CVR-MRICloud Operation Instructions for the MarkVCID Study
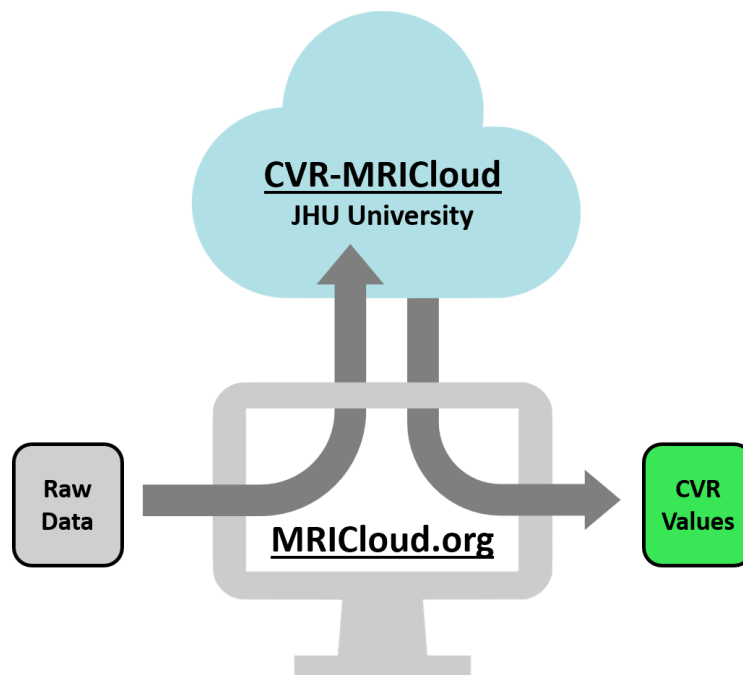
The contents of this document are intended to provide the MarkVCID sites a holistic set of instructions for processing CVR data with CVR-MRICloud. Questions may be sent to zbaker3@jhmi.edu.

CVR-MRICloud is a cloud-based processing tool which allows users to upload data online and then later download fully processed CVR data.

However, CVR-MRICloud requires users to execute a few preprocessing steps before uploading data. The following table lists the files and software needed to facilitate preprocessing:

Data Needed	Software Needed
• CVR BOLD scan (DICOM) • CO2 Trace (.fcd) • Site-specific scale and shift values (*scaleShift_<site>.txt*) • MPRAGE scan (DICOM) [optional]	• *vcidMprageEchoAvgr.m* • *flowtool_viewer.exe* • *preprocessGUI.m* • *Dcm2Analyze_v3.exe* • MATLAB (version R2016b or later)

Each site in the MarkVCID study will be sent their own *package.zip* that contains the above items in red text.

1. MPRAGE Processing

CVR-MRICloud needs segmented MPRAGE scan data to calculate results in MPRAGE and MNI subject space along with ROI-specific CVR values. ~~If these results are not desired, then users may skip to step 2.~~

Run *Dcm2Analyze_v3.exe*. You will see the following window:
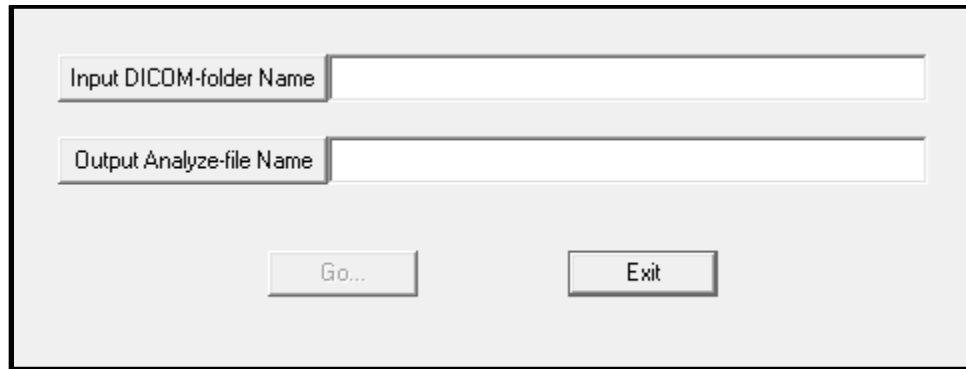
Click Input DICOM-folder Name and select the DICOM MPRAGE scan file(s). Click Output Analyze-file Name and select a directory where the converted scans should be placed. Click Go to convert scans from DICOM to ANALYZE format[1].

Open *vcidMprageEchoAvgr.m* in MATLAB and run the file[2]. You will see the following window:

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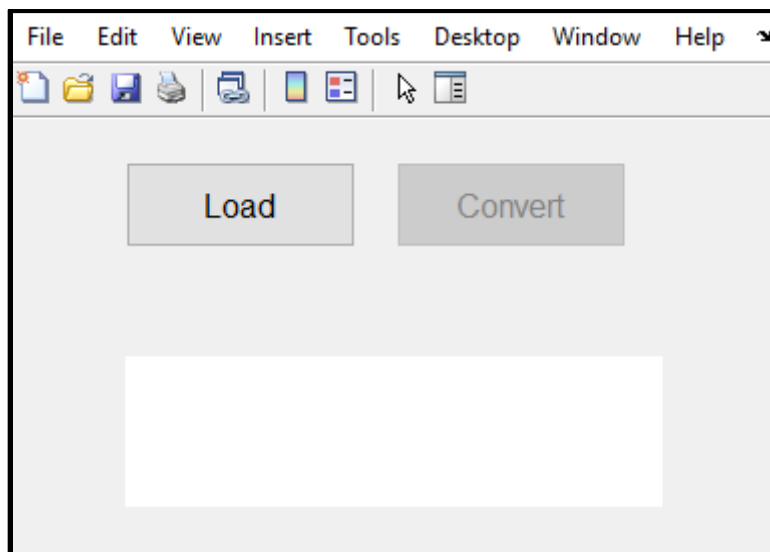
[1] ANALYZE format stores each MRI scan in two files with the same name. One of these files has the extension .hdr and one has the extension .img. Always keep these two files together and named identically.
[2] To run a MATLAB file, click the EDITOR tab and then click Run (button with green triangle).

Click Load and select the MPRAGE scan file with the .hdr extension. Then click Convert[3].

Navigate to https://braingps.mricloud.org/t1prep (make a free account if you do not already have one). Upload your MPRAGE .hdr and .img files you just converted (with the postfix '_avg'). Ignore Optional Information Fields and Select Processing Server. Under Select Slice Type choose Sagittal. Under Select Atlas choose Adult50-90yrs_287Labels_30atlases_M2_252_V10A. Include a job description under Description. Click Submit.

Once the webpage finishes uploading you can view your processing jobs under the My job status tab (https://braingps.mricloud.org/myjobstatus). Download the results once the processing is complete[4]. Results are downloaded as a zip file; do not alter this zip file beyond renaming it[5].

2. Preprocess CO2 Data

Open *flowtool_viewer.exe* and close the dialogue window. Click File -> Open and load your CO2 trace .fcd file. Ensure you are *only* viewing CO2 in mmHg:
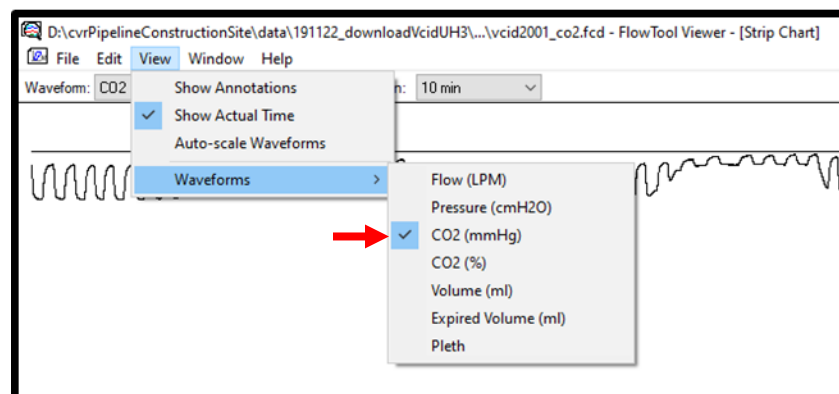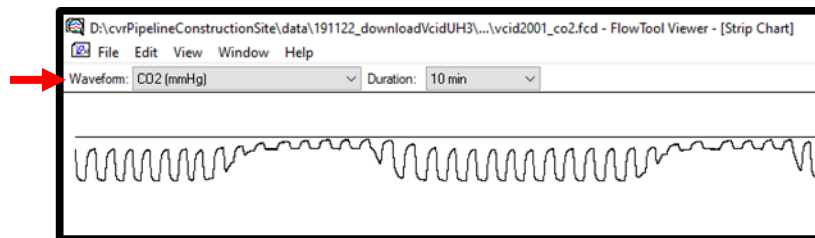

Click File -> Export -> Waveforms… to export the CO2 trace data into .TXT, .csv, or .txt format (it doesn't matter which).

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[3] This new MPRAGE scan will be placed in the same directory as the old one and the filenames will be postfixed with '_avg'.

[4] MPRAGE Segmentation jobs take anywhere from a few hours to a full day to run, depending on the job queue.

[5] https://braingps.mricloud.org/t1batch allows for batch segmentation of MPRAGE scans. To use results from this tool in CVR-MRICloud, extract (unzip) the results and rezip each 'target' into its own zip file.

