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editors@stata-journal.com

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Diagnostics for multiple imputation in Stata

Wesley Eddings
StataCorp
College Station, TX
weddings@stata.com

Yulia Marchenko
StataCorp
College Station, TX
ymarchenko@stata.com

Abstract. Our new command \texttt{midiagplots} makes diagnostic plots for multiple imputations created by \texttt{mi impute}. The plots compare the distribution of the imputed values with that of the observed values so that problems with the imputation model can be corrected before the imputed data are analyzed. We include an example and suggest extensions to other diagnostics.

\textbf{Keywords:} \texttt{st0263}, \texttt{midiagplots}, multiple imputation, diagnostics, model checking, imputed values, missing data, missing at random

1 Introduction

Multiple imputation (Rubin 1987) is a principled method for handling missing data, but it relies on a model for imputing the missing values. An inappropriate imputation model can lead to biased estimates, so it is important to check the model. A few simple checks are now available in our command \texttt{midiagplots}. Most of the methods are graphical, but there are also Kolmogorov–Smirnov tests for comparing the distribution of the observed values with the distribution of the imputed values. The foremost reference for the diagnostics is Abayomi, Gelman, and Levy (2008).

1.1 Methods for handling missing data

The theory of missing data assumes that missingness follows a probability model so that we may speak of the probability that data are missing. The probability model assumed to create the missing values is called the missing-data mechanism. To analyze incomplete data, we must make assumptions about the missing-data mechanism.

The default missing-data analysis in Stata is complete-case analysis, which makes a strong assumption about the missing-data mechanism. A complete-case analysis omits every observation that has a missing value for any of the model variables. So if we type \texttt{regress y x1 x2}, Stata will omit any observation that has a missing value for \texttt{y}, \texttt{x1}, or \texttt{x2}. Such omission is typically justified only if the data are missing completely at random (MCAR), the most stringent missing-data mechanism. The data are MCAR only if the missing values are like a simple random sample of all values so that missingness is not correlated with any variable, observed or unobserved.

MCAR is a severe restriction, and complete-case analysis may be biased if the data are not MCAR. A less restrictive method is multiple imputation, which may be performed under a weaker assumption, missing at random (MAR). An MAR mechanism
allows missingness to be correlated with observed variables so long as it remains conditionally independent of the unobserved values. So the observed variables must suffice for predicting missingness. If the MAR assumption does not hold, resulting in missingness being correlated with the unobserved values even after conditioning on the observed values, the data are said to be missing not at random (MNAR) or nonignorably missing. For rigorous definitions of the missing-data mechanisms, see Little and Rubin (2002, sec. 1.3).

1.2 Multiple imputation in Stata

Multiple imputation imputes each missing value multiple times. A regression model is created to predict the missing values from the observed values, and multiple predicted values are generated for each missing value to create the multiple imputations. Each imputation is a separate, filled-in dataset that can be analyzed on its own with standard methods. The separate results are then combined to produce a single multiple-imputation result. The method accounts for the uncertainty in the imputed values provided that the imputation and analysis models are appropriate. For more information, please see the documentation entry [mi] intro substantive and its references.

Multiple imputation was first added to Stata in the user-written packages mitools, ice, and mim (Carlin et al. 2003; Royston 2004; Carlin, Galati, and Royston 2008). The official mi commands were introduced in Stata 11 and expanded in Stata 12. The key commands are mi impute, for creating multiple imputations; mi estimate, for analyzing the multiple imputations; and special commands for managing the multiply imputed datasets. For more information on multiple imputation in Stata, type help mi.

mi impute requires the data to be MAR, so the missing values can be imputed using only the observed values and an imputation model.\textsuperscript{1} The MAR assumption is not testable, because it is not possible to check the distribution of the unobserved values. But if we tentatively assume MAR, it is possible to check the imputation model.

Our new command midiagplots helps check the fit of an imputation model. The command compares the imputed values with the observed ones, so implausible imputed values may be detected before the primary analysis. For continuous variables, there are three graphical methods (cumulative distribution functions, kernel density estimates, and histograms) and Kolmogorov–Smirnov tests; for categorical variables, there are both graphs and tables (of proportions or frequencies).

\textsuperscript{1} Multiple imputation itself does not require the MAR assumption. If the data are MNAR though, the probability model for the missing-data mechanism must be incorporated in the imputation model.
2 The midiagplots command

2.1 Syntax

\texttt{midiagplots [ \textit{impvars} ] [ \textit{if} ] [ , \textit{m(numlist)} \textit{plottype(plotspec)} sample(plotsample) ncategories(#) separate combine by(\textit{varlist}) sort(\textit{varlist}) tabfreq sleep(#) more ksmirnov nograph notable plotopts(plotopts) plot2opts(plotopts) plot3opts(plotopts) graph_options]}

2.2 Description

\texttt{midiagplots} performs diagnostics for multiply imputed data. By default, the command plots the distributions of continuous variables and tabulates categorical variables. A variable is considered categorical if it has no more than five distinct observed values; use the \texttt{ncategories(\#)} option to specify a different number of values.

