Package ‘MADSEQ’

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Type Package

Title Mosaic Aneuploidy Detection and Quantification using Massive Parallel Sequencing Data

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Author Yu Kong, Adam Auton, John Murray Greally

Maintainer Yu Kong <yu.kong@phd.einstein.yu.edu>

Description The MADSEQ package provides a group of hierarchical Bayesisan models for the detection of mosaic aneuploidy, the inference of the type of aneuploidy and also for the quantification of the fraction of aneuploid cells in the sample.

License GPL(>=2)

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MADSEQ-package

Mosaic Aneuploidy Detection using Massive Parallel Sequencing Data (MADSEQ)

Description

The MADSEQ package provides a group of hierarchical Bayesian models for the detection and quantification of mosaic aneuploidy using massive parallel sequencing data.

Details

MADSEQ is a group of hierarchical Bayesian models used for the detection and quantification of mosaic aneuploidy. The package takes bam file and vcf file as input. There are functions for the calculation of the coverage for the sequencing data; the normalization of the coverage to correct GC bias; the detection and quantification of mosaic aneuploidy and the inference of the type of aneuploidy (monosomy, mitotic trisomy, meiotic trisomy, loss of heterozygosity). The package also includes function to visualize the estimated distribution for detected mosaic aneuploidy. To fully understand how to use the MADSEQ package, please check the documentation. The manual explains what data do you need, and how to process the data to be ready for the model, what steps to follow and how to interpret the output from our model.

Author(s)

Yu Kong

References

Description
An S4 class MadSeq object

Usage
aneuploidy_chr18

Format
An MadSeq object

Value
MadSeq object returned from runMadSeq function, mitotic trisomy has been detected for the chromosome 18

Examples
## to load the data
data(aneuploidy_chr18)
## check statistics of the data
summary(aneuploidy_chr18)

Description
Accessing delta BIC of MadSeq object

Usage
deltaBIC(object)

## S4 method for signature 'MadSeq'
deltaBIC(object)

Arguments
object A MadSeq object returned by runMadSeq function

Value
A numeric vector containing deltaBIC values between selected model and other models
MadSeq-class

Author(s)
Yu Kong

See Also
MadSeq, runMadSeq

Examples

## load the example MadSeq object come with the package
data("aneuploidy_chr18")

## access deltaBIC
deltaBIC(aneuploidy_chr18)

## load the example MadSeq object come with the package
data("aneuploidy_chr18")

## access deltaBIC
deltaBIC(aneuploidy_chr18)

---

MadSeq-class  The MadSeq class

Description
An S4 class contains estimated result returned from runMadSeq function

Slots

- posterior: A matrix contains the posterior distribution from the selected model
- deltaBIC: A numeric vector contains the deltaBIC value between selected model and other models. The deltaBIC between models indicate the confidence level that selected model against other models: deltaBIC ~ [0,2]: Not worth more than a bare mention deltaBIC ~ [2,6]: Positive deltaBIC ~ [6,10]: Strong deltaBIC >10: Very Strong

Accessors

In the code below, x is a MadSeq object.

- posterior(x): Get the matrix containing posterior distribution of selected model.
- deltaBIC(x): Get the deltaBIC between selected model and other models

Summary

In the code below, x is a MadSeq object.

- summary(x): summarize the posterior distribution

MadSeq Methods

In the code below, x is a MadSeq object.

- plotMadSeq(x): Plot the posterior distribution of all parameters in selected model.
- plotFraction(x): Plot the estimated distribution of the fraction of aneuploid sample.
- plotMixture(x): Plot the distribution of AAF estimated from the selected model.
**normalizeCoverage**

Author(s)
Yu Kong

See Also
`runMadSeq`, `plotMadSeq`

---

**normalizeCoverage**  
**correct coverage bias due to GC content**

---

**Description**
function to normalize coverage by GC content and quantile normalization

**Usage**

```r
normalizeCoverage(object, ..., control = NULL, writeToFile = TRUE, destination = NULL, plot = TRUE)
```

**Arguments**

- **object**: A GRanges object returned from `prepareCoverageGC` function.
- **...**: additional GRanges object to pass. **Note1**: If there is only one Granges object given, then coverage will be corrected by GC content. If there are more than one GRanges object from multiple samples are given, the function will first quantile normalize coverage across samples, then correct coverage by GC content in each sample. **Note2**: If more than one GRanges object provided, make sure they are different samples sequenced by the same protocol, which means the targeted region is the same **Note3**: If your input samples contain female and male, we suggest you separate them to get a more accurate normalization.
- **control**: A GRanges object returned from `prepareCoverageGC` function. **Default value**: NULL. If you have a control normal sample, then put it here
- **writeToFile**: Boolean Default: TRUE. If TRUE, normalized coverage table for each sample provided will be written to destination specified, the file will be named as "sample_normed_depth.txt". If set to FALSE, a GRangesList object will be returned
- **destination**: A character, specify the path to the location where the normalized coverage table will be written. Default: NULL, the file will be written to current working directory
- **plot**: Boolean Default: TRUE. If TRUE, the coverage vs. GC content plot before and after normalization will be plotted And the average coverage for each chromosome before and after normalization will be plotted

**Value**
If `writeToFile` is set to TRUE, normalized coverage will be written to the destination. Otherwise, a GRangesList object containing each of input sample will be returned.
normalizeCoverage

Note

The normalize function works better when you have multiple samples sequenced using the same protocol, namely have the same targeted regions. And if you have female sample and male sample, the best way is to normalize them separately.

Author(s)

Yu Kong

References


See Also

prepareCoverageGC

Examples

```#
#------- if you deal with single sample
#-------
## 1. prepare coverage and gc
## specify the path to the location of bed file
target = system.file("extdata","target.bed",package="MADSEQ")

## specify the path to the bam file
aneuploidy_bam = system.file("extdata","aneuploidy.bam",package="MADSEQ")

## prepare coverage data for the aneuploidy sample
aneuploidy_cov_gc = prepareCoverageGC(target,aneuploidy_bam,"hg19")

## normalize the coverage
##---- if not write to file ----
aneuploidy_norm = normalizeCoverage(aneuploidy_cov_gc,writeToFile=FALSE)

## check the GRangesList and subset your sample
aneuploidy_norm
names(aneuploidy_norm)
aneuploidy_norm["aneuploidy_cov_gc"]

##---- if write to file ----
normalizeCoverage(aneuploidy_cov_gc,writeToFile=TRUE,destination=".")
```
normal_cov gc = prepareCoverageGC(target,normal_bam,"hg19")

## normalize the coverage
normed=normalizeCoverage(aneuploidy_cov gc,normal_cov gc,writeToFile=FALSE)
names(normed)
normed["aneuploidy_cov gc"]
normed["normal_cov gc"]
## or
normalizeCoverage(aneuploidy_cov gc,normal_cov gc,
            writeToFile=TRUE,destination=".")

## if you deal with multiple samples with a normal control
## specify the path to the location of bed file
target = system.file("extdata","target.bed",package="MADSEQ")

## specify the path to the bam file
aneuploidy_bam = system.file("extdata","aneuploidy.bam",package="MADSEQ")
normal_bam = system.file("extdata","normal.bam",package="MADSEQ")

## prepare coverage data for the samples
aneuploidy_cov gc = prepareCoverageGC(target,aneuploidy_bam,"hg19")
normal_cov gc = prepareCoverageGC(target,normal_bam,"hg19")

## normalize the coverage
normed = normalizeCoverage(aneuploidy_cov gc,
            control=normal_cov gc,writeToFile=FALSE)
## or
normalizeCoverage(aneuploidy_cov gc,control=normal_cov gc,
            writeToFile=TRUE,destination=".")

plotFraction

histogram for the fraction of aneuploid cells estimated by MadSeq model

Description
histogram of the posterior distribution of the fraction of aneuploid cells estimated by the selected model.

Usage
plotFraction(object, prob = 0.95)

## S4 method for signature 'MadSeq'
plotFraction(object, prob = 0.95)

Arguments

object A MadSeq object returned by runMadSeq function.
prob A numeric value between 0~1 specify the highest posterior interval (similar to credible interval) for the distribution. Default: 0.95.
Value

the histogram of posterior distribution of the fraction

Note

If normal model has been selected by runMadSeq function, no fraction plot will be produced by this function.

Author(s)

Yu Kong

See Also

runMadSeq, plotMadSeq, plotMixture

Examples

## load the example MadSeq object come with the package
data("aneuploidy_chr18")

## plot estimated fraction of aneuploid cells
plotFraction(aneuploidy_chr18)

plotMadSeq

density plot for posterior distribution of selected model

Description

plot the density plot for each of the parameters in the posterior distribution from selected model

Usage

plotMadSeq(object)

## S4 method for signature 'MadSeq'
plotMadSeq(object)

Arguments

object

A MadSeq object returned by runMadSeq function.

Value

the density plot for parameters in the posterior distribution of selected model.

