Computing Bremer support values

Bremer support

In this chapter, we assume that you are already familiar with conducting heuristic searches under the maximum parsimony (MP) criterion using PAUP* and with the computation of the strict consensus from all most parsimonious trees found. You probably also know that, as any other alignment-based phylogenetic method, MP can be combined with character re-sampling strategies such as bootstrapping and jackknifing to obtain statistical branch support values. In contrast, the so-called Bremer support is almost always combined with MP. Since it is not based on re-sampling, its statistical interpretation is less obvious, but is has some interesting properties that make it worth considering.

Basically, Bremer support is the difference in MP score between the globally best tree(s) found and the best tree(s) observed that lack the bipartition of interest. Two ways to compute Bremer support have been described in literature:

1. Search for the globally most parsimonious tree(s) of score X and compute the strict consensus between. Set N to 1 and also include trees of score X+N in the consensus. Increment N by 1 until the branch you are interested in collapses. Set the branch's support value to N.

2. Conduct heuristic searches under a negative constraint with disallows the bipartition of interest. Set the Bremer branch support to the difference between the best MP score under that condition and the globally best MP score.

Partitioned Bremer support

The second alternative has usually been considered more efficient. Before describing how to use our own Bremer support implementation, we have a look at the partitioned Bremer support. This is an elegant method to localize the origin of branch support if you have a dataset partitioned into, e.g., different loci or different codon positions. Computation follows the second method mentioned above, but best unconstrained and constrained MP scores are also computed after inclusion of each single partition only. In NEXUS documents, partitions can be defined in an assumptions block, e.g.:

```
begin assumptions;
     charset ITS1 = 15-327;
     charset 58S = 328-447;
     charset ITS2 = 448-791;
     charset total = ITS1 58S ITS2;
end;
```

Obviously, charset commands can even be defined by other charset commands. The "total" charset is convenient for re-inclusion of all characters used for computing the best tree, which need not represent all characters in the dataset. Note that NEXUS offers a convenient "each Nth character" syntax to define codon positions (with N=3, of course):

```
begin assumptions;
     charset pos1 = 1-747\3;
     charset pos2 = 2-747\3;
```

```
    charset pos3 = 3-747\3;
end;
```

The last character does not need to be finally included in the respective charset (e.g., character 747 of our example will only be included in pos3, as it should be).

Computation

Our brand-new Bremer implementation (http://www.goeker.org/scripts/) has to be invoked twice:

```
$ bremer.tcl strict_consensus.tre Bremer_logfile > batch_file
```

or, for partitioned support:

```
$ bremer.tcl strict_consensus.tre Bremer_logfile part1,part2,part3 > batch_file
```

After execution of the data file that the MP consensus tree "strict_consensus.tre" had been computed from and of the file "batch_file" with the heuristic search and negative constraints commands, PAUP* has produced a log file "Bremer_logfile" containing MP scores and constraint information. This file has to be converted:

```
$ bremer.tcl Bremer_logfile > Bremer_outfile
```

"Bremer_outfile" then contains the MP scores as well as the Bremer support values for each branch present in the strict consensus and for each partition.

References

- Baker, R.H., and DeSalle, R. 1997. Multiple sources of character information and the phylogeny of Hawaiian Drosophilids. Systematic Biology 46:654-673.

- Baker, R.H., Yu, X.B., and DeSalle, R. 1998. Assessing the relative contribution of molecular and morphological characters in simultaneous analysis trees. Molecular Phylogenetics and Evolution 9:427-436.

- Bremer, K. 1988. The limits of amino acid sequence data in angiosperm phylogenetic reconstruction. Evolution 42:795-803.

- Bremer, K. 1994. Branch support and tree stability. Cladistics 10: 295-304.

Exercises

- Compute Bremer support and partitioned Bremer support with your datasets. Include these support values in your tree graphics for presentation.

- What does (a) a negative Bremer branch support value due to an individual partition; (b) obtained from the whole dataset mean?

- What would happen if you conduct Bremer support computations based on the majority-rule consensus of all most parsimonious trees?

- Which effect does conducting less exhaustive heuristic searches have on (a) bootstrap support; (b) Bremer support?