

Package ‘MPXV’

December 5, 2022

Title Variable Number Tandem Repeats Analysis

Version 0.1.0

Description Analysis of calling Variable Number Tandem Repeats for the genome sequence of monkeypox virus and virus tracking.

LazyData true

Imports seqinr, stringr, Biostrings

RoxygenNote 7.2.1

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VNTRcaller	<i>Calling Variable Number Tandem Repeats (VNTR) for the genome sequence of monkeypox virus (MPXV)</i>
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Description

The function VNTRcaller estimates the copy numbers of VNTRs.

Usage

```
VNTRcaller(  
  data,  
  vntr = vntr,  
  match_s = match_s,  
  mismatch_s = mismatch_s,  
  regionStart = regionStart,  
  regionEnd = regionEnd,  
  baseonly = T,  
  fseqExtend = fseqExtend,  
  VNTRoutput = F,  
  tracker = F  
)
```

Arguments

data	MPXV sequences from a file in FASTA format
vntr	sequence of the repetitive unit
match_s	matching weight
mismatch_s	mismatching penalty
regionStart	starting position of a VNTR region
regionEnd	ending position of a VNTR region
baseonly	logical. If TRUE, only the letters of the nucleotide bases (i.e. A,C,G,T) are considered. If FALSE, the degenerate codes are also considered.
fseqExtend	the length of extended flanking sequence
VNTRoutput	logical. If TRUE, the output is written to .csv files.
tracker	logical. If TRUE, call function VNTRtracker .

Value

ID	name of MPXV sequences
r	copy of tandem repeats
match	number of matches
mismatch	number of mismatches
indel	number of insertions and deletions (indels)
score	alignment score of a VNTR region for a query strain
start_pos	starting position of the VNTR region for a query strain

References

Yang, H.-C. et al (2022) Monkeypox genome contains variable number tandem repeats enabling accurate virus tracking.

Pages H, Aboyoun P, Gentleman R, DebRoy S (2022) *Biostrings: Efficient manipulation of biological strings*. R package version 2.64.0.

Examples

```
## Read MPXV example sequences from a file in FASTA format.
MPXVseq <- read.fasta(system.file("extdata/MPXV_seq_example.fasta.gz", package = "MPXV"), as.string = T)

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

## parameter settings
match_s = 2
mismatch_s = -5
baseonly = TRUE
fseqExtend = 150
VNTRoutput = FALSE
tracker = FALSE

## computes the copy of the variable number tandem repeats
```

```
out <- VNTRcaller(data = MPXVseq, vntr = vntr,
                  regionStart = regionStart, regionEnd = regionEnd,
                  match_s = match_s, mismatch_s=mismatch_s,
                  baseonly = baseonly, fseqExtend = fseqExtend,
                  VNTRoutput = VNTRoutput,
                  tracker = tracker)
```

VNTRtracker	<i>Tracking the origin of monkeypox virus (MPXV) by using Variable Number Tandem Repeats (VNTR) markers</i>
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Description

The function VNTRtracker calculates the MPXV strain-strain genetic distance to track the origin of a given MPXV by using VNTRs.

Usage

```
VNTRtracker(r, file_name = "Tracking_output")
```

Arguments

r	A vector of copies of VNTR of MPXV.
file_name	Filename of the output.

Details

The four VNTR markers nt133095[A25R - A26L] (T), nt150560[A47R - A49R] (TATGATGGA), nt173267[B14R - B15L] (AT), and nt179074[B18R - B19R] (ATATACATT) are proposed to track the original of MPXV strains. Based on these four VNTRs, we calculate three distances (ploymorphism information content, entropy, and length of repetitive unit (see Yang et al. (2022)) between a query MPXV strain and the strains in our database.

Value

The output contains multiple columns, including accession ID, country name, collection date, clade, lineage, and three distances mentioned above.

References

Yang, H.-C. et al (2022) Monkeypox genome contains variable number tandem repeats enabling accurate virus tracking.

Examples

```
r=c(27,7,24,16)
```

```
VNTRtracker(r,
             file_name="Tracking_output")
```

```
#The output is a csv file with the file name given by the parameter "file_name".
```

```
#In this file, each row represents a strain in our database, and column variables contain accession ID, country name, collection date, clade, lineage, and three distances mentioned above.
```

```
#The rank of strains are ordered by ploymorphism information content distance (see Yang et al. (2022)) from low to high.
```

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