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
LazyLoad yes
biocViews SequencingData, SNPData, BiocViews
NeedsCompilation no

R topics documented:

cgdv17-package .................................................. 1
countVariants .................................................. 2
getRVS .......................................................... 3
padToReference ............................................... 3
raggedVariantSet-class ..................................... 4
variantGRanges ............................................... 5

Index

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

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

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/roranges 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)
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 = "function")

variantGRanges signature(rvs = "raggedVariantSet", delim = "GRanges", qthresh = "numeric", applier = "function")

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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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Index

*Topic **classes**
  raggedVariantSet-class, 4

*Topic **models**
  countVariants, 2
  getRVS, 3
  padToReference, 3
  variantGRanges, 5

*Topic **package**
  cgdv17-package, 1
  [,raggedVariantSet,ANY,ANY,ANY-method (raggedVariantSet-class). 4
  [,raggedVariantSet,ANY,ANY-method (raggedVariantSet-class). 4

  cgdv17 (cgdv17-package), 1
  cgdv17-package, 1
  countVariants, 2
  CY17 (cgdv17-package), 1

  getrd (getRVS), 3
  getRVS, 3

  h1 (cgdv17-package), 1

  padToReference, 3
  popvec (cgdv17-package), 1

  raggedVariantSet, 2, 4, 5
  raggedVariantSet-class, 4
  readVcf, 3

  sampleNames,raggedVariantSet-method (raggedVariantSet-class). 4
  show,raggedVariantSet-method (raggedVariantSet-class). 4

  variantGRanges, 5
  variantGRanges,raggedVariantSet,GRanges,missing,missing-method (raggedVariantSet-class). 4
  variantGRanges,raggedVariantSet,GRanges,numeric,funcion-method (raggedVariantSet-class). 4
  variantNames (variantGRanges), 5