Package ‘DuoClustering2018’

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Type Package

Title Data, Clustering Results and Visualization Functions From Duò et al (2018)

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Description Preprocessed experimental and simulated scRNA-seq data sets used for evaluation of clustering methods for scRNA-seq data in Duò et al (2018). Also contains results from applying several clustering methods to each of the data sets, and functions for plotting method performance.

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### ari_df

**Help function for computing ARI**

**Description**

Help function for computing ARI

**Usage**

```r
ari_df(x)
```

**Arguments**

- `x` A `data.frame` with clustering results.

**Value**

A `data.frame` with ARI values for each pair of runs.
Description

Clustering results for the performance evaluation of clustering methods for scRNA-seq data, corresponding to v1 of Duò et al. (2018).

Usage

clustering_summary_filteredExpr10_Koh_v1(metadata = FALSE)

Arguments

metadata Logical, whether only metadata should be returned

Details

These objects contain clustering results from the performance evaluation of clustering methods for scRNA-seq data. The clustering results are provided as a data.frame object containing 10 variables (columns) named dataset, method, cell, run, k, resolution, cluster, trueclass, est_k and elapsed. For further information see Duò et al. (2018).

Value

Returns a data.frame.

References


Examples

clustering_summary_filteredExpr10_Koh_v1()
**Description**

Clustering results for the performance evaluation of clustering methods for scRNA-seq data, corresponding to v2 of Duò et al. (2018).

**Usage**

`clustering_summary_filteredExpr10_Koh_v2(metadata = FALSE)`

**Arguments**

- `metadata` Logical, whether only metadata should be returned

**Details**

These objects contain clustering results from the performance evaluation of clustering methods for scRNA-seq data. The clustering results are provided as a `data.frame` object containing 10 variables (columns) named `dataset`, `method`, `cell`, `run`, `k`, `resolution`, `cluster`, `trueclass`, `est_k` and `elapsed`. For further information see Duò et al. (2018).

**Value**

Returns a `data.frame`.

**References**


**Examples**

`clustering_summary_filteredExpr10_Koh_v2()`
Description

Data package containing scRNA-seq data sets, clustering results and functions for summarizing the performance of different scRNA-seq clustering methods.

Details

This package contains publicly available scRNA-seq data sets and the accompanying results from clustering using general-purpose methods and scRNA-seq clustering methods. Several real data sets as well as simulated data sets are provided. The data sets have been used to evaluate the performance of clustering algorithms in our previous work and publication (Duò et al., F1000Research 2018). The data sets are available as SingleCellExperiment objects. For additional details on the data sets, see the help files for the respective data sets.

Additionally, the clustering results from the evaluation as well as functions for summarization and visualization of the clustering results are provided.

A description of the basic usage of the package for retrieving data sets and clustering results, and how to construct various plots summarizing the performance of different methods is outlined in the package vignettes.

Author(s)

Angelo Duò and Charlotte Sonesson

References


duo_clustering_all_parameter_settings_v1

Hyperparameter values

Description

Hyperparameter values for all clustering algorithms and data sets in v1 of Duo et al (F1000Research 2018)

Usage

duo_clustering_all_parameter_settings_v1(metadata = FALSE)
Arguments
metadata  Logical, whether only metadata should be returned

Details
List of hyperparameter values used for all clustering algorithms and data sets in v2 of Duò et al (F1000Research 2018).

Value
Returns a list with hyperparameter values for all data sets and methods.

References

Examples
duo_clustering_all_parameter_settings_v1()

duo_clustering_all_parameter_settings_v2

Hyperparameter values

Description
Hyperparameter values for all clustering algorithms and data sets in v2 of Duo et al (F1000Research 2018)

Usage
duo_clustering_all_parameter_settings_v2(metadata = FALSE)

Arguments
metadata  Logical, whether only metadata should be returned

Details
List of hyperparameter values used for all clustering algorithms and data sets in v2 of Duò et al (F1000Research 2018).

Value
Returns a list with hyperparameter values for all data sets and methods.
plot_entropy

References


Examples

duo_clustering_all_parameter_settings_v2()

plot_entropy(res, method_colors = NULL)

Description

Plot entropy of cluster assignments

Usage

plot_entropy(res, method_colors = NULL)

Arguments

res A data.frame with clustering results.
method_colors A named vector with colors to use for the different clustering methods. Can be NULL, in which case colors are chosen automatically.

