

# Package ‘CellaRepertorium’

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**Type** Package

**Title** Data structures, clustering and testing for single cell immune receptor repertoires (scRNAseq RepSeq/AIRR-seq)

**Version** 1.10.0

**Description** Methods to cluster and analyze high-throughput single cell immune cell repertoires, especially from the 10X Genomics VDJ solution. Contains an R interface to CD-HIT (Li and Godzik 2006). Methods to visualize and analyze paired heavy-light chain data. Tests for specific expansion, as well as omnibus oligoclonality under hypergeometric models.

**License** GPL-3

**Depends** R (>= 4.0)

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**Suggests** testthat, readr, knitr, rmarkdown, ggplot2, BiocStyle, ggdendro, broom, lme4, RColorBrewer, SingleCellExperiment, scater, broom.mixed, cowplot, igraph, ggraph

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 'ggplot2-utils.R' 'pairing-methods.R' 'reexports.R'  
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## R topics documented:

.cluster_permute_test . . . . .	3
canonicalize_cell . . . . .	4
canonicalize_cluster . . . . .	5
ccdb_ex . . . . .	7
ccdb_join . . . . .	7
cdhit . . . . .	8
cdhit_ccdb . . . . .	9
cland . . . . .	10
cluster_filterset . . . . .	11
cluster_germline . . . . .	12
cluster_permute_test . . . . .	12
cluster_plot . . . . .	14
cluster_test_by . . . . .	15
ContigCellDB . . . . .	16
contigs_qc . . . . .	18
crosstab_by_celltype . . . . .	19
cross_tab_tbl . . . . .	19
entropy . . . . .	20
equalize_ccdb . . . . .	21
fancy_name_contigs . . . . .	22
filter_cdb . . . . .	23
fine_clustering . . . . .	24
fine_cluster_seqs . . . . .	25
generate_pseudobulk . . . . .	26
guess_celltype . . . . .	27
hushWarning . . . . .	27

ig_chain_recode . . . . .	28
map_axis_labels . . . . .	29
pairing_tables . . . . .	30
plot_cluster_factors . . . . .	32
plot_permute_test . . . . .	33
purity . . . . .	34
rank_prevalence_ccdb . . . . .	34
rbind,ContigCellDB-method . . . . .	36
reexports . . . . .	36
right_join_warn . . . . .	37
split_cdb . . . . .	38
[[,ContigCellDB,character,missing-method . . . . .	38
\$/,ContigCellDB-method . . . . .	40

**Index** **41**

.cluster\_permute\_test *Cell permutation tests (internal)*

**Description**

Cell permutation tests (internal)

**Usage**

```
.cluster_permute_test(
  labels,
  covariates,
  strata,
  statistic,
  contrasts,
  n_perm,
  alternative,
  ...
)
```

**Arguments**

- labels            factor of length n
- covariates       data.frame of length n
- strata           factor
- statistic        function of label (vector) and covariate (data.frame). If this returns a vector, then by default each level will be compared against each other, pairwise, but see the next section.
- contrasts        an optional list of numeric vectors. Each will be dotted with the statistic, or optionally a matrix provided in which case each **row** would be tested one-by-one.

n_perm	number of permutations to run
alternative	character naming the direction statistic should be fall under the alternative hypothesis
...	passed along to statistic

**Value**

a list containing the observed value of the statistic, the permuted values of the statistic, its expectation (under independence), a p-value, and the Monte Carlo standard error (of the expected value).

---

canonicalize_cell	<i>Find a canonical contig to represent a cell</i>
-------------------	--

---

**Description**

Using filtering in `contig_filter_args` and sorting in `tie_break_keys` and order find a single, canonical contig to represent each cell Fields in `contig_fields` will be copied over to the `cell_tbl`.

**Usage**

```
canonicalize_cell(
  ccdb,
  contig_filter_args = TRUE,
  tie_break_keys = c("umis", "reads"),
  contig_fields = tie_break_keys,
  order = 1,
  overwrite = TRUE
)
```

**Arguments**

ccdb	<a href="#">ContigCellDB()</a>
contig_filter_args	an expression passed to <code>dplyr::filter()</code> . Unlike <code>filter</code> , multiple criteria must be & together, rather than using commas to separate. These act on <code>ccdb\$contig_tbl</code>
tie_break_keys	(optional) character naming fields in <code>contig_tbl</code> that are used sort the contig table in descending order. Used to break ties if <code>contig_filter_args</code> does not return a unique contig for each cluster
contig_fields	Optional fields from <code>contig_tbl</code> that will be copied into the <code>cluster_tbl</code> from the canonical contig.
order	The rank order of the contig, based on <code>tie_break_keys</code> to return. If <code>tie_break_keys</code> included an ordered factor (such as <code>chain</code> ) this could be used to return the second chain.
overwrite	logical – should non-key fields in <code>y</code> be overwritten using <code>x</code> , or should a suffix (".y") be added

**Value**

`ContigCellDB()` with some number of clusters/contigs/cells but with "canonical" values copied into `cell_tbl`

**See Also**

`canonicalize_cluster()`

**Examples**

```
# Report beta chain with highest umi-count, breaking ties with reads
data(ccdb_ex)
beta = canonicalize_cell(ccdb_ex, chain == 'TRB',
  tie_break_keys = c('umis', 'reads'),
  contig_fields = c('umis', 'reads', 'chain', 'v_gene', 'd_gene', 'j_gene'))
head(beta$cell_tbl)

# Stable: only adds fields to `cell_tbl`
stopifnot(dplyr::all_equal(beta$cell_tbl[ccdb_ex$cell_pk],
  ccdb_ex$cell_tbl[ccdb_ex$cell_pk], ignore_row_order = TRUE))

#Report cdr3 with highest UMI count, but only when > 5 UMIs support it
umi5 = canonicalize_cell(ccdb_ex, umis > 5,
  tie_break_keys = c('umis', 'reads'), contig_fields = c('umis', 'cdr3'))
stopifnot(all(umi5$cell_tbl$umis > 5, na.rm = TRUE))
```

---

`canonicalize_cluster` *Find a canonical contig to represent a cluster*

---

**Description**

Find a canonical contig to represent a cluster

**Usage**

```
canonicalize_cluster(
  ccdb,
  contig_filter_args,
  tie_break_keys = character(),
  order = 1,
  representative = ccdb$cluster_pk[1],
  contig_fields = c("cdr3", "cdr3_nt", "chain", "v_gene", "d_gene", "j_gene"),
  overwrite = TRUE
)
```

**Arguments**

ccdb	<a href="#">ContigCellDB()</a>
contig_filter_args	an expression passed to <a href="#">dplyr::filter()</a> . Unlike filter, multiple criteria must be & together, rather than using commas to separate. These act on <code>ccdb\$contig_tbl</code>
tie_break_keys	(optional) character naming fields in <code>contig_tbl</code> that are used sort the contig table in descending order. Used to break ties if <code>contig_filter_args</code> does not return a unique contig for each cluster
order	The rank order of the contig, based on <code>tie_break_keys</code> to return. If <code>tie_break_keys</code> included an ordered factor (such as <code>chain</code> ) this could be used to return the second chain.
representative	an optional field from <code>contig_tbl</code> that will be made unique. Serve as a surrogate <code>cluster_pk</code> .
contig_fields	Optional fields from <code>contig_tbl</code> that will be copied into the <code>cluster_tbl</code> from the canonical contig.
overwrite	logical – should non-key fields in <code>y</code> be overwritten using <code>x</code> , or should a suffix (".y") be added

**Value**

[ContigCellDB\(\)](#) with some number of clusters/contigs/cells but with "canonical" values copied into `cluster_tbl`

**See Also**

[canonicalize\\_cell\(\)](#) [left\\_join\\_warn\(\)](#)

