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

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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

Package:	cgdv17
Version:	0.0.9
Suggests:	
Imports:	Biobase, IRanges
Depends:	R (>= 2.14), VariantAnnotation, org.Hs.eg.db, methods
License:	Artistic 2.0
LazyLoad:	yes
biocViews:	genetics
Built:	R 2.15.0; ; 2012-03-09 12:45:57 UTC; unix

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```
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

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`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/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)
```

Arguments

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

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`raggedVariantSet-class`

Class `"raggedVariantSet"`

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` getter

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