

Rosalind

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*‘This Supplementary Material can be found at <https://github.com/darwinanddavis/rosalind>’

Overview

This document contains the code and solutions to the coding problem sets from the Rosalind database at <http://rosalind.info/problems/list-view/>

Install packages and set working dir

```
# install pcks
packages <- c("stringr","stringi","gsubfn")
if (require(packages)) {
  install.packages(packages,dependencies = T)
  require(packages)
}
lapply(packages,library,character.only=T)
```

Problems

DNA Counting DNA Nucleotides

```
s <- read.csv("rosalind_dna.txt",header=F,sep="," ,stringsAsFactors = F);s

## # A tibble: 1 x 1
##   V1
##   <chr>
## 1 AAGTGCTAGATCTGCGGGCCAACTCTCTATGACCCGAGACAGCCGGGCTCTCTTACACCGTAGGCATGAT~
str_count(s,c("A","C","G","T"))

## [1] 199 224 210 205
```

RNA Transcribing DNA into RNA

```
t <- read.csv("rosalind_rna.txt",header=F,sep="," ,stringsAsFactors = F);t

## # A tibble: 1 x 1
##   V1
##   <chr>
## 1 GAACGAGGAACGTCTTGCCACCATCCGATCTGAAACGGCAGGTACGTTTACAAAGTTCTCCAGTGTA AAC~
gsub("T","U",t)

## [1] "GAACGAGGAACGUCUUGCCACCAUCCGAUCUGAAACGGCAGGUACGUUUACAAAGUUCUCCAGUGUAAAACACGGUGCGGUGAAGAGUUC CCAAU~"
```

Complementing a Strand of DNA

```
require(stringi)
require(gsubfn)
```

```
# s <- read.csv(".txt",header=F,sep=",",stringsAsFactors = F);s
```

```
s <- "AAAACCCGGT"
```

```
sc <- c("A","T","C","G") # target units
```

```
sc2r <- c("T","A","G","C") # units to be replaced
```

```
s <- stringi::stri_reverse(s);s # reverse string
```

```
## [1] "TGGCCCAAAA"
```

```
s <- replace(s,sc,sc2r);s # replace
```

```
##           A           T           C           G  
## "TGGCCCAAAA"      "T"      "A"      "G"      "C"
```

```
# desired result: ACCGGGTTTT
```