

# Package ‘scoup’

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**License** GPL (>= 2)

**Title** Simulate Codons with Darwinian Selection Modelled as an OU Process

**Description** An elaborate molecular evolutionary framework that facilitates straightforward simulation of codon genetic sequences subjected to different degrees and/or patterns of Darwinian selection. The model was built upon the fitness landscape paradigm of Sewall Wright, as popularised by the mutation-selection model of Halpern and Bruno. This enabled realistic evolutionary process of living organisms to be reproduced seamlessly. For example, an Ornstein-Uhlenbeck fitness update algorithm is incorporated herein. Consequently, otherwise complex biological processes, such as the effect of the interplay between genetic drift and mutation on the inference of diversifying selection, may now be investigated with minimal effort. Frequency-dependent and deterministic fitness landscape update techniques are also available.

**Depends** R (>= 4.4), Matrix

**Imports** Biostrings, methods

**Suggests** BiocManager, BiocStyle, bookdown, htmltools, knitr, testthat (>= 3.0.0), yaml

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**Contact** <hassan.t.sadiq@gmail.com>

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**Author** Hassan Sadiq [aut, cre, cph] (ORCID:  
<<https://orcid.org/0000-0003-0192-7134>>)

**Maintainer** Hassan Sadiq <[hassan.t.sadiq@gmail.com](mailto:hassan.t.sadiq@gmail.com)>

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**35**

aaGamma

*Obtain Gamma Distributed Amino Acid Selection Coefficients***Description**

Obtain a vector of values from the Gamma distribution that may be conveniently used as amino acid selection coefficients.

**Usage**

```
aaGamma(vNvS, nsynVar)
```

**Arguments**

vNvS	Ratio of the variance of the coefficients of the non-synonymous codons relative to the variance of the synonymous selection coefficients. Can be assigned a value equal to zero to eliminate synonymous selection.
nsynVar	A non-negative value that corresponds to the variance of the coefficients of the non-synonymous codons. That is, the the between-amino-acid variance.

**Details**

Twenty random observations from a  $\text{Gamma}(1, 1/\sqrt{\text{nsynVar}})$  distribution are sampled as the amino acid selection coefficients. The associated variance of the synonymous coefficients (`synVar`) is calculated as  $\text{nsynVar}/\text{vNvS}$ . If  $\text{nsynVar} < 10^{-12}$ , all the amino acid coefficients will be equal to a single random draw from a  $\text{Gamma}(1, 1/\text{synVar})$  distribution.

**Value**

Returns an object of class `aminoSC`, a vector that at least contains the following components.

`coeffs` A vector of 20 numeric elements that represent the sampled amino acid coefficients. The coefficients are ordered in terms of the 1-letter amino acid IUPAC labels. That is, (A, C, . . . , W, Y).

`synVar` Variance of the selection coefficients of the synonymous codons.

`nsynVar` Variance of the selection coefficients of the non-synonymous codons.

**Author(s)**

Hassan Sadiq

**See Also**

An alternative approach for generating amino acid selection coefficients from a normal distribution `aaGauss`. There is `codonCoeffs` as well, a function designed to convert amino acid to codon selection coefficients.

**Examples**

```
test1 <- aaGamma(0.50, 1e-04)
coeffs(test1)
synVar(test1)
nsynVar(test1)

test2 <- aaGamma(1e-02, 0)
coeffs(test2)
synVar(test2)
nsynVar(test2)
```

aaGauss

*Obtain Gaussian Distributed Amino Acid Selection Coefficients***Description**

Obtain a vector of values from a Normal distribution that may be conveniently used as amino acid selection coefficients.

**Usage**

```
aaGauss(vNvS, nsynVar)
```

**Arguments**

vNvS	Ratio of the variance of the selection coefficients of the non-synonymous codons relative to the variance of the synonymous coefficients. It can be assigned a value equal to zero to eliminate synonymous selection.
nsynVar	A non-negative value that corresponds to the variance of the coefficients among the non-synonymous codons. That is, the between-amino-acid variance.

**Details**

An observation is sampled from a  $\text{Normal}(0, \text{nsynVar})$  distribution independently for each of the 20 amino acid residues. The variance of the synonymous selection coefficients ( $\text{synVar}$ ) is calculated as  $\text{nsynVar}/\text{vNvS}$ . If  $\text{nsynVar}$  is less than  $10^{-12}$ , all the amino acid coefficients will be equal to a single random draw from a  $\text{Normal}(0, \text{synVar})$  distribution.

**Value**

Returns an object of class `aminoSC`, a vector that at least contains the following component.

`coeffs` A vector of 20 numeric elements that represent the sampled amino acid coefficients. The coefficients are ordered in terms of the 1-letter amino acid IUPAC labels. That is, (A, C, . . . , W, Y).

`synVar` Variance of the selection coefficients of the synonymous codons.

`nsynVar` Variance of the selection coefficients of the non-synonymous codons.

**Author(s)**

Hassan Sadiq

**See Also**

An alternative sampling function, [aaGamma](#) is also available. The [codonCoeffs](#) function requires the output from this function (or from [aaGamma](#)).

**Examples**

```
case0 <- aaGauss(0.50, 1e-04)
nsynVar(case0)
synVar(case0)
coeffs(case0)

case1 <- aaGauss(1e-02, 0)
nsynVar(case1)
synVar(case1)
coeffs(case1)
```

alignsim

*Simulate Codon Sequence Alignment***Description**

Obtain an alignment of codon sequences that have been artificially subjected to natural selection, imposed as changes in the fitness landscape along the branches of a symmetric evolutionary tree.

**Usage**

```
alignsim(adaptIn, seqIn, ...)
```

**Arguments**

adaptIn	A list of class discrete, omega or ou.
seqIn	A list of class seqParameters.
...	Arguments to be passed to methods such as 'omega' and 'ou'. See modelIn and filename in details below.

**Details**

This is the primary function of the package. Codon sequence alignment be simulated in terms of the population genetics paradigm. Fitness landscape may be kept static or set to be renewed along the branches of a balanced phylogeny based on any of the three available methods: Ornstein-Uhlenbeck, frequency-dependent or deterministic. Other possible inputs include, modelIn: a hbParameters object. Only applicable when adaptIn is an ou object. filename: a string that specifies the full path of the file that will contain the simulated alignment in NEXUS format. Say it is given as "seq.nex", a file with that name will be printed in the working directory. When set as NA (default), no file will be saved. When set as NULL, a DNAStrngSet object will be returned.

**Value**

A NEXUS format file is saved in the specified (or working) directory. In addition, a scoup object that contains the following entries is returned.

`seqs` A matrix of integers between 1 and 61. The integers are the positions of the simulated codons within an ordered set of nucleotide triplets. The rows are the extant sequences and the columns are alignment sites.

`dNdS` A matrix of the corresponding site-wise (or codon-wise) dN/dS value for all the fitness landscapes utilised in the simulation.

`aInfo` A string of text that contains details of the parameter values that were used during simulation of the codon sequence alignment.

`cseq` A dataframe of the simulated codon sequence alignment.

`seqCOL` A DNASTringSet object with colorful sequences. Only applicable when `filename=NULL`.

**Author(s)**

Hassan Sadiq

**References**

Sadiq, H. et al. (in progress) *scoup: Simulate Codon Sequences with Darwinian Selection Incorporated as an Ornstein-Uhlenbeck Process*.

Pages H, Aboyoun P, Gentleman R, DebRoy S (2024). *Biostrings: Efficient manipulation of biological strings*. R package version 2.72.1, <https://bioconductor.org/packages/Biostrings>.

**See Also**

Complementary functions that are useful for defining the simulation parameters needed to successfully utilise this function. These include, (a.) `discreteInput`, (b.) `hbInput`, (c.) `ouInput`, (d.) `seqDetails` and (d.) `wInput`. See also `DNASTringSet` in the `Biostrings` package.

**Examples**

```
alignEntry <- seqDetails(c(ntaxa=8,nsite=10))

dsim <- alignsim(discreteInput(), alignEntry)
aInfo(dsim)
cseq(dsim)

wsim <- alignsim(wInput(), alignEntry, filename=NULL)
seqCOL(wsim)
dNdS(wsim)

osim <- alignsim(ouInput(), alignEntry, modelIn=hbInput())
osim
```

## Description

A numerical vector of values that are associated with the amino acid selection coefficients.

## Objects from the Class

Objects of this class (aminoSC) can be created by calls of the form `new("aminoSC", coeffs=..., synVar=..., nsynVar=...)`. The two amino acid sampling functions (that is, `aaGamma` and `aaGauss`) that are available in the `scoup` package return objects of this class.

## Slots

`coeffs`: numeric vector returned by the `coeffs` method.

`synVar`: numeric value returned by the `synVar` method.

`nsynVar`: numeric value returned by the `nsynVar` method.

## Methods

**coeffs** signature(`x = "aminoSC"`): vector of twenty values that correspond to the amino acid selection coefficients. The entries are ordered in increasing alphabetical order in terms of the one-letter IUPAC naming structure.

**nsynVar** signature(`x = "aminoSC"`): variance of the probability distribution where the returned amino acid selection coefficients were sampled.

**show** signature(`object = "aminoSC"`): summary of the contents of the aminoSC object including a snippet of the sampled coefficients as well as the values of the `synVar` ( $\sigma_s^2$ ) and the `nsynVar` ( $\sigma_n^2$ ) parameters.

**synVar** signature(`x = "aminoSC"`): variance of the uniform distribution where the synonymous selection coefficients should be sampled.

## Author(s)

Hassan Sadiq

## See Also

`aaGamma`, `aaGauss`

## Examples

```
aasc1 <- aaGamma(1e-10, 1e-04)
coeffs(aasc1)
show(aasc1)
```

---

`biTree`*Generate a Balanced Bifurcating Evolutionary Tree*

---

**Description**

Obtain an evolutionary tree that is such that all its internal nodes have exactly two offspring and all the branches on the tree have equal length.

**Usage**

```
biTree(ntaxa, bLength, terModel=NA)
```

**Arguments**

<code>ntaxa</code>	Number of extant taxa. It must be an integer ( $t$ ) that may be expressed as $2^m$ , where $m$ is itself a positive integer.
<code>bLength</code>	Branch length. All the branches of the generated tree will have the same length that is equal to the specified value.
<code>terModel</code>	A text that would be added as suffix to the extant taxa names. If set as NA (default), no suffix will be added. This is useful for assigning a model to the leaves in branch-specific analyses.

**Value**

`tree` A bifurcating tree in newick format.

**Author(s)**

Hassan Sadiq

**Examples**

```
biTree(16, 0.01, "{foreground}")
```

```
biTree(16, 0.01, "#1")
```

```
biTree(16, 0.01)
```

codonCoeffs

*Transform Amino Acid to Codon Selection Coefficients***Description**

Convert a 20-element vector of amino acid selection coefficients to a 61-element vector of codon selection coefficients.

**Usage**

```
codonCoeffs(s01x22, fixed=NULL)
```

**Arguments**

s01x22	A 22-element vector of class aminoSC.
fixed	A vector of integers between 1 and 20 that indicates which amino acid to assign positive coefficients to, based on the alphabetical order of the 1-letter IUPAC notation. That is, (1=A, 2=C, 3=D, ..., 19=W, 20=Y). All the other amino acids are assigned zero coefficients. This input is only necessary when the specified between-amino-acid variance is less than $10^{-12}$ . The default is NULL.

**Details**

Consider a vector of amino acid selection coefficients, ( $s_x$ :  $s_A$ ,  $s_C$ ,  $s_D$ , ...,  $s_W$ ,  $s_Y$ ) that are subset of s01x22. All the synonymous codons that encode each amino acid are assigned independently sampled values from  $\text{Uniform}(s_x - 3*\text{synVar}; s_x + 3*\text{synVar})$  distribution, where synVar is the synonymous variance and it is also retrieved from s01x22. For amino acids M and W, the corresponding codon coefficient is simply set equal to  $s_M$  and  $s_W$ , respectively. The output from the function is of the order ( $s_{(AAA)}$ ,  $s_{(AAC)}$ ,  $s_{(AAG)}$ , ...,  $s_{(TTC)}$ ,  $s_{(TTG)}$ ,  $s_{(TTT)}$ ), excluding the stop codons.

**Value**

Returns a codonvalues object that will contain the following.

coeffs A 61-element vector of codon selection coefficients ordered alphabetically with respect to the IUPAC nucleotide triplets nomenclature.

**Author(s)**

Hassan Sadiq

**See Also**

[aaGamma](#) and [aaGauss](#), functions useful for generating aminoSC objects.

**Examples**

```
# Example 1:
aasc1 <- aaGamma(1e-10, 1e-04)
ccfs0 <- codonCoeffs(aasc1)
coeffs(ccfs0)

# Example 2:
aasc2 <- aaGauss(1e-10, 1e-04)
ccfs1 <- codonCoeffs(aasc2)
coeffs(ccfs1)

# Example 3:
aasc3 <- aaGauss(1e-03, 0)
ccfs2 <- codonCoeffs(aasc3, c(2,6))
coeffs(ccfs2)
```

---

codonFreq

*Generate Codon Frequencies From Selection Coefficients*


---

**Description**

Obtain codon frequencies from specified selection coefficients in a way that accounts for the magnitude of the coefficients in the real number line.

**Usage**

```
codonFreq(sc01x61)
```

**Arguments**

sc01x61      Vector of sense codon selection coefficients that are ordered alphabetically in terms of the IUPAC nucleotide triplets nomenclature.

**Details**

This conversion to frequencies accommodates the magnitude and signs of the selection coefficients because the frequency for the  $i$ th codon is estimated as:

$$\pi_i = \begin{cases} \log(s_i) / \sum_{j=1}^{61} \log(s_j) & \text{if } s_j > 0 \quad \forall_j, \\ e^{s_i} / \sum_{j=1}^{61} e^{s_j} & \text{otherwise,} \end{cases}$$

where  $s_i \in \text{sc01x61}$  is the selection coefficient of the  $i$ th codon.

**Value**

Returns a codonvalues object that contains the following.

freqs A vector of 61 fractional values that sum to one and represent the frequencies of sense codons that are ordered alphabetically in terms of the IUPAC nucleotide triplets nomenclature.

**Author(s)**

Hassan Sadiq

**See Also**[codonCoeffs](#), a function that produces codon selection coefficients that may be used as an input.**Examples**

```
aaEG1 <- aaGamma(1e-03, 0)
csc01 <- codonCoeffs(aaEG1, 4)
cFq <- codonFreq(csc01)
freqs(cFq)
```

---

`codonMutation`*Construct a Codon Mutation Matrix*

---

**Description**

Build an instantaneous codon mutation matrix from a HKY85 DNA mutation matrix.

**Usage**

```
codonMutation(kappa=4, mrate=0.25)
```

**Arguments**

<code>kappa</code>	Transition to transversion rate between nucleotide pairs. Default value is 4.
<code>mrate</code>	Average rate at which mutation occurs between DNA pairs. Default value is 0.25.

**Details**

The mutation rate is set to zero for pairs of codons that differ by more than one nucleotide position or for two codons that do not differ. For a pair of codons that differ at one nucleotide position, the mutation rate is set to the corresponding mutation rate of the non-matching nucleotide pair. The nucleotide rate is obtained as proposed by Hasegawa, Kishino and Yano (1985).

**Value**

`codonMutate` Codon mutation matrix such that the rows and the columns are arranged with respect to the IUPAC naming structure of nucleotide triplets in alphabetical order.

**Author(s)**

Hassan Sadiq

## References

Hasegawa, M., Kishino, H. and Yano, T. (1985). Dating of the Human-Ape Splitting by a Molecular Clock of Mitochondria DNA, *Journal of Molecular Evolution* **22**: 160-174.

## See Also

Codon substitution matrix generating function [subsMatrix](#) and the fixation matrix generating function [fixMatrix](#).

## Examples

```
cm0 <- codonMutation()
head(cm0)
dim(cm0)
cm1 <- codonMutation(1, 0.032)
tail(cm1)
dim(cm1)
```

---

codonvalues-class      *Codon Frequencies and Selection Coefficients*

---

## Description

A numerical vector of values that correspond to the selection coefficients of the sense codons.

## Objects from the Class

Objects of this class (codonvalues) can be created by calls of the form `new("codonvalues", cdnums=...)`. Two codon-related transformation functions (that is, [codonCoeffs](#) and [codonFreq](#)) that are available in the [scoup](#) package return objects of this class.

## Slots

**cdnums**: vector of 61 values that could correspond to the selection coefficients or the frequencies of the sense codons depending on the method called.

## Methods

**coeffs** signature(`x = "codonvalues"`): vector of 61 values that correspond to the selection coefficients of the sense codons. The entries are ordered in increasing alphabetical order in terms of the IUPAC nucleotide triplets naming structure.

**freqs** signature(`x = "codonvalues"`): vector of 61 values that correspond to the frequencies of the sense codons. The entries are ordered in increasing alphabetical order in terms of the IUPAC nucleotide triplets naming structure.

**show** signature(`object = "codonvalues"`): prints the first six relevant (that is, coefficients or frequencies) codon values.

**Author(s)**

Hassan Sadiq

**See Also**[codonCoeffs](#), [codonFreq](#)**Examples**

```
aasc1 <- aaGamma(1e-10, 1e-04)
ccfs0 <- codonCoeffs(aasc1)
cFq <- codonFreq(ccfs0)
coeffs(ccfs0)
freqs(cFq)
```

---

`discrete-class`*Deterministic Simulation Model Input*

---

**Description**

Creates an object suitable for use when interested in generating an alignment of genetic sequences following the deterministic simulation technique available in the [scoup](#) package.

**Objects from the Class**

Objects can be created by calls of the form `new("discrete", lscape=..., sampler=..., nodeIndex=..., psize=..., t3mdl=..., kappa=..., mrate=...)`. Objects can also be created straightforwardly with the [discreteInput](#) function.

**Slots**

**lscape:** numeric matrix returned by the `lscape` method.

**sampler:** numeric value that can be set as 1 or 2. It indicates the probability distribution where the amino acid selection coefficients should be sampled.

**nodeIndex:** numeric input only relevant for implicit execution of the simulation algorithm. It is of no practical utility to the end-user.

**psize:** numeric value returned by the `effpop` method.

**t3mdl:** character input that may be used to specify suffix for the leaves on the returned phylogeny. It is intended to facilitate inference analyses with external software such as PAML or HyPhy.

**kappa:** numeric value returned by the `kappa` method.

**mrate:** numeric value returned by the `hky85mu` method.

## Methods

- aaSCupdate** signature(parameters="discrete"): background function that is not intended for end-use. It updates the amino acid selection coefficients intermittently during the sequence simulation process.
- alignsim** signature(adaptIn="discrete", seqIn="seqParameters"): primary simulation function available in the [scoup](#) package.
- effpop** signature(x="discrete"): effective population size.
- lscape** signature(x="discrete"): numerical matrix that contains parameters of the fitness landscape. The first row will contain the ratio of the variance of the non-synonymous to synonymous selection coefficients (vNvS) and the second row will contain the variance of the non-synonymous selection coefficients  $\sigma_n^2$ . The number of columns will be equal to the number of internal (bifurcating) stages. A phylogeny with  $2^m$  leaves will have m internal stages.
- sampler** signature(x="discrete"): probability distribution where the amino acid selection coefficients should be obtained.
- show** signature(object="discrete"): prints characteristics of the corresponding genetic sequence, including the population size and the number of extant taxa.
- sitesim** signature(parameters="discrete", nodeLength="numeric"): background function that is not to be used by an end-user. It generates the DNA data at each site independently.
- kappa** signature(x="discrete"): ratio of the rate of the transition to transversion of nucleotides.
- hky85mu** signature(x="discrete"): average nucleotide mutation rate.

## Author(s)

Hassan Sadiq

## See Also

[discreteInput](#), [codonMutation](#), [alignsim](#).

## Examples

```
dtest <- discreteInput()
effpop(dtest)
lscape(dtest)
sampler(dtest)
```

---

discreteInput

*Populate Deterministic Seascape Model Parameters*

---

## Description

Create an object that has a discrete class attribute. It is particularly useful for defining one of the possible inputs of the main simulation function `alignsim`, when interested in simulating codon sequences that evolve with fitness landscapes that change at every internal node.

