GenCplex Command

Description

Generates CPLEX input for a species tree and a set of gene trees. The trees must be specified in the rich newick format. Specifying more than one species thee will run the command multiple times with one execution per species tree.

The tool will generate three files for each pair of a species tree and all gene trees to the specified directory. The three file will be prefixed input, var and s cript with a number suffix. The suffix number corresponds to the species tree entry position in the input set parameter.

The input file is a mixed linear integer programming (MILP) formulation that CPLEX will read, and solve. However, because the number of variables and constraints in this file might be very big, and so manually typing commands to query CPLEX the optimization solution is not practical, the tool supplies with a script file, which you can use to ask CPLEX to load the problem, solve it. From the UNIX shell, you type: cat script# | cplex > output#, and all of CPLEX output is directed to the file output#. The purpose of the file var is to provide a mapping between the species (and gene) trees' nodes to variables in the MILP formulation.

Usage

gencplex {species_tree_ident1 [, species_tree_ident2...]} {gene_tree_ident1 [, gene_tree_ident2...]} w1 w2
out_dir

species_tree_ident1 [, species_tree_ident2]	Comma delimited set of species tree identifiers.	mandator y
gene_tree_ident1 [, gene_tree_ident2]	Comma delimited set of gene tree identifiers.	mandator y
w1	The weight for the number of deep coalescences.	mandator y
w2	The number of no coalescences.	mandator y
out_dir	Output directory	mandator y

Examples

#NEXUS
BEGIN NETWORKS;
Network st = ((((a:1,b:2),c:3),d:4),e:5);
Network gt = (((a:1,b:2,c:3),d:4),e:5);
END;
BEGIN PHYLONET;
gencplex {st} {gt} 2 2 "C:\temp\cplex";

Command References

 C. Than, R. Sugino, H. Innan, and L. Nakhleh. Efficient inference of bacterial strain trees from genome-scale multi-locus data. The 16th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Bioinformatics, 24:i123–i131, 2008.

See Also

• List of PhyloNet Commands