

# HEALTH AND RETIREMENT STUDY

## **Sensitive Health Data**

### **Blood-Based Biomarkers**

2014 Health and Retirement Study

Data Description and Usage

Version 1.0, December 2017

**To the researcher:** This data set is intended for exclusive use by you under the terms specified in the *Sensitive Health Data Use Agreement*. If there are any questions about this data set and its use, please contact the HRS Help Desk ([hqsquestions@umich.edu](mailto:hqsquestions@umich.edu)).

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## 1. Overview

The Health and Retirement Study (HRS) is a national longitudinal study of the economic, health, marital, and family status, as well as public and private support systems, of older Americans. The HRS is a rich source of longitudinal, cross-sectional data for researchers and policymakers who study aging. Funding for the Health and Retirement Study is provided by the National Institute on Aging at NIH (U01 AG009740), with supplemental support from the Social Security Administration. The study is conducted by the Institute for Social Research (ISR) at the University of Michigan.

## 2. Obtaining the Data

### 2a. Access to Sensitive Health Data

Although most HRS data sets are available to the public without restriction, certain HRS data sets contain sensitive respondent information and are only available under terms of a formal agreement negotiated between the researcher and HRS. To apply:

1. Create an account on the [HRS User Registration/File Download Web site](#), if you don't already have one
2. Download and complete the [Sensitive Data Access Use Agreement](#)
3. Submit the [Sensitive Data Order Form](#)
4. *If you did not attach your Agreement in Step 2 to the Order Form in Step 3*, send a signed copy of the Agreement via email to [h rsdatareq@umich.edu](mailto:h rsdatareq@umich.edu).
5. You will be notified when access to download the files has been granted.

The Health and Retirement Study will review your request, and based on the information that you provided when you registered at the [HRS Data Download System](#) Web site, verify your identity and institutional affiliation. Once this authentication process has been completed to our satisfaction, we will authorize access to the desired data set(s). We will communicate with you at the email address that you provided when you registered at the File Download Web site.

### 2b. How to Download

1. Once you receive your approval notification, login at the [HRS Data Download System](#) Web site.
2. In the **HRS Special Access Files** box on the right hand side of the page you will now see links to the data set(s) that you have requested.
3. Click on the appropriate link and follow instructions to download the file(s) you need.

### 2c. Publications Based on Sensitive Health Data

You must inform HRS of any papers, publications, or presentations based on this HRS sensitive health data set. Please send a copy of such publications in PDF format via e-mail to [h rsquestions@umich.edu](mailto:h rsquestions@umich.edu) with "Attn: Papers and Publications" in the subject line. If you wish, you may include a bibliographical reference.

As an alternative, you may transmit publications in paper format by postal mail:

Health and Retirement Study  
Attn: Papers and Publications  
The Institute for Social Research, Room 3410  
P.O. Box 1248  
Ann Arbor, Michigan 48106-1248

### 3. Data Set Content

This version of the *Blood-Based Biomarkers 2014* data set matches the current version of the tracker file (Tracker 2014)<sup>1</sup>. It has 7,352 records, which are uniquely identified by Household Identifier (HHID) and Person Number (PN). This document accompanies the HRS blood-based biomarker data collected and assayed from 2014. More detailed descriptions of the procedures for collection of the data and assay of the blood-based markers are available in *Documentation of Blood-Based Biomarkers in the 2014 Health and Retirement Study*, included with this distribution.

HRS began to collect blood-based biomarkers on half the sample in 2006, the other half of the sample provided biomarker data in 2008. The first group was asked for blood samples again in 2010 and 2014; the second group gave repeat samples in 2012 and 2016.

