Index

March 31, 2020

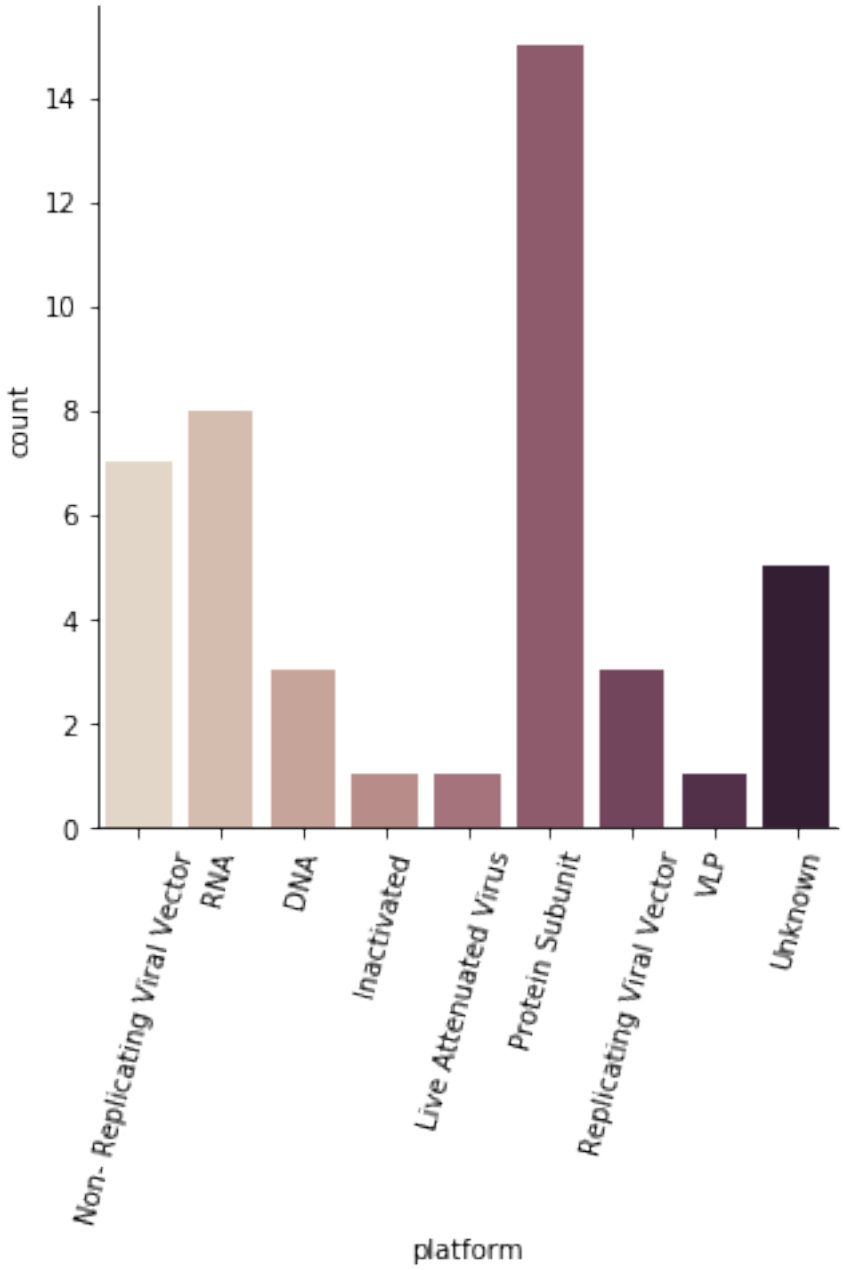
[1]:
```
{
    "tags": [
        "hide_input",
    ]
}

import pandas as pd

import tabula

import requests

from ggplot import *

import seaborn as sns

import matplotlib.pyplot as plt

import numpy as np

#url = 'https://milkeninstitute.org/sites/default/files/2020-03/
 ↪Covid19-Tracker-3-36-20-FINAL.pdf'

url = 'https://www.who.int/blueprint/priority-diseases/key-action/
 ↪novel-coronavirus-landscape-ncov.pdf?ua=1'

myfile = requests.get(url)
open('COVID19-data.pdf', 'wb').write(myfile.content)

#declare the path of your file
file_path = "COVID19-data.pdf"
#Convert your file
df = tabula.read_pdf(file_path, pages='all', lattice=True,multiple_tables=False)
#df = df[10]
#df = df.drop(index=0)
df = df[0]
df = df.dropna(axis=0,thresh=5)
```

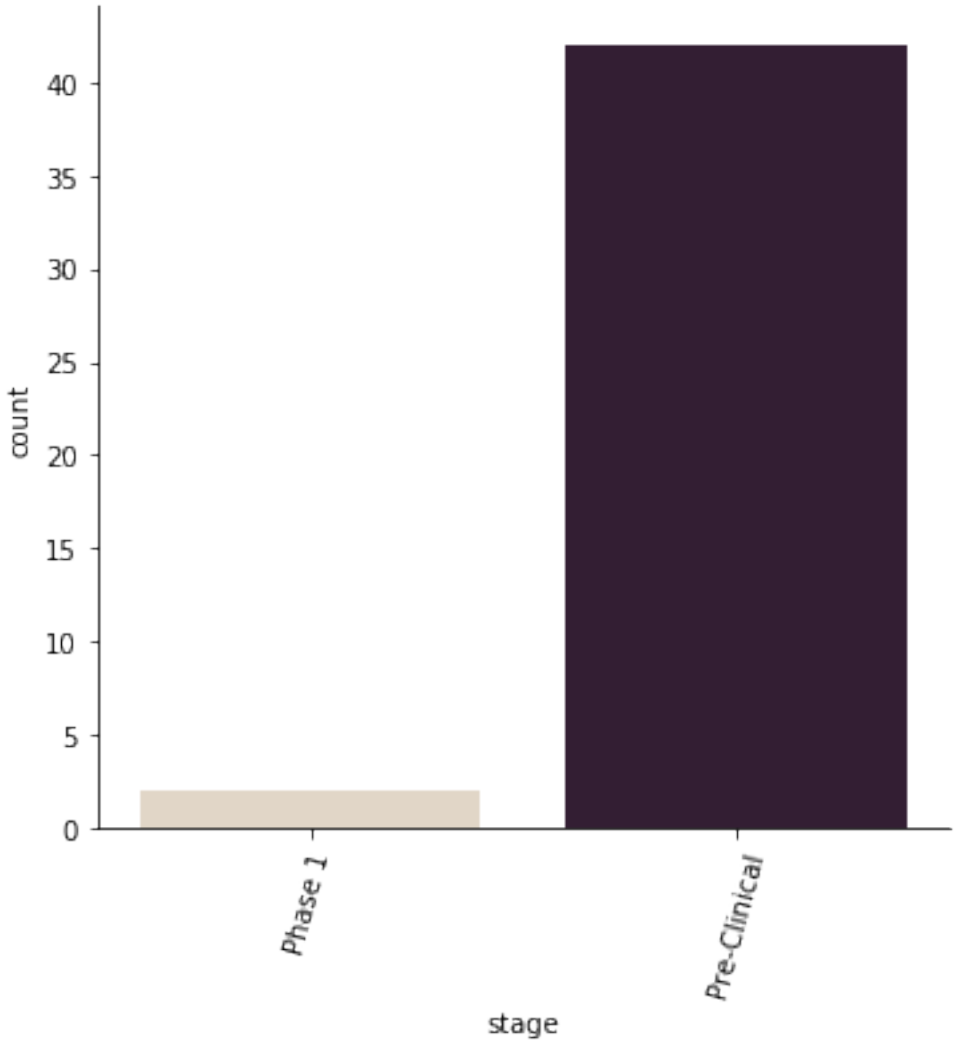
```
#%% Clean the data


df.columns = ['platform', 'type_product', 'developer', 'covid', 'stage',
              'other']

a = df['platform'].values
aa = df['stage'].values
b = []

for i in range(len(a)):
    #aa[i] = aa[i].replace('\r',' ')
    b.append(a[i].replace('\r',' '))
    if b[i] == 'Platform':
        b[i] = np.nan

df['platform'] = b

# Evaluate the different trial types
stages = ['Pre-Clinical', 'Phase 1', 'Phase 2', 'Phase 3']

c = df['stage'].values
stage_list = []

for i in range(len(c)):
    stage = c[i]
    for j in range(len(stages)):
        if stages[j] in stage:
            stage_list.append(stages[j])
    if len(stage_list)<i+1:
            stage_list.append(np.nan)


df['stage'] = stage_list


#%% Plot

chart = sns.catplot(x="platform", kind="count", palette="ch:.25", data=df);

chart.set_xticklabels(rotation=75)


chart2 = sns.catplot(x="stage", kind="count", palette="ch:.25", data=df);

chart2.set_xticklabels(rotation=75)
```

```
#%%
#plt.figure()
#plat_count = df['platform'].value_counts()
#chart3 = sns.barplot(plat_count.index, plat_count.values, alpha=0.
↪8,palette="ch:.25")
#plt.setp(chart3.get_xticklabels(), rotation=90)
#plt.xlabel('Vaccine Platform')
#plt.ylabel('Count')
```

```
Got stderr: Mar 27, 2020 10:31:19 AM
org.apache.pdfbox.pdmodel.font.PDCIDFontType2 <init>
INFO: OpenType Layout tables used in font BCDGEE+Calibri-Light are not
implemented in PDFBox and will be ignored
Mar 27, 2020 10:31:20 AM org.apache.pdfbox.pdmodel.font.PDCIDFontType2 <init>
INFO: OpenType Layout tables used in font BCDIEE+Calibri are not implemented in
PDFBox and will be ignored
```

[1]: <seaborn.axisgrid.FacetGrid at 0x1a183c3590>


14
12
10
8
6
4
2
0
count
Non- Replicating Viral Vector
RNA
DNA
Inactivated
Live Attenuated Virus
Protein Subunit
Replicating Viral Vector
VLP
Unknown
platform


40
35
30
25
20
15
10
5
0
count
Phase 1
Pre-Clinical
stage

[ ]: