physio_calc.py: New program to model cardiac & respiratory contributions to BOLD signal in AFNI

POSTER 136

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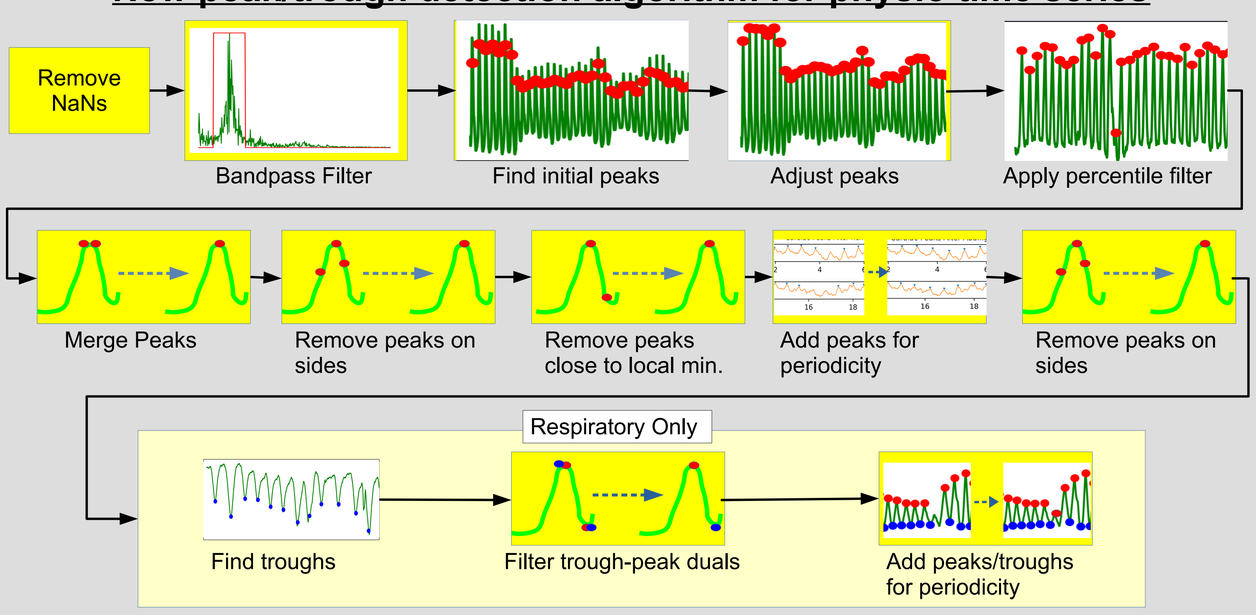
Introduction

FMRI allows researchers to model neuronal activity at different parts of the brain by analyzing BOLD signals. However blood oxygenation also varies with cardiac and respiratory cycles[1]. Glover et al.[1] present an algorithm for modeling such variation. This was previously implemented, with some modification, in RetroTS.py, creating slicewise regressors for FMRI processing. physio_calc.py is a newer approach to the same issue, implementing similar stages but improving the sub-algorithms, particularly for peak and trough detection. More modular design, new options, increased flexibility, and automatic quality control images have all been added, as well. Here, we describe both new and improved features of physio_calc.py, which is freely available in AFNI[2], demonstrating with both synthetic and real data.