**Usage**

```
discreteInput(defList=list())
```

**Arguments**

`defList` A list that may contain up to seven named entries. See **Details** for further information.

**Details**

If fully specified, `defList` will be a list with seven elements. The preferred list content include (a.) `p02xnodes`: a 2-row matrix with rows that are properly named as “vNvS” and “nsynVar”. Entries in the “vNvS” row should be the ratio of the variance of the non-synonymous selection coefficients to the variance of the synonymous coefficients. Entries in the “nsynVar” row should be the variance of the non-synonymous selection coefficients. The number of the matrix columns will be used to determine the number of internal nodes to assume for the simulation phylogeny. Each column of the matrix will be used to determine the parameters of the sampling distribution where the coefficient updates will be sampled at every node. Default is a  $2 \times 4$  matrix, wherein all the values in the “vNvS” row are equal to 1 and all the entries in the “nsynVar” row are equal to  $10^{-5}$ . (b.) `technique`: a binary integer that could be 1 for Gaussian or 2 for Gamma (default) distribution. It informs about the probability distribution to be used for updating the coefficients. (c.) `pSize`: (default = 1000) is the effective population size. (d.) `nodeIndex`: a nuisance input that is best left unspecified. It is updated within the `alignsim` operation. (e.) `leafModel`: a text that may be used to suffix the names of the terminal nodes (default = NA). (f.) `kappa`: transition to transversion rate between nucleotide pairs (default = 4). (g.) `mrRate`: average rate at which mutation occurs between DNA pairs (default = 0.25). Note that this function was not designed to be used in isolation. Its purpose is to complement the `alignsim` simulation function.

**Value**

A discrete object that contains the following.

`lscap` Matrix containing landscape parameters.

`sampler` Name of the sampling distribution used for selection coefficient updates.

`effpop` Effective population size.

`kappa` Transition to transversion rate between DNA pairs.

`hkyMu` Average DNA mutation rate.

**Author(s)**

Hassan Sadiq

**See Also**

[alignsim](#), [aaGamma](#), [aaGauss](#), [biTree](#), [codonMutation](#).

**Examples**

```
dtest <- discreteInput()
effpop(dtest)
lscape(dtest)
sampler(dtest)
```

---

dndsCalculator      *Estimate dN/dS Value Analytically*

---

**Description**

Obtain an analytical estimate for the ratio of non-synonymous to synonymous rate (dN/dS) of codon substitution.

**Usage**

```
dndsCalculator(pi01x61, q61x61, kappa, mrate)
```

**Arguments**

pi01x61	Vector of sense codon frequencies that are ordered alphabetically with respect to nucleotide triplets according to IUPAC nomenclature.
q61x61	A $61 \times 61$ matrix of sense codon instantaneous substitution rates, where the rows and the columns are ordered in terms of IUPAC-lettered nucleotide triplets.
kappa	Transition to transversion rate between nucleotide pairs suitable for the HKY85 DNA mutation model.
mrate	Average rate at which mutation occurs between DNA pairs suitable for the HKY85 DNA mutation model.

**Details**

The returned dN/dS estimate is obtained from the ratio of the following expressions.

$$dN = \frac{\sum_j \sum_{i \neq j} \pi_i A_{ij} I_N}{\sum_j \sum_{i \neq j} \pi_i \mu_{ij} I_N}, \quad dS = \frac{\sum_j \sum_{i \neq j} \pi_i A_{ij} I_S}{\sum_j \sum_{i \neq j} \pi_i \mu_{ij} I_S},$$

where  $A$  and  $\pi$  are the input codon frequency vector (pi01x61) and the instantaneous substitution rate matrix (q61x61), respectively. The notation  $\mu$  denotes codon mutation matrix (embedded as a function of the HKY85 nucleotide model) while  $I_S$  and  $I_N$  are Boolean matrices with ones at positions occupied by synonymous and non-synonymous codons, respectively.

**Value**

dnds An estimate for the corresponding dN/dS

**Author(s)**

Hassan Sadiq

## References

Spielman, S. J. and Wilke, C. O. (2015). The Relationship between dN/dS and Scaled Selection Coefficients, *Molecular Biology and Evolution* **32**(4): 1097-1108.

## See Also

Codon frequencies generating function [codonFreq](#), instantaneous substitution rate matrix function [subsMatrix](#) and the nucleotide to codon mutation matrix converter [codonMutation](#).

## Examples

```
aasc <- aaGauss(0.5, 1e-03)
codonsc <- codonCoeffs(aasc)
piFreq <- codonFreq(codonsc)
smat <- subsMatrix(codonsc, 1000, 4, 0.25)
dndsCalculator(piFreq, smat, 4, 0.25)
```

---

 fixMatrix

---

*Construct Fixation Rate Matrix*


---

## Description

Construct a  $61 \times 61$  matrix that contains the rate at which a mutant (column) codon gets fixed at a position previously occupied by a resident (row) codon for all the pairwise combinations of the 61 sense codons.

## Usage

```
fixMatrix(sc01x61, effpopsize)
```

## Arguments

`sc01x61` A vector of sense codon selection coefficients that are ordered alphabetically in terms of the IUPAC nucleotide triplets nomenclature.

`effpopsize` Effective population size.

## Details

If the additive fitness of a mutant codon ( $j$ ) relative to a resident codon ( $i$ ) is given by  $s_{ij} = (s_j - s_i)$ , then the rate at which codon  $j$  gets fixed in a codon position occupied by codon  $i$  can be expressed as follows.

$$f_{ij} = \begin{cases} \frac{1 - e^{-2s_{ij}}}{1 - e^{-2N_e s_{ij}}} & \text{if codons } i \text{ and } j \text{ differs only by one nucleotide,} \\ 0 & \text{otherwise,} \end{cases}$$

where  $s_i, s_j \in \text{sc01x61}$  and  $N_e$  (effpopsize) is the effective population size. If  $s_i - s_j = 0$ , then  $f_{ij} = 1$ .

**Value**

fixMtx A  $61 \times 61$  matrix of the fixation rates of the sense codons. The rows and columns are ordered alphabetically in terms of the IUPAC nucleotide triplets nomenclature. That is, AAA, AAC, AAG, ..., TTG, TTT.

**Author(s)**

Hassan Sadiq

**References**

Bershtein, S. and Serohijos, A. W. R. and Shakhnovich, E. I. (2017), Bridging the Physical Scales in Evolutionary Biology: From Protein Sequence Space to Fitness of Organisms and Populations, *Current Opinion in Structural Biology* **42**: 31-40.

Halpern, A. L. and Bruno, W. J. (1998). Evolutionary Distances for Protein-Coding Sequences: Modelling Site-Specific Residue Frequencies, *Molecular Biology and Evolution* **15**(7): 910-917.

