phenologyOverlap: computing overlap of phenology time series

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Note that this is a markdown document with some LaTeX in it. For a proper LaTeX-document, Sweave/knitr is the way to go; see https://github.com/yihui/knitr/blob/master/inst/examples/knitr-minimal.Rnw

This vignette covers . . . .

Example data

A small set of annotated example trees are included in the `phenologyOverlap` package.
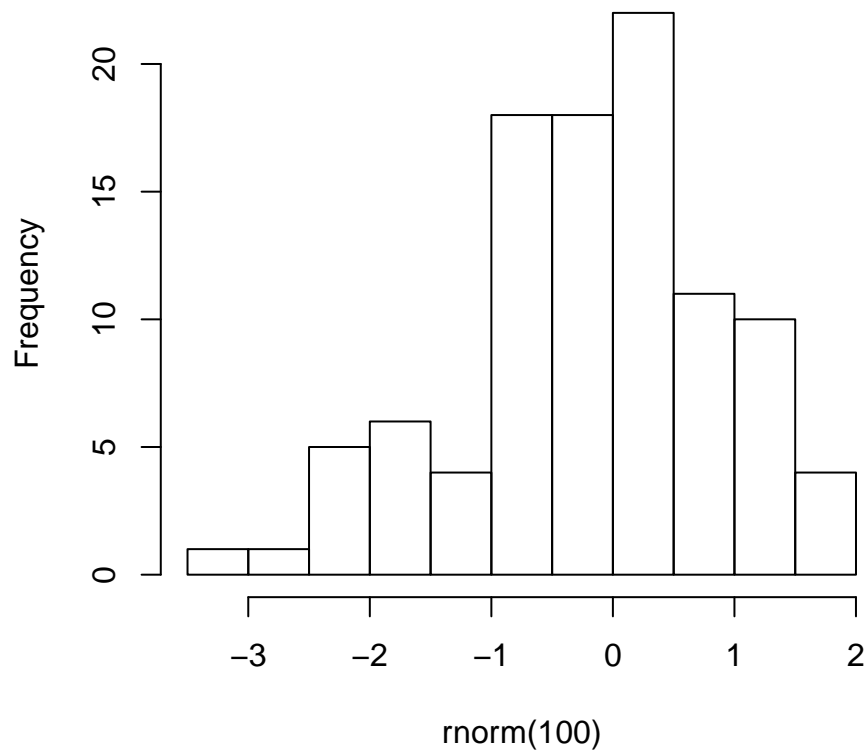
```r
# Load required packages
library(MASS)

# Load example data
data(mcycle)

hist(rnorm(100))
```

Histogram of rnorm(100)

Some equations are always useful:

$$\hat{o} = f(\vec{x}_1, \vec{x}_2)$$