

# Charnet Command

## Description

This command implements functions to compute the trees, tripartitions or clusters contained in a phylogenetic network. Please note that the clusters and tripartitions returned by this tool will not contain trivial ones, that is, clusters and tripartitions for the network’s root and leaves. The networks must be specified in the [Rich Newick Format](#).

## Usage

```
Charnet network_ident -m [tree|tri|cluster] [resultOutputFile]
```

network_ident	The name of the network to analyse.	mandatory
-m [tree tri cluster]	Characterization mode. One of tree, tri, or cluster.	mandatory
resultOutputFile	Optional file destination for command output.	optional

## Examples

```
#NEXUS

BEGIN NETWORKS;

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

END;

BEGIN PHYLONET;

Charnet net -m tree;

END;
```

## Command References

- 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.

## See Also

- [List of PhyloNet Commands](#)