

Biostrings Quick Overview

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October 30, 2018

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

| Function | Description |
|---|---|
| <code>length</code> | Return the number of sequences in an object. |
| <code>names</code> | Return the names of the sequences in an object. |
| <code>[</code> | Extract sequences from an object. |
| <code>head, tail</code> | Extract the first or last sequences from an object. |
| <code>rev</code> | Reverse the order of the sequences in an object. |
| <code>c</code> | Combine in a single object the sequences from 2 or more objects. |
| <code>width, nchar</code> | Return the sizes (i.e. number of letters) of all the sequences in an object. |
| <code>==, !=</code> | Element-wise comparison of the sequences in 2 objects. |
| <code>match, %in%</code> | Analog to <code>match</code> and <code>%in%</code> on character vectors. |
| <code>duplicated, unique</code> | Analog to <code>duplicated</code> and <code>unique</code> on character vectors. |
| <code>sort, order</code> | 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. |
| <code>relist, split, extractList</code> | Analog to <code>relist</code> and <code>split</code> on character vectors, except that the result is a <i>DNASetList</i> or <i>AASetList</i> object. <code>extractList</code> is a generalization of <code>relist</code> and <code>split</code> that supports <i>arbitrary</i> groupings. |

Table 1: Low-level manipulation of *DNASetList* and *AASetList* objects.

| Function | Description |
|--|---|
| <code>alphabetFrequency</code> <code>letterFrequency</code> | Tabulate the letters (all the letters in the alphabet for <code>alphabetFrequency</code> , only the specified letters for <code>letterFrequency</code>) in a sequence or set of sequences. |
| <code>uniqueLetters</code> | Extract the unique letters from a sequence or set of sequences. |
| <code>letterFrequencyInSlidingView</code> | Specialized version of <code>letterFrequency</code> that tallies the requested letter frequencies for a fixed-width view that is conceptually slid along the input sequence. |
| <code>consensusMatrix</code> | Computes the consensus matrix of a set of sequences. |
| <code>dinucleotideFrequency</code> <code>trinucleotideFrequency</code> <code>oligonucleotideFrequency</code> | Fast 2-mer, 3-mer, and k-mer counting for DNA or RNA. |
| <code>nucleotideFrequencyAt</code> | 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 <i>DNAStringSetList</i> or <i>AAStringSetList</i> 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 <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.**