Plotting Haplotype Networks with pegas

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1 Background

1.1 Layout Algorithm

```
R> data(woodmouse)
R> d <- dist.dna(woodmouse, "N")
R> nt <- rmst(d, quiet = TRUE)</pre>
```

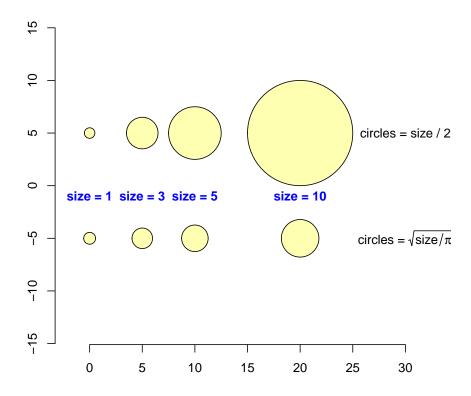
2 New Features in pegas 1.0

2.1 Improved "Replotting"

2.2 Haplotype Symbol Shapes

The area of a disc is πr^2 with r being the radius of the disc, so if we want the area of the symbols to be proportional to \mathtt{size} , we should square-root them. However, in practice this masks differences if most values in \mathtt{size} are not very different (see below). Instead, the diameters of the symbols (2r) are equal to the values in \mathtt{size} . If these are very heterogeneous, they could be transformed with $\mathtt{size} = \mathtt{sqrt}(\ldots)$ keeping in mind that the legend will be on this new scale.

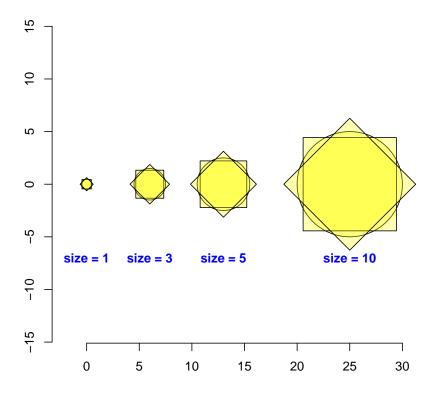
```
R> par(xpd = TRUE)
R> size <- c(1, 3, 5, 10)
R> x <- c(0, 5, 10, 20)
R> plot(0, 0, type="n", xlim=c(-2, 30), asp=1, bty="n", ann=FALSE)
```



For squares and diamonds, their areas are equal to the discs for the same values given to size:

```
R> x < -c(0, 6, 13, 25)
R> plot(0, 0, type="n", xlim=c(-2, 30), asp=1, bty="n", ann=FALSE)
R> other.args$y < -0
R> o < -mapply(symbols, x = x, circles = size/2, MoreArgs = other.args)
R> other.args$col < -"black"
R> other.args$add < -other.args$inches < -NULL
R> o < -mapply(pegas:::square, x = x, size = size, MoreArgs = other.args)
```

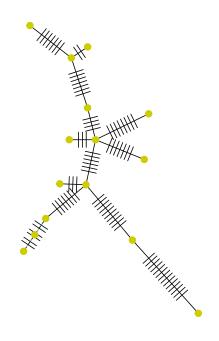
R> o <- mapply(pegas:::diamond, x = x, size = size, MoreArgs = other.args) R> text(x, -7, paste("size =", size), font = 2, col = "blue")



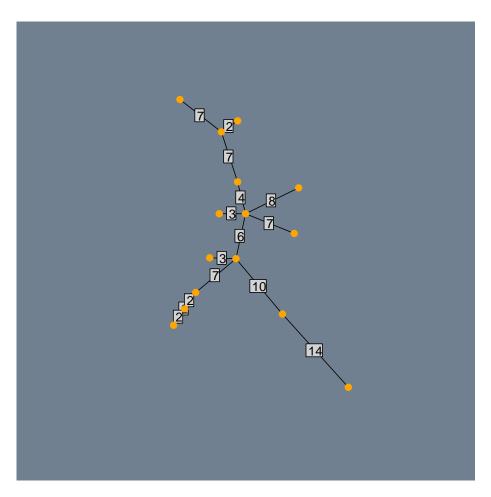
A diamond is simply a square rotated $45\,^\circ$ around its center.

2.3 Themes

R> plot(nt)



R> setHaploNetTheme("puma")
R> plot(nt)



R> setHaploNetTheme("tiger")
R> plot(nt)

