**QPP Scripts** June 2020, minorly updated February 2021

Keilholz MIND Lab, GATech and Emory, [shella.keilholz@bme.gatech.edu](mailto:shella.keilholz@bme.gatech.edu), bzyousefi@gmail.com

The folder **QPPv0620SD** contains **Matlab scripts with sample data**, respectively located in folders **QPPv0620** and **All\_preproc\_Data**, to detect multiple **Q**uasi-**P**eriodically recurring spatiotemporal **P**atterns **(QPPs)** of the brain’s intrinsic activity based on the following two methods:

**M1\_GrpFst**, for **fast detection of multiple QPPs, at the group level**, by concatenating all scans of all subjects and running the QPP algorithm (introduced by Majeed et al 2011) for a few randomly selected initial segments (folders **M1\_GrpFst\_HCPR3** and **M1\_GrpFst\_HCPR40** in **/QPPv0620SD/QPPv0620/**).

**M2\_S2GRbst**, for **robust detection of multiple QPPs**, which starts from subject level and runs the QPP algorithm for all possible initial segments; each group QPP is then obtained by fine-tune averaging the QPPs of subjects (folders **M2\_S2GRbst\_HCPR40** and **NIMG21\_S2GRbst\_HCP817** in /QPPv0620SD /QPPv0620/, the latter folder being the **scripts of Yousefi and Keilholz, NeuroImage, 2021**).

M2\_S2GRbst (introduced by Yousefi et al 2018 and Yousefi and Keilholz 2021) gives similar results to M1\_GrpFst, for the healthy adults of the high-quality Human Connectome Project (HCP) dataset, but takes more time, see the related supplementary analysis (SA) in M2\_S2GRbst\_HCPR40. Therefore, we suggest **using the M1\_GrpFst first on a new dataset and later trying M2\_S2GRbst to examine the robustness of the results. On any new dataset, always have in mind to start by revising the settings of the free parameters** such as the duration of QPPs.

**Note: If you** are accessing this document via the KeilholzLab drive, make a local copy of the codes and the sample data in your personal directory and be careful not to change anything in the QPPv0620SD. **If you** are accessing this document via the KeilholzLab github page, use your own copy of the HCP dataset or download 100 unrelated subjects from the HCP website (resting-state fMRI, preferably FIX-denoised and both days) and please apply our additional preprocessing described below - note, a small parcellated sample data is shared in the KeilholzLab github page, so that you can readily try parts of the QPP scripts.

**Start your first QPP analysis** by M1\_GrpFst\_HCPR3, which detects 5 group QPPs of 3 Randomly selected unrelated subjects from rsfMRI dataset of the HCP S900 with 2 scans included per subject. **QPP scripts are numbered based on the order that they should be run. The first script** (M10\_Params.m) **sets the parameters and paths that are saved in a .mat file** (Params\_~.mat) **and read by other scripts within the same folder** (e.g., M11\_~.m to M14\_~.m in M1\_GrpFst\_HCPR3).

Data for HCPR3 (B\_GWCR\_HCPR3.mat), located in /QPPv0620SD/All\_Preproc\_Data/, also shared in the KeilholzLab github page, has our own additional preprocessing and is parcellated (Non-parcellated additionally preprocessed data is located in folder /GWCR\_HCPR3/). Parameters and paths of the data and the additional preprocessing are set in P0\_~.m and saved in Preproc\_Params\_~.mat. This mat file is further read by P1\_~.m, which is the script that implements the additional preprocessing. Note that folder /QPPv0620SD/Utils/ contains all the required toolboxes, indices for parcellations, etc. Also, **note that Preproc\_Params\_~.mat is read by the postprocessing scripts and is needed along the data; it is the first item to set in M10\_Params.m for the QPP analysis.**

Go through all the items in M10\_Params.m. **As a reference for the QPP method, the free parameters or what is implemented by each part of the QPP scripts, “carefully” read Yousefi and Keilholz (2021).**

Run M10\_Params.m, M11\_GrpQPP.m and M12\_Plts and note the generated plots. These plots are also provided in /QPPv0620/Plts2Expect/.

If you are accessing the scripts via Keilholzlab github page and only have B\_GWCR\_HCPR3.mat, this is the last stage; switch to your own downloads of the HCP data, pick any few subjects, run our additional preprocessing, particularly generate Preproc\_Params\_~.mat, and proceed further with the QPP scripts.

Run M13\_GrpQPP\_VxSm and M14\_Plts and visualize QPPs in grayordinates by opening the cifiti files in HCP workbench.

M1\_GrpFst\_HCPR3 is suitable for start (e.g., as an intro or a demo), but the data is not long enough to get significant magnitudes for QPPs, particularly in the noncortical regions. So, we have not included much analysis in grayordinates for M1\_GrpFst\_HCPR3. More complete analyses in grayordinates are included in folders M1\_GrpFst\_HCPR40, M2\_S2GRbst\_HCPR40 and NIMG21\_S2GRbst\_HCP817.

M1\_GrpFst\_HCPR40 and M2\_S2GRbst\_HCPR40 are based on 40 randomly selected unrelated subjects from HCP S900 dataset with all 4 scans included per subject. Preprocessed data for HCPR40, applied by P0\_~.m, is also located in /All\_Preproc\_Data/ in the Keilholzlab drive.

You can start running scripts in M1\_GrpFst\_HCPR40, which takes some time. Meanwhile, browse scripts of M2\_S2GRbst\_HCPR40 and note the script differences with M1\_GrpFst\_HCPR40.

M2\_S2GRbst\_HCPR40, **which can be run after you start analyzing your own data with the first method**, takes more time compared to M1\_GrpFst\_HCPR40 but is more robust, as mentioned before. Both folders related to the second method (M2\_S2GRbst\_HCPR40 and NIMG21\_S2GRbst\_HCP817) have multiple supplementary analyses (SAs), which validate various choices in the pre-/post-processing or support some claims and statements in Yousefi and Keilholz 2021.

NIMG21\_S2GRbst\_HCP817, which contains the scripts of Yousefi and Keilholz 2021 and detects three QPPs of all subjects in HCPS900 dataset who had four complete scans (817 subjects), is minorly different in terms of division of scripts, compared to M2\_S2GRbst\_HCPR40; this made it easier to analyze a large number of subjects. Also, obtaining the threshold for significance of activity within QPPs is appearing as SA (NIMG21\_S2GRbst\_HCP817/SA/SA2\_SigActiv/) because this part was added in the revision process and we meant the scripts that generated the results of the publication to stay unchanged. **NIMG21\_Rslts2Share.mat** file, located in NIMG21\_S2GRbst\_HCP817 folder (if accessing via Keilholz lab drive, or located aside QPPv0620SD folder in seven subfiles if accessing via github) contains some parts of the published results in Yousefi and Keilholz 2021, which are QPPs 1-3 in grayordinates (variable named QPPv), indices of QPPs’ active vertices/voxels (QPPv\_io), QPPs’ summary maps (QPPv\_clst and QPPv\_te), QPPs in parcel space (QPP) and change in functional connectivity after regressing QPPs (dFC).

Finally, we recommend the current structure of the scripts for the QPP analysis, meaning, making a folder for each project, having a parameter mat file, etc. QPP scripts can be modified, simplified, or more scripts can be added, based on the study question. Current functions used throughout the scripts (located in /QPPv0620SD/QPPv0620/QPPfv0620/) can be used in different context, e.g., comparing QPPs between groups using Tcomp.