Cmpnets Command

Description

Computes the distance between two phylogenetic networks, based on their topologies. Three measures are currently implemented:

- Tree-based measure. (-m tree)
- Tripartition-based measure. (-m tri)
- Cluster-based measure. (-m cluster)
- Reduction-based measure (Nakhleh, L. (2010)). (-m luay)

The networks must be specified in the Rich Newick Format.

This program returns three numbers: the false negative rate (roughly, the trees/tripartitions/clusters found in the first network but not the second, divided by the number of trees/tripartitions/clusters in the first network), the false positive rate (roughly, the trees/tripartitions/clusters found in the second network but not the first, divided by the number of trees/tripartitions/clusters in the second network), and the average of the two rates (their sum divided by 2).

If reduction-based measure is used, this program returns only one number: the distance.

Usage

```
cmpnets network_ident1 network_ident2 -m [tree|tri|cluster|luay] [resultOutputFile]
```

network_ident1	The name of the first network.	mandatory
network_ident2	The name of the second network.	mandatory
-m [tree|tri|cluster|luay]	Characterization mode. One of `tree`, `tri`, `cluster, or luay`.	mandatory
resultOutputFile	Optional file destination for command output.	optional

Examples

```
#NEXUS

BEGIN NETWORKS;

Network net1 = ((a,(b,(c)x#1)),((d,x#1),e));
Network net2 = ((((a, (c)x#1), d), (b, x)), e);

END;


BEGIN PHYLONET;

Cmpnets net1 net2 -m cluster;

END;
```

Command References

- L. Nakhleh, J. Sun, T. Warnow, R. Linder, B.M.E. Moret, and A. Tholse. Towards the development of computational tools for evaluating phylogenetic network reconstruction methods. In Proc. *8th Pacific Symp. on Biocomputing (PSB03)*, pages 315--326. World Scientific Pub., 2003.

- B.M.E. Moret, L. Nakhleh, T. Warnow, C.R. Linder, A. Tholse, A. Padolina, J. Sun, and R. Timme. Phylogenetic networks: modeling, reconstructibility, and accuracy. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 1(1):13--23, 2004.

- L. Nakhleh and L.S.Wang. Phylogenetic networks, trees, and clusters. In Proceedings of the 2005 *International Workshop on Bioinformatics Research and Applications (IWBRA 05)*, pages 919--926, 2005. LNCS #3515.

- L. Nakhleh and L.S. Wang. Phylogenetic networks: properties and relationship to trees and clusters. *LNCS Transactions on Computational Systems Biology II*, pages 82--99, 2005. LNBI #3680.
- Nakhleh, L. (2010). A metric on the space of reduced phylogenetic networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)*, *7*(2), 218-222.

See Also

- List of PhyloNet Commands