

Biostrings Quick Overview

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November 13, 2013

Please note that *most* but *not all* the functionalities provided by the Biostrings package are listed in this document.

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	Put 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 <code>match</code> and <code>%in%</code> on character vectors.
duplicated, unique	Analog to <code>duplicated</code> and <code>unique</code> on character vectors.
sort, order	Analog to <code>sort</code> and <code>order</code> on character vectors, except that the ordering of DNA or Amino Acid sequences doesn't depend on the locale.
split, relist	Analog to <code>split</code> and <code>relist</code> on character vectors, except that the result is a <i>DNASet</i> or <i>AASet</i> object.

Table 1: Low-level manipulation of *DNASet* or *AASet* objects.

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	Translate the letters in a 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.

Table 2: Sequence editing.

Function	Description
alphabetFrequency letterFrequency	Tabulate the letters (all the letters in the alphabet for alphabetFrequency , only the specified letters for letterFrequency) of 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 3: **Counting / tabulating.**

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 findComplementedPalindromes	Find palindromic or complemented 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 <code>pairwiseAlignment</code>) 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.**

Function	Description
stringDist	Computes the matrix of Levenshtein edit distances, or Hamming distances, or pairwise alignment scores, for a set of strings.

Table 6: **Miscellaneous.**