Package: SICtools (via r-universe)

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Type Package

Title Find SNV/Indel differences between two bam files with near relationship

Version 1.43.1

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Description This package is to find SNV/Indel differences between two bam files with near relationship in a way of pairwise comparison thourgh each base position across the genome region of interest. The difference is inferred by fisher test and euclidean distance, the input of which is the base count (A,T,G,C) in a given position and read counts for indels that span no less than 2bp on both sides of indel region.

License GPL (>=2)

LazyLoad Yes

Depends R (>= 3.0.0), methods, Rsamtools (>= 1.18.1), doParallel (>= 1.0.8), Biostrings (>= 2.32.1), stringr (>= 0.6.2), matrixStats (>= 0.10.0), plyr (>= 1.8.3), GenomicRanges (>= 1.22.4), IRanges (>= 2.4.8)

Suggests knitr, RUnit, BiocGenerics

biocViews Alignment, Sequencing, Coverage, SequenceMatching, QualityControl, DataImport, Software, SNP, VariantDetection

VignetteBuilder knitr

Config/Bioconductor/UnsupportedPlatforms windows

Config/pak/sysreqs libbz2-dev libicu-dev liblzma-dev xz-utils zlib1g-dev

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`SICtools-package` *tools for SNV/Indel Comparison between two bam files with near relationship*

Description

This package is to find SNV/Indel differences between two bam files with near relationship in a way of pairwise comparison thourgh each base position across the genome region of interest. The difference is inferred by fisher test and euclidean distance, the input of which is the base count (A,T,G,C) in a given position and read counts for indels that span no less than 2bp on both sides of indel region called from samtools+bcftools

Details

Package:	SICtools
Type:	Package
Version:	1.0
Date:	2014-07-24
License:	GPL (>=2)
LazyLoad:	Yes

Author(s)

Xiaobin Xing

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indelDiff *main function to call indel difference between the bam files*

Description

test indel-read count differences at a given indel position between the two bam files. The indel position are obtained by samtools+bcftools first, and count the number of reads that span no less than 3bp of the indel boundary. The read-count matrix at a given indel region from the two bam files are tested by fisher exact test and euclidean distance. If nothing difference, NULL will be returned.

Usage

```
indelDiff(bam1, bam2, refFsa, regChr, regStart, regEnd, minBaseQuality = 13, minMapQuality = 0, nCores =
```

Arguments

bam1	the first bam file to be compared
bam2	the second bam file to be compared
refFsa	the reference fasta file used for bam1 and bam2 alignments
regChr	chromosome name of the region of interest, it should match the chromosome name in reference name
regStart	the start position (1-based) of the region of interest
regEnd	the end position (1-based) of the region of interest
minBaseQuality	the minimum base quality to be used for indel-read count
minMapQuality	the minimum read mapping quality to be used for indel-read count
nCores	number of thread used for calculate in parallel
pValueCutOff	p.value cutoff from fisher.test to display output. If there is no difference between two compared positions (p.value = 1 and d.value = 0), NULL will be returned even setting pValueCutOff = 1.
gtDistCutOff	euclidean distance cutoff from dist(,method='euclidean') to display output. If there is no difference between two compared positions (p.value = 1 and d.value = 0), NULL will be returned even setting gtDistCutOff = 0.
verbose	print progress on screen, default = TRUE.

Value

indelDiff: returns a data.frame with difference information: chromosome, position, reference genenotype, two alt genotypes, and their indel-read count for two bam files, p.value (fisher exact test of these read counts) and d.value (euclidean distance of these read counts)

Author(s)

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References

Li H.*, Handsaker B.*, Wysoker A., Fennell T., Ruan J., Homer N., Marth G., Abecasis G., Durbin R. and 1000 Genome Project Data Processing Subgroup (2009) The Sequence alignment/map (SAM) format and SAMtools. Bioinformatics, 25, 2078-9. [PMID: 19505943]

Examples

```
bam1 <- system.file(package='SICtools','extdata','example1.bam')
bam2 <- system.file(package='SICtools','extdata','example2.bam')
refFsa <- system.file(package='SICtools','extdata','example.ref.fasta')

indelDiff(bam1,bam2,refFsa,'chr07',828514,828914,pValueCutOff=1,gtDistCutOff=0)
```

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snpDiff *main function to test point differences between the two bam files*

Description

test base count (A,T,G,C) difference at a given position between the two bam files. The base count matrix is tested by fisher exact test and euclidean distance. If nothing difference, NULL will be returned.

Usage

```
snpDiff(bam1, bam2, refFsa, regChr, regStart, regEnd, minBaseQuality = 13, minMapQuality = 0, nCores = 1
```

Arguments

bam1	the first bam file to be compared
bam2	the second bam file to be compared
refFsa	the reference fasta file used for bam1 and bam2 alignments
regChr	chromosome name of the region of interest, it should match the chromosome name in reference name
regStart	the start position (1-based) of the region of interest
regEnd	the end position (1-based) of the region of interest
minBaseQuality	the minimum base quality to be used for base count
minMapQuality	the minimum read mapping quality to be used for base count
nCores	number of thread used for calculate in parallel
pValueCutOff	p.value cutoff from fisher.test to display output. If there is no difference between two compared positions (p.value = 1 and d.value = 0), NULL will be returned even setting pValueCutOff = 1.
baseDistCutOff	euclidean distance cutoff from dist(,method='euclidean') to display output. If there is no difference between two compared positions (p.value = 1 and d.value = 0), NULL will be returned even setting baseDistCutOff = 0.
verbose	print progress on screen, default = TRUE.

Value

snpDiff: returns a data.frame with difference information: chromosome, position, reference base, base count (A,C,G,T,N) for two bam files, p.value (fisher exact test of these base counts) and d.value (euclidean distance of these base counts)

Author(s)

Xiaobin Xing, <email:xiaobinxing0316@gmail.com>

References

Morgan M, Pages H, Obenchain V and Hayden N. Rsamtools: Binary alignment (BAM), FASTA, variant call (BCF), and tabix file import.

Examples

```
bam1 <- system.file(package='SICtools','extdata','example1.bam')
bam2 <- system.file(package='SICtools','extdata','example2.bam')
refFsa <- system.file(package='SICtools','extdata','example.ref.fasta')

snpDiff(bam1,bam2,refFsa,'chr04',962501,1026983,pValueCutOff=1,baseDistCutOff=0)
```

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