

# Package ‘comapr’

June 4, 2026

**Title** Crossover analysis and genetic map construction

**Version** 1.17.0

**Description** comapr detects crossover intervals for single gametes from their haplotype states sequences and stores the crossovers in GRanges object. The genetic distances can then be calculated via the mapping functions using estimated crossover rates for maker intervals. Visualisation functions for plotting interval-based genetic map or cumulative genetic distances are implemented, which help reveal the variation of crossovers landscapes across the genome and across individuals.

**biocViews** Software, SingleCell, Visualization, Genetics

**Depends** R (>= 4.1.0)

**Imports** methods, ggplot2, reshape2, dplyr, gridExtra, plotly, circlize, rlang, GenomicRanges, IRanges, foreach, BiocParallel, GenomeInfoDb, scales, RColorBrewer, tidyr, S4Vectors, utils, Matrix, grid, stats, SummarizedExperiment, plyr, Gviz

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## Contents

|                               |           |
|-------------------------------|-----------|
| .change_missing . . . . .     | 2         |
| .filterCOsExtra . . . . .     | 3         |
| .label_gt . . . . .           | 4         |
| bootstrapDist . . . . .       | 5         |
| calGeneticDist . . . . .      | 6         |
| coCount . . . . .             | 8         |
| comapr . . . . .              | 9         |
| combineHapState . . . . .     | 9         |
| correctGT . . . . .           | 10        |
| countBinState . . . . .       | 11        |
| countCOs . . . . .            | 12        |
| countGT . . . . .             | 13        |
| fill_fail . . . . .           | 14        |
| filterGT . . . . .            | 14        |
| findDupSamples . . . . .      | 15        |
| getAFTracks . . . . .         | 16        |
| getCellAFTrack . . . . .      | 17        |
| getCellCORange . . . . .      | 19        |
| getCellDPTrack . . . . .      | 20        |
| getDistortedMarkers . . . . . | 21        |
| getMeanDPTrack . . . . .      | 22        |
| getSNPDensityTrack . . . . .  | 23        |
| parents_genotype . . . . .    | 24        |
| perCellChrQC . . . . .        | 24        |
| permuteDist . . . . .         | 25        |
| perSegChrQC . . . . .         | 26        |
| plotCount . . . . .           | 27        |
| plotGeneticDist . . . . .     | 29        |
| plotGTFreq . . . . .          | 30        |
| plotWholeGenome . . . . .     | 30        |
| readColMM . . . . .           | 31        |
| readHapState . . . . .        | 32        |
| snp_genotype . . . . .        | 33        |
| snp_genotype_gr . . . . .     | 34        |
| twoSamples . . . . .          | 35        |
| <b>Index</b>                  | <b>36</b> |

---

|                 |   |
|-----------------|---|
| .change_missing | <i>change SNPs with genotype 'Fail' to NA</i> |
|-----------------|---|

---

### Description

change SNPs with genotype 'Fail' to NA

### Usage

```
.change_missing(s_gt, missing = "Fail")
```

**Arguments**

s\_gt            a column of labelled genotypes  
missing        the string used for encoding missing values default to Fail

**Details**

calculation.

**Value**

a vector of genotypes with Fail substituted by 'NA'

**Author(s)**

Ruqian Lyu

---

.filterCOsExtra            *Filter out doublet cells and uninformative SNPs*

---

**Description**

This function filter out cells that have been called too many crossovers due to diploid cell contamination or doublets. It also only keeps SNPs (rows) that ever contribute to a crossover interval. This function should be run for individual chromosomes and is called internally by 'readHapState'

**Usage**

```
.filterCOsExtra(  
  se,  
  minSNP = 30,  
  minlogllRatio = 200,  
  minCellSNP = 200,  
  bpDist = 100,  
  maxRawCO = 10,  
  biasTol = 0.45,  
  nmad = 1.5  
)
```

**Arguments**

se            the SummarizedExperiment object that contains the called haplotype state matrix in the assay field and haplotype segment information in the metadata field.  
minSNP        the crossover(s) will be filtered out if introduced by a segment that has fewer than 'minSNP' SNPs to support.  
minlogllRatio   the crossover(s) will be filtered out if introduced by a segment that has lower than 'minlogllRatio' to its reversed state.  
minCellSNP    the minimum number of SNPs detected for a cell to be kept, used with 'nmads'  
bpDist        the crossover(s) will be filtered out if introduced by a segment that is shorter than 'bpDist' basepairs.



**Details**

This function takes the a sample's genotype across each SNP marker in alleles and compare with genotypes of in-bred reference and alternative strains to. If the sample's genotype for a particular SNP marker is the same with the reference strain, it is labelled as Homo\_ref homogeneous reference for a particular SNP marker; if the sample's genotype is the same with the alternative strain it is labelled as Homo\_alt homogeneous alternative for a particular SNP marker; if the sample's genotype is heterozygous then it is labeled as Het heterozygous for this particular genotypes. If it does not fall in any of the three cases, it is labelled as the string specified by the argument 'missing'.

Note that the wrong/failed genotype is labelled as the string in 'missing' after this function. If there is a different label for failed genotype, provide the label using the 'missing' argument.

**Value**

a vector of labels Homo\_ref, Homo\_alt, Het indicating the progeny's genotypes across markers

**Author(s)**

Ruqian Lyu

---

|               |                      |
|---------------|----------------------|
| bootstrapDist | <i>bootstrapDist</i> |
|---------------|----------------------|

---

**Description**

Generating distribution of sample genetic distances

**Usage**

```
bootstrapDist(co_gr, B = 1000, mapping_fun = "k", group_by)
```

**Arguments**

|             |  |
|-------------|--|
| co_gr       | GRanges or RangedSummarizedExperiment object that contains the crossover counts for each marker interval across all samples. Returned by countCOs  |
| B           | integer the number of sampling times   |
| mapping_fun | character default to "k" (kosambi mapping function). It can be one of the mapping functions: "k","h"   |
| group_by    | the prefix for each group that we need to generate distributions for(only when co_gr is a GRanges object). Or the column name for 'colData(co_gr)' that contains the group factor (only when co_gr is a RangedSummarizedExperiment object) |

**Details**

It takes the crossover counts for samples in multiple groups that is returned by 'countCO'. It then draws samples from a group with replacement and calculate the distribution of relevant statistics.

**Value**

lists of numeric genetic distances for multiple samples

**Author(s)**

Ruqian Lyu

**Examples**

```
data(coCount)

bootsDiff <- bootstrapDist(coCount, group_by = "sampleGroup", B=10)
```

---

|                |                       |
|----------------|-----------------------|
| calGeneticDist | <i>calGeneticDist</i> |
|----------------|-----------------------|

---

**Description**

Calculate genetic distances of marker intervals or binned-chromosome. Given whether crossover happens in each marker interval, calculate the recombination fraction in samples and then derive the Haldane or Kosambi genetic distances via mapping functions.

