Package ‘cgdv17’

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Title Complete Genomics Diversity Panel, chr17 on 46 individuals
Version 0.12.0
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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, BioViews
NeedsCompilation no

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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

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**

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

```r
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 = "missing") getter
variantGRanges signature(rvs = "raggedVariantSet", delim = "GRanges", qthresh = "numeric", applier = "function") getter with quality threshold

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Examples

showClass("raggedVariantSet")
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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