Package ‘chimera’

July 13, 2015

Type Package
Title A package for secondary analysis of fusion products
Version 1.10.0
Date 31 March 2015
Author Raffaele A Calogero, Matteo Carrara, Marco Beccuti, Francesca Cordero
Maintainer Raffaele A Calogero <raffaele.calogero@unito.it>
Depends Biobase, GenomicRanges (>= 1.13.3), Rsamtools (>= 1.13.1), GenomicAlignments, methods, AnnotationDbi, BSgenome.Hsapiens.UCSC.hg19, TxDb.Hsapiens.UCSC.hg19.knownGene, Homo.sapiens
Suggests BiocParallel, geneplotter
Enhances Rsubread, BSgenome.Musculus.UCSC.mm9, TxDb.Musculus.UCSC.mm9.knownGene, BSgenome.Musculus.UCSC.mm10, TxDb.Musculus.UCSC.mm10.knownGene, Mus.musculus, BSgenome.Hsapiens.NCBI.GRCh38, TxDb.Hsapiens.UCSC.hg38.knownGene
Description This package facilitates the characterisation of fusion products events. It allows to import fusion data results from the following fusion finders: chimeraScan, bellerophontes, deFuse, FusionFinder, FusionHunter, mapSplice, tophat-fusion, FusionMap, STAR, Rsubread, fusionCatcher.

biocViews Infrastructure

SystemRequirements STAR, TopHat, bowtie and samtools are required for some functionalities

License Artistic-2.0
NeedsCompilation yes

R topics documented:

  chimera-package .................................................. 2
  bam2fastq .......................................................... 4
chimera-package

A package for secondary analysis of fusion products

Description

The package imports fusion results from tophat-fusion, tophat-fusion-post, mapSplice, deFuse, fusionmap, bellerophontes, fusionfinder, fusionhunter, STAR, Rsubread, fusionCatcher. The package was design to facilitate the characterisation of fusion products events. Data upload: outputs for the above indicated fusion detection tools can be imported using `importFusionData` in a list of `fSet` objects. `fset-class` offers various methods to extract information from the `fSet` objects. The fusion names can be extracted with `fusionName` function. The number of reads supporting a fusion event can be extracted with the `supportingReads` function.

Filtering: The imported fusion list can be filtered using `filterList`
Annotation: Oncofuse can be installed in chimera with the function `oncofuseInstallation`. Various information on the fusions location, on structural and functional domains affected by the fusion event as well as a prediction of the putative functional effect of the fusion on the cell can be obtained by using `oncofuseRun`.

`chimeraSeqs` generates the nucleotide sequence of a fusion transcript described in an fSet object. `chimeraSeqSet` does the same but on a list of fSet objects.

`fusionPeptides` allows to investigate if the fusion events generate also a fusion at protein level.

`subreadRun` allows to remap reads on the fused transcripts reconstructed with `chimeraSeqs`.

Validation GapFiller is a seed-and-extend local assembler capable to produce (in-silico) longer and highly accurate sequences from a collection of Next Generation Sequencing reads. It can be installed in chimera with the function `gapfillerInstallation`. The function `gapfillerRun` allows to check if reads mapped by `subreadRun` over a fused transcript generated with `chimeraSeqs` are able to reconstruct by de novo assembly the fusion break-point.

Export The function `prettyPrint` converts the information stored in a list of fSet objects in a dataframe structure that is saved as tab delimited file.

**Details**

<table>
<thead>
<tr>
<th>Package</th>
<th>chimera</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type</td>
<td>Package</td>
</tr>
<tr>
<td>Version</td>
<td>1.0</td>
</tr>
<tr>
<td>Date</td>
<td>2014-31-07</td>
</tr>
<tr>
<td>License</td>
<td>Artistic-2.0</td>
</tr>
</tbody>
</table>

**Author(s)**

Raffaele A Calogero Maintainer: Raffaele A Calogero <raffaele.calogero@unito.it>

**References**

bam2fastq

A function to extract pair end reads from the bam file generated with subreadRun function

Description

A function to extract pair end reads from the bam file generated with subread function. The output files are ready to be used for fusion validation with gapfiller.

Usage

bam2fastq(bam, filename="ready4gapfiller", ref, parallel=FALSE)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>bam</td>
<td>name of the bam file to be used for PE reads extraction</td>
</tr>
<tr>
<td>filename</td>
<td>base name for the PE fastq output data</td>
</tr>
<tr>
<td>ref</td>
<td>name of the fusion sequence that was used as reference</td>
</tr>
<tr>
<td>parallel</td>
<td>option that allow the use of BioParallel package</td>
</tr>
</tbody>
</table>

Value

PE fastq files

Author(s)

Raffaele A Calogero

Examples

```r
# if(require(Rsubread)){
# subreadRun(ebwt=paste(find.package(package="chimera"),"/examples/SULF2_ARFGEF2.fa",sep=""),
#     input1=paste(find.package(package="chimera"),"/examples/mcf7_sample_1.fq",sep=""),
#     input2=paste(find.package(package="chimera"),"/examples/mcf7_sample_2.fq",sep=""),
#     outfile.prefix="accepted_hits", alignment="se", cores=1)
# ref.name <- names(readDNAStringSet(paste(find.package(package="chimera"),"/examples/SULF2_ARFGEF2.fa",sep=""))
# bam2fastq(bam="accepted_hits.bam", filename="ready4gapfiller", ref=ref.name, parallel=F)
# }
```
breakpointOverlaps

A function to extract the reads overlapping to fusion breakpoint.

Description
A function to extract the reads overlapping to fusion breakpoint.

Usage
breakpointOverlaps(fset, plot=FALSE, ylim=NULL)

Arguments
- fset: An fSet object. The slots fusionRNA and fusionGA needs to be loaded
- plot: If FALSE plot is not printed
- ylim: If NULL it uses the full fusion transcript coverage to define the ylim of the plot. If setted it can be used to zoom in the plot to better see the structure of the coverage at the break point

Value
An object of GAlignment class. A plot of the fusion transcript coverage in blue and of the reads spanning over the break point in yellow.

Author(s)
Raffaele A Calogero

Examples
load(paste(find.package(package="chimera"), "/examples/fset_ARFGEF2-SULF2.rda", sep=""))
my.seq <- chimeraSeqs(my.fset)
my.fset <- addRNA(my.fset, my.seq)
tmp <- breakpointOverlaps(my.fset)

chimeraSeqs
A function to generate the nucleotide sequences of a fusion event

Description
A function generating the nucleotide sequences of a chimera.

Usage
chimeraSeqs(fset, extend=1000, type="transcripts")
chimeraSeqSet

Description

A function generating the nucleotide sequences of chimeras described in a list of fSet, i.e. the list generated using importFusionData function.

Usage

chimeraSeqSet(list, parallel=FALSE)
defuseTPTN

Arguments

  list  A list of fSet objects.
  parallel  If TRUE uses the BioParallel package

Value

A DNAStringSet encompassing the fusions described in a list of fSet objects. This object represents the ideal reference to remap reads over detected fusions. Remapping is required to validate fusions using GapFiller de novo reconstruction.

Author(s)

Raffaele A Calogero

See Also

  fusionName, importFusionData, gapfillerInstallation, gapfillerRun

Examples

  tmp <- importFusionData("fusionmap", paste(find.package(package="chimera"),"/examples/mcf7.FMFusionReport", sep=
  fusion.names <- fusionName(tmp)
  fusion.names
  myset <- tmp[1:3]
  tmp.seq <- chimeraSeqSet(myset, parallel=FALSE)
  # sapply(tmp.seq, function(x){writeXStringSet(x, "detected.fusions.fa", format="fasta", append=TRUE)))
filterList

A function to filter a list of fSet objects

Description

A function filtering a list of fSet objects on the basis of various parameters.

Usage

filterList(x,type=c("spanning.reads","fusion.names","intrinsic","annotated.genes","read.through"),

Arguments

x a list of fSet object
type filtering can be performed on the basis of spanning.reads: a minimal number of
spanning reads, fusion.names: a vector list of user defined fusion names, in-
trinsic: only fusion encompassing exon data are retained annotated.genes: only
fusion encompassing two annotated genes are retained read.through: only fu-
sion with different gene names are retained oncofuse: using the output of onco-
fuseRun various filtering option can be applied using oncofuse.type and onco-
fuse.threshold
oncofuse.output The output generated with oncofuseRun
query query is a number. In case spanning.reads is selected or a vector of fusion names
if the case fusion.names is selected. In case type is intrinsic query is NULL. In
the latter case fusion having one of the elements located in an intrinsic region
are discarded. In the case of oncofuse.type equal to passenger.prob or expres-
sion.gain query is the threshold number to be used for the filtering
oncofuse.type This refers to the filtering based on the output of oncofuse that can be generated
using the oncofuseRun function. g5CDS selects only fusions having the break-
point in 5' end gene CDS, g3CDS selects only fusions having the breakpoint in
3' end gene CDS, g5g3CDS selects only fusions having the breakpoint in both
gene CDSs, g5exon selects only fusions having the breakpoint in an exon of 5'
end gene, g3exon selects only fusions having the breakpoint in an exon of 3'
end gene, g5g3exon selects only fusions having the breakpoint in an exon of
both genes. In the case of oncofuse.type equal to driver.prob the filter will use
the probability of the fusion to be a tumor driver. In the case of oncofuse.type
equal to expression.gain the filter will use the score that suggests the presence
of a gain in expression
parallel option to run a parallel version of the function, default FALSE

Examples

tptn <- defuseTPTN()
**filterSamReads**

A function to filter SAM or BAM files

**Description**

A function to filter SAM or BAM files using picard-tools

**Usage**

```r
filterSamReads(input, output, filter=c("includeAligned","excludeAligned"))
```

**Arguments**

- **input**: SAM/BAM file to be validated
- **output**: file name in which to save the filtered results
- **filter**: type of filter

**Value**

A filtered SAM/BAM.

**Author(s)**

Raffaele A Calogero

**See Also**

- `picardInstallation`

**Examples**

```r
# filterSamReads(input="kd2_accepted_hits2.sam", output="kd2_accepted_hits2_mapped.sam", filter="includeAligned")
```
fSet

Class fSet, a class represent fusion data, and methods for processing it

Description

This is class representation for a fusion event.

Slots

- **fusionInfo** A list: fusionTool: the tool that has generated the fusions UniqueCuttingPositionCount: the number of unique cutting positions detected for the fusion. SeedCount: the number of reads overlapping the break-point, i.e. spanning reads (FusionMap, FusionHunter, mapSplice, Tophat-fusion, ChimeraScan, STAR, Rsubread, FusionCatcher). Both spanning and encompassing reads (Bellerophontes, FusionFinder). Encompassing reads, i.e. one read of a pair on gene 1, and the other on gene 2 (deFuse). RescuedCount: the number of reads overlapping the break-point rescued after identification of the break point (FusionMap). Encompassing reads (Tophat-fusionm Tophat-fusion-post, FusionCatcher, STAR). Both spanning and encompassing reads (ChimeraScan, Rsubread). SplicePattern: the splice pattern for a fusion junction FusionGene: the name of the fusion gene in the format gene1 -> gene2. frameShift: frameshift at break-point

- **fusionLoc** A GRangesList encompassing fusion locations for gene 1 and 2

- **fusionRNA** A DNAStringSet encompassing the fusion transcript that can be generated by chimeraSeqs function.

- **fusionGA** A GAlignments object encompassing positions for all reads mapping on the DNAStringSet located in fusionRNA slot

Methods

Standard generic methods:

- **fusionData(fSet)** An accessor function used to retrieve information for a fusion
- **fusionGRL(fSet)** An accessor function used to retrieve GRangesList encompassing fusion locations for gene 1 and 2
- **fusionRNA(fSet)** An accessor function used to extract the DNAStringSet
- **addRNA(fSet, rna)** An accessor function used to add the DNAStringSet to the fset object
- **fusionGA(fSet)** An accessor function used to extract the GAlignments object
- **addGA(fSet, bam)** An accessor function used to add the GAlignments object to the fSet object

Constructor

```r
newfSet newfSet(fusionInfo = list(), fusionLoc = GRangesList(), fusionRNA, fusionGA)
```

This creates a fSet object.

- fusionInfo A list of the fusion characteristics see above slot fusionInfo
- fusionLoc A GRangesList encompassing the fusion break points
fusionName A function to extract fusion names for a list of fSet object

Description
A function allowing extract fusion names from a list of fSet objects.

Usage
fusionName(list, parallel=FALSE)

Arguments
  list a list of fSet object
  parallel option to run a parallel version of the function, default FALSE

Examples
# creating a fusion report from output of fusionMap
tmp <- importFusionData("fusionmap", paste(find.package(package="chimera"),"/examples/mcf7.FMFusionReport", sep="", collapse=""))
# extracting the fusions names
fusion.names <- fusionName(tmp)
fusion.names
# extracting the fSet object ofr one of the fusions
myset <- tmp[[1]]
# constructing the fused sequence(s)
trs <- chimeraSeqs(myset, type="transcripts")
# adding the sequences to the fSet object
myset <- addRNA(myset, trs)
# extracting sequences from an fSet object
tmp.seq <- fusionRNA(myset)
# adding reads mapped on the fusion generated using tophatRun function
myset <- addGA(myset, paste(path.package(package="chimera"),"/examples/mcf7_trs_accepted_hits.bam",sep=""))
# extracting the GAlignments from an fSet object
ga <- fusionGA(myset)
**fusionPeptides**

**Author(s)**

Raffaele A Calogero

**Examples**

```r
tmp <- importFusionData("fusionmap", paste(find.package(package="chimera"), "/examples/mcf7.FM FusionReport", sep="/"))
fusion.names <- fusionName(tmp)
fusion.names
```

**Description**

A function to investigate the peptides involved in the fusion event.

**Usage**

```r
fusionPeptides(chimeraSeq.output, annotation="hsUCSC")
```

**Arguments**

- `chimeraSeq.output`  
  DNAStringSet encompassing the fusion event of interest, generated by chimeraSeq function
- `annotation`  
  The annotation used to retrieve the UCSC names of the transcripts involved in the fusion

**Value**

An list encompassing:

- **AAStringSet**  
  encompassing: fusion sequence, peptide from p1 and peptide from p2. In case the peptides are not in frame the AAStringSet will not contain the fusion sequence
- **DNAStringSet**  
  encompassing the fusion transcript

**Author(s)**

Raffaele A Calogero

**Examples**

```r
tmp <- importFusionData("fusionmap", paste(find.package(package="chimera"), "/examples/mcf7.FM FusionReport", sep="/"))
fusion.names <- fusionName(tmp)
fusion.names
myset <- tmp[1:3]
tmp.seq <- chimeraSeqSet(myset, parallel=FALSE)
tmpx <- lapply(tmp.seq,fusionPeptides)
```
**Description**


**Usage**

gapfillerInstallation(os=c("mac64","unix64"))

**Arguments**

- **os**  
  The supported operating systems

**Author(s)**

Raffaele A Calogero

**See Also**

gapfillerRun

**Examples**

#gapfillerInstallation(os="mac64")

---

**Description**

A function that uses GapFiller to confirm, by de novo assembly, the presence of the fusion break point. The function needs as input the fusion transcript generated by chimeraSeqs function and two fastq files corresponding to the reads mapping over the fusion transcript.

**Usage**

gapfillerRun(fusion.fa, seed1, seed2, gapfiller=NULL, seed.ins=200, seed.var=50, block.length=5, overlap=20, max.length=5000, slack=30, k=6, global.match=5)
**Arguments**

- `fusion.fa` fasta file with the fusion transcript
- `seed1` The R1 fastq of a pair-end
- `seed2` The R2 fastq of a pair-end
- `gapfiller` path to GapFiller executable program
- `seed.ins` seed reads insert size
- `seed.var` seed reads insert variation
- `block.length` length of perfect match
- `overlap` minimum suffix-prefix overlap
- `max.length` print only contigs <= max-length long
- `slack` number of overlaps: suffix-prefix overlap range is given by overlap, overlap + slack
- `k` length of the word used to hash
- `global.mismatch` maximum number of mismatches between mate and contig

**Value**

The program will write in a temporary directory contigs.fasta and contig.stats, which are used to evaluate if the de novo assembly allows the identification of the fusion break point. The function returns a list of three objects. The list is returned only in case that some of de novo assemblies cover the breakpoint junction. The list is made of:

- `contigs` which is a PairwiseAlignments object
- `junction.contigs` which is a DNAStringSet encompassing the sequences present in the contigs object
- `fusion` which is a DNAStringSet object encompassing the fusion transcript

**Author(s)**

Raffaele A Calogero

**See Also**

`chimeraSeqs`, `gapfillerInstallation`

**Examples**

```r
# tmp <- gapfillerRun(fusion.fa=paste(path.package("chimera", quiet = FALSE),"/examples/uc002xvp.1-243_uc002iyu
```
gapfillerWrap

A function to prepare files and to run gapfiller

Description

A function that uses GapFiller to confirm, by de novo assembly, the presence of the fusion break point. The function needs as input a list of fusion transcript generated by chimeraSeqSet function and the bam file containing the reads remapped over the fusion transcripts made using subreadRun.

Usage

gapfillerWrap(chimeraSeqSet.out, bam, parallel=c(FALSE,TRUE))

Arguments

- chimeraSeqSet.out: a list of DNAStringSet output from chimeraSeqSet
- bam: bam file containing the reads remapped over the fusion transcripts using Rsubread
- parallel: if FALSE FALSE no parallelization, if TRUE TRUE full parallelization, if FALSE TRUE only parallelization for internal functions

Value

The program will write in a temporary directory contigs.fasta and contig.stats, which are used to evaluate if the de novo assembly allows the identification of the fusion break point. The function returns for each fusion a list of three objects. The list is returned only in case that some of de novo assemblies cover the breakpoint junction. The list is made of:

- contigs: which is a PairwiseAlignments object
- junction.contigs: which is a DNAStringSet encompassing the sequences present in the contigs object
- fusion: which is a DNAStringSet object encompassing the fusion transcript

Author(s)

Raffaele A Calogero

See Also

chimeraSeqs, gapfillerInstallation, gapfillerRun

Examples

```r
#tmp <- importFusionData("star", "Chimeric.out.junction", org="hg19", min.support=100)
#myset <- tmp[1:4]
#tmp.seq <- chimeraSeqSet(myset, type="transcripts")
#tmp <- gapfillerWrap(chimeraSeqSet.out=trsx, bam="accepted_hits_mapped.bam", parallel=c(FALSE,TRUE))
```
importFusionData  

*A function to import fusion data detected by different fusion finders*

**Description**

A function to import in a list fusions data detected by bellerophontes, defuse, fusionfinder, fusionhunter, mapspliace, tophat-fusion, fusionmap, chimerascan, STAR, Rsubread, fusionCatcher. In the case of chimerascan and STAR output it is possible to load the data applying a filter on the minimal number of reads supporting a specific fusion. Both chimerascan and STAR accept data generated using human hg19, hg38, mouse mm9 and mm10 reference. IMPORTANT: please note that the it is important that the genome reference version used for the alignment is the same of that used for by chimera for annotation. Especially between hg38 and hg19 there are shifts in gene location.

**Usage**

`importFusionData(format, filename, ...)`

**Arguments**

- **format**  Format allows to select the data structure to be imported. One of the following keyword need to be associated to format parameter: bellerophontes, defuse, fusionfinder, fusionhunter, mapspliace, tophat-fusion, fusionmap, chimerascan, star, rsubread, fusioncatcher.

- **filename**  The file generated by one of the fusion finders defined in format

- **...**  Additional parameters: In case of rsubread min.distance, which indicates the minimal distance to consider a fusion within the same chromosome, is set to 700000 as default. In case of rsubread, chimerascan and STAR min.support, which indicates the minimal number of reads supporting a specific fusion, is set to 10 as default. Please remember that using low values as min.support, e.g. 1, will significantly increase the time for data import. In this case is strongly suggested to run the function as batch and, when available, using the parallel option, see below. In case of chimerascan, STAR, Rsubread, fusionmap, fusioncatcher, tophat-fusion, tophat-fusion-post, mapspliace, bellerophontes org, which indicates the organism to be used for annotation, has the following options: hg19, hg38, mm9, mm10. In case of STAR and Rsubread the upload can be parallelized using parallel=TRUE

**Author(s)**

Raffaele A Calogero

**Examples**

```r
tmp <- importFusionData("fusionmap", paste(find.package(package="chimera"),"/examples/mcf7.FMFusionReport"), min.support=10, org="hg19")
#download Edgren Chimeric.out.junction. This file encompass the results obtaines combined all cell lines used```

is.fSet

A function to evaluate if an object belongs to `fSet` class or not

**Description**

A function to evaluate if an object belongs to `fSet` class or not.

**Usage**

```r
is.fSet(x)
```

**Arguments**

- `x` an object

**Value**

If the object belongs to `fSet` class it returns `TRUE`, else it returned `FALSE`.

**Author(s)**

Raffaele A Calogero

**Examples**

```r
tmp <- importFusionData("fusionmap", paste(find.package(package="chimera"), "/examples/mcf7.FMFusionReport", sep=""), sep="")
is.fSet(tmp[[1]])
```

---

mhmakeRandomString

A function generating a random string

**Description**

A function generating a random string.

**Usage**

```r
mhmakeRandomString()
```

**Value**

- a string
newfSet

Author(s)
Raffaele A Calogero

Examples

tmp.file <- paste(HmakeRandomString(),".fa", sep="")

tmp <- newfSet()
tmp
oncofuseInstallation

A function to download oncofuse

Description

A function allowing the download of oncofuse in the chimera folder. Oncofuse requires java

Usage

oncofuseInstallation()

Author(s)

Raffaele A Calogero

See Also

oncofuseRun

Examples

#oncofuseInstallation()

oncofuseRun

A function to annotate fusions with Oncofuse. Oncofuse is a naive bayesian classifier. Its goal is to identify those fusion sequences with higher probability of being driver than passenger events

Description

A list of fSet objects can be annotated using the Oncofuse java application.

Usage

oncofuseRun(listfSet, tissue=c("EPI","HEM","MES","AVG"), org=c("hg19","hg38"), threads=1, plot=FALSE)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>listfSet</td>
<td>A list of fSets</td>
</tr>
<tr>
<td>tissue</td>
<td>Type of tissue in which the fusion was detected. EPI epithelial, HEM hematological, MES mesenchimal, AVG average expression</td>
</tr>
<tr>
<td>org</td>
<td>Supported genome assembly version. IMPORTANT: the genome version used for the fusion detection and for the oncofuse analysis need to be same</td>
</tr>
<tr>
<td>threads</td>
<td>number of threads that Oncofuse will use</td>
</tr>
</tbody>
</table>
plot: plotting the expression gain score versus the passenger mutation probability. For more info please see Shugay et al. Bioinformatics 2013:29,2539

type: listfSet a list of fSet objects or coordDf a dataframe of coordinates of fusions in the format required by Oncofuse

Value
The output is a dataframe containing the output of Oncofuse. For more info on Oncofuse please see Shugay et al. Bioinformatics 2013, 29, 2539.

Author(s)
Raffaele A Calogero

Examples
```r
#tmp <- importFusionData("fusionmap", paste(find.package(package="chimera"), "/examples/mcf7.FMFusionReport", sep=""))
#installOncofuse()
#of.out <- oncofuseRun(tmp, tissue="EPI")
```

---

### picardInstallation

**A function to download picard-tools**

**Description**
A function allowing the download of picard-tools in the chimera folder. Picard tools require java

**Usage**
```r
picardInstallation()
```

**Author(s)**
Raffaele A Calogero

**Examples**
```r
#picardInstallation()
```
plotCoverage

A function to plot the coverage of a fusion gene

Description
A function to plot the coverage of a fusion gene.

Usage

plotCoverage(fset, plot.type=c("exons","junctions"), junction.spanning=20, fusion.only=FALSE, xlab="nt", ylab="coverage", main="Blat of target coverage", col.box1="red", col.box2="green", ybox.lim=c(-4,-1))

Arguments

fset A fSet object
plot.type exons plot exons coverage as junctions plot coverage of junction between exons
junction.spanning number of nucleotides located upstream and downstream the junction/fusion location
fusion.only if TRUE only fusion coverage is plotted
xlab x-axis label
ylab y-axis label
main Plot title
col.box1 color of the box describing the first gene
col.box2 color of the box describing the second gene
ybox.lim y range defining the height of the box representing the exons

Author(s)
Raffaele A Calogero

See Also
fusionName, chimeraSeqs

Examples

