

# Package ‘fastText’

May 12, 2026

**Type** Package

**Title** Efficient Learning of Word Representations and Sentence Classification

**Version** 1.0.8

**Date** 2026-05-12

**URL** <https://github.com/mlampros/fastText>,  
<https://mlampros.github.io/fastText/>

**BugReports** <https://github.com/mlampros/fastText/issues>

**Description** An interface to the 'fastText' <<https://github.com/facebookresearch/fastText>> library for efficient learning of word representations and sentence classification. The 'fastText' algorithm is explained in detail in (i) ``Enriching Word Vectors with subword Information'', Piotr Bojanowski, Edouard Grave, Armand Joulin, Tomas Mikolov, 2017, <[doi:10.1162/tacl\\_a\\_00051](https://doi.org/10.1162/tacl_a_00051)>; (ii) ``Bag of Tricks for Efficient Text Classification'', Armand Joulin, Edouard Grave, Piotr Bojanowski, Tomas Mikolov, 2017, <[doi:10.18653/v1/e17-2068](https://doi.org/10.18653/v1/e17-2068)>; (iii) ``FastText.zip: Compressing text classification models'', Armand Joulin, Edouard Grave, Piotr Bojanowski, Matthijs Douze, Herve Jegou, Tomas Mikolov, 2016, <[doi:10.48550/arXiv.1612.03651](https://doi.org/10.48550/arXiv.1612.03651)>.

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**Encoding** UTF-8

**Imports** Rcpp (>= 1.0.0), ggplot2, grid, utils, glue, data.table, stats

**Depends** R(>= 3.2.3)

**LinkingTo** Rcpp

**Suggests** testthat, covr, knitr, rmarkdown

**VignetteBuilder** knitr

**RoxygenNote** 7.3.2

**NeedsCompilation** yes

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**Repository** CRAN

**Date/Publication** 2026-05-12 06:50:02 UTC

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---

fasttext\_interface      *Interface for the fasttext library*

---

## Description

Interface for the fasttext library

## Usage

```
fasttext_interface(
  list_params,
  path_output = "",
  MilliSecs = 100,
  path_input = "",
  remove_previous_file = TRUE,
  print_process_time = FALSE
)
```

**Arguments**

<code>list_params</code>	a list of valid parameters
<code>path_output</code>	a character string specifying the file path where the process-logs (or output in generally) should be saved
<code>MilliSecs</code>	an integer specifying the delay in milliseconds when printing the results to the specified <i>path_output</i>
<code>path_input</code>	a character string specifying the path to the input data file
<code>remove_previous_file</code>	a boolean. If TRUE, in case that the <i>path_output</i> is not an empty string (""), then an existing file with the same output name will be removed
<code>print_process_time</code>	a boolean. If TRUE then the processing time of the function will be printed out in the R session

**Details**

This function allows the user to run the various methods included in the fasttext library from within R

The "output" parameter which exists in the named list (see examples section) and is passed to the "list\_params" parameter of the "fasttext\_interface()" function, is a file path and not a directory name and will actually return two files (a \*.vec\* and a \*.bin\*) to the output directory.

**Value**

a vector of class character that includes the parameters and file paths used as input to the function

**References**

<https://github.com/facebookresearch/fastText>

<https://github.com/facebookresearch/fastText/blob/master/docs/supervised-tutorial.md>

**Examples**

```
## Not run:

library(fastText)

#####
# If the user intends to run the following examples then he / she must replace #
# the 'input', 'output', 'path_input', 'path_output', 'model' and 'test_data' file #
# paths depending on where the data are located or should be saved! #
# ( 'tempdir()' is used here as an example folder ) #
#####

# -----
# print information for the Usage of each function [ parameters ]
```

```

# -----

fastText::printUsage()
fastText::printTestUsage()
fastText::printTestLabelUsage()
fastText::printQuantizeUsage()
fastText::printPrintWordVectorsUsage()
fastText::printPrintSentenceVectorsUsage()
fastText::printPrintNgramsUsage()
fastText::printPredictUsage()
fastText::printNNUsage()
fastText::printDumpUsage()
fastText::printAnalogiesUsage()
fastText::print_parameters(command = "supervised")

# -----
# In case that the 'command' is one of 'cbow', 'skipgram' or 'supervised'
# -----

list_params <- list(
  command = "cbow",
  lr = 0.1,
  dim = 200,
  input = file.path(tempdir(), "doc.txt"),
  output = tempdir(),
  verbose = 2,
  thread = 1
)

res <- fasttext_interface(list_params,
  path_output = file.path(tempdir(), "model_logs.txt"),
  MilliSecs = 100
)

# -----
# 'supervised' training
# -----

list_params <- list(
  command = "supervised",
  lr = 0.1,
  dim = 200,
  input = file.path(tempdir(), "cooking.train"),
  output = file.path(tempdir(), "model_cooking"),
  verbose = 2,
  thread = 1
)

res <- fasttext_interface(list_params,
  path_output = file.path(tempdir(), "logs_supervise.txt"),
  MilliSecs = 5
)

```

```
# -----
# In case that the 'command' is 'predict'
# -----

list_params <- list(
  command = "predict",
  model = file.path(tempdir(), "model_cooking.bin"),
  test_data = file.path(tempdir(), "cooking.valid"),
  k = 1,
  th = 0.0
)

res <- fasttext_interface(list_params,
  path_output = file.path(tempdir(), "predict_valid.txt")
)

# -----
# In case that the 'command' is 'test' [ k = 5 , means that precision and recall are at 5 ]
# -----

list_params <- list(
  command = "test",
  model = file.path(tempdir(), "model_cooking.bin"),
  test_data = file.path(tempdir(), "cooking.valid"),
  k = 5,
  th = 0.0
)

res <- fasttext_interface(list_params) # It only prints 'Precision', 'Recall' to the R session

# -----
# In case that the 'command' is 'test-label' [ k = 5 , means that precision and recall are at 5 ]
# -----

list_params <- list(
  command = "test-label",
  model = file.path(tempdir(), "model_cooking.bin"),
  test_data = file.path(tempdir(), "cooking.valid"),
  k = 5,
  th = 0.0
)

res <- fasttext_interface(list_params, # prints also 'Precision', 'Recall' to R session
  path_output = file.path(tempdir(), "test_valid.txt")
)

# -----
# quantize function [ it will take a .bin file and return an .ftz file ]
# -----
```

```

# the quantize function is currently (01/02/2019) single-threaded
# https://github.com/facebookresearch/fastText/issues/353#issuecomment-342501742

list_params <- list(
  command = "quantize",
  input = file.path(tempdir(), "model_cooking.bin"),
  output = file.path(tempdir(), gsub(".bin", ".ftz", "model_cooking.bin"))
)

res <- fasttext_interface(list_params)

# -----
# quantize function [ by using the optional parameters 'qnorm' and 'qout' ]
# -----

list_params <- list(
  command = "quantize",
  input = file.path(tempdir(), "model_cooking.bin"),
  output = file.path(tempdir(), gsub(".bin", ".ftz", "model_cooking.bin")),
  qnorm = TRUE,
  qout = TRUE
)

res <- fasttext_interface(list_params)

# -----
# print-word-vectors [ each line of the 'queries.txt' must be a single word ]
# -----

list_params <- list(
  command = "print-word-vectors",
  model = file.path(tempdir(), "model_cooking.bin")
)

res <- fasttext_interface(list_params,
  path_input = file.path(tempdir(), "queries.txt"),
  path_output = file.path(tempdir(), "print_vecs_file.txt")
)

# -----
# print-sentence-vectors [ See also the comments in the main.cc file about the input-file ]
# -----

list_params <- list(
  command = "print-sentence-vectors",
  model = file.path(tempdir(), "model_cooking.bin")
)

res <- fasttext_interface(list_params,
  path_input = file.path(tempdir(), "text.txt"),

```

```
    path_output = file.path(tempdir(), "SENTENCE_VECs.txt")
  )

# -----
# print-ngrams      [ print to console or to output-file ]
# -----

list_params <- list(
  command = "skipgram", lr = 0.1, dim = 200,
  input = file.path(tempdir(), "doc.txt"),
  output = tempdir(), verbose = 2, thread = 1,
  minn = 2, maxn = 2
)

res <- fasttext_interface(list_params,
  path_output = file.path(tempdir(), "ngram_out.txt"),
  MilliSecs = 5
)

list_params <- list(
  command = "print-ngrams",
  model = file.path(tempdir(), "ngram_out.bin"),
  word = "word"
) # print n-grams for specific word

res <- fasttext_interface(list_params, path_output = "") # print output to console
res <- fasttext_interface(list_params,
  path_output = file.path(tempdir(), "NGRAMS.txt")
) # output to file

# -----
# 'nn' function
# -----

list_params <- list(
  command = "nn",
  model = file.path(tempdir(), "model_cooking.bin"),
  k = 20,
  query_word = "word"
) # a 'query_word' is required

res <- fasttext_interface(list_params,
  path_output = file.path(tempdir(), "nn_output.txt")
)

# -----
# analogies [ in the output file each analogy-triplet-result is separated with a newline ]
# -----

list_params <- list(
```

```

    command = "analogies",
    model = file.path(tempdir(), "model_cooking.bin"),
    k = 5
  )

  res <- fasttext_interface(list_params,
    path_input = file.path(tempdir(), "analogy_queries.txt"),
    path_output = file.path(tempdir(), "analogies_output.txt")
  )

  # -----
  # dump function [ the 'option' param should be one of 'args', 'dict', 'input' or 'output' ]
  # -----

  list_params <- list(
    command = "dump",
    model = file.path(tempdir(), "model_cooking.bin"),
    option = "args"
  )

  res <- fasttext_interface(list_params,
    path_output = file.path(tempdir(), "DUMP.txt")
  )

  ## End(Not run)

```

---

language\_identification

*Language Identification using fastText*

---

## Description

Language Identification using fastText

## Usage

```

language_identification(
  input_obj,
  pre_trained_language_model_path,
  k = 1,
  th = 0,
  threads = 1,
  verbose = FALSE
)

```

## Arguments

`input_obj` either a valid character string to a valid path where each line represents a different text extract or a vector of text extracts

pre_trained_language_model_path	a valid character string to the pre-trained language identification model path, for more info see <a href="https://fasttext.cc/docs/en/language-identification.html">https://fasttext.cc/docs/en/language-identification.html</a>
k	predict top k labels (1 by default)
th	probability threshold (0.0 by default)
threads	an integer specifying the number of threads to run in parallel. This parameter applies only if k > 1
verbose	if TRUE then information will be printed out in the console

**Value**

an object of class `data.table` which includes two or more columns with the names `'iso_lang_N'` and `'prob_N'` where `'N'` corresponds to 1 to `'k'` input parameter

**References**

<https://fasttext.cc/docs/en/language-identification.html> <https://becominghuman.ai/a-handy-pre-trained-model-for-language-identification-cadd89db9db8>

**Examples**

```
library(fastText)

vec_txt <- c(
  "Incapaz de distinguir la luna y la cara de esta chica,
    Las estrellas se ponen nerviosas en el cielo",
  "Unable to tell apart the moon and this girl's face,
    Stars are flustered up in the sky."
)

file_pretrained <- system.file("language_identification/lid.176.ftz", package = "fastText")

dtbl_out <- language_identification(
  input_obj = vec_txt,
  pre_trained_language_model_path = file_pretrained,
  k = 3,
  th = 0.0,
  verbose = TRUE
)
dtbl_out
```

---

plot\_progress\_logs      *Plot the progress of loss, learning-rate and word-counts*

---

**Description**

Plot the progress of loss, learning-rate and word-counts

**Usage**

```
plot_progress_logs(path_logs = "progress_data.txt", plot = FALSE)
```

**Arguments**

path_logs	a character string specifying a valid path to a file where the progress-logs are saved
plot	a boolean specifying if the loss, learning-rate and word-counts should be plotted

**Value**

an object of class data.frame that includes the progress logs with columns 'progress', 'words\_sec\_thread', 'learning\_rate' and 'loss'

**References**

[http://www.cookbook-r.com/Graphs/Multiple\\_graphs\\_on\\_one\\_page\\_\(ggplot2\)/](http://www.cookbook-r.com/Graphs/Multiple_graphs_on_one_page_(ggplot2)/)

**Examples**

```
## Not run:

library(fastText)

#-----
# the 'progress_data.txt' file corresponds to the 'path_output'
# parameter of the 'fasttext_interface()'. Therefore the user has
# to run first the 'fasttext_interface()' function to save the
# 'progress_data.txt' file to the desired folder.
#-----

res <- plot_progress_logs(
  path = file.path(tempdir(), "progress_data.txt"),
  plot = TRUE
)

## End(Not run)
```

---

printAnalogiesUsage    *Print Usage Information when the command equals to 'analogies'*

---

**Description**

Print Usage Information when the command equals to 'analogies'

**Usage**

```
printAnalogiesUsage(verbose = TRUE)
```

**Arguments**

verbose            if TRUE then information will be printed in the console

**Value**

It does not return a value but only prints the available parameters of the 'printAnalogiesUsage' function in the R session

**Examples**

```
library(fastText)
printAnalogiesUsage()
```

---

`printDumpUsage`            *Print Usage Information when the command equals to 'dump'*

---

**Description**

Print Usage Information when the command equals to 'dump'

**Usage**

```
printDumpUsage(verbose = TRUE)
```

**Arguments**

verbose            if TRUE then information will be printed in the console

**Value**

It does not return a value but only prints the available parameters of the 'printDumpUsage' function in the R session

**Examples**

```
library(fastText)
printDumpUsage()
```

---

printNNUsage	<i>Print Usage Information when the command equals to 'nn'</i>
--------------	--

---

**Description**

Print Usage Information when the command equals to 'nn'

**Usage**

```
printNNUsage(verbose = TRUE)
```

**Arguments**

verbose           if TRUE then information will be printed in the console

**Value**

It does not return a value but only prints the available parameters of the 'printNNUsage' function in the R session

**Examples**

```
library(fastText)
printNNUsage()
```

---

printPredictUsage	<i>Print Usage Information when the command equals to 'predict' or 'predict-prob'</i>
-------------------	---

---

**Description**

Print Usage Information when the command equals to 'predict' or 'predict-prob'

**Usage**

```
printPredictUsage(verbose = TRUE)
```

**Arguments**

verbose           if TRUE then information will be printed in the console

**Value**

It does not return a value but only prints the available parameters of the 'printPredictUsage' function in the R session

**Examples**

```
library(fastText)
printPredictUsage()
```

---

`printPrintNgramsUsage` *Print Usage Information when the command equals to 'print-ngrams'*

---

**Description**

Print Usage Information when the command equals to 'print-ngrams'

**Usage**

```
printPrintNgramsUsage(verbose = TRUE)
```

**Arguments**

`verbose`            if TRUE then information will be printed in the console

**Value**

It does not return a value but only prints the available parameters of the 'printPrintNgramsUsage' function in the R session

**Examples**

```
library(fastText)
printPrintNgramsUsage()
```

---

`printPrintSentenceVectorsUsage`  
*Print Usage Information when the command equals to 'print-sentence-vectors'*

---

**Description**

Print Usage Information when the command equals to 'print-sentence-vectors'

**Usage**

```
printPrintSentenceVectorsUsage(verbose = TRUE)
```

**Arguments**

verbose            if TRUE then information will be printed in the console

**Value**

It does not return a value but only prints the available parameters of the 'printPrintSentenceVectorsUsage' function in the R session

**Examples**

```
library(fastText)

printPrintSentenceVectorsUsage()
```

---

```
printPrintWordVectorsUsage
```

*Print Usage Information when the command equals to 'print-word-vectors'*

---

**Description**

Print Usage Information when the command equals to 'print-word-vectors'

**Usage**

```
printPrintWordVectorsUsage(verbose = TRUE)
```

**Arguments**

verbose            if TRUE then information will be printed in the console

**Value**

It does not return a value but only prints the available parameters of the 'printPrintWordVectorsUsage' function in the R session

**Examples**

```
library(fastText)

printPrintWordVectorsUsage()
```

---

printQuantizeUsage     *Print Usage Information when the command equals to 'quantize'*

---

**Description**

Print Usage Information when the command equals to 'quantize'

**Usage**

```
printQuantizeUsage(verbose = TRUE)
```

**Arguments**

verbose            if TRUE then information will be printed in the console

**Value**

It does not return a value but only prints the available parameters of the 'printQuantizeUsage' function in the R session

**Examples**

```
library(fastText)
printQuantizeUsage()
```

---

printTestLabelUsage     *Print Usage Information when the command equals to 'test-label'*

---

**Description**

Print Usage Information when the command equals to 'test-label'

**Usage**

```
printTestLabelUsage(verbose = TRUE)
```

**Arguments**

verbose            if TRUE then information will be printed in the console

**Value**

It does not return a value but only prints the available parameters of the 'printTestLabelUsage' function in the R session

**Examples**

```
library(fastText)
printTestLabelUsage()
```

---

printTestUsage	<i>Print Usage Information when the command equals to 'test'</i>
----------------	--

---

**Description**

Print Usage Information when the command equals to 'test'

**Usage**

```
printTestUsage(verbose = TRUE)
```

**Arguments**

verbose           if TRUE then information will be printed in the console

**Value**

It does not return a value but only prints the available parameters of the 'printTestUsage' function in the R session

**Examples**

```
library(fastText)
printTestUsage()
```

---

printUsage	<i>Print Usage Information for all parameters</i>
------------	---

---

**Description**

Print Usage Information for all parameters

**Usage**

```
printUsage(verbose = TRUE)
```

**Arguments**

verbose           if TRUE then information will be printed in the console

**Value**

It does not return a value but only prints the available parameters of the 'printUsage' function in the R session

**Examples**

```
library(fastText)

printUsage()
```

---

print_parameters	<i>Print the parameters for a specific command</i>
------------------	--

---

**Description**

Print the parameters for a specific command

**Usage**

```
print_parameters(command = "supervised")
```

**Arguments**

command	a character string specifying the command for which the parameters should be printed in the R session. It should be one of "skipgram", "cbow", "supervised", "test", "test-label" or "quantize"
---------	---

**Value**

It does not return a value but only prints the available parameters in the R session

**References**

<https://github.com/facebookresearch/fastText#full-documentation>  
<https://github.com/facebookresearch/fastText/issues/341#issuecomment-339783130>

**Examples**

```
## Not run:

library(fastText)

print_parameters(command = "supervised")

## End(Not run)
```

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