

# Sequence manipulation and scanning

*Benjamin Jean-Marie Tremblay*<sup>\*1</sup>

<sup>1</sup>University of Waterloo, Waterloo, Canada

<sup>\*</sup>b2tremblay@uwaterloo.ca

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## 1 Introduction

This vignette goes through generating your own sequences from a specified background model, shuffling sequences whilst maintaining a certain  $k$ -let size, and the scanning of sequences and scoring of motifs. For an introduction to sequence motifs, see the [introductory](#) vignette. For a basic overview of available motif-related functions, see the [motif manipulation](#) vignette. For advanced usage and analyses, see the [advanced usage](#) vignette.

## 2 Creating random sequences

The [Biostrings](#) package offers an excellent suite of functions for dealing with biological sequences. The [universalmotif](#) package hopes to help extend these by providing the `create_sequences()` and `shuffle_sequences()` functions. The first of these, `create_sequences()`, in its simplest form generates a set of letters in random order with `sample()`, then passes these strings to the [Biostrings](#) package. The number and length of sequences can be specified. The probabilities of individual letters can also be set.

The `freqs` option of `create_sequences()` also takes higher order backgrounds. In these cases the sequences are constructed in a Markov-style manner, where the probability of each letter (chosen by `sample()`) is based on which letters precede it.

```
library(universalmotif)
library(Biostrings)

## Create some DNA sequences for use with an external program (default
## is DNA):

sequences.dna <- create_sequences(seqnum = 500,
                                freqs = c(A=0.3, C=0.2, G=0.2, T=0.3))

## writeXStringSet(sequences.dna, "dna.fasta")
sequences.dna
#> A DNASTringSet instance of length 500
#>      width seq
#> [1] 100 GACAAGTCAGGTAATCAACGTCGAACTAAT...ATTCATAAAAGGTAATGTAATATAGCGAATA
#> [2] 100 GAGAATTGGGGATTATTCTCTCTCCTGCATA...TTGTCGCGTCTACATTCTGATATGTTCAATG
#> [3] 100 TTGAGAAATGATGCTGATTACCTATGTAGTG...AGATGAGGCGTATTCGTGTTTCGAGGATATTA
#> [4] 100 GGCTTTCGGGACAGGCGAACAACATCTGGCG...TCTACCCGCATTATGGGCAGAAAATAGATGG
#> [5] 100 AGTTCTAAGCCAGGAGTTACCCGCTAAGAAA...TCTCGCGACAGCATAAGAGTTGGTTGCTAAA
#> ...
#> [496] 100 ATATATCTCTCAACCAGAGTAGAACCTTGTA...GAATAAGTGATTTTTACTTACATGCAAATA
#> [497] 100 CCAACTACTTCATTCTGCTCTCTCGGAATGT...CACTTAAGTAAGAGGCAAGTTTTATTGTTT
#> [498] 100 CGTGACGTTCTTATCTATATACAGCTGTCCA...GATAAGTTACTACTTAAATATAGGGGACTG
#> [499] 100 ATCGAGTCTAAATTCCAGAATACTTTATATC...ACGCAGTAATGCGGTGCCTGGGCTACACCGT
#> [500] 100 CACCTAGCGCTCCACACAATTTATCCAAGGG...CTTACAGACGTTTTTCTCGTGATGTTATTG

## Amino acid:

create_sequences(alphabet = "AA")
#> A AAStringSet instance of length 100
```

```
#>      width seq
#> [1] 100 MHDVSVICIGPLYQGHFSGWYECWEHKDDD...RSQDRDAIQKDWVVKQYAIGQKICTLCNVH
#> [2] 100 CEPYSLNRWARERIVLRCHITVFDICDASG...CDTMNWQCLSRALLCHGMDYSHTIVKEKAK
#> [3] 100 WNCANQYNYRHERTQKSSFYKLATWVWRKH...AHVPRWCQMKNDQYHEQDCVYKIVQMRTYG
#> [4] 100 RFNHEKDNSHLKEGCCEVEQFWHVETVDDC...QKQNCYITNTKSMTDSWRTEGFGNAEHQNKF
#> [5] 100 QQHNQSRCDVNADYVLRQPTEFHYWWDRE...YPYRDWGETMWAILATRQNSAHLGIGLMWS
#> ... ..
#> [96] 100 RANWDYTFPTDNIRWAINWTKMHRWDPN...MDTAKLPEDNSVSMHFMKICEDNPNCNNND
#> [97] 100 IAFRLAESFQDIQYTGRLEQEFTGNINCD...DPYAAQNNPDIMGPHRDMFMCEKMWMCQLIS
#> [98] 100 KDVTTGATKDFHENEQWLRTHMAGGQAFFIT...AKSCFYQDIHWGSIYDKLQSWFFRTDTAWEK
#> [99] 100 PINKNVGGCFNVIWIGWKRIHAQTRCTGCS...CVAGFVKLILAYTWTDNEMRTVKCQAQVWI
#> [100] 100 LYMFCGMHECFQKMTCFEELMPHNRFYTIEI...FFLPEWFSNGCGPTTSFRAWMHRIYAHAKMA

## Any set of characters can be used

create_sequences(alphabet = paste(letters, collapse = ""))
#> A BStringSet instance of length 100
#>      width seq
#> [1] 100 mebjcdpykbvlnkdumtvrexllqgwpybh...oedpyczvovwyzaxfjzgvkbsxyfqluvx
#> [2] 100 nerufsrcolelyzdwbbqwisebedojysp...kceetmrmlntsxbmalqjotljvgbezazs
#> [3] 100 gxjkdnrtyvdavlahstuvbjmsejrmyvq...qxxxfrxijnsdzwhufvmvthzpwwdlyot
#> [4] 100 lcnbrlbdssstrioolmqgbogfcuclvvhj...mkyjltatuxrbysjrjuncnwxwodxka
#> [5] 100 vrbmimjanvypjynsnjmravjckwjxtvo...kyqnxvqfravetlrczlvjzmvopauye
#> ... ..
#> [96] 100 ruqykhiqlszbqkyqhormodgnzgcrelk...yyngbzhmtburarnknlgoxypvbrapvd
#> [97] 100 newwreuvwmzsuyomvnrpseidrskhqmz...akuopojigfsdleqwmgvcihizfakkaju
#> [98] 100 jqtevtftqjgegzzjloztfspkfaffcow...twzvlldolnqnvoyozemwzgcakvnidmyt
#> [99] 100 ucdxvwxcjywbllrfzyuiqepvfkmfnly...gsiupsawqcquwuybjauhfphxargeex
#> [100] 100 msfnjfwyqgoarwywhjvzairgobgtkum...brzdwwlicudycjtzcrxmediajnjqdhm
```

### 3 Shuffling sequences

When performing *de novo* motif searches or motif enrichment analyses, it is common to do so against a set of background sequences. In order to properly identify consistent patterns or motifs in the target sequences, it is important that there be maintained a certain level of sequence composition between the target and background sequences. This reduces results which are derived purely from differential letter frequency biases.

In order to avoid these results, typically it is desirable to use a set of background sequences which preserve a certain *k*-let size (such as dinucleotide or trinucleotide frequencies in the case of DNA sequences). Though for some cases a set of similar sequences may already be available for use as background sequences, usually background sequences are obtained by shuffling the target sequences, while preserving a desired *k*-let size. For this purpose, the most commonly used tool is likely uShuffle (Jiang et al. 2008). Despite this the *universalmotif* package aims to provide its own *k*-let shuffling capabilities for use within R via `shuffle_sequences()`.

The *universalmotif* offers three different methods for sequence shuffling: `euler`, `markov` and `linear`. The first method, `euler`, can shuffle sequences while preserving any desired *k*-let size. Exact letter counts will be preserved. However in order for this to be possible, the first and last letters will remain unshuffled.

## Sequence utilities

The second method, `markov` can only guarantee that the approximate `k`-let frequency will be maintained, but not that the original letter counts will be preserved. The `markov` method involves determining the original `k`-let frequencies, then creating a new set of sequences which will have approximately similar `k`-let frequency. As a result the counts for the individual letters will likely be different.

The third method `linear` preserves the original letter counts exactly, but uses a more crude shuffling technique. In this case the sequence is split into sub-sequences every `k`-let (of any size), which are then re-assembled randomly. This means that while shuffling the same sequence multiple times with `method = "linear"` will result in different sequences, they will all have started from the same set of sub-sequences (just re-assembled differently).

```
library(universalmotif)
data(ArabidopsisPromoters)

## Potentially starting off with some external sequences:
# library(Biostrings)
# ArabidopsisPromoters <- readDNASTringSet("ArabidopsisPromoters.fasta")

euler <- shuffle_sequences(ArabidopsisPromoters, k = 2, method = "euler")
markov <- shuffle_sequences(ArabidopsisPromoters, k = 2, method = "markov")
linear <- shuffle_sequences(ArabidopsisPromoters, k = 2, method = "linear")
k1 <- shuffle_sequences(ArabidopsisPromoters, k = 1)
```

Let us compare how the methods perform:

```
o.letter <- colSums(oligonucleotideFrequency(ArabidopsisPromoters,
                                              1, as.prob = FALSE))
e.letter <- colSums(oligonucleotideFrequency(euler, 1, as.prob = FALSE))
m.letter <- colSums(oligonucleotideFrequency(markov, 1, as.prob = FALSE))
l.letter <- colSums(oligonucleotideFrequency(linear, 1, as.prob = FALSE))

data.frame(original=o.letter, euler=e.letter, markov=m.letter, linear=l.letter)
#>   original euler markov linear
#> A    17384 17384  17360  17384
#> C     8081  8081   8116   8081
#> G     7583  7583   7593   7583
#> T    16952 16952  16931  16952

o.counts <- colSums(oligonucleotideFrequency(ArabidopsisPromoters,
                                              2, as.prob = FALSE))
e.counts <- colSums(oligonucleotideFrequency(euler, 2, as.prob = FALSE))
m.counts <- colSums(oligonucleotideFrequency(markov, 2, as.prob = FALSE))
l.counts <- colSums(oligonucleotideFrequency(linear, 2, as.prob = FALSE))

data.frame(original=o.counts, euler=e.counts, markov=m.counts, linear=l.counts)
#>   original euler markov linear
#> AA     6893  6893  6901  6429
#> AC     2614  2614  2631  2752
#> AG     2592  2592  2569  2615
#> AT     5276  5276  5240  5568
#> CA     3014  3014  3048  2934
#> CC     1376  1376  1364  1308
```

```
#> CG      1051  1051  1054  1091
#> CT      2621  2621  2646  2741
#> GA      2734  2734  2703  2661
#> GC      1104  1104  1163  1171
#> GG      1176  1176  1178  1192
#> GT      2561  2561  2539  2549
#> TA      4725  4725  4689  5343
#> TC      2977  2977  2952  2843
#> TG      2759  2759  2783  2679
#> TT      6477  6477  6490  6074
```

## 4 Calculating sequence background

Sequence backgrounds can be retrieved for DNA and RNA sequences with `oligonucleotide Frequency()` from *Biostrings*. Unfortunately, no such *Biostrings* function exists for other sequence alphabets. The *universalmotif* package provides `get_bkg()` to remedy this. Similarly, the `get_bkg()` function can calculate higher order backgrounds for any alphabet as well. It is recommended to use the original *Biostrings* for DNA and RNA sequences whenever possible though, as it is much faster than `get_bkg()`.

```
library(universalmotif)

## Background of DNA sequences:
dna <- create_sequences()
get_bkg(dna, k = 1:2, list.out = FALSE)
#>      A      C      G      T      AA      AC      AG
#> 0.24880000 0.25640000 0.25440000 0.24040000 0.06454545 0.06292929 0.06060606
#>      AT      CA      CC      CG      CT      GA      GC
#> 0.06040404 0.06454545 0.06494949 0.06626263 0.06090909 0.06090909 0.06494949
#>      GG      GT      TA      TC      TG      TT
#> 0.06727273 0.06151515 0.05888889 0.06383838 0.06000000 0.05747475

## Background of non DNA/RNA sequences:
qwerty <- create_sequences("QWERTY")
get_bkg(qwerty, k = 1:2, list.out = FALSE)
#>      E      Q      R      T      W      Y      EE
#> 0.16840000 0.16860000 0.16770000 0.16330000 0.16400000 0.16800000 0.02828283
#>      EQ      ER      ET      EW      EY      QE      QQ
#> 0.02828283 0.02919192 0.02868687 0.02565657 0.02868687 0.02888889 0.02878788
#>      QR      QT      QW      QY      RE      RQ      RR
#> 0.02767677 0.02747475 0.02858586 0.02757576 0.02848485 0.02737374 0.02848485
#>      RT      RW      RY      TE      TQ      TR      TT
#> 0.02797980 0.02777778 0.02787879 0.02626263 0.02868687 0.02787879 0.02686869
#>      TW      TY      WE      WQ      WR      WT      WW
#> 0.02606061 0.02727273 0.02808081 0.02616162 0.02575758 0.02666667 0.02878788
#>      WY      YE      YQ      YR      YT      YW      YY
#> 0.02838384 0.02808081 0.02919192 0.02909091 0.02585859 0.02777778 0.02737374
```

## 5 Scanning sequences for motifs

There are many motif-programs available with sequence scanning capabilities, such as [HOMER](#) and tools from the [MEME suite](#). The [universalmotif](#) package does not aim to supplant these, but rather provide convenience functions for quickly scanning a few sequences without needing to leave the R environment. Furthermore, these functions allow for taking advantage of the higher-order ([multifreq](#)) motif format described in the [advanced usage](#) vignette.

Two scanning-related functions are provided: `scan_sequences()` and `enrich_motifs()`. The latter simply runs `scan_sequences()` twice on a set of target and background sequences; see the [advanced usage](#) vignette. Given a motif of length `n`, `scan_sequences()` considers every possible `n`-length subset in a sequence and scores it using the PWM format. If the match surpasses the minimum threshold, it is reported. This is case regardless of whether one is scanning with a regular motif, or using the higher-order ([multifreq](#)) motif format (the [multifreq](#) matrix is converted to a PWM).

### 5.1 Regular scanning

Before scanning a set of sequences, one must first decide the minimum logodds threshold for retrieving matches. This decision is not always the same between scanning programs out in the wild, nor is it usually told to the user what the cutoff is or how it is decided. As a result, [universalmotif](#) aims to be as transparent as possible in this regard by allowing for complete control of the threshold. For more details on PWMs, see the [introductory](#) vignette.

One way is to set a cutoff between 0 and 1, then multiplying the highest possible PWM score to get a threshold. The `matchPWM()` function from the [Biostrings](#) package for example uses a default of 0.8 (shown as "80%"). This is quite arbitrary of course, and every motif will end up with a different threshold. For high information content motifs, there is really no right or wrong threshold; as they tend to have fewer non-specific positions. This means that incorrect letters in a match will be more punishing. To illustrate this, contrast the following PWMs:

```
library(universalmotif)
m1 <- create_motif("TATATATATA", nsites = 50, type = "PWM", pseudocount = 1)
m2 <- matrix(c(0.10,0.27,0.23,0.19,0.29,0.28,0.51,0.12,0.34,0.26,
               0.36,0.29,0.51,0.38,0.23,0.16,0.17,0.21,0.23,0.36,
               0.45,0.05,0.02,0.13,0.27,0.38,0.26,0.38,0.12,0.31,
               0.09,0.40,0.24,0.30,0.21,0.19,0.05,0.30,0.31,0.08),
             byrow = TRUE, nrow = 4)
m2 <- create_motif(m2, alphabet = "DNA", type = "PWM")
m1["motif"]
#>      T      A      T      A      T      A      T
#> A -5.672425  1.978626 -5.672425  1.978626 -5.672425  1.978626 -5.672425
#> C -5.672425 -5.672425 -5.672425 -5.672425 -5.672425 -5.672425 -5.672425
#> G -5.672425 -5.672425 -5.672425 -5.672425 -5.672425 -5.672425 -5.672425
#> T  1.978626 -5.672425  1.978626 -5.672425  1.978626 -5.672425  1.978626
#>      A      T      A
#> A  1.978626 -5.672425  1.978626
#> C -5.672425 -5.672425 -5.672425
#> G -5.672425 -5.672425 -5.672425
#> T -5.672425  1.978626 -5.672425
m2["motif"]
```

## Sequence utilities

```
#>           S           H           C           N           N           N
#> A -1.3219281  0.09667602 -0.12029423 -0.3959287  0.2141248  0.1491434
#> C  0.5260688  0.19976951  1.02856915  0.6040713 -0.1202942 -0.6582115
#> G  0.8479969 -2.33628339 -3.64385619 -0.9434165  0.1110313  0.5897160
#> T -1.4739312  0.66371661 -0.05889369  0.2630344 -0.2515388 -0.4102840
#>           R           N           N           V
#> A  1.0430687 -1.0732490  0.4436067  0.04222824
#> C -0.5418938 -0.2658941 -0.1202942  0.51171352
#> G  0.0710831  0.5897160 -1.0588937  0.29598483
#> T -2.3074285  0.2486791  0.3103401 -1.65821148
```

In the first example, sequences which do not have a matching base in every position are punished heavily. The maximum logodds score in this case is approximately 20, and for each incorrect position the score is reduced approximately by 5.7. This means that a threshold of zero would allow for at most three mismatches. At this point, it is up to you how many mismatches you would deem appropriate.

This thinking becomes impossible for the second example. In this case, mismatches are much less punishing; to the point that one must ask, what even constitutes a mismatch? The answer to this question is much more difficult in cases such as these. An alternative to manually deciding upon a threshold is to instead start with maximum P-value one would consider appropriate for a match. If, say, we want matches with a P-value of at most 0.001, then we can use `motif_pvalue()` to calculate the appropriate threshold (see the [advanced usage](#) vignette for details on motif P-values).

```
motif_pvalue(m2, pvalue = 0.001, progress = FALSE)
#> [1] 6.531
```

## 5.2 Higher-order scanning

The `scan_sequences()` function offers the ability to scan using the `multifreq` slot, if available. This allows to take into account inter-positional dependencies, and get matches which more faithfully represent the original sequences from which the motif originated. For more details on the `multifreq` slot, see the [advanced usage](#) vignette.

```
library(universalmotif)
library(Biostrings)
data(ArabidopsisPromoters)

## A 2-letter example:

motif.k2 <- create_motif("CWWWCC", nsites = 6)
sequences.k2 <- DNASTringSet(rep(c("CAAAACC", "CTTTTC"), 3))
motif.k2 <- add_multifreq(motif.k2, sequences.k2)
```

Regular scanning:

```
head(scan_sequences(motif.k2, ArabidopsisPromoters, RC = TRUE, verbose = 0,
                    threshold = 0.9, threshold.type = "logodds",
                    progress = FALSE))
#> motif sequence start stop score max.score score.pct match strand
```

## Sequence utilities

```
#> 1 motif AT4G28150 621 627 9.08 9.081843 99.99359 CTAAACC +
#> 2 motif AT1G19380 139 145 9.08 9.081843 99.99359 CTTATCC +
#> 3 motif AT1G19380 204 210 9.08 9.081843 99.99359 CTAAACC +
#> 4 motif AT1G03850 203 209 9.08 9.081843 99.99359 CTAATCC +
#> 5 motif AT5G01810 821 827 9.08 9.081843 99.99359 CATATCC +
#> 6 motif AT5G01810 840 846 9.08 9.081843 99.99359 CAAATCC +
```

Using 2-letter information to scan:

```
head(scan_sequences(motif.k2, ArabidopsisPromoters, use.freq = 2, RC = TRUE,
                    threshold = 0.9, threshold.type = "logodds",
                    verbose = 0, progress = FALSE))
#>  motif sequence start stop score max.score score.pct match strand
#> 1 motif AT4G12690 938 945 17.827 17.82933 99.99327 CAAAACC +
#> 2 motif AT2G37950 751 758 17.827 17.82933 99.99327 CAAAACC +
#> 3 motif AT1G49840 959 966 17.827 17.82933 99.99327 CTTTTC +
#> 4 motif AT1G77210 184 191 17.827 17.82933 99.99327 CAAAACC +
#> 5 motif AT1G77210 954 961 17.827 17.82933 99.99327 CAAAACC +
#> 6 motif AT3G57640 917 924 17.827 17.82933 99.99327 CTTTTC +
```