```r
tmp <- importFusionData("fusionmap", paste(find.package(package="chimera"),"/examples/mcf7.FMFusionReport", sep=""))
fusion.names <- fusionName(tmp)
myset <- tmp[13]
trs <- chimeraSeqs(myset, type="transcripts")
myset <- addRNA(myset, trs)
tmp.seq <- fusionRNA(myset)
myset <- addGA(myset, paste(path.package(package="chimera"),"/examples/mcf7_trs_accepted_hits.bam",sep=""))
ga <- fusionGA(myset)
plotCoverage(myset, plot.type="exons", col.box1="red", col.box2="green", ybox.lim=c(-4,-1))
```
prettyPrint

A function to represent a list of fSet as a dataframe

Description

A function reorganizing a list of fSet in a dataframe structure. The dataframe is then saved in a tab delimited file.

Usage

prettyPrint(list, filename, fusion.reads=c("all", "spanning"))

Arguments

list a list of fSet object
filename the name of the file in which the dataframe is printed
fusion.reads it allows to extract spanning reads associated to the SeedCount slot or all the detected reads associate to the RescuedCount

Author(s)

Raffaele A Calogero

Examples

#tmp <- importFusionData("fusionmap", paste(find.package(package="chimera"), "/examples/mcf7.FMFusionReport", sep=""))
#fusion.names <- fusionName(tmp)
#tmp1 <- filterlist(tmp, type="fusion.names", fusion.names[c(1,3,7)], parallel=FALSE)
#prettyPrint(tmp1, "tmp1.df.txt", fusion.reads="spanning")

removingErrorLine

A function to remove a line stopping SAM to BAM conversion

Description

A function to remove a line stopping SAM to BAM conversion

Usage

removingErrorLine(line.number, filenameIn, filenameOut)
*starInstallation*

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>line.number</td>
<td>line number to be removed</td>
</tr>
<tr>
<td>filenameIn</td>
<td>input file name</td>
</tr>
<tr>
<td>filenameOut</td>
<td>output file name</td>
</tr>
</tbody>
</table>

**Value**

SAM file without the error line

**Author(s)**

Raffaele A Calogero

**Examples**

```r
#removingErrorLine(14680066,"kd2_accepted_hits.sam","kd2_accepted_hits1.sam")
```

---

**Description**

A function allowing the download and installation of STAR (Dobin et al. Bioinformatics 2012) in chimera package folder. The function also creates soft links in the user bin folder to allow the call of the above mentioned program.

**Usage**

```r
starInstallation(binDir, os=c("unix","mac"))
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>binDir</td>
<td>The user bin folder</td>
</tr>
<tr>
<td>os</td>
<td>The supported operating systems</td>
</tr>
</tbody>
</table>

**Author(s)**

Raffaele A Calogero

**Examples**

```r
#starInstallation(binDir="/somewhere/inyourpc/bin", os="mac")
```
starReads  

*A function to extract reads info from STAR fusion output*

**Description**

A function producing a GRRangeList for the reads information, involved in a fusion event.

**Usage**

```r
starReads(fusion.report, parallel=FALSE)
```

**Arguments**

- `fusion.report`: STAR fusion output file
- `parallel`: option to run a parallel version of the function, default FALSE

**Author(s)**

Raffaele A Calogero

**Examples**

```r
#tmp <- starReads("Chimeric.out.junction", parallel=FALSE)
```

starRun  

*A function to generate a bam file for fusions coverage evaluation*

**Description**

A function mapping reads to a chimera sequence set. The bam produced by this remapping on a putative fusion will be used to plot the coverage data for all the fused constructs. The function assumes that STAR is installed and located in the path.

**Usage**

```r
starRun(input1, input2, cores=1, star= "STAR", samtools="samtools", fa, alignment=c("se","pe"), chimsegmen
```
subreadRun

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>input1</td>
<td>The R1 fastq of a pair-end</td>
</tr>
<tr>
<td>input2</td>
<td>The R2 fastq of a pair-end</td>
</tr>
<tr>
<td>cores</td>
<td>number of cores to be used by tophat with program name, e.g. /somewhere/tophat</td>
</tr>
<tr>
<td>star</td>
<td>full path of STAR with program name, e.g. /somewhere/STAR</td>
</tr>
<tr>
<td>samtools</td>
<td>full path of samtools</td>
</tr>
<tr>
<td>fa</td>
<td>full path and name of the fasta file of one of the set of fusions of interest, to be used to build the STAR database. The fusion nucleotide sequences was generated with the function chimeraSeqs</td>
</tr>
<tr>
<td>alignment</td>
<td>se means that both fastq files from the pair-end run are concatenated, pe means that tophat will use fastq files in pair-end mode</td>
</tr>
<tr>
<td>chimSegmentMin</td>
<td>STAR fusion parameter, see STAR manual</td>
</tr>
<tr>
<td>chimJunctionOverhangMin</td>
<td>STAR fusion parameter, see STAR manual</td>
</tr>
</tbody>
</table>

Value

The function create a folder called chimeraDB_time, where time is the time when the folder was created. STAR output will be located in the folder output_time, where time is the time when the folder was created. The bam file of interest is accepted_hits.bam.

Author(s)

Raffaele A Calogero

See Also

chimeraSeqs

Examples

```r
#starRun(input1=paste(find.package(package="chimera"),"/examples/mcf7_sample_1.fq",sep=""), input2=paste(find.package(package="chimera"),"/examples/mcf7_sample_2.fq",sep=""), cores=1)
```

Description

A function mapping reads to a chimera sequence set. The bam produced by this remapping on a putative fusion will be used to plot the coverage data for all the fused constructs. The function uses Rsdesktop aligner for MAC and UNIX OS. In case WINDOWS OS Rbowtie is used.

Usage

```r
subreadRun(ebwt,input1, input2, outfile.prefix="accepted_hits", alignment=c("se","pe"),cores=1)
```
supportingReads

**Arguments**

- **ebwt**: Full path and name of the fasta file of one of the set of fusions of interest, to be used to build the index database. The fusion nucleotide sequences can be generated with the function `chimeraSeqs`.
- **input1**: The R1 fastq of a pair-end.
- **input2**: The R2 fastq of a pair-end.
- **outfile.prefix**: Prefix of the output bam file. Default is `accepted_hits`.
- **alignment**: se means that both fastq files from the pair-end run are concatenated, pe means that tophat will use fastq files in pair-end mode.
- **cores**: Number of cores to be used by the aligner.

**Value**

Standard bam file output. The bam file name by default is `accepted_hits.bam`.

**Author(s)**

Raffaele A Calogero

**See Also**

`chimeraSeqs`

**Examples**

```r
if(require(Rsubread)){
  subreadRun(ebwt=paste(find.package(package="chimera"),"/examples/SULF2_ARFGEF2.fa",sep=""),
input1=paste(find.package(package="chimera"),"/examples/mcf7_sample_1.fq",sep=""),
input2=paste(find.package(package="chimera"),"/examples/mcf7_sample_2.fq",sep=""),
outfile.prefix="accepted_hits", alignment="se", cores=1)
}
```

**supportingReads**

A function to extract supporting reads values from a list of `fSet` object.

**Description**

A function extracting supporting reads values from a list of `fSet` objects. Please note that not all outputs of supported tools provides both spanning reads, i.e. pair-end reads having one of the two mates spanning over the break point, and encompassing reads, i.e. pair-end reads having the two mates mapping on the exons of the two transcripts involved in the fusion. The presence of both type of reads is mandatory to provide the full number of reads covering the junction region. To know which information are provided by the supported tool please check `fSet`.

**Usage**

```r
supportingReads(list, fusion.reads=c("encompassing","spanning"), parallel=FALSE)
```
**tophatInstallation**

**Arguments**

- `list` a list of fSet objects
- `fusion.reads` it allows to extract spanning reads associated to the SeedCount slot or encompassing reads associated to the RescuedCount
- `parallel` option to run a parallel version of the function, default FALSE

**Author(s)**

Raffaele A Calogero

**Examples**

```r
tmp <- importFusionData("fusionmap", paste(find.package(package="chimera"),"/examples/mcf7.FMFusionReport", sep=" "))
supporting.reads <- supportingReads(tmp, fusion.reads="spanning")
supporting.reads
```

**Description**

A function allowing the download and installation of tophat, bowtie and samtools in chimera package folder. The function also creates soft links in the user bin folder to allow the call of the above mentioned programs.

**Usage**

```r
tophatInstallation(binDir, os=c("unix","mac"))
```

**Arguments**

- `binDir` The user bin folder
- `os` The supported operating systems

**Author(s)**

Raffaele A Calogero

**Examples**

```r
#tophatInstallation(binDir="/somewhere/inyourpc/bin", os="mac")
```
tophatRun

A function to generate a bam file for fusions coverage evaluation

Description

A function mapping reads to a chimera sequence set. The bam produced by this remapping on a putative fusion will be used to plot the coverage data for all the fused constructs. The function assumes that tophat is installed and located in the path. To run TopHat a softlink to bowtie or bowtie2 need to located in the user bin dir

Usage

tophatRun(input1, input2, output, cores=1, bowtie=c("bowtie","bowtie2"), tophat= "tophat", ebwt=paste0("/", getwd(), "\nmychimera\nf.fa"), alignment=c("se","pe"))

Arguments

input1 The R1 fastq of a pair-end
input2 The R2 fastq of a pair-end
output Folder in which tophat will generate the output
cores number of cores to be used by tophat with program name, e.g. /somewhere/tophat
bowtie selecting bowtie or bowtie2 aligner
tophat full path of tophat
ebwt full path and name of the fasta file of one of the set of fusions of interest, to be used to build the bowtie database. The fusion nucleotide sequences was generated with the function chimeraSeqs
alignment se means that both fastq files from the pair-end run are concatenated, pe means that tophat will use fastq files in pair-end mode

Value

TopHat standard output. The bam file of interest is accepted_hits.bam. The bam file will be then loaded in the slot fusionsLoc of the fSetSummary object from which fusions were retrieved.

Author(s)

Raffaele A Calogero

See Also

chimeraSeqs

Examples

#tophatRun(input1=paste(find.package(package="chimera"),"/examples/mcf7_sample_1.fq",sep=""), input2=paste(find...
validateSamFile  

A function to validate SAM or BAM files

Description

A function to validate SAM or BAM files using picard-tools

Usage

validateSamFile(input, output, mode=c("VERBOSE", "SUMMARY"), max.output="100")

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>input</td>
<td>SAM/BAM file to be validated</td>
</tr>
<tr>
<td>output</td>
<td>file name in which to save the validation information</td>
</tr>
<tr>
<td>mode</td>
<td>Mode of output. Default value: VERBOSE</td>
</tr>
<tr>
<td>max.output</td>
<td>max number of reported error lines</td>
</tr>
</tbody>
</table>

Value

Validation information referring to a SAM/BAM file.

Author(s)

Raffaele A Calogero

See Also

picardInstallation

Examples

#validateSamFile(input=paste(find.package(package="chimera"),'/examples/mcf7_trs_accepted_hits.bam',sep=""), output= validation_results.txt, mode="summary", max.output=100)
Index

*Topic **classes**
  fSet, 10

*Topic **package**
  chimera-package, 2

*Topic **utilities**
  bam2fastq, 4
  breakpointOverlaps, 5
  chimeraSeqs, 5
  chimeraSeqSet, 6
  defuseTPTN, 7
  filterList, 8
  filterSamReads, 9
  fusionName, 11
  fusionPeptides, 12
  gapfillerInstallation, 13
  gapfillerRun, 13
  gapfillerWrap, 15
  importFusionData, 16
  is.fSet, 17
  MHHmakeRandomString, 17
  newfSet, 18
  oncofuseInstallation, 19
  oncofuseRun, 19
  picardInstallation, 20
  plotCoverage, 21
  prettyPrint, 22
  removingErrorLine, 22
  starInstallation, 23
  starReads, 24
  starRun, 24
  subreadRun, 25
  supportingReads, 26
  tophatInstallation, 27
  tophatRun, 28
  validateSamFile, 29

  addGA (fSet), 10
  addGA, fSet-method (fSet), 10
  addRNA (fSet), 10
  addRNA, fSet-method (fSet), 10

  bam2fastq, 4
  breakpointOverlaps, 5
  chimera (chimera-package), 2
  chimera-package, 2
  chimeraSeqs, 3, 5, 11, 14, 15, 21, 25, 26, 28
  chimeraSeqSet, 3, 6, 6
  defuseTPTN, 7
  filterList, 2, 8
  filterSamReads, 9
  fSet, 2, 3, 10, 26
  fSet-class (fSet), 10
  fusionData (fSet), 10
  fusionData, fSet-method (fSet), 10
  fusionGA (fSet), 10
  fusionGA, fSet-method (fSet), 10
  fusionGRL (fSet), 10
  fusionGRL, fSet-method (fSet), 10
  fusionName, 2, 6, 7, 11, 21
  fusionPeptides, 3, 11, 12
  fusionRNA (fSet), 10
  fusionRNA, fSet-method (fSet), 10
  gapfillerInstallation, 3, 7, 13, 14, 15
  gapfillerRun, 3, 7, 13, 15
  gapfillerWrap, 15

  importFusionData, 2, 7, 16
  is.fSet, 17
  MHHmakeRandomString, 17
  newfSet, 18
  newfSet, fSet-method (fSet), 10
  oncofuseInstallation, 3, 19
  oncofuseRun, 3, 11, 19, 19
  picardInstallation, 9, 20, 29
INDEX

plotCoverage, 21
prettyPrint, 3, II, 22

removingErrorLine, 22

starInstallation, 23
starReads, 24
starRun, 24
subreadRun, 3, 25
supportingReads, 2, 26

tophatInstallation, 27
tophatRun, 28

validateSamFile, 29