data-vis-report

March 8, 2018

1 White Swan AS Data Analysis Report

```
Date:    8 March 2018
Theme:   Data validation and visual analysis
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```

```
In [1]: import numpy as np
        import pandas as pd
        from matplotlib import pyplot as plt
        import seaborn as sns

        sns.set()

        %matplotlib inline
```

1.0.1 Load all datasets

```
In [40]: basmi_df = pd.read_excel('../data/clean_basmi.xls', index_col=(0,1))
         basmi_df['Drug'].replace(np.nan,'None', inplace=True)

         normed_bs_df = pd.read_excel('../data/bs_normed_full.xls', index_col=0)
         agg_bs_df = pd.read_excel('../data/bs_normed_agg.xls', index_col=0, header=[0,1])

         # Demographics Data
         demo_df = pd.read_excel('../data/demographics and Biologics data.xlsx')
```

1.1 Age Distribution

Show what the age distribution is for the patients' "Age at diagnosis". This will give us an idea of what age do patients enter the study

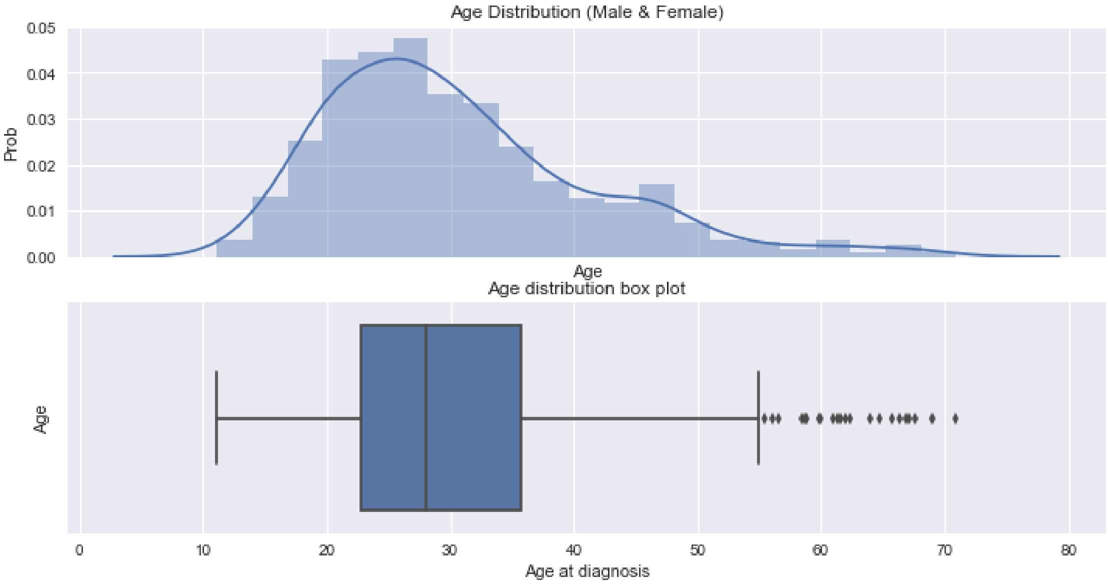
Process:

First, remove patients from demographics data that we do not have BASMI data for and remove patients with any missing data.

Then, plot the age distribution for males and females and afterwards split the process for both genders

```
In [16]: # Patients in BASMI dataset
         basmi_patient_ids = set(basmi_df.index.get_level_values('patient_id').unique().values)
```

```
# Patients in Demographics dataset
demo_patient_ids = set(demo_df['patient_id'].unique())

# Patients in BOTH datasets
overlap_patient_ids = basmi_patient_ids.intersection(demo_patient_ids)

# Keep only overlapping patient data
demo_df = demo_df[demo_df['patient_id'].isin(list(overlap_patient_ids))]

# Remove the rows with missing values
demo_df.dropna(how='any',inplace=True)

# Overall distribution Plot
age_at_entry = demo_df['Age at diagnosis']

fig, ax_1 = plt.subplots(nrows=2, ncols=1, figsize=(12,6), sharex=True)
sns.distplot(age_at_entry, ax=ax_1[0])
ax_1[0].set_title('Age Distribution (Male & Female)')
ax_1[0].set_xlabel('Age')
ax_1[0].set_ylabel('Prob')

sns.boxplot(age_at_entry, ax=ax_1[1])
ax_1[1].set_title('Age distribution box plot')
ax_1[1].set_ylabel('Age')

plt.show()
```

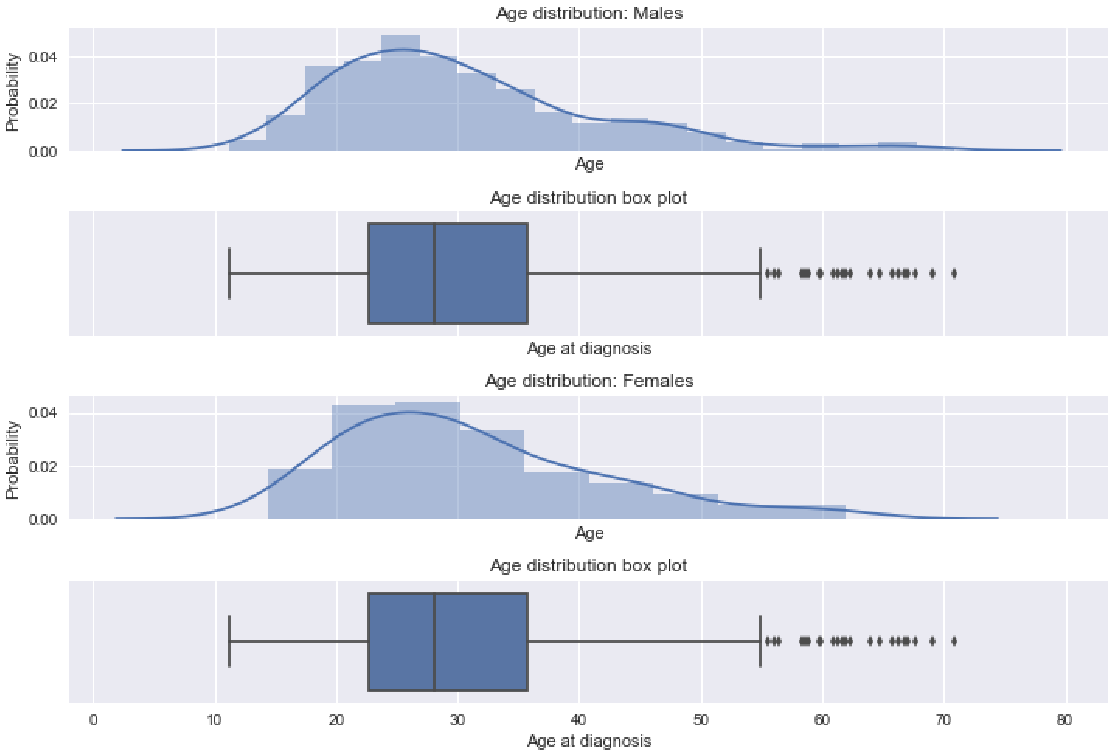


It is observed that the age distribution is slightly positively skewed. Furthermore, the modal age at entry is approximately 25 years. This is younger than expected (by me at least).

1.1.1 Age distribution by gender

Split the process up for males and females

```
In [17]: genders = demo_df['patient_gender_id']
         # Get male and female index
         male_ids = demo_df[genders == 'Male']['patient_id']
         female_ids = demo_df[genders == 'Female']['patient_id']

         # Get demographics about males and females
         male_demo_df = demo_df[demo_df['patient_id'].isin(male_ids)]
         female_demo_df = demo_df[demo_df['patient_id'].isin(female_ids)]

         # Plot age at entry distribution for males and females
         age_at_entry_male = male_demo_df['Age at diagnosis'].values
         age_at_entry_female = female_demo_df['Age at diagnosis'].values

         fig, ax_2 = plt.subplots(nrows=4,ncols=1,sharex=True, figsize=(12,8))
         plt.subplots_adjust(hspace=0.5)
         sns.distplot(age_at_entry_male, ax = ax_2[0])
         ax_2[0].set_title('Age distribution: Males')
         ax_2[0].set_xlabel('Age')
         ax_2[0].set_ylabel('Probability')
         sns.boxplot(age_at_entry, ax=ax_2[1])
         ax_2[1].set_title('Age distribution box plot')

