PCP Quality Assessment Protocol - Group report

• QA protocol: anatomical.

• Date and time: 2016-03-17, 12:07.

• Failed workflows: none.

• Image parameters:

Subject ID	Session	Scan ID	Image size (voxels)	Spacing (mm)	TR (ms)	Time steps
sub-01	single_session	T1w	176 × 256 × 256	1.000 × 0.977 × 0.977	N/A	1
sub-02	single_session	T1w	176 × 256 × 256	1.000 × 0.977 × 0.977	N/A	1
sub-03	single_session	T1w	176 × 256 × 256	1.000 × 0.977 × 0.977	N/A	1
sub-04	single_session	T1w	176 × 256 × 256	1.000 × 0.977 × 0.977	N/A	1
sub-05	single_session	T1w	176 × 256 × 256	1.000 × 0.977 × 0.977	N/A	1
sub-06	single_session	T1w	176 × 256 × 256	1.000 × 0.977 × 0.977	N/A	1
sub-07	single_session	T1w	176 × 256 × 256	1.000 × 0.977 × 0.977	N/A	1
sub-09	single_session	T1w	176 × 256 × 256	1.000 × 0.977 × 0.977	N/A	1
sub-10	single_session	T1w	176 × 256 × 256	1.000 × 0.977 × 0.977	N/A	1
sub-11	single_session	T1w	176 × 256 × 256	1.000 × 0.977 × 0.977	N/A	1
sub-12	single_session	T1w	176 × 256 × 256	1.000 × 0.977 × 0.977	N/A	1
sub-13	single_session	T1w	176 × 256 × 256 176 × 256 ×	1.000 × 0.977 × 0.977 1.000 × 0.977 ×	N/A	1
sub-14	single_session	T1w	256 176 × 256 ×	0.977 1.000 × 0.977 ×	N/A	1
sub-16	single_session	T1w	256 176 × 256 ×	0.977 1.000 × 0.977 ×	N/A	1
sub-17	single_session	T1w	256 176 × 256 ×	0.977 1.000 × 0.977 ×	N/A	1
sub-18	single_session	T1w	256 176 × 256 ×	0.977 1.000 × 0.977 ×	N/A	1
sub-20	single_session	T1w	256 176 × 256 ×	0.977 1.000 × 0.977 ×	N/A	1
sub-21	single_session	T1w	256 176 × 256 ×	0.977 1.000 × 0.977 ×	N/A	1
sub-23	single_session	T1w	256 176 × 256 ×	0.977 1.000 × 0.977 ×	N/A	1
sub-24	single_session	T1w	256 176 × 256 ×	0.977 1.000 × 0.977 ×	N/A	1
sub-25	single_session	T1w	256 176 × 256 ×	0.977 1.000 × 0.977 ×	N/A	1
sub-26 sub-28	single_session single_session	T1w T1w	256 176 × 256 ×	0.977 1.000 × 0.977 ×	N/A N/A	1
sub-26	single_session	T1w	256 176 × 256 ×	0.977 1.000 × 0.977 ×	N/A	1
545 23	5111g10_36331011	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	256	0.977	IN/C	•

2.5 le5

2.0

1.5

1.0

0.5

0.0

4.5

4.0

3.0

2.0

1.8

1.6

1.4

1.2

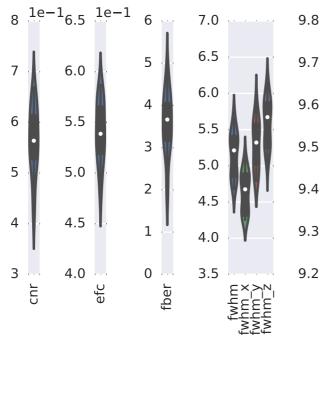
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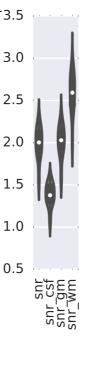
0.8

0.6

0.4

QC measures (single_session)



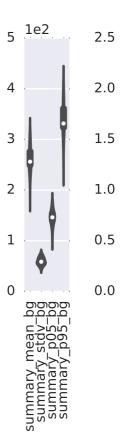


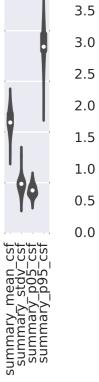
2.5

2.0

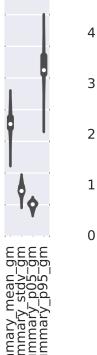
1.0

0.5





1e2



1e2

4.0

5 1e2

PCP Quality Assessment Protocol - QAP Anatomical Spatial Reports

After all processing has been completed, the designated output directory for the <code>qap_anatomical_spatial.py</code> workflow will contain a set of pdf files that contain the relevant reports for the set of scans undergoing quality assessment. The set of output pdfs includes one pdf file per input scan in the scan directory, e.g.: <code>qap_anatomical_spatial_sub-01.pdf</code>, which contains the T1 slice mosaic and QC metrics for that scan. There will also be a group report pdf in the main output directory, e.g.: <code>qap_anatomical_spatial_group.pdf</code>, that contains summary metrics for the entire set of scans.

For the individual scan reports:

The T1 Anatomical Slice Mosaic

This plot in the report for the scan being assessed, e.g.:

```
Anatomical reoriented, subject sub-01 (session_1_anat_1)
```

is the rendering of the axial slices from the 3D stack created by the workflow. This image can be used to eyeball the quality of the overall signal in the anatomical scan, as it will be obvious if there were any problem areas where there was signal dropout resulting from a bad shim or other sources of signal distortion.

The Spatial Metrics computed on the Anatomical Scan

The metrics displayed in the Summary Report, e.g.: QC measures (subject sub-01_session_1) were computed using the qap_anatomical_spatial.py workflow and have been displayed as violin plots. The stars in these plots denote where the score for the scans for this participant fall in the distribution of all scores for scans that were included as inputs to the anatomical-spatial workflow. If there are several scans per session for this individual, then the stars will be displayed adjacent to each other in the violin plot.

The metrics computed are as follows:

- 1. bg_size Background mask size
- 2. fg_size Foreground mask size
- 3. bg_mean Mean intensity of the background mask
- 4. fg_mean Mean intensity of the foreground mask
- 5. bg_std Standard deviation of the background mask
- 6. fg_std Standard deviation of the foreground mask
- 7. csf_size Cerebrospinal fluid mask size
- 8. gm_size Grey matter mask size
- 9. wm_size White matter mask size
- 10. csf_mean Mean intensity of the CSF mask
- 11. gm_mean Mean intensity of the grey matter mask
- 12. wm_mean Mean intensity of the white matter mask
- 13. csf_std Standard deviation of the CSF mask
- 14. gm_std Standard deviation of the grey matter mask
- 15. wm_std Standard deviation of the white matter mask
- 16. cnr Contrast to Noise Ratio
- 17. efc Entropy Focus Criterion
- 18. fber Foreground to Background Energy Ratio
- 19. fwhm Full-width half maximum smoothness of the voxels averaged across the three coordinate axes, and also for each axis [x,y,x]
- 20. qi1 Artifact Detection
- 21. snr Signal to Noise Ratio

All metrics are described in more detail in the <u>Taxonomy of QA Measures section</u> of the QAP documentation. Please refer to the QAP website for descriptions of these metrics.

For the group reports:

The violin plots included in the group report, e.g.: qqap_anatomical_spatial_group.pdf, are a graphical representation of the columnar values in the qap_anatomical_spatial.csv file that was created in the main output directory for the workflow. The scores for each metric described above were aggregated to create the distributions that were plotted in both the individual and group reports. Hence, the violin plots in the individual scan reports and the group reports are identical, except that the group reports do not contain any stars denoting individual scans. These group reports are intended to provide the user a means of visually inspecting the overall quality of the spatial data for that group of anatomical scans.