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PhysIO Wiki Main Page

This Wiki contains the most up-to date User Guide to the PhysIO Toolbox. It is most conveniently viewed online with gitlab-formatting. Its content can also be retrieved offline after downloading the toolbox, in folder `physio/wikidocs` as

- plain text `.md` markdown files
- as single HTML and PDF file: `documentation.{html,pdf}`

List of current Wiki files

- HOME: This page. Landing Page of PhysIO Wiki. Navigation to all other files and this explanation.
- FAQ: Frequently asked questions (for users) (also frequently updated!)
- QUICKSTART: Example script and how to use it on test data, Intro to Batch Editor GUI
- EXAMPLES: List and explanation of all examples available for download
- Manual: Detailed overview of the toolbox functionality, sub-pages following its modular structure
  - Read-In of Logfiles
  - *The following pages are under construction*
  - **TODO** Preprocessing Physiological Data
  - **TODO** Physiological Noise Modeling
  - **TODO** Performance Assessment
  - **TODO** Technical Documentation For developers, list of all functions, see header of `.m` files for now

Other sources of Documentation

Documentation for this toolbox is also provided in the following forms:

1. Overview and guide to further documentation: README.md and CHANGELOG.md
   - README.md: purpose, installation, getting started, pointer to more help
   - CHANGELOG.md: List of all toolbox versions and the respective release notes, i.e. major changes in functionality, bugfixes etc.

2. Within SPM: All toolbox parameters and their settings are explained in the Help Window of the SPM Batch Editor
3. Within Matlab: Extensive header at the start of each `tapas_physio_*` function and commenting
    - accessible via `help` and `doc` commands from Matlab command line
    - starting point for all parameters (comments within file): `edit tapas_physio_new`
    - also useful for developers (technical documentation)
4. Scientific Documentation: Our paper on the PhysIO Toolbox explains both the scientific background on physiological noise modeling, as well as the modular structure of the toolbox as comprehensivce yet succinct as we (and the reviewers) could.

Quickstart

Quickstart Manual

Purpose

This page provides simple walk-throughs of the SPM Batch Editor GUI, the scripts to run the main examples, and the most common output plots of the PhysIO Toolbox.

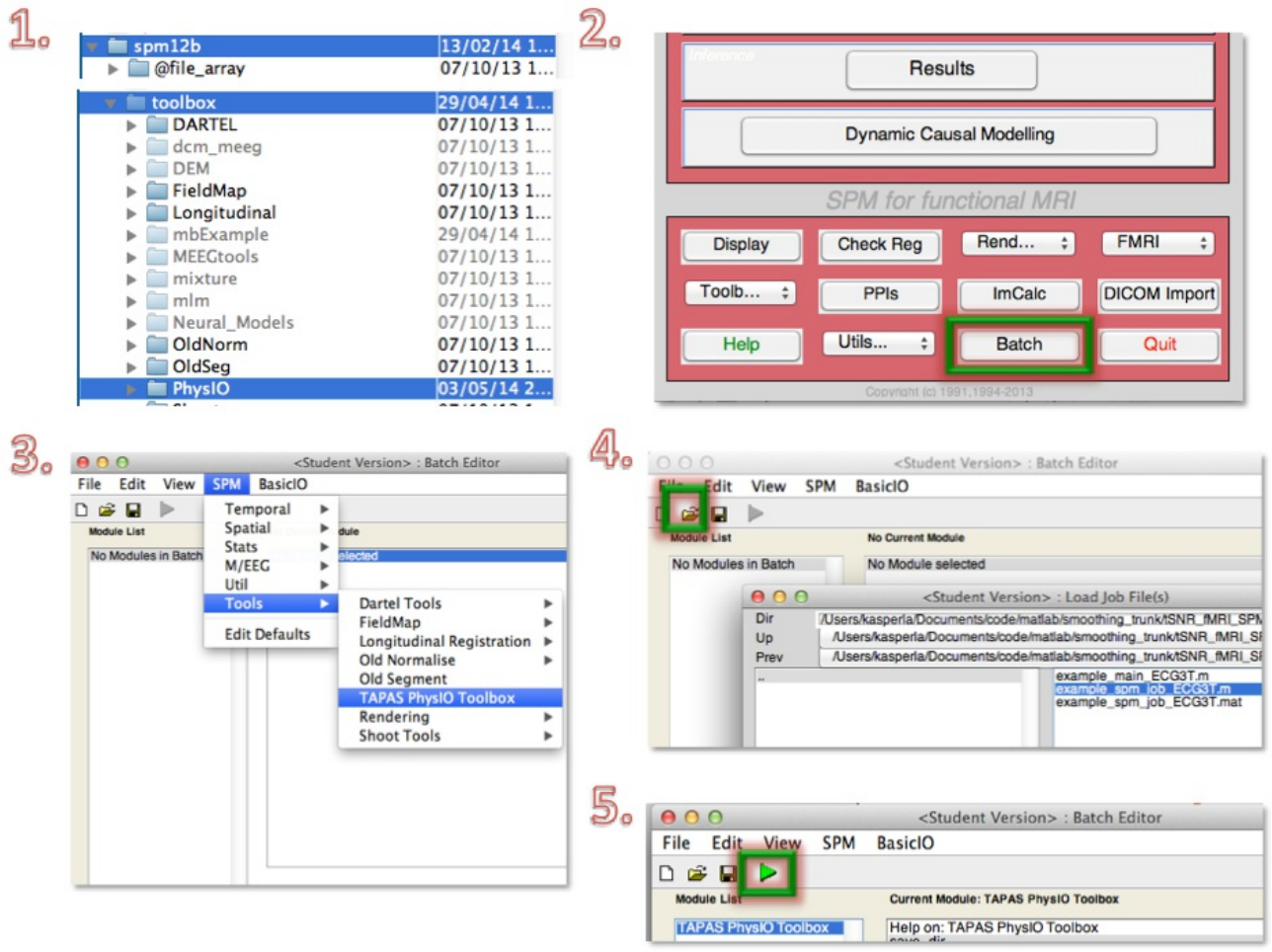
Requirements

- Download the latest PhysIO Toolbox version from the TAPAS software release page on GitHub.
- Download the example data by running `tapas_download_example_data()` in the `misc` subfolder of the TAPAS software download.

One-Page-Quickstart (with SPM)

...of SPM Batch Editor GUI for PhysIO Toolbox

1. Go to the `tapas/PhysIO` folder and run `tapas_physio_init()`
    - This should check whether PhysIO and SPM are properly installed, whether paths are set correctly, and whether the PhysIO code folder is properly linked (or copied, for Windows) to the sub-folder `spm/toolbox`, where SPM expects its Batch Editor toolboxes to reside.
2. (Re-)Start SPM (`spm fmri`) and open the Batch editor (Button Batch in SPM GUI).
3. The PhysIO Toolbox should now show up under SPM -> Tools -> TAPAS PhysIO Toolbox
4. Change directory (!) to `examples/Philips/ECG3T`-folder and open an example spm-job file with the Batch Editor, e.g : `example_philips_ecg3t_spm_job.m`
    - If you click on any of the various parameters, you will see a detailed description in the Help Box in the lower part of the Batch Editor window.
5. Press Play (in the Batch Editor)!
6. Feel free to try out the other batches in other vendor/device subfolders, which always end in `*_spm_job.m` or `*spm_job.mat`



One-Page-Quickstart (Matlab only, no SPM)

1. Go to the `tapas/PhysIO` folder and run `tapas_physio_init()`
2. Change Matlab directory to `examples/Philips/ECG3T`-folder
3. Open an example matlab script, e.g., `example_philips_ecg3t_matlab_script.m`
4. Press Play (in Matlab, or F5)!
5. Feel free to try out the other matlab scrupts in other vendor/device subfolders, which always end in `*_matlab_script.m`
    - A detailed documentation of all parameters is found in `tapas_physio_new.m`, next to each parameter, just open this file with Matlab or any editor.

Troubleshoot

1. If the PhysIO Toolbox does not show up in the SPM Batch Editor, the necessary matlab code-files cannot be found by SPM.
    - Manually copy the PhysIO Toolbox `PhysIO/code` folder to `spm/toolbox/PhysIO` (see Figure 1).
    - Note that this is only the `code` subfolder of PhysIO, i.e., the `tapas_physio*.m` files should be located directly in `spm/toolbox/PhysIO` (**not** `spm/toolbox/PhysIO/code`).

Readme

TAPAS PhysIO Toolbox

Current version: Release 2019a, v7.1.0

> Lars Kasper
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Translational Neuromodeling Unit (TNU)
Institute for Biomedical Engineering
University of Zurich and ETH Zurich

Download

- Please download the latest stable versions of the PhysIO Toolbox on GitHub as part of the TAPAS software releases of the TNU.
- Older versions are available on the TNU website.
- The latest bugfixes can be found in the GitHub Issue Forum or by request to the authors.
- Changes between all versions are documented in the CHANGELOG.

Purpose

The general purpose of this Matlab toolbox is the model-based physiological noise correction of fMRI data using peripheral measures of respiration and cardiac pulsation. It incorporates noise models of cardiac/respiratory phase (RETROICOR, Glover et al. 2000), as well as heart rate variability and respiratory volume per time (cardiac response function, Chang et. al, 2009, respiratory response function, Birn et al. 2006), and extended motion models. While the toolbox is particularly well integrated with SPM via the Batch Editor GUI, its simple output nuisance regressor text files can be incorporated into any major neuroimaging analysis package.

Core design goals for the toolbox were: *flexibility*, *robustness*, and *quality assurance* to enable physiological noise correction for large-scale and multi-center studies.

Some highlights:

1. Robust automatic preprocessing of peripheral recordings via iterative peak detection, validated in noisy data and patients.
2. Flexible support of peripheral data formats (Siemens, Philips, HCP, GE, Biopac, ...) and noise models (RETROICOR, RVHRCOR).
3. Fully automated noise correction and performance assessment for group studies.
4. Integration in fMRI pre-processing pipelines as SPM Toolbox (Batch Editor GUI).

The accompanying technical paper about the toolbox concept and methodology can be found at:
https://doi.org/10.1016/j.jneumeth.2016.10.019

Installation

Matlab

1. Unzip the TAPAS archive in your folder of choice
2. Open Matlab
3. Go to `/your/path/to/tapas/physio/code`
4. Run `tapas_physio_init()` in Matlab

Note: Step (4) executes the following steps, which you could do manually as well.

- Adds the `physio/code/` folder to your Matlab path
- Adds SPM to your Matlab path (you can enter it manually, if not found)
- Links the folder (Linux/Max) or copies the folder (Windows) `physio/code/` to `/your/path/to/SPM/toolbox/PhysIO`, if the PhysIO code is not already found there

Only the first point is necessary for using PhysIO standalone with Matlab. The other two points enable PhysIO's SPM integration, i.e., certain functionality (Batch Editor GUI, pipeline dependencies, model assessment via F-contrasts).

Getting Started

...following the installation, you can try out an example:

1. Download the TAPAS examples via running `tapas_download_example_data()` (found in `misc`-subfolder of TAPAS)
    - The PhysIO Example files will be downloaded to `tapas/examples/<tapas-version>/PhysIO`
2. Run `philips_ecg3t_matlab_script.m` in subdirectory `Philips/ECG3T`
3. See subdirectory `physio/docs` and the next two section of this document for help.

You may try any of the examples in the other vendor folders as well.

Contact/Support

We are very happy to provide support on how to use the PhysIO Toolbox. However, as every researcher, we only have a limited amount of time. So please excuse, if we might not provide a detailed answer to your request, but just some general pointers and templates. Before you contact us, please try the following:

1. A first look at the FAQ (which is frequently extended) might already answer your questions.
2. A lot of questions (before 2018) have also been discussed on our mailinglist tapas@sympa.ethz.ch, which has a searchable archive.
3. For new requests, we would like to ask you to submit them as issues on our github release page for TAPAS, which is also an up-to-date resource to user-driven questions (since 2018).

Documentation

Documentation for this toolbox is provided in the following forms

1. Overview and guide to further documentation: README.md and CHANGELOG.md
    - README.md: this file, purpose, installation, getting started, pointer to more help
    - CHANGELOG.md: List of all toolbox versions and the respective release notes, i.e. major changes in functionality, bugfixes etc.
2. User Guide: The markdown-based GitLab Wiki, including an FAQ
    - online (and frequently updated) at http://gitlab.ethz.ch/physio/physio-doc/wikis/home.
    - offline (with stables releases) as part of the toolbox in folder `physio/wikidocs`:
        - plain text `.md` markdown files
        - as single HTML and PDF file: `documentation.{html,pdf}`
3. Within SPM: All toolbox parameters and their settings are explained in the Help Window of the SPM Batch Editor
4. Within Matlab: Extensive header at the start of each `tapas_physio_*` function and commenting
    - accessible via `help` and `doc` commands from Matlab command line
    - starting point for all parameters (comments within file): `edit tapas_physio_new`
    - also useful for developers (technical documentation)

Background

The PhysIO Toolbox provides physiological noise correction for fMRI-data from peripheral measures (ECG/pulse oximetry, breathing belt). It is model-based, i.e. creates nuisance regressors from the physiological monitoring that can enter a General Linear Model (GLM) analysis, e.g. SPM8/12. Furthermore, for scanner vendor logfiles (PHILIPS, GE, Siemens), it provides means to statistically assess peripheral data (e.g. heart rate variability) and recover imperfect measures (e.g. distorted R-peaks of the ECG).

Facts about physiological noise in fMRI:

- Physiological noise can explain 20-60 % of variance in fMRI voxel time series (Birn2006, Hutton2011, Harvey2008)
  - Physiological noise affects a lot of brain regions (s. figure, e.g. brainstem or OFC), especially next to CSF, arteries (Hutton2011).
  - If not accounted for, this is a key factor limiting sensitivity for effects of interest.
- Physiological noise contributions increase with field strength; they become a particular concern at and above 3 Tesla (Kasper2009, Hutton2011).
- In resting state fMRI, disregarding physiological noise leads to wrong connectivity results (Birn2006).

Therefore, some kind of physiological noise correction is highly recommended for every statistical fMRI analysis.

Model-based correction of physiological noise:

- Physiological noise can be decomposed into periodic time series following heart rate and breathing cycle.
- The Fourier expansion of cardiac and respiratory phases was introduced as RETROICOR (RETROspective Image CORrection, Glover2000, see also Josephs1997).
- These Fourier Terms can enter a General Linear Model (GLM) as nuisance regressors, analogous to movement parameters.
- As the physiological noise regressors augment the GLM and explain variance in the time series, they increase sensitivity in all contrasts of interest.

Features of this Toolbox

Physiological Noise Modeling

- Modeling physiological noise regressors from peripheral data (breathing belt, ECG, pulse oximeter)
  - State of the art RETROICOR cardiac and respiratory phase expansion
  - Cardiac response function (Chang et al, 2009) and respiratory response function (Birn et al. 2006) modelling of heart-rate variability and respiratory volume per time influence on physiological noise
  - Flexible expansion orders to model different contributions of cardiac, respiratory and interaction terms (see Harvey2008, Hutton2011)
- Data-driven noise regressors
  - PCA extraction from nuisance ROIs (CSF, white matter), similar to aCompCor (Behzadi2007)

Automatization and Performance Assessment

- Automatic creation of nuisance regressors, full integration into standard GLMs, tested for SPM8/12 ("multiple_regressors.mat")
- Integration in SPM Batch Editor: GUI for parameter input, dependencies to integrate physiological noise correction in preprocessing pipeline
- Performance Assessment: Automatic F-contrast and tSNR Map creation and display for groups of physiological noise regressors, using SPM GLM tools

Flexible Read-in

The toolbox is dedicated to seamless integration into a clinical research s etting and therefore offers correction methods to recover physiological data from imperfect peripheral measures.

- General Electric
- Philips SCANPHYSLOG files (all versions from release 2.6 to 5.3)
- Siemens VB (files `.ecg`, `.resp`, `.puls`)
- Siemens VD (files `*_ECG.log`, `*_RESP.log`, `*_PULS.log`)

- Siemens Human Connectome Project (preprocessed files `*Physio_log.txt`)
- Biopac .mat-export
  - assuming the following variables (as columns): `data`, `isi`, `isi_units`, `labels`, `start_sample`, `units`
  - See `tapas_physio_read_physlogfiles_biopac_mat.m` for details
- Custom logfiles: should contain one amplitude value per line, one logfile per device. Sampling interval(s) are provided as a separate parameter to the toolbox.

Compatibility

- Matlab Toolbox
- Input:
  - Fully integrated to work with physiological logfiles for Philips MR systems (SCANPHYSLOG)
  - tested for General Electric (GE) log-files
  - implementation for Siemens log-files (both VB and VD/VE, CMRR multiband)
  - also: interface for 'Custom', i.e. general heart-beat time stamps & breathing volume time courses from other log formats
  - BioPac
  - ... (other upcoming formats)
- Output:
  - Nuisance regressors for mass-univariate statistical analysis with SPM5,8,12 or as text file for export to any other package
  - raw and processed physiological logfile data
  - Graphical Batch Editor interface to SPM
- Part of the TAPAS Software Collection of the Translational Neuromodeling Unit (TNU) Zurich:long term support and ongoing development

Contributors

- Lead Programmer:
  - Lars Kasper, TNU & MR-Technology Group, IBT, University of Zurich & ETH Zurich
- Project Team:
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  - Jakob Heinzle, TNU Zurich
  - Chloe Hutton, FIL London, UK (previously)
  - Miriam Sebold, Charite Berlin, Germany

References

Main Toolbox Reference

1. Kasper, L., Bollmann, S., Diaconescu, A.O., Hutton, C., Heinzle, J., Iglesias, S., Hauser, T.U., Sebold, M., Manjaly, Z.-M., Pruessmann, K.P., Stephan, K.E., 2017. The PhysIO Toolbox for Modeling Physiological Noise in fMRI Data. Journal of Neuroscience Methods 276, 56–72. doi:10.1016/j.jneumeth.2016.10.019

Related Papers (Implemented noise correction algorithms and optimal parameter choices)

RETROICOR

2. Glover, G.H., Li, T.Q. & Ress, D. Image-based method for retrospective correction of PhysIOlogical motion effects in fMRI: RETROICOR. Magn Reson Med 44, 162-7 (2000).

3. Hutton, C. et al. The impact of PhysIOlogical noise correction on fMRI at 7 T. NeuroImage 57, 101-112 (2011).

4. Harvey, A.K. et al. Brainstem functional magnetic resonance imaging: Disentangling signal from PhysIOlogical noise. Journal of Magnetic Resonance Imaging 28, 1337-1344 (2008).

aCompCor / Noise ROIs

5. Behzadi, Y., Restom, K., Liau, J., Liu, T.T., 2007. A component based noise correction method (CompCor) for BOLD and perfusion based fMRI. NeuroImage 37, 90–101. doi:10.1016/j.neuroimage.2007.04.042

RVT

6. Birn, R.M., Smith, M.A., Jones, T.B., Bandettini, P.A., 2008. The respiration response function: The temporal dynamics of fMRI s ignal fluctuations related to changes in respiration. NeuroImage 40, 644–654. doi:10.1016/j.neuroimage.2007.11.059

7. Jo, H.J., Saad, Z.S., Simmons, W.K., Milbury, L.A., Cox, R.W., 2010. Mapping sources of correlation in resting state FMRI, with artifact detection and removal. NeuroImage 52, 571–582. https://doi.org/10.1016/j.neuroimage.2010.04.246
regressor delay suggestions

HRV

8. Chang, C., Cunningham, J.P., Glover, G.H., 2009. Influence of heart rate on the BOLD signal: The cardiac response function. NeuroImage 44, 857–869. doi:10.1016/j.neuroimage.2008.09.029

9. Shmueli, K., van Gelderen, P., de Zwart, J.A., Horovitz, S.G., Fukunaga, M., Jansma, J.M., Duyn, J.H., 2007. Low-frequency fluctuations in the cardiac rate as a source of variance in the resting-state fMRI BOLD signal. NeuroImage 38, 306–320. https://doi.org/10.1016/j.neuroimage.2007.07.037
regressor delay suggestions

Motion (Censoring, Framewise Displacement)

10. Siegel, J.S., Power, J.D., Dubis, J.W., Vogel, A.C., Church, J.A., Schlaggar, B.L., Petersen, S.E., 2014. Statistical improvements in functional magnetic resonance imaging analyses produced by censoring high-motion data points. Hum. Brain Mapp. 35, 1981–1996. doi:10.1002/hbm.22307

11. Power, J.D., Barnes, K.A., Snyder, A.Z., Schlaggar, B.L., Petersen, S.E., 2012. Spurious but systematic correlations in functional connectivity MRI networks arise from subject motion. NeuroImage 59, 2142–2154. https://doi.org/10.1016/j.neuroimage.2011.10.018

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FAQ

Frequently Asked Questions (FAQ)

1. What is the PhysIO Toolbox?

PhysIO is a toolbox for model-based physiological noise correction of fMRI data.

PhysIO stands for Physiological Input/Output toolbox, which summarizes its core purpose. A quote from our paper:

> In short, the toolbox transforms physiological input, i.e. peripheral recordings, into physiological output, i.e. regressors encoding components of physiological noise [...] A modular Matlab implementation supports command-line operation and is compatible with all major fMRI analysis packages via the export of regressor text-files. For the Statistical Parametric Mapping SPM software package in particular, PhysIO features a full integration as a Batch Editor Tool, which allows user-friendly, GUI-based setup and inclusion into existing preprocessing and modeling pipelines.

2. How does PhysIO differ from other toolboxes for physiological noise correction for fMRI using peripheral recordings?

Citing from the introduction of our paper again

> ### Highlights
>
> - A Toolbox to integrate preprocessing of physiological data and fMRI noise modeling.
> - Robust preprocessing via iterative peak detection, shown for noisy data and patients.
> - Flexible support of peripheral data formats and noise models (RETROICOR, RVHRCOR).
> - Fully automated noise correction and performance assessment for group studies.
> - Integration in fMRI pre-processing pipelines as SPM Toolbox (Batch Editor GUI).

3. How do I cite PhysIO?

The **core reference for PhysIO** is: *The PhysIO Toolbox for Modeling Physiological Noise in fMRI Data* (http://dx.doi.org/10.1016/j.jneumeth.2016.10.019)

Please cite this paper if you use PhysIO in your work. Moreover, this paper is also a good source for more information on PhysIO (see next question).

A **standard snippet to include** in your method section could look like the following, assuming you use our specific implementation of RETROICOR, which uses Fourier expansions of different order for the estimated phases of cardiac pulsation (3rd order), respiration (4th order) and cardio--respiratory interactions (1st order) following (Harvey et al., 2008)

> Correction for physiological noise was performed via RETROICOR [1,2] using Fourier expansions of different order for the estimated phases of cardiac pulsation (3rd order), respiration (4th order) and cardio--respiratory interactions (1st order) [2]: The corresponding confound regressors were created using the Matlab PhysIO Toolbox ([4], open source code available as part of the TAPAS software collection: https://www.translationalneuromodeling.org/tapas).

1. Glover, G.H., Li, T.Q. & Ress, D. Image--based method for retrospective correction of PhysIOlogical motion effects in fMRI: RETROICOR. Magn Reson Med 44, 162-- 7 (2000).
2. Hutton, C. et al. The impact of PhysIOlogical noise correction on fMRI at 7 T. NeuroImage 57, 101--112 (2011).
3. Harvey, A.K. et al. Brainstem functional magnetic resonance imaging: Disentangling signal from PhysIOlogical noise. Journal of Magnetic Resonance Imaging 28, 1337--1344 (2008).
4. Kasper, L., Bollmann, S., Diaconescu, A.O., Hutton, C., Heinzle, J., Iglesias, S., Hauser, T.U., Sebold, M., Manjaly, Z.-M., Pruessmann, K.P., Stephan, K.E., 2017. The PhysIO Toolbox for Modeling Physiological Noise in fMRI Data. Journal of Neuroscience Methods 276, 56–72. doi:10.1016/j.jneumeth.2016.10.019

If you use **respiratory-volume-per time (RVT), heart--rate variability (HRV), noise ROIs or 12/24 regressor motion modeling**, also include the respective references:

5. Behzadi, Y., Restom, K., Liau, J., Liu, T.T., 2007. A component based noise correction method (CompCor) for BOLD and perfusion based fMRI. NeuroImage 37, 90–101. doi:10.1016/j.neuroimage.2007.04.042
6. Birn, R.M., Smith, M.A., Jones, T.B., Bandettini, P.A., 2008. The respiration response function: The temporal dynamics of fMRI s ignal fluctuations related to changes in respiration. NeuroImage 40, 644–654. doi:10.1016/j.neuroimage.2007.11.059 PhysIO Toolbox I Citing this work 20
7. Chang, C., Cunningham, J.P., Glover, G.H., 2009. Influence of heart rate on the BOLD signal: The cardiac response function.

NeuroImage 44, 857–869. doi:10.1016/j.neuroimage.2008.09.029

8. Siegel, J.S., Power, J.D., Dubis, J.W., Vogel, A.C., Church, J.A., Schlaggar, B.L., Petersen, S.E., 2014. Statistical improvements in functional magnetic resonance imaging analyses produced by censoring high-motion data points. Hum. Brain Mapp. 35, 1981–1996. doi:10.1002/hbm.22307

4. Where do I find more documentation for PhysIO?

- The paper describing its structure, objective and modules
- README.md in the main folder when downloading
    - For help on installation and getting started
- Quickstart
    - PDF (or markdown .md file)
    - Tutorial matlab-scripts
- Reference Manual (for developers)

5. I am using FSL, AFNI, BrainVoyager, etc., for my fMRI analyses. Do I need SPM for PhysIO to work?

No, the basic functionality of PhysIO, i.e. creating nuisance regressors for your GLM analysis, is available in plain Matlab. The following extra functionality related to automatizing and assessing noise correction, require the installation of SPM:

- GUI (SPM Batch Editor)
- Pipeline dependencies (automatic input of realignment parameters, feed-in of multiple regressors file to GLM)
- Model assessment via F-tests and automatic F-map/tSNR report
- Noise-ROIs model (read-in of nifti files via SPM)

6. I am using device X for physiological recordings. Does PhysIO support the physiological logfile format Y?

Currently, PhysIO natively supports the following physiological logfile types:

- Brain Imaging Data Structure (BIDS)
    - [Standard for peripheral recordings] (https://bids-specification.readthedocs.io/en/stable/04-modality-specific-files/06-physiological-and-other-continous-recordings.html)
    - both raw physiological traces and pre-computed pulse events are supported
- BioPac formats
    - Biopac `.mat`-export
        - assuming the following variables (as columns): `data`, `isi`, `isi_units`, `labels`, `start_sample`, `units`
        - See `tapas_physio_read_physlogfiles_biopac_mat.m` for details
    - Biopac `.txt`-export
        - assuming the following 4 columns, with one sample per row: respiratory, skin conductance (GSR), cardiac (PPG), and trigger signal (on/off)
- General Electric
- Philips SCANPHYSLOG files (`SCANPHYSLOG<DateTime>.log` ; all versions from release 2.6 to 5.3)
- Siemens formats
    - Siemens VB (files `.ecg`, `.resp`, `.puls`)
    - Siemens VD/VE (files `*_ECG.log`, `*_RESP.log`, `*_PULS.log`)

        - including CMRR-derived multiband-files
    - Siemens Human Connectome Project log files (preprocessed 3 column files `*_Physio_log.txt`)

See Read-In of Logfiles for a detailed description of the expected file formats.

Furthermore, physiological recordings can be entered via a *custom* data format, i.e., providing one text file per device. The files should contain one amplitude value per line. The corresponding sampling interval(s) are provided as a separate parameter in the toolbox.

If your favourite logfile format is not supported, please contact the developers. We try everything to accomodate the read-in flexibility of the toolbox to your needs.

7. I am running the toolbox for a lot of subjects / on a remote server without graphics. Can I somehow reproduce the output figures relevant to assess the data quality?

Yes you can, using the toolbox function `tapas_physio_review`. This function takes the physio-structure as an input argument, which is per default saved as `physio.mat` in the specified output folder of your batch job.

8. How do I interpret the various output plots of the toolbox?

Have a look at our publication: *The PhysIO Toolbox for Modeling Physiological Noise in fMRI Data* (http://dx.doi.org/10.1016/j.jneumeth.2016.10.019)

The figures there give a good overview of the toolbox output figures, in particular:

- Fig. S1 (supplementary): Philips Scan Timing Sync from `gradient_log` (explanation of `thresh.zero`, `thresh.sli`, `thresh.vol`, `thresh.vol_spacing`
- Fig. 3: Diagnostic Raw Time Series (cardiac cycle length curve, respiration histogram)
- Fig. 8C: Single Subject F-contrast results (cardiac regressors)
- Fig. 9: Group results/typical activation sites for F-contrasts of RETROICOR regressors (cardiac/resp/interaction)

9. I want to access subject's physiological measures, e.g. heart rate or respiratory volume (per time), before they enter the regressors. Where can I do that?

All intermediate data processing steps (e.g. filtering, cropping) of the peripheral data, including the computation of physiologically meaningful time courses, such as heart rate and respiratory volume, are saved in the substructure `ons_secs` ("onsets in seconds) of the physio-structure mentioned in question 7. This structure is typically saved in a file `physio.mat`.

`physio.ons_secs` then contains the different time courses, cropped to the acquisition window synchronized to your fMRI scan (the same values before synchronization/cropping, is found in `physio.ons_secs.raw`). Here are the most important ones:

- `ons_secs.t` = []; % time vector corresponding to c and r
- `ons_secs.c` = []; % raw cardiac waveform (ECG or PPU)
- `ons_secs.r` = []; % raw respiration amplitude time course
- `ons_secs.cpulse` = []; % onset times of cardiac pulse events (e.g. R-peaks)
- `ons_secs.fr` = []; % filtered respiration amplitude time series
- `ons_secs.c_sample_phase` = []; % phase in heart-cycle when each slice of each volume was acquired
- `ons_secs.r_sample_phase` = []; % phase in respiratory cycle when each slice of each volume was acquired
- `ons_secs.hr` = []; % [nScans,1] estimated heart rate at each scan
- `ons_secs.rvt` = []; % [nScans,1] estimated respiratory volume per time at each scan

- `ons_secs.c_outliers_high` = []; % onset of too long heart beats
- `ons_secs.c_outliers_low` = []; % onsets of too short heart beats
- `ons_secs.r_hist` = []; % histogram of breathing amplitudes

For a detailed list of all properties and their documentation, read the source code of `tapas_physio_new.m`

10. What is the order of the regressor columns in the multiple regressors file?

This depends on the physiological models (and their order) specified in the `model`-submodule of physio (or in the batch editor). The general order is outlined in Fig. 7A of the Main PhysIO Toolbox Paper. The []-brackets indicate the number of regressors:

1. RETROICOR cardiac regressors [2 x nOrderCardiac]
2. RETROICOR respiratory regressors [2 x nOrderRespiratory]
3. RETROICOR cardXResp interaction regressors [4 x nOrderCardiacXRespiratory]
4. HRV [nDelaysHRV]
5. RVT [nDelaysRVT]
6. Noise ROIs (PCA signatures and mean of each region) [nNoiseROIs x (nComponents+1)]
7. Other (included other text file) [nColumnsOtherFile]
8. Motion [6 or 12 or 24, depending on motion model]

If any of the models was not specified, the number of regressors is reduced accordingly.

11. How do I know whether the physiological noise correction worked?

The best way to assess the quality of the correction is an F-test over the respective physiological noise model regressors in the design matrix. Luckily, if you use SPM, the toolbox can create these contrasts and corresponding output plots with overlays of your brain automatically via calling the following function in the Matlab command window:

```
args = tapas_physio_report_contrasts(...
                'fileReport', 'physio.ps', ...
                'fileSpm', 'analysisFolder/SPM.mat', ...
                'filePhysIO', 'analysisFolder/physio.mat', ...
                'fileStructural', 'anatomyFolder/warpedAnatomy.nii')
```

Of course, you will have to adapt all paths to your `SPM.mat`, `physio.mat` and `anatomy.nii` files. There are more parameters to set (e.g. F-contrast thresholds), type `help tapas_physio_report_contrasts` for a list of options.

There should be whole-brain multiple-comparison corrected "activation" in physiological noise sites (similar to Fig. 8C or 9 in our paper.

If your F-contrast results differ or are absent, have a look at the *Diagnostic raw physiological time series*-plot and check whether it resembles Fig. 3 in the paper or whether there are any suspicious spikes in the heart cycle length.

Other than that, scan timing synchronisation is a major source of error, so always check the *Cutout actual scans* plot, whether the curves and scan events, TR etc. make sense.

12. Philips: I would like to use the gradient log for timing synchronization, but how do I set the thresholds?

Have a look at the following figure:

1. SUPPLEMENTARY MATERIAL

1.1. Figure S1

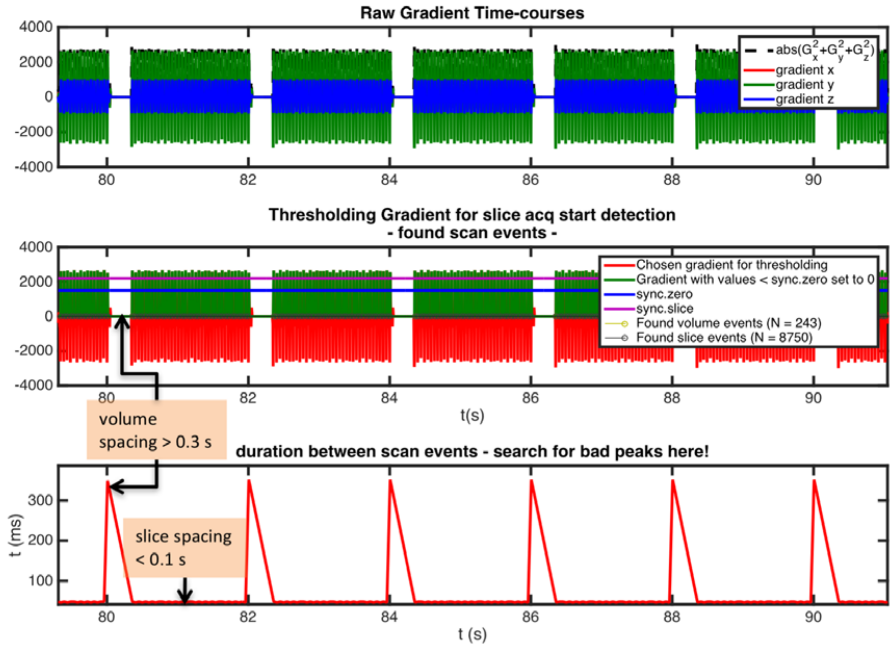

Figure S1: *Determining scan timing from gradient logging for Philips data (`sync.method = 'gradient_log'`). Besides cardiac and respiratory data, the Philips SCANPHYSLOG-file stores time courses of the x,y,z-gradients at a coarse temporal resolution (2 ms) (top). Their regularity, however, is sufficient to infer on slice and volume repetitions, and does not change over subjects. Thus, for each study, one only has to determine once which gradient shows the highest regularity (e.g. `sync.grad_direction = 'y'`, green curve), set lower thresholds for irrelevant and slice peaks (middle, `sync.zero = 1500`, blue line; `sync.slice = 2200`, magenta line), as well as volume peaks, if they differ from slice peaks (not shown, `sync.vol = []`). If volume peaks are not discernible, the non-equidistant slice spacing between volumes can be used to identify volume onsets (bottom, red curve, `sync.vol_spacing = 0.3` seconds).*

This figure can be found as figure S1 in the supplementary material of our paper.

The following heuristics might help with the threshold settings in the `sync` structure:

1. Note that these thresholds have to be set correctly only once for each functional sequence, i.e., usually once per study. Even small changes to scan geometry (e.g. slice tilt) between subjects shouldn't affect them significantly.

2. Setting the thresholds is an iterative procedure. You might start with the defaults, probably running into an error or warning

(`Warning: Invalid MinPeakHeight. There are no data points greater than MinPeakHeight.` or `Not enough volume/slice scan events found`). Then you inspect the figure output resembling the one above and adjust (usually lower) the thresholds in the order mentioned below.

3. There are three time courses in the upper of the three subplots shown in the figure. These time courses show the traces of the three gradient directions `x`, `y`, `z`. Choose the one as `sync.grad_direction` parameter that has the highest peaks and most regular features reflecting slice and/or volume scan events.

4. `sync.zero` has to be smaller than `sync.slice` and `sync.vol`. It should be about 4/5 of the typical peak height in the gradient trace. Note that you can set this thresholds (and all other) either in absolute values or relative to the maximum peak height. Set a value below 1, if you prefer the latter.

5. `sync.slice` should be about 9/10 of the typical peak height of a slice scan event.

6. `sync.vol`, if you set it, should be larger than `sync.slice`. It should be 9/10 of the peak height that stands out at the beginning of a volume, and is followed by some dozens of smaller peaks (for the slices) typically. It might be, however, that there is no such peak marking the start of a volume. If so, you might try `sync.vol_spacing` or leave it empty and rely on the slice thresholds exclusively

7. `sync.vol_spacing`, if set, should reflect the temporal spacing (in seconds), between the end of the previous volume and the start of the next one. The figure above gives some idea how to do that based on the bottom subplot that shows peak onset differences. If once every few seconds (your `TR`) you find an exposed peak, its height will give you the value for `sync.vol_spacing` (maybe reduce it by about 5-10ms to allow for timing inaccuracies).

13. How do I know which logfile type ('vendor') I have to choose?

- Typically, you will know your scanner manufacturer or the supplier of your peripheral recording device. The currently supported vendors can always be found in the SPM Batch Editor, as dropdown options for the vendor parameter in any PhysIO batch, and are also listed as cases in `tapas_physio_read_physlogfiles.m`.

- For Siemens, since there are a couple of formats, it is often helpful to check the extensions of the files (or the file name structure in general) see question 7.

- Sometimes you will have to look in the log files themselves and compare them to the examples provided on the Data Section of our homepage.

14. What does Parameter *XY* mean and what is its best setting?

Before you ask us directly, there are two simple ways to find out more about the parameters and options of the PhysIO toolbox:

- In SPM, you can use the Batch Editor as a Help GUI directly. If you open or create a TAPAS PhysIO Batch and click on any parameter, there will be useful information about its meaning and suitable values in the help window, located in the lower part of the Batch Editor.

- Within Matlab, type `edit tapas_physio_new`. This constructor function lists all parameters of the physio-structure with inline comments on their purpose and possible values.

15. I cannot find the answer to my question in the FAQ. Whom do I ask for help?

We are very happy to provide support on how to use the PhysIO Toolbox. However, as every researcher, we only have a limited amount of time. So please excuse, if we might not provide a detailed answer to your request, but just some general pointers and templates. Before you contact us, please try the following:

1. A first look at the FAQ (which is frequently extended) might already answer your questions.

2. A lot of questions have also been discussed on our mailinglist tapas@sympa.ethz.ch, which has a searchable archive.

3. For new requests, we would like to ask you to submit them as issues on our github release page for TAPAS.

Examples

Example Datasets for PhysIO

The following datasets are available to explore the read-in and modeling capabilities of PhysIO. They can be downloaded by running the function `tapas_download_example_data()` in Matlab, which is located in the `misc` subfolder of the TAPAS software release you downloaded (probably here).

Afterwards, the examples can be found in `tapas/examples/<tapasVersion>/PhysIO` as different subfolders (`vendor/device`) and shall be run directly from within these individual folders.

Besides the raw physiological logfiles, each example contains example scripts to run PhysIO as

- SPM job (`*spm_job.mat`)
- editable SPM job (`*spm_job.m`)
- plain matlab script (`*matlab_script.m`)

Brain Imaging Data Structure (BIDS)

CPULSE 3T

Courtesy of Hrvoje Stojic, Max Planck UCL Centre for Computational Psychiatry and Ageing Research, University College London

Vendor-computed (software: Spike2) cardiac pulse events from PPU (finger plethysmograph) data, Siemens 3T scanner, Multiband CMRR sequence

Description: This datasets contains the (compressed) tab-separated value (`.tsv.gz`) files as well as the meta-file (`.json`) holding sampling rate of the physiological recording, and its relative onset to scanning, in adherence with the BIDS standard for peripheral recordings files.

PPU 3T

Courtesy of Hrvoje Stojic, Max Planck UCL Centre for Computational Psychiatry and Ageing Research, University College London

PPU (finger plethysmograph) and breathing belt, Siemens 3T scanner, Nultiband CMRR sequence

Description: Similar to CPULSE3T (same acquisition system), but now with analog data instead of vendor-detected pulses, data from different subject

General Electric

PPU 3T

Courtesy of Steffen Bollmann, Kinderspital Zurich and ETH Zurich

PPU (finger plethysmograph) and breathing belt, General Electric 3T scanner

Description: Similar to PPU, but acquired on a GE system with two separate output logfiles for pulse oximetry and breathing amplitude, sampled with 40 Hz. The quality of the signal is particularly challenging, stemming from a patient population.

Philips

ECG 3T

Courtesy of Sandra Iglesias, Translational Neuromodeling Unit, ETH & University of Zurich

4-electrode ECG and breathing belt, Philips 3T Achieva scanner

Description: Standard example; shows how to use volume counting either from beginning or end of run to synchronize physiological logfile with acquisition onsets of fMRI scans.

ECG 7T

Courtesy of Zina-Mary Manjaly, University Hospital Zurich

4-electrode ECG and breathing belt, Philips 7T Achieva scanner

Description: The ECG data for ultra-high field data is typically much noisier than at 3 Tesla. Therefore, R-wave peaks are frequently missed by prospective trigger detection and not marked correctly in the logfile. This example shows how to select typical R-wave-peaks manually and let the algorithm find the heartbeat events.

PPU 3T

Courtesy of Diana Wotruba, University and University Hospital of Zurich

PPU (finger plethysmograph) and breathing belt, Philips 3T Achieva scanner

Description: Similar to ECG3T, but a plethysmograph instead of an ECG was used to monitor the cardiac pulsation. Example shows how to extract heart and breathing rate.

Siemens - VB

Siemens has different physiological logfile formats, for which examples are provided here. A detailed description of these formats is on a different wiki page.

This is the older Siemens log file format (also available via *manual recording*), which is part of software release *VB*, and can be determined by the file extensions `.resp`, `.ecg`, `.puls`, in combination with an optional `.dcm` DICOM header file for the first acquired volume.

A lot of 7T scanners still use this format.

ECG 3T

Courtesy of Miriam Sebold, Charite Berlin, and Quentin Huys, TNU Zurich

4-electrode ECG data, Siemens 3T scanner

Description: Similar to ECG 3T, but acquired on a Siemens system with only one logfile for ECG data. The quality of the signal is challenging, stemming from a patient population.

Siemens - HCP

The Human Connectome Project uses Siemens scanners, and the logfile format that comes with their published data seems to be pre-converted and custom (even though the documentation desribes the VB format). We have implemented an own reader for that and written a little tutorial for a single subject dataset of the HCP.

https://github.com/translationalneuromodeling/tapas/issues/6#issuecomment-361001716

If you download the whole dataset (including functional image files), this example with the additional batches mentioned below also demonstrates how to use the toolbox for model assessment using statistical maps (F-contrasts).

HCP (Subject 178748)

You will have to download the dataset from the HCP yourself, we just provide the matlab batches and the physiological logfile `tfMRI_MOTOR_LR_Physio_log.txt` here.

For consistency with the other example files, the batch files have been renamed compared to the blog entry:

- `batch_preproc.m` -> `batch_preproc.m`
- `batch_physio.m` -> `siemens_hcp_ppu3t_spm_job.m`
- `batch_glm.m` -> `batch_glm.m`

If you want to run the preproc and glm batch, place them on the same level as the subject folder `178748` for the downloaded data. The physio-batch shall reside in the same folder as the physiological logfile `tfMRI_MOTOR_LR_Physio_log.txt`.

Siemens - VD/VE Tics

This is the most recent logfile format of Siemens, included in Software releases *VD*, *VE* and sometimes referred to as the *Tics* format, because all time stamps in all files refer to the same reference point (start of the day) and count in the same intervals or "*tics*" of 2.5 ms from there.

You will recognize this file format via the extensions `_Info.log` (or `_AcquisitionInfo.log`), `_RESP.log`, `_ECG.log` and `_PULS.log`. Sometimes, it is also written into the DICOM header (`.dcm`) file of your functional data directly. In this case, use extractCMRRPhysio.m to convert it to the above separate files before using PhysIO.

Most modern Siemens scanners, such as the Prisma or 7T Terra, use this format.

There are a couple of variants for this format around (e.g., with the WIP Multiband Protocol that is distributed to multiple sites), and PhysIO tries to support all of them.

PPU 3T

Courtesy of Saskia Bollmann, Centre for Advanced Imaging, University of Queensland, Brisbane, Australia

Pulse oximetry and breathing belt data, Siemens Prisma 3T, logfile version `EJA_1`, multi-echo fMRI (3 echoes)

The UUID and date/time stamps were altered for anonymization.

Technical Documentation: Read-in Brain Imaging Data Structure (BIDS)

PhysIO supports physiological logfiles prepared according to the BIDS standard

- In brief, BIDS files are (optionally compressed) tab-separated values (`*.tsv[.gz]`) files that contain raw traces of peripheral recordings from cardiac and respiratory sources, as well as scan trigger events
- The header of the columns of this `*.tsv` file, as well as meta-information, such as sampling rate and relative onset of physiological logging to MRI scan onset is described in an accompanying `*.json` file
  - It is assumed to have the that this `*.json` file has the same name (apart from the extension) as the `*.tsv` file
  - If PhysIO does not find this file, you can manually enter the timing information in the `log_files` structure, and a default column order of (cardiac, respiratory, trigger) is assumed
- Example `*.tsv` file (with cardiac, respiratory, trigger column :

```
-0.949402 -0.00610382 0
-0.949402 -0.00610382 0
-0.951233 -0.00915558 0
-0.951233 -0.00915558 0
-0.953064 -0.0122073  0
-0.953064 -0.0122073  0
-0.95459  -0.0076297  1
-0.95459  -0.0076297  0
```

- Example `*.json` file:

```
{
  "SamplingFrequency": 50.0,
  "Columns": [
      "cardiac",
      "respiratory",
      "trigger"
  ],
  "StartTime": -255.45
}
```

- See `tapas_physio_read_physlogfiles_bids.m` for more details and technical documentation.

BioPac

Mat-file Export (`.mat`)

- assuming the following variables (as columns): `data`, `isi`, `isi_units`, `labels`, `start_sample`, `units`

- See `tapas_physio_read_physlogfiles_biopac_mat.m` for details

Single Text File Export (`.txt`)

```
RESP - RSP100C    GSR - EDA100C-MRI    PPG - PPG100C    Marker
-0.949402    -0.00610382    0.0134277    0
-0.949402    -0.00610382    0.0134277    0
...
-0.951233    -0.00915558    0.0204468    11
-0.951233    -0.00915558    0.0204468    11
-0.953064    -0.0122073    0.0259399    0
...
```

Custom

If you have logfile data from any other vendor than the ones specified below, you may still use it with PhysIO:

1. Export your traces from cardiac and breathing recording devices into 2 text files and select `log_files.vendor = 'Custom'`. The format is explained in `tapas_physio_new` or the help window of the Batch Editor:
    - 'Custom' expects the logfiles (separate files for cardiac and respiratory) to be plain text, with one cardiac (or respiratory) sample per row;
    - If heartbeat (R-wave peak) events are recorded as well, they have to be put as a 2nd column in the cardiac logfile by specifying a 1; 0 in all other rows, e.g.

      ```
      0.2  0
      0.4  1 <- cardiac pulse event
      0.2  0
      -0.3 0
      ```

2. You have to specify the sampling intervals for these log files (in seconds), via `log_files.sampling_interval`, e.g. [0.01 0.02] if you have 10 ms (100 Hz) and 20 ms (50 Hz) sampling intervals (frequencies) for cardiac and respiratory data, respectively
3. You will probably have to change `log_files.relative_start_acquisition`, if logging of your physiological recording device does not start synchronized to the first fMRI volume.

General Electric (GE)

- Very similar to custom format
- One text file each for ECG, pulse oximetry and respiratory data, e.g., `ECGData_epiRT_phys_0921201215_38_08` or `RespData_epiRT_phys_0921201215_38_08`
- One amplitude entry per line, e.g.,

  ```
  2626
  2649
  2673
  2699
  2727
  2755
  ```

- sampling rate is determined as a setting beforehand, has to be noted manually (not in log file)

Philips

- Physiology automatically recorded into `SCANPHYSLOG_<Date>_<Time>.log` (one file per scan) as soon as ECG is connected to scanner, and scan is started
- tabular text (ascii) format, different columns for ECG, pulse oximetry and breathing data
    - additionally, trigger events and gradient timecourses are logged, and can be used for synchronization by the toolbox

```
## <YourScannerLocation>, Release r32 (SWID 77)
## Mon 01-01-2011 12:00:01
## 2628 1214 775 387 -1024 -323 -780 -274 0
## Dockable table = FALSE
# v1raw v2raw  v1 v2  ppu resp  gx gy gz mark
-458 325  -494 2  0 -762  0 0 0 0000
-497 284  -527 -32  0 -745  0 0 0 0000
-533 251  -560 -68  0 -745  0 0 0 0000
-571 219  -592 -104  0 -745  0 0 0 0000
-606 190  -623 -139  0 -745  0 0 0 0000
```

- fixed sampling rate (2 ms for cable connection, 1/496 ms for Wi-Fi devices)

Siemens

Manual Recording

Physiological data collection on the Siemens scanners uses the physiological monitoring unit (PMU). The initial sampling is performed at 400 Hz, but through the PMU buffer the effective sampling intervals are ECG: 2.5 ms, RESP: 20 ms, PULS: 20 ms and EXT: 5 ms.

There are several ways to control the physiological data collection. The 'manual' version is available on all platforms. It uses the telnet mpcu/ideacmdtool to manually start and stop the log file acquisition. The log files (logFileName.ecg, logFileName.resp, logFileName.puls, logFileName.ext) are stored in `\MedCom\log`. More details on how to record these data can be found here or in the "Other Miscellaneous Topics" slides from the IDEA course.

An example of a .puls logfile is given below. The data are stored in one long line. The text between 5002 and 6002 forms the header, and the text between 5003 and 6003 the footer. Important information in the footer is the LogStartMDHTime and the LogStopMDHTime (in ms since midnight), which can be used to synchronize the logfiles with the dicom images using the AcquisitionTime in the dicom header (in hhmmss.ms). The values 5000 and 6000 are inserted into the signal trace and indicate trigger events. Note that only the modality which is selected to be displayed during the acquisition will have triggers.

```
1 2 40 280 5002 Logging PULSE signal: reduction factor = 1, PULS_SAMPLES_PER_SECOND = 50; PULS_SAMP
LE_INTERVAL = 20000 6002 1653 1593 1545 1510 1484 ...
ACQ FINISHED
 6002 3093 3096 3064 5000 3016 2926 5003
ECG  Freq Per: 0 0
PULS Freq Per: 66 906
RESP Freq Per: 18 3260
EXT  Freq Per: 0 0
ECG  Min Max Avg StdDiff: 0 0 0 0
PULS Min Max Avg StdDiff: 731 1113 914 1
RESP Min Max Avg StdDiff: 3080 4540 3779 73
EXT  Min Max Avg StdDiff: 0 0 0 0
NrTrig NrMP NrArr AcqWin: 0 0 0 0
LogStartMDHTime:  47029710
LogStopMDHTime:   47654452
LogStartMPCUTime: 47030087
LogStopMPCUTime:  47652240
6003
```

CMRR Sequence

The CMRR sequence on VD/VE also allows the automatic recording of physiological log files (to be selected in the sequence special card). For more information have a look at the manual. The physiological traces are stored in logFileName_PULS.log, logFileName_RESP, logFileName_ECG.log. Timing information is stored in logFileName_Info.log and external trigger events in logFileName_EXT.log.

An example of the current format (December 2017, Release 016a) for the logFileName_Info.log is given below:

```
UUID        = 7a16ea95-ac36-4ee3-9b76-bbb686ac07ca
ScanDate    = 20171206_150609
LogVersion  = EJA_1
LogDataType = ACQUISITION_INFO
NumSlices   = 48
NumVolumes  = 30
NumEchoes   = 3

VOLUME   SLICE   ACQ_START_TICS  ACQ_FINISH_TICS  ECHO

     0       0         21754755         21754762     0
     0      12         21754755         21754762     0
     0      24         21754755         21754762     0
     0      36         21754755         21754762     0
     0       0         21754763         21754770     1
     0      12         21754763         21754770     1
     0      24         21754763         21754770     1
     0      36         21754763         21754770     1
     0       0         21754771         21754779     2
     0      12         21754771         21754779     2
     0      24         21754771         21754779     2
     0      36         21754771         21754779     2
     0       5         21754787         21754795     0
     0      17         21754787         21754795     0
     0      29         21754787         21754795     0
     0      41         21754787         21754795     0
     0       5         21754795         21754803     1
     0      17         21754795         21754803     1
```

The accompanying logFileName_PULS.log looks like this:

```
UUID        = 7a16ea95-ac36-4ee3-9b76-bbb686ac07ca
ScanDate    = 20171206_150609
LogVersion  = EJA_1
LogDataType = PULS
SampleTime  = 2

ACQ_TIME_TICS  CHANNEL  VALUE  SIGNAL

     21747857     PULS   2086
     21747859     PULS   2076
     21747861     PULS   2071
     21747863     PULS   2057
     21747867     PULS   2038
     21747869     PULS   2024
     21747871     PULS   2010
     21747873     PULS   1991
     21747875     PULS   1976
     21747877     PULS   1962
```

PhysIO uses the logFileName_Info.log to synchronize the physiological traces with the data acquisition. Note that the reference slice does not yet take into account the multiband slice ordering, but just assumes an even distribution. Older version of the CMRR sequence produced slightly different output files, which might work. Please log an issue if you have a very different format that is not supported.

Human Connectome Project

Disclaimer: Most of the information below is a best guess from the developers, but without any guarantee of accuracy.

The physiological log file (`*paradigm*_Physio_log.txt`) distributed with the Human Connectome Project data contains respiratory and puls-oximeter data in one file. The first column marks when data acquisition is performed, the second and third contain the respiratory and puls-oximeter traces, respectively. The files are written at a sampling rate of 400Hz and start and end with the scan. PhysIO does provide a reader, you just need to select the appropriate option in the file format tab. An example is provided below:

```
1    1904    1756
1    1904    1756
1    1907    1754
1    1904    1756
1    1907    1756
1    1907    1756
1    1907    1758
1    1907    1760
1    1910    1760
1    1907    1762
1    1907    1762
1    1904    1764
1    1907    1766
1    1904    1766
1    1907    1768
1    1907    1768
1    1904    1768
1    1904    1770
1    1904    1770
1    1904    1772
1    1904    1772
1    1904    1776
1    1904    1776
1    1904    1778
1    1904    1780
```

Version History (Changelog)

RELEASE INFORMATION

Current Release

Current version: PhysIO Toolbox Release R2019a, v7.1.0

March 19, 2019

Minor Release Notes (R2019a, v7.1.0)

Added

- BIDS reader and example (Brain Imaging Data Structure, http://bids.neuroimaging.io/bids_spec.pdf) for `*_physio.tsv[.gz]/.json` files
- Added BioPac txt-File read-in and example
- Template example with all physio-fields for matlab script and settings as in default SPM batch
- Started unit testing framework in folder `tests`
  - example functions for findpeaks and BIDS readin
  - reference data saved with example data in subfolder `TestReferenceResults`
  - reference data reflects physio structure after running example scripts with PhysIO R2019a

Changed

- put all functions in `code` into subfolders relating to different modules: `readin`, `sync`, `preproc`, `model`, `assess`, `utils` (gitlab-issue #58)
  - updated deployment `tapas_physio_init` because of that
  - updated figure names to reflect respective code module
- matlab-script examples now contain more comments
  - fixed internal bug that prepended absolute paths to input logfiles in automatic example generation

- `tapas_physio_create_noise_rois_regressors` with more flexible ROI reslicing options (speed-up) and uses `spm_erode` (no Matlab image processing toolbox needed), thanks to a contribution by Benoît Béranger
- introduced semantic version numbers for all previous releases, and changed Release numbering to R style
- extended documentation (FAQ, new read-in BIDS)
- several bugfixes (Sep 18 - Mar 19), see GitHub Issues

Removed

- `tapas_physio_findpeaks` now refers to current Matlab signal processing toolbox implementation, instead of copy of older version
- some Matlab toolbox dependencies by custom simplified functions (e.g., `suptitle`)

Bugfix Release Notes (R2018.1.3, v7.0.3)

Changed

- fixed bug for matching of Philips SCANPHYSLOG-files (Gitlab #62), if physlogs were acquired on different days, but similar times

Bugfix Release Notes (R2018.1.2, v7.0.2)

Added

- BioPac txt-file reader (for single file, resp/cardiac/trigger data in different columns)

Changed

- fixed bug for 3D nifti array read-in in tapas_physio_create_noise_rois_regressors (github issue #24, gitlab #52)

Bugfix Release Notes (R2018.1.1, v7.0.1)

Changed

- documentation.{html,pdf} export nicer with different FAQ numbering

Major Release Notes (R2018.1, v7.0.0)

Added

- initialization function `tapas_physio_init()` to check Matlab paths, including SPM for batch processing
- Extended motion diagnostics via Framewise displacement (Power et al., 2012)
  - Outlier motion models generate 'spike' regressors from FD outliers (gitlab issue #)
- Censoring of intervals with bad physiological recordings in RETROICOR regressors (github issue #11, gitlab #36)
- Added examples of Siemens VD (Tics Format, Prisma) and Human Connectome Project (HCP) format

Changed

- Updated read-in examples of all vendors (Siemens, Philips, GE) to latest PhysIO Toolbox version.
- Updated `README.md` to reflect changes to example download, new references
- Extended Wiki documentation, in particular examples and read-in formats

Minor Release Notes (R2017.3, v6.3.0)

- Included references to external ETH gitlab physio-doc repo and wiki
- New Human Connectome Project reader for preprocessed Siemens 3-column logfiles (`*Physio_log.txt`)

- Updated Siemens Reader for Multiband patches(CMRR), versions EJA_1
  - including multi-echo data (4,5 columns)
  - multi-channel ECG data
  - significant speed up of read-in
  - generalized framework for later changes to format
  - interpolation of different sampling rates RESP/CARDIAC
- updated README about documentation, new support policy and TAPAS on GitHub
- extended FAQ

Minor Release Notes (R2017.2, v6.2.0)

- Included Markdown-based documentation via Wiki (also CITATION, LICENSE, CHANGELOG.md)
- Included FAQ in Wiki
- Split git repositories into public, dev, examples, and added wiki, to disentangle development from deployed toolbox code and data
- Bugfix and Typo correction
- Philips SCANPYHSLOG for their software release 5.1.7.

Minor Release Notes (R2017.1, v6.1.0)

- Substantially improved Siemens interface, both for VB/VD and 3T/7T releases
  - several bugfixes
  - based on extensive user feedback from Berlin and Brisbane
- New functionality tapas_physio_overlay_contrasts.m to display non-physio contrasts automatically as well

Major Release Notes (r904 / R2016.1, v6.0.0)

- Software version for accepted PhysIO Toolbox Paper: doi:10.1016/j.jneumeth.2016.10.019
- Tested and expanded versions of examples
- Improved stability by bugfixes and compatibility to Matlab R2016
- Slice-wise regressor creation
- Detection of constant physiological time series (detachment, clipping)
- Refactoring of report_contrasts and compute_tsnr_gains as standalone functionality
- Improved Read-in capabilities (Siemens respiration data, BioPac .mat)
- Migration from svn (r904) to git (tnurepository) for version control

Major Release Notes (r835, v5.0.0)

- Software version for Toolbox Paper submission
- Noise ROIs modeling
- Extended motion models (24 parameters, Volterra expansion)
- HRV/RVT models with optional multiple delay regressors
- Report_contrasts with automatic contrast generation for all regressor groups
- compute_tsnr_gains for individual physiological regressor groups

- consistent module naming (scan_timing, preproc)
- Visualisation improvement (color schemes, legends)

Minor Release Notes (r666, v4.1.0)

- Compatibility tested for SPM12, small bugfixes Batch Dependencies
- Cleaner Batch Interface with grouped sub-menus (cfg_choice)
- new model: 'none' to just read out physiological raw data and preprocess, without noise modelling
- Philips: Scan-timing via gradient log now automatized (gradient_log_auto)
- Siemens: Tics-Logfile read-in (proprietary, needs Siemens-agreement)
- All peak detections (cardiac/respiratory) now via auto_matched algorithm
- Adapt plots/saving for Matlab R2014b

Major Release Notes (r534, v4.0.0)

- Read-in of Siemens plain text log files; new example dataset for Siemens
- Speed up and debugging of auto-detection method for noisy cardiac data => new method thresh.cardiac.initial_cpulse_select.method = 'auto_matched'
- Error handling for temporary breathing belt failures (Eduardo Aponte, TNU Zurich)
- slice-wise regressors can be created by setting sqpar.onset_slice to a index vector of slices

Major Release Notes (r497, v3.0.0)

- SPM matlabbatch GUI implemented (Call via Batch -> SPM -> Tools -> TAPAS PhysIO Toolbox)
- improved, automatic heartbeat detection for noisy ECG now standard for ECG and Pulse oximetry (courtesy of Steffen Bollmann)
- QuickStart-Manual and PhysIO-Background presentation expanded/updated
- job .m/.mat-files created for all example datasets
- bugfixes cpulse-initial-select method-handling (auto/manual/load)

Major Release Notes (r429, v2.0.0)

- Cardiac and Respiratory response function regressors integrated in workflow (heart rate and breathing volume computation)
- Handling of Cardiac and Respiratory Logfiles only
- expanded documentation (Quickstart.pdf and Handbook.pdf)
- read-in of custom log files, e.g. for BrainVoyager peripheral data
- more informative plots and commenting (especially in tapas_physio_new).

Minor Release Notes (r354, v1.1.0)

- computation of heart and breathing rate in Philips/PPU/main_PPU.m
- prefix of functions with tapas_*

Major Release Notes (r241, v1.0.0)

- complete modularization of reading/preprocessing/regressor creation for peripheral physiological data

- manual selection of missed heartbeats in ECG/pulse oximetry (courtesy of Jakob Heinzle)
- support for logfiles from GE scanners (courtesy of Steffen Bollmann, KiSpi Zuerich)
- improved detection of pulse oximetry peaks (courtesy of Steffen Bollmann)
- improved documentation
- consistent function names (prefixed by "physio_")

NOTE: Your main_ECG/PPU.m etc. scripts from previous versions (<=r159) will not work with this one any more. Please adapt one of the example scripts for your needs (~5 min of work). The main benefit of this version is a complete new variable structure that is more sustainable and makes the code more readable.

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```
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```

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under certain conditions; type `show c' for details.
```

The hypothetical commands `show w' and` show c' should show the appropriate parts of the General Public License. Of course, your program's commands might be different; for a GUI interface, you would use an "about box".

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