

# BioFlow

## Introduction

The current package facilitates the work of bioinformaticians with the help of several functions. It can be used to replicate the central dogma of molecular biology “DNA -> RNA -> protein”.

The package has dependencies on two libraries: ggplot2 and stringr.

## Library Loading

Github Repository: [https://github.com/rforbiodatascience23/group\\_04\\_package.git](https://github.com/rforbiodatascience23/group_04_package.git)

```
library(BioFlow)
```

## Functions Description

### NucMerge

The function creates a random sequence of merged nucleotides based on the user-defined integer number. The input number is the number of the nucleotides that will be merged.

```
nucMerge(10)
#> [1] "ATGATTGGA"
```

Example of function usage:

### TranslatedDNA

The function translates DNA sequence into RNA. It takes a DNA string as an input. The function returns the translated RNA string.

```
TranslatedDNA("ATCG")
#> [1] "AUCG"
```

Example of function usage:

### seqToCodon

The function splits the nucleotides in the sequence into the codons of three. The sequence is given as a string input. It can be used for RNA and DNA.

```
seqToCodons("AUGAGG")
#> [1] "AUG" "AGG"
```

Example of function usage:

## TranslateCodon

The function translated codons into amino acids. The function takes only one string of three characters at a time that specifies a codon. The function result a corresponding amino acid in one letter format.

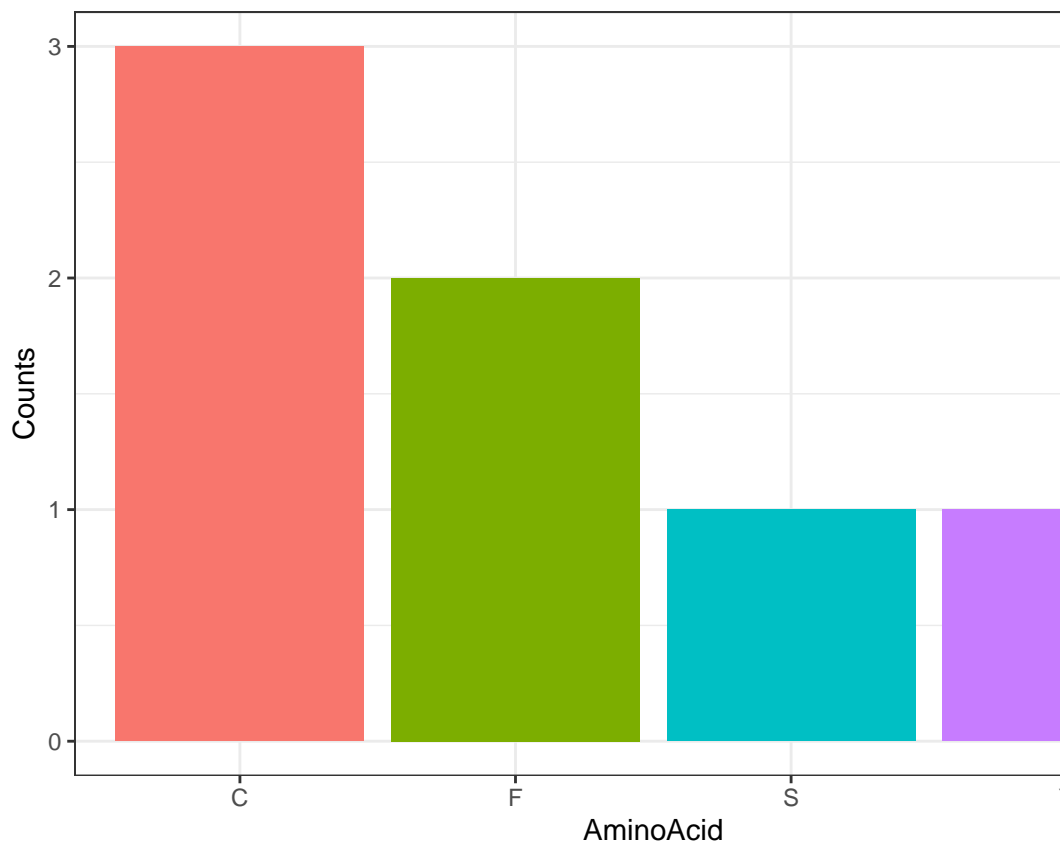
```
TranslateCodon("UUU")  
#> [1] "F"
```

Example of function usage:

## PlotAACount

The function plots amino acid counts based on the string input. It returns the bar plot in ggplot style with the colours established by the developers.

```
PlotAACount("FFSYCCC")
```



Example of function usage: