Package 'HiCool'

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Title HiCool

Description HiCool provides an R interface to process and normalize Hi-C paired-end fastq reads into .(m)cool files.
.(m)cool is a compact, indexed HDF5 file format specifically tailored for efficiently storing HiC-based data.
On top of processing fastq reads, HiCool provides a convenient reporting function to generate shareable reports summarizing Hi-C experiments and including quality controls.

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URL https://github.com/js2264/HiCool

BugReports https://github.com/js2264/HiCool/issues

Depends R (>= 4.2), HiCExperiment

Imports BiocIO, S4Vectors, GenomicRanges, IRanges, InteractionSet, vroom, basilisk.utils, basilisk, reticulate, rmarkdown, rmdformats, plotly, dplyr, stringr, sessioninfo, utils

Suggests HiContacts, HiContactsData, AnnotationHub, BiocFileCache, BiocStyle, testthat, knitr, rmarkdown

biocViews HiC, DNA3DStructure, DataImport

Encoding UTF-8

VignetteBuilder knitr

LazyData false

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

Config/testthat/edition 3

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`getLoops` *Finding loops in contact map*

Description

Find loops using chromosight

Usage

```
getLoops(
  x,
  resolution = NULL,
  output_prefix = file.path("chromosight", "chromo"),
  norm = "auto",
  max.dist = "auto",
  min.dist = "auto",
  min.separation = "auto",
  n.mads = 5L,
  pearson = "auto",
  nreads = "no",
  ncores = 1L
)
```

Arguments

`x`	A `HiCExperiment` object
`resolution`	Which resolution to use to search loops
`output_prefix`	Prefix to chromosight output (default: "chromosight/chromo")
`norm`	Normalization parameter for chromosight

min.dist, max.dist	Min and max distance to use to filter for significant loops
min.separation	Minimum separation between anchors of potential loops
n.mads	Number of MADs to use to filter relevant bins to search for loops
pearson	Minimum Pearson correlation score to use to filter for significant loops
nreads	Number of reads to subsample to before searching for loops
ncores	Number of cores for chromosight

Value

A HiCExperiment object with a new "loops" topologicalFeatures storing significant interactions identified by chromosight, and an additional chromosight_args metadata entry.

Examples

```
contacts_yeast <- contacts_yeast()
## Not run:
  contacts_yeast <- getLoops(contacts_yeast)
  metadata(contacts_yeast)$chromosight_args
  topologicalFeatures(contacts_yeast, 'loops')

## End(Not run)
```

HiCool *Processing Hi-C paired-end fastq files in R*

Description

HiCool::HiCool() automatically processes paired-end HiC sequencing files by performing the following steps:

1. Automatically setting up an appropriate conda environment using basilisk;
2. Mapping the reads to the provided genome reference using hicstuff and filtering of irrelevant pairs;
3. Filtering the resulting pairs file to remove unwanted chromosomes (e.g. chrM);
4. Binning the filtered pairs into a cool file at a chosen resolution;
5. Generating a multi-resolution mcool file;
6. Normalizing matrices at each resolution by iterative corretion using cooler.

The filtering strategy used by hicstuff is described in Cournac et al., BMC Genomics 2012.

Usage

```
HiCool(
  r1 = "~/repos/tinyMapper/tests/testHiC_R1.fq.gz",
  r2 = "~/repos/tinyMapper/tests/testHiC_R2.fq.gz",
  genome = "R64-1-1",
  restriction = "DpnII,HinfI",
  binning = NULL,
  iterative = TRUE,
  balancing_args = " --min-nnz 10 --mad-max 5 ",
  threads = 1L,
  exclude_chr = "Mito|chrM|MT",
  output = "HiCool",
  keep_bam = FALSE,
  build_report = TRUE,
  scratch = tempdir()
)

importHiCoolFolder(output, hash, resolution = NULL)

getHiCoolArgs(log)

getHicStats(log)
```

Arguments

r1	Path to fastq file (R1 read)
r2	Path to fastq file (R2 read)
genome	Genome used to map the reads on, provided either as a fasta file (in which case the bowtie2 index will be automatically generated), or as a prefix to a bowtie2 index (e.g. mm10 for mm10.*.bt2 files). Genome can also be a unique ID for the following references: hg38, mm10, dm6, R64-1-1, GRZc10, WBcel235, Galgal4.
restriction	Restriction enzyme(s) used in HiC (Default: "DpnII,HinfI")
binning	First resolution used to bin the final mcool file (Default: 10000 for hg38 and mm10, 1000 for dm6, R64-1-1, ...)
iterative	Should the read mapping be performed iteratively? (Default: TRUE)
balancing_args	Balancing arguments for cooler. See cooler documentation here for a list of all available balancing arguments. These defaults match those used by the 4DN consortium.
threads	Number of CPUs used for parallelization. (Default: 1)
exclude_chr	Chromosomes excluded from the final .mcool file. This will not affect the pairs file. (Default: "Mito|chrM|MT")
output	Output folder used by HiCool.
keep_bam	Should the bam files be kept? (Default: FALSE)
build_report	Should an automated report be computed? (Default: TRUE)
scratch	Path to temporary directory where processing will take place. (Default: tempdir())

hash	Unique 6-letter ID used to identify files from a specific HiCool processing run.
resolution	Resolution used to import the mcool file
log	Path to log file generated by hicstuff/hicool

Value

A CoolFile object with prefilled pairsFile and metadata slots.

HiCool utils

- importHiCoolFolder(folder, hash) automatically finds the different processed files associated with a specific HiCool::HiCool() processing hash ID.
- getHiCoolArgs() parses the log file generated by HiCool::HiCool() during processing to recover which arguments were used.
- getHicStats() parses the log file generated by HiCool::HiCool() during processing to recover pre-computed stats about pair numbers, filtering thresholds, etc.

Examples

```
r1 <- HiContactsData::HiContactsData(sample = 'yeast_wt', format = 'fastq_R1')
r2 <- HiContactsData::HiContactsData(sample = 'yeast_wt', format = 'fastq_R2')
hcf <- HiCool(r1, r2, genome = 'R64-1-1', output = './HiCool/')
hcf
getHiCoolArgs(metadata(hcf)$log)
getHicStats(metadata(hcf)$log)
readLines(metadata(hcf)$log)
```

HiCReport *HiC processing report*

Description

HiC processing report

Usage

```
HiCReport(x, output = NULL)
```

Arguments

x	an CoolFile object, generated from HiCool::HiCool() or HiCool::importHiCoolFolder(), or directly from calling HiCExperiment::CoolFile().
output	Path to save output HTML file.

Value

String to the generated HTML report file

Examples

```
mcool_path <- HiContactsData::HiContactsData('yeast_wt', 'mcool')
pairs_path <- HiContactsData::HiContactsData('yeast_wt', 'pairs.gz')
log_path <- HiContactsData::HiContactsData(sample = 'yeast_wt', format = 'HiCool_log')
cf <- CoolFile(mcool_path, pairs = pairs_path, metadata = list(log = log_path))
HiCReport(cf)
```

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