User's Manual
Hyperpolarized ^{129}Xenon MRI Analysis App

For Research Use Only

User's Manual

HP ^{129}Xe MRI Analysis App

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1 | Overview

Main Menus:

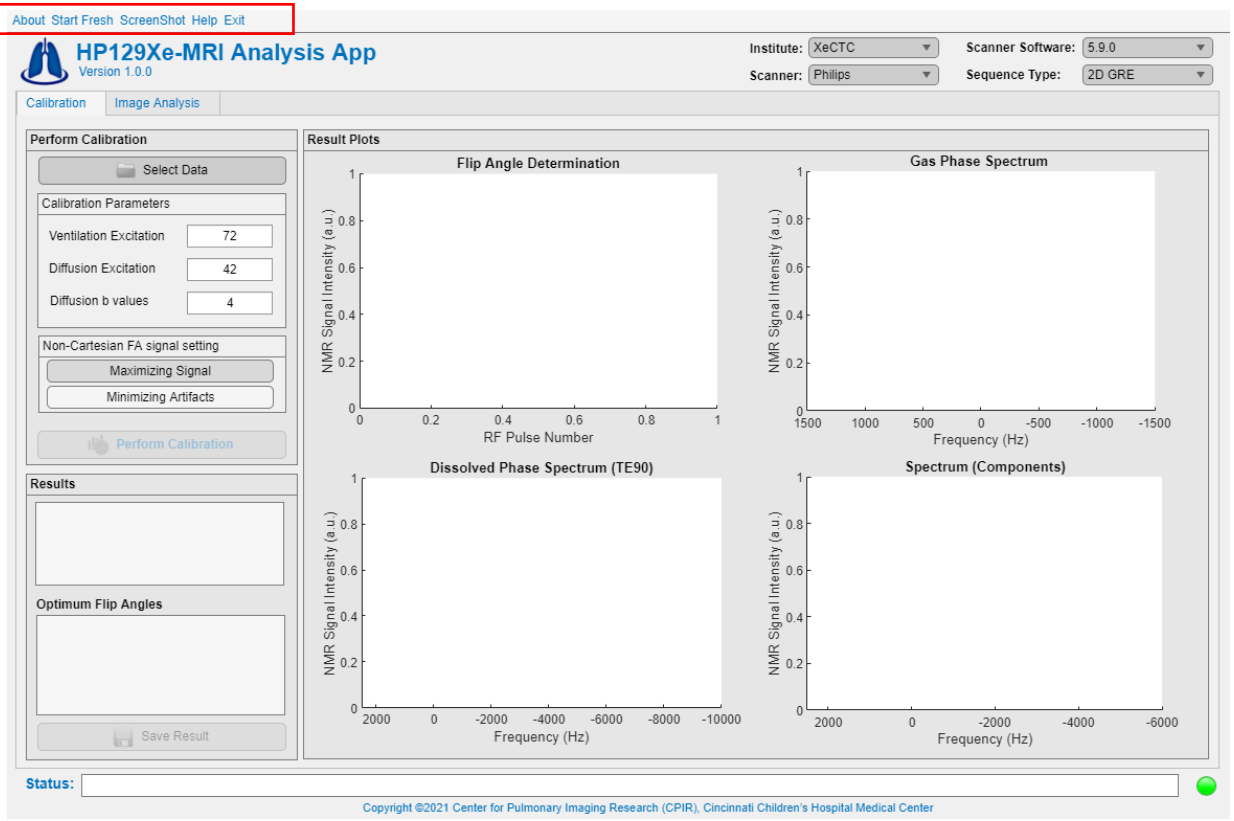
About: Provides an insightful overview of the application and its functionalities.

Start Fresh: Restores the app to its default settings and eliminates all variables. This feature proves beneficial when handling numerous subjects consecutively.

Screenshot: Captures the entire app window and saves it as a high-quality PNG file.

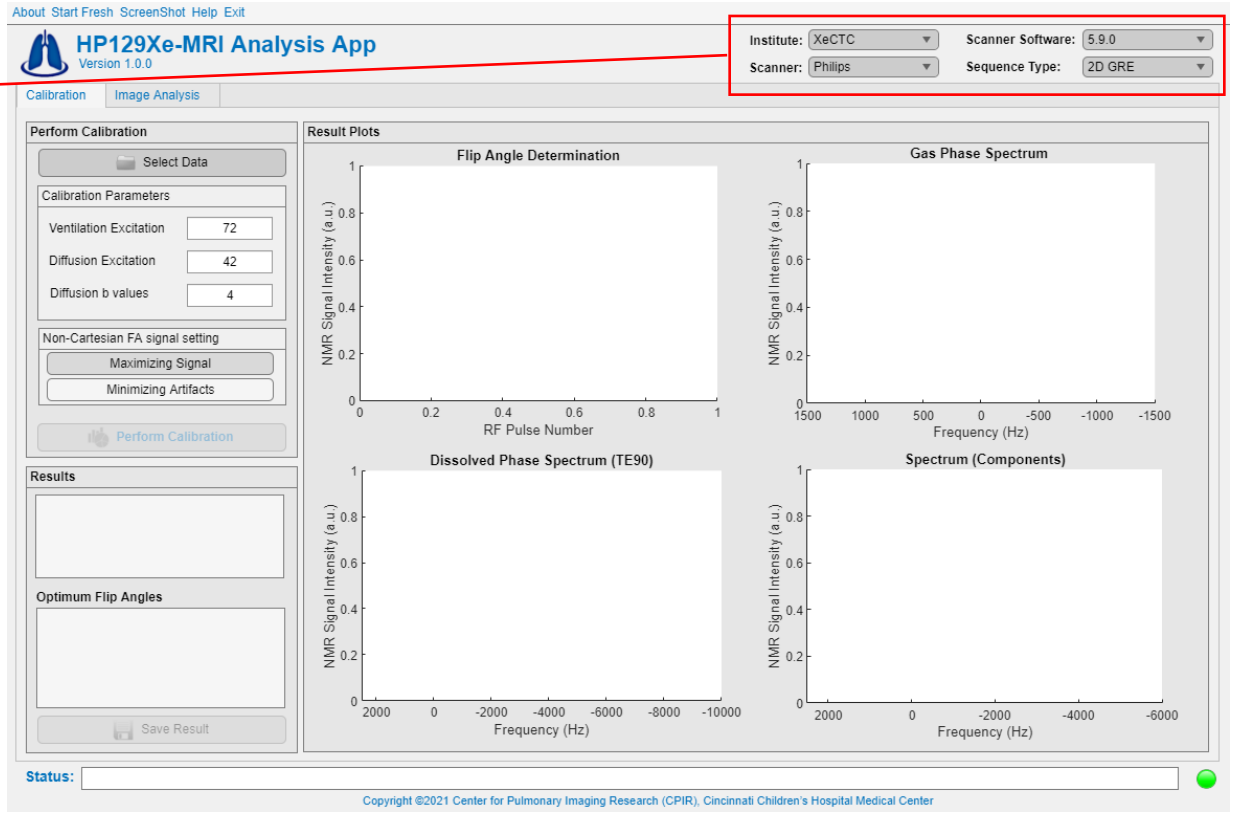
Help: Guides you to the comprehensive user manual, offering assistance and clarification.

Exit: Safely shuts down the application, concluding the user's session.



Institutes and Scanner Options:

These exceptional features allow for seamless customization of the application according to your specific requirements. They prove particularly valuable when working with multiple scanners, scanner software versions, and sequences.

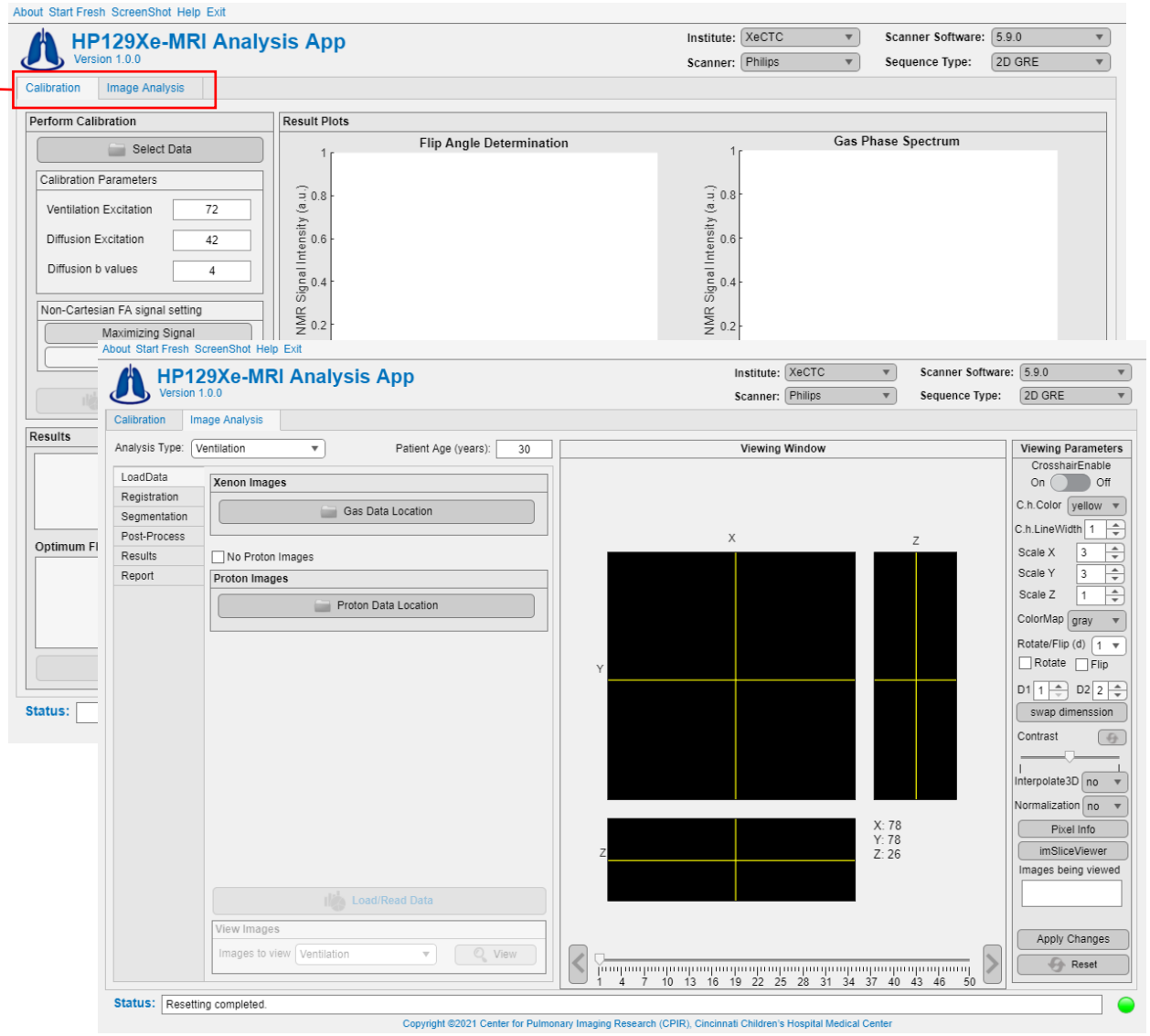


Main Tabs:

Calibrations: Manages flip angles and frequency calibration, ensuring precise adjustments for optimal acquisitions.

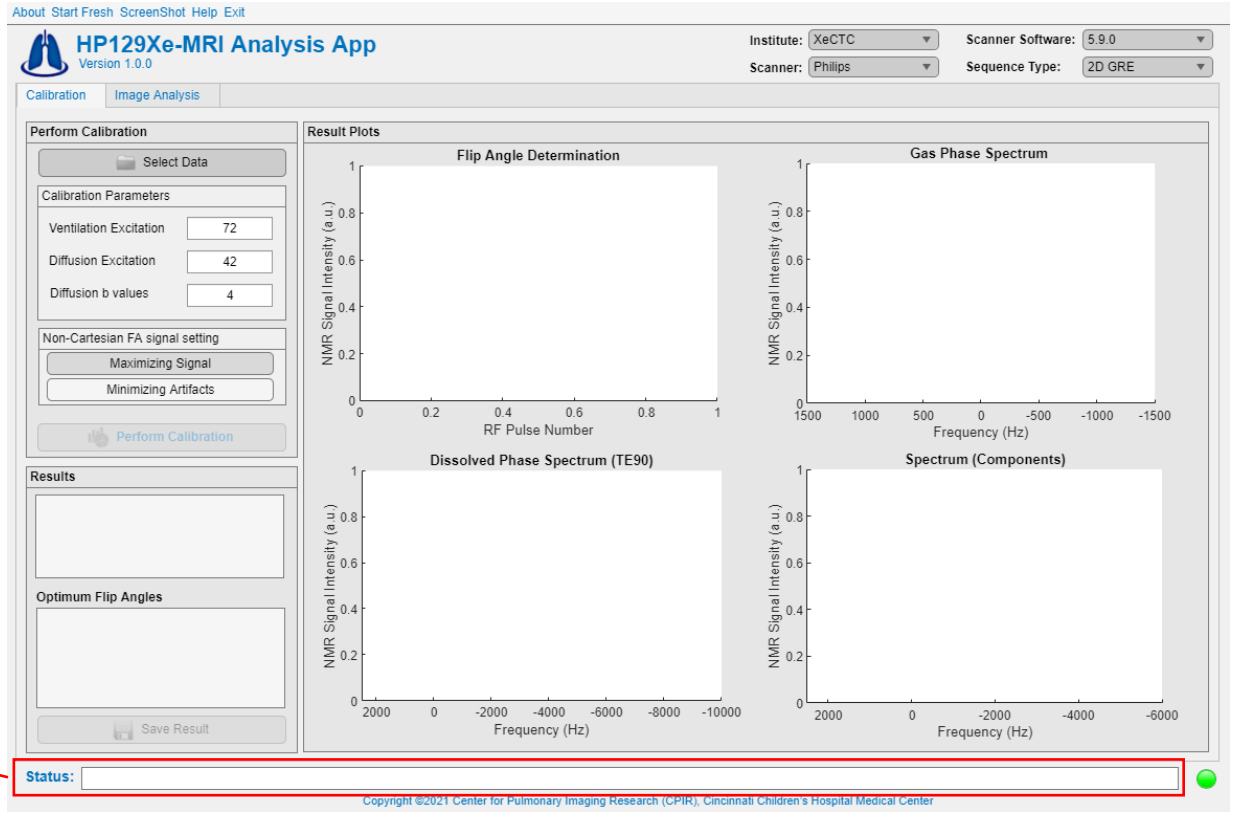
Image Analysis: Facilitates image reconstruction and conducts comprehensive post-processing analysis, enabling in-depth examination and evaluation.

Note: These two tabs operate independently from each other, maintaining separate sets of parameters. There is no parameter sharing between them, ensuring complete autonomy and flexibility.



Status Window:

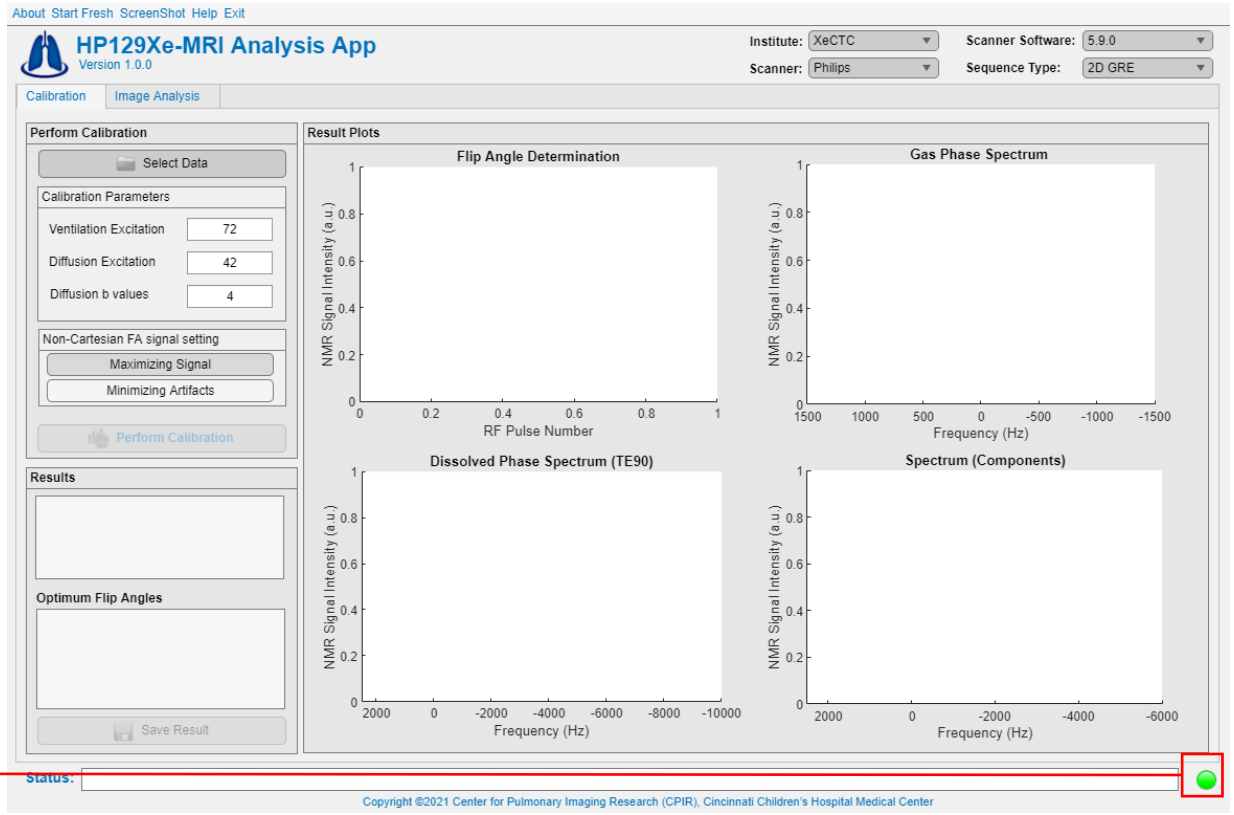
The status window presents a text box that provides real-time updates on tasks and displays error messages when necessary. It serves as a valuable tool for tracking progress and promptly addressing any issues that may arise.



Lamp:

Green: Signals that the app is ready for execution, indicating availability for use.

Red: Indicates that the app is currently unable to process tasks. It's important to note that if a bug occurs and the process halts midway, the lamp will not turn green until another task is initiated.



2 | Flip Angle and Frequency Calibration

2.1 | Input

Perform Calibration Analysis:

1- Select Data: Choose the flip angle calibration data from the available options (refer to Table 2.1 for supported data types).

2 – Perform Calibration: Read in the selected data and conduct essential fittings and calculations to obtain accurate results. The determined optimal flip angles and frequency parameters are subsequently entered prior to image acquisition.

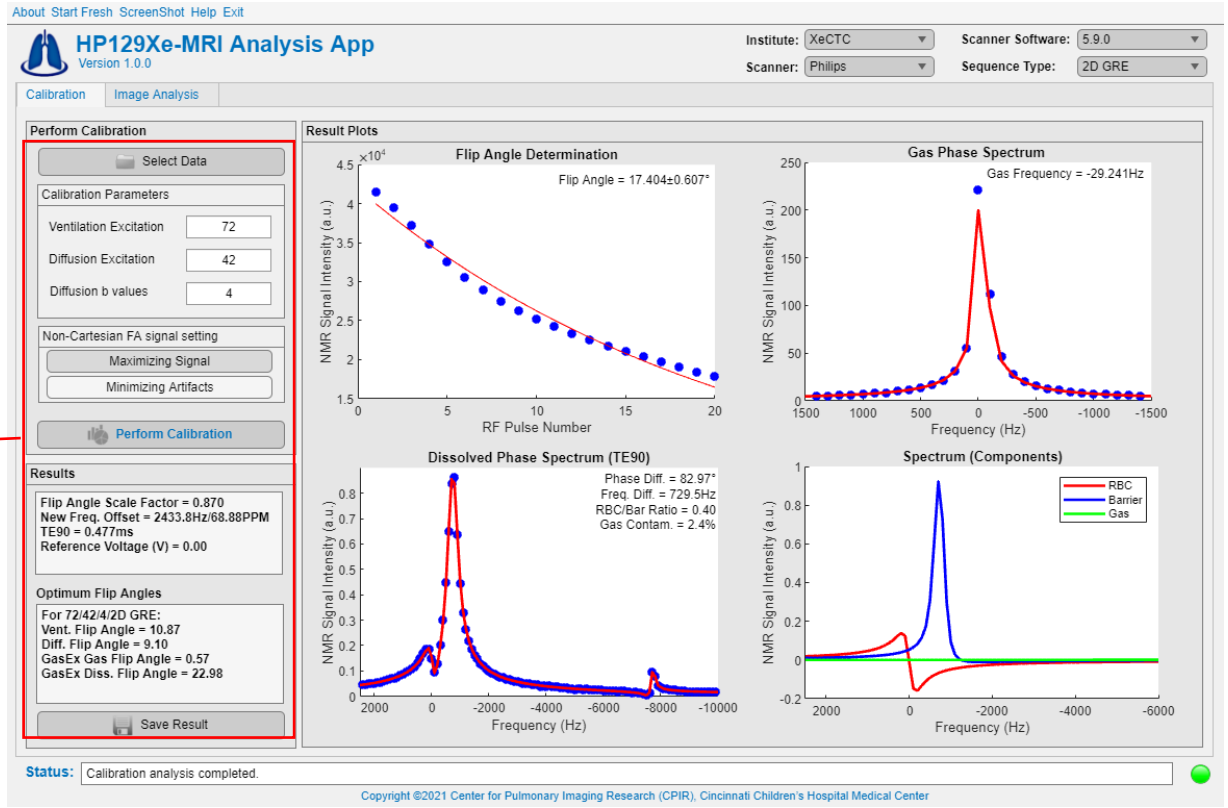


Table 2.1: Supported data type for Calibration analysis

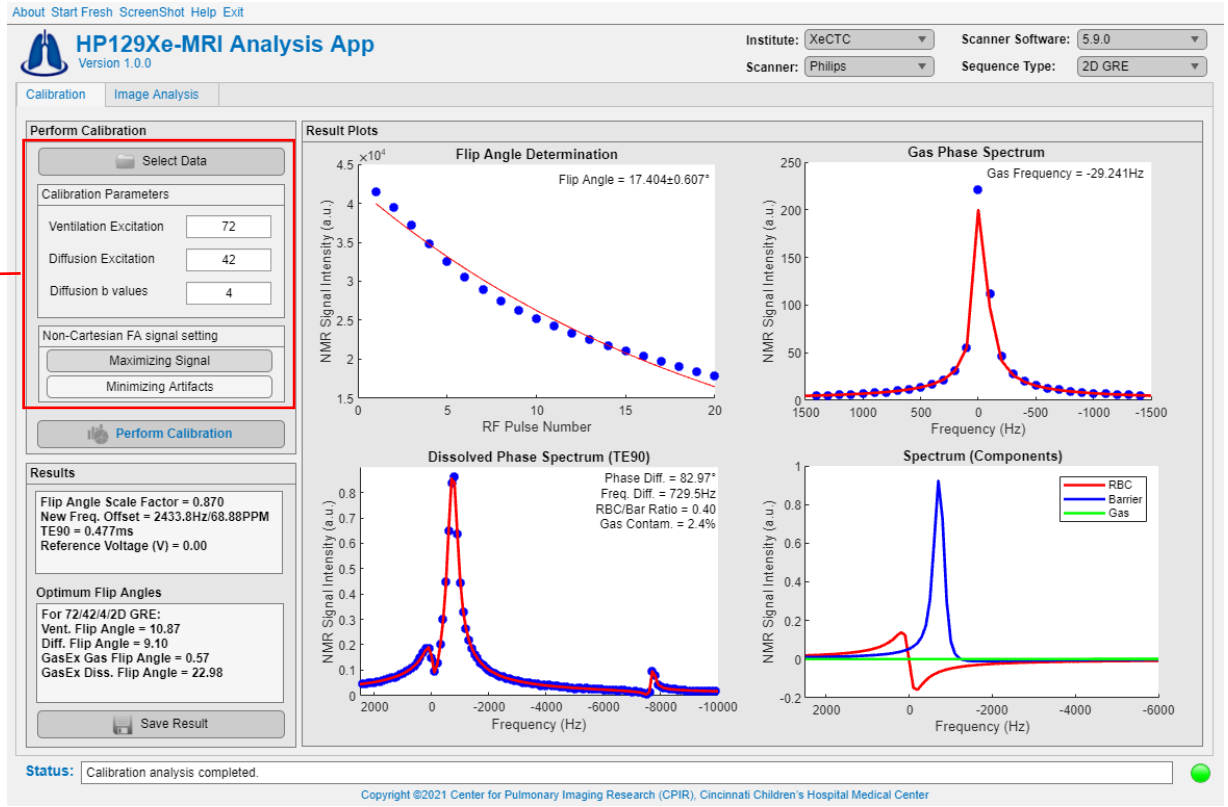
Scanner	Philips	Siemens	GE
Data Type	.data*/.list	.dat*	

* The data that needs to be selected!

