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 `script` 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.	mandatory
gene_tree_ident1 [, *gene_tree_ident2*...]	Comma delimited set of gene tree identifiers.	mandatory
w1	The weight for the number of deep coalescences.	mandatory
w2	The number of no coalescences.	mandatory
out_dir	Output directory	mandatory

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 Biololgy (ISMB)*. Bioinformatics, 24:i123–i131, 2008.

See Also

- List of PhyloNet Commands