R documentation

of 'man/VNTR.Genotype.Rd'

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VNTR.Genotype	*Genotyping Variable Number Tandem Repeats (VNTR) for the genome sequence of monkeypox virus (MPXV)*

Description

The funciton VNTR.Genotype computes the copy of the variable number tandem repeats.

Usage

```
VNTR.Genotype(data, vntr,
      regionStart, regionEnd,
      match_s = match_s,
      mismatch_s = mismatch_s,
      baseonly = True,
      VNTRoutput = False,
      finder = False)
```

Arguments

data	sequences from a file in FASTA format
vntr	variable number tandem repeat
match_s	matching weight
mismatch_s	mismatching penalty
regionStart	start position of VNTR region
regionEnd	end position of VNTR region
baseonly	logical. If TRUE, only uses the letters in base alphabet i.e. A,C,G,T.
VNTRoutput	logical. If TRUE, export output to .csv file.
finder	logical. If TRUE, call function STR_finder.

Value

ID	name of sequence
r	the copy of tandem repeats
match	the number of matches
mismatch	the number of mismatches
indel	the number of indels
score	alignment score of VNTR region for each query strain
start_pos	start position of the VNTR region for each query strain

References

PagC(s H, Aboyoun P, Gentleman R, DebRoy S (2022) *Biostrings: Efficient manipulation of biological strings*. R package version 2.64.0, https://bioconductor.org/packages/Biostrings.

Examples

```
## load example
data(example)


## VNTR
vntr <- c("T","TATGATGGA","AT","ATATACATT")
regionStart <- c(132436,150542,173240,178413)
regionEnd <- c(133216,151501,173320,179244)

## parameter settings
baseonly = T
match_s = 2
mismatch_s = -5
VNTRoutput = F
finder = F

## computes the copy of the variable number tandem repeats
out <- VNTR.Genotype(data = MPXVseq, vntr = vntr,
                     regionStart = regionStart, regionEnd = regionEnd,
                     match_s = match_s, mismatch_s=mismatch_s,
                     baseonly = baseonly,VNTRoutput = VNTRoutput,
                     finder = finder)
```

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