2.2 | Adjusting Parameters

Perform Calibration Analysis:

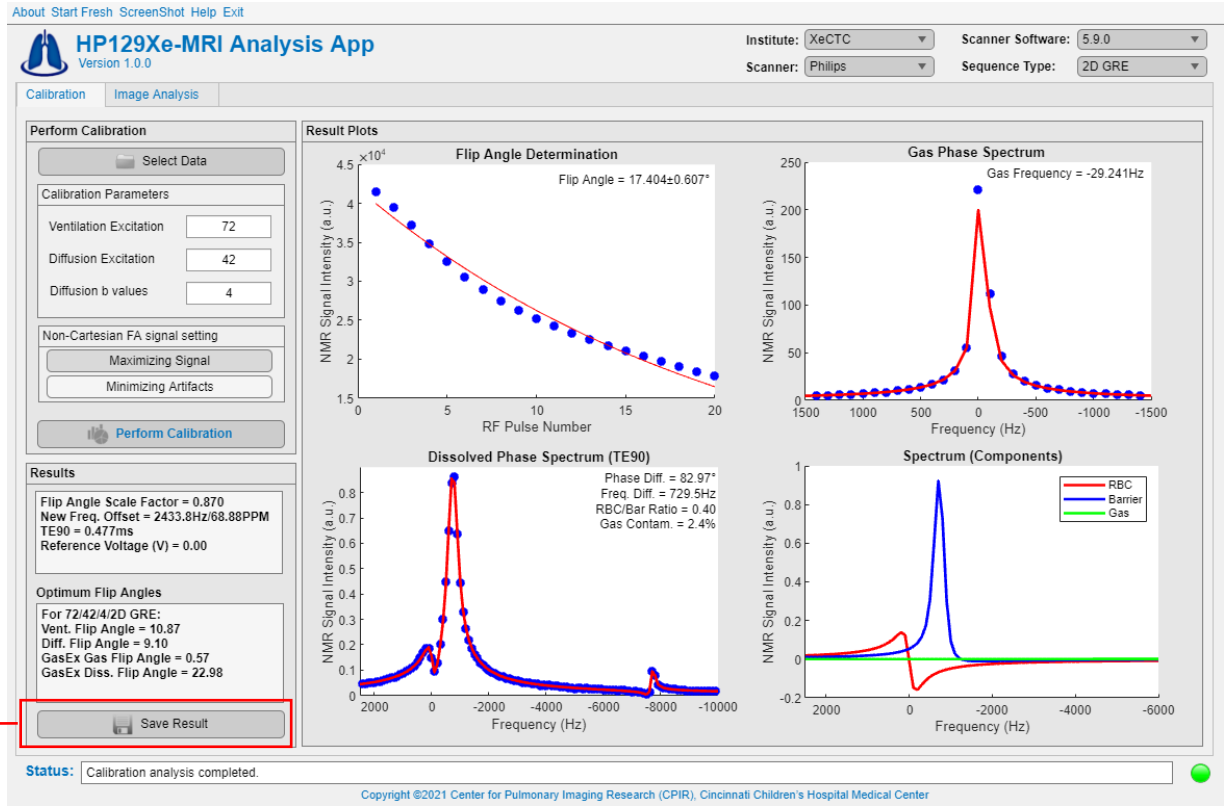
The calibration analysis allows for flexibility in adjusting parameters both before and after the analysis. These input parameters possess a dynamic property, meaning that any changes made to their values will automatically update the calculations. This enables effortless refinement and adaptation of the analysis based on parameter modifications.



2.3 | Save Results

Save Results:

Saves a screenshot of the entire app window as a PNG and PDF files in the data path.



3 | Image Analysis

3.1 | Inputs

Load Data:

1- Choose Analysis Type: Select the desired type of analysis from the available options.

2- Gas Data Selection: Choose the data file/s for analysis. If raw data is selected, reconstruction functions will be invoked to process the data.

3- Proton Data Selection: If proton data is available, select the corresponding data. Otherwise, check the "No Proton Images" box.

4- Load Data: Load the selected data for further processing and analysis.

5- Image Selection: Select the specific type of images to view.

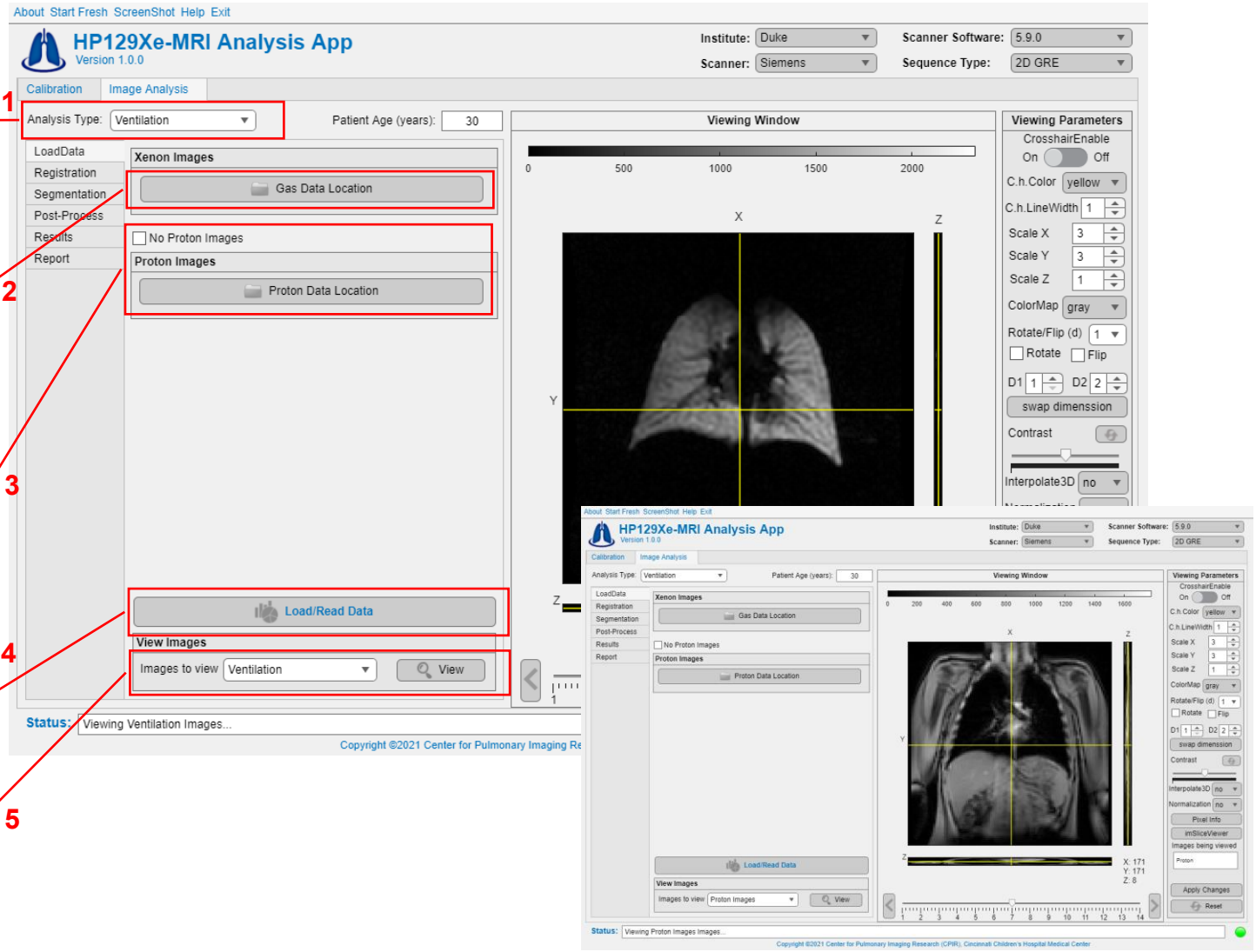


Table 3.1: Supported data type for image analysis

Data Type	DICOM (.dcm)		MATLAB (.mat)	Nifti (.nii or .nii.gz)	ISMRMD (.mrd or .h5)		Raw data															
	single	multiple	single	single	single		Philips						Siemens						GE			
					GRE	NC	GRE (.data)			NC (.data)			NC			NC			NC			NC		
							V	D	G	V	D	G	V	D	G	V	D	G	V	D	G	V	D	G
Supported?	yes	yes	yes	yes	yes	no	yes	yes	no	no	no	yes	no	no	no	no	no	no	no	no	no	no	no	no

GRE: Gradient Recall Echo, V: Ventilation, D: Diffusion, G: Gas Exchange

3.2 | Registration

Perform Registration:

1. Registration Type Selection: Choose the desired registration type, with "affine" being the recommended option for optimal results.

2. Image Resolution: If the two images have different voxel sizes, it is advisable to specify the image resolution for accurate registration. The ratio of the image sizes can also be used as a reference.

3. Slice Selection: In case the slices of the images do not align, you can specify the starting and ending slices of the matched region. Linear interpolation will be employed to adjust the number of slices accordingly.

4. Registration Process: Initiate the registration process for multimodal 3D medical images.

5. Image Selection: Select image type to view.

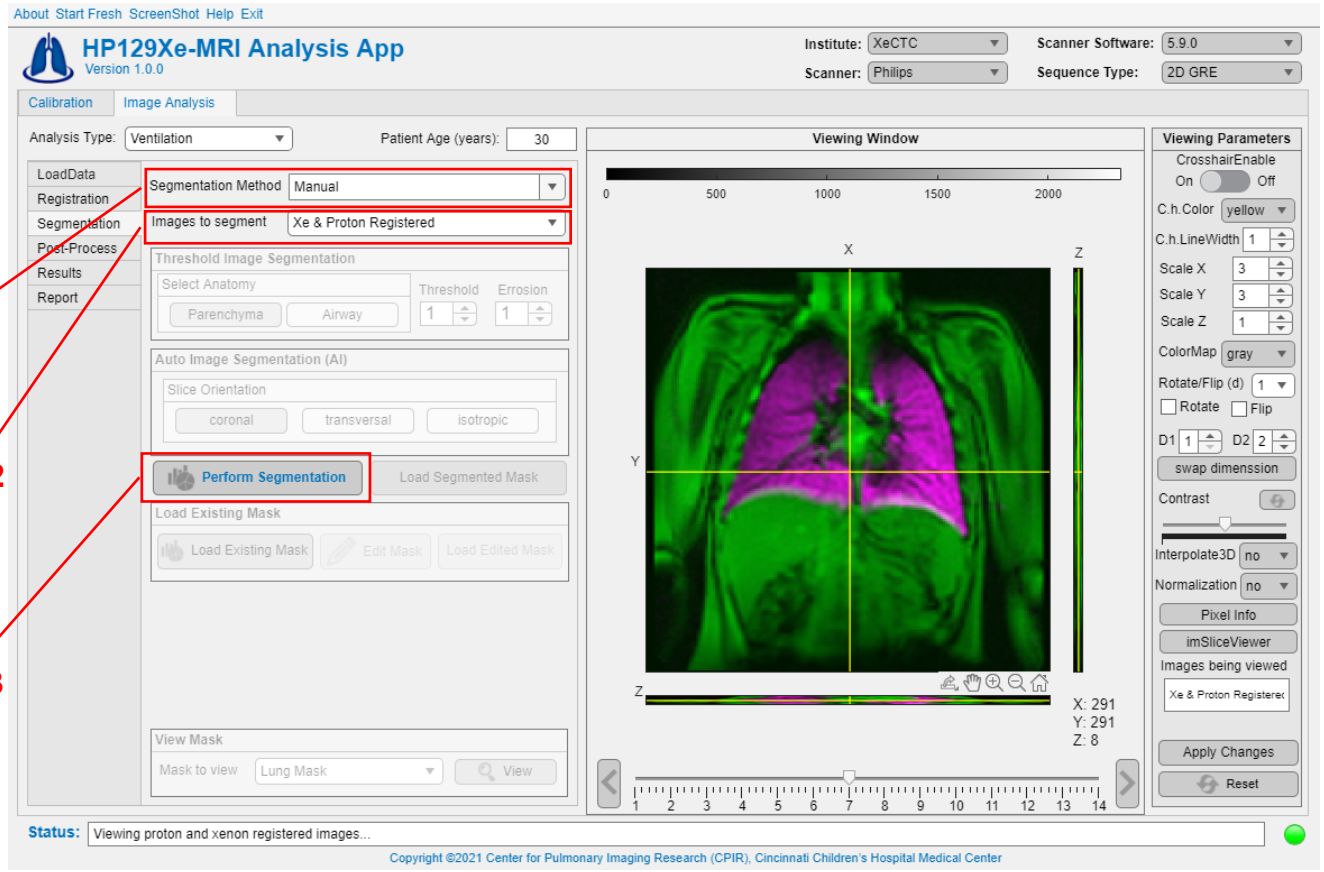
3.3 | Segmentation

Manual Segmentation:

1-Select "Manual Segmentation" from the dropdown menu.

2-Specify the image type for segmentation. Note that only grayscale images are accepted for freehand segmentation.

3-Initiate the segmentation process.



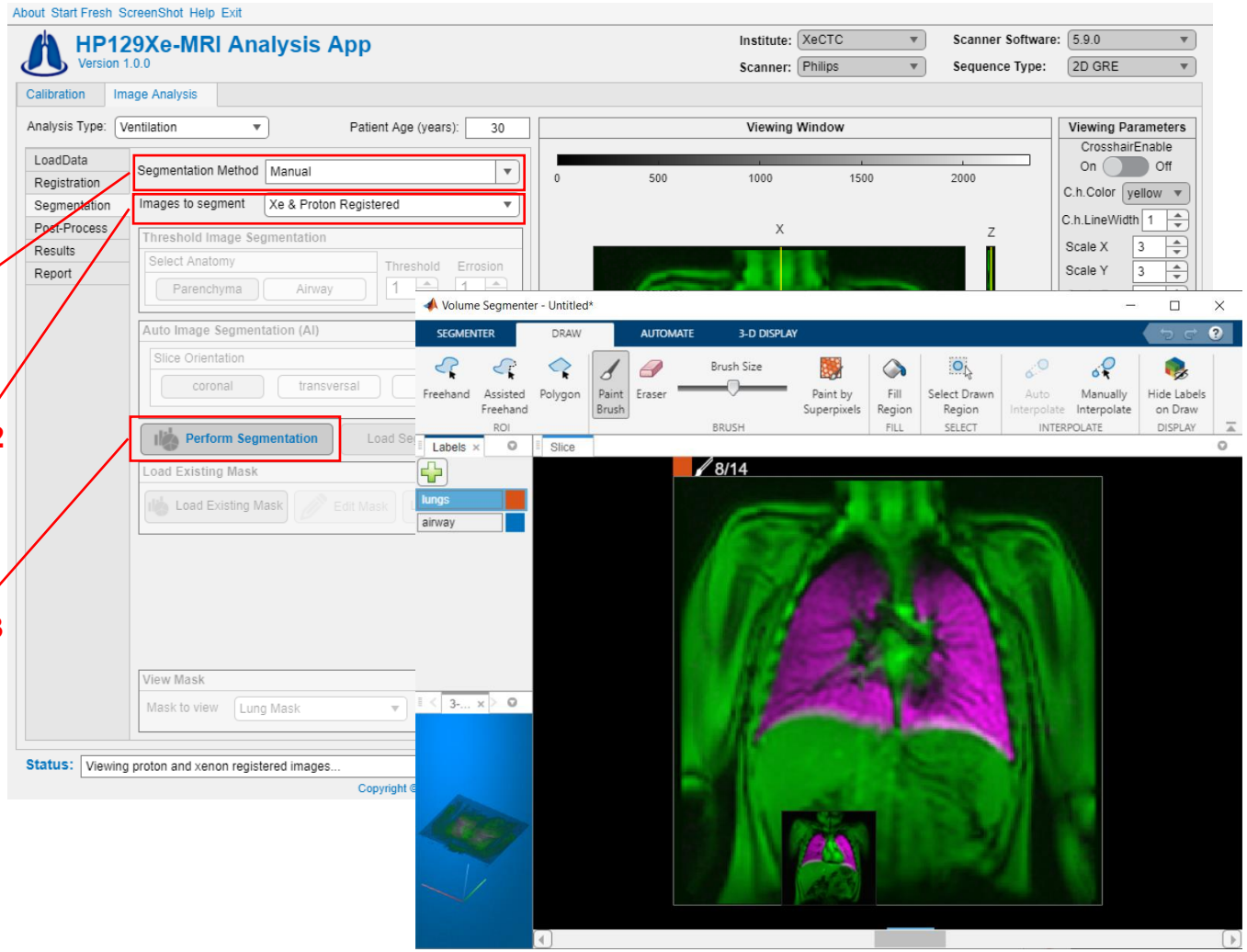
Manual Segmentation:

1-Select "Manual Segmentation" from the dropdown menu.

2-Specify the image type for segmentation. Note that only grayscale images are accepted for freehand segmentation.

3-Initiate the segmentation process.

Manual segmentation utilizes MATLAB's built-in App Volume Segmenter which offers many advanced segmentation tools.



Manual Segmentation:

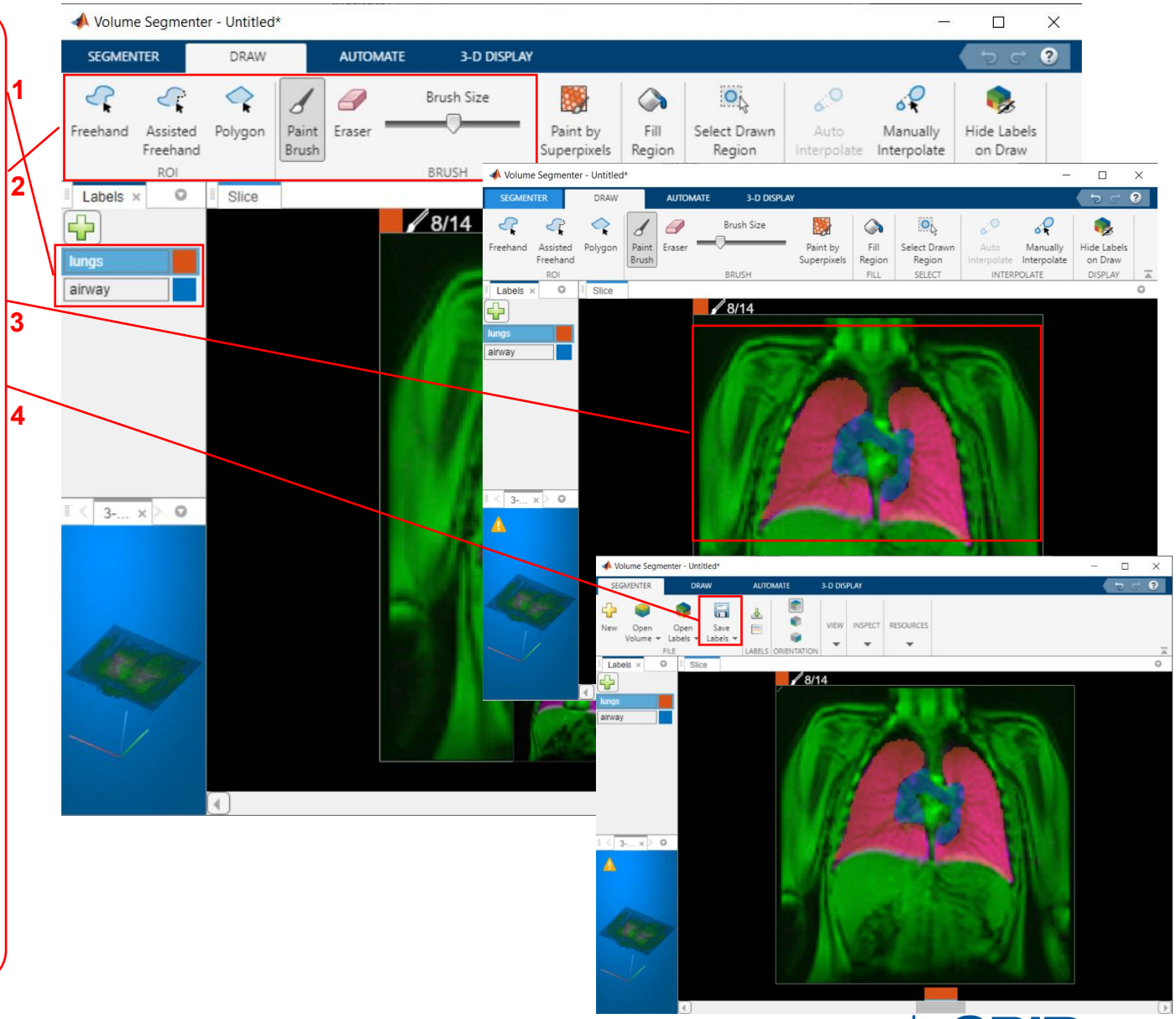
1-Create two labels for the lungs and airways.

2-Choose a drawing method such as Freehand, Paintbrush, etc.

3-Draw masks for the lungs and airways using the selected method.

4-After completing the masks, save them in the Xenon data folder with the filename "mask". Please ensure that the name of the mask is either "mask," "MASK," or "Mask," as any other name will not be uploadable.

