Package ‘cgdv17’

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Title Complete Genomics Diversity Panel, chr17 on 46 individuals
Version 0.14.0
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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
LazyLoad yes
biocViews SequencingData, SNPData, BiocViews
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
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

getRVS

acquire data for and construct a ragged variant set instance

Description

acquire data for and construct a ragged variant set instance

Usage

getRVS(packname, fns2samplenames = function(x)
gsub(".*\(NA\.....\).*", "\\1", x))

getr(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(rv, gr, qthresh = 160, applier = lapply)
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 = "function"): getter with quality threshold

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Examples

showClass("raggedVariantSet")
variantGRanges

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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