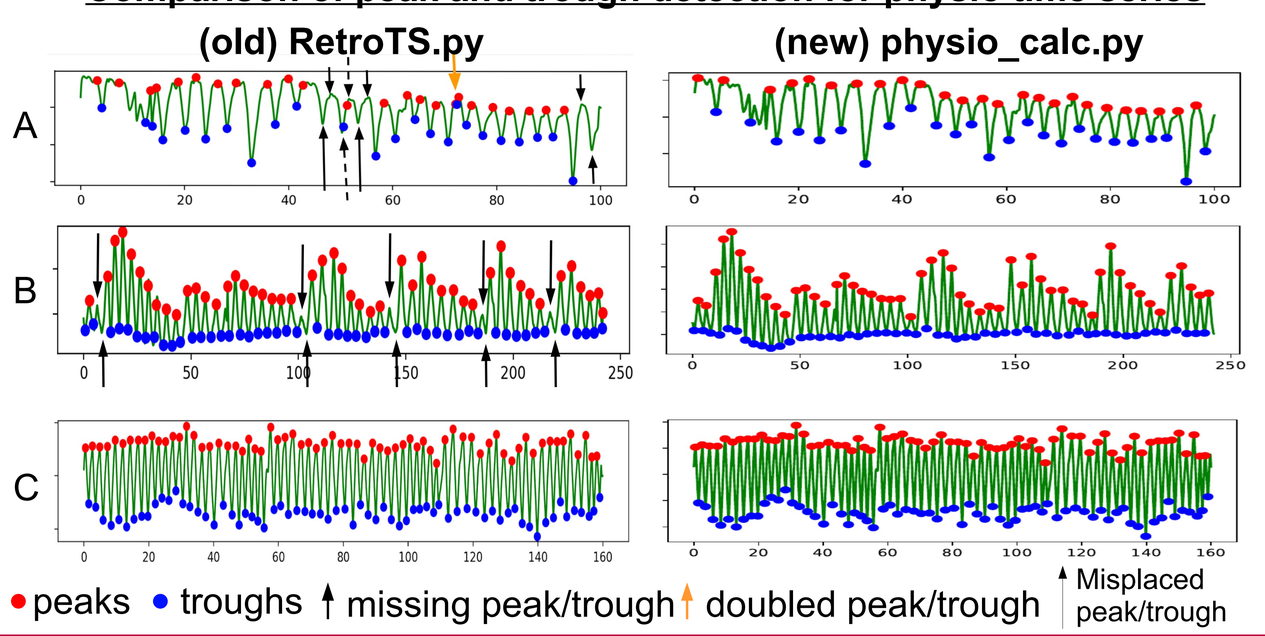
Methods

The physio_calc.py program contains several algorithmic improvements, in particular in finding peaks (and, in some cases, troughs) in the input physio time series. Finding peaks and troughs is a key aspect of the RETROICOR procedure. Figure 1 (left) shows the algorithmic steps now used. Figure 2 (right) shows a comparison of peak- and trough-finding between physio_calc.py and RetroTS.py. While both algorithms find the vast majority of peaks and troughs correctly for most time series, RetroTS.py misses some subtle ones, and physio_calc.py finds more of them reliably (leading to improved phase estimation).

New peak/trough detection algorithm for physio time series



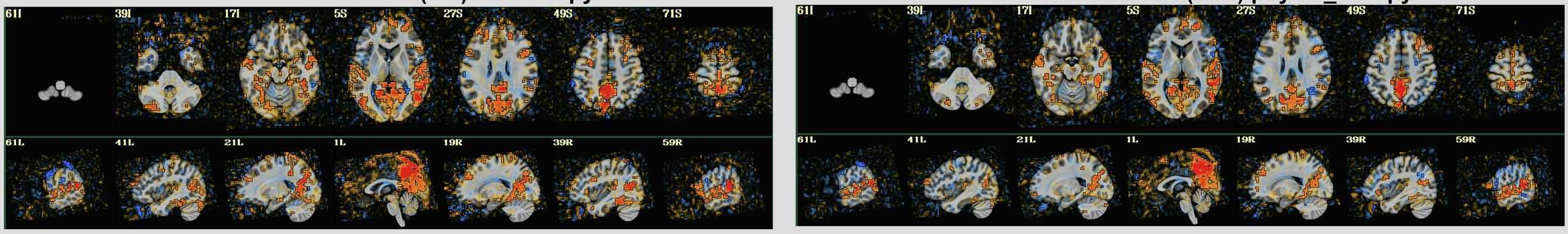
Comparison of peak and trough detection for physio time series



Results

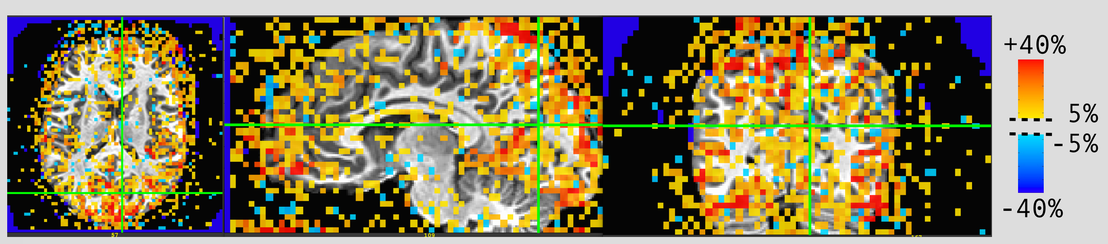
The physio_calc.py program estimates regressors to be used in FMRI processing, such as via AFNI's afni_proc.py pipeline tool. We show a comparison of real FMRI results using the old RetroTS.py (left) and new physio_calc.py (right), using seed-based maps of the default mode network (from afni_proc.py's QC HTML[3]. While results are similar, the higher correlation regions on the right appear to be more tightly constrained within GM and less noisy.

DMN correlation with (old) RetroTS.py | **DMN correlation with (new) physio_calc.py**



The algorithms can be directly compared in terms of variance reduction (likely due to filtering physiological features out). In the figure below, physio_calc.py tends to have a greater effect globally. Additionally, we show an example of command line syntax, which aims to balance processing flexibility with clarity.

Relative amount of variance reduction using physio_calc.py, compared to RetroTS.py.




```
# A command line example
physio_calc.py -do_fix_nan -freq 50                \
    -card_file cardiacTimeSeries.txt               \
    -resp_file respiratoryTimeSeries.txt           \
    -dset_epi  EPI.nii.gz  -RVT_lags 0 20          \
    -out_dir physio_results
```

Conclusion

Improvements in physio_calc.py (relative to RetroTS.py):

+ Improved sub-algorithms, particularly for signal peak and trough detection
+ More modular design and improved error handling
+ Greater flexibility across types of physio inputs
+ Options for fixing issues in the recorded time series (NaNs, gaps, 0s, etc.)
+ User control of respiration volume per time (RVT)[4] lags
+ Better noise reduction in FMRI practical examples (to be further tested)
+ Automatic quality control images created

Acknowledgment & References

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