Biostrings Quick Overview

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Most but not all functions defined in the Biostrings package are summarized here.

Function	Description
length	Return the number of sequences in an object.
names	Return the names of the sequences in an object.
[	Extract sequences from an object.
head, tail	Extract the first or last sequences from an object.
rev	Reverse the order of the sequences in an object.
c	Combine in a single object the sequences from 2 or more objects.
width, nchar	Return the sizes (i.e. number of letters) of all the sequences in an object.
==, !=	Element-wise comparison of the sequences in 2 objects.
match, %in%	Analog to match and %in% on character vectors.
duplicated, unique	Analog to duplicated and unique on character vectors.
sort, order	Analog to sort and order on character vectors, except that the ordering of DNA or Amino Acid sequences doesn't depend on the locale.
relist, split, extractList	Analog to relist and split on character vectors, except that the result is a *DNAStringSetList* or *AAStringSetList* object. extractList is a generalization of relist and split that supports *arbitrary* groupings.

Table 1: **Low-level manipulation of *DNAStringSet* and *AAStringSet* objects.**

Function	Description
alphabetFrequency letterFrequency	Tabulate the letters (all the letters in the alphabet for alphabetFrequency, only the specified letters for letterFrequency) in a sequence or set of sequences.
uniqueLetters	Extract the unique letters from a sequence or set of sequences.
letterFrequencyInSlidingView	Specialized version of letterFrequency that tallies the requested letter frequencies for a fixed-width view that is conceptually slid along the input sequence.
consensusMatrix	Computes the consensus matrix of a set of sequences.
dinucleotideFrequency trinucleotideFrequency oligonucleotideFrequency	Fast 2-mer, 3-mer, and k-mer counting for DNA or RNA.
nucleotideFrequencyAt	Tallies the short sequences formed by extracting the nucleotides found at a set of fixed positions from each sequence of a set of DNA or RNA sequences.

Table 2: **Counting / tabulating.**

Function	Description
reverse complement reverseComplement	Compute the reverse, complement, or reverse-complement, of a set of DNA sequences.
translate	Translate a set of DNA sequences into a set of Amino Acid sequences.
chartr replaceAmbiguities	Replace letters in a sequence or set of sequences.
subseq, subseq<- extractAt, replaceAt	Extract/replace arbitrary substrings from/in a string or set of strings.
replaceLetterAt	Replace the letters specified by a set of positions by new letters.
padAndClip, stackStrings	Pad and clip strings.
strsplit, unstrsplit	strsplit splits the sequences in a set of sequences according to a pattern. unstrsplit is the reverse operation i.e. a fast implementation of sapply(x, paste0, collapse=sep) for collapsing the list elements of a *DNAStringSetList* or *AAStringSetList* object.

Table 3: **Sequence transformation and editing.**

Function	Description
matchPattern countPattern	Find/count all the occurrences of a given pattern (typically short) in a reference sequence (typically long). Support mismatches and indels.
vmatchPattern vcountPattern	Find/count all the occurrences of a given pattern (typically short) in a set of reference sequences. Support mismatches and indels.
matchPDict countPDict whichPDict	Find/count all the occurrences of a set of patterns in a reference sequence. (whichPDict only identifies which patterns in the set have at least one match.) Support a small number of mismatches.
vmatchPDict vcountPDict vwhichPDict	[Note: vmatchPDict not implemented yet.] Find/count all the occurrences of a set of patterns in a set of reference sequences. (whichPDict only identifies for each reference sequence which patterns in the set have at least one match.) Support a small number of mismatches.
pairwiseAlignment	Solve (Needleman-Wunsch) global alignment, (Smith-Waterman) local alignment, and (ends-free) overlap alignment problems.
matchPWM countPWM	Find/count all the occurrences of a Position Weight Matrix in a reference sequence.
trimLRPatterns	Trim left and/or right flanking patterns from sequences.
matchLRPatterns	Find all paired matches in a reference sequence i.e. matches specified by a left and a right pattern, and a maximum distance between them.
matchProbePair	Find all the amplicons that match a pair of probes in a reference sequence.
findPalindromes	Find palindromic regions in a sequence.

Table 4: **String matching / alignments.**

Function	Description

`readBStringSet`
`readDNAStringSet`
`readRNAStringSet`
`readAAStringSet`
	Read ordinary/DNA/RNA/Amino Acid sequences from files (FASTA or FASTQ format).

`writeXStringSet`	Write sequences to a file (FASTA or FASTQ format).
`writePairwiseAlignments`	Write pairwise alignments (as produced by `pairwiseAlignment`) to a file ("pair" format).

`readDNAMultipleAlignment`
`readRNAMultipleAlignment`
`readAAMultipleAlignment`
	Read multiple alignments from a file (FASTA, "stockholm", or "clustal" format).

`write.phylip`	Write multiple alignments to a file (Phylip format).

Table 5: **I/O functions.**