

SEQR

FAST K-MER COUNTING

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K-MER COUNTING



- Analysing peptides sequences
- Counting occurrences of all k-length subsequences

seqR:: package for fast k-mer counting.

Algorithm description

Algorithm of seqR is based on hashtable that counts occurances of each k-mer in the sequence. The vector of elements is changed to integer representation for calculation of hash function and faster code execution. K-mers can be counted within specified alphabet, elements from outside of the alphabet are not counted. Implementation also allows to count gapped and positional kmers. Positional ones are related to its position (column index in the given sequence matrix), so, for example k-mer "abc" that starts on the first position is a different kmer than k-mer "abc" that starts on the second position. Original code was written in C++ and ported to R with Rcpp library. Parallelization was made with RcppParallel.

Function usage

count_kmers(s, d, alphabet, pos)

Params:

s Sequence Matrix (non-empty), each row denotes a sequence.

Sequences are represented as strings.

d Integer Vector of gaps in k-mer.

Length of this vector equals the length of k-mer + 1.

seaR

alphabet Alphabet string Vector.

pos Boolean value telling if k-mers are positional or not.

Returns:

Named Vector where names corresponds to k-mers and values to their counts.

Usage Example:

IMPLEMENTATION OVERVIEW



- Written in C++ with Rcpp library
- Parallelization with RcppParallel
- Hash table k-mer counting
- Integer sequence representation
- Gapped k-mers can be counted
- Counting over user defined alphabet

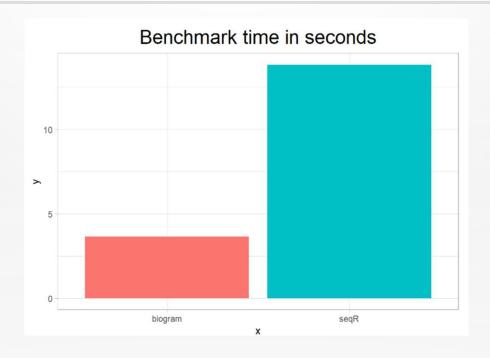
PACKAGE ELEMENTS



- Base Rcpp code
- Support for Windows, Linux and Mac OS
- Package Site
- Logo
- Cheetsheet
- Vignette

BENCHMARK







THANKS FOR YOUR ATTENTION