

# CGHnormaliter

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CGHnormaliter-package

*This package implements the CGHnormaliter algorithm which is a strategy for improved normalization of array Comparative Genomic Hybridization (aCGH) data.*

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## Description

CGHnormaliter is an iterative algorithm for normalization of aCGH data displaying imbalanced aberrations. First, provisory balanced copy numbers are identified and subsequently used for normalization based on LOWESS. These two steps are then iterated to refine the normalization. The assumption here is that the temporary exclusion of aberrations allows for a more appropriate calculation of the LOWESS regression curve. As a result, after normalization, the log<sub>2</sub> intensity ratios of the normals will generally be closer to zero and better reflect the biological reality.

## Details

Package: CGHnormaliter  
Type: Package  
Version: 1.1.0  
Date: 2009-06-25  
License: GPLv3 (<http://www.gnu.org/copyleft/gpl.html>)

The package contains two public functions. The function `CGHnormaliter` performs the iterative normalization of aCGH data, while the function `CGHnormaliter.write.table` prints normalized aCGH data to a file. See function documentation for details.

## Author(s)

Thomas W. Binsl, Bart P.P. van Houte, Hannes Hettling

## References

Bart P.P. van Houte, Thomas W. Binsl, Hannes Hettling, Walter Pirovano and Jaap Heringa. CGH-normaliter: an iterative strategy to enhance normalization of array CGH data with imbalanced aberrations. *BMC Genomics*, 10:401, 2009.

**See Also**

CGHcall, DNACopy

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CGHnormaliter      *Iterative normalization of aCGH data*

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**Description**

Implementation of an iterative algorithm for normalization of aCGH data displaying imbalanced aberrations.

**Usage**

```
CGHnormaliter(data, nchrom = 24, stop_threshold = 0.01, max_iterations = 5)
```

**Arguments**

<code>data</code>	Either a dataframe or character string containing a filename. See section Details for the format.
<code>nchrom</code>	Number of chromosomes.
<code>stop_threshold</code>	Threshold value for the mean difference between the LOWESS regression curves from two consecutive iterations. The iteration is terminated if this difference is below the <code>stop_threshold</code> for all samples.
<code>max_iterations</code>	Maximum number of iterations.

**Details**

The input should be either a `data.frame` or the file name of a tabseparated text file (text files must contain a header). The first four columns should contain the name, chromosome and the start and end position in bp for each array target respectively. The position columns must contain numbers only. Following these are two columns with the raw test and reference intensities for each of your samples. These intensities must be numeric as well. If the input type is a text file, missing values should be represented as 'NA' or an empty field. There is a `CGHnormaliter.write.table` method that prints the results in a tabular format.

**Value**

This function returns a matrix of objects of class `cghCall` with dimension (number of clones) \* (number of samples). Each object contains the following components (See section Examples on how to access them):

<code>normalized data</code>	A matrix with the normalized log2 intensity ratios for each profile.
<code>segments</code>	A matrix with the segments for each profile.
<code>calls</code>	A <code>data.frame</code> with the calls for each profile. Values are -1 (loss), 0 (normal) or 1 (gain).
<code>probabilities</code>	A <code>data.frame</code> with 3 columns of probe information (name, chromosome and position), followed by 3 columns with aberration probabilities for each sample.

**Author(s)**

Thomas W. Binsl, Bart P.P. van Houte, Hannes Hettling

**References**

Bart P.P. van Houte, Thomas W. Binsl, Hannes Hettling, Walter Pirovano and Jaap Heringa. CGH-normaliter: an iterative strategy to enhance normalization of array CGH data with imbalanced aberrations. BMC Genomics, 10:401, 2009.

**Examples**

```
data(Leukemia)
## Normalize the raw intensity values of the first 3 chromosomes.
result <- CGHnormaliter(Leukemia, nchrom=3)
## Get the normalized log2 intensity ratios, segments and calls
normalized.data <- copynumber(result)
segmented.data <- segmented(result)
called.data <- calls(result)
## Plot the normalization result of sample 2
plot(result[,2])
## Write the normalized log2 intensity ratios to file
CGHnormaliter.write.table(result)
```

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CGHnormaliter.write.table

*Print normalized data to a file*

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**Description**

This function stores the results of a CGHnormaliter normalization into a plain text file.

**Usage**

```
CGHnormaliter.write.table(result, file="normalized.txt")
```

**Arguments**

result	Result object of a CGHnormaliter normalization.
file	Filename to store the data in.

**Details**

This function prints the normalized log2 intensity ratios to a tabseparated file with the specified file name.

**Author(s)**

Thomas W. Binsl, Bart P.P. van Houte, Hannes Hettling

## References

Bart P.P. van Houte, Thomas W. Binsl, Hannes Hettling, Walter Pirovano and Jaap Heringa. CGH-normaliter: an iterative strategy to enhance normalization of array CGH data with imbalanced aberrations. *BMC Genomics*, 10:401, 2009.

## See Also

[CGHnormaliter](#)

## Examples

```
data(Leukemia)
## Normalize the intensity ratios
## Not run: result <- CGHnormaliter(Leukemia)
## Write the result to a file
## Not run: CGHnormaliter.write.table(result, "normalization_results.txt")
```

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Leukemia

*Array CGH experiment data on childhood acute lymphoblastic leukemia (ALL) in humans.*

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## Description

A dataframe containing 30180 rows and 10 columns, representing the array CGH data of 3 ALL samples.

## Usage

Leukemia

## Format

A dataframe containing the following 10 columns:

**CloneID** The unique identifiers of array elements.

**Chromosome** Chromosome number of each array element.

**Start** Chromosomal start position in bp of each array element.

**End** Chromosomal end position in bp of each array element.

**Case1.test** Background corrected test intensity values for sample 1.

**Case1.ref** Background corrected reference intensity values for sample 1.

**Case2.test** Background corrected test intensity values for sample 2.

**Case2.ref** Background corrected reference intensity values for sample 2.

**Case3.test** Background corrected test intensity values for sample 3.

**Case3.ref** Background corrected reference intensity values for sample 3.

## Source

Provided by the authors (see references).

**References**

Paulsson K, Heidenblad M, Morse H, Borg A, Fioretos T, Johansson B: Identification of cryptic aberrations and characterization of translocation breakpoints using array CGH in high hyperdiploid childhood acute lymphoblastic leukemia. *Leukemia* 2006, 20:2002-2007.

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