Value

A named list of ggplot2 objects

Author(s)

Angelo Duo, Charlotte Soneson

Examples

res <- clustering_summary_filteredExpr10_Koh_v2()
plots <- plot_entropy(res)
plot_k_diff  
*Plot differences between optimal, estimated and true number of clusters*

**Description**
Plot differences between optimal, estimated and true number of clusters

**Usage**

\[\text{plot\_k\_diff}(\text{res}, \text{method\_colors} = \text{NULL})\]

**Arguments**

- **res**  
  A data.frame with clustering results.

- **method\_colors**  
  A named vector with colors to use for the different clustering methods. Can be NULL, in which case colors are chosen automatically.

**Value**

A named list of ggplot2 objects

**Author(s)**
Angelo Duo, Charlotte Soneson

**Examples**

```
res <- clustering_summary_filteredExpr10_Koh_v1()
plots <- plot_k_diff(res)
```

---

plot_performance  
*Plot performance of clustering methods*

**Description**
Generate various plots of the agreement between each clustering and the true partitioning of the cells, quantified by the adjusted Rand index (ARI).

**Usage**

\[\text{plot\_performance}(\text{res}, \text{method\_colors} = \text{NULL})\]

**Examples**

```
res <- clustering_summary_filteredExpr10_Koh_v1()
plots <- plot_performance(res)
```
`plot_stability`

**Arguments**

- `res` A data.frame with clustering results.
- `method_colors` A named vector with colors to use for the different clustering methods. Can be `NULL`, in which case colors are chosen automatically.

**Value**

A named list of `ggplot2` objects

**Author(s)**

Angelo Duo, Charlotte Soneson

**Examples**

```r
res <- clustering_summary_filteredExpr10_Koh_v1()
plots <- plot_performance(res)
```

---

**Description**

Plot the stability of the clusterings obtained for each method

**Usage**

```r
plot_stability(res, method_colors = NULL)
```

**Arguments**

- `res` A data.frame with clustering results.
- `method_colors` A named vector with colors to use for the different clustering methods. Can be `NULL`, in which case colors are chosen automatically.

**Value**

A named list of `ggplot2` objects

**Author(s)**

Angelo Duo, Charlotte Soneson

**Examples**

```r
res <- clustering_summary_filteredExpr10_Koh_v1()
plots <- plot_stability(res)
```
plot_timing  

Plot timing of methods

Description

Plot the elapsed time for each clustering method

Usage

plot_timing(res, method_colors = NULL, scaleMethod = NULL)

Arguments

res
A data.frame with clustering results.

method_colors
A named vector with colors to use for the different clustering methods. Can be NULL, in which case colors are chosen automatically.

scaleMethod
Either NULL or one of the clustering methods in the result data.frame. If not NULL, a plot will be generated where all elapsed times are normalized by dividing with the time for scaleMethod. If NULL, this plot will not be generated.

Value

A named list of ggplot2 objects

Author(s)

Angelo Duo, Charlotte Soneson

Examples

res <- clustering_summary_filteredExpr10_Koh_v1()
plots <- plot_timing(res)

cce_full_Koh  

Koh data sets

Description

Gene or TCC counts for a scRNA-seq data set from Koh et al. (2016), consisting of in vitro cultured H7 embryonic stem cells (WiCell) and H7-derived downstream early mesoderm progenitors.
Usage

sce_full_Koh(metadata = FALSE)
sce_filteredExpr10_Koh(metadata = FALSE)
sce_filteredHVG10_Koh(metadata = FALSE)
sce_filteredM3Drop10_Koh(metadata = FALSE)
sce_full_KohTCC(metadata = FALSE)
sce_filteredExpr10_KohTCC(metadata = FALSE)
sce_filteredHVG10_KohTCC(metadata = FALSE)
sce_filteredM3Drop10_KohTCC(metadata = FALSE)

Arguments

metadata Logical, whether only metadata should be returned

Format

SingleCellExperiment

Details

This is a scRNA-seq data set originally from Koh et al. (2016). The data set consists of gene-level read counts or TCCs (transcript compatibility counts) of in vitro cultured human H7 embryonic stem cells (WiCell) and H7-derived downstream early mesoderm progenitors. It contains 9 subpopulations, defined by the cell phenotype given by the authors’ annotations. The data sets have been used to evaluate the performance of clustering algorithms in Duò et al. (2018).

