

Package: MorbiditySpainR (via r-universe)

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Type Package

Title Read and manipualte data from Encuesta de morbilidad
hospitalaria INE

Version 0.1.0

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Description Show data from Encuesta de morbilidad hospitalaria

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URL <https://github.com/rOpenSpain/MorbiditySpainR>

Encoding UTF-8

LazyData true

Imports readr, dplyr, ggplot2, seasonal, dplyr, lubridate, XLConnect

RoxygenNote 6.0.1

Suggests testthat, knitr, rmarkdown

VignetteBuilder knitr

Config/pak/sysreqs make default-jdk libx11-dev

Repository <https://ropenspain.r-universe.dev>

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AddDiagnosis1	<i>Add principal diagnosis to morbity data</i>
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Description

Add principal diagnosis following international classification of diseases

Usage

```
AddDiagnosis1(data)
```

Arguments

data	Morbidity data
------	----------------

Value

data frame with morbidity data prov_hosp, sexo, prov_res, diag_in, diag_ppal, motivo_alta, estancia, fecha_ingreso, edad, diag1

Examples

```
data <- data_ejemplo %>% AddDiagnosis1()
```

AddDiagnosis2	<i>Add secondary diagnosis to morbity data</i>
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Description

Add secondary diagnosis following international classification of diseases

Usage

```
AddDiagnosis2(data)
```

Arguments

data Morbidity data

Value

data frame with morbidity data prov_hosp, sexo, prov_res, diag_in, diag_ppal, motivo_alta, estancia, fecha_ingreso, edad, diag2

Examples

```
data <- data_ejemplo %>% AddDiagnosis2()
```

AddDiagnosis3	<i>Add specific diagnosis to morbidity data</i>
---------------	---

Description

Add specific diagnosis following international classification of diseases

Usage

```
AddDiagnosis3(data)
```

Arguments

data Morbidity data

Value

data frame with morbidity data prov_hosp, sexo, prov_res, diag_in, diag_ppal, motivo_alta, estancia, fecha_ingreso, edad, diag3

Examples

```
data <- data_ejemplo %>% AddDiagnosis3()
```

FilterDiagnosis1	<i>Filter morbidity by principal diagnosis</i>
------------------	--

Description

Filter morbidity by principal diagnosis following international classification of diseases

Usage

```
FilterDiagnosis1(data, diagnosis_id)
```

Arguments

data	Morbidity data
diagnosis_id	id of principal diagnosis

Details

Uses dplyr filter

Value

data frame with morbidity data prov_hosp, sexo, prov_res, diag_in, diag_ppal, motivo_alta, estancia, fecha_ingreso, edad

Examples

```
data <- data_ejemplo %>% FilterDiagnosis1(2)
```

FilterDiagnosis2	<i>Filter morbidity by secondary diagnosis</i>
------------------	--

Description

Filter morbidity by secondary diagnosis following international classification of diseases

Usage

```
FilterDiagnosis2(data, diagnosis_id)
```

Arguments

data	Morbidity data
diagnosis_id	id of secondary diagnosis

Details

Uses dplyr filter

Value

data frame with morbidity data prov_hosp, sexo, prov_res, diag_in, diag_ppal, motivo_alta, estancia, fecha_ingreso, edad

Examples

```
data <- data_ejemplo %>% FilterDiagnosis2(20)
```

FilterEmergency	<i>Filter morbidity by ER item</i>
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Description

Filter morbidity by ER

Usage

```
FilterEmergency(data)
```

Arguments

data	Morbidity data
------	----------------

Details

Uses dplyr filter

Value

data frame with morbidity data prov_hosp, sexo, prov_res, diag_in, diag_ppal, motivo_alta, estancia, fecha_ingreso, edad

Examples

```
data <- data_ejemplo %>% FilterEmergency()
```

FilterProvincia	<i>Filter morbidity by provincia</i>
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Description

Filter morbidity by provincia using official id of provincias

Usage

```
FilterProvincia(data, provincia)
```

Arguments

data	Morbidity data
provincia	ID of provincia

Details

Uses dplyr filter

Value

data frame with morbidity data prov_hosp, sexo, prov_res, diag_in, diag_ppal, motivo_alta, estancia, fecha_ingreso, edad

Examples

```
data <- data_ejemplo %>% FilterProvincia(28)
```

GetMorbiData	<i>Download and read morbidity data for several years</i>
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Description

Download morbidity data from INE ftp and parse it

Usage

```
GetMorbiData(y1 = 2005, y2 = 2015)
```

Arguments

year1	Begining year of morbidity data
year2	Ending year of morbidity data

Details

Uses ReadZip

Value

data frame with morbidity data prov_hosp, sexo, prov_res, diag_in, diag_ppal, motivo_alta, estancia, fecha_ingreso, edad

Examples

```
data <- GetMorbiData(y1=2010,y2=2011)
```

ReadZip

Download and read morbidity data

Description

Download morbidity data from INE ftp and parse it

Usage

```
ReadZip(year)
```

Arguments

year Year of morbidity data

Details

Uses read.fwf

Value

data frame with morbidity data prov_hosp, sexo, prov_res, diag_in, diag_ppal, motivo_alta, estancia, fecha_ingreso, edad

Examples

```
data <- ReadZip(2010)
```

ReadZip2015

Download and read morbidity data form year 2015

Description

Download morbidity data from INE ftp and parse it

Usage

```
ReadZip2015(year)
```

Arguments

year	Year of morbidity data
------	------------------------

Details

Uses script provided from INE

Value

data frame with morbidity data prov_hosp, sexo, prov_res, diag_in, diag_ppal, motivo_alta, estancia, fecha_ingreso, edad

Examples

```
data <- ReadZip(2015)
```

ReduceData

Reduce data to temporal serie

Description

Reduce morbidity data to temporal serie, including diagnosis, province or sex

Usage

```
ReduceData(data, provincia = TRUE, date = "day", diag = NULL,
  sex = FALSE)
```

Arguments

data	Morbidity data
date	day, month or year
diag	diag1, daig2, diag3, if NULL not reduced by diagnosis
sex	Boolean, reduce by sex
province	Boolean, reduce by provicia

Details

Uses group_by

Value

data frame with data serie of morbidity

Examples

```
data <- data_ejemplo %>% ReduceData(provincia = TRUE,date = "day")
```

SetPrevalence	<i>Calculate prevalence, relative values.</i>
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Description

Calculate prevalence, relative values by total population of preovince

Usage

```
SetPrevalence(data, pop = "total")
```

Arguments

data	Morbidity data
pop	total, male, females

Details

Uses poblacion

Value

relative values of prevalence

Examples

```
data <- data_ejemplo %>% ReduceData(provincia = TRUE,date="year") %>% SetPrevalence()
```

`TraduceCodigoEspecifico`*Get specific diagnosis*

Description

Get specific diagnosis following international classification of diseases

Usage

```
TraduceCodigoEspecifico(codigo)
```

Arguments

`codigo` code from morbidity data

Value

Specific diagnosis

Examples

```
data <- TraduceCodigoEspecifico(3019)
```

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