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 `Infer_ST` 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			
CalIntroRate	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

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