nhanes_imputation

April 13, 2020

1 Analyzing missing data in Python Statsmodels, a case study with the NHANES data

This notebook demonstrates several techniques for working with missing data in Python, using the Statsmodels library. The methods are illustrated using data from the NHANES (National Health and Nutrition Examination Study).

First we import the libraries that we will be using.

[1]:
```
import matplotlib.pyplot as plt
import seaborn as sns
import pandas as pd
import statsmodels.api as sm
import numpy as np
from statsmodels.imputation import mice
from statsmodels.imputation.bayes_mi import BayesGaussMI, MI
```

```
/nfs/kshedden/python3/lib/python3.7/site-
packages/statsmodels/compat/pandas.py:23: FutureWarning: The Panel class is
removed from pandas. Accessing it from the top-level namespace will also be
removed in the next version
  data_klasses = (pandas.Series, pandas.DataFrame, pandas.Panel)
```

Next we will load the data. The NHANES study encompasses multiple waves of data collection. Here we will only use the 2015-2016 data.

[2]:
```
url = "https://raw.githubusercontent.com/kshedden/statswpy/master/NHANES/merged/
 ↪nhanes_2015_2016.csv"
da = pd.read_csv(url)

# Retain a subset of columns for use below.
vars = ["BPXSY1", "RIDAGEYR", "RIAGENDR", "RIDRETH1", "DMDEDUC2", "BMXBMI",␣
 ↪"SMQ020"]
```

2 Multiple imputation

Here we demonstrate how to use multiple imputation to estimate a correlation coefficient when some data values are missing. Blood pressure and BMI are expected to be positively related, and we estimate the correlation between them below. A thorough understanding of the relationship between blood pressure and BMI should consider gender, BMI, and other possibly relevant factors. But for illustration, we focus here on the simple unadjusted correlation.

In the next cell, we determine how many values of these variables are missing:

[3]:
```
dx = da.loc[:, ["BPXSY1", "BMXBMI"]]

# Size of all data, including missing values
print(dx.shape)

# Number of missing values for each variable
print(pd.isnull(dx).sum(0))

# Number of cases that are missing both variables
print(pd.isnull(dx).prod(1).sum(0))
```

```
(5735, 2)
BPXSY1    334
BMXBMI     73
dtype: int64
19
```

Next, for comparison purposes, we estimate the correlation coefficient and its standard error using “complete case” analysis:

[4]:
```
dd = dx.dropna()
c = np.cov(dd.T)

r_cc = c[0, 1] / np.sqrt(c[0, 0] * c[1, 1])
print("Complete case estimate:       %f" % r_cc)
print("Complete case standard error: %f\n" % (1 / np.sqrt(dd.shape[0])))
```

```
Complete case estimate:       0.135201
Complete case standard error: 0.013676
```

Now we are ready to use multiple imputation. Statsmodels provides a Bayesian imputation framework using the Gaussian distribution (we will explore other ways to do imputation later).

Like most Bayesian methods, this approach utilizes prior distributions on the structural parameters of the model. If the data are approximately standardized (i.e. have zero mean and unit variance), then the default priors should work fine. But BMI and blood pressure are measured on scales with values ranging from around 10 to 200. Therefore, we scale the prior covariance matrices accordingly.

To use this approach, we first construct an imputation object and “burn” it in.

[5]:
```
bm = BayesGaussMI(dx, mean_prior=100*np.eye(2), cov_prior=100*np.eye(2))

for k in range(100):
    bm.update()
```

Now we are ready to draw samples from the imputation object, and use these samples to estimate the unknown parameter of interest (the correlation between blood pressure and BMI).