Note: There are several segmentation tools available, including thresholding and the option to add your own functions. Feel free to explore and find the most suitable tool for your needs. MATLAB's built-in App Volume Segmenter



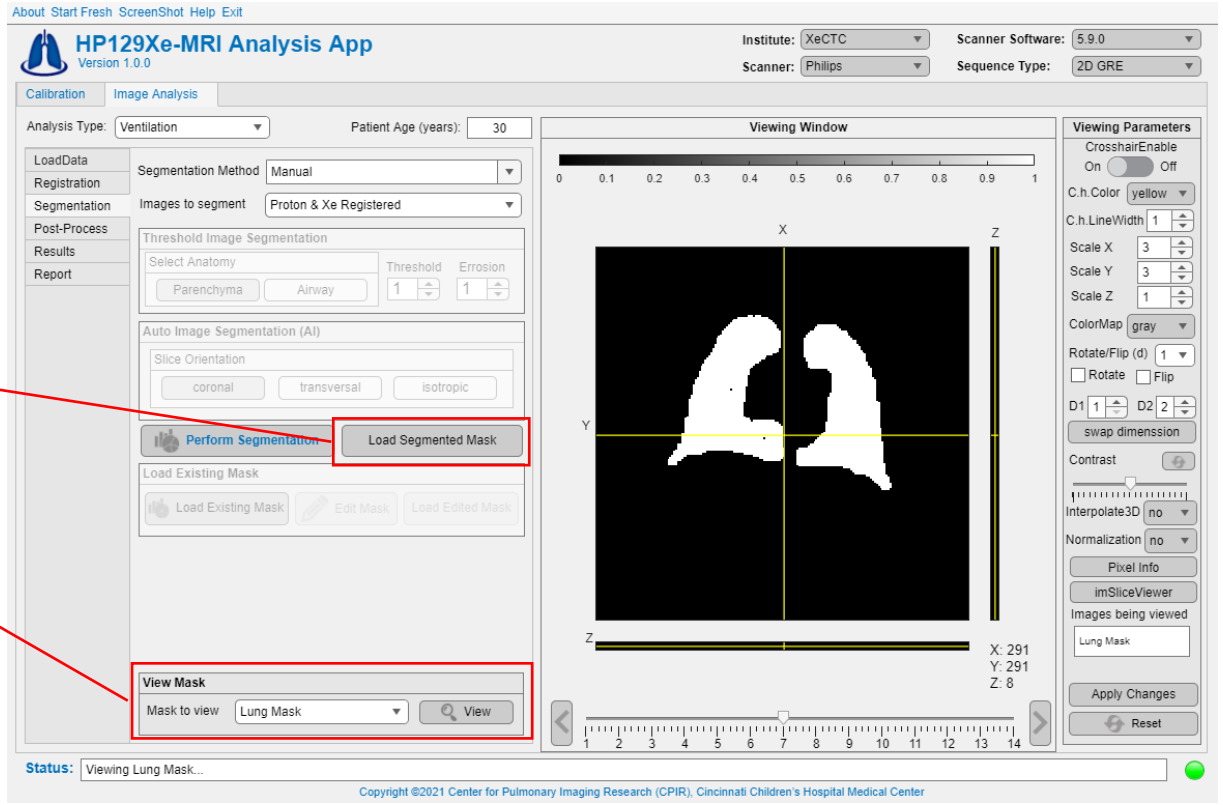
Cincinnati Children's
changing the outcome together

CPIR

Manual Segmentation:

1-Once you have saved the mask, click on "Load Segmented Mask" to automatically upload the mask.

2-You can view the lungs and airway mask by selecting the desired option from the "Viewing Mask" dropdown menu.



Threshold Segmentation:

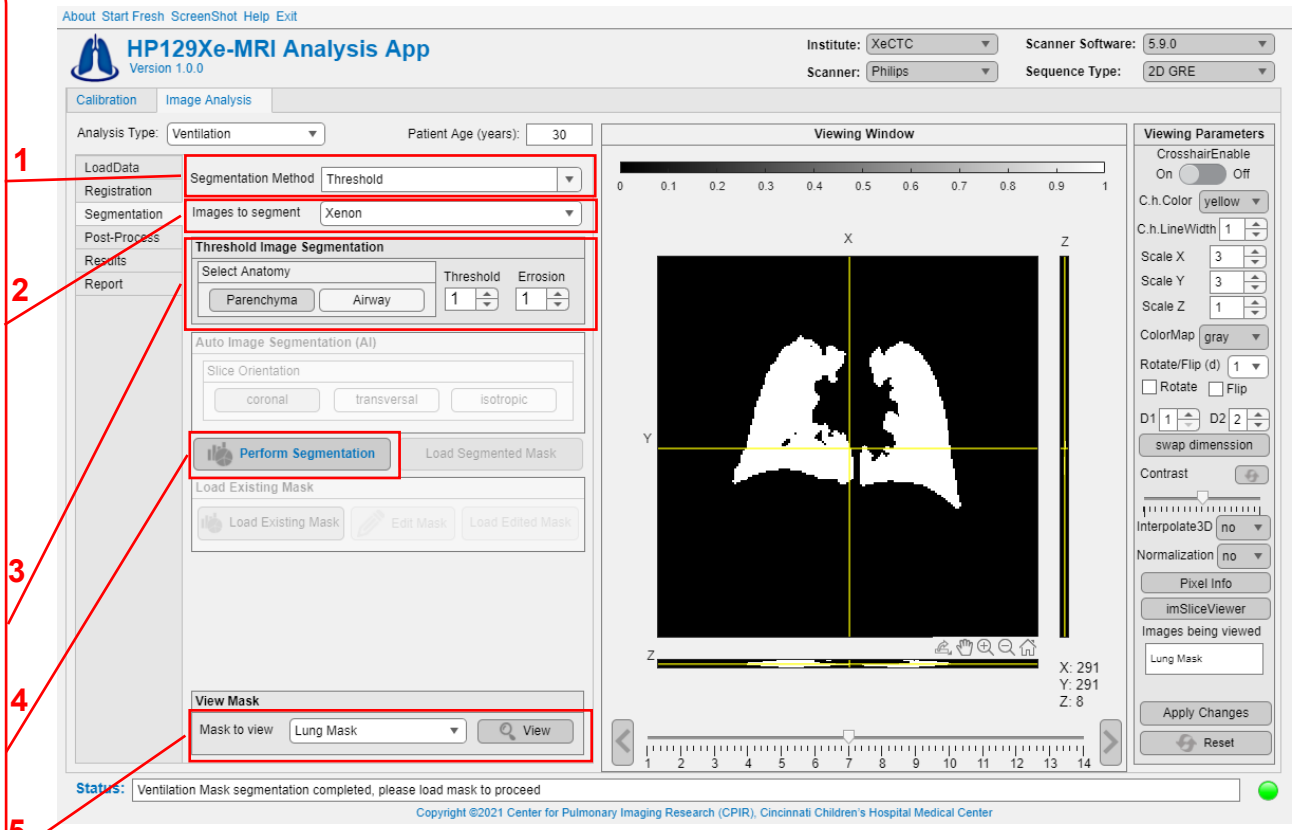
1-Select "Threshold Segmentation" from the dropdown menu.

2-Choose the images to be segmented. For the Threshold method, only grayscale images are accepted. Please note that the airway mask can only be drawn manually (refer to the next page for instructions).

3-Select the desired anatomy, threshold level, and erosion level.

4-Initiate the segmentation process.

5Image Selection: Choose the image type you want to view.



Threshold Segmentation:

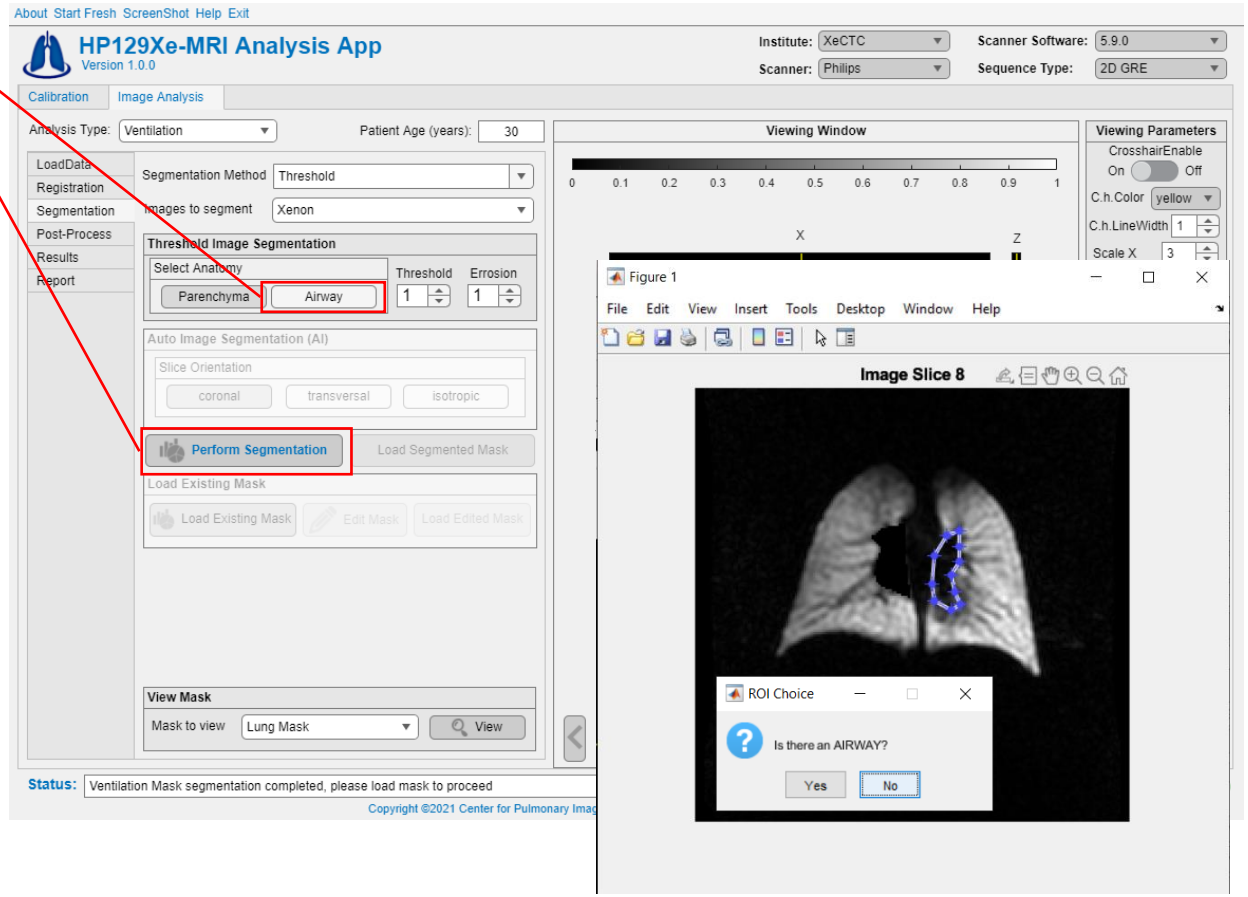
1-Select "Airway"

2- Initiate the segmentation process. The airway mask can only be drawn manually.

Begin drawing the boundaries of the airways by clicking and moving the mouse. You can adjust the points by holding the click and dragging them inward or outward. You can also move the entire region of interest (ROI) by click-holding and moving it. Once finished, double-click in the middle of the ROI.

From prompted, select "Yes" to segment another airway, or select "No" to proceed to the next slice.

Note: The analyst must possess sufficient knowledge about lung anatomy to accurately draw masks.



