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UCLA Brain Tumor Imaging Laboratory

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User Guide

This document was created for the rCBV_LeakageCorrection application developed by UCLA Brain Tumor Imaging Laboratory of the University of California Los Angeles. rCBV_LeakageCorrection is a standalone application developed in Matlab®R2016a.

Current Version: 2.1
Date: 8th November 2016

New Features

1. Allows loading and saving of sequences in DICOM format.

2. Creates the brain mask for the loaded perfusion sequences.

3. Calculates the injection time point for the perfusion sequence loaded.

4. Corrects the perfusion sequence for motion.

5. Registers the results to a T1 post contrast sequence for visualization.

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1 Installation

To install **rCBV_LeakageCorrection** click on the file rCBV_LeakageCorrection-installer. An installation window will open with the software version (see Figure 1). To begin the installation, click on **Next >**.

Figure 1: **rCBV_LeakageCorrection** main installation window

As shown in Figure 2, the following window will ask for a path to install the application. Select a folder where you have writing privileges. Once again click on **Next >**.
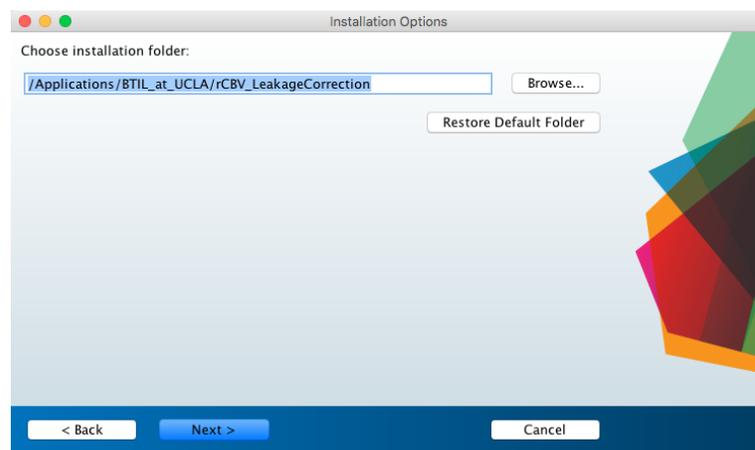

Figure 2: **rCBV_LeakageCorrection** installation options: installation folder

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> ✏️ **Note:** rCBV_LeakageCorrection requires the user to be able to install applications in the system. If you don't have these privileges, contact your system administrator.

rCBV_LeakageCorrection requires Matlab®R2016a Runtime. It is included in the installation package and will be installed if it is not on the system. If needed, choose an installation folder (Figure 3). After pressing **Next >** the license agreement for Matlab®R2016a Runtime will be displayed. Read and accept the terms by activating the radio button **Yes**.

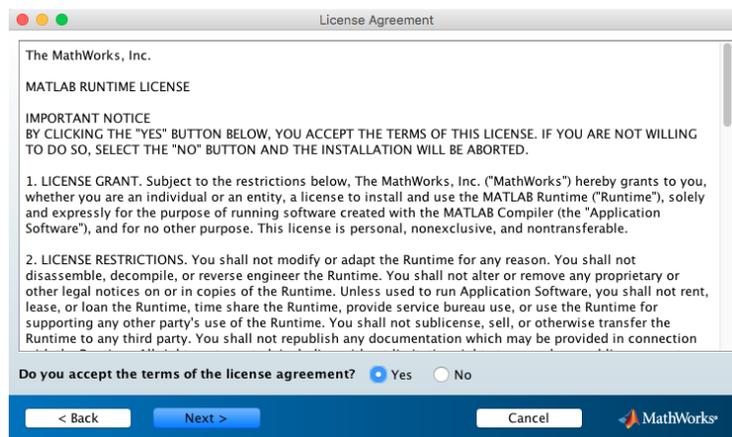Figure 3: rCBV_LeakageCorrection required software

Figure 4: rCBV_LeakageCorrection license agreement

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A final confirmation window will pop up with a summary of all software that is going to be installed and their paths (see Figure 5). If everything is correct, press **Install >** otherwise press **< Back** and correct. This will begin the installation process. The installation will take a few minutes.
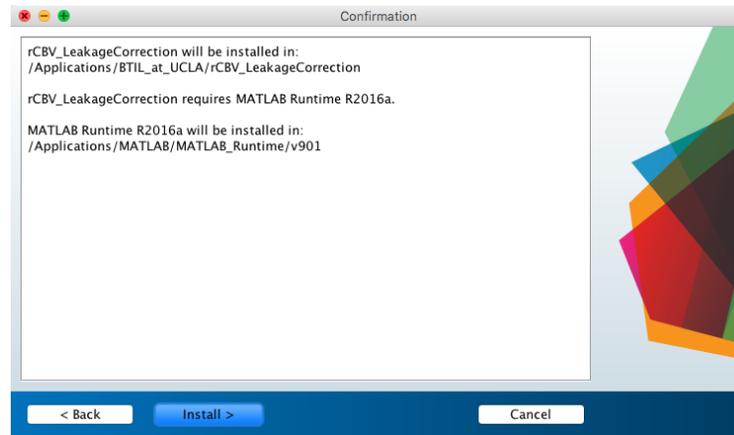

Figure 5: rCBV_LeakageCorrection confirmation

When the installation is complete, launch the application by clicking the rCBV_LeakageCorrection icon (Figure 6).

Figure 6: rCBV_LeakageCorrection icon

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2 Graphical User Interface

2.1 Main Window

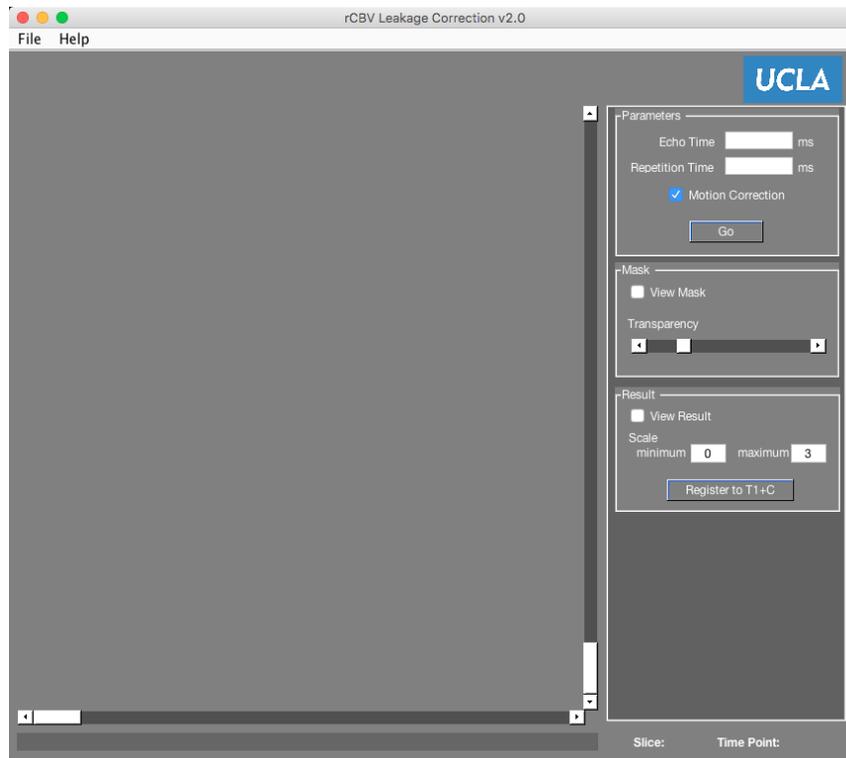Figure 7 shows the main window for the rCBV_LeakageCorrection application.

Figure 7: Main window

There are four major components of the GUI:

1. **Top Menu** - Handles file interaction (**_File_**) and allows the user to get the documentation when needed (**_Help_**).

2. **Control Panel** - Contains all functionality of the application. It will be explained in more detail in the following section.

3. **Image Axes** - Perfusion sequences and their masks are presented in here as well as the calculated rCBV leakage correction. The vertical slider switches among the different time points of the sequence and the horizontal changes the current slice.

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4. **Status Panel** - Displays the process being executed and the slice number and time point currently displayed on the image axes.

2.2 Control Panel

The control panel is used to operate the functionality and visualization of the sequences. It encapsulates three components.

2.2.1 Mask Control Panel

Figure 8 shows the panel to control the visualization of the mask. After a perfusion sequence and its mask have been loaded, they are displayed in the image axes overlaying the mask on the MRI sequence. In order to turn off this feature, the button "View Mask" should be unchecked. To control transparency of the overlay mask, use the slider.
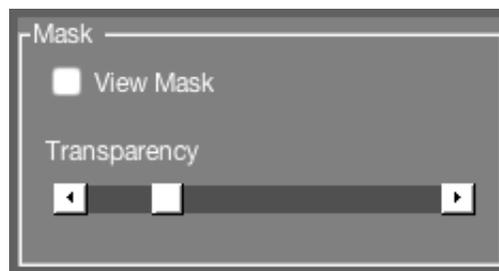
Figure 8: Mask control panel

2.2.2 Parameters Control Panel

To calculate the leakage correction two parameters are needed: echo time **TE** in milliseconds and repetition time **TR** in milliseconds. Once the parameters are inserted into their corresponding box, trigger the button **Go** to begin the calculation. Figure 9 shows the default values for these parameters.

The following processes will run in the background:

  i Brain mask calculation

  ii Motion correction (if the check box was active when the button **Go** was pressed).
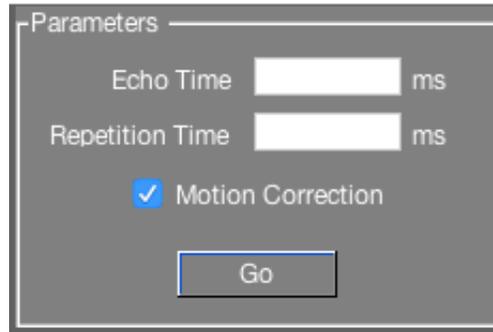
  iii Injection Point calculation

  iv Leakage correction

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Figure 9: Parameters control panel

2.2.3   Result Control Panel

The panel shown in Figure 10 allows the user to visualize the resulting images and to register this result to a T1 post contrast sequence for better visualization when triggering the button **Register to T1+C**. When the check button "View Result" is off the image axes will display the perfusion sequence (and the mask if "View Mask" check button is active). To customize the scale in which the result is displayed, the minimum and maximum can be changed.
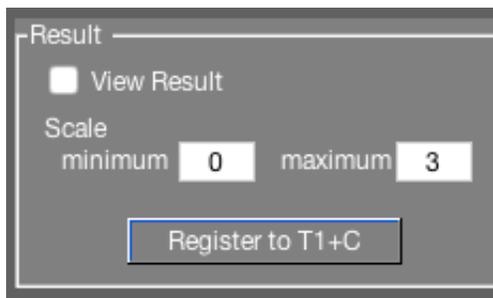

Figure 10: Result control panel

✎ **Note:** rCBV_LeakageCorrection does not allow showing the mask and the result simultaneously. Hence, if the result check box is triggered, the mask check box will automatically change to unchecked.

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Usage

The following section shows step-by-step usage of the rCBV_LeakageCorrection application.

3 Load Sequences

The following files can be use in this software:

- Perfusion Sequence: single 4D MRI file in NIfTI format

- Perfusion Sequence: directory containing DICOM 4D MRI Images

Load these by clicking on the top menu *File → Open NIfTI* or *Open DICOM*. (see Figure 11)
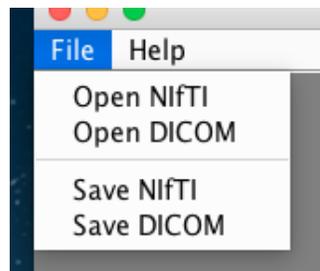

Figure 11: Open files

This action will prompt a message in the status panel

> ✐ **Note:** rCBV_LeakageCorrection does not support compressed DICOM images (.jpeg). To dejpeg them use osiriX (http://www.osirix-viewer.com/), DCMTK dcmdjpeg (http://support.dcmtk.org/docs/dcmdjpeg.html) or any appropriate tool to decompress the images.

