Package 'bioseq'

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Type Package

Title A Toolbox for Manipulating Biological Sequences

Version 0.1.1

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Description

Classes and functions to work with biological sequences (DNA, RNA and amino acid sequences).
Implements S3 infrastructure to work with biological sequences.
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.

License GPL-3

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

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

Encoding UTF-8

LazyData true

Depends R (>= 3.1.0)

Imports methods, vctrs, tibble, ape, crayon, dplyr, pillar, stringr, readr, rlang

Suggests knitr, rmarkdown, testthat (>= 2.1.0), covr

VignetteBuilder knitr

RoxygenNote 6.1.1

NeedsCompilation no

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Repository CRAN

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R topics documented:

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aa *Build an amino acid (AA) vector*

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 *AliView: DNA sequences viewer*

Description

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

Usage

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

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. Bioinformatics30(22): 3276-3278.

See Also

Other GUI wrappers: seaview

alphabets *Biological alphabets*

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.

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as-tibble-ape *Convert DNAbin/AAbin to tibble*

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` *Convert bioseq DNA, RNA and AA to tibble*

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 *Coercion to an amino acid (AA) vector*

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 *Coerce to AAbin*

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 *Coerce tibble to AAbin*

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 *Coercion to DNA vector*

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

x	An object.
...	Other parameters.

Value

A DNAbin object.

See Also

Other conversions: as-tibble-ape, as-tibble-bioseq, as_AAbin, 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

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

A DNAbin object.

as_rna *Coercion to RNA vector*

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 *Coerce to seqinr alignment*

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 *Genetic code tables*

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 *Build a DNA vector*

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 *DNA sequences (rbcL) for various Fragilaria*

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 *Genetic code tables*

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. Condylostoma 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

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`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 *Test if the object is a RNA vector*

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 *Amino acid (AA) vector constructor*

Description

Amino acid (AA) vector constructor

Usage

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

Arguments

x	a character vector.

new_dna *DNA vector constructor*

Description

DNA vector constructor

Usage

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

Arguments

x	a character vector.

new_rna *RNA vector constructor*

Description

RNA vector constructor

Usage

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

Arguments

x	a character vector.

read_fasta *Read sequences in FASTA format*

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` *Reverse and complement sequences*

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 *Build a RNA vector*

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 *SeaView: DNA sequences and phylogenetic tree viewer*

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 = options("bioseq.seaview.exec"))
```

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 *Replace matched patterns in sequences*

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.

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

`x`	a DNA, RNA or AA vector of sequences to clustered.
`threshold`	Threshold value (range in [0, 1]).
`method`	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 diastance 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",
       "CGTCATACGCAGTAAAAACTACTGATG",
       "CTTCATACGCAGTAAAAACTACTGATG",
       "CTTCATATGCAGTAAAAACTACTGATG",
       "CTTCATACGCAGTAAAAACTACTGATG",
       "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 collapsew ill be coerced to the type of input vectors with a warning if some character have to 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("TTTTTTTT", "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 *Count the number of matches in sequences*

Description

Count the number of matches in sequences

Usage

```
seq_count_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

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.

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` *Crop sequences using delimiting patterns*

Description

Crop sequences using delimiting patterns

Usage

```
seq_crop_pattern(x, pattern_in, pattern_out)
```

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).

Value

A cropped DNA, RNA or AA 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.

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_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("ACGTTAAAAAGTGTAGCCCCCGT", "CTCGAAATGA")
seq_crop_pattern(x, pattern_in = "AAAA", pattern_out = "CCCC")
```

`seq_crop_position` *Crop sequences between two positions*

Description

Crop sequences between two positions

Usage

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

Arguments

`x`	a DNA, RNA or AA vector.
`position_in`	an integer giving the position where to start cropping.
`position_out`	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` *Detect the presence of patterns in sequences*

Description

Detect the presence of patterns in sequences

Usage

```
seq_detect_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 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.

See Also

`stri_detect` from **stringi** and `str_detect` from **stringr** 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")))
seq_detect_pattern(x, "^A.{2}T")
```

`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.

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` *Extract a region between two positions in sequences*

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("ACGTTAGTGTAGCCGT", "CTCGAAATGA")
seq_extract_position(x, 3, 8)
```

seq_nchar *Count the number of character in sequences*

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-----","TTGCCTAGKTGAACC"))
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` *Remove matched patterns in sequences*

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.

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("ACGTTAGTGTAGCCGT", "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` *Spell out sequences*

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 *Split sequences*

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.

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 *Compute G+C content*

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-----","TTGCCTAGKTGAACC"))

seq_stat_gc(x)
```

seq_stat_prop *Compute proportions for characters*

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 *Translate DNA/RNA sequences into amino acids*

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` *Write sequences in FASTA format*

Description

Write sequences in FASTA format

Usage

```
write_fasta(x, file, append = FALSE)
```

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.

See Also

Other input/output operations: `read_fasta`

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