Package ‘chimera’

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Type Package
Title A package for secondary analysis of fusion products
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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 Rsamtools, BSgenome.Mmusculus.UCSC.mm9,
TxDb.Mmusculus.UCSC.mm9.knownGene,
BSgenome.Mmusculus.UCSC.mm10,
TxDb.Mmusculus.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 fu-
sion data results from the following fusion finders: chimeraScan, bellerophontes, deFuse, Fusion-
Finder, 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:

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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**

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</table>

**Author(s)**

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

**References**


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**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)`
breakpointOverlaps

Arguments

bam name of the bam file to be used for PE reads extraction
filename base name for the PE fastq output data
ref name of the fusion sequence that was used as reference
parallel option that allow the use of BioParallel package

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

```r
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.
chimeraSeqs

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")

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>fset</td>
<td>A fSet object.</td>
</tr>
<tr>
<td>extend</td>
<td>number of nucleotides used to extend a genomic region that is not an annotated gene. Default is 1000 nts</td>
</tr>
<tr>
<td>type</td>
<td>Chimera can be build at transcript level, i.e. transcript level will generate multiple fusion transcripts depending of the number of transcripts associated to each of the two genes involved in the fusion.</td>
</tr>
</tbody>
</table>

Value
A DNAStringSet encompassing the fusions generated using all the isoforms for each gene involved in the fusion. The name of each element of the DNAStringSet has the following format: gene1-lengthOfGeneFragment:gene2-lengthOfGeneFragment. In case the fusion junction is located in an intronic sequence, a warning is provided. The presence of a partial intron in the fusion is an indication that the fusion does not generate an active chimeric peptide.

Author(s)
Raffaele A Calogero

See Also
fusionName, chimeraSeqSet
chimeraSeqSet

A function to generates DNAStringSet encompassing fusion sequences

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)

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 <- chimeraSeqs(myset, type="transcripts")
#writeXStringSet(tmp.seq, paste(sub(":\","_",fusion.names[13])), ".fa", sep=""), format="fasta")

# sapply(tmp.seq, function(x){writeXStringSet(x, "detected.fusions.fa", format="fasta", append=TRUE))
defuseTPTN

Description

A function that generate a list of fSet objects encopassing 60 experimentally validated fusions and 61 false fusions.

Usage

defuseTPTN()

Value

An list of fSet objects: Experimentally validated fusions 1-60, fish validated fusions 1-14, false fusions 61-121.

Author(s)

Raffaele A Calogero

Examples

tptn <-defuseTPTN()

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", "intronic", "annotated.genes", "read.through", "passenger.prob", "g3CDS", "g5g3CDS", "g5exon", "g3exon", "g5g3exon", "oncofuse.type", "oncofuse.threshold"))

Arguments

x a list of fSet object
type filtering can be performed on the basis of spanning.read: a minimal number of spanning reads, fusion.names: a vector list of user defined fusion names, intronic: only fusion encompassing exon data are retained annotated.genes: only fusion encompassing two annotated genes are retained read.through: only fusion with different gene names are retained oncofuse: using the output of oncofuseRun various filtering option can be applied using oncofuse.type and oncofuse.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 intronic query is NULL. In the latter case fusion having one of the elements located in an intronic region are discarded. In the case of oncofuse.type equal to passenger.prob or expression.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 breakpoint 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

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)
tmp2 <- filterList(tmp, type="spanning.reads", query=2, parallel=FALSE)
#tmp3 <- filterList(tmp, type="intronic")
#tmp4 <- filterList(tmp, type="annotated.genes", parallel=FALSE)
#tmp5 <- filterList(tmp, type="read.through", parallel=FALSE)
#csdf.of <- oncofuseRun(csdf.e, tissue="EPI")
#tmp6 <- filterList(csdf.e[1:100],oncofuse.output=csdf.of, type="oncofuse", oncofuse.type="g5g3CDS", parallel=FALSE)
#tmp7 <- filterList(csdf.e[1:100],oncofuse.output=csdf.of, type="oncofuse", oncofuse.type="passenger.prob"}

filterSamReads

A function to filter SAM or BAM files

Description

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

Usage

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")
```

---

### 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, Rsusread, FusionCatcher). Both spanning and encompassing reads (Bellerophontes, FusionFinder). Encompassing reads, i.e. one read of a pair on gene 1, and the other on gene2 (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, Rsusread). 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
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)
fusionPeptides

Arguments

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>list</td>
<td>a list of fSet object</td>
</tr>
<tr>
<td>parallel</td>
<td>option to run a parallel version of the function, default FALSE</td>
</tr>
</tbody>
</table>

Author(s)

Raffaele A Calogero

Examples

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

---

fusionPeptides

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

Description

A function extracting the donor and the acceptor peptides involved in the fusion.

Usage

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

Arguments

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>chimeraSeq.output</td>
<td>DNAStringSet encompassing the fusion event of interest, generated by chimeraSeq function</td>
</tr>
<tr>
<td>annotation</td>
<td>The annotation used to retrieve the UCSC names of the transcripts involved in the fusion</td>
</tr>
</tbody>
</table>

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

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)
tmpx <- lapply(tmp.seq,fusionPeptides)
A function to download a compiled version of GapFiller

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")

A function to confirm fusion break point by de novo assembly

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.mismatch=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 DNAMapSet encompassing the sequences present in the contigs object
- **fusion** which is a DNAMapSet 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.4-1031_R1.fastq", sep=""))
```
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 transcripts 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

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

Description

A function to import a list fusions data detected by bellerophonites, defuse, fusionfinder, fusionhunter, mapsplice, 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: bellerophonites, defuse, fusionfinder, fusionhunter, mapsplice, 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, mapsplice, bellerophonites 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

tmp <- importFusionData("fusionmap", paste(find.package(package="chimera"),"/examples/mcf7.FMFusionReport", sep=""), org="hg19")
#min.support allow to retrieve only the subset of fusions supported by a user defined minimal number of junctions
#tmp <- importFusionData("chimerascan", "edgren_cs10.bedpe", min.support=10, org="hg19")
#download Edgren Chimeric.out.junction. This file encompass the results obtaines combined all cell lines used by Edgren
#download.file("http://sourceforge.net/projects/ochguiextras/files/chimera/Chimeric.out.junction.zip"/download)
#unzip("Chimeric.out.junction.zip")
#tmp <- importFusionData("star", "Chimeric.out.junction", org="hg19", min.support=100)
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
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=""), org="hg19")
is.fSet(tmp[[1]])
```

---

MHmakeRandomString  
A function generating a random string

Description
A function generating a random string.

