

# Package ‘cgdv17’

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

**Version** 0.8.0

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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

```

**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

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countVariants	<i>count variants in a raggedVariantSet instance</i>
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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)**

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getRVS	<i>acquire data for and construct a ragged variant set instance</i>
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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 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	<i>create a <code>snpStats SnpMatrix</code> 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	<code>raggedVariantSet</code> instance
gr	<code>GRanges</code> instance
qthresh	quality lower bound for retention of variant
applier	lapply like function

**Author(s)**

VJ Carey <stvjc@channing.harvard.edu>

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raggedVariantSet-class  
Class "raggedVariantSet"

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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 = '')`  
getter

**variantGRanges** `signature(rvs = "raggedVariantSet", delim = "GRanges", qthresh = "numeric", applier = '')`  
getter with quality threshold

### Author(s)

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### Examples

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

---

variantGRanges      *acquire a list of GRanges recording variants and locations*

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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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