

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.

```
library(dowser)
```

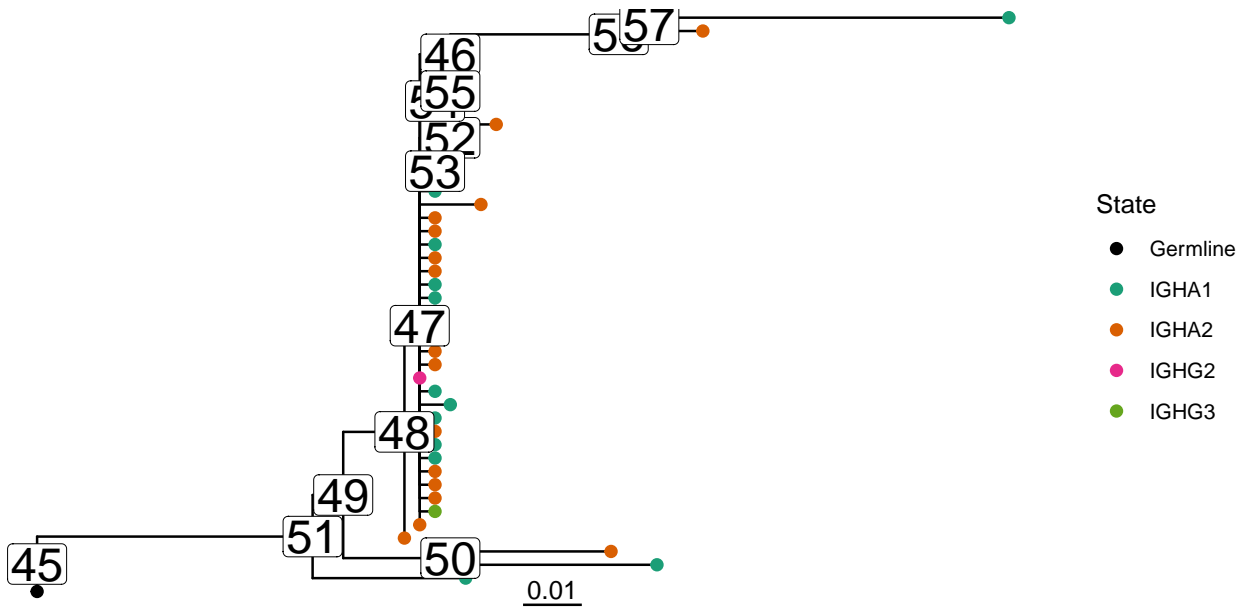
```
data(ExampleClones)
```

```
# 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]]
```

3128



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

```
print(sequence)
```

```
##
```

```
## "GAGGTGCAGCTGGTGGAGTCTGGGGGA...GGCTTGGTVCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTC
```