Using the *laser* package: data input & formats

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Data input

Laser operates on sets of branching times derived from ultrametric phylogenetic trees. Perhaps the most common input data format is the Newick (or parenthetic) tree format:

```
(((human:1.0, chimp:1.0):2.0, (gorilla:1.5, orang:1.5):1.5):8.0, dog:11.0);
```

If you have a single tree that you would like to analyze in laser, create a text file containing the Newick tree only, as displayed above. Note that if you typically work with other data formats (e.g., trees from Nexus or the *.con consensus file from MrBayes), you will have to delete all of the text except the actual tree and the terminal semicolon.

If the above tree is stored in file 'apes.tre', then we generate a numeric vector of branching times with the following commands:

```
library(laser)
data <- getBtimes(file = 'apes.tre')
```

`data` now contains a numeric vector of branching times. We can visualize the lineage-through-time plot for `data` by calling:

```
plotLtt(data)
```

If you have multiple input trees, perhaps from another phylogenetic simulation package (e.g., Phyl-O-Gen), each tree should reside on a separate line of text, and the file should include nothing else. As an example, here we view the contents of a file 'apetrees.tre':

```
(((human:1.0, chimp:1.0):2.0, (gorilla:1.5, orang:1.5):1.5):7.0, dog:10.0);
(((human:1.0, chimp:1.0):2.0, (gorilla:1.5, orang:1.5):1.5):8.0, dog:11.0);
(((human:0.5, chimp:0.5):2.0, (gorilla:1.0, orang:1.0):1.5):8.0, dog:10.5);
(((human:1.0, chimp:1.0):2.0, (gorilla:1.5, orang:1.5):1.5):6.5, dog:9.5);
(((human:0.5, chimp:0.5):4.0, (gorilla:2.0, orang:2.0):2.5):6.0, dog:10.5);
```

To create a matrix of branching times for these trees, where each row is a different tree & each column is a speciation event, we call:

```
x <- getBtimes.batch(file = 'apetrees.tre')
```

Thus, for the 'apetrees.tre' example, we have a 5-row, 4 column matrix (5 trees and $N - 1 = 4$ branching times). To plot log-lineages-through-time for the second tree in x, call:

```
plotLtt(x[2, ])
```

And for the k'th tree: `plotLtt(x[k, ])`

Alternatively, you might have a set of branching times without a corresponding tree:

100, 80, 40, 30, 20, 10, 5, 4, 2.2, 1.7, 0.9, 0,3

If you have a file containing branching times as such, simply scan them into R using the function scan:

```
data <- scan(file = '*.txt')
```

`data` is now a vector containing the branching times and can be visualized using `plotLtt(data)`.

Analyses

Basic analyses in laser are covered in the html documentation included with the R package. An overview of the statistical framework employed can be found in:

Rabosky, D. 2006. Likelihood methods for inferring temporal shifts in diversification rates. *Evolution* 60:1152-1164