An Example of mi Usage

Ben Goodrich and Jonathan Kropko, for this version, based on earlier versions written by Yu-Sung Su, Masanao Yajima, Maria Grazia Pittau, Jennifer Hill, and Andrew Gelman

06/16/2014

There are several steps in an analysis of missing data. Initially, users must get their data into R. There are several ways to do so, including the `read.table`, `read.csv`, `read.fwf` functions plus several functions in the `foreign` package. All of these functions will generate a `data.frame`, which is a bit like a spreadsheet of data. http://cran.r-project.org/doc/manuals/R-data.html for more information.

```r
options(width = 65)
suppressMessages(library(mi))
data(nlsyV, package = "mi")
```

From there, the first step is to convert the `data.frame` to a `missing_data.frame`, which is an enhanced version of a `data.frame` that includes metadata about the variables that is essential in a missing data context.

```r
mdf <- missing_data.frame(nlsyV)
```

## NOTE: In the following pairs of variables, the missingness pattern of the first is a subset of the second.  Please verify whether they are in fact logically distinct variables.

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
</tr>
</tbody>
</table>

The `missing_data.frame` constructor function creates a `missing_data.frame` called `mdf`, which in turn contains seven `missing_variable`s, one for each column of the `nlsyV` dataset.

The most important aspect of a `missing_variable` is its class, such as `continuous`, `binary`, and `count` among many others (see the table in the Slots section of the help page for `missing_variable-class`). The `missing_data.frame` constructor function will try to guess the appropriate class for each `missing_variable`, but rarely will it correspond perfectly to the user's intent. Thus, it is very important to call the `show` method on a `missing_data.frame` to see the initial guesses.

```r
show(mdf) # momrace is guessed to be ordered
```

## Object of class missing_data.frame with 400 observations on 7 variables

## There are 20 missing data patterns

## Append '@patterns' to this missing_data.frame to access the corresponding pattern for every observation.
and to modify them, if necessary, using the `change` function, which can be used to change many things about a `missing_variable`, so see its help page for more details. In the example below, we change the class of the `momrace` (race of the mother) variable from the initial guess of `ordered-categorical` to a more appropriate unordered-categorical and change the income `nonnegative-continuous`.

```r
mdf <- change(mdf, y = c("income", "momrace"), what = "type", 
              to = c("non", "un"))
```

Once all of the `missing_variables` are set appropriately, it is useful to get a sense of the raw data, which can be accomplished by looking at the `summary`, `image`, and/or `hist` of a `missing_data.frame`.

```r
summary(mdf)
```

```r
# ppvtr.36  first  b.marr
# Min. : 41.00 Min. :0.0000 Min. :0.0000
```
Next we use the `mi` function to do the actual imputation, which has several extra arguments that, for example, govern how many independent chains to utilize, how many iterations to conduct, and the maximum amount of time the user is willing to wait for all the iterations of all the chains to finish. The imputation step can be quite time consuming, particularly if there are many missing variables and if many of them are categorical. One important way in which the computation time can be reduced is by imputing in parallel, which is highly recommended and is implemented in the `mi` function by default on non-Windows machines. If users encounter problems running `mi` with parallel processing, the problems are likely due to the machine exceeding available RAM. Sequential processing can be used instead for `mi` by using the `parallel=FALSE` option.

```r
rm(nlsyV)  # good to remove large unnecessary objects to save RAM
options(mc.cores = 2)
imputations <- mi(mdf, n.iter = 30, n.chains = 4, max.minutes = 20)
show(imputations)
```

`## Object of class mi with 4 chains, each with 30 iterations. ## Each chain is the evolution of an object of missing_data.frame class with 400 observations on 7 variables.`

The next step is very important and essentially verifies whether enough iterations were conducted. We want the mean of each completed variable to be roughly the same for each of the 4 chains.

```r
round(mipply(imputations, mean, to.matrix = TRUE), 3)
```

`## chain:1 chain:2 chain:3 chain:4 ## ppvtr.36 0.003 0.004 0.010 0.007 ## first 1.435 1.435 1.435 1.435 ## b.marr 1.685 1.688 1.685 1.685 ## income 9.547 9.564 9.512 9.515 ## momage 0.000 0.000 0.000 0.000 ## momed 2.053 2.053 2.067 2.053 ## momrace 2.292 2.277 2.260 2.283 ## missing_ppvtr.36 0.188 0.188 0.188 0.188 ## missing_b.marr 0.030 0.030 0.030 0.030`

4
If so — and when it does in the example depends on the pseudo-random number seed — we can proceed to diagnosing other problems. For the sake of example, we continue our 4 chains for another 5 iterations by calling

```r
imputations <- mi(imputations, n.iter = 5)
```

to illustrate that this process can be continued until convergence is reached.

Next, the plot of an object produced by `mi` displays, for all missing_variables (or some subset thereof), a histogram of the observed, imputed, and completed data, a comparison of the completed data to the fitted values implied by the model for the completed data, and a plot of the associated binned residuals. There will be one set of plots on a page for the first three chains, so that the user can get some sense of the sampling variability of the imputations. The `hist` function yields the same histograms as `plot`, but groups the histograms for all variables (within a chain) on the same plot. The `image` function gives a sense of the missingness patterns in the data.

```r
plot(imputations)
```
## Warning: algorithm did not converge
## Warning in .local(y, data, ...): bayesglm() did not converge for variable income:is_zero on iteration 36
## Warning: algorithm did not converge
## Warning in .local(y, data, ...): bayesglm() did not converge for variable income:is_zero on iteration 36
## Warning: algorithm did not converge
## Warning in .local(y, data, ...): bayesglm() did not converge for variable income:is_zero on iteration 36
plot(imputations, y = c("ppvtr.36", "momrace"))
hist(imputations)
image(imputations)
summary(imputations)

## $ppvtr.36
## $ppvtr.36$is_missing
## missing
## FALSE  TRUE
## 325  75
##
## $ppvtr.36$imputed
## Min. 1st Qu. Median  Mean 3rd Qu.  Max.
## -1.3604 -0.3738  0.0517  0.0205  0.3501  1.3273
##
## $ppvtr.36$observed
## Min. 1st Qu. Median  Mean 3rd Qu.  Max.
## -1.2019  0.3192  0.0285  0.0000  0.3494  1.2321
##
##
## $first$
## $first$is_missing
## [1] "all values observed"
##
## $first$observed
##
## 1 2
## 226 174
##
##
##
## $b.marr
## $b.marr$crosstab
##
## observed imputed
## 0  456  45
## 1 1096  3
##
## $income
## $income$is_missing
## missing
## FALSE  TRUE
##  318   82
##
## $income$imputed
##   Min. 1st Qu. Median  Mean 3rd Qu.  Max.
##
## $income$observed
##   Min. 1st Qu. Median  Mean 3rd Qu.  Max.
##
##
## $momage
## $momage$is_missing
## [1] "all values observed"
##
## $momage$observed
##   Min. 1st Qu. Median  Mean 3rd Qu.  Max.
## -1.21377 -0.27468  0.03835  0.00000  0.35137  1.29046
##
##
## $momed
## $momed$crosstab
##
## observed imputed
## 1  472  43
## 2  540  60
## 3  324  35
## 4  104  22
##
##
## $momrace
## $momrace$crosstab
##
## observed imputed
## 1  220  141
## 2  320  122
## 3  592  205
Finally, we pool over $m = 5$ imputed datasets – pulled from across the 4 chains – in order to estimate a descriptive linear regression of test scores ($ppvtr.36$) at 36 months on a variety of demographic variables pertaining to the mother of the child.

```
analysis <- pool(ppvtr.36 ~ first + b.marr + income + momage + momed + momrace, 
data = imputations, m = 5)
display(analysis)
```

```
## bayesglm(formula = ppvtr.36 ~ first + b.marr + income + momage + 
##         momed + momrace, data = imputations, m = 5)
## coef.est coef.se
## (Intercept) 80.79 7.57
## first1 4.26 1.72
## b.marr1 5.47 2.47
## income 0.00 0.00
## momage -0.12 0.31
## momed.L 10.72 3.11
## momed.Q 1.08 2.35
## momed.C 0.85 1.76
## momrace2 -6.16 3.69
## momrace3 11.75 2.92
## n = 390, k = 10
## residual deviance = 93528.0, null deviance = 142095.8 (difference = 48567.8)
## overdispersion parameter = 239.8
## residual sd is sqrt(overdispersion) = 15.49
```

The rest is optional and only necessary if you want to perform some operation that is not supported by the mi package, perhaps outside of R. Here we create a list of data.frames, which can be saved to the hard disk and / or exported in a variety of formats with the foreign package. Imputed data can be exported to Stata by using the mi2stata function instead of complete.
dfs <- complete(imputations, m = 2)