

# **Bio::Tools::Phylo::PAML HOWTO**

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## Accessing Tree data

First we'll just describe how to access data for a topology for a single model or where NSsites=0. In this case we'll just want to get the tree(s) associated with a give result. In this code we loop through all the `Bio::Tree::Tree` associated with the `Bio::Tools::Phylo::PAML::Result`.

```
use Bio::Tools::Phylo::PAML;

my $outcodeml = shift(@ARGV);
my $paml_parser = new Bio::Tools::Phylo::PAML(-file => $outcodeml,
                                              -dir => ".");
if( my $result = $paml_parser->next_result() ) {
  while ( my $tree = $result->next_tree ) {
    for my $node ( $tree->get_nodes ) {
      my $id;
      # first we do some work to figure out what the ID should be.
      # for a leaf or tip node this is just the taxon label
      if( $node->is_Leaf() ) {
        $id = $node->id;
      } else {
```

```

        $ns_result->model_description, "\n";
while ( my $tree = $ns_result->next_tree ) {
  for my $node ( $tree->get_nodes ) {
    my $id;
    # first we do some work to figure out what the ID should be.
    # for a leaf or tip node this is just the taxon label
    if( $node->is_Leaf() ) {
      $id = $node->id;
    } else {
      # for the internal nodes it is just the name of all the sub-nodes
      # put together, much like how Sanderson represents internal nodes
      # in r8s
      $id = "(" . join(",", map { $_->id } grep { $_->is_Leaf }
        $node->get_all_Descendents) . ")";
    }
    if( ! $node->ancestor || ! $node->has_tag('t') ) {
      # skip when no values have been associated with this node
    }
  }
}

```