As an aside: the previous example involved calling `create_motif()` and `add_multifreq()` separately. In this case however this could have been simplified to just calling `create_motif()` and using the `add_multifreq` option:

```
library(universalmotif)
library(Biostrings)

sequences <- DNAStringSet(rep(c("CAAAACC", "CTTTTC"), 3))
motif <- create_motif(sequences, add_multifreq = 2:3)
```

## 6 Testing for motif positional preferences in sequences

The *universalmotif* package provides the `motif_peaks()` function, which can test for positionally preferential motif sites in a set of sequences. This can be useful, for example, when trying to determine whether a certain transcription factor binding site is more often than not located at a certain distance from the transcription start site (TSS). The `motif_peaks()` function finds density peaks in the input data, then creates a null distribution from randomly generated peaks to calculate peak P-values.

```
library(universalmotif)
data(ArabidopsisMotif)
data(ArabidopsisPromoters)

hits <- scan_sequences(ArabidopsisMotif, ArabidopsisPromoters, RC = FALSE,
                      verbose = 0, progress = FALSE, threshold = 0.8,
                      threshold.type = "logodds")

res <- motif_peaks(hits$start,
```



## Sequence utilities

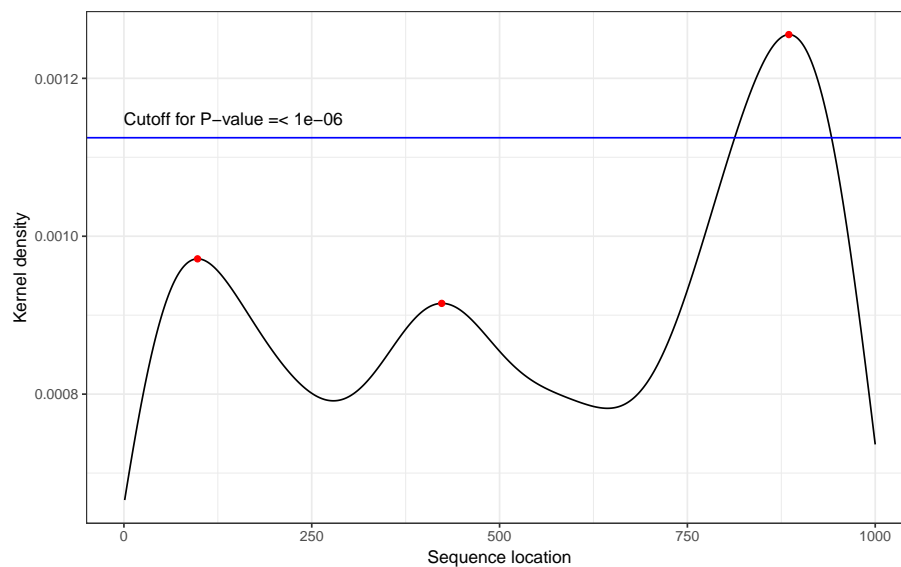
```
seq.length = unique(width(ArabidopsisPromoters)),
seq.count = length(ArabidopsisPromoters)

## Significant peaks:
res$Peaks
#>   Peak Pval
#> 1  885    0
```

Using the datasets provided in this package, a significant motif peak was found at 885 bases in the input promoters, or 115 bases away from the TSS. If you'd like to simply know the locations of any peaks, this can be done by setting `max.p = 1`.

The function can also output a plot:

```
res$Plot
```



In this plot, red dots are used to indicate density peaks and the blue line shows the P-value cutoff.

## Session info

```
#> R version 3.6.0 (2019-04-26)
#> Platform: x86_64-apple-darwin15.6.0 (64-bit)
#> Running under: OS X El Capitan 10.11.6
#>
#> Matrix products: default
#> BLAS:   /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRblas.0.dylib
#> LAPACK: /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRlapack.dylib
#>
#> locale:
#> [1] C/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
```

