ThReshold selection.

Knecmab

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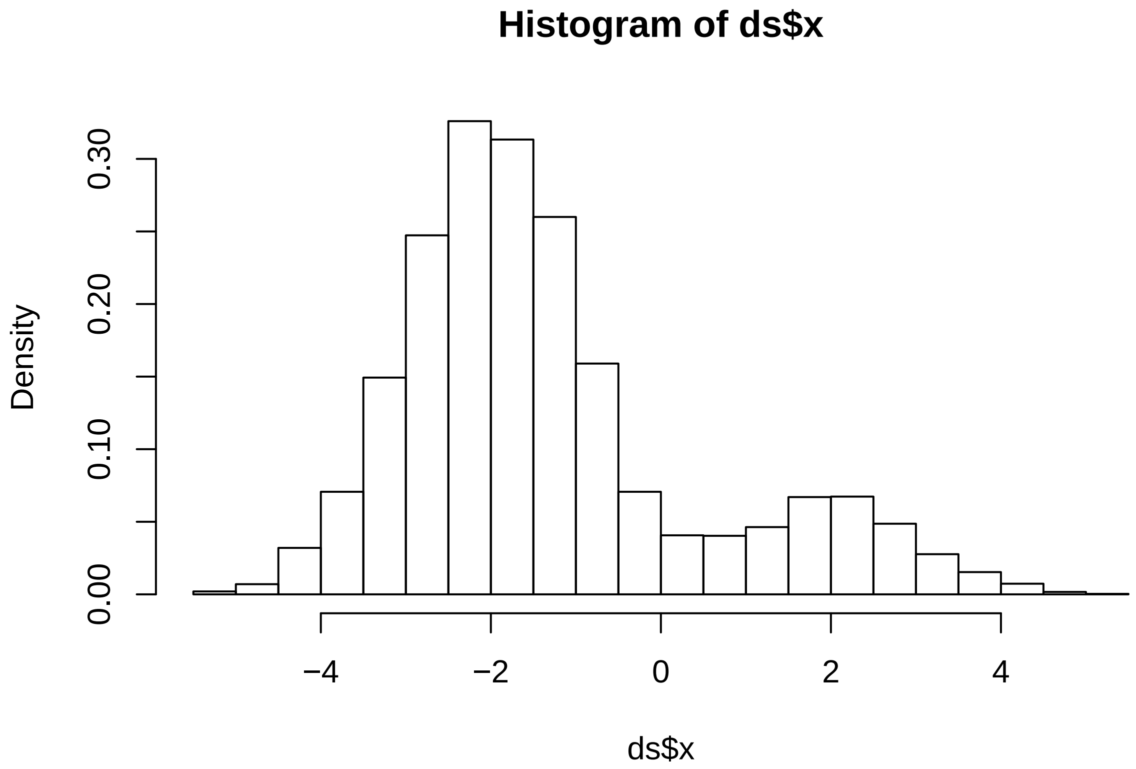
ThReshold selection for bi-modal data.

First lets load the package and get a data set.

```
require(threshold)
ds <- twoGaussians(seed=123)
hist(ds$x, breaks='Scott', freq=FALSE)
```



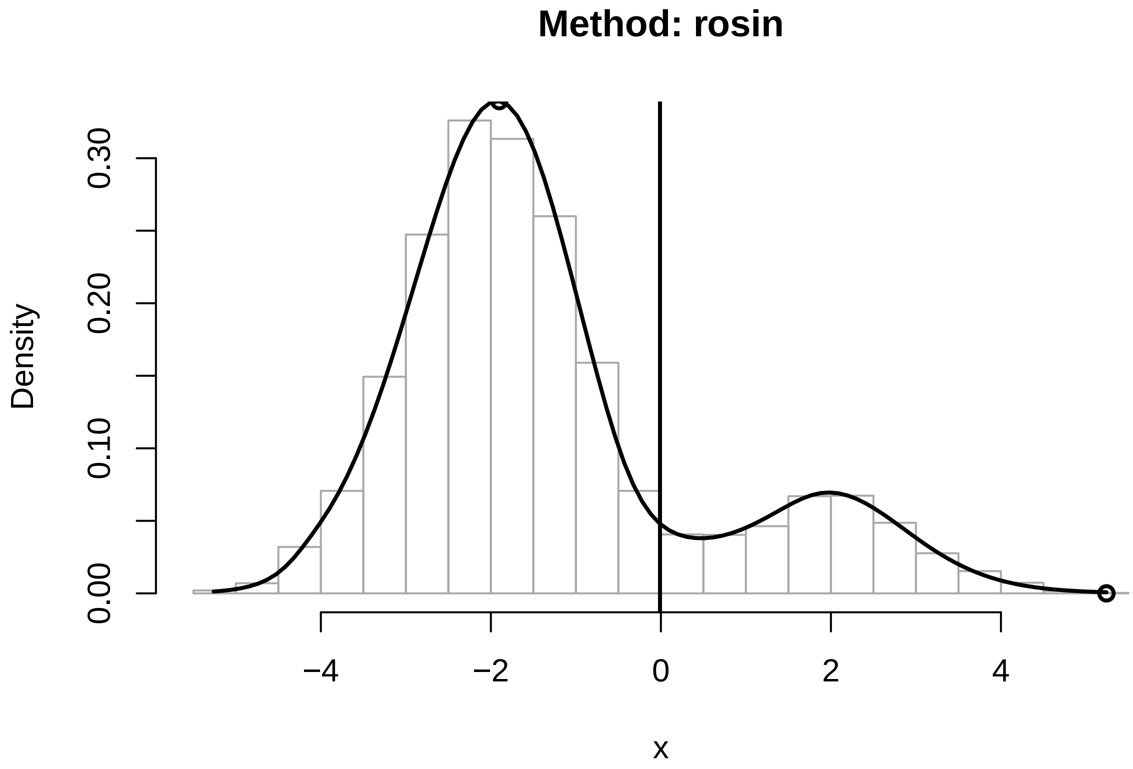
And see what the different threshold selection methods do.

`rosin` threshold:

```
th_rosin <- find_threshold(ds$x, method="rosin")
th_rosin
```

```
## [1] "Threshold(s): -0.0105547"
## [1] "Method: rosin"
```

```r
plot.threshold(th_rosin)
```

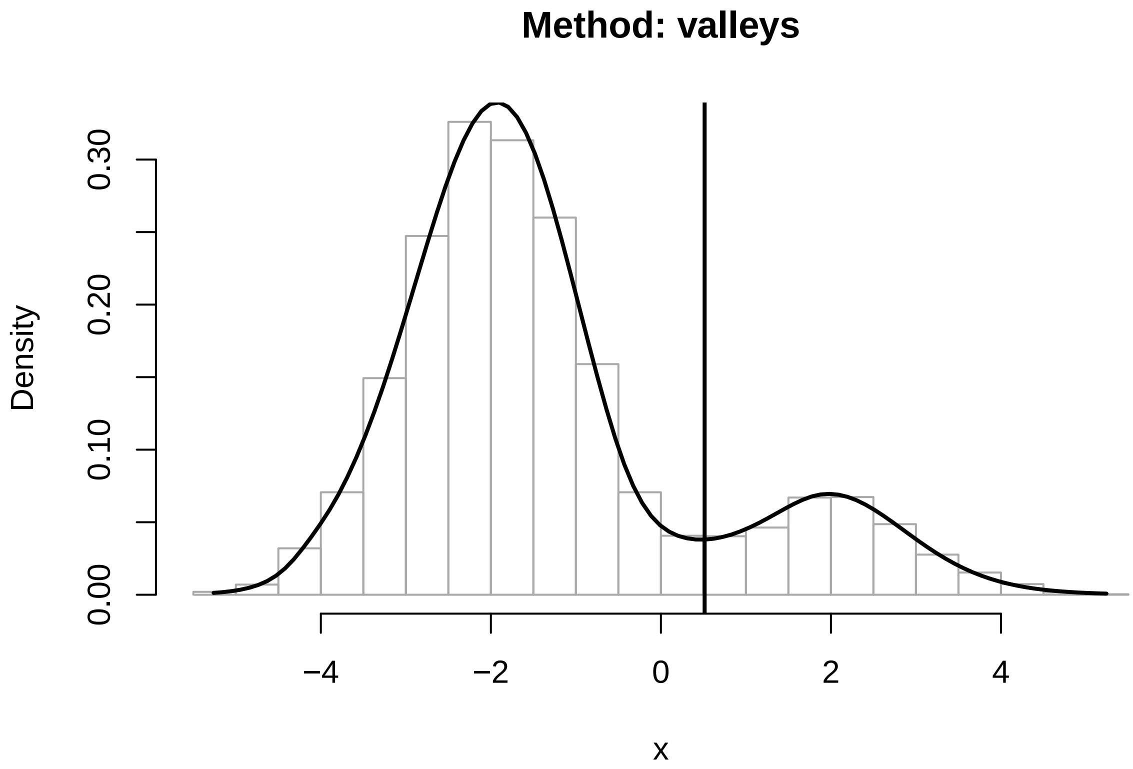


`valleys` threshold:

```r
th_valleys <- find_threshold(ds$x, method="valleys")
th_valleys
```

```
## [1] "Threshold(s): 0.514605"
## [1] "Method: valleys"
```

```r
plot(th_valleys)
```

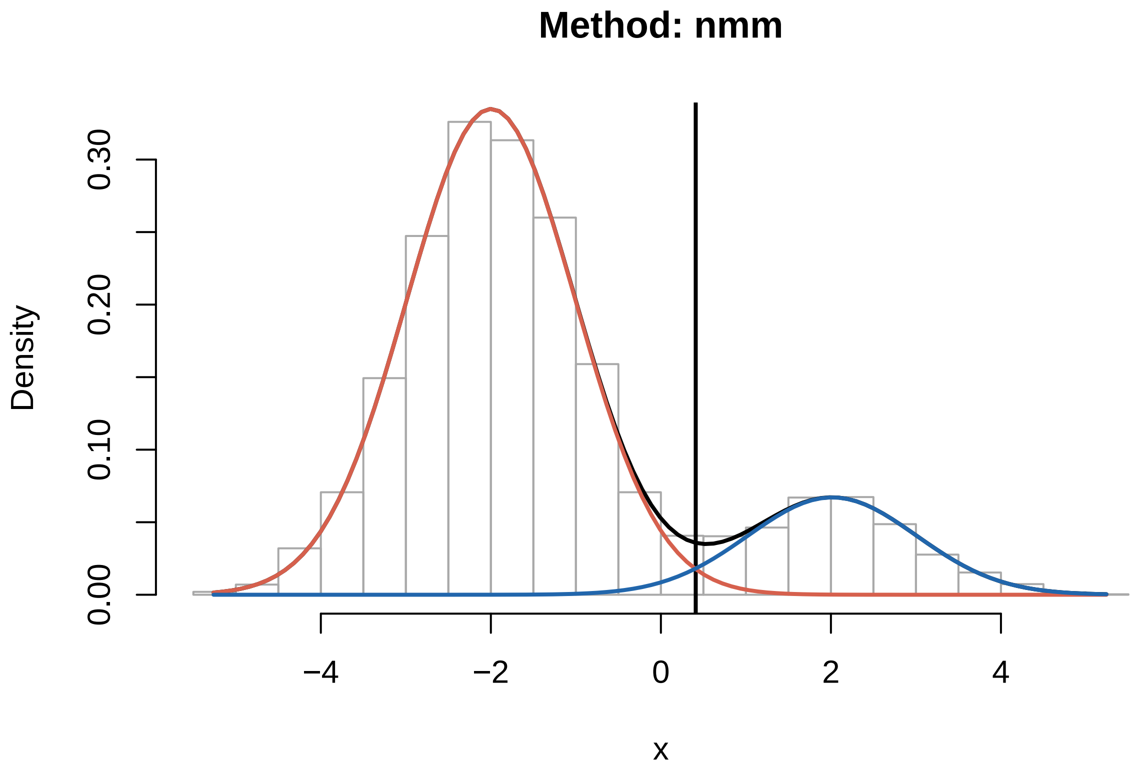


`nmm` threshold:

```
th_nmm <- find_threshold(ds$x, method="nmm")
th_nmm
```

```
## [1] "Threshold(s): 0.409573"
## [1] "Method: nmm"
```

```
plot(th_nmm)
```

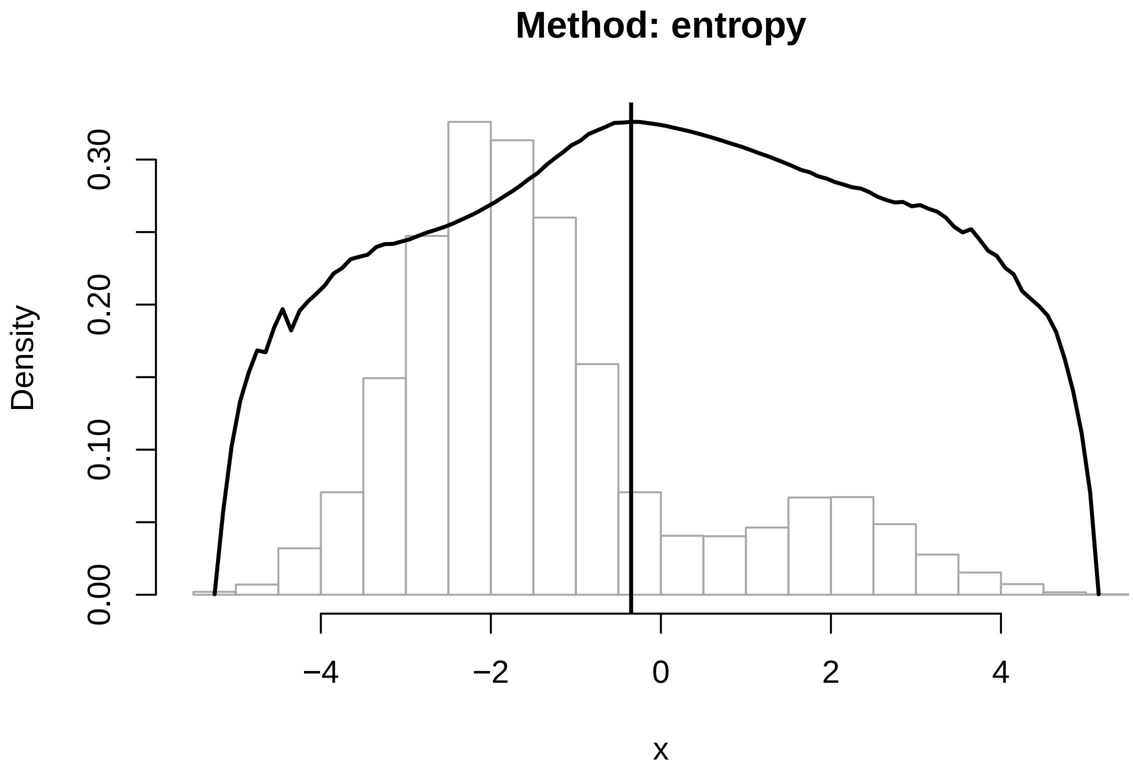


`entropy` threshold:

```
th_entropy <- find_threshold(ds$x, method="entropy")
th_entropy
```

```
## [1] "Threshold(s): -0.35"
## [1] "Method: entropy"
```

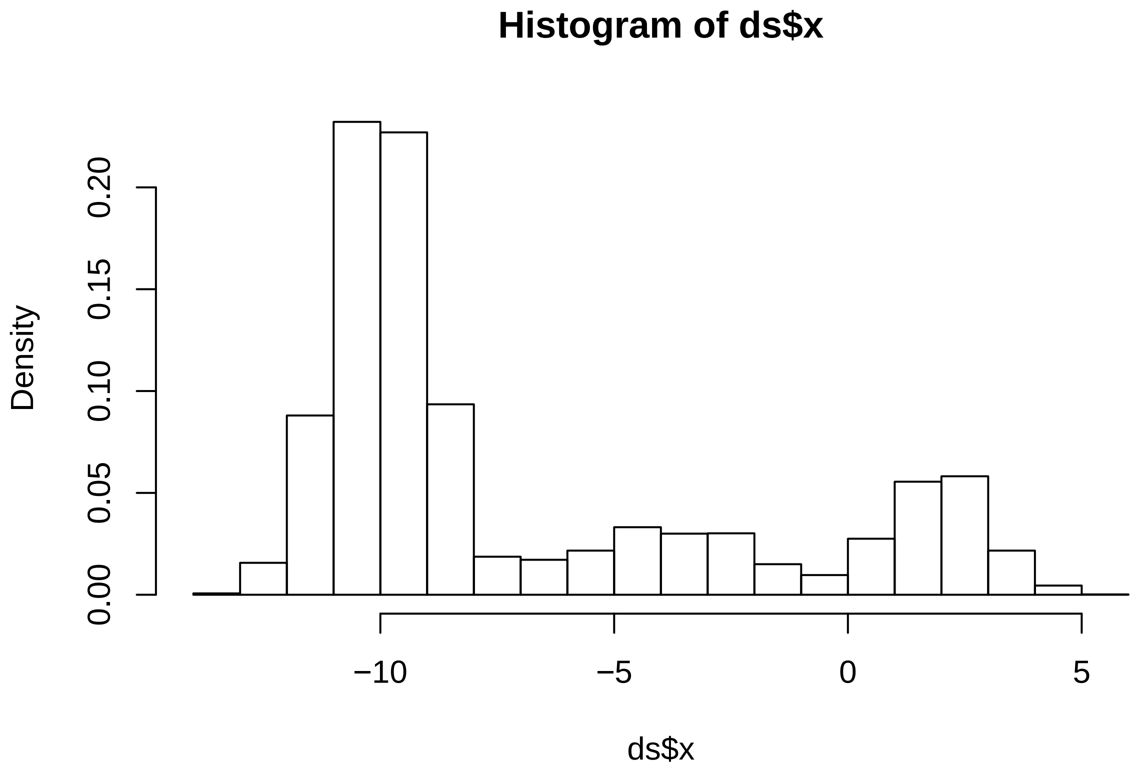
```
plot(th_entropy)
```



ThReshold selection for tri-modal data.

First lets load the package and get a data set.

```
require(threshold)
ds <- threeGaussians(seed=123)
hist(ds$x, breaks='Scott', freq=FALSE)
```



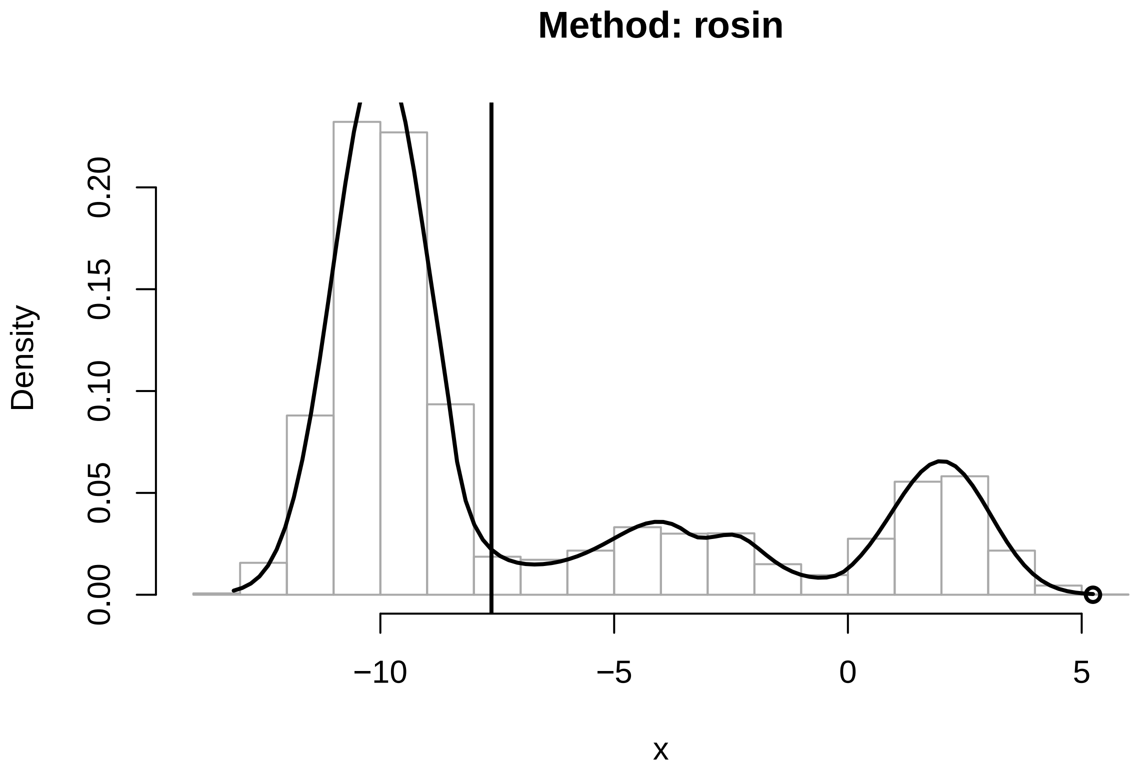
And see what the different threshold selection methods do.

`rosin` threshold:

```
th_rosin <- find_threshold(ds$x, method="rosin")
th_rosin
```

```
## [1] "Threshold(s): -7.62386"
## [1] "Method: rosin"
```

```
plot.threshold(th_rosin)
```

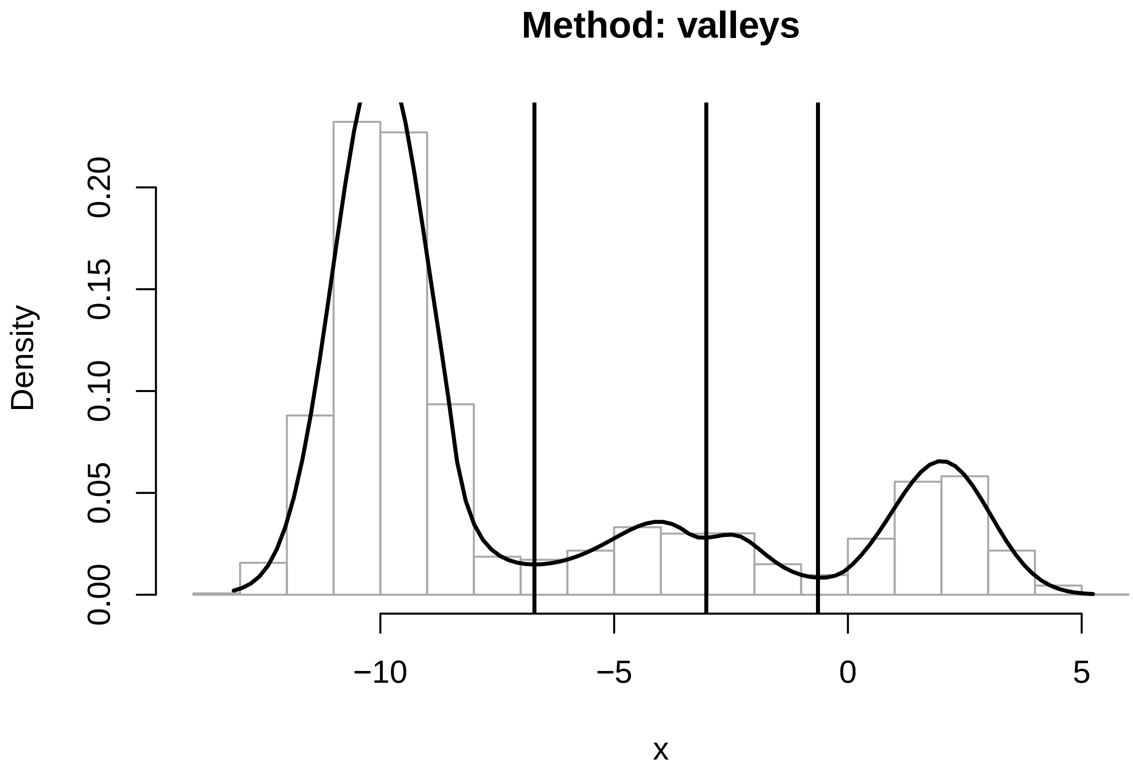


`valleys` threshold:

```
th_valleys <- find_threshold(ds$x, method="valleys")
th_valleys
```

```
## [1] "Threshold(s): -6.70494"  "Threshold(s): -3.02925"
## [3] "Threshold(s): -0.640056"
## [1] "Method: valleys"
```

```
plot(th_valleys)
```



`nmm` threshold:

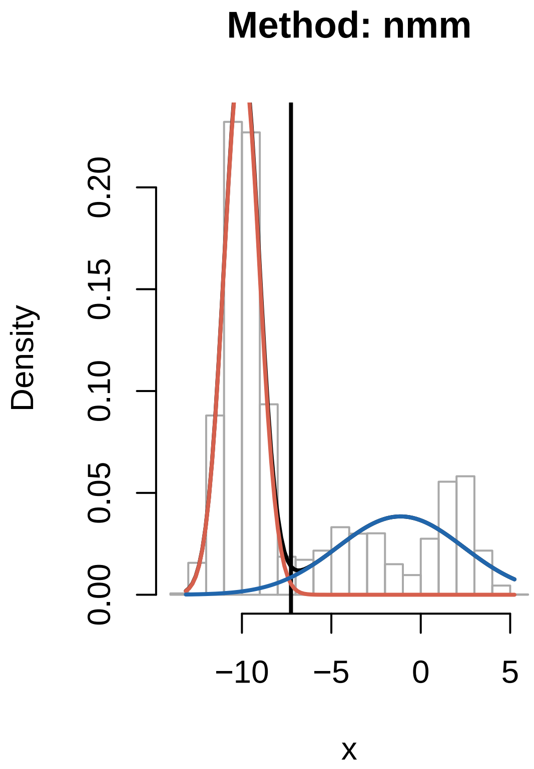
```
th_nmm.g2 <- find_threshold(ds$x, method="nmm", G=2)
th_nmm.g2
```

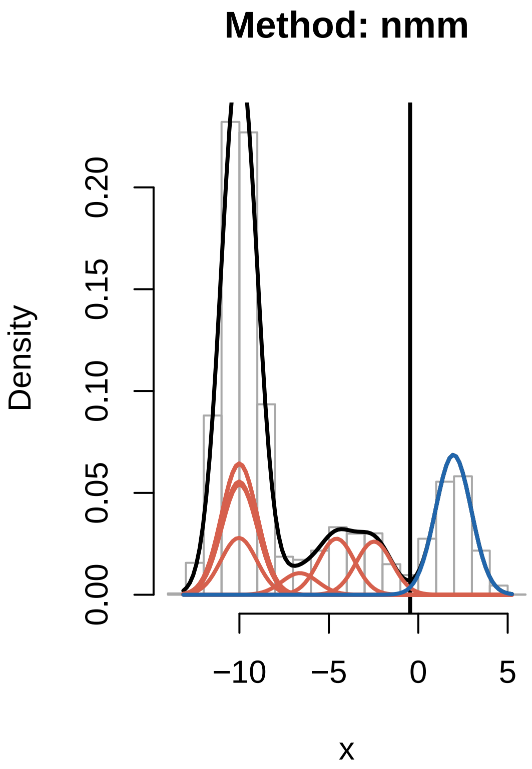
```
## [1] "Threshold(s): -7.25629"
## [1] "Method: nmm"
```

```
th_nmm.g9 <- find_threshold(ds$x, method="nmm", G=9)
th_nmm.g9
```

```
## [1] "Threshold(s): -0.456272"
## [1] "Method: nmm"
```

```
par(mfrow=c(1,2))
plot(th_nmm.g2)
plot(th_nmm.g9)
```



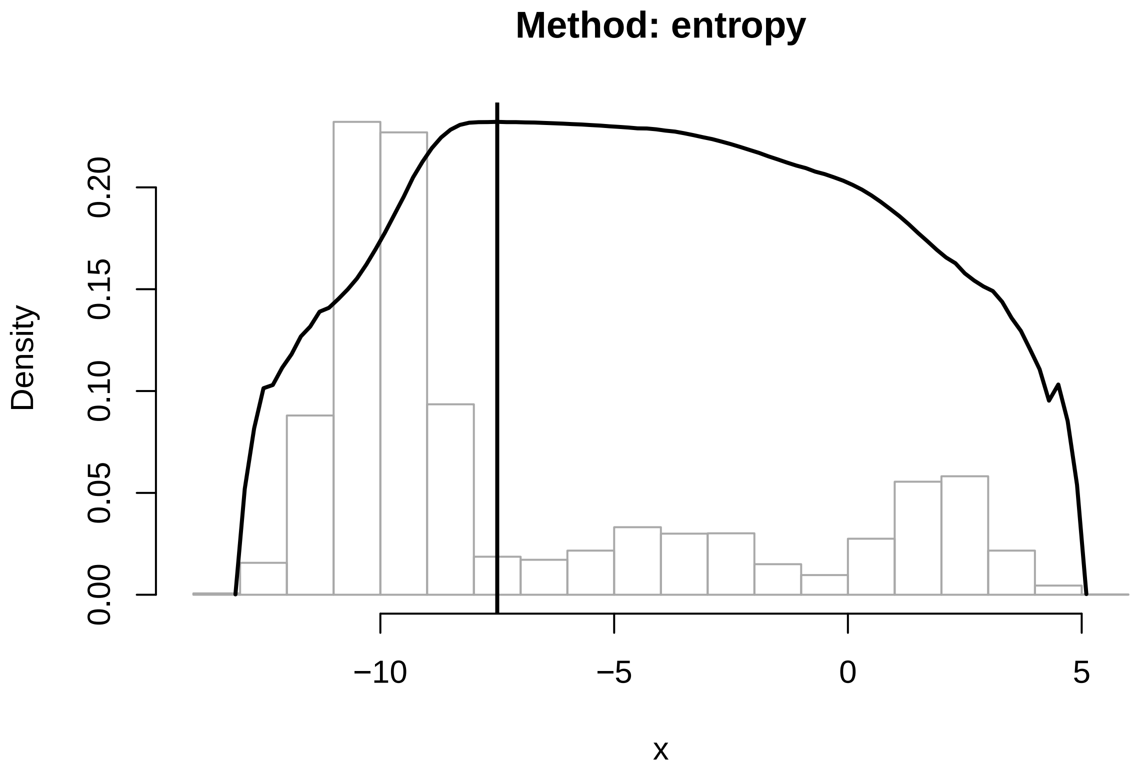


`entropy` threshold:

```
th_entropy <- find_threshold(ds$x, method="entropy")
th_entropy
```

```
## [1] "Threshold(s): -7.5"
## [1] "Method: entropy"
```

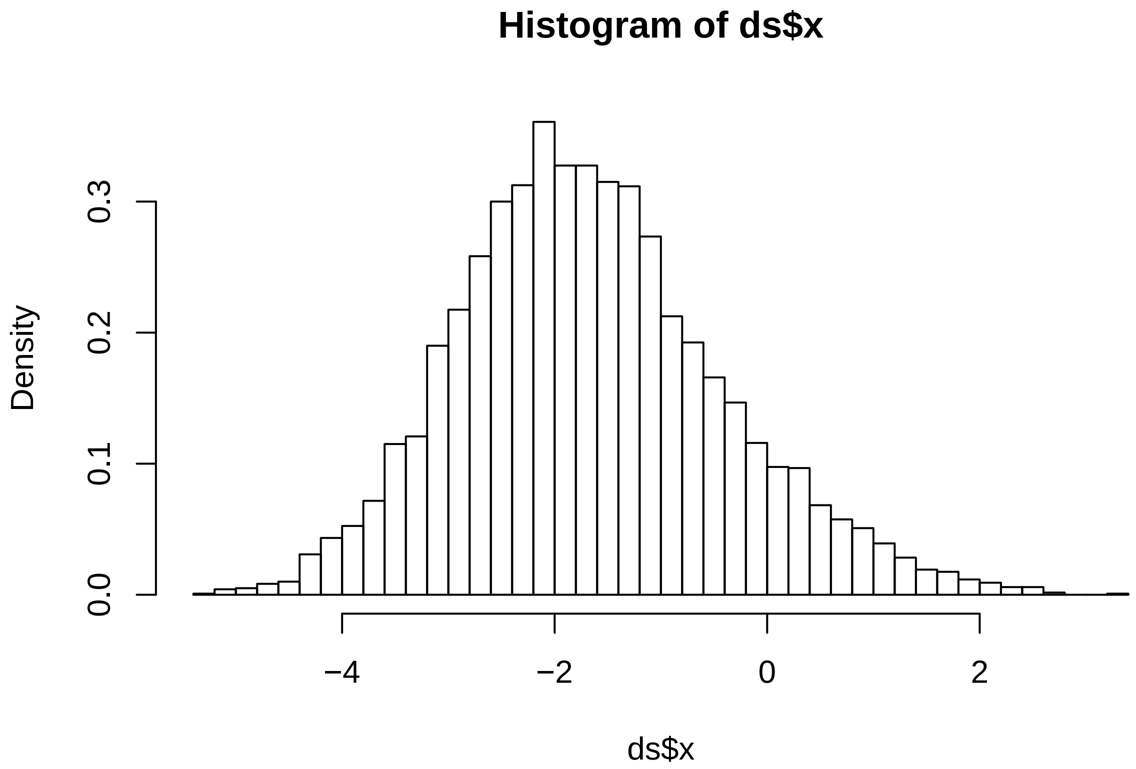
```
plot(th_entropy)
```



ThReshold selection for uni-modal data.

First lets load the package and get a data set.

```r
require(threshold)
ds <- twoGaussians(seed=123, m.pos=0)
hist(ds$x, breaks='Scott', freq=FALSE)
```



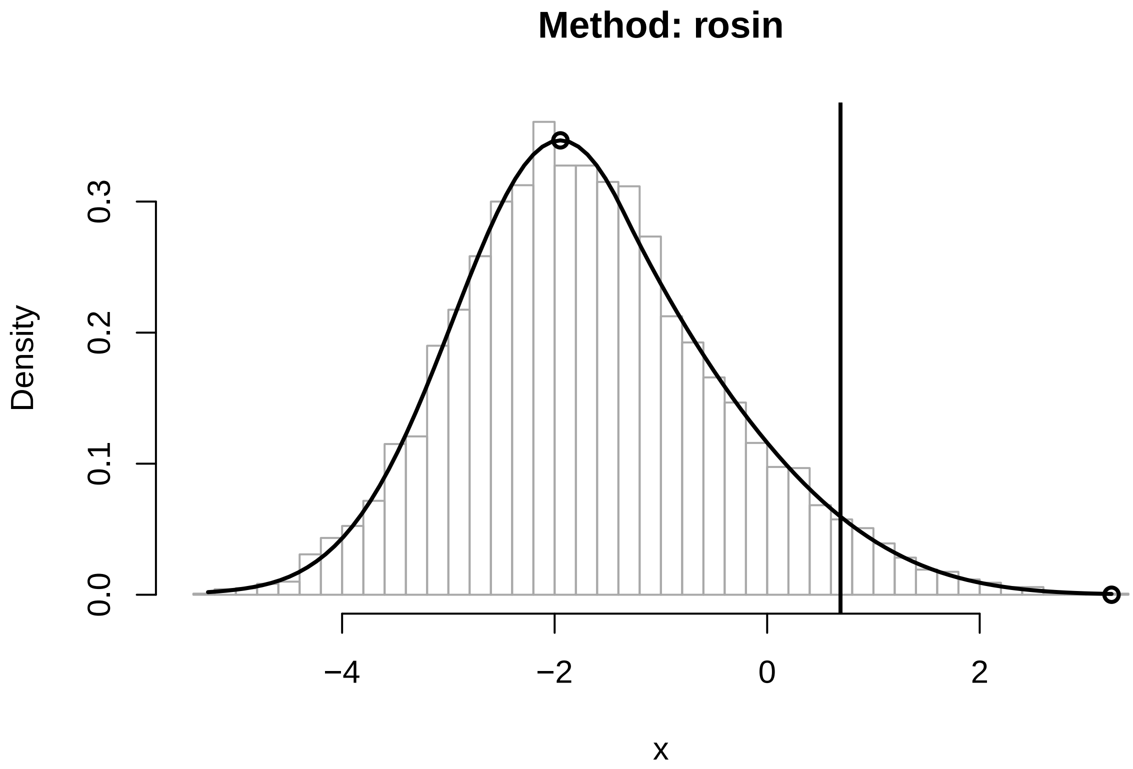
And see what the different threshold selection methods do.

`rosin` threshold:

```
th_rosin <- find_threshold(ds$x, method="rosin")
th_rosin
```

```
## [1] "Threshold(s): 0.690083"
## [1] "Method: rosin"
```

```
plot.threshold(th_rosin)
```

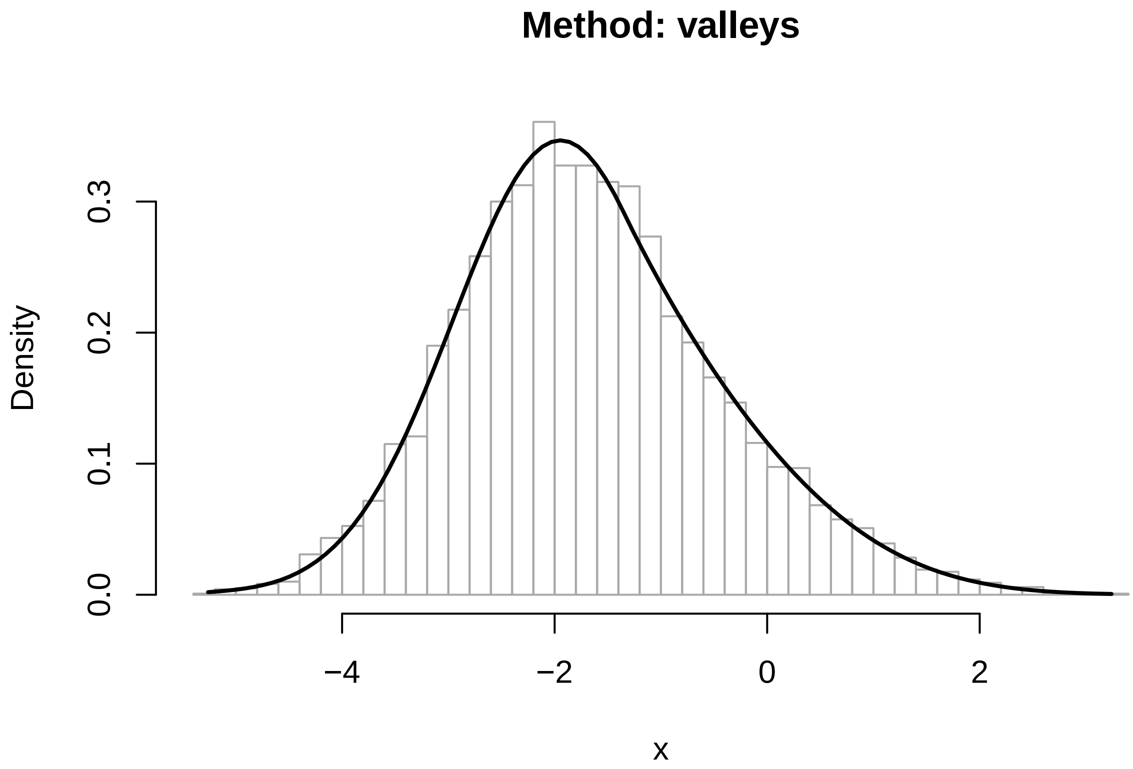


`valleys` threshold:

```
th_valleys <- find_threshold(ds$x, method="valleys")
th_valleys
```

```
## [1] "Threshold(s): NA"
## [1] "Method: valleys"
```

```
plot(th_valleys)
```

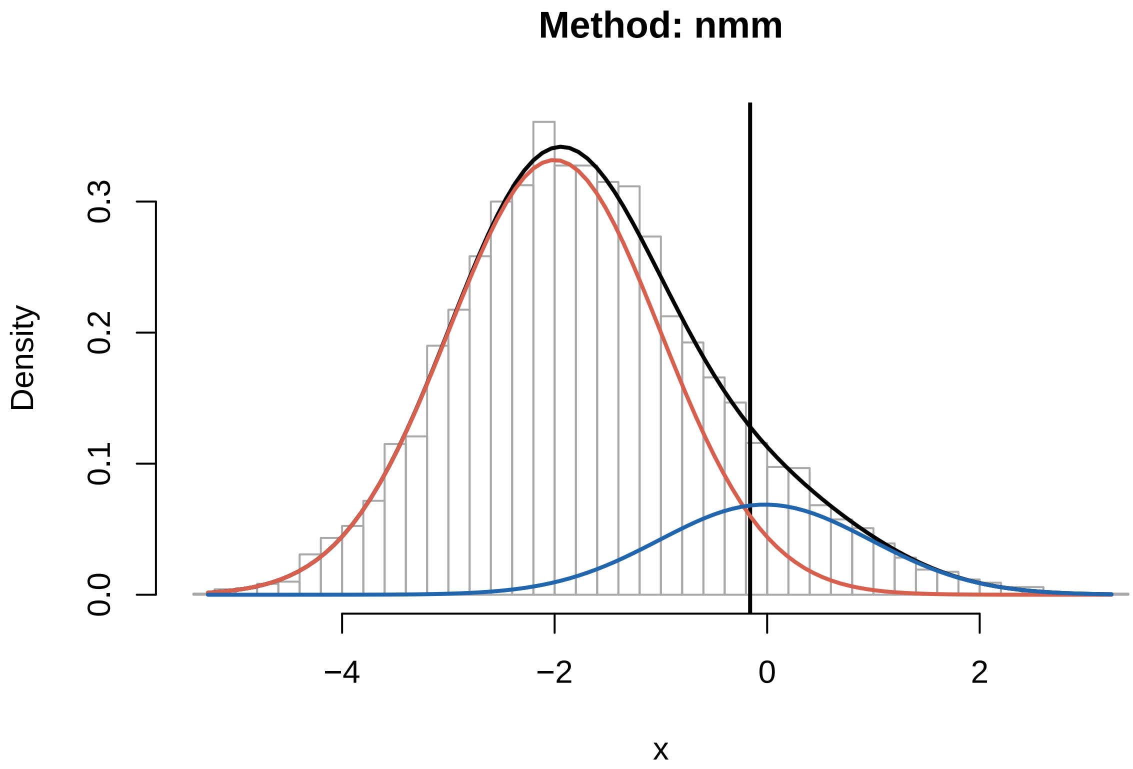


`nmm` threshold:

```
th_nmm <- find_threshold(ds$x, method="nmm")
th_nmm
```

```
## [1] "Threshold(s): -0.160236"
## [1] "Method: nmm"
```

```
plot(th_nmm)
```

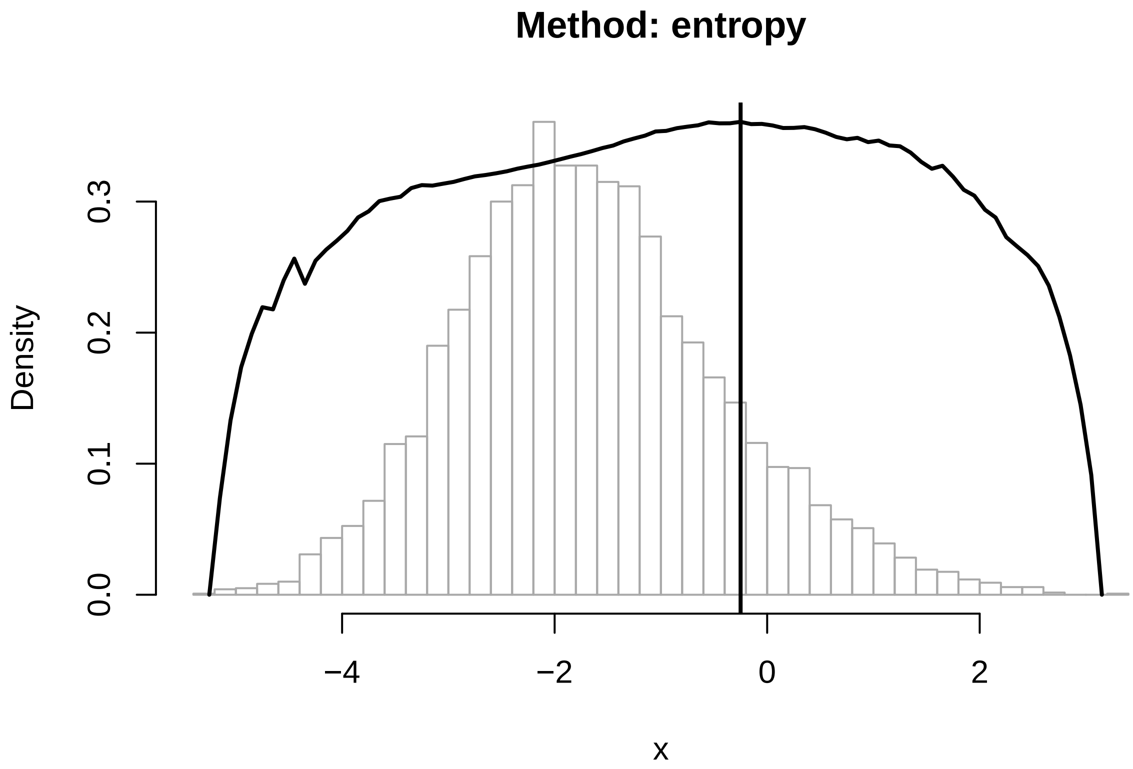


entropy threshold:

```
th_entropy <- find_threshold(ds$x, method="entropy")
th_entropy
```

```
## [1] "Threshold(s): -0.25"
## [1] "Method: entropy"
```

```
plot(th_entropy)
```



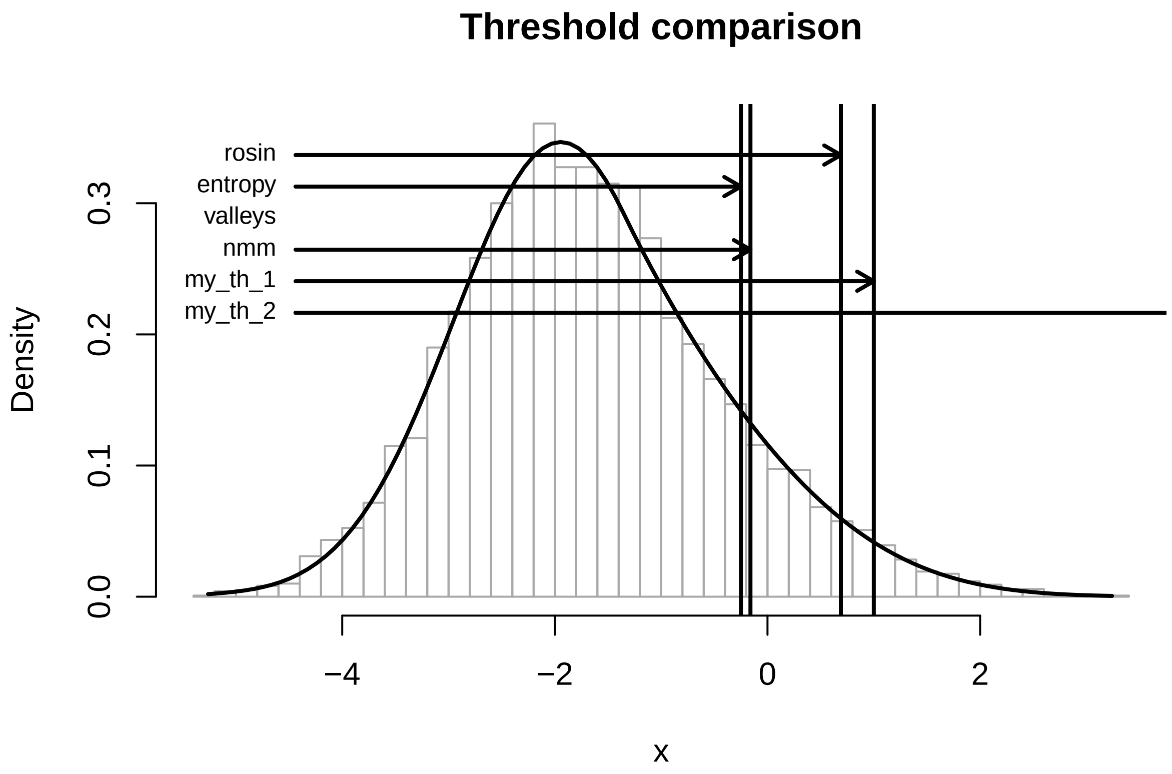
ThReshold selection - run all at once.

```
ths <- find_threshold(ds$x, method=c("rosin", "entropy", "valleys", "nmm"))
ths
```

```
## $rosin
## [1] "Threshold(s): 0.690083"
## [1] "Method: rosin"
##
## $entropy
## [1] "Threshold(s): -0.25"
## [1] "Method: entropy"
##
## $valleys
## [1] "Threshold(s): NA"
## [1] "Method: valleys"
##
## $nmm
## [1] "Threshold(s): -0.160236"
## [1] "Method: nmm"
##
## attr(,"class")
## [1] "threshold_list"
```

```
plot(ths)
plot(ths)


# You might also want to compare it to another set of thresholds.
plot(ths, ths_add=list('my_th_1'=c(1),
                       'my_th_2'=c(4, 4.2)))
```


Threshold comparison
rosin
entropy
valleys
nmm
my_th_1
my_th_2
Density
x