Package: RChASM (via r-universe)

June 5, 2026

Title Detection of Chromosomal Aneuploidies in Ancient DNA Studies

Version 1.0.1

Description An R implementation of ChASM (Chromosomal Aneuploidy Screening Methodology): a statistically rigorous Bayesian approach for screening data sets for autosomal and sex chromosomal aneuploidies. This package takes as input the number of (deduplicated) reads mapping to chromosomes 1-22 and the X and Y chromosomes, and models these using a Dirichlet-multinomial distribution. From this, This package returns posterior probabilities of sex chromosomal karyotypes (XX, XY, XXY, XYY, XXX and X) and full autosomal aneuploidies (trisomy 13, trisomy 18 and trisomy 21). This package also returns two diagnostic statistics: (i) a posterior probability addressing whether contamination between XX and XY may explain the observed sex chromosomal aneuploidy, and (ii) a chi-squared statistic measuring whether the observed read counts are too divergent from the underlying distribution (and may represent abnormal sequencing/quality issues).

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Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

Imports checkmate, cowplot, dplyr, EnvStats, ggplot2, ggrepel, ggsci, ggstar, magrittr, matrixStats, mclust, rstatix, sirt, stringr, tibble, tidyr, readr

LazyData true

Suggests knitr, rmarkdown, extraDistr

VignetteBuilder knitr

Depends R (>= 3.5.0)

URL https://jonotuke.github.io/RChASM/, https://github.com/jonotuke/RChASM

BugReports https://github.com/jonotuke/RChASM/issues

Config/pak/sysreqs libcairo2-dev cmake libfontconfig1-dev libfreetype6-dev make libicu-dev libpng-dev libuv1-dev libx11-dev

Repository https://jonotuke.r-universe.dev

Date/Publication 2026-04-30 20:38:48 UTC

RemoteUrl https://github.com/jonotuke/rchasm

RemoteRef HEAD

RemoteSha 6cf17e35826caaddf2ef62b6f0f16d9cc5966616

Contents

`adjustA` *Adjusts alpha vector for contamination karyotypes*

Description

Adjusts alpha vector for contamination karyotypes

Usage

```
adjustA(a, c1, c2, g, correction = 1e-06)
```

Arguments

a	vector to change
c1	X multiplier for karyotype 1
c2	X multiplier for karyotype 2
g	mixing parameter
correction	error rate for Y mapping for non-Y karyotypes

Value

adjusted alpha vector

---

bound *bounds number to be in [0,1] (contamination estimation)*

Description

bounds number to be in [0,1] (contamination estimation)

Usage

```
bound(x)
```

Arguments

x	number

Value

bounded number

---

callKaryotypes *Take prior and observed counts and calls karyotypes and Z-scores*

Description

Take prior and observed counts and calls karyotypes and Z-scores

Usage

```
callKaryotypes(indat, inDirichlet, p_contamination = 0.1)
```

Arguments

indat	full input tibble
inDirichlet	associated Dirichlet parameters
p_contamination	the assumed probability of contamination

Value

karyotype calls

---

combineData *combine data*

Description

Combine both autosomal and sex chromosomal analyses into one output

Usage

```
combineData(calls.auto, calls.sca, z.scores, printMissingIDs = FALSE)
```

Arguments

calls.auto	a list or predefined piped string of sample IDs to look for
calls.sca	the autosomal karyotype calls for the samples
z.scores	the sex chromosomal karyotype calls for the samples
printMissingIDs	print the IDs of individuals not in all 3 input files (or just numbers)?

Value

combined data

ddirichletultinomial *calculate Dirichlet probabilities with filtering*

Description

calculate Dirichlet probabilities with filtering

Usage

```
ddirichletultinomial(nvector, avector, cvector, log = TRUE, correction = 1e-06)
```

Arguments

nvector	observed read counts
avector	alpha vector to change
cvector	change vector for new karyotype
log	return value in log space
correction	error rate for Y mapping for non-Y karyotypes

Value

Dirichlet probabilities

dirichlet.mle_filter *calculate Dirichlet parameters with filtering*

Description

calculate Dirichlet parameters with filtering

Usage

```
dirichlet.mle_filter(y, whichK)
```

Arguments

y	input values
whichK	which parameter to return

Value

parameters

`estimateGamma` *Estimate contamination from XX and XY based on observed counts*

Description

Estimate contamination from XX and XY based on observed counts

Usage

```
estimateGamma(nvector, avector, c1, c2, correction)
```

Arguments

`nvector`	observed read counts
`avector`	vector to change
`c1`	X multiplier for karyotype 1
`c2`	X multiplier for karyotype 2
`correction`	error rate for Y mapping for non-Y karyotypes

Value

estimated contamination

`example_data` *example_data*

Description

An example data set for RChASM

Usage

```
example_data
```

Format

A data frame with 266 rows and 26 variables:

Source

"Ben Rohrlach"

filterOutliers *filter for outliers*

Description

filter for outliers

Usage

```
filterOutliers(v)
```

Arguments

v	vector to filter

Value

vector for filtering

makeC *make c vector for new karyotypes*

Description

make c vector for new karyotypes

Usage

```
makeC(x, y, n)
```

Arguments

x	value to replace 1
y	location to make replacement
n	length of vector

Value

c vector

makeDirichlet *function to make a Dirichlet prior*

Description

function to make a Dirichlet prior

Usage

```
makeDirichlet(
  indat,
  refType,
  min_reads = 30000,
  max_reads = 1e+09,
  show_plot = TRUE
)
```

Arguments

indat	full input tibble
refType	"auto"="autosomal"; "sca"="sex chromosomal"; "diagnostic"
min_reads	min number of reads per sample
max_reads	max number of reads per sample
show_plot	boolean to show plot

Value

Dirichlet prior

makeZscores *Calculates Z-scores per chromosome*

Description

Calculates Z-scores per chromosome

Usage

```
makeZscores(indat, refType = "auto", min_reads = 30000, max_reads = 1e+09)
```

Arguments

indat	full input tibble
refType	"auto"="autosomal"; "sca"="sex chromosomal"; "diagnostic"
min_reads	min number of reads per sample
max_reads	max number of reads per sample

Value

Z-scores

`plot_diagnostic` *Plots diagnostic plots*

Description

Plots diagnostic plots

Usage

```
plot_diagnostic(IDs, inChASM, addLabels = FALSE)
```

Arguments

`IDs`	a list or predefined piped string of sample IDs to look for
`inChASM`	parameter object
`addLabels`	add "A", "B" and "C" to the plot panels?

Value

plots

Examples

```
example_calls <- runChASM(rawReadCountsIn = example_data)
plot_diagnostic(IDs = 'Ind_255_1', inChASM = example_calls, addLabels = TRUE)
```

`printChASM` *A function to print the result of the combined analysis to screen*

Description

A function to print the result of the combined analysis to screen

Usage

```
printChASM(inChASM, lines = 20)
```

Arguments

`inChASM`	the result of a full ChASM analysis (output from runChASM)
`lines`	the number of lines to print to screen

Value

print output

Examples

```
example_calls <- runChASM(rawReadCountsIn = example_data)
printChASM(inChASM = example_calls, lines = 10)
```

`processReadCounts` *processReadCounts*

Description

Task: takes read counts and makes useful file

Usage

```
processReadCounts(
  rawReadCountsIn,
  refType,
  minTotal = 1000,
  minSamplesPerProtocol = 30
)
```

Arguments

`rawReadCountsIn`	the reads counts via KP
`refType`	for capture, use only on-target (F)?
`minTotal`	minimum number of protocol counts to be included
`minSamplesPerProtocol`	"auto"="autosomal"; "sca"="sex chromosomal"

Value

outreadcounts

runChASM *Title*

Description

Title

Usage

```
runChASM(
  rawReadCountsIn,
  minSamplesPerProtocol = 30,
  min_reads = 60000,
  max_reads = 1e+09,
  p_contamination = 0.01,
  show_plot = TRUE,
  printMissingIDs = FALSE
)
```

Arguments

rawReadCountsIn	the reads counts for each chromosome
minSamplesPerProtocol	minimum number of reads per protocol for parameter estimation
min_reads	the minimum number of reads for Dirichlet parameter estimation
max_reads	the maximum number of reads for Dirichlet parameter estimation
p_contamination	the probability of a sample yielding significant contamination
show_plot	show the clustering plot for sex chromosomal aneuploidy Dirichlet estimation?
printMissingIDs	when combining karyotype calls, return names that are missing (or just the number of missing IDs)?

Value

summary

Examples

```
runChASM(rawReadCountsIn = example_data)
```

saveChASM *A function for saving the results of a ChASM analysis as a tsv*

Description

A function for saving the results of a ChASM analysis as a tsv

Usage

```
saveChASM(inChASM, file, sort_by_samplename = FALSE)
```

Arguments

inChASM	the result of a full ChASM analysis (output from runChASM)
file	the full path and file name to place output
sort_by_samplename	reorder alphabetically by sample names?

Value

saves results

Examples

```
example_calls <- runChASM(rawReadCountsIn = example_data)
## Not run:
saveChASM(inChASM = example_calls)

## End(Not run)
```

summary_calls *summary_calls*

Description

Combine both autosomal and sex chromosomal analyses into one output

Usage

```
summary_calls(
  inChASM,
  minTotal = 60000,
  minPosterior = 0.95,
  ignoreUnusual = FALSE,
  printProtocol = FALSE
)
```

Arguments

inChASM	the result of combining both autosomal and sca analyses
minTotal	minimum total for autosomal or sca analyses
minPosterior	minimum value maxP can take (i.e. minimum posterior probability accepted)
ignoreUnusual	filter our unusual observations?
printProtocol	print protocol column?

Value

combined calls

Examples

```
example_calls <- runChASM(rawReadCountsIn = example_data)
summary_calls(inChASM = example_calls, minTotal = 6e4, minPosterior = 0.95)
```

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