         sns.distplot(age_at_entry_female, ax = ax_2[2] )
         ax_2[2].set_title('Age distribution: Females')
         ax_2[2].set_xlabel('Age')
         ax_2[2].set_ylabel('Probability')
         sns.boxplot(age_at_entry, ax=ax_2[3])
         ax_2[3].set_title('Age distribution box plot')
         plt.show()
```



It is seen that the shape of the two histograms are similar. Hence, there is not a massive difference between the age at entry of males and females. Notice that females are diagnosed at an earlier stage than males, although this is only a marginal difference.

2 BS Score Over Time

Now we look at how the `BS` score progresses over time for the average patient.

A more complete analysis can be found in the `bs-over-time.ipynb` notebook.

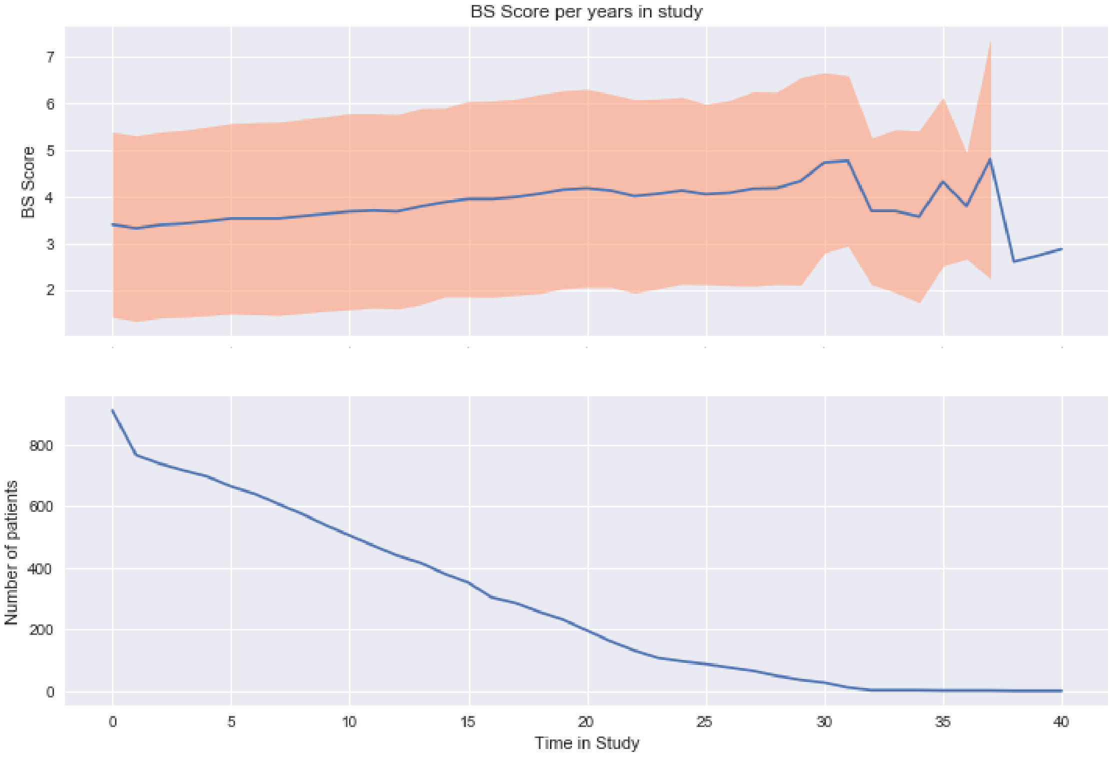
To do this, we first *normalized* the patient timelines so that the year in which the patient entered the study is set to 0 and the next year is 1 and so forth. Then the *average* BS score is calculated for each year in the study as well as the number of patients that were included in the study for that many years.

For example, if patient A started in May 1998 and patient B started in June 2007 then the BS score of patient A in 1998 will be averaged with the BS score of patient B in 2007 for the year 0 in graph below, as 1998 and 2007 were the respective "0th" year in the study.

If either patient had more than 1 measurement in their first year in the study, these measurements are averaged for that year to attain a single score per year in study, per patient.

```
In [19]: std_bs = agg_bs_df['BS', 'std']
         mean_bs = agg_bs_df['BS','mean']
         num_patients = agg_bs_df['count','len']
```

```
def plot_bs_over_time(mean_bs, std_bs, num_patients):
    fig = plt.figure(figsize=(12,8))
    ax1 = plt.subplot(211)
    plt.plot(mean_bs)
    plt.fill_between(mean_bs.index, y1=mean_bs+std_bs, y2=mean_bs-std_bs, color='lights
    plt.setp(ax1.get_xticklabels(), fontsize=0)
    plt.title('BS Score per years in study')
    ax1.set_ylabel('BS Score')

    ax2 = plt.subplot(212, sharex=ax1)
    plt.plot(num_patients)
    ax2.set_xlabel('Time in Study')
    ax2.set_ylabel('Number of patients')

    plt.show()

plot_bs_over_time(mean_bs, std_bs, num_patients)

print(f'Number of patients in study at year 0 vs year 30 = {num_patients.loc[30]} / {nu
```



