Demonstration of nLTTstat functions

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2016-09-14

Both `nLTTstat` and `nLTTstat_exact` calculate the nLTT statistic value. The nLTT statistic is a measure of mismatch between two phylogenies.

In this vignette:

- an introduction of the data we work on
- a demo of how to use the function itself

General setup

Load all libraries:

```
library(nLTT) # nolint
```

Use the heigest warning level:

```
options(warn = 2)
```

Set the random number generator seed:

```
set.seed(42)
```

Setting a random number generator seed makes the results reproducible.

The data we work on will be:

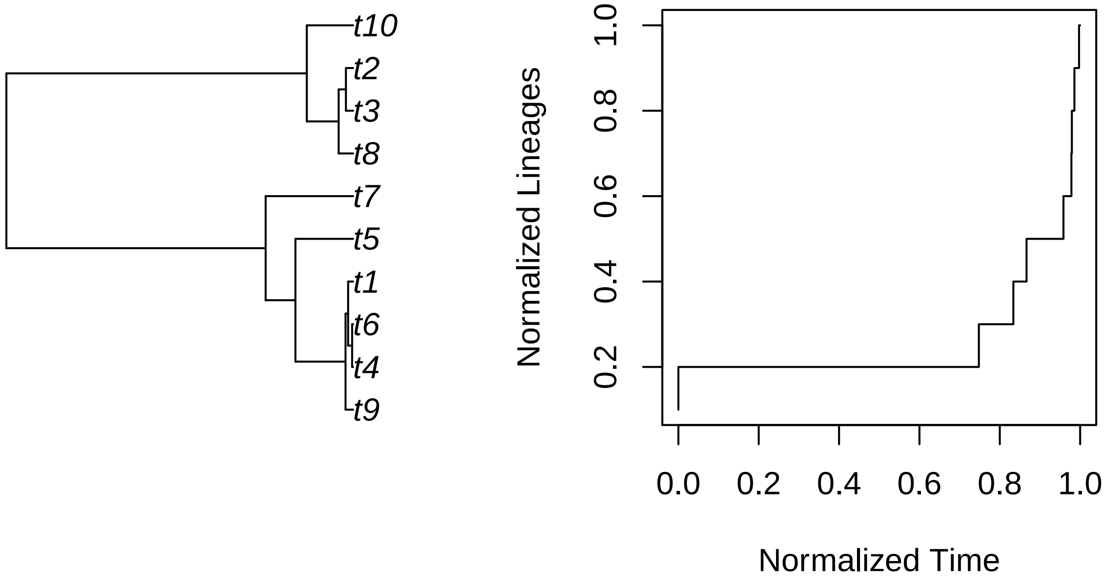
- a focal phylogeny, called 'the species tree'
- multiple other phylogenies to be compared to the species tree, called 'the posterior'

First we construct the focal species tree:

```
species_tree <- ape::rcoal(n = 10)
```

Here the phylogeny and nLTT plot are displayed:

```
par(mfrow = c(1, 2))
ape::plot.phylo(species_tree)
nLTT::nltt_plot(species_tree)
```



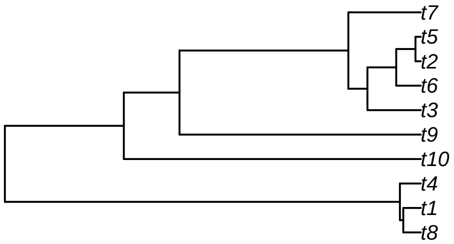
```
par(mfrow = c(1, 1))
```

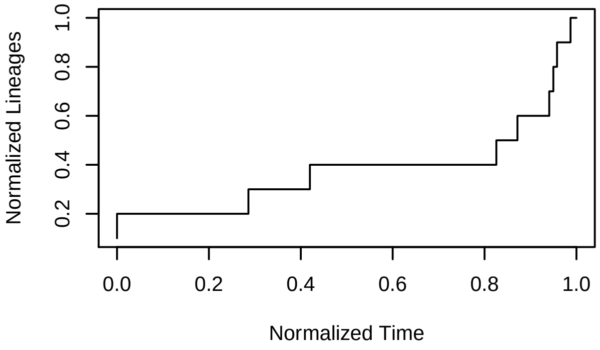
Then we collect four possible posterior species trees:

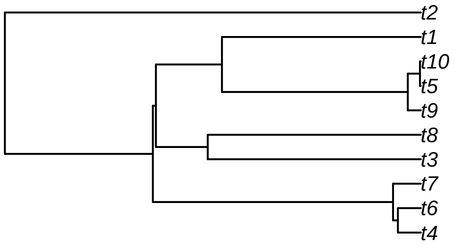
```
posteriors <- c(
  ape::rcoal(n = 10),
  ape::rcoal(n = 10),
  species_tree,
  ape::rcoal(n = 10)
)
```

Here these phylogenies and nLTT plots are displayed:

```
par(mfrow = c(4, 2))
for (p in posteriors) {
  ape::plot.phylo(p, cex = 1)
  nLTT::nltt_plot(p)
}
```


t7
t5
t2
t6
t3
t9
t10
t4
t1
t8


Normalized Lineages
0.2
0.4
0.6
0.8
1.0
0.0
0.2
0.4
0.6
0.8
1.0
Normalized Time


t2
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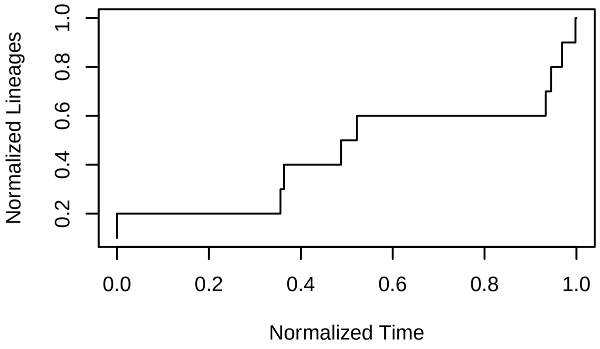
Normalized Lineages
0.2
0.4
0.6
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0.8
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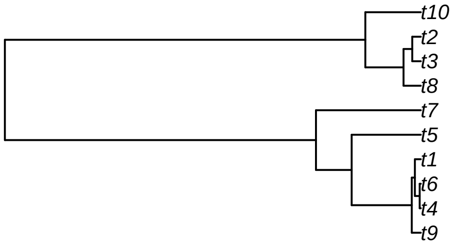
Normalized Time


t10
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t8
t7
t5
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t6
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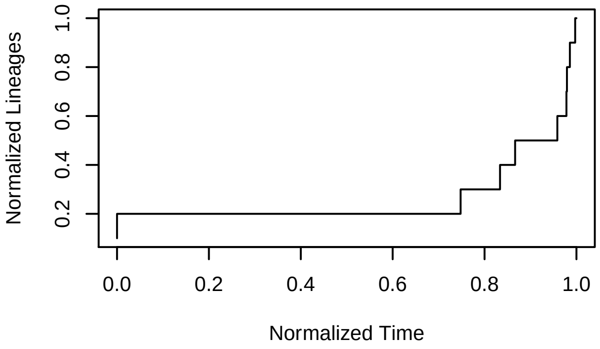
t9


Normalized Lineages
0.2
0.4
0.6
0.8
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0.2
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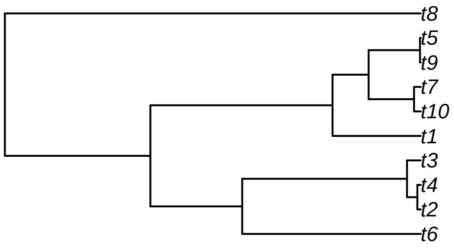
0.6
0.8
1.0
Normalized Time


t8
t5
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t7
t10
t1
t3
t4
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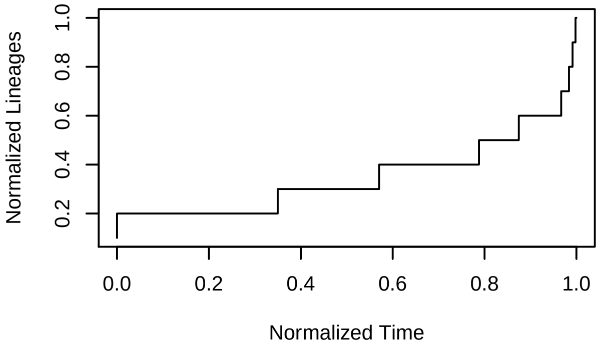
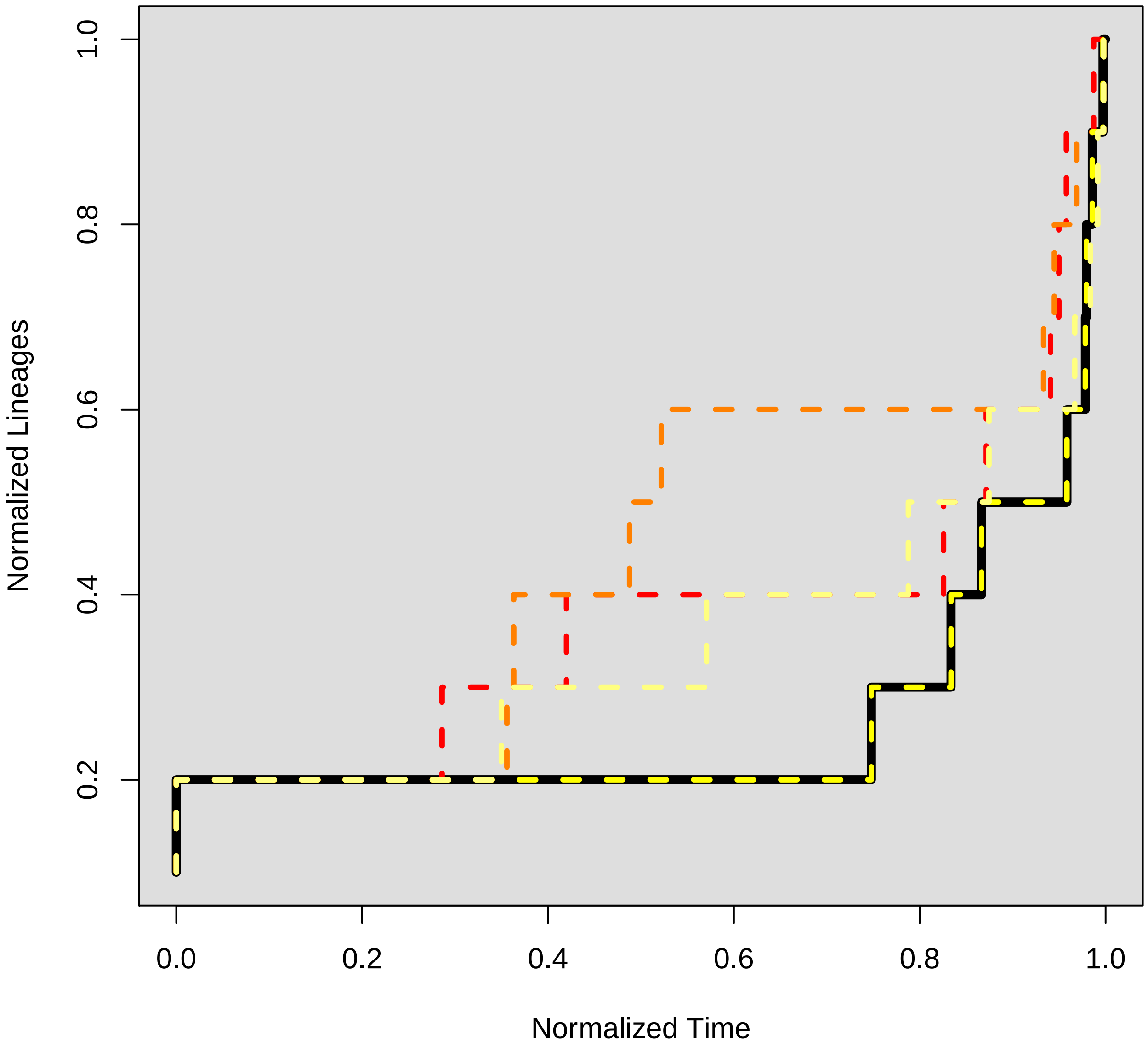

Normalized Lineages
0.2
0.4
0.6
0.8
1.0
0.0
0.2
0.4
0.6
0.8
1.0
Normalized Time

```
par(mfrow = c(1, 1))
```

Here we display the nLTT plots of both the original species tree (thicker lines) and its posteriors:

```
# Set the plot area
nLTT::nltt_plot(species_tree)
# Set the background to light grey
rect(par("usr")[1],par("usr")[3],par("usr")[2],par("usr")[4], col = colors()[240])
# Draw the species tree
nLTT::nltt_lines(species_tree, lwd = 5)
# Draw the posteriors
col_index <- 1
for (p in posteriors) {
  nLTT::nltt_lines(p, lwd = 3, lty = 2, col = grDevices::heat.colors(n = 4)[col_index])
  col_index <- col_index + 1
}
```



The nLTT statistic

The nLTT package supplies two version of calculating the nLTT statistic: exact or approximated.

First, we calculate both nLTT statistic between original species tree and each posterior tree:

```
nltt_stats_exact  <- rep(x = 0, times = length(posteriors))
nltt_stats_approx <- rep(x = 0, times = length(posteriors))
i <- 1
for (p in posteriors) {
  nltt_stats_exact[i]  <- nLTTstat_exact(species_tree, p)
  nltt_stats_approx[i] <- nLTTstat(species_tree, p)
  i <- i + 1
}
```

One of the posterior tree is a copy of the input phylogeny. This allows us to check our algorithm: the final nLTT statistic should be zero for that posterior tree.

