# 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.)

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

**CoalHMM Methods**

<table>
<thead>
<tr>
<th>Name</th>
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</tr>
</thead>
<tbody>
<tr>
<td>HmmCommand</td>
<td>Uses a hidden Markov to assign a species tree to each locus in data coming from a species network.</td>
<td>3.5.4</td>
</tr>
<tr>
<td>Package</td>
<td>Description</td>
<td>Version</td>
</tr>
<tr>
<td>--------------</td>
<td>-----------------------------------------------------------------------------------------------------------------------------------------------</td>
<td>---------</td>
</tr>
<tr>
<td>VI_coalHMM</td>
<td>Black box variational inference of continuous parameters on a species tree under the coalescent with recombination using coalHMM.</td>
<td>3.8.3</td>
</tr>
<tr>
<td><strong>Characterizing and Comparing Phylogenetic Trees/Networks Based on Their Topologies</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Charnet</td>
<td>Computes the trees, tripartitions and clusters contained in a phylogenetic network.</td>
<td>3.0.0</td>
</tr>
<tr>
<td>Cmpnets</td>
<td>Computes the distance between two phylogenetic networks based on their topologies.</td>
<td>3.0.0</td>
</tr>
<tr>
<td>LCA</td>
<td>Computes the least common ancestor of a group of nodes in a tree.</td>
<td>3.0.0</td>
</tr>
<tr>
<td>MAST</td>
<td>Computes a Maximum Agreement Subtree of a pair of trees.</td>
<td>3.0.0</td>
</tr>
<tr>
<td>SymmetricDifference</td>
<td>Computes the symmetric difference, also known as the Robinson-Foulds (RF) distance, between two trees.</td>
<td>3.0.0</td>
</tr>
<tr>
<td>SummarizeNetworks</td>
<td>Computes the common structures with their proportions given a set of networks (with their proportion).</td>
<td>3.8.0</td>
</tr>
</tbody>
</table>