```
Number of patients in study at year 0 vs year 30 = 28 / 910
```

Interpretation Firstly, we can observe a approximately linear increase in BS score as time in study increases, while the number of patients in study also decreases approximately linearly. These observations are in line with what we expected.

Secondly, we can see that at around the 30 year mark there are very few patients in the study (28 vs 910 at start), which shows corresponding erratic measurements

We can see a high variability in the average BS score per year in study. This could be motivated by the fact that we are taking an average over patients that are in different phases of disease progression. For example, patient A might join the study with a BS score of 2 and patient B might join with a BS score of 4.2 - vastly different stages in disease progression, but both will be considered in the calculation of the mean BS score for `year-in-study = 0`.

Also, at the last few datapoints we only have 1 patient in the study, and thus the standard deviation is not defined.

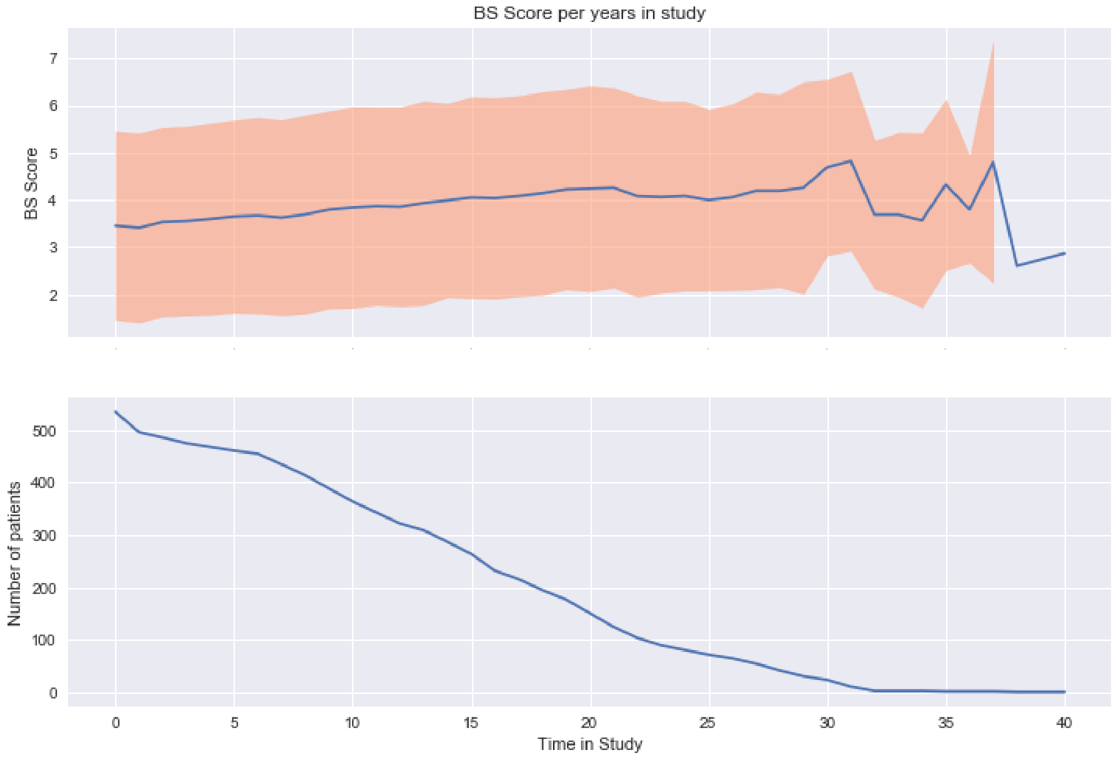
2.1 Repeat the above analysis for both males and females

The first step is to identify which patients are male and female.

```
In [20]: demo_df = pd.read_excel('../data/demographics and Biologics data.xlsx')

         # Get patient ids of males and females
         genders = demo_df['patient_gender_id'].values

         # Get male and female index
         male_ids = demo_df[genders == 'Male']['patient_id']
         female_ids = demo_df[genders == 'Female']['patient_id']

         # # Get BS dataset of males and females
         male_bs_df = normed_bs_df.loc[male_ids]
         female_bs_df = normed_bs_df.loc[female_ids]
```

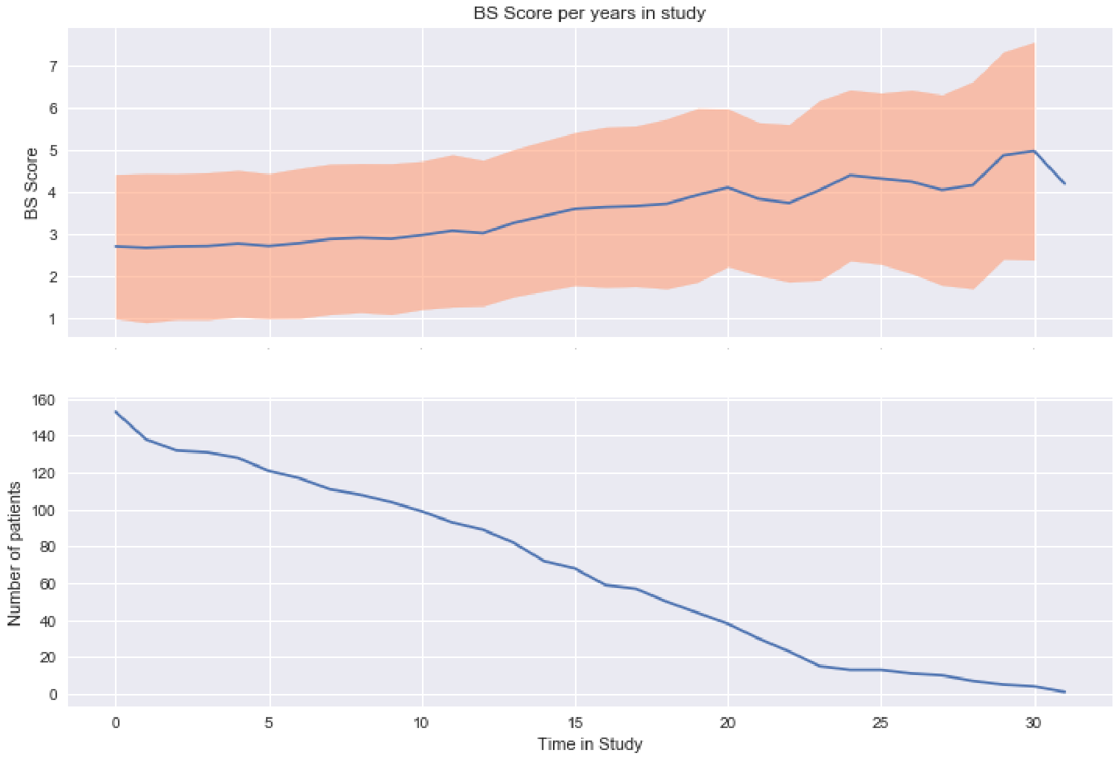
2.2 Plot BS score over time for males

```
In [21]: agg_male_df = (male_bs_df.groupby('norm_years')
                                  .agg({'BS': ['mean','std'], 'norm_years': len})
                                  .rename(columns={'norm_years': 'count'}))

         std_bs = agg_male_df['BS', 'std']
         mean_bs = agg_male_df['BS','mean']
         num_patients = agg_male_df['count','len']

         plot_bs_over_time(mean_bs, std_bs, num_patients)
```



2.3 Plot BS over time for females

```
In [22]: agg_female_df = (female_bs_df.groupby('norm_years')
                             .agg({'BS': ['mean','std'], 'norm_years': len})
                             .rename(columns={'norm_years': 'count'}))

         std_bs = agg_female_df['BS', 'std']
         mean_bs = agg_female_df['BS','mean']
         num_patients = agg_female_df['count','len']

         plot_bs_over_time(mean_bs, std_bs, num_patients)
```



2.4 Average duration of treatment (days)

What is the average duration spent by a patient on a specific drug or no medication at all?

```
In [41]: # List of drugs
         drugs = [d for d in basmi_df['Drug'].unique() ]

         # DataFrame to hold descriptive info
         drugs_duration_df = pd.DataFrame(index = drugs, columns = ['avg_days','median_days','st

         drugs_days = {drug: [] for drug in drugs}
         for group, group_df in basmi_df.groupby(['Drug','patient_id']):

             start = min(group_df.index.get_level_values('Date'))
             end = max(group_df.index.get_level_values('Date'))

             days = pd.Timedelta(end-start).days

             drugs_days[group[0]].append(days)

         for drug,days in drugs_days.items():
             drugs_duration_df.loc[drug] = [np.mean(days), np.median(days),np.std(days), len(day
drugs_duration_df
```

```
{'None': [], 'Infliximab': [], 'Adalimumab': [], 'Etanercept': [], 'Certolizumab Pegol': [], 'Go
```

```
Out[41]:                     avg_days median_days std_dev_days count
         None                 4355.49        4026      3243.97   907
         Infliximab           3132.58        3256      890.052    12
         Adalimumab            1763.2        1843      1155.04    75
         Etanercept           2489.46      2677.5      1063.13    50
         Certolizumab Pegol        11          11            0     1
         Golimumab              405.5         361      381.702     8
         Rituximab               1291        1291          850     2
```