Package: NameNeedle (via r-universe)

October 12, 2024

Version 1.2.7

Date 2023-08-19

Title Using Needleman-Wunsch to Match Sample Names

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Description The Needleman-Wunsch global alignment algorithm can be
used to find approximate matches between sample names in
different data sets. See Wang et al. (2010)
<doi:10.4137/CIN.S5613>.

Depends R (>= 3.0)

Imports stats

Suggests Biostrings

License Apache License (== 2.0)

URL http://oompa.r-forge.r-project.org/

NeedsCompilation no

Repository CRAN

Date/Publication 2023-08-19 19:42:31 UTC

Contents

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cellLineNames-data   *Cell Line Names*

Description

This dataset contains vectors of cell line names that are used to demonstrate how to use the **Name-Needle** package.

Usage

```
data(cellLineNames)
```

Format

This dataset contains four objects: three character vectors (sf2Names, rppaNames, and illuNames) and one factor (illuType).

Details

The three character vectors, sf2Names, rppaNames, and illuNames contain the names of cell lines used in three different but related experiments. The factor, illuType, indicates whether the cell lines named in the illuNames vector were derived from lung cancer (with the value "Lung") or from head and neck cancer ("HNSCC").

Examples

```
data(cellLineNames)
head(rppaNames)
head(sf2Names)
head(illuNames)
summary(illuType)
```

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needles   *Needleman-Wunsch simple global alignment algorithm*

Description

The Needleman-Wunsch simple gap algorithm was one of the first methods introduced for global alignment of biological sequences. The same algorithm can be used to match cell line names or sample names from two related data sets; we provide examples in the documentation, using data that accompanies this package.

While the **NameNeedle** package can be used for biological sequence alignment, the **Biostrings** package from Bioconductor contains much more sophisticated tools for that problem.

Usage

```
needles(pattern, subject, params=defaultNeedleParams)
needleScores(pattern, subjects, params=defaultNeedleParams)
defaultNeedleParams
```

Arguments

pattern   character string to be matched

subject   character string to be matched against

subjects   character vector where matches are sought

params   list containing four required components. The default values are specified by
                 the object `defaultNeedleParams`, which contains the following values:

```
$ MATCH   : num 1
$ MISMATCH: num -1
$ GAP     : num -1
$ GAPCHAR : chr "*"
```

Details

The Needleman-Wunsch global alignment algorithm was one of the first algorithms used to align
DNA, RNA, or protein sequences. The basic algorithm uses dynamic programming to find an opti-
mal alignment between two sequences, with parameters that specify penalties for mismatches and
gaps and a reward for exact matches. More elaborate algorithms (not implemented here) make use
of matrices with different penalties depending on different kinds of mismatches. The version im-
plemented here is based on the Perl implementation in the first section of Chapter 3 of the book
BLAST.

Value

The `needles` function returns a list with five components:

score   The raw alignment score.

align1   The final (optimal) alignment for the `pattern`.

align2   The final (optimal) alignment for the `subject`.

sm   The score matrix.

dm   The backtrace matrix.

The `needleScores` function returns a numeric vector the same length as the `subjects` argument,
with each entry equal to the corresponding raw alignment score.

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References

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Wang J, Byers LA, Yordy JS, Liu W, Shen L, Baggerly KA, Giri U, Myers JN, Ang KK, Story MD, Girard L, Minna JD, Heymach JV, Coombes KR.
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See Also

The **Biostrings** package from Bioconductor used to contain a function called needwunQS that provided a simple gap implementation of Needleman-Wunsch, similar to the one presented here. That function has been deprecated in favor of a more elaborate interface called pairwiseAlignment that incorporates a variety of other alignment methods in addition. While pairwiseAlignment is much more useful for applications to biological sequences, it is serious overkill for the application we have in mind for matching cell line or other sample names.

Examples

```
data(cellLineNames)
myParam <- defaultNeedleParams
myParam$MATCH <- 2
myParam$MISMATCH <- -2
needles(sf2Names[2], illuNames[1], myParam)
scores <- needleScores(sf2Names[6], illuNames, myParam)
w <- which(scores == max(scores))
w
sf2Names[6]

needles(sf2Names[6], illuNames[w], myParam)
```

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