

# Package ‘Dune’

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**Title** Improving replicability in single-cell RNA-Seq cell type discovery

**Version** 1.17.0

**Description** Given a set of clustering labels, Dune merges pairs of clusters to increase mean ARI between labels, improving replicability.

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`.adjustedRandIndex`     *adjustedRandIndex*

**Description**

`adjustedRandIndex`

**Usage**

`.adjustedRandIndex(tab)`

**Arguments**

`tab`                    The confusion matrix

**Value**

The ARI

`ARIImp`                    *ARI improvement*

**Description**

Compute the ARI improvement over the ARI merging procedure

**Usage**

`ARIImp(merger, unclustered = NULL)`

**Arguments**

merger            the result from having run [Dune](#) on the dataset  
 unclustered      The value assigned to unclustered cells. Default to NULL

**Value**

a vector with the mean ARI between methods at each merge

**See Also**

ARItrend

**Examples**

```
data("clusMat", package = "Dune")
merger <- Dune(clusMat = clusMat)
plot(0:nrow(merger$merges), ARIImp(merger))
```

---

 ARIs

*ARI Matrix*


---

**Description**

ARI Matrix

**Usage**

```
ARIs(clusMat, unclustered = NULL)
```

**Arguments**

clusMat            The clustering matrix with a row per cell and a column per clustering label type  
 unclustered      The value assigned to unclustered cells. Default to NULL

**Details**

In the ARI matrix where each cell  $i,j$  is the adjusted Rand Index between columns  $i$  and  $j$  of the original `clusMat`. If `unclustered` is not NULL, the cells which have been assigned to the unclustered cluster will not be counted towards computing the ARI.

**Value**

The ARI matrix

**Examples**

```
data("clusMat", package = "Dune")
ARIs(clusMat)
```

---

ARItrend *ARI improvement plot*

---

### Description

A plot to see how ARI improves over merging

### Usage

```
ARItrend(merger, unclustered = NULL)
```

### Arguments

merger            the result from having run [Dune](#) on the dataset  
 unclustered      The value assigned to unclustered cells. Default to NULL

### Value

a [ggplot](#) object

### Examples

```
data("clusMat", package = "Dune")
merger <- Dune(clusMat = clusMat)
ARItrend(merger)
```

---

clusMat *A clustering matrix used to demonstrate the ari-merging process.*

---

### Description

A clustering matrix used to demonstrate the ari-merging process.

### Usage

```
clusMat
```

### Format

An object of class `matrix` (inherits from `array`) with 100 rows and 5 columns.

### Details

This matrix has 100 samples with 5 cluster labels. Cluster labels 2 through 5 are modified versions of cluster label 1, where some clusters from label 1 were broken down into smaller clusters. It is just a toy dataset that can be re-generated with the code in [https://github.com/HectorRDB/Pipeline\\_Brain/blob/master/Sandbox](https://github.com/HectorRDB/Pipeline_Brain/blob/master/Sandbox).

---

clusterConversion	<i>clusterConversion</i>
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---

**Description**

Find the conversion between the old cluster and the final clusters

**Usage**

```
clusterConversion(merger, p = 1, average_n = NULL, n_steps = NULL)
```

**Arguments**

merger	the result from having run <a href="#">Dune</a> on the dataset
p	A value between 0 and 1. We stop when the metric used for merging has improved by p of the final total improvement. Default to 1 (i.e running the full merging).
average_n	Alternatively, you can specify the average number of clusters you want to have.
n_steps	Finally, you can specify the number of merging steps to do before stopping.

**Details**

If more than one of p, average\_n and n\_steps is specified, then the order of preference is n\_steps, then average\_n then p.

**Value**

A list containing a matrix per clustering method, with a column for the old labels and a column for the new labels.

**Examples**

```
data("clusMat", package = "Dune")
merger <- Dune(clusMat = clusMat)
clusterConversion(merger)[[2]]
```

---

ConfusionEvolution	<i>Plot the evolution of the ConfusionPlot as merging happens</i>
--------------------	-------------------------------------------------------------------

---

**Description**

Animated version of [ConfusionPlot](#)

**Usage**

```
ConfusionEvolution(merger, unclustered = NULL, x, y, state_length = 1)
```

**Arguments**

merger	the result from having run <a href="#">Dune</a> on the dataset
unclustered	The value assigned to unclustered cells. Default to NULL
x	The name of the first cluster label to plot
y	The name of the second cluster label to plot
state_length	Time between steps. Default to 1. See <a href="#">transition_states</a> for details.

**Details**

See [ConfusionPlot](#) and [animate](#).

**Value**

a `gganim` object

**Examples**

```
## Not run:
data("clusMat", package = "Dune")
merger <- Dune(clusMat = clusMat)
ConfusionEvolution(merger, x = "A", y = "B")
## End(Not run)
```

---

ConfusionPlot	<i>Plot confusion matrix</i>
---------------	------------------------------

---

**Description**

A plot to visualize how alike two clustering labels are

**Usage**

```
ConfusionPlot(x, y = NULL)
```

**Arguments**

x	A vector of clustering labels or a matrix of clustering labels. See details.
y	Optional. Another vector of clustering labels

**Value**

a `ggplot` object

**Examples**

```
data("nuclei", package = "Dune")
ConfusionPlot(nuclei[, c("SC3", "Monocle")])
```

---

Dune

*Dune*

---

## Description

Compute the Metric between every pair of clustering labels after merging every possible pair of clusters. Find the one that improves the Metric merging the most, merge the pair. Repeat until there is no improvement.

## Usage

```
Dune(clusMat, ...)  
  
## S4 method for signature 'matrix'  
Dune(  
  clusMat,  
  unclustered = NULL,  
  verbose = FALSE,  
  parallel = FALSE,  
  BPPARAM = BiocParallel::bpparam(),  
  metric = "NMI"  
)  
  
## S4 method for signature 'data.frame'  
Dune(  
  clusMat,  
  unclustered = NULL,  
  verbose = FALSE,  
  parallel = FALSE,  
  BPPARAM = BiocParallel::bpparam(),  
  metric = "NMI"  
)  
  
## S4 method for signature 'SummarizedExperiment'  
Dune(  
  clusMat,  
  cluster_columns,  
  unclustered = NULL,  
  verbose = FALSE,  
  parallel = FALSE,  
  BPPARAM = BiocParallel::bpparam(),  
  metric = "NMI"  
)
```

## Arguments

<code>clusMat</code>	the matrix of samples by clustering labels.
<code>...</code>	parameters including:
<code>unclustered</code>	The value assigned to unclustered cells. Default to NULL
<code>verbose</code>	Whether or not the print cluster merging as it happens.

<code>parallel</code>	Logical, defaults to FALSE. Set to TRUE if you want to parallelize the fitting.
<code>BPPARAM</code>	object of class <code>bpparamClass</code> that specifies the back-end to be used for computations. See <code>bpparam</code> in <code>BiocParallel</code> package for details. Won't be used if <code>parallel</code> is FALSE.
<code>metric</code>	The metric that is tracked to decide which clusters to merge. For now, either ARI and NMI are accepted. Default to NMI. See details.
<code>cluster_columns</code>	if <code>clusMat</code> is a <a href="#">SummarizedExperiment</a> , then this defines the columns of <code>colData</code> that are outputs from a clustering algorithm.

## Details

The Dune algorithm merges pairs of clusters in order to improve the mean adjusted Rand Index or the mean normalized mutual information with other clustering labels. It returns a list with five components.: #'

- `initialMat`: The initial matrix of cluster labels
- `currentMat`: The final matrix of cluster labels
- `merges`: The step-by-step detail of the merges, recapitulating which clusters where merged in which cluster label
- `impMetric`: How much each merge improved the mean Metric between the cluster label that has been merged and the other cluster labels.
- `metric`: The metric that was used to find the merges.

## Value

A list with four components: the initial matrix of clustering labels, the final matrix of clustering labels, the merge info matrix and the Metric improvement vector.

## See Also

`clusterConversion` `ARIImp`

## Examples

```
data("clusMat", package = "Dune")
merger <- Dune(clusMat = clusMat)
# clusters 11 to 14 from cluster label 5 and 3 are subset of cluster 2 from
# other cluster labels. Designing cluster 2 as unclustered therefore means we
# do fewer merges.
merger2 <- Dune(clusMat = clusMat, unclustered = 2)
merger$merges
merger2$merges
```



---

functionTracking	<i>Track the evolution of a function along merging</i>
------------------	--------------------------------------------------------

---

**Description**

For a given ARI merging, compute the evolution on the function  $f$

**Usage**

```
functionTracking(merger, f, p = 1, n_steps = NULL, ...)
```

**Arguments**

merger	the result from having run <a href="#">Dune</a> on the dataset
f	the function used. It must takes as input a clustering matrix and return a value
p	A value between 0 and 1. We stop when the metric used for merging has improved by $p$ of the final total improvement. Default to 1 (i.e running the full merging).
n_steps	Alternatively, you can specify the number of merging steps to do before stopping.
...	additional arguments passed to f

**Value**

a vector of length the number of merges

**Examples**

```
# Return the number of clusters for the fourth cluster label
data("clusMat", package = "Dune")
merger <- Dune(clusMat = clusMat)
f <- function(clusMat, i) dplyr::n_distinct(clusMat[, i])
functionTracking(merger, f, i = 4)
```

---

intermediateMat	<i>Find the clustering matrix that we would get if we stopped the ARI merging early</i>
-----------------	-----------------------------------------------------------------------------------------

---

**Description**

Find the clustering matrix that we would get if we stopped the ARI merging early

**Usage**

```
intermediateMat(merger, p = 1, average_n = NULL, n_steps = NULL)
```

**Arguments**

merger	the result from having run <a href="#">Dune</a> on the dataset
p	A value between 0 and 1. We stop when the metric used for merging has improved by p of the final total improvement. Default to 1 (i.e running the full merging).
average_n	Alternatively, you can specify the average number of clusters you want to have.
n_steps	Finally, you can specify the number of merging steps to do before stopping.

**Details**

If more than one of p, average\_n and n\_steps is specified, then the order of preference is n\_steps, then average\_n then p.

**Value**

A data.frame with the same dimensions as the currentMat of the merger argument, plus one column with cell names, related to the rownames of the original input

**Examples**

```
data("clusMat", package = "Dune")
merger <- Dune(clusMat = clusMat)
head(intermediateMat(merger, n_steps = 1))
```

---

NMIImp

*NMI improvement*


---

**Description**

Compute the NMI improvement over the NMI merging procedure

**Usage**

```
NMIImp(merger, unclustered = NULL)
```

**Arguments**

merger	the result from having run <a href="#">Dune</a> on the dataset
unclustered	The value assigned to unclustered cells. Default to NULL

**Value**

a vector with the mean NMI between methods at each merge

**See Also**

NMItrend

**Examples**

```
data("clusMat", package = "Dune")
merger <- Dune(clusMat = clusMat)
plot(0:nrow(merger$merges), NMIImp(merger))
```

---

 NMI<sub>s</sub>
*NMI Matrix*


---

**Description**

NMI Matrix

**Usage**

```
NMIs(clusMat, unclustered = NULL)
```

**Arguments**

clusMat	The clustering matrix with a row per cell and a column per clustering label type
unclustered	The value assigned to unclustered cells. Default to NULL

**Details**

In the NMI matrix where each cell **i,j** is the normalized mutual information between columns **i** and **j** of the original clusMat. If unclustered is not NULL, the cells which have been assigned to the unclustered cluster will not be counted towards computing the NMI.

**Value**

The NMI matrix

**Examples**

```
data("clusMat", package = "Dune")
NMIs(clusMat)
```

---

 NMI<sub>trend</sub>
*NMI improvement plot*


---

**Description**

A plot to see how NMI improves over merging

**Usage**

```
NMItrend(merger, unclustered = NULL)
```

**Arguments**

merger	the result from having run <a href="#">Dune</a> on the dataset
unclustered	The value assigned to unclustered cells. Default to NULL

**Value**

a [ggplot](#) object

**Examples**

```
data("clusMat", package = "Dune")
merger <- Dune(clusMat = clusMat)
NMItrend(merger)
```

---

nuclei	<i>Cluster labels for a subset of the allen Smart-Seq nuclei dataset</i>
--------	--------------------------------------------------------------------------

---

**Description**

Cluster labels for a subset of the allen Smart-Seq nuclei dataset

**Usage**

```
nuclei
```

**Format**

An object of class `data.frame` with 1744 rows and 7 columns.

**Details**

This matrix of clusters was obtained by running 3 clustering algorithms on a brain snRNA-Seq dataset from Tasic et .al (<https://doi.org/10.1038/s41586-018-0654-5>). This dataset was then sub-setted to the GABAergic neurons. Code to reproduce all this can be found in the github repository from the Dune paper ([https://github.com/HectorRDB/Dune\\_Paper](https://github.com/HectorRDB/Dune_Paper)).

---

plotARIs	<i>Plot an heatmap of the ARI matrix</i>
----------	------------------------------------------

---

**Description**

We can compute the ARI between pairs of cluster labels. This function plots a matrix where a cell is the adjusted Rand Index between cluster label of row *i* and cluster label of column *j*.

**Usage**

```
plotARIs(clusMat, unclustered = NULL, values = TRUE, numericalLabels = FALSE)
```

**Arguments**

<code>clusMat</code>	The clustering matrix with a row per cell and a column per clustering label type
<code>unclustered</code>	The value assigned to unclustered cells. Default to <code>NULL</code>
<code>values</code>	Whether to also display the ARI values. Default to <code>TRUE</code> .
<code>numericalLabels</code>	Whether labels are numerical values. Default to <code>FALSE</code> .

**Value**

a `ggplot` object

**Examples**

```
data("clusMat", package = "Dune")
merger <- Dune(clusMat = clusMat)
plotARIs(merger$initialMat)
plotARIs(merger$currentMat)
```

---

plotNMIs

*Plot an heatmap of the NMI matrix*


---

**Description**

We can compute the NMI between pairs of cluster labels. This function plots a matrix where a cell is the Normalized Mutual Information between cluster label of row  $i$  and cluster label of column  $j$ .

**Usage**

```
plotNMIs(clusMat, unclustered = NULL, values = TRUE, numericalLabels = FALSE)
```

**Arguments**

clusMat	The clustering matrix with a row per cell and a column per clustering label type
unclustered	The value assigned to unclustered cells. Default to NULL
values	Whether to also display the ARI values. Default to TRUE.
numericalLabels	Whether labels are numerical values. Default to FALSE.

**Value**

a `ggplot` object

**Examples**

```
data("clusMat", package = "Dune")
merger <- Dune(clusMat = clusMat, metric = "NMI")
plotNMIs(merger$initialMat)
plotNMIs(merger$currentMat)
```

---

plotPrePost

*Plot the reduction in cluster size for an ARI merging with Dune*


---

**Description**

Plot the reduction in cluster size for an ARI merging with Dune

**Usage**

```
plotPrePost(merger)
```

**Arguments**

merger                    The output from an ARI merging, by calling [Dune](#)

**Value**

a [ggplot](#) object #' @importFrom dplyr mutate

**Examples**

```
data("clusMat", package = "Dune")
merger <- Dune(clusMat = clusMat)
plotPrePost(merger)
```

---

whenToStop

*When to Stop*

---

**Description**

When to Stop

**Usage**

```
whenToStop(merger, p = 1, average_n = NULL)
```

**Arguments**

merger                    the result from having run [Dune](#) on the dataset

p                            A value between 0 and 1. We stop when the metric used for merging has improved by p of the final total improvement. Default to 1 (i.e running the full merging).

average\_n                Alternatively, you can specify the average number of clusters you want to have.

**Details**

The [Dune](#) process improves the metric. This return the first merging step after which the metric has been improved by p of the total. Setting p = 1 just return the number of merges.

**Value**

An integer giving the step where to stop.

**Examples**

```
data("clusMat", package = "Dune")
merger <- Dune(clusMat = clusMat)
whenToStop(merger, p = .5)
```

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