For the sce_full_Koh data set, all genes except those with zero counts across all cells are retained. The gene counts are gene-level length-scaled TPM values derived from Salmon (Patro et al. (2017)) quantifications (see Soneson and Robinson (2018)). For the TCC data set we estimated transcripts compatibility counts using kallisto as an alternative to the gene-level count matrix (Bray et al. (2016), Ntranos et al. (2016)).

The scater package was used to perform quality control of the data sets (McCarthy et al. (2017)). Features with zero counts across all cells, as well as all cells with total count or total number of detected features more than 3 median absolute deviations (MADs) below the median across all cells (on the log scale), were excluded.

The sce_full_Koh data set consists of 531 cells and 48,981 features, and the sce_full_KohTCC data set of 531 cells and 811,938 features. The filteredExpr, filteredHVG and filteredM3Drop10 are further reduced data sets. For each of the filtering methods, we retained 10 percent of the number of genes (with a non-zero count in at least one cell) in the original data sets.

For the filteredExpr data sets, only the genes/TCCs with the highest average expression (log-normalized count) value across all cells were retained. Using the Seurat package (Satija et al. (2015)), the filteredHVG data sets were filtered on the variability of the features and only the most highly variable ones were retained. Finally, the M3Drop package was used to model the dropout rate of the genes as a function of the mean expression level using the Michaelis-Menten equation and select variables to retain for the filteredM3Drop10 data sets (Andrews and Hemberg (2018)).

The scater package was used to normalize the count values, based on normalization factors calculated by the deconvolution method from the scran package (Lun et al. (2016)).
This data set is provided as a SingleCellExperiment object (Lun and Risso (2017)). Raw data files for the original data set (SRP073808) are available from https://www.ncbi.nlm.nih.gov/sra?term=SRP073808.

**Value**

Returns a SingleCellExperiment object.

**References**


**Examples**

sce_filteredHVG10_Koh()
sce_full_Kumar

Kumar data sets

Description
Gene or TCC counts for scRNA-seq data set from Kumar et al. (2014), consisting of mESCs with various genetic perturbations which are cultured in different media.

Usage
sce_full_Kumar(metadata = FALSE)
sce_filteredExpr10_Kumar(metadata = FALSE)
sce_filteredHVG10_Kumar(metadata = FALSE)
sce_filteredM3Drop10_Kumar(metadata = FALSE)
sce_full_KumarTCC(metadata = FALSE)
sce_filteredExpr10_KumarTCC(metadata = FALSE)
sce_filteredHVG10_KumarTCC(metadata = FALSE)
sce_filteredM3Drop10_KumarTCC(metadata = FALSE)

Arguments
metadata Logical, whether only metadata should be returned

Format
SingleCellExperiment

Details
This is a scRNA-seq data set originally from Kumar et al. (2014). The data set consists of gene-level read counts or TCCs (transcript compatibility counts) for mESCs from Mus musculus with various genetic perturbations which are cultured in different media. It contains 3 subpopulations, defined by the cell phenotype given by the authors’ annotations. The data sets have been used to evaluate the performance of clustering algorithms in Duò et al. (2018).

For the sce_full_Kumar data set, all genes except those with zero counts across all cells are retained. The gene counts are gene-level length-scaled TPM values derived from Salmon (Patro et al. (2017)) quantifications (see Soneson and Robinson (2018)). For the TCC data set we estimated transcripts compatibility counts using kallisto as an alternative to the gene-level count matrix (Bray et al. (2016), Ntranos et al. (2016)).

The scater package was used to perform quality control of the data sets (McCarthy et al. (2017)). Features with zero counts across all cells, as well as all cells with total count or total number of detected features more than 3 median absolute deviations (MADs) below the median across all cells (on the log scale), were excluded. Additionally, cells with a large fraction of ERCC reads were filtered out.

The sce_full_Kumar data set consists of 246 cells and 45,159 features, the sce_full_KumarTCC data set of 246 cells and 803,405 features, respectively. The filteredExpr, filteredHVG and
filteredM3Drop10 are further reduced data sets. For each filtering method, we retained 10 percent of the original number of genes (with a non-zero count in at least one cell) in the original data sets.

For the filteredExpr data sets, only the genes/TCCs with the highest average expression (log-normalized count) value across all cells were retained. Using the Seurat package, the filteredHVG data sets were filtered on the variability of the features and only the most highly variable ones were retained (Satija et al. (2015)). Finally, the M3Drop package was used to model the dropout rate of the genes as a function of the mean expression level using the Michaelis-Menten equation and select variables to retain for the filteredM3Drop10 data sets (Andrews and Hemberg (2018)).

The scater package was used to normalize the count values, based on normalization factors calculated by the deconvolution method from the scran package (Lun et al. (2016)). This data set is provided as a SingleCellExperiment object (Lun and Risso (2017)). For further information on the SingleCellExperiment class, see the corresponding manual. Raw data files for the original data set (GSE60749) are available from https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE60749.

Value

Returns a SingleCellExperiment object.

References


sce_full_SimKumar4easy

Examples

sce_filteredExpr10_Kumar()

sce_full_SimKumar4easy

SimKumar data sets

Description

Gene counts for scRNA-seq data sets simulated with the splatter package.

Usage

sce_full_SimKumar4easy(metadata = FALSE)
sce_filteredExpr10_SimKumar4easy(metadata = FALSE)
sce_filteredHVG10_SimKumar4easy(metadata = FALSE)
sce_filteredM3Drop10_SimKumar4easy(metadata = FALSE)
sce_full_SimKumar4hard(metadata = FALSE)
sce_filteredExpr10_SimKumar4hard(metadata = FALSE)
sce_filteredHVG10_SimKumar4hard(metadata = FALSE)
sce_filteredM3Drop10_SimKumar4hard(metadata = FALSE)
sce_full_SimKumar8hard(metadata = FALSE)
sce_filteredExpr10_SimKumar8hard(metadata = FALSE)
sce_filteredHVG10_SimKumar8hard(metadata = FALSE)
sce_filteredM3Drop10_SimKumar8hard(metadata = FALSE)

Arguments

metadata Logical, whether only metadata should be returned

Format

SingleCellExperiment

Details

Using one subpopulation of the sce_full_Kumar data set as input, scRNA-seq data with known group structure was simulated with the splatter package from Zappia et al. (2017). The simulated data have been used to evaluate the performance of clustering algorithms in Duò et al. (2018).

Three data sets have been generated, each consisting of 500 cells and approximately 43,000 features, with varying degree of cluster separability. The sce_full_SimKumar4easy data set consists of 4 subpopulations with relative abundances 0.1, 0.15, 0.5 and 0.25, and probabilities of differential expression set to 0.05, 0.1, 0.2 and 0.4 for the four subpopulations, respectively. The sce_full_SimKumar4hard data set consists of 4 subpopulations with relative abundances 0.2, 0.15, 0.4 and 0.25, and probabilities of differential expression 0.01, 0.05, 0.05 and 0.08. Finally, the sce_full_SimKumar8hard data set consists of 8 subpopulations with relative abundances 0.13,
0.07, 0.1, 0.05, 0.4, 0.1, 0.1 and 0.05, and probabilities of differential expression equal to 0.03, 0.03, 0.05, 0.05, 0.07, 0.08 and 0.1, respectively.

The scater package was used to perform quality control of the data sets (McCarthy et al. (2017)). Features with zero counts across all cells, as well as cells with total count or total number of detected features more than 3 median absolute deviations (MADs) below the median across all cells (on the log scale), were excluded. The filteredExpr, filteredHVG and filteredM3Drop10 are further reduced data sets. For each of the filtering method, we retained 10 percent of the original number of genes (with a non-zero count in at least one cell) in the original data sets.

For the filteredExpr data sets, only the genes with the highest average expression (log-normalized count) value across all cells were retained. Using the Seurat package, the filteredHVG data sets were filtered on the variability of the features and only the most highly variable ones were retained (Satija et al. (2015)). Finally, the M3Drop package was used to model the dropout rate of the genes as a function of the mean expression level using the Michaelis-Menten equation and select variables to retain for the filteredM3Drop10 data sets (Andrews and Hemberg (2018)).

The scater package was used to normalize the count values, based on normalization factors calculated by the deconvolution method from the scran package (Lun et al. (2016)). This data set is provided as a SingleCellExperiment object (Lun and Risso (2017)). For further information on the SingleCellExperiment class, see the corresponding manual.

Value

Returns a SingleCellExperiment object.

References


Examples

sce_filteredExpr10_SimKumar4easy()
sce_full_Trapnell

Description

Gene or TCC counts for scRNA-seq data set from Trapnell et al. (2014), consisting of primary myoblasts over a time course of serum-induced differentiation.

Usage

sce_full_Trapnell(metadata = FALSE)
sce_filteredExpr10_Trapnell(metadata = FALSE)
sce_filteredHVG10_Trapnell(metadata = FALSE)
sce_filteredM3Drop10_Trapnell(metadata = FALSE)
sce_full_TrapnellTCC(metadata = FALSE)
sce_filteredExpr10_TrapnellTCC(metadata = FALSE)
sce_filteredHVG10_TrapnellTCC(metadata = FALSE)
sce_filteredM3Drop10_TrapnellTCC(metadata = FALSE)

Arguments

metadata Logical, whether only metadata should be returned

Format

SingleCellExperiment

Details

This is a scRNA-seq data set originally from Trapnell et al. (2014). The data set consists of gene-level read counts or TCCs (transcript compatibility counts) from human primary myoblasts over a time course of serum-induced differentiation. It contains 3 subpopulations, defined by the cell phenotype given by the authors' annotations. The data sets have been used to evaluate the performance of clustering algorithms in Duò et al. (2018).

For the sce_full_Trapnell data set, all genes except those with zero counts across all cells are retained. The gene counts are gene-level length-scaled TPM values derived from Salmon (Patro et al. (2017)) quantifications (see Soneson and Robinson (2018)). For the TCC data set we estimated transcripts compatibility counts using kallisto as an alternative to the gene-level count matrix (Bray et al. (2016), Ntranos et al. (2016)).

The scater package was used to perform quality control of the data sets (McCarthy et al. (2017)). Features with zero counts across all cells, as well as all cells with total count or total number of detected features more than 3 median absolute deviations (MADs) below the median across all cells (on the log scale), were excluded. Additionally, cells that were classified as doublets or debris were filtered out.

The sce_full_Trapnell data set consists of 222 cells and 41,111 features, the sce_full_TrapnellTCC data set of 227 cells and 684,953 features, respectively. The filteredExpr, filteredHVG and
filteredM3Drop10 are further reduced data sets. For each of the filtering method, we retained 10 percent of the original number of genes (with a non-zero count in at least one cell) in the original data sets.

For the filteredExpr data sets, only the genes/TCCs with the highest average expression (log-normalized count) value across all cells were retained. Using the Seurat package, the filteredHVG data sets were filtered on the variability of the features and only the most highly variable ones were retained (Satija et al. (2015)). Finally, the M3Drop package was used to model the dropout rate of the genes as a function of the mean expression level using the Michaelis-Menten equation and select variables to retain for the filteredM3Drop10 data sets (Andrews and Hemberg (2018)).

The scater package was used to normalize the count values, based on normalization factors calculated by the deconvolution method from the scran package (Lun et al. (2016)).

This data set is provided as a SingleCellExperiment object (Lun and Risso (2017)). For further information on the SingleCellExperiment class, see the corresponding manual. Raw data files for the original data set (GSE52529) are available from https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE52529.

Value

Returns a SingleCellExperiment object.

References


Examples

sce_filteredExpr10_Trappnell()

sce_full_Zhengmix4eq  Zheng data sets

Description

Gene counts for scRNA-seq data sets from Zheng et al. (2017), consisting of pre-sorted cell types combined into three artificial data sets with different cell proportions.

Usage

sce_full_Zhengmix4eq(metadata = FALSE)
sce_filteredExpr10_Zhengmix4eq(metadata = FALSE)
sce_filteredHVG10_Zhengmix4eq(metadata = FALSE)
sce_filteredM3Drop10_Zhengmix4eq(metadata = FALSE)
sce_full_Zhengmix4uneq(metadata = FALSE)
sce_filteredExpr10_Zhengmix4uneq(metadata = FALSE)
sce_filteredHVG10_Zhengmix4uneq(metadata = FALSE)
sce_filteredM3Drop10_Zhengmix4uneq(metadata = FALSE)
sce_full_Zhengmix8eq(metadata = FALSE)
sce_filteredExpr10_Zhengmix8eq(metadata = FALSE)
sce_filteredHVG10_Zhengmix8eq(metadata = FALSE)
sce_filteredM3Drop10_Zhengmix8eq(metadata = FALSE)

Arguments

metadata  Logical, whether only metadata should be returned

Format

SingleCellExperiment

Details

This is a scRNA-seq data set originally from Zheng et al. (2017). The data set consists of eight pre-sorted cell types (B-cells, naive cytotoxic T-cells, CD14 monocytes, regulatory T-cells, CD56 NK cells, memory T-cells, CD4 T-helper cells and naive T-cells) from Homo sapiens combined into three artificial data sets with different cell proportions. The annotated cell type (obtained by pre-sorting of the cells) is used as the true cell label. The data sets have been used to evaluate the performance of clustering algorithms in Duò et al. (2018).

For the Zhengmix4eq data set, randomly selected B-cells, CD14 monocytes, naive cytotoxic T-cells and regulatory T-cells were combined in equal proportions (1,000 cells per subpopulation). The Zhengmix4uneq data set consists of four cell types, combined in unequal proportions (1,000 B-cells, 500 naive cytotoxic T-cells, 2,000 CD14 monocytes and 3,000 regulatory T-cells). For the
Zhengmix8eq data set, all eight populations were combined in approximately equal proportions (400–600 cells per population).

For the sce_full_Zhengmix4eq, sce_full_Zhengmix4uneq and sce_full_Zhengmix8eq data set, all genes except those with zero counts across all cells are retained. The gene counts are unique molecular identifiers (UMIs) counts. The scater package was used to perform quality control of the data (McCarthy et al. (2017)). Features with zero counts across all cells, as well as all cells with total count or total number of detected features more than 3 median absolute deviations (MADs) below the median across all cells (on the log scale), were excluded.

The sce_full_Zhengmix4eq data set consists of 3,994 cells and 15,568 features, the sce_full_Zhengmix4uneq data set of 6,498 cells and 16,443 features and the sce_full_Zhengmix8eq of 3,994 cells and 16,443 features, respectively. The filteredExpr, filteredHVG and filteredM3Drop10 are further reduced data sets. For each of the filtering method, we retained 10 percent of the original number of genes (with a non-zero count in at least one cell) in the original data sets.

For the filteredExpr data sets, only the genes with the highest average expression (log-normalized count) value across all cells were retained. Using the Seurat package, the filteredHVG data sets were filtered on the variability of the features and only the most highly variable ones were retained (Satija et al. (2015)). Finally, the M3Drop package was used to model the dropout rate of the genes as a function of the mean expression level using the Michaelis-Menten equation and select variables to retain for the filteredM3Drop10 data sets (Andrews and Hemberg (2018)).

The scater package was used to normalize the count values, based on normalization factors calculated by the deconvolution method from the scran package (Lun et al. (2016)). This data set is provided as a SingleCellExperiment object (Lun and Risso (2017)). For further information on the SingleCellExperiment class, see the corresponding manual. Raw data files or the original data sets are available from https://support.10xgenomics.com/single-cell-gene-expression/datasets.

Value

Returns a SingleCellExperiment object.

References


Examples

sce_filteredExpr10_Zhengmix4eq()

shannon_entropy  

Calculate Shannon entropy

Description

Calculate Shannon entropy

Usage

shannon_entropy(cluster_assignments)

Arguments

cluster_assignments

A vector with cluster assignments

Value

The Shannon entropy of the assignment vector
Index

* datasets

clustering_summary_filteredExpr10_Koh_v1, 3
clustering_summary_filteredExpr10_Koh_v2, clustering_summary_filteredExpr10_SimKumar4easy_v1
(clustering_summary_filteredExpr10_Koh_v1), 3
clustering_summary_filteredExpr10_KohTCC_v1, clustering_summary_filteredExpr10_SimKumar4hard_v1
(clustering_summary_filteredExpr10_Koh_v1), 3
clustering_summary_filteredExpr10_KohTCC_v2, clustering_summary_filteredExpr10_SimKumar8hard_v1
(clustering_summary_filteredExpr10_Koh_v1), 3
duo_clustering_all_parameter_settings_v1, clustering_summary_filteredExpr10_Trapnell_v1
(clustering_summary_filteredExpr10_Koh_v1), 3
duo_clustering_all_parameter_settings_v2, clustering_summary_filteredExpr10_Trapnell_v2
(clustering_summary_filteredExpr10_Koh_v1), 4
sce_full_Koh, 10
sce_full_Kumar, 13
sce_full_SimKumar4easy, 15
sce_full_Trapnell, 17
sce_full_Zhengmix4eq, 19

ari_df, 2

clustering_summary_filteredExpr10_Koh_v1, 3
clustering_summary_filteredExpr10_Koh_v2, 4
clustering_summary_filteredExpr10_KohTCC_v1, clustering_summary_filteredExpr10_Trapnell_v1
(clustering_summary_filteredExpr10_Koh_v1), 3
clustering_summary_filteredExpr10_KohTCC_v2, clustering_summary_filteredExpr10_Trapnell_v2
(clustering_summary_filteredExpr10_Koh_v1), 4
clustering_summary_filteredExpr10_Kumar_v1, clustering_summary_filteredExpr10_TrapnellTCC_v1
(clustering_summary_filteredExpr10_Koh_v1), 3
clustering_summary_filteredExpr10_Kumar_v2, clustering_summary_filteredExpr10_TrapnellTCC_v2
(clustering_summary_filteredExpr10_Koh_v1), 4
clustering_summary_filteredExpr10_KumarTCC_v1, clustering_summary_filteredExpr10_Zhengmix4eq_v1
(clustering_summary_filteredExpr10_Koh_v1), 3
clustering_summary_filteredExpr10_KumarTCC_v2, clustering_summary_filteredExpr10_Zhengmix4eq_v2
(clustering_summary_filteredExpr10_Koh_v1), 4
clustering_summary_filteredExpr10_KumarTCC_v4, clustering_summary_filteredExpr10_Zhengmix4uneq_v1
(clustering_summary_filteredExpr10_Koh_v1), 3
clustering_summary_filteredExpr10_Zhengmix4uneq
(clustering_summary_filteredExpr10_Koh_v2), (clustering_summary_filteredExpr10_Koh_v2), 4

clustering_summary_filteredExpr10_Zhengmix8eq
(clustering_summary_filteredExpr10_Koh_v1), (clustering_summary_filteredExpr10_Koh_v1), 3

clustering_summary_filteredExpr10_Zhengmix8uneq
(clustering_summary_filteredExpr10_Koh_v2)
clustering_summary_filteredM3Drop10_Kumar_v2 clustering_summary_filteredM3Drop10_Zhengmix4uneq_v2
(clustering_summary_filteredExpr10_Koh_v2), (clustering_summary_filteredExpr10_Koh_v2),
4
clustering_summary_filteredM3Drop10_KumarTCC clustering_summary_filteredM3Drop10_Zhengmix8eq_v1
(clustering_summary_filteredExpr10_Koh_v1), (clustering_summary_filteredExpr10_Koh_v1),
3
clustering_summary_filteredM3Drop10_KumarTCC clustering_summary_filteredM3Drop10_Zhengmix8eq_v2
(clustering_summary_filteredExpr10_Koh_v2), (clustering_summary_filteredExpr10_Koh_v2),
4
clustering_summary_filteredM3Drop10_SimKumar4easy_v1
(clustering_summary_filteredExpr10_Koh_v1),
3
duo_clustering_all_parameter_settings_v1,
5
duo_clustering_all_parameter_settings_v2,
6
duoClustering2018,
5
clustering_summary_filteredM3Drop10_SimKumar4hard_v1
(clustering_summary_filteredExpr10_Koh_v1),
3
do_stability,
9
plot_stability,
9
plot_entropy,
7
plot_k_diff,
8
plot_performance,
8
plot_performance,
8
plot_timing,
10
clustering_summary_filteredM3Drop10_SimKumar8hard_v1
(clustering_summary_filteredExpr10_Koh_v1),
3
sce_filteredExpr10_Koh (sce_full_Koh),
10
sce_filteredExpr10_KohTCC
4
sce_filteredExpr10_KohTCC
4
sce_filteredExpr10_Kumar
4
(sce_full_Kumar),
10
sce_filteredExpr10_Kumar
4
(sce_full_Kumar),
13
sce_filteredExpr10_SimKumar4easy
15
sce_filteredExpr10_SimKumar4easy
15
sce_filteredExpr10_SimKumar4hard
15
sce_filteredExpr10_SimKumar4hard
15
sce_filteredExpr10_Trapnell
15
sce_filteredExpr10_Trapnell
15
sce_filteredExpr10_TrapnellTCC
15
sce_filteredExpr10_TrapnellTCC
15
sce_filteredExpr10_Trapnell
15
sce_filteredExpr10_Trapnell
15
sce_filteredExpr10_TrapnellTCC
15
sce_filteredExpr10_Trapnell
15
sce_filteredExpr10_Zhengmix4eq
19
sce_filteredExpr10_Zhengmix4eq
19
sce_filteredExpr10_Zhengmix4uneq
19
sce_filteredExpr10_Zhengmix4uneq
19
sce_filteredExpr10_Zhengmix4eq_v2
19
sce_filteredExpr10_Zhengmix4eq_v2
19
sce_filteredHVG10_Koh
10
(sce_full_Koh),
10
(sce_full_HVG10_KohTCC
3
(sce_full_hvg10_KohTCC
3
(sce_full_koh),
10
sce_filteredHVG10_Koh
10
(sce_full_Koh),
10
sce_filteredHVG10_Koh
10
(sce_full_Koh),
10
sce_filteredHVG10_Koh
10
(sce_full_Koh),
10
sce_filteredHVG10_Koh
10
(sce_full_Koh),
10
sce_filteredHVG10_Koh
10
(sce_full_Koh),
10
sce_filteredHVG10_Koh
10
(sce_full_Koh),
10
sce_filteredHVG10_Kumar (sce_full_Kumar), 13
sce_filteredHVG10_KumarTCC (sce_full_Kumar), 13
sce_filteredHVG10_SimKumar4easy (sce_full_SimKumar4easy), 15
sce_filteredHVG10_SimKumar4hard (sce_full_SimKumar4easy), 15
sce_filteredHVG10_SimKumar8hard (sce_full_SimKumar4easy), 15
sce_filteredHVG10_Trapnell (sce_full_Trapnell), 17
sce_filteredHVG10_TrapnellTCC (sce_full_Trapnell), 17
sce_filteredHVG10_Zhengmix4eq (sce_full_Zhengmix4eq), 19
sce_filteredHVG10_Zhengmix4uneq (sce_full_Zhengmix4eq), 19
sce_filteredHVG10_Zhengmix8eq (sce_full_Zhengmix4eq), 19
sce_filteredM3Drop10_Koh (sce_full_Koh), 10
sce_filteredM3Drop10_KohTCC (sce_full_Koh), 10
sce_filteredM3Drop10_Kumar (sce_full_Kumar), 13
sce_filteredM3Drop10_KumarTCC (sce_full_Kumar), 13
sce_filteredM3Drop10_SimKumar4easy (sce_full_SimKumar4easy), 15
sce_filteredM3Drop10_SimKumar4hard (sce_full_SimKumar4easy), 15
sce_filteredM3Drop10_SimKumar8hard (sce_full_SimKumar4easy), 15
sce_filteredM3Drop10_Trapnell (sce_full_Trapnell), 17
sce_filteredM3Drop10_TrapnellTCC (sce_full_Trapnell), 17
sce_filteredM3Drop10_Zhengmix4eq (sce_full_Zhengmix4eq), 19
sce_filteredM3Drop10_Zhengmix4uneq (sce_full_Zhengmix4eq), 19
sce_filteredM3Drop10_Zhengmix8eq (sce_full_Zhengmix4eq), 19
sce_full_Koh, 10
callen_KohTCC (sce_full_Koh), 10
sce_full_Kumar, 13
sce_full_KumarTCC (sce_full_Kumar), 13
sce_full_SimKumar4easy, 15
callen_SimKumar4hard
(sce_full_SimKumar4easy), 15
callen_SimKumar8hard
(sce_full_SimKumar4easy), 15
sce_full_Trapnell, 17
callen_TrapnellTCC
(sce_full_Trapnell), 17
callen_Zhengmix4eq, 19
callen_Zhengmix4uneq
(sce_full_Zhengmix4eq), 19
callen_Zhengmix8eq
(sce_full_Zhengmix4eq), 19
shannon_entropy, 21