ThReshold selection.

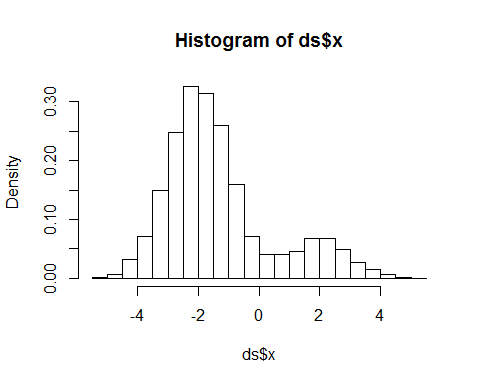
Knecmab

Tuesday, November 18, 2014

# 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)



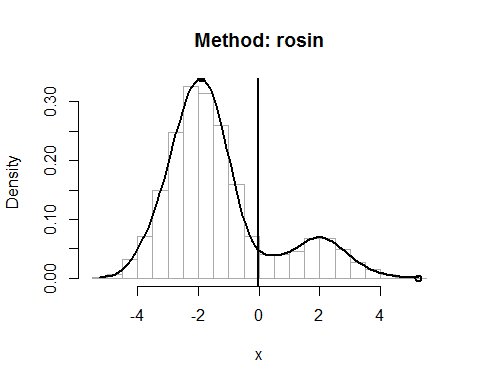
And see what the different threshold selection methods do.

rosin threshold:

th\_rosin <- find\_threshold(ds$x, method="rosin")  
th\_rosin

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

plot.threshold(th\_rosin)

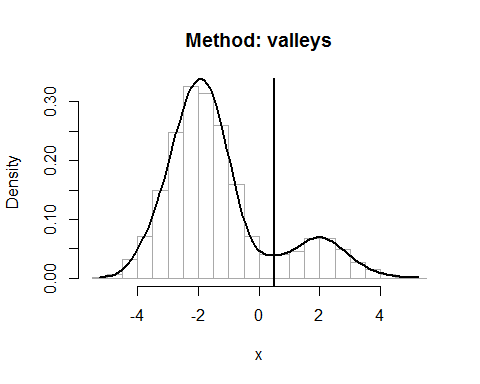


valleys threshold:

th\_valleys <- find\_threshold(ds$x, method="valleys")  
th\_valleys

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

plot(th\_valleys)

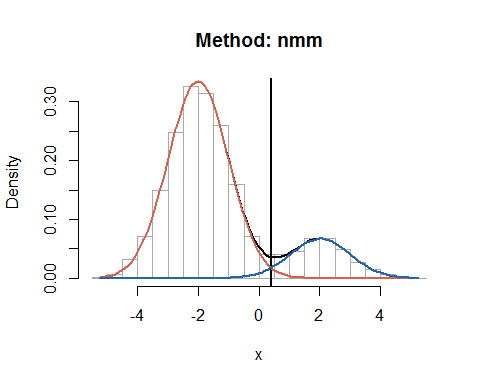


nmm threshold:

th\_nmm <- find\_threshold(ds$x, method="nmm")  
th\_nmm

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

plot(th\_nmm)

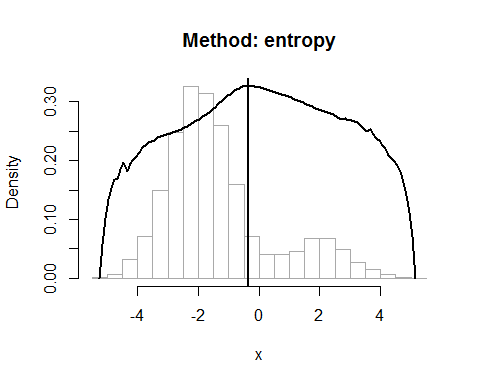


entropy threshold:

th\_entropy <- find\_threshold(ds$x, method="entropy")  
th\_entropy

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

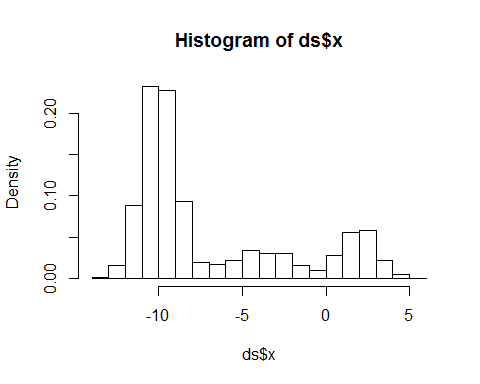
plot(th\_entropy)



# 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)



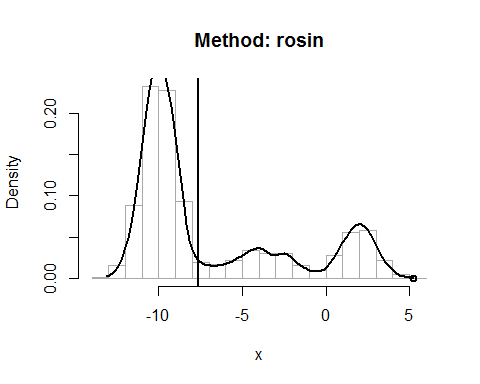
And see what the different threshold selection methods do.

rosin threshold:

th\_rosin <- find\_threshold(ds$x, method="rosin")  
th\_rosin

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

plot.threshold(th\_rosin)

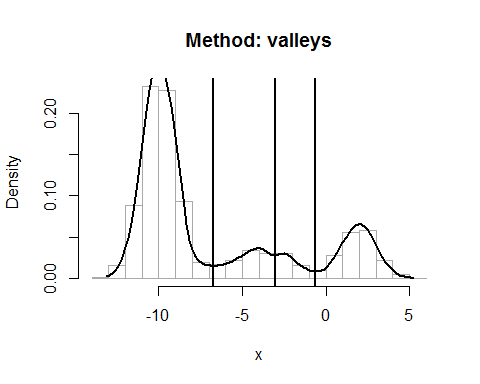


valleys threshold:

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:

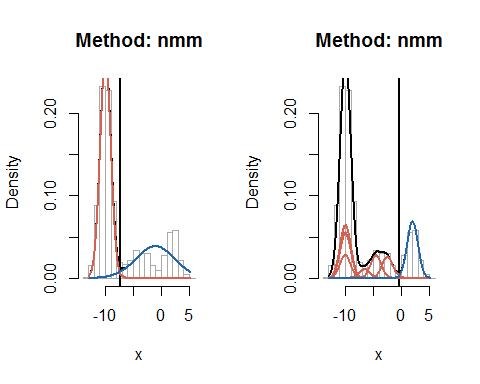
th\_nmm.g2 <- find\_threshold(ds$x, method="nmm", G=2)  
th\_nmm.g2

## [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)

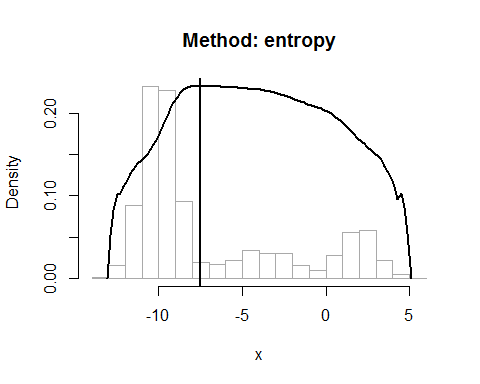


entropy threshold:

th\_entropy <- find\_threshold(ds$x, method="entropy")  
th\_entropy

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

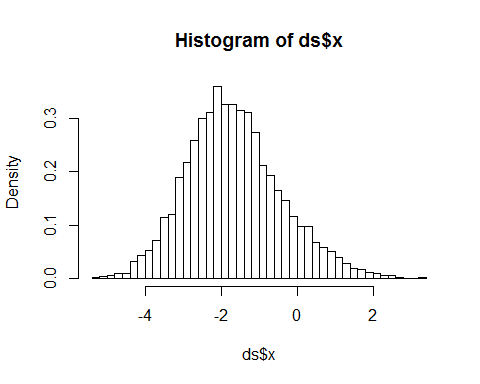
plot(th\_entropy)



# ThReshold selection for uni-modal data.

First lets load the package and get a data set.

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



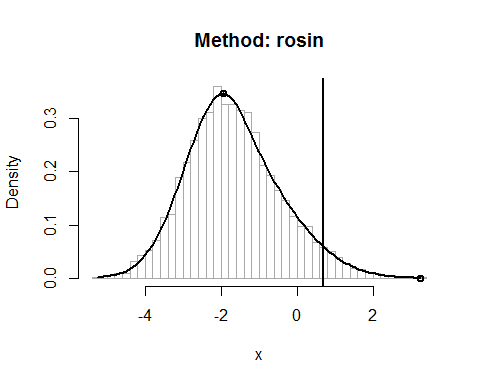
And see what the different threshold selection methods do.

rosin threshold:

th\_rosin <- find\_threshold(ds$x, method="rosin")  
th\_rosin

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

plot.threshold(th\_rosin)

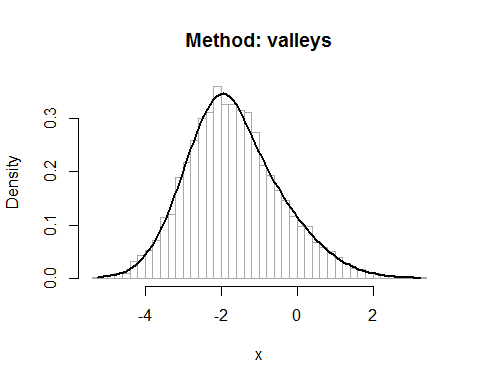


valleys threshold:

th\_valleys <- find\_threshold(ds$x, method="valleys")  
th\_valleys

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

plot(th\_valleys)

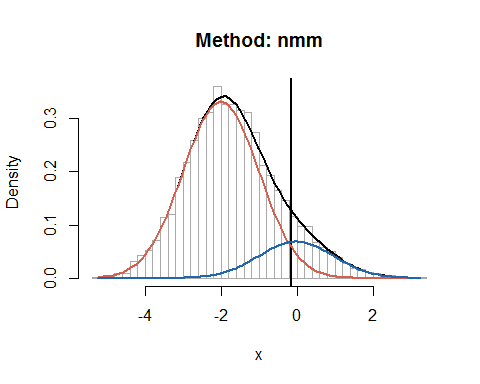


nmm threshold:

th\_nmm <- find\_threshold(ds$x, method="nmm")  
th\_nmm

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

plot(th\_nmm)

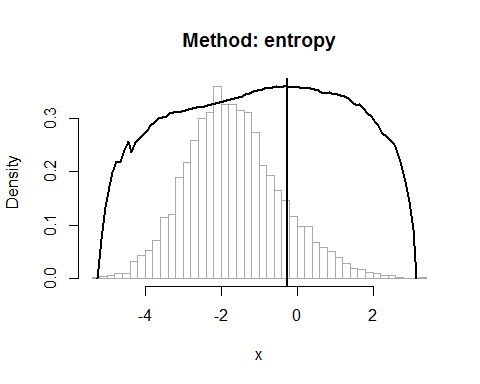


entropy threshold:

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)))

