Package 'RobustCNV'

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Type Package

Title A Package for Copy Number Variant Analysis of Targeted Capture Sequencing Data

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Description A copy number variant tool using robust regression for normalization and DNA-copy for segmentation.

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LazyData TRUE

Imports DNAcopy,
MASS,
IRanges,

Suggests WGCNA,
knitr

VignetteBuilder knitr

R topics documented:

`callSegments` *Make calls on segments based on a cutoff calculated from segment SD and a tuning factor.*

Description

Make calls on segments based on a cutoff calculated from segment SD and a tuning factor.

Usage

```
callSegments(gsegments, normCoverage, tuning = 0.8)
```

Arguments

`gsegments`	a dataframe with columns: Sample,Chromosome,Start,End,NumProbes,Segment,SegmentMean
`normCoverage`	a vector or dataframe containing normalized coverage
`tuning`	a parameter for adjusting sensitivity, higher values are less sensitive, more specific.

Value

A new dataframe with a "SegmentCall" column consisting of (-, 0, +).

Examples

```
## Not run:
callSegments(gsegments, normCoverage)
callSegments(gsegments, normCoverage, tuning=.2)

## End(Not run)
```

`formatForNexus` *Create an output formatted for Nexus compatibility.*

Description

Create an output formatted for Nexus compatibility.

Usage

```
formatForNexus(perIntervalCalls)
```

Arguments

`perIntervalCalls`	a data.frame containing per-interval calls

Value

A data.frame formatted for Nexus compatibility

Examples

```
## Not run:
formatForNexus(perIntervalCalls)

## End(Not run)
```

`plotGCBias` *Plot GC bias plot*

Description

Plot GC bias plot

Usage

```
plotGCBias(sampleName, pGC, coverage)
```

Arguments

`sampleName`	sample name
`pGC`	vector of percent GC for each interval
`coverage`	vector of per-interval coverage

Value

A gc-score value which is the sum of abs(predicted values).

Examples

```
## Not run:
plotGCBias(sampleName, pGC, coverage)

## End(Not run)
```

plotGenomeIntervalCalls *Make genome plots.*

Description

Make genome plots.

Usage

```
plotGenomeIntervalCalls(perIntervalCalls, main = "")
```

Arguments

perIntervalCalls	data.frame containing per-Interval calls and other data.
main	title of plot.

Value

nothing.

Examples

```
## Not run:
plotGenomeIntervalCalls(perIntervalCalls)

## End(Not run)
```

plotSampleClusters *Make sample-cluster plots.*

Description

Make sample-cluster plots.

Usage

```
plotSampleClusters(rawNormalCoverage, rawTumorCoverage)
```

Arguments

rawNormalCoverage	Data.frame containing raw coverage for normal samples
rawTumorCoverage	Data.frame containing raw coverage for tumor samples

Value

nothing.

Examples

```
## Not run:
plotSampleClusters(rawNormalCoverage, rawTumorCoverage)

## End(Not run)
```

`robustNorm` *Normalize coverage data.*

Description

Do a normalization with interval length, gcContent and panel of normals using a robust regression strategy followed by a GC correction using loess.

Usage

```
robustNorm(y, x, ilengths, pGC, idx = NA)
```

Arguments

`y`	a vector of coverage values for the sample of interest.
`x`	a dataframe or matrix with coverage values for normal samples (columns are samples).
`ilengths`	a vector of interval lengths.
`pGC,`	the percent GC content for each interval
`idx`	a vector used to subset the input during model generation only (all intervals are reported)

Value

A new vector normalized against the panel of normals, interval lengths, and for GC content

Examples

```
## Not run:
robustNorm(y, x, ilengths, pGC)

## End(Not run)
```

segment *Segment normalized log2 coverage values for one or more samples.*

Description

Segment normalized log2 coverage values for one or more samples.

Usage

```
segment(normCoverage, orderedChrom, maploc, idx = NA)
```

Arguments

normCoverage	a data.frame or matrix with normalized coverage. Columns should be samples.
orderedChrom	a vector of ordered factors indicating the chromosome, must be nrow(norm.coverage) long.
maploc	a vector containing chromosome locus for intervals (end of each interval)
idx	segments can be called using a subset of targeted intervals, idx provides the subset.

Value

A new dataframe with columns: Sample, Chromosome, Start, End, NumProbes, SegmentMean, SegmentCall

Examples

```
## Not run:
segment(normalizedTumorCoverage, orderedChrom, maploc)

## End(Not run)
```

summarizeIntervalCalls *Summarize interval level calls to gene level call. This is an interval function that is used by summarizeToGeneCalls.*

Description

Summarize interval level calls to gene level call. This is an interval function that is used by summarizeToGeneCalls.

Usage

```
summarizeIntervalCalls(x)
```

Arguments

x	a vector of calls for a single gene

Value

A data.frame containing QC metrics

Examples

```
## Not run:
CNVqc(data)

## End(Not run)
```

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summarizeToGeneCalls *Summarize per-IntervalCalls to gene level calls.*

Description

Summarize per-IntervalCalls to gene level calls.

Usage

```
summarizeToGeneCalls(perIntervalCalls)
```

Arguments

perIntervalCalls	a vector of calls for a single gene

Value

A data.frame containing calls summarized to gene level

Examples

```
## Not run:
CNVqc(data)

## End(Not run)
```

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