

# Package ‘cgdv17’

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**Title** Complete Genomics Diversity Panel, chr17 on 46 individuals

**Version** 0.26.0

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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

**git\_url** <https://git.bioconductor.org/packages/cgdv17>

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 cgdv17-package

*Complete Genomics Diversity Panel, chr17 on 46 individuals*


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## 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

## Index:

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

## Author(s)

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 countVariants

*count variants in a raggedVariantSet instance*


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## Description

count variants in a raggedVariantSet instance

**Usage**

```
countVariants(rvs, delim, qthresh = 160, applier = lapply)
```

**Arguments**

rvs	instance of <a href="#">raggedVariantSet</a>
delim	GRanges instance
qthresh	quality threshold for keeping a variant in count
applier	lapply-like function

**Author(s)**

VJ Carey <stvjc@channing.harvard.edu>

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getRVS

*acquire data for and construct a ragged variant set instance*

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**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 <a href="#">raggedVariantSet</a>
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

**Author(s)**

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padToReference	<i>create a snpStats SnpMatrix instance by padding a ragged variant set to reference alleles wherever a variant is not recorded</i>
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**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	<i>Class "raggedVariantSet"</i>
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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

**Author(s)**

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**Examples**

```
showClass("raggedVariantSet")
```

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variantGRanges	<i>acquire a list of GRanges recording variants and locations</i>
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**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	<a href="#">raggedVariantSet</a> instance
delim	GRanges instance for confinement
qthresh	lower bound on quality
applier	lapply like function

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