

Expanding phylogeny to include taxa without sequence data using available taxonomic information

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##Use PASTIS to merge consensus tree and clade membership data to expand phylogenetic analyses

Call “pastis” package and “phytools” package for reading trees

```
require(pastis)
require(treeio)
```

Read in the summary tree

```
tree <- read.newick("IschnuraExpanded.tree")
```

#Creating .csv file for inputting into pastis

```
clade_dat <- data.frame(taxon = tree$tip.label)
clade_dat$clade <- rownames(clade_dat)
```

Add clade data for each species in expanded phylogeny

```
added_taxa <- data.frame(taxon = c("Ischnura_abyssinica",
                                   "Ischnura_sp.a",
                                   "Ischnura_aralensis",
                                   "Ischnura_chingaza",
                                   "Ischnura_cyane",
                                   "Ischnura_forcipata",
                                   "Ischnura_genei",
                                   "Ischnura_indivisa",
                                   "Ischnura_rubilio"),
                        clade = c(42,43,42,44,45,46,47,48,49))
```

```
clade_membership <- rbind(clade_dat, added_taxa)
```

Write .taxa file for pastis analysis

```
write.table(clade_membership, file = "IschnuraExpanded.taxa",
            sep = ",", row.names=FALSE, col.names = TRUE, quote=FALSE)
```

Create constraint tree without branch lengths

```
IschnuraExpandedConstraint.tree <- tree
IschnuraExpandedConstraint.tree$edge.length <- NULL
write.tree(IschnuraExpandedConstraint.tree, "IschnuraExpandedConstraint.
tree")
```

Create PastisData object (with tree, taxa list and sequences)

```

IschnuraExpanded = read_input(
  constraint_tree = "IschnuraExpandedConstraint.tree",
  taxa_list = "IschnuraExpanded.taxa",
  missing_clades = "IschnuraExpanded.missingclades",
  sequences = "concatenated.fasta",
  output_template = "IschnuraExpanded.template"
)

```

Adjust variables

```

IschnuraExpanded$taxa_list$taxon <- factor(IschnuraExpanded$taxa_list$
  taxon)
IschnuraExpanded$taxa_list$clade <- factor(IschnuraExpanded$taxa_list$
  clade)

```

Create input file for Mr Bayes (need to go into .nexus file and remove directory from filename at bottom of document)

```

pastis_simple(pastisData = IschnuraExpanded,
  base_name = "IschnuraExpanded",
  paraphyly_constrains = TRUE,
  monophyly_constrains = TRUE,
  omit_sequences = FALSE
)

```