Open *preprocessGUI.m* in MATLAB and run the file[6]. You will see the following window:
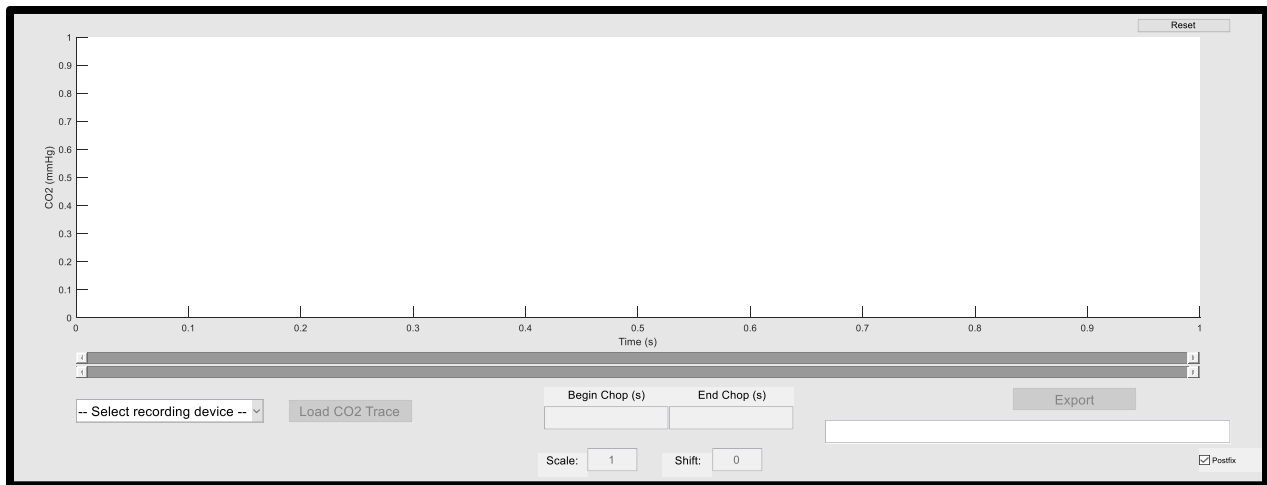
Under -- Select recording device -- pick Philips NM3, then click Load CO2 Trace and select the CO2 trace data that was previously exported. The trace will be displayed in its entirety:
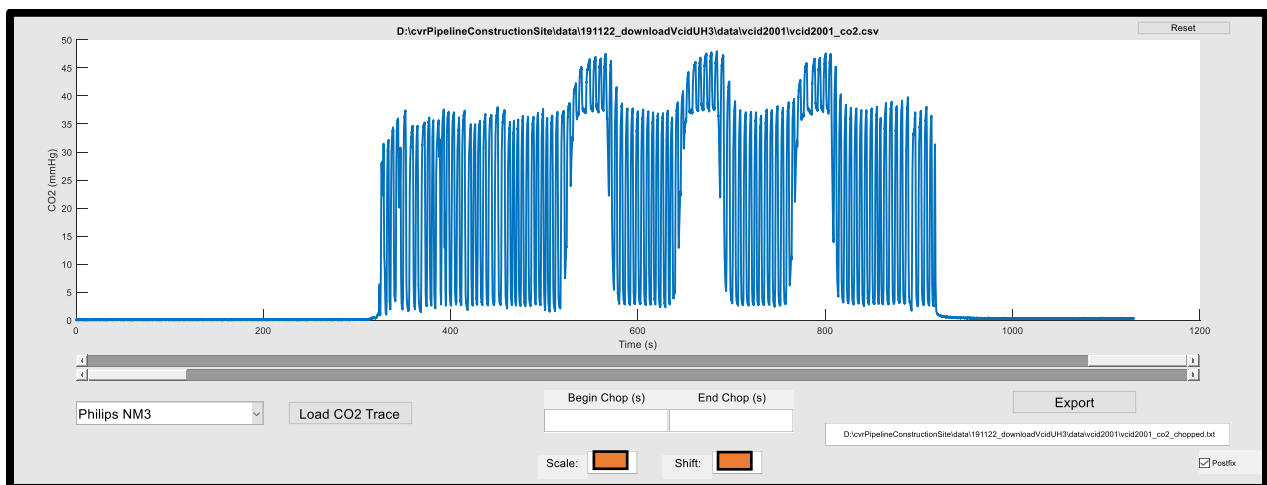

First, replace the Scale and Shift fields (orange boxes) with the values in the appropriate site's *scaleShift.txt* file. **Do not skip this step.**

Next, use the Begin Chop (s) and End Chop (s) fields or the slider bars to truncate the CO2 trace. The CO2 trace data should be truncated to include the gas challenges as well as all uninterrupted breathing before and after the challenges. The goal is to include as much **realistic** breathing information as possible.

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[6] To run a MATLAB file, click the EDITOR tab and then click Run (button with green triangle).
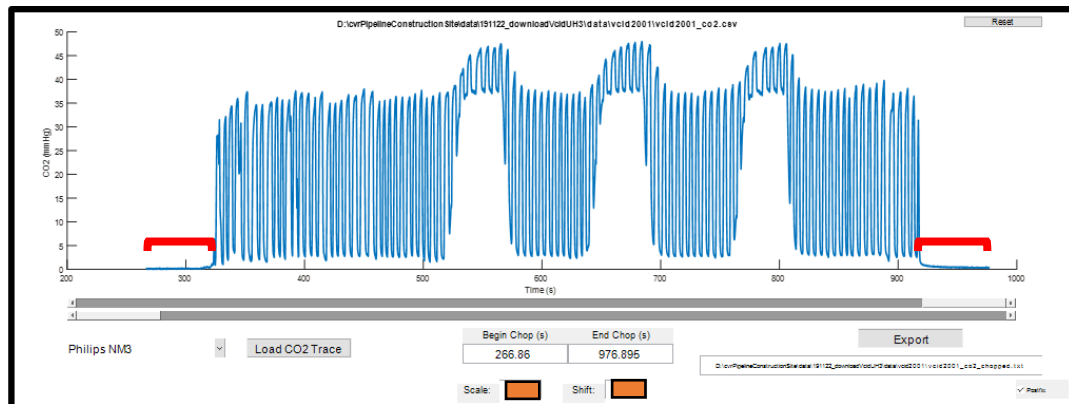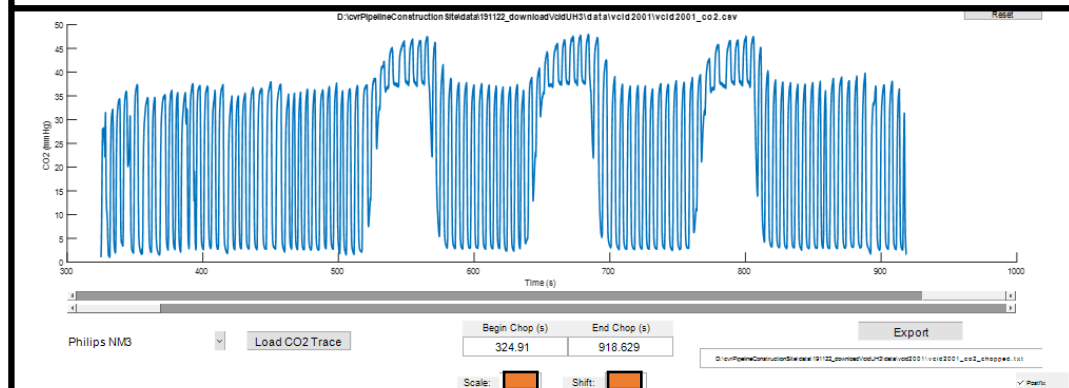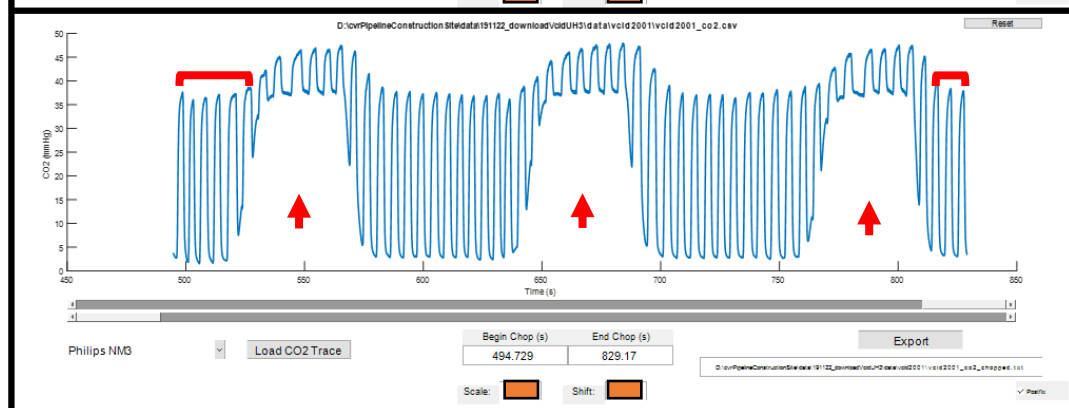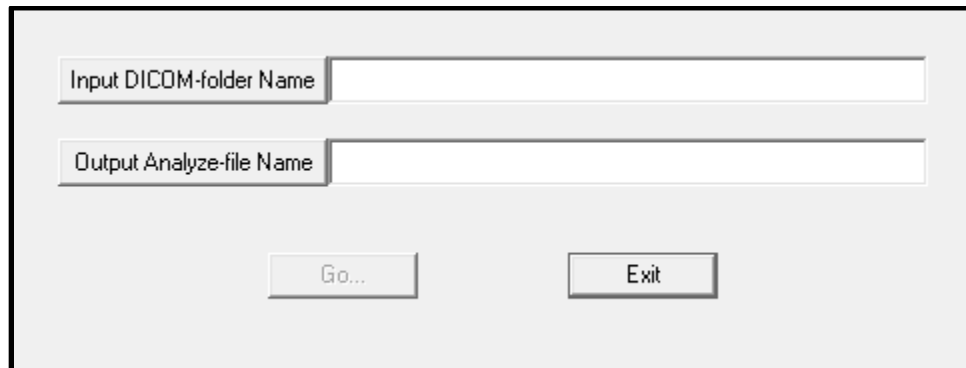
In the above figure, the top truncation is incorrect because the patient's breathing is not being recorded at the beginning and end of the trace. The bottom truncation is incorrect because the trace is truncated *too close* to the gas challenges (red arrows). The rule of thumb states: **"The CO2 trace data should be truncated with *at least* 60 seconds of recording before and after the BOLD scan's start and end respectively."**

Once you have inputted the scale/shift values and truncated the CO2 trace, click export.

3. CVR Processing

Run *Dcm2Analyze_v3.exe*. You will see the following window:

Click Input DICOM-folder Name and select the DICOM CVR BOLD scan file(s). Click Output Analyze-file Name and select a directory where the converted scans should be placed. Click Go to convert scans from DICOM to ANALYZE format[7].

Navigate to https://braingps.mricloud.org/cvr.v3 (make a free account if you do not already have one). Upload the CVR BOLD .hdr and .img files you just converted. Also upload the .txt file of the CO2 trace file you truncated, scaled, and shifted (likely postfixed with '*_scaleShift_chopped*'). If MPRAGE processing (step 1) was done, upload the zip file from T1-MultiAtlas analysis. Keep the Repetition time (s) and CO2 trace sample rate (Hz) fields at 1.5 and 100 respectively. For Select Processing Server choose VCID. Include a job description under Description. Click Submit.

Once the webpage finishes uploading you can view your processing jobs under the My job status tab (https://braingps.mricloud.org/myjobstatus). Download the results once the processing is complete[8].

The results of CVR-MRICloud are downloaded as a zip file. The extracted (unzipped) contents of a successful job will have 3 subdirectories (Globalshift_maps, MATLAB_figures, and Voxelshift_maps) and 3 text files (bold And Etco2 Signal, cvr results, and EtCO2 Stats). The Globalshift_maps and Voxelshift_maps subdirectories contain all the CVR and BAT maps produced by CVR-MRICloud (including maps in MPRAGE and MNI subject space if MPRAGE Processing was done)[9,10]. The MATLAB_figures subdirectory contains MATLAB figures used to check for proper EtCO2 shifting. The cvr results text file contains the whole-brain CVR value (along with ROI-specific CVR values if MPRAGE Processing was done). The bold And Etco2 Signal text file contains the whole-brain BOLD signal and the synchronized EtCO2 signal. The EtCO2 Stats text file reports the mean EtCO2 value, the average top and bottom 25% of the EtCO2 signal, and the time shift used to align the EtCO2 signal with the whole-brain BOLD signal.

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[7] ANALYZE format stores each MRI scan in two files with the same name. One of these files has the extension .hdr and one has the extension .img. Always keep these two files together and named identically.

[8] CVR-MRICloud jobs take anywhere from 30 minutes to a few hours to run, depending on the job queue.

[9] CVR maps are calculated with two different methods. Globalshift: CVR found using the EtCO2 curve aligned with the whole-brain BOLD signal. Voxelshift: CVR found using the EtCO2 curve aligned with each voxel's BOLD signal.

[10] CVR maps containing the phrase '*_rel_*' are relative maps; all values are divided by the map's average CVR value. This rule does not apply to BAT maps, which always contain the phrase '*_rel_*'. This is because they report the Bolus Arrival Time relative to the average BAT.