Data Science Capstone Project Presentation

In fulfillment of Simplilearn Master Data Science Certification course

Project_name: Healthcare - NIDDK (National Institute of Diabetes and Digestive and Kidney Diseases)

Presenter:***Samuel_Y._Ntsua***

Trainer and Mentor : **TBD**

install packages :

remotezip : for query and downloand zip folder from a url

plotly, seaborn : interactive graphs

cufflinks : connects plotly with pandas to create graphs and charts of dataframes directly

textblob : process textual data

missingno : visualize missing data

scikit-learn : missing data treatment and model evaluation

pandas-profiling: detailed EDA.

** In addition tho these, we will be installing other libraries down the road, as and when they are needed.

In [1]:
```
# %pip install remotezip cufflinks plotly textblob seaborn missingno  # Comented out because this is needed only once.
# %pip install pandas_profiling[notebook]
# %conda install -c conda-forge scikit-learn pandas-profiling
```

In [2]:
```
# Checking content of zip folder so I can determine a strategy to load files
```

In [3]:
```
%lsmagic
```

Out[3]:
```
Available line magics:
%alias  %alias_magic  %autoawait  %autocall  %automagic  %autosave  %bookmark  %cd  %clear  %cls  %colors  %conda  %confi
g  %connect_info  %copy  %ddir  %debug  %dhist  %dirs  %doctest_mode  %echo  %ed  %edit  %env  %gui  %hist  %history  %ki
```

```
llbgscripts  %ldir  %less  %load  %load_ext  %loadpy  %logoff  %logon  %logstart  %logstate  %logstop  %ls  %lsmagic  %ma
cro  %magic  %matplotlib  %mkdir  %more  %notebook  %page  %pastebin  %pdb  %pdef  %pdoc  %pfile  %pinfo  %pinfo2  %pip
%popd  %pprint  %precision  %prun  %psearch  %psource  %pushd  %pwd  %pycat  %pylab  %qtconsole  %quickref  %recall  %reh
ashx  %reload_ext  %ren  %rep  %rerun  %reset  %reset_selective  %rmdir  %run  %save  %sc  %set_env  %store  %sx  %system
%tb  %time  %timeit  %unalias  %unload_ext  %who  %who_ls  %whos  %xdel  %xmode

Available cell magics:
%%!  %%HTML  %%SVG  %%bash  %%capture  %%cmd  %%debug  %%file  %%html  %%javascript  %%js  %%latex  %%markdown  %%perl  %
%prun  %%pypy  %%python  %%python2  %%python3  %%ruby  %%script  %%sh  %%svg  %%sx  %%system  %%time  %%timeit  %%writefi
le

Automagic is ON, % prefix IS NOT needed for line magics.
```

In [4]:

```
# Ignore harmless warnings
import warnings
warnings.filterwarnings('ignore')
# Imports
import os, pandas as pd, numpy as np, seaborn as sns, plotly.express as px, cufflinks as cf, matplotlib.pyplot as plt, mi
#os.listdir("Project2")
```

** Check the content of the ziped folder located on github

In [5]:

```
# from remotezip import RemoteZip
# with RemoteZip('https://github.com/Simplilearn-Edu/Data-Science-Capstone-Projects/raw/master/Project_2.zip') as hczip :
#     for hcfiles in hczip.infolist():
#         print(hcfiles.filename)
```

**Now that we see the contents, we can grab the specific file we need for this project.

In [6]:

```
# with RemoteZip('https://github.com/Simplilearn-Edu/Data-Science-Capstone-Projects/raw/master/Project_2.zip') as hczip :
#    hczip.extract('Project 2/Healthcare - Diabetes/health care diabetes.csv')
```

The file is now downloaded to my local machine at 'Project 2/Healthcare - Diabetes/health care diabetes.csv'

We can now load it with pandas

In [7]:

```
hc_df = pd.read_csv('Project 2/Healthcare - Diabetes/health care diabetes.csv')
```

Exploratory Data Analysis

** Descriptive analysis and data understanding

In [8]:
```
hc_df.shape
```

Out[8]:
```
(768, 9)
```

In [9]:
```
type(hc_df)
```

Out[9]:
```
pandas.core.frame.DataFrame
```

In [10]:
```
hc_df.dtypes
```

Out[10]:
```
Pregnancies                   int64
Glucose                       int64
BloodPressure                 int64
SkinThickness                 int64
Insulin                       int64
BMI                         float64
DiabetesPedigreeFunction    float64
Age                           int64
Outcome                       int64
dtype: object
```

** Visual exploration and checking for missing data

The project instruction indicates that a value of 0 in

Glucose, BloodPressure, SkinThickness, Insulin, BMI are actually missing values

So let's go ahead and set the 0s to np.nan

In [11]:
```
# hc_df.columns = hc_df.columns.map(str.lower) # all column names to lowercase
zcol = ['Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI']
#hc_df=hc_df[hc_df[zcol].astype(float)]
#hc_df=hc_df.astype({'Glucose':float, 'BloodPressure':float, 'SkinThickness':float, 'Insulin':float, 'BMI':float})
```

In [12]:
```
hc_df
```

Out[12]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72	35	0	33.6	0.627	50	1
1	1	85	66	29	0	26.6	0.351	31	0
2	8	183	64	0	0	23.3	0.672	32	1

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
3	1	89	66	23	94	28.1	0.167	21	0
4	0	137	40	35	168	43.1	2.288	33	1
...	...	...	...	...	...	...	...	...	...
763	10	101	76	48	180	32.9	0.171	63	0
764	2	122	70	27	0	36.8	0.340	27	0
765	5	121	72	23	112	26.2	0.245	30	0
766	1	126	60	0	0	30.1	0.349	47	1
767	1	93	70	31	0	30.4	0.315	23	0

768 rows × 9 columns

In [13]:
```
hc_df[hc_df[zcol]==0]=np.nan
```

In [14]:
```
hc_df.isnull().sum()
```

Out[14]:
```
Pregnancies                   0
Glucose                       5
BloodPressure                35
SkinThickness               227
Insulin                     374
BMI                          11
DiabetesPedigreeFunction      0
Age                           0
Outcome                       0
dtype: int64
```

** The same information as above, but now in percentge

In [15]:
```
round(100*(hc_df.isnull().sum() / len(hc_df)))
```

Out[15]:
```
Pregnancies                  0.0
Glucose                      1.0
BloodPressure                5.0
SkinThickness               30.0
Insulin                     49.0
```

```
BMI                         1.0
DiabetesPedigreeFunction    0.0
Age                         0.0
Outcome                     0.0
dtype: float64
```

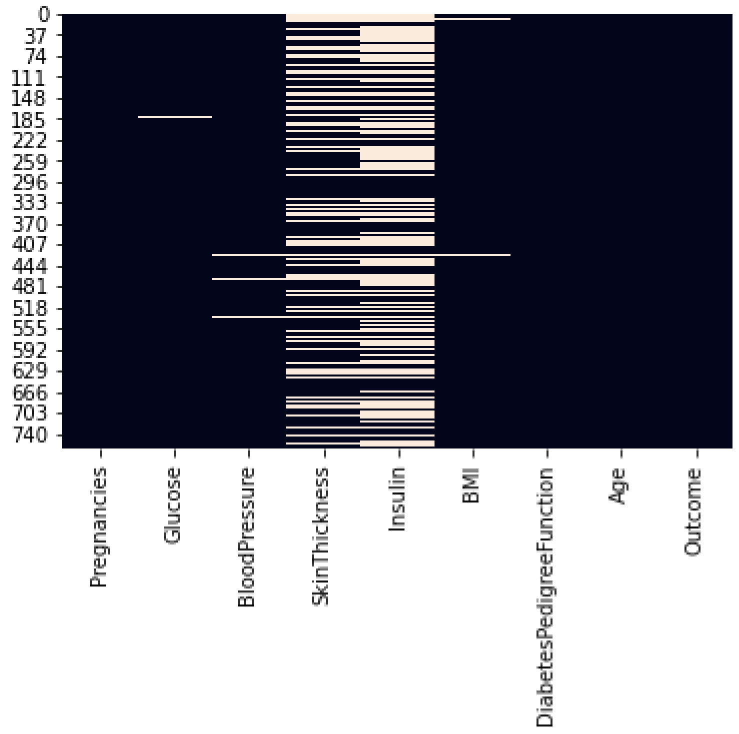
In [16]:
```
# %history -g -f cmd_hist.py
```

In [17]:
```
# %lsmagic
%matplotlib inline
```

To visually see how missing value in one column is related to another column, * let's plot the heatmap of the missingness.

