Package 'binmapr'

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Type Package

Title Call Marker from Snp Data using Binmap

Description The raw NGS (Next Generation Sequencing) variants called from GBS (Genotyping by Sequencing) / WES (Whole Exon Sequencing)/ WGS (Whole Genome Sequencing) may include many error sites. The 'binmapr' could fix the potential error sites and generate highly confident markers for downstream analysis, such as QTL (quantitative trait locus) mapping, genetic map construction.
Davey, J.W. (2011) <doi:10.1038/nrg3012>.

Version 0.1.3

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License Artistic-2.0

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

NeedsCompilation no

URL https://github.com/xuzhougeng/binmapr

BugReports https://github.com/xuzhougeng/binmapr/issues

Depends R (>= 3.5.0)

Imports vcfR

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Repository CRAN

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R topics documented:

`batchCallGeno` *Genotyping all sample by chromsome*

Description

The genotype of each sample will be called according to their allele depth, and then the potential error will be fixed.

Usage

```
batchCallGeno(x, CHROM, outdir = ".", window.size = 15,
  low.count = 6, high.count = 24, fix.size = 5, pos.start = 6,
  pdf.height = 4, pdf.width = 8)
```

Arguments

`x`	GT matrix
`CHROM`	chromosome vector
`outdir`	outdir
`window.size`	parameter of callWindowGeno
`low.count`	parameter of callWindowGeno
`high.count`	parameter of callWindowGeno
`fix.size`	parameter of fixGenoError
`pos.start`	position start index, for exmaple, the pos.start of chr1_1234 is 6, chr01_1234 is 7
`pdf.height`	pdf width
`pdf.width`	pdf width

Value

A list object including genotype of each chromosome. It will also create PDF and CSV of these genotype.

Author(s)

Zhougeng xu

Examples

```
data(geno)
GT <- as.matrix(geno[1:100,5:6])
row.names(GT) <- paste0(geno$CHR[1:100], "_", geno$POS[1:100])
temp_dir <- tempdir()
gt <- batchCallGeno(GT, "chr01",  outdir = temp_dir, pos.start = 7)
```

`calcFreqFromAd` *Calculate the frequcy of AD*

Description

Calculate the frequcy of AD

Usage

```
calcFreqFromAd(x, min.depth = 10, max.depth = 200)
```

Arguments

`x`	AD matrix
`min.depth`	minimum depth to infer the genotype, if depth lower than it, it will be conside as NA
`max.depth`	maximum depth to infer the genotype, if depth larger than it, it will be conside as NA

Value

matrix contains. The alt/(alt+ref) will be caculted from the allele depth

Author(s)

Zhou-geng Xu

Examples

```
AD <- matrix(data = c("30,1","1,30","0,0","15,15"), nrow = 2)
row.names(AD) <- c("chr1_1","chr1_100")
colnames(AD) <- c("A","B")
freq <- calcFreqFromAd(AD)
```

`callGtFromAd` *call genotype from AD*

Description

call genotype from AD

Usage

```
callGtFromAd(x, min.depth = 10, max.depth = 200, low = 0.2,
  high = 0.8)
```

Arguments

`x`	AD matrix
`min.depth`	minimum depth to infer the genotype, if depth lower than it, it will be conside as NA
`max.depth`	maximum depth to infer the genotype, if depth larger than it, it will be conside as NA
`low`	threshold to infer one parent, encoded as 0
`high`	threshold to infer another parent, encoded as 2

Value

matrix contains. The allele depth will convet to genotype

Author(s)

Zhougeng Xu

Examples

```
AD <- matrix(data = c("30,1","1,30","0,0","15,15"), nrow = 2)
row.names(AD) <- c("chr1_1","chr1_100")
colnames(AD) <- c("A","B")
geno <- callGtFromAd(AD)
```

callWindowGeno *Call genotype by fix-size window*

Description

Call genotype by fix-size window

Usage

```
callWindowGeno(x, window.size = 15, low = 6, high = 24)
```

Arguments

x	a vector object, storing genotype information
window.size	default is 15
low	default is 6
high	default is 24

