

Package ‘bioseq’

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Type Package

Title A Toolbox for Manipulating Biological Sequences

Version 0.1.5

Description

Classes and functions to work with biological sequences (DNA, RNA and amino acid sequences). Implements S3 infrastructure to work with biological sequences as described in Keck (2020) <[doi:10.1111/2041-210X.13490](https://doi.org/10.1111/2041-210X.13490)>. Provides a collection of functions to perform biological conversion among classes (transcription, translation) and basic operations on sequences (detection, selection and replacement based on positions or patterns). The package also provides functions to import and export sequences from and to other package formats.

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URL <https://fkeck.github.io/bioseq/>

BugReports <https://github.com/fkeck/bioseq/issues>

Encoding UTF-8

LazyData true

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VignetteBuilder knitr

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<i>aa</i>	<i>Build an amino acid (AA) vector</i>
-----------	--

Description

aa() build a AA vector from a character vector.

Usage

aa(...)

Arguments

... character to turn into AA. Can be a set of name-value pairs.

Value

vector of class bioseq_aa

See Also

Other classes: [dna\(\)](#), [rna\(\)](#)

Examples

```
aa("AGGTGC", "TTCGA")

aa(Seq_1 = "AGGTGC", Seq_2 = "TTCGA")

x <- c("AGGTGC", "TTCGA")
aa(x)
```

aliview	<i>AliView: DNA sequences viewer</i>
---------	--------------------------------------

Description

This function uses AliView (Larsson, 2014) to visualize DNA sequences. The software must be installed on the computer.

Usage

```
aliview(
  x,
  aliview_exec = getOption("bioseq.aliview.exec", default = "aliview")
)
```

Arguments

x a DNA, RNA or AA vector. Alternatively a DNABin or AABin object.
aliview_exec a character string giving the path of the program.

Details

By default, the function assumes that the executable is installed in a directory located on the PATH. Alternatively the user can provide an absolute path to the executable (i.e. the location where the software was installed/uncompressed). This information can be stored in the global options settings using `options(bioseq.aliview.exec = "my_path_to_aliview")`.

References

Larsson, A. (2014). AliView: a fast and lightweight alignment viewer and editor for large data sets. *Bioinformatics* 30(22): 3276-3278.

See Also

Other GUI wrappers: [seaview\(\)](#)

alphabets	<i>Biological alphabets</i>
-----------	-----------------------------

Description

List of the allowed characters for each type of sequences.

DNA

A C G T W S M K R Y B D H V N -

RNA

A C G U W S M K R Y B D H V N -

AA

A C D E F G H I K L M N P Q R S T V W Y B X Z J U O * -

References

Nomenclature Committee of the International Union of Biochemistry (NC-IUB) (1986). Proc. Natl. Acad. Sci. USA. 83 (1): 4–8.

Nomenclature and Symbolism for Amino Acids and Peptides. IUPAC-IUB Joint Commission on Biochemical Nomenclature. 1983.

as-tibble-ape	<i>Convert DNABin/AAbin to tibble</i>
---------------	---------------------------------------

Description

These methods convert sequences from **ape** formats DNABin and AAbin to tibbles.

Usage

```
as_tibble.DNABin(x, label = "label", sequence = "sequence", ...)
```

```
as_tibble.AABin(x, label = "label", sequence = "sequence", ...)
```

Arguments

x	a DNABin or AAbin object.
label	Name of the column that stores the sequence labels in the returned tibble.
sequence	Name of the column that stores the sequences in the returned tibble.
...	Not used.

Value

A tibble with two columns (if name is not NULL, the default) or one column (otherwise).

See Also

Other conversions: [as-tibble-bioseq](#), [as_AAbin\(\)](#), [as_DNABin\(\)](#), [as_aa\(\)](#), [as_dna\(\)](#), [as_rna\(\)](#), [as_seqinr_alignment\(\)](#)

Examples

```
require(ape)
require(tibble)
x <- rDNABin(nrow = 10, ncol = 25)
as_tibble.DNABin(x)
```

as-tibble-bioseq	<i>Convert bioseq DNA, RNA and AA to tibble</i>
------------------	---

Description

Convert bioseq DNA, RNA and AA to tibble

Usage

```
as_tibble.bioseq_dna(x, label = "label", sequence = "sequence", ...)
as_tibble.bioseq_rna(x, label = "label", sequence = "sequence", ...)
as_tibble.bioseq_aa(x, label = "label", sequence = "sequence", ...)
```

Arguments

x	a DNA, RNA or AA vector.
label	Name of the column that stores the sequence labels in the returned tibble.
sequence	Name of the column that stores the sequences in the returned tibble.
...	Not used.

Value

A tibble with two columns (if name is not NULL, the default) or one column (otherwise).

See Also

Other conversions: [as-tibble-ape](#), [as_AABin\(\)](#), [as_DNABin\(\)](#), [as_aa\(\)](#), [as_dna\(\)](#), [as_rna\(\)](#), [as_seqinr_alignment\(\)](#)

Examples

```
require(tibble)
x <- dna(A = "ACGTTAGTGTAGCCGT", B = "CTCGAAATGA", C = NA)
as_tibble(x)
```

as_aa	<i>Coercion to an amino acid (AA) vector</i>
-------	--

Description

Coercion to an amino acid (AA) vector

Usage

```
as_aa(x)
```

Arguments

x An object to coerce.

Value

An amino acid vector of class `bioseq_aa`

See Also

Other conversions: [as-tibble-ape](#), [as-tibble-bioseq](#), [as_AAbin\(\)](#), [as_DNAbin\(\)](#), [as_dna\(\)](#), [as_rna\(\)](#), [as_seqinr_alignment\(\)](#)

as_AAbin	<i>Coerce to AAbin</i>
----------	------------------------

Description

Coerce to AAbin

Usage

```
as_AAbin(x, ...)
```

Arguments

x An object.
... Other parameters.

Value

An AAbin object.

See Also

Other conversions: [as-tibble-ape](#), [as-tibble-bioseq](#), [as_DNAbin\(\)](#), [as_aa\(\)](#), [as_dna\(\)](#), [as_rna\(\)](#), [as_seqinr_alignment\(\)](#)

as_AAbin.tbl_df	<i>Coerce tibble to AAbin</i>
-----------------	-------------------------------

Description

Coerce tibble to AAbin

Usage

```
## S3 method for class 'tbl_df'
as_AAbin(x, sequences, labels = NULL, ...)
```

Arguments

- x a tibble.
- sequences Name of the tibble column that stores the sequences.
- labels Name of the tibble column that stores the sequence labels.
- ... Other params.

Value

An AAbin object.

as_dna	<i>Coercion to DNA vector</i>
--------	-------------------------------

Description

Coercion to DNA vector

Usage

```
as_dna(x)
```

Arguments

- x An object to coerce.

Value

A DNA vector of class bioseq_dna

See Also

Other conversions: [as-tibble-ape](#), [as-tibble-bioseq](#), [as_AAbin\(\)](#), [as_DNAbin\(\)](#), [as_aa\(\)](#), [as_rna\(\)](#), [as_seqinr_alignment\(\)](#)

`as_DNABin`*Coerce to DNABin*

Description

Coerce to DNABin

Usage

```
as_DNABin(x, ...)
```

Arguments

<code>x</code>	An object.
<code>...</code>	Other parameters.

Value

A DNABin object.

See Also

Other conversions: [as-tibble-ape](#), [as-tibble-bioseq](#), [as_ABin\(\)](#), [as_aa\(\)](#), [as_dna\(\)](#), [as_rna\(\)](#), [as_seqinr_alignment\(\)](#)

`as_DNABin.tbl_df`*Coerce tibble to DNABin*

Description

Coerce tibble to DNABin

Usage

```
## S3 method for class 'tbl_df'  
as_DNABin(x, sequences, labels = NULL, ...)
```

Arguments

<code>x</code>	a tibble.
<code>sequences</code>	Name of the tibble column that stores the sequences.
<code>labels</code>	Name of the tibble column that stores the sequence labels.
<code>...</code>	Other params.

Value

A DNABin object.

as_rna	<i>Coercion to RNA vector</i>
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Description

Coercion to RNA vector

Usage

```
as_rna(x)
```

Arguments

x	An object to coerce.
---	----------------------

Value

A RNA vector of class `bioseq_rna`

See Also

Other conversions: [as-tibble-ape](#), [as-tibble-bioseq](#), [as_AAbin\(\)](#), [as_DNAbin\(\)](#), [as_aa\(\)](#), [as_dna\(\)](#), [as_seqinr_alignment\(\)](#)

as_seqinr_alignment	<i>Coerce to seqinr alignment</i>
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Description

Coerce to seqinr alignment

Usage

```
as_seqinr_alignment(x, ...)
```

Arguments

x	An object.
...	Other parameters.

Value

An alignment object.

See Also

Other conversions: [as-tibble-ape](#), [as-tibble-bioseq](#), [as_AAbin\(\)](#), [as_DNAbin\(\)](#), [as_aa\(\)](#), [as_dna\(\)](#), [as_rna\(\)](#)

dic_genetic_codes	<i>Genetic code tables</i>
-------------------	----------------------------

Description

The function returns a list of named vectors with Start, Stop and Full_name attributes.

Usage

```
dic_genetic_codes()
```

Value

A list of genetic code tables for DNA/RNA translation.

dna	<i>Build a DNA vector</i>
-----	---------------------------

Description

`dna()` build a DNA vector from a character vector.

Usage

```
dna(...)
```

Arguments

... characters to turn into DNA. Can be a set of name-value pairs.

Value

a vector of class `bioseq_dna`

See Also

Other classes: [aa\(\)](#), [rna\(\)](#)

Examples

```
dna("AGGTGC", "TTCGA")

dna(Seq_1 = "AGGTGC", Seq_2 = "TTCGA")

x <- c("AGGTGC", "TTCGA")
dna(x)
```

fragilaria	<i>DNA sequences (rbcL) for various Fragilaria</i>
------------	--

Description

An unparsed FASTA of DNA sequences (rbcL) for various strains of *Fragilaria* retrieved from NCBI.

Usage

```
fragilaria
```

Format

A long character vector (unparsed FASTA).

Source

GenBank <https://www.ncbi.nlm.nih.gov/genbank/> using the following search term: "(rbcL) AND *Fragilaria*"

See Also

[read_fasta](#) to parse these data.

genetic-codes	<i>Genetic code tables</i>
---------------	----------------------------

Description

List of all genetic code tables available in `bioseq`. The number in bold can be used to select a table in appropriate functions.

Available genetic codes

1. Standard
2. Vertebrate Mitochondrial
3. Yeast Mitochondrial
4. Mold Mitochondrial; Protozoan Mitochondrial; Coelenterate Mitochondrial; Mycoplasma; Spiroplasma
5. Invertebrate Mitochondrial
6. Ciliate Nuclear; Dasycladacean Nuclear; Hexamita Nuclear
9. Echinoderm Mitochondrial; Flatworm Mitochondrial
10. Euplotid Nuclear

- 11. Bacterial, Archaeal and Plant Plastid
- 12. Alternative Yeast Nuclear
- 13. Ascidian Mitochondrial
- 14. Alternative Flatworm Mitochondrial
- 15. Blepharisma Macronuclear
- 16. Chlorophycean Mitochondrial
- 21. Trematode Mitochondrial
- 22. Scenedesmus obliquus Mitochondrial
- 23. Thraustochytrium Mitochondrial
- 24. Pterobranchia Mitochondrial
- 25. Candidate Division SR1 and Gracilibacteria
- 26. Pachysolen tannophilus Nuclear
- 27. Karyorelict Nuclear
- 28. Condyllostoma Nuclear
- 29. Mesodinium Nuclear
- 30. Peritrich Nuclear
- 31. Blastocrithidia Nuclear
- 32. Balanophoraceae Plastid
- 33. Cephalodiscidae Mitochondrial

References

Andrzej (Anjay) Elzanowski and Jim Ostell at National Center for Biotechnology Information (NCBI), Bethesda, Maryland, U.S.A. <https://www.ncbi.nlm.nih.gov/Taxonomy/taxonomyhome.html/index.cgi?chapter=tgencodes>

is_aa

Test if the object is an amino acid vector

Description

This function returns TRUE for objects of class bioseq_aa

Usage

```
is_aa(x)
```

Arguments

x An object.

Value

Logical.

Examples

```
x <- c("AGGTGC", "TTCGA")
is_aa(x)
y <- aa(x)
is_aa(x)
```

is_dna

Test if the object is a DNA vector

Description

This function returns TRUE for objects of class bioseq_dna

Usage

```
is_dna(x)
```

Arguments

x An object.

Value

Logical.

Examples

```
x <- c("AGGTGC", "TTCGA")
is_dna(x)
y <- dna(x)
is_dna(y)
```

is_rna	<i>Test if the object is a RNA vector</i>
--------	---

Description

This function returns TRUE for objects of class bioseq_rna

Usage

```
is_rna(x)
```

Arguments

x	An object.
---	------------

Value

Logical.

Examples

```
x <- c("AGGTGC", "TTCGA")
is_rna(x)
y <- rna(x)
is_rna(x)
```

new_aa	<i>Amino acid (AA) vector constructor</i>
--------	---

Description

Amino acid (AA) vector constructor

Usage

```
new_aa(x = character())
```

Arguments

x	a character vector.
---	---------------------

new_dna	<i>DNA vector constructor</i>
---------	-------------------------------

Description

DNA vector constructor

Usage

```
new_dna(x = character())
```

Arguments

x	a character vector.
---	---------------------

new_rna	<i>RNA vector constructor</i>
---------	-------------------------------

Description

RNA vector constructor

Usage

```
new_rna(x = character())
```

Arguments

x	a character vector.
---	---------------------

read_fasta	<i>Read sequences in FASTA format</i>
------------	---------------------------------------

Description

Read sequences in FASTA format

Usage

```
read_fasta(file, type = "DNA")
```

Arguments

file	A path to a file, a connection or a character string.
type	Type of data. Can be "DNA" (the default), "RNA" or "AA".

Value

A DNA, RNA or AA vector (depending on type argument).

See Also

Other input/output operations: [write_fasta\(\)](#)

rev_complement	<i>Reverse and complement sequences</i>
----------------	---

Description

Reverse and complement sequences

Usage

```
seq_complement(x)
```

```
seq_reverse(x)
```

Arguments

x a DNA or RNA vector. Function seq_reverse also accepts AA vectors.

Value

A reverse or complement sequence (same class as the input).

See Also

Other biological operations: [seq_rev_translate\(\)](#), [seq_translate\(\)](#), [transcription](#)

Examples

```
x <- dna("ACTTTGGCTAAG")
seq_reverse(x)
seq_complement(x)
```

rna	<i>Build a RNA vector</i>
-----	---------------------------

Description

rna() build a RNA vector from a character vector.

Usage

```
rna(...)
```

Arguments

... characters to turn into RNA. Can be a set of name-value pairs.

Value

a vector of class bioseq_rna

See Also

Other classes: [aa\(\)](#), [dna\(\)](#)

Examples

```
rna("AGGUGC", "UUCGA")

rna(Seq_1 = "AGGUGC", Seq_2 = "UUCGA")

x <- c("AGGTGC", "TTCGA")
rna(x)
```

seaview	<i>SeaView: DNA sequences and phylogenetic tree viewer</i>
---------	--

Description

This function opens SeaView (Gouy, Guindon & Gascuel, 2010) to visualize biological sequences and phylogenetic trees. The software must be installed on the computer.

Usage

```
seaview(
  x,
  seaview_exec = getOption("bioseq.seaview.exec", default = "seaview")
)
```

Arguments

- `x` a DNA, RNA or AA vector. Alternatively a DNABin or AABin object or a phylogenetic tree (class phylo).
- `seaview_exec` a character string giving the path of the program.

Details

By default, the function assumes that the executable is installed in a directory located on the PATH. Alternatively the user can provide an absolute path to the executable (i.e. the location where the software was installed/uncompressed). This can be stored in the global options settings using `options(bioseq.seaview.exec = "my_path_to_seaview")`.

References

Gouy M., Guindon S. & Gascuel O. (2010) SeaView version 4 : a multiplatform graphical user interface for sequence alignment and phylogenetic tree building. *Molecular Biology and Evolution* 27(2):221-224.

See Also

Other GUI wrappers: [aliview\(\)](#)

seq-replace	<i>Replace matched patterns in sequences</i>
-------------	--

Description

Replace matched patterns in sequences

Usage

```
seq_replace_pattern(x, pattern, replacement)
```

Arguments

- `x` a DNA, RNA or AA vector.
- `pattern` a DNA, RNA or AA vectors (but same as `x`) or a character vector of regular expressions, or a list. See section Patterns.
- `replacement` a vector of replacements.

Value

A vector of same class as `x`.

Patterns

It is important to understand how patterns are treated in **bioseq**.

Patterns are recycled along the sequences (usually the `x` argument). This means that if a pattern (vector or list) is of length > 1 , it will be replicated until it is the same length as `x`. The reverse is not true and a vector of patterns longer than a vector of sequences will raise a warning.

Patterns can be DNA, RNA or AA vectors (but they must be from the same class as the sequences they are matched against). If patterns are DNA, RNA or AA vectors, they are disambiguated prior to matching. For example `pattern_dna("ARG")` will match AAG or AGG.

Alternatively, patterns can be a simple character vector containing regular expressions.

Vectors of patterns (DNA, RNA, AA or regex) can also be provided in a list. In that case, each vector of the list will be collapsed prior matching, which means that each vector element will be used as an alternative pattern. For example `pattern_list(c("AAA", "CCC"), "GG")` will match AAA or CCC in the first sequence, GG in the second sequence, AAA or CCC in the third, and so on following the recycling rule.

@section Fuzzy matching: When `max_error` is greater than zero, the function perform fuzzy matching. Fuzzy matching does not support regular expression.

See Also

`stri_replace` from **stringi** and `str_replace` from **stringr** for the underlying implementation.

Other string operations: `seq_combine()`, `seq_count_pattern()`, `seq_crop_pattern()`, `seq_crop_position()`, `seq_detect_pattern()`, `seq_extract_pattern()`, `seq_extract_position()`, `seq_remove_pattern()`, `seq_remove_position()`, `seq_replace_position()`, `seq_split_kmer()`, `seq_split_pattern()`

Examples

```
x <- dna("ACGTTAGTGTAGCCGT", "CTCGAAATGA")
seq_replace_pattern(x, dna("AAA"), dna("GGGGGG"))
seq_replace_pattern(x, "^A.{2}T", "TTTTTT")
```

seq_cluster

Cluster sequences by similarity

Description

Cluster sequences by similarity

Usage

```
seq_cluster(x, threshold = 0.05, method = "complete")
```

Arguments

<code>x</code>	a DNA, RNA or AA vector of sequences to clustered.
<code>threshold</code>	Threshold value (range in $[0, 1]$).
<code>method</code>	the clustering method (see details).

Details

The function uses **ape** [dist.dna](#) and [dist.aa](#) functions to compute pairwise distances among sequences and [hclust](#) for clustering.

Computing a full pairwise distance matrix can be computationally expensive. It is recommended to use this function for moderate size dataset.

Supported methods are:

- "single" (= Nearest Neighbour Clustering)
- "complete" (= Farthest Neighbour Clustering)
- "average" (= UPGMA)
- "mcquitty" (= WPGMA)

Value

An integer vector with group memberships.

See Also

Function [seq_consensus](#) to compute consensus and representative sequences for clusters.

Other aggregation operations: [seq_consensus\(\)](#)

Examples

```
x <- c("-----TACGCAGTAAAAGCTACTGATG",
      "CGTCATACGCAGTAAAACTACTGATG",
      "CTTCATACGCAGTAAAACTACTGATG",
      "CTTCATATGCAGTAAAACTACTGATG",
      "CTTCATACGCAGTAAAACTACTGATG",
      "CGTCATACGCAGTAAAAGCTACTGATG",
      "CTTCATATGCAGTAAAAGCTACTGACG")
x <- dna(x)
seq_cluster(x)
```

seq_combine

Combine multiple sequences

Description

Combine multiple sequences

Usage

```
seq_combine(..., sep = "", collapse = NULL)
```

Arguments

...	One or more vectors of sequences (DNA, RNA, AA). They must all be of the same type. Short vectors are recycled.
sep	String to insert between input vectors.
collapse	If not NULL, combine everything with this string as separator.

Details

The strings `sep` and `collapse` will be coerced to the type of input vectors with a warning if some character have to be replaced.

Value

A vector of sequences (if `collapse` is NULL). A vector with a single sequence, otherwise.

See Also

[stri_join](#) from **stringi** and [str_c](#) from **stringr** for the underlying implementation.

Other string operations: [seq_replace](#), [seq_count_pattern\(\)](#), [seq_crop_pattern\(\)](#), [seq_crop_position\(\)](#), [seq_detect_pattern\(\)](#), [seq_extract_pattern\(\)](#), [seq_extract_position\(\)](#), [seq_remove_pattern\(\)](#), [seq_remove_position\(\)](#), [seq_replace_position\(\)](#), [seq_split_kmer\(\)](#), [seq_split_pattern\(\)](#)

Examples

```
x <- dna("ACGTTAGTGTAGCCGT", "CTCGAAATGA")
y <- dna("TTTTTTTTT", "AAAAAAAAA")
seq_combine(x, y)
seq_combine(y, x, sep = "CCCCC")
seq_combine(y, x, sep = "CCCCC", collapse = "GGGGG")
```

seq_consensus

Find a consensus sequence for a set of sequences.

Description

Find a consensus sequence for a set of sequences.

Usage

```
seq_consensus(x, method = "chr_majority", weights = NULL, gaps = TRUE)
```

Arguments

x	a DNA, RNA or AA vector.
method	the consensus method (see Details).
weights	an optional numeric vector of same length as x giving a weight for each input sequence.
gaps	logical. Should the gaps ("-") taken into account.

Details

"chr_majority", "chr_ambiguity", "seq_centrality", "seq_majority"

For chr_ambiguity gap character always override other characters. Use gaps = FALSE to ignore gaps.

Value

A consensus sequence

See Also

Other aggregation operations: [seq_cluster\(\)](#)

Examples

```
x <- c("-----TACGCAGTAAAAGCTACTGATG",
      "CGTCATACGCAGTAAAAACTACTGATG",
      "CTTCATACGCAGTAAAAACTACTGATG",
      "CTTCATATGCAGTAAAAACTACTGATG",
      "CTTCATACGCAGTAAAAACTACTGATG",
      "CGTCATACGCAGTAAAAGCTACTGATG",
      "CTTCATATGCAGTAAAAGCTACTGACG")
x <- dna(x)
seq_consensus(x)
```

seq_count_pattern	<i>Count the number of matches in sequences</i>
-------------------	---

Description

Count the number of matches in sequences

Usage

```
seq_count_pattern(x, pattern)
```

Arguments

<code>x</code>	a DNA, RNA or AA vector.
<code>pattern</code>	a DNA, RNA or AA vectors (but same as <code>x</code>) or a character vector of regular expressions, or a list. See section Patterns.

Value

An integer vector.

Patterns

It is important to understand how patterns are treated in **bioseq**.

Patterns are recycled along the sequences (usually the `x` argument). This means that if a pattern (vector or list) is of length > 1 , it will be replicated until it is the same length as `x`. The reverse is not true and a vector of patterns longer than a vector of sequences will raise a warning.

Patterns can be DNA, RNA or AA vectors (but they must be from the same class as the sequences they are matched against). If patterns are DNA, RNA or AA vectors, they are disambiguated prior to matching. For example `pattern dna("ARG")` will match AAG or AGG.

Alternatively, patterns can be a simple character vector containing regular expressions.

Vectors of patterns (DNA, RNA, AA or regex) can also be provided in a list. In that case, each vector of the list will be collapsed prior matching, which means that each vector element will be used as an alternative pattern. For example `pattern list(c("AAA", "CCC"), "GG")` will match AAA or CCC in the first sequence, GG in the second sequence, AAA or CCC in the third, and so on following the recycling rule.

@section Fuzzy matching: When `max_error` is greater than zero, the function perform fuzzy matching. Fuzzy matching does not support regular expression.

See Also

[stri_count](#) from **stringi** and [str_count](#) from **stringr** for the underlying implementation.

Other string operations: [seq_replace](#), [seq_combine\(\)](#), [seq_crop_pattern\(\)](#), [seq_crop_position\(\)](#), [seq_detect_pattern\(\)](#), [seq_extract_pattern\(\)](#), [seq_extract_position\(\)](#), [seq_remove_pattern\(\)](#), [seq_remove_position\(\)](#), [seq_replace_position\(\)](#), [seq_split_kmer\(\)](#), [seq_split_pattern\(\)](#)

Examples

```
x <- dna("ACGTTAGTGTAGCCGT", "CTCGAAATGA")
seq_count_pattern(x, dna("AAA"))
seq_count_pattern(x, "T.G")
```

seq_crop_pattern	<i>Crop sequences using delimiting patterns</i>
------------------	---

Description

Crop sequences using delimiting patterns

Usage

```
seq_crop_pattern(
  x,
  pattern_in,
  pattern_out,
  max_error_in = 0,
  max_error_out = 0,
  include_patterns = TRUE
)
```

Arguments

x	a DNA, RNA or AA vector to be cropped.
pattern_in	patterns defining the beginning (left-side).
pattern_out	patterns defining the end (right-side).
max_error_in, max_error_out	numeric values ranging from 0 to 1 and giving the maximum error rate allowed between the target sequence and pattern_in/pattern_out. Error rate is relative to the length of the pattern.
include_patterns	logical. Should the matched pattern sequence included in the returned sequences?

Value

A cropped DNA, RNA or AA vector. Sequences where patterns are not detected returns NA.

Fuzzy matching

When max_error_in or max_error_out are greater than zero, the function perform fuzzy matching. Fuzzy matching does not support regular expression.

Patterns

It is important to understand how patterns are treated in **bioseq**.

Patterns are recycled along the sequences (usually the x argument). This means that if a pattern (vector or list) is of length > 1, it will be replicated until it is the same length as x. The reverse is not true and a vector of patterns longer than a vector of sequences will raise a warning.

Patterns can be DNA, RNA or AA vectors (but they must be from the same class as the sequences they are matched against). If patterns are DNA, RNA or AA vectors, they are disambiguated prior to matching. For example `pattern dna("ARG")` will match AAG or AGG.

Alternatively, patterns can be a simple character vector containing regular expressions.

Vectors of patterns (DNA, RNA, AA or regex) can also be provided in a list. In that case, each vector of the list will be collapsed prior matching, which means that each vector element will be used as an alternative pattern. For example `pattern list(c("AAA", "CCC"), "GG")` will match AAA or CCC in the first sequence, GG in the second sequence, AAA or CCC in the third, and so on following the recycling rule.

@section Fuzzy matching: When `max_error` is greater than zero, the function perform fuzzy matching. Fuzzy matching does not support regular expression.

See Also

`stri_extract` from **stringi**, `str_extract` from **stringr** and `afind` from **stringdist** for the underlying implementation.

Other string operations: `seq_replace`, `seq_combine()`, `seq_count_pattern()`, `seq_crop_position()`, `seq_detect_pattern()`, `seq_extract_pattern()`, `seq_extract_position()`, `seq_remove_pattern()`, `seq_remove_position()`, `seq_replace_position()`, `seq_split_kmer()`, `seq_split_pattern()`

Examples

```
x <- dna("ACGTAAAAAGTGTAGCCCCCGT", "CTCGAAATGA")
seq_crop_pattern(x, pattern_in = "AAAA", pattern_out = "CCCC")
```

seq_crop_position	<i>Crop sequences between two positions</i>
-------------------	---

Description

Crop sequences between two positions

Usage

```
seq_crop_position(x, position_in = 1, position_out = -1)
```

Arguments

<code>x</code>	a DNA, RNA or AA vector.
<code>position_in</code>	an integer giving the position where to start cropping.
<code>position_out</code>	an integer giving the position where to stop cropping.

Value

A cropped DNA, RNA or AA vector.

See Also

[stri_sub](#) from **stringi** and [str_sub](#) from **stringr** for the underlying implementation.

Other string operations: [seq_replace](#), [seq_combine\(\)](#), [seq_count_pattern\(\)](#), [seq_crop_pattern\(\)](#), [seq_detect_pattern\(\)](#), [seq_extract_pattern\(\)](#), [seq_extract_position\(\)](#), [seq_remove_pattern\(\)](#), [seq_remove_position\(\)](#), [seq_replace_position\(\)](#), [seq_split_kmer\(\)](#), [seq_split_pattern\(\)](#)

Examples

```
x <- dna("ACGTTAGTGTAGCCGT")

# Drop the first 3 nucleotides (ACG)
seq_crop_position(x, position_in = 4)

# Crop codon between position 4 and 6
seq_crop_position(x, position_in = 4, position_out = 6)
```

seq_detect_pattern	<i>Detect the presence of patterns in sequences</i>
--------------------	---

Description

Detect the presence of patterns in sequences

Usage

```
seq_detect_pattern(x, pattern, max_error = 0)
```

Arguments

x	a DNA, RNA or AA vector.
pattern	a DNA, RNA or AA vectors (but same as x) or a character vector of regular expressions, or a list. See section Patterns.
max_error	numeric value ranging from 0 to 1 and giving the maximum error rate allowed between the target sequence and the pattern. Error rate is relative to the length of the pattern.

Value

A logical vector.

Patterns

It is important to understand how patterns are treated in **bioseq**.

Patterns are recycled along the sequences (usually the `x` argument). This means that if a pattern (vector or list) is of length > 1 , it will be replicated until it is the same length as `x`. The reverse is not true and a vector of patterns longer than a vector of sequences will raise a warning.

Patterns can be DNA, RNA or AA vectors (but they must be from the same class as the sequences they are matched against). If patterns are DNA, RNA or AA vectors, they are disambiguated prior to matching. For example `pattern_dna("ARG")` will match AAG or AGG.

Alternatively, patterns can be a simple character vector containing regular expressions.

Vectors of patterns (DNA, RNA, AA or regex) can also be provided in a list. In that case, each vector of the list will be collapsed prior matching, which means that each vector element will be used as an alternative pattern. For example `pattern_list(c("AAA", "CCC"), "GG")` will match AAA or CCC in the first sequence, GG in the second sequence, AAA or CCC in the third, and so on following the recycling rule.

@section Fuzzy matching: When `max_error` is greater than zero, the function perform fuzzy matching. Fuzzy matching does not support regular expression.

See Also

[stri_detect](#) from **stringi**, [str_detect](#) from **stringr** and [afind](#) from **stringdist** for the underlying implementation.

Other string operations: [seq_replace](#), [seq_combine\(\)](#), [seq_count_pattern\(\)](#), [seq_crop_pattern\(\)](#), [seq_crop_position\(\)](#), [seq_extract_pattern\(\)](#), [seq_extract_position\(\)](#), [seq_remove_pattern\(\)](#), [seq_remove_position\(\)](#), [seq_replace_position\(\)](#), [seq_split_kmer\(\)](#), [seq_split_pattern\(\)](#)

Examples

```
x <- dna(c("ACGTTAGTGTAGCCGT", "CTCGAAATGA"))
seq_detect_pattern(x, dna(c("CCG", "AAA")))

# Regular expression
seq_detect_pattern(x, "^A.{2}T")

# Fuzzy matching
seq_detect_pattern(x, dna("AGG"), max_error = 0.2)
# No match. The pattern has three character, the max_error
# has to be > 1/3 to allow one character difference.

seq_detect_pattern(x, dna("AGG"), max_error = 0.4)
# Match
```

`seq_disambiguate_IUPAC`*Disambiguate biological sequences*

Description

This function finds all the combinations of sequences corresponding to a given vector of sequences with ambiguities (IUPAC codes).

Usage

```
seq_disambiguate_IUPAC(x)
```

Arguments

`x` a DNA, RNA or AA vector

Value

A list of DNA, RNA or AA vectors (depending on the input) giving all possible combinations.

See Also

Other op-misc: [seq_nchar\(\)](#), [seq_nseq\(\)](#), [seq_spellout\(\)](#), [seq_stat_gc\(\)](#), [seq_stat_prop\(\)](#)

Examples

```
x <- dna(c("AYCTGW", "CTTN"))
seq_disambiguate_IUPAC(x)

y <- seq_transcribe(x)
seq_disambiguate_IUPAC(y)

z <- aa("YJSNAALNX")
z <- seq_translate(y)
seq_disambiguate_IUPAC(z)
```

`seq_extract_pattern`*Extract matching patterns from sequences*

Description

Extract matching patterns from sequences

Usage

```
seq_extract_pattern(x, pattern)
```

Arguments

x	a DNA, RNA or AA vector.
pattern	a DNA, RNA or AA vectors (but same as x) or a character vector of regular expressions, or a list. See section Patterns.

Value

A list of vectors of same class as x.

Patterns

It is important to understand how patterns are treated in **bioseq**.

Patterns are recycled along the sequences (usually the x argument). This means that if a pattern (vector or list) is of length > 1, it will be replicated until it is the same length as x. The reverse is not true and a vector of patterns longer than a vector of sequences will raise a warning.

Patterns can be DNA, RNA or AA vectors (but they must be from the same class as the sequences they are matched against). If patterns are DNA, RNA or AA vectors, they are disambiguated prior to matching. For example pattern dna("ARG") will match AAG or AGG.

Alternatively, patterns can be a simple character vector containing regular expressions.

Vectors of patterns (DNA, RNA, AA or regex) can also be provided in a list. In that case, each vector of the list will be collapsed prior matching, which means that each vector element will be used as an alternative pattern. For example pattern list(c("AAA", "CCC"), "GG") will match AAA or CCC in the first sequence, GG in the second sequence, AAA or CCC in the third, and so on following the recycling rule.

@section Fuzzy matching: When max_error is greater than zero, the function perform fuzzy matching. Fuzzy matching does not support regular expression.

See Also

[stri_extract](#) from **stringi** and [str_extract](#) from **stringr** for the underlying implementation.

Other string operations: [seq_replace](#), [seq_combine\(\)](#), [seq_count_pattern\(\)](#), [seq_crop_pattern\(\)](#), [seq_crop_position\(\)](#), [seq_detect_pattern\(\)](#), [seq_extract_position\(\)](#), [seq_remove_pattern\(\)](#), [seq_remove_position\(\)](#), [seq_replace_position\(\)](#), [seq_split_kmer\(\)](#), [seq_split_pattern\(\)](#)

Examples

```
x <- dna("ACGTTAGTGTAGCCGT", "CTCGAAATGA")
seq_extract_pattern(x, dna("AAA"))
seq_extract_pattern(x, "T.G")
```

seq_extract_position	<i>Extract a region between two positions in sequences</i>
----------------------	--

Description

Extract a region between two positions in sequences

Usage

```
seq_extract_position(x, position_in, position_out)
```

Arguments

x	a DNA, RNA or AA vector.
position_in	an integer giving the position where to start to extract.
position_out	an integer giving the position where to stop to extract.

Value

A vector of same class as x.

See Also

[stri_extract](#) from **stringi** and [str_extract](#) from **stringr** for the underlying implementation.

Other string operations: [seq_replace](#), [seq_combine\(\)](#), [seq_count_pattern\(\)](#), [seq_crop_pattern\(\)](#), [seq_crop_position\(\)](#), [seq_detect_pattern\(\)](#), [seq_extract_pattern\(\)](#), [seq_remove_pattern\(\)](#), [seq_remove_position\(\)](#), [seq_replace_position\(\)](#), [seq_split_kmer\(\)](#), [seq_split_pattern\(\)](#)

Examples

```
x <- dna("ACGTTAGTG TAGCCGT", "CTCGAAATGA")
seq_extract_position(x, 3, 8)
```

seq_nchar	<i>Count the number of character in sequences</i>
-----------	---

Description

Count the number of character in sequences

Usage

```
seq_nchar(x, gaps = TRUE)
```

Arguments

`x` a DNA, RNA or AA vector.
`gaps` if FALSE gaps are ignored.

Value

An integer vector giving the size of each sequence of `x`.

See Also

Other op-misc: [seq_disambiguate_IUPAC\(\)](#), [seq_nseq\(\)](#), [seq_spellout\(\)](#), [seq_stat_gc\(\)](#), [seq_stat_prop\(\)](#)

Examples

```
x <- dna(c("ATGCAGA", "GGR-----", "TTCCTAGKTGAACC"))
seq_nchar(x)
seq_nchar(x, gaps = FALSE)
```

seq_nseq

Number of sequences in a vector

Description

This is an alias for `length`.

Usage

```
seq_nseq(x)
```

Arguments

`x` a DNA, RNA or AA vector.

Value

an integer.

See Also

Other op-misc: [seq_disambiguate_IUPAC\(\)](#), [seq_nchar\(\)](#), [seq_spellout\(\)](#), [seq_stat_gc\(\)](#), [seq_stat_prop\(\)](#)

seq_remove_pattern	<i>Remove matched patterns in sequences</i>
--------------------	---

Description

Remove matched patterns in sequences

Usage

```
seq_remove_pattern(x, pattern)
```

Arguments

x	a DNA, RNA or AA vector.
pattern	a DNA, RNA or AA vectors (but same as x) or a character vector of regular expressions, or a list. See section Patterns.

Value

A vector of same class as x.

Patterns

It is important to understand how patterns are treated in **bioseq**.

Patterns are recycled along the sequences (usually the x argument). This means that if a pattern (vector or list) is of length > 1, it will be replicated until it is the same length as x. The reverse is not true and a vector of patterns longer than a vector of sequences will raise a warning.

Patterns can be DNA, RNA or AA vectors (but they must be from the same class as the sequences they are matched against). If patterns are DNA, RNA or AA vectors, they are disambiguated prior to matching. For example pattern dna("ARG") will match AAG or AGG.

Alternatively, patterns can be a simple character vector containing regular expressions.

Vectors of patterns (DNA, RNA, AA or regex) can also be provided in a list. In that case, each vector of the list will be collapsed prior matching, which means that each vector element will be used as an alternative pattern. For example pattern list(c("AAA", "CCC"), "GG") will match AAA or CCC in the first sequence, GG in the second sequence, AAA or CCC in the third, and so on following the recycling rule.

@section Fuzzy matching: When max_error is greater than zero, the function perform fuzzy matching. Fuzzy matching does not support regular expression.

See Also

[str_remove](#) from **stringr** for the underlying implementation.

Other string operations: [seq_replace](#), [seq_combine\(\)](#), [seq_count_pattern\(\)](#), [seq_crop_pattern\(\)](#), [seq_crop_position\(\)](#), [seq_detect_pattern\(\)](#), [seq_extract_pattern\(\)](#), [seq_extract_position\(\)](#), [seq_remove_position\(\)](#), [seq_replace_position\(\)](#), [seq_split_kmer\(\)](#), [seq_split_pattern\(\)](#)

Examples

```
x <- dna("ACGTTAGTGTAGCCGT", "CTCGAAATGA")
seq_remove_pattern(x, dna("AAA"))
seq_remove_pattern(x, "^A.{2}T")
```

seq_remove_position *Remove a region between two positions in sequences.*

Description

Remove a region between two positions in sequences.

Usage

```
seq_remove_position(x, position_in, position_out)
```

Arguments

x a DNA, RNA or AA vector.

position_in an integer giving the position where to start to remove.

position_out an integer giving the position where to stop to remove.

Value

A vector of same class as x.

See Also

[str_remove](#) from **stringr** for the underlying implementation.

Other string operations: [seq_replace](#), [seq_combine\(\)](#), [seq_count_pattern\(\)](#), [seq_crop_pattern\(\)](#), [seq_crop_position\(\)](#), [seq_detect_pattern\(\)](#), [seq_extract_pattern\(\)](#), [seq_extract_position\(\)](#), [seq_remove_pattern\(\)](#), [seq_replace_position\(\)](#), [seq_split_kmer\(\)](#), [seq_split_pattern\(\)](#)

Examples

```
x <- dna("ACGTTAGTGTAGCCGT", "CTCGAAATGA")
seq_remove_position(x, 2, 6)
seq_remove_position(x, 1:2, 3:4)
```

seq_replace_position *Replace a region between two positions in sequences*

Description

Replace a region between two positions in sequences

Usage

```
seq_replace_position(x, position_in, position_out, replacement)
```

Arguments

x	a DNA, RNA or AA vector.
position_in	an integer giving the position where to start to replace.
position_out	an integer giving the position where to stop to replace.
replacement	a vector of replacements.

Value

A vector of same class as x.

See Also

[stri_replace](#) from **stringi** and [str_replace](#) from **stringr** for the underlying implementation.

Other string operations: [seq_replace](#), [seq_combine\(\)](#), [seq_count_pattern\(\)](#), [seq_crop_pattern\(\)](#), [seq_crop_position\(\)](#), [seq_detect_pattern\(\)](#), [seq_extract_pattern\(\)](#), [seq_extract_position\(\)](#), [seq_remove_pattern\(\)](#), [seq_remove_position\(\)](#), [seq_split_kmer\(\)](#), [seq_split_pattern\(\)](#)

Examples

```
x <- dna("ACGTTAGTG TAGCCGT", "CTCGAAATGA")
seq_replace_position(x, c(5, 2), 6, "-----")
```

seq_rev_translate *Reverse translate amino acid sequences*

Description

The function perform reverse translation of amino acid sequences. Such operation does not exist in nature but is provided for completeness. Because of codon degeneracy it is expected to produce many ambiguous nucleotides.

Usage

```
seq_rev_translate(x, code = 1)
```

Arguments

- x an amino acid sequence (bioseq_aa)
- code an integer indicating the genetic code to use for reverse translation (default 1 uses the Standard genetic code). See Details.

Details

Gaps (-) are interpreted as unknown amino acids (X) but can be removed prior to the translation with the function seq_remove_gap.

Value

a vector of DNA sequences.

See Also

Other biological operations: [rev_complement](#), [seq_translate\(\)](#), [transcription](#)

Examples

```
x <- dna("ACTTTGGCTAAG")
y <- seq_translate(x)
z <- seq_rev_translate(y)
z
# There is a loss of information during the reverse translation
all.equal(x, z)
```

seq_spellout	<i>Spell out sequences</i>
--------------	----------------------------

Description

This function spells out nucleotides and amino acids in sequences.

Usage

```
seq_spellout(x, short = FALSE, collapse = " - ")
```

Arguments

- x a DNA, RNA or AA vector
- short logical. If TRUE, the function will return 3-letters short names for amino acids (ignored for DNA and RNA).
- collapse a character vector to separate the results. Set to NULL to avoid collapsing the results.

Value

A character vector if collapse is not NULL. A list of character vectors otherwise.

See Also

Other op-misc: [seq_disambiguate_IUPAC\(\)](#), [seq_nchar\(\)](#), [seq_nseq\(\)](#), [seq_stat_gc\(\)](#), [seq_stat_prop\(\)](#)

Examples

```
x <- dna("ACGT")
seq_spellout(x)

x <- rna("ACGU")
seq_spellout(x)

x <- aa("ACGBTX")
seq_spellout(x)
```

seq_split_kmer

Split sequences into k-mers

Description

Split sequences into k-mers

Usage

```
seq_split_kmer(x, k)
```

Arguments

x	A DNA, RNA or AA vector.
k	an integer giving the size of the k-mer.

Value

a list of k-mer vectors of same class as x.

See Also

[seq_split_pattern](#).

Other string operations: [seq_replace](#), [seq_combine\(\)](#), [seq_count_pattern\(\)](#), [seq_crop_pattern\(\)](#), [seq_crop_position\(\)](#), [seq_detect_pattern\(\)](#), [seq_extract_pattern\(\)](#), [seq_extract_position\(\)](#), [seq_remove_pattern\(\)](#), [seq_remove_position\(\)](#), [seq_replace_position\(\)](#), [seq_split_pattern\(\)](#)

Examples

```
x <- dna(a = "ACGTTAGTGTAGCCGT", b = "CTCGAAATGA")
seq_split_kmer(x, k = 5)
```

seq_split_pattern	<i>Split sequences</i>
-------------------	------------------------

Description

Split sequences

Usage

```
seq_split_pattern(x, pattern)
```

Arguments

x	a DNA, RNA or AA vector.
pattern	a DNA, RNA or AA vectors (but same as x) or a character vector of regular expressions, or a list. See section Patterns.

Value

A list of vectors of same class as x.

Patterns

It is important to understand how patterns are treated in **bioseq**.

Patterns are recycled along the sequences (usually the x argument). This means that if a pattern (vector or list) is of length > 1, it will be replicated until it is the same length as x. The reverse is not true and a vector of patterns longer than a vector of sequences will raise a warning.

Patterns can be DNA, RNA or AA vectors (but they must be from the same class as the sequences they are matched against). If patterns are DNA, RNA or AA vectors, they are disambiguated prior to matching. For example pattern dna("ARG") will match AAG or AGG.

Alternatively, patterns can be a simple character vector containing regular expressions.

Vectors of patterns (DNA, RNA, AA or regex) can also be provided in a list. In that case, each vector of the list will be collapsed prior matching, which means that each vector element will be used as an alternative pattern. For example pattern list(c("AAA", "CCC"), "GG") will match AAA or CCC in the first sequence, GG in the second sequence, AAA or CCC in the third, and so on following the recycling rule.

@section Fuzzy matching: When max_error is greater than zero, the function perform fuzzy matching. Fuzzy matching does not support regular expression.

See Also

[stri_split](#) from **stringi** and [str_split](#) from **stringr** for the underlying implementation.

Other string operations: [seq_replace](#), [seq_combine\(\)](#), [seq_count_pattern\(\)](#), [seq_crop_pattern\(\)](#), [seq_crop_position\(\)](#), [seq_detect_pattern\(\)](#), [seq_extract_pattern\(\)](#), [seq_extract_position\(\)](#), [seq_remove_pattern\(\)](#), [seq_remove_position\(\)](#), [seq_replace_position\(\)](#), [seq_split_kmer\(\)](#)

Examples

```
x <- dna(a = "ACGTTAGTGTAGCCGT", b = "CTCGAAATGA")
seq_split_pattern(x, dna("AAA"))
seq_split_pattern(x, "T.G")
```

seq_stat_gc	<i>Compute G+C content</i>
-------------	----------------------------

Description

Compute G+C content

Usage

```
seq_stat_gc(x)
```

Arguments

x a DNA or RNA

Details

Ambiguous characters (other than S and W) are ignored.

Value

A numeric vector of G+C proportions.

See Also

Other op-misc: [seq_disambiguate_IUPAC\(\)](#), [seq_nchar\(\)](#), [seq_nseq\(\)](#), [seq_spellout\(\)](#), [seq_stat_prop\(\)](#)

Examples

```
x <- dna(c("ATGCAGA", "GGR-----", "TGCCTAGKTGAACC"))

seq_stat_gc(x)
```

seq_stat_prop	<i>Compute proportions for characters</i>
---------------	---

Description

Compute proportions for characters

Usage

```
seq_stat_prop(x, gaps = FALSE)
```

Arguments

x	a DNA, RNA or AA vector.
gaps	if FALSE gaps are ignored.

Value

A list of vectors indicating the proportion of characters in each sequence.

See Also

Other op-misc: [seq_disambiguate_IUPAC\(\)](#), [seq_nchar\(\)](#), [seq_nseq\(\)](#), [seq_spellout\(\)](#), [seq_stat_gc\(\)](#)

Examples

```
x <- dna(c("ATGCAGA", "GGR-----", "TTGCCTAGKTGAACC"))
seq_stat_prop(x)
seq_stat_prop(x, gaps = TRUE)
```

seq_translate	<i>Translate DNA/RNA sequences into amino acids</i>
---------------	---

Description

Translate DNA/RNA sequences into amino acids

Usage

```
seq_translate(x, code = 1, codon_frame = 1, codon_init = FALSE)
```

Arguments

x	a vector of DNA (bioseq_dna) or RNA (bioseq_rna).
code	an integer indicating the genetic code to use for translation (default 1 uses the Standard genetic code). See Details.
codon_frame	an integer giving the nucleotide position where to start translation.
codon_init	a logical indicating whether the first codon is evaluated as a possible codon start and translated to methionine.

Details

Several genetic codes can be used for translation. See [genetic-codes](#) to get the list of available genetic codes and their ID number.

Gaps (-) are interpreted as unknown nucleotides (N) but can be removed prior to the translation with the function `seq_remove_gap`.

The function deals with ambiguities on both sides. This means that if ambiguous codons cannot be translated to amino acid, they are translated to the most specific ambiguous amino acids (X in the most extreme case).

Value

An amino acid vector (bioseq_aa).

See Also

Other biological operations: [rev_complement](#), [seq_rev_translate\(\)](#), [transcription](#)

Examples

```
x <- dna(c("ATGCAGA", "GGR", "TTGCCTAGKTGAACC", "AGGNGC", "NNN"))
seq_translate(x)
```

transcription

Transcribe DNA, reverse-transcribe RNA

Description

Transcribe DNA, reverse-transcribe RNA

Usage

```
seq_transcribe(x)
```

```
seq_rev_transcribe(x)
```

Arguments

x A vector of DNA for seq_transcribe, a vector of RNA for seq_rev_transcribe

Value

A vector of RNA for seq_transcribe, a vector of DNA for seq_rev_transcribe

See Also

Other biological operations: [rev_complement](#), [seq_rev_translate\(\)](#), [seq_translate\(\)](#)

write_fasta	<i>Write sequences in FASTA format</i>
-------------	--

Description

Write sequences in FASTA format

Usage

```
write_fasta(x, file, append = FALSE, line_length = 80, block_length = 10)
```

Arguments

x a DNA, RNA or AA vector.
file a path to a file or a connection.
append a logical. If TRUE append the data to the file. If FALSE (default), overwrite the file.
line_length length (in number of character) of one line (excluding spaces separating blocks). Use Inf to avoid line breaks.
block_length length (in number of character) of one block. Use the same value as line_length or Inf to avoid block separation.

See Also

Other input/output operations: [read_fasta\(\)](#)

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