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robmarkcole / Useful-python-for-medical-physics

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Useful-python-for-medical-physics / Experiments in ipython notebooks / pyEclipseDVH / Bladder\_plan\_comparison 5-4-2017.ipynb

 robmarkcole Various edits to remove old work

2c4aa84 on 5 Apr 2017

1 contributor

448 lines (447 sloc) 78.2 KB

```
In [1]: from pyEclipseDVH_v2 import List_txt, Load_patient, get_dmin, get_dmax, get_d_metric, Load_files_t
o_df
%matplotlib inline
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt

In [2]: Prescription = 36.0 # Gy

In [3]: def diff_to_prescribed(dose, Prescribed_dose):
        return 100.0 + 100.0*(dose-Prescribed_dose)/Prescribed_dose

In [4]: txt_files = List_txt()
txt_files

Out[4]: ['Planned_plan_RC_export.txt', 'Replan_RC_export.txt']

In [5]: multi_df = Load_files_to_df(txt_files)

Planned_plan_RC_export.txt loaded          patID:X12345 PlanID:Planned and number of structures is 6
Replan_RC_export.txt loaded          patID:X12345 PlanID:Replanned and number of structures is 5

In [6]: multi_df.to_csv('All_data.csv')
```

For processing, drop the patID level since it is unchanged and this causes errors in my custom get\_dose functions]

```
In [7]: multi_df.columns = multi_df.columns.droplevel()
multi_df.head()
```

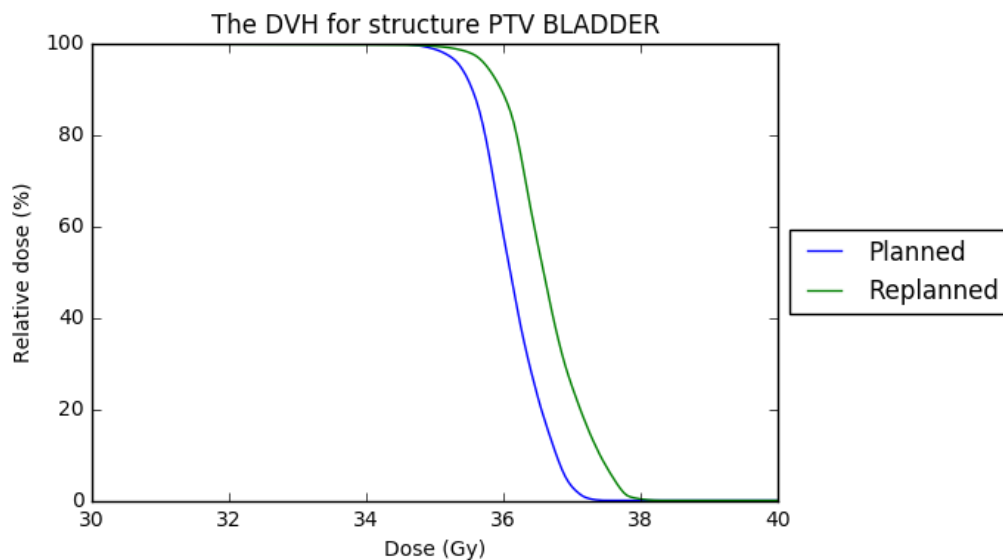
Out[7]:

planID	Planned						Replanned				
Structure	BODY	CTV36Gy	L Femoral Head	PTV BLADDER	R Femoral Head	Rectum	CTV36Gy	L Femoral Head	PTV BLADDER	R Femoral Head	Rectum
Dose (Gy)											
0.00	100.000000	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
0.05	99.967853	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
0.10	99.710568	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0

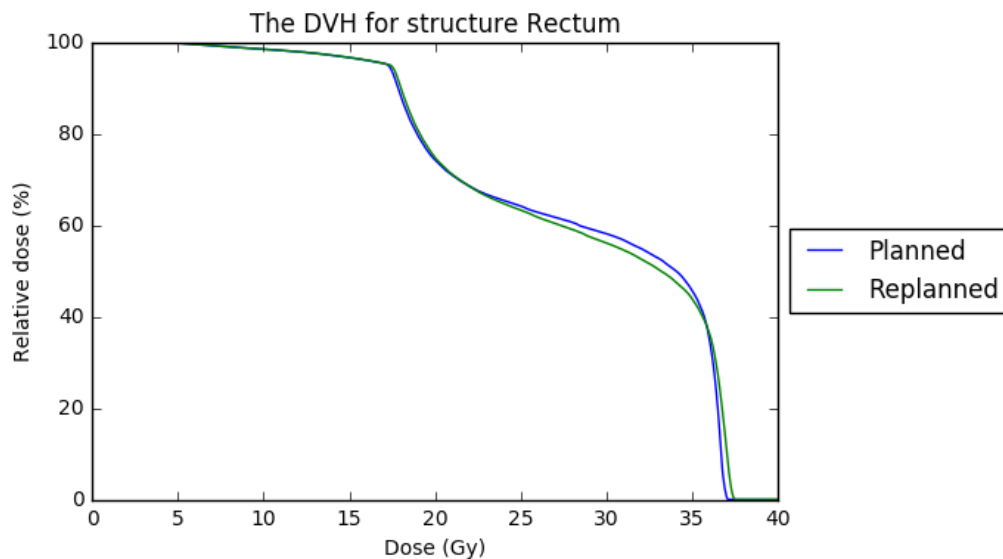
<b>0.15</b>	98.967167	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
<b>0.20</b>	96.848389	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0

```
In [8]: def plot_structure(structure, xlim):
        multi_df.xls(structure, level='Structure', axis=1).plot()
        plt.legend(loc='center left', bbox_to_anchor=(1, 0.5))
        plt.title('The DVH for structure ' + structure)
        plt.ylabel('Relative dose (%)')
        plt.xlim(xlim)
        return

        structure = 'PTV BLADDER'
        plot_structure(structure, xlim=[30,40])
```



```
In [9]: structure = 'Rectum'
        plot_structure(structure, xlim=[0,40])
```



```
In [10]: def d50(df):
         return diff_to_prescribed(get_d_metric(df, 50.0), Prescription)
```

```
In [11]: d50_df = multi_df.apply(d50)      # function of form lambda function that takes a single argument
```

```
In [15]: d50_df
```

```
Out[15]: planID      Structure
         Planned      BODY          2.650682
          CTV36Gy      99.967557
          L Femoral Head 61.680973
          PTV BLADDER  100.271376
```

```
      R Femoral Head      60.645708
      Rectum              94.564767
Replanned CTV36Gy        101.221269
      L Femoral Head      61.565716
      PTV BLADDER         101.619544
      R Femoral Head      61.015640
      Rectum              92.089050
dtype: float64
```

```
In [22]: for item in d50_df.index.values:
          print(item)
```

```
('Planned', 'BODY')
('Planned', 'CTV36Gy')
('Planned', 'L Femoral Head')
('Planned', 'PTV BLADDER')
('Planned', 'R Femoral Head')
('Planned', 'Rectum')
('Replanned', 'CTV36Gy')
('Replanned', 'L Femoral Head')
('Replanned', 'PTV BLADDER')
('Replanned', 'R Femoral Head')
('Replanned', 'Rectum')
```

```
In [25]: d50_df[('Planned', 'CTV36Gy')]
```

```
Out[25]: 99.967557445299192
```

```
In [26]: d50_df[('Replanned', 'CTV36Gy')]
```

```
Out[26]: 101.22126906797547
```

```
In [ ]:
```