Package 'R2019nCoV'

February 29, 2020

Title Analysis of 2019-nCoV Virus

Version 0.1.0

Description Since December 2019, Wuhan City, Hubei Province has continued to carry out surveillance of influenza and related diseases, and found multiple cases of viral pneumonia, all of which were diagnosed with viral pneumonia / pulmonary infection. On January 12, 2020, the World Health Organization officially named the new coronavirus causing the pneumonia epidemic in Wuhan as ``2019 New Coronavirus (2019-nCoV)''. The current epidemic situation is very serious, here we developed an R package for 2019-nCoV analysis(Real-time monitoring and Visualization) by querying real-time statistics of 2019-nCoV virus cases from <https://view.inews.qq.com/g2/getOnsInfo?name=disease_h5&callback=1580373566110> and performing follow-up analysis.

Depends R (>= 3.5.0)

License Artistic-2.0

Encoding UTF-8

LazyData true

Language en-US

Imports jsonlite, ggplot2, dplyr, pinyin, maps

Suggests spelling, knitr, rmarkdown

RoxygenNote 7.0.0

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

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| china_line_data | *a data.frame which is the border map data of China from http://nfgis.nsdi.gov.cn* |

Description

a data.frame which is the border map data of China from http://nfgis.nsdi.gov.cn

Usage

```
china_line_data
```

Format

a data.frame

| china_map_data | *a data.frame which is the detailed map data of China from http://nfgis.nsdi.gov.cn* |

Description

a data.frame which is the detailed map data of China from http://nfgis.nsdi.gov.cn

Usage

```
china_map_data
```

Format

a data.frame

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geneSEQ *a string which is the sequence of 2019-nCoV*

Description

a string which is the sequence of 2019-nCoV

Usage

```
geneSEQ
```

Format

a string

---

getDataFrame *Getting data.frame of detailed real-time statistical numbers of every provinces of China of 2019-nCoV virus cases*

Description

Getting data.frame of detailed real-time statistical numbers of every provinces of China of 2019-nCoV virus cases

Usage

```
getDataFrame(x)
```

Arguments

x   a R2019-nCoV object, i.e. the result of function get_2019nCoV

Value

a data.frame object which contains detailed real-time statistics of 2019-nCoV virus cases

Examples

```
x <- get_2019nCoV()
df <- getDataFrame(x)
```

---

getMap   *Getting real-time monitoring map of the 2019-nCoV virus*

Description

Getting real-time monitoring map of the 2019-nCoV virus

Usage

```
getMap(x)
```

Arguments

x   a R2019-nCoV object, i.e. the result of function get_2019nCoV

Value

a ggplot2 object which shows the real-time monitoring map of the 2019-nCoV virus

Examples

```
x <- get_2019nCoV()
map <- getMap(x)
```

---

getSeq   *Getting   the   gene   sequence   of   2019-nCoV   virus*
                                (i.e.GenBank:MN908947)

Description

Getting the gene sequence of 2019-nCoV virus (i.e.GenBank:MN908947)

Usage

```
getSeq()
```

Value

a string which is the gene sequence of 2019-nCoV

Examples

```
Seq <- getSeq()
```

---

get_2019nCoV   *Getting R2019-nCoV object and checking real-time monitoring num-*
                                  bers of the 2019-nCoV virus

---

Description

Getting R2019-nCoV object and checking real-time monitoring numbers of the 2019-nCoV virus

Usage

```
get_2019nCoV()
```

Value

a R2019-nCoV object for further use

Examples

```
x <- get_2019nCoV()
```

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