**Examples**

```
library(dplyr)
data(ccdb_ex)
ccdb_ex_small = ccdb_ex
ccdb_ex_small$cell_tbl = ccdb_ex_small$cell_tbl[1:200,]
ccdb_ex_small = cdhit_ccdb(ccdb_ex_small,
  sequence_key = 'cdr3_nt', type = 'DNA', cluster_name = 'DNA97',
  identity = .965, min_length = 12, G = 1)
ccdb_ex_small = fine_clustering(ccdb_ex_small, sequence_key = 'cdr3_nt', type = 'DNA')

# Canonicalize with the medoid contig is probably what is most common
ccdb_medoid = canonicalize_cluster(ccdb_ex_small)

# But there are other possibilities.
# To pass multiple "AND" filter arguments must use &
ccdb_umi = canonicalize_cluster(ccdb_ex_small,
  contig_filter_args = chain == 'TRA' & length > 500, tie_break_keys = 'umis',
  contig_fields = c('chain', 'length'))
ccdb_umi$cluster_tbl %>% dplyr::select(chain, length) %>% summary()
```

---

ccdb_ex	<i>A preconstructed ContigClusterDB from the contigs_qc data</i>
---------	--

---

**Description**

A preconstructed ContigClusterDB from the contigs\_qc data

**Usage**

```
data(ccdb_ex)
```

**Format**

```
ccdb_ex = ContigCellDB_10XVDJ(contigs_qc, contig_pk = c('pop', 'sample', 'barcode',
'contig_id'), cell_pk = c('pop', 'sample', 'barcode'))
```

**See Also**

[contigs\\_qc](#)

---

ccdb_join	<i>Join dataframe or SingleCellExperiment object with ContigCellDB object</i>
-----------	---

---

**Description**

Join dataframe or SingleCellExperiment object with ContigCellDB object

**Usage**

```
ccdb_join(template, ccdb, join_fun = dplyr::left_join, by = ccdb$cell_pk)
```

**Arguments**

template	data.frame or SingleCellExperiment object to be joined with ccdb.
ccdb	A ContigCellDB object.
join_fun	Function used for the join operation.
by	A character vector of variables to join by.

**Value**

[ContigCellDB\(\)](#)

**Examples**

```
data(ccdb_ex)
to_join = dplyr::bind_rows(ccdb_ex$cell_tbl[1:10,],
dplyr::tibble(barcode = c('extra1', 'extra2'), sample = LETTERS[1:2],
pop = LETTERS[1:2]))
ccdb_join(to_join, ccdb_ex)
```

---

cdhit

*R interface to CDHIT/CDHITest*


---

**Description**

CDHIT is a greedy algorithm to cluster amino acid or DNA sequences based on a minimum identity. By default, in this package it is configured perform ungapped, global alignments with no clipping at start or end. The `identity` is the number of identical characters in alignment divided by the full length of the shorter sequence. Set `s < 1` to change the minimum coverage of the shorter sequence, which will allow clipping at start or end. Changing `G = 0` changes the meaning of the `identity` to be the number of identical characters in the alignment divided by the length of the alignment. In this case, you must also set the alignment coverage controls `aL`, `AL`, `aS`, `AS`.

**Usage**

```
cdhit(
  seqs,
  identity = NULL,
  kmerSize = NULL,
  min_length = 6,
  s = 1,
  G = 1,
  only_index = FALSE,
  showProgress = interactive(),
  ...
)
```

**Arguments**

<code>seqs</code>	AAseq or DNaseq
<code>identity</code>	minimum proportion identity
<code>kmerSize</code>	word size. If <code>NULL</code> , it will be chosen automatically based on the identity. You may need to lower it below 5 for AAseq with identity less than .7.
<code>min_length</code>	Minimum length for sequences to be clustered. An error if something smaller is passed.
<code>s</code>	fraction of shorter sequence covered by alignment.
<code>G</code>	1 for global alignment, 0 for local. If doubt, pick global.
<code>only_index</code>	if <code>TRUE</code> only return the integer cluster indices, otherwise return a tibble.

showProgress show a status bar  
 ... other arguments that can be passed to cdhit, see <https://github.com/weizhongli/cdhit/wiki/3.-User's-Guide#CDHIT> for details. These will override any default values.

## Details

CDHit is by Fu, Niu, Zhu, Wu and Li (2012). The R interface is originally by Thomas Lin Pedersen and was transcribed here because it is not exported from the package FindMyFriends, which is orphaned.

## Value

vector of integer of length seqs providing the cluster ID for each sequence, or a tibble. See details.

## Examples

```
fasta_path = system.file('extdata', 'demo.fasta', package='CellaRepertorium')
aaseq = Biostrings::readAAStringSet(fasta_path)
# 100% identity, global alignment
cdhit(aaseq, identity = 1, only_index = TRUE)[1:10]
# 100% identity, local alignment with no padding of endpoints
cdhit(aaseq, identity = 1, G = 0, aL = 1, aS = 1, only_index = TRUE)[1:10]
# 100% identity, local alignment with .9 padding of endpoints
cdhit(aaseq, identity = 1, G = 0, aL = .9, aS = .9, only_index = TRUE)[1:10]
# a tibble
tbl = cdhit(aaseq, identity = 1, G = 0, aL = .9, aS = .9, only_index = FALSE)
```

---

cdhit\_ccdb

*Use `cdhit()` to cluster a `ContigCellDB()`*

---

## Description

See <https://github.com/weizhongli/cdhit/wiki/3.-User's-Guide#CDHIT> for details on other potential arguments to ... These will override any default values.

## Usage

```
cdhit_ccdb(
  ccdb,
  sequence_key,
  type = c("DNA", "AA"),
  cluster_pk = "cluster_idx",
  ...
)
```

**Arguments**

ccdb	An object of class <code>ContigCellDB()</code>
sequence_key	character naming the column in the <code>contig_tbl</code> containing the sequence to be clustered
type	one of 'DNA' or 'AA'
cluster_pk	character specifying key, and name for the clustering.
...	Arguments passed on to <code>cdhit</code>
	<code>identity</code> minimum proportion identity
	<code>kmerSize</code> word size. If NULL, it will be chosen automatically based on the <code>identity</code> . You may need to lower it below 5 for AAseq with <code>identity</code> less than .7.
	<code>min_length</code> Minimum length for sequences to be clustered. An error if something smaller is passed.
	<code>s</code> fraction of shorter sequence covered by alignment.
	<code>showProgress</code> show a status bar
	<code>G</code> 1 for global alignment, 0 for local. If doubt, pick global.

**Value**

`ContigCellDB()`

**See Also**

`cdhit()`

**Examples**

```
data(ccdb_ex)
res = cdhit_ccdb(ccdb_ex, 'cdr3_nt', type = 'DNA',
  cluster_name = 'DNA97', identity = .965, min_length = 12, G = 1)
res$cluster_tbl
res$contig_tbl
res$cluster_pk
```

---

cland

*Cluster "And" intersection*

---

**Description**

For each contig present in both X and Y, a new cluster is defined that combines cluster identities in both X and Y. In the resulting `ContigCellDB`, two contigs are in the same cluster if they are in the same cluster in X and the same cluster in Y. X and Y must have matching `contig_pk`. The `contig_tbl` has fields from X for contigs present in both X and Y. The `cell_tbl` from X is carried forward unchanged, while the `cluster_tbl` in the result contains the mapping between the ancestral clustering, and the derived.

**Usage**

```
cland(X, Y, new_pk)
```

**Arguments**

X	ContigCellDB
Y	ContigCellDB
new_pk	optional character naming the new pk.

**Examples**

```
data(ccdb_ex)
ccdb_germ = cluster_germline(ccdb_ex, cluster_pk = 'germline_idx')
ccdb_cdr3 = cdhit_ccdb(ccdb_ex, 'cdr3_nt', type = 'DNA',
cluster_name = 'DNA97', identity = .965, min_length = 12, G = 1)
ccdb_cdr3 = cland(ccdb_cdr3, ccdb_germ)
```

---

cluster\_filterset      *A filtration of clusters*

---

**Description**

Return clusters that match all provided conditions

**Usage**

```
cluster_filterset(min_number = 0, min_freq = 0, white_list = NULL)
```

**Arguments**

min_number	integer	At least this many cells
min_freq	numeric	At least this frequency
white_list	data.frame	keyed by cluster_pk that must match

**Value**

object representing the filtration (currently a list)

**Examples**

```
cluster_filterset(min_number = 1, min_freq = 0)
```

---

cluster_germline	<i>Cluster contigs by germline properties</i>
------------------	---

---

### Description

Cluster contigs by germline properties

### Usage

```
cluster_germline(
  ccdb,
  segment_keys = c("v_gene", "j_gene", "chain"),
  cluster_pk = "cluster_idx"
)
```

### Arguments

ccdb	<a href="#">ContigCellDB()</a>
segment_keys	fields in contig_tbl that identify a cluster
cluster_pk	name of cluster to be added to cluster_tbl

### Value

[ContigCellDB\(\)](#)

### Examples

```
data(ccdb_ex)
ccdb_ex = cluster_germline(ccdb_ex)
ccdb_ex$cluster_tbl
```

---

cluster_permute_test	<i>Tests for independence between labels and covariates using permutation of cells</i>
----------------------	--

---

### Description

This tests a statistic for association between labels (for instance, cluster/clonal ID) and covariates (for instance, subject or treatment) by permuting the link between the two. Each observation represents a cell. `statistic` is any function of labels

**Usage**

```
cluster_permute_test(
  ccdb,
  cell_covariate_keys,
  cell_label_key = ccdb$cluster_pk,
  cell_stratify_keys,
  statistic,
  contrasts = NULL,
  n_perm,
  alternative = c("two.sided", "less", "greater"),
  sanity_check_strata = TRUE,
  ...
)
```

**Arguments**

ccdb	ContigCellDB
cell_covariate_keys	character naming fields in ccdb\$cell_tbl
cell_label_key	character naming a single field in ccdb\$cell_tbl
cell_stratify_keys	optional character naming fields in ccdb\$cell_tbl under which permutations of cell_label_key will occur. This means that the test will occur conditional on these covariates. Must be disjoint from cell_covariate_keys.
statistic	function of label (vector) and covariate (data.frame). If this returns a vector, then by default each level will be compared against each other, pairwise, but see the next section.
contrasts	an optional list of numeric vectors. Each will be dotted with the statistic, or optionally a matrix provided in which case each <b>row</b> would be tested one-by-one.
n_perm	number of permutations to run
alternative	character naming the direction statistic should be fall under the alternative hypothesis
sanity_check_strata	logical, should cell_stratify_keys be checked for sanity?
...	passed to statistic

**Value**

a list containing the observed value of the statistic, the permuted values of the statistic, its expectation (under independence), a p-value, and the Monte Carlo standard error (of the expected value).

**See Also**

[purity\(\)](#)

**Examples**

```

library(dplyr)
# covariate should name one or more columns in `cell_tbl`

cluster_idx = c(1, 1, 1, 2, 2, 3, 3)
subject = c('A', 'A', 'B', 'B', 'B', 'C', 'C')
contig_tbl = tibble(contig_pk = seq_along(cluster_idx), cluster_idx, subject)
ccdb_test = ContigCellDB(contig_tbl = contig_tbl, contig_pk = 'contig_pk',
cell_pk = c('contig_pk', 'subject', 'cluster_idx'), cluster_pk = 'cluster_idx')
ccdb_test$cell_tbl

clust_test = cluster_permute_test(ccdb_test, 'subject', 'cluster_idx',
statistic = purity, n_perm = 50)
library(ggplot2)
plot_permute_test(perm_test = clust_test)
tidy.PermuteTest(clust_test)

```

---

cluster\_plot

*Make a plot showing properties of the clustering*


---

**Description**

The number of elements per cluster and the average distance between the medoid and other elements are plotted.

**Usage**

```
cluster_plot(cdb, return_plotlist = FALSE)
```

**Arguments**

`cdb` A fine\_clustering ContigCellDB object

`return_plotlist` should a list of ggplot2 plots be returned. If FALSE, a cowplot composite is returned.

**Value**

a cowplot composite or a list of plots.

**Examples**

```

library(dplyr)
data(ccdb_ex)
ccdb_ex_small = ccdb_ex
ccdb_ex_small$cell_tbl = ccdb_ex_small$cell_tbl[1:200,]
ccdb_ex_small = cdhit_ccdb(ccdb_ex_small,
sequence_key = 'cdr3_nt', type = 'DNA', cluster_name = 'DNA97',
identity = .965, min_length = 12, G = 1)

```

```

ccdb_ex_small = fine_clustering(ccdb_ex_small, sequence_key = 'cdr3_nt', type = 'DNA')

# Canonicalize with the medoid contig is probably what is most common
ccdb_medoid = canonicalize_cluster(ccdb_ex_small)

# But there are other possibilities.
# To pass multiple "AND" filter arguments must use &
ccdb_umi = canonicalize_cluster(ccdb_ex_small,
contig_filter_args = chain == 'TRA' & length > 500, tie_break_keys = 'umis',
contig_fields = c('chain', 'length'))
ccdb_umi$cluster_tbl %>% dplyr::select(chain, length) %>% summary()
cluster_plot(ccdb_ex_small)

```

---

cluster_test_by	<i>Test clusters for differential usage</i>
-----------------	---

---

## Description

Typically one will want to stratify by chain by calling `cluster_test_by`, as this will calculate the number of cell "trials" separately depending on the chain recovered.

## Usage

```

cluster_test_by(ccdb, fields = "chain", tbl = "cluster_tbl", ...)

cluster_logistic_test(
  formula,
  ccdb,
  filterset = cluster_filterset(),
  contig_filter_args = TRUE,
  tie_break_keys = c("umis", "reads"),
  add_cluster_tbl = FALSE,
  keep_fit = FALSE,
  fitter = glm_glmmer,
  silent = FALSE
)

```

## Arguments

<code>ccdb</code>	<a href="#">ContigCellDB()</a>
<code>fields</code>	character naming fields in <code>tbl</code>
<code>tbl</code>	one of <code>contig_tbl</code> , <code>cell_tbl</code> or <code>cluster_tbl</code>
<code>...</code>	passed to <code>cluster_logistic_test</code>
<code>formula</code>	the <b>right-hand side</b> of a glmer or glm-style formula.
<code>filterset</code>	a call to <a href="#">cluster_filterset()</a> that will be used to subset clusters.

<code>contig_filter_args</code>	an expression passed to <code>dplyr::filter()</code> . Unlike <code>filter</code> , multiple criteria must be & together, rather than using commas to separate. These act on <code>ccdb\$contig_tbl</code>
<code>tie_break_keys</code>	(optional) character naming fields in <code>contig_tbl</code> that are used sort the contig table in descending order. Used to break ties if <code>contig_filter_args</code> does not return a unique contig for each cluster
<code>add_cluster_tbl</code>	logical should the output be joined to the <code>cluster_tbl</code> ?
<code>keep_fit</code>	logical as to whether the fit objects should be returned as a list column
<code>fitter</code>	a function taking arguments <code>formula</code> , <code>data</code> , <code>is_mixed</code> and <code>keep_fit</code> that is run on each cluster. Should return a <code>tibble</code> or <code>data.frame</code>
<code>silent</code>	logical. Should warnings from fitting functions should be suppressed?

**Value**

table with one row per cluster/term.

**Functions**

- `cluster_test_by`: split `ccdb` and conduct tests within strata

**Examples**

```
library(dplyr)
data(ccdb_ex)
ccdb_ex = cluster_germline(ccdb_ex)
trav1 = filter(ccdb_ex$cluster_tbl, v_gene == 'TRAV1')
cluster_logistic_test(~pop + (1|sample), ccdb_ex,
  filterset = cluster_filterset(white_list= trav1))
# Fixed effect analysis of each cluster, by chain
prev4 = ccdb_ex$contig_tbl %>% group_by(cluster_idx) %>%
  summarize(n()) %>% filter(`n()`>= 4)
cluster_test_by(ccdb = ccdb_ex, fields = 'chain',
  tbl = 'cluster_tbl', formula = ~ pop, filterset = cluster_filterset(white_list= prev4))
```

**Description**

Construct a ContigCellDB

**Usage**

```
ContigCellDB(
  contig_tbl,
  contig_pk,
  cell_tbl,
  cell_pk,
  cluster_tbl,
  cluster_pk = character(),
  equalize = TRUE
)

ContigCellDB_10XVDJ(
  contig_tbl,
  contig_pk = c("barcode", "contig_id"),
  cell_pk = "barcode",
  ...
)
```

**Arguments**

<code>contig_tbl</code>	a data frame of contigs, and additional fields describing their properties
<code>contig_pk</code>	character vector naming fields in <code>contig_tbl</code> that uniquely identify a row/contig
<code>cell_tbl</code>	a data frame of cell barcodes, and (optional) additional fields describing their properties
<code>cell_pk</code>	character vector naming fields in <code>cell_tbl</code> that uniquely identify a cell barcode
<code>cluster_tbl</code>	A data frame that provide cluster assignments for each contig
<code>cluster_pk</code>	If <code>cluster_tbl</code> was provided, a character vector naming fields in <code>cluster_tbl</code> that uniquely identify a cluster
<code>equalize</code>	logical. Should the contig, cells and clusters be equalized by taking the intersection of their common keys?
<code>...</code>	passed to <a href="#">ContigCellDB()</a>

**Value**

ContigCellDB

**Functions**

- `ContigCellDB_10XVDJ`: provide defaults that correspond to identifiers in 10X VDJ data

**Accessors/mutators**

See [\\$,ContigCellDB-method](#) for more on how to access and mutate slots. See [mutate\\_cdb\(\)](#) and [filter\\_cdb\(\)](#) for endomorphic filtering/mutation methods See [split\\_cdb\(\)](#) to split into a list, and [rbind.ContigCellDB\(\)](#) for the inverse operation.

**See Also**

[\\$,ContigCellDB-method](#)

**Examples**

```
data(contigs_qc)
contigs_qc

cdb = ContigCellDB(contigs_qc, contig_pk = c('barcode', 'pop', 'sample', 'contig_id'),
  cell_pk = c('barcode', 'pop', 'sample'))
cdb

# everything that was in contigs_qc
cdb$contig_tbl

# Only the cell_pk are included by default (until clustering/canonicalization)
cdb$cell_tbl

# Empty, since no cluster_pk was specified
cdb$cluster_tbl

# Keys
cdb$contig_pk
cdb$cell_pk
cdb$cluster_pk
```

---

contigs\_qc

*Filtered and annotated contigs of TCR from mice*

---

**Description**

Data for c57bl6 and balbc mice TCR were downloaded from 10x Genomics website as shown in `system.file('script/10XMouseTCR_v3_chem.R', package = 'CellaRepertorium')`. Additional processing of these data is done in the vignette `mouse_tcell_qc` and are serialized to serve as an examples for other vignettes and documentation.

**Usage**

```
data(contigs_qc)
```

**Format**

A data frame of 3399 contigs and 22 fields, all except 4 are originally defined in <https://support.10xgenomics.com/single-cell-vdj/software/pipelines/latest/output/annotation#contig>. The following fields were defined ex post facto.

1. anno\_file: Path to original csv file
2. pop: Mouse strain.

3. sample: An artificial "replicate" from the original data defined by subsampling with replacement
4. celltype: The putative cell type of the contig.

---

crosstab\_by\_celltype *Count contig UMIs by celltype*

---

### Description

Count contig UMIs by celltype

### Usage

```
crosstab_by_celltype(ccdb)
```

### Arguments

ccdb                    A ContigCellDB object

### Value

a table, keyed by cell\_pk counting UMIs per celltype

### See Also

[guess\\_celltype\(\)](#)

### Examples

```
data(ccdb_ex)
nrow(ccdb_ex$cell_tbl)
total_umi = crosstab_by_celltype(ccdb_ex)
nrow(total_umi)
```

---

cross\_tab\_tbl                    *Generate a 2d cross tab using arbitrary numbers of columns as factors*

---

### Description

As many rows as unique combs of x\_fields As many columns as unique combs of y\_fields No NA.

### Usage

```
cross_tab_tbl(tbl, x_fields, y_fields)
```

**Arguments**

tbl	data.frame
x_fields	character fields in tbl
y_fields	character fields in tbl

**Value**

tibble

**Examples**

```
cross_tab_tbl(mtcars, c('cyl', 'gear'), 'carb')
```

---

entropy

*Calculate the entropy of a vector*

---

**Description**

Calculate the entropy of a vector

**Usage**

```
entropy(v, pseudo_count = length(v)/1000, na.action = na.fail)
```

```
np(v, p = 0.05, pseudo_count = p/5, na.action = na.fail)
```

```
modal_category(v, na.action = na.fail)
```

**Arguments**

v	categorical vector
pseudo_count	number of pseudo counts to add on, to stabilize empty categories
na.action	how to handle NA values
p	proportion threshold

**Value**

the sample entropy

**Functions**

- np: The number of categories exceeding p proportion of the total
- modal\_category: The modal category of v. Ties are broken by lexicographic order of the factor levels.

**Examples**

```

v2 = gl(2, 4)
v4 = gl(4, 4)
stopifnot(entropy(v2) < entropy(v4))
v_empty = v2[1:4] #empty level 2
stopifnot(is.finite(entropy(v_empty))) # pseudo_count

np(v4, p = .2, pseudo_count = 0)
np(v4, p = .25, pseudo_count = 0)
np(v4, p = .25, pseudo_count = .0001)

modal_category(v4)
modal_category(v4[-1])

```

---

equalize\_ccdb

*Take the intersection of keys in tables in x*


---

**Description**

The cells in `cell_tbl`, and clusters in `cluster_tbl` can potentially be a superset of the `contig_tbl`.

**Usage**

```
equalize_ccdb(x, cell = TRUE, contig = TRUE, cluster = TRUE, sort = FALSE)
```

**Arguments**

<code>x</code>	<code>ContigCellDB()</code>
<code>cell</code>	logical equalize cells
<code>contig</code>	logical equalize contigs
<code>cluster</code>	logical equalize clusters
<code>sort</code>	logical should equalized fields also be <code>order()</code> ed by their primary keys?

**Details**

- `equalize_ccdb(x, cell = TRUE)` trims cells that aren't in `contig_tbl` or `cluster_tbl`.
- `equalize_ccdb(x, cluster = TRUE)` trims clusters that aren't in `contig_tbl`.
- `equalize_ccdb(x, contig = TRUE)` trims contigs that aren't `cell_tbl` or `cluster_tbl`.

**Value**

`ContigCellDB()`

**Default equalization**

Modification to `contig_tbl` (with `$`) always equalizes contigs and clusters. Modification to `cell_tbl` equalizes only contigs. Modification to `cluster_tbl` equalizes contigs and clusters.

**Examples**

```

library(dplyr)
tbl = tibble(clust_idx = gl(3, 2), cell_idx = rep(1:3, times = 2), contig_idx = 1:6)
ccdb = ContigCellDB(tbl, contig_pk = c('cell_idx', 'contig_idx'),
cell_pk = 'cell_idx', cluster_pk = 'clust_idx')
# 3 cells
ccdb
ccdb$cell_tbl = bind_rows(ccdb$cell_tbl, tibble(cell_idx = 0))
# 4 cells now
ccdb
# 3 cells again
equalize_ccdb(ccdb)
# remove all contigs from cell 1, and one contig from cell 2
ccdb$contig_tbl = ccdb$contig_tbl[-c(1, 2, 4),]
# no changes to cell_tbl yet
ccdb
# trim cell_tbl to 2 cells, keep all clusters
equalize_ccdb(ccdb, cluster = FALSE)
# trim both cells and clusters
equalize_ccdb(ccdb, cluster = TRUE)

```

---

fancy\_name\_contigs      *Generate a legible name for a series of contigs*

---

**Description**

Generate a legible name for a series of contigs

**Usage**

```
fancy_name_contigs(contig_tbl, prefix)
```

**Arguments**

contig_tbl	An all_contig_annotations.csv file, output from VDJ Cell ranger. Importantly, this should contain columns chain, v_gene, d_gene, j_gene
prefix	an optional prefix added to each contig, eg, possibly a sample id.

