

automatically removing high missing patients or features

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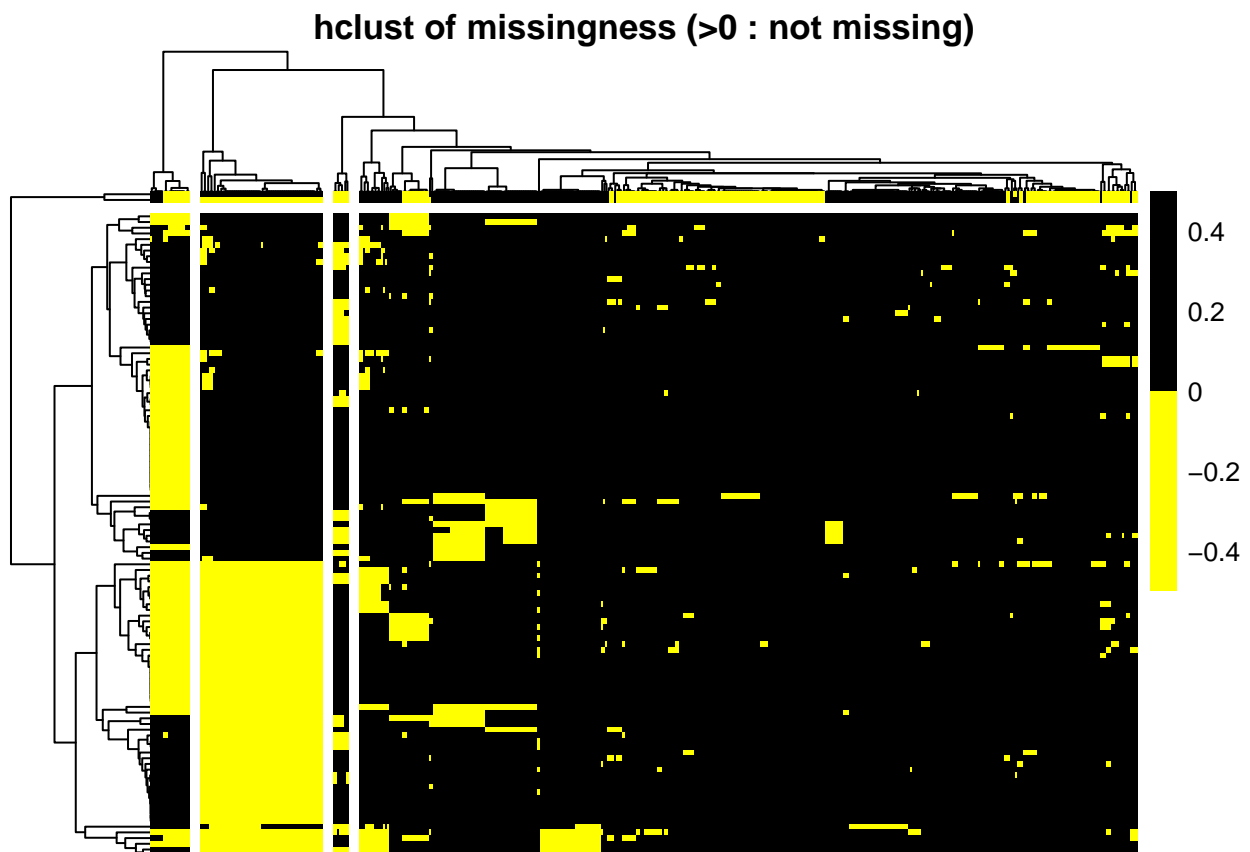
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using Jaccard distance

```
c1 <- clusterMiss(ds1, dis_measure = list('row'='jaccard', 'col'='jaccard'), numCluster = c('row'=2, 'col'=2))

## raw input dimension: 126 520
## dimension after removing full missing cols/rows: 126 484
## matrix used for clustering: 115 438
## using jaccard,jaccard distance

## Metric: 'jaccard'; comparing: 115 vectors.
## Metric: 'jaccard'; comparing: 438 vectors.
```



```
## [1] "row groups:"
## pt_groups
```

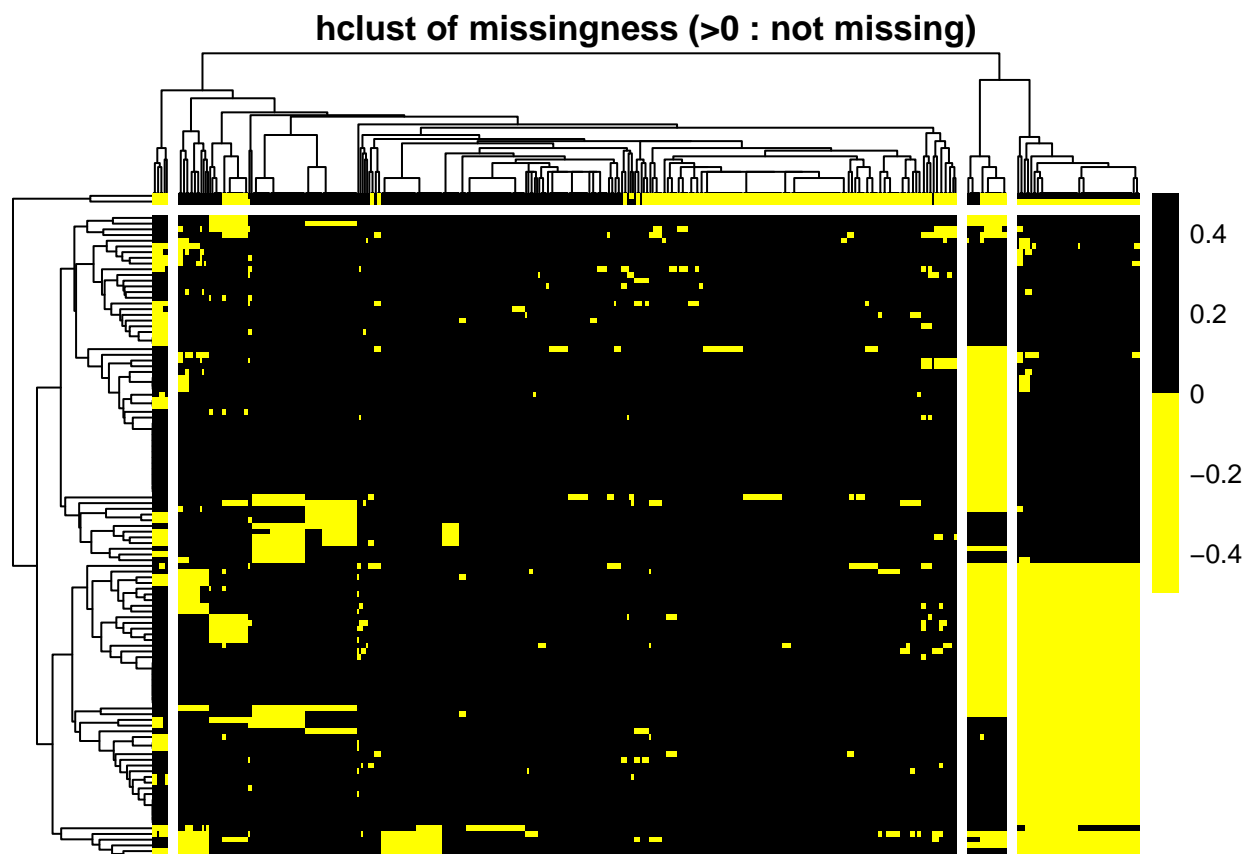
```
## 1 2
## 113 2
## [1] "column groups:"
## ft_groups
## 1 2 3 4
## 357 7 56 18
## [1] "summary of percent non-missing values among excluded items in the original matrix"
## G028915-264866-401004 G028915-266618-423025
## 0.6198347 0.5061983
## summary for 81 items
## Min. 1st Qu. Median Mean 3rd Qu. Max.
## 0.4683 0.5159 0.5794 0.5684 0.5873 0.7619
## [1] "summary of percent non-missing values after removing patients and samples with high missing"
## summary for 124 items
## Min. 1st Qu. Median Mean 3rd Qu. Max.
## 0.8065 0.9404 0.9851 0.9648 1.0000 1.0000
## summary for 403 items
## Min. 1st Qu. Median Mean 3rd Qu. Max.
## 0.7823 0.9516 0.9839 0.9648 0.9919 1.0000
```

using euclidian distance

this is an option; but not the default setting

```
c1 <- clusterMiss(ds1, dis_measure = list('row'='euclidean', 'col'='euclidean'), numCluster = c('row'=2, 'col'=2))

## raw input dimension: 126 520
## dimension after removing full missing cols/rows: 126 484
## matrix used for clustering: 115 438
## using euclidean,euclidean distance
```



```
## [1] "row groups:"
## pt_groups
##   1   2
## 113   2
## [1] "column groups:"
## ft_groups
##   1   2   3   4
## 357   7  56  18
## [1] "summary of percent non-missing values among excluded items in the original matrix"
## G028915-264866-401004 G028915-266618-423025
##           0.6198347           0.5061983
## summary for 81 items
##   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.4683  0.5159  0.5794  0.5684  0.5873  0.7619
## [1] "summary of percent non-missing values after removing patients and samples with high missing"
## summary for 124 items
##   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.8065  0.9404  0.9851  0.9648  1.0000  1.0000
## summary for 403 items
##   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.7823  0.9516  0.9839  0.9648  0.9919  1.0000
```