The diagnostics compare the distributions of the observed, imputed, and completed values. (The completed data combine the observed and imputed data.) If the distributions differ greatly (possibly after conditioning on predictors of missingness), we may suspect a problem with the imputation model.

By default, there is one plot or table per imputed variable per imputation. A typical command is

\texttt{. midiagplots age income, m(1/5) sample(all) plottype(cumul)}

The option \texttt{m(1/5)} requests diagnostics for the first five imputations; the other options specify all samples (observed, imputed, and completed) and plots of cumulative distribution functions. (The choice for \texttt{sample()} is the default; we are assuming that \texttt{age} and \texttt{income} are continuous.)

Each plot would show three overlaid cumulative distribution functions, one for each of the observed, imputed, and completed samples. There would be 10 plots, 5 for \texttt{age} and 5 for \texttt{income}. By default, \texttt{midiagplots} shows one plot at a time and waits for three seconds before going on to the next plot; you can change the waiting time with the \texttt{sleep()} option. Or you can specify \texttt{more}, which pauses after each plot until you press a key. You can \texttt{combine} the plots across imputations into one figure or \texttt{separate} the samples for each imputation into separate plots. The \texttt{separate} option is especially useful for \texttt{plottype(histogram)}.

For categorical variables, \texttt{midiagplots} displays tables. Each table shows the distributions of the observed, imputed, and completed samples. Proportions are shown by default; to see frequencies instead, use the \texttt{tabfreq} option. Use \texttt{plottype(histogram)} to supplement the tables with histograms. (For categorical variables, the other plot types are not available.)

The most useful multiple-imputation diagnostics are graphical, but \texttt{midiagplots} also includes significance tests. The \texttt{ksmirnov} option uses the Kolmogorov–Smirnov
Multiple-imputation diagnostics

test to compare the observed and imputed distributions; a significant result means that
the distribution of the imputed data differs significantly from that of the observed data.
The results of ksmirnov should not be taken too seriously though, because the imputed
data are not independent of the observed data and because the distributions will differ
for MAR data even if the imputation model is correct (Abayomi, Gelman, and Levy
2008, 280).

If no impvars are specified, the command defaults to all variables registered as im-
puted.

midiagplots works only with mi data that have been mi set. Data from ice may
be converted to mi data with the official command mi import ice.

2.3 Options

m(numlist) specifies which imputations to use. The default is m(1).

plottype(plotspec) specifies the type of plot. plotspec is one of

kdensity [, kden_opts] | histogram [, hist_opts] | cumul [, cumul_opts]

kdensity requests kernel density estimates, the default. kden_opts are any of the
options allowed by twoway kdensity; see [G-2] graph twoway kdensity.

histogram requests histograms. The discrete option is automatically applied
to categorical variables. hist_opts are any of the options allowed by twoway
histogram; see [G-2] graph twoway histogram.

cumul requests plots of cumulative distribution functions. Plots of cumulative
distribution functions may be desirable because they do not require tuning, unlike
histograms and kernel density estimates (which are affected by the number of
bins or the bandwidth). cumul_opts are freq, equal, and connect_opts; see

Options specified in plotspec are applied to each plot.

sample(plotsample) specifies which samples to plot. plotsample may be all or any
combination of observed, imputed, and completed. The default is sample(all).
The option does not affect tables for categorical variables, which always show all
three samples.

ncategories(#) specifies that variables with no more than # distinct values should
be considered categorical. The default is ncategories(5).

separate requests a separate plot for each plotsample; the separate plots are presented in
one figure. By default, the distributions are instead overlaid onto one plot. separate
may not be specified with combine or with twoway’s legend() option.

combine combines all of a variable’s imputation plots into one figure. combine implies all
imputations, unless m() is specified. combine may not be specified with separate.
by(varlist) requests separate diagnostics for the subgroups defined by varlist; also see the by() option of twoway.

sort(varlist) sorts the data on the variables in varlist. Without sorting, plots may depend slightly on the active mi style if there are tied observations. If there are no ties, sorting has no effect.

tabfreq requests that tables display frequencies instead of proportions. Plots are not affected.

sleep(#) specifies a length of # milliseconds between the plots. The default is sleep(3000).

more causes Stata to pause after each plot until you press a key.

ksmirnov requests Kolmogorov–Smirnov statistics comparing the observed and imputed distributions of each continuous variable in impvars. Tests are not reported for categorical variables. ksmirnov may not be combined with by().

nograph suppresses all graphs and is intended for use with ksmirnov.

notable suppresses the tables produced by default for categorical variables.

plot1opts(plotopts) modifies the plot of the observed values.

plot2opts(plotopts) modifies the plot of the imputed values.

plot3opts(plotopts) modifies the plot of the completed values.

plotopts are any of the options documented in \[G-3\] connect_options, \[G-2\] graph twoway histogram, or \[G-2\] graph twoway kdensity applicable to the specified plottype().

graph_options specify the overall look of the graph. If the separate option is used, then graph_options are any of the options documented in \[G-2\] graph combine. Otherwise, graph_options are twoway_options—any of the options documented in \[G-3\] twoway_options.

3 Example

We will use a study of breast cancer that has illustrated multiple imputation in several other Stata Journal articles (Royston 2004; Carlin, Galati, and Royston 2008). There are 686 patients, and the outcome is recurrence-free survival. The data were modified by Royston (2004, 234) to have 20% of the values MCAR. We want to impute the missing predictors, check the imputations, and fit a model to predict recurrence-free survival. Because we are imputing survival data, the imputation model should include as predictors the censoring indicator and the Nelson–Aalen estimate of the cumulative hazard (White, Royston, and Wood 2011, 384). The Nelson–Aalen estimate is available in \sts generate.
Carlin, Galati, and Royston (2008, 62–64) used ice to impute the five missing predictors `mx1`, `mx4a`, `mx5e`, `mx6`, and `mhormon`. We will use mi impute chained.

```
. mi set wide
. mi register imputed mx1 mx4a mx5e mx6 mhormon
. set seed 912346
. mi impute chained (regress) mx1 mx5e (pmm) mx6
  > (logit) mx4a mhormon = _d cumhaz, add(5)
Conditional models:
  mx6: pmm mx6 i.mx4a i.mhormon mx1 mx5e _d cumhaz
  mx4a: logit mx4a mx6 i.mhormon mx1 mx5e _d cumhaz
  mhormon: logit mhormon mx6 i.mx4a mx1 mx5e _d cumhaz
  mx1: regress mx1 mx6 i.mx4a i.mhormon mx5e _d cumhaz
  mx5e: regress mx5e mx6 i.mx4a i.mhormon mx1 _d cumhaz
Performing chained iterations ...
Multivariate imputation Imputations = 5
Chained equations added = 5
Imputed: m=1 through m=5 updated = 0
Initialization: monotone Iterations = 50
  burn-in = 10
mx1: linear regression
mx5e: linear regression
mx6: predictive mean matching
mx4a: logistic regression
mhormon: logistic regression
```

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(complete + incomplete = total; imputed is the minimum across m of the number of filled-in observations.)
Figure 1 gives a diagnostic plot for \(mx_1\), patients' ages in years:

```
. midiaqpplots mx1
(M = 5 imputations)
(imputed: mx1 mx4a mx5e mx6 mhormon)
```

In figure 1, the observed ages are bimodal, but the imputed values are unimodal (as we would expect from a linear imputation model with normal errors). To correct the discrepancy, we may reimpute the variable by predictive mean matching (\texttt{mi impute pmm}), which does not assume normality. For more information, please see the documentation entry [\texttt{MI}] \texttt{mi impute pmm}.

```
. mi impute chained (regress) mx5e (pmm) mx1 mx6 (logit) mx4a
  > mhormon = _d cumhaz, replace

Conditional models:
  mx6: pmm mx6 i.mx4a i.mhormon mx1 mx5e _d cumhaz
  mx4a: logit mx4a mx6 i.mhormon mx1 mx5e _d cumhaz
  mhormon: logit mhormon mx6 i.mx4a mx1 mx5e _d cumhaz
  mx1: pmm mx1 mx6 i.mx4a i.mhormon mx5e _d cumhaz
  mx5e: regress mx5e mx6 i.mx4a i.mhormon mx1 _d cumhaz

Performing chained iterations ...  

Multivariate imputation Imputations =  5
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mx5e: linear regression
mx1: predictive mean matching
mx6: predictive mean matching
mx4a: logistic regression
mhormon: logistic regression
```
Multiple-imputation diagnostics

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(complete + incomplete = total; imputed is the minimum across m of the number of filled-in observations.)

```
. midaagplots mx1
(M = 5 imputations)
(imputed: mx1 mx4a mx5e mx6 mhormon)
```

Figure 2. Patients' ages imputed by predictive mean matching

We see in figure 2 that ages (mx1) imputed by method pmm no longer have a unimodal distribution, resulting in a distribution that more closely matches the observed distribution. We did not specify the knn() option, so mi impute pmm used the default setting of one “nearest neighbor”. Using more than one nearest neighbor would decrease variance but increase bias.
The imputations for variable \( mx5e \) could also be improved because they include values that are impossible in the observed data (figure 3):

```stata
.midiagplots mx5e, plottype(histogram) separate
(M = 5 imputations)
(imputed: mx1 mx4a mx5e mx6 mhormon)
```

![Graph showing observed and imputed values of \( mx5e \).](image)

Figure 3. The imputed values of \( mx5e \) lie outside \((0, 1)\)

The variable \( mx5e \) in figure 3 is an exponential transformation \( f(x) = \exp(-0.12x) \) of the patient’s number of positive lymph nodes, and the transformation always produces observed data between 0 and 1. (Every patient in the study had at least one positive node.) The imputation model, however, does not respect the bounds, and some of the imputed values lie outside \((0, 1)\).

