How to use cghMCR

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1 Overview

This vignette demonstrate how to use cghMCR to locate minimum common regions (MCR) across arrayCGH profiles derived from different samples. MCR was initially proposed by Dr. Lynda Chin's lab (Aguirre et. al. 2004) to identify chromosome regions showing common gains/losses across samples using arrayCGH platform. The cghMCR pacakge implements the algorithm.

2 Getting Started

The example data used in this vignette are artificially constructed following the *Agilent* arrayCGH format within 5000 probes to maintain speed.

2.1 Read the sample data

The sample data are stroed in the *data* subdirectory and can be read in using read.Agilent of *marray*.

```
> require("cghMCR")
```

```
Loading required package: cghMCR
Loading required package: DNAcopy
Loading required package: marray
Loading required package: limma
```

Attaching package: 'cghMCR'

```
The following object(s) are masked from package:DNAcopy : plot.DNAcopy
```

[1] TRUE > sampleData <- r</pre>

```
Reading ... /tmp/Rinst.15943/cghMCR/sampledata/sample1.agi
Reading ... /tmp/Rinst.15943/cghMCR/sampledata/sample2.agi
Reading ... /tmp/Rinst.15943/cghMCR/sampledata/sample3.agi
```

sampleData has three samples with intensity measures for 5000 probes.

> maNsamples(sampleData)

[1] 3

> length(maLabels(maGnames(sampleData)))

[1] 5000

It normally takes a few steps such as quality assessment and normalization before engaging data analysis. Here we conduct a loess normalization that is supported by marray. Readers are referred to packages marray and limma for further information.

```
> normedData <- maNorm(sampleData, norm = "loess")</pre>
```

2.2 Identify chromosome segments

For each sample, we need to first identify chromosome segments having similar intensity measures. The function getSegments is a wrapper around the main functions provided by DNAcopy that are capable of detecting chromosome regions within which probe intensities remain similar.

```
> segments <- getSegments(normedData)
```

```
Analyzing: X.tmp.Rinst.15943.cghMCR.sampledata.sample1.agi
Analyzing: X.tmp.Rinst.15943.cghMCR.sampledata.sample2.agi
Analyzing: X.tmp.Rinst.15943.cghMCR.sampledata.sample3.agi
```

Results from the segmentation analysis (segments) is a list with three elements:

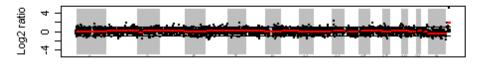
```
> names(segments)
```

```
[1] "data" "output" "call"
```

The *data* element contain the normalized data, the *output* element contains the chromosome segments identified, and the *call* elements contains the function call with parameters passed indicated. Now, let's plot the original data and the segments to see what the segments look like.

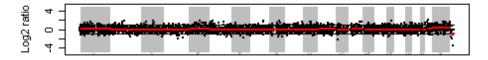
```
> plot(segments)
```

C..PROGRA.1.R.R.22.1.0.library.cghMCR.sampledata.sample1.agi



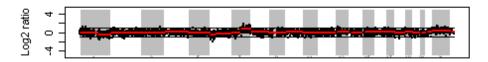
Chromsome

C..PROGRA.1.R.R.22.1.0.library.cghMCR.sampledata.sample2.agi



Chromsome

C..PROGRA.1.R.R.22.1.0.library.cghMCR.sampledata.sample3.agi



Chromsome

Figure 1:

2.3 Identify MCRs

The element - output of the segments object generated in the previous section contains the segmentation data and will be used to get the MCRs. The parameter margin is numeric indicating how many basepairs should two adjancent segments be allowed to apart to be considered as one locus. Parameters gain.threshold and loss.threshold are also numerics indicating the minimum positive or maximum negative values for chromsome segments to be considered as gains or losses.

```
> cghmcr <- cghMCR(segments, margin = 0, gain.threshold = 0.8,
+ loss.threshold = -0.8)
> mcrs <- MCR(cghmcr)</pre>
```

Using the above settings, we get four MCRs but only one (on chromosome 7) of them are common to two samples.

To include probe ids for the MCRs identified, we can call the function mergeMCR-Probes to have probe ids within each MCR appended. Multiple probes are separated by a ",".

3 Session Information

The version number of R and packages loaded for generating the vignette were:

```
R version 2.2.0, 2005-10-06, x86_64-unknown-linux-gnu
```

```
attached base packages:

[1] "tools" "methods" "stats" "graphics" "grDevices" "utils"

[7] "datasets" "base"

other attached packages:
 cghMCR marray limma DNAcopy

"1.1.0" "1.9.1" "2.2.0" "1.4.0"
```

4 References

Aguirre, AJ, C. Brennan, G. Bailey, R. Sinha, B. Feng, C. Leo, Y. Zhang, J. Zhang, N. Bardeesy, C. Cauwels, C. Cordon-Cardo, MS Redston, RA DePinho and L. Chin. High-resolution Characterization of the Pancreatic Adenocarcinoma Genome. Proc Natl Acad Sci U S A. 2004. 101(24):9067-9072.