Package 'cgdv17'

January 9, 2013

Title Complete Genomics Diversity Panel, chr17 on 46 individuals

Version 0.0.18

Author VJ Carey <stvjc@channing.harvard.edu>

Description Complete Genomics Diversity Panel, chr17 on 46 individuals

Suggests

Imports Biobase, IRanges

Depends R (>= 2.15), VariantAnnotation, org.Hs.eg.db, methods,GGtools, TxDb.Hsapiens.UCSC.hg19.knownGene, parallel

Maintainer VJ Carey <stvjc@channing.harvard.edu>

License Artistic 2.0

LazyLoad yes

biocViews genetics

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

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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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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

Author(s)

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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/rowdata where row data 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

Author(s)

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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/rowdata, 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 = "mis
    getter

variantGRanges signature(rvs = "raggedVariantSet", delim = "GRanges", qthresh = "numeric", applier = "fun
    getter with quality threshold

Author(s)

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Examples

showClass("raggedVariantSet")

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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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