[6]:
```
rv = []
for k in range(200):
    bm.update()

    # After calling bm.update, we can access bm.mean and bm.cov,
    # which are draws from the posterior distribution of the
    # Gaussian mean and covariance parameters given the data.
    # We can also access the underlying data frame dx, which
    # has now been imputed so that there are no missing values.
    r = bm.cov[0, 1] / np.sqrt(bm.cov[0, 0] * bm.cov[1, 1])

    rv.append(r)

rv = np.asarray(rv)
```

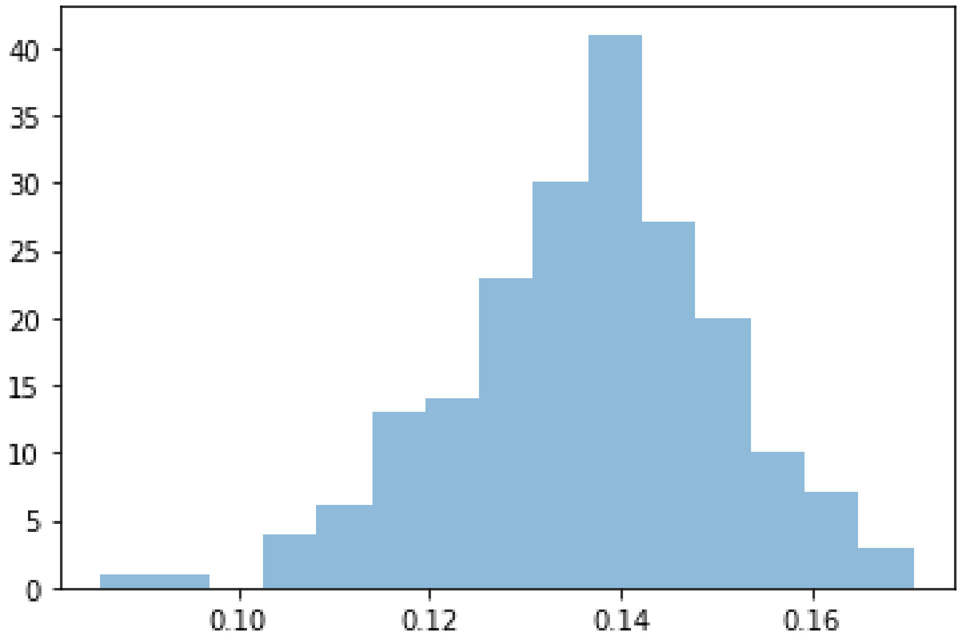
Based on these posterior samples, we can estimate the posterior mean and posterior variance of the correlation coefficient between BMI and blood pressure.

[7]:
```
print("Mean: ", rv.mean())
print("SD:   ", rv.std())
```

```
Mean:  0.13646846202360918
SD:    0.013897382582866182
```

We can also view the histogram of the draws from the posterior distribution.

[8]:
```
_ = plt.hist(rv, bins=15, alpha=0.5)
```



3 Simulation study to assess "information" in partially observed records

Next we use a small simulation study to better understand the performance characteristics of this type of multiple imputation. We take the NHANES data for BMI and blood and introduce increasingly greater fractions of missing values into the data. Then we use multiple imputation (MI) and complete case analysis to estimate the correlation coefficient between blood pressure and BMI, and the standard error of this statistic.

[9]:
```
for f in 0.2, 0.4, 0.6:

    # Introduce missing values, at rate equal to f.
        dy = dx.copy()
        for j in 0, 1:
                ii = np.flatnonzero(np.random.uniform(size=dy.shape[0]) < f)
                dy.iloc[ii, j] = np.nan

        # Complete cases
        dc = dy.dropna()

    # Set up an imputer
        bm = BayesGaussMI(dy, mean_prior=100*np.eye(2), cov_prior=100*np.eye(2))

    # Burn in the imputer
        for k in range(100):
            bm.update()

    # Generate 200 samples from the posterior distribution of the
    # covariance matrix
        rv = []
        for k in range(200):
            bm.update()
            r = bm.cov[0, 1] / np.sqrt(bm.cov[0, 0] * bm.cov[1, 1])
            rv.append(r)
        rv = np.asarray(rv)

    # The mean and standard deviation based on the multiply
    # imputed data, and the standard deviation for complete
    # case analysis (which is computed theoretically as
    # 1/sqrt(sample size)).
        print(rv.mean(), rv.std(), 1/np.sqrt(dc.shape[0]))
```

```
0.1294361670803976 0.016092986661808424 0.016534008228581126
0.1435750916781924 0.020289440775454495 0.022107884414269093
0.15221923818886549 0.03388342050090585 0.032879797461071454
```

Next we have a modified version of the simulation above. We introduce missing values into BMI and SBP, and then impute the missing values multiple times. We then take the mean of log transformed BMI for each dataset, and the sampling variance of this quantity. Finally, we use the combining rules to produce an estimate of the overall uncertainty in the estimate of the expected value of log BMI. Since we are imputing BMI, but analyzing log BMI, we cannot simply use the covariance matrix from the MI procedure, as in the example above.

[10]:
```
for f in 0.2, 0.4, 0.6:

    # Introduce missing values, at rate equal to f.
        dy = dx.copy()
        for j in 0, 1:
                ii = np.flatnonzero(np.random.uniform(size=dy.shape[0]) < f)
                dy.iloc[ii, j] = np.nan

    # Set up an imputer
        bm = BayesGaussMI(dy, mean_prior=100*np.eye(2), cov_prior=100*np.eye(2))

    # Burn in the imputer
        for k in range(100):
            bm.update()

    # Generate 200 samples from the posterior distribution of the
    # covariance matrix
        lm = []
        for k in range(200):
            bm.update()
            lbmi = np.log(bm.data.BMXBMI)
            lm.append([lbmi.mean(), lbmi.var()/len(lbmi)])
        lm = np.asarray(lm)

        print(lm[:, 0].mean(), np.sqrt(lm[:, 1].mean() + lm[:, 0].var()))
```

```
/nfs/kshedden/python3/lib/python3.7/site-packages/pandas/core/series.py:853:
RuntimeWarning: invalid value encountered in log
  result = getattr(ufunc, method)(*inputs, **kwargs)

3.3536019378556396 0.0036617845448228474
3.3536123951751136 0.004235657494170672
3.3426949926268628 0.005606378154698827
```

The goal of any imputation analysis is to recover information from "partially observed" cases. Here, a partially observed case is a person for whom either the blood pressure or BMI value (but not both) is missing. Depending on the specific statistic that is being calculated (or model that is being fit), the benefit of recovering information from partially observed observations can be substantial, or quite small.

Since the missing data values are introduced into random locations, and the MI procedure is itself stochastic, the results of this simulation study will vary from run to run. In general, the complete case standard error and MI "standard error" (which is actually a posterior standard deviation) are quite similar, but the complete case standard error tends to be the slightly larger of the two. In this setting, the observations with only one value contribute to the MI analysis but not to the complete case analysis. It turns out that retaining these cases only provides a small amount of information that is relevant for estimating the correlation coefficient.

4 Multiple imputation for regression

The MI class can automate the process of applying multiple imputation to a dataset and using the "combining rules" to produce a single set of parameter estimates and standard errors. We will illustrate this for the task of using linear regression to explore the conditional relationship of blood pressure given BMI, age, and gender.

First, we subset the data that we will be using.

[11]:
```
dx = da.loc[:, ["BPXSY1", "BMXBMI", "RIDAGEYR", "RIAGENDR"]]

print(dx.shape)
print(pd.isnull(dx).sum(0))
```

```
(5735, 4)
BPXSY1      334
BMXBMI       73
RIDAGEYR      0
RIAGENDR      0
dtype: int64
```

Only a handful of values are missing, so for illustration purposes, we introduce additional missing values into the age and BMI variables.

[12]:
```
ii = np.flatnonzero(np.random.uniform(size=dx.shape[0]) < 0.1)
dx.loc[ii, "RIDAGEYR"] = np.nan

ii = np.random.uniform(size=dx.shape[0]) < 0.1
dx.loc[ii, "BMXBMI"] = np.nan

print(pd.isnull(dx).sum(0))
```

```
BPXSY1      334
BMXBMI      603
RIDAGEYR    588
RIAGENDR      0
dtype: int64
```

Now we are ready to go:

[13]:
```
v = np.r_[100, 30, 40, 1]
bm = BayesGaussMI(dx, mean_prior=np.diag(v), cov_prior=np.diag(v))

def model_kwds_fn(x):
    return {"data": x}
```

```
mi = MI(bm, sm.OLS, formula="BPXSY1 ~ BMXBMI + RIDAGEYR + RIAGENDR",
        burn=0, model_kwds_fn=model_kwds_fn)
mir = mi.fit()

print(mir.summary())
```

```
                 Results: Ordinary least squares
=================================================================
Method:                    MI           Sample size:         5735
Model:                     OLS          Num. imputations     20
Dependent variable:        BPXSY1
-----------------------------------------------------------------
           Coef.  Std.Err.    t    P>|t|   [0.025   0.975]   FMI
-----------------------------------------------------------------
Intercept 99.8122   1.3192 75.6611 0.0000 97.2266 102.3977 0.1679
BMXBMI     0.3062   0.0348  8.7974 0.0000  0.2379   0.3744 0.2323
RIDAGEYR   0.4557   0.0125 36.5261 0.0000  0.4313   0.4802 0.1285
RIAGENDR  -3.7659   0.4494 -8.3804 0.0000 -4.6467  -2.8852 0.0913
=================================================================
```

Note that the multiple imputation results show the full sample size, indicating that no cases were dropped (as in a complete case analysis).

5 MICE

Multiple Imputation with Chained Equations (MICE) is a regression-based framework for imputing missing values that allows us to specify arbitrary regression models for imputing each variable's missing values from the other variables.

One common workflow with MICE is to create a set of imputed datasets, then save them as files. They can then be retrieved later and used in an MI analysis using the "combining rules". This workflow is illustrated below.

[14]:
```
dx = da.copy()
dx = dx.loc[:, ["BMXBMI", "BPXSY1", "RIAGENDR", "RIDAGEYR"]]

# Recode to 0 (male), 1 (female)
dx.RIAGENDR -= 1

# Introduce some missing values
for k in range(dx.shape[1]):
    ii = np.flatnonzero(np.random.uniform(size=dx.shape[0]) < 0.1)
    dx.iloc[ii, k] = np.nan

imp_data = mice.MICEData(dx)
imp_data.set_imputer("BMXBMI", "RIDAGEYR + RIAGENDR")
imp_data.set_imputer("RIAGENDR", "BPXSY1 + RIDAGEYR + BMXBMI", model_class=sm.
 ↪GLM,
                     init_kwds={"family": sm.families.Binomial()})

for j in range(10):
    imp_data.update_all()

    # Uncomment this line to save the files.
    #imp_data.to_csv('data%02d.csv' % j)
```

Another common workflow is to combine the data imputation, modeling and results combination together.

[15]:
```
dx = da.copy()
dx = dx.loc[:, ["BMXBMI", "BPXSY1", "RIAGENDR", "RIDAGEYR"]]

# Recode to 0 (male), 1 (female)
dx.RIAGENDR -= 1

# Introduce some missing values
for k in range(dx.shape[1]):
    ii = np.flatnonzero(np.random.uniform(size=dx.shape[0]) < 0.1)
    dx.iloc[ii, k] = np.nan

imp_data = mice.MICEData(dx)
imp_data.set_imputer("BMXBMI", "RIDAGEYR + RIAGENDR")
imp_data.set_imputer("RIAGENDR", "BPXSY1 + RIDAGEYR + BMXBMI", model_class=sm.
 ↪GLM,
                     init_kwds={"families": sm.families.Binomial()})

mi = mice.MICE("BPXSY1 ~ RIDAGEYR + RIAGENDR + BMXBMI", sm.OLS, imp_data,␣
 ↪n_skip=1)
result = mi.fit(10, 10)

print(result.summary())
```

```
                         Results: MICE
================================================================
Method:                    MICE       Sample size:         5734
Model:                     OLS        Scale                258.93
Dependent variable:        BPXSY1     Num. imputations     10
----------------------------------------------------------------
           Coef.  Std.Err.    t     P>|t|   [0.025  0.975]  FMI
----------------------------------------------------------------
Intercept 96.5985   1.1731 82.3454 0.0000 94.2992 98.8977 0.2068
RIDAGEYR   0.4673   0.0133 35.1179 0.0000  0.4412  0.4934 0.2507
RIAGENDR  -3.7378   0.5062 -7.3842 0.0000 -4.7299 -2.7457 0.2880
BMXBMI     0.2682   0.0363  7.3813 0.0000  0.1970  0.3395 0.3235
```

==