PESTICA4/SLOMOCO Manual

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What is PESTICA?

- For many years, researchers used pulse and respiratory equipment to "estimate" physiologic noise in EPI by measuring the timing of the physiologic cycles
- PESTICA accomplishes the same, determines the timing of the physiologic cycles, so can be used in place of physiologic monitoring equipment
  - *PESTICA == physiologic monitor for cardiac and respiration*
  - *Useful when external monitoring is unavailable or imperfect*

- Physiologic EStimation by Temporal ICA
  - Beall and Lowe, "Isolating physiologic noise sources with independently determined spatial measures." Neuroimage, 2007 Oct 1;37(4):1286-300

What is PESTICA?

- Physiologic EStimation by Temporal ICA
    - **1.** Performs slice-wise temporal ICA,
    - 2. Identifies noise component per slice using averaged spatial mixing matrix,
    - 3. Normalizes and assembles noise components
        - Resulting two timecourses look a lot like a pulse trace and a respiratory trace

- PESTICA software includes optimizations to account for more variance with fewer regressors than RETROICOR
- PESTICA3 includes SLOMOCO scripts for a powerful slice-wise motion correction
- PESTICA4 also handles SMS (MB) acquisition in both PESTICA and SLOMOCO. Note this requires the correct slice timestamps in the input EPI data
    - Check genSMStimeshiftfile.m and its help

How to run PESTICA

- First time only: modify setup_pestica.sh
  - Define PESTICA_DIR as the directory where PESTICA4 is unzipped.
- Next, source setup_pestica.sh (or put in .bashrc/.tcshrc to always run it)

- Next, go to the working directory where EPI data is stored.
- Type, "run_pestica.sh –d <EPI file name here>"
- The directory named "pestica4" will be generated under the working directory
  - output file is <inputfilename>.retroicor_pestica+orig.
  - coupling_ret_card(or resp)_pestica+orig store the goodness of fit per coefficient
- Optional: if you have monitored pulse/respiration files, these can be used instead of PESTICA with the "-p" option:
  - "run_pestica.sh –d <2d EPI file name here> -p <physio file name>"

Optional: PESTICA using PMU data

- Why would you do this?
- If you have PMU data files for each EPI dataset, and they are good quality, the PESTICA scripts can be directed to use these PMU data files instead of running the ICA estimation
- To direct the PESTICA scripts to used your monitored pulse/respiration files instead of ICA decomposition, use the "-p" option:
  - "run_pestica.sh –d <2d EPI file name here> -p <physio file name>"
- Equivalent results as using ICA decomposition, but benefit of ground truth with your PMU data files
- It is also possible that the EPI data contain artifacts that interfere with the ICA decomposition or the timing is insufficient to fully sample cardiac cycles, in which case, only the monitored PMU data files can give a suitable correction.

Update from PESTICA2

- Intermediate version of PESTICA3
  - SMS/Multiband acquisition is added, all previous only performed with singleband (SB) EPI (conventional)
  - New PESTICA templates are generated from 240 subjects.
  - The performance is improved.
    - See 2016 HBM poster, *PESTICA3.0; Evaluation of a new physiologic estimation by temporal ICA*
  - Not published in public

- PESTICA4
  - Numerous minor issues have been debugged
  - The process is accelerated and running time is reduced
    - In case of 3T SB 2d EPI data set (2x2x4mm, 31slc, 128 reps), PESTICA is done under 15 mins, and SLOMOCO under 35mins
  - New directory structures and output names are proposed.
    - Easy to version control

From 2016 HBM poster, PESTICA3.0

Correlation	PESTICA2	PESTICA3
Card. PMU	0.32 ± 0.19	0.41 ± 0.20
Resp. PMU	0.41 ± 0.16	0.41 ± 0.21

Table 1. Correlation between PMU signals and different version of PESTICA

Cycle(Hz)	PMU	PESTICA2	PESTICA3
Card	0.96 ± 0.12	1.00 ± 0.05*	0.96 ± 0.11
Resp.	3.77 ± 0.47	4.15 ± 0.72**	3.64 ± 0.47

Table 2. Mean and standard deviation of average cardiac and respiratory cycle of PMU and different PESTICA signals over 23 subjects. * and ** indicate the difference from PMU was significant ($p < 0.05$, and 0.01, respectively)

Example of PESTICA using 3T HCP Lifespan protocol

Card PMU	Estimated card	Resp PMU	Estimated resp
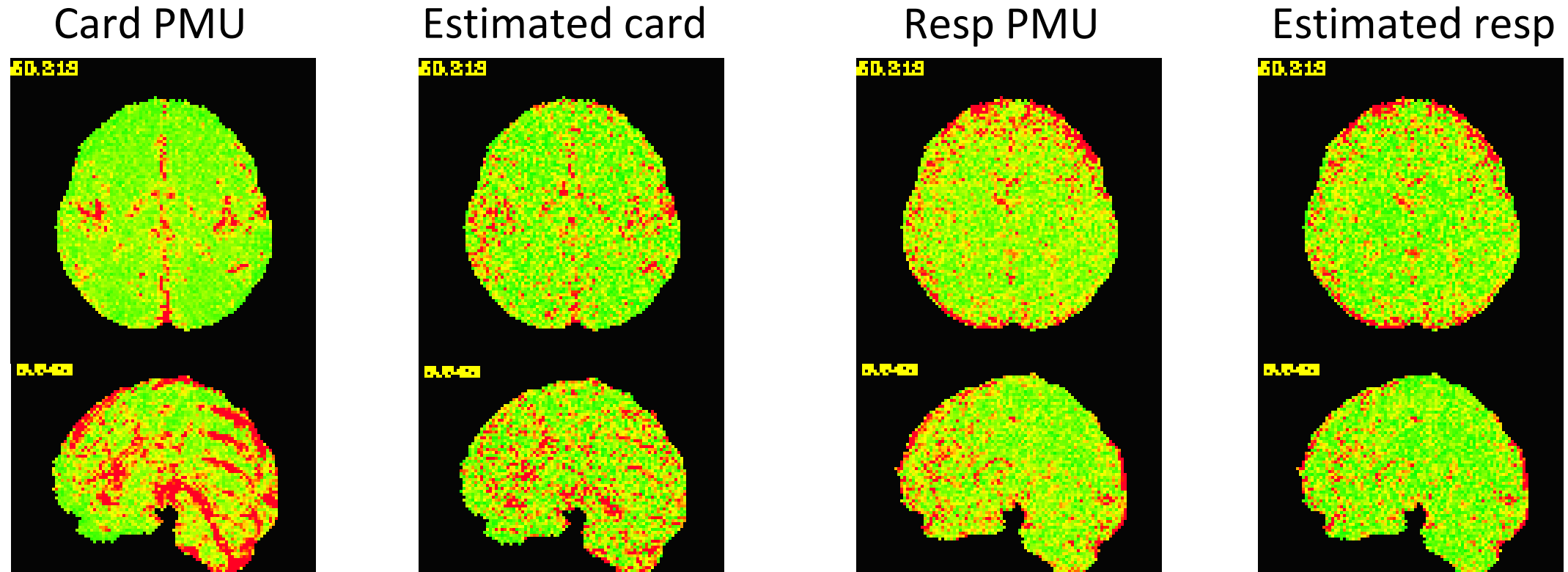
T-score map with correlation of PMU/PESTICA and EPI signal,
shown in coupling_ret_card/resp_pestica+orig

What is SLOMOCO?

- SLice-Oriented MOtion COrrection
  - Beall and Lowe, "SimPACE: generating simulated motion corrupted BOLD data with synthetic-navigated acquisition for the development and evaluation of SLOMOCO: a new, highly effective slicewise motion correction.", Neuroimage, 2014 Nov(1);101;21-34

- Slomoco decomposes problem into in-plane and out-of-plane
  1. runs in-plane motion correction and stores output (uses output on next steps)
  2. runs out-of-plane correction on each slice independently (ignores output)
  3. normalizes and filters the resulting motion parameters
  4. uses resulting parameters to determine voxel-specific regressors for a second motion correction applied to in-plane corrected data.

- It is recommended to run slomoco after physiologic correction, or if using PESTICA scripts, it can be run with SLOMOCO+physiologic corrections "in parallel" for enhanced efficiency

How to run SLOMOCO

- It is recommended but not required to run SLOMOCO *with* PESTICA
  - Involves first running PESTICA (PESTICA4), then running SLOMOCO with the option to "include" the PESTICA output in the final regression
  - Alternatively, can be run without PESTICA or any physiologic correction

- Basic usage: *slicemoco_newalgorithm.sh –d <epi name>*
  - Note, does not include any physiologic regressors

- SLOMOCO+PESTICA usage: *slicemoco_newalgorithm.sh –d <epi name> -r*
  - PESTICA option can be either "-r" to use ICA-estimated or "-p" to use PMU-estimated
  - Requires first running PESTICA appropriately, then ignoring the output corrected datafile

- The directory named "*slmoco4*" will be generated under the working directory
  - output file is *<inputfilename>.slicemocoxy_afni.slomoco_pestica+orig.*
  - slomoco_pestica_coupling_maps show the goodness of fit

Example of SLOMOCO using 3T HCP Lifespan protocol

Slomoco_Coupling_pmu
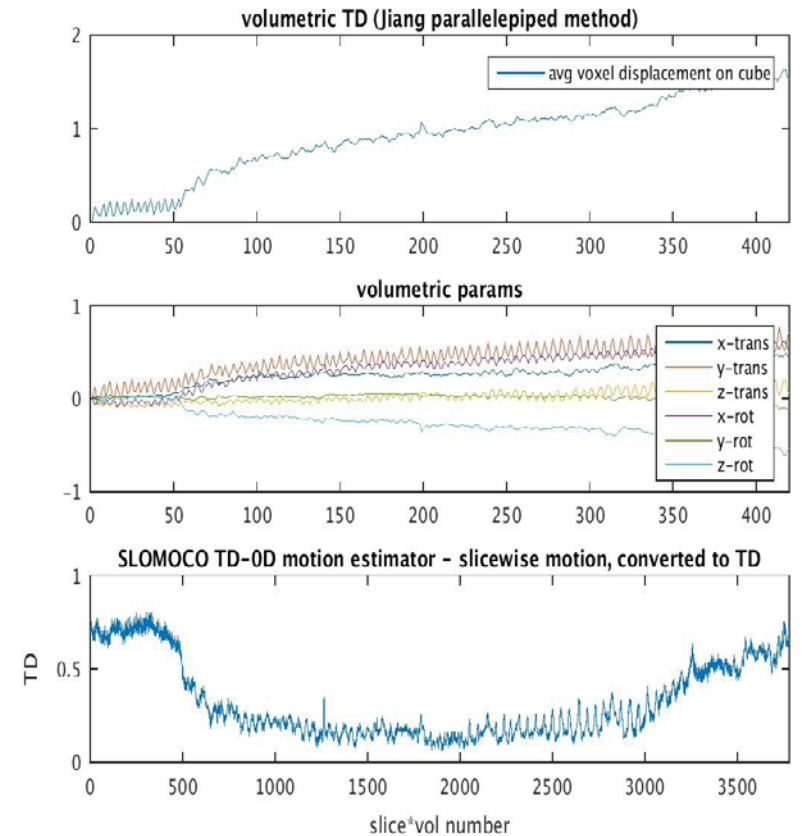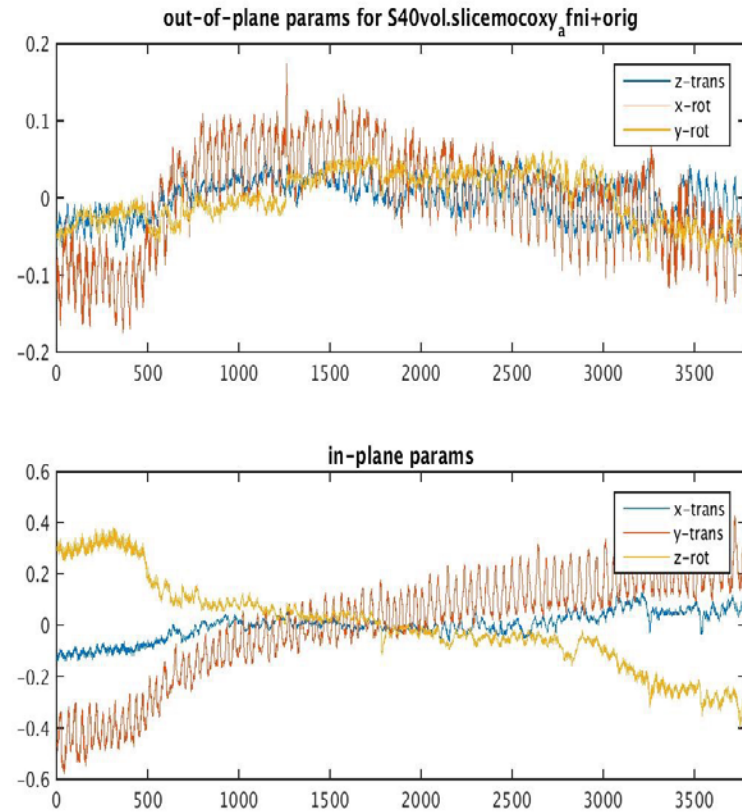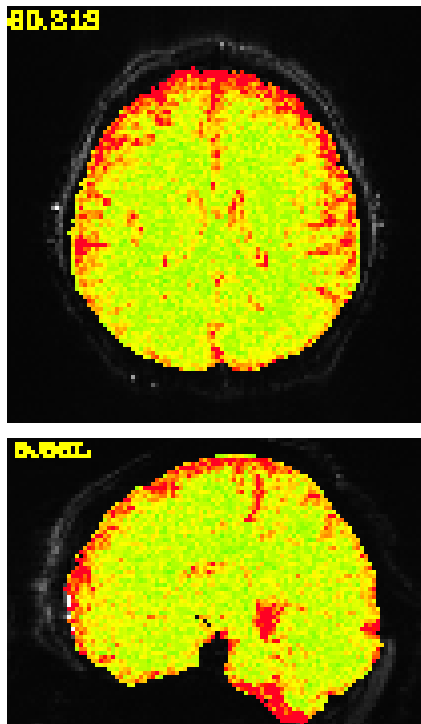
Question and Answer

- Feel free to modify, please share your findings on the message board at http://www.nitrc.org/projects/pestica

- RVT is not available in PESTICA because the resulting ICA-derived signal amplitudes are not accurate.

- Please cite the original papers when using PESTICA and/or SLOMOCO

- Contact Wanyong Shin, Wanyong.shin@gmail.com, if you have a question
  - To assist in a prompt response, please provide relevant details (command line used, verify PESTICA is set up, error you obtain)