

ThReshold selection for one-class classifiers.

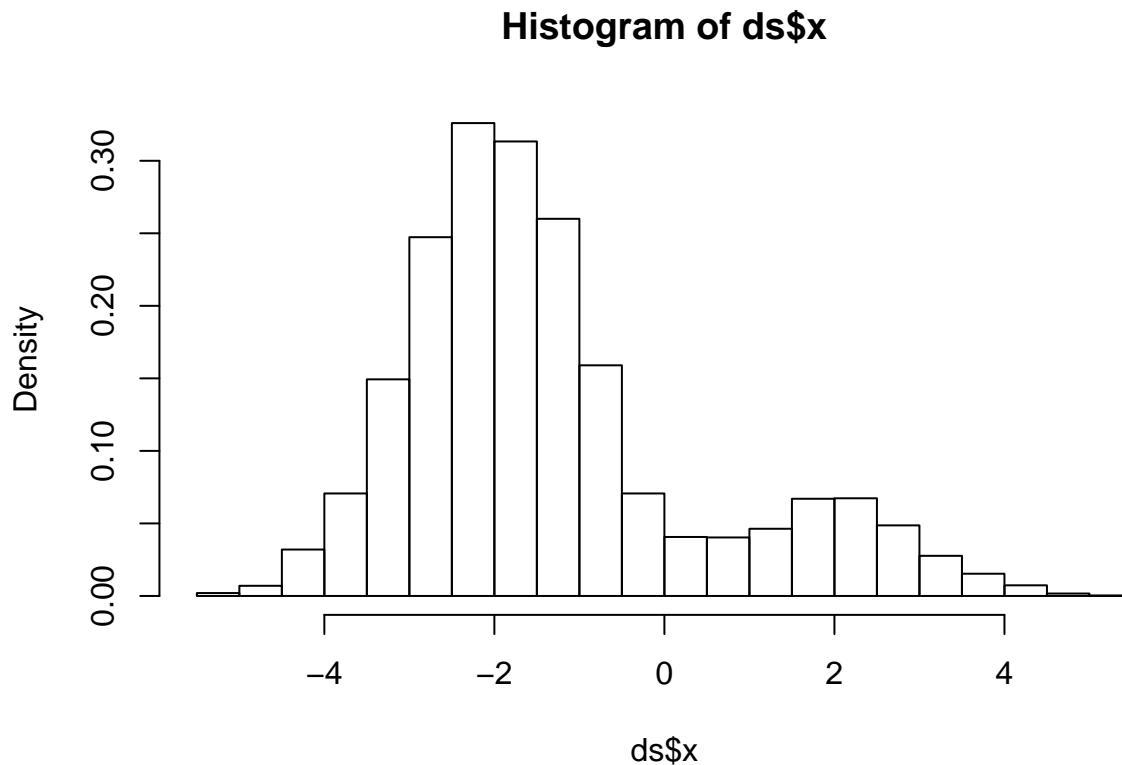
Knecmab

Tuesday, November 18, 2014

ThReshold selection

First lets load the package and get a data set.

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



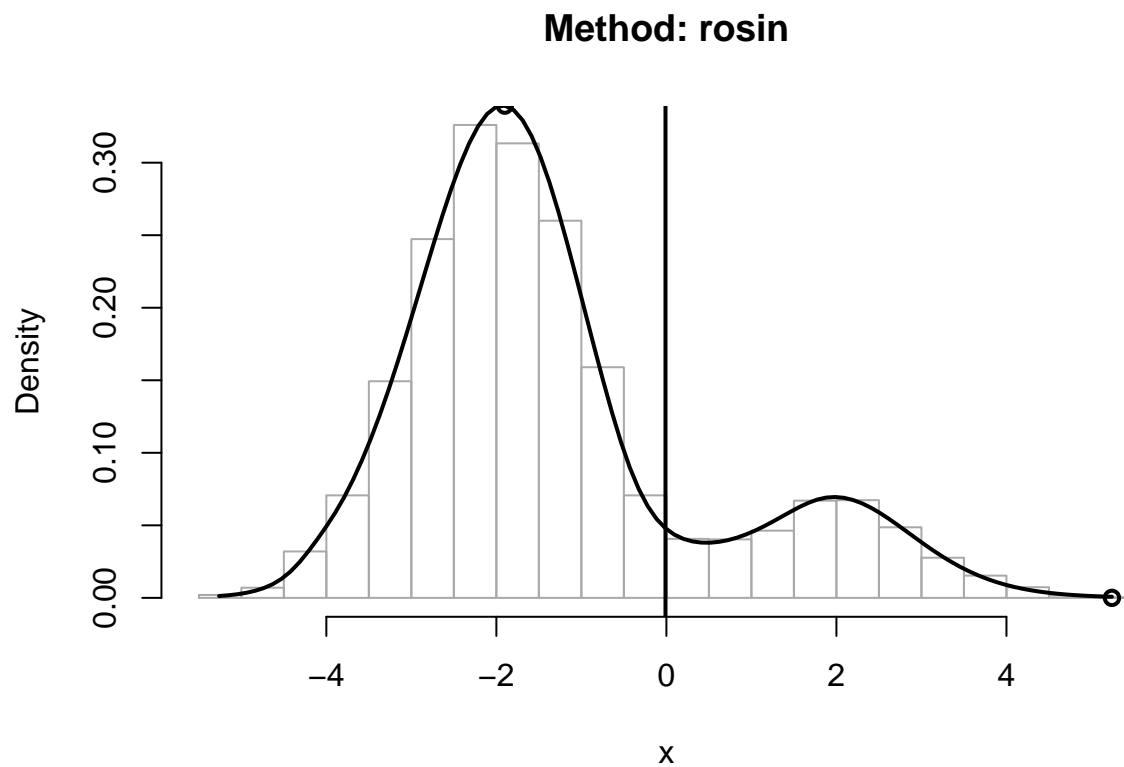
And see what the different threshold selection methods do.

rosin threshold:

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

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

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

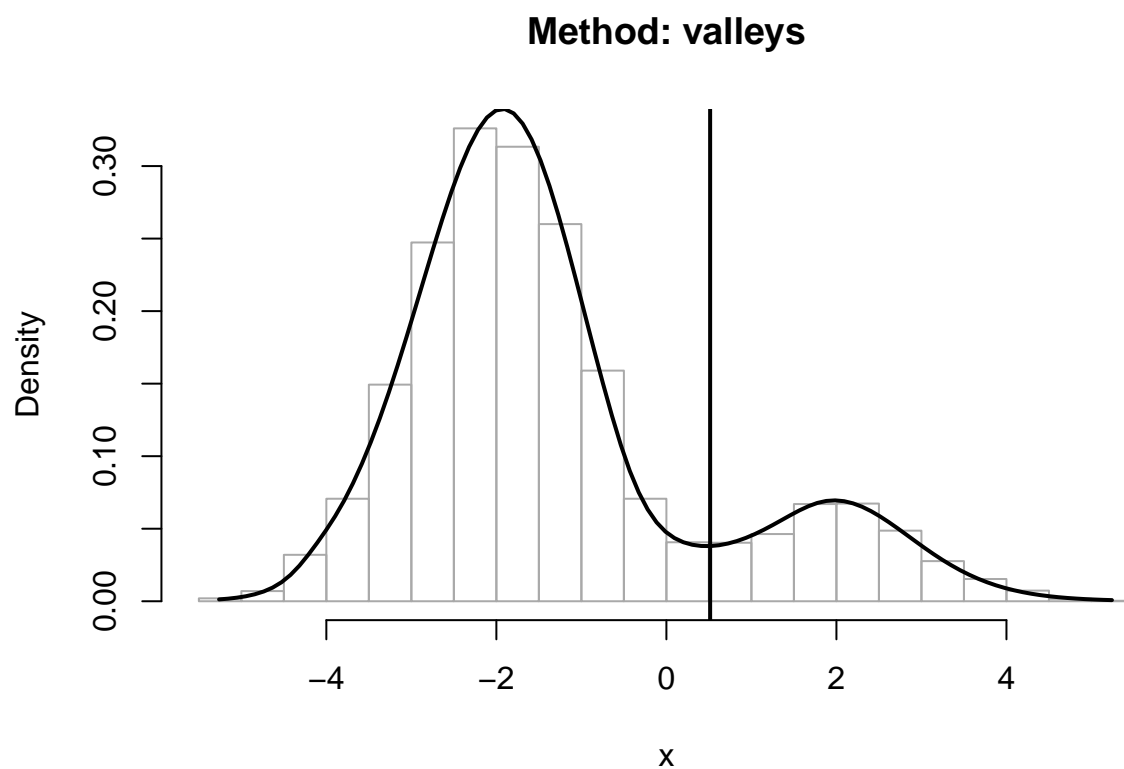


valleys threshold:

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

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

```
plot(th_valleys)
```

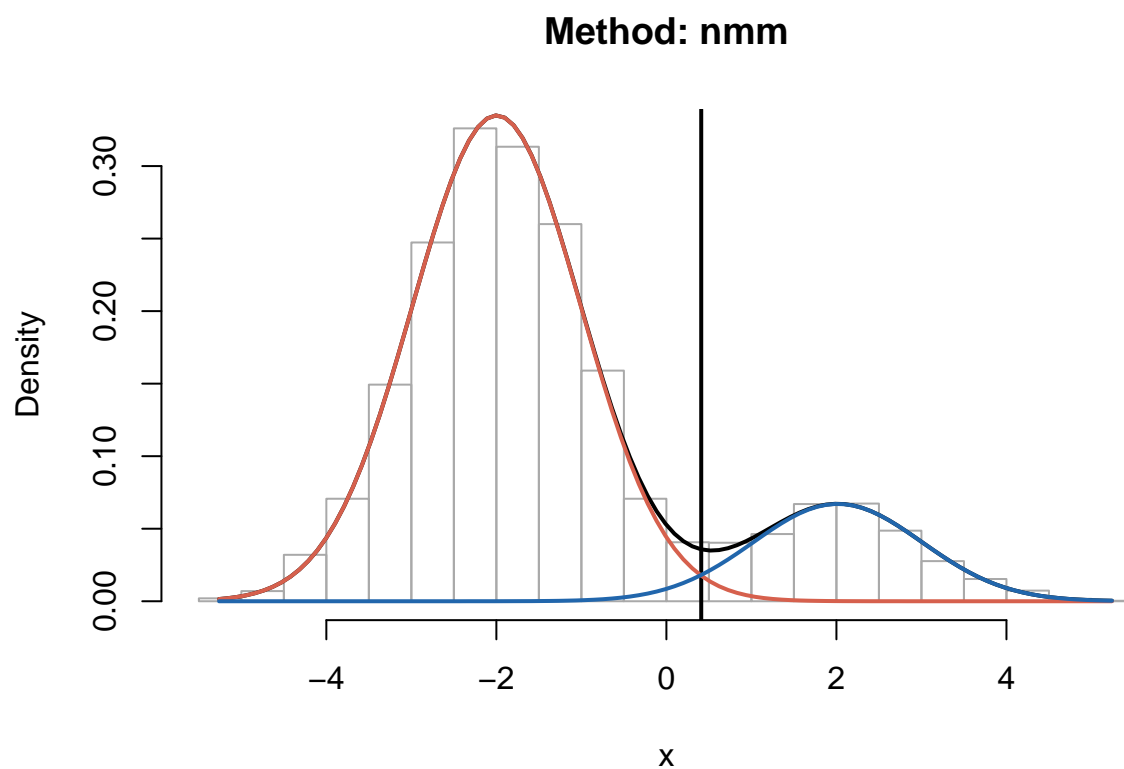


nmv threshold:

```
th_nmv <- find_threshold(ds$x, method="nmv")  
th_nmv
```

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

```
plot(th_nmv)
```



entropy threshold:

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

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

```
plot(th_entropy)
```