An open dialogue (Figure 12) will pop. Depending on the option selected, the dialogue will show the title *"Open perfusion file"* for NIfTI or *"Pick the main directory"* for DICOM. After loading the perfusion sequence, the images will be displayed on the axes (see Figure 13).
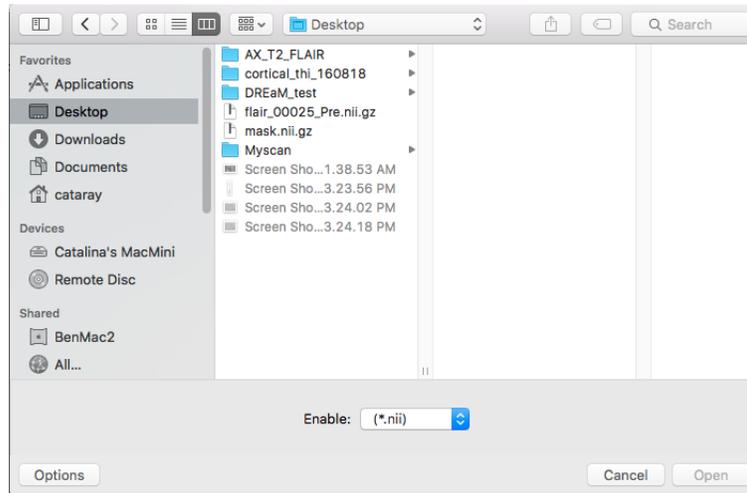
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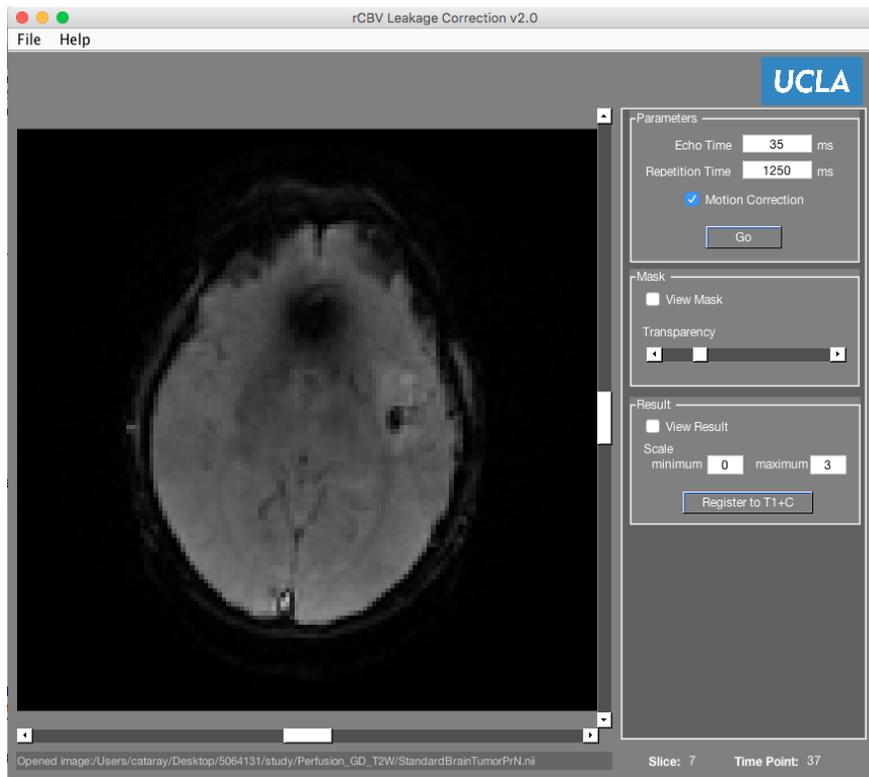*Center for Computer Vision and Imaging Biomarkers*
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Figure 12: Open dialogue

Figure 13: Displayed perfusion sequence

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> ✎ **Note:** Matlab®R2016a is not fully supported in OS X El Capitan causing multiple bugs. The open and save dialogues don't display the titles as a result of this.

The status panel will be updated showing the path to the last image loaded. After opening, the middle slice and time point will be displayed by default and the status panel will report this information. The sliders can be used to change between time points and slices (vertical and horizontal respectively).

4 Process Sequences

To begin processing the sequence it is necessary have two parameters in the control panel (section 2.2.2):

- **TE:** echo time in milliseconds.

- **TR:** repetition time in milliseconds.

If the images uploaded are in DICOM format, this parameters will be read from the header, otherwise the user will need to input them. There is also the option to activate or deactivate the motion correction. Click on **Go** to start calculating. The processes performed internally are listed in section 2.2.2).

