Package ‘cgdv17’

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Title Complete Genomics Diversity Panel, chr17 on 46 individuals
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Description Complete Genomics Diversity Panel, chr17 on 46 individuals
Depends R (>= 2.15), methods, VariantAnnotation (>= 1.15.15)
Imports BiocGenerics, S4Vectors, IRanges, GenomicRanges, Biobase
Suggests parallel, GGtools, TxDb.Hsapiens.UCSC.hg19.knownGene, org.Hs.eg.db, illuminaHumanv1.db
License Artistic-2.0
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biocViews SequencingData, SNPData, BioViews
NeedsCompilation no

R topics documented:

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- cgdv17-package Complete Genomics Diversity Panel, chr17 on 46 individuals

Description

Complete Genomics Diversity Panel, chr17 on 46 individuals, illustrating subject-specific variant sets

Details
countVariants

countVariants

count variants in a raggedVariantSet instance

getRVS

acquire data for and construct a ragged variant set instance

padToReference

create a snpStats SnpMatrix instance by padding a ragged variant set to reference alleles wherever a variant is not recorded

raggedVariantSet-class

Class "raggedVariantSet"

variantGRanges

acquire a list of GRanges recording variants and locations

see vignette; CY17 is an ExpressionSet on individuals from CEU and YRI overlapping with the diversity set, popvec enumerates source populations, h1 is an exemplar VCF header structure

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countVariants count variants in a raggedVariantSet instance

Description

count variants in a raggedVariantSet instance

Usage

countVariants(rvs, delim, qthresh = 160, applier = lapply)

Arguments

rvs instance of raggedVariantSet
delim GRanges instance
qthresh quality threshold for keeping a variant in count
applier lapply-like function
getRVS

Acquire data for and construct a ragged variant set instance

Description

Acquire data for and construct a ragged variant set instance

Usage

getRVS(parameters)

getrd(x, id)

Arguments

packname: string naming package where the resources are found
fns2samplenames: function to transform filenames to sample name tokens
x: instance of raggedVariantSet
id: character to select sample

Details

Currently very specialized, as the protocol for managing collections of VCF files with discrepant variant sets per subject is not clear.

Assumes the package has inst/rowranges where row ranges of readVcf results are held.

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padToReference

Create a snpStats SnpMatrix instance by padding a ragged variant set to reference alleles wherever a variant is not recorded

Description

Create a snpStats SnpMatrix instance by padding a ragged variant set to reference alleles wherever a variant is not recorded.

Usage

padToReference(parameters)
raggedVariantSet-class

Arguments

rv          raggedVariantSet instance
gr          GRanges instance
qthresh     quality lower bound for retention of variant
applier     lapply like function

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Description

manage information on non-aligned variant sets from multiple VCFs

Objects from the Class

Objects can be created by calls of the form new("raggedVariantSet", ...).

Slots

filenames: files will be held in inst/rowranges, named here
sampleNames: names of samples managed

Methods

[ signature(x = "raggedVariantSet", i = "ANY", j = "ANY", drop = "ANY"): familiar
subsetting syntax
sampleNames signature(object = "raggedVariantSet"): getter
show signature(object = "raggedVariantSet"): concise report
variantGRanges signature(rvs = "raggedVariantSet", delim = "GRanges", qthresh = "missing", applier = "missing"): getter
variantGRanges signature(rvs = "raggedVariantSet", delim = "GRanges", qthresh = "numeric", applier = "numeric"): getter with quality threshold

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Examples

showClass("raggedVariantSet")
variantGRanges

acquire a list of GRanges recording variants and locations

Description

acquire a list of GRanges recording variants and locations

Usage

variantGRanges(rvs, delim, qthresh = 160, applier = lapply)

variantNames(rvs, delim, qthresh = 160, applier = lapply)

Arguments

rvs raggedVariantSet instance
delim GRanges instance for confinement
qthresh lower bound on quality
applier lapply like function

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