

# Package ‘CellMentor’

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**Type** Package

**Title** Supervised Non-negative Matrix Factorization for Dimensional Reduction in Single-Cell Analysis

**Version** 1.0.0

**Description**

Implements supervised cell type-aware non-negative matrix factorization (NMF) for dimensional reduction in single-cell RNA sequencing analysis. The package provides methods for incorporating cell type information into the dimensionality reduction process, enabling improved visualization and downstream analysis of single-cell data while preserving biological structure. CellMentor employs a unique loss function that simultaneously minimizes variation within known cell populations while maximizing distinctions between different cell types, enabling effective transfer of learned patterns from labeled reference datasets to new unlabeled data.

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magrittr, graphics, RMTstat, sparsesvd, cluster, skmeans,  
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**BugReports** <https://github.com/petrenkokate/CellMentor/issues>

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CellMentor	<i>CellMentor: Cell-Type Aware Dimensionality Reduction for Single-Cell RNA-Seq</i>
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## Description

CellMentor is a supervised dimensionality reduction method based on non-negative matrix factorization (NMF) that integrates cell type labels directly into its optimization objective. By minimizing variation within known populations while maximizing distinctions between types, CellMentor produces low-dimensional embeddings optimized for cell type identification in single-cell RNA sequencing analysis.

Tests different combinations of hyperparameters using RunCSFNMF to find the optimal configuration. The function performs a grid search over specified parameter ranges, evaluating the model's performance for each combination. Parameters `alpha` and `beta` are kept equal during optimization. The rank (`k`) can be provided, taken from an existing object, or determined automatically using `SelectRank`.

**Usage**

```

CellMentor(
  object,
  k = NULL,
  init_methods = c("regulated"),
  alpha_range = c(1, 5),
  beta_range = c(1, 5),
  gamma_range = c(0.1),
  delta_range = c(1),
  n_iter = 1,
  verbose = TRUE,
  num_cores = 1,
  seed = 1
)

```

**Arguments**

object	CSFNMF object containing reference and query data matrices, with required matrices for data and ref under object@matrices.
k	Optional rank value (number of factors). If NULL: - Uses existing rank from object if available - Otherwise determines automatically using SelectRank
init_methods	Vector of initialization methods to test. Options: - "uniform": Random uniform initialization - "regulated": Cell-type guided initialization - "NNDSVD": Non-negative Double SVD - "skmeanGenes": Gene clustering-based - "skmeanCells": Cell clustering-based Default: c("regulated")
alpha_range	Vector of alpha values to test. Controls within-class scatter (cell similarity within the same type). Default: c(0.1, 0.5, 1)
beta_range	Vector of beta values to test. Controls between-class scatter (cell separation between different types). Default: c(1, 2, 5)
gamma_range	Vector of sparsity parameter values to test. Controls sparsity of the factorization. Default: c(0, 0.1)
delta_range	Vector of orthogonality parameter values to test. Controls orthogonality between factors. Default: c(0, 0.5)
n_iter	Number of repetitions per configuration for averaging results (default: 3).
verbose	Logical; whether to show progress messages during optimization. Default: TRUE
num_cores	Number of cores to use for parallel processing. If > 1, parameter combinations are tested in parallel. Default: 1
seed	Random seed

**Value**

List containing: - best\_params: List with the overall best parameter configuration: \* k: Selected rank \* init\_method: Best initialization method \* alpha: Best alpha parameter \* beta: Best beta parameter \* gamma: Best gamma value \* delta: Best delta value \* accuracy: Best achieved accuracy \* loss: Corresponding loss value - results: Data frame of all combinations tested, including:

\* `init_method`: Initialization method used \* `alpha`: Alpha parameter value \* `beta`: Beta parameter value \* `gamma`: Gamma parameter value \* `delta`: Delta parameter value \* `accuracy`: Achieved accuracy \* `loss`: Final loss value \* `convergence_iter`: Number of iterations for convergence - `best_model`: CSFNMF model object trained with the best parameters.

### Key Features

- **Supervised NMF Framework:** Incorporates labels via discriminative constraints
- **Superior Cell Type Separation:** Maximally separable embeddings
- **Robust Batch Handling:** Preserves biology while mitigating technical effects
- **Rare Population Detection:** Sensitive to low-frequency types
- **Automated Parameter Optimization:** Built-in hyperparameter tuning

### Two-Phase Workflow

1. **Decomposition (Training):** Learn  $W$  (genes  $\times$  K) and  $H$  (K  $\times$  cells)
2. **Projection (Inference):** Project queries with non-negative least squares

### Main Functions

- `CellMentor` — supervised NMF / hyperparameter search
- `project_data` — project queries using learned  $W$
- `CreateCSFNMFObject` — initialize a CellMentor object

### Getting Help

- Package docs: `help(package = "CellMentor")`
- GitHub: <https://github.com/petrenkokate/CellMentor>
- Issues: <https://github.com/petrenkokate/CellMentor/issues>

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### References

Hevdeli, O., Petrenko, E., & Aran, D. (2025). CellMentor: Cell-Type Aware Dimensionality Reduction for Single-cell RNA-Sequencing Data. *bioRxiv*. doi:10.1101/2025.06.17.660094

### See Also

Useful links:

- <https://github.com/petrenkokate/CellMentor>
- Report bugs at <https://github.com/petrenkokate/CellMentor/issues>

## Examples

```
data(obj_toy, package = "CellMentor")
# Run lightweight CellMentor
result <- CellMentor(
  object      = obj_toy,
  k           = 2,
  init_methods = "regulated",
  alpha_range = 1,
  beta_range  = 1,
  gamma_range = 0.1,
  delta_range = 1,
  n_iter      = 1,
  verbose     = FALSE,
  num_cores   = 1
)

# Inspect results (should run in <10 seconds)
names(result)
if ("best_params" %in% names(result)) {
  print(result$best_params)
}
```

---

cm\_annotation

*Access cell annotations from a CellMentor object*

---

## Description

Retrieve cell type or metadata annotations.

## Usage

```
cm_annotation(x)
```

## Arguments

x                    A CellMentor object.

## Value

A data frame containing cell annotations.

## Examples

```
data(obj_toy, package = "CellMentor")
cm_annotation(obj_toy)
```

cm\_rank                      *Access the rank of a CellMentor object*

---

### **Description**

Retrieve the factorization rank used during CSFNMF training.

### **Usage**

```
cm_rank(x)
```

### **Arguments**

x                      A CellMentor object.

### **Value**

A numeric value representing the selected rank.

### **Examples**

```
## Not run:  
# Access the rank of the model  
cm_rank(cs_obj)  
  
## End(Not run)
```

---

CreateCSFNMFobject      *Create CSFNMF Object for Cell Type Analysis*

---

### **Description**

Creates and initializes a Constrained Supervised Factorization NMF (CSFNMF) object for analyzing single-cell RNA sequencing data. This is the main function for starting analysis with CellMentor.

### **Usage**

```
CreateCSFNMFobject(  
  ref_matrix,  
  ref_celltype,  
  data_matrix,  
  norm = TRUE,  
  most.variable = TRUE,  
  scale = TRUE,  
  scale_by = "cells",
```

```

    gene_list = NULL,
    verbose = TRUE,
    num_cores = 1
)

```

### Arguments

ref_matrix	Reference matrix (genes × cells) with known cell types
ref_celltype	Vector of cell type labels for reference cells
data_matrix	Query matrix (genes × cells) to be analyzed
norm	Logical: perform normalization (default: TRUE)
most.variable	Logical: select variable genes (default: TRUE)
scale	Logical: perform scaling (default: TRUE)
scale_by	Character: scaling method, either "cells" or "genes" (default: "cells")
gene_list	Optional vector of genes to include (default: NULL)
verbose	Logical: show progress messages (default: TRUE)
num_cores	Integer: number of cores for parallel processing (default: 1)

### Value

A CSFNMF object containing processed data and annotations

### Examples

```

data(ref_matrix_toy, qry_matrix_toy, ref_celltype_toy, package = "CellMentor")
obj <- CreateCSFNMFobject(ref_matrix_toy, ref_celltype_toy, qry_matrix_toy,
                          norm = FALSE, most.variable = FALSE, scale = FALSE,
                          verbose = FALSE, num_cores = 1)
inherits(obj, "csfnmf")

```

---

data_matrix	<i>Access the query (data) matrix from a RefDataList object</i>
-------------	---

---

### Description

Retrieve the single-cell expression matrix for the query dataset.

### Usage

```
data_matrix(x)
```

### Arguments

x	A RefDataList object.
---	-----------------------

**Value**

A sparse `Matrix::Matrix` object representing query data.

**Examples**

```
data(obj_toy, package = "CellMentor")
data_matrix(matrices(obj_toy))
```

---

H

*Access the H matrix*

---

**Description**

Retrieve the H matrix (cell embeddings) from a CellMentor object.

**Usage**

```
H(x)
```

**Arguments**

x                    A CellMentor object.

**Value**

A numeric matrix representing the H (cell embeddings) matrix.

**Examples**

```
data(obj_toy, package = "CellMentor")
H(obj_toy)
```

---

h.baron\_dataset

*Load Baron Human Pancreas Dataset (Deprecated)*

---

**Description**

This function has been renamed. Please use `hBaronDataset()` instead.

**Usage**

```
h.baron_dataset()
```

**Value**

A list containing the dataset

---

hBaronDataset	<i>Load Baron Human Pancreas Dataset</i>
---------------	--

---

**Description**

Loads and processes the Baron et al. human pancreas single-cell RNA-seq dataset

**Usage**

```
hBaronDataset()
```

**Value**

A list containing:

data	Expression matrix with genes as rows and cells as columns
celltypes	Named vector of cell type annotations

**Examples**

```
# Load Baron human pancreas dataset
baron <- hBaronDataset()

# Check dimensions
dim(baron$data)

# View cell type distribution
table(baron$celltypes)
```

---

matrices	<i>Access the RefDataList from a CSFNMF object</i>
----------	--

---

**Description**

Retrieve the RefDataList structure containing both reference and query matrices.

**Usage**

```
matrices(x)
```

**Arguments**

x	A csfnmf or traincsfnmf object.
---	---------------------------------

**Value**

A RefDataList object containing the reference and query matrices.

**Examples**

```
data(obj_toy, package = "CellMentor")
matrices(obj_toy)
```

---

muraro_dataset	<i>Load Muraro Pancreas Dataset</i>
----------------	-------------------------------------

---

**Description**

Loads and processes the Muraro et al. pancreas single-cell RNA-seq dataset

**Usage**

```
muraro_dataset()
```

**Value**

A list containing:

data	Expression matrix with genes as rows and cells as columns
celltypes	Named vector of cell type annotations

**Examples**

```
# Load Muraro pancreas dataset
muraro <- muraro_dataset()

# Check dataset dimensions
dim(muraro$data)

# View available cell types
table(muraro$celltypes)

# Check number of cells per type
sort(table(muraro$celltypes), decreasing = TRUE)
```

---

obj_toy	<i>Tiny prebuilt CSFNMF object for accessors (optional)</i>
---------	---

---

**Description**

Tiny prebuilt CSFNMF object for accessors (optional)

**Usage**

```
obj_toy
```

**Format**

An object of class `csfnmf` built on the toy matrices.

**Details**

Only provided to make accessor examples immediate. For real analyses, construct objects from your own data.

**Examples**

```
data(obj_toy, package = "CellMentor")
inherits(obj_toy, "csfnmf")
```

---

project_data	<i>Project Data onto NMF Basis Matrix</i>
--------------	---

---

**Description**

Projects new data onto the learned basis matrix ( $W$ ) using non-negative least squares (NNLS). This function is used to obtain cell-type signatures ( $H$  matrix) for new query data using the gene weights ( $W$  matrix) learned during training. The projection is performed in chunks to manage memory efficiently, with optional parallel processing.

**Usage**

```
project_data(W, X, seed = 1, num_cores = 1, chunk_size = 1000, verbose = TRUE)
```

**Arguments**

W	Basis matrix (genes × rank) containing learned gene weights
X	Data matrix (genes × cells) to be projected. Must have same number of genes (rows) as W
seed	Random seed for reproducibility (default: 1)
num_cores	Number of cores for parallel processing (default: 1). If > 1, processing is parallelized across chunks
chunk_size	Number of cells to process in each chunk (default: 1000). Smaller chunks use less memory but may be slower
verbose	Logical; whether to show progress bar (default: TRUE)

**Details**

The projection is performed using non-negative least squares (NNLS) to solve the optimization problem:  $\min \|X - WH\|^2$  subject to  $H \geq 0$ , for each cell in the input matrix X. The resulting H matrix contains the cell-type signatures for the query data.

For memory efficiency, cells are processed in chunks. The `chunk_size` parameter can be adjusted based on available memory. Parallel processing can be enabled by setting `num_cores > 1`.

**Value**

A Matrix object (rank × cells) containing the projection coefficients. The rows correspond to factors (rank) and columns to cells. Additional processing information is stored in attributes: - `num_chunks`: Number of chunks processed - `chunk_size`: Size of chunks used - `num_cores`: Number of cores used

**Examples**

```
# Minimal, fast example (no external data)
set.seed(1)

# Dimensions
genes <- paste0("Gene", seq_len(50))
k     <- 3   # rank
cells <- 10

# Non-negative basis W (genes x k)
W_ex <- matrix(abs(rnorm(length(genes) * k, sd = 0.5)),
               nrow = length(genes), ncol = k,
               dimnames = list(genes, paste0("k", seq_len(k))))

# Generate a non-negative H_true and synthetic data X = W * H + noise
H_true <- matrix(abs(rnorm(k * cells, sd = 0.5)), nrow = k, ncol = cells)
X_ex   <- W_ex %*% H_true + matrix(rexp(length(genes) * cells, rate = 20),
                                   nrow = length(genes), ncol = cells,
                                   dimnames = list(genes, paste0("cell", seq_len(cells))))

# Project (rank x cells)
```

```

H_est <- project_data(
  W = W_ex,
  X = X_ex,
  num_cores = 1,      # keep examples fast & deterministic
  chunk_size = 5,
  verbose = FALSE
)

dim(H_est)           # should be k x cells

```

---

ref\_matrix                      *Access the reference matrix from a RefDataList object*

---

### Description

Retrieve the single-cell expression matrix for the reference dataset.

### Usage

```
ref_matrix(x)
```

### Arguments

x                      A RefDataList object.

### Value

A sparse Matrix::Matrix object representing reference data.

### Examples

```

data(obj_toy, package = "CellMentor")
ref_matrix(matrices(obj_toy))

```

---

ref\_matrix\_toy                      *Tiny toy matrices and labels for runnable examples*

---

### Description

Tiny toy matrices and labels for runnable examples

### Usage

```

ref_matrix_toy

qry_matrix_toy

ref_celltype_toy

```

**Format**

- `ref_matrix_toy`: numeric matrix (50 genes x 12 cells), `dimnames` set.
- `qry_matrix_toy`: numeric matrix (50 genes x 8 cells), `dimnames` set.
- `ref_celltype_toy`: character vector of length 12, names match `colnames(ref_matrix_toy)`.

An object of class `matrix` (inherits from `array`) with 50 rows and 8 columns.

An object of class `character` of length 12.

**Details**

These are minimal, non-biological toy data with shared gene IDs across reference and query for fast runnable examples and tests.

**Examples**

```
data(ref_matrix_toy, package = "CellMentor")
data(qry_matrix_toy, package = "CellMentor")
data(ref_celltype_toy, package = "CellMentor")
dim(ref_matrix_toy); dim(qry_matrix_toy)
head(ref_celltype_toy)
```

---

W

*Access the W matrix*

---

**Description**

Retrieve the W matrix (gene loadings) from a `CellMentor` object.

**Usage**

```
W(x)
```

**Arguments**

`x` A `CellMentor` object (e.g., `traincsfnmf` or `csfnmf`).

**Value**

A numeric matrix representing the W (gene loadings) matrix.

**Examples**

```
data(obj_toy, package = "CellMentor")
W(obj_toy)
```

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