Package: DoAbsolute (via r-universe)

July 21, 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

Contents

`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

`max.as.seg.count`
: Maximum number of allelic segments. Samples with a higher segment count will be flagged as 'failed'. Default: 1500

`max.non.clonal`
: Maximum genome fraction that may be modeled as non-clonal (subclonal SCNA). Solutions implying greater values will be discarded. Default: 0.05

`max.neg.genome`
: 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

`copy.num.type`
: The type of copy number to be handled. Either total or allelic. Total is what this package for. Default: "total"

`min.mut.af`
: Minimum mutation allelic fraction. Mutations with lower allelic fractions will be filtered out before analysis. Default: 0.1

`min.no.mut`
: 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

`verbose`
: if `TRUE`, print extra info. Default: `FALSE`

`nThread`
: number of cores used for computation. Default: 1L

`keepAllResult`
: if `TRUE`, clean all results, otherwise clean result directory and keep most important results. Default: `TRUE`

`recover`
: if `TRUE`, recover previous unfinished work. This is helpful when program stop unexpectedly when `clean.temp` 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)

Shixiang Wang w_shixiang@163.com

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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