Package: SADEG (via r-universe)

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Type Package

Title Stability Analysis in Differentially Expressed Genes

Version 1.0.0

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Description We analyzed the nucleotide composition of genes with a special emphasis on stability of DNA sequences. Besides, in a variety of different organisms unequal use of synonymous codons, or codon usage bias, occurs which also show variation among genes in the same genome. Seemingly, codon usage bias is affected by both selective constraints and mutation bias which allows and enables us to examine and detect changes in these two evolutionary forces between genomes or along one genome. Therefore, we determined the codon adaptation index (CAI), effective number of codons (ENC) and codon usage analysis with calculation of the relative synonymous codon usage (RSCU), and subsequently predicted the translation efficiency and accuracy through GC-rich codon usages. Furthermore, we estimated the relative stability of the DNA sequence following calculation of the average free energy (Delta G) and Dimer base-stacking energy level.

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LazyData true

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`SADEG.ACGT` *SADEG.ACGT*

Description

Number and frequencies of occurrence of each nucleotide.

Usage

```
SADEG.ACGT(Nucleotide_Sequence)
```

Arguments

`Nucleotide_Sequence`	Nucleotide Sequence

Details

The Number of occurrence of each nucleotide.(A, T, C, and G). Furtheremore, The frequencies of occurrence of each nucleotide. (A

Value

Table which first row represent number of each nucleotide and row 2 represent percentage of each nucleotide.

Author(s)

Babak Khorsand

Examples

```
SADEG.ACGT("actagtcacgatcag")
```

`SADEG.CAI` *SADEG.CAI*

Description

Codon Adaption Index

Usage

```
SADEG.CAI(Nucleotide_Sequence)
```

Arguments

`Nucleotide_Sequence`	Nucleotide Sequence

Details

Geometric mean of the RSCU values presented as relative adaptiveness value (w), The CAI for a gene is then defined as the geometric mean of w values for codons in that gene excluding methionine, tryptophan, and stop codons.

Value

CAI

Author(s)

Babak Khorsand

Examples

```
SADEG.CAI(Nucleotide_Sequence="atggctgctgcagcggccagtcacgatcagaggtaagttgtcgcagcatgt")
```

`SADEG.CodonUsage` *SADEG.CodonUsage*

Description

Frequency of occurrence of each Amino acids codons.

Usage

```
SADEG.CodonUsage(Nucleotide_Sequence)
```

Arguments

`Nucleotide_Sequence`	Nucleotide Sequence

Details

Frequency of occurrence of each Amino acids codons.

Value

CodonUsage

Author(s)

Babak Khorsand

Examples

```
SADEG.CodonUsage(Nucleotide_Sequence="atggctgcagcggccagtcacgatcagaggtaagttgtc")
```

`SADEG.Dimer` *SADEG.Dimer*

Description

Number and frequency of each Dimers

Usage

```
SADEG.Dimer(Nucleotide_Sequence)
```

Arguments

`Nucleotide_Sequence`	Nucleotide Sequence

Details

Count the number of each Dimers and calculate frequencies of them.

Value

Table which first row represent number of each Dimers and row 2 represent percentage of each Dimers.

Author(s)

Babak Khorsand

Examples

```
SADEG.Dimer("actagtcacgatcag")
```

`SADEG.DimerStackingEnergy`

SADEG.DimerStackingEnergy

Description

Sum of Stacking energy of each Dimers.

Usage

```
SADEG.DimerStackingEnergy(Nucleotide_Sequence)
```

Arguments

`Nucleotide_Sequence`	Nucleotide Sequence

Details

Count the number of each Dimers and multiply by related stacking energy.

Value

Sum of Stacking energy of each Dimers.

Author(s)

Babak Khorsand

Examples

```
SADEG.DimerStackingEnergy("actagtcacgatcag")
```

`SADEG.EENC` *SADEG.EENC*

Description

Expected Effective Number Of Codon

Usage

```
SADEG.EENC(Nucleotide_Sequence)
```

Arguments

`Nucleotide_Sequence`	Nucleotide Sequence

Details

ENC analysis was used to quantify the absolute codon usage bias by determining the degree of codon usage bias exhibited by the coding sequences, regardless of gene length and the number of amino acids. ENC values ranged between 20 and 61. ENC value of 20, indicates extreme codon usage bias using only one of the possible synonymous codons for the corresponding amino acid and value 61 denotes no bias using all possible synonymous codons equally for the corresponding amino acid. A smaller ENC value correlates with the larger extension of codon preference in a gene. It is also generally accepted that when the ENC value is less than or equal to 35, genes tend to have a significant codon bias.

Value

EENC

Author(s)

Babak Khorsand

Examples

```
SADEG.EENC(Nucleotide_Sequence="atggctgctgcagcggccagtcacgatcagaggtaagttgtcgcagcatgt")
```

SADEG.GC *SADEG.GC*

Description

GC content.

Usage

```
SADEG.GC(Nucleotide_Sequence)
```

Arguments

`Nucleotide_Sequence`	Nucleotide Sequence

Details

GC content : Sum of frequencies of G and C.

Value

GC content

Author(s)

Babak Khorsand

Examples

```
SADEG.GC("actagtcacgatcag")
```

SADEG.GC1 *SADEG.GC1*

Description

GC1 content.

Usage

```
SADEG.GC1(Nucleotide_Sequence)
```

Arguments

`Nucleotide_Sequence`	Nucleotide Sequence

Details

GC1 content : Sum of frequencies of G and C at the first position of each codon.

Value

GC1

Author(s)

Babak Khorsand

Examples

```
SADEG.GC1(Nucleotide_Sequence="atggctgctgcagcggccagtcacgatcagaggtaagttgtcgcagcatgt")
```

`SADEG.GC12` *SADEG.GC12*

Description

GC12 content.

Usage

```
SADEG.GC12(Nucleotide_Sequence)
```

Arguments

`Nucleotide_Sequence`	Nucleotide Sequence

Details

GC12 content : Sum of frequencies of G and C at first and second position of each codon.

Value

GC12

Author(s)

Babak Khorsand

Examples

```
SADEG.GC12(Nucleotide_Sequence="atggctgctgcagcggccagtcacgatcagaggtaagttgtcgcagcatgt")
```

`SADEG.GC2` *SADEG.GC2*

Description

GC2 content.

Usage

```
SADEG.GC2(Nucleotide_Sequence)
```

Arguments

`Nucleotide_Sequence`	Nucleotide Sequence

Details

GC2 content : Sum of frequencies of G and C at the second position of each codon.

Value

GC2

Author(s)

Babak Khorsand

Examples

```
SADEG.GC2(Nucleotide_Sequence="atggctgctgcagcggccagtcacgatcagaggtaagttgtcgcagcatgt")
```

`SADEG.GC3` *SADEG.GC3*

Description

GC3 content.

Usage

```
SADEG.GC3(Nucleotide_Sequence)
```

Arguments

`Nucleotide_Sequence`	Nucleotide Sequence

Details

GC3 content : Sum of frequencies of G and C at the third position of each codon.

Value

GC3

Author(s)

Babak Khorsand

Examples

```
SADEG.GC3(Nucleotide_Sequence="atggctgctgcagcggccagtcacgatcagaggtaagttgtcgcagcatgt")
```

`SADEG.ReverseComplement`

SADEG.ReverseComplement

Description

Complement of the reversed sequence.

Usage

```
SADEG.ReverseComplement(Nucleotide_Sequence)
```

Arguments

`Nucleotide_Sequence`	Nucleotide Sequence

Details

Complement of the reversed sequence. (atcagt -> Reverse: tgacta -> Reverse-Complement: actgat)

Value

Reverse-Complement

Author(s)

Babak Khorsand

Examples

```
SADEG.ReverseComplement("actagtcacgatcag")
```

`SADEG.RSCU` *SADEG.RSCU*

Description

Relative Synonymous Codon Usage

Usage

```
SADEG.RSCU(Nucleotide_Sequence)
```

Arguments

`Nucleotide_Sequence`	Nucleotide Sequence

Details

The Relative Synonymous Codon Usage (RSCU) is the number of times a codon appears in a gene divided by the number of expected occurrences under equal codon usage.

Value

RSCU

Author(s)

Babak Khorsand

Examples

```
SADEG.RSCU(Nucleotide_Sequence="atggctgcagcggccagtcacgatcagaggtaagttgtc")
```

`SADEG.StackingEnergy` *SADEG.StackingEnergy*

Description

Average free energy

Usage

```
SADEG.StackingEnergy(Nucleotide_Sequence)
```

Arguments

`Nucleotide_Sequence`	Nucleotide Sequence

Details

Average free energy value was obtained via multiplying average energy of each dimer from each sequence in number of stacked bases. In order to designate and identify a product-favored process, minus sign was denoted before the average free energy (AFE) value. Lastly, all relevant stacked bases in each gene cumulatively defined the total stacking energy for respective sequences.

Value

StackingEnergy

Author(s)

Babak Khorsand

Examples

```
SADEG.StackingEnergy("actagtcacgatcag")
```

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