Package 'DEploid.utils'

December 19, 2024

Title 'DEploid' Data Analysis and Results Interpretation

Version 0.0.1

Description 'DEploid' (Zhu et.al. 2018 <doi:10.1093/bioinformatics/btx530>)
is designed for deconvoluting mixed genomes with unknown
proportions. Traditional phasing programs are limited to diploid organisms.
Our method modifies Li and Stephen's algorithm with Markov chain Monte Carlo
(MCMC) approaches, and builds a generic framework that allows haloptype
searches in a multiple infection setting. This package provides R functions
to support data analysis and results interpretation.

Depends R (>= 3.1.0)

Imports Rcpp (>= 0.11.2), scales (>= 0.4.0), magrittr (>= 1.5),
combinat

Suggests knitr, rmarkdown(>= 1.6), circlize, testthat (>= 0.9.0)

LinkingTo Rcpp

RoxygenNote 7.3.2

Encoding UTF-8

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License Apache License (>= 2)

NeedsCompilation yes

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Repository CRAN

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Contents

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computeObsWSAF   *Compute observed WSAF*

Description

Compute observed allele frequency within sample from the allele counts.

Usage

```
computeObsWSAF(alt, ref)
```

Arguments

alt	Numeric array of alternative allele count.
ref	Numeric array of reference allele count.

Value

Numeric array of observed allele frequency within sample.

See Also

[histWSAF](#) for histogram.

Examples

```
# Example 1
refFile <- system.file("extdata", "PG0390-C.test.ref", package = "DEploid.utils")
altFile <- system.file("extdata", "PG0390-C.test.alt", package = "DEploid.utils")
PG0390CoverageTxt <- extractCoverageFromTxt(refFile, altFile)
obsWSAF <- computeObsWSAF(PG0390CoverageTxt$altCount, PG0390CoverageTxt$refCount)

# Example 2
vcfFile <- system.file("extdata", "PG0390-C.test.vcf.gz", package = "DEploid.utils")
```

```
PG0390CoverageVcf <- extractCoverageFromVcf(vcfFile, "PG0390-C")
obsWSAF <- computeObsWSAF(PG0390CoverageVcf$altCount, PG0390CoverageVcf$refCount)
```

---

extractCoverageFromTxt

Extract read counts from plain text file

Description

Extract read counts from tab-delimited text files of a single sample.

Usage

```
extractCoverageFromTxt(refFileName, altFileName)
```

Arguments

refFileName   Path of the reference allele count file.

altFileName   Path of the alternative allele count file.

Value

A data.frame contains four columns: chromosomes, positions, reference allele count, alternative allele count.

Note

The allele count files must be tab-delimited. The allele count files contain three columns: chromosomes, positions and allele count.

Examples

```
refFile <- system.file("extdata", "PG0390-C.test.ref", package = "DEploid.utils")
altFile <- system.file("extdata", "PG0390-C.test.alt", package = "DEploid.utils")
PG0390 <- extractCoverageFromTxt(refFile, altFile)
```

```
extractCoverageFromVcf
```
                                  Extract VCF information

Description

Extract VCF information

Usage

```
extractCoverageFromVcf(filename, samplename)
```

Arguments

filename   VCF file name.

samplename   Sample name

Value

A dataframe list with members of haplotypes, proportions and log likelihood of the MCMC chain.

- CHROM SNP chromosomes.

- POS SNP positions.

- refCount reference allele count.

- altCount alternative allele count.

See Also

- extractCoverageFromVcf

- extractCoverageFromTxt

Examples

```
vcfFile = system.file("extdata", "PG0390-C.test.vcf.gz", package = "DEploid.utils")
vcf = extractCoverageFromVcf(vcfFile, "PG0390-C")
```

---

extractPLAF *Extract PLAF*

Description

Extract population level allele frequency (PLAF) from text file.

Usage

```
extractPLAF(plafFileName)
```

Arguments

plafFileName   Path of the PLAF text file.

Value

A numeric array of PLAF

Note

The text file must have header, and population level allele frequency recorded in the "PLAF" field.

Examples

```
plafFile <- system.file("extdata", "labStrains.test.PLAF.txt", package = "DEploid.utils")
plaf <- extractPLAF(plafFile)
```

---

haplotypePainter *Painting haplotype according the reference panel*

Description

Plot the posterior probabilities of a haplotype given the refernece panel.

Usage

```
haplotypePainter(
  posteriorProbabilities,
  title = "",
  labelScaling,
  numberOfInbreeding = 0
)
```

Arguments

posteriorProbabilities

Posterior probabilities matrix with the size of number of loci by the number of reference strain.

title   Figure title.

labelScaling   Scaling parameter for plotting.

numberOfInbreeding

Number of inbreading strains

Value

No return value called for side effects

---

histWSAF   *WSAF histogram*

Description

Produce histogram of the allele frequency within sample.

Usage

```
histWSAF(
  obsWSAF,
  exclusive = TRUE,
  title = "Histogram 0<WSAF<1",
  cex.lab = 1,
  cex.main = 1,
  cex.axis = 1
)
```

Arguments

obsWSAF   Observed allele frequency within sample

exclusive   When TRUE 0 < WSAF < 1; otherwise 0 <= WSAF <= 1.

title   Histogram title

cex.lab   Label size.

cex.main   Title size.

cex.axis   Axis text size.