From 2006 through 2012, the dried blood spot (DBS) samples were assayed for 5 biomarkers. In 2014 a sixth was added, IL-6 which is a cytokine indicator of inflammation. The biomarkers available now in the 2014 release include the following:

- Total cholesterol (TC) an indicator of lipid levels
- High Density Lipoprotein cholesterol (HDL), an indicator of lipid levels
- Glycosylated hemoglobin (HbA1c), an indicator of glycemic control over the past 2-3 months
- C-reactive protein (CRP), a general marker of systemic inflammation
- Cystatin C, an indicator of kidney functioning.<sup>2</sup>

### 4. If You Need to Know More

This document is intended to serve as a brief overview of the *Blood-Based Biomarkers 2014* data set. If you have questions or concerns that are not adequately covered here or on our Web site, or if you have any comments, please contact us. We will do our best to provide answers. Health and Retirement Study public release data and additional information about the study are available on the Internet. To access public data or to find out more about restricted data products and procedures, visit the [HRS Web site](http://hrsonline.isr.umich.edu). If you need to contact us, you may do so by one of the methods listed below.

Internet: Help Desk at the HRS Web site (<http://hrsonline.isr.umich.edu>)

E-mail: [hrsquestions@umich.edu](mailto:hrsquestions@umich.edu)

Postal Service:

Health and Retirement Study  
The Institute for Social Research  
426 Thompson Street, 3050 ISR  
Ann Arbor, Michigan 48104

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<sup>1</sup> The HRS tracker file is created to facilitate the use of HRS data within and across waves. It contains one record for every person who was ever eligible to be interviewed in any wave. The tracker file version used in preparation of this dataset (Tracker 2014, Final v1.0) covers all types of interviews (core, exit, and post-exit) for 1992 through the 2014 interviewing year.

<sup>2</sup> The IL-6 data will be released when we have data from VBS available to make an equivalent value.

# Appendix: Installation

## 1. Distribution Set

The *Blood-Based Biomarkers 2014* data set is packaged for distribution in a .ZIP file, BIOMK14BL.zip. In order to keep the contents secure, the .ZIP file has been encrypted using WinZIP 256 bit AES encryption. Extract the data file(s), the program statement file(s) matching your analysis environment, the data description (this file), and the codebook file. If you require a special file format or experience system problems, please contact the [HRS Help Desk](#). If all files are decompressed, they will require approximately 5 MB of free space on your storage device.

### 1-1. Windows Environment

Copy the ZIP file to the Windows folder where you plan to do your work Use a third-party<sup>3</sup> file compression/decompression tool such as **WinZIP** or **7-zip** to extract the ZIP folder contents. When you are prompted for the pass-phrase, respond with the character string that you received via e-mail. The output will be the files listed in Table A1.

### 1-2. UNIX/Linux Environment

Copy the ZIP file to the folder where you plan to do your work. Use the ZIP file decompression software installed on your system, (e.g. **7z**, **gunzip**) to decrypt and decompress the ZIP folder contents. When you are prompted for the pass-phrase, respond with the character string that you received via e-mail. The output will be the files listed in Table A-1.

### 1-3. Macintosh OS X Environment (10.4.x and above)

Copy the ZIP file to the folder where you plan to do your work and use **stuffit** to decrypt and decompress the ZIP folder contents. When you are prompted for the pass-phrase, respond with the character string that you received via e-mail. The output will be the files listed in Table A-1.

Table A-1: Contents of Distribution Package

| Directory <sup>4</sup> | File                       | Type                            |
|------------------------|----------------------------|---------------------------------|
| c:\biom\data\          | BIOMK14BL.da               | Data files (ASCII text)         |
| c:\biom\docs\          | BIOMK14BL.txt              | Codebook files (ASCII text)     |
| c:\biom\sas\           | BIOMK14BL.sas              | SAS program statements          |
| c:\biom\spss\          | BIOMK14BL.sps              | SPSS program statements         |
| c:\biom\stata\         | BIOMK14BL.dct/BIOMK14BL.do | Stata dictionary and "do" files |

## 2. Program Statements

Each data file comes with associated SPSS, SAS or Stata program statements to read the data. Files containing SPSS statements are named with an .sps extension, those with SAS statements with an .sas extension, and those with Stata statements with .do and .dct extensions. The files are keyed on Household Identifier, Other Person Number and Sub-Household Identifier. See the appendix for usage details.

