HN analysis part 2 - ANALYSIS 15-12-2016

December 15, 2016

```
In [1]: import pandas as pd
        import numpy as np
        import matplotlib.pyplot as plt
        %matplotlib inline
        from scipy import stats
        from scipy.stats import wilcoxon  # must import explicitly
        import seaborn as sns
        sns.set(style="whitegrid", palette="pastel", color_codes=True)
```

0.1 Helper functions

```
In [2]: def diff_percent(Dm,AAA):
            return 100*((Dm-AAA)/AAA)

        print(diff_percent(105.0,100.0))

5.0
```

```
In [3]: def my_wilcox(data):                        # helper function to return p-value
            z_stat, p_val = wilcoxon(data)    # if only 1 value passed
            #z_stat, p_val = wilcoxon(data.as_matrix())    # if only 1 value passed
            return p_val

In [4]: my_wilcox([1,2,3,4,6,7,2,352,3])

C:\Users\RCole02.ROYALSURREY\AppData\Local\Continuum\Anaconda3\lib\site-packages\sc
  warnings.warn("Warning: sample size too small for normal approximation.")

Out[4]: 0.0075792819433897285

In [5]: def query_data(df, Col, structure, metric):    # helper function to get data
            return df[Col][(df['structure'] == structure) & (df['metric'] == metric
```

1 Start analysis

```
In [6]: HN_df = pd.read_csv('HN_df_clean_28_11.csv')  # read in the cleaned data
        HN_df['Dm-AAA'] = HN_df['Dm'] - HN_df['AAA'] # get abs diff
        HN_df['Dm-AAA%'] = diff_percent(HN_df['Dm'], HN_df['AAA'])
```

Exclude Case5 which has 54 Gy prescription

```
In [7]: to_exclude = ['Case5', 'Case7']  # has prescription of 54 Gy
        to_include = list(set(HN_df['Case'].unique()) - set(to_exclude))
        HN_df = HN_df[HN_df['Case'].isin(to_include)]
        HN_df['Case'].unique()

Out[7]: array(['Case1', 'Case2', 'Case3', 'Case4', 'Case6', 'Case8', 'Case9',
               'Case10'], dtype=object)

In [8]: HN_df.head()

Out[8]:     Case structure metric        AAA         Dm    Dm-AAA    Dm-AAA%
        0  Case1      PTV2    D2%  65.392496  64.671451 -0.721045  -1.102642
        1  Case1      PTV2    D5%  61.221910  60.574434 -0.647476  -1.057589
        2  Case1      PTV2   D50%  56.935482  56.306392 -0.629090  -1.104918
        3  Case1      PTV2   D95%  52.908380  53.783883  0.875503   1.654753
        4  Case1      PTV2   D99%  38.261698  45.021250  6.759552  17.666628
```

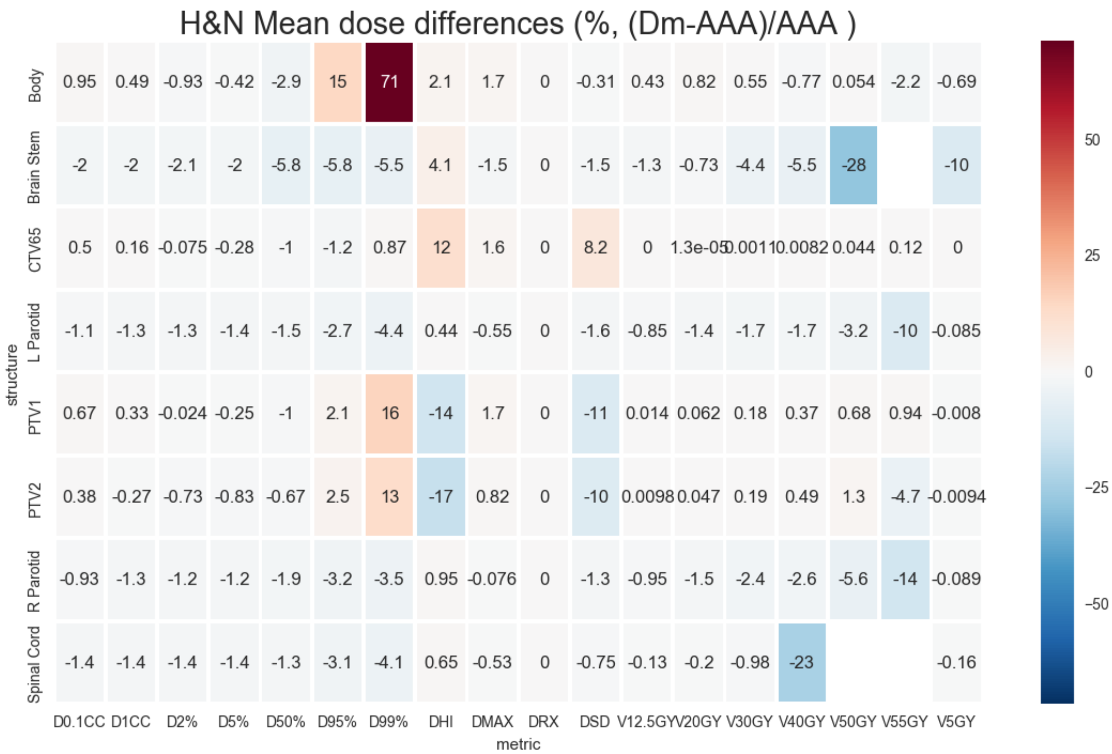
Everything imported OK

1.1 Get mean dose differences

```
In [9]: mean_diff_table = HN_df.groupby(['structure', 'metric'],as_index=False).mea

In [10]: #metrics_of_interest = [ 'D95%', 'D50%', 'D99%', 'D0.1CC', 'DMAX']  # use
         metrics_of_interest = mean_diff_table.columns                           # use a

In [11]: plt.figure(figsize=(14, 8))
         ax1 = sns.heatmap(mean_diff_table[metrics_of_interest], annot=True, linewi
         ax1.set_title('H&N Mean dose differences (%, (Dm-AAA)/AAA )', size='xx-lar
         plt.savefig('H&N Mean dose difference.png', dpi=200)
```



1.2 Get wilcoxon p value of differences

```
In [12]: metrics_of_interest = [ 'D95%', 'D50%', 'D0.1CC', 'DMAX']  # use limited s
         #HN_df['structure'].unique()  # all structures
         structures_of_interest = ['PTV1', 'PTV2', 'CTV65', 'L Parotid', 'R Parotic
```

```
In [13]: i = len(structures_of_interest)
         j = len(metrics_of_interest)
         wilcox_data = np.zeros((i,j))  # init an empty array
```

```
In [14]: d = HN_df  # for convenience just copy

         j = 0
         for structure in structures_of_interest:
             i = 0
             for metric in metrics_of_interest:
                 A =  d[(d['structure'] == structure) & (d['metric'] == metric)]
                 D =  A['Dm-AAA%']
                 wilcox_data[j][i] = my_wilcox(D.values)
                 i = i + 1
             j = j+ 1
```

```
C:\Users\RCole02.ROYALSURREY\AppData\Local\Continuum\Anaconda3\lib\site-packages\sc
  warnings.warn("Warning: sample size too small for normal approximation.")
```

In [15]:
```
wilcox_data_df = pd.DataFrame(data=wilcox_data,     # values
...                  index=structures_of_interest,    # 1st column as index
...                  columns=metrics_of_interest)  # 1st row as the column nam
```

In [16]:
```
# Keep for plotting all p-vals

#confidence = 1.0
#plt.figure(figsize=(16, 8))
#ax2 = sns.heatmap(wilcox_data_df[wilcox_data_df<confidence], annot=True,
#ax2.set_title('HN p- value for mean dose differences (%) by structure and
#plt.savefig('HN p value for mean dose differences.png', dpi=500)
```

In [17]:
```
sub_diff_table = mean_diff_table[metrics_of_interest].loc[structures_of_in
```

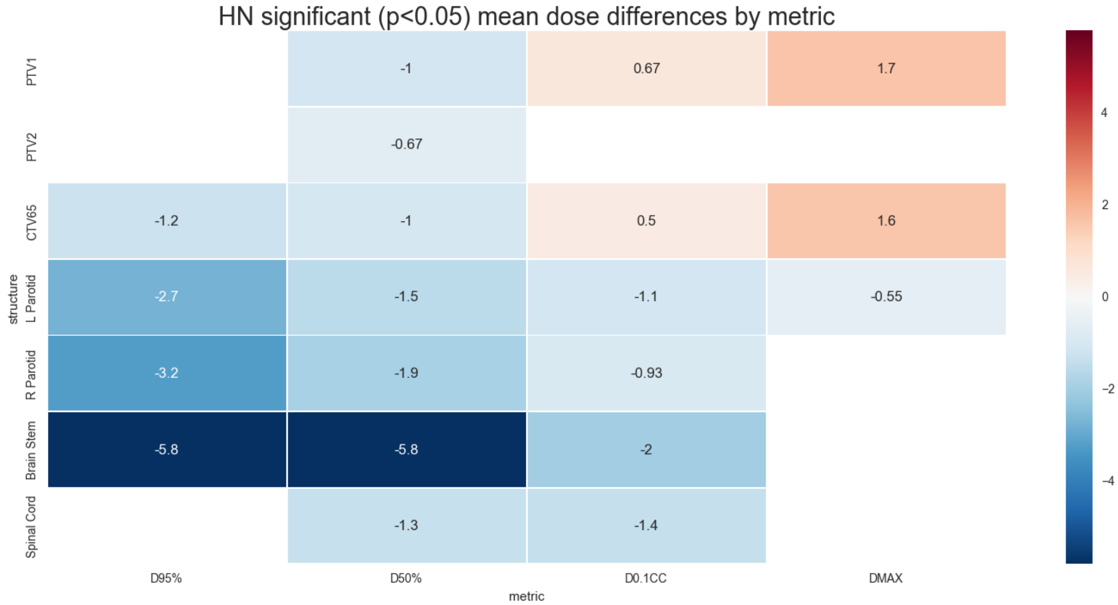
In [18]:
```
plt.figure(figsize=(18, 8))
data = sub_diff_table[wilcox_data_df<0.05]
mask = np.zeros_like(data, dtype=np.bool)   # create a mask
mask[np.triu_indices_from(mask)] = True

ax3 = sns.heatmap(data, annot=True, linewidths=.5, center=0) #  mask=mask,
ax3.set_title('HN significant (p<0.05) mean dose differences by metric', s

#plt.savefig('HN significant mean dose differences by metric.png', dpi=500
print('Mean differences')
print(sub_diff_table)
print('*****************')
print('p-vals of differences')
print(wilcox_data_df)
```

```
Mean differences
metric            D95%      D50%    D0.1CC      DMAX
structure
PTV1          2.104196 -1.041277  0.674281  1.666932
PTV2          2.514504 -0.665242  0.377605  0.819839
CTV65        -1.239658 -1.039090  0.496371  1.584108
L Parotid    -2.725370 -1.549682 -1.059832 -0.545207
R Parotid    -3.243811 -1.857180 -0.934542 -0.076388
Brain Stem   -5.783298 -5.783946 -2.001884 -1.487810
Spinal Cord -3.117142 -1.316931 -1.364837 -0.534718
*****************
p-vals of differences
                  D95%      D50%    D0.1CC      DMAX
PTV1          0.400814  0.011719  0.011719  0.035692
PTV2          0.092892  0.035692  0.483840  0.123485
CTV65         0.017290  0.011719  0.035692  0.017290
L Parotid     0.035692  0.011719  0.011719  0.035692
R Parotid     0.035692  0.017290  0.017290  0.483840
Brain Stem    0.017290  0.011719  0.011719  0.068704
```

```
Spinal Cord  0.092892  0.017290  0.011719  0.326989
```



2 Investigate differences

```
In [22]: def AAA_diff_plot(Dm, AAA, structure, metric, *args, **kwargs):
             Dm      = np.asarray(Dm)    # convert to arrays
             AAA      = np.asarray(AAA)
             z_stat, p_val = wilcoxon(Dm, AAA)

             diff_pct = diff_percent(Dm, AAA)
             AAA_norm_pct = diff_percent(AAA, AAA.mean()) # how far is a measuremen

             plt.scatter(AAA_norm_pct, diff_pct, linewidths=3, *args, **kwargs)

             plt.axhline(diff_pct.mean(), color='red', linestyle='--')  # horitz li
             plt.axvline(0, color='k', linestyle='--')  # v line

             plt.title('Dm ' + str(np.round(diff_pct.mean(), decimals = 3)) + ' % m
             plt.ylabel('Dm - AAA difference (%)')
             plt.xlabel('AAA - AAA.mean difference (%)')

In [23]: structure = 'PTV1'
         metric = 'D50%'
         plt.figure(figsize=(6, 4))
         #bland_altman_plot(query_data(HN_df, 'Dm', structure, metric), query_data
         AAA_diff_plot(query_data(HN_df, 'Dm', structure, metric), query_data(HN_df
```

```
plt.show()
HN_df[(HN_df['structure'] == structure) & (HN_df['metric'] == metric)]
```

```
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```

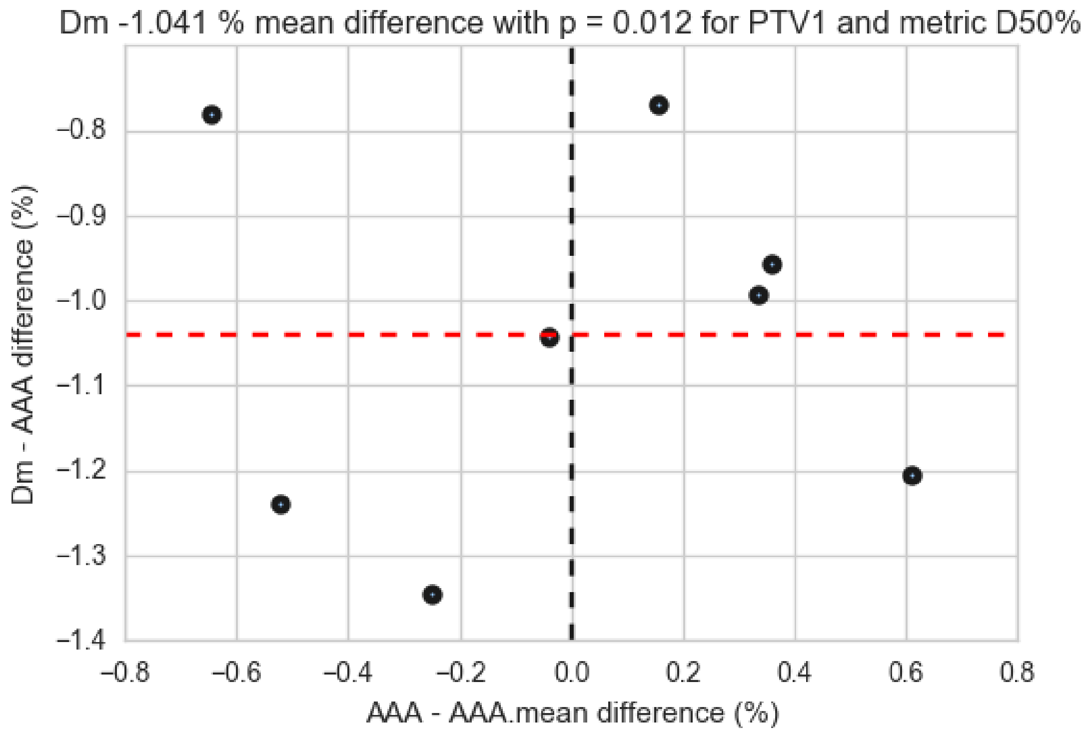

Out[23]:

	Case	structure	metric	AAA	Dm	Dm-AAA	Dm-AAA%
20	Case1	PTV1	D50%	68.559571	67.733731	-0.825840	-1.204558
164	Case2	PTV1	D50%	68.250510	67.725632	-0.524878	-0.769047
308	Case3	PTV1	D50%	68.372452	67.693337	-0.679114	-0.993257
452	Case4	PTV1	D50%	68.388653	67.734436	-0.654217	-0.956616
740	Case6	PTV1	D50%	67.787586	66.948429	-0.839157	-1.237922
1028	Case8	PTV1	D50%	68.116240	67.405729	-0.710511	-1.043086
1262	Case9	PTV1	D50%	67.705087	67.176668	-0.528418	-0.780471
1406	Case10	PTV1	D50%	67.973479	67.059061	-0.914418	-1.345257

In [24]:
```
structure = 'PTV1'
metric = 'DMAX'
plt.figure(figsize=(6, 4))
AAA_diff_plot(query_data(HN_df, 'Dm', structure, metric), query_data(HN_df
#bland_altman_plot(query_data(HN_df, 'Dm', structure, metric), query_data
plt.show()
HN_df[(HN_df['structure'] == structure) & (HN_df['metric'] == metric)]
```

```
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  warnings.warn("Warning: sample size too small for normal approximation.")
```

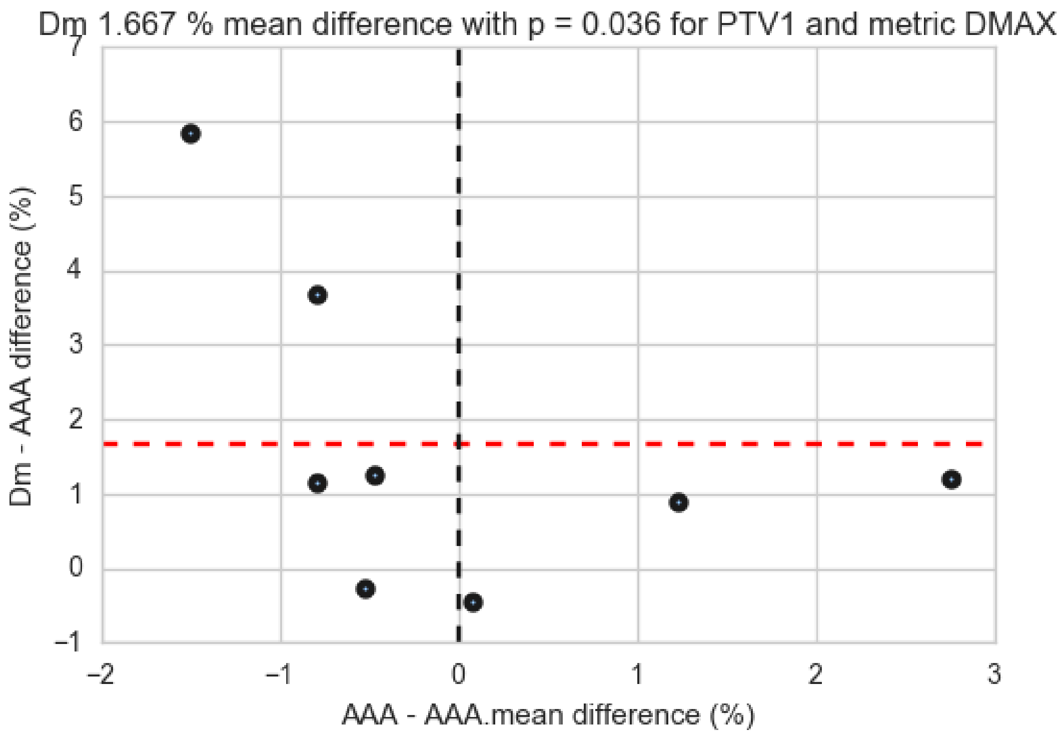

Out[24]:

	Case	structure	metric	AAA	Dm	Dm-AAA	Dm-AAA%
25	Case1	PTV1	DMAX	73.32000	72.99500	-0.32500	-0.443262
169	Case2	PTV1	DMAX	75.28158	76.19172	0.91014	1.208981
313	Case3	PTV1	DMAX	74.16500	74.83000	0.66500	0.896649
457	Case4	PTV1	DMAX	72.92000	73.83500	0.91500	1.254800
745	Case6	PTV1	DMAX	72.16110	76.38675	4.22565	5.855856
1033	Case8	PTV1	DMAX	72.68118	73.52631	0.84513	1.162791
1267	Case9	PTV1	DMAX	72.68118	75.34659	2.66541	3.667263
1411	Case10	PTV1	DMAX	72.87621	72.68118	-0.19503	-0.267618

In [ ]: