

# Package ‘Vega’

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**Type** Package

**Title** An R package for copy number data segmentation

**Version** 1.4.0

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**Description** Vega (Variational Estimator for Genomic Aberrations) is an algorithm that adapts a very popular variational model (Mumford and Shah) used in image segmentation so that chromosomal aberrant regions can be efficiently detected.

**Depends** R (>= 2.10)

**License** GPL-2

**LazyLoad** yes

**biocViews** aCGH, DNACopyNumber

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Vega-package	<i>An R package for copy number data segmentation</i>
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## Description

Vega (Variational Estimator for Genomic Aberrations) is an algorithm that adapts a very popular variational model (Mumford and Shah) used in image segmentation so that chromosomal aberrant regions can be efficiently detected.

## Details

Package: Vega  
Type: Package  
Version: 1.0  
License: GPL-2  
LazyLoad: yes  
biocViews: aCGH, DNACopyNumber

### Author(s)

Sandro Morganella, Luigi Cerulo, Giuseppe Viglietto, Michele Ceccarelli Maintainer: Sandro Morganella <morganellaalx@gmail.com>

### References

Morganella S. et al. (2010). VEGA: Variational segmentation for copy number detection, Bioinformatics.

### Examples

```
# Load the data for Granta-519 Cell Line
data(G519);

# Start Vega segmentation on all chromosomes of G519 data and save the results in G519_segmentation.txt tab
seg <- vega(CNVdata=G519, chromosomes=c(1:22, "X", "Y"), out_file_name="G519_segmentation.txt", beta=0.5, r
```

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G519

*Granta-519 Data*

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### Description

LRR for Granta-519 Cell Line data (published in DeLeeuw et al. (2004). Comprehensive whole genome array CGH profiling of mantle cell lymphoma model genomes, Human Molecular Genetics, 13(17):1827-1837).

### Usage

```
data(G519)
```

### Format

A matrix containing four columns: chromosome, start and end probe positions, observed Log R Ratio.

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plotSegmentation	<i>Plot observations and the respective segmentation.</i>
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### Description

This function allows to plot the observed data superimposing the respective segmentation. By the parameter 'opt' the user can plot the LRR mean values of each segment or the computed aberration kind. In plot window the gain and the loss are identified by a line having value of 1 and -1 respectively.

### Usage

```
plotSegmentation(CNVdata, segmentation, chromosomes, opt = 0)
```

### Arguments

CNVdata	The data matrix.
segmentation	The computed segmentation.
chromosomes	The chromosomes that have to be plotted.
opt	If opt=0 (default) then the LRR mean values are plotted, if opt=1 the computed labels are plotted.

### Note

If the argument opt=1 then gains and losses are identified by 1 and -1 respectively.

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### References

Morganella S. et al. (2010). VEGA: Variational segmentation for copy number detection, Bioinformatics.

### Examples

```
# Import the data
data(G519)

# Compute the segmentation for all chromosomes
seg <- vega(G519, c(1:22, "X", "Y"))

# Plot the results for all chromosomes in terms of mean of LRRs
plotSegmentation(G519, seg, c(1:22, "X", "Y"), opt=0)

# Plot the results for all chromosomes in terms of aberration kinds
plotSegmentation(G519, seg, c(1:22, "X", "Y"), opt=1)
```

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vega

*This function computes, saves and returns the copy number segmentation on the aCGH data passed as argument.*

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### Description

This function computes the segmentation of the copy number data passed as argument. 'vega' function returns the computed segmentation and save it as a tab delimited file. Users need just to use this function.

### Usage

```
vega(CNVdata, chromosomes, out_file_name = "", beta = 0.5, min_region_size = 2)
```

### Arguments

CNVdata	This argument is matrix containing the data that have to be analyzed. This matrix must have 4 columns: <ul style="list-style-type: none"><li>- the first row indicates the chromosome;</li><li>- the second row indicates the start bp of the probe;</li><li>- the third row indicates the end bp of the probe;</li><li>- the fourth row reports the measured Log R Ratio;</li></ul>
chromosomes	This is a vector containing the chromosome sthathave to be analyzed. By using <code>c(1:22, "X", "Y")</code> the whole genome will be segmented.
out_file_name	This is the file name used to save the computed segmentation.
beta	This argument is used for the stop condition definition.
min_region_size	This argument specifies the minimum size for the segmented regions.

### Value

segmentation This is a data frame containing the computed segmentation.

### Author(s)

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### References

Morganella S. et al. (2010). VEGA: Variational segmentation for copy number detection, Bioinformatics.

### Examples

```
# Load the data for Granta-519 Cell Line
data(G519);

# Start Vega segmentation on all chromosomes of G519 data
```

```
v <- vega(CNVdata=G519, chromosomes=c(1:22, "X", "Y"), beta=0.5, min_region_size=2);
```

```
# Start Vega segmentation on chromosomes 8 of G519 data and save the results in G519_segmentation_chr8.txt  
v <- vega(CNVdata=G519, chromosomes=c(8), out_file_name="G519_segmentation_chr8.txt", beta=0.5, min_region.
```

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