
| InferNetwork_ML_CV | Infers a phylogenetic network from gene trees under maximum likelihood with cross-validation. | here | 3.5.2 |
| InferNetwork_ML | Infers a phylogenetic network from gene trees under maximum likelihood. | here | 3.4.0 |
| InferNetwork_MP | Infers a phylogenetic network from gene trees under the MDC criterion. | here | 3.4.0 |
| InferNetwork_MP_Allopp | Infers an allopolyploid network from gene trees under the MDC criterion. | | 3.8.3 |
| NetMerger | Merge subnetworks inferred by MCMC_SEQ or MCMC_BiMarkers to a full network. | here | |
| Methods for Species Tree (not Networks) Inference | | | |
| Infer_ST_Bootstrap | Infers a species tree using bootstrap with existing <i>Infer_ST</i> commands. | | 3.0.0 |
| Infer_ST_DV | Infers a species tree from gene trees using the "Democratic Vote" method. | | 3.0.0 |
| Infer_ST_GLASS | Infers a species tree using the GLASS method of Mossel and Roch. | here | 3.0.0 |
| Infer_ST_MC | Infers a species tree from gene trees using greedy consensus (allows for gene trees with multiple alleles in species and for unrooted gene trees). | | 3.0.0 |
| Infer_ST_MDC | Infers a species tree from gene tree topologies using the "Minimize Deep Coalescence" (MDC) criterion. | here | 3.0.0 |
| Infer_ST_MDC_Time | Infers a species tree from gene trees with coalescent times using the MDC criterion. | | 3.0.0 |
| Infer_ST_MDC_UR | Infers a species tree from unrooted gene tree topologies using the MDC criterion. | here | 3.0.0 |
| GenCPLEX | Generates CPLEX input for a species tree and a set of gene trees. | here | 3.0.0 |
| GenST | Generates species tree topologies based on maximal sets of compatible clusters. | here | 3.0.0 |
| Methods for Analyzing Species Trees/Networks with Respect to Locus-specific Data | | | |
| CallIntroRate | Quantifies the introgression probability for each reticulation branch in a given phylogenetic network. | here | 3.6.0 |
| ExploreHypothesis_GibbsSampling | Uses Gibbs Sampling to explore the hypothesis of the evolutionary history from a collection of gene trees. | here | 3.6.0 |
| DeepCoalCount_network | Counts the number of extra lineages contributed by a phylogenetic network and a set of gene trees. | here | 3.3.0 |
| DeepCoalCount_AlloppNet | Counts the number of extra lineages contributed by an allopolyploid network and a set of gene trees. | | 3.8.3 |
| CalGTProb | Computes the likelihood of a phylogenetic network given a collection of gene trees. | here | 3.3.0 |
| ProcessGT | Refines and roots gene trees with respect to a rooted binary species tree under the MDC criterion. | here | 3.0.0 |
| RIATAHGT | Detects and reconstructs horizontal gene transfer events from phylogenetic incongruence. | here | 3.0.0 |
| CountCoal | Computes the number of coalescent scenarios that can explain the incongruence observed between two trees. | here | 3.0.0 |
| DeepCoalCount_tree | Counts the number of extra lineages contributed by a species tree and a set of gene trees. | here | 3.0.0 |
| Methods for Simulating Locus Data on Phylogenetic Networks (and Trees) | | | |
| SimGTinNetwork | Simulates gene trees under the multispecies network coalescent (automates the 'ms' program on an arbitrary phylogenetic network). | here | 3.6.1 |
| SimBiMarkersinNetwork | Simulates bi-marker alleles under the multispecies network coalescent. | here | 3.6.1 |
| CoalHMM Methods | | | |
| HmmCommand | Uses a hidden Markov to assign a species tree to each locus in data coming from a species network. | | 3.5.4 |

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| VI_coalHMM | Black box variational inference of continuous parameters on a species tree under the coalescent with recombination using coalHMM. | | 3.8.3 |
| Characterizing and Comparing Phylogenetic Trees/Networks Based on Their Topologies | | | |
| Charnet | Computes the trees, tripartitions and clusters contained in a phylogenetic network. | | 3.0.0 |
| Cmpnets | Computes the distance between two phylogenetic networks based on their topologies. | | 3.0.0 |
| LCA | Computes the least common ancestor of a group of nodes in a tree. | | 3.0.0 |
| MAST | Computes a Maximum Agreement Subtree of a pair of trees. | | 3.0.0 |
| SymmetricDifference | Computes the symmetric difference, also known as the Robinson-Foulds (RF) distance, between two trees. | | 3.0.0 |
| SummarizeNetworks | Computes the common structures with their proportions given a set of networks (with their proportion). | here | 3.8.0 |