Package ‘HTSeqGenie’

November 20, 2016

Imports  
BiocGenerics (>= 0.2.0), S4Vectors (>= 0.9.25), IRanges (>= 1.21.39), GenomicRanges (>= 1.23.21), Rsamtools (>= 1.8.5), Biostrings (>= 2.24.1), chipseq (>= 1.6.1), hwriter (>= 1.3.0), Cairo (>= 1.5.5), GenomicFeatures (>= 1.9.31), BiocParallel, parallel, tools, rtracklayer (>= 1.17.19), GenomicAlignments, VariantTools (>= 1.7.7), GenomeInfoDb, SummarizedExperiment, methods

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License  Artistic-2.0
Title  A NGS analysis pipeline.
Type  Package
LazyLoad  yes
Author  Gregoire Pau, Jens Reeder
Description  Libraries to perform NGS analysis.
Version  4.4.0
Depends  R (>= 3.0.0), gmapR (>= 1.8.0), ShortRead (>= 1.19.13), VariantAnnotation (>= 1.8.3)
Suggests  TxDb.Hsapiens.UCSC.hg19.knownGene, LungCancerLines, org.Hs.eg.db
RoxygenNote  5.0.1
NeedsCompilation  no

R topics documented:

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annotateVariants

Description
Calculate and process Variants

Usage
analyzeVariants()

Value
Nothing

Author(s)
Jens Reeder

annotateVariants
Annotate variants via vep

Description
Annotate variants via vep

Usage
annotateVariants(vcf.file)

Arguments
vcf.file A character vector pointing to a VCF (or gzipped VCF) file
buildGenomicFeaturesFromTxDb

Value
Path to a vcf file with variant annotations

Author(s)
Jens Reeder

Description
Build genomic features from a TxDb object

Usage
buildGenomicFeaturesFromTxDb(txdb)

Arguments
txdb  A TxDb object.

Value
A list named list of GRanges objects containing the biological entities to account for.

Author(s)
Gregoire Pau

Examples
## Not run:
library("TxDb.Hsapiens.UCSC.hg19.knownGene")
txdb <- TxDb.Hsapiens.UCSC.hg19.knownGene
genomic_features <- buildGenomicFeaturesFromTxDb(txdb)
## End(Not run)
**callVariantsGATK**  
*Variant calling via GATK*

**Description**
Call variants via GATK using the pipeline framework. Requires a GATK compatible genome with a name matching the alignment genome to be installed in `path.gatk_genome`.

**Usage**
callVariantsGATK(bam.file)

**Arguments**
- **bam.file**  
  Path to bam.file

**Value**
Path to variant file

**Author(s)**
Jens Reeder

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**checkGATKJar**  
*Check for the GATK jar file*

**Description**
Check for the GATK jar file

**Usage**
checkGATKJar(path = getOption("gatk.path"))

**Arguments**
- **path**  
  Path to the GATK jar file

**Value**
TRUE if tool can be called, FALSE otherwise
### detectRRNA

**Detect rRNA Contamination in Reads**

**Description**

Returns a named vector indicating if a read ID has rRNA contamination or not.

**Usage**

```r
detectRRNA(lreads, remove_tmp_dir = TRUE, save_dir = NULL)
```

**Arguments**

- `lreads`: A list of ShortReadQ objects
- `remove_tmp_dir`: boolean indicating whether or not to delete temp directory of gsnap results
- `save_dir`: Save directory

**Details**

Given a genome and fastq data, each read in the fastq data is aligned against the rRNA sequences for that genome.

**Value**

A named logical vector indicating if a read has rRNA contamination.

**Author(s)**

Cory Barr

---

### excludeVariantsByRegions

**Filter variants by regions**

**Description**

Filter variants by regions.

**Usage**

```r
excludeVariantsByRegions(variants, mask)
```

**Arguments**

- `variants`: Variants as Vranges, GRanges or VCF object
- `mask`: region to mask, given as GRanges

**Details**

This function can be used to filter variants in a given region, e.g. low complexity and repeat regions.
Value

The filtered variants

Author(s)

Jens Reeder

---

gatk

description

Run a command from the GATK

Usage

gatk(gatk.jar.path = getOption("gatk.path"), method, args, maxheap = "4g")

Arguments

gatk.jar.path Path to the gatk jar file
method Name of the gatk method, e.g. UnifiedGenotyper
args additional args passed to gatk
maxheap Maximal heap space allocated for java, GATK recommends 4G heap for most of its apps

Details

Execute the GATK jar file using the method specified as arg. Stops if the command executed fails.

