



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

For Research Use Only



User's Manual
HP ¹²⁹Xe MRI Analysis App

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Center for Pulmonary Imaging Research
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1 | Overview

Main Menu:

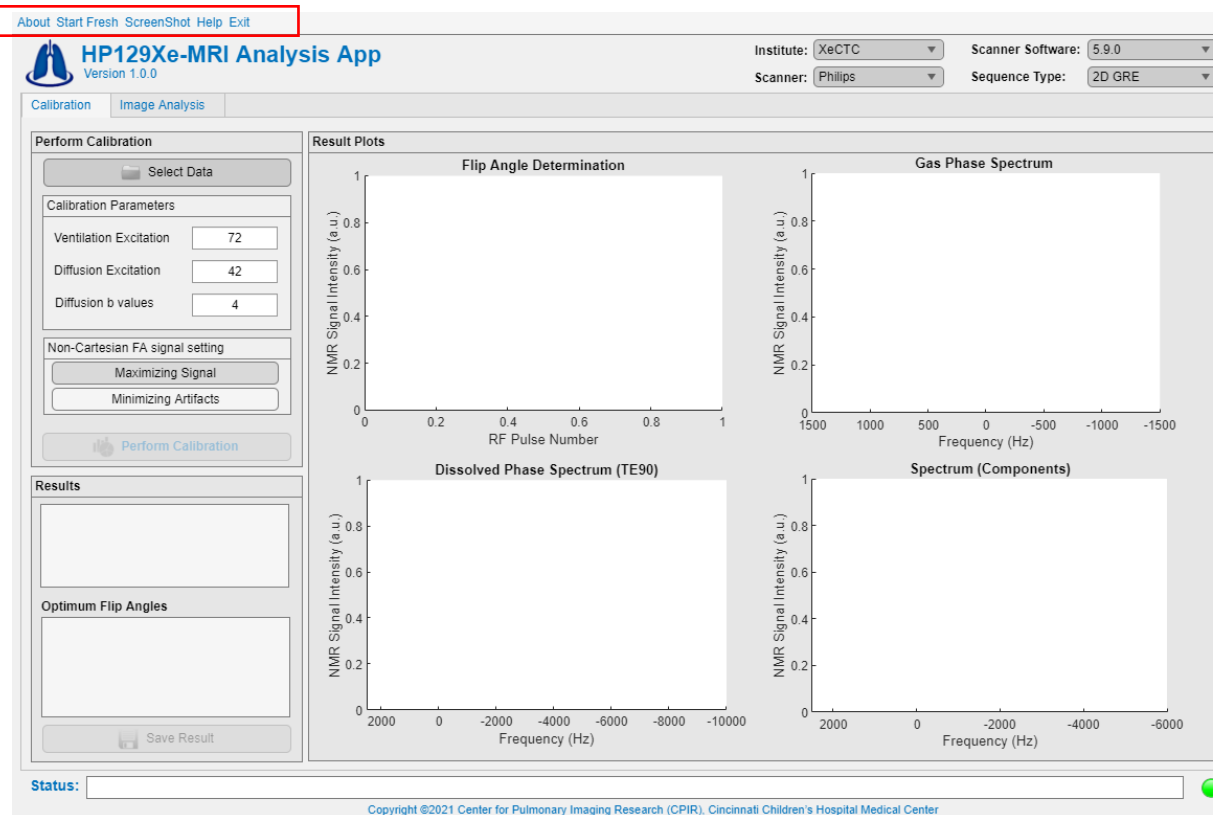
About: Provides an insightful overview of the application and its functionalities.

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.

About Start Fresh ScreenShot Help Exit

HP129Xe-MRI Analysis App
Version 1.0.0

Institute: XeCTC Scanner Software: 5.9.0
Scanner: Philips Sequence Type: 2D GRE

Calibration Image Analysis

Perform Calibration

Select Data

Calibration Parameters

Ventilation Excitation: 72
Diffusion Excitation: 42
Diffusion b values: 4

Non-Cartesian FA signal setting
Maximizing Signal
Minimizing Artifacts

Perform Calibration

Results

Optimum Flip Angles

Save Result

Result Plots

Flip Angle Determination

NMR Signal Intensity (a.u.) vs RF Pulse Number

Gas Phase Spectrum

NMR Signal Intensity (a.u.) vs Frequency (Hz)

Dissolved Phase Spectrum (TE90)

NMR Signal Intensity (a.u.) vs Frequency (Hz)

Spectrum (Components)

NMR Signal Intensity (a.u.) vs Frequency (Hz)

Status:

