

# Package ‘stringdist’

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**Maintainer** Mark van der Loo <mark.vanderloo@gmail.com>

**License** GPL-3

**Title** Approximate String Matching, Fuzzy Text Search, and String Distance Functions

**LazyData** no

**Type** Package

**LazyLoad** yes

**Description** Implements an approximate string matching version of R's native 'match' function. Also offers fuzzy text search based on various string distance measures. Can calculate various string distances based on edits (Damerau-Levenshtein, Hamming, Levenshtein, optimal sting alignment), qgrams (q-gram, cosine, jaccard distance) or heuristic metrics (Jaro, Jaro-Winkler). An implementation of soundex is provided as well. Distances can be computed between character vectors while taking proper care of encoding or between integer vectors representing generic sequences. This package is built for speed and runs in parallel by using 'openMP'. An API for C or C++ is exposed as well. Reference: MPJ van der Loo (2014) <doi:10.32614/RJ-2014-011>.

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**Author** Mark van der Loo [aut, cre] (<<https://orcid.org/0000-0002-9807-4686>>),  
Jan van der Laan [ctb],  
R Core Team [ctb],  
Nick Logan [ctb],  
Chris Muir [ctb],  
Johannes Gruber [ctb]

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stringdist-package     *A package for string distance calculation and approximate string matching.*

---

## Description

The **stringdist** package offers fast and platform-independent string metrics. Its main purpose is to compute various string distances and to do approximate text matching between character vectors. As of version 0.9.3, it is also possible to compute distances between sequences represented by integer vectors.

## Details

A typical use is to match strings that are not precisely the same. For example

```
amatch(c("hello", "g'day"), c("hi", "hallo", "ola"), maxDist=2)
```

returns `c(2, NA)` since "hello" matches closest with "hallo", and within the maximum (optimal string alignment) distance. The second element, "g'day", matches closest with "ola" but since the distance equals 4, no match is reported.

A second typical use is to compute string distances. For example

```
stringdist(c("g'day"), c("hi", "hallo", "ola"))
```

Returns `c(5, 5, 4)` since these are the distances between "g'day" and respectively "hi", "hallo", and "ola".

A third typical use would be to compute a `dist` object. The command

```
stringdistmatrix(c("foo", "bar", "boo", "baz"))
```

returns an object of class `dist` that can be used by clustering algorithms such as `stats::hclust`.

A fourth use is to compute string distances between general sequences, represented as integer vectors (which must be stored in a `list`):

```
seq_dist( list(c(1L, 1L, 2L)), list(c(1L, 2L, 1L), c(2L, 3L, 1L, 2L)) )
```

The above code yields the vector `c(1, 2)` (the first shorter first argument is recycled over the longer second argument)

Besides documentation for each function, the main topics documented are:

- [stringdist-metrics](#) – string metrics supported by the package
- [stringdist-encoding](#) – how encoding is handled by the package
- [stringdist-parallelization](#) – on multithreading

## Acknowledgements

- The code for the full Damerau-Levenshtein distance was adapted from Nick Logan's [public github repository](#).
- C code for converting UTF-8 to integer was copied from the R core for performance reasons.
- The code for soundex conversion and string similarity was kindly contributed by Jan van der Laan.

## Citation

If you would like to cite this package, please cite the [R Journal Paper](#):

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Or use `citation('stringdist')` to get a bibtex item.

## Description

`afind` slides a window of fixed width over a string `x` and computes the distance between the each window and the sought-after pattern. The location, content, and distance corresponding to the window with the best match is returned.

**Usage**

```
afind(
  x,
  pattern,
  window = NULL,
  value = TRUE,
  method = c("osa", "lv", "dl", "hamming", "lcs", "qgram", "cosine", "running_cosine",
    "jaccard", "jw", "soundex"),
  useBytes = FALSE,
  weight = c(d = 1, i = 1, s = 1, t = 1),
  q = 1,
  p = 0,
  bt = 0,
  nthread = getOption("sd_num_thread")
)
```

```
grab(x, pattern, maxDist = Inf, value = FALSE, ...)
```

```
grabl(x, pattern, maxDist = Inf, ...)
```

```
extract(x, pattern, maxDist = Inf, ...)
```

**Arguments**

x	strings to search in
pattern	strings to find (not a regular expression). For grab, grabl, and extract this must be a single string.
window	width of moving window.
value	toggle return matrix with matched strings.
method	Matching algorithm to use. See <a href="#">stringdist-metrics</a> .
useBytes	Perform byte-wise comparison. See <a href="#">stringdist-encoding</a> .
weight	For method='osa' or 'dl', the penalty for deletion, insertion, substitution and transposition, in that order. When method='lv', the penalty for transposition is ignored. When method='jw', the weights associated with characters of a, characters from b and the transposition weight, in that order. Weights must be positive and not exceed 1. weight is ignored completely when method='hamming', 'qgram', 'cosine', 'Jaccard', 'lcs', or 'soundex'.
q	q-gram size, only when method is 'qgram', 'jaccard', or 'cosine'.
p	Winklers 'prefix' parameter for Jaro-Winkler distance, with $0 \leq p \leq 0.25$ . Only when method is 'jw'
bt	Winkler's boost threshold. Winkler's prefix factor is only applied when the Jaro distance is larger than bt. Applies only to method='jw' and $p > 0$ .
nthread	Number of threads used by the underlying C-code. A sensible default is chosen, see <a href="#">stringdist-parallelization</a> .
maxDist	Only windows with distance $\leq$ maxDist are considered a match.
...	passed to afind.

## Details

Matching is case-sensitive. Both `x` and `pattern` are converted to UTF-8 prior to search, unless `useBytes=TRUE`, in which case the distances are measured bytewise.

Code is parallelized over the `x` variable: each value of `x` is scanned for every element in `pattern` using a separate thread (when `nthread` is larger than 1).

The functions `grab` and `grabl` are approximate string matching functions that somewhat resemble base R's `grep` and `grep1`. They are implemented as convenience wrappers of `afind`.