Value

vector

Author(s)

Zhougeng Xu

Examples

```
data(geno)
GT <- geno[,5]
names(GT) <- paste0(geno$CHR, "_", geno$POS)
genos <- callWindowGeno(GT)
```

fixGenoError *Fix potential genotype error*

Description

Fix potential genotype error

Usage

```
fixGenoError(geno, fix.size = 10)
```

Arguments

geno	a vector object, storing genotyping information
fix.size	the size of short genotpe error

Value

vector contains error-fixed genotype

Author(s)

Zhougeng Xu, Guangwei Li

Examples

```
genos <- c(1,1,1,1,1,0,1,1,1,1,1,0)
fixGenoError(genos, fix.size = 2)
```

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geno *Rice QTL genotype data*

Description

Data from "Three representative inter and intra-subspecific crosses reveal the genetic architecture of reproductive isolation in rice."

Usage

```
data(geno)
```

Format

An object of class `"cross"`; see `read.cross`.

References

Li, G. et al. (2017) The Plant Journal 92, 349–362. (PubMed)

Examples

```
data(geno)
```

getAdFromVcf *get the AD from vcf*

Description

get the AD from vcf

Usage

```
getAdFromVcf(file, keep = NULL, chromosome = NULL)
```

Arguments

file	vcf file path
keep	a vector store high confidence site, format should be "chr_1"
chromosome	vector, which chromosome to use if it is NULL, all chromosome will be include in analysis

Value

a list with AD and CHROM

Author(s)

Zhougeng Xu

Examples

```
library(vcfR)
data(vcfR_test)
orig_dir <- getwd()
temp_dir <- tempdir()
setwd( temp_dir )
write.vcf( vcfR_test, file = "test.vcf.gz" )
ad <- getAdFromVcf("test.vcf.gz")
ad
# return is full of NA, because the origin vcf don't have INFO/AD
setwd( orig_dir )
```

pheno *Rice QTL phenotype data*

Description

Data from "Three representative inter and intra-subspecific crosses reveal the genetic architecture of reproductive isolation in rice."

Usage

```
data(pheno)
```

Format

An object of class `"cross"`; see `read.cross`.

References

Li, G. et al. (2017) The Plant Journal 92, 349–362. (PubMed)

Examples

```
data(pheno)
```

plotGeno *genotype plotting*

Description

genotype plotting

Usage

```
plotGeno(geno, pos.start = 6, xlab = "position", ylab = NULL,
  title = NULL)
```

Arguments

`geno`	genotype vector
`pos.start`	position start index, for exmaple, the pos.start of chr1_1234 is 6
`xlab`	x lab
`ylab`	y lab
`title`	title

Value

a genotype distribution by the chromsome

Author(s)

Zhougeng Xu

Examples

```
geno <- c(1,1,1,1,0,0,0,2,2,2)
names(geno) <- c("1_1","1_100","1_200","1_210","1_230","1_300","1_500","1_600","1_700","1_1000")
plotGeno(geno, pos.start = 3)
```

`plotQtl` *QTL mapping plot*

Description

QTL mapping plot

Usage

```
plotQtl(pos, pvalue, ylab = "LOD", chr.name = "", ymax = 10,
  threshold = 2, ...)
```

Arguments

`pos`	position of each p value
`pvalue`	p value
`ylab`	y lab
`chr.name`	chromosome name
`ymax`	y max
`threshold`	QTL threshold
`...`	other parameter pass to base::plot

Value

a LOD distribution by the chromsome

Author(s)

Zhougeng Xu

Examples

```
pos <- c(1,100,200,210,230,300,500,600,700,1000)
pvalue <- c(0.1,0.05,0.05,0.05,0.01,0.001,0.01,0.05,0.05,0.1)
plotQtl(pos, pvalue, ymax = 3)
```

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