Phylogenetic Tree HOWTO

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Nodes and specific data, like bootstrap vfifi

```
print "lca is ",$lca->id, " for ", join(",",map { $_->id } @orig82 71"Efda d.2z/ }_

@nodes = grep { $_->id =~ /a|z/ } $tree->get_nodes;
@orig = @nodes;
while( @nodes > 1 ) {
  my $lca = $tree->get_lca(-nodes => [shift @nodes, shift @nodes]%ca d.2z/ } $tzTa(
```

6. Making Images of Trees

You can also make images of trees. If you have the module SVG::Graph installed you can create an SVG image of your tree. The example below uses TreeIO to get a Tree object and then its tree is written to an image file.

```
use Bio::TreeIO;
my $in = new Bio::TreeIO(-file => 'input',
                         -format => 'newick');
my $out = new Bio::TreeIO(-file => '>mytree.svg',
                          -format => 'svggraph');

while( my $tree = $in->next_tree ) {
    $out->write_tree($tree);
}
```

Alternatively you could use an output format of "tabtree", this option will create an ASCII drawing of the tree.

7. Constructing Trees

Pairwise distances for all sequences in an alignment can be computed with `Bio::Align::DNAStatistics` and and `Bio::Align::ProteinStatistics`. There are several different methods implemented. For DNA

Non-parametric bootstrapping is one method to test the consistency of the data with the optimal tree. A set of subreplicates are generated from the alignment using the method from `Bio::Align::Utilities` called `bootstrap_replicates`. One passes in an alignment object and the count of the number of replicates to generate.

```
use Bio::Align::Utilities qw(:all);
my $replicates = bootstrap_replicates($aln,$count);
```

8. Advanced Topics

Eddy SR, Durbin R, Krogh A, Mitchison G, "Biological Sequence Analysis" 1998. Cambridge Univ Press, Cambridge, UK.

10. Additional Information

Here's a list of the relevant modules. If you have questions or comments that aren't addressed herein then write the Bioperl community at bioperl-l@bioperl.org.

Related Modules

Bio/TreeIO.pm [http://doc.bioperl.org/releases/bioperl-1.4/Bio/TreeIO.html]
Bio/Tree/Tree.pm [http://doc.bioperl.org/releases/bioperl-1.4/Bio/Tree/Tree.html]
Bio/Align/DN