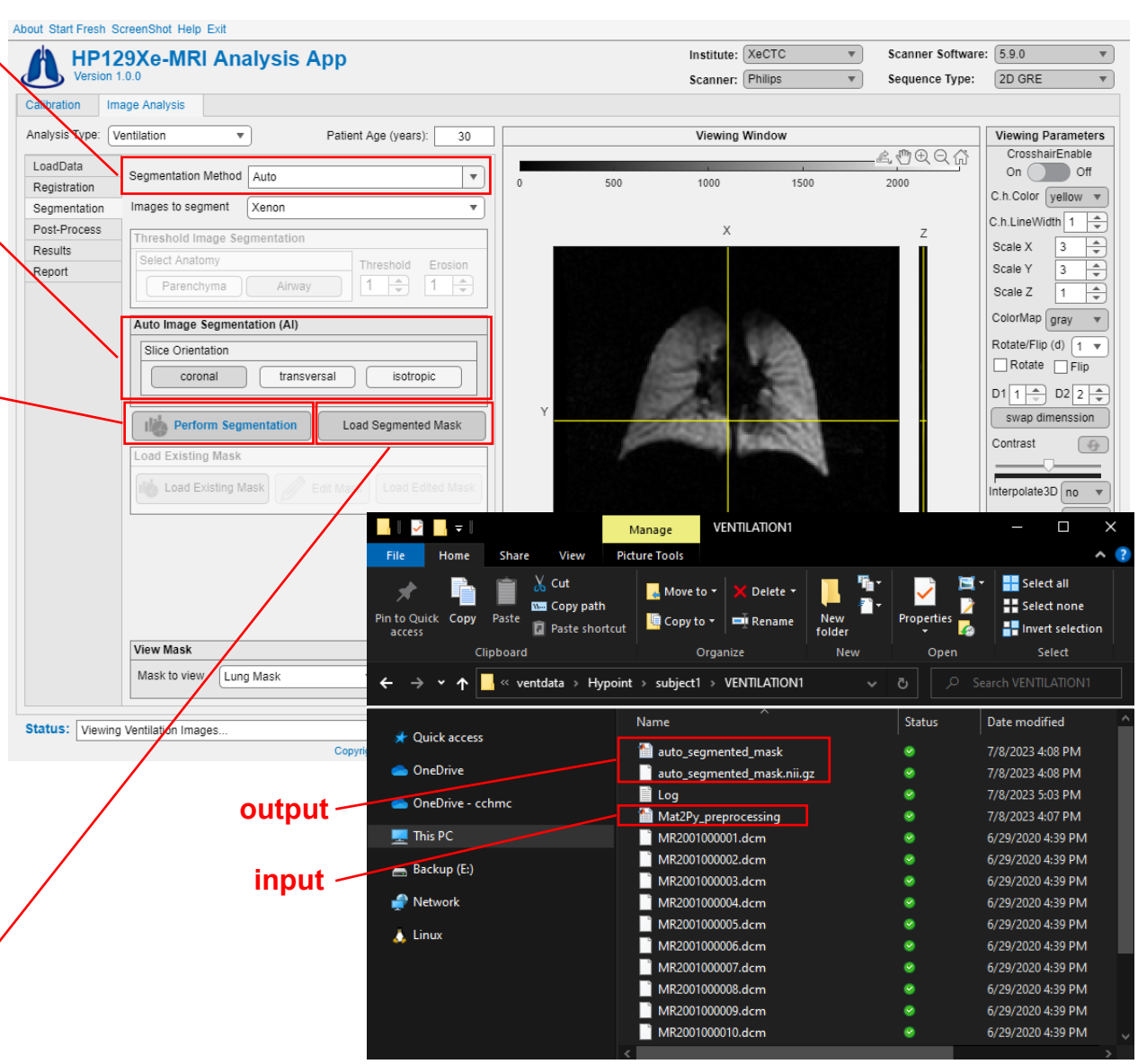
Auto Segmentation:

1-Choose "Auto" from the dropdown menu. Please note that Auto segmentation is not supported for Diffusion analysis.

2-Select the slice orientation. Transversal orientation is not supported for any type of analysis in this current release.

3-Initiate the segmentation process. This will call the appropriate .exe applications. Please ensure that you manually add these files as they cannot be found on the GitHub account. Refer to the GitHub instructions for downloading these applications. Once the process begins, a prompt window will appear. Choose the MATLAB file named "Mat2Py_preprocessing". The resulting mask will be saved in the data folder as "auto_segmented_mask" in both .mat and .nii formats.

4-Load the segmented mask.



3.4 | post-Processing

Post-Processing: Ventilation

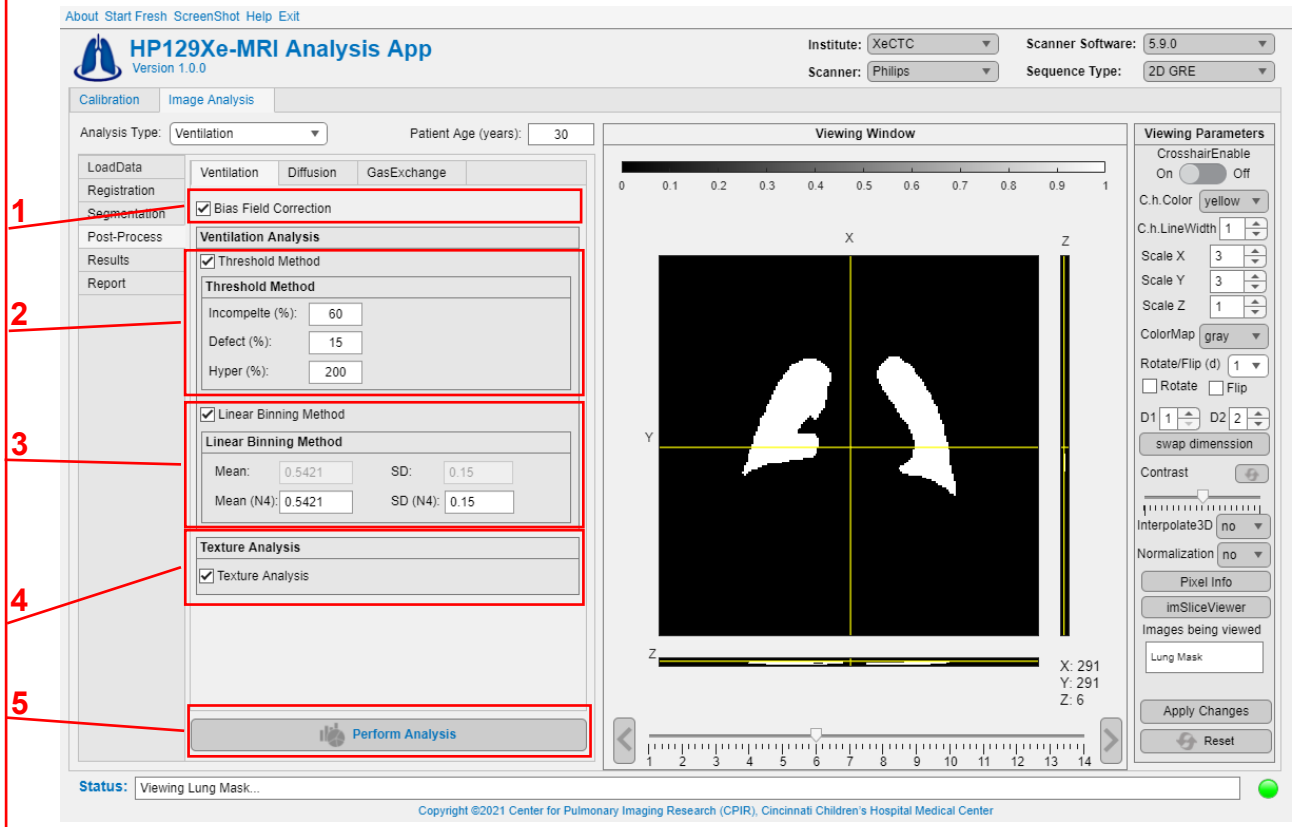
1- Choose "Bias Field Correction" if required.

2-Specify threshold values. The default values are recommended.

3-Specify the means and standard deviations of the healthy reference distribution for linear binning analysis.

4-Select "Texture Analysis" if desired.

5-Initiate the analysis.



Post-Processing: Diffusion

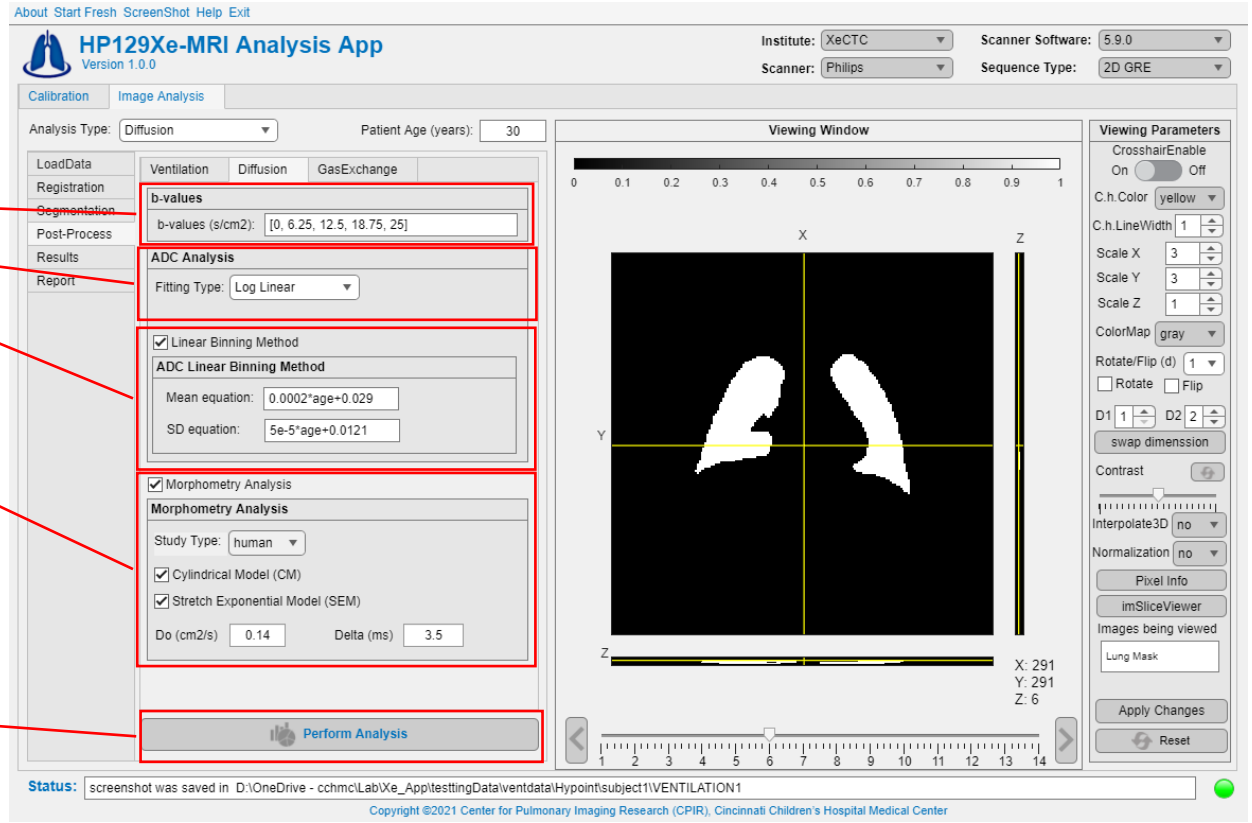
1-Enter the b-values.

2-Choose the type of fitting.

3-Specify the means and standard deviations of the healthy reference distribution for linear binning analysis.

4-Select the desired morphometry settings. Please note that morphometry analysis requires a minimum of 4 b-values.

5-Initiate the analysis.

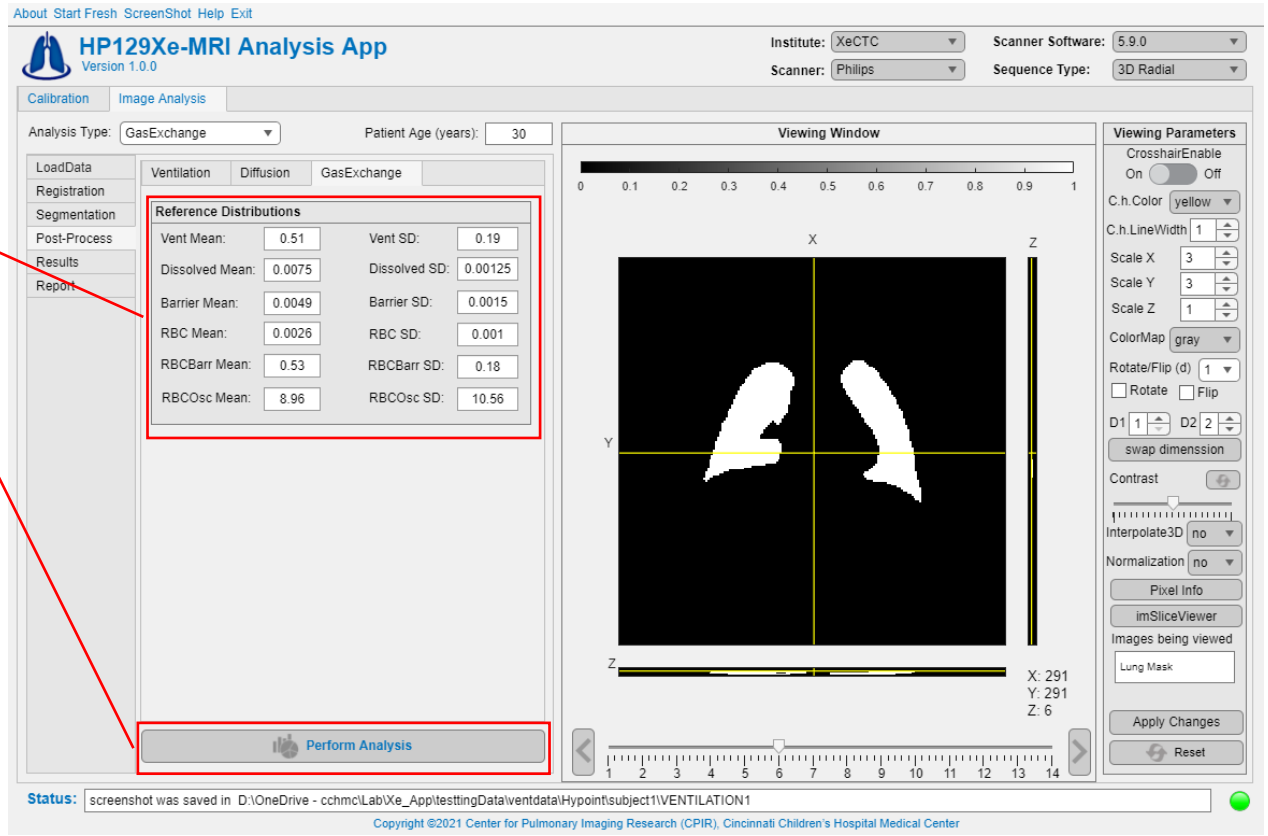


Post-Processing: Gas Exchange

1-Provide the means and standard deviations of the healthy reference distribution.

