

# GLAD package: Gain and Loss Analysis of DNA

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# 1 Overview

This document presents an overview of the GLAD package (Gain and Loss Analysis of DNA). This package is devoted to the analysis of Array Comparative Genomic Hybridization (array CGH) (Pinkel et al., 1998; Snijders et al., 2001; Solinas-Toldo et al., 1997; Ishkanian et al., 2004). The methodology for detecting the breakpoints delimiting altered regions in genomic patterns and assigning a status (normal, gained or lost) to each chromosomal region described in the paper Hupé et al. (2004) is implemented in this package. Some graphical functions are provided as well.

## 2 Data

### 2.1 Public data set

We used the public data set described in Snijders et al. (2001). The data corresponds to 15 human cell strains with known karyotypes (12 fibroblast cell strains, 2 chorionic villus cell strains, 1 lymphoblast cell strain) from the NIGMS Human Genetics Cell Repository (<http://locus.umdj.edu/nigms>). Each cell strain has been hybridized on CGH arrays of 2276 BACs, spotted in triplicates. Two array CGH profiles from the data obtained by Veltman et al. (2003) are available.

### 2.2 Bladder cancer data

Bladder cancer data from tumors collected at Henri Mondor Hospital (Créteil, France) (Billerey et al., 2001) have been hybridized on CGH arrays composed of 2464 BACs (Radvanyi, Pinkel et al., unpublished results). In this data, only the log-ratios are provided and no information about clones is available since the data is not yet published. This data allows only some graphical functionalities to be shown and will be used as a support to illustrate some functions for array normalization (not yet available in the current version of the package).

## 3 GLAD classes

### 3.1 arrayCGH

This class stores raw values after images analysis. The object `arrayCGH` is a list with at least a `data.frame` named `arrayValues` and a vector named `arrayDesign`. The `data.frame` `arrayValues` must contain the following fields:

**Col** Vector of columns coordinates.

**Row** Vector of rows coordinates.

... Other elements can be added.

The vector `arrayDesign` is composed of 4 values: `c(arrayCol, arrayRow, SpotCol, SpotRow)`. The array CGH is represented by `arrayRow*arrayCol` blocs and each bloc is composed of `SpotRow*SpotCol` spots. N.B.: `Col` takes the values in `1:arrayRow*SpotRow` and `Row` takes the values in `1:arrayCol*SpotCol`

### 3.2 profileCGH and profileChr

This class stores synthetic values related to each clone available on the `arrayCGH`. The object `profileChr` corresponds to data of only one chromosome. Objects `profileCGH` and `profileChr` are composed of a list with the first element `profileValues` which is a `data.frame` with the following columns names:

**LogRatio** Test over Reference log-ratio.

**PosOrder** The rank position of each clone on the genome.

**PosBase** The base position of each clone on the genome.

**Chromosome** Chromosome name.

**Clone** The name of the corresponding clone.

... Other elements can be added.

LogRatio, Chromosome and PosOrder are compulsory.

To create those objects you can use the function *as.profileCGH*.

## 4 Analysis of array CGH profile

Two functions are available: *glad* and *daglad*. The second one is an improvement of the first one which was originally described in Hupé et al. (2004). We recommend to use the *daglad* function. For fast computation use the option *smoothfunc=haarseg*.

### 4.1 Segmentation algorithms

Two algorithms are available for data segmentation:

- AWS (Polzehl and Spokoiny, 2000, 2002)
- HaarSeg (Ben-Yaacov and Eldar, 2008)

### 4.2 The *glad* function

A result of the GLAD methodology on cell line gm13330 (Snijders et al., 2001) is presented in **Figure 1**.

```
> data(snijders)
> profileCGH <- as.profileCGH(gm13330)
> res <- glad(profileCGH, mediancenter=FALSE,
+             smoothfunc="lawsglad", bandwidth=10, round=1.5,
+             model="Gaussian", lkern="Exponential", qlambda=0.999,
+             base=FALSE,
+             lambdabreak=8, lambdacluster=8, lambdaclusterGen=40,
+             type="tricubic", param=c(d=6),
+             alpha=0.001, msize=2,
+             method="centroid", nmax=8,
+             verbose=FALSE)

[1] "Smoothing for each Chromosome"
[1] "Optimization of the Breakpoints"
[1] "Results Preparation"

>
```

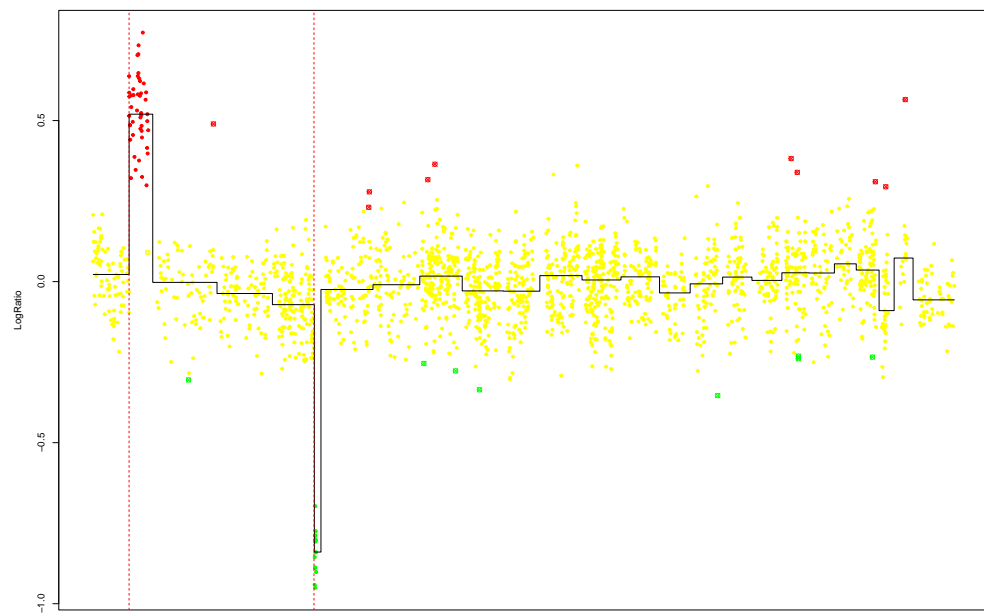


Figure 1: Results of glad on cell line gm13330 (Snijders data).

### 4.3 The *daglad* function

The algorithm implemented in this function is a slightly modified version of the GLAD algorithm.

```
> data(veltman)
> profileCGH <- as.profileCGH(P9)
> profileCGH <- daglad(profileCGH, mediancenter=FALSE, normalrefcenter=FALSE, genomestep=FALSE,
+                       smoothfunc="lawsglad", lkern="Exponential", model="Gaussian",
+                       qlambda=0.999, bandwidth=10, base=FALSE, round=1.5,
+                       lambdabreak=8, lambdaclusterGen=40, param=c(d=6), alpha=0.001, msize=2,
+                       method="centroid", nmin=1, nmax=8,
+                       amplicon=1, deletion=-5, deltaN=0.2, forceGL=c(-0.3,0.3), nbsigma=3,
+                       MinBkpWeight=0.35, CheckBkpPos=TRUE)

[1] "Smoothing for each Chromosome"
[1] "Optimization of the Breakpoints and DNA copy number calling"
[1] "Check Breakpoints Position"
[1] "Results Preparation"

>
>
```

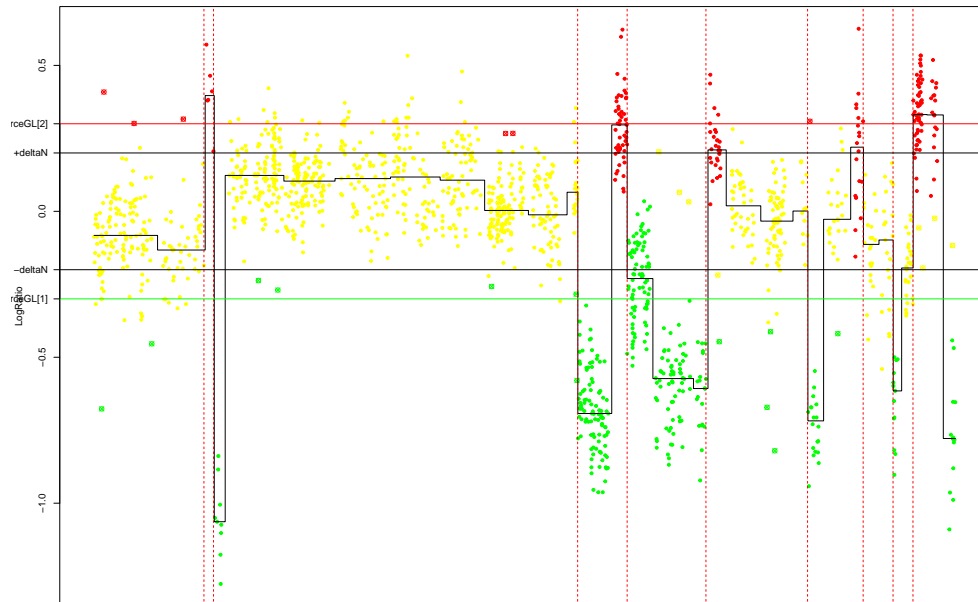


Figure 2: Results of daglad on the patient P9 (Veltman data).

The *daglad* function allows to choose some threshold to help the algorithm to identify the status of the genomic regions. The thresholds are given in the following parameters:

- deltaN
- forceGL

- deletion
- amplicon

Comparing **Figure 2** and **Figure 3** shows the influence of two different sets of parameters.

```
> data(veltman)
> profileCGH <- as.profileCGH(P9)
> profileCGH <- daglad(profileCGH, mediancenter=FALSE, normalrefcenter=FALSE, genomestep=FALSE,
+                       smoothfunc="lawsglad", lkern="Exponential", model="Gaussian",
+                       qlambda=0.999, bandwidth=10, base=FALSE, round=1.5,
+                       lambdabreak=8, lambdaclusterGen=40, param=c(d=6), alpha=0.001, msize=2,
+                       method="centroid", nmin=1, nmax=8,
+                       amplicon=1, deletion=-5, deltaN=0.10, forceGL=c(-0.15,0.15), nbsigma=3,
+                       MinBkpWeight=0.35, CheckBkpPos=TRUE)

[1] "Smoothing for each Chromosome"
[1] "Optimization of the Breakpoints and DNA copy number calling"
[1] "Check Breakpoints Position"
[1] "Results Preparation"

>
>
```

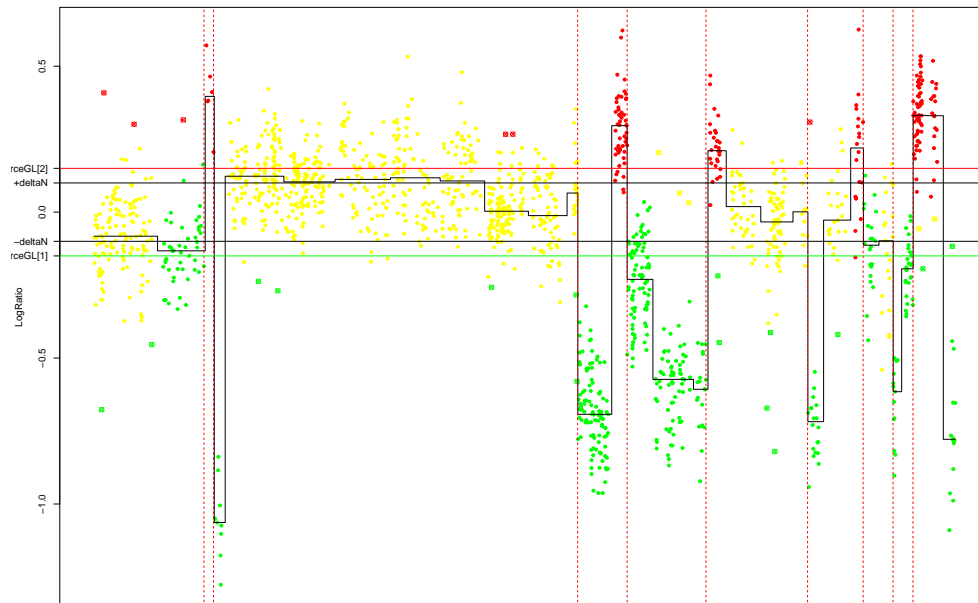


Figure 3: Results of daglad on the patient P9 (Veltman data) - Influence of the thresholds.

The *daglad* function allows a smoothing step over the whole genome (if *genomestep=TRUE*) where all the chromosomes are concatenated together. During this step, the cluster which corresponds to the Normal DNA level is identified: the thresholds used in the function (*deltaN*, *forceGL*, *amplicon*, *deletion*) are then compared to the median of this cluster.

## 4.4 Tuning parameters

The most important parameters are:

- *lambdabreak*
- *lambdacluster*
- *lambdaclusterGen*
- *param*  $c(d = 6)$

Decreasing those parameters will lead to a higher number of breakpoints identified. For arrays experiments with very small Signal to Noise ratio it is recommended to use a small value of *param* like  $d = 3$  or less.

## 5 Graphical functions

### 5.1 Plot of raw array data

```
> data(arrayCGH)
> # object of class arrayCGH
>
> array <- list(arrayValues=array2, arrayDesign=c(4,4,21,22))
> class(array) <- "arrayCGH"
```

```
> arrayPlot(array, "Log2Rat", bar="none")
```

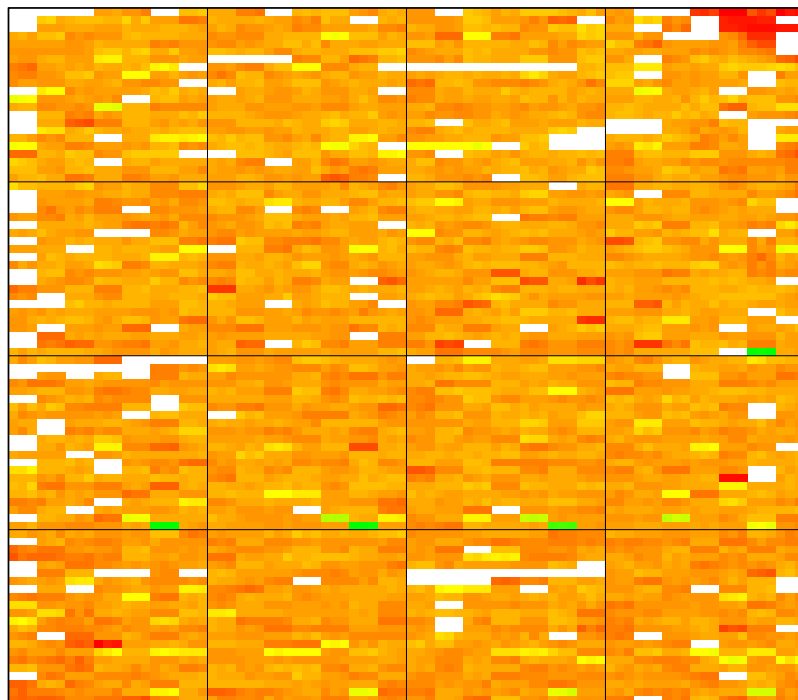


Figure 4: Spatial image of array CGH



```
> arrayPersp(array,"Log2Rat", box=FALSE, theta=110, phi=40, bar=FALSE)
```



Figure 5: Perspective image of array CGH

## 5.2 Plot of genomic profile

```
[1] "Smoothing for each Chromosome"  
[1] "Optimization of the Breakpoints"  
[1] "Results Preparation"
```

```
> plotProfile(res, unit=3, Bkp=TRUE, labels=FALSE, Smoothing="Smoothing", plotband=FALSE, cyto
```

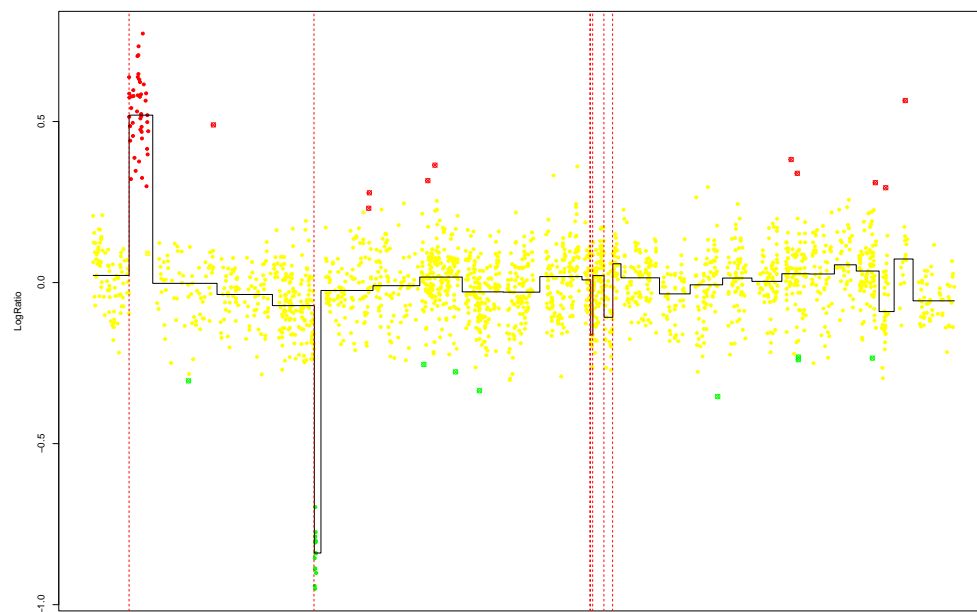


Figure 6: Genomic profile on the whole genome

```
> plotProfile(res, unit=3, Bkp=TRUE, labels=FALSE, Smoothing="Smoothing", cytoband = cytoband)
```