Usage
MHmakeRandomString()

Value
a string

Author(s)
Raffaele A Calogero

Examples
```r
tmp.file <- paste(MHmakeRandomString(), ".fa", sep="")
```
newfSet

A constructor for fSet class objects

Description

A function to create a new fSet object

Usage

newfSet(fusionInfo = list(fusionTool = NA, UniqueCuttingPositionCount = 0, SeedCount = 0, RescuedCount = 0, SplicePattern = NA, FusionGene = NA, frameShift = NA),
fusionLoc = GRangesList(),
fusionRNA = DNAStringSet(),
fusionGA = GAlignments())

Arguments

fusionInfo A list of the fusion characteristics see fSet class slot fusionInfo
fusionLoc A GRangesList encompassing the fusion break points
fusionRNA A DNAStringSet encompassing the fusion transcript
fusionGA A GAlignments encompassing the location of reads mapping on the fusion transcript

Value

An object of fSet class

Author(s)

Raffaele A Calogero

Examples

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, type=c("listfSet","coordDf"))

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>
<tr>
<td>plot</td>
<td>plotting the expression gain score versus the passenger mutation probability. For more info please see Shugay et al. Bioinformatics 2013:29,2539</td>
</tr>
<tr>
<td>type</td>
<td>listfSet a list of fSet objects or coordDf a dataframe of coordinates of fusions in the format required by Oncofuse</td>
</tr>
</tbody>
</table>
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

#tmp <- importFusionData("fusionmap", paste(find.package(package="chimera"), "/examples/mcf7.FMFusionReport"))
#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

picardInstallation()

Author(s)

Raffaele A Calogero

Examples

#picardInstallation()

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**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=...
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"))
removingErrorLine

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

```r
#tmp <- importFusionData("fusionmap", paste(find.package(package="chimera"),"/examples/mcf7.FMFusionReport"))
#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

```r
removingErrorLine(line.number, filenameIn, filenameOut)
```

Arguments

*line.number*  
line number to be removed

*filenameIn*  
input file name

*filenameOut*  
output file name

Value

SAM file without the error line

Author(s)

Raffaele A Calogero

Examples

```r
#removingErrorLine(14680066,"kd2_accepted_hits.sam","kd2_accepted_hits1.sam")
```
starInstallation  A function to download STAR

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

Arguments
binDir The user bin folder
os The supported operating systems

Author(s)
Raffaele A Calogero

Examples
#starInstallation(binDir="/somewhere/inyourpc/bin", os="mac")

starReads  A function to extract reads info from STAR fusion output

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

Usage
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
#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

starRun(input1, input2, cores=1, star= "STAR", samtools="samtools", fa, alignment=c("se","pe"), chimSegmentMin=0, chimJunctionOverhangMin=20)

Arguments

input1 The R1 fastq of a pair-end
input2 The R2 fastq of a pair-end
cores number of cores to be used by tophat with program name, e.g. /somewhere/tophat
star full path of STAR with program name, e.g. /somewhere/STAR
samtools full path of samtools
fa 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
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
chimSegmentMin STAR fusion parameter, see STAR manual
chimJunctionOverhangMin STAR fusion parameter, see STAR manual

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

#starRun(input1=paste(find.package(package="chimera"),"/examples/mcf7_sample_1.fq",sep=""), input2=paste(f
subreadRun

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 uses Rsubread aligner for MAC and UNIX OS. In case WINDOWS OS Rbowtie is used.

Usage

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

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ebwt</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 index database. The fusion nucleotide sequences can be generated with the function chimeraSeqs</td>
</tr>
<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>outfile.prefix</td>
<td>Prefix of the output bam file. Default is accepted_hits</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>cores</td>
<td>Number of cores to be used by the aligner</td>
</tr>
</tbody>
</table>

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

supportingReads(list, fusion.reads=c("encompassing","spanning"), parallel=FALSE)

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

tmp <- importFusionData("fusionmap", paste(find.package(package="chimera"),"/examples/mcf7.FMFusionReport", sep=""), org="hg19")
supporting.reads <- supportingReads(tmp, fusion.reads="spanning")
supporting.reads

tophatInstallation

A function to download tophat, bowtie and samtools

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

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

Arguments

- binDir: The user bin folder
- os: The supported operating systems
Author(s)
Raffaele A Calogero

Examples
#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=paste(getwd(), "mychimera.fa", sep="/"), 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(paste(find.package(package="chimera"), "/examples/mcf7_sample_2.fq", sep=""), sep=","), output="..."
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

input
SAM/BAM file to be validated

output
file name in which to save the validation information

mode
Mode of output. Default value: VERBOSE

max.output
max number of reported error lines

Value

Validation information referring to a SAM/BM file.

Author(s)
Raffaele A Calogero

See Also

picardInstallation

Examples

#validateSamFile(input=paste(find.package(package="chimera"),"/examples/mcf7_trs_accepted_hits.bam",sep=""))
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