<sup>3</sup> The built-in Windows decompression utility will not process AES-256bit encrypted zip files; it halts with "an unexpected error is keeping you from copying the file".

<sup>4</sup> While a specific setup is not required for using HRS files, we have traditionally suggested a directory structure for the Windows environment. By using this directory structure (or a Unix equivalent), you will not have to change the path name references in your data descriptor files. If you use a different structure, just change the directory references in the program files.

### *2-1. Using the Files with SAS*

To create a SAS system file for a particular data set, two file types must be present for that data set -- .sas program statement files and .da data files. To create a SAS system file, load the BIOMK14BL.sas file into the SAS Program Editor. If the \*.sas file is located in "c:\biom\sas" and the data file is located in "c:\biom\data", you can run the file as is. A SAS system will be saved to directory "c:\biom\sas". If the files are not located in the specified directories, you will need to edit the BIOMK14BL.sas file to reflect the proper path names prior to running the file.

### *2-2. Using the Files with SPSS*

To create an SPSS system file for a particular data set, two file types must be present for that data set -- BIOMK14BL.sps program statement files and .da data files. To create an SPSS system file, open the \*.sps file in SPSS as an SPSS Syntax File. If the \*.sps file is located in "c:\biom\spss" and the data file is located in "c:\biom\data", you can run the file as is. An SPSS system file will be saved to directory "c:\biom\spss". If the files are not located in the specified directories, you will need to edit the BIOMK14BL.sps file to reflect the proper path names prior to running the file.

### *2-3. Using the Files with Stata*

To use Stata with a particular data set, the following three file types must be present for that data set -- .dct files, .do files, and .da data files. Files with the suffix ".da" contain the raw data for Stata to read. Files with the suffix ".dct" are Stata dictionaries used by Stata to describe the data. Files with the suffix ".do" are short Stata programs ("do files") which you may use to read in the data. Load the .do file into Stata and then submit it. If the \*.do and .dct files are located in "c:\biom\stata" and the data file is located in "c:\biom\data", you can run the .do file as is. If the files are not located in these directories, you must edit the BIOMK14BL.do and BIOMK14BL.dct files to reflect the proper path names before you run the files.

### 3. Non-Windows Environments

Non-Microsoft users should modify the default Windows file structure syntax to match that of their own operating system. The following examples should work for both Macintosh OS X and any Unix/Linux distribution. Open the SAS program file(s), SPSS syntax file(s) or the Stata do/dct files in an ASCII editor and make the changes indicated below.

#### 3-1. SPSS in an OSX environment

In this example, we assume that the user has extracted the files from the *Respondent Date of Birth* data set and placed them in a **Desktop** folder called **biom** with the ASCII data file stored in subfolder **data** and the syntax file in subfolder **spss**. Then the commands in the syntax file would be modified to look like this:

```
FILE HANDLE biom /name='Desktop/biom/data/biom.da' RECL=221.
DATA LIST FILE= biom/
HHID 1-6(A)
[rest of syntax file goes here]
.
execute.
SAVE /outfile 'Desktop/biom/spss/biom.sav' .
Execute.
```

#### 3-2. STATA in an OS X Environment

In the following example we assume that:

- The username is “user1”
- The encrypted zip file containing *Respondent Date of Birth* data has been copied to the user’s desktop from the CDRom sent by HRS.
- The user has decrypted /decompressed the zip file (use Stuffit for OS X) into a desktop folder named **biom**
- The statistical package is stata

File BIOMK14BL.do should be modified as follows:

*Change...*

```
infile using c:\biom\stata\biom.dct
```

*To...*

```
infile using /Users/user1/Desktop/biom/stata/biom.dct
```

*Change...*

```
save c:\biom\stata\biom.dta
```

*To...*

```
save /Users/user1/Desktop/biom/stata/biom.dta
```

File BIOMK14BL.dct should be modified as follows:

*Change...*

```
dictionary using c:\biom\data\biom.da {...}
```

*To...*

```
dictionary using /Users/user1/Desktop/biom/data/biom.da {...}
```