

Genetic Functions

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Prerequisites

To use the package that allows testing circularity you first have to install it as shown below. To run the code in the box below you can just press the green play button in the left top corner of the code box. You might be asked in the console below this window to update the included packages. Afterwards it might take a while to install all 3 packages.

```
install.packages("Rcpp", repos = "https://packages.othr.de/cran/" )
install.packages("devtools", repos = "https://packages.othr.de/cran/")
devtools::install_github("StarmanMartin/GCATR", ref = "Testing")
```

Get codon type

As with other functions there is three ways to provide input vectors/codons You can provide the input as an R vector, as a string split by spaces or stating the tuple length. The example below demonstrates the first two ways. The last way is demonstrated in the code sample below this one.

```
code_as_vector <- c("ACG", "AGU", "CGU")
code_as_split_string <- c("ACG AGU CGU")
```

The code snippet below demonstrates how the function `code_get_acid` can be used to determine whether a code uses DNA or RNA bases. You can execute the snippet below by clicking the green button to the right of the box. The code below should return DNA as this how the function works, when neither U nor T is used in the code.

```
GCATR::code_get_acid("ACGGCA",3)
## [1] "DNA"
```

Likewise this example should return DNA as it uses the base T.

```
GCATR::code_get_acid(c("ACG", "ATT"))  
## [1] "DNA"
```

This example uses the base U and thus returns RNA.

```
GCATR::code_get_acid(c("ACG", "AUU"))  
## [1] "RNA"
```

The last example returns NONE as neither RNA nor DNA bases are used.

```
GCATR::code_get_acid(c("343", "123"))  
## [1] "NONE"
```

Get DNA and RNA bases

These two functions demonstrated below respectively return the DNA and RNA bases as a vector.

```
GCATR::get_dna_bases()  
## [1] "T" "C" "A" "G"  
GCATR::get_rna_bases()  
## [1] "U" "C" "A" "G"
```

Get RNA Codon Table

As the name suggests this function returns a data table containing all 64 rna codons. These two functions demonstrated below respectively return the DNA and RNA bases as a vector.

```
GCATR::get_rna_codon_table()  
##      U      C      A      G  
## U_U "UUU" "UCU" "UAU" "UGU"  
## U_C "UUC" "UCC" "UAC" "UGC"  
## U_A "UUA" "UCA" "UAA" "UGA"  
## U_G "UUG" "UCG" "UAG" "UGG"  
## C_U "CUU" "CCU" "CAU" "CGU"  
## C_C "CUC" "CCC" "CAC" "CGC"  
## C_A "CUA" "CCA" "CAA" "CGA"  
## C_G "CUG" "CCG" "CAG" "CGG"  
## A_U "AUU" "ACU" "AAU" "AGU"  
## A_C "AUC" "ACC" "AAC" "AGC"  
## A_A "AUA" "ACA" "AAA" "AGA"  
## A_G "AUG" "ACG" "AAG" "AGG"  
## G_U "GUU" "GCU" "GAU" "GGU"  
## G_C "GUC" "GCC" "GAC" "GGC"  
## G_A "GUA" "GCA" "GAA" "GGA"  
## G_G "GUG" "GCG" "GAG" "GGG"
```

Get RNA Codon list

This functions returns all RNA codons as a list.

```
GCATR::get_rna_codon_list()
```

```
## [1] "UUU" "UCU" "UAU" "UGU" "UUC" "UCC" "UAC" "UGC" "UUA" "UCA" "UAA" "UGA"
## [13] "UUG" "UCG" "UAG" "UGG" "CUU" "CCU" "CAU" "CGU" "CUC" "CCC" "CAC" "CGC"
## [25] "CUA" "CCA" "CAA" "CGA" "CUG" "CCG" "CAG" "CGG" "AUU" "ACU" "AAU" "AGU"
## [37] "AUC" "ACC" "AAC" "AGC" "AUA" "ACA" "AAA" "AGA" "AUG" "ACG" "AAG" "AGG"
## [49] "GUU" "GCU" "GAU" "GGU" "GUC" "GCC" "GAC" "GGC" "GUA" "GCA" "GAA" "GGA"
## [61] "GUG" "GCG" "GAG" "GGG"
```