

# Package ‘MSA2dist’

May 14, 2024

**Type** Package

**Title** MSA2dist calculates pairwise distances between all sequences of a DNStringSet or a AAStringSet using a custom score matrix and conducts codon based analysis

**Version** 1.9.0

**Description** MSA2dist calculates pairwise distances between all sequences of a DNStringSet or a AAStringSet using a custom score matrix and conducts codon based analysis. It uses scoring matrices to be used in these pairwise distance calculations which can be adapted to any scoring for DNA or AA characters. E.g. by using literal distances MSA2dist calculates pairwise IUPAC distances.

**License** GPL-3 + file LICENSE

**Encoding** UTF-8

**LazyData** false

**biocViews** Alignment, Sequencing, Genetics, GO

**Depends** R (>= 4.4.0)

**Imports** Rcpp, Biostrings, GenomicRanges, IRanges, ape, doParallel, dplyr, foreach, methods, parallel, pwalgn, rlang, seqinr, stats, stringi, stringr, tibble, tidyr, utils

**Suggests** rmarkdown, knitr, devtools, testthat, ggplot2, BiocStyle

**LinkingTo** Rcpp, RcppThread

**VignetteBuilder** knitr

**NeedsCompilation** yes

**SystemRequirements** C++11

**URL** <https://gitlab.gwdg.de/mpievolbio-it/MSA2dist>,  
<https://mpievolbio-it.pages.gwdg.de/MSA2dist/>

**BugReports** <https://gitlab.gwdg.de/mpievolbio-it/MSA2dist/issues>

**RoxygenNote** 7.3.1

**git\_url** <https://git.bioconductor.org/packages/MSA2dist>

**git\_branch** devel  
**git\_last\_commit** 98bd32e  
**git\_last\_commit\_date** 2024-04-30  
**Repository** Bioconductor 3.20  
**Date/Publication** 2024-05-13  
**Author** Kristian K Ullrich [aut, cre] (<<https://orcid.org/0000-0003-4308-9626>>)  
**Maintainer** Kristian K Ullrich <ullrich@evolbio.mpg.de>

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aa2selfscore	<i>aa2selfscore</i>
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---

**Description**

This function return the selfscore from an AAStrngSet.

**Usage**

```
aa2selfscore(aa, scorematrix = "BLOSUM62")
```

**Arguments**

aa	AAStrngSet [mandatory]
scorematrix	score matrix to use [default: BLOSUM62]

**Value**

data.frame

**Author(s)**

Kristian K Ullrich

**See Also**

[XStringSet-class](#), [substitution\\_matrices](#)

**Examples**

```
data(woodmouse, package="ape")
#cds2aa(dnabin2dnastring(woodmouse), shorten=TRUE,
#genetic.code=Biostrings::getGeneticCode("2"))
woodmouse |> dnabin2dnastring() |> cds2aa(shorten=TRUE,
genetic.code=Biostrings::getGeneticCode("2")) |> aa2selfscore()
```

---

aabin2aastring	<i>aabin2aastring</i>
----------------	-----------------------

---

**Description**

This function converts an ape AAbin into AAStrngSet.

**Usage**

```
aabin2aastring(aabin)
```

**Arguments**

aabin	ape AAbin [mandatory]
-------	-----------------------

**Value**

An object of class AAStrngSet

**Author(s)**

Kristian K Ullrich

**See Also**

[as.alignment as.DNAbin.alignment AAStrngSet](#)

**Examples**

```
data(woodmouse, package="ape")
## convert into AAStrngSet
#aabin2aastring(ape::trans(woodmouse, 2))
ape::trans(woodmouse, 2) |> aabin2aastring()
```

---

AAMatrix-data	<i>AAMatrix-data</i>
---------------	----------------------

---

**Description**

getAAMatrix() from the alakazam package.

**Usage**

```
data(AAMatrix)
```

**Format**

an object of class `matrix`

**Value**

score matrix

**References**

Gupta N, Vander Heiden J, Uduman M, Gadala-Maria D, Yaari G, Kleinstein S (2015) Change-O: a toolkit for analyzing large-scale B cell immunoglobulin repertoire sequencing data. *Bioinformatics*. **31**(20), 3356-3358.

**Examples**

```
data("AAMatrix", package="MSA2dist")
```

---

aastring2aabin	<i>aastring2aabin</i>
----------------	-----------------------

---

**Description**

This function converts a `AAStringSet` into an `ape DNABin`.

**Usage**

```
aastring2aabin(aa)
```

**Arguments**

aa                      `AAStringSet` [mandatory]

**Value**

An object of class `DNABin`

**Author(s)**

Kristian K Ullrich

**See Also**

[as.alignment](#) [as.DNABin.alignment](#)

**Examples**

```
## define two cds sequences
cds1 <- Biostrings::DNAString("ATGCAACATTGC")
cds2 <- Biostrings::DNAString("ATG---CATTGC")
cds1.cds2.aln <- c(Biostrings::DNAStringSet(cds1),
  Biostrings::DNAStringSet(cds2))
## convert into AAbin
#aastring2aabin(cds2aa(cds1.cds2.aln))
cds1.cds2.aln |> cds2aa() |> aastring2aabin()
```

---

aastring2aln

*aastring2aln*


---

**Description**

This function converts a AAStringSet into an seqinr alignment.

**Usage**

```
aastring2aln(aa)
```

**Arguments**

aa                    AAStringSet [mandatory]

**Value**

An object of class alignment which is a list with the following components:  
 nb the number of aligned sequences  
 nam a vector of strings containing the names of the aligned sequences  
 seq a vector of strings containing the aligned sequences  
 com a vector of strings containing the commentaries for each sequence or NA if there are no comments

**Author(s)**

Kristian K Ullrich

**See Also**

[as.alignment](#)

**Examples**

```
## define two cds sequences
cds1 <- Biostrings::DNAString("ATGCAACATTGC")
cds2 <- Biostrings::DNAString("ATG---CATTGC")
cds1.cds2.aln <- c(Biostrings::DNAStringSet(cds1),
  Biostrings::DNAStringSet(cds2))
#aastring2aln(cds2aa(cds1.cds2.aln))
cds1.cds2.aln |> cds2aa() |> aastring2aln()
```

---

aastring2dist

*aastring2dist*


---

**Description**

This function calculates pairwise distances for all combinations of a AAStringSet.

**Usage**

```
aastring2dist(
  aa,
  threads = 1,
  symmetric = TRUE,
  score = NULL,
  mask = NULL,
  region = NULL
)
```

**Arguments**

aa	AAStringSet [mandatory]
threads	number of parallel threads [default: 1]
symmetric	symmetric score matrix [default: TRUE]
score	score matrix use a score matrix to calculate distances [mandatory]
mask	IRanges object indicating masked sites [default: NULL]
region	IRanges object indicating region to use for dist calculation (by default all sites are used) [default: NULL]

**Value**

A data.frame of pairwise distance values distSTRING, sites used sitesUsed and region used regionUsed

**Author(s)**

Kristian K Ullrich

**See Also**[dnastring2dist](#)**Examples**

```
## load example sequence data
data("hiv", package="MSA2dist")
#astring2dist(cds2aa(hiv), score=granthamMatrix())
hiv |> cds2aa() |> astring2dist(score=granthamMatrix())
## create mask
mask1 <- IRanges::IRanges(start=c(11,41,71), end=c(20,50,80))
## use mask
hiv |> cds2aa() |> astring2dist(score=granthamMatrix(), mask=mask1)
## use region
region1 <- IRanges::IRanges(start=c(1,75), end=c(45,85))
hiv |> cds2aa() |> astring2dist(score=granthamMatrix(), region=region1)
## use mask and region
hiv |> cds2aa() |> astring2dist(score=granthamMatrix(),
  mask=mask1, region=region1)
## use asymmetric score matrix
myscore <- granthamMatrix()
myscore[5, 6] <- 0
h <- hiv |> cds2aa() |> astring2dist(score=myscore, symmetric=FALSE)
h$distSTRING[1:2, 1:2]
```

---

addmask2string*addmask2string*

---

**Description**

This function adds mask information as an IRanges object, START and END information, to a DNASTringSet or an AAStringSet and puts them into the metadata information. This information can be used to restrict the distance calculation to specific regions of the DNASTringSet or the AAStringSet.

**Usage**

```
addmask2string(seq, mask = NULL, append = TRUE)
```

**Arguments**

seq	DNASTringSet or AAStringSet [mandatory]
mask	IRanges object [mandatory]
append	indicate if mask should be appended or overwritten [default: TRUE]

**Value**

An object of class DNASTringSet or AAStringSet



**Author(s)**

Kristian K Ullrich

**See Also**[addregion2string](#), [addpop2string](#), [addpos2string](#)**Examples**

```
## load example sequence data
data(iupac, package="MSA2dist")
iupac.aa <- iupac |> cds2aa(shorten = TRUE)
## create mask
mask1 <- IRanges::IRanges(start=c(1,41), end=c(20,50))
## add mask
iupac.aa <- iupac.aa |> addmask2string(mask=mask1)
#(iupac.aa |> slot("metadata"))$mask
iupac.aa |> getmask()
## append mask
mask2 <- IRanges::IRanges(start=c(21), end=c(30))
iupac.aa <- iupac.aa |> addmask2string(mask=mask2)
#(iupac.aa |> slot("metadata"))$mask
iupac.aa |> getmask()
## overwrite mask
iupac.aa <- iupac.aa |> addmask2string(mask=mask2, append=FALSE)
#(iupac.aa |> slot("metadata"))$mask
iupac.aa |> getmask()
## reduce by mask
#iupac.aa.region <- iupac.aa |> string2region(mask=
#   (iupac.aa |> slot("metadata"))$mask)
iupac.aa.region <- iupac.aa |> string2region(mask=
  getmask(iupac.aa))
#iupac.aa.region |> slot("metadata")
iupac.aa.region |> getmask()
```

---

addpop2string

---

*addpop2string*


---

**Description**

This function adds population information to a DNASTringSet or an AASTringSet and puts them into the metadata information.

\_\_Note\_\_: All unassigned sequences will be put into pop "unassigned"!

Do not use "unassigned" as a population name!

\_\_Note\_\_: Names in a population in the poplist must match sequence names!

\_\_Note\_\_: Duplicated assignments are allowed!

**Usage**

```
addpop2string(seq, poplist)
```

**Arguments**

seq	DNASet or AASet [mandatory]
poplist	named list of populations either as index or names per population (do not mix index and names in one population) [mandatory]

**Value**

An object of class DNASet or AASet

**Author(s)**

Kristian K Ullrich

**See Also**

[addmask2string](#), [addregion2string](#), [addpos2string](#)

**Examples**

```
## load example sequence data
data(iupac, package="MSA2dist")
iupac.aa <- iupac |> cds2aa(shorten = TRUE)
## create poplist
poplist <- list(FRA = grep("Mmd.FRA", names(iupac)),
               GER = grep("Mmd.GER", names(iupac)),
               IRA = grep("Mmd.IRA", names(iupac)),
               AFG = grep("Mmm.AFG", names(iupac)))
iupac.aa <- iupac.aa |> addpop2string(poplist)
#(iupac.aa |> slot("metadata"))$pop.integer
iupac.aa |> popinteger()
#(iupac.aa |> slot("metadata"))$pop.names
iupac.aa |> popnames()
## mixing index and names
poplist <- list(FRA = names(iupac)[grep("Mmd.FRA", names(iupac))],
               GER = grep("Mmd.GER", names(iupac)),
               IRA = names(iupac)[grep("Mmd.IRA", names(iupac))],
               AFG = grep("Mmm.AFG", names(iupac)))
iupac.aa <- iupac.aa |> addpop2string(poplist)
iupac.aa |> popinteger()
iupac.aa |> popnames()
## leaving out some sequences which will be assigned as "unassigned"
poplist <- list(FRA = names(iupac)[grep("Mmd.FRA", names(iupac))],
               GER = grep("Mmd.GER", names(iupac)),
               IRA = names(iupac)[grep("Mmd.IRA", names(iupac))])
iupac.aa <- iupac.aa |> addpop2string(poplist)
iupac.aa |> popinteger()
iupac.aa |> popnames()
```

---

addpos2string	<i>addpos2string</i>
---------------	----------------------

---

## Description

This function adds GenomicRanges information, CHROM, START and END to a DNASTringSet or an AAStringSet and puts them into the metadata information. This information can be used to find overlaps with a chromosome wide mask.

## Usage

```
addpos2string(seq, chrom = NULL, start = NULL, end = NULL)
```

## Arguments

seq	DNASTringSet or AAStringSet [mandatory]
chrom	chromosome name [mandatory]
start	start position [mandatory]
end	end position [mandatory]

## Value

An object of class DNASTringSet or AAStringSet

## Author(s)

Kristian K Ullrich

## See Also

[addmask2string](#), [addregion2string](#), [addpop2string](#)

## Examples

```
## load example sequence data
data(iupac, package="MSA2dist")
## add position
iupac <- iupac |> addpos2string(chrom="chr1", start=1, end=1000)
#(iupac |> slot("metadata"))$GRanges
iupac |> getpos()
```

---

addregion2string	<i>addregion2string</i>
------------------	-------------------------

---

## Description

This function adds region information as an IRanges object, START and END information, to a DNASTringSet or an AAStringSet and puts them into the metadata information. This information can be used to restrict the distance calculation to specific regions of the DNASTringSet or the AAStringSet.

## Usage

```
addregion2string(seq, region = NULL, append = TRUE)
```

## Arguments

seq	DNASTringSet or AAStringSet [mandatory]
region	IRanges object [mandatory]
append	indicate if region should be appended or overwritten [default: TRUE]

## Value

An object of class DNASTringSet or AAStringSet

## Author(s)

Kristian K Ullrich

## See Also

[addmask2string](#), [addpop2string](#), [addpos2string](#)

## Examples

```
## load example sequence data
data(iupac, package="MSA2dist")
iupac.aa <- iupac |> cds2aa(shorten = TRUE)
## create region
region1 <- IRanges::IRanges(start=c(1,41), end=c(20,50))
## add region
iupac.aa <- iupac.aa |> addregion2string(region=region1)
#(iupac.aa |> slot("metadata"))$region
iupac.aa |> region()
## append region
region2 <- IRanges::IRanges(start=c(21), end=c(30))
iupac.aa <- iupac.aa |> addregion2string(region=region2)
#(iupac.aa |> slot("metadata"))$region
iupac.aa |> region()
```

```
## overwrite region
iupac.aa <- iupac.aa |> addregion2string(region=region2, append=FALSE)
#(iupac.aa |> slot("metadata"))$region
iupac.aa |> region()
## reduce by region
#iupac.aa.region <- iupac.aa |> string2region(region=
#   (iupac.aa |> slot("metadata"))$region)
iupac.aa.region <- iupac.aa |> string2region(region=
  region(iupac.aa))
#iupac.aa.region |> slot("metadata")
iupac.aa.region |> region()
```

---

aln2aastring

aln2aastring

---

## Description

This function converts a seqinr alignment into an AASTringSet.

## Usage

```
aln2aastring(aln)
```

## Arguments

aln                      seqinr alignment [mandatory]

## Value

An object of class AASTringSet

## Author(s)

Kristian K Ullrich

## See Also

[as.alignment AASTringSet](#)

## Examples

```
## define two cds sequences
cds1 <- Biostrings::DNAString("ATGCAACATTGC")
cds2 <- Biostrings::DNAString("ATG---CATTGC")
cds1.cds2.aln <- c(Biostrings::DNAStringSet(cds1),
  Biostrings::DNAStringSet(cds2))
#aastring2aln(cds2aa(cds1.cds2.aln))
cds1.cds2.aln |> cds2aa() |> aastring2aln() |> aln2aastring()
```

---

aln2dnastring	<i>aln2dnastring</i>
---------------	----------------------

---

## Description

This function converts a seqinr alignment into an DNASTringSet.

## Usage

```
aln2dnastring(aln)
```

## Arguments

aln                      seqinr alignment [mandatory]

## Value

An object of class DNASTringSet

## Author(s)

Kristian K Ullrich

## See Also

[as.alignment DNASTringSet](#)

## Examples

```
## define two cds sequences
cds1 <- Biostrings::DNASTring("ATGCAACATTGC")
cds2 <- Biostrings::DNASTring("ATG---CATTGC")
cds1.cds2.aln <- c(Biostrings::DNASTringSet(cds1),
  Biostrings::DNASTringSet(cds2))
## convert into alignment
#dnastring2aln(cds1.cds2.aln)
cds1.cds2.aln |> dnastring2aln()
## convert back into DNASTringSet
#aln2dnastring(dnastring2aln(cds1.cds2.aln))
cds1.cds2.aln |> dnastring2aln() |> aln2dnastring()
```

---

`cds2aa`*cds2aa*

---

## Description

This function translates a `DNASet` into an `AASet`.

## Usage

```
cds2aa(  
  cds,  
  shorten = FALSE,  
  frame = 1,  
  framelist = NULL,  
  genetic.code = NULL,  
  return.cds = FALSE  
)
```

## Arguments

<code>cds</code>	<code>DNASet</code> [mandatory]
<code>shorten</code>	shorten all sequences to multiple of three [default: FALSE]
<code>frame</code>	indicates the first base of a the first codon [default: 1]
<code>framelist</code>	supply vector of frames for each entry [default: NULL]
<code>genetic.code</code>	The genetic code to use for the translation of codons into Amino Acid letters [default: NULL]
<code>return.cds</code>	return shorten cds instead of aa [default: FALSE]

## Value

`AASet`

## Author(s)

Kristian K Ullrich

## See Also

[XStringSet-class](#), [translate](#)

## Examples

```
## define two cds sequences  
cds1 <- Biostrings::DNAString("ATGCAACATTGC")  
cds2 <- Biostrings::DNAString("ATG---CATTGC")  
cds1.cds2.aln <- c(Biostrings::DNAStringSet(cds1),  
  Biostrings::DNAStringSet(cds2))
```

```
#cds2aa(cds1.cds2.aln)
cds1.cds2.aln |> cds2aa()
## alternative genetic code
data(woodmouse, package="ape")
#cds2aa(dnabin2dnastring(woodmouse), shorten=TRUE)
woodmouse |> dnabin2dnastring() |> cds2aa(shorten=TRUE)
#cds2aa(dnabin2dnastring(woodmouse), shorten=TRUE,
#genetic.code=Biostrings::getGeneticCode("2"))
woodmouse |> dnabin2dnastring() |> cds2aa(shorten=TRUE,
genetic.code=Biostrings::getGeneticCode("2"))
woodmouse |> dnabin2dnastring() |> cds2aa(shorten=TRUE, return.cds=TRUE) |>
cds2aa(genetic.code=Biostrings::getGeneticCode("2"))
```

---

cds2codonaln

*cds2codonaln*


---

## Description

This function takes two single sequence DNASTring's or two single sequence DNASTringSet's, converts them into aa, calculates a global alignment and converts this alignment back into a codon alignment.

## Usage

```
cds2codonaln(
  cds1,
  cds2,
  type = "global",
  substitutionMatrix = "BLOSUM62",
  gapOpening = 10,
  gapExtension = 0.5,
  remove.gaps = FALSE,
  ...
)
```

## Arguments

cds1	single sequence DNASTringSet or DNASTring [mandatory]
cds2	single sequence DNASTringSet or DNASTring [mandatory]
type	type of alignment (see <a href="#">pairwiseAlignment</a> ) [default: global]
substitutionMatrix	substitution matrix representing the fixed substitution scores for an alignment (see <a href="#">pairwiseAlignment</a> ) [default: BLOSUM62]
gapOpening	the cost for opening a gap in the alignment (see <a href="#">pairwiseAlignment</a> ) [default: 10]
gapExtension	the incremental cost incurred along the length of the gap in the alignment (see <a href="#">pairwiseAlignment</a> ) [default: 0.5]



`remove.gaps`      specify if gaps in the codon alignment should be removed [default: FALSE]  
`...`                other cds2aa parameters

**Value**

codon alignment as `DNAStringSet`

**Author(s)**

Kristian K Ullrich

**References**

Pagès, H et al. (2014) Biostrings: Efficient manipulation of biological strings. *R package version, 2(0)*.

**See Also**

[pairwiseAlignment](#)

**Examples**

```
## define two cds sequences
cds1 <- Biostrings::DNAString("ATGCAACATTGC")
cds2 <- Biostrings::DNAString("ATGCATTGC")
cds2codonaln(cds1, cds2)
```

---

<code>cdsstring2codonaln</code>	<i>cdsstring2codonaln</i>
---------------------------------	---------------------------

---

**Description**

This function takes two sequences as `DNAStringSet`, and their corresponding `AAStringSet`, calculates a global alignment and converts this alignment back into a codon alignment.

**Usage**

```
cdsstring2codonaln(
  cds,
  aa,
  type = "global",
  substitutionMatrix = "BLOSUM62",
  gapOpening = 10,
  gapExtension = 0.5,
  remove.gaps = FALSE
)
```

**Arguments**

<code>cds</code>	two sequences DNASTringSet [mandatory]
<code>aa</code>	two sequences AAStringSet [mandatory]
<code>type</code>	type of alignment (see <a href="#">pairwiseAlignment</a> ) [default: global]
<code>substitutionMatrix</code>	substitution matrix representing the fixed substitution scores for an alignment (see <a href="#">pairwiseAlignment</a> ) [default: BLOSUM62]
<code>gapOpening</code>	the cost for opening a gap in the alignment (see <a href="#">pairwiseAlignment</a> ) [default: 10]
<code>gapExtension</code>	the incremental cost incurred along the length of the gap in the alignment (see <a href="#">pairwiseAlignment</a> ) [default: 0.5]
<code>remove.gaps</code>	specify if gaps in the codon alignment should be removed [default: FALSE]

**Value**

codon alignment as DNASTringSet

**Author(s)**

Kristian K Ullrich

**References**

Pagès, H et al. (2014) Biostrings: Efficient manipulation of biological strings. *R package version, 2(0)*.

**See Also**

[pairwiseAlignment](#)

**Examples**

```
## define two cds sequences
cds <- Biostrings::DNASTringSet(c("ATGCAACATTGC", "ATGCATTGC"))
names(cds) <- c("cds1", "cds2")
## get protein alignment
aa <- MSA2dist::cds2aa(cds)
cdsstring2codonaln(cds, aa)
```

---

codon2numberAMBIG	<i>codon2numberAMBIG</i>
-------------------	--------------------------

---

**Description**

This function converts a codon into a number, but accept N and -.

**Usage**

```
codon2numberAMBIG(codon)
```

**Arguments**

codon	[mandatory]
-------	-------------

**Value**

An object of class `numeric`

**Author(s)**

Kristian K Ullrich

**See Also**

[GENETIC\\_CODE](#)

**Examples**

```
#unlist(lapply(names(Biostrings::GENETIC_CODE), codon2numberAMBIG))
names(Biostrings::GENETIC_CODE) |> codon2numberAMBIG()
```

---

codon2numberTCAG	<i>codon2numberTCAG</i>
------------------	-------------------------

---

**Description**

This function converts a codon into a number.

**Usage**

```
codon2numberTCAG(codon)
```

**Arguments**

codon	[mandatory]
-------	-------------

**Value**

An object of class `numeric`

**Author(s)**

Kristian K Ullrich

**See Also**

[GENETIC\\_CODE](#)

**Examples**

```
#unlist(lapply(names(Biostrings::GENETIC_CODE), codon2numberTCAG))
names(Biostrings::GENETIC_CODE) |> codon2numberTCAG()
```

---

codonmat2pnps

*codonmat2pnps*

---

**Description**

This function calculates pn/ps according to *Nei and Gojobori (1986)*.

**Usage**

```
codonmat2pnps(codonmat)
```

**Arguments**

codonmat            codon matrix of two columns to be compared [mandatory]

**Value**

An object of class `pnps` which is a list with the following components:

- seq1 sequence1 name
- seq2 sequence2 name
- Codons sequence2 name
- Compared sequence2 name
- Ambiguous sequence2 name
- Indels sequence2 name
- Ns sequence2 name
- Sd sequence2 name
- Sn sequence2 name
- S sequence2 name
- N sequence2 name
- ps sequence2 name
- pn sequence2 name
- pnps sequence2 name

ds sequence2 name  
 dn sequence2 name  
 dn ds sequence2 name

## Author(s)

Kristian K Ullrich

## References

Nei and Gojobori. (1986) Simple methods for estimating the numbers of synonymous and nonsynonymous nucleotide substitutions. *Mol. Biol. Evol.*, **3**(5), 418-426.

Ganeshan et al. (1997) Human immunodeficiency virus type 1 genetic evolution in children with different rates of development of disease. *J. Virology*. **71**(1), 663-677.

Yang et al. (2000) Codon-substitution models for heterogeneous selection pressure at amino acid sites. *Genetics*. **155**(1), 431-449.

## See Also

[kaks](#)

## Examples

```
## load example sequence data
data("hiv", package="MSA2dist")
#codonmat2pnps(dnastring2codonmat(hiv)[,c(1, 2)])
(hiv |> dnastring2codonmat())[,c(1, 2)] |> codonmat2pnps()
```

---

codonmat2xy

*codonmat2xy*

---

## Description

This function calculates average behavior of each codon for all pairwise comparisons for indels, syn, and nonsyn mutations according to *Nei and Gojobori (1986)*.

## Usage

```
codonmat2xy(codonmat, threads = 1)
```

## Arguments

codonmat	codon matrix obtained via <a href="#">dnastring2codonmat</a> [mandatory]
threads	number of parallel threads [default: 1]

**Value**

A data.frame object with the following components:

- Codon Codon index
- n number of comparison
- SynSum Sum of syn
- NonSynSum Sum of nonsyn
- IndelSum Sum of indels
- SynMean average syn per codon
- NonSynMean average nonsyn per codon
- IndelMean average indels per codon
- CumSumSynMean cumulative average syn per codon
- CumSumNonSynMean cumulative average nonsyn per codon
- CumSumIndelMean cumulative indels per codon

**Author(s)**

Kristian K Ullrich

**References**

Nei and Gojobori. (1986) Simple methods for estimating the numbers of synonymous and nonsynonymous nucleotide substitutions. *Mol. Biol. Evol.*, **3**(5), 418-426.

Ganeshan et al. (1997) Human immunodeficiency virus type 1 genetic evolution in children with different rates of development of disease. *J. Virology*. **71**(1), 663-677.

Yang et al. (2000) Codon-substitution models for heterogeneous selection pressure at amino acid sites. *Genetics*. **155**(1), 431-449.

**See Also**

[dnastring2codonmat](#) [codonmat2pnps](#) [dnastring2kaks](#) [kaks](#)

**Examples**

```
## load example sequence data
data("hiv", package="MSA2dist")
#codonmat2xy(dnastring2codonmat(hiv))
hiv |> dnastring2codonmat() |> codonmat2xy()
#codonmat2xy(dnastring2codonmat(hiv), threads=2)
hiv |> dnastring2codonmat() |> codonmat2xy(threads=2)
```

---

compareCodons	<i>compareCodons</i>
---------------	----------------------

---

### Description

This function compares two codons and returns the number of syn and non-syn sites according to *Nei and Gojobori (1986)*.

### Usage

```
compareCodons(codA, codB)
```

### Arguments

codA	codon A [mandatory]
codB	codon B [mandatory]

### Value

vector of syn and non-syn sites

### Author(s)

Kristian K Ullrich

### References

Nei and Gojobori. (1986) Simple methods for estimating the numbers of synonymous and nonsynonymous nucleotide substitutions. *Mol. Biol. Evol.*, **3**(5), 418-426.

Ganeshan et al. (1997) Human immunodeficiency virus type 1 genetic evolution in children with different rates of development of disease. *J. Virology*. **71**(1), 663-677.

Yang et al. (2000) Codon-substitution models for heterogeneous selection pressure at amino acid sites. *Genetics*. **155**(1), 431-449.

### See Also

[kaks](#)

### Examples

```
compareCodons("AAA", "TTA")
compareCodons("AAA", "TAT")
compareCodons("AAA", "ATT")
compareCodons("AAA", "TTT")
## load example sequence data
data("hiv", package="MSA2dist")
compareCodons(dnastring2codonmat(hiv)[1,1], dnastring2codonmat(hiv)[1,2])
```

---

dnabin2dnastring	<i>dnabin2dnastring</i>
------------------	-------------------------

---

**Description**

This function converts an ape DNABin into a DNASTringSet.

**Usage**

```
dnabin2dnastring(dnabin)
```

**Arguments**

dnabin	ape DNABin [mandatory]
--------	------------------------

**Value**

An object of class DNASTringSet

**Author(s)**

Kristian K Ullrich

**See Also**

[as.alignment](#) [as.DNABin.alignment](#) [DNASTringSet](#)

**Examples**

```
data(woodmouse, package="ape")
## convert into DNASTringSet
#dnabin2dnastring(woodmouse)
woodmouse |> dnabin2dnastring()
```

---

dnastring2aln	<i>dnastring2aln</i>
---------------	----------------------

---

**Description**

This function converts a DNASTringSet into an seqinr alignment.

**Usage**

```
dnastring2aln(dna)
```



**Arguments**

dna                      DNASTringSet [mandatory]

**Value**

An object of class alignment which is a list with the following components:  
 nb the number of aligned sequences  
 nam a vector of strings containing the names of the aligned sequences  
 seq a vector of strings containing the aligned sequences  
 com a vector of strings containing the commentaries for each sequence or NA if there are no comments

**Author(s)**

Kristian K Ullrich

**See Also**

[as.alignment](#)

**Examples**

```
## define two cds sequences
cds1 <- Biostrings::DNASTring("ATGCAACATTGC")
cds2 <- Biostrings::DNASTring("ATG---CATTGC")
cds1.cds2.aln <- c(Biostrings::DNASTringSet(cds1),
  Biostrings::DNASTringSet(cds2))
## convert into alignment
#dnastring2aln(cds1.cds2.aln)
cds1.cds2.aln |> dnastring2aln()
```

---

dnastring2codonmat	<i>dnastring2codonmat</i>
--------------------	---------------------------

---

**Description**

This function converts a DNASTringSet into a codon matrix.

**Usage**

```
dnastring2codonmat(cds, shorten = FALSE, frame = 1, framelist = NULL)
```

**Arguments**

cds                      DNASTringSet [mandatory]  
 shorten                shorten all sequences to multiple of three [default: FALSE]  
 frame                   indicates the first base of a the first codon [default: 1]  
 framelist               supply vector of frames for each entry [default: NULL]

**Value**

An object of class alignment which is a list with the following components:

- nb the number of aligned sequences
- nam a vector of strings containing the names of the aligned sequences
- seq a vector of strings containing the aligned sequences
- com a vector of strings containing the commentaries for each sequence or NA if there are no comments

**Author(s)**

Kristian K Ullrich

**See Also**

[as.alignment](#)

**Examples**

```
## define two cds sequences
cds1 <- Biostrings::DNAString("ATGCAACATTGC")
cds2 <- Biostrings::DNAString("ATG---CATTGC")
cds1.cds2.aln <- c(Biostrings::DNAStringSet(cds1),
  Biostrings::DNAStringSet(cds2))
## convert into alignment
#dnastring2codonmat(cds1.cds2.aln)
cds1.cds2.aln |> dnastring2codonmat()
## use frame 2 and shorten to circumvent multiple of three error
cds1 <- Biostrings::DNAString("-ATGCAACATTGC-")
cds2 <- Biostrings::DNAString("-ATG---CATTGC-")
cds1.cds2.aln <- c(Biostrings::DNAStringSet(cds1),
  Biostrings::DNAStringSet(cds2))
cds1.cds2.aln |> dnastring2codonmat(frame=2, shorten=TRUE)
```

---

dnastring2dist

*dnastring2dist*

---

**Description**

This function calculates pairwise distances for all combinations of a DNAStringSet.

**Usage**

```
dnastring2dist(
  dna,
  model = "IUPAC",
  threads = 1,
  symmetric = TRUE,
  score = NULL,
```

```

    mask = NULL,
    region = NULL,
    ...
)

```

### Arguments

<code>dna</code>	DNAStrngSet [mandatory]
<code>model</code>	specify model either "IUPAC" or any model from <code>ape::dist.dna</code> [default: IUPAC]
<code>threads</code>	number of parallel threads [default: 1]
<code>symmetric</code>	symmetric score matrix [default: TRUE]
<code>score</code>	score matrix use score matrix to calculate distances [default: NULL]
<code>mask</code>	IRanges object indicating masked sites [default: NULL]
<code>region</code>	IRanges object indicating region to use for dist calculation. Default is null, meaning all sites are used [default: NULL]
<code>...</code>	other <code>ape::dist.dna</code> parameters (see <a href="#">dist.dna</a> )

### Value

A data.frame of pairwise distance values `distSTRING` and sites used `sitesUsed`

### Author(s)

Kristian K Ullrich

### See Also

[dist.dna](#)

### Examples

```

## load example sequence data
data("hiv", package="MSA2dist")
#dnastring2dist(hiv, model="IUPAC")
hiv |> dnastring2dist(model="IUPAC")
#dnastring2dist(hiv, model="K80")
hiv |> dnastring2dist(model="K80")
data("woodmouse", package="ape")
#dnastring2dist(dnabin2dnastring(woodmouse), score=iupacMatrix())
woodmouse |> dnabin2dnastring() |> dnastring2dist()
#dnastring2dist(hiv, model = "IUPAC", threads = 2)
hiv |> dnastring2dist(model = "IUPAC", threads = 2)
## create mask
mask1 <- IRanges::IRanges(start=c(1,61,121), end=c(30,90,150))
## use mask
hiv |> dnastring2dist(model="IUPAC", mask=mask1)
## use region
region1 <- IRanges::IRanges(start=c(1,139), end=c(75,225))

```

```

hiv |> dnastring2dist(model="IUPAC", region=region1)
## use mask and region
hiv |> dnastring2dist(model="IUPAC", mask=mask1, region=region1)
## use asymmetric score matrix
myscore <- iupacMatrix()
myscore[1, 4] <- 0.5
(hiv |> dnastring2dist(score=myscore, symmetric=FALSE))$distSTRING[1:2, 1:2]

```

---

dnastring2dnabin	<i>dnastring2dnabin</i>
------------------	-------------------------

---

## Description

This function converts a DNASTringSet into an ape DNABin.

## Usage

```
dnastring2dnabin(dna)
```

## Arguments

dna                      DNASTringSet [mandatory]

## Value

An object of class DNABin

## Author(s)

Kristian K Ullrich

## See Also

[as.alignment as.DNABin.alignment](#)

## Examples

```

## define two cds sequences
cds1 <- Biostrings::DNASTring("ATGCAACATTGC")
cds2 <- Biostrings::DNASTring("ATG---CATTGC")
cds1.cds2.aln <- c(Biostrings::DNASTringSet(cds1),
  Biostrings::DNASTringSet(cds2))
## convert into DNABin
#dnastring2dnabin(cds1.cds2.aln)
cds1.cds2.aln |> dnastring2dnabin()

```

---

dnastring2kaks	<i>dnastring2kaks</i>
----------------	-----------------------

---

## Description

This function calculates Ka/Ks (pN/pS) for all combinations of a DNASTringSet. If the sequences in the DNASTringSet are not a multiple-sequence alignment, pairwise codon alignments can be calculated on the fly. Models used and implemented according to *Li (1993)* (using seqinr) or *Nei and Gojobori (1986)* (own implementation) or models from KaKs\_Calculator2 ported to MSA2dist with Rcpp.

## Usage

```
dnastring2kaks(
  cds,
  model = "Li",
  threads = 1,
  isMSA = TRUE,
  sgc = "1",
  verbose = FALSE,
  ...
)
```

## Arguments

cds	DNASTringSet coding sequence alignment [mandatory]
model	specify codon model either "Li" or "NG86" or one of KaKs_Calculator2 model "NG", "LWL", "LPB", "MLWL", "MLPB", "GY", "YN", "MYN", "MS", "MA", "GNG", "GLWL", "GLPB", "GMLWL", "GMLPB", "GYN", "GMYN" [default: Li]
threads	number of parallel threads [default: 1]
isMSA	cds DNASTringSet represents MSA [default: TRUE]
sgc	standard genetic code (for KaKs Calculator models) [default: 1]
verbose	verbosity (for KaKs Calculator models) [default: FALSE]
...	other codon alignment parameters

## Value

A data.frame of KaKs values

## Author(s)

Kristian K Ullrich

## References

- "MS/MA/GNG/GLWL/GLPB/GMLWL/GMLPB/GYN:" Wang et al. (2010) KaKs\_Calculator 2.0: a toolkit incorporating gamma-series methods and sliding window strategies. *Genomics, proteomics & bioinformatics*. **8(1)**, 77-80.
- "Li/LWL:" Li et al. (1985) A new method for estimating synonymous and nonsynonymous rates of nucleotide substitution considering the relative likelihood of nucleotide and codon changes. *Mol. Biol. Evol.*, **2(2)**, 150-174.
- "Li/LPB:" Li (1993). Unbiased estimation of the rates of synonymous and nonsynonymous substitution. *Journal of molecular evolution*, 36(1), pp.96-99.
- "NG86/NG:" Nei and Gojobori. (1986) Simple methods for estimating the numbers of synonymous and nonsynonymous nucleotide substitutions. *Mol. Biol. Evol.*, **3(5)**, 418-426.
- "LPB:" Pamilo and Bianchi. (1993) Evolution of the Zfx and Zfy genes: Rates and interdependence between genes. *Mol. Biol. Evol.*, **10**, 271-281.
- "MLWL/MLPB:" Tzeng et al. (2004). Comparison of three methods for estimating rates of synonymous and nonsynonymous nucleotide substitutions. *Mol. Biol. Evol.*, **21(12)**, 2290-2298.
- "GY:" Goldman and Yang (1994). A codon-based model of nucleotide substitution for protein-coding DNA sequences. *Mol. Biol. Evol.*, **11(5)** 725-736.
- "YN:" Yang et al. (2000) Codon-substitution models for heterogeneous selection pressure at amino acid sites. *Genetics*. **155(1)**, 431-449.
- "MYN:" Zhang et al. (2006). Computing Ka and Ks with a consideration of unequal transitional substitutions. *BMC evolutionary biology*, **6(1)**, 1-10.
- "data(hiv):" Ganeshan et al. (1997) Human immunodeficiency virus type 1 genetic evolution in children with different rates of development of disease. *J. Virology*. **71(1)**, 663-677.
- Wang et al. (2009). gamma-MYN: a new algorithm for estimating Ka and Ks with consideration of variable substitution rates. *Biology Direct*, **4(1)**, 1-18.

