Analyse case7 dicompyler-core 28-11-2016

November 28, 2016

Metrics show high PTV dose and low brain stem dose in this case

In [1]:
```
%matplotlib inline
import os
import numpy as np
import dicom as dicom
from dicompylercore import dicomparser, dvh, dvhcalc
import matplotlib.pyplot as plt
import urllib.request
import os.path
from ipywidgets import FloatSlider, interactive, interact
from scipy.misc import imresize
from scipy import interpolate
from pylinac.core.image import ArrayImage
import copy
import scipy.ndimage.filters as spf
```

1 Helpers

In [3]:
```
def f_info(file_):    # pass a dicomparser object, e.g. AAA
    print('****')
    print('position = ' + str( file_.GetDoseData()['position']  ))
    print('dosegridscaling = ' + str( file_.GetDoseData()['dosegridscaling'
    print('frames = ' + str( file_.GetDoseData()['frames']  ))
    print('rows = ' + str( file_.GetDoseData()['rows']  ))
    print('columns = ' + str( file_.GetDoseData()['columns']  ))
    print('pixelspacing = ' + str( file_.GetDoseData()['pixelspacing']  ))
    #print('GridFrameOffsetVector = ' + str( file_.ds.GridFrameOffsetVecto
    print('dosemax (pix) = ' + str( file_.GetDoseData()['dosemax']  ))
    print('dosemax (Gy) = ' + str( file_.GetDoseData()['dosemax'] * file_.G
    #print('samplesperpixel = ' + str( file_.GetDoseData()['samplesperpixel
```

In [4]:
```
def get_dose_array(rtdose):   # e.g. rtdose = AAA dicomparser object, retur
    x = rtdose.GetDoseData()['rows']
    y = rtdose.GetDoseData()['columns']
    z = rtdose.GetDoseData()['frames']
    rtdose_array = np.zeros((x, y, z))  # create 3d array for data
```

```
        planes = (np.array(rtdose.ds.GridFrameOffsetVector) * rtdose.ds.ImageOr
        for i, plane in enumerate(planes):  # put dose data in 3d array
            rtdose_array[:, :, i] = rtdose.GetDoseGrid(plane)
        rtdose_array = rtdose_array* rtdose.GetDoseData()['dosegridscaling']
        return(rtdose_array)

    # plt.imshow(get_dose_array(AAA)[:,:, 50]);   # exampleusage
```

1.1 Analysis

```
In [5]: Structures_set = dicomparser.DicomParser('Case7_structures.dcm')
        AAA = dicomparser.DicomParser('Case7_dose_AAA.dcm')    # a dicomparser obje
        Dm = dicomparser.DicomParser('Case7_dose_Dm.dcm')

In [6]: f_info(AAA)

****
position = ['-244.4338517', '-178.5440886', '-216.25']
dosegridscaling = 6.501e-5
frames = 135
rows = 107
columns = 192
pixelspacing = ['2.5', '2.5']
dosemax (pix) = 1066131.0
dosemax (Gy) = 69.30917631


In [7]: f_info(Dm)

****
position = ['-245.6838517', '-179.7940886', '-216.25']
dosegridscaling = 7.8024484e-5
frames = 135
rows = 108
columns = 193
pixelspacing = ['2.5', '2.5']
dosemax (pix) = 942825.0
dosemax (Gy) = 73.5634341273
```

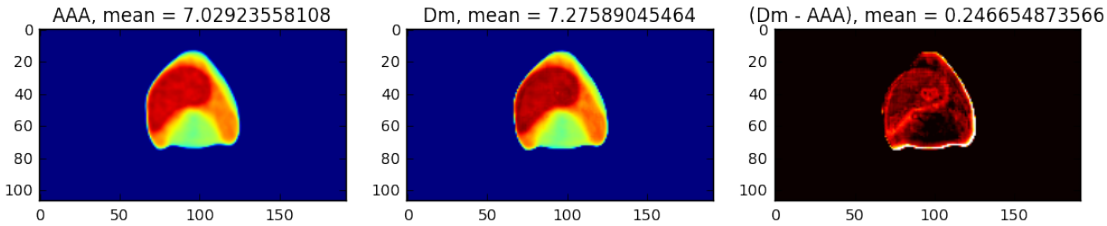
1.1.1 Get dose grids, crop array to match

```
In [8]: AAA_dose = get_dose_array(AAA)
        print(AAA_dose.shape)
        x = AAA_dose.shape[0]
        y = AAA_dose.shape[1]
        print('***')

        Dm_dose = get_dose_array(Dm)
```

```
        print(Dm_dose.shape)
        Dm_dose = Dm_dose[:x,:y, :]  # put on same grid
        print(Dm_dose.shape)
```

```
(107, 192, 135)
***
(108, 193, 135)
(107, 192, 135)
```

In [9]:
```
        y = FloatSlider(
            value=75,
            min=0,
            max=135,
            step=1,
            description='Slice Position in numpy:',
        )

        def showdoseboth(z):

            AAA_display = AAA_dose[:,:,z]
            Dm_display  = Dm_dose[:,:,z]
            cmin = min(AAA_display.min(), Dm_display.min())  # use identical colour
            cmax = max(AAA_display.max(), Dm_display.max())  # use identical colour

            f, (ax1, ax2, ax3) = plt.subplots(1, 3, figsize=(12, 18))

            ax1.imshow(AAA_display, vmin = cmin, vmax = cmax)  # , vmin=0, vmax=cma
            ax1.set_title('AAA, mean = ' + str(np.mean(AAA_display)))

            ax2.imshow(Dm_display,  vmin = cmin, vmax = cmax)     # , vmin=0,vmax=c
            ax2.set_title('Dm, mean = ' + str(np.mean(Dm_display)))

            # Difference analysis
            difference_display = (Dm_display - AAA_display)
            ax3.imshow(difference_display, cmap='hot', vmin = 0.0, vmax = 10.0) #
            ax3.set_title('(Dm - AAA), mean = ' + str(np.mean(difference_display)))

            plt.show()


        interactive(showdoseboth, z=75)
```



1.2 DVH analysis

```
In [10]: structures = Structures_set.GetStructures()  # returns a dict of structure

         for i, structure in enumerate(structures):
             print(str(i+1) +  '    ' + structures[structure]['name'])
```

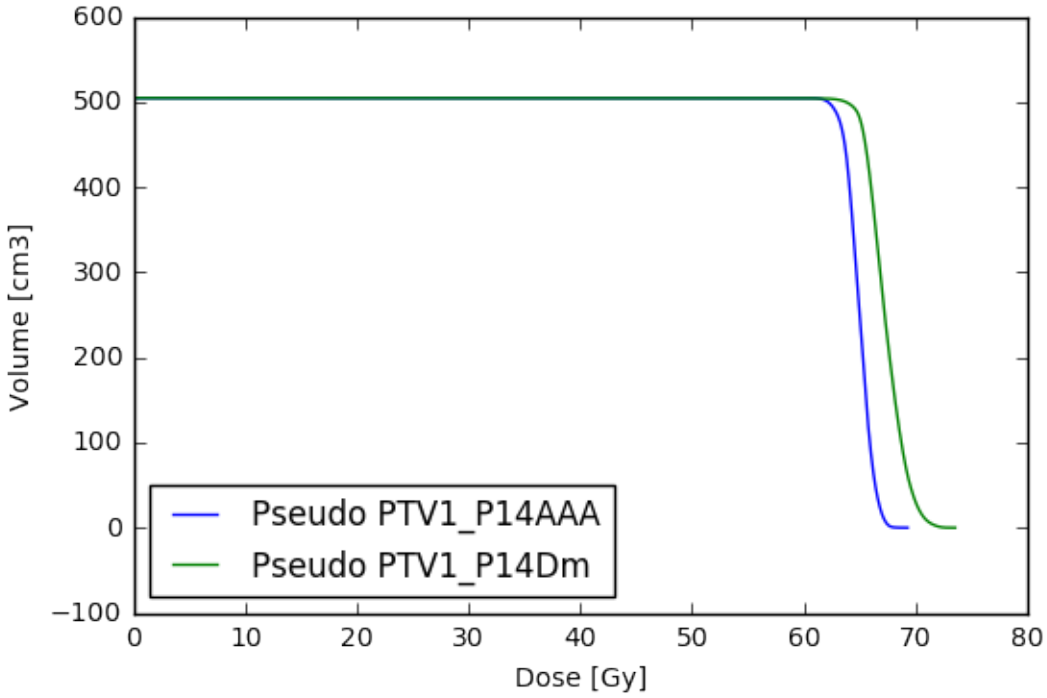
```
1    GTV_P8
2    GTVn_P2
3    GTV + 15mm_P1
4    GTVn + 10mm_P1
5    CTV65_P12
6    CTV54_P8
7    L Parotid_P14
8    R Parotid_P14
9    L Lens_P12
10    R Lens_P12
11    L Orbit_P12
12    R Orbit_P12
13    Brain Stem_P14
14    Spinal Cord_P14
15    BS + 3mm_P9
16    BS + 5mm_P13
17    Body_P14
18    Lt Par edit_P14
19    PTV1_P13
20    PTV1 edit_P13
21    PTV2_P13
22    PTV2 edit_P13
23    Pseudo Midline14
24    Pseudo Oral Ca14
25    Pseudo PostBrai2
26    Pseudo Post_P12
27    Rt Par edit_P14
28    SC + 3mm_P14
29    SC + 5mm_P14
30    Pseudo PTV1_P14
31    Pseudo PTV2_P14
```

```
32   Left Couch Bar_6
33   Right Couch Bar6
34   Artifact_P2
35   Annulus1_P3
36   Dose 6175[cGy]_4
37   Dose 5130[cGy]_4
38   missing1_P1
39   missing2_P1
```

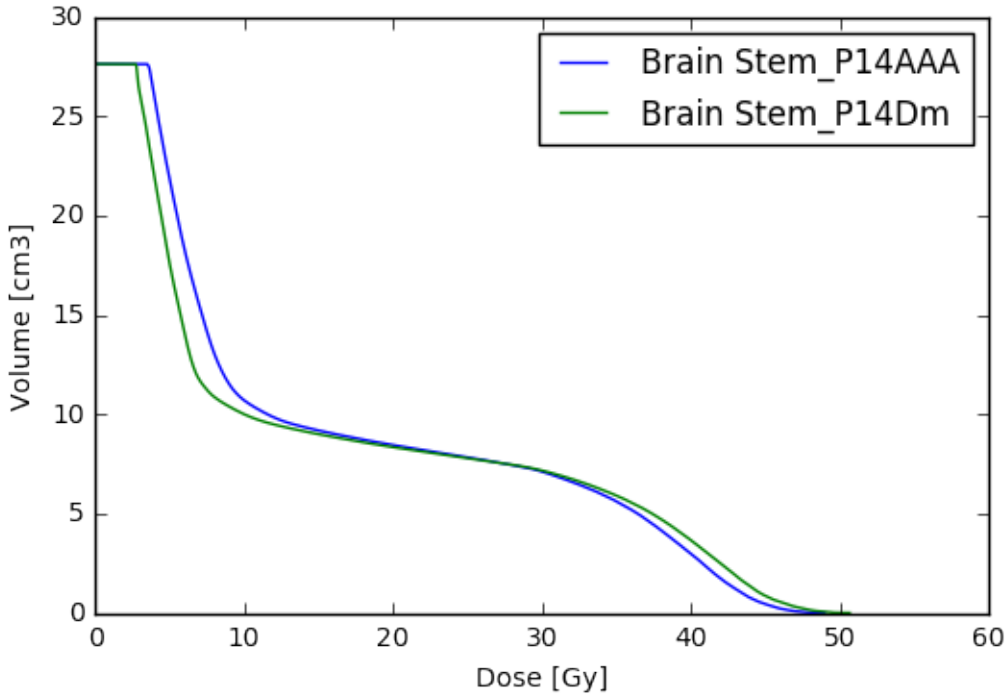
```
In [12]: def compare_dvh(key=1):
             structure = Structures_set.GetStructures()[key]
             AAA_ = dvh.DVH.from_dicom_dvh(AAA.ds, key, name=structure['name'] + 'A
             Dm_ = dvh.DVH.from_dicom_dvh(Dm.ds, key, name=structure['name'] + 'Dm'
             AAA_.compare(Dm_)
```

```
In [13]: compare_dvh(key=30)
```

```
Structure:  Pseudo PTV1_P14AAA Pseudo PTV1_P14Dm          Rel Diff       Abs diff
-----
DVH Type:  cumulative, abs dose: Gy, abs volume: cm3
Volume:           504.47 cm3        504.47 cm3         +0.00 %          +0.00
Max:               69.31 Gy          73.57 Gy          +6.15 %          +4.26
Min:               59.58 Gy          57.79 Gy          -3.00 %          -1.79
Mean:              64.99 Gy          67.37 Gy          +3.67 %          +2.38
D100:               0.00 Gy           0.00 Gy          +0.00 %          +0.00
D98:               62.59 Gy          64.43 Gy          +2.94 %          +1.84
D95:               63.18 Gy          65.06 Gy          +2.98 %          +1.88
D2cc:              67.68 Gy          71.90 Gy          +6.24 %          +4.22
```




```
In [14]: compare_dvh(key=13)

Structure:  Brain Stem_P14AAA  Brain Stem_P14Dm          Rel Diff       Abs diff
-----
DVH Type:  cumulative, abs dose: Gy, abs volume: cm3
Volume:            27.62 cm3         27.62 cm3         +0.00 %          +0.00
Max:               48.97 Gy          50.64 Gy          +3.41 %          +1.67
Min:                3.45 Gy           2.66 Gy         -22.90 %          -0.79
Mean:              15.97 Gy          15.37 Gy          -3.76 %          -0.60
D100:               0.00 Gy           0.00 Gy          +0.00 %          +0.00
D98:                3.71 Gy           2.82 Gy         -23.99 %          -0.89
D95:                3.90 Gy           2.96 Gy         -24.10 %          -0.94
D2cc:              41.52 Gy          42.79 Gy          +3.06 %          +1.27
```


Brain Stem_P14AAA
Brain Stem_P14Dm
Volume [cm3]
Dose [Gy]
0
5
10
15
20
25
30
0
10
20
30
40
50
60

In [ ]: