

# Package ‘SCFA’

November 18, 2025

**Type** Package

**Title** SCFA: Subtyping via Consensus Factor Analysis

**Version** 1.21.0

**Description** Subtyping via Consensus Factor Analysis (SCFA) can efficiently remove noisy signals from consistent molecular patterns in multi-omics data.

SCFA first uses an autoencoder to select only important features and then repeatedly performs factor analysis to represent the data with different numbers of factors.

Using these representations, it can reliably identify cancer subtypes and accurately predict risk scores of patients.

**License** LGPL

**Encoding** UTF-8

**LazyData** true

**Depends** R (>= 4.0)

**Imports** matrixStats, BiocParallel, torch (>= 0.3.0), coro, igraph,  
Matrix, cluster, psych, glmnet, RhpcBLASctl, stats, utils,  
methods, survival

**RoxygenNote** 7.1.1

**biocViews** Survival, Clustering, Classification

**Suggests** knitr, rmarkdown, BiocStyle

**VignetteBuilder** knitr

**URL** <https://github.com/duct317/SCFA>

**BugReports** <https://github.com/duct317/SCFA/issues>

**git\_url** <https://git.bioconductor.org/packages/SCFA>

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**Author** Duc Tran [aut, cre],  
Hung Nguyen [aut],  
Tin Nguyen [fnd]  
**Maintainer** Duc Tran <duct@nevada.unr.edu>

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|     |            |
|-----|------------|
| GBM | <i>GBM</i> |
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Description

GBM dataset, including microRNA and survival data.

Usage

GBM

Format

A list with two items:

**data** List of microRNA data matrix.

**survival** Survival information.

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|------|-------------|
| SCFA | <i>SCFA</i> |
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Description

The main function to perform subtyping. It takes a list of data matrices as the input and outputs the subtype for each patient

Usage

SCFA(dataList, k = NULL, max.k = 5, ncores = 10L, seed = NULL)

**Arguments**

|                       |                                                                                                          |
|-----------------------|----------------------------------------------------------------------------------------------------------|
| <code>dataList</code> | List of data matrices. In each matrix, rows represent samples and columns represent genes/features.      |
| <code>k</code>        | Number of clusters, leave as default for auto detection.                                                 |
| <code>max.k</code>    | Maximum number of cluster                                                                                |
| <code>ncores</code>   | Number of processor cores to use.                                                                        |
| <code>seed</code>     | Seed for reproducibility, you still need to use <code>set.seed</code> function for full reproducibility. |

**Value**

A numeric vector containing cluster assignment for each sample.

**Examples**

```
#Load example data (GBM dataset)
data("GBM")
#List of one matrix (microRNA data)
dataList <- GBM$data
#Survival information
survival <- GBM$survival
library(survival)
#Generating subtyping result
set.seed(1)
subtype <- SCFA(dataList, seed = 1, ncores = 2L)
#Perform survival analysis on the result
coxFit <- coxph(Surv(time = Survival, event = Death) ~ as.factor(subtype), data = survival, ties="exact")
coxP <- round(summary(coxFit)$sctest[3], digits = 20)
print(coxP)
```

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SCFA.class

*SCFA.class*


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**Description**

Perform risk score prediction on input data. This function requires training data with survival information. The output is the risk scores of patients in testing set.

**Usage**

```
SCFA.class(dataListTrain, trainLabel, dataListTest, ncores = 10L, seed = NULL)
```

**Arguments**

|                            |                                                                                                              |
|----------------------------|--------------------------------------------------------------------------------------------------------------|
| <code>dataListTrain</code> | List of training data matrices. In each matrix, rows represent samples and columns represent genes/features. |
| <code>trainLabel</code>    | Survival information of patient in training set in form of Surv object.                                      |
| <code>dataListTest</code>  | List of testing data matrices. In each matrix, rows represent samples and columns represent genes/features.  |
| <code>ncores</code>        | Number of processor cores to use.                                                                            |
| <code>seed</code>          | Seed for reproducibility, you still need to use <code>set.seed</code> function for full reproducibility.     |

**Value**

A vector of risk score predictions for patient in test set.

**Examples**

```
#Load example data (GBM dataset)
data("GBM")
#List of one matrix (microRNA data)
dataList <- GBM$data
#Survival information
survival <- GBM$survival
library(survival)
#Split data to train and test
set.seed(1)
idx <- sample.int(nrow(dataList[[1]]), round(nrow(dataList[[1]])/2) )
survival$Survival <- survival$Survival - min(survival$Survival) + 1 # Survival time must be positive
trainList <- lapply(dataList, function(x) x[idx, ] )
trainSurvival <- Surv(time = survival[idx,]$Survival, event = survival[idx,]$Death)
testList <- lapply(dataList, function(x) x[-idx, ] )
testSurvival <- Surv(time = survival[-idx,]$Survival, event = survival[-idx,]$Death)
#Perform risk prediction
result <- SCFA.class(trainList, trainSurvival, testList, seed = 1, ncores = 2L)
#Validation using concordance index
c.index <- concordance(coxph(testSurvival ~ result))$concordance
print(c.index)
```

# Index

## \* **datasets**

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