cnr-04-cc3

December 2, 2021

1 TUMOR - CNR - TOWARD HISTOGRAM ANALYSIS - CC3 SUB-JECT

Created: 2021.11.10 / Updated: 2021.12.02

ver: 0.02

• standarize ROI colors in images and histograms

2 GLOBAL VARIABLES

```
[4]: HOME_DIR = pathlib.Path(os.getcwd()).parent
DATA_DIR = HOME_DIR / 'data'
RESULTS_DIR = DATA_DIR / 'results'
PLOT_DIR = DATA_DIR / 'plots'
TABLE_DIR = DATA_DIR / 'tables'

CURRENT_NOTEBOOK_NAME = 'cnr-04-cc3'
CURRENT_NOTEBOOK_NUMBER = CURRENT_NOTEBOOK_NAME.split('-')[1]
```

3 GET LIST ALL CC3 IMAGES

```
[5]: SUB = 'CC3'
[6]: files = list(RESULTS_DIR.glob(f"*{SUB}*.nii.gz"))
     files
[6]: [PosixPath('/home/marek/Dropbox/p1ext4_P/no_work/TUMOR-CNR/tumor-cnr-
     git/data/results/CC3_t2_bladder.nii.gz'),
     PosixPath('/home/marek/Dropbox/p1ext4_P/no_work/TUMOR-CNR/tumor-cnr-
     git/data/results/CC3_t2.nii.gz'),
     PosixPath('/home/marek/Dropbox/p1ext4_P/no_work/TUMOR-CNR/tumor-cnr-
     git/data/results/CC3_t2_roi_dilated2.nii.gz'),
      PosixPath('/home/marek/Dropbox/p1ext4_P/no_work/TUMOR-CNR/tumor-cnr-
     git/data/results/CC3_t2_roi.nii.gz'),
      PosixPath('/home/marek/Dropbox/p1ext4_P/no_work/TUMOR-CNR/tumor-cnr-
     git/data/results/CC3_t2_roi_cm.nii.gz'),
      PosixPath('/home/marek/Dropbox/p1ext4_P/no_work/TUMOR-CNR/tumor-cnr-
     git/data/results/CC3_t2_roi_dilated_ball3.nii.gz')]
[7]: # print only names
     _ = [print(f'{k+1}) {f.name}') for k, f in enumerate(sorted(files))]
    1) CC3_t2.nii.gz
    2) CC3_t2_bladder.nii.gz
    3) CC3_t2_roi.nii.gz
    4) CC3_t2_roi_cm.nii.gz
    5) CC3_t2_roi_dilated2.nii.gz
    6) CC3_t2_roi_dilated_ball3.nii.gz
    3.1 LOAD ALL IMAGES
[8]: # image
     img = nib.load(RESULTS_DIR / f'{SUB}_t2.nii.gz').get_fdata()
```

```
[8]: # image
img = nib.load(RESULTS_DIR / f'{SUB}_t2.nii.gz').get_fdata()
# roi
roi = nib.load(RESULTS_DIR / f'{SUB}_t2_roi.nii.gz').get_fdata()
# dilated 2
dil2 = nib.load(RESULTS_DIR / f'{SUB}_t2_roi_dilated2.nii.gz').get_fdata()
# ball3
bal3 = nib.load(RESULTS_DIR / f'{SUB}_t2_roi_dilated_ball3.nii.gz').get_fdata()
# bladder
bla = nib.load(RESULTS_DIR / f'{SUB}_t2_bladder.nii.gz').get_fdata()
```

3.1.1 CREATE LIST OFLOADED IMAGES AND LIST OF THEIR NAMES

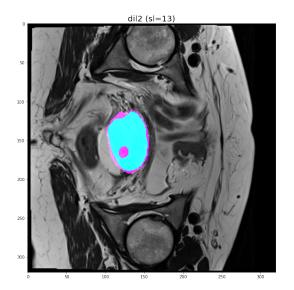
```
[9]: masks = [dil2, bal3]
names = ['dil2', 'bal3']

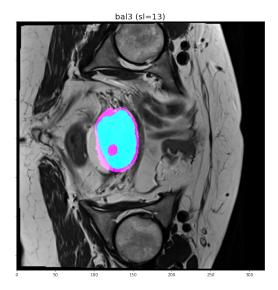
# only dil and bal images; neither img nor roi
MASKS_CNT = len(masks)
```

3.1.2 BASIC INFO ABOUT IMAGES

```
[10]: f1.im_info(img, 'img')
      f1.im_info(roi, 'roi')
      f1.im_info(bla, 'bladder')
      print()
      for i,n in zip(masks, names):
          f1.im_info(i,name=n)
     *** IMG ***,
                     max=1640.0, min=0.0, mean=443.37, shape=(320, 320, 28),
     #voxels=2867200
                     max=1.0, min=0.0, mean=0.01, shape=(320, 320, 28),
     *** ROI ***,
     #voxels=2867200
                             \max=1.0, \min=0.0, \max=0.00, \max=(320, 320, 28),
     *** BLADDER ***,
     #voxels=2867200
     *** DIL2 ***,
                     \max=1.0, \min=0.0, \max=0.01, \sup=(320, 320, 28),
     #voxels=2867200
     *** BAL3 ***,
                     max=1.0, min=0.0, mean=0.02, shape=(320, 320, 28),
     #voxels=2867200
```

3.1.3 DISPLAY ALL MASKS OVERLAYED ON IMAGE AND ROI FOR SELECTED SLICE

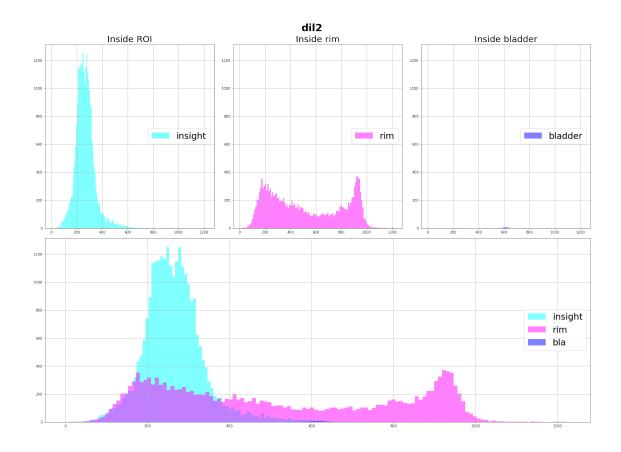




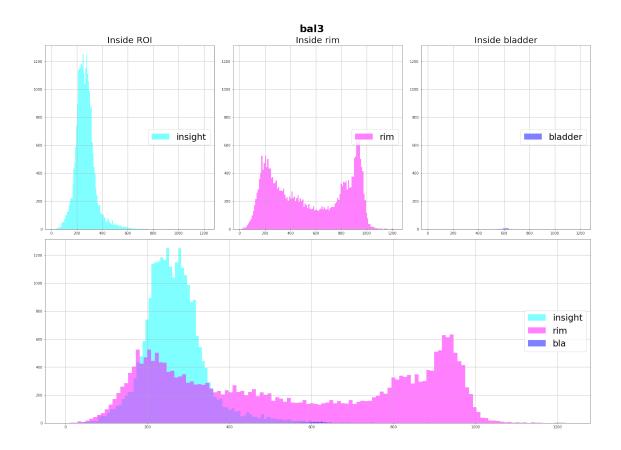
4 PLOT HISTOGRAMS FOR ALL MASKS

Saved figure:

../data/plots/04-CC3-dil2.png



Saved figure: ../data/plots/04-CC3-bal3.png



[13]: utils.print_date(5)

02-Dec-2021 19:10:42

- [14]: utils.save_notebook_as_html(file_name=CURRENT_NOTEBOOK_NAME, cleaning_delay=2)
- [15]: utils.save_notebook_as_pdf(file_name=CURRENT_NOTEBOOK_NAME, cleaning_delay=2)