**Value**

character

**Examples**

```

library(dplyr)
contig_anno_path = system.file('extdata', 'all_contig_annotations_balbc_1.csv.xz',
package = 'CellaRepertorium')
contig_anno = readr::read_csv(contig_anno_path)
contig_anno = contig_anno %>% mutate(fancy_name =

```

```
fancy_name_contigs(., prefix = 'b6_1')
stopifnot(!any(duplicated(contig_anno$fancy_name)))
```

---

filter_cdb	<i>Create new or update existing columns of ContigCellDB tables</i>
------------	---

---

## Description

Create new or update existing columns of ContigCellDB tables

## Usage

```
filter_cdb(ccdb, ..., tbl = "contig_tbl")
```

```
mutate_cdb(ccdb, ..., tbl = "contig_tbl")
```

## Arguments

ccdb	<a href="#">ContigCellDB()</a>
...	name and value pair of column that will be updated
tbl	character. One of contig_tbl, cell_tbl or cluster_tbl, naming the table to be updated.

## Value

ContigCellDB object with updated table

## Functions

- filter\_cdb: Filter rows of a table in a ContigCellDB object

## See Also

[dplyr::mutate\(\)](#)

[dplyr::filter\(\)](#)

## Examples

```
data(ccdb_ex)
subset_contig = filter_cdb(ccdb_ex, full_length, productive == 'True',
high_confidence, chain != 'Multi', nchar(cdr3) > 5)
subset_cell = filter_cdb(ccdb_ex, sample == 4, tbl = 'cell_tbl')
data(ccdb_ex)
new_contig = mutate_cdb(ccdb_ex, new_col = 1)
new_cell = mutate_cdb(ccdb_ex, new_col = 1, tbl = 'contig_tbl')
```

---

fine_clustering	<i>Perform additional clustering of sequences within groups</i>
-----------------	---

---

**Description**

Perform additional clustering of sequences within groups

**Usage**

```
fine_clustering(
  ccdb,
  sequence_key,
  type,
  max_affinity = NULL,
  keep_clustering_details = FALSE,
  ...
)
```

**Arguments**

ccdb	A <a href="#">ContigCellDB()</a> object
sequence_key	character naming column in contig_tbl with sequence
type	'AA' or 'DNA'
max_affinity	numeric naming the maximal affinity for the sparse affinity matrix that is constructed. Not currently used.
keep_clustering_details	logical – should output of fine_cluster_seqs be kept as a list column
...	Arguments passed on to <a href="#">fine_cluster_seqs</a>
big_memory_brute	attempt to cluster more than 4000 sequences? Clustering is quadratic, so this will take a long time and might exhaust memory
method	one of 'substitutionMatrix' or 'levenshtein'
substitution_matrix	a character vector naming a substitution matrix available in Biostrings, or a substitution matrix itself

**Value**

[ContigCellDB\(\)](#) object with updated contig\_tbl and cluster\_tbl

**Examples**

```
library(dplyr)
data(ccdb_ex)
ccdb_ex_small = ccdb_ex
ccdb_ex_small$cell_tbl = ccdb_ex_small$cell_tbl[1:200,]
ccdb_ex_small = cdhit_ccdb(ccdb_ex_small,
  sequence_key = 'cdr3_nt', type = 'DNA', cluster_name = 'DNA97',
```

```

identity = .965, min_length = 12, G = 1)
ccdb_ex_small = fine_clustering(ccdb_ex_small, sequence_key = 'cdr3_nt', type = 'DNA')

# Canonicalize with the medoid contig is probably what is most common
ccdb_medoid = canonicalize_cluster(ccdb_ex_small)

# But there are other possibilities.
# To pass multiple "AND" filter arguments must use &
ccdb_umi = canonicalize_cluster(ccdb_ex_small,
contig_filter_args = chain == 'TRA' & length > 500, tie_break_keys = 'umis',
contig_fields = c('chain', 'length'))
ccdb_umi$cluster_tbl %>% dplyr::select(chain, length) %>% summary()

```

---

fine_cluster_seqs	<i>Calculate distances and perform hierarchical clustering on a set of sequences</i>
-------------------	--

---

## Description

The distances between AA sequences is defined to be  $1 - \text{score} / \max(\text{score})$  times the median length of the input sequences. The distances between nucleotide sequences is defined to be  $\text{edit\_distance} / \max(\text{edit\_distance})$  times the median length of input sequences.

## Usage

```

fine_cluster_seqs(
  seqs,
  type = "AA",
  big_memory_brute = FALSE,
  method = "levenshtein",
  substitution_matrix = "BLOSUM100",
  cluster_fun = "none",
  cluster_method = "complete"
)

```

## Arguments

seqs	character vector, DNASTringSet or AAStringSet
type	character either AA or DNA specifying type of seqs
big_memory_brute	attempt to cluster more than 4000 sequences? Clustering is quadratic, so this will take a long time and might exhaust memory
method	one of 'substitutionMatrix' or 'levenshtein'
substitution_matrix	a character vector naming a substitution matrix available in Biostrings, or a substitution matrix itself
cluster_fun	character, one of "hclust" or "none", determining if distance matrices should also be clustered with hclust
cluster_method	character passed to hclust

**Value**

list

**See Also**[hclust\(\)](#), [Biostrings::stringDist\(\)](#)**Examples**

```
fasta_path = system.file('extdata', 'demo.fasta', package='CellaRepertorium')
aaseq = Biostrings::readAAStringSet(fasta_path)[1:100]
cls = fine_cluster_seqs(aaseq, cluster_fun = 'hclust')
plot(cls$cluster)
```

---

generate\_pseudobulk    *Generate "pseudobulk" data from a ContigCellDB*

---

**Description**

Tabulate contigs with a unique combination of class\_keys per total\_keys. For instance, total\_keys might be a sample identifier, and class\_keys might be the V- and J- gene identities. The idea is that this might mimic the data generated in a bulk experiment.

**Usage**

```
generate_pseudobulk(ccdb, class_keys, total_keys, type = c("cell", "umi"))
```

**Arguments**

ccdb	<a href="#">ContigCellDB()</a>
class_keys	character naming fields in contig_tbl that define unique classes of the repertoire
total_keys	character naming fields to be conditioned upon when calculating the total.
type	one of "cell" or "umi"

**Details**

This function is currently rather 10x-specific, in that it is assumed that columns barcode and umi exist.

**Value**

tibble

**Examples**

```
data(ccdb_ex)
ccdb_ex = cluster_germline(ccdb_ex)
pseudo = generate_pseudobulk(ccdb_ex, c('v_gene', 'j_gene', 'chain'), c('pop', 'sample'))
```

---

guess_celltype	<i>Guess the cell type of a contig from the chain ID</i>
----------------	--

---

**Description**

This function is likely dependent on annotations from 10X and may change or break as their pipeline changes.

**Usage**

```
guess_celltype(chain)
```

**Arguments**

chain            character which will be parsed to try to infer celltype

**Value**

contig table with celltype column

**See Also**

[crosstab\\_by\\_celltype\(\)](#)

**Examples**

```
data(ccdb_ex)
table(guess_celltype(ccdb_ex$contig_tbl$chain))
```

---

hushWarning	<i>Selectively muffle warnings based on output</i>
-------------	--

---

**Description**

Selectively muffle warnings based on output

**Usage**

```
hushWarning(expr, regexp)
```

**Arguments**

expr            an expression  
regexp          a regexp to be matched (with str\_detect)

**Value**

the result of expr

**Examples**

```
CellaRepertorium::hushWarning(warning('Beware the rabbit'), 'rabbit')
CellaRepertorium::hushWarning(warning('Beware the rabbit'), 'hedgehog')
```

---

ig_chain_recode	<i>Categorize the pairing present in a cell</i>
-----------------	---

---

**Description**

For each cell (defined by `ccdb$cell_pk`) count the number of each level of `chain_key` occurs, and cross tabulate. Also for each cell, paste together all values `chain_key`. Return a tibble, keyed by cells that includes the counts of the chains, the `raw_chain_type` and any additional output from running `chain_recode_fun`.