## Sequence utilities

```
#>
#> attached base packages:
#> [1] stats4      parallel    stats      graphics  grDevices  utils      datasets
#> [8] methods    base
#>
#> other attached packages:
#> [1] TFBSTools_1.22.0      ggplot2_3.1.1      ggtree_1.16.0
#> [4] MotifDb_1.26.0        Biostrings_2.52.0   XVector_0.24.0
#> [7] IRanges_2.18.0        S4Vectors_0.22.0    BiocGenerics_0.30.0
#> [10] universalmotif_1.2.1 BiocStyle_2.12.0
#>
#> loaded via a namespace (and not attached):
#> [1] VGAM_1.1-1           colorspace_1.4-1
#> [3] grImport2_0.1-5      GenomicRanges_1.36.0
#> [5] base64enc_0.1-3      rGADEM_2.32.0
#> [7] bit64_0.9-7          AnnotationDbi_1.46.0
#> [9] splines_3.6.0        R.methodsS3_1.7.1
#> [11] motifStack_1.28.0    knitr_1.22
#> [13] ade4_1.7-13          jsonlite_1.6
#> [15] splitstackshape_1.4.8 Rsamtools_2.0.0
#> [17] seqLogo_1.50.0       gridBase_0.4-7
#> [19] annotate_1.62.0      G0.db_3.8.2
#> [21] png_0.1-7            R.oo_1.22.0
#> [23] BiocManager_1.30.4   readr_1.3.1
#> [25] compiler_3.6.0       httr_1.4.0
#> [27] rvcheck_0.1.3        assertthat_0.2.1
#> [29] Matrix_1.2-17        lazyeval_0.2.2
#> [31] htmltools_0.3.6      tools_3.6.0
#> [33] gtable_0.3.0         glue_1.3.1
#> [35] TFMPvalue_0.0.8      GenomeInfoDbData_1.2.1
#> [37] reshape2_1.4.3       dplyr_0.8.0.1
#> [39] tinytex_0.12         Rcpp_1.0.1
#> [41] Biobase_2.44.0       Logolas_1.8.0
#> [43] ape_5.3              nlme_3.1-139
#> [45] rtracklayer_1.43.3   ggseqlogo_0.1
#> [47] gbRd_0.4-11          xfun_0.6
#> [49] CNEr_1.20.0          stringr_1.4.0
#> [51] ps_1.3.0             powerLaw_0.70.2
#> [53] gtools_3.8.1         XML_3.98-1.19
#> [55] zlibbioc_1.30.0      MASS_7.3-51.4
#> [57] scales_1.0.0         BSgenome_1.52.0
#> [59] hms_0.4.2            SummarizedExperiment_1.14.0
#> [61] RColorBrewer_1.1-2   yaml_2.2.0
#> [63] memoise_1.1.0        MotIV_1.40.0
#> [65] SQUAREM_2017.10-1    stringi_1.4.3
#> [67] RSQLite_2.1.1        highr_0.8
#> [69] tidytree_0.2.4       caTools_1.17.1.2
#> [71] BiocParallel_1.18.0  bibtex_0.4.2
#> [73] GenomeInfoDb_1.20.0  Rdpack_0.11-0
#> [75] rlang_0.3.4          pkgconfig_2.0.2
#> [77] matrixStats_0.54.0   bitops_1.0-6
```

## Sequence utilities

```
#> [79] evaluate_0.13          lattice_0.20-38
#> [81] purrr_0.3.2           htmlwidgets_1.3
#> [83] GenomicAlignments_1.20.0 treeio_1.8.0
#> [85] labeling_0.3          bit_1.1-14
#> [87] processx_3.3.1        tidyselect_0.2.5
#> [89] plyr_1.8.4            magrittr_1.5
#> [91] bookdown_0.9          R6_2.4.0
#> [93] DelayedArray_0.10.0   DBI_1.0.0
#> [95] pillar_1.3.1          withr_2.1.2
#> [97] KEGGREST_1.24.0       RCurl_1.95-4.12
#> [99] tibble_2.1.1          crayon_1.3.4
#> [101] rmarkdown_1.12        jpeg_0.1-8
#> [103] grid_3.6.0            data.table_1.12.2
#> [105] blob_1.1.1            digest_0.6.18
#> [107] xtable_1.8-4          tidyr_0.8.3
#> [109] R.utils_2.8.0         munsell_0.5.0
#> [111] DirichletMultinomial_1.26.0
```

## References

Jiang, M., J. Anderson, J. Gillespie, and M. Mayne. 2008. "uShuffle: A Useful Tool for Shuffling Biological Sequences While Preserving K-Let Counts." *BMC Bioinformatics* 9 (192).