

Package: DoAbsolute (via r-universe)

December 19, 2024

Title Automate Absolute Copy Number Calling

Version 2.2.0

Description Provide an easy interface to automate estimation of absolute copy number, purity, ploidy using 'ABSOLUTE'.

Depends R (>= 3.5)

Imports foreach, doParallel, data.table

Suggests ABSOLUTE

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Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.0

Repository <https://shixiangwang.r-universe.dev>

RemoteUrl <https://github.com/ShixiangWang/DoAbsolute>

RemoteRef HEAD

RemoteSha ae20c68792702ff3f144f774b3031b0ab6825b38

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DoAbsolute *Automate ABSOLUTE calling for multiple samples in parallel way*

Description

An example can be found at [README](#). If calling for a sample failed, the error message will be written to `error.log` under `result` directory.

Usage

```

DoAbsolute(
  Seg,
  Maf = NULL,
  sigma.p = 0,
  max.sigma.h = 0.2,
  min.ploidy = 0.5,
  max.ploidy = 10,
  primary.disease = NA,
  platform = c("SNP_6.0", "Illumina_WES", "SNP_250K_STY"),
  temp.dir = file.path(tempdir(), "Absolute"),
  clean.temp = FALSE,
  results.dir = getwd(),
  max.as.seg.count = 1500,
  max.non.clonal = 0.05,
  max.neg.genome = 0.005,
  copy.num.type = c("total", "allelic"),
  min.mut.af = 0.1,
  min.no.mut = 5,
  verbose = FALSE,
  nThread = 1L,
  keepAllResult = TRUE,
  recover = FALSE
)

```

Arguments

Seg	a data.frame or a file (path) contains columns "Sample", "Chromosome", "Start", "End", "Num_Probes", "Segment_Mean".
Maf	MAF, default is NULL, can provided as data.frame or file path.
sigma.p	Provisional value of excess sample level variance used for mode search. Default: 0
max.sigma.h	Maximum value of excess sample level variance (Eq. 6). Default: 0.2
min.ploidy	Minimum ploidy value to consider. Solutions implying lower ploidy values will be discarded. Default: 0.5
max.ploidy	Maximum ploidy value to consider. Solutions implying greater ploidy values will be discarded. Default: 10
primary.disease	Primary disease of the sample. Default: NA
platform	one of "SNP_6.0", "Illumina_WES", "SNP_250K_STY". Default: "SNP_6.0"
temp.dir	directory path used to store tempory files. Default: Absolute subdirectory under tempdir()
clean.temp	if TRUE, auto-clean temp dir at the end. Default: FALSE
results.dir	directory path used to store result files. Default: work directory

<code>max.as.seg.count</code>	Maximum number of allelic segments. Samples with a higher segment count will be flagged as 'failed'. Default: 1500
<code>max.non.clonal</code>	Maximum genome fraction that may be modeled as non-clonal (subclonal SCNA). Solutions implying greater values will be discarded. Default: 0.05
<code>max.neg.genome</code>	Maximum genome fraction that may be modeled as non-clonal with copy-ratio below that of clonal homozygous deletion. Solutions implying greater values will be discarded. Default: 0.005
<code>copy.num.type</code>	The type of copy number to be handled. Either total or allelic. Total is what this package for. Default: "total"
<code>min.mut.af</code>	Minimum mutation allelic fraction. Mutations with lower allelic fractions will be filtered out before analysis. Default: 0.1
<code>min.no.mut</code>	Minor allele frequency file, or NULL if one is not available. This specifies the data for somatic point mutations to be used by ABSOLUTE. Default: 5
<code>verbose</code>	if TRUE, print extra info. Default: FALSE
<code>nThread</code>	number of cores used for computation. Default: 1L
<code>keepAllResult</code>	if TRUE, clean all results, otherwise clean result directory and keep most important results. Default: TRUE
<code>recover</code>	if TRUE, recover previous unfinished work. This is helpful when program stop unexpectedly when <code>clean.temp</code> is FALSE. Default: FALSE

Details

ABSOLUTE is a famous software developed by Broad Institute, however the `RunAbsolute` function is designed for computing one sample each time and set no default values. **DoAbsolute** help user set default parameters according to [ABSOLUTE documentation](#), provide an uniform interface to input data easily and run `RunAbsolute` parallelly.

More detail about how to analyze ABSOLUTE results please see [this link](#).

Author(s)

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References

Carter, Scott L., et al. "Absolute quantification of somatic DNA alterations in human cancer." *Nature biotechnology* 30.5 (2012): 413.

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