Value

0 for success, stops otherwise

Author(s)

Jens Reeder
generateSingleGeneDERs

Description
Generate DEXSeq-ready exons

Usage
generateSingleGeneDERs(txdb)

Arguments

- `txdb` A transcript DB object

Details
generateSingleGeneDERs() generates exons by: 1) disjoining the whole exon set 2) keeping only the exons of coding regions 3) keeping only the exons that belong to unique genes

Value
single gene DERs

getRRNAIds

Detect reads that look like rRNA

Description
Detect reads that look like rRNA

Usage
getRRNAIds(file1, file2 = NULL, tmp_dir, rRNADb)

Arguments

- `file1` FastQ file of forward reads
- `file2` FastQ file of reverse reads in paired-end sequencing, NULL otherwise
- `tmp_dir` temporary directory used for storing the gsnaps results
- `rRNADb` Name of the rRNA sequence database. Must exist in the gsnaps genome directory

Value
IDs of reads flagged as rRNA
getTabDataFromFile  
Load tabular data from the NGS pipeline result directory

Description
Load tabular data from the NGS pipeline result directory

Usage
getTabDataFromFile(save_dir, object_name)

Arguments
- save_dir: A character string containing an NGS pipeline output directory.
- object_name: A character string containing the regular expression matching a filename in dir_path

Value
A data frame.

hashCoverage  
Hashing function for coverage

Description
Hashing function for coverage

Usage
hashCoverage(cov)

Arguments
- cov: A SimpleRleList object

Value
A numeric

Author(s)
Gregoire Pau
**hashVariants**

*Hashing function for variants*

**Description**

Hashing function for variants

**Usage**

```
hashVariants(var)
```

**Arguments**

- `var` A GRanges object

**Value**

A numeric

**Author(s)**

Gregoire Pau

---

**hashVector**

*Hashing function for vector*

**Description**

Hashing function for vector

**Usage**

```
hashVector(x)
```

**Arguments**

- `x` A vector

**Value**

A numeric

**Author(s)**

Gregoire Pau
Description

The HTSeqGenie package is a robust and efficient software to analyze high-throughput sequencing experiments in a reproducible manner. It supports the RNA-Seq and Exome-Seq protocols and provides: quality control reporting (using the ShortRead package), detection of adapter contamination, read alignment versus a reference genome (using the gmapR package), counting reads in genomic regions (using the GenomicRanges package), and read-depth coverage computation.

Package content

To run the pipeline:

- runPipeline

To access the pipeline output data:

- getTabDataFromFile

To build the genomic features object:

- buildGenomicFeaturesFromTxDb
- TP53GenomicFeatures

Examples

```r
## Not run:
## build genome and genomic features
tp53Genome <- TP53Genome()
tp53GenomicFeatures <- TP53GenomicFeatures()

## get the FASTQ files
fastq1 <- system.file("extdata/H1993_TP53_subset2500_1.fastq.gz", package="HTSeqGenie")
fastq2 <- system.file("extdata/H1993_TP53_subset2500_2.fastq.gz", package="HTSeqGenie")

## run the pipeline
save_dir <- runPipeline(
  ## input
  input_file=fastq1,
  input_file2=fastq2,
  paired_ends=TRUE,
  quality_encoding="illumina1.8",

  ## output
  save_dir="test",
  prepend_str="test",
  overwrite_save_dir="erase",

  ## aligner
  path_gsnap_genomes=path(directory(tp53Genome)),
  alignReads.genome=genome(tp53Genome),
  alignReads.additional_parameters="--indel-penalty=1 --novelsplicing=1 --distant-splice-penalty=1",
)
```
isSparse

## gene model
path.genomic_features=dirname(tp53GenomicFeatures),
countGenomicFeatures.gfeatures=basename(tp53GenomicFeatures)
)

## End(Not run)

---

isSparse

### Description
Check coverage for sparseness

### Usage
isSparse(cov, threshold = 0.1)

### Arguments
- **cov**: A cov object as SimpleRleList
- **threshold**: Fraction of number of runs over total length

### Details
Some Rle related operations become very slow when they are dealing with data that violates their sparseness assumption. This method provides an estimate about whether the data is dense or sparse. More precisely it checks if the fraction of the number of runs over the total length is smaller than a threshold

### Value
Boolean whether this object is dense or sparse

### Author(s)
Jens Reeder

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markDuplicates

### Description
Mark duplicates in bam

### Usage
markDuplicates(bamfile, outfile = NULL, path = getOption("picard.path"))
### Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>bamfile</td>
<td>Name of input bam file</td>
</tr>
<tr>
<td>outfile</td>
<td>Name of output bam file</td>
</tr>
<tr>
<td>path</td>
<td>Full path to MarkDuplicates jar</td>
</tr>
</tbody>
</table>

### Details

Use MarkDuplicates from PicardTools to mark duplicate alignments in bam file.

### Value

Path to output bam file

### Author(s)

Jens Reeder
**realignIndels**

**Description**
Realign indels in pipeline context

**Usage**
`realignIndels()`

**Details**
High level function call to realign indels in the analyzed.bam file using GATK

**Value**
Nothing

**Author(s)**
Jens Reeder

---

**realignIndelsGATK**

**Description**
Realign indels using the GATK tools RealignerTargetCreator and IndelRealigner. Requires a GATK compatible genome with a name matching the alignment genome to be installed in `path.gatk_genome`

**Usage**
`realignIndelsGATK(bam.file)`

**Arguments**
- `bam.file` Path to bam.file

**Details**
Since GATKs IndelRealigner is not parallelized, we run it in parallel per chromosome.

**Value**
Path to realigned bam file

**Author(s)**
Jens Reeder
runPipeline  

Run the NGS analysis pipeline

Description

Run the NGS analysis pipeline

Usage

runPipeline(...)

Arguments

... A list of parameters. See the vignette for details.

Details

This function starts the pipeline. It first preprocesses the input FASTQ reads, align them, count the read overlaps with genomic features and compute the coverage. See the vignette for details.

Value

The path to the NGS output directory.

Author(s)

Jens Reeder, Gregoire Pau

See Also

TP53Genome, TP53GenomicFeatures

Examples

```r
## Not run:
## build genome and genomic features
tp53Genome <- TP53Genome()
tp53GenomicFeatures <- TP53GenomicFeatures()

## get the FASTQ files
fastq1 <- system.file("extdata/H1993_TP53_subset2500_1.fastq.gz", package="HTSeqGenie")
fastq2 <- system.file("extdata/H1993_TP53_subset2500_2.fastq.gz", package="HTSeqGenie")

## run the pipeline
save_dir <- runPipeline(
  ## input
  input_file=fastq1,
  input_file2=fastq2,
  paired_ends=TRUE,
  quality_encoding="illumina1.8",

  ## output
  save_dir="test",
  prepend_str="test",
)```

runPipelineConfig

overwrite_save_dir="erase",

## aligner
path.gsnap_genomes=path(directory(tp53Genome)),
alignReads.genome=genome(tp53Genome),
alignReads.additional_parameters="--indel-penalty=1 --novelsplicing=1 --distant-splice-penalty=1",

## gene model
path.genomic_features=dirname(tp53GenomicFeatures),
countGenomicFeatures.gfeatures=basename(tp53GenomicFeatures)
)

## End(Not run)

runPipelineConfig

Run the NGS analysis pipeline

Description

Run the NGS analysis pipeline from a configuration file

Usage

runPipelineConfig(config_filename, config_update)

Arguments

config_filename
Path to a pipeline configuration file

config_update
A list of name value pairs that will update the config parameters

Details

This is the launcher function for all pipeline runs. It will do some preprocessing steps, then aligns the reads, counts overlap with genomic Features such as genes, exons etc and applies a variant caller.

Value

Nothing

Author(s)

Jens Reeder, Gregoire Pau
**setupTestFramework**  
*setup test framework*

**Description**

setup test framework

**Usage**

```r
setupTestFramework(config.filename, config.update = list(),
    testname = "test", package = "HTSeqGenie", use.TP53Genome = TRUE)
```

**Arguments**

- `config.filename`: configuration file
- `config.update`: update list of config values
- `testname`: name of test case
- `package`: name of package
- `use.TP53Genome`: Boolean indicating the use of the TP53 genome as template config

**Value**

the created temp directory

---

**TP53GenomicFeatures**  
*Demo genomic features around the TP53 gene*

**Description**

Build the genomic features of the TP53 demo region

**Usage**

```r
TP53GenomicFeatures()
```

**Details**

Returns a list of genomic features (gene, exons, transcripts) annotating a region of UCSC hg19 sequence centered on the region of the TP53 gene, with 1 Mb flanking sequence on each side. This is intended as a test/demonstration to run the NGS pipeline in conjunction with the LungCancerLines data package.

**Value**

A list of GRanges objects containing the genomic features

**Author(s)**

Gregoire Pau
vcfStat

See Also
TP53Genome, buildGenomicFeaturesFromTxDb, runPipeline

vcfStat Compute stats on a VCF file

Description
Compute stats on a VCF file

Usage
vcfStat(vcf.filename)

Arguments
vcf.filename A character pointing to a VCF (or gzipped VCF) file

Value
A numeric vector

Author(s)
Gregoire Pau

wrap.callVariants Variant calling

Description
Call Variants in the pipeline framework

Usage
wrap.callVariants(bam.file)

Arguments
bam.file Aligned reads as bam file

Details
A wrapper around VariantTools callVariant framework.

Value
Variants as Vranges

Author(s)
Jens Reeder
**Description**
Write variants to VCF file

**Usage**
```
writeVCF(variants.vranges, filename)
```

**Arguments**
- `variants.vranges`: Genomic Variants as VRanges object
- `filename`: Name of vcf file to write

**Value**
VCF file name

**Author(s)**
Jens Reeder
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