**Usage**

```
ig_chain_recode(tbl)

tcr_chain_recode(tbl)

enumerate_pairing(ccdb, chain_key = "chain", chain_recode_fun = NULL)
```

**Arguments**

<code>tbl</code>	output from <code>enumerate_pairing</code> containing TRA/TRB or IGH/IHK/IHL columns
<code>ccdb</code>	ContigCellDB
<code>chain_key</code>	character naming the field in the <code>contig_tbl</code> identifying chain
<code>chain_recode_fun</code>	a function that operates on the output of this function that further reduces the chain combinations to some other summary. Set to 'guess' to apply functions that may work for 10X data or NULL to skip. See <code>CellaRepertorium::tcr_chain_recode</code> for an example.

**Value**

a tibble keyed by cells.

**Functions**

- `ig_chain_recode`: Recode a table with IG chains
- `tcr_chain_recode`: Recode a table with TCR chains

**Examples**

```
data(ccdb_ex)
enumerate_pairing(ccdb_ex)
enumerate_pairing(ccdb_ex, chain_recode_fun = 'guess')
```

---

map_axis_labels	<i>Color axis labels</i>
-----------------	--------------------------

---

**Description**

Color axis labels

**Usage**

```
map_axis_labels(
  plt,
  label_data_x = NULL,
  label_data_y = NULL,
  aes_label,
  scale = ggplot2::scale_color_hue(aesthetics = "axis_color")
)
```

**Arguments**

plt	ggplot2::ggplot() object
label_data_x	data.frame() containing the mapping between x-axis labels and aes_label
label_data_y	data.frame() containing the mapping between y-axis labels and aes_label
aes_label	character or bare symbol giving the column in label_data to be mapped
scale	ggplot2 discrete color

**Value**

plt with axis text modified

**Examples**

```
require(ggplot2)
require(dplyr)
plt = ggplot(mpg, aes(x = manufacturer, y = drv)) + geom_jitter()
label_data = mpg %>% select(manufacturer) %>% unique() %>%
mutate(euro = manufacturer %in% c('audi', 'volkswagen'))
map_axis_labels(plt, label_data_x = label_data, aes_label = euro)
```

---

pairing_tables	<i>Generate a list of tables representing clusters paired in cells</i>
----------------	--

---

### Description

A contingency table of every combination of `cluster_idx` up to `table_order` is generated. Combinations that are found in at least `min_expansion` number of cells are reported. All cells that have these combinations are returned, as well as cells that only have `orphan_level` of matching `cluster_idx`.

### Usage

```
pairing_tables(
  ccdb,
  ranking_key = "grp_rank",
  table_order = 2,
  min_expansion = 2,
  orphan_level = 1,
  cluster_keys = character(),
  cluster_whitelist = NULL,
  cluster_blacklist = NULL
)
```

### Arguments

<code>ccdb</code>	ContigCellDB
<code>ranking_key</code>	field in <code>ccdb\$contig_tbl</code> giving the ranking of each contig per cell. Probably generated by a call to <code>rank_prevalence_ccdb()</code> or <code>rank_chain_ccdb()</code> .
<code>table_order</code>	Integer larger than 1. What order of <code>cluster_idx</code> will be paired, eg, <code>order = 2</code> means that the first and second highest ranked contigs will be sought and paired in each cell
<code>min_expansion</code>	the minimal number of times a pairing needs to occur for it to be reported
<code>orphan_level</code>	Integer in interval <code>[1, table_order]</code> . Given that at least <code>min_expansion</code> cells are found that have <code>table_order</code> chains identical, how many <code>cluster_idx</code> pairs will we match on to select other cells. Example: <code>orphan_level=1</code> means that cells that share just a single chain with an expanded pair will be reported.
<code>cluster_keys</code>	optional character naming additional columns in <code>ccdb\$cluster_tbl</code> to be reported in the pairing
<code>cluster_whitelist</code>	a table of pairings or clusters that should always be reported. Here the clusters must be named "cluster_idx.1", "cluster_idx.2" (if order-2 pairs are being selected) rather than with "ccdb\$cluster_pk"
<code>cluster_blacklist</code>	a table of pairings or clusters that will never be reported. Must be named as per <code>cluster_whitelist</code> .

**Details**

For example, if `table_order=2` and `min_expansion=2` then heavy/light or alpha/beta pairs found two or more times will be returned (as well as alpha-alpha pairs, etc, if those are present). If `orphan_level=1` then all cells that share just a single chain with an expanded clone will be returned.

The `cluster_idx.1_fct` and `cluster_idx.2_fct` fields in `cell_tbl`, `idx1_tbl`, `idx2_tbl` are cast to factors and ordered such that pairings will tend to occur along the diagonal when they are cross-tabulated. This facilitates plotting.

**Value**

list of tables. The `cell_tbl` is keyed by the `cell_identifiers`, with fields "cluster\_idx.1", "cluster\_idx.2", etc, IDing the contigs present in each cell. "cluster\_idx.1\_fct" and "cluster\_idx.2\_fct" cast these fields to factors and are reordered to maximize the number of pairs along the diagonal. The `idx1_tbl` and `idx2_tbl` report information (passed in about the `cluster_idx` by `feature_tbl`.) The `cluster_pair_tbl` reports all pairings found of contigs, and the number of times observed.

**See Also**

[rank\\_prevalence\\_ccdb\(\)](#)

**Examples**

```
library(dplyr)
tbl = tibble(clust_idx = gl(3, 2), cell_idx = rep(1:3, times = 2), contig_idx = 1:6)
ccdb = ContigCellDB(tbl, contig_pk = c('cell_idx', 'contig_idx'),
cell_pk = 'cell_idx', cluster_pk = 'clust_idx')
# add `grp_rank` to ccdb$contig_tbl indicating how frequent a cluster is
ccdb = rank_prevalence_ccdb(ccdb, tie_break_keys = character())
# using `grp_rank` to determine pairing
# no pairs found twice
pt1 = pairing_tables(ccdb)
# all pairs found, found once.
pt2 = pairing_tables(ccdb, min_expansion = 1)
pt2$cell_tbl
tbl2 = bind_rows(tbl, tbl %>% mutate(cell_idx = rep(4:6, times = 2)))
ccdb2 = ContigCellDB(tbl2, contig_pk = c('cell_idx', 'contig_idx'), cell_pk = 'cell_idx',
cluster_pk = 'clust_idx') %>% rank_prevalence_ccdb(tie_break_keys = character())
#all pairs found twice
pt3 = pairing_tables(ccdb2, min_expansion = 1)
pt3$cell_tbl
ccdb2$contig_tbl = ccdb2$contig_tbl %>%
  mutate(umis = 1, reads = 1, chain = rep(c('TRA', 'TRB'), times = 6))
ccdb2 = rank_chain_ccdb(ccdb2, tie_break_keys = character())
pt4 = pairing_tables(ccdb2, min_expansion = 1, table_order = 2)
```

---

plot\_cluster\_factors *Visualization of pairs of cluster factor*

---

### Description

With factors, a pair of variables present in the `contig_tbl` and the `cluster_tbl`, generate and plot cross-tabs of the number of contigs, or its pearson residual.