In [18]:
```
sns.heatmap(hc_df.isnull(),cbar=False)
```

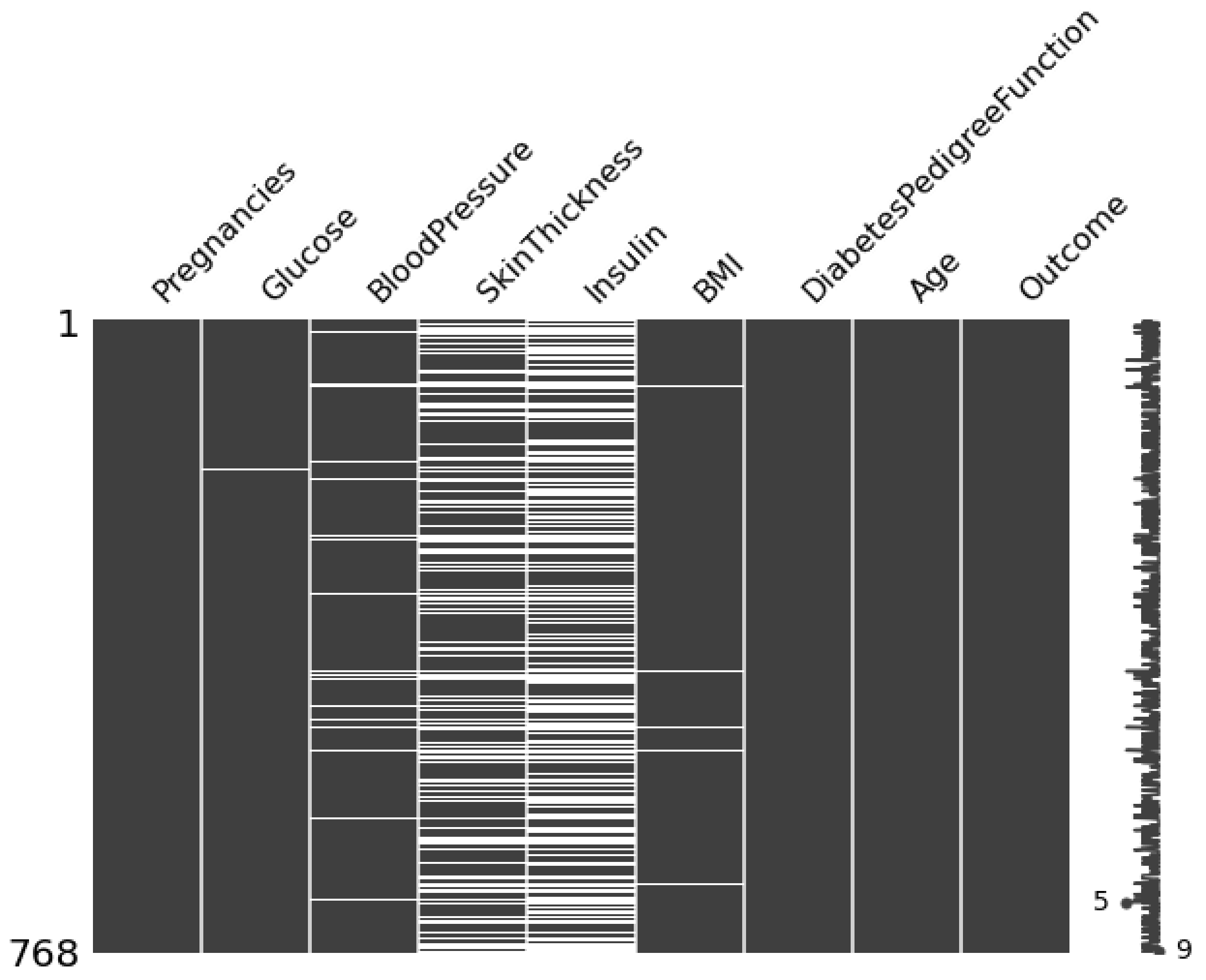
Out[18]:
```
<AxesSubplot:>
```



** Furthermore, we can use missno's matrix to highlight places in each column where data is missing.

```
In [19]: missno.matrix(hc_df,figsize=(10,6))
```

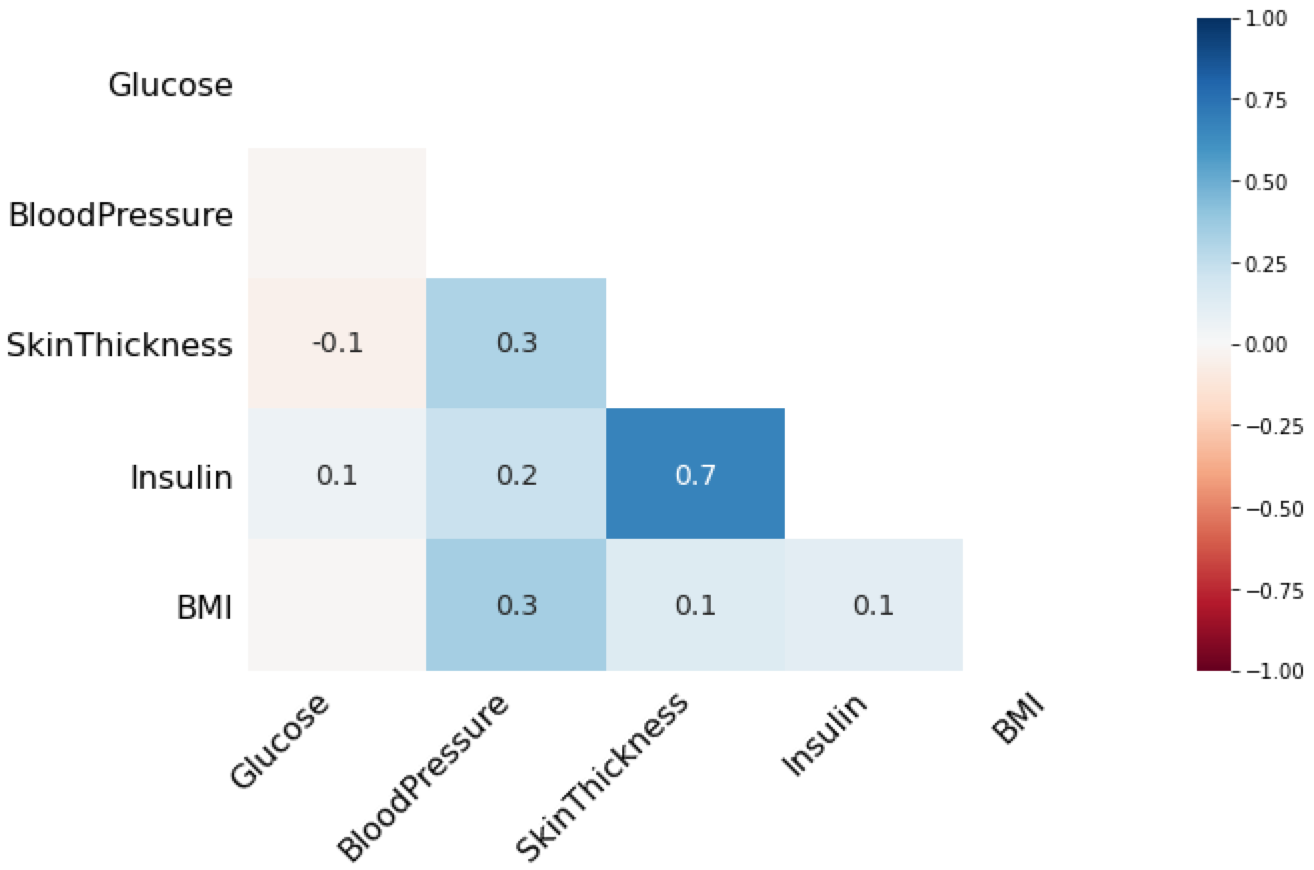
```
Out[19]: <AxesSubplot:>
```



Dropping missing a missing value from a column leads to dropping all other valid values in the row corresponding to the missing value.
Dropping valid data will then lead to bias in the results.
To avoid such problem, we need to examine how much good data will be thrown out when a targeted missing data is dropped.
A correlation metrix between the missing variables can tell us the how one missing value is related to other non-missing values.
Below, we see the missno heatmap of missingness correlated matrix.

```
In [20]: missno.heatmap(hc_df,figsize=(10,6))
```

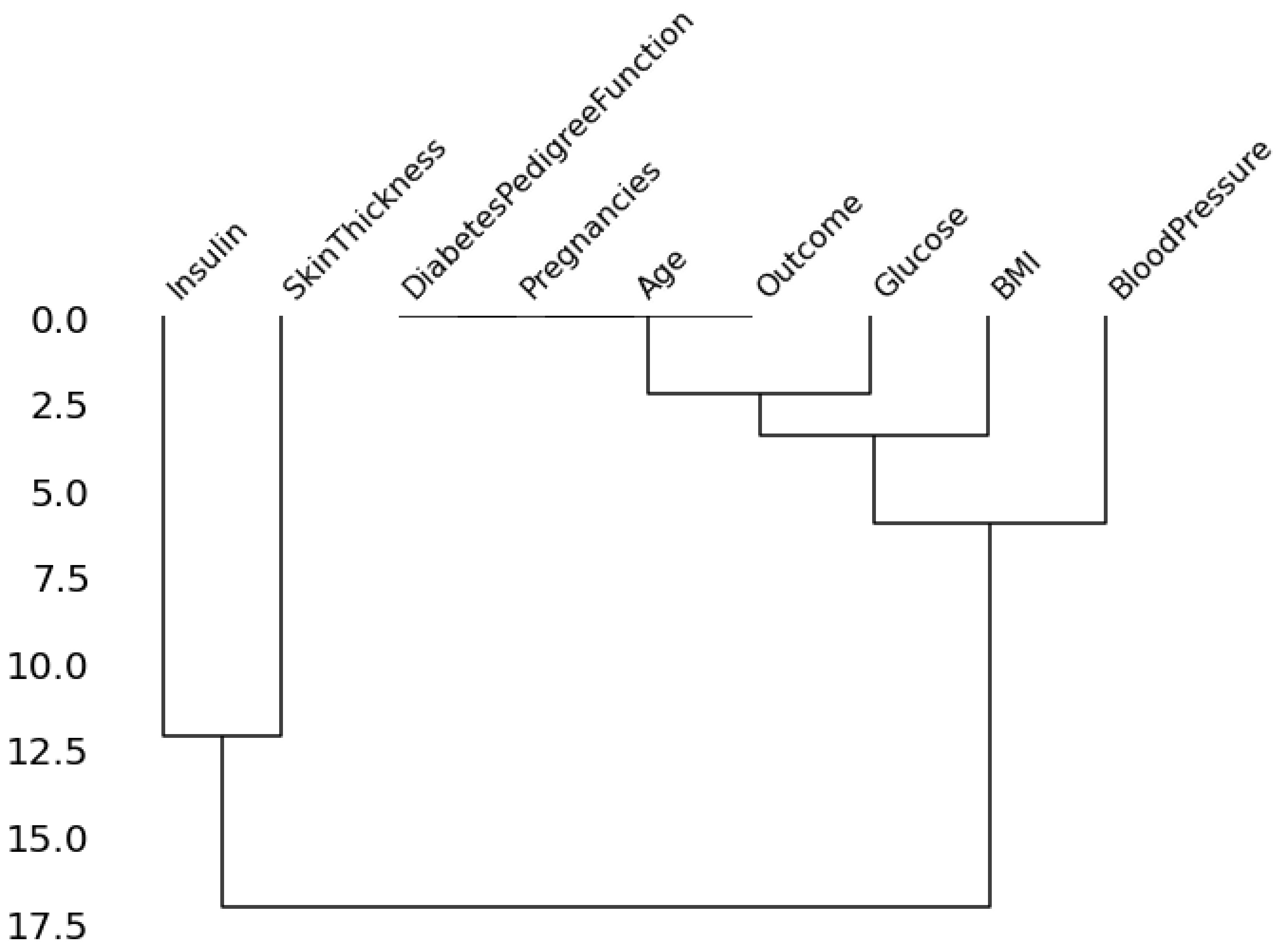
```
Out[20]: <AxesSubplot:>
```



** Likewise, a dendogram also show how one missing value in one column is related to non-missing value in another column.

```
In [21]: missno.dendrogram(hc_df,figsize=(10,6))
```

```
Out[21]: <AxesSubplot:>
```



From the graphs above we can observe that:

(1) `Insuline` and `SkinThinckness` are correlated (corr coef =0.7)

(2) There are more missing data in `Insulin` and `SkinThickness` , but

each time `Insulin` is missing `SkinThickness` is also missing, however, not the other way round.

In theory, given this correlation, the absence of one of `Insulin` or `SkinThickness` will not affect the ability to predict

the `Outcome` varibale. That is, one of the correlated variable can be expressed in termes of the other.

But if we were to drop one, further analysis is needed to determine the one that is not a `principal component` contributing

variation to `Outcome` . Furthermore, when two variables are correlated, it do not necessarily mean one of then is useless.

In fact ,in this dataset, the measures of `Insulin` or `SkinThickness` were observed naturally as they occured on the patients.

These observations suggest that dropping these missing values can lead to loosing data pont that would otherwise

contribute to the accuracy of our analysis results.
So for now we continue our analysis without dropping any variable.

** Going forward, we need to figure out how to handle the missing values then.

Do we fill them with mean values? Probably not. Why?
Although replacing almost half of the values with the mean value is not going the affect the mean of that same variable,
it however reduces it's standard error, and so affecting its relationship with other variables in the dataset.
Doing so will likely tilt the imputed mean towards the observed mean.

Replacing missing values with the mean constitute a quick fix that will get me the project
completed quickly, but it comes with flawed prediction capabilities.

As such, I would not opt for that option.
What else can be done without loosing predictive capability of the data?

Now let's look at two other treatment methods of missing values:
multiple imputation (`mi`) and maximum likelihood estimate (`mle`).
`maximum likelihood estimate mle`:
`mle` takes the row on which data is missing, then compare the non-missing values of that row to other non-missing
value in the same column (within variable), then determins the closet of the set of non-missing values (the likelyhood),
and finally look up the corresponding value in the missing value's column to replace the actual missing value.
Another way to view this is, if two subject have the same values of parameter except that one is missing for a subject,
it is logical to replace the missing value with the corresponding parameter of the other subject.
Problem with `mle` treatment of missing value
`mle` does not impute data.
Given the description of the method above, it is clear that the replacement of the missing value is `linear` in nature,
and therefore `mle` applies to linear models only.
`multiple imputation mi`:
As the name suggests, `mi` imputes multiple times, that is, it takes multiple and different samples (of same size)
from the original data (nonparametric bootstrap), compute an estimator $\hat{X_{i}}$ of the missing value from each sample,
then based on the assumption that, the missing value we are trying to figure out follows the same distribution as $\hat{X_{i}}$,
we compute an estimate $\bar{x}$ of the missing value.
Statistical software like Stata, SAS, SPSS and R implement various computation methods of `mi` .
** In Python I am going to use scikit-learn implimentation (IterativeImputer), even though it is still experimental as of today.

In [22]:
```
from sklearn.experimental import enable_iterative_imputer
from sklearn.impute import IterativeImputer
```

In [23]:
```
imp = IterativeImputer(random_state=100)
imp.fit(hc_df)
```

Out[23]:
```
IterativeImputer(random_state=100)
```

In [24]:
```
imputed_hc_df = pd.DataFrame(imp.transform(hc_df), columns=hc_df.columns)
```

In [25]:
```
round(100*(imputed_hc_df.isnull().sum() / len(imputed_hc_df)))
```

Out[25]:
```
Pregnancies                 0.0
Glucose                     0.0
BloodPressure               0.0
SkinThickness               0.0
Insulin                     0.0
BMI                         0.0
DiabetesPedigreeFunction    0.0
Age                         0.0
Outcome                     0.0
dtype: float64
```

Now that we have full dataset, we can steam forward with more data exploration.

** Let's look at the Mean, std, min, max and quantiles of `before imputation` , for both `Outcome` ==0 and `Outcome` ==1

In [26]:
```
hc_df.describe().T
```

Out[26]:

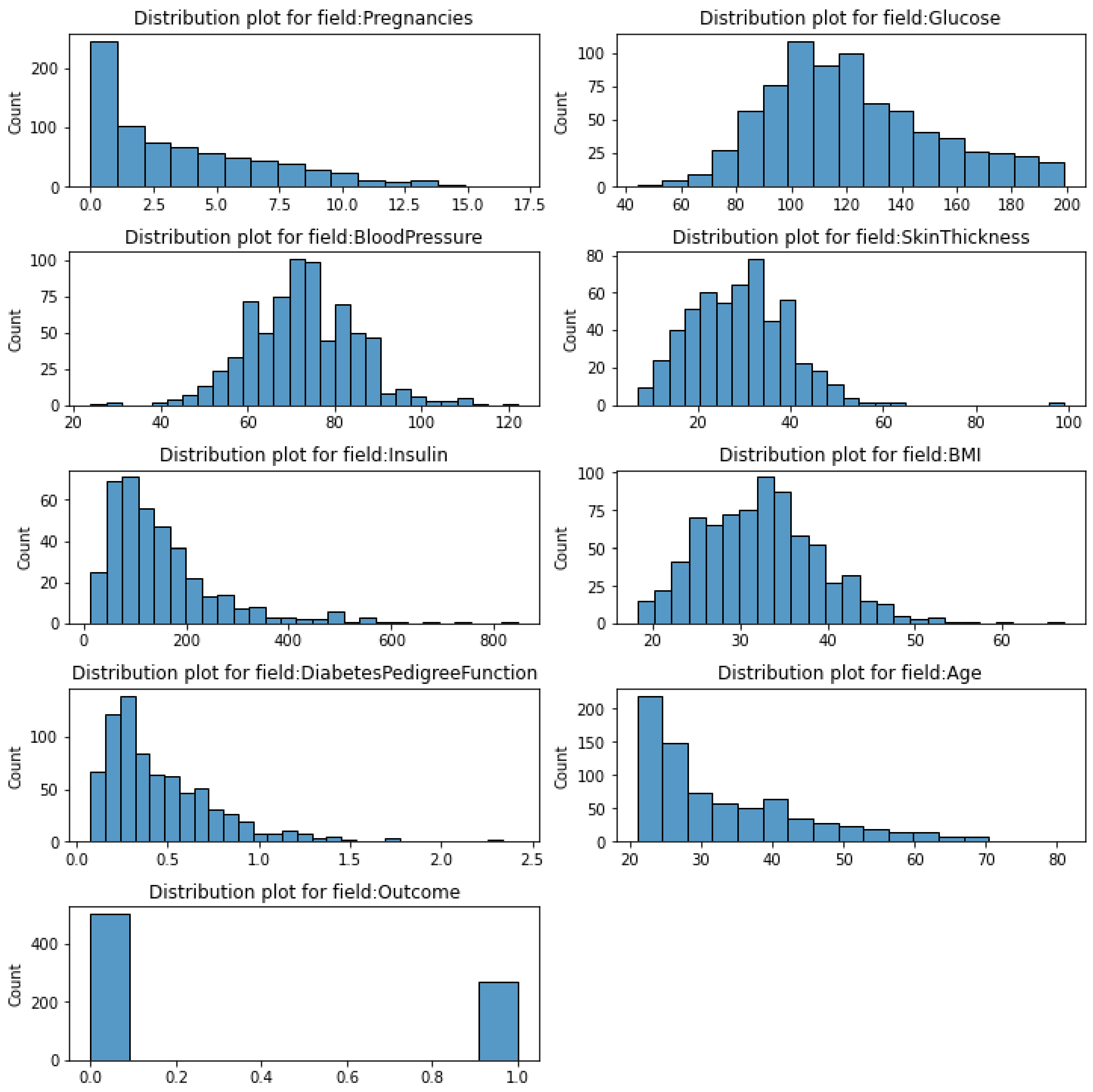
	count	mean	std	min	25%	50%	75%	max
Pregnancies	768.0	3.845052	3.369578	0.000	1.00000	3.0000	6.00000	17.00
Glucose	763.0	121.686763	30.535641	44.000	99.00000	117.0000	141.00000	199.00
BloodPressure	733.0	72.405184	12.382158	24.000	64.00000	72.0000	80.00000	122.00
SkinThickness	541.0	29.153420	10.476982	7.000	22.00000	29.0000	36.00000	99.00
Insulin	394.0	155.548223	118.775855	14.000	76.25000	125.0000	190.00000	846.00

	count	mean	std	min	25%	50%	75%	max
BMI	757.0	32.457464	6.924988	18.200	27.50000	32.3000	36.60000	67.10
DiabetesPedigreeFunction	768.0	0.471876	0.331329	0.078	0.24375	0.3725	0.62625	2.42
Age	768.0	33.240885	11.760232	21.000	24.00000	29.0000	41.00000	81.00
Outcome	768.0	0.348958	0.476951	0.000	0.00000	0.0000	1.00000	1.00

The above output of `mean` and `max` implies that there are some extremes values in the dataset.
For instance, `Pregnancies` has a max value of 17.
This suggests someone in the dataset was pregnant 17 times! Is this realistc?
`Insulin` also seems to have an extreme case.
Let's look at the historgram of the variable to see if there are extreme cases to worry about.

