

Reconstruct intermediate sequences

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Dowser automatically reconstructs intermediate sequences as part of the `getTrees` function. These are stored in the `nodes` list contained in each `phylo` object.

First, collapse internal nodes with identical sequences using the `collapseNodes`. This will significantly clean up the visualization. You could alternatively run `getTrees` with `collapse=TRUE`. Then, visualize the trees using `plotTrees` but with the `node_nums` parameter set. This will display the ID number of each internal node.

To obtain the IMGT-gapped sequence for each reconstructed node, specify the clone ID and node number in the `getNodeSeq` function.

To obtain all observed and reconstructed sequences for all clones, use the `getAllSeqs` function.

You can save the output of `getAllSeqs` as a fasta file using the `dfToFasta` function.

```
library(dowser)

data(ExampleClones)

# Collapse nodes with identical sequences. This will
trees = collapseNodes(ExampleClones[1:2,])

# Plot trees with node ID numbers
plots = plotTrees(trees, tips="c_call", tipsize=2, node_nums=TRUE, labels=7)

plots[[1]]

sequence = getNodeSeq(trees, node=50, clone=3128)

print(sequence)

# Get all sequences as a data frame
all_sequences = getAllSeqs(trees)

head(all_sequences)
```

Saving sequences to a file

The `dfToFasta` function can be used to save a dataframe of sequences as a fasta file:

```
# Save all sequences as a fasta file
```

```
dfToFasta(all_sequences, file="all_sequences.fasta", id="node_id", columns=c("clone_id","locus
```