**Usage**

```
calGeneticDist(
  co_count,
  bin_size = NULL,
  mapping_fun = "k",
  ref_genome = "mm10",
  group_by = NULL,
  chrom_info = NULL
)

## S4 method for signature 'GRanges,missing,ANY,ANY,missing'
calGeneticDist(
  co_count,
  bin_size = NULL,
  mapping_fun = "k",
  ref_genome = "mm10",
  group_by = NULL,
  chrom_info = NULL
)

## S4 method for signature 'GRanges,numeric,ANY,ANY,missing'
calGeneticDist(
  co_count,
  bin_size = NULL,
  mapping_fun = "k",
  ref_genome = "mm10",
  group_by = NULL,
  chrom_info = NULL
)

## S4 method for signature 'GRanges,missing,ANY,ANY,character'
calGeneticDist(
```

```
    co_count,
    bin_size = NULL,
    mapping_fun = "k",
    ref_genome = "mm10",
    group_by = NULL,
    chrom_info = NULL
)

## S4 method for signature 'GRanges,numeric,ANY,ANY,character'
calGeneticDist(
  co_count,
  bin_size = NULL,
  mapping_fun = "k",
  ref_genome = "mm10",
  group_by = NULL,
  chrom_info = NULL
)

## S4 method for signature 'RangedSummarizedExperiment,missing,ANY,ANY,missing'
calGeneticDist(
  co_count,
  bin_size = NULL,
  mapping_fun = "k",
  ref_genome = "mm10",
  group_by = NULL,
  chrom_info = NULL
)

## S4 method for signature
## 'RangedSummarizedExperiment,missing,ANY,ANY,character'
calGeneticDist(
  co_count,
  bin_size = NULL,
  mapping_fun = "k",
  ref_genome = "mm10",
  group_by = NULL,
  chrom_info = NULL
)

## S4 method for signature
## 'RangedSummarizedExperiment,numeric,ANY,ANY,character'
calGeneticDist(
  co_count,
  bin_size = NULL,
  mapping_fun = "k",
  ref_genome = "mm10",
  group_by = NULL,
  chrom_info = NULL
)

## S4 method for signature 'RangedSummarizedExperiment,numeric,ANY,ANY,missing'
calGeneticDist(
```

```

    co_count,
    bin_size = NULL,
    mapping_fun = "k",
    ref_genome = "mm10",
    group_by = NULL,
    chrom_info = NULL
  )

```

### Arguments

|                          |   |
|--------------------------|---|
| <code>co_count</code>    | GRange or RangedSummarizedExperiment object, returned by countCO  |
| <code>bin_size</code>    | The binning size for grouping marker intervals into bins. If not supplied, the original marker intervals are returned with converted genetic distances based on recombination rate  |
| <code>mapping_fun</code> | The mapping function to use, can be one of "k" or "h" (kosambi or haldane)  |
| <code>ref_genome</code>  | The reference genome name. It is used to fetch the chromosome size information from UCSC database.  |
| <code>group_by</code>    | character vector contains the unique prefix of sample names that are used for defining different sample groups. Or the column name in <code>colData(co_count)</code> that specify the group factor. If missing all samples are assumed to be from one group       |
| <code>chrom_info</code>  | A user supplied data.frame containing two columns with column names <code>chrom</code> and <code>size</code> , describing the chromosome names and lengths if not using <code>ref_genome</code> from UCSC. If supplied, the <code>'ref_genome'</code> is ignored. |

### Value

GRanges object GRanges for marker intervals or binned intervals with Haldane or Kosambi centi-Morgans

### Examples

```

data(coCount)
dist_se <- calGeneticDist(coCount)
# dist_se <- calGeneticDist(coCount, group_by="sampleGroup")

```

---

|                      |  |
|----------------------|--|
| <code>coCount</code> | <i>RangedSummarizedExperiment object containing the crossover counts across samples for the list of SNP marker intervals</i> |
|----------------------|--|

---

### Description

RangedSummarizedExperiment object containing the crossover counts across samples for the list of SNP marker intervals

### Usage

```
data(coCount)
```

**Format**

An object of class `RangedSummarizedExperiment` with 3 rows and 10 columns.

---

|        |                       |
|--------|-----------------------|
| comapr | <i>comapr package</i> |
|--------|-----------------------|

---

**Description**

crossover inference package

**Details**

See the README on [GitLab](#)

---

|                 |                        |
|-----------------|------------------------|
| combineHapState | <i>combineHapState</i> |
|-----------------|------------------------|

---

**Description**

combine two ‘`RangedSummarizedExperiment`’ objects, each contains the haplotype state for a list of SNPs across a set of cells. The combined result will have cells from two individuals and merged list of SNPs from the two.

**Usage**

```
combineHapState(rse1, rse2, groupName = c("Sample1", "Sample2"))
```

**Arguments**

|           |   |
|-----------|---|
| rse1      | the first ‘ <code>RangedSummarizedExperiment</code> ’                               |
| rse2      | the second ‘ <code>RangedSummarizedExperiment</code> ’                              |
| groupName | a character vector of length 2 that contains the first and the second group’s names |

**Value**

A ‘`RangedSummarizedExperiment`’ that contains the cells and SNPs in both ‘rse’

**Author(s)**

Ruqian Lyu

**Examples**

```

BiocParallel::register(BiocParallel::SnowParam(workers = 1))
demo_path <- paste0(system.file("extdata",package = "comapr"),"/")
s1_rse_state <- readHapState("s1",chroms=c("chr1"),
                           path=demo_path,barcodeFile=NULL,minSNP = 0,
                           minlogllRatio = 50,
                           bpDist = 100,maxRawCO=10,
                           minCellsNP = 1)

s2_rse_state <- readHapState("s2",chroms=c("chr1"),
                           path=demo_path,
                           barcodeFile=paste0(demo_path,"s2_barcode.txt"),
                           minSNP = 0,
                           minlogllRatio = 50,
                           bpDist = 100,maxRawCO=10,
                           minCellsNP = 1)

sb <- combineHapState(s1_rse_state,s2_rse_state)

```

---

correctGT

*correctGT*


---

**Description**

function for formatting and correction genotypes of markers

**Usage**

```
correctGT(gt_matrix, ref, alt, failed = "Fail", wrong_label = "Homo_ref")
```

**Arguments**

|             |   |
|-------------|---|
| gt_matrix   | the input genotype matrix of markers by samples with rownames as marker IDs and column names as sample IDs                          |
| ref         | a vector of genotypes of the inbred reference strain  |
| alt         | a vector of genotypes of the inbred alternative strain  |
| failed      | what was used for encoding failed genotype calling such as "Fail" in example data snp_geno  |
| wrong_label | what would be considered a wrong genotype label for example Homo_ref which should not be in the possible genotypes of BC1F1 samples |

**Details**

This function changes genotype in alleles to genotype labels, change Homo\_ref to Hets/Fail, infer Failed genotype, and change "Failed" to NA for counting crossover later

This function changes genotype in alleles to labels by calling internal functions lable\_gt, and changes the wrong genotype Homo\_ref to Fail by calling .change\_missing.

**Value**

a genotype data.frame of sample genotypes with dimension as the input 'gt\_matrix' with genotypes converted to labels and failed calls are changed to NA.

**Author(s)**

Ruqian Lyu

**Examples**

```

data(snp_geno_gr)
data(parents_geno)
snp_gt_crt <- correctGT(gt_matrix = GenomicRanges::mcols(snp_geno_gr),
                       ref = parents_geno$ref,
                       alt = parents_geno$alt,
                       fail = "Fail",
                       wrong_label = "Homo_ref")

```

---

|               |                      |
|---------------|----------------------|
| countBinState | <i>countBinState</i> |
|---------------|----------------------|

---

**Description**

Bins the chromosome into supplied number of bins and find the state of the chromosome bins across all gamete cells

**Usage**

```
countBinState(chr, snpAnno, viState, genomeRange, ntile = 5)
```

**Arguments**

|             |  |
|-------------|--|
| chr         | character, the chromosome to check                                   |
| snpAnno     | data.frame, the SNP annotation for the supplied chromosome           |
| viState     | dgTMatrix/Matrix, the viterbi state matrix, output from 'sgcocaller' |
| genomeRange | GRanges object with seqlengths information for the genome            |
| ntile       | integer, how many tiles the chromosome is binned into                |

**Details**

This function is used for checking whether chromosome segregation pattern obeys the expected ratio.

**Value**

a data.frame that contains chromosome bin segregation ratio

**Author(s)**

Ruqian Lyu

**Examples**

```

library(IRanges)
library(S4Vectors)

chrom_info <- GenomeInfoDb::getChromInfoFromUCSC("mm10")
seq_length <- chrom_info$size
names(seq_length) <- chrom_info$chrom

dna_mm10_gr <- GenomicRanges::GRanges(
  seqnames = Rle(names(seq_length)),
  ranges = IRanges(1, end = seq_length, names = names(seq_length)),
  seqlengths = seq_length)

GenomeInfoDb::genome(dna_mm10_gr) <- "mm10"
demo_path <- system.file("extdata",package = "comapr")
sampleName <- "s1"
chr <- "chr1"
vi_mtx <- Matrix::readMM(file = paste0(demo_path,"/", sampleName, "_",
                                       chr, "_vi.mtx"))

snpAnno <- read.table(file = paste0(demo_path,"/", sampleName,
                                     "_", chr, "_snpAnnot.txt"),
                      stringsAsFactors = FALSE,
                      header = TRUE)

countBinState(chr = "chr1",snpAnno = snpAnno,
viState = vi_mtx,genomeRange = dna_mm10_gr, ntile = 1)

```

countCOs

*countCOs***Description**

Count number of COs within each marker interval COs identified in the interval overlapping missing markers are distributed according to marker interval base-pair sizes. Genotypes encoded with "0" are treated as missing value.

**Usage**

```

countCOs(geno)

## S4 method for signature 'GRanges'
countCOs(geno)

## S4 method for signature 'RangedSummarizedExperiment'
countCOs(geno)

```

**Arguments**

geno GRanges object or RangedSummarizedExperiment object with genotype matrix that has SNP positions in the rows and cells/samples in the columns

**Value**

GRanges object or RangedSummarizedExperiment with markers-intervals as rows and samples in columns, values as the number of COs estimated for each marker interval

**Author(s)**

Ruqian Lyu

**Examples**

```
data(twoSamples)
cocount <- countCOs(twoSamples)
```

---

countGT

*countGT*

---

**Description**

count how many samples have genotypes calls across markers and count how many markers that each individual has called genotypes for. This function helps identify poor samples or poor markers for filtering. It can also generate plots that help identify outlier samples/markers

**Usage**

```
countGT(geno, plot = TRUE, interactive = FALSE)
```

**Arguments**

|             |   |
|-------------|---|
| geno        | the genotype data.frame of markers by samples from output of function correctGT |
| plot        | it determines whether a plot will be generated, defaults to TRUE                |
| interactive | it determines whether an interactive plot will be generated                     |

**Value**

A list of two elements including n\_markers and n\_samples

**Author(s)**

Ruqian Lyu

**Examples**

```
data(snp_geno_gr)
genotype_counts <- countGT(GenomicRanges::mcols(snp_geno_gr))
```

---

|           |   |
|-----------|---|
| fill_fail | <i>Infer the genotype of failed SNPs If we have a Fail in the genotype data and the Fail in a block of either Home_alt, or Het, we fill in the Fails using values of the ones adjacent to it, otherwise they remain as "Fail" to indicate missing values.</i> |
|-----------|---|

---

### Description

Infer the genotype of failed SNPs If we have a Fail in the genotype data and the Fail in a block of either Home\_alt, or Het, we fill in the Fails using values of the ones adjacent to it, otherwise they remain as "Fail" to indicate missing values.

### Usage

```
fill_fail(s_gt, fail = "Fail", chr = NULL)
```

### Arguments

|      |  |
|------|--|
| s_gt | a column of labelled genotypes   |
| fail | the string that is used for encoding failed genotype results, default to Fail  |
| chr  | the factor vector indicating which chromosomes the markers are on, default to NULL which means the input markers are all on the same chromosome. |

### Value

a vector of genotypes with Failed genotype imputed or changed to 'NA' if not imputable

### Author(s)

Ruqian Lyu

---

|          |                 |
|----------|-----------------|
| filterGT | <i>filterGT</i> |
|----------|-----------------|

---

### Description

Filter markers or samples that have too many missing values

### Usage

```
filterGT(geno, min_markers = 5, min_samples = 3)

## S4 method for signature 'matrix,numeric,numeric'
filterGT(geno, min_markers = 5, min_samples = 3)

## S4 method for signature 'GRanges,numeric,numeric'
filterGT(geno, min_markers = 5, min_samples = 3)
```

**Arguments**

geno                    the genotype data.frame of markers by samples from output of function correctGT  
 min\_markers            the minimum number of markers for a sample to be kept  
 min\_samples            the minimum number of samples for a marker to be kept

**Details**

This function takes the geno data.frame and filter the data.frame by the provided cut-offs.

**Value**

The filtered genotype matrix

**Author(s)**

Ruqian Lyu

**Examples**

```
data(snp_genog)
corrected_genog <- filterGT(snp_genog, min_markers = 30, min_samples = 2)
```

---

|                |                       |
|----------------|-----------------------|
| findDupSamples | <i>findDupSamples</i> |
|----------------|-----------------------|

---

**Description**

Find the duplicated samples by look at the number of matching genotypes in all pair-wise samples

**Usage**

```
findDupSamples(geno, threshold = 0.99, in_text = FALSE)
```

**Arguments**

geno                    the genotype data.frame of markers by samples from output of function correctGT  
 threshold              the frequency cut-off of number of matching genotypes out of all genotypes for determining whether the pair of samples are duplicated, defaults to 0.99. NAs are regarded as same genotypes for two samples if they both have NA for a marker.  
 in\_text                whether text of frequencies should be displayed in the heatmap cells

**Value**

The paris of duplicated samples.

**Author(s)**

Ruqian Lyu

**Examples**

```

data(snp_genotype)
or_genotype <- snp_genotype[,grep("X",colnames(snp_genotype))]
rownames(or_genotype) <- paste0(snp_genotype$CHR,"_",snp_genotype$POS)
or_genotype[,1] <- or_genotype[,5]
cr_genotype <- correctGT(or_genotype,ref = snp_genotype$C57BL.6J,
                        alt = snp_genotype$FVB.NJ..i.)
dups <- findDupSamples(cr_genotype)

```

---

getAFTracks

*getAFTracks*


---

**Description**

Generate the raw alternative allele frequencies tracks for all cells in the columns of provided 'co\_count'

**Usage**

```

getAFTracks(
  chrom = "chr1",
  path_loc = "./output/firstBatch/WC_522/",
  sampleName = "WC_522",
  nwindow = 80,
  barcodeFile,
  co_count,
  snp_track = NULL
)

```

**Arguments**

|             |   |
|-------------|---|
| chrom       | the chromosome  |
| path_loc    | the path prefix to the output files from sscocaller including "*_totalCount.mtx" and "_altCount.mtx"  |
| sampleName  | the sample name, which is the prefix of sscocaller's output files   |
| nwindow     | the number of windows for binning the chromosome  |
| barcodeFile | the barcode file containing the list of cell barcodes used as the input file for sscocaller   |
| co_count    | 'GRange' or 'RangedSummarizedExperiment' object, returned by countCO that contains the crossover intervals and the number of crossovers in each cell.                       |
| snp_track   | the SNP position track which is used for obtaining the SNP chromosome locations. It could be omitted and the SNP positions will be acquired from the "*_snpAnnot.txt" file. |

**Value**

a list object, in which each element is a list of two items with the cell's alternative allele frequency DataTrack and the called crossover ranges.

**Author(s)**

Ruqian Lyu

**Examples**

```

demo_path <- system.file("extdata",package = "comapr")
s1_rse_state <- readHapState("s1",chrom=c("chr1"),
                           path=demo_path,barcodeFile=NULL,minSNP = 0,
                           minlogllRatio = 50,
                           bpDist = 100,maxRawCO=10,
                           minCellSNP = 0)
s1_counts <- countCOs(s1_rse_state)

af_co_tracks <- getAFTracks(chrom ="chr1",
                           path_loc = demo_path,
                           sampleName = "s1",
                           barcodeFile = file.path(demo_path,
                                                    "s1_barcodes.txt"),
                           co_count = s1_counts)

```

getCellAFTrack

*getCellAFTrack Generates the DataTracks for plotting AF and crossover regions*

**Description**

It plots the raw alternative allele frequencies and highlight the crossover regions for the selected cell.

It plots the raw alternative allele frequencies and highlight the crossover regions for the selected cell.

**Usage**

```

getCellAFTrack(
  chrom = "chr1",
  path_loc = "./output/firstBatch/WC_522/",
  sampleName = "WC_522",
  nwindow = 80,
  barcodeFile,
  cellBarcode,
  co_count,
  snp_track = NULL,
  chunk = 1000L
)

```

```

getCellAFTrack(
  chrom = "chr1",
  path_loc = "./output/firstBatch/WC_522/",
  sampleName = "WC_522",
  nwindow = 80,

```

```

barcodeFile,
cellBarcode,
co_count,
snp_track = NULL,
chunk = 1000L
)

```

### Arguments

|             |   |
|-------------|---|
| chrom       | the chromosome  |
| path_loc    | the path prefix to the output files from sscocaller including "*_totalCount.mtx" and "_altCount.mtx"  |
| sampleName  | the sample name, which is the prefix of sscocaller's output files   |
| nwindow     | the number of windows for binning the chromosome  |
| barcodeFile | the barcode file containing the list of cell barcodes used as the input file for sscocaller   |
| cellBarcode | the selected cell barcode   |
| co_count    | 'GRange' or 'RangedSummarizedExperiment' object, returned by countCO that contains the crossover intervals and the number of crossovers in each cell.                       |
| snp_track   | the SNP position track which is used for obtaining the SNP chromosome locations. It could be omitted and the SNP positions will be acquired from the "*_snpAnnot.txt" file. |
| chunk       | An integer scalar indicating the chunk size to use, i.e., number of rows to read at any one time.   |

### Value

The DataTrack object defined in [DataTrack](#)

The DataTrack object defined in [DataTrack](#)

### Author(s)

Ruqian Lyu

### Examples

```

demo_path <- paste0(system.file("extdata", package = "comapr"), "/")
s1_rse_state <- readHapState("s1", chroms=c("chr1"),
                           path=demo_path, barcodeFile=NULL, minSNP = 0,
                           minlogllRatio = 50,
                           bpDist = 100, maxRawCO=10,
                           minCellsNP = 0)
s1_counts <- countCOs(s1_rse_state)
af_co_tracks <- getCellAFTrack(chrom = "chr1",
                              path_loc = demo_path,
                              sampleName = "s1",
                              barcodeFile = paste0(demo_path,
                                                    "s1_barcodes.txt"),
                              cellBarcode = "BC1",
                              co_count = s1_counts)

demo_path <- paste0(system.file("extdata", package = "comapr"), "/")

```

```

s1_rse_state <- readHapState("s1",chroms=c("chr1"),
                           path=demo_path,barcodeFile=NULL,minSNP = 0,
                           minlogllRatio = 50,
                           bpDist = 100,maxRawCO=10,
                           minCellsNP = 0)
s1_counts <- countCOs(s1_rse_state)
af_co_tracks <- getCellAFTrack(chrom ="chr1",
                              path_loc = demo_path,
                              sampleName = "s1",
                              barcodeFile = paste0(demo_path,
                                                    "s1_barcode.txt"),
                              cellBarcode = "BC1",
                              co_count = s1_counts)

```

---

|                |                       |
|----------------|-----------------------|
| getCellCORange | <i>getCellCORange</i> |
|----------------|-----------------------|

---

## Description

It finds the crossover intervals for a selected cell

## Usage

```
getCellCORange(co_count, cellBarcode)
```

## Arguments

|             |   |
|-------------|---|
| co_count    | ‘GRanges’ or ‘RangedSummarizedExperiment’ object, |
| cellBarcode | the selected cell’s barcode                       |

## Value

GRRange object containing the crossover intervals for the selected cell

## Author(s)

Ruqian Lyu

## Examples

```

demo_path <-paste0(system.file("extdata",package = "comapr"),"/")
s1_rse_state <- readHapState("s1",chroms=c("chr1"),
                           path=demo_path,barcodeFile=NULL,minSNP = 0,
                           minlogllRatio = 50,
                           bpDist = 100,maxRawCO=10,
                           minCellsNP = 0)
s1_counts <- countCOs(s1_rse_state)

co_ranges <- getCellCORange(cellBarcode = "BC1",
                           co_count = s1_counts)

```

---

|                |  |
|----------------|--|
| getCellDPTrack | <i>getCellDPTrack Generates the DataTrack for plotting DP of a selected cell</i> |
|----------------|--|

---

### Description

It plots the total allele counts for the selected cell.

### Usage

```
getCellDPTrack(
  chrom = "chr1",
  path_loc = "./output/firstBatch/WC_522/",
  sampleName = "WC_522",
  nwindow = 80,
  barcodeFile,
  cellBarcode,
  snp_track = NULL,
  chunk = 1000L,
  log = TRUE,
  plot_type = "hist"
)
```

### Arguments

|             |   |
|-------------|---|
| chrom       | the chromosome  |
| path_loc    | the path prefix to the output files from sscocaller including "*_totalCount.mtx"  |
| sampleName  | the sample name, which is the prefix of sscocaller's output files   |
| nwindow     | the number of windows for binning the chromosome  |
| barcodeFile | the barcode file containing the list of cell barcodes used as the input file for sscocaller   |
| cellBarcode | the selected cell barcode   |
| snp_track   | the SNP position track which is used for obtaining the SNP chromosome locations. It could be omitted and the SNP positions will be acquired from the "*_snpAnnot.txt" file. |
| chunk       | A integer scalar indicating the chunk size to use, i.e., number of rows to read at any one time.  |
| log         | whether the histogram of SNP density should be plotted on log scale (log10)   |
| plot_type   | the DataTrack plot type, default to be 'hist'   |

### Value

The DataTrack object defined in [DataTrack](#)

### Author(s)

Ruqian Lyu

**Examples**

```

demo_path <- system.file("extdata",package = "comapr")
s1_rse_state <- readHapState("s1",chrom=c("chr1"),
                           path=demo_path,barcodeFile=NULL,minSNP = 0,
                           minlogllRatio = 50,
                           bpDist = 100,maxRawCO=10,
                           minCellSNP = 0)
s1_counts <- countCOs(s1_rse_state)
dp_co_tracks <- getCellDPTrack(chrom ="chr1",
                              path_loc = demo_path,
                              sampleName = "s1",
                              barcodeFile = file.path(demo_path,
                                                         "s1_barcodes.txt"),
                              cellBarcode = "BC1")

```

---

getDistortedMarkers    *getDistortedMarkers*

---

**Description**

Marker segregation distortion detection using chisq-test

**Usage**

```
getDistortedMarkers(geno, p = c(0.5, 0.5), adj.method = "BH")
```

**Arguments**

|            |   |
|------------|---|
| geno       | the genotype data.frame of markers by samples from output of function correctGT |
| p          | the expected genotype ratio in a numeric vector, defaults to c(0.5,0.5)         |
| adj.method | Methods to adjust for multiple comparisons, defaults to "BH"                    |

**Details**

We expect the genotypes to appear with the frequencies of 1:1 homo\_alt:hets. We use `chisq.test` for finding markers that have genotypes among samples that are significantly different from the 1:1 ratio and report them

**Value**

data.frame with each row representing one SNP marker and columns containing the `chisq.test` results

**Author(s)**

Ruqian Lyu

**Examples**

```

data(parents_genom)
data(snp_genom_gr)
corrected_genom <- correctGT(gt_matrix = GenomicRanges::mcols(snp_genom_gr),
ref = parents_genom$ref,alt = parents_genom$alt,fail = "Fail",
wrong_label = "Homo_ref")
GenomicRanges::mcols(snp_genom_gr) <- corrected_genom
corrected_genom <- filterGT(snp_genom_gr, min_markers = 30,min_samples = 2)
pvalues <- getDistortedMarkers(GenomicRanges::mcols(corrected_genom))

```

---

getMeanDPTrack

*getMeanDPTrack*


---

**Description**

Generate the mean DP (Depth) DataTrack (from Gviz) for cells

**Usage**

```

getMeanDPTrack(
  chrom = "chr1",
  path_loc,
  nwindow = 80,
  sampleName,
  barcodeFile,
  plot_type = "hist",
  selectedBarcodes = NULL,
  snp_track = NULL,
  log = TRUE
)

```

**Arguments**

|                  |   |
|------------------|---|
| chrom            | the chromosome  |
| path_loc         | the path prefix to the output files from sscocaller including "*_totalCount.mtx" and "_altCount.mtx"  |
| nwindow          | the number of windows for binning the chromosome  |
| sampleName       | the sample name, which is the prefix of sscocaller's output files   |
| barcodeFile      | the barcode file containing the list of cell barcodes used as the input file for sscocaller   |
| plot_type        | the DataTrack plot type, default to be 'hist'   |
| selectedBarcodes | the selected cell barcodes which should be the barcodes that have been called crossovers for. If not supplied then all cells are counted.                                   |
| snp_track        | the SNP position track which is used for obtaining the SNP chromosome locations. It could be omitted and the SNP positions will be acquired from the "*_snpAnnot.txt" file. |
| log              | whether the histogram of SNP density should be plotted on log scale (log10)   |

**Value**

DataTrack object plotting the mean DP histogram for windowed chromosomes

**Author(s)**

Ruqian Lyu

**Examples**

```
demo_path <- paste0(system.file("extdata", package = "comapr"), "/")
meanDP_track <- getMeanDPTrack(chrom = "chr1",
                               path_loc = demo_path,
                               sampleName = "s1",
                               barcodeFile = paste0(demo_path,
                                                       "s1_barcodes.txt"))
```

---

getSNPDensityTrack      *getSNPDensityTrack*

---

**Description**

Generate the SNP density DataTrack (from 'Gviz') for selected chromosome

**Usage**

```
getSNPDensityTrack(
  chrom = "chr1",
  sampleName = "s1",
  path_loc = ".",
  nwindow = 80,
  plot_type = "hist",
  log = TRUE
)
```