Here we put the results in a data frame and display it as a table:

```
nltt_stats <- data.frame(
  id = seq(1, length(nltt_stats_exact)),
  nltt_stat_exact = nltt_stats_exact,
  nltt_stat_approx = nltt_stats_approx
)
knitr::kable(nltt_stats)
```

id	nltt_stat_exact	nltt_stat_approx
1	0.1108467	0.1114308
2	0.1775316	0.1774595
3	0.0000000	0.0000000
4	0.0846390	0.0863506

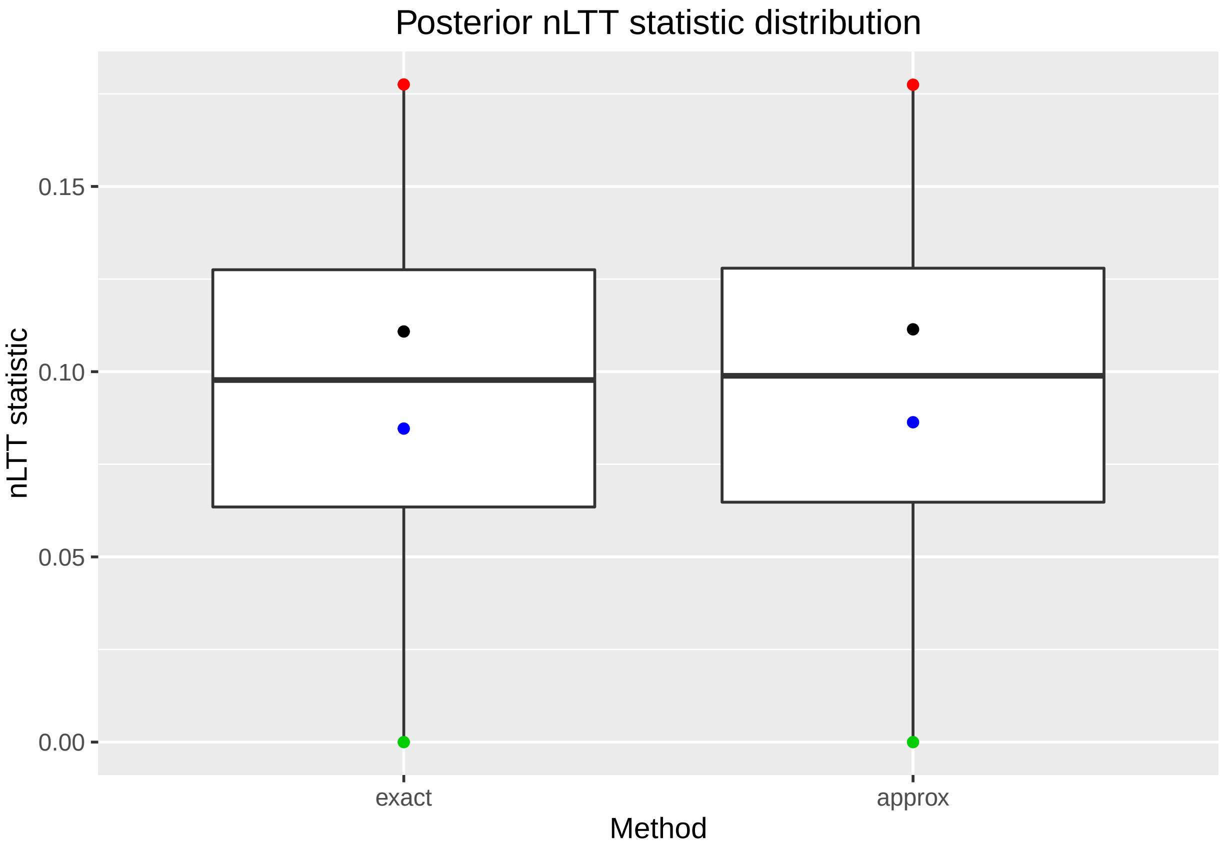
The date frame shows that both methods result in appoximately the same values.

Melting this data for the next plot:

```
df <- reshape2::melt(
  nltt_stats,
  id.vars = c("id"),
  measure.vars = c( "nltt_stat_exact", "nltt_stat_approx")
)
names(df) <- c("id", "method", "nltt_stat")
df$id <- as.factor(df$id)
df$method <- plyr::revalue(
  df$method,
  c("nltt_stat_exact" = "exact", "nltt_stat_approx" = "approx")
)
```

Plotting the methods in a boxplot:

```
ggplot2::ggplot(
  data = df,
  ggplot2::aes(x = df$method, y = df$nltt_stat)
) + ggplot2::geom_boxplot(
) + ggplot2::geom_point(color = df$id
) + ggplot2::scale_y_continuous(name = "nLTT statistic"
) + ggplot2::scale_x_discrete(name = "Method"
) + ggplot2::ggtitle("Posterior nLTT statistic distribution")
```


Posterior nLTT statistic distribution
nLTT statistic
exact
approx
Method