### Usage

```
plot_cluster_factors(
  ccdb,
  factors,
  type = c("heatmap", "network"),
  statistic = c("pearson", "contigs"),
  ncluster = 0,
  chaintype
)
```

### Arguments

<code>ccdb</code>	A ContigCellDB object.
<code>factors</code>	character length 2 of fields present
<code>type</code>	Type of visualization, a heatmap or a node-edge network plot
<code>statistic</code>	Cluster characteristics visualized by pearson residuals or raw contig counts
<code>ncluster</code>	integer. Omit factors that occur less than nclusters. For clarity of visualization.
<code>chaintype</code>	Character in <code>ccdb\$contig_tbl\$chain</code> . If passed will subset contigs belonging to specified chain (IGH,IGK,IGL,TRA,TRB)

### Value

A `ggraph` object if `type == 'network'`, and a `ggplot` object if `type == 'heatmap'`

### See Also

`canonicalize_cluster` to "roll-up" additional contig variables into the 'cluster\_tbl'

### Examples

```
library(ggraph)
data(ccdb_ex)
ccdb_germline_ex = cluster_germline(ccdb_ex, segment_keys = c('v_gene', 'j_gene', 'chain'),
  cluster_pk = 'segment_idx')
ccdb_germline_ex = fine_clustering(ccdb_germline_ex, sequence_key = 'cdr3_nt', type = 'DNA')
plot_cluster_factors(ccdb_germline_ex, factors = c('v_gene', 'j_gene'),
  statistic = 'pearson', type = 'network', ncluster = 10, chaintype = 'TRB')
```

```
plot_cluster_factors(ccdb_germline_ex, factors = c('v_gene', 'j_gene'),
  statistic = 'contigs', type = 'heatmap')
plot_cluster_factors(ccdb_germline_ex, factors = c('v_gene', 'j_gene'),
  statistic = 'contigs', type = 'network', ncluster = 10)
```

---

plot\_permute\_test      *Plot a histogram of permuted vs observed test statistic*

---

### Description

Plot a histogram of permuted vs observed test statistic

### Usage

```
plot_permute_test(perm_test)

## S3 method for class 'PermuteTestList'
tidy(x, ...)

## S3 method for class 'PermuteTest'
tidy(x, ...)

## S3 method for class 'PermuteTest'
print(x, ...)

## S3 method for class 'PermuteTestList'
print(x, max = 3, ...)
```

### Arguments

perm_test	PermuteTest or PermuteTestList output from cluster_permute_test()
x	PermuteTestList
...	ignored
max	maximum number of components to print

### Methods (by generic)

- tidy: return permutations run using a sequence of contrasts as a tibble
- tidy: return permutations as a tibble
- print: pretty-print
- print: pretty-print

### See Also

cluster\_permute\_test

---

purity	<i>Calculate number of cluster-subject singletons for the purposes of permutation testing</i>
--------	---

---

### Description

Calculate number of cluster-subject singletons for the purposes of permutation testing

### Usage

```
purity(cluster_idx, subject)
```

### Arguments

cluster_idx	factor-like cluster variable
subject	factor-like subject

### Value

average number of singletons

### See Also

[cluster\\_permute\\_test\(\)](#)

### Examples

```
message("see example(cluster_permute_test)")
```

---

rank_prevalence_ccdb	<i>Rank contigs, per cell, by experiment-wide prevalence of cluster_pk, which is added as the prevalence field</i>
----------------------	--

---

### Description

Rank contigs, per cell, by experiment-wide prevalence of cluster\_pk, which is added as the prevalence field

**Usage**

```
rank_prevalence_ccdb(
  ccdb,
  contig_filter_args = TRUE,
  tie_break_keys = c("umis", "reads")
)

rank_chain_ccdb(
  ccdb,
  contig_filter_args = TRUE,
  tie_break_keys = c("umis", "reads"),
  chain_key = "chain",
  contig_fields = tie_break_keys,
  chain_levels = c("IGL", "IGK", "TRA", "TRB", "IGH")
)
```

**Arguments**

ccdb	<a href="#">ContigCellDB()</a>
contig_filter_args	an expression passed to <a href="#">dplyr::filter()</a> . Unlike filter, multiple criteria must be & together, rather than using commas to separate. These act on <code>ccdb\$contig_tbl</code>
tie_break_keys	(optional) character naming fields in <code>contig_tbl</code> that are used sort the contig table in descending order. Used to break ties if <code>contig_filter_args</code> does not return a unique contig for each cluster
chain_key	character naming the field in <code>contig_tbl</code> to be sorted on.
contig_fields	Optional fields from <code>contig_tbl</code> that will be copied into the <code>cluster_tbl</code> from the canonical contig.
chain_levels	an optional character vector providing the sort order of the chain column in <code>tbl</code> . If set to length zero, then the the ordering will be alphabetical

**Value**

ContigCellDB with modified `contig_tbl`

**Functions**

- `rank_chain_ccdb`: return a canonical contig by chain type, with TRB/IGH returned first. By default, ties are broken by umis and reads.

**Examples**

```
data(ccdb_ex)
ccdb_ex = cluster_germline(ccdb_ex)
rank_prev = rank_prevalence_ccdb(ccdb_ex)
rank_prev$contig_tbl
rank_chain = rank_chain_ccdb(ccdb_ex)
rank_chain$contig_tbl
```

---

```
rbind, ContigCellDB-method
```

*Combine ContigCellDB along rows (contigs, cells or clusters).*

---

### Description

The union of the rows in each of the objects is taken, thus removing any rows that has an exact duplicate. This includes all fields, not just the primary key for that table. The union of the various primary keys is taken.

### Usage

```
## S4 method for signature 'ContigCellDB'
rbind(..., deparse.level = 1)
```

### Arguments

```
...          ContigCellDB()
deparse.level ignored
```

### Value

```
ContigCellDB()
```

### Examples

```
data(ccdb_ex)
splat = split_cdb(ccdb_ex, 'chain', 'contig_tbl')
unite = equalize_ccdb(rbind(splat$TRA, splat$TRB), sort = TRUE)
stopifnot(all.equal(unite, ccdb_ex))
```

---

```
reexports
```

*Turn an object into a tidy tibble*

---

### Description

Turn an object into a tidy tibble

### Usage

```
tidy(x, ...)
```

### Arguments

```
x          An object to be converted into a tidy tibble::tibble().
...       Additional arguments to tidying method.
```

**Value**

A `tibble::tibble()` with information about model components.

**Methods**

No methods found in currently loaded packages.

---

right_join_warn	<i>Perform a <code>dplyr::left_join()</code> but check for non-key overlapping fields</i>
-----------------	---

---

**Description**

Perform a `dplyr` join, but either warn if the two tables share non-key fields. If `overwrite = TRUE`, then shared columns will pull from `x` otherwise a suffix will be added to `y`. To perform this check, `by` must be specified, and it is an error if it is not.

**Usage**

```
right_join_warn(...)
```

```
left_join_warn(x, y, by, overwrite = FALSE, join = left_join, ...)
```

**Arguments**

<code>...</code>	passed to joining function
<code>x</code>	A pair of data frames, data frame extensions (e.g. a tibble), or lazy data frames (e.g. from <code>dbplyr</code> or <code>dtplyr</code> ). See <i>Methods</i> , below, for more details.
<code>y</code>	A pair of data frames, data frame extensions (e.g. a tibble), or lazy data frames (e.g. from <code>dbplyr</code> or <code>dtplyr</code> ). See <i>Methods</i> , below, for more details.
<code>by</code>	character specifying columns in <code>x</code> and <code>y</code> to key on.
<code>overwrite</code>	logical – should non-key fields in <code>y</code> be overwritten using <code>x</code> , or should a suffix (" <code>.y</code> ") be added
<code>join</code>	function giving the type of join to perform, eg, left, right, inner, outer.

