Package ‘HTSeqGenie’

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1.21.39), GenomicRanges (&gt;= 1.23.21), Rsamtools (&gt;= 1.8.5),
Biostrings (&gt;= 2.24.1), chipseq (&gt;= 1.6.1), hwriter (&gt;= 1.3.0),
Cairo (&gt;= 1.5.5), GenomicFeatures (&gt;= 1.9.31), BiocParallel,
parallel, tools, rtracklayer (&gt;= 1.17.19), GenomicAlignments,
VariantTools (&gt;= 1.7.7), GenomeInfoDb, SummarizedExperiment,
methods

Maintainer  Jens Reeder &lt;reeder.jens@gene.com&gt;
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 (&gt;= 3.0.0), gmapR (&gt;= 1.8.0), ShortRead (&gt;= 1.19.13),
VariantAnnotation (&gt;= 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

annotateVariants()

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
Value
Path to a vcf file with variant annotations

Author(s)
Jens Reeder

---

**buildGenomicFeaturesFromTxDb**

*Build genomic features from a TxDb object*

---

**Description**
Build genomic features from a TxDb object

**Usage**

```r
defineGenomicFeaturesFromTxDb(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**

```r
## 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

---

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**

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**

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

---

**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**

```r
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

**Description**

Detect reads that look like rRNA

**Usage**

```r
getRRNAIds(file1, file2 = NULL, tmp_dir, rRNADb)
```

**Arguments**

- **file1**: FastQ file of forward reads
- **file2**: FastQ of reverse reads in paired-end sequencing, NULL otherwise
- **tmp_dir**: temporary directory used for storing the gsnap results
- **rRNADb**: Name of the rRNA sequence database. Must exist in the gsnap 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**
```r
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**
```r
hashCoverage(cov)
```

**Arguments**
- `cov` A `SimpleRleList` object

**Value**
A numeric

**Author(s)**
Gregoire Pau
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<th><strong>Hashing function for variants</strong></th>
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**Description**

Hashing function for variants

**Usage**

`hashVariants(var)`

**Arguments**

- **var**  
  A GRanges object

**Value**

A numeric

**Author(s)**

Gregoire Pau

<table>
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**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

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

markDuplicates

Description
Mark duplicates in bam

Usage
markDuplicates(bamfile, outfil null, path = getOption("picard.path"))
Arguments

- **bamfile**: Name of input bam file
- **outfile**: Name of output bam file
- **path**: Full path to MarkDuplicates jar

Details

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

Value

Path to output bam file

Author(s)

Jens Reeder

Description

Mark duplicates in pipeline context

Usage

```r
markDups()
```

Details

High level function call to mark duplicates in the analyzed.bam file of a pipeline run.

Value

Nothing

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**
Realigning 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

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

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

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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