If the parameters are not introduced before clicking the button or the ones used do not give a solution the error message shown on Figure 14 will pop-up.
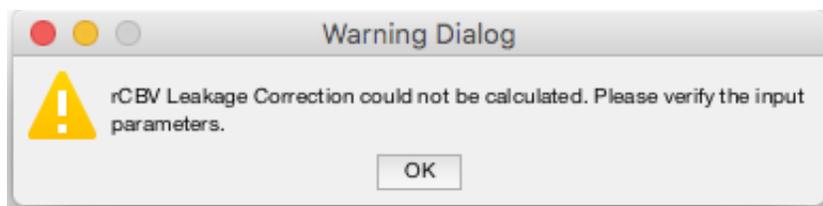

Figure 14: Warning message for parameters

When the calculation begins, the status bar will display the current process. Once it is done, it will be updated to "rCBV Leakage correction finished".

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To visualize the output, use the result control panel (section 2.2.3). Activate the View Result check button and update the scale to better interpret what is being displayed. Once again the middle slice is presented as default, but the horizontal slider allows the user to inspect the entire sequence.
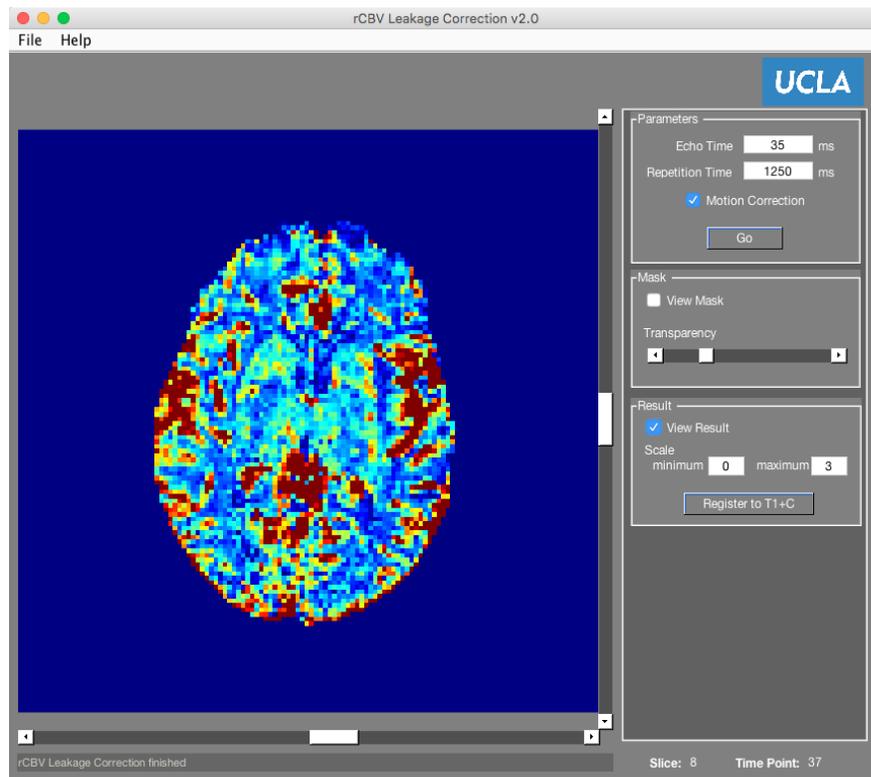

Figure 15: Result visualization

At this point you can proceed to save the results (see section 2.2.3), but version 2.0 offers the possibility to register the result to a post contrast T1 sequence by triggering the ***Register to T1+C*** button. This option is only useful when DICOM images are loaded since the header is needed. If triggered when a NIfTI file has been loaded an error message will pop-up when saving the files fail due to the lack of a header file.

A open dialogue will pop-up with the title ***Pick the T1 main directory***: choose the directory containing the DICOM images of the post contrast T1 sequence. The result of this operation would be folder named ***color_overlay*** containing the register images. The result will be displayed in the axes for inspection.
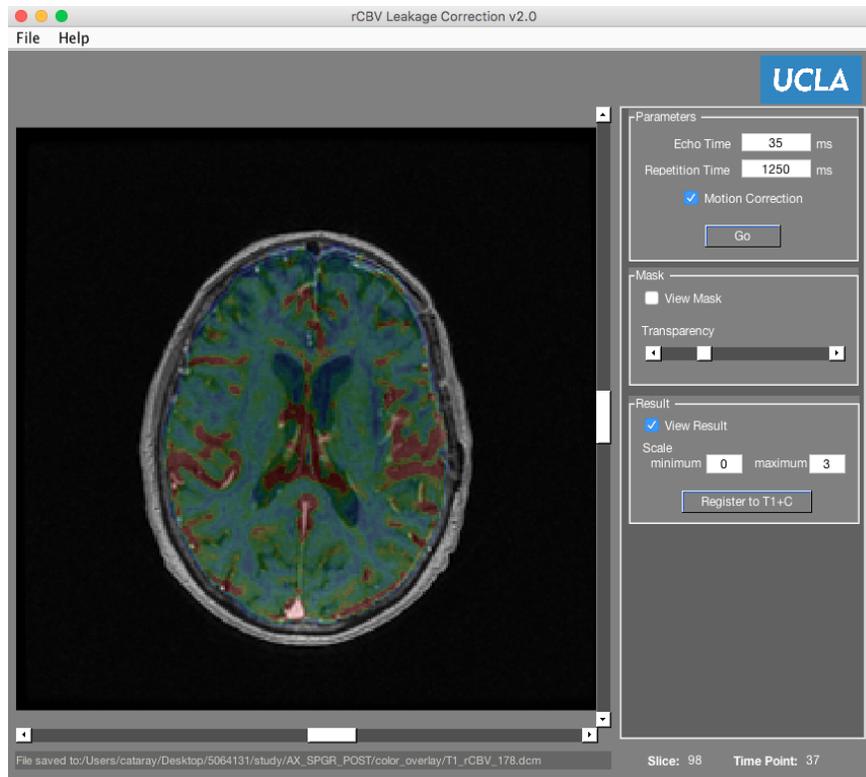
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Figure 16: Registration Result

5   Save Results

To save the results click on the top menu **File → Save NIfTI** or **Save DICOM**.

Figure 17: Save file

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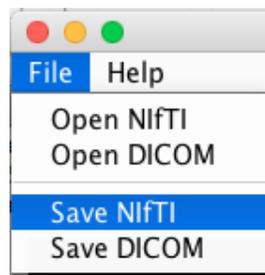
A save dialogue similar to the one presented in Figure 18 will pop up. For NIfTI, select the location where the file will be stored and its name and click on **Save**. For DICOM, select the folder where the images will be stored and click on **Save**.
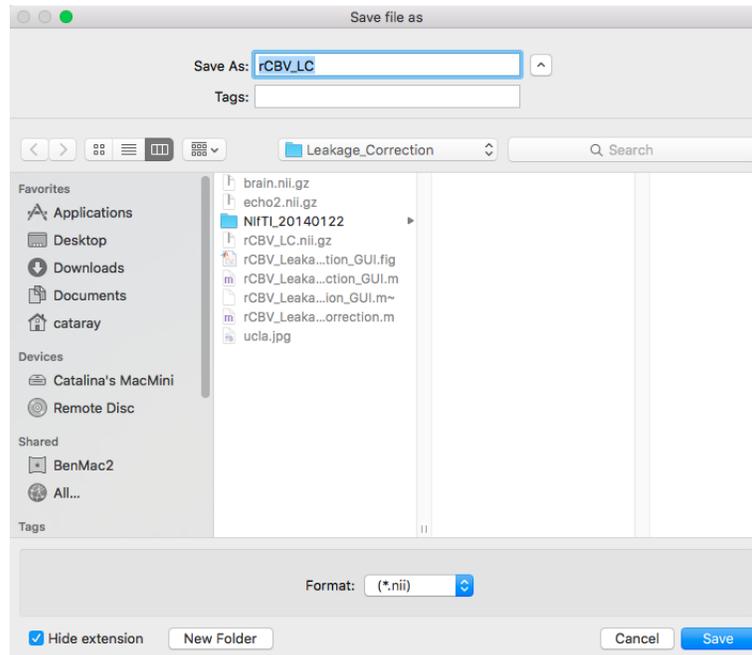

Figure 18: Save dialogue

The status bar will be updated to show the path and name of the files created.

This concludes the process. Close the application or load a new sequence to start again.

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References and Support

For more information:

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ii Leu K, Boxerman JL, Lai A, et al. Bidirectional Contrast agent leakage correction of dynamic susceptibility contrast (DSC)-MRI improves cerebral blood volume estimation and survival prediction in recurrent glioblastoma treated with bevacizumab. J Magn Reson Imaging 2016

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