Package: DEploid.utils (via r-universe)

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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

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NeedsCompilation yes

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RemoteUrl https://github.com/cran/DEploid.utils

RemoteRef HEAD

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Contents

`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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