Author(s)

Yu Kong

Yu Kong
plotMixture

See Also

runMadSeq, plotFraction, plotMixture

Examples

## load the example MadSeq object come with the package
data("aneuploidy_chr18")

## plot the posterior distribution
plotMadSeq(aneuploidy_chr18)

---

plotMixture  
density plot for the posterior distribution of alternative allele frequency estimated from the selected model

Description

density plot presents the posterior distribution of alternative allele frequency (AAF) estimated from selected model

Usage

plotMixture(object)

## S4 method for signature 'MadSeq'
plotMixture(object)

Arguments

object  A MadSeq object returned by runMadSeq function.

Value

density plot for the posterior distribution of AAF

Author(s)

Yu Kong
Yu Kong

See Also

runMadSeq, plotMadSeq, plotFraction

Examples

## load the example MadSeq object come with the package
data("aneuploidy_chr18")

## plot the distribution of estimated AAF
plotMixture(aneuploidy_chr18)
**posterior**  
*Accessing posterior distribution of MadSeq object*

**Description**  
An S4 method to access the posterior distribution of MadSeq object

**Usage**  
```r
posterior(object)
```

## S4 method for signature 'MadSeq'
```r
posterior(object)
```

**Arguments**

- **object**: A MadSeq object returned by `runMadSeq` function

**Value**

A matrix containing posterior distribution of selected model

**Author(s)**

Yu Kong

**See Also**

`MadSeq`, `runMadSeq`

**Examples**

```r
## load the example MadSeq object come with the package
data("aneuploidy_chr18")

## access posterior distribution
posterior(aneuploidy_chr18)
```

---

**prepareCoverageGC**  
*get sequencing coverage and GC content for targeted regions*

**Description**  
Given a bam file and a bed file containing targeted regions, return sequencing coverage and GC content for each targeted region

**Usage**

```r
prepareCoverageGC(target_bed, bam, genome_assembly = "hg19")
```
prepareHetero

Arguments

target_bed  A character, specify the path to the location of bed file containing targeted regions.
bam  character, path to the bam file. Please make sure that bam file is sorted, and the index bam is present
genome_assembly  A character, indicating the assembly number of your genome. Default:"hg19". To see available genome_assembly, use available.genomes from BSgenome package

Value

a GRanges object with at least two mcols: depth and GC, each range indicating a targeted region

Note

The bam file should be sorted and indexed.

Author(s)

Yu Kong

See Also

normalizeCoverage

Examples

## specify the path to the location of bed file
target = system.file("extdata","target.bed",package="MADSEQ")

## specify the path to the bam file
aneuploidy_bam = system.file("extdata","aneuploidy.bam",package="MADSEQ")
normal_bam = system.file("extdata","normal.bam",package="MADSEQ")

## prepare coverage data for the samples
aneuploidy_cov_gc = prepareCoverageGC(target,aneuploidy_bam,"hg19")
normal_cov_gc = prepareCoverageGC(target,normal_bam,"hg19")

prepareHetero  prepare heterozygous sites for aneuploidy detection

Description

given the vcf file and bed file containing targeted region, generate processed heterozygous sites for furthur analysis

Usage

prepareHetero(vcffile, target_bed, genome = "hg19", writeToFile = TRUE, destination = NULL)
prepareHetero

Arguments

vcffile A character, specify the path to the location of the vcf.gz file of your sample. 

Note: the vcf file need to be compressed by bgzip. The tool is part of tabix package, can be download from [http://www.htslib.org/](http://www.htslib.org/)

target_bed A character, specify the path to the location of bed file containing targeted regions.

genome A character, specify the assembly of your genome. Default: hg19. To see available genome assembly, use available.genomes from BSgenome package

writeToFile Boolean Default: TRUE. If TRUE, processed table containing heterozygous sites will be written to destination specified, the file will be named as 'sample_filtered_heterozygous.txt'. If set to FALSE, a GRanges object containing processed heterozygous sites will be returned

destination A character, specify the path to the location where the processed heterozygous sites table will be written. Default: NULL, the file will be written to current working directory

Value

If writeToFile is set to TRUE, processed table will be written to the destination. Otherwise, a GRanges object containing each of input sample will be returned.

Note

1. The vcf file you provided need to be compressed by bgzip
2. The vcf file should contain depth and allelic depth for variants in the FORMAT field

Author(s)

Yu Kong

See Also

runMadSeq

Examples

```r
## specify the path to the vcf.gz file for the aneuploidy sample
aneuploidy_vcf = system.file("extdata","aneuploidy.vcf.gz", package="MADSEQ")
target = system.file("extdata","target.bed", package="MADSEQ")

##------ if not write to file ------
aneuploidy_hetero=prepareHetero(aneuploidy_vcf, target, writeToFile=FALSE)

##------ if write to file ------
prepareHetero(aneuploidy_vcf, target, writeToFile=TRUE, destination=".")
```
runMadSeq  

Model to detect and quantify mosaic aneuploidy

Description

Take in the heterozygous sites and coverage information, use different models (normal, monosomy, mitotic trisomy, meiotic trisomy, loss of heterozygosity) to fit the data, and select the model fit the data best according to BIC value and return estimation of the fraction of aneuploid cells.

