

Package ‘DECIPHER’

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Type Package

Title Database Enabled Code for Ideal Probe Hybridization Employing R

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Microarray, QualityControl, qPCR, Alignment, WholeGenome,
Microbiome

Description A toolset for deciphering and managing biological sequences.

Depends R (>= 2.13.0), Biostrings (>= 2.35.12), RSQLite (>= 1.0.0),
stats, parallel

Imports methods, DBI, S4Vectors, IRanges, XVector

LinkingTo Biostrings, RSQLite, S4Vectors, IRanges, XVector

License GPL-3

NeedsCompilation yes

R topics documented:

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Description

Database Enabled Code for Ideal Probe Hybridization Employing R (DECIPHER) is a software toolset that can be used for deciphering and managing biological sequences efficiently using the R statistical programming language. The program is designed to be used with non-destructive workflows that guide the user through the process of importing, maintaining, analyzing, manipulating, and exporting a massive amount of sequences. Some functionality of the program is provided on-line through web tools. DECIPHER is an ongoing project at the University of Wisconsin - Madison and is freely available for download.

Details

Package: DECIPHER
 Type: Package
 Depends: R (>= 2.13.0), Biostrings (>= 2.35.12), RSQLite (>= 1.0), stats, parallel
 Imports: methods, DBI, S4Vectors, IRanges, XVector
 LinkingTo: Biostrings, RSQLite, S4Vectors, IRanges, XVector
 License: GPL-3
 LazyLoad: yes

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| Array2Matrix | Create a Matrix Representation of a Microarray |
| BrowseDB | View A Database Table In A Web Browser |
| BrowseSeqs | View Sequences In A Web Browser |
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| CalculateEfficiencyPCR | Predict Amplification Efficiency of Primer Sequences |
| ConsensusSequence | Create A Consensus Sequence |
| CorrectFrameshifts | Corrects Frameshift Errors In Protein Coding |

| | |
|---------------------|--|
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| DB2Seqs | Export Database Sequences to a FASTA or FASTQ File |
| deltaGrules | Free Energy of Hybridization of Probe/Target Quadruplets |
| deltaHrules | Change in Enthalpy of Hybridization of Primer/Target Quadruplets in Solution |
| deltaSrules | Change in Entropy of Hybridization of Primer/Target Quadruplets in Solution |
| DesignArray | Design a set of DNA Microarray Probes for Detecting Sequences |
| DesignPrimers | Design Primers Targeting a Specific Group of Sequences |
| DesignProbes | Design FISH Probes Targeting a Specific Group of Sequences |
| DesignSignatures | Design PCR Primers for Amplifying Group-Specific Signatures |
| DigestDNA | Simulate Restriction Digestion of DNA |
| Disambiguate | Expand Ambiguities into All Permutations of a DNAStrngSet |
| DistanceMatrix | Calculate the Distance Between Sequences |
| FindChimeras | Find Chimeras In A Sequence Database |
| FindSynteny | Finds Synteny In A Sequence Database |
| FormGroups | Forms Groups By Rank |
| HEC_MI | Mutual Information for Protein Secondary Structure Prediction |
| IdClusters | Cluster Sequences By Distance or Sequence |
| IdConsensus | Create Consensus Sequences by Groups |
| IdentifyByRank | Identify By Taxonomic Rank |
| IdLengths | Determine the Number of Bases, Nonbases, and Width of Each Sequence |
| MaskAlignment | Masks Highly Variable Regions of An Alignment |
| MeltDNA | Simulate Melting of DNA |
| MIQS | MIQS Amino Acid Substitution Matrix |
| MODELS | Available Models of DNA Evolution |
| NNLS | Sequential Coordinate-wise Algorithm for the Non-negative Least Squares Problem |
| OrientNucleotides | Orient nucleotide sequences |
| PredictHEC | Predict Protein Secondary Structure |
| RESTRICTION_ENZYMES | Common Restriction Enzyme's Cut Sites |
| SearchDB | Obtain Specific Sequences from A Database |
| Seqs2DB | Add Sequences from Text File to Database |
| StaggerAlignment | Produce a Staggered Alignment |
| Synteny-class | Synteny blocks and hits |
| TerminalChar | Determine the Number of Terminal Characters |
| TileSeqs | Form a Set of Tiles for Each Group of Sequences |

Author(s)

Erik Wright

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Add2DB

Add Data To A Database

Description

Adds a data.frame to a database table by row.names.

Usage

```
Add2DB(myData,  
        dbFile,  
        tblName = "DNA",  
        clause = "",  
        verbose = TRUE)
```

Arguments

| | |
|---------|--|
| myData | Data frame containing information to be added to the dbFile. |
| dbFile | A SQLite connection object or a character string specifying the path to the database file. |
| tblName | Character string specifying the table in which to add the data. |
| clause | An optional character string to append to the query as a clause. |
| verbose | Logical indicating whether to display each query as it is sent to the database. |

Details

Data contained in myData will be added to the tblName by its respective row.names.

Value

Returns TRUE if the data was added successfully, or FALSE otherwise.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

See Also

[Seqs2DB](#), [SearchDB](#), [BrowseDB](#)

Examples

```
# Create a sequence database
gen <- system.file("extdata", "Bacteria_175seqs.gen", package="DECIPHER")
dbConn <- dbConnect(SQLite(), ":memory:")
Seqs2DB(gen, "GenBank", dbConn, "Bacteria")

# Identify the sequence lengths
l <- IdLengths(dbConn)

# Add lengths to the database
Add2DB(l, dbConn)

# View the added lengths
BrowseDB(dbConn)
dbDisconnect(dbConn)
```

AdjustAlignment

*Improve An Existing Alignment By Adjusting Gap Placements***Description**

Makes small adjustments by shifting groups of gaps left and right to find their optimal positioning in a multiple sequence alignment.

Usage

```
AdjustAlignment(myXStringSet,
               perfectMatch = 5,
               mismatch = 0,
               gapLetter = -3,
               gapOpening = -0.1,
               gapExtension = 0,
               substitutionMatrix = NULL,
               shiftPenalty = -0.2,
               threshold = 0.1,
               weight = 1,
               processors = NULL)
```

Arguments

| | |
|--------------|---|
| myXStringSet | An AStringSet, DNASTringSet, or RNASTringSet object of aligned sequences. |
| perfectMatch | Numeric giving the reward for aligning two matching nucleotides in the alignment. Only used for DNASTringSet or RNASTringSet inputs. |
| mismatch | Numeric giving the cost for aligning two mismatched nucleotides in the alignment. Only used for DNASTringSet or RNASTringSet inputs. |
| gapLetter | Numeric giving the cost for aligning gaps to letters. A lower value (more negative) encourages the overlapping of gaps across different sequences in the alignment. |

| | |
|--------------------|--|
| gapOpening | Numeric giving the cost for opening or closing a gap in the alignment. |
| gapExtension | Numeric giving the cost for extending an open gap in the alignment. |
| substitutionMatrix | Either a substitution matrix representing the substitution scores for an alignment or the name of the amino acid substitution matrix to use in alignment. The latter may be one of the following: "BLOSUM45", "BLOSUM50", "BLOSUM62", "BLOSUM80", "BLOSUM100", "PAM30", "PAM40", "PAM70", "PAM120", "PAM250", or "MIQS". The default (NULL) will use the perfectMatch and misMatch penalties for DNA/RNA or "MIQS" for AA. (See examples section below.) |
| shiftPenalty | Numeric giving the cost for every additional position that a group of gaps is shifted. |
| threshold | Numeric specifying the improvement in score required to permanently apply an adjustment to the alignment. |
| weight | A numeric vector of weights for each sequence, or a single number implying equal weights. |
| processors | The number of processors to use, or NULL (the default) for all available processors. |

Details

The process of multiple sequence alignment often results in the integration of small imperfections into the final alignment. Some of these errors are obvious by-eye, which encourages manual refinement of automatically generated alignments. However, the manual refinement process is inherently subjective and time consuming. AdjustAlignment refines an existing alignment in a process similar to that which might be applied manually, but in a repeatable and much faster fashion. This function shifts all of the gaps in an alignment to the left and right to find their optimal positioning. The optimal position is defined as the position that maximizes the alignment "score", which is determined by the input parameters. The resulting alignment will be similar to the input alignment but with many imperfections eliminated. Note that the affine gap penalties here are different from the more flexible penalties used in [AlignProfiles](#), and have been optimized independently.

Value

An XStringSet of aligned sequences.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

References

ES Wright (2015) "DECIPHER: harnessing local sequence context to improve protein multiple sequence alignment". BMC Bioinformatics, doi:10.1186/s12859-015-0749-z.

See Also

[AlignSeqs](#), [AlignTranslation](#), [StaggerAlignment](#)

Examples

```
# a trivial example
aa <- AAStringSet(c("ARN-PK", "ARRP-K"))
aa
AdjustAlignment(aa)

# a real example
fas <- system.file("extdata", "Streptomyces_ITS_aligned.fas", package="DECIPHER")
dna <- readDNASTringSet(fas)
adjustedDNA <- AdjustAlignment(dna)
BrowseSeqs(adjustedDNA, highlight=1)
adjustedDNA==dna # most sequences were adjusted
```

AlignDB

*Align Two Sets of Aligned Sequences In A Sequence Database***Description**

Merges the two separate sequence alignments in a database. The aligned sequences must have separate identifiers in the same table or be located in different database tables.

Usage

```
AlignDB(dbFile,
        tblName = "DNA",
        identifier = "",
        type = "DNASTringSet",
        add2tbl = "DNA",
        batchSize = 10000,
        perfectMatch = 5,
        misMatch = 0,
        gapOpening = -13,
        gapExtension = -1,
        gapPower = -1,
        terminalGap = -5,
        normPower = 1,
        substitutionMatrix = NULL,
        processors = NULL,
        verbose = TRUE)
```

Arguments

| | |
|---------|---|
| dbFile | A SQLite connection object or a character string specifying the path to the database file. |
| tblName | Character string specifying the table(s) where the sequences are located. If two tblNames are provided then the sequences in both tables will be aligned. |

| | |
|--------------------|--|
| identifier | Optional character string used to narrow the search results to those matching a specific identifier. If "" then all identifiers are selected. If two identifiers are provided then the set of sequences matching each identifier will be aligned. |
| type | The type of XStringSet being processed. This should be (an abbreviation of) one of "AAStringSet", "DNAStringSet", or "RNAStringSet". |
| add2tbl | Character string specifying the table name in which to add the aligned sequences. |
| batchSize | Integer specifying the number of sequences to process at a time. |
| perfectMatch | Numeric giving the reward for aligning two matching nucleotides in the alignment. Only used when type is DNAStringSet or RNAStringSet. |
| misMatch | Numeric giving the cost for aligning two mismatched nucleotides in the alignment. Only used when type is DNAStringSet or RNAStringSet. |
| gapOpening | Numeric giving the cost for opening a gap in the alignment. |
| gapExtension | Numeric giving the cost for extending an open gap in the alignment. |
| gapPower | Numeric specifying the exponent to use in the gap cost function. |
| terminalGap | Numeric giving the cost for allowing leading and trailing gaps ("- or ." characters) in the alignment. Either two numbers, the first for leading gaps and the second for trailing gaps, or a single number for both. |
| normPower | Numeric giving the exponent that controls the degree of normalization applied to scores by column occupancy. A normPower of 0 does not normalize the scores, which results in all columns of the profiles being weighted equally, and is the optimal value for aligning fragmentary sequences. A normPower of 1 normalizes the score for aligning two positions by their column occupancy (1 - fraction of gaps). A normPower greater than 1 more strongly discourages aligning with "gappy" regions of the alignment. |
| substitutionMatrix | Either a substitution matrix representing the substitution scores for an alignment or the name of the amino acid substitution matrix to use in alignment. The latter may be one of the following: "BLOSUM45", "BLOSUM50", "BLOSUM62", "BLOSUM80", "BLOSUM100", "PAM30", "PAM40", "PAM70", "PAM120", "PAM250", or "MIQS". The default (NULL) will use the perfectMatch and misMatch penalties for DNA/RNA or "MIQS" for AA. (See examples section below.) |
| processors | The number of processors to use, or NULL (the default) for all available processors. |
| verbose | Logical indicating whether to display progress. |

Details

Sometimes it is useful to align two large sets of sequences, where each set of sequences is already aligned but the two sets are not aligned to each other. AlignDB first builds a profile of each sequence set in increments of batchSize so that the entire sequence set is not required to fit in memory. Next the two profiles are aligned using dynamic programming. Finally, the new alignment is applied to all the sequences as they are incrementally added to the add2tbl.

Two identifiers or tblNames must be provided, indicating the two sets of sequences to align. The sequences corresponding to the first identifier and tblName will be aligned to those of

the second identifier or tblName. The aligned sequences are added to add2tbl under a new identifier formed from the concatenation of the two identifiers or tblNames. (See examples section below.)

Value

Returns the number of newly aligned sequences added to the database.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

References

ES Wright (2015) "DECIPHER: harnessing local sequence context to improve protein multiple sequence alignment". BMC Bioinformatics, doi:10.1186/s12859-015-0749-z.

See Also

[AlignProfiles](#), [AlignSeqs](#), [AlignTranslation](#)

Examples

```
gen <- system.file("extdata", "Bacteria_175seqs.gen", package="DECIPHER")
fas <- system.file("extdata", "Bacteria_175seqs.fas", package="DECIPHER")

# Align two tables and place result into a third
dbConn <- dbConnect(SQLite(), ":memory:")
Seqs2DB(gen, "GenBank", dbConn, "Seqs1", tblName="Set1")
Seqs2DB(fas, "FASTA", dbConn, "Seqs2", tblName="Set2")
AlignDB(dbConn, tblName=c("Set1", "Set2"), add2tbl="AlignedSets")
l <- IdLengths(dbConn, "AlignedSets", add2tbl=TRUE)
BrowseDB(dbConn, tblName="AlignedSets") # all sequences have the same width
dbDisconnect(dbConn)

# Align two identifiers and place the result in the same table
dbConn <- dbConnect(SQLite(), ":memory:")
Seqs2DB(gen, "GenBank", dbConn, "Seqs1")
Seqs2DB(fas, "FASTA", dbConn, "Seqs2")
AlignDB(dbConn, identifier=c("Seqs1", "Seqs2"))
l <- IdLengths(dbConn, add2tbl=TRUE)
BrowseDB(dbConn) # note the sequences with a new identifier
dbDisconnect(dbConn)
```

AlignProfiles

*Align Two Sets of Aligned Sequences***Description**

Aligns two sets of one or more aligned sequences by first generating representative profiles, then aligning the profiles with dynamic programming, and finally merging the two aligned sequence sets.

Usage

```
AlignProfiles(pattern,
              subject,
              p.weight = 1,
              s.weight = 1,
              p.struct = NULL,
              s.struct = NULL,
              perfectMatch = 5,
              misMatch = 0,
              gapOpening = -13,
              gapExtension = -1,
              gapPower = -1,
              terminalGap = -5,
              restrict = -1000,
              anchor = 0.7,
              normPower = 1,
              substitutionMatrix = NULL,
              structureMatrix = NULL,
              processors = NULL)
```

Arguments

| | |
|--------------|---|
| pattern | An AAStringSet, DNASTringSet, or RNASTringSet object of aligned sequences to use as the pattern. |
| subject | A XStringSet object of aligned sequences to use as the subject. Must match the type of the pattern. |
| p.weight | A numeric vector of weights for each sequence in the pattern to use in generating a profile, or a single number implying equal weights. |
| s.weight | A numeric vector of weights for each sequence in the subject to use in generating a profile, or a single number implying equal weights. |
| p.struct | Either NULL (the default), or a list of matrices with one list element per sequence in the pattern. (See details section below.) |
| s.struct | Either NULL (the default), or a list of matrices with one list element per sequence in the subject. (See details section below.) |
| perfectMatch | Numeric giving the reward for aligning two matching nucleotides in the alignment. Only used for DNASTringSet or RNASTringSet inputs. |

| | |
|---------------------------------|---|
| <code>misMatch</code> | Numeric giving the cost for aligning two mismatched nucleotides in the alignment. Only used for <code>DNAStringSet</code> or <code>RNAStringSet</code> inputs. |
| <code>gapOpening</code> | Numeric giving the cost for opening a gap in the alignment. |
| <code>gapExtension</code> | Numeric giving the cost for extending an open gap in the alignment. |
| <code>gapPower</code> | Numeric specifying the exponent to use in the gap cost function. (See details section below.) |
| <code>terminalGap</code> | Numeric giving the cost for allowing leading and trailing gaps ("-" or ".") characters) in the alignment. Either two numbers, the first for leading gaps and the second for trailing gaps, or a single number for both. |
| <code>restrict</code> | Numeric specifying the lowest relative score to consider when aligning. The default (-1000) will align most inputs that can reasonably be globally aligned without any loss in accuracy. Input sequences with high similarity could be more restricted (e.g., -500), whereas a pattern and subject with little overlap should be less restricted (e.g., -10000). (See details section below.) |
| <code>anchor</code> | Numeric giving the fraction of sequences with identical k-mers required to become an anchor point, or NA to not use anchors. Alternatively, a matrix specifying anchor regions. (See details section below.) |
| <code>normPower</code> | Numeric giving the exponent that controls the degree of normalization applied to scores by column occupancy. A <code>normPower</code> of 0 does not normalize the scores, which results in all columns of the profiles being weighted equally, and is the optimal value for aligning fragmentary sequences. A <code>normPower</code> of 1 normalizes the score for aligning two positions by their column occupancy (1 - fraction of gaps). A <code>normPower</code> greater than 1 more strongly discourages aligning with “gappy” regions of the alignment. |
| <code>substitutionMatrix</code> | Either a substitution matrix representing the substitution scores for an alignment or the name of the amino acid substitution matrix to use in alignment. The latter may be one of the following: “BLOSUM45”, “BLOSUM50”, “BLOSUM62”, “BLOSUM80”, “BLOSUM100”, “PAM30”, “PAM40”, “PAM70”, “PAM120”, “PAM250”, or “MIQS”. The default (NULL) will use the perfectMatch and misMatch penalties for DNA/RNA or “MIQS” for AA. (See examples section below.) |
| <code>structureMatrix</code> | A structure matrix if <code>p.struct</code> and <code>s.struct</code> are supplied, or NULL otherwise. (See examples section below.) |
| <code>processors</code> | The number of processors to use, or NULL (the default) for all available processors. |

Details

Profiles are aligned using dynamic programming, a variation of the Needleman-Wunsch algorithm for global alignment. The dynamic programming method requires order $N \times M$ time and memory space where N and M are the width of the pattern and subject. This method works by filling in a matrix of the possible “alignment space” by considering all matches, insertions, and deletions between two sequence profiles. The highest scoring alignment is then used to add gaps to each of the input sequence sets.

Heuristics can be useful to improve performance on long input sequences. The `restrict` parameter can be used to dynamically constrain the possible “alignment space” to only paths that will likely include the final alignment, which in the best case can improve the speed from quadratic time to linear time. The degree of restriction is important, and if the sequences are not mostly overlapping then `restrict` should be relaxed (more negative than the default). For example, if aligning a pattern to a much longer subject then `restrict` should be set to $-1e10$ to prevent restriction.

The argument `anchor` can be used to split the global alignment into multiple sub-alignments. This can greatly decrease the memory requirement for long sequences when appropriate anchor points can be found. Anchors are 15-mer (for DNA/RNA) or 7-mer (for AA) subsequences that are shared between at least anchor fraction of pattern(s) and subject(s). Anchored ranges are extended along the length of each sequence in a manner designed to split the alignment into sub-alignments that can be separately solved. For most input sequences `anchor` has no effect on accuracy, but anchoring can be disabled by setting `anchor=NA`.

Alternatively, `anchor` can be a matrix with 4 rows and one column per anchor. The first two rows correspond to the anchor start and end positions in the pattern sequence(s), and the second two rows are the equivalent anchor region in the subject sequence(s). Anchors specified in this manner must be strictly increasing (non-overlapping) in both sequences, and have an anchor width of at least two positions. Note that the anchors do not have to be equal length, in which case the anchor regions will also be aligned. Manually splitting the alignment into more subtasks can sometimes make it more efficient, but typically automatic anchoring is effective.

The arguments `p.struct` and `s.struct` may be used to provide secondary structure probabilities. Each list element must contain a matrix with dimensions $q \times w$, where q is the number of possible secondary structure states, and w is the width of the unaligned pattern sequence. Values in each matrix represent the probability of the given state at that position in the sequence. A `structureMatrix` must be supplied along with the structures. The function `PredictHEC` can be used to predict secondary structure probabilities in the format required by `AlignProfiles`.

