Reconstruct intermediate sequences

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Contents

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

First, collapse internal nodes with identical sequences using the \texttt{collapseNodes}. This will significantly clean up the visualization. You could alternatively run \texttt{getTrees} with \texttt{collapse=TRUE}. Then, visualize the trees using \texttt{plotTrees} but with the \texttt{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 \texttt{getSeq} function.

\begin{verbatim}
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, labelsize=7)

plots[[1]]
\end{verbatim}
sequence = getSeq(trees, node=50, clone=3128)

print(sequence)

## "GAGGTGCAGCTGGTAGCCGGGGA...GGCTTGGTACAGCCAGGGCCTCTCTGACTCTCCTGTAAGCTTCTGATTGGAACTTT..."