

Reading Human Fertility Database and Human Mortality Database data into R

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Abstract

The features and usage of the `HMDHFDplus` package are demonstrated for reading data from the Human Mortality Database, the Human Fertility Database, and other similarly formatted sources directly from the database Websites into R.

1 Motivation

The Human Fertility Database (2015) and Human Mortality Database (2015) are two widely used data sources for the comparative and historical study of fertility and mortality. Both databases offer the option to download data in bulk in a few different formats. After a bulk download, users can then set up local databases in a variety of convenient ways, such as that described by Minton (2015) for R (R Development Core Team 2012) users. Another option for R users is to read data directly into an interactive session from the respective database websites. This is handy for small examples, lightweight reproducibility, and rapid prototyping. The `HMDHFDplus` package provides easy direct access to the databases using a simple standard set of arguments. Issues such as authentication and fixing column classes are handled automatically. Analogous functions are also made available for databases using similar formatting standards. At this time, these databases include the Japanese Mortality Database (2015), the Canadian Human Mortality Database (2015), and the Human Fertility Collection (2015).¹ This report outlines the basic features and provides usage examples.

¹The Human Life-Table Database (2015) may also be incorporated in the future.

2 Installation

The HMDHFDplus package is hosted by and can be installed directly from `github`.² Two external dependencies help R handle `html` parsing and database authentication, and these must be installed first in order for HMDHFDplus to properly install. These two dependencies are `cURL` and `XML`, and their installation unfortunately depends on one's operating system at this time.

In Linux and similar systems, open the Terminal and run:

```
sudo apt-get install libcurl
sudo apt-get install libxml2-dev
```

Then install HMDHFDplus using:

```
library(devtools)
install_github("timriffe/TR1/TR1/HMDHFDplus")
```

This is the simplest case. For Windows, Mac, or other special cases, the process is different steps are required. Please consult the `README`³ file on the `github` repository for more details, and contact the maintainer if necessary.

3 Usage and examples

Load the package using:

```
library(HMDHFDplus)
```

The two main functions of interest are `readHMDweb()` and `readHFDweb()`, and both functions have the same essential arguments. These two functions only require the user to supply country codes, data item names, and database authentication parameters.⁴ It helps to be familiar with HMD and HFD file naming conventions. To retrieve the population codes used in any of these databases, run:

```
getHFDcountries()
getHFCcountries()
getHMDcountries()
getJMDprefectures()
getCHMDprovinces()
```

²The package is under the following url: <http://github.com/timriffe/TR1/tree/master/TR1/HMDHFDplus>. This report, as well as a useful `README` document, can be found under <http://github.com/timriffe/TR1>.

³The `README` is at the foot of the main repository page: <https://github.com/timriffe/TR1>

⁴The HFD also allows users to extract data from former updates, which may be useful for strict replication purposes. In order to make use of this feature, users must note the 8-digit date code associated with the specific country series update. By default, `readHFDweb()` extracts the most recent update.

This returns vectors of the standard numerical or letter codes used to identify population units.

The functions used for reading data into R from the Web use a common set of required arguments. In interactive R sessions, the following will prompt the user to enter a username and password into the console (no quotes) each time the function is run:

```
# for HMD:
USmales <- readHMDweb(CNTRY = "USA", item = "mltper_1x1")
# for HFD (will need to re-enter username and password)
USfert <- readHFDweb(CNTRY = "USA", item = "asfrRR")
```

Manually entering a username and password can become tedious for larger data-grabs, so these can also be given explicitly in the arguments, like so:

```
USmales <- readHMDweb(CNTRY = "USA", item = "mltper_1x1", username =
"myusername", password = "mypassword")
USfert <- readHFDweb(CNTRY = "USA", item = "asfrRR", username =
"myusername", password = "mypassword")
```

There is a security trade-off in this case, because the username and password may inadvertently be saved within your R script. I suggest two alternatives in this case. First, in an interactive R session, define your username once at the beginning of the script, but without saving them as text within the script, like so:

```
pw <- userInput()
us <- userInput()
USmales <- readHMDweb(CNTRY = "USA", item = "mltper_1x1", username = us,
password = pw)
```

The two objects `pw` and `us` can in this case be recycled throughout the following R session. Second, For more frequent users, I recommend defining your HMD and HFD passwords in the `.Rprofile` file, such that they are defined and ready to use at the start of R sessions. The above HMD code will return data such as the following: `data.frame`:

```
head(USmales)
```

	Year	Age	mx	qx	ax	lx	dx	Lx	Tx	ex	OpenInterval
1	1933	0	0.06859	0.06515	0.23	100000	6515	94978	5916978	59.17	FALSE
2	1933	1	0.01004	0.00999	0.50	93485	934	93018	5822000	62.28	FALSE
3	1933	2	0.00467	0.00466	0.50	92551	431	92336	5728982	61.90	FALSE
4	1933	3	0.00333	0.00333	0.50	92120	307	91967	5636646	61.19	FALSE
5	1933	4	0.00254	0.00253	0.50	91814	233	91697	5544679	60.39	FALSE
6	1933	5	0.00209	0.00209	0.50	91581	191	91485	5452982	59.54	FALSE

This `data.frame` differs from the original HMD `mltper_1x1` file in that the `Age` column is integer, and a new `OpenInterval` column has been added, which contains the value `TRUE` for age 110. HFD `Age` and `Cohort` columns are modified in a similar way for more intuitive and immediate use of these columns as integers. Likewise, abridged ages, such as "5-9" are coerced as integers of the lower interval bound, as 5. Finally, HMD Population files, obtained via

```

USpop <- readHMDweb("USA","Population",username = us, password = pw)
head(USpop)

```

	Year	Age	OpenInterval	Female1	Male1	Total1	Female2	Male2	Total2
1	1933	0	FALSE	984472.3	1015362	1999834	937185.8	968955.4	1906141
2	1933	1	FALSE	1040496.0	1064088	2104584	970696.5	993352.8	1964049
3	1933	2	FALSE	1093043.8	1117527	2210571	1062002.5	1083452.4	2145455
4	1933	3	FALSE	1107994.3	1135047	2243041	1095555.1	1121220.2	2216775
5	1933	4	FALSE	1130624.4	1179514	2310138	1105999.3	1132665.9	2238665
6	1933	5	FALSE	1168930.6	1228225	2397156	1141944.4	1197735.4	2339680

, where columns ending in 1 indicate January 1st estimates and columns ending in 2 indicate December 31st estimates, and the `Year` and `Age` columns are coerced to an integer class. The JMD, CHMD, and HFC are all called in similar ways, but without authentication:

```

# 31 columns!
USasfrB0 <- readHFC("USA","ASFRstand_B0")
# 5x5 male lifetables for Aomori prefecture:
Aomori <- readJMDweb("02","mltper_5x5")
# 5x5 lifetables for Alberta:
ALB <- readCHMDweb("alb","mltper_5x5")

```

The JMD and CHMD follow the same formatting standards and naming conventions as the HMD, although the data products available are a subset of those produced by the HMD. The HFC follows different standards and conventions than the HFD.

4 Conclusions

Reading data directly from HMD, HFD and similar databases directly from the web into R is made easy with the `HMDHFDplus` package. Common R pitfalls are removed by coercing columns to useful classes by default. At this time, utilities are provided for reading data from the HMD, JMD, CHMD, HFD, and HFC websites, and this list may expand in the future as new databases arise in the same spirit.

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