The gap cost function is based on the observation that gap lengths are best approximated by a Zipfian distribution (Chang & Benner, 2004). The cost of inserting a gap of length L is equal to: $\text{gapOpening} + \text{gapExtension} \times \sum(\text{seq_len}(L - 1)^{\text{gapPower}}$ when $L > 1$, and gapOpen when $L = 1$. This function effectively penalizes shorter gaps significantly more than longer gaps when $\text{gapPower} < 0$, and is equivalent to the affine gap penalty when gapPower is 0 .

Value

An `XStringSet` of aligned sequences.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

References

- Chang, M. S. S., & Benner, S. A. (2004). Empirical Analysis of Protein Insertions and Deletions Determining Parameters for the Correct Placement of Gaps in Protein Sequence Alignments. *Journal of Molecular Biology*, **341**(2), 617-631.
- Needleman S., Wunsch, C. (1970). A general method applicable to the search for similarities in the amino acid sequence of two proteins. *Journal of Molecular Biology*, **48**(3), 443-453.

ES Wright (2015) "DECIPHER: harnessing local sequence context to improve protein multiple sequence alignment". BMC Bioinformatics, doi:10.1186/s12859-015-0749-z.

See Also

[AlignDB](#), [AlignSeqs](#), [AlignSynteny](#), [AlignTranslation](#), [MIQS](#)

Examples

```
# align two sets of sequences
db <- system.file("extdata", "Bacteria_175seqs.sqlite", package="DECIPHER")
dna1 <- SearchDB(db, remove="common", limit=100) # the first 100 sequences
dna2 <- SearchDB(db, remove="common", limit="100,100") # the rest
alignedDNA <- AlignProfiles(dna1, dna2)
BrowseSeqs(alignedDNA, highlight=1)

# specify a DNA substitution matrix
subMatrix <- matrix(0,
                    nrow=4, ncol=4,
                    dimnames=list(DNA_BASES, DNA_BASES))
diag(subMatrix) <- 5 # perfectMatch
alignedDNA.defaultSubM <- AlignProfiles(dna1, dna2, substitutionMatrix=subMatrix)
all(alignedDNA.defaultSubM==alignedDNA)

# specify a different DNA substitution matrix
subMatrix2 <- matrix(c(12, 3, 5, 3, 3, 12, 3, 6, 5, 3, 11, 3, 3, 6, 3, 9),
                    nrow=4, ncol=4,
                    dimnames=list(DNA_BASES, DNA_BASES))
alignedDNA.alterSubM <- AlignProfiles(dna1, dna2, substitutionMatrix=subMatrix2)
all(alignedDNA.alterSubM==alignedDNA)

# anchors are found automatically by default, but it is also
# possible to specify anchor regions between the sequences
anchors <- matrix(c(774, 788, 752, 766), nrow=4)
anchors
subseq(dna1, anchors[1, 1], anchors[2, 1])
subseq(dna2, anchors[3, 1], anchors[4, 1])
alignedDNA2 <- AlignProfiles(dna1, dna2, anchor=anchors)
```

AlignSeqs

Align A Set of Unaligned Sequences

Description

Performs profile-to-profile alignment of multiple unaligned sequences following a guide tree.

Usage

```
AlignSeqs(myXStringSet,
          guideTree = NULL,
          iterations = 1,
          refinements = 1,
          gapOpening=c(-16, -12),
          gapExtension=c(-2, -1),
          structures = NULL,
          FUN = AdjustAlignment,
          levels = c(0.95, 0.7, 10, 5),
          processors = NULL,
          verbose = TRUE,
          ...)
```

Arguments

| | |
|--------------|--|
| myXStringSet | An AStringSet, DNASTringSet, or RNASTringSet object of unaligned sequences. |
| guideTree | Either NULL or a data.frame giving the ordered tree structure in which to align profiles. If NULL then a guide tree will be automatically constructed based on the order of shared k-mers. |
| iterations | Number of iteration steps to perform. During each iteration step the guide tree is regenerated based on the alignment and the sequences are realigned. |
| refinements | Number of refinement steps to perform. During each refinement step groups of sequences are realigned to rest of the sequences, and the best of these two alignments (before and after realignment) is kept. |
| gapOpening | Single numeric giving the cost for opening a gap in the alignment, or two numbers giving the minimum and maximum costs. In the latter case the cost will be varied depending upon whether the groups of sequences being aligned are nearly identical or maximally distant. |
| gapExtension | Single numeric giving the cost for extending an open gap in the alignment, or two numbers giving the minimum and maximum costs. In the latter case the cost will be varied depending upon whether the groups of sequences being aligned are nearly identical or maximally distant. |
| structures | Either a list of secondary structure probabilities matching the structureMatrix, such as that output by PredictHEC, or NULL to generate the structures automatically. Only applicable if myXStringSet is an AStringSet. |
| FUN | A function to be applied after each profile-to-profile alignment. (See details section below.) |
| levels | Numeric with four elements specifying the levels above which to apply FUN. (See details section below.) |
| processors | The number of processors to use, or NULL (the default) for all available processors. |
| verbose | Logical indicating whether to display progress. |

... Further arguments to be passed directly to [AlignProfiles](#), including `perfectMatch`, `misMatch`, `gapPower`, `terminalGap`, `restrict`, `anchor`, `normPower`, `substitutionMatrix`, and `structureMatrix`.

Details

The profile-to-profile method aligns a sequence set by merging profiles along a guide tree until all the input sequences are aligned. This process has three main steps: (1) If `guideTree=NULL`, an initial single-linkage guide tree is constructed based on a distance matrix of shared k-mers. If an initial `guideTree` is provided then the `guideTree` should be provided in the output given by `IdClusters` with ascending levels of cutoff. (2) If `iterations` is greater than zero, then a UPGMA guide tree is built based on the initial alignment and the sequences are re-aligned along this tree. This process repeated `iterations` times or until convergence. (3) If `refinements` is greater than zero, then groups of sequences are iteratively realigned to the full-alignment. This process generates two alignments, the best of which is chosen based on its sum-of-pairs score. This refinement process is repeated `refinements` times, or until no improvement can be made.

The FUN function is applied during each of the three steps based on levels. The purpose of levels is to speed-up the alignment process by not running FUN on the alignment when it is unnecessary. The default levels specify that FUN should be run on the sequences when the initial tree is above 0.95 average dissimilarity, when the iterative tree is above 0.7 average dissimilarity, and after every tenth improvement made during refinement. The final element of levels prevents FUN from being applied at any point to less than 5 sequences. The FUN function is always applied just before returning the alignment, independently of the first three values of levels. The default FUN is `AdjustAlignment`, but FUN accepts any function that takes in an `XStringSet` as its first argument, and `weights`, `processors`, and `substitutionMatrix` as optional arguments. For example, the default FUN could be altered to not perform any function by setting it equal to `FUN=function(x, ...) return(x)` where x is an `XStringSet`.

Value

An `XStringSet` of aligned sequences.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

References

ES Wright (2015) "DECIPHER: harnessing local sequence context to improve protein multiple sequence alignment". *BMC Bioinformatics*, doi:10.1186/s12859-015-0749-z.

See Also

[AdjustAlignment](#), [AlignDB](#), [AlignProfiles](#), [AlignSyteny](#), [AlignTranslation](#), [IdClusters](#), [StaggerAlignment](#)

Examples

```
db <- system.file("extdata", "Bacteria_175seqs.sqlite", package="DECIPHER")
dna <- SearchDB(db, remove="all")
alignedDNA <- AlignSeqs(dna)
BrowseSeqs(alignedDNA, highlight=1)
```

AlignSynteny

Pairwise Aligns Syntenic Blocks

Description

Performs pairwise alignment of all blocks of synteny between sets of sequences.

Usage

```
AlignSynteny(synteny,
             dbFile,
             tblName = "DNA",
             identifier = "",
             verbose = TRUE,
             ...)
```

Arguments

| | |
|------------|---|
| synteny | An object of class "Synteny". |
| dbFile | A SQLite connection object or a character string specifying the path to the database file. |
| tblName | Character string specifying the table where the sequences are located that were used to create the object synteny. |
| identifier | Optional character string used to narrow the search results to those matching a specific identifier, or an integer sequence corresponding to indices of rownames(synteny). If "" (the default), then all identifiers are selected from synteny. |
| verbose | Logical indicating whether to display progress. |
| ... | Further arguments to be passed directly to AlignProfiles , including perfectMatch, misMatch, gapPower, terminalGap, restrict, normPower, and substitutionMatrix. |

Details

AlignSynteny will extract all sequence regions belonging to syntenic blocks in synteny, and perform pairwise alignment with [AlignProfiles](#). Hits are used to anchor the alignment such that only the regions between anchors are aligned.

Value

A list with elements for each pair of identifiers in synteny. Each list element contains a DNAStrngSetList one pairwise alignment per syntenic block.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

See Also

[FindSynteny](#), [Synteny-class](#)

Examples

```
db <- system.file("extdata", "Influenza.sqlite", package="DECIPHER")
synteny <- FindSynteny(db, minScore=50)
DNA <- AlignSynteny(synteny, db)
names(DNA)
DNA[[1]] # the first set of pairwise alignments
DNA[[1]][[1]] # the first block of synteny between H9N2 & H5N1
unlist(DNA[[2]]) # a DNASTringSet of synteny between H9N2 & H2N2
```

AlignTranslation

Align Sequences By Their Amino Acid Translation

Description

Performs alignment of a set of DNA or RNA sequences by aligning their corresponding amino acid sequences.

Usage

```
AlignTranslation(myXStringSet,
                 sense = "+",
                 direction = "5' to 3'",
                 readingFrame = NA,
                 asAAStringSet = FALSE,
                 geneticCode = GENETIC_CODE,
                 ...)
```

Arguments

| | |
|--------------|--|
| myXStringSet | A DNASTringSet or RNASTringSet object of unaligned sequences. |
| sense | Single character specifying sense of the input sequences, either the positive ("+") coding strand or negative ("-") non-coding strand. |
| direction | Direction of the input sequences, either "5' to 3'" or "3' to 5'". |
| readingFrame | Numeric vector giving a single reading frame for all of the sequences, or an individual reading frame for each sequence in myXStringSet. The readingFrame can be either 1, 2, 3 to begin translating on the first, second, and third nucleotide position, or NA (the default) to guess the reading frame. (See details section below.) |

| | |
|---------------|--|
| asAAStringSet | Logical determining whether to return the aligned translation as an AAStringSet rather than the input type. Incomplete starting and ending codons will be translated into the mask character ("+"). |
| geneticCode | Named character vector in the same format as GENETIC_CODE (the default), which represents the standard genetic code. |
| ... | Further arguments to be passed directly to AlignSeqs , including gapOpening, gapExtension, gapPower, terminalGap, restrict, anchor, normPower, substitutionMatrix, structureMatrix, guideTree, iterations, refinements, structures, FUN, and levels. |

Details

Alignment of proteins is often more accurate than alignment of their coding nucleic acid sequences. This function aligns the input nucleic acid sequences via aligning their translated amino acid sequences. First, the input sequences are translated according to the specified sense, direction, and readingFrame. The resulting amino acid sequences are aligned using [AlignSeqs](#), and this alignment is reverse translated into the original sequence type, sense, and direction. Not only is alignment of protein sequences more accurate, but aligning translations will ensure that the reading frame is maintained in the nucleotide sequences.

If the readingFrame is NA (the default) then an attempt is made to guess the reading frame of each sequence based on the number of stop codons in the translated amino acids. For each sequence, the first reading frame will be chosen (either 1, 2, or 3) without stop codons, except in the last position. If the number of stop codons is inconclusive for a sequence then the reading frame will default to 1. The entire length of each sequence is translated in spite of any stop codons identified. Note that this method is only constructive in circumstances where there is a substantially long coding sequence with at most a single stop codon expected in the final position, and therefore it is preferable to specify the reading frame of each sequence if it is known.

Value

An XStringSet matching the input type.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

References

ES Wright (2015) "DECIPHER: harnessing local sequence context to improve protein multiple sequence alignment". BMC Bioinformatics, doi:10.1186/s12859-015-0749-z.

See Also

[AlignDB](#), [AlignProfiles](#), [AlignSeqs](#), [AlignSynteny](#), [CorrectFrameshifts](#)

Examples

```

# first three sequences translate to MFITP*
# and the last sequence translates as MF-TP*
rna <- RNAStringSet(c("AUGUUCAUCACCCCUAA", "AUGUUCAUAACUCCUUGA",
"AUGUUCAUUACACCGUAG", "AUGUUUACCCCAUAA"))
RNA <- AlignSeqs(rna, verbose=FALSE)
RNA

RNA <- AlignTranslation(rna, verbose=FALSE)
RNA

AA <- AlignTranslation(rna, asAAStringSet=TRUE, verbose=FALSE)
AA

# example of aligning many protein coding sequences:
fas <- system.file("extdata", "50S_ribosomal_protein_L2.fas", package="DECIPHER")
dna <- readDNAStrngSet(fas)
DNA <- AlignTranslation(dna) # align the translation then reverse translate
DNA

```

AmplifyDNA

Simulate Amplification of DNA by PCR

Description

Predicts the amplification efficiency of theoretical PCR products (amplicons) given one or more primer sequences.

Usage

```

AmplifyDNA(primers,
            myDNAStrngSet,
            maxProductSize,
            annealingTemp,
            P,
            ions = 0.2,
            includePrimers=TRUE,
            minEfficiency = 0.001,
            ...)

```

Arguments

| | |
|----------------|---|
| primers | A DNAStrngSet object or character vector with one or more unaligned primer sequences in 5' to 3' orientation. |
| myDNAStrngSet | A DNAStrngSet object or character vector with unaligned template DNA sequences in 5' to 3' orientation. |
| maxProductSize | Integer specifying the maximum length of PCR products (amplicons) in nucleotides. |

| | |
|----------------|---|
| annealingTemp | Numeric specifying the annealing temperature used in the PCR reaction. |
| P | Numeric giving the molar concentration of primers in the reaction. |
| ions | Numeric giving the molar sodium equivalent ionic concentration. Values may range between 0.01M and 1M. |
| includePrimers | Logical indicating whether to include the primer sequences in the theoretical PCR products. (See details section below.) |
| minEfficiency | Numeric giving the minimum amplification efficiency of PCR products to include in the output (default 0.1%). (See details section below.) |
| ... | Additional arguments to be passed directly to <code>CalculateEfficiencyPCR</code> , including <code>batchSize</code> , <code>taqEfficiency</code> , <code>maxDistance</code> , <code>maxGaps</code> , and <code>processors</code> . |

Details

Exponential amplification in PCR requires the annealing and elongation of two primers from target sites on opposing strands of the template DNA. If the template DNA sequence (e.g., chromosome) is known then predictions of theoretical amplicons can be obtained from in silico simulations of amplification. AmplifyDNA first searches for primer target sites on the template DNA, and then calculates an amplification efficiency from each target site using `CalculateEfficiencyPCR`. Ambiguity codes (IUPAC_CODE_MAP) are supported in the primers, but not in `myDNAStringSet` to prevent trivial matches (e.g., runs of N's).

If `taqEfficiency` is TRUE (the default), the amplification efficiency of each primer is defined as the product of hybridization efficiency and elongation efficiency. Amplification efficiency must be at least `minEfficiency` for a primer to be amplified in silico. Overall amplification efficiency of the PCR product is then calculated as the geometric mean of the two (i.e., forward and reverse) primers' efficiencies. Finally, amplicons are generated if the two primers are within `maxProductSize` nucleotides downstream of each other.

Potential PCR products are returned, either with or without including the primer sequences in the amplicon. The default (`includePrimers=TRUE`) is to incorporate the primer sequences as would normally occur during amplification. The alternative is to return the complete template sequence including the target sites, which may not exactly match the primer sequences. Note that amplicons may be duplicated when different input primers can amplify the same region of DNA.

Value

A `DNAStrngSet` object containing potential PCR products, sorted from highest-to-lowest amplification efficiency. The sequences are named by their predicted amplification efficiency followed by the index of each primer in `myDNAStringSet`. (See examples section below.)

Note

The program `OligoArrayAux` (<http://mfold.rna.albany.edu/?q=DINAMelt/OligoArrayAux>) must be installed in a location accessible by the system. For example, the following code should print the installed `OligoArrayAux` version when executed from the R console:

```
system("hybrid-min -V")
```

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

References

ES Wright et al. (2013) "Exploiting Extension Bias in PCR to Improve Primer Specificity in Ensembles of Nearly Identical DNA Templates." *Environmental Microbiology*, doi:10.1111/1462-2920.12259.

See Also

[CalculateEfficiencyPCR](#), [DesignPrimers](#), [DesignSignatures](#), [MeltDNA](#)

Examples

```
data(yeastSEQCHR1)

# not run (must have OligoArrayAux installed first):

# match a single primer that acts as both the forward and reverse
primer1 <- "TGGAAGCTGAAACG"
## Not run: AmplifyDNA(primer1, yeastSEQCHR1, annealingTemp=55, P=4e-7, maxProductSize=500)

# perform a typical amplification with two primer sequences:
primer2 <- c("GGCTGTTGTTGGTGT", "TGTCATCAGAACACCAA")
## Not run: AmplifyDNA(primer2, yeastSEQCHR1, annealingTemp=55, P=4e-7, maxProductSize=500)

# perform a multiplex PCR amplification with multiple primers:
primers <- c(primer1, primer2)
## Not run: AmplifyDNA(primers, yeastSEQCHR1, annealingTemp=55, P=4e-7, maxProductSize=500)
```

Array2Matrix

Create a Matrix Representation of a Microarray

Description

Converts the output of DesignArray into the sparse matrix format used by NNLS.

Usage

```
Array2Matrix(probes,
             verbose = TRUE)
```

Arguments

| | |
|---------|---|
| probes | A set of microarray probes in the format output by DesignArray. |
| verbose | Logical indicating whether to display progress. |

Details

A microarray can be represented by a matrix of hybridization efficiencies, where the rows represent each of the probes and the columns represent each the possible templates. This matrix is sparse since microarray probes are designed to only target a small subset of the possible templates.

Value

A list specifying the hybridization efficiency of each probe to its potential templates.

| | |
|----------|--|
| i | Element's row index in the sparse matrix. |
| j | Element's column index in the sparse matrix. |
| x | Non-zero elements' values representing hybridization efficiencies. |
| dimnames | A list of two components: the names of each probe, and the names of each template. |

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

References

ES Wright et al. (2013) Identification of Bacterial and Archaeal Communities From Source to Tap. Water Research Foundation, Denver, CO.

DR Noguera, et al. (2014). Mathematical tools to optimize the design of oligonucleotide probes and primers. Applied Microbiology and Biotechnology. doi:10.1007/s00253-014-6165-x.

See Also

[DesignArray, NNLS](#)

Examples

```
fas <- system.file("extdata", "Bacteria_175seqs.fas", package="DECIPHER")
dna <- readDNAStrngSet(fas)
names(dna) <- 1:length(dna)
probes <- DesignArray(dna)
A <- Array2Matrix(probes)
```

BrowseDB

View A Database Table In A Web Browser

Description

Opens an html file in a web browser to show the contents of a table in a database.

Usage

```
BrowseDB(dbFile,
          htmlFile = paste(tempdir(), "/db.html", sep = ""),
          openURL = interactive(),
          tblName = "DNA",
          identifier = "",
          limit = -1,
```

```
orderBy = "row_names",
maxChars = 50,
clause="")
```

Arguments

| | |
|------------|--|
| dbFile | A SQLite connection object or a character string specifying the path to the database file. |
| htmlFile | Character string giving the location where the html file should be written. |
| openURL | Logical indicating whether the htmlFile should be opened in a web browser. |
| tblName | Character string specifying the table to view. |
| identifier | Optional character string used to narrow the search results to those matching a specific identifier. If "" then all identifiers are selected. |
| limit | Number of results to display. The default (-1) does not limit the number of results. |
| orderBy | Character string giving the column name for sorting the results. Defaults to the order of entries in the database. Optionally can be followed by " ASC" or " DESC" to specify ascending (the default) or descending order. |
| maxChars | Maximum number of characters to display in each column. |
| clause | An optional character string to append to the query as a clause. |

Value

Creates an html table containing all the fields of the database table and (if openURL is TRUE) opens it in the web browser for viewing.

Returns htmlFile if the html file was written successfully.

Note

If viewing a table containing sequences, the sequences are purposefully not shown in the output.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

See Also

[BrowseSeqs](#)

Examples

```
db <- system.file("extdata", "Bacteria_175seqs.sqlite", package="DECIPHER")
BrowseDB(db)
```


Description

Opens an html file in a web browser to show the sequences in an XStringSet.

Usage

```
BrowseSeqs(myXStringSet,
           htmlFile = paste(tempdir(), "/myXStringSet.html", sep = ""),
           openURL = interactive(),
           colorPatterns = TRUE,
           highlight = NA,
           patterns = c("-", alphabet(myXStringSet, baseOnly=TRUE)),
           colors = substring(rainbow(length(patterns),
                                     v=0.8, start=0.9, end=0.7), 1, 7),
           colWidth = Inf,
           ...)
```

Arguments

| | |
|---------------|--|
| myXStringSet | A XStringSet object of sequences. |
| htmlFile | Character string giving the location where the html file should be written. |
| openURL | Logical indicating whether the htmlFile should be opened in a web browser. |
| colorPatterns | Logical specifying whether to color matched patterns, or an integer vector providing pairs of start and stop boundaries for coloring. |
| highlight | Numeric specifying which sequence in the set to use for comparison or NA to color all sequences (default). If highlight is 0 then positions differing from the consensus sequence are highlighted. |
| patterns | Either an AStringSet, DNStringSet, or RNStringSet object, or a character vector containing regular expressions to be colored in the XStringSet. Regular expressions are searched sequentially with multiple matches allowed, even within other previously matched patterns. (See details section below.) |
| colors | Character vector providing the color for each of the matched patterns. Typically a character vector with elements of 7 characters: “#” followed by the red, blue, green values in hexadecimal (after rescaling to 0 ... 255). Positions given background color are also given white font. |
| colWidth | Integer giving the maximum number of nucleotides wide the display can be before starting a new page. Must be a multiple of 20 (e.g., 100), or Inf (the default) to display all the sequences in one set of rows. |
| ... | Additional arguments to adjust the appearance of the consensus sequence at the base of the display. Passed directly to ConsensusSequence for an AStringSet, DNStringSet, or RNStringSet, or to consensusString for a BStringSet. |

Details

BrowseSeqs converts an XStringSet into html format for viewing in a web browser. If patterns are supplied then they are matched as regular expressions, and colored according to colors. Some web browsers cannot quickly display a large amount colored text, so it is recommended to use `color = FALSE` or to highlight a sequence when viewing a large XStringSet. Highlighting will only show all of the characters in the highlighted sequence, and convert all matching positions in the other sequences into dots without color.

Patterns are not matched across column breaks, so multi-character patterns should be carefully considered when `colWidth` is less than the maximum sequence length. Patterns are matched sequentially in the order provided, so it is feasible to use nested patterns such as `c("ACCTG", "CC")`. In this case the "CC" could be colored differently inside the previously colored "ACCTG". Note that patterns overlapping the boundaries of a previously matched pattern will not be matched. For example, "ACCTG" would not be matched if `patterns=c("CC", "ACCTG")`.

Value

Creates an html file containing sequence data and (if `openURL` is TRUE) opens it in a web browser for viewing. The layout has the sequence name on the left, position legend on the top, cumulative number of nucleotides on the right, and consensus sequence on the bottom.

Returns `htmlFile` if the html file was written successfully.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

See Also

[BrowseDB](#), [ConsensusSequence](#)

Examples

```
db <- system.file("extdata", "Bacteria_175seqs.sqlite", package="DECIPHER")
dna <- SearchDB(db)
BrowseSeqs(dna, colWidth=100, highlight=1)

# color bases in alternating groups with a different color scheme
BrowseSeqs(dna[1:5],
  colorPatterns=seq(1, width(dna)[1], 10),
  patterns=c("A", "C", "G", "T", "-"),
  colors=c("#1E90FF", "#32CD32", "#9400D3", "#000000", "#EE3300"))

# color all restriction sites
data(RESTRICTION_ENZYMES)
sites <- RESTRICTION_ENZYMES
sites <- gsub("[^A-Z]", "", sites) # remove non-letters
sites <- DNASTringSet(sites)
rc_sites <- DNASTringSet(sites)
w <- which(sites != rc_sites)
sites <- c(sites, rc_sites[w])
sites <- sites[order(nchar(sites))] # match shorter sites first
```

```
dna <- SearchDB(db, remove="all") # unaligned sequences
BrowseSeqs(dna, patterns=sites)
```

CalculateEfficiencyArray

Predict the Hybridization Efficiency of Probe/Target Sequence Pairs

Description

Calculates the Gibbs free energy and hybridization efficiency of probe/target pairs at varying concentrations of the denaturant formamide.

Usage

```
CalculateEfficiencyArray(probe,
                        target,
                        FA = 0,
                        dGini = 1.96,
                        Po = 10^-2.0021,
                        m = 0.1731,
                        temp = 42,
                        deltaGrules = NULL)
```

Arguments

| | |
|-------------|--|
| probe | A DNASTringSet object or character vector with pairwise-aligned probe sequences in 5' to 3' orientation. |
| target | A DNASTringSet object or character vector with pairwise-aligned target sequences in 5' to 3' orientation. |
| FA | A vector of one or more formamide concentrations (as percent v/v). |
| dGini | The initiation free energy. The default is 1.96 [kcal/mol]. |
| Po | The effective probe concentration. |
| m | The m-value defining the linear relationship of denaturation in the presence of formamide. |
| temp | Equilibrium temperature in degrees Celsius. |
| deltaGrules | Free energy rules for all possible base pairings in quadruplets. If NULL, defaults to the parameters obtained using NimbleGen microarrays and a Linear Free Energy Model developed by Yilmaz <i>et al.</i> |

Details

This function calculates the free energy and hybridization efficiency (HE) for a given formamide concentration ([FA]) using the linear free energy model given by:

$$HE = Po * exp[-(dG_0 + m * FA)/RT]/(1 + Po * exp[-(dG_0 + m * FA)/RT])$$

The probe and target input sequences must be aligned in pairs, such that the first probe is aligned to the first target, second-to-second, and so on. Ambiguity codes in the IUPAC_CODE_MAP are accepted in probe and target sequences. Any ambiguities will default to perfect match pairings by inheriting the nucleotide in the same position on the opposite sequence whenever possible. If the ambiguity results in a mismatch then “T”, “G”, “C”, and “A” are substituted, in that order. For example, if a probe nucleotide is “S” (“C” or “G”) then it will be considered a “C” if the target nucleotide in the same position is a “C”, otherwise the ambiguity will be interpreted as a “G”.

If deltaGrules is NULL then the rules defined in data(deltaGrules) will be used. Note that deltaGrules of the same format may be customized for any application and specified as an input.

Value

A matrix with the predicted Gibbs free energy (dG) and hybridization efficiency (HE) at each concentration of formamide ([FA]).

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

References

Yilmaz LS, Loy A, Wright ES, Wagner M, Noguera DR (2012) Modeling Formamide Denaturation of Probe-Target Hybrids for Improved Microarray Probe Design in Microbial Diagnostics. PLoS ONE 7(8): e43862. doi:10.1371/journal.pone.0043862.

See Also

[deltaGrules](#)

Examples

```
probes <- c("AAAAACGGGGAGCGGGGGATACTG", "AAAAACTCAACCCGAGGAGCGGGG")
targets <- c("CAACCCGGGGAGCGGGGGATACTG", "TCGGGCTCAACCCGAGGAGCGGGG")
result <- CalculateEfficiencyArray(probes, targets, FA=0:40)
dG0 <- result[, "dG_0"]
HE0 <- result[, "HybEff_0"]
plot(result[1, 1:40], xlab="[FA]", ylab="HE", main="Probe/Target # 1", type="l")
```

`CalculateEfficiencyFISH`*Predict Thermodynamic Parameters of Probe/Target Sequence Pairs*

Description

Calculates the Gibbs free energy, formamide melt point, and hybridization efficiency of probe/target (DNA/RNA) pairs.

Usage

```
CalculateEfficiencyFISH(probe,  
                        target,  
                        temp,  
                        P,  
                        ions,  
                        FA,  
                        batchSize = 1000)
```

Arguments

| | |
|-----------|--|
| probe | A DNASTringSet object or character vector with unaligned probe sequences in 5' to 3' orientation. |
| target | A DNASTringSet object, RNASTringSet, or character vector with unaligned target or non-target sequences in 5' to 3' orientation. The DNA base Thymine will be treated the same as Uracil. |
| temp | Numeric specifying the hybridization temperature, typically 46 degrees Celsius. |
| P | Numeric giving the molar concentration of probes during hybridization. |
| ions | Numeric giving the molar sodium equivalent ionic concentration. Values may range between 0.01M and 1M. Note that salt correction is not available for thermodynamic rules of RNA/RNA interactions, which were determined at 1 molar concentration. |
| FA | Numeric concentration (as percent v/v) of the denaturant formamide in the hybridization buffer. |
| batchSize | Integer specifying the number of probes to simulate hybridization per batch. See the Description section below. |

Details

Hybridization of pairwise probe/target (DNA/RNA) pairs is simulated *in silico*. Gibbs free energies are obtained from system calls to OligoArrayAux, which must be properly installed (see the Notes section below). Probe/target pairs are sent to OligoArrayAux in batches of batchSize, which prevents systems calls from being too many characters. Note that OligoArrayAux does not support degeneracy codes (non-base letters), although they are accepted without error. Any sequences with ambiguity should be expanded into multiple permutations with [Disambiguate](#) before input.

Value

A matrix of predicted hybridization efficiency (HybEff), formamide melt point (F_{Am}), and free energy (ddG1 and dG1) for each probe/target pair of sequences.

Note

The program OligoArrayAux (<http://mfold.rna.albany.edu/?q=DINAMelt/OligoArrayAux>) must be installed in a location accessible by the system. For example, the following code should print the installed OligoArrayAux version when executed from the R console:

```
system("hybrid-min -V")
```

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

References

ES Wright et al. (2014) "Automated Design of Probes for rRNA-Targeted Fluorescence In Situ Hybridization Reveals the Advantages of Using Dual Probes for Accurate Identification." Applied and Environmental Microbiology, doi:10.1128/AEM.01685-14.

See Also

[DesignProbes](#), [TileSeqs](#)

Examples

```
probe <- c("GGGCTTTCACATCAGACTTAAGAAACC", "CCCCACGCTTTCGCGCC")
target <- reverseComplement(DNAStringSet(probe))
# not run (must have OligoArrayAux installed first):
## Not run: CalculateEfficiencyFISH(probe, target, temp=46, P=250e-9, ions=1, FA=35)
```

CalculateEfficiencyPCR

Predict Amplification Efficiency of Primer Sequences

Description

Calculates the amplification efficiency of primers from their hybridization efficiency and elongation efficiency at the target site.

Usage

```
CalculateEfficiencyPCR(primer,
                      target,
                      temp,
                      P,
                      ions,
                      batchSize = 1000,
                      taqEfficiency = TRUE,
                      maxDistance = 0.4,
                      maxGaps = 2,
                      processors = NULL)
```

Arguments

| | |
|---------------|---|
| primer | A DNASTringSet object or character vector with unaligned primer sequences in 5' to 3' orientation. |
| target | A DNASTringSet object or character vector with unaligned target or non-target sequences in 5' to 3' orientation. |
| temp | Numeric specifying the annealing temperature used in the PCR reaction. |
| P | Numeric giving the molar concentration of primers in the reaction. |
| ions | Numeric giving the molar sodium equivalent ionic concentration. Values may range between 0.01M and 1M. |
| batchSize | Integer specifying the number of primers to simulate hybridization per batch. See the Description section below. |
| taqEfficiency | Logical determining whether to make use of elongation efficiency and maxDistance to increase predictive accuracy for <i>Taq</i> DNA Polymerase amplifying primers with mismatches near the 3' terminus. Note that this should be set to FALSE if using a high-fidelity polymerase with 3' to 5' exonuclease activity. |
| maxDistance | Numeric specifying the maximal fraction of mismatched base pairings on a rolling basis beginning from the 3' end of the primer. Only used if taqEfficiency is TRUE. |
| maxGaps | Integer specifying the maximum number of insertions or deletions (indels) in the primer/target alignment. Only used if taqEfficiency is TRUE. |
| processors | The number of processors to use, or NULL (the default) for all available processors. |

Details

Amplification of pairwise primer/target pairs is simulated *in silico*. A complex model of hybridization is employed that takes into account the side reactions resulting from probe-folding, target-folding, and primer-dimer formation. The resulting hybridization efficiency is multiplied by the elongation efficiency to predict the overall efficiency of amplification.

Free energy is obtained from system calls to OligoArrayAux, which must be properly installed (see the Notes section below). Primer/target pairs are sent to OligoArrayAux in batches of batchSize, which prevents systems calls from being too many characters. Note that OligoArrayAux does not

support degeneracy codes (non-base letters), although they are accepted without error. Any sequences with ambiguity should be expanded into multiple permutations with [Disambiguate](#) before input.

Value

A vector of predicted efficiencies for amplifying each primer/target pair of sequences.

Note

The program OligoArrayAux (<http://mfold.rna.albany.edu/?q=DINAMelt/OligoArrayAux>) must be installed in a location accessible by the system. For example, the following code should print the installed OligoArrayAux version when executed from the R console:

```
system("hybrid-min -V")
```

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

References

ES Wright et al. (2013) "Exploiting Extension Bias in PCR to Improve Primer Specificity in Ensembles of Nearly Identical DNA Templates." *Environmental Microbiology*, doi:10.1111/1462-2920.12259.

See Also

[AmplifyDNA](#), [DesignPrimers](#), [DesignSignatures](#)

Examples

```
primers <- c("AAAACGGGAGCGGGGG", "AAAACTCAACCCGAGGAGCGCGT")
targets <- reverseComplement(DNAStringSet(primers))
# not run (must have OligoArrayAux installed first):
## Not run: CalculateEfficiencyPCR(primers, targets, temp=75, P=4e-7, ions=0.225)
```

ConsensusSequence

Create A Consensus Sequence

Description

Forms a consensus sequence representing a set of sequences.

Usage

```
ConsensusSequence(myXStringSet,
                  threshold = 0.05,
                  ambiguity = TRUE,
                  noConsensusChar = "+",
                  minInformation = 0.75,
                  ignoreNonBases = FALSE,
                  includeTerminalGaps = FALSE)
```

Arguments

| | |
|----------------------------------|---|
| <code>myXStringSet</code> | An <code>AAStringSet</code> , <code>DNAStrngSet</code> , or <code>RNAStrngSet</code> object of aligned sequences. |
| <code>threshold</code> | Numeric giving the maximum fraction of sequence information that can be lost in the consensus sequence. |
| <code>ambiguity</code> | Logical specifying whether to consider ambiguity as split between their respective nucleotides. Degeneracy codes are specified in the <code>IUPAC_CODE_MAP</code> . |
| <code>noConsensusChar</code> | Single character from the sequence's alphabet giving the base to use when there is no consensus in a position. |
| <code>minInformation</code> | Minimum fraction of information required to form consensus in each position. |
| <code>ignoreNonBases</code> | Logical specifying whether to count gap ("-"), mask ("+"), and unknown (".") characters towards the consensus. |
| <code>includeTerminalGaps</code> | Logical specifying whether or not to include terminal gaps ("- or "." characters on each end of the sequence) into the formation of consensus. |

Details

Two key parameters control the degree of consensus: `threshold` and `minInformation`. The default `threshold` (0.05) means that at most 5% of sequences will not be represented by the consensus sequence at any given position. The default `minInformation` (0.75) specifies that at least 75% of sequences must contain the information in the consensus, otherwise the `noConsensusChar` is used. If the specified `threshold` results in the choice of an ambiguity code that does not represent `minInformation` fraction of the sequences, then the `noConsensusChar` is used.

If `ambiguity = TRUE` (the default) then degeneracy codes are split between their respective bases according to the `IUPAC_CODE_MAP` for DNA/RNA, or `AMINO_ACID_CODE` for AA. For example, an "R" in a `DNAStrngSet` would count as half an "A" and half a "G". If `ambiguity = FALSE` then degeneracy codes are not considered in forming the consensus. For an `AAStringSet` input, the lack of degeneracy codes generally results in "X" in positions with mismatches, unless the `threshold` is set higher than 0.05 (the default).

If `includeNonBases = TRUE` (the default) then gap ("-"), mask ("+"), and unknown (".") characters are counted towards the consensus, otherwise they are omitted from calculation of the consensus. Note that gap ("-") and unknown (".") characters are treated interchangeably as gaps when forming the consensus sequence. For this reason, the consensus of a position with all unknown (".") characters will be a gap ("-"). Also, note that if consensus is formed between different length sequences then it will represent only the longest sequences at the end. For this reason the consensus sequence is generally based on a sequence alignment so that all of the sequences will have equal lengths.

Value

An XStringSet with a single consensus sequence matching the input type.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

See Also

[Disambiguate](#), [IdConsensus](#), [Seqs2DB](#)

Examples

```
dna <- DNASTringSet(c("ANGCT-", "-ACCT-"))
ConsensusSequence(dna)
# returns "ANSCT-"

aa <- AAStringSet(c("ANQIH-", "ADELW."))
ConsensusSequence(aa)
# returns "ABZJX-"
```

CorrectFrameshifts *Corrects Frameshift Errors In Protein Coding Sequences*

Description

Corrects the reading frame to mitigate the impact of frameshift errors caused by insertions or deletions in unaligned nucleotide sequences.

Usage

```
CorrectFrameshifts(myXStringSet,
                  myAAStringSet,
                  type = "indels",
                  acceptDistance = 0.01,
                  rejectDistance = 0.60,
                  maxComparisons = 10,
                  gapOpening = -13,
                  gapExtension = -1,
                  frameShift = -15,
                  geneticCode = GENETIC_CODE,
                  substitutionMatrix = "MIQS",
                  verbose = TRUE,
                  processors = NULL)
```

Arguments

| | |
|--------------------|---|
| myXStringSet | A DNAStr ingSet or RNAStr ingSet of unaligned protein coding sequences in 5' to 3' orientation. |
| myAAStringSet | An AAStringSet of reference sequences having accurate translations. |
| type | Character string indicating the type of result desired. This should be (an abbreviation of) one of "indels", "sequences", or "both". (See details section below.) |
| acceptDistance | Numeric giving the maximum distance from a reference sequence that is acceptable to skip any remaining comparisons. |
| rejectDistance | Numeric giving the maximum distance from a reference sequence that is allowed when correcting frameshifts. Sequences in myXStringSet that are greater than rejectDistance from the nearest reference sequence will only have their length trimmed from the 3'-end to a multiple of 3 nucleotides without any frameshift correction. |
| maxComparisons | The number of reference comparisons to make before stopping the search for a closer reference sequence. |
| gapOpening | Numeric giving the cost for opening a gap between the query and reference sequences. |
| gapExtension | Numeric giving the cost for extending an open gap between the query and reference sequences. |
| frameShift | Numeric giving the cost for shifting between frames of the query sequence. |
| geneticCode | Named character vector in the same format as GENETIC_CODE (the default), which represents the standard genetic code. |
| substitutionMatrix | Either a substitution matrix representing the substitution scores for matching two amino acids or the name of the amino acid substitution matrix. The latter may be one of the following: "BLOSUM45", "BLOSUM50", "BLOSUM62", "BLOSUM80", "BLOSUM100", "PAM30", "PAM40", "PAM70", "PAM120", "PAM250", or "MIQS" (the default). |
| verbose | Logical indicating whether to display progress. |
| processors | The number of processors to use, or NULL (the default) for all available processors. |

Details

Accurate translation of protein coding sequences can be greatly disrupted by one or two nucleotide phase shifts that occasionally occur during DNA sequencing. These frameshift errors can potentially be corrected through comparison with other unshifted protein sequences. This function uses a set of reference amino acid sequences (AAStringSet) to find and correct frameshift errors in a set of nucleotide sequences (myXStringSet). First, three frame translation of the nucleotide sequences is performed, and the nearest reference sequence is selected. Then the optimal reading frame at each position is determined based on a variation of the Guan & Uberbacher method. Putative insertions and/or deletions (indels) are returned in the result, typically with close proximity to the true indel locations.

If type is "sequences" or "both", then frameshifts are corrected by adding N's and/or removing nucleotides. Note that this changes the nucleotide sequence, and the new sequence often has minor errors because the exact location of the indel(s) cannot be determined. However, the original frameshifts that disrupted the entire downstream sequence are reduced to local perturbations. All of the returned nucleotide sequences will have a reading frame starting from the first position. This allows direct translation, and in practice works well if there is a similar reference myAAStringSet with the correct reading frame. Hence it is more important that myAAStringSet contain a wide variety of sequences than it is that it contain a lot of sequences.

Multiple inputs control the time required for frameshift correction. The number of sequences in the reference set (myAAStringSet) will affect the speed of the first search for similar sequences. Assessing frameshifts in the second step requires order $N \times M$ time, where N and M are the lengths of the query (myXStringSet) and reference sequences. Two parameters control the number of assessments that are made for each sequence: (1) `maxComparisons` determines the maximum number of reference sequences to compare to each query sequence, and (2) `acceptDist` defines the maximum distance between a query and reference that is acceptable before continuing to the next query sequence. A lower value for `maxComparisons` or a higher value for `acceptDist` will accelerate frameshift correction, potentially at the expense of some accuracy.

Value

If type is "indels" then the returned object is a list with the same length as myXStringSet. Each element is a list with four components:

| | |
|------------|--|
| insertions | Approximate positions of inserted nucleotides, which could be removed to correct the reading frame. |
| deletions | Approximate positions of deleted nucleotides, which could be added back to correct the reading frame. |
| distance | The amino acid distance from the nearest reference sequence, between 0 and 1. |
| index | The integer index of the reference sequence that was used for frame correction, or 0 if no reference sequence was within <code>rejectDistance</code> . |

If type is "sequences" then the returned object is an XStringSet of the same type as the input (myXStringSet). Nucleotides are added or deleted as necessary to correct for frameshifts. The returned sequences all have a reading frame starting from position 1, so that they can be translated directly.

If type is "both" then the returned object is a list with two components: one for the "indels" and the other for the "sequences".

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

References

Guan, X., & Uberbacher, E. C. (1996). Alignments of DNA and protein sequences containing frameshift errors. *Computer Applications in the Biosciences : CABIOS*, **12**(1), 31-40.

See Also

[AlignTranslation](#), [OrientNucleotides](#)

Examples

```
fas <- system.file("extdata", "50S_ribosomal_protein_L2.fas", package="DECIPHER")
dna <- readDNAStrngSet(fas)

# introduce artificial indels
n_ins <- 2 # insertions per sequence
shifted <- replaceAt(dna,
  lapply(width(dna),
    sample,
    n_ins),
  sample(DNA_BASES,
    n_ins,
    replace=TRUE))
n_dels <- 1 # deletions per sequence
shifted <- replaceAt(shifted,
  RangesList(lapply(width(shifted),
    function(x) {
      IRanges(sample(x,
        n_dels),
        width=1)
    })))

# to make frameshift correction more challenging,
# only supply 20 reference amino acid sequences
s <- sample(length(dna), 20)
x <- CorrectFrameshifts(shifted,
  translate(dna[s]),
  type="both")

# there was a wide range of distances
# to the nearest reference sequence
quantile(unlist(lapply(x[[1]], `[\`, "distance")))

# none of the sequences were > rejectDistance
# from the nearest reference sequence
length(which(unlist(lapply(x[[1]], `[\`, "index"))==0))

# the number of indels was generally correct
table(unlist(lapply(x[[1]], function(x) {
  length(x$insertions)}))/length(shifted)
table(unlist(lapply(x[[1]], function(x) {
  length(x$deletions)}))/length(shifted)

# align and display the translations
AA <- AlignTranslation(x$sequences,
  readingFrame=1,
  asAAStringSet=TRUE)
BrowseSeqs(AA)
```

| | |
|----------------|-----------------------------------|
| CreateChimeras | <i>Create Artificial Chimeras</i> |
|----------------|-----------------------------------|

Description

Creates artificial random chimeras from a set of sequences.

Usage

```
CreateChimeras(myDNAStringSet,  
               numChimeras = 10,  
               numParts = 2,  
               minLength = 80,  
               maxLength = Inf,  
               minChimericRegionLength = 30,  
               randomLengths = TRUE,  
               includeParents = TRUE,  
               processors = NULL,  
               verbose = TRUE)
```

Arguments

| | |
|--------------------------------------|---|
| <code>myDNAStringSet</code> | A <code>DNAStringSet</code> object with aligned sequences. |
| <code>numChimeras</code> | Number of chimeras desired. |
| <code>numParts</code> | Number of chimeric parts from which to form a single chimeric sequence. |
| <code>minLength</code> | Minimum length of the complete chimeric sequence. |
| <code>maxLength</code> | Maximum length of the complete chimeric sequence. |
| <code>minChimericRegionLength</code> | Minimum length of the chimeric region of each sequence part. |
| <code>randomLengths</code> | Logical specifying whether to create random length chimeras in addition to random breakpoints. |
| <code>includeParents</code> | Whether to include the parents of each chimera in the output. |
| <code>processors</code> | The number of processors to use, or <code>NULL</code> (the default) for all available processors. |
| <code>verbose</code> | Logical indicating whether to display progress. |

Details

Forms a set of random chimeras from the input set of (typically good quality) sequences. The chimeras are created by merging random sequences at random breakpoints. These chimeras can be used for testing the accuracy of the [FindChimeras](#) or other chimera finding functions.

Value

A DNAStrngSet object containing chimeras. The names of the chimeras are specified as "parent #1 name [chimeric region] (distance from parent to chimera), ...".

If includeParents = TRUE then the parents of the chimeras are included at the end of the result. The parents are trimmed to the same length as the chimera if randomLengths = TRUE. The names of the parents are specified as "parent #1 name [region] (distance to parent #2, ...)".

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

See Also

[FindChimeras](#), [Seqs2DB](#)

Examples

```
db <- system.file("extdata", "Bacteria_175seqs.sqlite", package="DECIPHER")
dna <- SearchDB(db)
chims <- CreateChimeras(dna)
BrowseSeqs(chims)
```

DB2Seqs

Export Database Sequences to a FASTA or FASTQ File

Description

Exports a database containing sequences to a FASTA or FASTQ formatted file of sequence records.

Usage

```
DB2Seqs(file,
         dbFile,
         tblName = "DNA",
         identifier = "",
         type = "BStringSet",
         limit = -1,
         replaceChar = "-",
         nameBy = "description",
         orderBy = "row_names",
         removeGaps = "none",
         append = FALSE,
         width = 80,
         compress = FALSE,
         chunkSize = 1e5,
         clause = "",
         verbose = TRUE)
```

Arguments

| | |
|-------------|---|
| file | Character string giving the location where the file should be written. |
| dbFile | A SQLite connection object or a character string specifying the path to the database file. |
| tblName | Character string specifying the table in which to extract the data. |
| identifier | Optional character string used to narrow the search results to those matching a specific identifier. If "" then all identifiers are selected. |
| type | The type of XStringSet (sequences) to export to a FASTA formatted file or QualityScaledXStringSet to export to a FASTQ formatted file. This should be (an unambiguous abbreviation of) one of "DNAStrngSet", "RNAStrngSet", "AAStrngSet", "BStringSet", "QualityScaledDNAStrngSet", "QualityScaledRNAStrngSet", "QualityScaledAAStrngSet", or "QualityScaledBStringSet". (See details section below.) |
| limit | Number of results to display. The default (-1) does not limit the number of results. |
| replaceChar | Optional character used to replace any characters of the sequence that are not present in the XStringSet's alphabet. Not applicable if type=="BStringSet". (See details section below.) |
| nameBy | Character string giving the column name(s) for identifying each sequence record. If more than one column name is provided, the information in each column is concatenated, separated by pairs of colons ("::"), in the order specified. |
| orderBy | Character string giving the column name for sorting the results. Defaults to the order of entries in the database. Optionally can be followed by " ASC" or " DESC" to specify ascending (the default) or descending order. |
| removeGaps | Determines how gaps ("- or ." characters) are removed in the sequences. This should be (an unambiguous abbreviation of) one of "none", "all" or "common". |
| append | Logical indicating whether to append the output to the existing file. |
| width | Integer specifying the maximum number of characters per line of sequence. Not applicable when exporting to a FASTQ formatted file. |
| compress | Logical specifying whether to compress the output file using gzip compression. |
| chunkSize | Number of lines of the file to write at a time. Cannot be less than the total number of sequences if removeGaps is "common". |
| clause | An optional character string to append to the query as a clause. |
| verbose | Logical indicating whether to display status. |

Details

Sequences are exported into either a FASTA or FASTQ file as determined by the type of sequences. If type is an XStringSet then sequences are exported to FASTA format. Quality information for QualityScaledXStringSets are interpreted as PredQuality scores before export to FASTQ format.

If type is "BStringSet" (the default) then sequences are exported to a FASTA file exactly the same as they were when imported. If type is "DNAStrngSet" then all U's are converted to T's before export, and vice-versa if type is "RNAStrngSet". All remaining characters not in the XStringSet's alphabet are converted to replaceChar.

Value

Writes a FASTA or FASTQ formatted file containing the sequence records in the database.
Returns the number of sequence records written to the file.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

Examples

```
db <- system.file("extdata", "Bacteria_175seqs.sqlite", package="DECIPHER")
tf <- tempfile()
DB2Seqs(tf, db, limit=10)
file.show(tf)
unlink(tf)
```

DECIPHER-defunct

Defunct functions in package 'DECIPHER'

Description

These functions are defunct and no longer available.

Details

The following functions are defunct; use the replacement indicated below:

- BrowseSequences: [BrowseSeqs](#)
- Amplify: [AmplifyDNA](#)

deltaGrules

Free Energy of Hybridization of Probe/Target Quadruplets on Microarrays

Description

An 8D array with four adjacent base pairs of the probe and target sequences at a time. Each dimension has five elements defining the residue at that position ("A", "C", "G", "T", or "-"). The array contains the standard Gibbs free energy change of probe binding (dG, [kcal/mol]) for every quadruple base pairing.

Usage

```
data(deltaGrules)
```


References

SantaLucia, J., Jr., & Hicks, D. (2004) The Thermodynamics of DNA Structural Motifs. Annual Review of Biophysics and Biomolecular Structure, 33(1), 415-440. doi:10.1146/annurev.biophys.32.110601.141800.

Examples

```
data(deltaSrules)
# dS of primer = AGCT / target = A-CT pairing
deltaSrules["A", "G", "C", "T", "A", "-", "C", "T"]
```

DesignArray

Design a set of DNA Microarray Probes for Detecting Sequences

Description

Chooses the set of microarray probes maximizing sensitivity and specificity to each target consensus sequence.

Usage

```
DesignArray(myDNAStringSet,
            maxProbeLength = 24,
            minProbeLength = 20,
            maxPermutations = 4,
            numRecordedMismatches = 500,
            numProbes = 10,
            start = 1,
            end = NULL,
            maxOverlap = 5,
            hybridizationFormamide = 10,
            minMeltingFormamide = 15,
            maxMeltingFormamide = 20,
            minScore = -1e+12,
            processors = NULL,
            verbose = TRUE)
```

Arguments

myDNAStringSet A DNAStringSet object of aligned consensus sequences.

maxProbeLength The maximum length of probes, not including the poly-T spacer. Ideally less than 27 nucleotides.

minProbeLength The minimum length of probes, not including the poly-T spacer. Ideally more than 18 nucleotides.

maxPermutations
The maximum number of probe permutations required to represent a target site. For example, if a target site has an 'N' then 4 probes are required because probes cannot be ambiguous. Typically fewer permutations are preferable because this requires less space on the microarray and simplifies interpretation of the results.

| | |
|------------------------|--|
| numRecordedMismatches | The maximum number of recorded potential cross-hybridizations for any target site. |
| numProbes | The target number of probes on the microarray per input consensus sequence. |
| start | Integer specifying the starting position in the alignment where potential forward primer target sites begin. Preferably a position that is included in most sequences in the alignment. |
| end | Integer specifying the ending position in the alignment where potential reverse primer target sites end. Preferably a position that is included in most sequences in the alignment. |
| maxOverlap | Maximum overlap in nucleotides between target sites on the sequence. |
| hybridizationFormamide | The formamide concentration (% vol/vol) used in hybridization at 42 degrees Celsius. Note that this concentration is used to approximate hybridization efficiency of cross-amplifications. |
| minMeltingFormamide | The minimum melting point formamide concentration (% vol/vol) of the designed probes. The melting point is defined as the concentration where half of the template is bound to probe. |
| maxMeltingFormamide | The maximum melting point formamide concentration (% vol/vol) of the designed probes. Must be greater than the minMeltingFormamide. |
| minScore | The minimum score of designed probes before exclusion. A greater minScore will accelerate the code because more target sites will be excluded from consideration. However, if the minScore is too high it will prevent any target sites from being recorded. |
| processors | The number of processors to use, or NULL (the default) for all available processors. |
| verbose | Logical indicating whether to display progress. |

Details

The algorithm begins by determining the optimal length of probes required to meet the input constraints while maximizing sensitivity to the target consensus sequence at the specified hybridization formamide concentration. This set of potential target sites is then scored based on the possibility of cross-hybridizing to the other non-target sequences. The set of probes is returned with the minimum possibility of cross-hybridizing.

Value

A data.frame with the optimal set of probes matching the specified constraints. Each row lists the probe's target sequence (name), start position, length in nucleotides, start and end position in the sequence alignment, number of permutations, score, melt point in percent formamide at 42 degrees Celsius, hybridization efficiency (hyb_eff), target site, and probe(s). Probes are designed such that the stringency is determined by the equilibrium hybridization conditions and not subsequent washing steps.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

References

ES Wright et al. (2013) Identification of Bacterial and Archaeal Communities From Source to Tap. Water Research Foundation, Denver, CO.

DR Noguera, et al. (2014). Mathematical tools to optimize the design of oligonucleotide probes and primers. Applied Microbiology and Biotechnology. doi:10.1007/s00253-014-6165-x.

See Also

[Array2Matrix](#), [NLS](#)

Examples

```
fas <- system.file("extdata", "Bacteria_175seqs.fas", package="DECIPHER")
dna <- readDNASTringSet(fas)
names(dna) <- 1:length(dna)
probes <- DesignArray(dna)
probes[1,]
```

DesignPrimers

Design PCR Primers Targeting a Specific Group of Sequences

Description

Assists in the design of primer sets targeting a specific group of sequences while minimizing the potential to cross-amplify other groups of sequences.

Usage

```
DesignPrimers(tiles,
              identifier = "",
              start = 1,
              end = NULL,
              minLength = 17,
              maxLength = 26,
              maxPermutations = 4,
              minCoverage = 0.9,
              minGroupCoverage = 0.2,
              annealingTemp = 64,
              P = 4e-07,
              monovalent = 0.07,
              divalent = 0.003,
              dNTPs = 8e-04,
              minEfficiency = 0.8,
```

```
worstScore = -Inf,
numPrimerSets = 0,
minProductSize = 75,
maxProductSize = 1200,
maxSearchSize = 1500,
batchSize = 1000,
maxDistance = 0.4,
primerDimer = 1e-07,
ragged5Prime = TRUE,
taqEfficiency = TRUE,
induceMismatch = FALSE,
processors = NULL,
verbose = TRUE)
```

Arguments

| | |
|------------------|--|
| tiles | A set of tiles representing each group of sequences, as in the format created by the function TileSeqs. |
| identifier | Optional character string used to narrow the search results to those matching a specific identifier. Determines the target group(s) for which primers will be designed. If "" then all identifiers are selected. |
| start | Integer specifying the starting position in the alignment where potential forward primer target sites begin. Preferably a position that is included in most sequences in the alignment. |
| end | Integer specifying the ending position in the alignment where potential reverse primer target sites end. Preferably a position that is included in most sequences in the alignment. |
| minLength | Integer providing the minimum length of primers to consider in the design. |
| maxLength | Integer providing the maximum length of primers to consider in the design, which must be less than or equal to the maxLength of tiles. |
| maxPermutations | Integer providing the maximum number of permutations considered as part of a forward or reverse primer set. |
| minCoverage | Numeric giving the minimum fraction of the target group's sequences that must be covered with the primer set. |
| minGroupCoverage | Numeric giving the minimum fraction of the target group that must have sequence information (not terminal gaps) in the region covered by the primer set. |
| annealingTemp | Numeric indicating the desired annealing temperature that will be used in the PCR experiment. |
| P | Numeric giving the molar concentration of primers in the reaction. |
| monovalent | The molar concentration of monovalent ([Na] and [K]) ions in solution that will be used to determine a sodium equivalent concentration. |
| divalent | The molar concentration of divalent ([Mg]) ions in solution that will be used to determine a sodium equivalent concentration. |

| | |
|----------------|---|
| dNTPs | Numeric giving the molar concentration of free nucleotides added to the solution that will be used to determine a sodium equivalent concentration. |
| minEfficiency | Numeric giving the minimum efficiency of hybridization desired for the primer set. Note that an efficiency of 99% (0.99) will greatly lower predicted specificity of the primer set, however an efficiency of 50% (0.5) may be too low in actuality to amplify the target group due to error in melt temperature predictions. |
| worstScore | Numeric specifying the score cutoff to remove target sites from consideration. For example, a worstScore of -5 will remove all primer sets scoring below -5, although this may eventually result in no primer sets meeting the design criteria. |
| numPrimerSets | Integer giving the optimal number of primer sets (forward and reverse primer sets) to design. If set to zero then all possible forward and reverse primers are returned, but the primer sets minimizing potential cross-amplifications are not chosen. |
| minProductSize | Integer giving the minimum number of nucleotides desired in the PCR product. |
| maxProductSize | Integer giving the maximum number of nucleotides desired in the PCR product. |
| maxSearchSize | Integer giving the maximum number of nucleotides to search for false priming upstream and downstream of the expected binding site. |
| batchSize | Integer specifying the number of primers to simulate hybridization per batch that is passed to CalculateEfficiencyPCR. |
| maxDistance | Numeric specifying the maximal fraction of mismatched base pairings on a rolling basis beginning from the 3' end of the primer. |
| primerDimer | Numeric giving the maximum amplification efficiency of potential primer-dimer products. |
| ragged5Prime | Logical specifying whether the 5' end or 3' end of primer permutations targeting the same site should be varying lengths. |
| taqEfficiency | Logical determining whether to make use of elongation efficiency and maxDistance to increase predictive accuracy for <i>Taq</i> DNA Polymerase amplifying primers with mismatches near the 3' terminus. Note that this should be set to FALSE if using a high-fidelity polymerase with 3' to 5' exonuclease activity. |
| induceMismatch | Logical or integer specifying whether to induce a mismatch in the primer with the template DNA. If TRUE then a mismatch is induced at the 6th primer position. If an integer value is provided between 2 and 6 then a mismatch is induced in that primer position, where the 3'-end is defined as position 1. |
| processors | The number of processors to use, or NULL (the default) for all available processors. |
| verbose | Logical indicating whether to display progress. |

Details

Primers are designed for use with *Taq* DNA Polymerase to maximize sensitivity and specificity for the target group of sequences. The design makes use of *Taq*'s bias against certain 3' terminal mismatch types in order to increase specificity further than can be achieved with hybridization efficiency alone.

Primers are designed from a set of tiles to target each identifier while minimizing affinity for all other tiled groups. Arguments provide constraints that ensure the designed primer sets meet

the specified criteria as well as being optimized for the particular experimental conditions. A search is conducted through all tiles in the same alignment position to estimate the chance of cross-amplification with a non-target group.

If numPrimers is greater than or equal to one then the set of forward and reverse primers that minimizes potential false positive overlap is returned. This will also initiate a thorough search through all target sites upstream and downstream of the expected binding sites to ensure that the primers do not bind to nearby positions. Lowering the maxSearchSize will speed up the thorough search at the expense of potentially missing an unexpected target site. The number of possible primer sets assessed is increased with the size of numPrimers.

Value

A different data.frame will be returned depending on number of primer sets requested. If no primer sets are required then columns contain the forward and reverse primers for every possible position scored by their potential to amplify other identified groups. If one or more primer sets are requested then columns contain information for the optimal set of forward and reverse primers that could be used in combination to give the fewest potential cross-amplifications.

Note

The program OligoArrayAux (<http://mfold.rna.albany.edu/?q=DINAMelt/OligoArrayAux>) must be installed in a location accessible by the system. For example, the following code should print the installed OligoArrayAux version when executed from the R console:

```
system("hybrid-min -V")
```

To install OligoArrayAux from the downloaded source folder on Unix-like platforms, open the shell (or Terminal on Mac OS) and type:

```
cd oligoarrayaux # change directory to the correct folder name
./configure
make
sudo make install
```

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

References

ES Wright et al. (2013) "Exploiting Extension Bias in PCR to Improve Primer Specificity in Ensembles of Nearly Identical DNA Templates." Environmental Microbiology, doi:10.1111/1462-2920.12259.

See Also

[AmplifyDNA](#), [CalculateEfficiencyPCR](#), [DesignSignatures](#), [TileSeqs](#)

Examples

```

db <- system.file("extdata", "Bacteria_175seqs.sqlite", package="DECIPHER")
# not run (must have OligoArrayAux installed first):
## Not run: tiles <- TileSeqs(db, identifier=c("Acinetobacter","Pseudomonas"))
## Not run: primers <- DesignPrimers(tiles, identifier="Acinetobacter", start=280, end=420,
    minProductSize=50, numPrimerSets=1)
## End(Not run)

```

DesignProbes

Design FISH Probes Targeting a Specific Group of Sequences

Description

Assists in the design of single or dual probes targeting a specific group of sequences while minimizing the potential to cross-hybridize with other groups of sequences.

Usage

```

DesignProbes(tiles,
             identifier = "",
             start = 1,
             end = NULL,
             minLength = 17,
             maxLength = 26,
             maxPermutations = 4,
             minCoverage = 0.9,
             minGroupCoverage = 0.2,
             hybTemp = 46,
             P = 2.5e-07,
             Na = 1,
             FA = 35,
             minEfficiency = 0.5,
             worstScore = -Inf,
             numProbeSets = 0,
             batchSize = 1000,
             target = "SSU",
             verbose = TRUE)

```

Arguments

| | |
|------------|---|
| tiles | A set of tiles representing each group of sequences, as in the format created by the function <code>TileSeqs</code> . |
| identifier | Optional character string used to narrow the search results to those matching a specific identifier. Determines the target group(s) for which probes will be designed. If "" then all identifiers are selected. |

| | |
|------------------|--|
| start | Integer specifying the starting position in the alignment where potential target sites begin. Preferably a position that is included in most sequences in the alignment. |
| end | Integer specifying the ending position in the alignment where potential target sites end. Preferably a position that is included in most sequences in the alignment. |
| minLength | Integer providing the minimum length of probes to consider in the design. |
| maxLength | Integer providing the maximum length of probes to consider in the design, which must be less than or equal to the maxLength of tiles. |
| maxPermutations | Integer providing the maximum number of probe permutations required to reach the desired coverage of a target site. |
| minCoverage | Numeric giving the minimum fraction of the target group's sequences that must be covered by the designed probe(s). |
| minGroupCoverage | Numeric giving the minimum fraction of the target group that must have sequence information (not terminal gaps) in the target site's region. |
| hybTemp | Numeric specifying the hybridization temperature, typically 46 degrees Celsius. |
| P | Numeric giving the molar concentration of probes during hybridization. |
| Na | Numeric giving the molar sodium concentration in the hybridization buffer. Values may range between 0.01M and 1M. Note that salt correction from 1 molar is not available for the thermodynamic rules of RNA/RNA interactions. |
| FA | Numeric concentration (as percent v/v) of the denaturant formamide in the hybridization buffer. |
| minEfficiency | Numeric giving the minimum equilibrium hybridization efficiency desired for designed probe(s) at the defined experimental conditions. |
| worstScore | Numeric specifying the score cutoff to remove target sites from consideration. For example, a worstScore of -5 will remove all probes scoring below -5, although this may eventually result in no probes meeting the design criteria. |
| numProbeSets | Integer giving the optimal number of dual probe sets to design. If set to zero then all potential single probes are returned, and the probe sets minimizing potential false cross-hybridizations are not chosen. |
| batchSize | Integer specifying the number of probes to simulate hybridization per batch that is passed to CalculateEfficiencyFISH. |
| target | The target molecule used in the generation of tiles. Either "SSU" for the small-subunit rRNA, "LSU" for the large-subunit rRNA, or "Other". Used to determine the domain for dG3 calculations, which is plus or minus 200 nucleotides of the target site if "Other". |
| verbose | Logical indicating whether to display progress. |

Details

Probes are designed to maximize sensitivity and specificity to the target group(s) (identifier(s)). If numProbeSets > 0 then that many pairs of probes with minimal cross-hybridization overlap are returned, enabling increased specificity with a dual-color approach.

Probes are designed from a set of tiles to target each identifier while minimizing affinity for all other tiled groups. Arguments provide constraints that ensure the designed probes meet the specified criteria as well as being optimized for the particular experimental conditions. A search is conducted through all tiles in the same alignment position to estimate the chance of cross-hybridization with a non-target group.

Two models are used in design, both of which were experimentally calibrated using denaturation profiles from 5 organisms belonging to all three domains of life. Probe lengths are chosen to meet the `minEfficiency` using a fast model of probe-target hybridization. Candidate probes are then confirmed using a slower model that also takes into account probe-folding and target-folding. Finally, probes are scored for their inability to cross-hybridize with non-target groups by using the fast model and taking into account any mismatches.

Value

A different `data.frame` will be returned depending on number of primer sets requested. If no probe sets are required then columns contain the designed probes for every possible position scored by their potential to cross-hybridize with other identified groups. If one or more probe sets are requested then columns contain information for the optimal set of probes (probe one and probe two) that could be used in combination to give the fewest potential cross-hybridizations.

Note

The program `OligoArrayAux` (<http://mfold.rna.albany.edu/?q=DINAMelt/OligoArrayAux>) must be installed in a location accessible by the system. For example, the following code should print the installed `OligoArrayAux` version when executed from the R console:

```
system("hybrid-min -V")
```

To install `OligoArrayAux` from the downloaded source folder on Unix-like platforms, open the shell (or Terminal on Mac OS) and type:

```
cd oligoarrayaux # change directory to the correct folder name
./configure
make
sudo make install
```

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

References

ES Wright et al. (2014) "Automated Design of Probes for rRNA-Targeted Fluorescence In Situ Hybridization Reveals the Advantages of Using Dual Probes for Accurate Identification." *Applied and Environmental Microbiology*, doi:10.1128/AEM.01685-14.

See Also

[CalculateEfficiencyFISH](#), [TileSeqs](#)

Examples

```
db <- system.file("extdata", "Bacteria_175seqs.sqlite", package="DECIPHER")
# not run (must have OligoArrayAux installed first):
## Not run: tiles <- TileSeqs(db, identifier=c("Acinetobacter","Pseudomonas"))
## Not run: probes <- DesignProbes(tiles, identifier="Acinetobacter", start=280, end=420)
```

DesignSignatures

Design PCR Primers for Amplifying Group-Specific Signatures

Description

Aids the design of pairs of primers for amplifying a unique “signature” from each group of sequences. Signatures are distinct PCR products that can be differentiated by their length, melt temperature, or sequence.

Usage

```
DesignSignatures(dbFile,
                 tblName = "DNA",
                 identifier = "",
                 focusID = NA,
                 type = "melt",
                 resolution = 0.5,
                 levels = 10,
                 enzymes = NULL,
                 minLength = 17,
                 maxLength = 26,
                 maxPermutations = 4,
                 annealingTemp = 64,
                 P = 4e-07,
                 monovalent = 0.07,
                 divalent = 0.003,
                 dNTPs = 8e-04,
                 minEfficiency = 0.8,
                 ampEfficiency = 0.5,
                 numPrimerSets = 100,
                 minProductSize = 70,
                 maxProductSize = 400,
                 kmerSize = 8,
                 searchPrimers = 500,
                 maxDictionary = 20000,
                 primerDimer = 1e-07,
                 pNorm = 1,
                 taqEfficiency = TRUE,
                 processors = NULL,
                 verbose = TRUE)
```

Arguments

| | |
|-----------------|--|
| dbFile | A SQLite connection object or a character string specifying the path to the database file. |
| tblName | Character string specifying the table where the DNA sequences are located. |
| identifier | Optional character string used to narrow the search results to those matching a specific identifier. Determines the target group(s) for which primers will be designed. If "" then all identifiers are selected. |
| focusID | Optional character string specifying which of the identifiers will be used in the initial step of designing primers. If NA (the default), then the identifier with the most sequence information is used as the focusID. |
| type | Character string indicating the type of signature being used to differentiate the PCR products from each group. This should be (an abbreviation of) one of "melt", "length", or "sequence". |
| resolution | Numeric specifying the "resolution" of the experiment, or a vector giving the boundaries of bins. (See details section below.) |
| levels | Numeric giving the number of "levels" that can be distinguished in each bin. (See details section below.) |
| enzymes | Named character vector providing the cut sites of one or more restriction enzymes. Cut sites must be delineated in the same format as RESTRICTION_ENZYMES . |
| minLength | Integer providing the minimum length of primers to consider in the design. |
| maxLength | Integer providing the maximum length of primers to consider in the design. |
| maxPermutations | Integer providing the maximum number of permutations allowed in a forward or reverse primer to attain greater coverage of sequences. |
| annealingTemp | Numeric indicating the desired annealing temperature that will be used in the PCR experiment. |
| P | Numeric giving the molar concentration of primers in the reaction. |
| monovalent | The molar concentration of monovalent ([Na] and [K]) ions in solution that will be used to determine a sodium equivalent concentration. |
| divalent | The molar concentration of divalent ([Mg]) ions in solution that will be used to determine a sodium equivalent concentration. |
| dNTPs | Numeric giving the molar concentration of free nucleotides added to the solution that will be used to determine a sodium equivalent concentration. |
| minEfficiency | Numeric giving the minimum efficiency of hybridization desired for the primer set. |
| ampEfficiency | Numeric giving the minimum efficiency required for theoretical amplification of the primers. Note that ampEfficiency must be less than or equal to minEfficiency. Lower values of ampEfficiency will allow for more PCR products, although very low values are unrealistic experimentally. |
| numPrimerSets | Integer giving the optimal number of primer sets (forward and reverse primer sets) to design. |
| minProductSize | Integer giving the minimum number of nucleotides desired in the PCR product. |

| | |
|----------------|--|
| maxProductSize | Integer giving the maximum number of nucleotides desired in the PCR product. |
| kmerSize | Integer giving the size of k-mers to use in the preliminary search for potential primers. |
| searchPrimers | Numeric specifying the number of forward and reverse primers to use in searching for potential PCR products. A lower value will result in a faster search, but potentially neglect some useful primers. |
| maxDictionary | Numeric giving the maximum number of primers to search for simultaneously in any given step. |
| primerDimer | Numeric giving the maximum amplification efficiency of potential primer-dimer products. |
| pNorm | Numeric specifying the power ($p > 0$) used in calculating the L^p -norm when scoring primer pairs. By default ($p = 1$), the score is equivalent to the average divergence between pairwise signatures. When $p < 1$, many small divergences will be preferred over fewer large divergences, and vice-versa when $p > 1$. This enables prioritizing primer pairs that will yield a greater number of unique signatures ($p < 1$), or fewer distinct, but more dissimilar, signatures ($p > 1$). |
| taqEfficiency | Logical determining whether to make use of elongation efficiency to increase predictive accuracy for <i>Taq</i> DNA Polymerase amplifying primers with mismatches near the 3' terminus. Note that this should be set to FALSE if using a high-fidelity polymerase with 3' to 5' exonuclease activity. |
| processors | The number of processors to use, or NULL (the default) for all available processors. |
| verbose | Logical indicating whether to display progress. |

Details

Signatures are group-specific PCR products that can be differentiated by either their melt temperature profile, length, or sequence. DesignSignatures assists in finding the optimal pair of forward and reverse primers for obtaining a distinguishable signature from each group of sequences. Groups are delineated by their unique identifier in the database. The algorithm works by progressively narrowing the search for optimal primers: (1) the most frequent k-mers are found; (2) these are used to design primers initially matching the focusID group; (3) the most common forward and reverse primers are selected based on all of the groups, and ambiguity is added up to maxPermutations; (4) a final search is performed to find the optimal forward and reverse primer. Pairs of primers are scored by the distance between the signatures generated for each group, which depends on the type of experiment.

The arguments resolution and levels control the theoretical resolving power of the experiment. The signature for a group is discretized or grouped into "bins" each with a certain magnitude of the signal. Here resolution determines the separation between distinguishable "bins", and levels controls the range of values in each bin. A high-accuracy experiment would have many bins and/or many levels. While levels is interpreted similarly for every type of experiment, resolution is treated differently depending on type. If type is "melt", then resolution can be either a vector of different melt temperatures, or a single number giving the change in temperatures that can be differentiated. A high-resolution melt (HRM) assay would typically have a resolution between 0.25 and 1 degree Celsius. If type is "length" then resolution is either the number of bins between the minProductSize and maxProductSize, or the bin boundaries. For example, resolution can

be lower (wider bins) at long lengths, and higher (narrower bins) at shorter lengths. If type is "sequence" then resolution sets the k-mer size used in differentiating amplicons. Oftentimes, 4 to 6-mers are used for the classification of amplicons.

The signatures can be diversified by using a restriction enzyme to digest the PCR products when type is "melt" or "length". If enzymes are supplied then the an additional search is made to find the best enzyme to use with each pair of primers. In this case, the output includes all of the primer pairs, as well as any enzymes that will digest the PCR products of that primer pair. The output is re-scored to rank the top primer pair and enzyme combination. Note that enzymes is inapplicable when type is "sequence" because restriction enzymes do not alter the sequence of the DNA. Also, it is recommended that only a subset of the available RESTRICTION_ENZYMES are used as input enzymes in order to accelerate the search for the best enzyme.

Value

A data.frame with the top-scoring pairs of forward and reverse primers, their score, the total number of PCR products, and associated columns for the restriction enzyme (if enzyme is not NULL).

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

References

Coming soon!

See Also

[AmplifyDNA](#), [CalculateEfficiencyPCR](#), [DesignPrimers](#), [DigestDNA](#), [Disambiguate](#), [MeltDNA](#), [RESTRICTION_ENZYMES](#)

Examples

```
# below are suggested inputs for different types of experiments
db <- system.file("extdata", "Bacteria_175seqs.sqlite", package="DECIPHER")

## Not run:
# High Resolution Melt (HRM) assay:
primers <- DesignSignatures(db,
  resolution=seq(80, 100, 0.25), # degrees Celsius
  minProductSize=55, # base pairs
  maxProductSize=400)

# Primers for next-generation sequencing:
primers <- DesignSignatures(db,
  type="sequence",
  minProductSize=300, # base pairs
  maxProductSize=700,
  resolution=5, # 5-mers
  levels=5)

# Primers for community fingerprinting:
```



```

primers <- DesignSignatures(db,
  type="length",
  levels=2, # presence/absence
  minProductSize=200, # base pairs
  maxProductSize=1400,
  resolution=c(seq(200, 700, 3),
    seq(705, 1000, 5),
    seq(1010, 1400, 10)))

# Primers for restriction fragment length polymorphism (RFLP):
data(RESTRICTION_ENZYMES)
myEnzymes <- RESTRICTION_ENZYMES[c("EcoRI", "HinfI", "SalI")]
primers <- DesignSignatures(db,
  type="length",
  levels=2, # presence/absence
  minProductSize=200, # base pairs
  maxProductSize=600,
  resolution=c(seq(50, 100, 3),
    seq(105, 200, 5),
    seq(210, 600, 10)),
  enzymes=myEnzymes)

## End(Not run)

```

 DigestDNA

 Simulate Restriction Digestion of DNA

Description

Restriction enzymes can be used to cut double-stranded DNA into fragments at specific cut sites. DigestDNA performs an *in-silico* restriction digest of the input DNA sequence(s) given one or more restriction sites.

Usage

```

DigestDNA(sites,
  myDNAStringSet,
  type = "fragments",
  strand = "both",
  processors = NULL)

```

Arguments

| | |
|----------------|---|
| sites | A character vector of DNA recognition sequences and their enzymes' corresponding cut site(s). |
| myDNAStringSet | A DNAStringSet object or character vector with one or more sequences in 5' to 3' orientation. |
| type | Character string indicating the type of results desired. This should be (an abbreviation of) either "fragments" or "positions". |

| | |
|------------|---|
| strand | Character string indicating the strand(s) to cut. This should be (an abbreviation of) one of "both", "top", or "bottom". The top strand is defined as the input DNASTringSet sequence, and the bottom strand is its reverse complement. |
| processors | The number of processors to use, or NULL (the default) for all available processors. |

Details

In the context of a restriction digest experiment with a known DNA sequence, it can be useful to predict the expected DNA fragments *in-silico*. Restriction enzymes make cuts in double-stranded DNA at specific positions near their recognition site. The recognition site may be somewhat ambiguous, as represented by the IUPAC_CODE_MAP. Cuts that occur at different positions on the top and bottom strands result in sticky-ends, whereas those that occur at the same position result in fragments with blunt-ends. Multiple restriction sites can be supplied to simultaneously digest the DNA. In this case, sites for the different restriction enzymes may be overlapping, which could result in multiple close-proximity cuts that would not occur experimentally. Also, note that cut sites will not be matched to non-DNA_BASES in myDNASTringSet.

Value

DigestDNA can return two types of results: cut positions or the resulting DNA fragments corresponding to the top, bottom, or both strands. If type is "positions" then the output is a list with the cut location(s) in each sequence in myDNASTringSet. The cut location is defined as the position after the cut relative to the 5'-end. For example, a cut at 6 would occur between positions 5 and 6, where the respective strand's 5' nucleotide is defined as position 1.

If type is "fragments" (the default), then the result is a DNASTringSetList. Each element of the list contains the top and/or bottom strand fragments after digestion of myDNASTringSet, or the original sequence if no cuts were made. Sequences are named by whether they originated from the top or bottom strand, and list elements are named based on the input DNA sequences. The top strand is defined by myDNASTringSet as it is input, whereas the bottom strand is its reverse complement.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

See Also

[DesignSignatures](#), [RESTRICTION_ENZYMES](#)

Examples

```
# digest hypothetical DNA sequences with BamHI
data(RESTRICTION_ENZYMES)
site <- RESTRICTION_ENZYMES[c("BamHI")]
dna <- DNASTringSet(c("AAGGATCCAA", "GGGATCAT"))
dna # top strand
reverseComplement(dna) # bottom strand
names(dna) <- c("hyp1", "hyp2")
d <- DigestDNA(site, dna)
```

```
d # fragments in a DNASetList
unlist(d) # all fragments as one DNASetList

# Restriction digest of Yeast Chr. 1 with EcoRI and EcoRV
data(yeastSEQCHR1)
sites <- RESTRICTION_ENZYMES[c("EcoRI", "EcoRV")]
seqs <- DigestDNA(sites, yeastSEQCHR1)
seqs[[1]]

pos <- DigestDNA(sites, yeastSEQCHR1, type="positions")
str(pos)
```

Disambiguate

Expand Ambiguities into All Permutations of a DNASetList

Description

Performs the inverse function of `ConsensusSequence` by expanding any ambiguities present in sequences.

Usage

```
Disambiguate(myXStringSet)
```

Arguments

`myXStringSet` A `DNASetList` or `RNAStringSet` object of sequences.

Details

Ambiguity codes in the `IUPAC_CODE_MAP` can be used to represent multiple nucleotides at a single position. Using these letters, multiple oligonucleotide permutations can be represented with a single ambiguous sequence. This function expands each sequence in the `DNASetList` input into all of its permutations. Note that sequences with many ambiguities can result in a very large number of potential permutations.

Value

A `DNASetList` or `RNAStringSetList` with one element for each sequence in `myXStringSet`.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

See Also

[ConsensusSequence](#)

Examples

```
dna <- DNASTringSet(c("ACST", "NNN"))
dna_list <- Disambiguate(dna)
dna_list[[1]]
dna_list[[2]]
unlist(dna_list)

rna <- RNASTringSet(c("ACGU", "AGAU")) # 2 permutations
rna <- ConsensusSequence(rna) # "ASRU"
Disambiguate(rna) # 4 permutations
```

DistanceMatrix *Calculate the Distances Between Sequences*

Description

Calculates a distance matrix for an XStringSet. Each element of the distance matrix corresponds to the dissimilarity between two sequences in the XStringSet.

Usage

```
DistanceMatrix(myXStringSet,
               includeTerminalGaps = FALSE,
               penalizeGapLetterMatches = TRUE,
               penalizeGapGapMatches = FALSE,
               correction = "none",
               processors = NULL,
               verbose = TRUE)
```

Arguments

myXStringSet An XStringSet object of aligned sequences (DNASTringSet, RNASTringSet, or AAStringSet).

includeTerminalGaps
 Logical specifying whether or not to include terminal gaps ("- characters on each end of the sequence) into the calculation of distance.

penalizeGapLetterMatches
 Logical specifying whether or not to consider gap-to-letter matches as mismatches. If FALSE, then gap-to-letter matches are not included in the total length used to calculate distance.

penalizeGapGapMatches
 Logical specifying whether or not to consider gap-to-gap matches as mismatches. If FALSE (the default), then gap-to-gap matches are not included in the total length used to calculate distance.

correction The substitution model used for distance correction. This should be (an abbreviation of) either "none" or "Jukes-Cantor".

| | |
|------------|--|
| processors | The number of processors to use, or NULL (the default) for all available processors. |
| verbose | Logical indicating whether to display progress. |

Details

The uncorrected distance matrix represents the hamming distance between each of the sequences in `myXStringSet`. Ambiguity can be represented using the characters of the `IUPAC_CODE_MAP` for `DNAStringSet` and `RNAStringSet` inputs, or using the `AMINO_ACID_CODE` for an `AAStringSet` input. For example, the distance between an 'N' and any other nucleotide base is zero. The letters B (N or D), J (I or L), Z (Q or E), and X (any letter) are degenerate in the `AMINO_ACID_CODE`.

If `includeTerminalGaps = FALSE` then terminal gaps ("- or ." characters) are not included in sequence length. This can be faster since only the positions common to each pair of sequences are compared. Sequences with no overlapping region in the alignment are given a value of NA, unless `includeTerminalGaps = TRUE`, in which case distance is 100%.

Penalizing gap-to-gap and gap-to-letter mismatches specifies whether to penalize these special mismatch types and include them in the total length when calculating distance. Both "-" and "." characters are interpreted as gaps. The default behavior is to calculate distance as the fraction of positions that differ across the region of the alignment shared by both sequences (not including gap-to-gap matches).

The elements of the distance matrix can be referenced by `dimnames` corresponding to the names of the `XStringSet`. Additionally, an attribute named "correction" specifying the method of correction used can be accessed using the function `attr`.

Value

A symmetric matrix where each element is the distance between the sequences referenced by the respective row and column. The `dimnames` of the matrix correspond to the names of the `XStringSet`.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

See Also

[IdClusters](#)

Examples

```
# defaults compare intersection of internal ranges:
dna <- DNAStringSet(c("ANGCT-", "-ACCT-"))
d <- DistanceMatrix(dna)
# d[1,2] is 1 base in 4 = 0.25

# compare the entire sequence ranges:
dna <- DNAStringSet(c("ANGCT-", "-ACCT-"))
d <- DistanceMatrix(dna, includeTerminalGaps=TRUE,
                    penalizeGapGapMatches=TRUE)
# d[1,2] is now 3 bases in 6 = 0.50
```

```
# compare union of internal ranges:
dna <- DNASTringSet(c("ANGCT-", "-ACCT-"))
d <- DistanceMatrix(dna, includeTerminalGaps=TRUE,
                    penalizeGapGapMatches=FALSE)
# d[1,2] is now 2 bases in 5 = 0.40

# gap ("-") and unknown (".") characters are interchangeable:
dna <- DNASTringSet(c("ANGCT.", ".ACCT-"))
d <- DistanceMatrix(dna, includeTerminalGaps=TRUE,
                    penalizeGapGapMatches=FALSE)
# d[1,2] is still 2 bases in 5 = 0.40
```

FindChimeras

Find Chimeras In A Sequence Database

Description

Finds chimeras present in a database of sequences. Makes use of a reference database of (presumed to be) good quality sequences.

Usage

```
FindChimeras(dbFile,
             tblName = "DNA",
             identifier = "",
             dbFileReference,
             tblNameReference = "DNA",
             batchSize = 100,
             minNumFragments = 20000,
             tb.width = 5,
             multiplier = 20,
             minLength = 70,
             minCoverage = 0.6,
             overlap = 100,
             minSuspectFragments = 6,
             showPercentCoverage = FALSE,
             add2tbl = FALSE,
             maxGroupSize = -1,
             minGroupSize = 100,
             excludeIDs = NULL,
             verbose = TRUE)
```

Arguments

| | |
|---------|---|
| dbFile | A SQLite connection object or a character string specifying the path to the database file to be checked for chimeric sequences. |
| tblName | Character string specifying the table in which to check for chimeras. |

| | |
|---------------------|---|
| identifier | Optional character string used to narrow the search results to those matching a specific identifier. If "" then all identifiers are selected. |
| dbFileReference | A SQLite connection object or a character string specifying the path to the reference database file of (presumed to be) good quality sequences. A 16S reference database is available from DECIPHER.cee.wisc.edu . |
| tblNameReference | Character string specifying the table with reference sequences. |
| batchSize | Number sequences to tile with fragments at a time. |
| minNumFragments | Number of suspect fragments to accumulate before searching through other groups. |
| tb.width | A single integer [1..14] giving the number of nucleotides at the start of each fragment that are part of the trusted band. |
| multiplier | A single integer specifying the multiple of fragments found out-of-group greater than fragments found in-group in order to consider a sequence a chimera. |
| minLength | Minimum length of a chimeric region in order to be considered as a chimera. |
| minCoverage | Minimum fraction of coverage necessary in a chimeric region. |
| overlap | Number of nucleotides at the end of the sequence that the chimeric region must overlap in order to be considered a chimera. |
| minSuspectFragments | Minimum number of suspect fragments belonging to another group required to consider a sequence a chimera. |
| showPercentCoverage | Logical indicating whether to list the percent coverage of suspect fragments in each chimeric region in the output. |
| add2tbl | Logical or a character string specifying the table name in which to add the result. |
| maxGroupSize | Maximum number of sequences searched in a group. A value of less than 0 means the search is unlimited. |
| minGroupSize | The minimum number of sequences in a group to be considered as part of the search for chimeras. May need to be set to a small value for reference database with mostly small groups. |
| excludeIDs | Optional character vector of identifier(s) to exclude from database searches, or NULL (the default) to not exclude any. |
| verbose | Logical indicating whether to display progress. |

Details

FindChimeras works by finding suspect fragments that are uncommon in the group where the sequence belongs, but very common in another group where the sequence does not belong. Each sequence in the dbFile is tiled into short sequence segments called fragments. If the fragments are infrequent in their respective group in the dbFileReference then they are considered suspect. If enough suspect fragments from a sequence meet the specified constraints then the sequence is flagged as a chimera.

The default parameters are optimized for full-length 16S sequences (> 1,000 nucleotides). Shorter 16S sequences require two parameters that are different than the defaults: `minLength = 40`, and `minSuspectFragments = 2`.

Groups are determined by the identifier present in each database. For this reason, the groups in the `dbFile` should exist in the groups of the `dbFileReference`. The reference database is assumed to contain many sequences of only good quality.

If a reference database is not present then it is feasible to create a reference database by using the input database as the reference database. Removing chimeras from the reference database and then iteratively repeating the process can result in a clean reference database.

For non-16S sequences it may be necessary to optimize the parameters for the particular sequences. The simplest way to perform an optimization is to experiment with different input parameters on artificial chimeras such as those created using [CreateChimeras](#). Adjusting input parameters until the maximum number of artificial chimeras are identified is the easiest way to determine new defaults.

Value

A `data.frame` containing only the sequences that meet the specifications for being chimeric. The `chimera` column contains information on the chimeric region and to which group it belongs. The `row.names` of the `data.frame` correspond to those of the sequences in the `dbFile`.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

References

ES Wright et al. (2012) "DECIPHER: A Search-Based Approach to Chimera Identification for 16S rRNA Sequences." *Applied and Environmental Microbiology*, doi:10.1128/AEM.06516-11.

See Also

[CreateChimeras](#), [Add2DB](#)

Examples

```
db <- system.file("extdata", "Bacteria_175seqs.sqlite", package="DECIPHER")
# It is necessary to set dbFileReference to the file path of the
# 16S reference database available from DECIPHER.cae.wisc.edu
chimeras <- FindChimeras(db, dbFileReference=db)
```


FindSynteny

*Finds Synteny In A Sequence Database***Description**

Finds syntenic blocks between groups of sequences in a database.

Usage

```
FindSynteny(dbFile,
            tblName = "DNA",
            identifier = "",
            useFrames = TRUE,
            alphabet = c("MF", "ILV", "A", "C", "WYQHP", "G", "TSN", "RK", "DE"),
            geneticCode = GENETIC_CODE,
            sepCost = -0.01,
            gapCost = -0.2,
            shiftCost = -20,
            codingCost = -3,
            maxSep = 5000,
            maxGap = 5000,
            minScore = 200,
            dropScore = -100,
            maskRepeats = TRUE,
            verbose = TRUE)
```

Arguments

| | |
|-------------|--|
| dbFile | A SQLite connection object or a character string specifying the path to the database file. |
| tblName | Character string specifying the table where the sequences are located. |
| identifier | Optional character string used to narrow the search results to those matching a specific identifier. If "" then all identifiers are selected. |
| useFrames | Logical specifying whether to use 6-frame amino acid translations to help find more distant hits. If FALSE then faster but less sensitive to distant homology. |
| alphabet | Character vector of amino acid groupings used to reduce the 20 standard amino acids into smaller groups. Alphabet reduction helps to find more distant homologies between sequences. A non-reduced amino acid alphabet can be used by setting alphabet equal to AA_STANDARD. |
| geneticCode | Either a character vector giving the genetic code to use in translation, or a list containing one genetic code for each identifier. If a list is provided then it must be named by the corresponding identifiers in the database. |
| sepCost | Cost per nucleotide separation between hits to apply when chaining hits into blocks. |
| gapCost | Cost for gaps between hits to apply when chaining hits into blocks. |

| | |
|-------------|---|
| shiftCost | Cost for shifting between different reading frames when chaining reduced amino acid hits into blocks. |
| codingCost | Cost for switching between coding and non-coding hits when chaining hits into blocks. |
| maxSep | Maximal separation (in nucleotides) between hits in the same block. |
| maxGap | The maximum number of gaps between hits in the same block. |
| minScore | The minimum score required for a chain of hits to become a block. |
| dropScore | The change from maximal score required to stop extending blocks. |
| maskRepeats | Logical specifying whether to “soft” mask repeats when searching for hits. |
| verbose | Logical indicating whether to display progress. |

Details

Long nucleotide sequences, such as genomes, are often not collinear, or may be composed of many smaller segments (e.g., contigs). FindSynteny searches for “hits” between sequences that can be chained into collinear “blocks” of synteny. Hits are defined as k-mer exact nucleotide matches or k-mer matches in a reduced amino acid alphabet (if useFrames is TRUE). Hits are chained into blocks as long as they are: (1) within the same sequence, (2) within maxSep and maxGap distance, and (3) help maintain the score above minScore. Blocks are extended from their first and last hit until their score drops below dropScore from the maximum that was reached. This process results in a set of hits and blocks stored in an object of class “Synteny”.

Value

An object of class “Synteny”.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

See Also

[AlignSynteny](#), [Synteny-class](#)

Examples

```
db <- system.file("extdata", "Influenza.sqlite", package="DECIPHER")
synteny <- FindSynteny(db, minScore=50)
synteny
pairs(synteny) # scatterplot matrix
```

FormGroups

Forms Groups By Rank

Description

Agglomerates sequences into groups within a certain size range based on taxonomic rank.

Usage

```
FormGroups(dbFile,
           tblName = "DNA",
           goalSize = 1000,
           minGroupSize = 500,
           maxGroupSize = 10000,
           add2tbl = FALSE,
           verbose = TRUE)
```

Arguments

| | |
|--------------|---|
| dbFile | A SQLite connection object or a character string specifying the path to the database file. |
| tblName | Character string specifying the table where the rank information is located. |
| goalSize | Number of sequences required in each group to stop adding more sequences. |
| minGroupSize | Minimum number of sequences in each group required to stop trying to recombine with a larger group. |
| maxGroupSize | Maximum number of sequences in each group allowed to continue agglomeration. |
| add2tbl | Logical or a character string specifying the table name in which to add the result. |
| verbose | Logical indicating whether to print database queries and other information. |

Details

FormGroups uses the “rank” field in the dbFile table to group sequences with similar taxonomic rank. Rank information must be present in the tblName, such as that created when importing sequences from a GenBank formatted file. The rank information must not contain repeated taxonomic names belonging to different lineages.

Beginning with the least common ranks, the algorithm agglomerates groups with similar ranks until the goalSize is reached. If the group size is below minGroupSize then further agglomeration is attempted with a larger group. If additional agglomeration results in a group larger than maxGroupSize then the agglomeration is undone so that the group is smaller.

Value

Returns a data.frame of rank and id for each group. If add2tbl is not FALSE then the tblName is updated with the group as the identifier.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

See Also

[IdentifyByRank](#)

Examples

```
db <- system.file("extdata", "Bacteria_175seqs.sqlite", package="DECIPHER")
g <- FormGroups(db, goalSize=10, minGroupSize=5, maxGroupSize=20)
```

HEC_MI

Mutual Information for Protein Secondary Structure Prediction

Description

Arrays containing values of mutual information for single residues (HEC_MI1) and pairs of residues (HEC_MI2) located within 10 residues of the position being predicted (position "0"). The arrays have dimensions corresponding to the 20 (standard) amino acids, positions (-10 to 10), and states (helix ("H"), sheet ("E"), or coil ("C")).

Usage

```
data("HEC_MI1")
data("HEC_MI2")
```

Format

The format of HEC_MI1 is: num [1:20, 1:21, 1:3] 0.04264 -0.00117 0.02641 0.08264 -0.04876 ...
- attr(*, "dimnames")=List of 3 ..\$: chr [1:20] "A" "R" "N" "D"\$: chr [1:21] "-10" "-9" "-8"
"-7"\$: chr [1:3] "H" "E" "C"

The format of HEC_MI2 is: num [1:20, 1:20, 1:21, 1:21, 1:3] 2.56 -Inf -Inf -Inf -Inf ... - attr(*,
"dimnames")=List of 5 ..\$: chr [1:20] "A" "R" "N" "D"\$: chr [1:20] "A" "R" "N" "D"\$:
chr [1:21] "-10" "-9" "-8" "-7"\$: chr [1:21] "-10" "-9" "-8" "-7"\$: chr [1:3] "H" "E" "C"

Details

The values in each matrix were derived based on a set of 15,201 proteins in the ASTRAL Compendium (Chandonia, 2004). The 8-states assigned by the Dictionary of Protein Secondary Structure (DSSP) were reduced to 3-states via H = G, H, or I; E = E; and C = B, S, C, or T.

References

Chandonia, J. M. (2004). The ASTRAL Compendium in 2004. *Nucleic Acids Research*, **32(90001)**, 189D-192. doi:10.1093/nar/gkh034.

Examples

```

data(HEC_MI1)
# the contribution of an arginine ("R")
# located 3 residues left of center
# to a helical ("H") state at the center
HEC_MI1["R", "-3", "H"]

data(HEC_MI2)
# the contribution of arginine and lysine ("K")
# located at positions -1 and +1, respectively
# to a coil ("C") state at the center position
HEC_MI2["R", "K", "-1", "1", "C"]

matplot(-10:10, t(HEC_MI1[, , "H"]),
        type="l", col=1:8, lty=rep(1:3, each=8),
        xlab="Amino Acid Position Relative to Center",
        ylab="Log-Odds of Helix at Center Position")
legend("bottomleft",
       lwd=1, col=1:8, lty=rep(1:3, each=8),
       legend=dimnames(HEC_MI1)[[1]], ncol=2)

```

IdClusters

Cluster Sequences By Distance or Sequence

Description

Groups the sequences represented by a distance matrix into clusters of similarity.

Usage

```

IdClusters(myDistMatrix = NULL,
          method = "UPGMA",
          cutoff = -Inf,
          showPlot = FALSE,
          asDendrogram = FALSE,
          myXStringSet = NULL,
          model = MODELS,
          processors = NULL,
          verbose = TRUE)

```

Arguments

| | |
|---------------------------|---|
| <code>myDistMatrix</code> | A symmetric $N \times N$ distance matrix with the values of dissimilarity between N sequences, or NULL if method is "inexact". |
| <code>method</code> | An agglomeration method to be used. This should be (an abbreviation of) one of "complete", "single", "UPGMA", "WPGMA", "NJ", "ML", or "inexact". (See details section below.) |

| | |
|--------------|---|
| cutoff | A vector with the maximum edge length separating the sequences in the same cluster. Multiple cutoffs may be provided in ascending or descending order. If <code>asDendrogram=TRUE</code> or <code>showPlot=TRUE</code> then only one cutoff may be specified. (See details section below.) |
| showPlot | Logical specifying whether or not to plot the resulting dendrogram. Not applicable if <code>method='inexact'</code> . |
| asDendrogram | Logical. If <code>TRUE</code> then the object returned is of class <code>dendrogram</code> . Not applicable if <code>method='inexact'</code> . |
| myXStringSet | If <code>method</code> is "ML", the <code>DNAStrngSet</code> or <code>RNAStrngSet</code> used in the creation of <code>myDistMatrix</code> . If <code>method</code> is "inexact", the <code>DNAStrngSet</code> , <code>RNAStrngSet</code> , or <code>AAStringSet</code> to cluster. Not applicable for other methods. |
| model | One or more of the available <code>MODELS</code> of DNA evolution. Only applicable if <code>method</code> is "ML". |
| processors | The number of processors to use, or <code>NULL</code> (the default) for all available processors. |
| verbose | Logical indicating whether to display progress. |

Details

`IdClusters` groups the input sequences into clusters using a set dissimilarities representing the distance between N sequences. Initially a phylogenetic tree is formed using the specified method. Then each leaf (sequence) of the tree is assigned to a cluster based on its edge lengths to the other sequences. The available clustering methods are described as follows:

Ultrametric methods: The method `complete` assigns clusters using complete-linkage so that sequences in the same cluster are no more than `cutoff` percent apart. The method `single` assigns clusters using single-linkage so that sequences in the same cluster are within `cutoff` of at least one other sequence in the same cluster. `UPGMA` (the default) or `WPGMA` assign clusters using average-linkage which is a compromise between the sensitivity of complete-linkage clustering to outliers and the tendency of single-linkage clustering to connect distant relatives that do not appear to be closely related. `UPGMA` produces an unweighted tree, where each leaf contributes equally to the average edge lengths, whereas `WPGMA` produces a weighted result.

Additive methods: `NJ` uses the Neighbor-Joining method proposed by Saitou and Nei that does not assume lineages evolve at the same rate (the molecular clock hypothesis). The `NJ` method is typically the most phylogenetically accurate of the above distance-based methods. `ML` creates a neighbor-joining tree and then iteratively maximizes the likelihood of the tree given the aligned sequences (`myXStringSet`). This is accomplished through a combination of optimizing edge lengths with Brent's method and improving tree topology with nearest-neighbor interchanges (NNIs). When `method="ML"`, one or more `MODELS` of DNA evolution must be specified. Model parameters are iteratively optimized to maximize likelihood, except base frequencies which are empirically determined. If multiple models are given, the best model is automatically chosen based on BIC calculated from the likelihood and the sample size (defined as the number of variable sites in the DNA sequence).

Sequence-only method: `inexact` uses a greedy incremental algorithm to directly assign sequences to clusters without a distance matrix. First the sequences are ordered by length and the longest sequence becomes the first cluster seed. If the second sequence is less than `cutoff` percent distance

then it is added to the cluster, otherwise it becomes a new cluster representative. The remaining sequences are matched to cluster representatives using an ordered k-mer strategy, and then compared to the top hits with pairwise alignment. This approach, finding the closest cluster representatives followed by pairwise alignment to obtain the percent identity, is repeated until all sequences belong to a cluster. This process results in clusters with members generally separated by less than cutoff distance.

Cutoffs may be provided in ascending or descending order, except for `inexact` clustering, which requires descending cutoffs. If multiple cutoffs are provided in *descending* order then clustering at each new value of cutoff is continued within the prior cutoff's clusters. In this way clusters at lower values of cutoff are completely contained within their umbrella clusters at higher values of cutoff. This is useful for defining taxonomy, where lower level groups (e.g., genera) are expected not to straddle multiple higher level groups (e.g., families). If multiple cutoffs are provided in *ascending* order then clustering at each level of cutoff is independent of the prior level. This may result in fewer clusters for NJ and ML methods, but will have no impact on ultrametric methods.

Value

If `asDendrogram=FALSE` (the default), then a `data.frame` is returned with a column for each cutoff specified. This `data.frame` has dimensions $N * M$, where each one of N sequences is assigned to a cluster at the M -level of cutoff. The `row.names` of the `data.frame` correspond to the `dimnames` of `myDistMatrix`. If `asDendrogram=TRUE`, returns an object of class `dendrogram` that can be used for further manipulation and plotting. Leaves of the dendrogram are randomly colored by cluster number.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

References

- Felsenstein, J. (1981) Evolutionary trees from DNA sequences: a maximum likelihood approach. *Journal of Molecular Evolution*, **17(6)**, 368-376.
- Ghodsi, M., Liu, B., & Pop, M. (2011) DNACLUST. *BMC Bioinformatics*, **12(1)**, 271. doi:10.1186/1471-2105-12-271.
- Saitou, N. and Nei, M. (1987) The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution*, **4(4)**, 406-425.

See Also

[DistanceMatrix](#), [Add2DB](#), [MODELS](#)

Examples

```
# using the matrix from the original paper by Saitou and Nei
m <- matrix(0,8,8)
m[2:8,1] <- c(7, 8, 11, 13, 16, 13, 17)
m[3:8,2] <- c(5, 8, 10, 13, 10, 14)
m[4:8,3] <- c(5, 7, 10, 7, 11)
m[5:8,4] <- c(8, 11, 8, 12)
```

```

m[6:8,5] <- c(5, 6, 10)
m[7:8,6] <- c(9, 13)
m[8,7] <- c(8)

# returns an object of class "dendrogram"
myClusters <- IdClusters(m, cutoff=10, method="NJ", showPlot=TRUE, asDendrogram=TRUE)

# example of specifying a cutoff
# returns a data frame
IdClusters(m, cutoff=c(2,6,10,20))

```

IdConsensus

Create Consensus Sequences by Groups

Description

Forms a consensus sequence representing the sequences in each group.

Usage

```

IdConsensus(dbFile,
            tblName = "DNA",
            identifier = "",
            type = "DNAStrngSet",
            colName = "id",
            add2tbl = FALSE,
            verbose = TRUE,
            ...)

```

Arguments

| | |
|------------|---|
| dbFile | A SQLite connection object or a character string specifying the path to the database file. |
| tblName | Character string specifying the table in which to form consensus. |
| identifier | Optional character string used to narrow the search results to those matching a specific identifier. If "" then all identifiers are selected. |
| type | The type of XStringSet (sequences) to use in forming consensus. This should be (an abbreviation of) one of "DNAStrngSet", "RNAStrngSet", "AAStrngSet", or "BStringSet". |
| colName | Column containing the group name of each sequence. |
| add2tbl | Logical or a character string specifying the table name in which to add the result. |
| verbose | Logical indicating whether to display progress. |
| ... | Additional arguments to be passed directly to ConsensusSequence for an AAStrngSet, DNAStrngSet, or RNAStrngSet, or to consensusString for a BStringSet. |

Details

Creates a consensus sequence for each of the distinct groups defined in `colName`. The resulting `XStringSet` contains as many consensus sequences as there are distinct groups in `colName`. For example, it is possible to create a set of consensus sequences with one consensus sequence for each "id" in the `tblName`.

Value

An `XStringSet` object containing the consensus sequence for each group. The names of the `XStringSet` contain the number of sequences and name of each group.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

See Also

[Seqs2DB](#)

Examples

```
db <- system.file("extdata", "Bacteria_175seqs.sqlite", package="DECIPHER")
con <- IdConsensus(db, colName="id", noConsensusChar="N")
BrowseSeqs(con)
```

IdentifyByRank

Identify By Taxonomic Rank

Description

Identifies sequences by a specific level of their taxonomic rank.

Usage

```
IdentifyByRank(dbFile,
               tblName = "DNA",
               level = Inf,
               add2tbl = FALSE,
               verbose = TRUE)
```

Arguments

| | |
|----------------------|---|
| <code>dbFile</code> | A <code>SQLite</code> connection object or a character string specifying the path to the database file. |
| <code>tblName</code> | Character string specifying the table where the rank information is located. |
| <code>level</code> | Level of the taxonomic rank. (See details section below.) |
| <code>add2tbl</code> | Logical or a character string specifying the table name in which to add the result. |
| <code>verbose</code> | Logical indicating whether to print database queries and other information. |

Details

IdentifyByRank simply identifies a sequence by a specific level of its taxonomic rank. Requires that rank information be present in the tblName, such as that created when importing sequences from a GenBank formatted file.

The input parameter level should be a non-zero integer giving the “level” of the taxonomic rank to choose as the identifier. Negative levels are interpreted as that being many levels from the last level in each rank.

If the specified level of rank does not exist then the closest rank is chosen. Therefore, the default level (Inf) will always select the last taxonomic level (e.g., species).

Value

A data.frame with the rank and corresponding identifier as "id".

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

See Also

[FormGroups](#)

Examples

```
db <- system.file("extdata", "Bacteria_175seqs.sqlite", package="DECIPHER")
ids <- IdentifyByRank(db)
```

IdLengths

Determine the Number of Bases, Nonbases, and Width of Each Sequence

Description

Counts the number of bases (A, C, G, T) and ambiguities/degeneracies in each sequence.

Usage

```
IdLengths(dbFile,
          tblName = "DNA",
          identifier = "",
          type = "DNAStringSet",
          add2tbl = FALSE,
          batchSize = 10000,
          verbose = TRUE)
```

Arguments

| | |
|------------|---|
| dbFile | A SQLite connection object or a character string specifying the path to the database file. |
| tblName | Character string specifying the table where the sequences are located. |
| identifier | Optional character string used to narrow the search results to those matching a specific identifier. If "" then all identifiers are selected. |
| type | The type of XStringSet being processed. This should be (an abbreviation of) one of "DNAStringSet" or "RNAStringSet". |
| add2tbl | Logical or a character string specifying the table name in which to add the result. |
| batchSize | Integer specifying the number of sequences to process at a time. |
| verbose | Logical indicating whether to display progress. |

Value

A data.frame with the number of bases ("A", "C", "G", or "T"), nonbases, and width of each sequence. The width is defined as the sum of bases and nonbases in each sequence. The row.names of the data.frame correspond to the "row_names" in the tblName of the dbFile.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

See Also

[Add2DB](#)

Examples

```
db <- system.file("extdata", "Bacteria_175seqs.sqlite", package="DECIPHER")
l <- IdLengths(db)
```

MaskAlignment

Masks Highly Variable Regions of An Alignment

Description

Automatically masks poorly aligned regions of an alignment based on sequence conservation and gap frequency.

Usage

```
MaskAlignment(myXStringSet,
              windowSize = 5,
              threshold = 1,
              maxFractionGaps = 0.2,
              showPlot = FALSE)
```

Arguments

| | |
|-----------------|---|
| myXStringSet | An AAStrngSet, DNAStrngSet, or RNAStrngSet object of aligned sequences. |
| windowSize | Integer value specifying the size of the region to the left and right of the center-point to use in calculating the moving average. |
| threshold | Numeric giving the average entropy in bits from 0 to 2 below which a region is masked. |
| maxFractionGaps | Numeric specifying the maximum fraction of gaps in an alignment column to be masked. |
| showPlot | Logical specifying whether or not to show a plot of the positions that were kept or masked. |

Details

Poorly aligned regions of a multiple sequence alignment may lead to incorrect results in downstream analyses, and require extra processing time. One method to mitigate their effects is to mask columns of the alignment that may be poorly aligned, such as highly-variable regions or regions with many insertions and deletions (gaps).

Highly variable regions are detected by their signature of having low information content. A moving average of `windowSize` nucleotides to the left and right of the center-point is applied to smooth noise in the information content signal along the sequence. Regions dropping below `threshold` bits or more than `maxFractionGaps` are masked in the returned alignment.

Value

A `MultipleAlignment` object of the input type with masked columns where the input criteria are met.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

See Also

[AlignSeqs](#), [IdClusters](#)

Examples

```
fas <- system.file("extdata", "Streptomyces_ITS_aligned.fas", package="DECIPHER")
dna <- readDNAStrngSet(fas)
masked_dna <- MaskAlignment(dna, showPlot=TRUE)

# display only unmasked nucleotides for use in downstream analyses
not_masked <- as(masked_dna, "DNAStrngSet")
BrowseSeqs(not_masked)

# display only masked nucleotides that are covered by the mask
masked <- masked_dna
colmask(masked, append="replace", invert=TRUE) <- colmask(masked)
```

```
masked <- as(masked, "DNAStrngSet")
BrowseSeqs(masked)

# display the complete DNA sequence set including the mask
masks <- lapply(width(colmask(masked_dna)), rep, x="+")
masks <- unlist(lapply(masks, paste, collapse=""))
masked_dna <- replaceAt(dna, at=IRanges(colmask(masked_dna)), value=masks)
BrowseSeqs(masked_dna)
```

MeltDNA

Simulate Melting of DNA

Description

The denaturation of double-stranded DNA occurs over a range of temperatures. Beginning from a helical state, DNA will transition to a random-coil state as temperature is increased. MeltDNA predicts the positional helicity, melt curve, or its negative derivate at different temperatures.

Usage

```
MeltDNA(myDNAStrngSet,
        type = "derivative",
        temps = 50:100,
        ions = 0.2)
```

Arguments

| | |
|---------------|--|
| myDNAStrngSet | A DNAStrngSet object or character vector with one or more sequences in 5' to 3' orientation. |
| type | Character string indicating the type of results desired. This should be (an abbreviation of) one of "derivative curves", "melt curves", or "positional probabilities". |
| temps | Numeric vector of temperatures (in degrees Celsius). |
| ions | Numeric giving the molar sodium equivalent ionic concentration. Values must be at least 0.01M. |

Details

When designing a high resolution melt (HRM) assay, it is useful to be able to predict the results before performing the experiment. Multi-state models of DNA melting can provide near-qualitative agreement with experimental DNA melt curves obtained with quantitative PCR (qPCR). MeltDNA employs the algorithm of Tostesen et al. (2003) with an approximation for loop entropy that runs in nearly linear time and memory, which allows very long DNA sequences (up to 100,000 base pairs) to be analyzed.

Denaturation is a highly cooperative process whereby regions of double-stranded DNA tend to melt together. For short sequences (< 100 base pairs) there is typically a single transition from a helical to random-coil state. Longer sequences may exhibit more complex melting behavior with multiple peaks, as domains of the DNA melt at different temperatures. The melting curve represents the

average fractional helicity (Theta) at each temperature, and can be used for genotyping with high resolution melt analysis.

Value

MeltDNA can return three types of results: positional helicity, melting curves, or the negative derivative of the melting curves. If type is "position", then a list is returned with one component for each sequence in myDNAStringSet. Each list component contains a matrix with the probability of helicity (Theta) at each temperature (rows) and every position in the sequence (columns).

If type is "melt", then a matrix with the average Theta across the entire sequence is returned. This matrix has a row for each input temperature (temps), and a column for each sequence in myDNAStringSet. For example, the value in element [3, 4] is the average helicity of the fourth input sequence at the third input temperature. If type is "derivative" then the values in the matrix are the derivative of the melt curve at each temperature.

Note

MeltDNA uses nearest neighbor parameters from SantaLucia (1998).

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

References

- SantaLucia, J. (1998). A unified view of polymer, dumbbell, and oligonucleotide DNA nearest-neighbor thermodynamics. *Proceedings of the National Academy of Sciences*, 95(4), 1460-1465.
- Tostesen, E., et al. (2003). Speed-up of DNA melting algorithm with complete nearest neighbor properties. *Biopolymers*, 70(3), 364-376. doi:10.1002/bip.10495.

See Also

[AmplifyDNA](#), [CalculateEfficiencyPCR](#), [DesignSignatures](#)

Examples

```
fas <- system.file("extdata", "IDH2.fas", package="DECIPHER")
dna <- readDNAStringSet(fas)

# plot the melt curve for the two alleles
temps <- seq(85, 100, 0.2)
m <- MeltDNA(dna,
             type="melt", temps=temps, ions=0.1)
matplot(temps, m,
        type="l", xlab="Temperature (\u00B0C)", ylab="Average Theta")
legend("topright", names(dna), lty=seq_along(dna), col=seq_along(dna))

# plot the negative derivative curve for a subsequence of the two alleles
temps <- seq(80, 95, 0.25)
m <- MeltDNA(subseq(dna, 492, 542),
```

```

        type="derivative", temps=temps)
matplot(temps, m,
        type="l", xlab="Temperature (\u00B0C)", ylab="-d(Theta)/dTemp")
legend("topright", names(dna), lty=seq_along(dna), col=seq_along(dna))

# plot the positional helicity profile for the IDH2 allele
temps <- seq(90.1, 90.5, 0.1)
m <- MeltDNA(dna[1],
            type="position", temps=temps, ions=0.1)
matplot(seq_len(dim(m[[1]])[2]), t(m[[1]]),
        type="l", xlab="Nucleotide Position", ylab="Theta")
temps <- formatC(temps, digits=1, format="f")
legend("topright", legend=paste(temps, "\u00B0C", sep=""),
        col=seq_along(temps), lty=seq_along(temps), bg="white")

```

MIQS

MIQS Amino Acid Substitution Matrix

Description

The MIQS amino acid substitution matrix defined by Yamada & Tomii (2014).

Usage

```
data("MIQS")
```

Format

The format is: num [1:25, 1:25] 3.2 -1.3 -0.4 -0.4 1.5 -0.2 -0.4 0.4 -1.2 -1.3 ... - attr(*, "dim-names")=List of 2 ..\$: chr [1:25] "A" "R" "N" "D"\$: chr [1:25] "A" "R" "N" "D" ...

Details

Substitution matrix values represent the log-odds of observing an aligned pair of amino acids versus the likelihood of finding the pair by chance. Values in the MIQS matrix are in units of third-bits ($\log(\text{odds ratio}) * 3/\log(2)$).

Source

Yamada, K., & Tomii, K. (2014). Revisiting amino acid substitution matrices for identifying distantly related proteins. *Bioinformatics*, **30(3)**, 317-325. doi:10.1093/bioinformatics/btt694.

Examples

```

data(MIQS)
MIQS["A", "R"] # score for A/R pairing

data(BLOSUM62)
plot(BLOSUM62[1:20, 1:20], MIQS[1:20, 1:20])
abline(a=0, b=1)

```

Description

The MODELS character vector contains the models of DNA evolution that can be used by `IdClusters`.

Usage

MODELS

Details

Six models of DNA evolution are available, with or without the discrete Gamma rates distribution. These are described in order of increasing number of parameters as follows:

JC69 (Jukes and Cantor, 1969) The simplest substitution model that assumes equal base frequencies (1/4) and equal mutation rates.

K80 (Kimura, 1980) Assumes equal base frequencies, but distinguishes between the rate of transitions and transversions.

T92 (Tamura, 1992) In addition to distinguishing between transitions and transversions, a parameter is added to represent G+C content bias.

F81 (Felsenstein, 1981) Assumes equal mutation rates, but allows all bases to have different frequencies.

HKY85 (Hasegawa, Kishino and Yano, 1985) Distinguishes transitions from transversions and allows bases to have different frequencies.

TN93 (Tamura and Nei, 1993) Allows for unequal base frequencies and distinguishes between transversions and the two possible types of transitions (i.e., A <-> G & C <-> T).

+G (Yang, 1993) Specifying a model+G4 adds a single parameter to any of the above models to relax the assumption of equal rates among sites in the DNA sequence. The single parameter specifies the shape of the Gamma Distribution. The continuous distribution is represented with 2-10 discrete rates and their respective probabilities as determined by the Laguerre Quadrature method (Felsenstein, 2001). For example, specifying a model+G8 would represent the continuous Gamma Distribution with eight rates and their associated probabilities.

References

- Felsenstein, J. (1981). Evolutionary trees from DNA sequences: a maximum likelihood approach. *Journal of Molecular Evolution*, **17(6)**, 368-376.
- Felsenstein, J. (2001). Taking Variation of Evolutionary Rates Between Sites into Account in Inferring Phylogenies. *Journal of molecular evolution*, **53(4-5)**, 447-455.
- Hasegawa, M., Kishino H., Yano T. (1985). Dating of human-ape splitting by a molecular clock of mitochondrial DNA. *Journal of Molecular Evolution*, **22(2)**, 160-174.
- Jukes, T. and Cantor C. (1969). *Evolution of Protein Molecules*. New York: Academic Press. pp. 21-132.

Kimura, M. (1980). A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. *Journal of Molecular Evolution*, **16**(2), 111-120.

Tamura, K. (1992). Estimation of the number of nucleotide substitutions when there are strong transition-transversion and G+C content biases. *Molecular Biology and Evolution*, **9**(4), 678-687.

Tamura, K. and Nei M. (1993). Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. *Molecular Biology and Evolution*, **10**(3), 512-526.

Yang, Z. (1993). Maximum-likelihood estimation of phylogeny from DNA sequences when substitution rates differ over sites. *Molecular Biology and Evolution*, **10**(6), 1396-1401.

See Also

[IdClusters](#)

Examples

MODELS

| | |
|------|--|
| NNLS | <i>Sequential Coordinate-wise Algorithm for the Non-negative Least Squares Problem</i> |
|------|--|

Description

Consider the linear system $Ax = b$ where $A \in R^{m \times n}$, $x \in R^n$, and $b \in R^m$. The technique of least squares proposes to compute x so that the sum of squared residuals is minimized. NNLS solves the least squares problem $\min \|Ax = b\|^2$ subject to the constraint $x \geq 0$. This implementation of the Sequential Coordinate-wise Algorithm uses a sparse input matrix A , which makes it efficient for large sparse problems.

Usage

```
NNLS(A,
      b,
      precision = sqrt(.Machine$double.eps),
      processors = NULL,
      verbose = TRUE)
```

Arguments

| | |
|-----------|---|
| A | List representing the sparse matrix with integer components i and j, numeric component x. The fourth component, dimnames, is a list of two components that contains the names for every row (component 1) and column (component 2). |
| b | Numeric matrix for the set of observed values. (See details section below.) |
| precision | The desired accuracy. |

| | |
|------------|--|
| processors | The number of processors to use, or NULL (the default) for all available processors. |
| verbose | Logical indicating whether to display progress. |

Details

The input b can be either a matrix or a vector of numerics. If it is a matrix then it is assumed that each column contains a set of observations, and the output x will have the same number of columns. This allows multiple NNLS problems using the same A matrix to be solved simultaneously, and greatly accelerates computation relative to solving each sequentially.

Value

A list of two components:

| | |
|-----|---|
| x | The matrix of non-negative values that best explains the observed values given by b . |
| res | A matrix of residuals given by $Ax - b$. |

References

Franc, V., et al. (2005). Sequential coordinate-wise algorithm for the non-negative least squares problem. *Computer Analysis of Images and Patterns*, 407-414.

See Also

[Array2Matrix](#), [DesignArray](#)

Examples

```
# unconstrained least squares:
A <- matrix(c(1, -3, 2, -3, 10, -5, 2, -5, 6), ncol=3)
b <- matrix(c(27, -78, 64), ncol=1)
x <- solve(crossprod(A), crossprod(A, b))

# Non-negative least squares:
w <- which(A > 0, arr.ind=TRUE)
A <- list(i=w[,"row"], j=w[,"col"], x=A[w,
      dimnames=list(1:dim(A)[1], 1:dim(A)[2]))
x_nonneg <- NNLS(A, b)

# compare the unconstrained and constrained solutions:
cbind(x, x_nonneg$x)

# the input value "b" can also be a matrix:
b2 <- matrix(b, nrow=length(b), ncol=2) # repeat b in two columns
x_nonneg <- NNLS(A, b2) # solution is repeated in two output columns
```

OrientNucleotides *Orient nucleotide sequences*

Description

Orients nucleotide sequences to match the directionality and complementarity of specified reference sequences.

Usage

```
OrientNucleotides(myXStringSet,
                  reference = which.max(width(myXStringSet)),
                  type = "sequences",
                  orientation = "all",
                  threshold = 0.05,
                  verbose = TRUE,
                  processors = NULL)
```

Arguments

| | |
|--------------|--|
| myXStringSet | A DNAStrngSet or RNAStrngSet of unaligned sequences. |
| reference | The index of reference sequences with the same (desired) orientation. By default the first sequence with maximum width will be used. |
| type | Character string indicating the type of results desired. This should be (an abbreviation of) either "sequences", "orientations", or "both". |
| orientation | Character string(s) indicating the allowed reorientation(s) of non-reference sequences. This should be (an abbreviation of) either "all", "reverse", "complement", and/or "both" (for reverse complement). |
| threshold | Numeric giving the decrease in k-mer distance required to adopt the alternative orientation. |
| verbose | Logical indicating whether to display progress. |
| processors | The number of processors to use, or NULL (the default) for all available processors. |

Details

Biological sequences can sometimes have inconsistent orientation that interferes with their analysis. OrientNucleotides will reorient sequences by changing their directionality and/or complementarity to match specified reference sequences in the same set. The process works by finding the k-mer distance between the reference sequence(s) and each allowed orientation of the sequences. Alternative orientations that lessen the distance by at least threshold are adopted. Note that this procedure requires a moderately similar reference sequence be available for each sequence that needs to be reoriented. Sequences for which a corresponding reference is unavailable will most likely be left alone because alternative orientations will not pass the threshold. For this reason, it is recommended to specify several markedly different sequences as references.

Value

OrientNucleotides can return two types of results: the relative orientations of sequences and/or the reoriented sequences. If type is "sequences" (the default) then the reoriented sequences are returned. If type is "orientations" then a character vector is returned that specifies whether sequences were reversed ("r"), complemented ("c"), reversed complemented ("rc"), or in the same orientation ("") as the reference sequences (marked by NA). If type is "both" then the output is a list with the first component containing the "orientations" and the second component containing the "sequences".

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

See Also

[CorrectFrameshifts](#)

Examples

```
db <- system.file("extdata", "Bacteria_175seqs.sqlite", package="DECIPHER")
dna <- SearchDB(db, remove="all")
DNA <- dna # 175 sequences

# reorient subsamples of the first 169 sequences
s <- sample(169, 30)
DNA[s] <- reverseComplement(dna[s])
s <- sample(169, 30)
DNA[s] <- reverse(dna[s])
s <- sample(169, 30)
DNA[s] <- complement(dna[s])

DNA <- OrientNucleotides(DNA, reference=170:175)
DNA==dna
```

PredictHEC

Predict Protein Secondary Structure

Description

Predicts 3-state protein secondary structure based on the primary (amino acid) sequence using the GOR IV method (Garnier et al., 1996).

Usage

```
PredictHEC(myAAStringSet,
           type = "states",
           windowSize = 7,
           background = c(H = -0.12, E = -0.25, C = 0.23),
           HEC_MI1 = NULL,
           HEC_MI2 = NULL)
```

Arguments

| | |
|---------------|---|
| myAAStringSet | An AAStringSet object of sequences. |
| type | Character string indicating the type of results desired. This should be (an unambiguous abbreviation of) one of "states", "scores", or "probabilities". |
| windowSize | Numeric specifying the number of residues to the left or right of the center position to use in the prediction. |
| background | Numeric vector with the background "scores" for each of the three states (H, E, and C). |
| HEC_MI1 | An array of dimensions 20 x 21 x 3 giving the mutual information for single residues. |
| HEC_MI2 | An array of dimensions 20 x 20 x 21 x 21 x 3 giving the mutual information for pairs of residues. |

Details

The GOR (Garnier-Osguthorpe-Robson) method is an information-theory method for prediction of secondary structure based on the primary sequence of a protein. Version IV of the method makes 3-state predictions based on the mutual information contained in single residues and pairs of residues within windowSize residues of the position being assigned. This approach is about 65% accurate, and is one of the most accurate methods for assigning secondary structure that only use a single sequence. This implementation of GOR IV does not use decision constants or the number of contiguous states when assigning the final state. Note that characters other than the standard 20 amino acids are not assigned a state.

Value

If type is "states" (the default), then the output is a character vector with the secondary structure assignment ("H", "E", or "C") for each residue in myAAStringSet.

Otherwise, the output is a list with one element for each sequence in myAAStringSet. Each list element contains a matrix with dimensions 3 (H, E, or C) by the number of residues in the sequence. If type is "scores", then values in the matrix represent log-odds "scores". If type is "probabilities" then the values represent the normalized probabilities of the three states at a position.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

References

Garnier, J., Gibrat, J. F., & Robson, B. (1996). GOR method for predicting protein secondary structure from amino acid sequence. *Methods in Enzymology*, **266**, 540-553.

See Also

[HEC_MI1](#), [HEC_MI2](#)

Examples

```
fas <- system.file("extdata", "50S_ribosomal_protein_L2.fas", package="DECIPHER")
dna <- readDNASTringSet(fas)
aa <- translate(dna)
hec <- PredictHEC(aa)
head(hec)
```

RESTRICTION_ENZYMES *Common Restriction Enzyme's Cut Sites*

Description

A character vector of common restriction sites named by the restriction enzyme that cuts at each site. Sequence specificity is listed in 5' to 3' orientation based on the IUPAC_CODE_MAP. The cut site is either signified by a “/” for palindromic sites, or two numbers giving the position of the top and bottom cut positions relative to the site's 3'-end.

Usage

```
data(RESTRICTION_ENZYMES)
```

Format

The format is: Named chr [1:224] "GACGT/C" "G/GTACC" "GT/MKAC" ... - attr(*, "names")= chr [1:224] "AatII" "Acc65I" "AccI" "AciI" ...

Source

Restriction enzymes sold by [New England BioLabs](#).

Examples

```
data(RESTRICTION_ENZYMES)
```

SearchDB *Obtain Specific Sequences from A Database*

Description

Returns the set of sequences meeting the search criteria.

Usage

```
SearchDB(dbFile,
         tblName = "DNA",
         identifier = "",
         type = "XStringSet",
         limit = -1,
         replaceChar = "-",
         nameBy = "row_names",
         orderBy = "row_names",
         countOnly = FALSE,
         removeGaps = "none",
         clause = "",
         verbose = TRUE)
```

Arguments

| | |
|-------------|--|
| dbFile | A SQLite connection object or a character string specifying the path to the database file. |
| tblName | Character string specifying the table where the sequences are located. |
| identifier | Optional character string used to narrow the search results to those matching a specific identifier. If "" (the default) then all identifiers are selected. |
| type | The type of XStringSet (sequences) to return. This should be (an unambiguous abbreviation of) one of "XStringSet", "DNAStrngSet", "RNAStrngSet", "AAStringSet", "BStringSet", "QualityScaledXStringSet", "QualityScaledDNAStrngSet", "QualityScaledRNAStrngSet", "QualityScaledAAStringSet", or "QualityScaledBStringSet". If type is "XStringSet" or "QualityScaledXStringSet" then an attempt is made to guess the type of sequences based on their composition. |
| limit | Number of results to display. The default (-1) does not limit the number of results. |
| replaceChar | Optional character used to replace any characters of the sequence that are not present in the XStringSet's alphabet. Not applicable if type=="BStringSet". (See details section below.) |
| nameBy | Character string giving the column name for naming the XStringSet. |
| orderBy | Character string giving the column name for sorting the results. Defaults to the order of entries in the database. Optionally can be followed by " ASC" or " DESC" to specify ascending (the default) or descending order. |
| countOnly | Logical specifying whether to return only the number of sequences. |
| removeGaps | Determines how gaps ("- " or ". " characters) are removed in the sequences. This should be (an unambiguous abbreviation of) one of "none", "all" or "common". |
| clause | An optional character string to append to the query as a clause. |
| verbose | Logical indicating whether to display queries as they are sent to the database. |

Details

If type is "DNAStrngSet" then all U's are converted to T's before creating the DNAStrngSet, and vice-versa if type is "RNAStrngSet". All remaining characters not in the XStrngSet's alphabet are converted to replaceChar. Quality information is interpreted as PredQuality scores.

Value

An XStrngSet or QualityScaledXStrngSet with the sequences that meet the specified criteria. The names of the object correspond to the value in the nameBy column of the database.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

See Also

[Seqs2DB](#), [DB2Seqs](#)

Examples

```
db <- system.file("extdata", "Bacteria_175seqs.sqlite", package="DECIPHER")
# get all sequences in the default table:
dna <- SearchDB(db)
# select a random sequence:
dna <- SearchDB(db, orderBy="random()", limit=1)
# remove gaps from "Mycobacterium" sequences:
dna <- SearchDB(db, identifier="Mycobacterium", removeGaps="all")
# provide a more complex query:
dna <- SearchDB(db, nameBy="description", orderBy="bases", removeGaps="common",
               clause="where nonbases is 0")
```

Seqs2DB

Add Sequences from Text File to Database

Description

Adds sequences to a database.

Usage

```
Seqs2DB(seqs,
        type,
        dbFile,
        identifier,
        tblName = "DNA",
        chunkSize = 1e5,
        replaceTbl = FALSE,
        verbose = TRUE)
```


Arguments

| | |
|------------|--|
| seqs | A connection object or a character string specifying the file path to the file containing the sequences, an XStringSet object if type is XStringSet, or a QualityScaledXStringSet object if type is QualityScaledXStringSet. |
| type | The type of the sequences (seqs) being imported. This should be (an unambiguous abbreviation of) one of "FASTA", "FASTQ", "GenBank", "XStringSet", or "QualityScaledXStringSet". |
| dbFile | A SQLite connection object or a character string specifying the path to the database file. If the dbFile does not exist then a new database is created at this location. |
| identifier | Character string specifying the "id" to give the imported sequences in the database. |
| tblName | Character string specifying the table in which to add the sequences. |
| chunkSize | Number of lines of the seqs to read at a time. |
| replaceTbl | Logical. If FALSE (the default) then the sequences are appended to any already existing in the table. If TRUE then any sequences already in the table are overwritten. |
| verbose | Logical indicating whether to display each query as it is sent to the database. |

Details

Sequences are imported into the database in chunks of lines specified by chunkSize. The sequences can then be identified by searching the database for the identifier provided. Sequences are added to the database verbatim, so that no sequence information is lost when the sequences are exported from the database. The sequence names are recorded into a column named "description" in the database.

Value

The total number of sequences in the database table is returned after import.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

See Also

[SearchDB](#), [DB2Seqs](#)

Examples

```
gen <- system.file("extdata", "Bacteria_175seqs.gen", package="DECIPHER")
dbConn <- dbConnect(SQLite(), ":memory:")
Seqs2DB(gen, "GenBank", dbConn, "Bacteria")
BrowseDB(dbConn)
dna <- SearchDB(dbConn, nameBy="description")
dbDisconnect(dbConn)
```

StaggerAlignment *Produce a Staggered Alignment*

Description

Staggers overlapping characters in a multiple sequence alignment that are better explained by multiple insertions than multiple deletions.

Usage

```
StaggerAlignment(myXStringSet,
                 tree = NULL,
                 threshold = 3,
                 fullLength = FALSE,
                 processors = NULL,
                 verbose = TRUE)
```

Arguments

| | |
|--------------|--|
| myXStringSet | An AAStrngSet, DNAStrngSet, or RNAStrngSet object of aligned sequences. |
| tree | A bifurcating dendrogram representing the evolutionary relationships between sequences, such as that created by IdClusters . The root should be the topmost node of the tree. |
| threshold | Numeric giving the ratio of insertions to deletions that must be met to stagger a region of the alignment. Specifically, the number of insertions divided by deletions must be less than threshold to stagger. |
| fullLength | Logical specifying whether the sequences are full-length (TRUE), or terminal gaps should be treated as missing data (FALSE, the default). Either a single logical, a vector with one logical per sequence, or a list with right and left components containing logicals for the right and left sides of the alignment. |
| processors | The number of processors to use, or NULL (the default) for all available processors. |
| verbose | Logical indicating whether to display progress. |

Details

Multiple sequence aligners typically maximize true homologies at the expense of increased false homologies. `StaggerAlignment` creates a “staggered alignment” which separates regions of the alignment that are likely not homologous into separate regions. This re-balances the trade-off between true positives and false positives by decreasing the number of false homologies at the loss of some true homologies. The resulting alignment is less aesthetically pleasing because it is widened by the introduction of many gaps. However, in an evolutionary sense a staggered alignment is more correct because each aligned position represents a hypothesis about evolutionary events: overlapping characters between any two sequences represent positions common to their ancestor sequence that may have evolved through substitution.

The single parameter threshold controls the degree of staggering. Its value represents the ratio of insertions to deletions that must be crossed in order to stagger a region. A threshold of 1 would mean any region that could be better explained by separate insertions than deletions should be staggered. A higher value for threshold makes it more likely to stagger, and vice-versa. A very high value would conservatively stagger most regions with gaps, resulting in few false homologies but also fewer true homologies. The default value (3) is intended to remove more false homologies than it eliminates in true homologies. It may be preferable to tailor the threshold depending on the purpose of the alignment, as some downstream procedures (such as tree building) may be more or less sensitive to false homologies.

Value

An XStringSet of aligned sequences.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

References

Coming soon!

See Also

[AdjustAlignment](#), [AlignSeqs](#), [IdClusters](#)

Examples

```
db <- system.file("extdata", "Bacteria_175seqs.sqlite", package="DECIPHER")
dna <- SearchDB(db, remove="all")
alignedDNA <- AlignSeqs(dna)
staggerDNA <- StaggerAlignment(alignedDNA)
BrowseSeqs(staggerDNA, highlight=1)
```

Synteny

Synteny blocks and hits

Description

Syntenic blocks are DNA segments composed of conserved hits occurring in the same order on two sequences. The two sequences are typically chromosomes of different species that are hypothesized to contain homology. Class "Synteny" provides objects and functions for storing and viewing syntenic blocks and hits that are shared between sequences.

Usage

```
## S3 method for class 'Synteny'
pairs(x,
      bounds = TRUE,
      boxBlocks = FALSE,
      labels = abbreviate(rownames(x), 9),
      gap = 0.5,
      line.main = 3,
      cex.labels = NULL,
      font.labels = 1,
      ...)

## S3 method for class 'Synteny'
plot(x,
     labels = abbreviate(rownames(x), 9),
     ...)

## S3 method for class 'Synteny'
print(x,
      quote = FALSE,
      right = TRUE,
      ...)
```

Arguments

| | |
|-------------|--|
| x | An object of class “Synteny”. |
| bounds | Logical specifying whether to plot sequence boundaries as horizontal or vertical lines. |
| boxBlocks | Logical indicating whether to draw a rectangle around hits belonging to the same block of synteny. |
| labels | Character vector providing names corresponding to each “identifier” for labels on the diagonal. |
| gap | Distance between subplots, in margin lines. |
| line.main | If main is specified, line.main provides the line argument to mtext. |
| cex.labels | Magnification of labels on the diagonal. |
| font.labels | Font of labels on the diagonal. |
| quote | Logical indicating whether to print the output surrounded by quotes. |
| right | Logical specifying whether to right align strings. |
| ... | Other graphical parameters for pairs or plot, including: main, cex.main, font.main, and oma. Other arguments for print, including print.gap and max. |

Details

Objects of class Synteny are stored as square matrices of list elements with dimnames giving the “identifier” of the corresponding sequences. The synteny matrix can be separated into three parts:

along, above, and below the diagonal. Each list element along the diagonal contains an integer vector with the width of the sequence(s) belonging to that “identifier”. List elements above the diagonal (column $j > \text{row } i$) each contain a matrix with “hits” corresponding to matches between sequences i and j . List elements below the diagonal each contain a matrix with “blocks” of synteny between sequences j and i .

The `pairs` method creates a scatterplot matrix from a Synteny object. Dot plots above the diagonal show hits between identifier i and j , where forward hits are colored in black, and hits to the reverse strand of identifier j are colored in red. Plots below the diagonal show blocks of synteny colored by their score, from green (highest scoring) to blue to magenta (lowest scoring). The `plot` method displays a block view of the sequence groups in the same order as the input object (`x`). The endpoints of each block are connected by a pair of lines, which can cross if one block corresponds to the opposite strand of the other sequence.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

See Also

[AlignSynteny](#), [FindSynteny](#)

Examples

```
# a small example:
dbConn <- dbConnect(SQLite(), ":memory:")
s1 <- DNASTringSet("ACTAGACCCAGACCGATAAACGGACTGGACAAG")
s3 <- reverseComplement(s1)
s2 <- c(s1, s3)
Seqs2DB(c(c(s1, s2), s3),
        "XStringSet",
        dbConn,
        c("s1", "s2", "s2", "s3"))
syn <- FindSynteny(dbConn, minScore=1)
syn # Note: > 100% hits because of sequence reuse across blocks
pairs(syn, boxBlocks=TRUE)
plot(syn)
dbDisconnect(dbConn)

# a larger example:
db <- system.file("extdata", "Influenza.sqlite", package="DECIPHER")
synteny <- FindSynteny(db, minScore=50)
class(synteny) # 'Synteny'
synteny

# accessing parts
i <- 1
j <- 2
synteny[i, i][[1]] # width of sequences in i
synteny[j, j][[1]] # width of sequences in j
head(synteny[i, j][[1]]) # hits between i & j
synteny[j, i][[1]] # blocks between i & j
```

```
# plotting
pairs(synteny) # dot plots
plot(synteny) # block view
```

TerminalChar*Determine the Number of Terminal Characters*

Description

Counts the number of terminal characters for every sequence in an XStringSet. Terminal characters are defined as a specific character repeated at the beginning and end of a sequence.

Usage

```
TerminalChar(myXStringSet,
             char = "")
```

Arguments

myXStringSet An XStringSet object of sequences.

char A single character giving the terminal character to count, or an empty character ("") indicating to count both gap ("-") and unknown (".") characters.

Value

A matrix containing the results for each sequence in its respective row. The first column contains the number of leading char, the second contains the number of trailing char, and the third contains the total number of characters in-between.

Author(s)

Erik Wright <DECIPHER@cae.wisc.edu>

See Also

[IdLengths](#)

Examples

```
db <- system.file("extdata", "Bacteria_175seqs.sqlite", package="DECIPHER")
dna <- SearchDB(db)
t <- TerminalChar(dna)
```

 TileSeqs

Form a Set of Tiles for Each Group of Sequences.

Description

Creates a set of tiles that represent each group of sequences in the database for downstream applications.

Usage

```
TileSeqs(dbFile,
         tblName = "DNA",
         identifier = "",
         minLength = 26,
         maxLength = 27,
         maxTilePermutations = 10,
         minCoverage = 0.9,
         add2tbl = FALSE,
         verbose = TRUE,
         ...)
```

Arguments

| | |
|---------------------|---|
| dbFile | A SQLite connection object or a character string specifying the path to the database file. |
| tblName | Character string specifying the table of sequences to use for forming tiles. |
| identifier | Optional character string used to narrow the search results to those matching a specific identifier. If "" then all identifiers are selected. |
| minLength | Integer providing the minimum number of nucleotides in each tile. Typically the same or slightly less than maxLength. |
| maxLength | Integer providing the maximum number of nucleotides in each tile. Tiles are designed primarily for this length, which should ideally be slightly greater than the maximum length of oligos used in downstream functions. |
| maxTilePermutations | Integer specifying the maximum number of tiles in each target site. |
| minCoverage | Numeric providing the fraction of coverage that is desired for each target site in the group. For example, a minCoverage of 0.9 request that additional tiles are added until 90% of the group is represented by the tile permutations. |
| add2tbl | Logical or a character string specifying the table name in which to add the result. |
| verbose | Logical indicating whether to display progress. |
| ... | Additional arguments to be passed directly to SearchDB. |

Details

TileSeqs will create a set of overlapping tiles representing each target site in an alignment of sequences. The most common tile permutations are added until the desired minimum group coverage is obtained. The dbFile is assumed to contain DNASTringSet sequences (any U's are converted to T's).

Target sites with one more more tiles not meeting a set of requirements are marked with misprime equals TRUE. Requirements include minimum group coverage, minimum length, and maximum length. Additionally, tiles are required not to contain more than four runs of a single base or four di-nucleotide repeats.

Value

A data.frame with a row for each tile, and multiple columns of information. The row_names column gives the row number. The start, end, start_aligned, and end_aligned columns provide positioning of the tile in a consensus sequence formed from the group. The column misprime is a logical specifying whether the tile meets the specified constraints. The columns width and id indicate the tile's length and group of origin, respectively.

The coverage field gives the fraction of sequences containing the tile in the group that encompass the tile's start and end positions in the alignment, whereas groupCoverage contains the fraction of all sequences in the group containing a tile at their respective target site. For example, if only a single sequence out of 10 has information (no gap) in the first alignment position, then coverage would be 100% (1.0), while groupCoverage would be 10% (0.1).

The final column, target_site, provides the sequence of the tile.

Note

If add2tbl is TRUE then the tiles will be added to the database table that currently contains the sequences used for tiling. The added tiles may cause interference when querying a table of sequences. Therefore, it is recommended to add the tiles to their own table, for example, by using add2tbl="Tiles".

Author(s)

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See Also

[DesignPrimers](#)

Examples

```
db <- system.file("extdata", "Bacteria_175seqs.sqlite", package="DECIPHER")
tiles <- TileSeqs(db, identifier="Pseudomonas")
```


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