In [27]:
```
plt.figure(figsize=(10, 10))

for i, c in enumerate(hc_df.columns):
    plt.subplot(5,2,i+1)
    sns.histplot(hc_df[c])
    plt.title('Distribution plot for field:' + c)
    plt.xlabel('')
    plt.tight_layout(pad=0.4, w_pad=0.5, h_pad=1.0)
```


Distribution plot for field:Pregnancies
Count
0
100
200
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
Distribution plot for field:Glucose
Count
0
25
50
75
100
40
60
80
100
120
140
160
180
200
Distribution plot for field:BloodPressure
Count
0
25
50
75
100
20
40
60
80
100
120
Distribution plot for field:SkinThickness
Count
0
20
40
60
80
20
40
60
80
100
Distribution plot for field:Insulin
Count
0
20
40
60
0
200
400
600
800
Distribution plot for field:BMI
Count
0
25
50
75
100
20
30
40
50
60
Distribution plot for field:DiabetesPedigreeFunction
Count
0
50
100
0.0
0.5
1.0
1.5
2.0
2.5
Distribution plot for field:Age
Count
0
50
100
150
200
20
30
40
50
60
70
80
Distribution plot for field:Outcome
Count
0
200
400
0.0
0.2
0.4
0.6
0.8
1.0

Looking at the graph above, two cases of `Pregnancies` and `Insulin` need explanation:

`Pregnancies` : Even though it seems unusual for humans to be pregnant 17 times, the the graph shows no gap between the max value of 17 and the rest of the group. This suggest it is not an outlier case.

`Insulin` : there are a few observations in the same region as the max value of 846.
Even though these values are extremely high, the `75 percentile` shows that 75% of the data has value less than 190
Furthermore, the `mean of 155` and `standard deviation of 118` shows that the bulk of the data are within normal range.
Thus, the values of `Insulin` in the region of 800 will not significantly affect the overall statistical validity of that variable.
`SkinThickness` and `MBI` seem a little skewed, but not to the level that warrant correction before analysis.

** Mean, std, min, max and quantiles of `before imputation` , for `Outcome==0`

```
In [28]: hc_df[hc_df['Outcome']==0].describe().T
```

Out[28]:

	count	mean	std	min	25%	50%	75%	max
Pregnancies	500.0	3.298000	3.017185	0.000	1.00000	2.000	5.00000	13.000
Glucose	497.0	110.643863	24.776906	44.000	93.00000	107.000	125.00000	197.000
BloodPressure	481.0	70.877339	12.161223	24.000	62.00000	70.000	78.00000	122.000
SkinThickness	361.0	27.235457	10.026491	7.000	19.00000	27.000	33.00000	60.000
Insulin	264.0	130.287879	102.482237	15.000	66.00000	102.500	161.25000	744.000
BMI	491.0	30.859674	6.560737	18.200	25.60000	30.100	35.30000	57.300
DiabetesPedigreeFunction	500.0	0.429734	0.299085	0.078	0.22975	0.336	0.56175	2.329
Age	500.0	31.190000	11.667655	21.000	23.00000	27.000	37.00000	81.000
Outcome	500.0	0.000000	0.000000	0.000	0.00000	0.000	0.00000	0.000

** Mean, std, min, max and quantiles of `before imputation` , for `Outcome==1`

```
In [29]: hc_df[hc_df['Outcome']==1].describe().T
```

Out[29]:

	count	mean	std	min	25%	50%	75%	max
Pregnancies	268.0	4.865672	3.741239	0.000	1.7500	4.000	8.000	17.00

	count	mean	std	min	25%	50%	75%	max
Glucose	266.0	142.319549	29.599199	78.000	119.0000	140.000	167.000	199.00
BloodPressure	252.0	75.321429	12.299866	30.000	68.0000	74.500	84.000	114.00
SkinThickness	180.0	33.000000	10.327595	7.000	27.0000	32.000	39.000	99.00
Insulin	130.0	206.846154	132.699898	14.000	127.5000	169.500	239.250	846.00
BMI	266.0	35.406767	6.614982	22.900	30.9000	34.300	38.925	67.10
DiabetesPedigreeFunction	268.0	0.550500	0.372354	0.088	0.2625	0.449	0.728	2.42
Age	268.0	37.067164	10.968254	21.000	28.0000	36.000	44.000	70.00
Outcome	268.0	1.000000	0.000000	1.000	1.0000	1.000	1.000	1.00

`Differences` of (Mean, std, min, max and quantiles) `before and after inputation` :

- We compute and compare the differences for `Outcome==0` and `Outcome==1`

** Computation for `Outcome==0`

In [30]:
```
round(imputed_hc_df[imputed_hc_df['Outcome']==0].describe().T -  hc_df[hc_df['Outcome']==0].describe().T ,4)
```

Out[30]:

	count	mean	std	min	25%	50%	75%	max
Pregnancies	0.0	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0
Glucose	3.0	-0.0608	-0.0550	0.0000	0.0000	0.0000	0.0000	0.0
BloodPressure	19.0	-0.0802	-0.1986	0.0000	0.4921	0.0000	0.0000	0.0
SkinThickness	139.0	-0.2774	-0.8908	0.0000	1.0000	-0.2169	-0.8233	0.0
Insulin	236.0	-3.3301	-18.9441	-34.5017	7.8282	7.5000	-4.6201	0.0
BMI	9.0	-0.0049	-0.0590	0.0000	0.1500	0.1147	0.0000	0.0
DiabetesPedigreeFunction	0.0	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0
Age	0.0	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0
Outcome	0.0	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0

** Comment for `Outcome==0` :

- `count` : We successfully augmented the count for `SkinThickness` , `Insulin` , `BloodPressure` , `Glucose and MBI` as shown in the first column of the table above
- `mean` , `std` , `min` , `max and quantiles` : Given the magnitude of range (`max - min`) shown in the `before inputation` , `744-14 for Insulin, for instance` , it appears the before/after difference for `mean` , `std` , `min` , `max and quantiles` are quite small.

** Computation for `Outcome==1`

In [31]:
```
round(imputed_hc_df[imputed_hc_df['Outcome']==1].describe().T -  hc_df[hc_df['Outcome']==1].describe().T ,4)
```

Out[31]:

	count	mean	std	min	25%	50%	75%	max
Pregnancies	0.0	0.0000	0.0000	0.0	0.0000	0.0000	0.0000	0.0
Glucose	2.0	0.0003	-0.1110	0.0	0.0000	0.5000	0.0000	0.0
BloodPressure	16.0	-0.0706	-0.3211	0.0	0.0000	-0.5000	-2.0000	0.0
SkinThickness	88.0	-0.4615	-1.1542	0.0	0.0000	0.0000	-1.1387	0.0
Insulin	138.0	-6.1658	-29.5186	0.0	3.4362	8.5752	0.9089	0.0
BMI	2.0	-0.0049	-0.0239	0.0	0.0000	0.0000	-0.1500	0.0
DiabetesPedigreeFunction	0.0	0.0000	0.0000	0.0	0.0000	0.0000	0.0000	0.0
Age	0.0	0.0000	0.0000	0.0	0.0000	0.0000	0.0000	0.0
Outcome	0.0	0.0000	0.0000	0.0	0.0000	0.0000	0.0000	0.0

** Comment for `Outcome==1` :

- `count` : We successfully augmented the count for `SkinThickness` , `Insulin` , `BloodPressure` , `Glucose and MBI` as shown in the first column of the table above
- `mean` , `std` , `min` , `max and quantiles` : Given the magnitude of range (`max - min`) shown in the `before inputation` , `846-14 for Insulin, for instance` , it appears the before/after difference for `mean` , `std` , `min` , `max and quantiles` are quite small.

In conclusion, we can say the imputation has successfully improved the data without loosing any case.

But that does not mean that a thoughfully imputed dataset garantees a representative analysis result.

If there are significantly more of a particular outcome that others, the analysis results will be skeweb

if the dataset is not balance or a probability weight is not introduced.

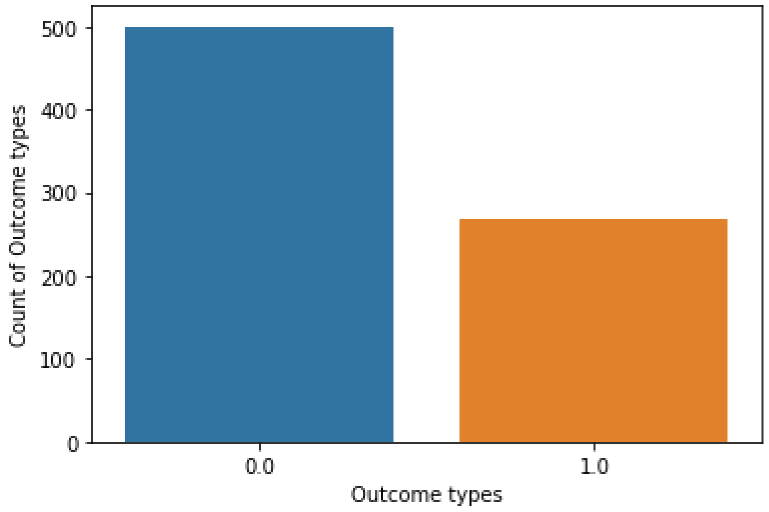
Let's see how balanced is the data after imputation.

In [32]:
```
print("Count for Outcome types : \n", imputed_hc_df['Outcome'].value_counts())
```

```
Count for Outcome types :
 0.0    500
1.0    268
Name: Outcome, dtype: int64
```

In [33]:
```
sns.countplot(imputed_hc_df['Outcome'])
plt.xlabel('Outcome types')
plt.ylabel('Count of Outcome types')
```

Out[33]:
```
Text(0, 0.5, 'Count of Outcome types')
```



The graph above show that about `2/3` of `Outcome` is `0` or `negative outcome` .
This implies that if we were to predict a 0 (negative outcome), we would have achieve an accuracy of 75% with the imbalanced data.

The data is imbalanced. Data imbalance can be addressed during (a) the analysis and interpretation
of results, including resampling methods or (b) at the model performance and evaluation metrics level, including chaging the metric and penalizing the algorithm computing the metric.

For this project, we are going to utilize the resampling method

to balance the dataset.

! pip install imbalanced-learn

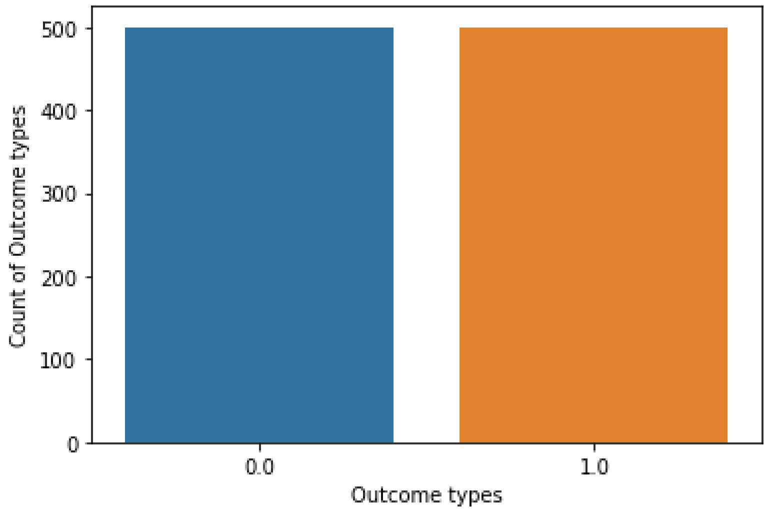
In [34]:
```
from sklearn.utils import resample
outcome_maj = imputed_hc_df[imputed_hc_df.Outcome==0]
outcome_min = imputed_hc_df[imputed_hc_df.Outcome==1]
upsample_outcome_min = resample(outcome_min, replace =True, n_samples = outcome_maj.shape[0], random_state= 9876)
#We can now put the balanced and imputed dataset together
bal_imp_hc_df = pd.concat([outcome_maj, upsample_outcome_min])
# Count
```

In [35]:
```
print('Count of the values of Outcome :\n',bal_imp_hc_df.Outcome.value_counts())
```

```
Count of the values of Outcome :
 0.0    500
1.0    500
Name: Outcome, dtype: int64
```

In [36]:
```
sns.countplot(bal_imp_hc_df.Outcome)
plt.xlabel('Outcome types')
plt.ylabel('Count of Outcome types')
```

Out[36]:
```
Text(0, 0.5, 'Count of Outcome types')
```



After oversampling the minority class, we now have `Outcome` values to be 50/50.

In [37]:

```
print('The shape of the data after oversampling \n {}'.format(bal_imp_hc_df.shape))
```

```
The shape of the data after oversampling 
 (1000, 9)
```

In [38]:

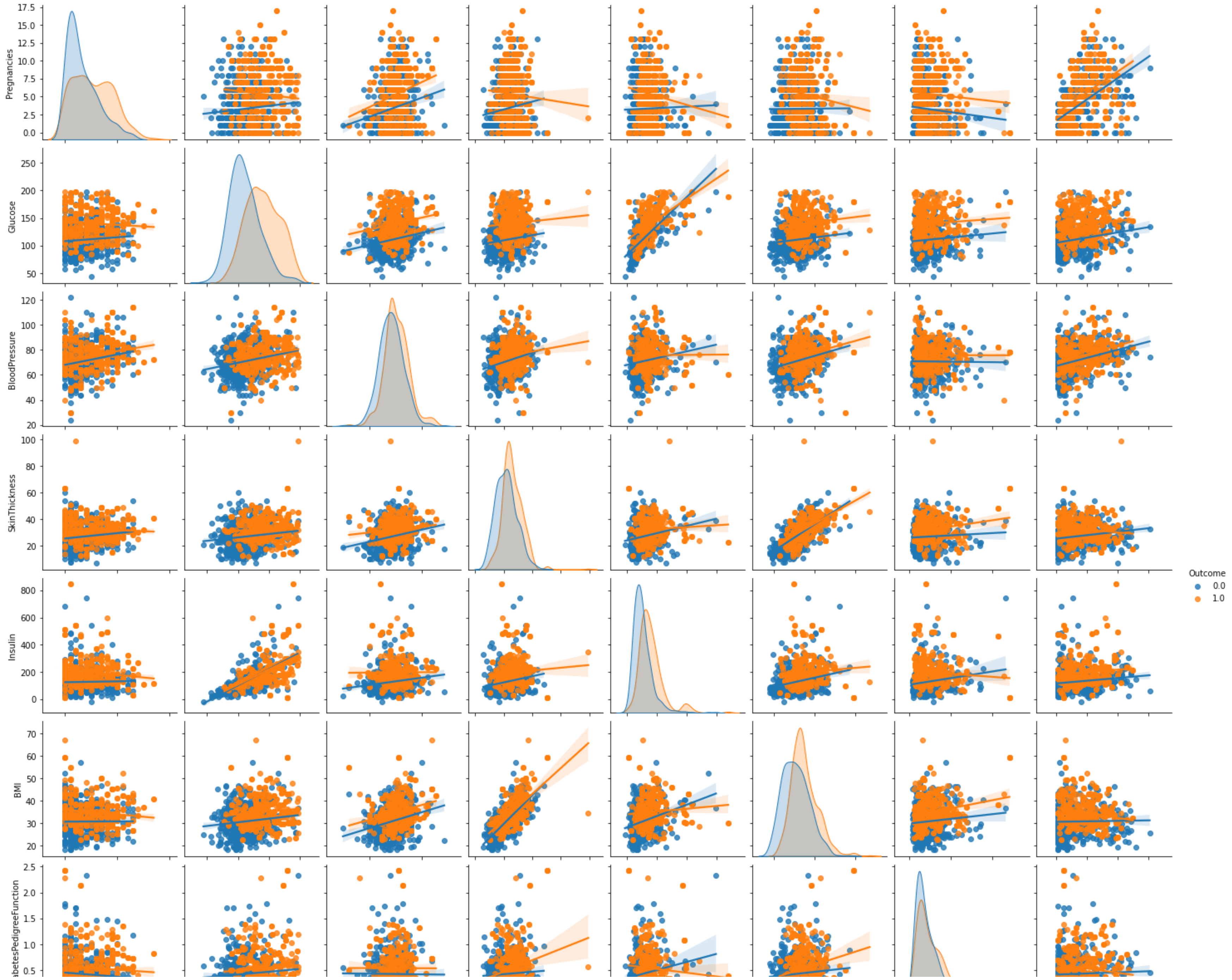
```
bal_imp_hc_df.info()
```

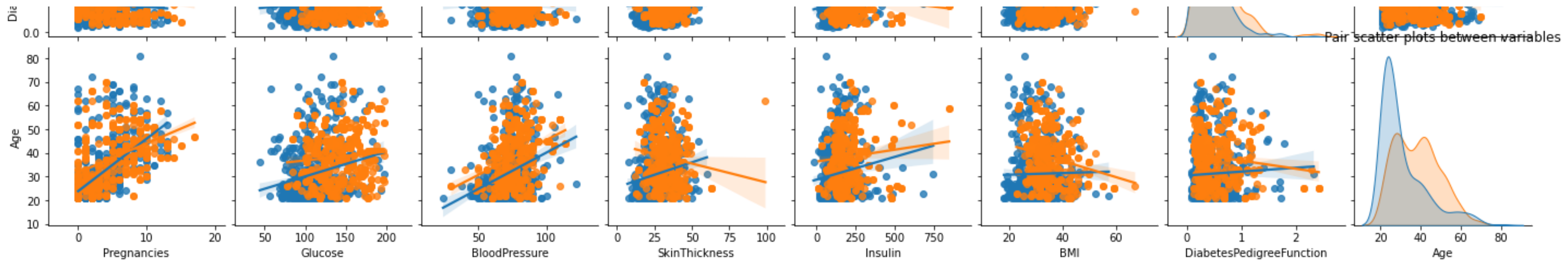
```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 1000 entries, 1 to 124
Data columns (total 9 columns):
 #   Column                    Non-Null Count  Dtype  
---  ------                    --------------  -----  
 0   Pregnancies               1000 non-null   float64
 1   Glucose                   1000 non-null   float64
 2   BloodPressure             1000 non-null   float64
 3   SkinThickness             1000 non-null   float64
 4   Insulin                   1000 non-null   float64
 5   BMI                       1000 non-null   float64
 6   DiabetesPedigreeFunction  1000 non-null   float64
 7   Age                       1000 non-null   float64
 8   Outcome                   1000 non-null   float64
dtypes: float64(9)
memory usage: 94.3 KB
```