## See Also

[kaks](#)

## Examples

```
## load example sequence data
data("hiv", package="MSA2dist")
#dnastring2kaks(hiv, model="Li")
hiv |> dnastring2kaks(model="Li")
#dnastring2kaks(hiv, model="NG86")
hiv |> dnastring2kaks(model="NG86")
#dnastring2kaks(hiv, model="NG86", threads=2)
hiv |> dnastring2kaks(model="NG86", threads=2)

## define three unaligned cds sequences
cds1 <- Biostrings::DNAString("ATGCAACATTGC")
cds2 <- Biostrings::DNAString("ATGCATTGC")
cds3 <- Biostrings::DNAString("ATGCAATGC")
cds_sequences <- Biostrings::DNAStringSet(list(cds1, cds2, cds3))
```

```
names(cds_sequences) <- c("cds1", "cds2", "cds3")
## set isMSA to FALSE to automatically create pairwise codon alignments
#dnastring2kaks(cds_sequences, model="Li", isMSA=FALSE)
cds_sequences |> dnastring2kaks(model="Li", isMSA=FALSE)
```

---

GENETIC_CODE_TCAG	<i>GENETIC_CODE_TCAG</i>
-------------------	--------------------------

---

## Description

GENETIC\_CODE from Biostrings extended by codon number and number of syn sites.

## Usage

```
codon2number(codon)
```

## Arguments

codon	codon [mandatory]
-------	-------------------

## Value

An object of class `numeric`

## Author(s)

Kristian K Ullrich

## See Also

[GENETIC\\_CODE](#)

## Examples

```
GENETIC_CODE_TCAG
```

---

getmask	<i>getmask</i>
---------	----------------

---

## Description

This function shows the mask slot from a DNASTringSet or an AAStringSet metadata information.

## Usage

```
getmask(seq)
```

## Arguments

seq	DNASTringSet or AAStringSet [mandatory]
-----	---

## Value

IRanges information from metadata

## Author(s)

Kristian K Ullrich

## See Also

[addpop2string](#)

## Examples

```
## load example sequence data
data(iupac, package="MSA2dist")
iupac.aa <- iupac |> cds2aa(shorten = TRUE)
## create mask
mask1 <- IRanges::IRanges(start=c(1,41), end=c(20,50))
## add mask
iupac.aa <- iupac.aa |> addmask2string(mask=mask1)
#(iupac.aa |> slot("metadata"))$mask
iupac.aa |> getmask()
```



---

getpos	<i>getpos</i>
--------	---------------

---

## Description

This function shows the position slot from a DNASTringSet or an AAStringSet metadata information.

## Usage

```
getpos(seq)
```

## Arguments

seq	DNASTringSet or AAStringSet [mandatory]
-----	---

## Value

GenomicRanges information from metadata

## Author(s)

Kristian K Ullrich

## See Also

[addpop2string](#)

## Examples

```
## load example sequence data
data(iupac, package="MSA2dist")
## add position
iupac <- iupac |> addpos2string(chrom="chr1", start=1, end=1000)
#(iupac |> slot("metadata"))$GRanges
iupac |> getpos()
```

---

globalDeletion	<i>globalDeletion</i>
----------------	-----------------------

---

### Description

This function returns a DNASTringSet reduced by all sites containing any gaps ("-", "+", ".") or missing ("N") sites.

### Usage

```
globalDeletion(dna)
```

### Arguments

dna	DNASTringSet [mandatory]
-----	--------------------------

### Value

DNASTringSet

### Author(s)

Kristian K Ullrich

### Examples

```
## define two cds sequences
cds1 <- Biostrings::DNASTring("ATGCAACATTGC")
cds2 <- Biostrings::DNASTring("ATG---CATTGC")
cds1.cds2.aln <- c(Biostrings::DNASTringSet(cds1),
  Biostrings::DNASTringSet(cds2))
globalDeletion(cds1.cds2.aln)
```

---

granthamMatrix	<i>granthamMatrix</i>
----------------	-----------------------

---

### Description

This function creates a granthamMatrix object to be used with the rcpp\_distSTRING function. By default, the grantham matrix is defined as from Grantham 1974. (see <https://link.springer.com/article/10.1007/s00335-017-9704-9>)

### Usage

```
granthamMatrix()
```

**Value**

matrix

**Author(s)**

Kristian K Ullrich

**References**

Grantham R. (1974). Amino Acid Difference Formula to Help Explain Protein Evolution. *Science*, **185**(4154), 862-864.

**See Also**

[aastring2dist](#), [dist.dna](#)

**Examples**

```
granthamMatrix()
```

---

hiv-data

*hiv-data*

---

**Description**

Example cds sequences from HIV-1 sample 136 patient 1 from Sweden envelope glycoprotein (env) gene, V3 region as DNASTringSet.

**Usage**

```
data(hiv)
```

**Format**

an object of class DNASTringSet see [XStringSet-class](#)

**References**

Yang et al. (2000) Codon-substitution models for heterogeneous selection pressure at amino acid sites. *Genetics*. **155**(1), 431-449.

**Examples**

```
data("hiv", package="MSA2dist")
```

indices2kaks

*indices2kaks***Description**

This function calculates Ka/Ks (pN/pS) for all combinations given in an indices list of a DNASTringSet. If the sequences in the DNASTringSet are not a multiple-sequence alignment, pairwise codon alignments can be calculated on the fly. Models used and implemented according to *Li (1993)* (using seqinr) or *Nei and Gojobori (1986)* (own implementation) or models from KaKs\_Calculator2 ported to MSA2dist with Rcpp.

**Usage**

```
indices2kaks(
  cds,
  indices,
  model = "Li",
  threads = 1,
  isMSA = TRUE,
  sgc = "1",
  verbose = FALSE,
  ...
)
```

**Arguments**

cds	DNASTringSet coding sequence alignment [mandatory]
indices	list list of indices to calculate Ks/Ks [mandatory]
model	specify codon model either "Li" or "NG86" or one of KaKs_Calculator2 model "NG", "LWL", "LPB", "MLWL", "MLPB", "GY", "YN", "MYN", "MS", "MA", "GNG", "GLWL", "GLPB", "GMLWL", "GMLPB", "GYN", "GMYN" [default: Li]
threads	number of parallel threads [default: 1]
isMSA	cds DNASTringSet represents MSA [default: TRUE]
sgc	standard genetic code (for KaKs Calculator models) [default: 1]
verbose	verbosity (for KaKs Calculator models) [default: FALSE]
...	other codon alignment parameters

**Value**

A data.frame of KaKs values

**Author(s)**

Kristian K Ullrich

## References

- "MS/MA/GNG/GLWL/GLPB/GMLWL/GMLPB/GYN:" Wang et al. (2010) KaKs\_Calculator 2.0: a toolkit incorporating gamma-series methods and sliding window strategies. *Genomics, proteomics & bioinformatics*. **8(1)**, 77-80.
- "Li/LWL:" Li et al. (1985) A new method for estimating synonymous and nonsynonymous rates of nucleotide substitution considering the relative likelihood of nucleotide and codon changes. *Mol. Biol. Evol.*, **2(2)**, 150-174.
- "Li/LPB:" Li (1993). Unbiased estimation of the rates of synonymous and nonsynonymous substitution. *Journal of molecular evolution*, 36(1), pp.96-99.
- "NG86/NG:" Nei and Gojobori. (1986) Simple methods for estimating the numbers of synonymous and nonsynonymous nucleotide substitutions. *Mol. Biol. Evol.*, **3(5)**, 418-426.
- "LPB:" Pamilo and Bianchi. (1993) Evolution of the Zfx and Zfy genes: Rates and interdependence between genes. *Mol. Biol. Evol.*, **10**, 271-281.
- "MLWL/MLPB:" Tzeng et al. (2004). Comparison of three methods for estimating rates of synonymous and nonsynonymous nucleotide substitutions. *Mol. Biol. Evol.*, **21(12)**, 2290-2298.
- "GY:" Goldman and Yang (1994). A codon-based model of nucleotide substitution for protein-coding DNA sequences. *Mol. Biol. Evol.*, **11(5)** 725-736.
- "YN:" Yang et al. (2000) Codon-substitution models for heterogeneous selection pressure at amino acid sites. *Genetics*. **155(1)**, 431-449.
- "MYN:" Zhang et al. (2006). Computing Ka and Ks with a consideration of unequal transitional substitutions. *BMC evolutionary biology*, **6(1)**, 1-10.
- "data(hiv):" Ganeshan et al. (1997) Human immunodeficiency virus type 1 genetic evolution in children with different rates of development of disease. *J. Virology*. **71(1)**, 663-677.
- Wang et al. (2009). gamma-MYN: a new algorithm for estimating Ka and Ks with consideration of variable substitution rates. *Biology Direct*, **4(1)**, 1-18.

## See Also

[kaks](#)

## Examples

```
## load example sequence data
data("hiv", package="MSA2dist")
## create indices
idx <- list(c(2, 3), c(5,7,9))
#indices2kaks(hiv, idx, model="Li")
hiv |> indices2kaks(idx, model="Li")
#indices2kaks(hiv, idx, model="NG86")
hiv |> indices2kaks(idx, model="NG86")
#indices2kaks(hiv, idx, model="NG86", threads=2)
hiv |> indices2kaks(idx, model="NG86", threads=2)

## define three unaligned cds sequences
cds1 <- Biostrings::DNAString("ATGCAACATTGC")
cds2 <- Biostrings::DNAString("ATGCATTGC")
```

```

cds3 <- Biostrings::DNASTring("ATGCAATGC")
cds_sequences <- Biostrings::DNASTringSet(list(cds1, cds2, cds3))
names(cds_sequences) <- c("cds1", "cds2", "cds3")
## create indices
idx <- list(c(1, 2), c(1,3))
## set isMSA to FALSE to automatically create pairwise codon alignments
#indices2kaks(cds_sequences, idx, model="Li", isMSA=FALSE)
cds_sequences |> indices2kaks(idx, model="Li", isMSA=FALSE)

```

---

iupac-data

*iupac-data*


---

### Description

Example IUPAC sequences created with `angsd` from different house mouse (*Mus musculus*) sub-populations from Harr et al. (2016) `DNASTringSet`.

### Usage

```
data(iupac)
```

### Format

an object of class `DNASTringSet` see [XStringSet-class](#)

### References

Harr et al. (2016) Genomic resources for wild populations of the house mouse, *Mus musculus* and its close relative *Mus spretus*. *Scientific data*. **3**(1), 1-14.

### Examples

```
data("iupac", package="MSA2dist")
```

---

iupacMatrix

*iupacMatrix*


---

### Description

This function creates a `iupacMatrix` object to be used with the `rcpp_distSTRING` function. By default, the `iupac` matrix is defined as literal distance obtained from Chang et al. 2017. (see <https://link.springer.com/article/10.1007/s00335-017-9704-9>)

### Usage

```
iupacMatrix()
```

**Value**

score matrix

**Author(s)**

Kristian K Ullrich

**References**

Chang,P. L.,Kopania,E.,Keeble,S.,Sarver,B. A.,Larson, E.,Orth,A,... & Dean,M. D. (2017). Whole exome sequencing of wild-derived inbred strains of mice improves power to link phenotype and genotype. *Mammalian genome*,**28(9-10)**,416-425.

**See Also**

[dnastring2dist,dist.dna](#)

**Examples**

```
iupacMatrix()
```

---

makePostalignedSeqs	<i>makePostalignedSeqs</i>
---------------------	----------------------------

---

**Description**

This function is a fork from an internal function from Biostrings

**Usage**

```
makePostalignedSeqs(x)
```

**Arguments**

x	x
---	---

**Value**

get internal function makePostalignedSeqs

**Author(s)**

Kristian K Ullrich

**See Also**

[pairwiseAlignment](#), [cds2codonaln](#)

**Examples**

```
## define two cds sequences
cds1 <- Biostrings::DNAString("ATGCAACATTGC")
cds2 <- Biostrings::DNAString("ATGCATTGC")
makePostalignedSeqs(pwalign::pairwiseAlignment(
  cds2aa(Biostrings::DNAStringSet(cds1)),
  cds2aa(Biostrings::DNAStringSet(cds2))))
```

---

pal2nal

*pal2nal*


---

**Description**

This function takes an AASTringSet alignment and its corresponding coding sequences DNASTringSet and converts the protein alignment into a codon alignment.

**Usage**

```
pal2nal(pal, nal, remove.gaps = FALSE)
```

**Arguments**

pal	AAStringSet [mandatory]
nal	DNASTringSet [mandatory]
remove.gaps	specify if gaps in the codon alignment should be removed [default: FALSE]

**Value**

codon alignment as DNASTringSet

**Author(s)**

Kristian K Ullrich

**References**

Pagès, H et al. (2014) Biostrings: Efficient manipulation of biological strings. *R package version*, **2(0)**.

**See Also**

[pairwiseAlignment](#)



### Examples

```
## define two cds sequences
cds <- Biostrings::DNAStringSet(c("ATGCAACATTGC", "ATGCATTGC"))
names(cds) <- c("cds1", "cds2")
## get protein alignment
aa <- MSA2dist::cds2aa(cds)
msa <- makePostalignedSeqs(pwalign::pairwiseAlignment(aa[1], aa[2]))[[1L]]
names(msa) <- names(aa)
## get codon alignment
nal <- MSA2dist::pal2nal(pal=msa, nal=cds)
nal
```

---

popinteger

*popinteger*

---

### Description

This function shows the population integer slot from a DNAStringSet or an AAStrngSet metadata information.

### Usage

```
popinteger(seq)
```

### Arguments

seq                      DNAStringSet or AAStrngSet [mandatory]

### Value

population integer from metadata

### Author(s)

Kristian K Ullrich

### See Also

[addpop2string](#)

### Examples

```
## load example sequence data
data(iupac, package="MSA2dist")
iupac.aa <- iupac |> cds2aa(shorten = TRUE)
## create poplist
poplist <- list(FRA = grep("Mmd.FRA", names(iupac)),
               GER = grep("Mmd.GER", names(iupac)),
```

```

      IRA = grep("Mmd.IRA", names(iupac)),
      AFG = grep("Mmm.AFG", names(iupac)))
iupac.aa <- iupac.aa |> addpop2string(poplist)
popinteger(iupac.aa)

```

---

popnames

*popnames*


---

## Description

This function shows the population names slot from a DNASTringSet or an AAStringSet metadata information.

## Usage

```
popnames(seq)
```

## Arguments

```
seq          DNASTringSet or AAStringSet [mandatory]
```

## Value

population names from metadata

## Author(s)

Kristian K Ullrich

## See Also

[addpop2string](#)

## Examples

```

## load example sequence data
data(iupac, package="MSA2dist")
iupac.aa <- iupac |> cds2aa(shorten = TRUE)
## create poplist
poplist <- list(FRA = grep("Mmd.FRA", names(iupac)),
  GER = grep("Mmd.GER", names(iupac)),
  IRA = grep("Mmd.IRA", names(iupac)),
  AFG = grep("Mmm.AFG", names(iupac)))
iupac.aa <- iupac.aa |> addpop2string(poplist)
popnames(iupac.aa)

```

---

rcpp_distSTRING	<i>rcpp_distSTRING</i>
-----------------	------------------------

---

**Description**

calculates pairwise distances using a score matrix

**Usage**

```
rcpp_distSTRING(dnavector, scoreMatrix, ncores = 1L, symmetric = 1L)
```

**Arguments**

dnavector	StringVector [mandatory]
scoreMatrix	NumericMatrix [mandatory]
ncores	number of cores [default: 1]
symmetric	symmetric score matrix [default: 1]

**Value**

list

**Author(s)**

Kristian K Ullrich

**Examples**

```
## load example sequence data
data("hiv", package="MSA2dist")
rcpp_distSTRING(dnavector=as.character(hiv), scoreMatrix=iupacMatrix())
```

---

rcpp_KaKs	<i>rcpp_KaKs</i>
-----------	------------------

---

**Description**

calculates KaKs as implemented in KaKs Calculator 2.0 MSA2dist with Rcpp.

**Usage**

```
rcpp_KaKs(cdsstr, sgc = "1", method = "YN", verbose = FALSE)
```

**Arguments**

cdsstr	StringVector [mandatory]
sgc	standard genetic code to use [default: 1]
method	KaKs Calculator 2.0 codon model [default: YN]
verbose	specify if verbose output [default: FALSE]

**Value**

list

**Author(s)**

Kristian K Ullrich

**References**

Wang et al. (2010) KaKs\_Calculator 2.0: a toolkit incorporating gamma-series methods and sliding window strategies. *Genomics, proteomics & bioinformatics*. **8(1)**, 77-80.

**Examples**

```
## load example sequence data
data("hiv", package="MSA2dist")
rcpp_KaKs(cdsstr=as.character(hiv[1:3]))
```

---

```
rcpp_pairwiseDeletionAA
      rcpp_pairwiseDeletionAA
```

---

**Description**

returns number of AA sites used

**Usage**

```
rcpp_pairwiseDeletionAA(aavector, ncores = 1L, symmetric = 1L)
```

**Arguments**

aavector	StringVector [mandatory]
ncores	number of cores [default: 1]
symmetric	symmetric score matrix [default: 1]

**Value**

list

**Author(s)**

Kristian K Ullrich

**Examples**

```
## load example sequence data
data("hiv", package="MSA2dist")
h <- hiv |> cds2aa() |> as.character()
rcpp_pairwiseDeletionAA(aavector=h, ncores=1)
```

---

```
rcpp_pairwiseDeletionDNA
      rcpp_pairwiseDeletionDNA
```

---

**Description**

returns number of DNA sites used

**Usage**

```
rcpp_pairwiseDeletionDNA(dnavector, ncores = 1L, symmetric = 1L)
```

**Arguments**

dnavector	StringVector [mandatory]
ncores	number of cores [default: 1]
symmetric	symmetric score matrix [default: 1]

**Value**

list

**Author(s)**

Kristian K Ullrich

**Examples**

```
## load example sequence data
data("woodmouse", package="ape")
w <- woodmouse |> dnabin2dnastring() |> as.character()
rcpp_pairwiseDeletionDNA(dnavector=w, ncores=1)
```

---

region	<i>region</i>
--------	---------------

---

### Description

This function shows the region slot from a DNASTringSet or an AAStringSet metadata information.

### Usage

```
region(seq)
```

### Arguments

seq	DNASTringSet or AAStringSet [mandatory]
-----	---

### Value

region IRanges object from metadata

### Author(s)

Kristian K Ullrich

### See Also

[addpop2string](#)

### Examples

```
## load example sequence data
data(iupac, package="MSA2dist")
iupac.aa <- iupac |> cds2aa(shorten = TRUE)
## create region
region1 <- IRanges::IRanges(start=c(1,41), end=c(20,50))
## add region
iupac.aa <- iupac.aa |> addregion2string(region=region1)
iupac.aa |> region()
```

---

regionused	<i>regionused</i>
------------	-------------------

---

## Description

This function shows the region used slot from a DNASTringSet or an AAStringSet metadata information.

## Usage

```
regionused(seq)
```

## Arguments

seq	DNASTringSet or AAStringSet [mandatory]
-----	---

## Value

population names from metadata

## Author(s)

Kristian K Ullrich

## See Also

[addpop2string](#)

## Examples

```
## load example sequence data
data("hiv", package="MSA2dist")
## create mask
mask1 <- IRanges::IRanges(start=c(11,41,71), end=c(20,50,80))
## use mask
hiv.region <- hiv |> cds2aa() |> string2region(mask=mask1)
#(hiv.region |> slot("metadata"))$regionUsed
hiv.region |> regionused()
```

---

string2region	<i>string2region</i>
---------------	----------------------

---

### Description

This function subsets a DNASTringSet or an AAStringSet by a mask and region given one or both options as IRanges.

### Usage

```
string2region(seq, mask = NULL, region = NULL, add = TRUE)
```

### Arguments

seq	DNASTringSet or AAStringSet [mandatory]
mask	IRanges object indicating masked sites [default: NULL]
region	IRanges object indicating region to use for dist calculation (by default all sites are used) [default: NULL]
add	indicate if mask and region should be added to metadata [default: TRUE]

### Value

A list object with the following components:  
 DNASTringSet or AAStringSet  
 regionUsed

### Author(s)

Kristian K Ullrich

### See Also

[dnastring2dist](#)

### Examples

```
## load example sequence data
data("hiv", package="MSA2dist")
## create mask
mask1 <- IRanges::IRanges(start=c(11,41,71), end=c(20,50,80))
## use mask
hiv.region <- hiv |> cds2aa() |> string2region(mask=mask1)
#(hiv.region |> slot("metadata"))$regionUsed
hiv.region |> regionused()
## use region
region1 <- IRanges::IRanges(start=c(1,75), end=c(45,85))
hiv.region <- hiv |> cds2aa() |> string2region(region=region1)
```



```
##(hiv.region |> slot("metadata"))$regionUsed
hiv.region |> regionused()
## use mask and region
hiv.region <- hiv |> cds2aa() |> string2region(mask=mask1, region=region1)
##(hiv.region |> slot("metadata"))$regionUsed
hiv.region |> regionused()
```

---

subString
-----------

---

<i>subString</i>
------------------

---

## Description

This function gets a subsequence from a DNAString, RNAString, AAString, BString, DNAStringSet, RNAStringSet, AAStringSet, BStringSet object from the Biostrings package.

## Usage

```
subString(x, s, e)
```

## Arguments

x	DNAStringSet, RNAString, AAString, BString, DNAStringSet, RNAStringSet, AAStringSet, BStringSet [mandatory]
s	start vector [mandatory]
e	end vector [mandatory]

## Value

subsequence of an Biostrings object

## Author(s)

Kristian K Ullrich

## See Also

[subseq](#)

## Examples

```
## define two cds sequences
cds1 <- Biostrings::DNAString("ATGCAACATTGC")
cds2 <- Biostrings::DNAString("ATG---CATTGC")
cds1.cds2.aln <- c(Biostrings::DNAStringSet(cds1),
  Biostrings::DNAStringSet(cds2))
subString(cds1.cds2.aln, c(1,7), c(3,12))
```

uptriidx

*uptriidx*

---

**Description**

This function returns upper tri index for usage with `pivot_long` reduction.

**Usage**

```
uptriidx(n, diag = FALSE)
```

**Arguments**

n	dimension of initial matrix [mandatory]
diag	indicate if diag should be retained [default: FALSE]

**Value**

list of positions

**Author(s)**

Kristian K Ullrich

**Examples**

```
uptriidx(10)
```

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