## Value

For `afind`: a list of three matrices, each with `length(x)` rows and `length(pattern)` columns. In each matrix, element  $(i, j)$  corresponds to `x[i]` and `pattern[j]`. The names and description of each matrix is as follows.

- `location`. [integer], location of the start of best matching window. When `useBytes=FALSE`, this corresponds to the location of a UTF code point in `x`, possibly after conversion from its original encoding.
- `distance`. [character], the string distance between `pattern` and the best matching window.
- `match`. [character], the first, best matching window.

For `grab`, an integer vector, indicating in which elements of `x` a match was found with a distance `<= maxDist`. The matched values when `value=TRUE` (equivalent to `grep`).

For `grabl`, a logical vector, indicating in which elements of `x` a match was found with a distance `<= maxDist`. (equivalent to `grep1`).

For `extract`, a character matrix with `length(x)` rows and `length(pattern)` columns. If match was found, element  $(i, j)$  contains the match, otherwise it is set to NA.

## Running cosine distance

This algorithm gains efficiency by using that two consecutive windows have a large overlap in their q-gram profiles. It gives the same result as the "cosine" distance, but much faster.

## See Also

Other matching: `amatch()`

## Examples

```
texts = c("When I grow up, I want to be"
          , "one of the harvesters of the sea"
          , "I think before my days are gone"
          , "I want to be a fisherman")
patterns = c("fish", "gone", "to be")

afind(texts, patterns, method="running_cosine", q=3)

grabl(texts, "grew", maxDist=1)
extract(texts, "harvested", maxDist=3)
```

---

amatch

*Approximate string matching*


---

## Description

Approximate string matching equivalents of R's native `match` and `%in%`.

## Usage

```
amatch(
  x,
  table,
  nomatch = NA_integer_,
  matchNA = TRUE,
  method = c("osa", "lv", "dl", "hamming", "lcs", "qgram", "cosine", "jaccard", "jw",
             "soundex"),
  useBytes = FALSE,
  weight = c(d = 1, i = 1, s = 1, t = 1),
  maxDist = 0.1,
  q = 1,
  p = 0,
  bt = 0,
  nthread = getOption("sd_num_thread")
)

ain(x, table, ...)
```

## Arguments

<code>x</code>	elements to be approximately matched: will be coerced to character unless it is a list consisting of integer vectors.
<code>table</code>	lookup table for matching. Will be coerced to character unless it is a list consisting of integer vectors.
<code>nomatch</code>	The value to be returned when no match is found. This is coerced to integer.
<code>matchNA</code>	Should NA's be matched? Default behaviour mimics the behaviour of base <code>match</code> , meaning that NA matches NA (see also the note on NA handling below).
<code>method</code>	Matching algorithm to use. See <a href="#">stringdist-metrics</a> .
<code>useBytes</code>	Perform byte-wise comparison. See <a href="#">stringdist-encoding</a> .
<code>weight</code>	For <code>method='osa'</code> or <code>'dl'</code> , the penalty for deletion, insertion, substitution and transposition, in that order. When <code>method='lv'</code> , the penalty for transposition is ignored. When <code>method='jw'</code> , the weights associated with characters of a, characters from b and the transposition weight, in that order. Weights must be positive and not exceed 1. <code>weight</code> is ignored completely when <code>method='hamming'</code> , <code>'qgram'</code> , <code>'cosine'</code> , <code>'Jaccard'</code> , <code>'lcs'</code> , or <code>'soundex'</code> .

maxDist	Elements in <code>x</code> will not be matched with elements of <code>table</code> if their distance is larger than <code>maxDist</code> . Note that the maximum distance between strings depends on the method: it should always be specified.
q	q-gram size, only when method is 'qgram', 'jaccard', or 'cosine'.
p	Winkler's 'prefix' parameter for Jaro-Winkler distance, with $0 \leq p \leq 0.25$ . Only when method is 'jw'
bt	Winkler's boost threshold. Winkler's prefix factor is only applied when the Jaro distance is larger than <code>bt</code> . Applies only to <code>method='jw'</code> and <code>p&gt;0</code> .
nthread	Number of threads used by the underlying C-code. A sensible default is chosen, see <a href="#">stringdist-parallelization</a> .
...	parameters to pass to <code>amatch</code> (except <code>nomatch</code> )

### Details

`ain` is currently defined as

```
ain(x, table, ...) <- function(x, table, ...) amatch(x, table, nomatch=0, ...) > 0
```

### Value

`amatch` returns the position of the closest match of `x` in `table`. When multiple matches with the same smallest distance metric exist, the first one is returned. `ain` returns a logical vector of length `length(x)` indicating whether an element of `x` approximately matches an element in `table`.

### Note on NA handling

R's native `match` function matches NA with NA. This may feel inconsistent with R's usual NA handling, since for example `NA==NA` yields NA rather than TRUE. In most cases, one may reason about the behaviour under NA along the lines of "if one of the arguments is NA, the result shall be NA", simply because not all information necessary to execute the function is available. One uses special functions such as `is.na`, `is.null` *etc.* to handle special values.

The `amatch` function mimics the behaviour of `match` by default: NA is matched with NA and with nothing else. Note that this is inconsistent with the behaviour of `stringdist` since `stringdist` yields NA when at least one of the arguments is NA. The same inconsistency exists between `match` and `adist`. In `amatch` this behaviour can be controlled by setting `matchNA=FALSE`. In that case, if any of the arguments in `x` is NA, the `nomatch` value is returned, regardless of whether NA is present in `table`. In `match` the behaviour can be controlled by setting the `incomparables` option.

### See Also

Other matching: `afind()`

### Examples

```
# lets see which sci-fi heroes are stringdistantly nearest
amatch("leia",c("uhura","leela"),maxDist=5)

# we can restrict the search
```

```

amatch("leia",c("uhura","leela"),maxDist=1)

# we can match each value in the find vector against values in the lookup table:
amatch(c("leia","uhura"),c("ripley","leela","scully","trinity"),maxDist=2)

# setting nomatch returns a different value when no match is found
amatch("leia",c("uhura","leela"),maxDist=1,nomatch=0)

# this is always true if maxDist is Inf
ain("leia",c("uhura","leela"),maxDist=Inf)

# Let's look in a neighbourhood of maximum 2 typo's (by default, the OSA algorithm is used)
ain("leia",c("uhura","leela"), maxDist=2)

```

---

phonetic

*Phonetic algorithms*

---

## Description

Translate strings to phonetic codes. Similar sounding strings should get similar or equal codes.

## Usage

```
phonetic(x, method = c("soundex"), useBytes = FALSE)
```

## Arguments

x	a character vector whose elements are phonetically encoded.
method	name of the algorithm used. The default is "soundex".
useBytes	Perform byte-wise comparison. useBytes=TRUE is faster but may yield different results depending on character encoding. For more information see the documentation of <a href="#">stringdist</a> .

## Details

Currently, only the soundex algorithm is implemented. Note that soundex coding is only meaningful for characters in the ranges a-z and A-Z. Soundex coding of strings containing non-printable ascii or non-ascii characters may be system-dependent and should not be trusted. If non-ascii or non-printable ascii characters are encountered, a warning is emitted.

## Value

The returns value depends on the method used. However, all currently implemented methods return a character vector of the same length of the input vector. Output characters are in the system's native encoding.



**References**

- The Soundex algorithm implemented is the algorithm used by the [National Archives](#). This algorithm differs slightly from the original algorithm patented by R.C. Russell (US patents 1261167 (1918) and 1435663 (1922)).

**See Also**

[printable\\_ascii](#), [stringdist-package](#)

**Examples**

```
# The following examples are from The Art of Computer Programming (part III, p. 395)
# (Note that our algorithm is specified different from the one in TACP, see references.)
phonetic(c('Euler', 'Gauss', 'Hilbert', 'Knuth', 'Lloyd', 'Lukasiewicz', 'Wachs'), method='soundex')
```

---

printable_ascii	<i>Detect the presence of non-printable or non-ascii characters</i>
-----------------	---

---

**Description**

Detect the presence of non-printable or non-ascii characters

**Usage**

```
printable_ascii(x)
```

**Arguments**

x                    a character vector

**Details**

Printable ASCII characters consist of space, A-Z, a-z, 0-9 and the characters

```
! " " # $ % & ' ( ) * + , . / : ; < = > ? @ [ ] \ ^ _ ` { | } ~ -
```

Note that this excludes tab (as it is a control character).

**Value**

A logical indicating which elements consist solely of printable ASCII characters.

## Examples

```
# define o-umlaut
ouml <- intToUtf8("0x00F6")
x <- c("Motorhead", paste0("Mot",ouml,"rhead"))
# second element contains a non-ascii character
printable_ascii(x)

# Control characters (like carriage return) are also excluded
printable_ascii("abc\r")
```

---

qgrams

*Get a table of qgram counts from one or more character vectors.*


---

## Description

Get a table of qgram counts from one or more character vectors.

## Usage

```
qgrams(..., .list = NULL, q = 1L, useBytes = FALSE, useNames = !useBytes)
```

## Arguments

...	any number of (named) arguments, that will be coerced to character with <code>as.character</code> .
.list	Will be concatenated with the ... argument(s). Useful for adding character vectors named 'q' or 'useNames'.
q	size of q-gram, must be non-negative.
useBytes	Determine byte-wise qgrams. <code>useBytes=TRUE</code> is faster but may yield different results depending on character encoding. For ASCII it is identical. See also <a href="#">stringdist</a> under Encoding issues.
useNames	Add q-grams as column names. If <code>useBytes=useNames=TRUE</code> , the q-byte sequences are represented as 2 hexadecimal numbers per byte, separated by a vertical bar ( ).

## Value

A table with  $q$ -gram counts. Detected  $q$ -grams are column names and the argument names as row names. If no argument names were provided, they will be generated.

## Details

The input is converted to character. If `useBytes=TRUE`, each element is converted to utf8 and then to integer as in [stringdist](#). Next, the data is passed to the underlying routine.

Strings with less than  $q$  characters and elements containing NA are skipped. Using `q=0` therefore counts the number of empty strings "" occurring in each argument.

**See Also**[stringdist](#), [amatch](#)**Examples**

```

qgrams('hello world',q=3)

# q-grams are counted uniquely over a character vector
qgrams(rep('hello world',2),q=3)

# to count them separately, do something like
x <- c('hello', 'world')
lapply(x,qgrams, q=3)

# output rows may be named, and you can pass any number of character vectors
x <- "I will not buy this record, it is scratched"
y <- "My hovercraft is full of eels"
z <- c("this", "is", "a", "dead","parrot")
qgrams(A = x, B = y, C = z,q=2)

# a tonque twister, showing the effects of useBytes and useNames
x <- "peter piper picked a peck of pickled peppers"
qgrams(x, q=2)
qgrams(x, q=2, useNames=FALSE)
qgrams(x, q=2, useBytes=TRUE)
qgrams(x, q=2, useBytes=TRUE, useNames=TRUE)

```

---

seq\_amatch

*Approximate matching for integer sequences.*


---

**Description**

For a list of integer vectors `x`, find the closest matches in a list of integer or numeric vectors in `table`.

**Usage**

```

seq_amatch(
  x,
  table,
  nomatch = NA_integer_,
  matchNA = TRUE,
  method = c("osa", "lv", "dl", "hamming", "lcs", "qgram", "cosine", "jaccard", "jw"),
  weight = c(d = 1, i = 1, s = 1, t = 1),

```

```

    maxDist = 0.1,
    q = 1,
    p = 0,
    bt = 0,
    nthread = getOption("sd_num_thread")
)

seq_ain(x, table, ...)

```

### Arguments

x	(list of) integer or numeric vector(s) to be approximately matched. Will be converted with <code>as.integer</code> .
table	(list of) integer or numeric vector(s) serving as lookup table for matching. Will be converted with <code>as.integer</code> .
nomatch	The value to be returned when no match is found. This is coerced to integer.
matchNA	Should NA's be matched? Default behaviour mimics the behaviour of base <code>match</code> , meaning that NA matches NA. With NA, we mean a missing entry in the list, represented as <code>NA_integer_</code> . If one of the integer sequences stored in the list has an NA entry, this is just treated as another integer (the representation of <code>NA_integer_</code> ).
method	Matching algorithm to use. See <a href="#">stringdist-metrics</a> .
weight	For <code>method='osa'</code> or <code>'dl'</code> , the penalty for deletion, insertion, substitution and transposition, in that order. When <code>method='lv'</code> , the penalty for transposition is ignored. When <code>method='jw'</code> , the weights associated with integers in elements of a, integers in elements of b and the transposition weight, in that order. Weights must be positive and not exceed 1. <code>weight</code> is ignored completely when <code>method='hamming', 'qgram', 'cosine', 'Jaccard',</code> or <code>'lcs'</code> .
maxDist	Elements in x will not be matched with elements of table if their distance is larger than <code>maxDist</code> . Note that the maximum distance between strings depends on the method: it should always be specified.
q	q-gram size, only when method is <code>'qgram', 'jaccard',</code> or <code>'cosine'</code> .
p	Winkler's prefix parameter for Jaro-Winkler distance, with $0 \leq p \leq 0.25$ . Only when method is <code>'jw'</code>
bt	Winkler's boost threshold. Winkler's prefix factor is only applied when the Jaro distance is larger than <code>bt</code> . Applies only to <code>method='jw'</code> and <code>p&gt;0</code> .
nthread	Number of threads used by the underlying C-code. A sensible default is chosen, see <a href="#">stringdist-parallelization</a> .
...	parameters to pass to <code>seq_amatch</code> (except <code>nomatch</code> )

### Value

`seq_amatch` returns the position of the closest match of x in table. When multiple matches with the same minimal distance metric exist, the first one is returned. `seq_ain` returns a logical vector of length `length(x)` indicating whether an element of x approximately matches an element in table.

**Notes**

seq\_ain is currently defined as

```
seq_ain(x, table, ...) <- function(x, table, ...) amatch(x, table, nomatch=0, ...) > 0
```

All input vectors are converted with `as.integer`. This causes truncation for numeric vectors (e.g. `pi` will be treated as 3L).

**See Also**

[seq\\_dist](#), [seq\\_sim](#), [seq\\_qgrams](#)

**Examples**

```
x <- list(1:3, c(3:1), c(1L, 3L, 4L))
table <- list(
  c(5L, 3L, 1L, 2L)
  , 1:4
)
seq_amatch(x, table, maxDist=2)

# behaviour with missings
seq_amatch(list(c(1L, NA_integer_, 3L), NA_integer_), list(1:3), maxDist=1)

## Not run:
# Match sentences based on word order. Note: words must match exactly or they
# are treated as completely different.
#
# For this example you need to have the 'hashr' package installed.
x <- "Mary had a little lamb"
x.words <- strsplit(x, "[[:blank:]]+")
x.int <- hashr::hash(x.words)
table <- c("a little lamb had Mary",
          "had Mary a little lamb")
table.int <- hashr::hash(strsplit(table, "[[:blank:]]+"))
seq_amatch(x.int, table.int, maxDist=3)

## End(Not run)
```

---

seq\_dist

*Compute distance metrics between integer sequences*

---

**Description**

`seq_dist` computes pairwise string distances between elements of `a` and `b`, where the argument with less elements is recycled. `seq_distmatrix` computes the distance matrix with rows according to `a` and columns according to `b`.

**Usage**

```
seq_dist(
  a,
  b,
  method = c("osa", "lv", "dl", "hamming", "lcs", "qgram", "cosine", "jaccard", "jw"),
  weight = c(d = 1, i = 1, s = 1, t = 1),
  q = 1,
  p = 0,
  bt = 0,
  nthread = getOption("sd_num_thread")
)

seq_distmatrix(
  a,
  b,
  method = c("osa", "lv", "dl", "hamming", "lcs", "qgram", "cosine", "jaccard", "jw"),
  weight = c(d = 1, i = 1, s = 1, t = 1),
  q = 1,
  p = 0,
  bt = 0,
  useNames = c("names", "none"),
  nthread = getOption("sd_num_thread")
)
```

**Arguments**

a	(list of) integer or numeric vector(s). Will be converted with <code>as.integer(target)</code>
b	(list of) integer or numeric vector(s). Will be converted with <code>as.integer(source)</code> . Optional for <code>seq_distmatrix</code> .
method	Distance metric. See <a href="#">stringdist-metrics</a>
weight	For <code>method='osa'</code> or <code>'dl'</code> , the penalty for deletion, insertion, substitution and transposition, in that order. When <code>method='lv'</code> , the penalty for transposition is ignored. When <code>method='jw'</code> , the weights associated with characters of a, characters from b and the transposition weight, in that order. Weights must be positive and not exceed 1. <code>weight</code> is ignored completely when <code>method='hamming', 'qgram', 'cosine', 'Jaccard', or 'lcs'</code>
q	Size of the $q$ -gram; must be nonnegative. Only applies to <code>method='qgram', 'jaccard' or 'cosine'</code> .
p	Prefix factor for Jaro-Winkler distance. The valid range for $p$ is $0 \leq p \leq 0.25$ . If $p=0$ (default), the Jaro-distance is returned. Applies only to <code>method='jw'</code> .
bt	Winkler's boost threshold. Winkler's prefix factor is only applied when the Jaro distance is larger than <code>bt</code> Applies only to <code>method='jw'</code> and $p>0$ .
nthread	Maximum number of threads to use. By default, a sensible number of threads is chosen, see <a href="#">stringdist-parallelization</a> .
useNames	label the output matrix with <code>names(a)</code> and <code>names(b)</code> ?

**Value**

seq\_dist returns a numeric vector with pairwise distances between a and b of length  $\max(\text{length}(a), \text{length}(b))$ .

For seq\_distmatrix there are two options. If b is missing, the `dist` object corresponding to the  $\text{length}(a) \times \text{length}(a)$  distance matrix is returned. If b is specified, the  $\text{length}(a) \times \text{length}(b)$  distance matrix is returned.

If any element of a or b is `NA_integer_`, the distance with any matched integer vector will result in NA. Missing values in the sequences themselves are treated as a number and not treated specially (Also see the examples).

**Notes**

Input vectors are converted with `as.integer`. This causes truncation for numeric vectors (e.g. pi will be treated as 3L).

**See Also**

[seq\\_sim](#), [seq\\_amatch](#), [seq\\_qgrams](#)

**Examples**

```
# Distances between lists of integer vectors. Note the postfix 'L' to force
# recycled over (\code{a})
a <- list(c(102L, 107L)) # fu
b <- list(c(102L,111L,111L),c(102L,111L,111L)) # foo, fo
seq_dist(a,b)

# translate strings to a list of integer sequences
a <- lapply(c("foo", "bar", "baz"),utf8ToInt)
seq_distmatrix(a)

# Note how missing values are treated. NA's as part of the sequence are treated
# as an integer (the representation of NA_integer_).
a <- list(NA_integer_,c(102L, 107L))
b <- list(c(102L,111L,111L),c(102L,111L,NA_integer_))
seq_dist(a,b)

## Not run:
# Distance between sentences based on word order. Note: words must match exactly or they
# are treated as completely different.
#
# For this example you need to have the 'hashr' package installed.
a <- "Mary had a little lamb"
a.words <- strsplit(a,"[[:blank:]]+")
a.int <- hashr::hash(a.words)
b <- c("a little lamb had Mary",
      "had Mary a little lamb")
b.int <- hashr::hash(strsplit(b,"[[:blank:]]+"))
seq_dist(a.int,b.int)

## End(Not run)
```

---

`seq_qgrams`*Get a table of qgram counts for integer sequences*

---

**Description**

Get a table of qgram counts for integer sequences

**Usage**

```
seq_qgrams(..., .list = NULL, q = 1L)
```

**Arguments**

<code>...</code>	Any number of (named) arguments that will be coerced with <code>as.integer</code>
<code>.list</code>	Will be concatenated with the <code>...</code> argument(s). Useful for adding integer vectors named 'q'.
<code>q</code>	The size of q-gramming.

**Value**

A matrix containing q-gram profiles. Columns 1 to q contain the encountered q-grams. The ensuing (named) columns contain the q-gram counts per vector. Run the example for a simple overview.

Missing values in integer sequences are treated as any other number.

**See Also**

[seq\\_dist](#), [seq\\_amatch](#)

**Examples**

```
# compare the 2-gram overlap between sequences 1:3 and 2:4
seq_qgrams(x = 1:3, y=2:4,q=2)

# behavior when NA's are present.
seq_qgrams(1:3,c(1,NA,2),NA_integer_)
```



---

seq\_sim *Compute similarity scores between sequences of integers*

---

### Description

Compute similarity scores between sequences of integers

### Usage

```
seq_sim(
  a,
  b,
  method = c("osa", "lv", "dl", "hamming", "lcs", "qgram", "cosine", "jaccard", "jw"),
  q = 1,
  ...
)
```

### Arguments

a	list of integer vectors (target)
b	list of integer vectors (source). Optional for seq_distmatrix.
method	Method for distance calculation. The default is "osa", see <a href="#">stringdist-metrics</a> .
q	Size of the $q$ -gram; must be nonnegative. Only applies to method='qgram', 'jaccard' or 'cosine'.
...	additional arguments are passed on to <a href="#">seq_dist</a> .

### Value

A numeric vector of length  $\max(\text{length}(a), \text{length}(b))$ . If one of the entries in a or b is NA\_integer\_, all comparisons with that element result in NA. Missings occurring within the sequences are treated as an ordinary number (the representation of NA\_integer\_).

### See Also

[seq\\_dist](#), [seq\\_amatch](#)

### Examples

```
L1 <- list(1:3,2:4)
L2 <- list(1:3)
seq_sim(L1,L2,method="osa")

# note how missing values are handled (L2 is recycled over L1)
L1 <- list(c(1L,NA_integer_,3L),2:4,NA_integer_)
L2 <- list(1:3)
seq_sim(L1,L2)
```

---

stringdist

---

*Compute distance metrics between strings*


---

### Description

stringdist computes pairwise string distances between elements of a and b, where the argument with less elements is recycled. stringdistmatrix computes the string distance matrix with rows according to a and columns according to b.

### Usage

```
stringdist(
  a,
  b,
  method = c("osa", "lv", "dl", "hamming", "lcs", "qgram", "cosine", "jaccard", "jw",
             "soundex"),
  useBytes = FALSE,
  weight = c(d = 1, i = 1, s = 1, t = 1),
  q = 1,
  p = 0,
  bt = 0,
  nthread = getOption("sd_num_thread")
)
```

```
stringdistmatrix(
  a,
  b,
  method = c("osa", "lv", "dl", "hamming", "lcs", "qgram", "cosine", "jaccard", "jw",
             "soundex"),
  useBytes = FALSE,
  weight = c(d = 1, i = 1, s = 1, t = 1),
  q = 1,
  p = 0,
  bt = 0,
  useNames = c("none", "strings", "names"),
  nthread = getOption("sd_num_thread")
)
```

### Arguments

a	R object (target); will be converted by <code>as.character</code>
b	R object (source); will be converted by <code>as.character</code> This argument is optional for <code>stringdistmatrix</code> (see section Value).
method	Method for distance calculation. The default is "osa", see <a href="#">stringdist-metrics</a> .
useBytes	Perform byte-wise comparison, see <a href="#">stringdist-encoding</a> .

weight	For method='osa' or 'dl', the penalty for deletion, insertion, substitution and transposition, in that order. When method='lv', the penalty for transposition is ignored. When method='jw', the weights associated with characters of a, characters from b and the transposition weight, in that order. Weights must be positive and not exceed 1. weight is ignored completely when method='hamming', 'qgram', 'cosine', 'Jaccard', 'lcs', or soundex.
q	Size of the $q$ -gram; must be nonnegative. Only applies to method='qgram', 'jaccard' or 'cosine'.
p	Prefix factor for Jaro-Winkler distance. The valid range for p is $0 \leq p \leq 0.25$ . If p=0 (default), the Jaro-distance is returned. Applies only to method='jw'.
bt	Winkler's boost threshold. Winkler's prefix factor is only applied when the Jaro distance is larger than bt. Applies only to method='jw' and $p > 0$ .
nthread	Maximum number of threads to use. By default, a sensible number of threads is chosen, see <a href="#">stringdist-parallelization</a> .
useNames	Use input vectors as row and column names?

### Value

For stringdist, a vector with string distances of size  $\max(\text{length}(a), \text{length}(b))$ .

For stringdistmatrix: if both a and b are passed, a  $\text{length}(a) \times \text{length}(b)$  matrix. If a single argument a is given an object of class `dist` is returned.

Distances are nonnegative if they can be computed, NA if any of the two argument strings is NA and Inf when `maxDist` is exceeded or, in case of the hamming distance, when the two compared strings have different length.

### See Also

[stringsim](#), [qgrams](#), [amatch](#), [afind](#)

### Examples

```
# Simple example using optimal string alignment
stringdist("ca", "abc")

# computing a 'dist' object
d <- stringdistmatrix(c('foo', 'bar', 'boo', 'baz'))
# try plot(hclust(d))

# The following gives a matrix
stringdistmatrix(c("foo", "bar", "boo"), c("baz", "buz"))

# An example using Damerau-Levenshtein distance (multiple editing of substrings allowed)
stringdist("ca", "abc", method="dl")

# string distance matching is case sensitive:
stringdist("ABC", "abc")
```

```

# so you may want to normalize a bit:
stringdist(tolower("ABC"),"abc")

# stringdist recycles the shortest argument:
stringdist(c('a','b','c'),c('a','c'))

# stringdistmatrix gives the distance matrix (by default for optimal string alignment):
stringdist(c('a','b','c'),c('a','c'))

# different edit operations may be weighted; e.g. weighted substitution:
stringdist('ab','ba',weight=c(1,1,1,0.5))

# Non-unit weights for insertion and deletion makes the distance metric asymmetric
stringdist('ca','abc')
stringdist('abc','ca')
stringdist('ca','abc',weight=c(0.5,1,1,1))
stringdist('abc','ca',weight=c(0.5,1,1,1))

# Hamming distance is undefined for
# strings of unequal lengths so stringdist returns Inf
stringdist("ab","abc",method="h")
# For strings of equal length it counts the number of unequal characters as they occur
# in the strings from beginning to end
stringdist("hello","HeLl0",method="h")

# The lcs (longest common substring) distance returns the number of
# characters that are not part of the lcs.
#
# Here, the lcs is either 'a' or 'b' and one character cannot be paired:
stringdist('ab','ba',method="lcs")
# Here the lcs is 'surey' and 'v', 'g' and one 'r' of 'surgery' are not paired
stringdist('survey','surgery',method="lcs")

# q-grams are based on the difference between occurrences of q consecutive characters
# in string a and string b.
# Since each character abc occurs in 'abc' and 'cba', the q=1 distance equals 0:
stringdist('abc','cba',method='qgram',q=1)

# since the first string consists of 'ab','bc' and the second
# of 'cb' and 'ba', the q=2 distance equals 4 (they have no q=2 grams in common):
stringdist('abc','cba',method='qgram',q=2)

# Wikipedia has the following example of the Jaro-distance.
stringdist('MARTHA','MATHRA',method='jw')
# Note that stringdist gives a _distance_ where wikipedia gives the corresponding
# _similarity measure_. To get the wikipedia result:
1 - stringdist('MARTHA','MATHRA',method='jw')

# The corresponding Jaro-Winkler distance can be computed by setting p=0.1
stringdist('MARTHA','MATHRA',method='jw',p=0.1)
# or, as a similarity measure
1 - stringdist('MARTHA','MATHRA',method='jw',p=0.1)

```

```
# This gives distance 1 since Euler and Gauss translate to different soundex codes.
stringdist('Euler', 'Gauss', method='soundex')
# Euler and Ellery translate to the same code and have distance 0
stringdist('Euler', 'Ellery', method='soundex')
```

---

stringdist-encoding     *String metrics in stringdist*

---

## Description

This page gives an overview of encoding handling in **stringst**.

## Encoding in stringdist

All character strings are stored as a sequence of bytes. An encoding system relates a byte, or a short sequence of bytes to a symbol. Over the years, many encoding systems have been developed, and not all OS's and softwares use the same encoding as default. Similarly, depending on the system R is running on, R may use a different encoding for storing strings internally.

The **stringdist** package is designed so users in principle need not worry about this. Strings are converted to UTF-32 (unsigned integer) by default prior to any further computation. This means that results are encoding-independent and that strings are interpreted as a sequence of symbols, not as a sequence of pure bytes. In functions where this is relevant, this may be switched by setting the `useBytes` option to `TRUE`. However, keep in mind that results will then likely depend on the system R is running on, except when your strings are pure ASCII. Also, for multi-byte encodings, results for byte-wise computations will usually differ from results using encoded computations.

Prior to **stringdist** version 0.9, setting `useBytes=TRUE` could give a significant performance enhancement. Since version 0.9, translation to integer is done by C code internal to **stringdist** and the difference in performance is now negligible.

## Unicode normalisation

In utf-8, the same (accented) character may be represented as several byte sequences. For example, an u-umlaut can be represented with a single byte code or as a byte code representing 'u' followed by a modifier byte code that adds the umlaut. The **stringi** package of Gagolevski and Tartanus offers unicode normalisation tools.

## Some tips on character encoding and transliteration

Some algorithms (like `soundex`) are defined only on the printable ASCII character set. This excludes any character with accents for example. Translating accented characters to the non-accented ones is a form of transliteration. On many systems running R (but not all!) you can achieve this with

`iconv(x, to="ASCII//TRANSLIT"),`

where `x` is your character vector. See the documentation of `iconv` for details.

The `stringi` package (Gagolewski and Tartanus) should work on any system. The command `stringi::stri_trans_general(x, "Latin-ASCII")` transliterates character vector `x` to ASCII.

## References

- The help page of [Encoding](#) describes how R handles encoding.
- The help page of `iconv` has a good overview of base R's encoding conversion options. The capabilities of `iconv` depend on the system R is running on. The `stringi` package offers platform-independent encoding and normalization tools.

## See Also

- Functions using re-encoding: `stringdist`, `stringdistmatrix`, `amatch`, `ain`, `qgrams`
- Encoding related: `printable_ascii`

---

stringdist-metrics      *String metrics in **stringdist***

---

## Description

This page gives an overview of the string dissimilarity measures offered by `stringdist`.

## String Metrics

String metrics are ways of quantifying the dissimilarity between two finite sequences, usually text strings. Over the years, many such measures have been developed. Some are based on a mathematical understanding of the set of all strings that can be composed from a finite alphabet, others are based on more heuristic principles, such as how a text string sounds when pronounced by a native English speaker.

The terms 'string metrics' and 'string distance' are used more or less interchangeably in literature. From a mathematical point of view, string metrics often do not obey the demands that are usually required from a distance function. For example, it is not true for all string metrics that a distance of 0 means that two strings are the same (e.g. in the  $q$ -gram distance). Nevertheless, string metrics are very useful in practice and have many applications.

The metric you need to choose for an application strongly depends on both the nature of the string (what does the string represent?) and the cause of dissimilarities between the strings you are measuring. For example, if you are comparing human-typed names that may contain typo's, the Jaro-Winkler distance may be of use. If you are comparing names that were written down after hearing them, a phonetic distance may be a better choice.

Currently, the following distance metrics are supported by `stringdist`.

Method name	Description
<code>osa</code>	Optimal string alignment, (restricted Damerau-Levenshtein distance).

lv	Levenshtein distance (as in R's native <code>adist</code> ).
dl	Full Damerau-Levenshtein distance.
hamming	Hamming distance (a and b must have same nr of characters).
lcs	Longest common substring distance.
qgram	$q$ -gram distance.
cosine	cosine distance between $q$ -gram profiles
jaccard	Jaccard distance between $q$ -gram profiles
jw	Jaro, or Jaro-Winkler distance.
soundex	Distance based on soundex encoding (see below)

### A short description of string metrics supported by stringdist

See [Van der Loo \(2014\)](#) for an extensive description and references. The review papers of Navarro (2001) and Boytsov (2011) provide excellent technical overviews of respectively online and offline string matching algorithms.

The **Hamming distance** (`method='hamming'`) counts the number of character substitutions that turns b into a. If a and b have different number of characters the distance is Inf.

The **Levenshtein distance** (`method='lv'`) counts the number of deletions, insertions and substitutions necessary to turn b into a. This method is equivalent to R's native `adist` function.

The **Optimal String Alignment distance** (`method='osa'`) is like the Levenshtein distance but also allows transposition of adjacent characters. Here, each substring may be edited only once. (For example, a character cannot be transposed twice to move it forward in the string).

The **full Damerau-Levenshtein distance** (`method='dl'`) is like the optimal string alignment distance except that it allows for multiple edits on substrings.

The **longest common substring** (`method='lcs'`) is defined as the longest string that can be obtained by pairing characters from a and b while keeping the order of characters intact. The **lcs-distance** is defined as the number of unpaired characters. The distance is equivalent to the edit distance allowing only deletions and insertions, each with weight one.

A  **$q$ -gram** (`method='qgram'`) is a subsequence of  $q$  consecutive characters of a string. If  $x$  ( $y$ ) is the vector of counts of  $q$ -gram occurrences in a (b), the  **$q$ -gram distance** is given by the sum over the absolute differences  $|x_i - y_i|$ . The computation is aborted when  $q$  is larger than the length of any of the strings. In that case Inf is returned.

The **cosine distance** (`method='cosine'`) is computed as  $1 - x \cdot y / (\|x\| \|y\|)$ , where  $x$  and  $y$  were defined above.

Let  $X$  be the set of unique  $q$ -grams in a and  $Y$  the set of unique  $q$ -grams in b. The **Jaccard distance** (`method='jaccard'`) is given by  $1 - |X \cap Y| / |X \cup Y|$ .

The **Jaro distance** (`method='jw'`,  $p=0$ ), is a number between 0 (exact match) and 1 (completely dissimilar) measuring dissimilarity between strings. It is defined to be 0 when both strings have length 0, and 1 when there are no character matches between a and b. Otherwise, the Jaro distance is defined as  $1 - (1/3)(w_1 m / |a| + w_2 m / |b| + w_3 (m - t) / m)$ . Here,  $|a|$  indicates the number of characters in a,  $m$  is the number of character matches and  $t$  the number of transpositions of matching characters. The  $w_i$  are weights associated with the characters in a, characters in b and with transpositions. A character  $c$  of a matches a character from b when  $c$  occurs in b, and the index of  $c$  in a differs less than  $\max(|a|, |b|) / 2 - 1$  (where we use integer division) from the index of  $c$  in b. Two matching characters are transposed when they are matched but they occur in different order in string a and b.

The **Jaro-Winkler distance** (method=`jw`,  $0 < p \leq 0.25$ ) adds a correction term to the Jaro-distance. It is defined as  $d - l \cdot p \cdot d$ , where  $d$  is the Jaro-distance. Here,  $l$  is obtained by counting, from the start of the input strings, after how many characters the first character mismatch between the two strings occurs, with a maximum of four. The factor  $p$  is a 'prefix' factor, which in the work of Winkler is often chosen 0.1.

For the **soundex** distance (method=`'soundex'`), strings are translated to a soundex code (see [phonetic](#) for a specification). The distance between strings is 0 when they have the same soundex code, otherwise 1. Note that soundex recoding is only meaningful for characters in the ranges a-z and A-Z. A warning is emitted when non-printable or non-ascii characters are encountered. Also see [printable\\_ascii](#).

The **running\_cosine** distance is an implementation of the cosine distance especially meant for fuzzy text search as in [afind](#). In fuzzy search a window of  $n$  characters slides across a (long) string while for each position of the window the distance between the part of the string in the window and a search pattern is computed. The (position of) the window with the shortest distance to the search pattern is returned. Sliding the window with a single position only affects the  $q$ -grams at the beginning and end of the window, and the 'running cosine' distance uses this and a few other tricks to save calculations.

## References

- MPJ van der Loo (2014) *The stringdist package for approximate string matching*. The R Journal **6**(1) 111-122.
- L. Boytsov (2011). *Indexing methods for approximate dictionary searching: comparative analyses*. ACM Journal of experimental algorithmics **16** 1-88.
- G. Navarro (2001). *A guided tour to approximate string matching*. ACM Computing Surveys **33** 31-88.

## See Also

- Functions applying string metrics to text: [stringdist](#), [stringdistmatrix](#), [amatch](#)
- Functions applying string metrics to integer sequences: [seq\\_dist](#), [seq\\_distmatrix](#), [seq\\_amatch](#)
- Encoding issues: [stringdist-encoding](#)

---

stringdist-parallelization

*Multithreading and parallelization in **stringdist***

---

## Description

This page describes how **stringdist** uses parallel processing.



### Multithreading and parallelization in stringdist

The core functions of **stringdist** are implemented in C. On systems where openMP is available, **stringdist** will automatically take advantage of multiple cores. The [section on OpenMP](#) of the [Writing R Extensions](#) manual discusses on what systems OpenMP is available (at the time of writing more or less anywhere except on OSX).

By default, the number of threads to use is taken from `options('sd_num_thread')`. When the package is loaded, the value for this option is determined as follows:

- If the environment variable `OMP_NUM_THREADS` is set, this value is taken.
- Otherwise, the number of available cores is determined with `parallel::detectCores()`. If this fails, the number of threads is set to 1 (with a message). If the nr of detected cores exceeds three, the number of used cores is set to  $n - 1$ .
- If available, the environment variable `OMP_THREAD_LIMIT` is determined and The number of threads is set to the lesser of `OMP_THREAD_LIMIT` and the number of detected cores.

The latter step makes sure that on machines with  $n > 3$  cores,  $n - 1$  cores are used. Some benchmarking showed that using all cores is often slower in such cases. This is probably because at least one of the threads will be shared with the operating system.

Functions that use multithreading have an option named `nthread` that controls the maximum number of threads to use. If you need to do large calculations, it is probably a good idea to benchmark the performance on your machine(s) as a function of '`nthread`', for example using the [microbenchmark](#) package of Mersmann.

### See Also

- Functions running multithreaded: [stringdist](#), [stringdistmatrix](#), [amatch](#), [ain](#)

---

stringdist\_api

*Calling stringdist from C or C++*

---

### Description

As of version 0.9.5.0 several C level functions can be linked to and called from C code in other R packages.

A description of the API can be found in [stringdist\\_api.pdf](#).

---

`stringsim`*Compute similarity scores between strings*

---

### Description

`stringsim` computes pairwise string similarities between elements of character vectors `a` and `b`, where the vector with less elements is recycled. `stringsimmatrix` computes the string similarity matrix with rows according to `a` and columns according to `b`.

### Usage

```
stringsim(  
  a,  
  b,  
  method = c("osa", "lv", "dl", "hamming", "lcs", "qgram", "cosine", "jaccard", "jw",  
             "soundex"),  
  useBytes = FALSE,  
  q = 1,  
  ...  
)
```

```
stringsimmatrix(  
  a,  
  b,  
  method = c("osa", "lv", "dl", "hamming", "lcs", "qgram", "cosine", "jaccard", "jw",  
             "soundex"),  
  useBytes = FALSE,  
  q = 1,  
  ...  
)
```

### Arguments

<code>a</code>	R object (target); will be converted by <code>as.character</code> .
<code>b</code>	R object (source); will be converted by <code>as.character</code> .
<code>method</code>	Method for distance calculation. The default is "osa", see <a href="#">stringdist-metrics</a> .
<code>useBytes</code>	Perform byte-wise comparison, see <a href="#">stringdist-encoding</a> .
<code>q</code>	Size of the $q$ -gram; must be nonnegative. Only applies to <code>method='qgram'</code> , <code>'jaccard'</code> or <code>'cosine'</code> .
<code>...</code>	additional arguments are passed on to <a href="#">stringdist</a> and <a href="#">stringdistmatrix</a> respectively.

## Details

The similarity is calculated by first calculating the distance using `stringdist`, dividing the distance by the maximum possible distance, and subtracting the result from 1. This results in a score between 0 and 1, with 1 corresponding to complete similarity and 0 to complete dissimilarity. Note that complete similarity only means equality for distances satisfying the identity property. This is not the case e.g. for q-gram based distances (for example if q=1, anagrams are completely similar). For distances where weights can be specified, the maximum distance is currently computed by assuming that all weights are equal to 1.

## Value

`stringsim` returns a vector with similarities, which are values between 0 and 1 where 1 corresponds to perfect similarity (distance 0) and 0 to complete dissimilarity. NA is returned when `stringdist` returns NA. Distances equal to Inf are truncated to a similarity of 0. `stringsimmatrix` works the same way but, equivalent to `stringdistmatrix`, returns a similarity matrix instead of a vector.

## Examples

```
# Calculate the similarity using the default method of optimal string alignment
stringsim("ca", "abc")

# Calculate the similarity using the Jaro-Winkler method
# The p argument is passed on to stringdist
stringsim('MARTHA','MATHRA',method='jw', p=0.1)
```

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