Value

histogram

Examples

```
# Example 1
refFile <- system.file("extdata", "PG0390-C.test.ref", package = "DEploid.utils")
altFile <- system.file("extdata", "PG0390-C.test.alt", package = "DEploid.utils")
PG0390CoverageTxt <- extractCoverageFromTxt(refFile, altFile)
obsWSAF <- computeObsWSAF(PG0390CoverageTxt$altCount, PG0390CoverageTxt$refCount)
histWSAF(obsWSAF)
myhist <- histWSAF(obsWSAF, FALSE)

# Example 2
vcfFile <- system.file("extdata", "PG0390-C.test.vcf.gz", package = "DEploid.utils")
PG0390CoverageVcf <- extractCoverageFromVcf(vcfFile, "PG0390-C")
obsWSAF <- computeObsWSAF(PG0390CoverageVcf$altCount, PG0390CoverageVcf$refCount)
histWSAF(obsWSAF)
myhist <- histWSAF(obsWSAF, FALSE)
```

---

plotAltVsRef   *Plot coverage*

Description

Plot alternative allele count vs reference allele count at each site.

Usage

```
plotAltVsRef(
  ref,
  alt,
  title = "Alt vs Ref",
  exclude.ref = c(),
  exclude.alt = c(),
  potentialOutliers = c(),
  cex.lab = 1,
  cex.main = 1,
  cex.axis = 1
)
```

Arguments

ref	Numeric array of reference allele count.
alt	Numeric array of alternative allele count.
title	Figure title, "Alt vs Ref" by default
exclude.ref	Numeric array of reference allele count at sites that are not deconvoluted.
exclude.alt	Numeric array of alternative allele count at sites that are not deconvoluted
potentialOutliers	
	Potential outliers

```
cex.lab          Label size.
cex.main         Title size.
cex.axis         Axis text size.
```

Value

No return value called for side effects

Examples

```
# Example 1
refFile <- system.file("extdata", "PG0390-C.test.ref", package = "DEploid.utils")
altFile <- system.file("extdata", "PG0390-C.test.alt", package = "DEploid.utils")
PG0390CoverageTxt <- extractCoverageFromTxt(refFile, altFile)
plotAltVsRef(PG0390CoverageTxt$refCount, PG0390CoverageTxt$altCount)

# Example 2
vcfFile <- system.file("extdata", "PG0390-C.test.vcf.gz", package = "DEploid.utils")
PG0390CoverageVcf <- extractCoverageFromVcf(vcfFile, "PG0390-C")
plotAltVsRef(PG0390CoverageVcf$refCount, PG0390CoverageVcf$altCount)
```

```
plotObsExpWSAF                  Plot WSAF
```

Description

Plot observed alternative allele frequency within sample against expected WSAF.

Usage

```
plotObsExpWSAF(
  obsWSAF,
  expWSAF,
  title = "WSAF(observed vs expected)",
  cex.lab = 1,
  cex.main = 1,
  cex.axis = 1
)
```

Arguments

```
obsWSAF          Numeric array of observed WSAF.
expWSAF          Numeric array of expected WSAF.
title            Figure title.
cex.lab          Label size.
cex.main         Title size.
cex.axis         Axis text size.
```

Value

No return value called for side effects

---

plotProportions *Plot proportions*

Description

Plot the MCMC samples of the proportion, indexed by the MCMC chain.

Usage

```
plotProportions(
  proportions,
  title = "Components",
  cex.lab = 1,
  cex.main = 1,
  cex.axis = 1
)
```

Arguments

proportions	Matrix of the MCMC proportion samples. The matrix size is number of the MCMC samples by the number of strains.
title	Figure title.
cex.lab	Label size.
cex.main	Title size.
cex.axis	Axis text size.

Value

No return value called for side effects

---

plotWSAFvsPLAF *Plot WSAF vs PLAF*

Description

Plot allele frequencies within sample against population level.

Usage

```
plotWSAFvsPLAF(
  plaf,
  obsWSAF,
  expWSAF = c(),
  potentialOutliers = c(),
  title = "WSAF vs PLAF",
  cex.lab = 1,
  cex.main = 1,
  cex.axis = 1
)
```

Arguments

`plaf`	Numeric array of population level allele frequency.
`obsWSAF`	Numeric array of observed altenative allele frequencies within sample.
`expWSAF`	Numeric array of expected WSAF from model.
`potentialOutliers`	
	Potential outliers
`title`	Figure title, "WSAF vs PLAF" by default
`cex.lab`	Label size.
`cex.main`	Title size.
`cex.axis`	Axis text size.

Value

No return value called for side effects

Examples

```
# Example 1
refFile <- system.file("extdata", "PG0390-C.test.ref", package = "DEploid.utils")
altFile <- system.file("extdata", "PG0390-C.test.alt", package = "DEploid.utils")
PG0390CoverageTxt <- extractCoverageFromTxt(refFile, altFile)
obsWSAF <- computeObsWSAF(PG0390CoverageTxt$altCount, PG0390CoverageTxt$refCount)
plafFile <- system.file("extdata", "labStrains.test.PLAF.txt", package = "DEploid.utils")
plaf <- extractPLAF(plafFile)
plotWSAFvsPLAF(plaf, obsWSAF)

# Example 2
vcfFile <- system.file("extdata", "PG0390-C.test.vcf.gz", package = "DEploid.utils")
PG0390CoverageVcf <- extractCoverageFromVcf(vcfFile, "PG0390-C")
obsWSAF <- computeObsWSAF(PG0390CoverageVcf$altCount, PG0390CoverageVcf$refCount)
plafFile <- system.file("extdata", "labStrains.test.PLAF.txt", package = "DEploid.utils")
plaf <- extractPLAF(plafFile)
plotWSAFvsPLAF(plaf, obsWSAF)
```

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