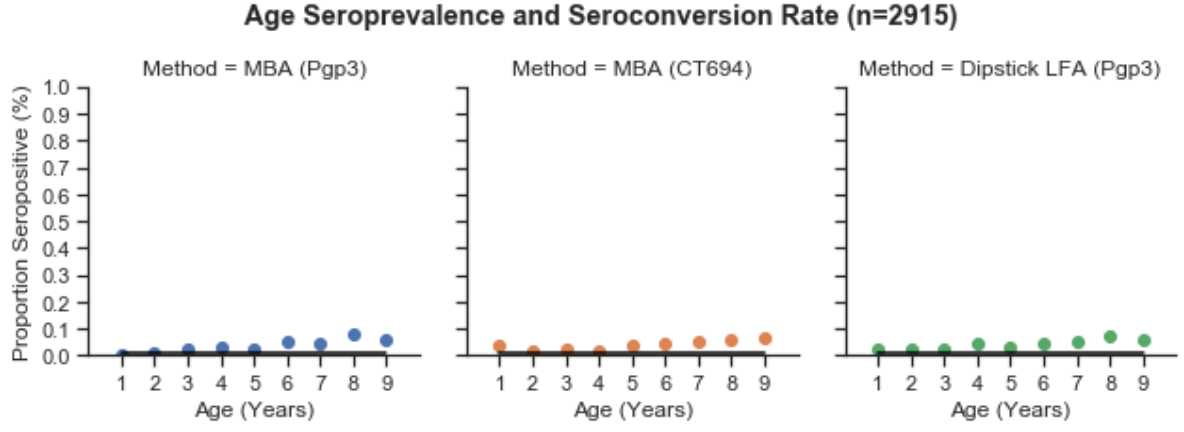
In [1]:
```
%load_ext watermark
%watermark -a "Jessica Randall"
```

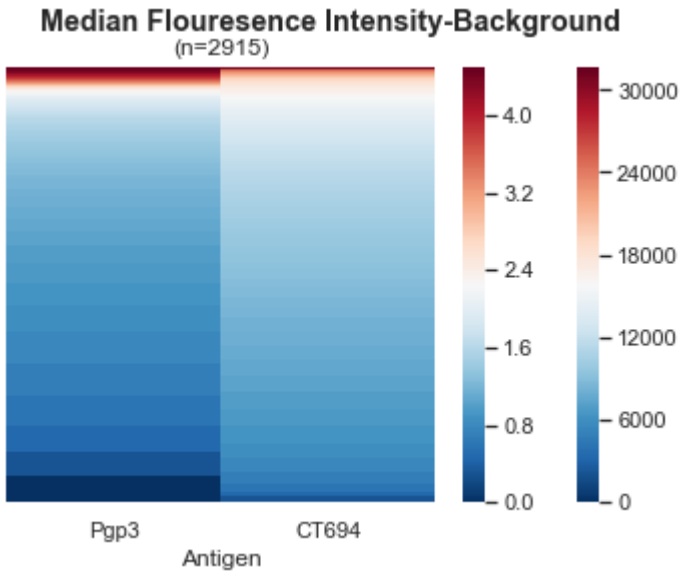
```
Jessica Randall
```

In [2]:
```
#import libraries
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import matplotlib.gridspec as gridspec
import numpy as np
```

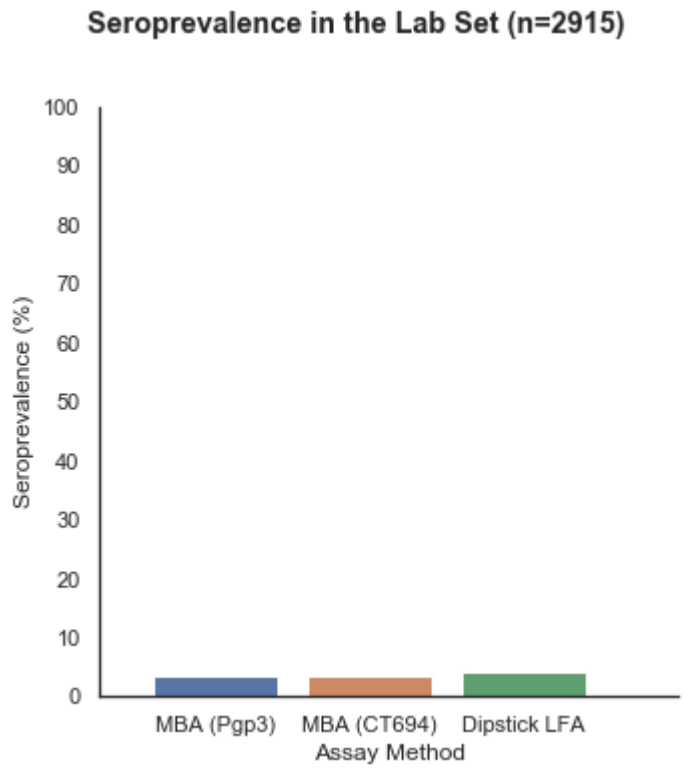
In [3]:
```
#Age Seroprevalence and Seroconversion Rate

#read in the dataframes
ageprev=pd.read_csv("ageseroprev.csv") #age seroprevalence in the lab set all
 percentages are listed as whole numbers without '%' signs for ease of graphin
g
ageprev.dropna()
ageprev

#set style
sns.set(style="ticks", color_codes=True)

#read in SCR data with each age graph
scrfacet=pd.read_csv("scrtable.csv") #age seroprevalence in the lab set
scrfacet

#plot a facetgrid
l=sns.FacetGrid(scrfacet, col="Method", hue="Method", sharex=True, sharey=True
, xlim=[0,10], ylim=[0, 1.0])
l=(l.map(plt.plot,"Age (Years)","MeanSCRAllAge",color='black').set(xlim=(0,10
), ylim=(0,1.0),

#specify tick marks
xticks=[1,2,3,4,5,6,7,8,9],
yticks=[0,0.1,0.3,0.5,0.7,0.9,1.0]))

#scatter plot
l=(l.map(plt.scatter,"Age (Years)","Proportion Seropositive (%)").set(xlim=(0,
10), ylim=(0,1.0),

#specify tick marks
xticks=[1,2,3,4,5,6,7,8,9],
yticks=[0,0.1,0.2,0.3,0.4,0.5,0.6,0.7,0.8,0.9,1.0]))

#define axes
plt.suptitle('Age Seroprevalence and Seroconversion Rate (n=2915)', fontweight
='bold',  y=1.08)
plt.ylabel=("Proportion Seropositive (%)")

#save graph as jpeg
l.savefig("scrfacets.png",bbox_inches='tight', dpi=700, frameon=True)
```



In [4]:
```
#MFI HeatMap

#set style
sns.set(style="white")

#read in both dataframes
#heatmap not log transformed
heatmapnolog=pd.read_csv("heatmapnolog.csv")
#heatmap log transformed
heatmaplog=pd.read_csv("heatmaplog.csv")

#define figure name
h = plt.figure()

#graph both log transformed and untransformed data to get both axes
ax=sns.heatmap(heatmapnolog, cmap=("RdBu_r"),cbar=True, xticklabels=True, ytic
klabels=False)
ax=sns.heatmap(heatmaplog, cmap=("RdBu_r"),cbar=True, xticklabels=True, ytickl
abels=False)

#define axes
ax.invert_yaxis()
plt.xlabel("Antigen")
plt.title("(n=2915)")
plt.suptitle('Median Flouresence Intensity-Background', fontweight='bold' )
plt.locator_params(nbins=10)
plt.show()

#save and export all lines to jpeg
h.savefig("mfiheatmap.png", bbox_inches='tight', dpi=300, frameon=True)
```



In [5]:
```
#Seroprevalence in the Lab Dataset

#read in lab seroprevalence graph data
seroprevlab=pd.read_csv("seroprevlab.csv")

#setup a category plot graph
h =sns.catplot(x='Assay Method', y='Seroprevalence (%)', data=seroprevlab, kin
d="bar").set(xlim=(0,4), ylim=(0,100), yticks=[0,10, 20, 30,40,50,60,70,80,90,
100])

#define axes
plt.suptitle('Seroprevalence in the Lab Set (n=2915)', fontweight='bold', y=1.
08)
plt.axis([-0.75, 3, 0, 100])
plt.show()

#save as a jpeg
h.savefig("seroposlab.jpeg", bbox_inches='tight', dpi=300, frameon=True)
```



In [6]:
```
#Seroprevalence in Field Dataset

#read in the dataframe
seroposfieldeu=pd.read_csv("seroprevfield.csv")
seroposfieldeu #seropositivity across assays in the field set

#graph a category plot
s = sns.catplot(x='Assay Method', y=' Seroprevalence (%)',
                data=seroposfieldeu, kind="bar").set(xlim=(0,4),
                ylim=(0,100),

#define ticks and axes
yticks=[0,10, 20, 30,40,50,60,70,80,90,100])
plt.axis([-0.75, 3, 0, 100])
plt.xticks(rotation=45)
plt.axis([-1, 4, 0, 100])
plt.suptitle('Seroprevalence in the Field Set (n=1914)',
             fontweight='bold', y=1.08)
plt.show()

#save as jpeg
s.savefig("seroposfield.jpeg", bbox_inches='tight', dpi=300, frameon=True)
```