McCandlish, D. M. (2011), Visualizing Fitness Landscapes, *Evolution* **65**(6): 1544-1558.

**See Also**

[codonCoeffs](#), [aaGamma](#), [aaGauss](#).

**Examples**

```
aasc <- aaGauss(0.5, 1e-03)
codonsc <- codonCoeffs(aasc)
fixMatrix(codonsc, 1000)
```

---

hbInput

*Generate Halpern-Bruno Substitution Model Parameters*

---

**Description**

Create a hbParameters object that contains values necessary to construct a Halpern-Bruno mutation-selection codon substitution model.

**Usage**

```
hbInput(hbVector=0)
```

**Arguments**

hbVector A named vector that provides values of the parameters necessary to successfully create a codon substitution model for simulation of genetic sequences. See **Details** for further information.

## Details

When fully specified, `hbVector` will be a six-element named vector. That is, `hbVector=c(Ne, meth, vNvS, nsynVar, kappa, mrate)`. `Ne` is an integer that represents the effective population size (default = 1000). `meth` is a binary integer that indicates the probability distribution from where the initial selection coefficients must be sampled. It can be 1 for a truncated Gaussian or 2 for a Gamma (default) distribution. `vNvS` is the ratio of the variance of the non-synonymous to synonymous selection coefficients. Default value is 1. The user can set the variance of the non-synonymous selection coefficients with `nsynVar` (default is  $10^{-5}$ ). `kappa` is the transition to transversion rate between nucleotide pairs (default = 4). `mrate` is the average rate at which mutation occurs between DNA pairs (default = 0.25). This function was not intended for independent use. Rather as a complement to the `alignsim` simulation function.

## Value

A `hbParameters` object that contains the following.

`psize` Effective population size.

`vNvS` Ratio of the variance of the non-synonymous to the synonymous selection coefficients.

`nsVar` Variance of the non-synonymous selection coefficients.

`sampler` Probability distribution for generating the initial selection coefficients.

`kappa`: Nucleotide transition to transversion rate ratio.

`hky85mu`: Mean nucleotide mutation rate.

## Author(s)

Hassan Sadiq

## See Also

Selection coefficients sampling functions, [aaGamma](#) and [aaGauss](#), codon mutation matrix constructor [codonMutation](#) as well as the primary simulation function [alignsim](#).

## Examples

```
h0 <- hbInput()
vNvS(h0)
h0

h1 <- hbInput(c(Ne=100, meth=2, vNvS=1e-08, nsynVar=1e-08))
sampler(h1)
```

---

hbParameters-class      *Halpern-Bruno Mutation-Selection Evolutionary Model Input*

---

### Description

Creates an object of class (hbParameters) that contains the principal entries necessary to construct a Halpern-Bruno mutation-selection evolutionary model.

### Objects from the Class

Objects of this class can be created by calls of the form `new("hbParameters", psize=??, vNvS=??, sampler=??, nsynVar=??, kappa=??, mrate=??, words=??)`. The object is an important input of the `alignsim` function when interested in simulating sequences with respect to the Ornstein-Uhlenbeck framework.

### Slots

**psize**: numeric value returned by the `effpop` method.  
**vNvS**: numeric value returned by the `vNvS` method.  
**sampler**: numeric value that can be set as 1 or 2. It indicates the probability distribution where the amino acid selection coefficients should be sampled.  
**nsynVar**: numeric value returned by the `nsynVar` method.  
**kappa**: numeric value returned by the `kappa` method.  
**mrate**: numeric value returned by the `hky85mu` method.  
**words**: comments about the specified Halpern-Bruno model parameters. It is a character format string that is eventually added to the simulated sequence for reference.

### Methods

**effpop** signature(`x = "hbParameters"`): effective population size.  
**nsynVar** signature(`x = "hbParameters"`): variance of the non-synonymous selection coefficients  $\sigma_n^2$ .  
**sampler** signature(`x = "hbParameters"`): probability distribution where the amino acid selection coefficients should be randomly retrieved.  
**show** signature(`object = "hbParameters"`): prints characteristics of the defined model including the population size, the `vNvS` and the  $\sigma_n^2$ .  
**vNvS** signature(`x = "hbParameters"`): ratio of the variance of the non-synonymous to synonymous selection coefficients.  
**kappa** signature(`x = "hbParameters"`): ratio of the rate of the transition to transversion of nucleotides.  
**hky85mu** signature(`x = "hbParameters"`): average nucleotide mutation rate.

### Author(s)

Hassan Sadiq

**See Also**

[alignsim](#), [hbInput](#)

**Examples**

```
h1 <- hbInput(c(Ne=100, meth=2, vNvS=1e-08, nsynVar=1e-08))
sampler(h1)
h1
```

---

omega-class

*Frequency-Dependent Evolutionary Model Specification*

---

**Description**

Creates an object that contains the inputs that are necessary to define a frequency-dependent evolutionary algorithm and subsequently simulate genetic sequence alignment based on the framework using the [alignsim](#) function in the [scoup](#) package.

**Objects from the Class**

Objects of this class can be created by calls of the form `new("omega", nsynVar=..., psize=..., sampler=..., aaPlus=..., vNvS=..., kappa=..., mrate=...)`. The object is an important input of the [alignsim](#) function when interested in simulating sequences with respect to the frequency-dependent framework. The [wInput](#) function in the [scoup](#) package returns this kind of object.

**Slots**

**nsynVar**: numeric value returned by the `nsynVar` method.

**psize**: numeric value returned by the `effpop` method.

**sampler**: numeric value that can be set as 1 or 2. It indicates the probability distribution where the amino acid selection coefficients should be sampled.

**aaPlus**: indices of the amino acids (after the corresponding one-letter IUPAC names are arranged in increasing alphabetical order) that should be assigned non-zero `vNvS`.

**vNvS**: numeric value returned by the `vNvS` method.

**kappa**: numeric value returned by the `kappa` method.

**mrate**: numeric value returned by the `hky85mu` method.

**Methods**

**alignsim** signature(`adaptIn="omega", seqIn="seqParameters"`): primary simulation function availed in the [scoup](#) package.

**effpop** signature(`x="omega"`): effective population size.

**lscape** signature(`x="omega"`): IUPAC one-letter notations of the amino acids that were assigned non-zero `vNvS` values.

**nsynVar** signature(x="omega"): variance of the non-synonymous selection coefficients  $\sigma_n^2$ .

**sampler** signature(x="omega"): probability distribution where the amino acid selection coefficients should be randomly retrieved.

**show** signature(object="omega"): prints the vNvS and the count of amino acids that had positive vNvS values.

**sitesim** signature(parameters="omega", nodeLength="numeric"): background function that is not available to end-user. It generates the DNA data at each site independently.

**vNvS** signature(x="omega"): ratio of the variance of the non-synonymous to synonymous selection coefficients.

**kappa** signature(x="omega"): ratio of the rate of the transition to transversion of nucleotides.

**hky85mu** signature(x="omega"): average nucleotide mutation rate.

### Author(s)

Hassan Sadiq

### See Also

[alignsim](#), [wInput](#)

### Examples

```
w1 <- wInput(list(aaPlus=c(4,2,11), nsynVar=10))
lscape(w1)
w1
```

---

ou-class

*Ornstein-Uhlenbeck Stochastic Simulation Model Object*

---

### Description

Contains the inputs that are necessary to define an Ornstein-Uhlenbeck (OU) evolutionary process.

### Objects from the Class

Class ou objects can be created by calls of the form `new("ou", var=??, theta=??, mu=??, words=??)`. This type of object is returned by the `ouInput` function in the `scoup` package. It is an important input of the `alignsim` function when interested in codon sequences that evolved following the OU framework.

### Slots

**var**: numeric value returned by the `asymVar` method.

**theta**: numeric value returned by the `reversion` method.

**mu**: numeric value returned by the `asymMean` method.

**words**: descriptive text that contains details of the set parameter values. Useful as reference comments to be included in the generated sequence alignment.

## Methods

**aaSCupdate** signature(parameters = "ou"): background function that is not intended for end-use. It updates the amino acid selection coefficients intermittently during the sequence simulation process.

**alignsim** signature(adaptIn="ou", seqIn="seqParameters"): primary simulation function available in the [scoup](#) package.

**asymMean** signature(x="ou"): asymptotic mean,  $\mu$ , of the OU evolutionary algorithm.

**asymVar** signature(x="ou"): asymptotic variance,  $\Sigma^2$ , of the OU evolutionary framework.

**reversion** signature(x="ou"): reversion parameter,  $\theta$ , that acts as a selective pull in the OU process.

**show** signature(object="ou"): prints the values of  $\Sigma^2$ ,  $\mu$  and  $\theta$ .

**sitesim** signature(parameters="ou", nodeLength="numeric"): background function that is not to be used by an end-user. It generates the DNA data at each site independently.

## Author(s)

Hassan Sadiq

## See Also

[alignsim](#), [ouInput](#).

## Examples

```
o1 <- ouInput( c(eVar=1e-02, Theta=10))
asymMean(o1)
asymVar(o1)
```

---

ouEvolve

*Simulate the Trend of an Ornstein-Uhlenbeck Process*

---

## Description

Simulate the next state of an Ornstein-Uhlenbeck (OU) process for a given value.

## Usage

```
ouEvolve(xInit, deltaT, sysTheta, asymptoteVar, asymptoteMew)
```

## Arguments

xInit	Starting point of the OU process.
deltaT	Jump size.
sysTheta	Reversion rate.
asymptoteVar	Asymptotic variance.
asymptoteMew	Asymptotic mean.

**Details**

The state at time  $k$  (that is,  $x_{t_k}$ ) of a process that evolves according to an OU algorithm can be expressed as an observation from a Gaussian distribution as follows.

$$x_{t_k} \sim \text{Normal}\left(\mu + (x_{t_{k-1}} - \mu) e^{-\theta \Delta t}; \frac{\sigma^2}{2\theta} (1 - e^{-2\theta \Delta t})\right)$$

Observe that when time interval (deltaT)  $\Delta t = t_k - t_{k-1}$  approaches infinity, the asymptotic mean (asymptoteMew) and the asymptotic variance (asymptoteVar) of the distribution are  $\mu$  and  $\Sigma^2 = \sigma^2/2\theta$  respectively, where  $\theta$  is the reversion rate.

**Value**

xnew A scalar that represents the updated state of the OU process.

**Author(s)**

Hassan Sadiq

**References**

Uhlenbeck, G. E. and Ornstein, L. S. (1930), On the Theory of the Brownian Motion, *Physical Review* **36**: 823-841.

**Examples**

```
x0 <- 0.015
xvec <- c()
xvec[1] <- x0
for(k in seq(2,100)){
  xstate <- ouEvolve(x0, 0.002, 10, 0.001, 0)
  xvec[k] <- xstate
  x0 <- xstate
}
plot(xvec, type="l")
```

---

ouInput

---

*Populate Parameters of the Ornstein-Uhlenbeck Algorithm*


---

**Description**

Create an ou object that will contain the parameters necessary to simulate a codon sequence alignment that evolves according to an Ornstein-Uhlenbeck (OU) process.

**Usage**

```
ouInput(ouVector=0)
```

## Arguments

`ouVector` A vector that contains carefully named elements. Each element represents a parameter in an OU model. See **Details** for more information.

## Details

In its full form, `ouVector` is a three-element vector. Its contents each represents part of the parameters required to implement an OU process. The vector contents include, `eMean`, `eVar` and `Theta`. Input `eMean` is the asymptotic mean ( $\mu$ ) and zero is its default value. `eVar` denotes the asymptotic variance ( $\Sigma^2$ ). It has a 0.01 default value. `Theta` (default = 0.01) represents the reversion rate ( $\theta$ ). This function was aimed as a complement to `alignsim`, not for use in isolation.

## Value

An `ou` object that contains the following.

`asymMean` Asymptotic mean of the OU process.

`asymVar` Asymptotic variance of the OU process.

`reversion` Reversion rate of the OU process.

## Author(s)

Hassan Sadiq

## References

Uhlenbeck, G. E. and Ornstein, L. S. (1930), On the Theory of the Brownian Motion, *Physical Review* **36**: 823-841.

## See Also

The Ornstein-Uhlenbeck state generating function `ouEvolve` and the `alignsim` simulation function.

## Examples

```
o0 <- ouInput()
reversion(o0)
o0

o1 <- ouInput( c(eVar=1e-02, Theta=10))
asymMean(o1)
asymVar(o1)
```

---

scoup

*Simulate Codons with Darwinian Selection Added as an OU Process*

---

## Description

The primary objective of this package is to facilitate more rigorous understanding of phylogenetic inferences of natural selection from codon sequences. Concepts from the Halpern-Bruno mutation-selection model and the Ornstein-Uhlenbeck stochastic process were creatively fused such that the end-product is a novelty with respect to computational genetic simulation. Users are able to seamlessly adjust the model parameters to mimic complex evolutionary procedures that may have been otherwise infeasible. For example, it is possible to explicitly interrogate the concepts of static and changing fitness landscapes with regards to Darwinian natural selection in the context of DNA sequences. The ratio of the variance in selection coefficients,  $vN/vS$ , is presented as a new measure of the net selection effect acting on genetic sequences. This package could be very useful for generating more appropriate test data sets for validation of likelihood-based ( $\omega$ ) codon models of evolution.

## Details

Three simulation algorithms are available. (a.) The Ornstein-Uhlenbeck simulation technique. This technique was built around the stochastic Brownian motion evolutionary paradigm. Explicit parameters exist to control the extent of drift, mutation and selection that are acting on the biological system. (b.) The frequency-dependent approach where every substitution event that corresponds to a shift in the fitness landscape. (c.) The deterministic method where the model parameters may be fixed for each internal node of the phylogeny.

## Author(s)

Hassan Sadiq

## References

Halpern, A. L. and Bruno, W. J. (1998). Evolutionary Distances for Protein-Coding Sequences: Modelling Site-Specific Residue Frequencies, *Molecular Biology and Evolution* **15**(7): 910-917.

Sadiq, H. et al. (in progress) scoup: *Simulate Codon Sequences with Darwinian Selection Incorporated as an Ornstein-Uhlenbeck Process*.

Uhlenbeck, G. E. and Ornstein, L. S. (1930), On the Theory of the Brownian Motion, *Physical Review* **36**: 823-841.

---

`scoup-class`*Output from the `scoup::alignsim` Genetic Sequence Simulator*

---

### Description

Stores the results from a successful implementation of any of the simulation algorithms available in the `scoup` package.

### Objects from the Class

Objects can be created by calls of the form `new("scoup", seqs=..., DNDS=..., aInfo=..., cseq=..., seqCOL=...)`.

### Slots

`seqs`: numerical matrix returned by the `seqs` method.

`DNDS`: numerical matrix returned by the `dNds` method.

`aInfo`: character phrase returned by the `aInfo` method.

`cseq`: data frame returned by the `cseq` method.

`seqCOL`: `DNAStrngSet` object returned by the `seqCOL` method.

### Methods

**aInfo** `signature(x="scoup")`: details of the parameters used to execute the simulation process. This includes, the branch length of all the nodes of the balanced phylogeny, the name of the probability distribution where the amino acid selection coefficients were sampled as well as the (`vNVS` & non-synonymous selection) parameter set used at each internal node ("generation") stage.

**cseq** `signature(x="scoup")`: data frame that contains the simulated genetic sequence.

**dNds** `signature(x="scoup")`: analytical estimates of the magnitude of the imposed selection effect. It is calculated node-wise as the ratio of the non-synonymous to synonymous substitutions.

**seqCOL** `signature(x="scoup")`: a `DNAStrngSet` version of the simulated genetic sequence alignment.

**seqs** `signature(x="scoup")`: expression of the simulated sequence as a matrix of integers, where each entry corresponds to the position of the associated codon in an an alphabetically increasing ordered set of the DNA triplets of the 61 sense codons.

**show** `signature(object="scoup")`: sentence that contains the number of codon sites and the number of extant taxa that make up the simulated genetic sequence alignment.

### Author(s)

Hassan Sadiq

**See Also**

Simulation function [alignsim](#).

**Examples**

```
alignEntry <- seqDetails(c(ntaxa=8,nsite=10))
dsim <- alignsim(discreteInput(), alignEntry)
aInfo(dsim)
cseq(dsim)
```

---

seqDetails

*Populate Sequence Alignment Information*


---

**Description**

Create a seqParameters object that contains features of the sequence that needs to be simulated.

**Usage**

```
seqDetails(seqVector=0)
```

**Arguments**

seqVector      A named vector that provides characteristics of the intended sequence alignment. See **Details** for further information.

**Details**

If fully specified, seqVector should be a four-element named vector. That is, seqVector = c(ntaxa, nsite, blength, terModel). ntaxa should be of the form  $2^m$ , where m is an integer. It corresponds to the number of extant taxa, default is 64. nsite, also an integer (default = 250), is the number of codon sites. blength is the length of each branch on the balanced symmetric tree that will be used for the simulation (default = 0.10). terModel is a text that will be added as a suffix to the leaf names on the phylogeny (default = NA). It is meant to facilitate assignment of models to the terminal nodes for branch-wise selection analyses. The purpose of this function is to complement alignsim.

**Value**

A seqParameters object that contains the following.

sites    Number of alignment sites.

ntaxa    Number of extant taxa.

nodes    Number of internal (bifurcating) stages on the evolutionary tree. A tree with  $2^m$  leaves will have m internal stages.

branchL    Length of the branches on the phylogeny.

phylogeny    Evolutionary tree in newick format.

details    Text that describes the evolutionary tree.

**Author(s)**

Hassan Sadiq

**See Also**

The codon sequence simulator [alignsim](#) and [biTree](#), the balanced evolutionary tree generator.

**Examples**

```
t0 <- seqDetails()
sites(t0)

t1 <- seqDetails(c(ntaxa=16, nsite=10, blength=0.20, terModel=" #1"))
details(t1)
```

---

seqParameters-class     *Simulated Codon Sequence Structure*

---

**Description**

A S4 object that contains information about the structure (that is, size, length, etc) of the simulated genetic sequence.

**Objects from the Class**

This is the object class of the output from the [seqDetails](#) function. It is a core input of the [alignsim](#) function. Objects can be created by calls of the form `new("seqParameters", sites=??, taxa=??, nodes=??, branchL=??, phylogeny=??, details=??)`.

**Slots**

**sites:** numeric value returned by the `sites` method.  
**taxa:** numeric value returned by the `taxa` method.  
**nodes:** numeric value returned by the `nodes` method.  
**branchL:** numeric value returned by the `branchL` method.  
**phylogeny:** character returned by the `phylogeny` method.  
**details:** character returned by the `details` method.

**Methods**

**alignsim** signature(adaptIn="discrete", seqIn="seqParameters"): an option of the primary simulation function in the [scoup](#) package. This setting activates the deterministic framework.

**alignsim** signature(adaptIn="omega", seqIn="seqParameters"): an option of the primary simulation function in the [scoup](#) package. This setting activates the frequency-dependent framework.

**alignsim** signature(adaptIn="ou", seqIn="seqParameters"): an option of the primary simulation function in the [scoup](#) package. This setting activates the Ornstein-Uhlenbeck framework.

**branchL** signature(xo="seqParameters"): branch length. Only balanced evolutionary trees are permitted. Therefore, all tree nodes have the same length.

**details** signature(xo="seqParameters"): note that contain the important parameter settings that generated the corresponding data. It is added as comments to the saved output.

**nodes** signature(xo="seqParameters"): number of internal (bifurcating) stages of the balanced phylogeny. An evolutionary tree with  $2^m$  extant taxa will have  $m$  nodes.

**phylogeny** signature(xo="seqParameters"): newick string of the phylogeny utilised for the codon sequence simulation.

**show** signature(object="seqParameters"): summary descriptive details about the corresponding sequence alignment.

**sites** signature(xo="seqParameters"): number of codon sites that make up the sequence.

**taxa** signature(xo="seqParameters"): number of leaves on the phylogeny.

### Author(s)

Hassan Sadiq

### See Also

Codon sequence simulator [alignsim](#) and the sequence preparatory function [seqDetails](#).

### Examples

```
t0 <- seqDetails()
sites(t0)
```

---

seqWriter

*Write Numeric Codon Alignment to a NEXUS File*

---

### Description

Save numeric codon alignment matrix to a file in NEXUS format. It is particularly useful when data with site partitions is required.

### Usage

```
seqWriter(alignmentMatrix, treeInfo=NA, addText="", fileTag=NULL)
```

**Arguments**

alignmentMatrix	A numerical matrix of codon sequence alignment that is similar to the seqs matrix from the output of alignsim. The rows of the matrix should each correspond to an extant taxa and the columns should be the alignments sites. The entries of the matrix should be integers between 1 and 61 and they will be decoded in terms of the ordered IUPAC sense codon triplets. That is, 1=AAA, 2=AAC, 3=AAG, 4=AAT, 5=ACA, ..., 57=TGT, 58=TTA, 59=TTC, 60=TTG, TTT.
treeInfo	Phylogeny to be printed with the sequence. If unspecified (default = NA) a balanced phylogeny with branch length = 0.10 and number of extant taxa set as the number of rows of the input alignmentMatrix will be used.
addText	A string of comments to be printed with the alignment (default = "").
fileTag	Full path to where the output file should be printed. It should be a string (default = NULL). If not provided, the NEXUS file returned will be saved as cranrSeqs.nex in a temporary directory.

**Value**

NULL A NEXUS file with codon alignment printed therein will be saved in a temporary (or specified) directory.

**Author(s)**

Hassan Sadiq

**See Also**

Simulation function [alignsim](#).

**Examples**

```
sqAlign <- alignsim(ouInput(), seqDetails(), hbInput(), NA)
seqWriter(seqs(sqAlign))
```

---

subsMatrix

*Build Mutation-Selection Codon Substitution Matrix*


---

**Description**

Construct an instantaneous codon substitution matrix based on the mutation-selection framework.

**Usage**

```
subsMatrix(sc01x61, effpopsiize, kappa, mrate)
```

**Arguments**

sc01x61	Vector of selection coefficients associated with the 61 sense codons, ordered alphabetically according to the nucleotide triplets and the IUPAC naming structure.
effpopsize	Effective population size.
kappa	Transition to transversion rate between nucleotide pairs suitable for the HKY85 DNA mutation model.
mrate	Average rate at which mutation occurs between DNA pairs suitable for the HKY85 DNA mutation model.

**Details**

Given an arbitrary scaling constant ( $k$ ), codon fixation rates ( $f_{ij}$ ) and mutation rates ( $m_{ij}$ ), the instantaneous rate by which codon  $i$  is substituted by another codon  $j$  may be expressed as follows.

$$q_{ij} = \begin{cases} k \times m_{ij} \times f_{ij} & \text{if } i \text{ and } j \text{ differs by only one nucleotide,} \\ 0 & \text{if } i \text{ and } j \text{ differs by more than one nucleotide,} \end{cases}$$

and  $q_{ii} = -\sum_j q_{ij}$ . The corresponding HKY85 nucleotide mutation matrix from which  $m_{ij}$  is obtained is such that the transition to transversion rate,  $\kappa = \text{kappa}$ , the average rate,  $\mu = \text{mrate}$  and the equilibrium frequencies are equal.

**Value**

mainMatrix Instantaneous codon substitution matrix such that the rows and the columns are arranged with respect to the IUPAC naming structure of nucleotide triplets in alphabetical order.

**Author(s)**

Hassan Sadiq

**References**

- Halpern, A. L. and Bruno, W. J. (1998). Evolutionary Distances for Protein-Coding Sequences: Modelling Site-Specific Residue Frequencies, *Molecular Biology and Evolution* **15**(7): 910-917.
- Hasegawa, M., Kishino, H. and Yano, T. (1985). Dating of the Human-Ape Splitting by a Molecular Clock of Mitochondria DNA, *Journal of Molecular Evolution* **22**: 160-174.

**See Also**

Selection coefficients conversion function [codonCoeffs](#) and fixation matrix generating function [fixMatrix](#).

**Examples**

```
aacoeffs <- aaGauss(1e-03, 0)
codonsc <- codonCoeffs(aacoeffs)
subsMatrix(codonsc, 1000, 4, 0.25)
```

---

wInput

---

*Populate Frequency-Dependent Simulation Model Parameters*


---

### Description

Create an omega object. The utility is for defining the parameters that are necessary for simulating codon sequences that mimic the evolutionary process described by the frequency-dependent models.

### Usage

```
wInput(wList=list())
```

### Arguments

**wList** A list that may contain up to seven named entries. See **Details** for further information.

### Details

In its full form, **wList** will contain seven named elements. The elements include (a.) **pSize**: an integer that represents the effective population size (default = 1000). (b.) **vNvS**: a numerical value that corresponds to the ratio of the variance of the non-synonymous to the synonymous selection coefficients (default = 1). (c.) **aaPlus**: its default is a vector of integers between 1 and 20, inclusive. It gives the indices, if the one-letter IUPAC amino acid notations were ordered alphabetically, of the residues that should be assigned non-zero coefficient variances. (d.) **technique**: it informs of the preferred probability distribution where the selection coefficients should be sampled. It could be set as 1 for Gaussian or 2 for Gamma (default) distribution. (e.) **nsynVar**: variance of the non-synonymous selection coefficients. This is a complementary function to **alignsim**. (f.) **kappa**: transition to transversion rate between nucleotide pairs (default = 4). (g.) **mrRate**: average rate at which mutation occurs between DNA pairs (default = 0.25).

### Value

An omega object that contains the following.

**nsynVar** Variance of the non-synonymous selection coefficients.

**technique** Probability density function for sampling the amino acid selection coefficients.

**aaPlus** Indices of the amino acids to be assigned non-zero coefficient variance values.

**vNvS** Ratio of the variance of the non-synonymous to the synonymous selection coefficients.

**pSize** Effective population size.

**kappa** Nucleotide transition to transversion ratio.

**mrRate** Average nucleotide mutation rate.

### Author(s)

Hassan Sadiq

## References

Goldman, N. and Yang, Z. (1994), A Codon-Based Model of Nucleotide Substitution for Protein-Coding DNA Sequences, *Molecular Biology and Evolution* **11**(5): 725-736.

Muse, S. V. and Gaut, B. S. (1994), A Likelihood Approach for Comparing Synonymous and Nonsynonymous Nucleotide Substitution Rates, with Application to the Chloroplast Genome, *Molecular Biology and Evolution* **11**(5): 715-724.

## See Also

Sequence simulation function [alignsim](#) as well as selection coefficient conversion functions [aaGamma](#) and [aaGauss](#).

## Examples

```
w0 <- wInput()
vNvS(w0)
w0

w1 <- wInput(list(aaPlus=c(4,2,11), nsynVar=10))
lscape(w1)
w1
```

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