**Arguments**

|            |  |
|------------|--|
| chrom      | the chromosome   |
| sampleName | the sample name, which is the prefix of sscocaller's output files                                    |
| path_loc   | the path prefix to the output files from sscocaller including "*_totalCount.mtx" and "_altCount.mtx" |
| nwindow    | the number of windows for binning the chromosome   |
| plot_type  | the DataTrack plot type, default to be 'hist'  |
| log        | whether the histogram of SNP density should be plotted on log scale (log10)                          |

**Value**

DataTrack object plotting the SNP density histogram

**Author(s)**

Ruqian Lyu

**Examples**

```
demo_path <- system.file("extdata", package = "comapr")
snp_track <- getSNPDensityTrack(chrom = "chr1",
                                path_loc = demo_path,
                                sampleName = "s1")
```

---

|              |   |
|--------------|---|
| parents_geno | <i>Parents' genotype for F1 samples in 'snp_geno'</i> |
|--------------|---|

---

**Description**

Parents' genotype for F1 samples in 'snp\_geno'

**Usage**

```
data(parents_geno)
```

**Format**

A data.frame:

**C57BL.6J** genotype of reference mouse train across markers

**FVB.NJ.i.** genotype of alternative mouse train across markers

---

|              |                     |
|--------------|---------------------|
| perCellChrQC | <i>perCellChrQC</i> |
|--------------|---------------------|

---

**Description**

A function that parses output ('\_viSegInfo.txt') from 'sgccaller' <https://gitlab.svi.edu.au/biocellgen-public/sgccaller> and generate cell cell (per chr) summary statistics

**Usage**

```
perCellChrQC(
  sampleName,
  chroms = c("chr1", "chr7", "chr15"),
  path,
  barcodeFile = NULL,
  doPlot = TRUE
)
```

**Arguments**

|             |   |
|-------------|---|
| sampleName  | the name of the sample to parse which is used as prefix for finding relevant files for the underlying sample        |
| chroms      | the character vectors of chromosomes to parse. Multiple chromosomes' results will be concated together.             |
| path        | the path to the files, with name patterns *chrom_vi.mtx, *chrom_viSegInfo.txt, end with slash                       |
| barcodeFile | defaults to NULL, it is assumed to be in the same directory as the other files and with name sampleName_barcode.txt |
| doPlot      | whether a plot should returned, default to TRUE   |

**Value**

a list object that contains the data.frame with summarised statistics per chr per cell and a plot (if doPlot)

**Author(s)**

Ruqian Lyu

**Examples**

```
demo_path <- system.file("extdata", package = "comapr")
pcQC <- perCellChrQC(sampleName="s1", chroms=c("chr1"),
  path=demo_path,
  barcodeFile=NULL)
```

---

permutDist

*permutDist*


---

**Description**

Permutation test of two sample groups

**Usage**

```
permutDist(co_gr, B = 100, mapping_fun = "k", group_by)
```

**Arguments**

|             |   |
|-------------|---|
| co_gr       | GRanges or RangedSummarizedExperiment object that contains the crossover counts for each marker interval across all samples. Returned by countCOs   |
| B           | integer the number of sampling times  |
| mapping_fun | character default to "k" (kosambi mapping function). It can be one of the mapping functions: "k", "h"   |
| group_by    | the prefix for each group that we need to generate distributions for (only when co_gr is a GRanges object). Or the column name for 'colData(co_gr)' that contains the group factor (only when co_gr is a RangedSummarizedExperiment object) |

**Details**

It shuffles the group labels for the samples and calculate a difference between two groups after shuffling.

**Value**

A list of three elements. 'permutes' of length B with numeric differences of permuted group differences, 'observed\_diff' the observed genetic distances of two groups, 'nSample', the number of samples in the first and second group.

**Author(s)**

Ruqian Lyu

**Examples**

```
data(coCount)
perms <- permuteDist(coCount, group_by = "sampleGroup", B=10)
```

---

perSegChrQC

*perSegChrQC*

---

**Description**

Plots the summary statistics of segments that are generated by 'sgcocaller' <https://gitlab.svi.edu.au/biocellgen-public/sgcocaller> which have been detected by finding consecutive viter states along the list of SNP markers.

**Usage**

```
perSegChrQC(
  sampleName,
  chroms = c("chr1", "chr7", "chr15"),
  path,
  barcodeFile = NULL,
  maxRawCO = 10
)
```

**Arguments**

|             |   |
|-------------|---|
| sampleName  | the name of the sample to parse which is used as prefix for finding relevant files for the underlying sample        |
| chroms      | the vector of chromosomes   |
| path        | the path to the files, with name patterns *chrom_vi.mtx, *chrom_viSegInfo.txt, end with slash                       |
| barcodeFile | defaults to NULL, it is assumed to be in the same directory as the other files and with name sampleName_barcode.txt |
| maxRawCO    | if a cell has more than 'maxRawCO' number of raw crossovers called across a chromosome, the cell is filtered out#'  |

**Details**

It provides guidance in filtering out close double crossovers that are not likely biological but due to technical reasons as well as crossovers that are supported by fewer number of SNPs at the ends of the chromosomes.

**Value**

Histogram plots for statistics summarized across all Viterbi state segments

**Author(s)**

Ruqian Lyu

**Examples**

```
demo_path <- system.file("extdata", package = "comapr")
s1_rse_qc <- perSegChrQC(sampleName="s1",
                        chroms=c("chr1"),
                        path=demo_path, maxRawCO=10)
```

---

plotCount

*plotCount*

---

**Description**

Plot the number of COs per sample group or per chromosome

**Usage**

```
plotCount(
  co_count,
  by_chr = FALSE,
  group_by = "sampleGroup",
  plot_type = "error_bar"
)

## S4 method for signature 'RangedSummarizedExperiment,missing,missing'
plotCount(
  co_count,
  by_chr = FALSE,
  group_by = "sampleGroup",
  plot_type = "error_bar"
)

## S4 method for signature 'RangedSummarizedExperiment,missing,character'
plotCount(
  co_count,
  by_chr = FALSE,
  group_by = "sampleGroup",
  plot_type = "error_bar"
```

```

)

## S4 method for signature 'RangedSummarizedExperiment,logical,character'
plotCount(
  co_count,
  by_chr = FALSE,
  group_by = "sampleGroup",
  plot_type = "error_bar"
)

## S4 method for signature 'RangedSummarizedExperiment,logical,missing'
plotCount(
  co_count,
  by_chr = FALSE,
  group_by = "sampleGroup",
  plot_type = "error_bar"
)

## S4 method for signature 'GRanges,logical,missing'
plotCount(
  co_count,
  by_chr = FALSE,
  group_by = "sampleGroup",
  plot_type = "error_bar"
)

## S4 method for signature 'GRanges,missing,missing'
plotCount(
  co_count,
  by_chr = FALSE,
  group_by = "sampleGroup",
  plot_type = "error_bar"
)

## S4 method for signature 'GRanges,missing,character'
plotCount(
  co_count,
  by_chr = FALSE,
  group_by = "sampleGroup",
  plot_type = "error_bar"
)

## S4 method for signature 'GRanges,logical,character'
plotCount(
  co_count,
  by_chr = FALSE,
  group_by = "sampleGroup",
  plot_type = "error_bar"
)

```

### Arguments

co\_count                    GRange or RangedSummarizedExperiment object, returned by countCO

|           |   |
|-----------|---|
| by_chr    | whether it should plot each chromosome separately   |
| group_by  | the column name in 'colData(co_count)' that specify the grouping factor. Or the character vector contains the unique prefix of sample names that are used for defining different sample groups. If missing all samples are assumed to be from one group |
| plot_type | determines what type the plot will be, choose from "error_bar" or "hist". Only relevant when by_chr=TRUE  |

**Value**

ggplot object

**Examples**

```
demo_path <- paste0(system.file("extdata", package = "comapr"), "/")
s1_rse_state <- readHapState("s1", choms=c("chr1"),
                           path=demo_path, barcodeFile=NULL, minSNP = 0,
                           minlogllRatio = 50,
                           bpDist = 100, maxRawCO=10,
                           minCellsNP = 0)
s1_count <- countCOs(s1_rse_state)
plotCount(s1_count)
```

---

|                 |                        |
|-----------------|------------------------|
| plotGeneticDist | <i>plotGeneticDist</i> |
|-----------------|------------------------|

---

**Description**

Plotting the calculated genetic distanced for each bin or marker interval supplied by the GRanges object

**Usage**

```
plotGeneticDist(gr, bin = TRUE, chr = NULL, cumulative = FALSE)
```

**Arguments**

|            |   |
|------------|---|
| gr         | GRanges object with genetic distances calculated for marker intervals                                 |
| bin        | TRUE or FALSE, indicating whether the supplied GRRange objecct is for binned interval                 |
| chr        | the specific chrs selected to plot  |
| cumulative | TRUE or FALSE, indicating whether it plots the bin-wise genetic distances or the cumulative distances |

**Value**

ggplot2 plot

**Author(s)**

Ruqian Lyu

**Examples**

```
data(coCount)
dist_se <- calGeneticDist(coCount)
plotGeneticDist(SummarizedExperiment::rowRanges(dist_se))
```

---

plotGTFreq

*plotGTFreq*


---

**Description**

Function to plot the genotypes for all samples faceted by genotype

**Usage**

```
plotGTFreq(geno)
```

**Arguments**

geno                    the genotype data.frame of markers by samples from output of function correctGT

**Value**

A ggplot object

**Author(s)**

Ruqian Lyu

**Examples**

```
data(snp_geno)
or_geno <- snp_geno[,grep("X",colnames(snp_geno))]
rownames(or_geno) <- paste0(snp_geno$CHR,"_",snp_geno$POS)
or_geno[1,] <- rep("Fail",dim(or_geno)[2])
cr_geno <- correctGT(or_geno,ref = snp_geno$C57BL.6J,
                    alt = snp_geno$FVB.NJ..i.)
ft_gt <- filterGT(cr_geno)
plotGTFreq(ft_gt)
```

---

plotWholeGenome

*Plot cumulative genetic distances across the genome*


---

**Description**

This function takes the calculated genetic distances for all marker intervals across all chromosomes provided and plot the cumulative genetic distances

**Usage**

```
plotWholeGenome(gr)
```

**Arguments**

`gr` GRanges object with genetic distances calculated for marker intervals

**Value**

A ggplot object

**Examples**

```
data(coCount)
dist_se <- calGeneticDist(coCount)
plotWholeGenome(SummarizedExperiment::rowRanges(dist_se))
```

---

|           |                  |
|-----------|------------------|
| readColMM | <i>readColMM</i> |
|-----------|------------------|

---

**Description**

Modified the 'Matrix::readMM' function for reading matrices stored in the Harwell-Boeing or MatrixMarket formats but only reads selected column.

**Usage**

```
readColMM(file, which.col, chunk = 1000L)
```

**Arguments**

`file` the name of the file to be read from as a character scalar. Those storing matrices in the MatrixMarket format usually end in ".mtx".

`which.col` An integer scalar, the column index

`chunk` An integer scalar indicating the chunk size to use, i.e., number of rows to read at any one time.

**Details**

See [readMM](#)

**Value**

A sparse matrix object that inherits from the "Matrix" class which the original dimensions. To get the vector of the specified column, one need to subset the matrix to select the column with the same index.

**Author(s)**

Ruqian Lyu

**Examples**

```
demo_path <- paste0(system.file("extdata", package = "comapr"), "/")
readColMM(file = paste0(demo_path, "s1_chr1_vi.mtx"), which.col=2, chunk=2)
```

---

|                           |                     |
|---------------------------|---------------------|
| <code>readHapState</code> | <i>readHapState</i> |
|---------------------------|---------------------|

---

### Description

A function that parses the viterbi state matrix (in .mtx format), barcode.txt and snpAnno.txt files for each individual.

### Usage

```
readHapState(
  sampleName,
  chroms = c("chr1"),
  path,
  barcodeFile = NULL,
  minSNP = 30,
  minlogllRatio = 200,
  bpDist = 100,
  maxRawCO = 10,
  nmad = 1.5,
  minCellSNP = 200,
  biasTol = 0.45
)
```

### Arguments

|                            |  |
|----------------------------|--|
| <code>sampleName</code>    | the name of the sample to parse which is used as prefix for finding relevant files for the underlying sample   |
| <code>chroms</code>        | the character vectors of chromosomes to parse. Multiple chromosomes' results will be concatenated together.  |
| <code>path</code>          | the path to the files, with name patterns <code>*chrom_vi.mtx</code> , <code>*chrom_viSegInfo.txt</code> , end with slash  |
| <code>barcodeFile</code>   | if NULL, it is assumed to be in the same directory as the other files and with name <code>sampleName_barcode.txt</code>  |
| <code>minSNP</code>        | the crossover(s) will be filtered out if introduced by a segment that has fewer than 'minSNP' SNPs to support.   |
| <code>minlogllRatio</code> | the crossover(s) will be filtered out if introduced by a segment that has lower than 'minlogllRatio' to its reversed state.  |
| <code>bpDist</code>        | the crossover(s) will be filtered out if introduced by a segment that is shorter than 'bpDist' basepairs. It can be a single value or a vector that is the same length and order with 'chroms'.  |
| <code>maxRawCO</code>      | if a cell has more than 'maxRawCO' number of raw crossovers called across a chromosome, the cell is filtered out   |
| <code>nmad</code>          | how many mean absolute deviations lower than the median number of SNPs per cell for a cell to be considered as low coverage cell and filtered. Only effective when number of cells are larger than 10. When effective, this or 'minCellSNP', whichever is larger, is applied |
| <code>minCellSNP</code>    | the minimum number of SNPs detected for a cell to be kept, used with 'nmads'   |

**biasTol** the SNP's haplotype ratio across all cells is assumed to be 1:1. This argument can be used for removing SNPs that have a biased haplotype. i.e. almost always inferred to be haplotype state 1. It specifies a bias tolerance value, SNPs with haplotype ratios deviating from 0.5 smaller than this value are kept. Only effective when number of cells are larger than 10

### Value

a RangedSummarizedExperiment with rowRanges as SNP positions that contribute to crossovers in any cells. colData contains cells annotation including barcodes and sampleName.

### Author(s)

Ruqian Lyu

### Examples

```
demo_path <- system.file("extdata", package = "comapr")
s1_rse_state <- readHapState(sampleName="s1", chroms=c("chr1"),
  path=paste0(demo_path, "/"),
  barcodeFile=NULL, minSNP = 0, minlogllRatio = 50,
  bpDist = 100, maxRawCO=10, minCellSNP=3)
s1_rse_state
```

---

snp\_geno

*Markers by genotype results for a group of samples*

---

### Description

Markers by genotype results for a group of samples

### Usage

```
data(snp_geno)
```

### Format

A data frame with columns:

**C57BL.6J** genotype of reference mouse train across markers

**FVB.NJ.i** genotype of alternative mouse train across markers

**POS** SNP marker base-pair location

**CHR** SNP marker chromosome location

**X100** a mouse sample

**X101** a mouse sample

**X102** a mouse sample

**X103** a mouse sample

**X104** a mouse sample

**X105** a mouse sample

**X106** a mouse sample

**X107** a mouse sample  
**X108** a mouse sample  
**X109** a mouse sample  
**X110** a mouse sample  
**X111** a mouse sample  
**X112** a mouse sample  
**X113** a mouse sample  
**X92** a mouse sample  
**X93** a mouse sample  
**X94** a mouse sample  
**X95** a mouse sample  
**X96** a mouse sample  
**X97** a mouse sample  
**X98** a mouse sample  
**X99** a mouse sample  
**rsID** the SNP ID

### Source

Statistics Canada. Table 001-0008 - Production and farm value of maple products, annual. <http://www5.statcan.gc.ca/cansim/>

---

snp\_genogr

*Markers by genotype results for a group of samples*

---

### Description

Markers by genotype results for a group of samples

### Usage

```
data(snp_genogr)
```

### Format

A GRanges object:

**X100** a mouse sample  
**X101** a mouse sample  
**X102** a mouse sample  
**X103** a mouse sample  
**X104** a mouse sample  
**X105** a mouse sample  
**X106** a mouse sample  
**X107** a mouse sample

**X108** a mouse sample  
**X109** a mouse sample  
**X110** a mouse sample  
**X111** a mouse sample  
**X112** a mouse sample  
**X113** a mouse sample  
**X92** a mouse sample  
**X93** a mouse sample  
**X94** a mouse sample  
**X95** a mouse sample  
**X96** a mouse sample  
**X97** a mouse sample  
**X98** a mouse sample  
**X99** a mouse sample  
**rsID** the SNP ID

#### Source

TBD

---

|            |   |
|------------|---|
| twoSamples | <i>RangedSummarizedExperiment</i> object containing the Viterbi states SNP markers for samples from two groups. 'colData(twoSamples)' contains the sample group factor. |
|------------|---|

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#### Description

RangedSummarizedExperiment object containing the Viterbi states SNP markers for samples from two groups. 'colData(twoSamples)' contains the sample group factor.

#### Usage

```
data(twoSamples)
```

#### Format

An object of class RangedSummarizedExperiment with 6 rows and 10 columns.

# Index

## \* datasets

coCount, 8  
 parents\_geno, 24  
 snp\_geno, 33  
 snp\_geno\_gr, 34  
 twoSamples, 35

## \* internal

.change\_missing, 2  
 .filterCOsExtra, 3  
 .label\_gt, 4  
 fill\_fail, 14  
 .change\_missing, 2  
 .filterCOsExtra, 3  
 .label\_gt, 4

bootstrapDist, 5

calGeneticDist, 6

calGeneticDist, GRanges, missing, ANY, ANY, character-method  
 (calGeneticDist), 6

calGeneticDist, GRanges, missing, ANY, ANY, missing-method  
 (calGeneticDist), 6

calGeneticDist, GRanges, numeric, ANY, ANY, character-method  
 (calGeneticDist), 6

calGeneticDist, GRanges, numeric, ANY, ANY, missing-method  
 (calGeneticDist), 6

calGeneticDist, RangedSummarizedExperiment, missing, ANY, ANY, character-method  
 (calGeneticDist), 6

calGeneticDist, RangedSummarizedExperiment, missing, ANY, ANY, missing-method  
 (calGeneticDist), 6

calGeneticDist, RangedSummarizedExperiment, numeric, ANY, ANY, character-method  
 (calGeneticDist), 6

calGeneticDist, RangedSummarizedExperiment, numeric, ANY, ANY, missing-method  
 (calGeneticDist), 6

coCount, 8

comapr, 9

combineHapState, 9

correctGT, 10

countBinState, 11

countCOs, 12

countCOs, GRanges-method (countCOs), 12

countCOs, RangedSummarizedExperiment-method  
 (countCOs), 12

countGT, 13

DataTrack, 18, 20

fill\_fail, 14

filterGT, 14

filterGT, GRanges, numeric, numeric-method  
 (filterGT), 14

filterGT, matrix, numeric, numeric-method  
 (filterGT), 14

findDupSamples, 15

getAFTracks, 16

getCellAFTrack, 17

getCellCORange, 19

getCellDPTrack, 20

getDistortedMarkers, 21

getMeanDPTrack, 22

getSNPDensityTrack, 23

parent\_geno, 24

perCellChrQC, 24

perCellDist, 25

perSegChrQC, 26

plotCount, 27

plotCount, GRanges, logical, character-method  
 (plotCount), 27

plotCount, GRanges, logical, missing-method

plotCount, GRanges, missing, character-method

plotCount, GRanges, missing, missing-method

plotCount, GRanges, missing, missing-method

plotCount, RangedSummarizedExperiment, logical, character-

method (plotCount), 27

plotCount, RangedSummarizedExperiment, logical, missing-me-

thod (plotCount), 27

plotCount, RangedSummarizedExperiment, missing, character-

method (plotCount), 27

plotCount, RangedSummarizedExperiment, missing, missing-me-

thod (plotCount), 27

plotGeneticDist, 29

plotGTFreq, 30

plotWholeGenome, 30

readColMM, 31

readHapState, [32](#)

readMM, [31](#)

snp\_geno, [33](#)

snp\_geno\_gr, [34](#)

twoSamples, [35](#)