**Value**

data.frame or tibble

**Functions**

- `right_join_warn`: perform a `dplyr::right_join()`

**Examples**

```
left_join_warn(mtcars, mtcars, by = 'mpg')
left_join_warn(mtcars, mtcars, by = 'mpg', overwrite = TRUE)
```

---

split_cdb	<i>Split into a list of <a href="#">ContigCellDB()</a> by named fields</i>
-----------	--

---

**Description**

Split into a list of [ContigCellDB\(\)](#) by named fields

**Usage**

```
split_cdb(ccdb, fields, tbl = "contig_tbl", drop = FALSE, equalize = TRUE)
```

**Arguments**

ccdb	<a href="#">ContigCellDB()</a>
fields	character naming fields in tbl
tbl	one of contig_tbl, cell_tbl or cluster_tbl
drop	logical indicating if levels that do not occur should be dropped (if f is a factor or a list).
equalize	logical. Should the contig, cells and clusters be equalized by taking the intersection of their common keys?

**Value**

list of [ContigCellDB](#)

**Examples**

```
data(ccdb_ex)
splat = split_cdb(ccdb_ex, 'chain', 'contig_tbl')
stopifnot(all(splat$TRA$contig_tbl$chain == 'TRA'))
stopifnot(all(splat$TRB$contig_tbl$chain == 'TRB'))
```

---

[[,ContigCellDB,character,missing-method	<i>data.frame-like mutation/accessor generics for ContigCellDB objects</i>
--	--

---

**Description**

A [ContigCellDB](#) pretend to be a `cell_tbl` data.frame in several regards. This is to enable nesting [ContigCellDB](#) objects in the `colData` of a `SingleCellExperiment` and so that various plotting functionality in `scater` can do something sensible.

**Usage**

```
## S4 method for signature 'ContigCellDB,character,missing'  
x[[i, j, ...]]  
  
## S4 method for signature 'ContigCellDB,ANY,missing,ANY'  
x[i, j, ..., drop = TRUE]  
  
## S4 method for signature 'ContigCellDB'  
dim(x)  
  
## S4 method for signature 'ContigCellDB'  
dimnames(x)  
  
## S4 method for signature 'ContigCellDB'  
nrow(x)  
  
## S4 method for signature 'ContigCellDB'  
ncol(x)
```

**Arguments**

x	ContigCellDB
i	integer or character index
j	ignored
...	ignored
drop	ignored

**Details**

If x a ContigCellDB, then dim(x) and dimnames(x) return dim(x\$cell\_tbl) and dimnames(x\$cell\_tbl), respectively, and x[[col]] returns x\$cell\_tbl[[col]]. Likewise indexing with x[i,] returns cells indexed by i. Finally as.data.frame(x) returns x\$cell\_tbl.

**Value**

See details.

**Examples**

```
data(ccdb_ex)  
ccdb_ex[1:10,]  
head(ccdb_ex[['barcode']])  
dim(ccdb_ex)  
dimnames(ccdb_ex)
```

---

\$,ContigCellDB-method *Access public members of ContigCellDB object.*

---

### Description

Modification to members will trigger various forms of equalization. See [equalize\\_ccdb\(\)](#) for details.

### Usage

```
## S4 method for signature 'ContigCellDB'
x$name

## S4 replacement method for signature 'ContigCellDB'
x$name <- value
```

### Arguments

x	A ContigCellDB object
name	a slot of a ContigCellDB object (one of c('contig_tbl', 'cell_tbl', 'contig_pk', 'cell_pk', 'cluster_tbl', 'cluster_pk'))
value	The value assigned to a slot of ContigCellDB object

### Value

Update or return a slot of [ContigCellDB\(\)](#)

### See Also

[equalize\\_ccdb\(\)](#)

### Examples

```
data(ccdb_ex)
ccdb_ex$contig_tbl
ccdb_ex$cell_tbl
ccdb_ex$cluster_tbl
data(ccdb_ex)
ccdb_ex$contig_pk = c("sample", "barcode", "contig_id") # 'pop' is technically redundant with 'sample'
# Take a subset of ccdb_ex
ccdb_ex
ccdb_ex$contig_tbl = dplyr::filter(ccdb_ex$contig_tbl, pop == 'b6')
ccdb_ex
```

# Index

\* **datasets**  
  ccdb\_ex, 7  
  contigs\_qc, 18  
  .cluster\_permute\_test, 3  
[,ContigCellDB,ANY,missing,ANY-method  
  ([[,ContigCellDB,character,missing-method),  
  38  
[,ContigCellDB,ANY,missing-method  
  ([[,ContigCellDB,character,missing-method),  
  38  
[[,ContigCellDB,character,missing-method,  
  38  
\$,ContigCellDB-method, 40  
\$<-,ContigCellDB-method  
  (\$,ContigCellDB-method), 40  
  
Biostrings::stringDist(), 26  
  
canonicalize\_cell, 4  
canonicalize\_cell(), 6  
canonicalize\_cluster, 5  
canonicalize\_cluster(), 5  
ccdb\_ex, 7  
ccdb\_join, 7  
cdhit, 8, 10  
cdhit(), 9, 10  
cdhit\_ccdb, 9  
cland, 10  
cluster\_filterset, 11  
cluster\_filterset(), 15  
cluster\_germline, 12  
cluster\_logistic\_test  
  (cluster\_test\_by), 15  
cluster\_permute\_test, 12  
cluster\_permute\_test(), 34  
cluster\_plot, 14  
cluster\_test\_by, 15  
ContigCellDB, 16  
ContigCellDB(), 4–7, 9, 10, 12, 15, 17, 21,  
  23, 24, 26, 35, 36, 38, 40  
  
ContigCellDB-mutate  
  (\$,ContigCellDB-method), 40  
ContigCellDB\_10XVDJ (ContigCellDB), 16  
contigs\_qc, 7, 18  
cross\_tab\_tbl, 19  
cross\_tab\_by\_celltype, 19  
crosstab\_by\_celltype(), 27  
  
data, frame(), 29  
dim,ContigCellDB-method  
  ([[,ContigCellDB,character,missing-method),  
  38  
dimnames,ContigCellDB-method  
  ([[,ContigCellDB,character,missing-method),  
  38  
dplyr::filter(), 4, 6, 16, 23, 35  
dplyr::mutate(), 23  
  
entropy, 20  
enumerate\_pairing (ig\_chain\_recode), 28  
equalize\_ccdb, 21  
equalize\_ccdb(), 40  
  
fancy\_name\_contigs, 22  
filter\_cdb, 23  
filter\_cdb(), 17  
fine\_cluster\_seqs, 24, 25  
fine\_clustering, 24  
  
generate\_pseudobulk, 26  
ggplot2::ggplot(), 29  
guess\_celltype, 27  
guess\_celltype(), 19  
  
hclust(), 26  
hushWarning, 27  
  
ig\_chain\_recode, 28  
  
left\_join\_warn (right\_join\_warn), 37  
left\_join\_warn(), 6

map\_axis\_labels, 29  
modal\_category (entropy), 20  
mutate\_cdb (filter\_cdb), 23  
mutate\_cdb(), 17

ncol, ContigCellDB-method  
    ([[, ContigCellDB, character, missing-method),  
    38  
np (entropy), 20  
nrow, ContigCellDB-method  
    ([[, ContigCellDB, character, missing-method),  
    38

order(), 21

pairing\_tables, 30  
plot\_cluster\_factors, 32  
plot\_permute\_test, 33  
print.PermuteTest (plot\_permute\_test),  
    33  
print.PermuteTestList  
    (plot\_permute\_test), 33  
purity, 34  
purity(), 13

rank\_chain\_ccdb (rank\_prevalence\_ccdb),  
    34  
rank\_chain\_ccdb(), 30  
rank\_prevalence\_ccdb, 34  
rank\_prevalence\_ccdb(), 30, 31  
rbind, ContigCellDB-method, 36  
rbind.ContigCellDB  
    (rbind, ContigCellDB-method), 36  
rbind.ContigCellDB(), 17  
reexports, 36  
right\_join\_warn, 37

split\_cdb, 38  
split\_cdb(), 17

tcrc\_chain\_recode (ig\_chain\_recode), 28  
tibble::tibble(), 36, 37  
tidy (reexports), 36  
tidy.PermuteTest (plot\_permute\_test), 33  
tidy.PermuteTestList  
    (plot\_permute\_test), 33