N-gram analysis of biological sequences in R

N-grams (k-mers) are vectors of n characters derived from input sequences, widely used in genomics, transcriptomics and proteomics. Despite the continuous interest in the sequence analysis, there are only a few tools tailored for comparative n-gram studies. Furthermore, the volume of n-gram data is usually very large, making its analysis in **R** especially challenging.

The CRAN package *biogram* [Burdukiewicz et al., 2015] facilitates incorporating n-gram data in the **R** workflows. Aside from the efficient extraction and storage of n-grams, the package offers also a feature selection method designed specifically for this type of data. QuiPT (Quick Permutation Test) uses several filtering criteria such as information gain (mutual information) to choose significant n-grams. To speed up the computation and allow precise estimation of small p-values, QuiPT uses analytically derived distributions instead of a large number of permutations. In addition to this, *biogram* contains tools designed for reducing the dimensionality of the amino acid alphabet [Murphy et al., 2000], further scaling down the feature space.

To illustrate the usage of n-gram data in the analysis of biological sequences, we present two case studies performed solely in **R**. The first, prediction of amyloids, short proteins associated with the number of clinical disorders as Alzheimer's or Creutzfeldt-Jakob's diseases [Fändrich, 2012], employs random forests [Wright and Ziegler, 2015] trained on n-grams. The second, detection of signal peptides orchestrating an extracellular transport of proteins, utilizes more complicated probabilistic framework (Hidden semi-Markov model,) but still uses n-gram data for training.

References

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