In [39]:

```
sns.pairplot(bal_imp_hc_df, hue='Outcome', diag_kind='kde', kind = 'reg')
plt.title('Pair scatter plots between variables')
```

Out[39]:
```
Text(0.5, 1.0, 'Pair scatter plots between variables')
```





Frem the pairplot above, it appears there is a slight correlation between :

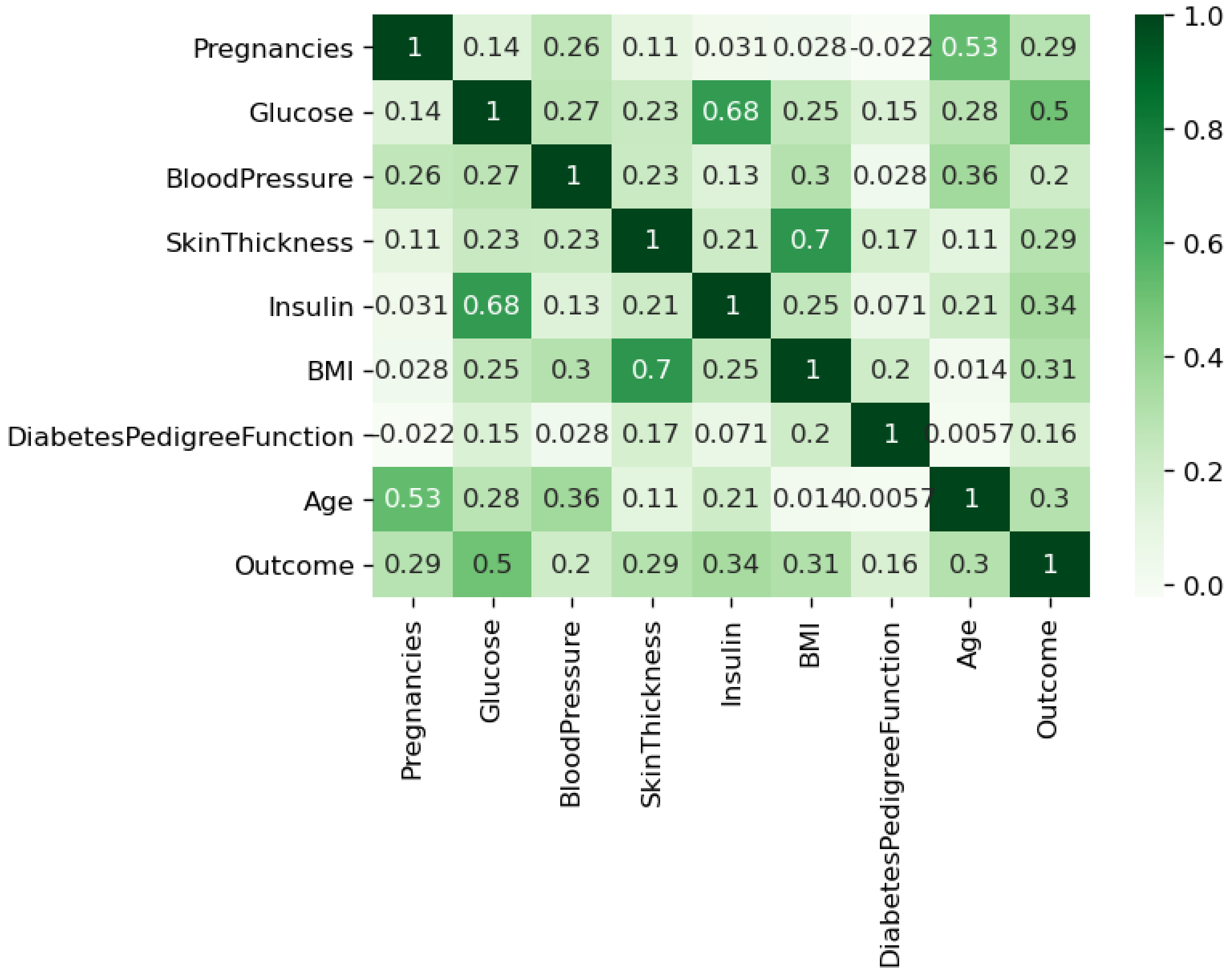
a-) `Glucose and Insulin`

b-) `SkinThickness and BMI`

Let's graph the correlation matrix too to confirm the above observation.

In [40]:
```
# Correlation heatmap
plt.figure(dpi=120)
sns.heatmap(bal_imp_hc_df.corr(), annot=True,cmap='Greens')
```

Out[40]:
```
<AxesSubplot:>
```



```
In [41]: bal_imp_hc_df.corr()['Outcome']
```

```
Out[41]: Pregnancies                 0.287039
         Glucose                     0.497589
         BloodPressure               0.204070
```

```
SkinThickness               0.291594
Insulin                     0.344833
BMI                         0.308442
DiabetesPedigreeFunction    0.160550
Age                         0.300631
Outcome                     1.000000
Name: Outcome, dtype: float64
```

As expected, the correlation matrix show the highest correlated pairs are :

`Glucose` and `Insulin` 0.68

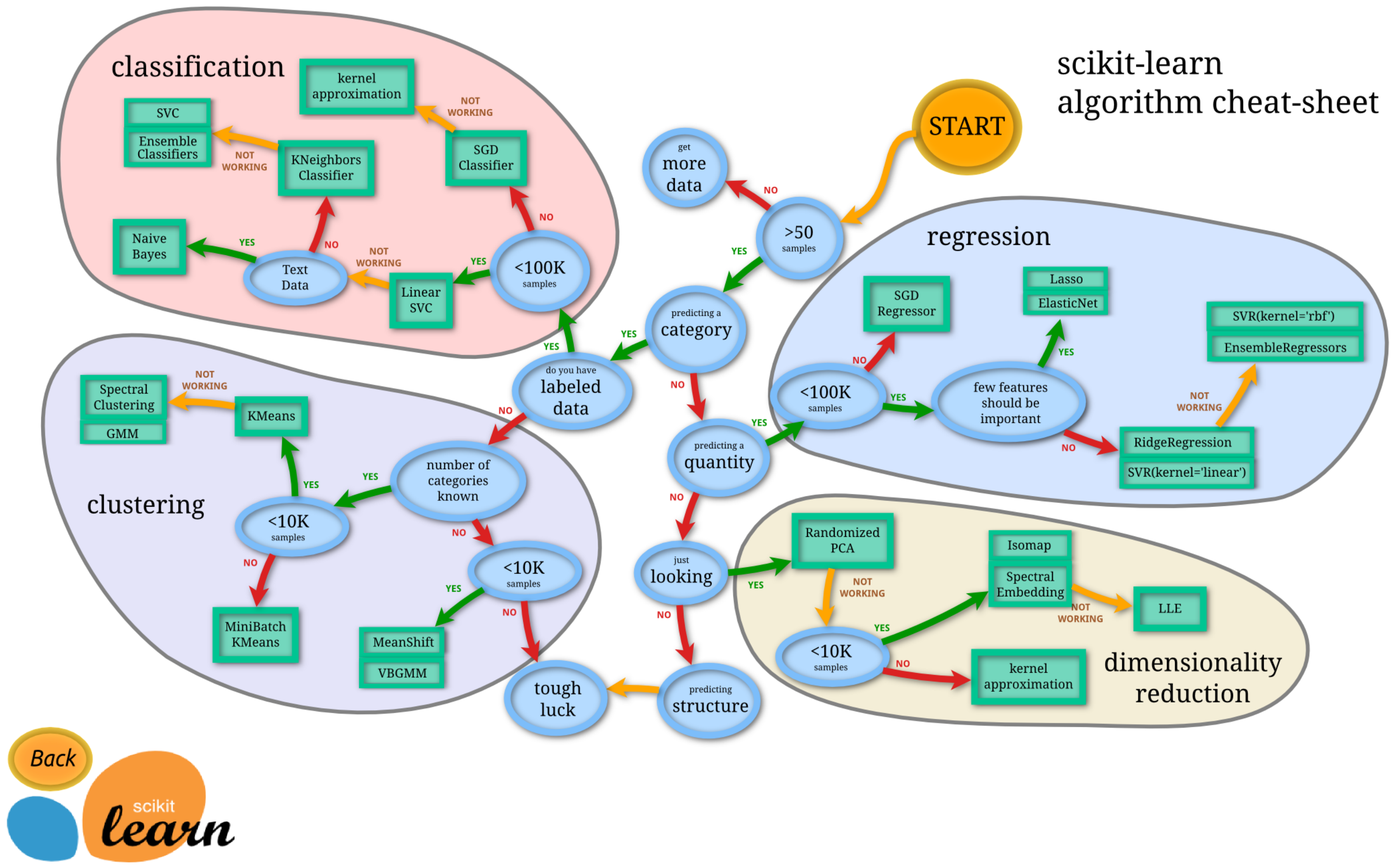
`SkinThickness` and `BMI` 0.7

The lest correlated pair are `Age` and `DiabetesPedigreeFunction` 0.0057.

Taking the factors individually, the most correlated to `Outcome` is `Glucose` (no surprise there)
followed by `Insulin` , then `BMI` , then `Age` , then `Pregnancies` and `Skinthickness` and
the least correlated with `Outcome` is `DiabetesPedigreeFunction` .
This ranking also gives us a rought indication of the princial components that, together, would bring the most variations
to `Outcome` , thus the best prediction power.

Data Modeling

Our data has labels, that is, `Outcome` variable.
We can therefore use a supervised learning algorithms to try to understand the relationship between:
(a) 'Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI', 'DiabetesPedigreeFunction', 'Age' on one side and
(b) `Outcome` on the other side.
Given the variables in `(a)` , we are trying to determine if a patient has diabetes `(Outcome ==1)` or not `(Outcome==0)`
This is a classification problem.
Now, which of the classification algorithms will give us the best prediction model?
The figure below from scikit-lean website shows us the path decide.



To figure out which classification model will yield the best prediction of `Outcome` ,
we can train test a few classification model then evaluate the performance then choose the highest performing model.

Strategies for model building and selection.

We will attempt several models to see their performance using Area Under the Curve score (AUC).
We will then choose the best performing model (or combination of model).

** Following scikit-learn's diagram above, I will model the data with the following 5 `estimators` :
1) Support Vector machines (SVM)
2) KNeighbors Classifier
3) three (3) Ensemble Classifiers (RandomForestClassifier, ExtraTreesClassifier and XGBoost)

In the first round of model selection, I will look at the `performance report card` of the `estimators` :
`precision` , `recall` and `f1-score` . The top 3 estimators will then be further evaluated by `parameter tuning` for their individual best performance on the data
Then they will be ranked by their `AUC score` .

** Split,Train and evaluate

In [42]:
```
## Model algorights to test on data

from sklearn.svm import SVC
from sklearn.neighbors import KNeighborsClassifier
from sklearn.ensemble import RandomForestClassifier, ExtraTreesClassifier
import xgboost as xgb # !pip install xgboost (if not already installed)
from xgboost import XGBClassifier

# Methods for model Selection
from sklearn.model_selection import train_test_split, KFold, cross_val_score,GridSearchCV
# Methods for model performance evaluation
from sklearn.metrics import classification_report, roc_auc_score, accuracy_score, mean_squared_error
```

In [43]:
```
X, y = bal_imp_hc_df.drop('Outcome',axis=1), bal_imp_hc_df['Outcome']
X_train, X_test, y_train, y_test = train_test_split( X , y, test_size=0.3, random_state=9876)
```

In [44]:
```
print(f'Shape of the training and testing splits: \n X_train ==> {X_train.shape} \n X_test ==> {X_test.shape} \n y_train
```

```
Shape of the training and testing splits:
 X_train ==> (700, 8)
 X_test ==> (300, 8)
 y_train ==> (700,)
 y_test ==> (300,)
```

Performance report card:Precision, recall and f1-score

Performance report card: Support Vector Machines

In [45]:
```
model = SVC()
model.fit(X_train, y_train)
y_train_hat = model.predict(X_train)
y_test_hat = model.predict(X_test)

print(model)
print(f'Train performance \n ====================================================' )
print(classification_report(y_train, y_train_hat))

print(f'Test performance \n ====================================================' )
print(classification_report(y_test, y_test_hat))

print(f'Roc_auc score \n ====================================================' )
print(roc_auc_score(y_test, y_test_hat))
```

```
SVC()
Train performance
 ====================================================
              precision    recall  f1-score   support

         0.0       0.80      0.69      0.74       346
         1.0       0.73      0.83      0.78       354

    accuracy                           0.76       700
   macro avg       0.77      0.76      0.76       700
weighted avg       0.77      0.76      0.76       700

Test performance
 ====================================================
              precision    recall  f1-score   support

         0.0       0.76      0.64      0.69       154
         1.0       0.67      0.79      0.73       146

    accuracy                           0.71       300
   macro avg       0.72      0.71      0.71       300
weighted avg       0.72      0.71      0.71       300

Roc_auc score
 ====================================================
0.7120174346201744
```

Performance report card: K-Neighbors

In [46]:
```
model = KNeighborsClassifier()
```

```
model.fit(X_train, y_train)
y_train_hat = model.predict(X_train)
y_test_hat = model.predict(X_test)

print(model)
print(f'Train performance \n =====================================================' )
print(classification_report(y_train, y_train_hat))

print(f'Test performance \n =====================================================' )
print(classification_report(y_test, y_test_hat))

print(f'Roc_auc score \n =====================================================' )
print(roc_auc_score(y_test, y_test_hat))
```

```
KNeighborsClassifier()
Train performance
 =====================================================
              precision    recall  f1-score   support

         0.0       0.88      0.75      0.81       346
         1.0       0.79      0.90      0.84       354

    accuracy                           0.83       700
   macro avg       0.83      0.82      0.82       700
weighted avg       0.83      0.83      0.82       700

Test performance
 =====================================================
              precision    recall  f1-score   support

         0.0       0.84      0.66      0.74       154
         1.0       0.71      0.86      0.78       146

    accuracy                           0.76       300
   macro avg       0.77      0.76      0.76       300
weighted avg       0.77      0.76      0.76       300

Roc_auc score
 =====================================================
0.7626756804838997
```

Performance report card: Random Forest

In [47]:

```
model = RandomForestClassifier(n_jobs=-1,random_state=9876)
model.fit(X_train, y_train)
y_train_hat = model.predict(X_train)
y_test_hat = model.predict(X_test)
```

```
print(model)
print(f'Train performance \n ====================================================' )
print(classification_report(y_train, y_train_hat))

print(f'Test performance \n ====================================================' )
print(classification_report(y_test, y_test_hat))

print(f'Roc_auc score \n ====================================================' )
print(roc_auc_score(y_test, y_test_hat))
```

```
RandomForestClassifier(n_jobs=-1, random_state=9876)
Train performance
 ====================================================
              precision    recall  f1-score   support

         0.0       1.00      1.00      1.00       346
         1.0       1.00      1.00      1.00       354

    accuracy                           1.00       700
   macro avg       1.00      1.00      1.00       700
weighted avg       1.00      1.00      1.00       700

Test performance
 ====================================================
              precision    recall  f1-score   support

         0.0       0.94      0.76      0.84       154
         1.0       0.79      0.95      0.86       146

    accuracy                           0.85       300
   macro avg       0.86      0.85      0.85       300
weighted avg       0.86      0.85      0.85       300

Roc_auc score
 ====================================================
0.8524728695961572
```

Performance report card: Extra Trees

In [48]:

```
model = ExtraTreesClassifier(random_state=9876)
model.fit(X_train, y_train)
y_train_hat = model.predict(X_train)
y_test_hat = model.predict(X_test)
print(model)
print(f'Train performance \n ====================================================' )
print(classification_report(y_train, y_train_hat))
print(f'Test performance \n ====================================================' )
print(classification_report(y_test, y_test_hat))

print(f'Roc_auc score \n ====================================================' )
print(roc_auc_score(y_test, y_test_hat))
```

```
ExtraTreesClassifier(random_state=9876)
Train performance
 ====================================================
              precision    recall  f1-score   support

         0.0       1.00      1.00      1.00       346
         1.0       1.00      1.00      1.00       354

    accuracy                           1.00       700
   macro avg       1.00      1.00      1.00       700
weighted avg       1.00      1.00      1.00       700

Test performance
 ====================================================
              precision    recall  f1-score   support

         0.0       0.91      0.80      0.85       154
         1.0       0.81      0.92      0.86       146

    accuracy                           0.86       300
   macro avg       0.86      0.86      0.86       300
weighted avg       0.86      0.86      0.86       300

Roc_auc score
 ====================================================
0.8582547589396905
```

Performance report card: XGBoost

In [49]:

```
model = XGBClassifier(random_state=9876)
model.fit(X_train, y_train)
y_train_hat = model.predict(X_train)
y_test_hat = model.predict(X_test)

print(model)
print(f'Train performance \n ====================================================' )
print(classification_report(y_train, y_train_hat))

print(f'Test performance \n ====================================================' )
print(classification_report(y_test, y_test_hat))
print(f'Roc_auc score \n ====================================================' )
print(roc_auc_score(y_test, y_test_hat))
```

```
[00:01:43] WARNING: C:/Users/Administrator/workspace/xgboost-win64_release_1.4.0/src/learner.cc:1095: Starting in XGBoost
1.3.0, the default evaluation metric used with the objective 'binary:logistic' was changed from 'error' to 'logloss'. Exp
licitly set eval_metric if you'd like to restore the old behavior.
XGBClassifier(base_score=0.5, booster='gbtree', colsample_bylevel=1,
              colsample_bynode=1, colsample_bytree=1, gamma=0, gpu_id=-1,
              importance_type='gain', interaction_constraints='',
              learning_rate=0.300000012, max_delta_step=0, max_depth=6,
              min_child_weight=1, missing=nan, monotone_constraints='()',
              n_estimators=100, n_jobs=8, num_parallel_tree=1,
              random_state=9876, reg_alpha=0, reg_lambda=1, scale_pos_weight=1,
              subsample=1, tree_method='exact', validate_parameters=1,
              verbosity=None)
Train performance
 ====================================================
              precision    recall  f1-score   support

         0.0       1.00      1.00      1.00       346
         1.0       1.00      1.00      1.00       354

    accuracy                           1.00       700
   macro avg       1.00      1.00      1.00       700
weighted avg       1.00      1.00      1.00       700

Test performance
 ====================================================
              precision    recall  f1-score   support

         0.0       0.93      0.75      0.83       154
         1.0       0.78      0.94      0.85       146

    accuracy                           0.84       300
   macro avg       0.86      0.85      0.84       300
weighted avg       0.86      0.84      0.84       300

Roc_auc score
 ====================================================
0.8458014588151574
```

Parameter tuning: Model optimization.

Out of the 5 algorithms tested above, I will retain the best 3 AUC score.

Random forest, XGBoost and ExtraTrees

I will tune their parameters to increase AUC score, by uing cross-validation method `GridSearchCV` .

In [50]:
```
from sklearn.model_selection import GridSearchCV, KFold
```

Parameter tuning: Random forest

In [51]:
```
params = {
    'n_estimators': [100, 200, 400],
    'criterion': ['gini', 'entropy'],
    'min_samples_split': [1,2,4,5],
    'min_samples_leaf': [1,2,4,5],
    'max_leaf_nodes': [4,10,20,50,None]
}

rf_gs = GridSearchCV(RandomForestClassifier(n_jobs=-1,random_state=9876), params, n_jobs=-1, cv=KFold(n_splits=3), scorir
rf_gs.fit(X_train, y_train)
y_pred = rf_gs.predict(X_test)
print(f'Best score for Random Forest:, {rf_gs.best_score_} \n Best parameters found for Random Forest: {rf_gs.best_params
```

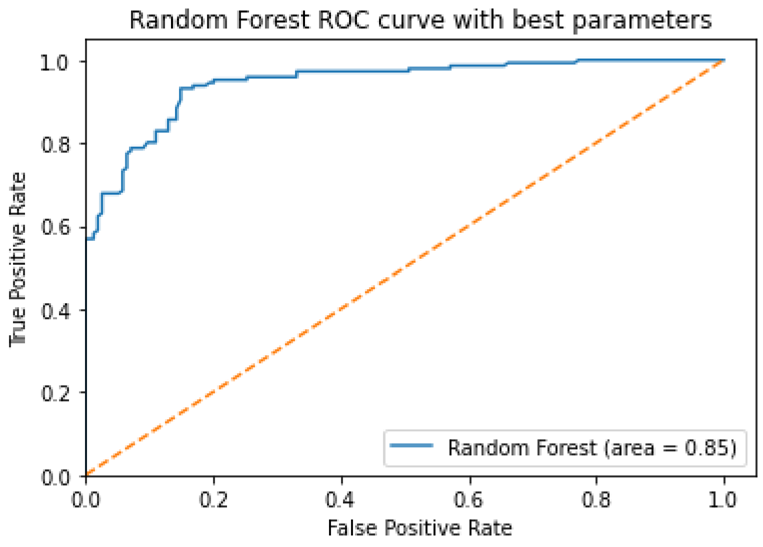
```
Best score for Random Forest:, 0.9211961442955007
 Best parameters found for Random Forest: {'criterion': 'gini', 'max_leaf_nodes': None, 'min_samples_leaf': 1, 'min_sampl
es_split': 2, 'n_estimators': 400}
```

AUC score: Randon Forest

In [52]:
```
from sklearn.metrics import roc_auc_score
from sklearn.metrics import roc_curve
rf_roc_auc = roc_auc_score(y_test, rf_gs.predict(X_test))
fpr, tpr, thresholds = roc_curve(y_test, rf_gs.predict_proba(X_test)[:,1])

plt.figure()
plt.plot(fpr, tpr, label='Random Forest (area = %0.2f)' % rf_roc_auc)
plt.plot([0, 1], [0, 1],'--')
plt.xlim([0.0, 1.05])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Random Forest ROC curve with best parameters')
plt.legend(loc="lower right")
plt.savefig('RF_ROC')
print('Area Under Curve: %.3f' % rf_roc_auc)
plt.show()
```

```
Area Under Curve: 0.853
```



Parameter tuning: XGBoost

In [53]:

```
params = {
    'n_estimators': [100, 200, 400],
    'learning_rate': [0.01,0.05,0.1],
    'booster': ['gbtree', 'gblinear'],
    'gamma': [0, 0.5, 1],
    'reg_alpha': [0, 0.5, 1],
    'base_score': [0.2, 0.5, 1]
}

xgb_gs = GridSearchCV(XGBClassifier(n_jobs=-1, random_state=9876), params, n_jobs=-1, cv=KFold(n_splits=3), scoring='roc_
xgb_gs.fit(X_train, y_train)
print(f'Best score for XGBoost:, {xgb_gs.best_score_} \n Best parameters found for XGBoost: {xgb_gs.best_params_}')
```

```
[00:06:11] WARNING: C:/Users/Administrator/workspace/xgboost-win64_release_1.4.0/src/learner.cc:1095: Starting in XGBoost
1.3.0, the default evaluation metric used with the objective 'binary:logistic' was changed from 'error' to 'logloss'. Exp
licitly set eval_metric if you'd like to restore the old behavior.
Best score for XGBoost:, 0.8942791755040348
 Best parameters found for XGBoost: {'base_score': 0.2, 'booster': 'gbtree', 'gamma': 0, 'learning_rate': 0.1, 'n_estimat
ors': 200, 'reg_alpha': 1}
```

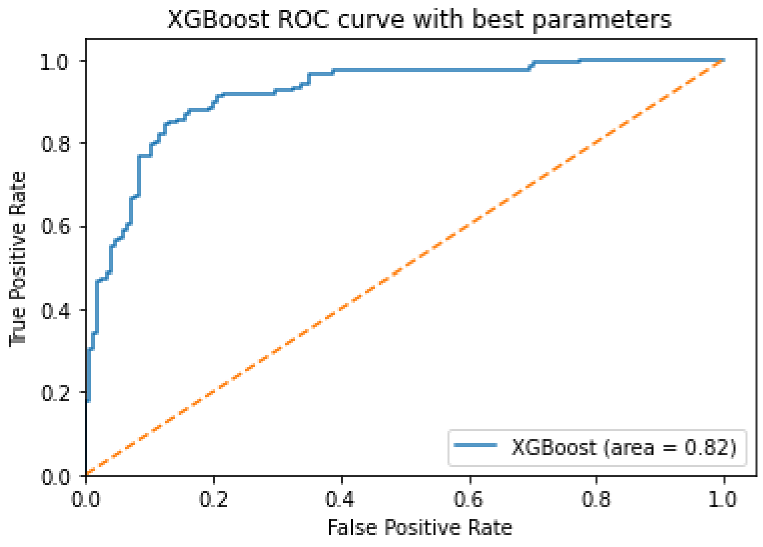
AUC score: XGBoost

In [54]:

```
xgb_roc_auc = roc_auc_score(y_test, xgb_gs.predict(X_test))
fpr, tpr, thresholds = roc_curve(y_test, xgb_gs.predict_proba(X_test)[:,1])
```

```
plt.figure()
plt.plot(fpr, tpr, label='XGBoost (area = %0.2f)' % xgb_roc_auc)
plt.plot([0, 1], [0, 1],'--')
plt.xlim([0.0, 1.05])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('XGBoost ROC curve with best parameters')
plt.legend(loc="lower right")
plt.savefig('XGB_ROC')
print('Area Under Curve: %.3f' % xgb_roc_auc)
plt.show()
```

```
Area Under Curve: 0.819
```



Parameter tuning: Extra Trees

In [55]:
```
params = {
    'n_estimators': [100, 200, 400],
    'criterion': ['gini', 'entropy'],
    'min_samples_split': [1,2,4,6],
    'min_samples_leaf': [1,2,4,6],
    'max_leaf_nodes': [4,10,20,40,None]
}

et_gs = GridSearchCV(ExtraTreesClassifier(n_jobs=-1, random_state=9876), params, n_jobs=-1, cv=KFold(n_splits=3), scoring
et_gs.fit(X_train, y_train)
print(f'Best score for ExtraTrees:, {et_gs.best_score_} \n Best parameters found for ExtraTrees: {et_gs.best_params_}')
```

```
Best score for ExtraTrees:, 0.9333230375818872
 Best parameters found for ExtraTrees: {'criterion': 'entropy', 'max_leaf_nodes': None, 'min_samples_leaf': 1, 'min_sampl
es_split': 2, 'n_estimators': 400}
```

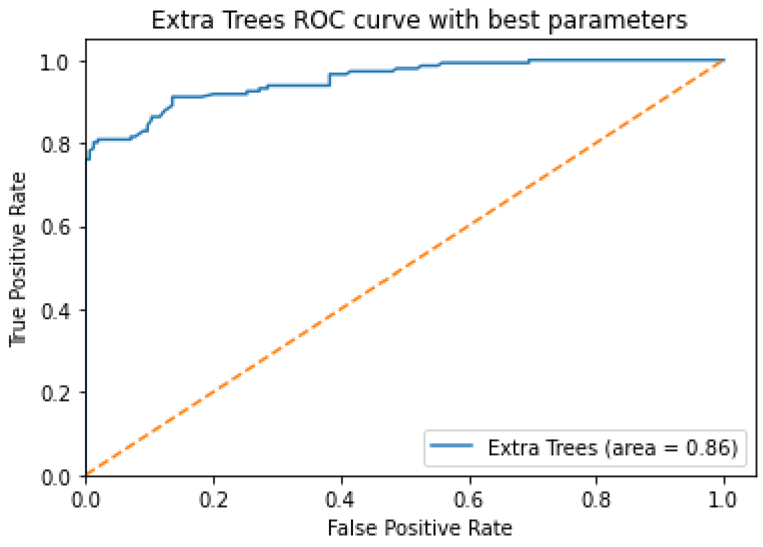
AUC score: Extra Trees

In [56]:

```
et_roc_auc = roc_auc_score(y_test, et_gs.predict(X_test))
fpr, tpr, thresholds = roc_curve(y_test, et_gs.predict_proba(X_test)[:,1])

plt.figure()
plt.plot(fpr, tpr, label='Extra Trees (area = %0.2f)' % et_roc_auc)
plt.plot([0, 1], [0, 1],'--')
plt.xlim([0.0, 1.05])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Extra Trees ROC curve with best parameters')
plt.legend(loc="lower right")
plt.savefig('ET_ROC')
print('Area Under Curve: %.3f' % et_roc_auc)
plt.show()
```

```
Area Under Curve: 0.855
```



Conclusion: Model selection

We can see that Extra Trees has the best ability to predict with this dataset.

With a AUC score of 86%, Extra Trees perfomed better than Random Forest 85%, then XGBoost with 82%.

KNN didn't even make ti to the top 3

```
In [ ]:
```