# Package 'edm1.sequence'

July 29, 2024

Title	Set	of	tools	to	manipul	ate	time	series
-------	-----	----	-------	----	---------	-----	------	--------

**Version** 2.0.0.0

**Description** Provides set of functions to manipulate time series dataset; create variables that designates the value of the individual at n-x, handle missing values...

License GPL (==3)

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

RoxygenNote 7.3.1

Imports stringr

# **Contents**

Index		9
	sequence_na_med2	7
	sequence_na_med1	
	sequence_na_mean2	5
	sequence_na_mean1	4
	historic_sequence2	2
	historic_sequence1	

historic\_sequence1 historic\_sequence1

# Description

Allow to perform a pivot wider on a sequencial dataset (here the type is dataframe), each variable will be dupplicated in a column to show the value to this variable at n-1 for each individual, see examples.

#### Usage

```
historic_sequence1(inpt_datf, bf_ = 1)
```

# **Arguments**

inpt\_datf is the input dataframe
bf\_ is the number of previous value of the individual it will search for, see examples

2 historic\_sequence2

```
set.seed(123)
var1 < - round(runif(n = 14, min = 100, max = 122))
set.seed(123)
var2 \leftarrow round(runif(n = 14, min = 14, max = 20))
datf <- data.frame("ids" = c(20, 20, 20, 20, 19, 19, 19, 18, 18, 18, 18,
                       17, 17, 17),
               "individual" = c("oui", "non", "peut1", "peut2", "oui", "peut1", "peut2"),
               "var1" = var1,
                "var2" = var2)
print(datf)
  ids individual var1 var2
  20 oui 106 16
           non 117
  20
2
                     19
         peut1 109 16
3
  20
         peut2 119 19
4
  20
           oui 121
5
  19
                     20
6 19
         peut1 101
                    14
7 19
         peut2 112
                    17
8 18
          oui 120 19
9 18
           non 112 17
10 18
         peut1 110
                    17
11 18
         peut2 121
                     20
12 17
          oui 110
                    17
13 17
          peut1 115
                     18
14 17
         peut2 113
                     17
historic_sequence1(inpt_datf = datf, bf_ = 2)
 id_seq individual var1-1 var1-2 var2-1 var2-2
        oui 121 120 20 19
1
    20
                                NA
2
                   NA
                         112
     20
             non
                                       17
                   101
                                14
3
     20
                         110
                                      17
           peut1
                                17
4
     20
                  112
                         121
                                      20
           peut2
5
                   120
                         110
                                19
     19
                                      17
            oui
                   110
                         115
                                17
                                      18
6
    19
           peut1
           peut2
    19
                  121
                         113
                                20
                                      17
historic_sequence1(inpt_datf = datf, bf_ = 3)
 id_seq individual var1-1 var1-2 var1-3 var2-1 var2-2 var2-3
1
    20
            oui 121 120 110 20 19 17
2
                   NA
                         112
                                      NA
                                             17
                                                  NA
     20
             non
                                NA
                                     14 17
17 20
3
                   101 110 115
    20
          peut1
                                                  18
4
    20
          peut2 112
                         121 113
                                                   17
```

historic\_sequence2 3

#### **Description**

Allow to perform a pivot wider on a sequencial dataset (here the type is dataframe), each variable will be dupplicated in a column to show the value to this variable at n - 1 for each individual, see examples.

#### Usage

```
historic_sequence2(inpt_datf, bf_ = 1)
```

#### **Arguments**

```
is the input dataframe
inpt_datf
bf_
                  is the number of previous value of the individual it will search for, see examples
```

# **Examples**

19

```
set.seed(123)
var1 < - round(runif(n = 14, min = 100, max = 122))
set.seed(123)
var2 \leftarrow round(runif(n = 14, min = 14, max = 20))
datf <- data.frame("ids" = c(20, 20, 20, 20, 19, 19, 19, 18, 18, 18, 18,
                            17, 17, 17),
                  "individual" = c("oui", "non", "peut1", "peut2",
                                    "oui", "peut1", "peut2"),
                  "var1" = var1,
                  "var2" = var2)
print(datf)
   ids individual var1 var2
1
   20 oui 106 16
2
   20
             non 117 19
          peut1 109 16
3
   20
          peut2 119 19
   20
5
  19
            oui 121
         peut1 101
peut2 112
6
  19
                         14
7
   19
                         17
           oui 120
8
   18
                         19
9
             non 112
                         17
   18
10 18
          peut1 110
                         17
11 18
          peut2 121
                         2.0
12
   17
             oui 110
                         17
13
   17
            peut1
                   115
                         18
   17
            peut2
                   113
                         17
print(historic_sequence2(inpt_datf = datf, bf_ = 2))
  id_seq individual var1-0 var1-1 var1-2 var2-0 var2-1 var2-2
1
              oui 106 121 120
                                           16 20
                                                          19
      20
2
      20
                       117
                                      112
                                                            17
                               NA
                                              19
                                                     NA
                non
      20
                      109
                            101
                                     110
                                                            17
3
                                             16
                                                     14
             peut1
4
      20
              peut2 119 112 121
                                             19
                                                    17
                                                            20

    oui
    121
    120
    110
    20
    19

    peut1
    101
    110
    115
    14
    17

    peut2
    112
    121
    113
    17
    20

5
      19
                                                            17
6
     19
            peut1
                                                            18
```

17

4 sequence\_na\_mean1

```
print(historic_sequence2(inpt_datf = datf, bf_ = 3))
 id_seq individual var1-0 var1-1 var1-2 var1-3 var2-0 var2-1 var2-2 var2-3
1
                       121 120
                                   110 16 20 19 17
     2.0
            oui
                 106
2
     20
                   117
                               112
                                            19
                                                  NA
                                                        17
             non
                         NA
                                     NA
                                                              NA
3
                  109
                         101
                              110
                                           16
                                                       17
     20
                                     115
                                                 14
                                                             18
           peut1
4
     20
                  119
                       112 121
                                    113
                                          19
                                                 17
                                                        20
                                                             17
           peut2
```

```
sequence_na_mean1 sequence_na_mean1
```

### **Description**

In a dataframe generated by the function historic\_sequence1, convert all NA to the mean of the values at the same variable for the individual at the id where the NA occurs, see examples (only accepts numeric variables)

# Usage

```
sequence_na_mean1(inpt_datf, bf_)
```

### **Arguments**

```
inpt_datf is the input dataframe
```

```
set.seed(123)
var1 < - round(runif(n = 14, min = 100, max = 122))
set.seed(123)
var2 \leftarrow round(runif(n = 14, min = 14, max = 20))
datf <- data.frame("ids" = c(20, 20, 20, 20, 19, 19, 19, 18, 18, 18, 18,
17, 17, 17),
"individual" = c("oui", "non", "peut1", "peut2",
"oui", "peut1", "peut2"),
"var1" = var1,
"var2" = var2)
datf <- historic_sequence1(inpt_datf = datf, bf_ = 2)</pre>
datf[3, 4] <- NA
datf[6, 4] <- NA
datf[1, 3] <- NA
print(datf)
  id_seq individual var1-1 var1-2 var2-1 var2-2
1
                                  20
     20
              oui
                    NA 120
                                           19
2
      20
                             112
                                            17
                       NA
                                     NA
               non
     20
                                            17
3
                      101
                                     14
             peut1
                              NA
4
     20
             peut2
                     112
                             121
                                     17
                                            20
5
     19
              oui
                     120
                             110
                                    19
                                            17
6
     19
             peut1
                      110
                             NA
                                    17
                                            18
7
     19
             peut2
                     121
                            113
                                    20
                                            17
```

sequence\_na\_mean2 5

```
print(sequence_na_mean1(inpt_datf = datf, bf_ = 2))
 id_seq individual var1-1 var1-2 var2-1 var2-2
     20 oui 115 120.0 20
1
                   112 112.0
                                 17
2
     20
             non
     20 peut1
20 peut2
                   101 105.5
                                14
3
                                        17
           peut2 112 121.0
4
                                17
                                        2.0
                   120 110.0
5
     19
            oui
                                19
                                       17
    19 peut1 110 105.5
19 peut2 121 113.0
6
                                17
                                       18
                                20
                                       17
```

```
sequence_na_mean2 sequence_na_mean2
```

# Description

In a dataframe generated by the function historic\_sequence1, convert all NA to the mean of the values at the same variable for the individual at the id where the NA occurs, see examples (only accepts numeric variables)

# Usage

```
sequence_na_mean2(inpt_datf, bf_)
```

# Arguments

```
inpt_datf is the input dataframe

bf_ is how at how many n -1 we look for the value of the variables for the individual at time index n
```

```
set.seed(123)
var1 < - round(runif(n = 14, min = 100, max = 122))
set.seed(123)
var2 \leftarrow round(runif(n = 14, min = 14, max = 20))
datf <- data.frame("ids" = c(20, 20, 20, 20, 19, 19, 19, 18, 18, 18,
17, 17, 17),
"individual" = c("oui", "non", "peut1", "peut2",
"oui", "peut1", "peut2"),
"var1" = var1,
"var2" = var2)
datf <- historic_sequence2(inpt_datf = datf, bf_ = 2)</pre>
datf[3, 4] \leftarrow NA
datf[6, 4] <- NA
datf[1, 3] <- NA
print(datf)
 id_seq individual var1-0 var1-1 var1-2 var2-0 var2-1 var2-2
     20 oui NA 121 120 16 NA
1
     20
             non 117
                           NA 112
                                         19
                                               NA
                                                      17
3
     20
           peut1 109 NA 110
                                         16
                                               14
                                                      17
```

6 sequence\_na\_med1

```
20
                    119
                         112
                                121
                                      19
                                             17
                                                    20
            peut2
5
     19
                    121
                          120
                                110
                                       20
                                             19
                                                    17
            oui
6
     19
            peut1
                    101
                          NA
                                115
                                       14
                                             17
                                                    18
7
                    112
     19
                          121
                                113
                                       17
                                             20
                                                    17
            peut2
print(sequence_na_mean2(inpt_datf = datf, bf_ = 2))
 id_seg individual var1-0
                        var1-1 var1-2 var2-0 var2-1 var2-2
1
     20
             oui 117 121.0000
                                120
                                        16
                                              18
             non 117 114.5000
2
     20
                                 112
                                        19
                                               18
                                                     17
3
                   109 108.3333
                                110
                                        16
                                                     17
     20
          peut1
4
     20
          peut2 119 112.0000
                                121
                                        19
                                              17
                                                     20
5
     19
           oui 121 120.0000
                                110 20
                                              19
                                                     17
    19 peut1 101 108.3333
19 peut2 112 121.0000
                                       14 17
                                115
6
                                                     18
                                        17
7
                                113
                                               20
                                                     17
```

```
sequence_na_med1 sequence_na_med1
```

# **Description**

In a dataframe generated by the function historic\_sequence1, convert all NA to the median of the values at the same variable for the individual at the id where the NA occurs, see examples (only accepts numeric variables)

# Usage

```
sequence_na_med1(inpt_datf, bf_)
```

#### **Arguments**

```
inpt_datf is the input dataframe

bf_ is how at how many n - -1 we look for the value of the variables for the individual at time index n
```

```
set.seed(123)
var1 <- round(runif(n = 14, min = 100, max = 122))
set.seed(123)
var2 <- round(runif(n = 14, min = 14, max = 20))

datf <- data.frame("ids" = c(20, 20, 20, 20, 19, 19, 19, 18, 18, 18, 18, 17, 17, 17),
  "individual" = c("oui", "non", "peut1", "peut2",
  "oui", "peut1", "peut2"),
  "var1" = var1,
  "var2" = var2)
datf <- historic_sequence1(inpt_datf = datf, bf_ = 2)
datf[3, 4] <- NA
datf[6, 4] <- NA
datf[1, 3] <- NA
print(datf)</pre>
```

sequence\_na\_med2 7

```
id_seq individual var1-1 var1-2 var2-1 var2-2
             oui NA 120 20
non NA 112 NA
     20
                                NA
2
     20
                                       17
    20 peut1 101
20 peut2 112
                                14
3
                                       17
                          NA
                                17
                        121
4
                                       20
                   120 110
            oui
5
    19
                                19
                                       17
          peut1
                                17
6
    19
                   110
                         NA
                                       18
    19
           peut2 121 113
                                20
                                       17
print(sequence_na_med1(inpt_datf = datf, bf_ = 2))
 id_seq individual var1-1 var1-2 var2-1 var2-2
     20 oui 115 120.0 20
1
     20
2
             non 112 112.0
                                17
                                       17
    20 peut1 101 105.5
20 peut2 112 121.0
19 oui 120 110.0
                                14
3
                                       17
4
                                17
                                       20
           oui 120 110.0 19
5
                                       17
     19 peut1 110 105.5
19 peut2 121 113.0
                              17
6
                                       18
                                20
                                       17
```

```
sequence_na_med2 sequence_na_med2
```

### **Description**

In a dataframe generated by the function historic\_sequence2, convert all NA to the median of the values at the same variable for the individual at the id where the NA occurs, see examples (only accepts numeric variables)

#### Usage

```
sequence_na_med2(inpt_datf, bf_)
```

### **Arguments**

inpt\_datf is the input dataframe

bf\_ is how at how many n -1 we look for the value of the variables for the individual at time index n

```
set.seed(123)
var1 <- round(runif(n = 14, min = 100, max = 122))
set.seed(123)
var2 <- round(runif(n = 14, min = 14, max = 20))
datf <- data.frame("ids" = c(20, 20, 20, 20, 19, 19, 19, 18, 18, 18, 17, 17, 17),
"individual" = c("oui", "non", "peut1", "peut2",
"oui", "peut1", "peut2"),
"var1" = var1,
"var2" = var2)
datf <- historic_sequence2(inpt_datf = datf, bf_ = 2)</pre>
```

8 sequence\_na\_med2

```
datf[3, 4] <- NA
datf[6, 4] <- NA
datf[1, 3] <- NA
print(datf)</pre>
```

	id_seq	individual	var1-0	var1-1	var1-2	var2-0	var2-1	var2-2
1	20	oui	NA	121	120	16	20	19
2	20	non	117	NA	112	19	NA	17
3	20	peut1	109	NA	110	16	14	17
4	20	peut2	119	112	121	19	17	20
5	19	oui	121	120	110	20	19	17
6	19	peut1	101	NA	115	14	17	18
7	19	peut2	112	121	113	17	20	17

print(sequence\_na\_med2(inpt\_datf = datf, bf\_ = 2))

	id_seq	individual	var1-0	var1-1	var1-2	var2-0	var2-1	var2-2
1	20	oui	120	121.0	120	16	20	19
2	20	non	117	114.5	112	19	18	17
3	20	peut1	109	109.0	110	16	14	17
4	20	peut2	119	112.0	121	19	17	20
5	19	oui	121	120.0	110	20	19	17
6	19	peut1	101	109.0	115	14	17	18
7	19	peut2	112	121.0	113	17	20	17

# Index

```
historic_sequence1, 1
historic_sequence2, 2
sequence_na_mean1, 4
sequence_na_mean2, 5
sequence_na_med1, 6
sequence_na_med2, 7
```