To handle the outlying imputed values, we will reimpute \( mx5e \) by using predictive mean matching. Method \texttt{pmm} guarantees that the imputed values lie within the extremes of the observed data.
Multiple-imputation diagnostics

. mi impute chained (pmm) mx1 mx6 mx5e (logit) mx4a
> mhormon = _d cumhaz, replace

Conditional models:
  mx6: pmm mx6 i.mx4a i.mhormon mx1 mx5e _d cumhaz
  mx4a: logit mx4a mx6 i.mhormon mx1 mx5e _d cumhaz
  mhormon: logit mhormon mx6 i.mx4a mx1 mx5e _d cumhaz
  mx1: pmm mx1 mx6 i.mx4a i.mhormon mx5e _d cumhaz
  mx5e: pmm mx5e mx6 i.mx4a i.mhormon mx1 _d cumhaz

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(complete + incomplete = total; imputed is the minimum across m of the number of filled-in observations.)
The imputations for \( \text{mx5e} \) in figure 4 now lie in \((0, 1)\).

There is another way to handle the transformation: instead of imputing the transformed variable \( \text{mx5e} \), we could impute \( \text{mx5} \), the untransformed number of positive nodes, and then transform the imputations by using \( f(x) = \exp(-0.12x) \) to produce values lying in \((0, 1)\).
We can use the `combine` option to check all imputations for variable `mx6` (concentration of progesterone receptors). The `combine` option combines all imputations into one graph shown in figure 5:

```
. midiagplots mx6, combine
(M = 5 imputations)
(imputed: mx1 mx4a mx5e mx6 mhormon)
(all imputations assumed with combine)
```

Figure 5. Kernel density estimates for progesterone receptor concentration (mx6) for all imputations

So far we have examined only the continuous variables, but `midiagplots` supports categorical variables too. By default, there is no graph; instead, the command tabulates the observed, imputed, and completed distributions. Let us tabulate the binary variables `mx4a` (tumor grade) and `mhormon` (hormonal therapy) for the fourth imputation:
Proportions of `mx4a` for \( m = 4 \)

\[
\begin{array}{c|ccc}
 & \text{Observed} & \text{Imputed} & \text{Completed} \\
\hline
0 & 0.102 & 0.093 & 0.101 \\
1 & 0.898 & 0.907 & 0.899 \\
\end{array}
\]

Proportions of `mhormon` for \( m = 4 \)

\[
\begin{array}{c|ccc}
 & \text{Observed} & \text{Imputed} & \text{Completed} \\
\hline
0 & 0.643 & 0.628 & 0.640 \\
1 & 0.357 & 0.372 & 0.360 \\
\end{array}
\]

For each variable, the three distributions are similar. To tabulate frequencies instead of proportions, use the `tabfreq` option.

Once we are satisfied with our imputation model, we can fit an analysis model with `mi estimate: stcox`.

\[ \text{Carlin, Galati, and Royston (2008, 64)} \text{ used fractional polynomials to model the variables `mx1` and `mx6`. For the other variables, our estimates are similar to theirs.} \]
Multiple-imputation diagnostics

4 Conclusion

midiagplots adds to Stata several multiple-imputation diagnostics, and the command may be extended as new diagnostics are published. Extensions may include plots of fitted values and residuals (Abayomi, Gelman, and Levy 2008; Marchenko and Eddings 2011), propensity score diagnostics (Raghunathan and Bondarenko 2007), and cross-validation (Gelman, King, and Liu 1998, 853–855).

midiagplots and other diagnostics can help check an imputation model provided that the data are MAR. But the diagnostics cannot check the MAR assumption itself. If the assumption is in doubt, an MNAR model may be used.

MNAR models are not identifiable though, for the same reason that the MAR assumption is not testable. So it is important to perform a sensitivity analysis—to make assumptions to identify the MNAR model and then vary the assumptions to see how the conclusions change. For an introduction to MNAR selection models and pattern-mixture models, see chapter 10 of Enders (2010).

5 References


About the authors

Wes Eddings is a senior statistician at StataCorp.

Yulia Marchenko is the director of biostatistics at StataCorp.