Usage

```r
runMadSeq(hetero, coverage, target_chr, adapt = 10000, burnin = 10000, 
nChain = 2, nStep = 10000, thinSteps = 2, checkConvergence = FALSE, 
plot = TRUE)
```

Arguments

- `hetero` A character specify the location of processed heterozygous table returned by `prepareHetero` function, or A GRanges object returned by `prepareHetero` function
- `coverage` A character specify the location of normalized coverage table returned by `normalizeCoverage` function, or A GRanges object from the GRangesList returned by `normalizeCoverage` function. Look up your sample by `names(GRangesList)`, and subset your the normalized coverage for your sample by `GRangesList['sample_name']`. For more details, please check the example.
- `target_chr` A character specify the chromosome number you want to detect. **Note:** Please check your assembly, use contig name "chr1" or "1" accordingly.
- `adapt` A integer indicate the adaption steps for the MCMC sampling. Default: 10000
- `burnin` A integer indicate burnin steps for the MCMC sampling. Default: 10000. If the posterior distribution is not converged, increasing burnin steps can be helpful.
- `nChain` A integer indicate the number of chains for the MCMC sampling. Default: 2. **Note:** More than 1 chain is required if checkConvergence is set to TRUE.
- `nStep` A integer indicate the number of steps to be recorded for the MCMC sampling. Default: 10000. Generally, the more steps you record, the more accurate the estimation is.
- `thinSteps` A integer indicate the number of steps to "thin" (thinSteps=1) means save every step. Default: 2.
- `checkConvergence` A Boolean indicate whether to check the convergence of independent MCMC chains. If your data is not converged, you may increase adaption step and burnin step. Default: FALSE
- `plot` A Boolean. If TRUE, the alternative allele frequency (AAF) for each heterozygous site along the target chromosome will be plotted.

Value

An S4 object of class `MadSeq` containing the posterior distribution for the selected model, and deltaBIC between five models.
Note

1. If you didn’t write normalized coverage into file, please subset the normalized coverage GRanges object from the GRangesList object returned from the normalizeCoverage function.
2. When specify target_chr, please make sure it consist with the contig names in your sequencing data, example: “chr1” and “1”.
3. If checkConvergence set to TRUE, the nChain has to be >2
4. If it shows that your chains are not converged, helpful options are increasing the adapt and burnin steps.
5. Because the model is an MCMC sampling process, it can take a very long time to finish. Running in the background or HPC is recommended.

Author(s)

Yu Kong

References


See Also

MadSeq, plotMadSeq, plotFraction, plotMixture

Examples

```r
## The following example is for the case that normalized coverage and
## processed heterozygous sites have not been written to files. For more
## examples, please check the documentation.

### Prepare Heterozygous Sites
aneuploidy_vcf = system.file("extdata","aneuploidy.vcf.gz",package="MADSEQ")
target = system.file("extdata","target.bed",package="MADSEQ")
aneuploidy_hetero = prepareHetero(aneuploidy_vcf,target, writeToFile=FALSE)

### Prepare Normalized Coverage
aneuploidy_bam = system.file("extdata","aneuploidy.bam",package="MADSEQ")
normal_bam = system.file("extdata","normal.bam",package="MADSEQ")
aneuploidy_cov_gc = prepareCoverageGC(target,aneuploidy_bam,"hg19")
normal_cov_gc = prepareCoverageGC(target,normal_bam,"hg19")
normed = normalizeCoverage(aneuploidy_cov_gc, control=normal_cov_gc,writeToFile=FALSE)
aneuploidy_normed_cov = normed[["aneuploidy_cov_gc"]]

### check chromosome18
```
```r
aneuploidy_chr18 = runMadSeq(aneuploidy_hetero, aneuploidy_normed_cov,
    target_chr="chr18", adapt=100, burnin=200,
    nChain =1, nStep = 1000, thinSteps=1)
```

## Summary

**Description**

An S4 method to summarize statistics for `MadSeq` object

**Usage**

```r
## S4 method for signature 'MadSeq'
summary(object)
```

**Arguments**

- **object**: A `MadSeq` object returned by `runMadSeq` function

**Value**

A table containing statistics for each parameters in the selected model

**Author(s)**

Yu Kong

**Examples**

```r
## load the example MadSeq object come with the package
data("aneuploidy_chr18")

## show statistics
summary(aneuploidy_chr18)
```
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