Package 'ProbeDeveloper'

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Type Package

Title Develop Hybridization Probes

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Description This tool can develop hybridization probes for target sequences based on melting temperature value calculated by R package 'TmCalculator' <https://CRAN.R-project.org/package=TmCalculator> and methods extended from Beliveau, B. J.,(2018) <doi:10.1073/pnas.1714530115>, and those hybridization probes can be used to capture specific target regions in fluorescence in situ hybridization and next generation sequence experiments.

License GPL (>= 2)

Imports TmCalculator (>= 1.0.0),Biostrings(>= 2.12.0)

Depends R (>= 2.10)

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ProbeDeveloper-package *Develop Hybridization Probes*

Description

This tool can develop hybridization probes for target sequences based on melting temperature value calculated by R package 'TmCalculator' <https://CRAN.R-project.org/package=TmCalculator> and methods extended from Beliveau, B. J.,(2018) <doi:10.1073/pnas.1714530115>, which can be used to capture specific target regions in fluorescence in situ hybridization and next generation sequence experiments.

Author(s)

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References

Beliveau B J, Kishi J Y, Nir G, et al. (2018). OligoMiner: A rapid, flexible environment for the design of genome-scale oligonucleotide in situ hybridization probes. bioRxiv.

ProbeMake *Make probes*

Description

ProbeMake searches for probes with a FASTA-formatted input file containing the target sequence. And it allows users to specify allowable ranges of probe length, percent GC content, and adjust melting temperature calculated using nearest neighbor thermodynamics. Candidate probe sequences passing all checks are outputted in BED format.

Usage

```
ProbeMake(fafile, LN = 90, ln = 60, TM = 80, tm = 60, CG = 70, cg = 30, gap = 0,
method = "S2L",direction = "3to5",prohibitseq=NULL,nn_table = "DNA_NN4",
tmm_table = "DNA_TMM1", imm_table = "DNA_IMM1",de_table = "DNA_DE1",
dnac1 = 25, dnac2 = 25, Na = 50,K = 0, Tris = 0, Mg = 0, dNTPs = 0, saltcorr = 5)
```

Arguments

fafile	Input file with a FASTA format read by function readDNAStringSet in R package 'Biostrings'
LN	The maximum allowed probe length, default is 90
ln	The minimum allowed probe length, default is 60
TM	The maximum allowed melting temperature, default is 80
tm	The minimum allowed melting temperature, default is 60
CG	The maximum allowed percent GC content, default is 70
cg	The minimum allowed percent GC content, default is 30
gap	The minimum gap between adjacent probes, default is 0
method	'S2L' is used to design probe extending from minimal probe length to the maximum until passing all checks, conversely 'L2S' make probe from maximal probe length to the minimum. Default is 'S2L'
direction	Design probes from 3 to 5 end of target sequence or from 5 to 3 end, default is '3to5'
prohibitseq	Prohibited sequence list, e.g prohibitseq=c("GGGGG","CCCCC"), default is NULL
nn_table	Thermodynamic NN values, eight tables are implemented. For DNA/DNA hybridizations: DNA_NN1,DNA_NN2,DNA_NN3,DNA_NN4 For RNA/RNA hybridizations: RNA_NN1,RNA_NN2,RNA_NN3 For RNA/DNA hybridizations: R_DNA_NN1 Default: DNA_NN4
tmm_table	Thermodynamic values for terminal mismatches. Default: DNA_TMM1
imm_table	Thermodynamic values for internal mismatches, may include insosine mismatches. Default: DNA_IMM1
de_table	Thermodynamic values for dangling ends: DNA_DE1(default),RNA_DE1
dnac1	Concentration of the higher concentrated strand [nM]. Typically this will be the primer (for PCR) or the probe. Default: 25
dnac2	Concentration of the lower concentrated strand [nM]. Default: 25
Na	Millimolar concentration of Na. Default: 50
K	Millimolar concentration of K. Default: 0
Tris	Millimolar concentration of Tris. Default: 0
Mg	Millimolar concentration of Mg
dNTPs	Millimolar concentration of dNTPs. Default: 50
saltcorr	Type of salt correction. Default: 5.

Value

Returns a bed file in the format TargetID <tab> Chr <tab> Start <tab> End <tab> Sequence <tab> Tm <tab> GC

Author(s)

Junhui Li

References

Beliveau B J, Kishi J Y, Nir G, et al. (2017). OligoMiner: A rapid, flexible environment for the design of genome-scale oligonucleotide in situ hybridization probes. bioRxiv.

Examples

```
data(samplefa)
ProbeMake(samplefa,LN=90,ln=60,TM=80,tm=70,CG=80,cg=20,gap=0,method="S2L",direction='3to5')
```

---

samplefa *sample data for target sequence region with class 'DNAStringSet'*

Description

Class 'DNAStringSet' sample data read by function readDNAStringSet in R package 'Biostrings' from fasta format, there are two target sequence resion in this data

Usage

```
data("samplefa")
```

Format

Formal class 'DNAStringSet' [package "Biostrings"] with 5 slots

Class 'DNAStringSet' sample data read by function readDNAStringSet in R package 'Biostrings' from fasta format, which is from ncbiRefSeq database for Homo Sapiens with referece genome version hg19

Examples

```
data(samplefa)
```

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