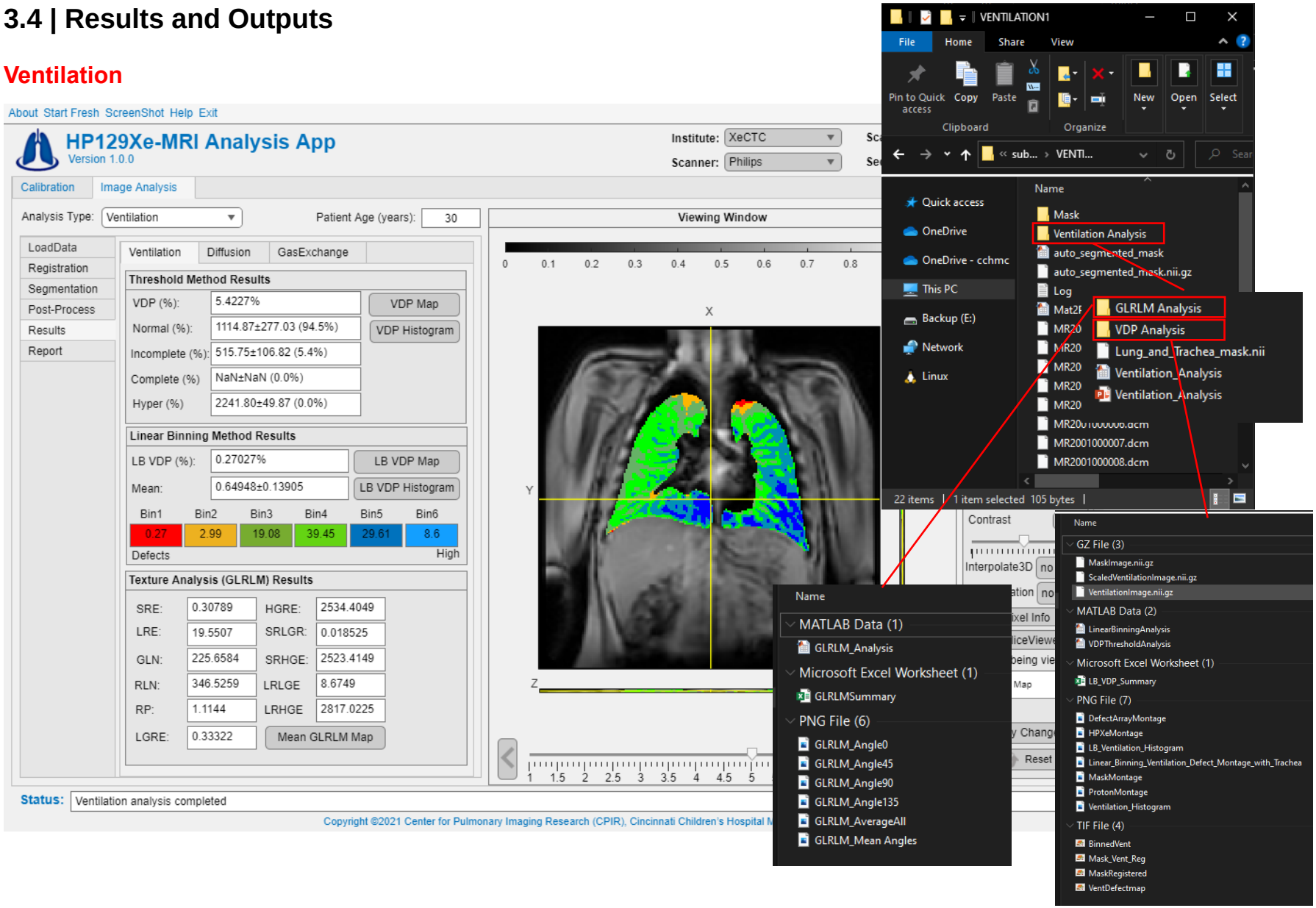
2-Initiate the analysis.

Note: The gas exchange analysis is complex and has been specifically coded for the CCHMC institute. We recommend implementing your own analysis pipeline using our analysis pipeline as a reference to meet your specific needs.