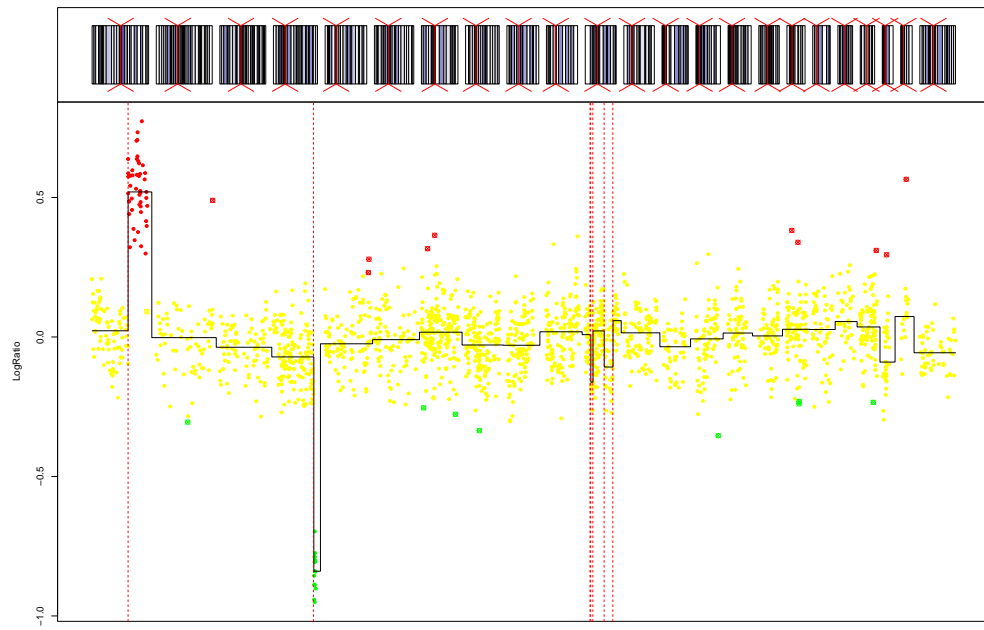


Figure 7: Genomic profile on the whole genome and cytogenetic banding

```

> text <- list(x=c(90000,200000),y=c(0.15,0.3),labels=c("NORMAL","GAIN"), cex=2)
> plotProfile(res, unit=3, Bkp=TRUE, labels=TRUE, Chromosome=1,
+ Smoothing="Smoothing", plotband=FALSE, text=text, cytoband = cytoband)

```



Figure 8: Genomic profile for chromosome 1

```

> text <- list(x=c(90000,200000),y=c(0.15,0.3),labels=c("NORMAL","GAIN"), cex=2)
> plotProfile(res, unit=3, Bkp=TRUE, labels=TRUE, Chromosome=1,
+ Smoothing="Smoothing", text=text, main="Chromosome 1", cytoband = cytoband)

```

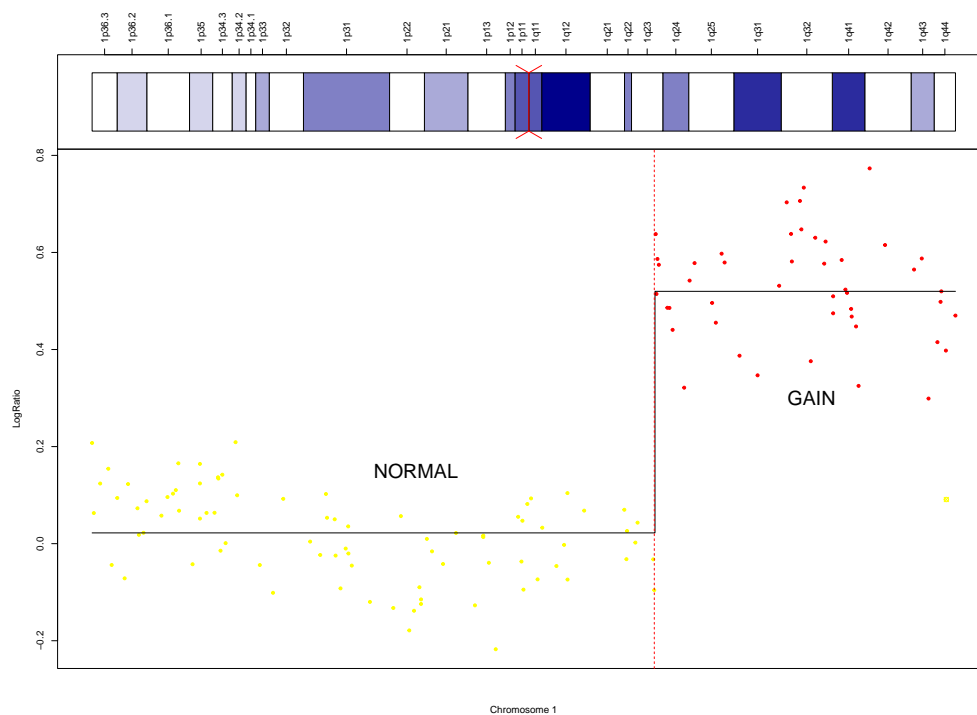


Figure 9: Genomic profile for chromosome 1 and cytogenetic banding with labels

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