

# Package ‘eoR’

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**Type** Package

**Title** Data Management Package (Exposure and Occurrence Data in R)

**Version** 0.4.0

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**Description** This data management package provides some helper classes for publicly available data sources (HMD, DESTATIS) in Demography. Similar to ideas developed in the Bioconductor project <<https://bioconductor.org>> we strive to encapsulate data in easy to use S4 objects.

If original data is provided in a text file, the resulting S4 object contains all information from that text file. But the information is somehow structured (header, footer, etc).

Further the classes provide methods to make a subset for selected calendar years or selected regions. The resulting subset objects still contain the original header and footer information.

**License** GPL-3

**URL** <https://github.molgen.mpg.de/walke/eoR>

**Encoding** UTF-8

**Depends** R (>= 3.2.0)

**Imports** methods, data.table

**LazyData** no

**RoxygenNote** 6.1.1

**NeedsCompilation** no

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EX1-class	<i>EX1 class for HMD exposure files 1x1</i>
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### Description

The class EX1 stores HMD exposure information in a systematic way.

The header-method gets the raw header information of an EX1 object

The ex1-method gets the exposure information of an EX1 object

The content-method gets the exposure table information of an EX1 object

The region-method gets the regional information of an EX1 object

The protocol-method gets the protocol information of an EX1 object

The Exposure1-constructor creates an EX1 object

The length-method gets the number of rows int the EX1 ex1 data.table

The selectYears-method gets a subset of an EX1 object

The readEX1x1-method reads all information from the file 1x1 exposure table

### Usage

```
## S4 method for signature 'EX1'
header(object)
```

```
## S4 method for signature 'EX1'
ex1(object)
```

```
## S4 method for signature 'EX1'
content(object)
```

```
## S4 method for signature 'EX1'
region(object)
```

```
## S4 method for signature 'EX1'
protocol(object)
```

```
Exposure1(header, ex1, content, region, protocol)
```

```

## S4 method for signature 'EX1'
length(x)

## S4 method for signature 'EX1'
show(object)

## S4 method for signature 'EX1'
selectYears(object, selectYears)

readEX1x1(infile)

```

### Arguments

object	EX1-object
header	vector
ex1	data.table
content	character
region	character
protocol	character
x	EX1-object
selectYears	vector
infile	character file name

### Details

This EX1 class fits to Human Mortality Database (HMD) 1x1 period exposure tables. See <https://www.mortality.org/> for data details. An EX1 instance stores the raw header, the content, the version protocol and regional information and the exposure table as a data.table object. The validation adds a pure numeric age AgeLow to the exposure table. Try demo(EX1) for a demonstration.

### Value

The header-method returns the raw header information

The ex1-method returns the exposure table

The content-method returns the content information

The region-method returns the regional information

The protocol-method returns the protocol information

The Exposure1-constructor returns an EX1 object

The length-method returns the number of rows

The selectYears-method returns an EX1 object

The readEX1x1-method returns an EX1 object

**Slots**

content describes the content  
 region regional entity  
 header includes the raw header information  
 ex1 stores the exposure table (data.table)  
 protocol contains the protocol information

**Examples**

```

e1 <- readEX1x1(file.path(system.file(package="eoR"), "extdata", "DEUTNP.Exposures_1x1m.txt"))
header(e1)
ex1(e1)[, table(Year)]
  
```

---

 header

*AllGenerics*


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**Description**

The header-method gets the header of an object  
 The footer-method gets the footer of an object  
 The content-method gets the content of an object  
 The region-method gets the region of an object  
 The protocol-method gets the protocol of an object  
 The selectYears-method gets a subset of an object  
 The selectRegion-method gets a subset of an object  
 The lt1-method gets the life table lt1 of an LT1 object  
 The ex1-method gets the exposure table ex1 of an EX1 object  
 The rd1-method gets the regional death count table rd1 of an RD1 object  
 The rd1total-method gets the total sum death count table rd1total of an RD1 object  
 The re1-method gets the regional exposure table re1 of an RE1 object  
 The re1total-method gets the regional total sum exposure table re1total of an RE1 object

**Usage**

```

header(object)

footer(object)

content(object)

region(object)
  
```

protocol(object)  
selectYears(object, selectYears)  
selectRegion(object, selectRegion)  
lt1(object)  
ex1(object)  
rd1(object)  
rd1total(object)  
re1(object)  
re1total(object)

**Arguments**

object	object
selectYears	vector of integer
selectRegion	vector of character

**Value**

The header-method returns the header of an object  
The footer-method returns the footer of an object  
The content-method returns the content of an object  
The region-method returns the region of an object  
The protocol-method returns the protocol of an object  
The selectYears-method returns a subset of an object  
The selectRegion-method returns a subset of an object  
The lt1-method returns the life table lt1 of an LT1 object  
The ex1-method returns the exposure table ex1 of an EX1 object  
The rd1-method returns the regional death count table rd1 of an RD1 object  
The rd1total-method returns the total sum death count table rd1total of an RD1 object  
The er1-method returns the regional exposure table re1 of an RE1 object  
The er1total-method returns the regional total sum exposure table re1total of an RE1 object

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 LT1-class

*LT1 class for HMD life-tables 1x1*


---

### Description

The class LT1 stores HMD life table information in a systematic way.

The header-method gets the raw header information of an LT1 object

The lt1-method gets the life table information of an LT1 object

The content-method gets the life table information of an LT1 object

The region-method gets the regional information of an LT1 object

The protocol-method gets the protocol information of an LT1 object

The LTable1-constructor creates an LT1 object

The length-method gets the number of rows int the LT1 lt1 data.table

The selectYears-method gets a subset of an LT1 object

The readLT1x1-method reads all information from the file 1x1 period life table

### Usage

```
## S4 method for signature 'LT1'
header(object)
```

```
## S4 method for signature 'LT1'
lt1(object)
```

```
## S4 method for signature 'LT1'
content(object)
```

```
## S4 method for signature 'LT1'
region(object)
```

```
## S4 method for signature 'LT1'
protocol(object)
```

```
LTable1(header, lt1, content, region, protocol)
```

```
## S4 method for signature 'LT1'
length(x)
```

```
## S4 method for signature 'LT1'
show(object)
```

```
## S4 method for signature 'LT1'
selectYears(object, selectYears)
```

```
readLT1x1(infile)
```

**Arguments**

object	LT1-object
header	vector
lt1	data.table
content	character
region	character
protocol	character
x	LT1-object
selectYears	vector
infile	character file name

**Details**

This LT1 class fits to Human Mortality Database (HMD) 1x1 period life tables. See <https://www.mortality.org/> for data details. An LT1 instance stores the raw header, the content, the version protocol and regional information and the life table as a data.table object. The validation adds a pure numeric age AgeLow to the life table. Try `demo(LT1)` for a demonstration.

**Value**

The `header`-method returns the raw header information

The `lt1`-method returns the life-table

The `content`-method returns the content information

The `region`-method returns the regional information

The `protocol`-method returns the protocol information

The `LTable1`-constructor returns an LT1 object

The `length`-method returns the number of rows

The `selectYears`-method returns an LT1 object

The `readLT1x1`-method returns an LT1 object

**Slots**

`content` describes the content

`region` regional entity

`header` includes the raw header information

`lt1` stores the life table (data.table)

`protocol` contains the protocol information

**Examples**

```
o1 <- readLT1x1(file.path(system.file(package="eOR"), "extdata", "DEUTNP.fltper_1x1m.txt"))
header(o1)
lt1(o1)[, table(Year)]
```

---

 RD1-class

*RD1 class for 'GENESIS-Tabelle: 12613-02-02-4'*


---

### Description

The class RD1 stores GENESIS table information in a systematic way.

The header-method gets the raw header information of an RD1 object

The footer-method gets the raw footer information of an RD1 object

The rd1-method gets the death count table information of an RD1 object

The rd1total-method gets the death count total sums table information of an RD1 object

The content-method gets the death count table information of an RD1 object

The region-method gets the regional information of an RD1 object

The protocol-method gets the protocol information of an RD1 object

The RegDeath1-constructor creates an RD1 object

The length-method gets the number of rows int the RD1 rd1 data.table

The selectYears-method gets a subset of an RD1 object

The selectRegion-method gets a subset of an RD1 object

The readRegDeath-method reads all information from 'GENESIS-Tabelle: 12613-02-02-4'

### Usage

```
## S4 method for signature 'RD1'
header(object)
```

```
## S4 method for signature 'RD1'
footer(object)
```

```
## S4 method for signature 'RD1'
rd1(object)
```

```
## S4 method for signature 'RD1'
rd1total(object)
```

```
## S4 method for signature 'RD1'
content(object)
```

```
## S4 method for signature 'RD1'
region(object)
```

```
## S4 method for signature 'RD1'
protocol(object)
```

```
RegDeath1(header, footer, rd1, rd1total, content, region, protocol)
```



```

## S4 method for signature 'RD1'
length(x)

## S4 method for signature 'RD1'
show(object)

## S4 method for signature 'RD1'
selectYears(object, selectYears)

## S4 method for signature 'RD1'
selectRegion(object, selectRegion)

readRegDeath(infile)

```

### Arguments

object	RD1-object
header	vector
footer	vector
rd1	data.table
rd1total	data.table
content	character
region	character
protocol	character
x	RD1-object
selectYears	vector
selectRegion	vector
infile	character file name

### Details

This RD1 class fits to the GENESIS table 12613-02-02-4. See <https://www.regionalstatistik.de/genesis/online> for data details. An RD1 instance stores the raw header, the raw footer, the content, the version protocol and regional information and the death count information as a data.table object. Further it stores a second data.table with the total sums information. Try `demo(RD1)` for a demonstration.

### Value

The header-method returns the raw header information

The footer-method returns the raw footer information

The rd1-method returns the death count table

The rd1total-method returns the death count total sums table

The content-method returns the content information

The region-method returns the regional information  
 The protocol-method returns the protocol information  
 The RegDeath1-constructor returns an RD1 object  
 The length-method returns the number of rows  
 The selectYears-method returns an RD1 object  
 The selectRegion-method returns an RD1 object  
 The readRegDeath-method returns an RD1 object

### Slots

content describes the content  
 region regional entity  
 header includes the raw header information  
 footer includes the raw footer information  
 rd1 stores the death count table (data.table)  
 rd1total stores the death count total sums table (data.table)  
 protocol contains the protocol information

### Examples

```
d1 <- readRegDeath(file.path(system.file(package="eOR"), "extdata", "12613-02-02-4m.csv"))
header(d1)
footer(d1)
rd1(d1)[, table(Year)]
```

---

 RE1-class

*RE1 class for 'GENESIS-Tabelle: 12411-03-03-4'*


---

### Description

The class RE1 stores GENESIS table information in a systematic way.  
 The header-method gets the raw header information of an RE1 object  
 The footer-method gets the raw footer information of an RE1 object  
 The re1-method gets the exposure table information of an RE1 object  
 The re1total-method gets the exposure total sums table information of an RE1 object  
 The content-method gets the exposure table information of an RE1 object  
 The region-method gets the regional information of an RE1 object  
 The protocol-method gets the protocol information of an RE1 object  
 The RegExp1-constructor creates an RE1 object  
 The length-method gets the number of rows int the RE1 re1 data.table  
 The selectYears-method gets a subset of an RE1 object  
 The selectRegion-method gets a subset of an RE1 object  
 The readRegExp-method reads all information from 'GENESIS-Tabelle: 12411-03-03-4'

**Usage**

```

## S4 method for signature 'RE1'
header(object)

## S4 method for signature 'RE1'
footer(object)

## S4 method for signature 'RE1'
re1(object)

## S4 method for signature 'RE1'
re1total(object)

## S4 method for signature 'RE1'
content(object)

## S4 method for signature 'RE1'
region(object)

## S4 method for signature 'RE1'
protocol(object)

RegExp1(header, footer, re1, re1total, content, region, protocol)

## S4 method for signature 'RE1'
length(x)

## S4 method for signature 'RE1'
show(object)

## S4 method for signature 'RE1'
selectYears(object, selectYears)

## S4 method for signature 'RE1'
selectRegion(object, selectRegion)

readRegExp(infile)

```

**Arguments**

object	RE1-object
header	vector
footer	vector
re1	data.table
re1total	data.table
content	character
region	character

protocol	character
x	RE1-object
selectYears	vector
selectRegion	vector
infile	character file name

### Details

This RE1 class fits to the GENESIS table 12411-03-03-4. See <https://www.regionalstatistik.de/genesis/online> for data details. An RE1 instance stores the raw header, the raw footer, the content, the version protocol and regional information and the exposure information as a `data.table` object. Further it stores a second `data.table` with the total sums information. Try `demo(RE1)` for a demonstration.

### Value

The `header`-method returns the raw header information  
 The `footer`-method returns the raw footer information  
 The `re1`-method returns the exposure table  
 The `re1total`-method returns the exposure total sums table  
 The `content`-method returns the content information  
 The `region`-method returns the regional information  
 The `protocol`-method returns the protocol information  
 The `RegExp1`-constructor returns an RE1 object  
 The `length`-method returns the number of rows  
 The `selectYears`-method returns an RE1 object  
 The `selectRegion`-method returns an RE1 object  
 The `readRegExp`-method returns an RE1 object

### Slots

`content` describes the content  
`region` regional entity  
`header` includes the raw header information  
`footer` includes the raw footer information  
`re1` stores the exposure table (`data.table`)  
`re1total` stores the exposure total sums table (`data.table`)  
`protocol` contains the protocol information

### Examples

```
r1 <- readRegExp(file.path(system.file(package="eoR"), "extdata", "12411-03-03-4m.csv"))
header(r1)
footer(r1)
re1(r1)[, table(Year)]
```

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