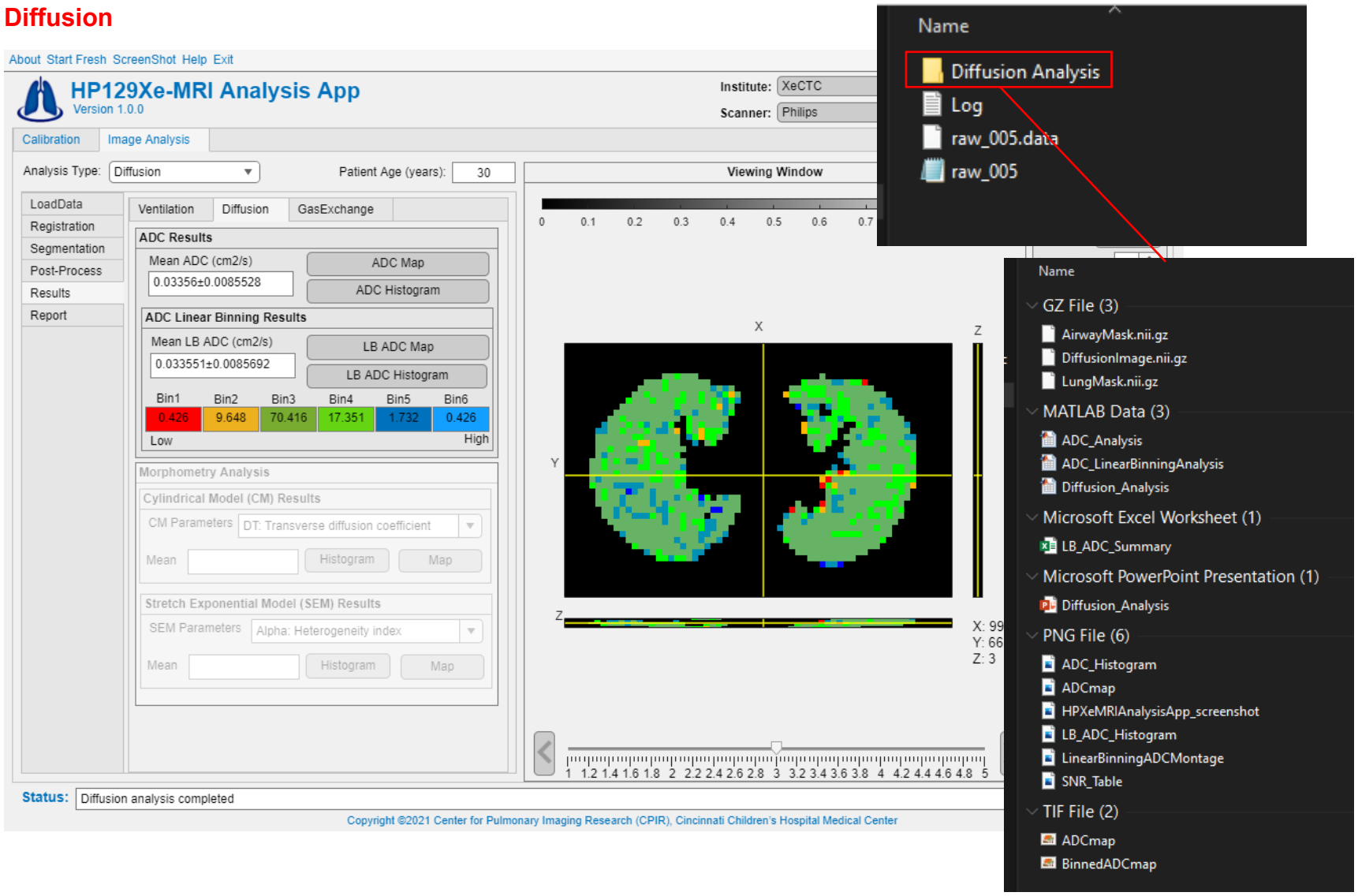


3.4 | Results and Outputs

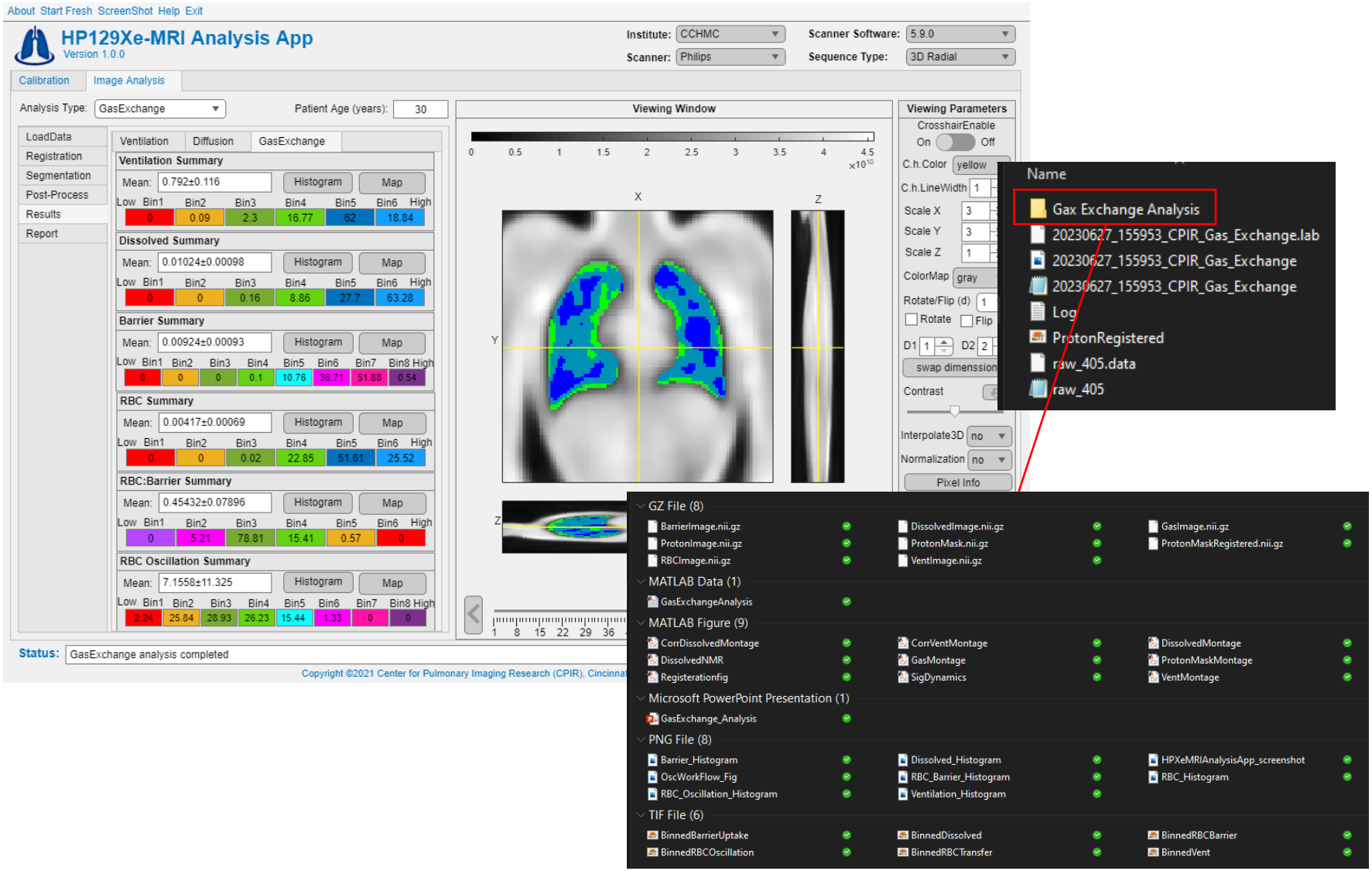
Ventilation



Diffusion


About Start Fresh ScreenShot Help Exit
HP129Xe-MRI Analysis App
Version 1.0.0
Institute: XeCTC
Scanner: Philips
Calibration
Image Analysis
Analysis Type: Diffusion
Patient Age (years): 30
LoadData
Registration
Segmentation
Post-Process
Results
Report
Ventilation
Diffusion
GasExchange
ADC Results
Mean ADC (cm2/s)
0.03356±0.0085528
ADC Map
ADC Histogram
ADC Linear Binning Results
Mean LB ADC (cm2/s)
0.033551±0.0085692
LB ADC Map
LB ADC Histogram
Bin1 Bin2 Bin3 Bin4 Bin5 Bin6
0.426 9.648 70.416 17.351 1.732 0.426
Low
High
Morphometry Analysis
Cylindrical Model (CM) Results
CM Parameters
DT: Transverse diffusion coefficient
Mean
Histogram
Map
Stretch Exponential Model (SEM) Results
SEM Parameters
Alpha: Heterogeneity index
Mean
Histogram
Map
Viewing Window
0 0.1 0.2 0.3 0.4 0.5 0.6 0.7
X
Y
Z
1 1.2 1.4 1.6 1.8 2 2.2 2.4 2.6 2.8 3 3.2 3.4 3.6 3.8 4 4.2 4.4 4.6 4.8 5
Status: Diffusion analysis completed
Copyright ©2021 Center for Pulmonary Imaging Research (CPIR), Cincinnati Children's Hospital Medical Center
Name
Diffusion Analysis
Log
raw_005.data
raw_005
Name
GZ File (3)
AirwayMask.nii.gz
DiffusionImage.nii.gz
LungMask.nii.gz
MATLAB Data (3)
ADC_Analysis
ADC_LinearBinningAnalysis
Diffusion_Analysis
Microsoft Excel Worksheet (1)
LB_ADC_Summary
Microsoft PowerPoint Presentation (1)
Diffusion_Analysis
PNG File (6)
ADC_Histogram
ADCmap
HPXeMRIAnalysisApp_screenshot
LB_ADC_Histogram
LinearBinningADCMontage
SNR_Table
TIF File (2)
ADCmap
BinnedADCmap

Gas Exchange



3.6 | Patient Report

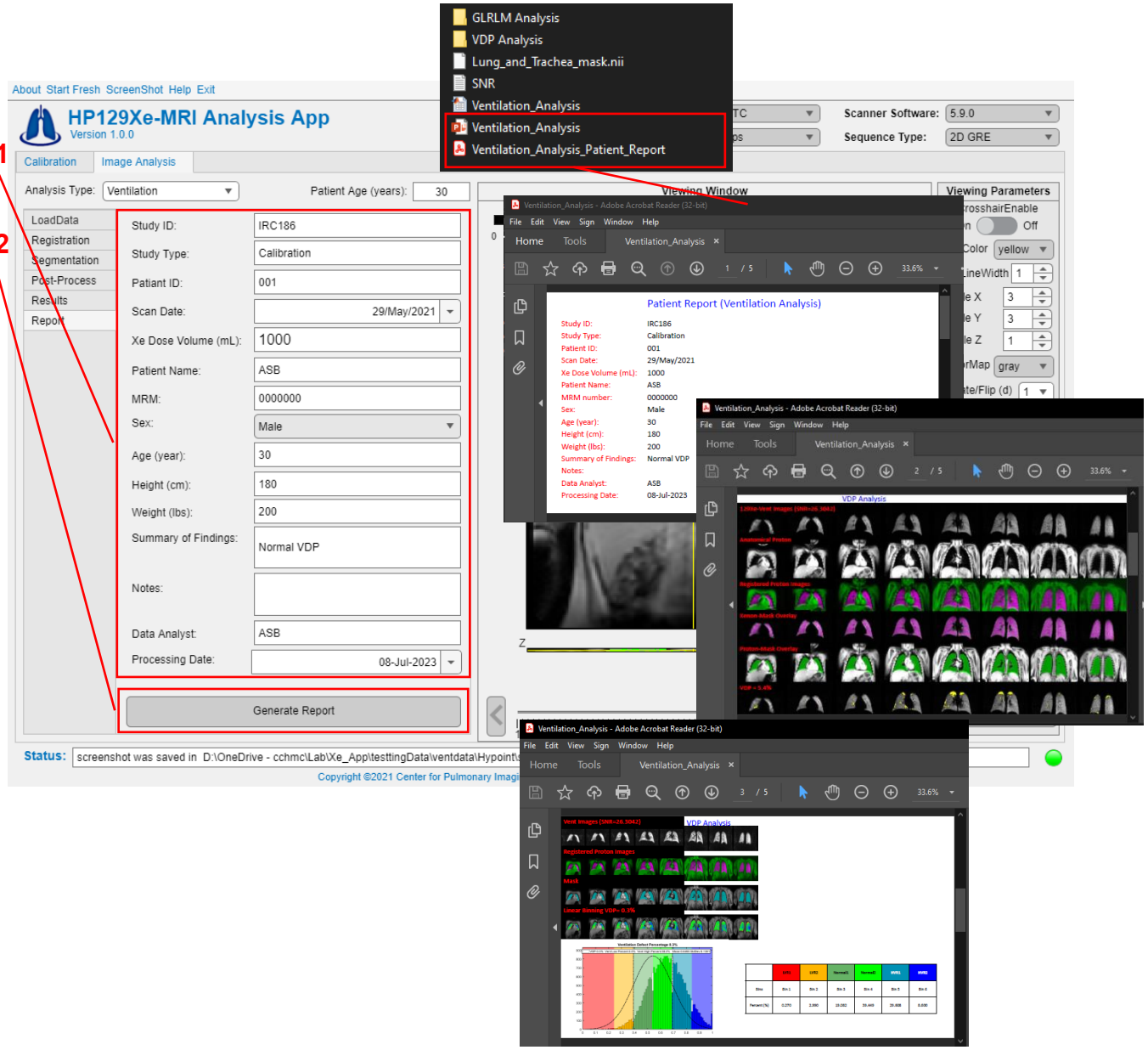
Patient Report

1-Complete the patient report information.

2-Generate the report.

This will generate .ppt and .pdf files containing all patient information and a summary of the findings.

Additionally, we recommend opening the analysis PowerPoint file to address any misalignments or make any desired additions before generating the report.



3.6 | Viewing Window

4 | Code Structure

4.1 | Folders

The app skeleton consists of the complete layout and interface.

Necessary functions for Calibration analysis

Necessary functions for Diffusion analysis

Necessary functions for Gas Exchange analysis

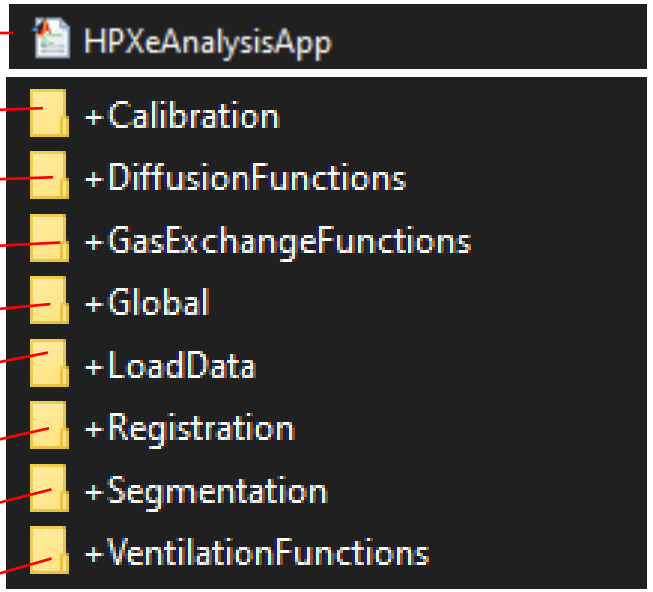
Global function that are used in all analyses.

Necessary functions for loading and reconstruction of images

Necessary functions for performing Registration.

Necessary functions for performing

Necessary functions for ventilation analysis



4.2 | Code Hierarchy

Here are the main and submain functions:

Calibration analysis: `StartCalibrationAnalysis()`
- `Calibration.XeCTC_Calibration()`
- `Calibration.Xe_duke_UVA_calibration()`

Load Data: `LoadData.LoadReadData()`
- **(.dcm)** `LoadData.DICOM_Load()`
- **(.mat)** `load()`
- **(.nii or .nii.gz)** `LoadData.load_nii()`
- **(Philips/.data)** `LoadData.LoadData_Gas_VentDiff_Philips_GRE()`
- **(Philips/.data)** `LoadData.LoadData_Gas_GasExchange_Philips_Sin()`

Registration: `Registration.PerformRegistration()`
- `Registration.GeneralRegisterProton_to_Xenon()`
- `Registration.GasExchange_RegisterProton_to_Xenon()`

Segmentation: `Segmentation.PerformSegmentation()`
- `Segmentation.PerformManualThresholdSegmentation()`
- `Segmentation.preprocess_images_for_auto_segmentation()`

Analysis:
`VentilationFunctions.Ventilation_Analysis()`
`DiffusionFunctions.Diffusion_Analysis()`
`GasExchangeFunctions.GasExchange_Analysis()`

4.2 | Implement Your Own Functions

The application is entirely open source, allowing users to fully customize and modify it according to their needs. Although the built-in features offer essential functionality for a comprehensive analysis pipeline, they should be adequate. However, users who already have in-house code for HP 129Xe analysis can easily integrate their existing functions into the application framework. They have the option to duplicate and modify the existing functions or introduce their own. Let's consider an example of adding a new function:

```
function [Ventilation, Diffusion, GasExchange, Proton] = LoadReadData(MainInput)
    if strcmp(MainInput.XeDataext,'.dcm') == 1
        ...
    elseif strcmp(MainInput.XeDataext,'.mat') == 1
        ...
    elseif strcmp(MainInput.XeDataext,'.nii') == 1 || strcmp(MainInput.XeDataext,'.gz') == 1
        ...
    %---------------------- add new read load function here --------------------
    % elseif strcmp(MainInput.XeDataType,'add DataType') == 1
    %     if strcmp(MainInput.AnalysisType,'Ventilation') == 1
    %       %  add load/read function here
    %     elseif strcmp(MainInput.AnalysisType,'Diffusion') == 1
    %       %  add load/read function here
    %     elseif strcmp(MainInput.AnalysisType,'GasExchange') == 1
    %       %  add load/read function here
    %     end
    end
end
```

4 | Debugging

As the application is entirely developed in MATLAB, the debugging procedure remains consistent with debugging any other MATLAB code. However, we additionally offer a script specifically designed for debugging the functions outside the application framework. This script serves multiple purposes, including function development, addition, and testing, allowing users to evaluate new functions before integrating them into the application.

5 | Report Issues

If you encounter any problems, kindly create an issue on our GitHub account, and our team of authors will collaborate with you to address and resolve the issue promptly.