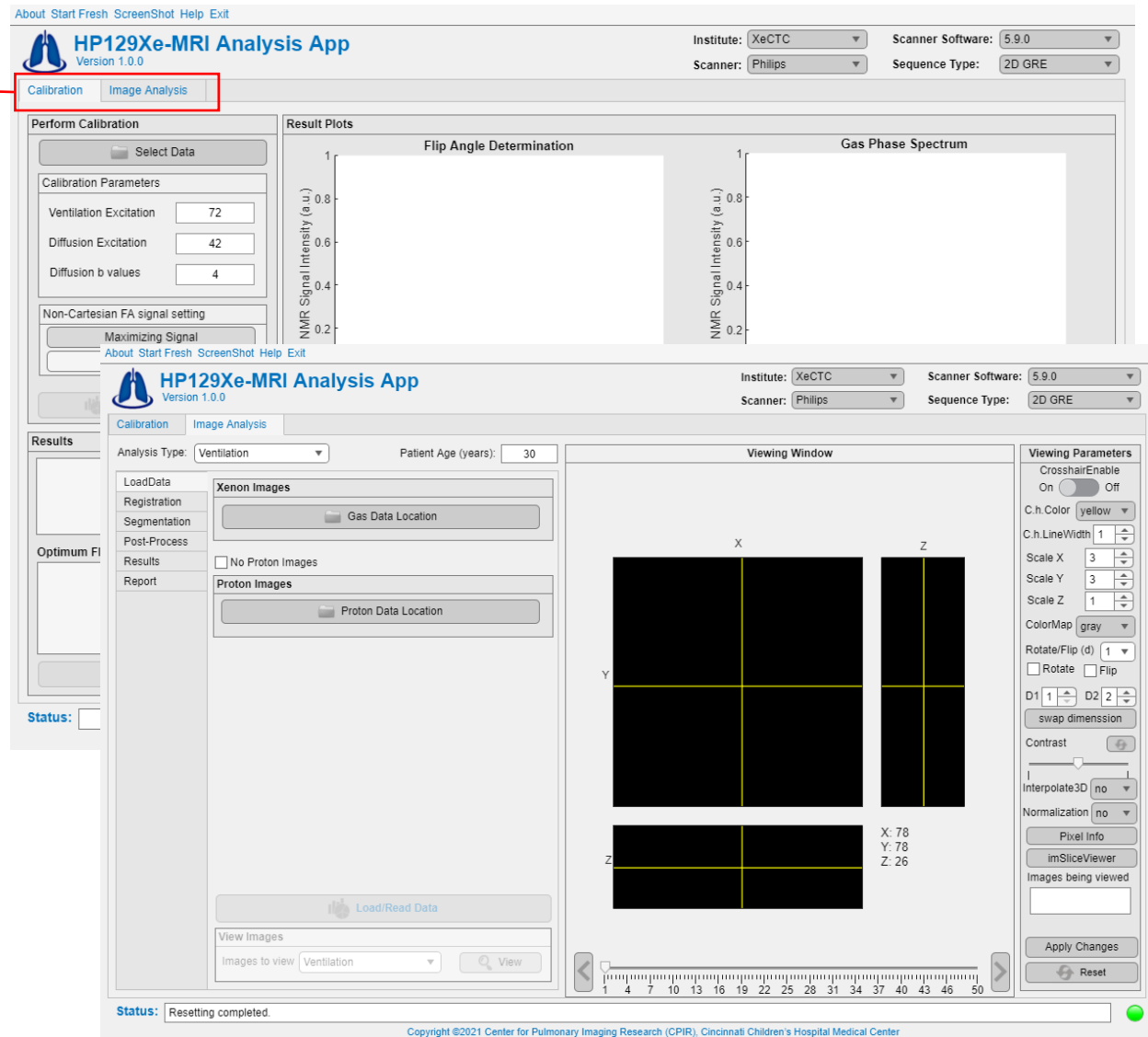
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Main Tabs:

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.

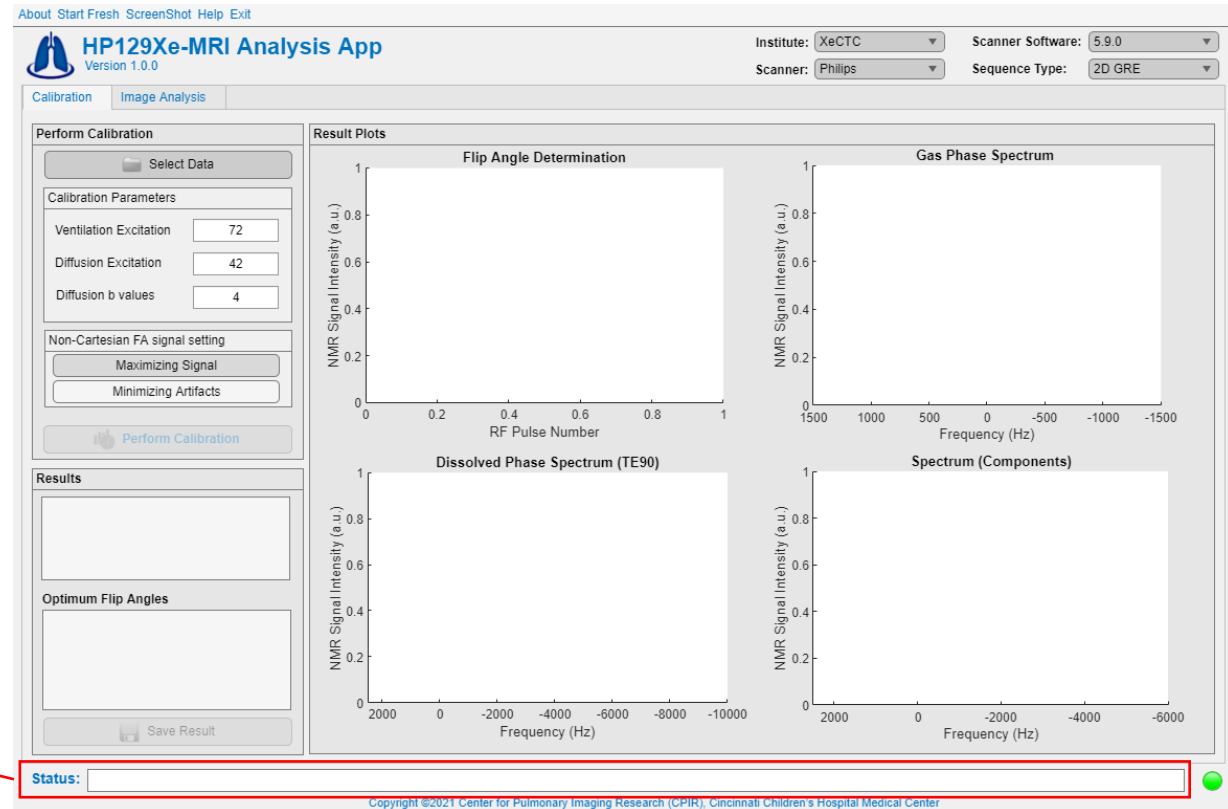


The screenshot displays the HP129Xe-MRI Analysis App interface, which is divided into two main sections: Calibration and Image Analysis. The top section, titled "HP129Xe-MRI Analysis App Version 1.0.0", includes a menu bar (About, Start Fresh, ScreenShot, Help, Exit) and a header area with dropdown menus for Institute (XeCTC), Scanner (Philips), Scanner Software (5.9.0), and Sequence Type (2D GRE). The main content area is split into two tabs: Calibration and Image Analysis. The Calibration tab is active, showing a "Perform Calibration" section with a "Select Data" button and "Calibration Parameters" (Ventilation Excitation: 72, Diffusion Excitation: 42, Diffusion b values: 4). It also includes a "Non-Cartesian FA signal setting" section with a "Maximizing Signal" button. The "Result Plots" section contains two graphs: "Flip Angle Determination" and "Gas Phase Spectrum", both showing NMR Signal Intensity (a.u.) on the y-axis. The Image Analysis tab is also visible, showing a "Viewing Window" with X, Y, and Z axes, a "Viewing Parameters" panel on the right, and a "Status" bar at the bottom indicating "Resetting completed."



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.

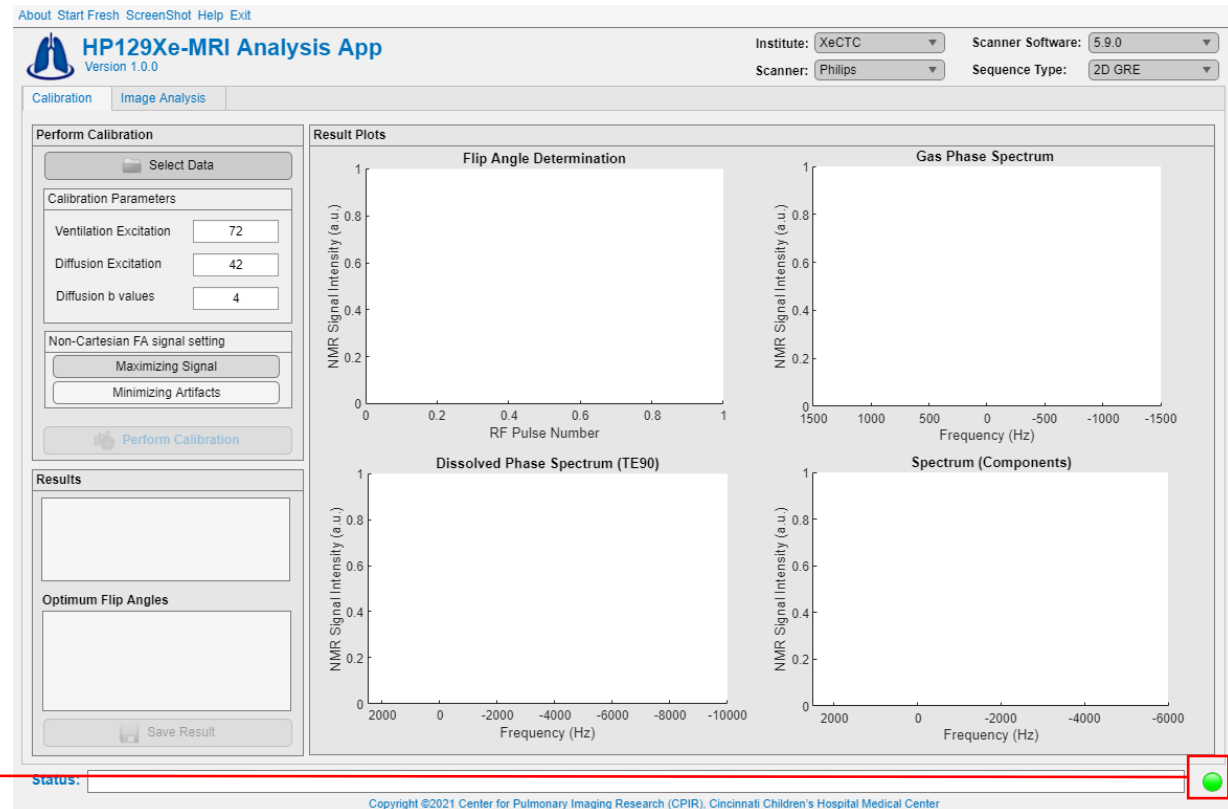




Lamp:

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.

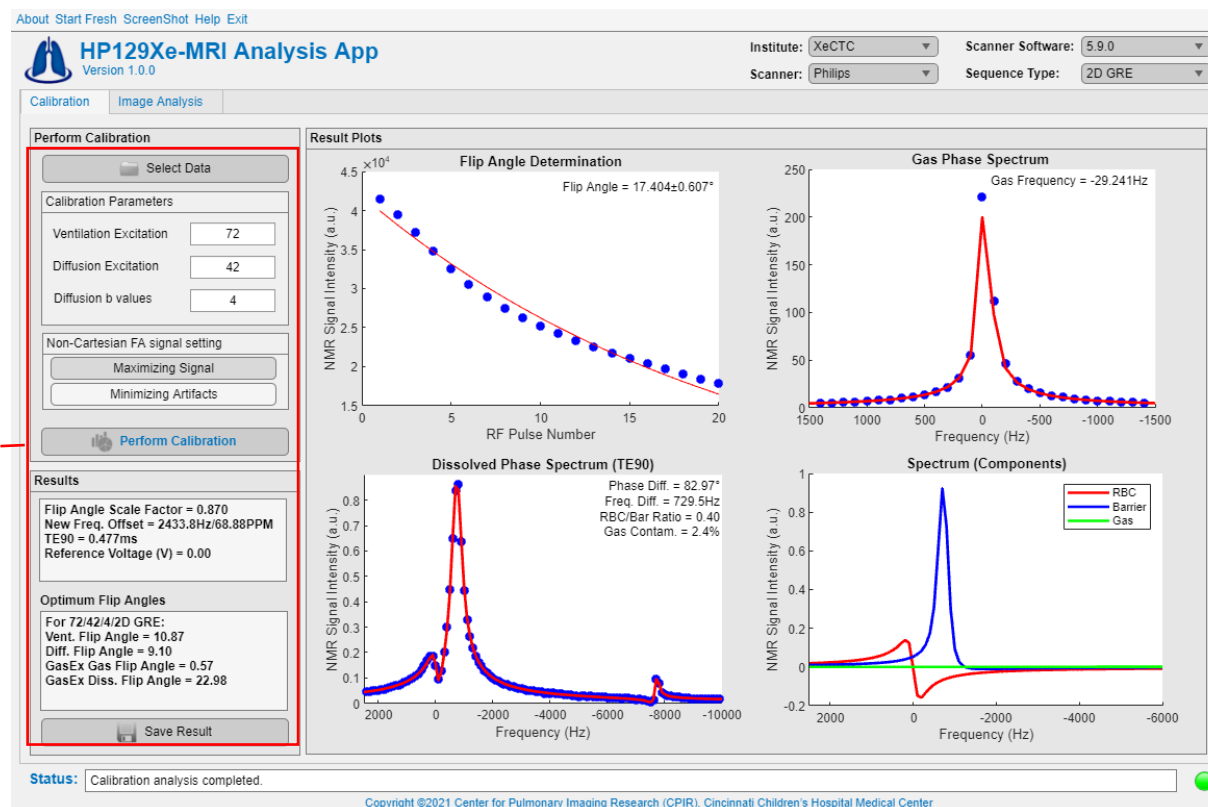


Table 2.1: Supported data type for Calibration analysis

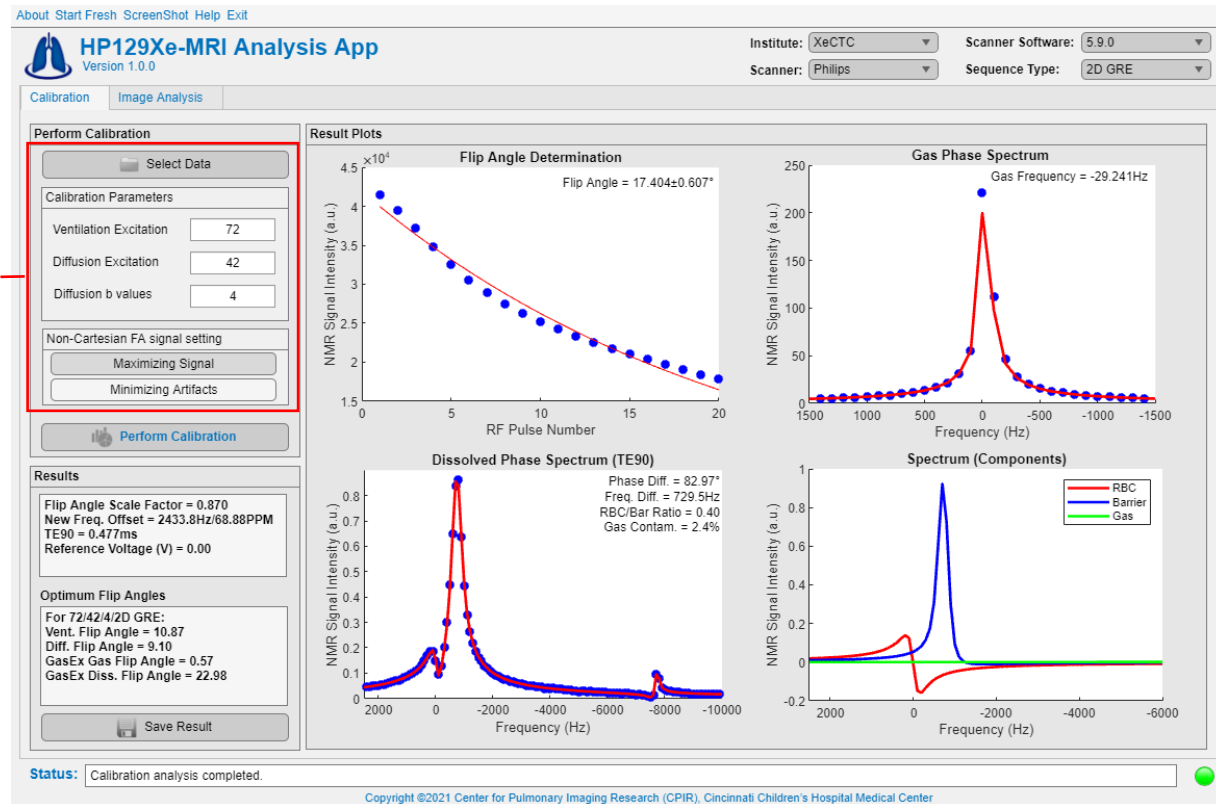
Scanner	Philips	Siemens	GE
Data Type	.data*/.list	.dat*	

* 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.

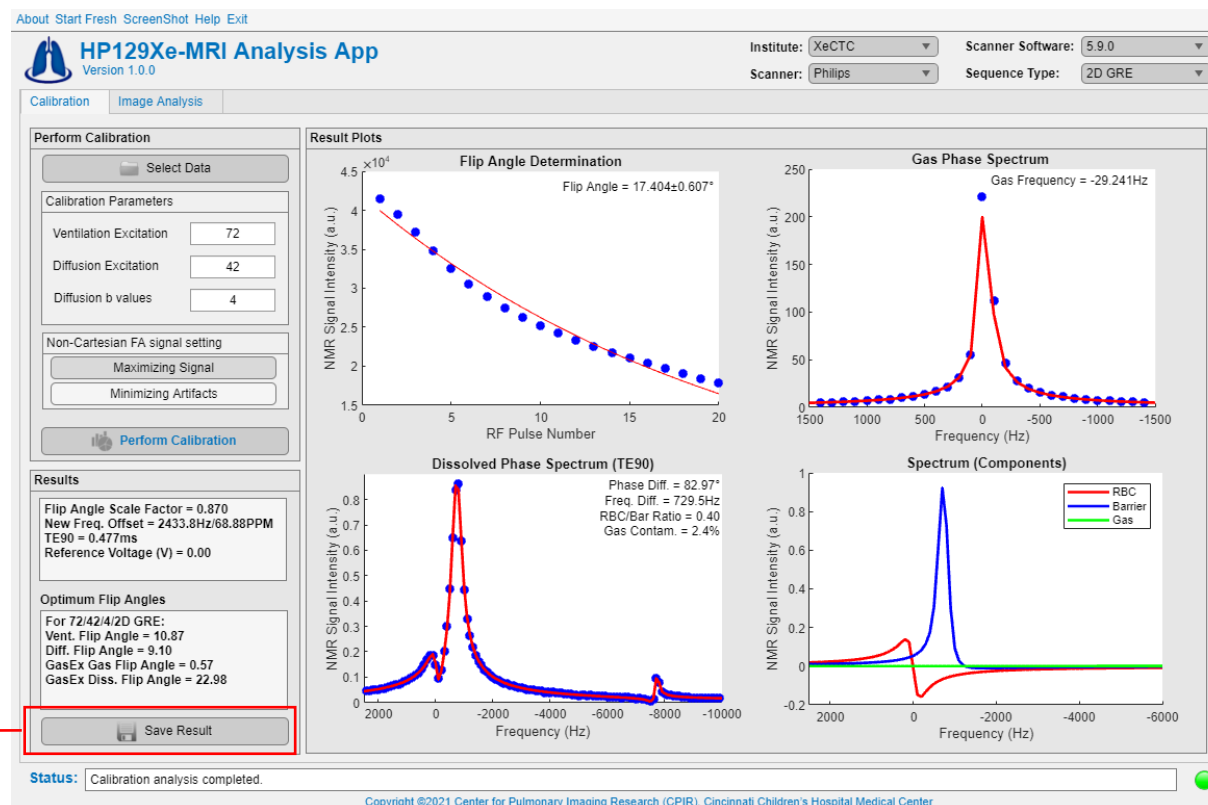




2.3 | Save Results

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.

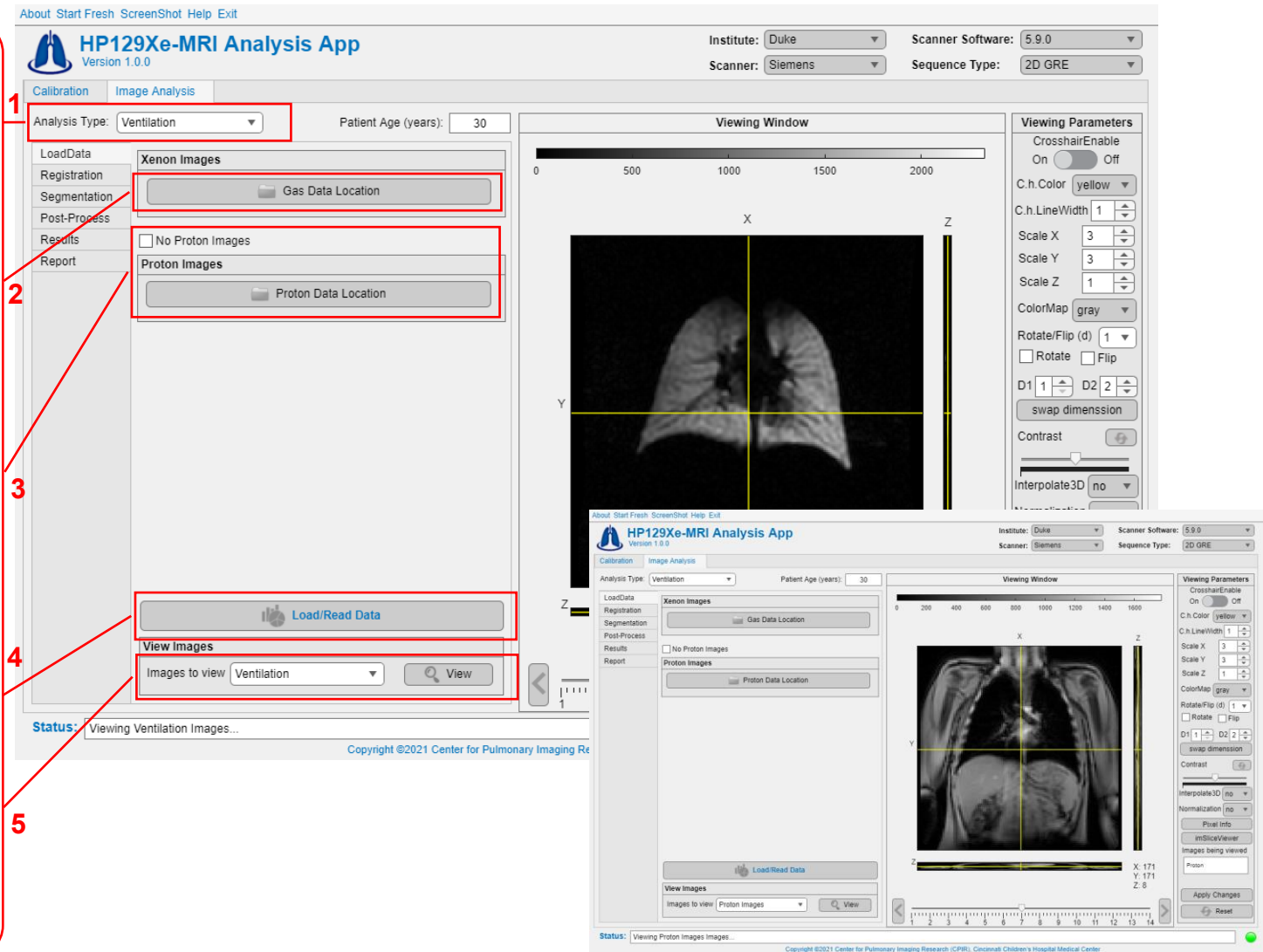




Table 3.1: Supported data type for image analysis

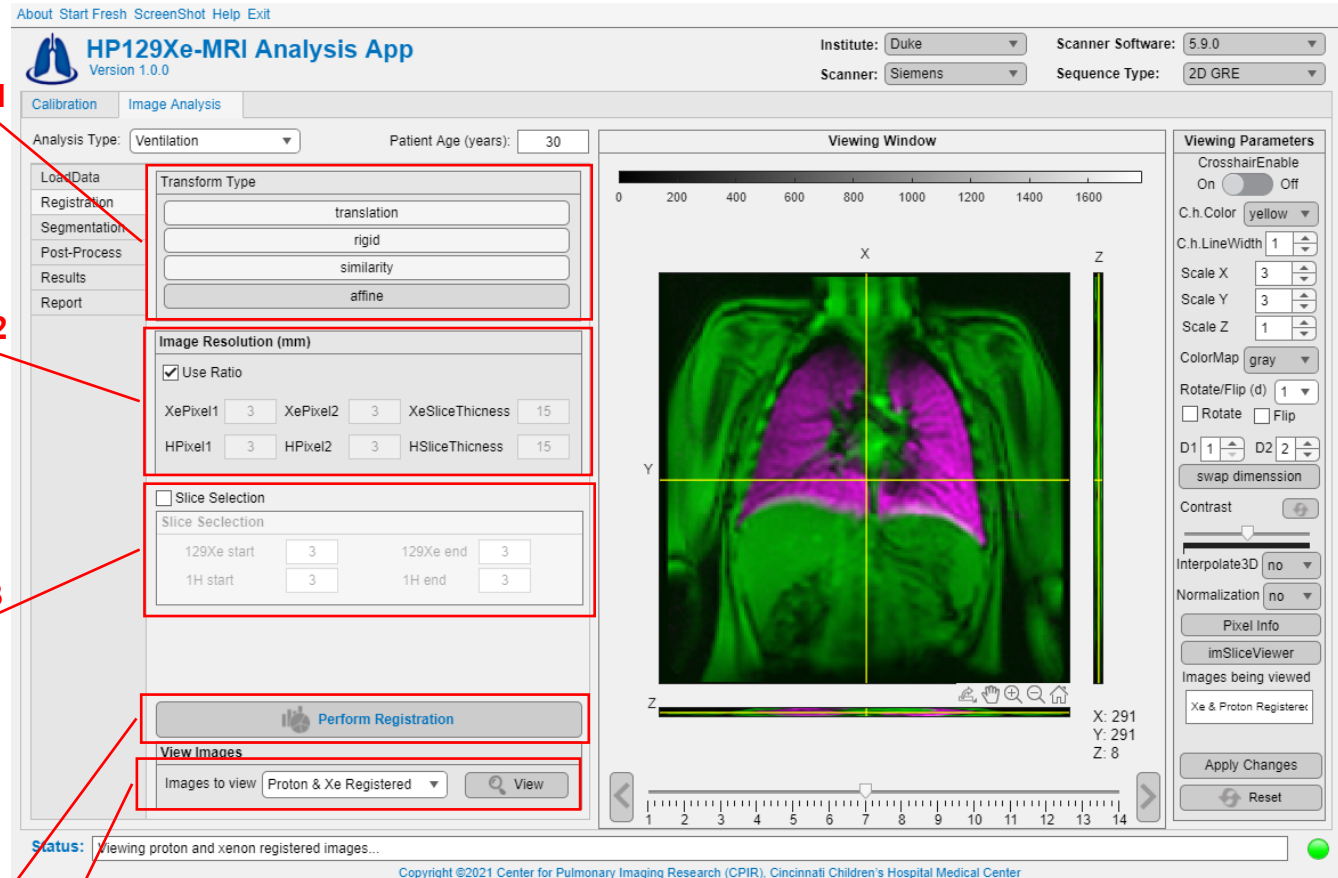
Data Type	DICOM (.dcm)		MATLAB (.mat)	Nifti (.nii or .nii.gz)	ISMRMD (.mrd or .h5)		Raw data																	
	single	multiple	single	single	single		Philips						Siemens						GE					
					GRE	NC	GRE (.data)			NC (.data)			NC			NC			NC			NC		
							V	D	G	V	D	G	V	D	G	V	D	G	V	D	G	V	D	G
Supported?	yes	yes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

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.

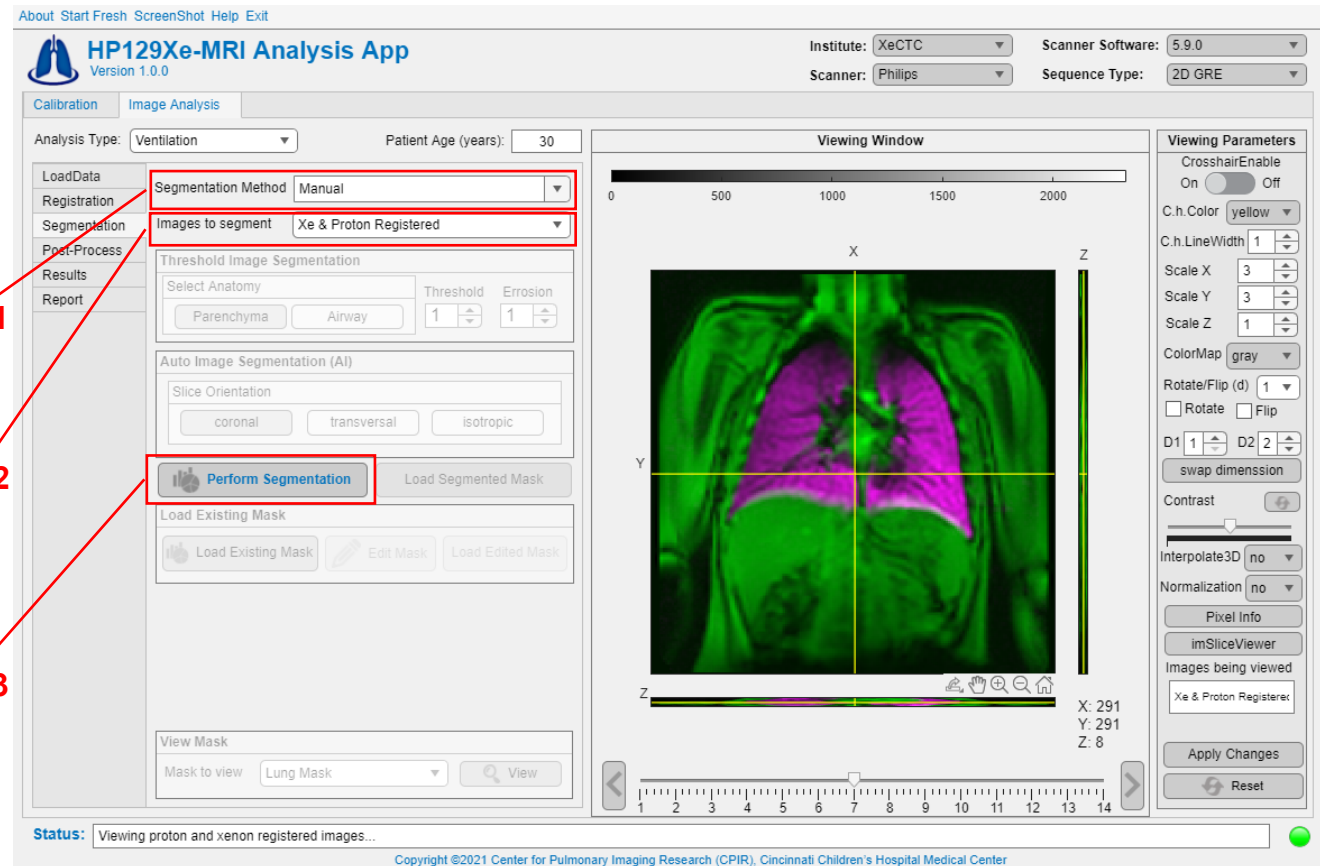




3.3 | Segmentation

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.





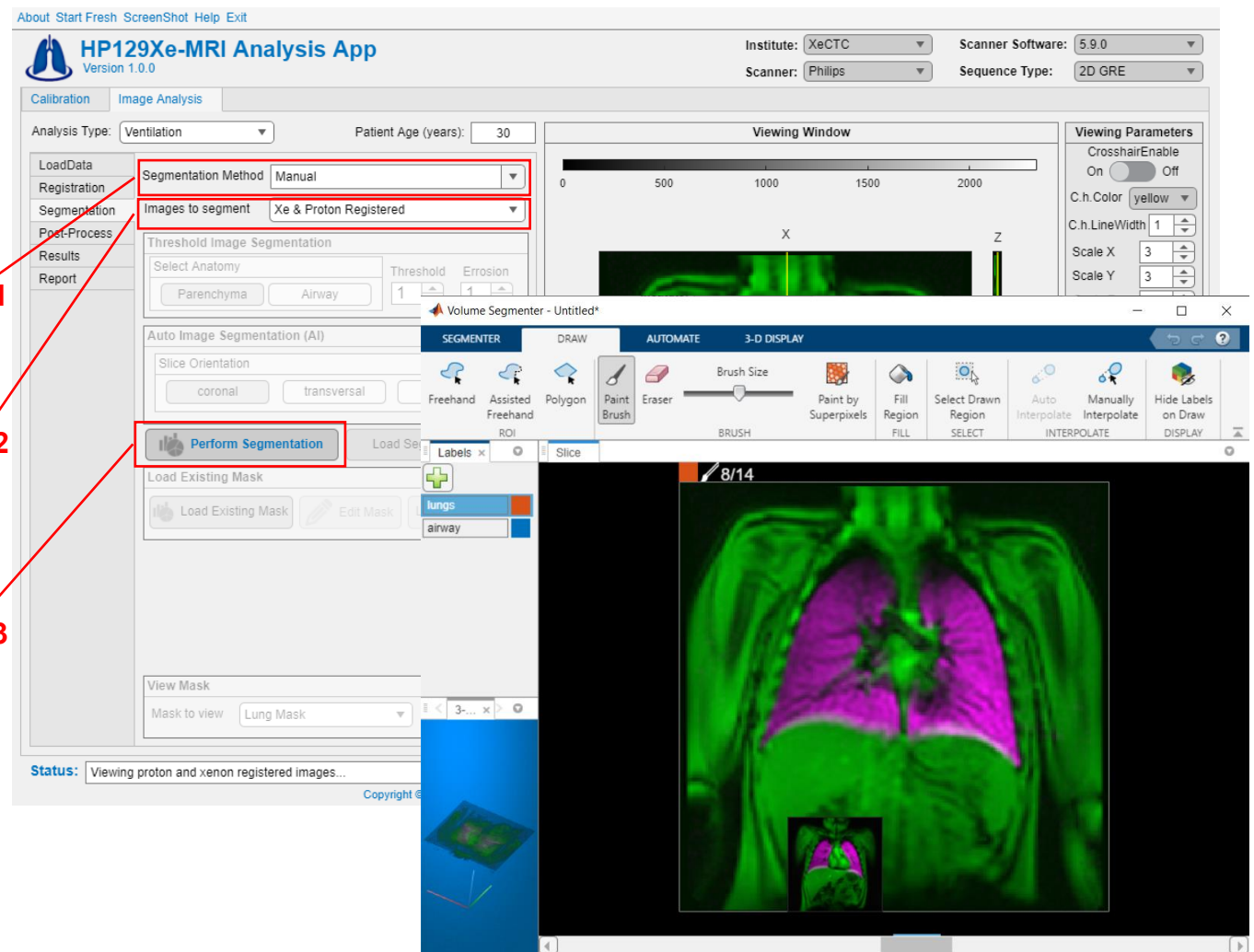
Manual Segmentation:

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:

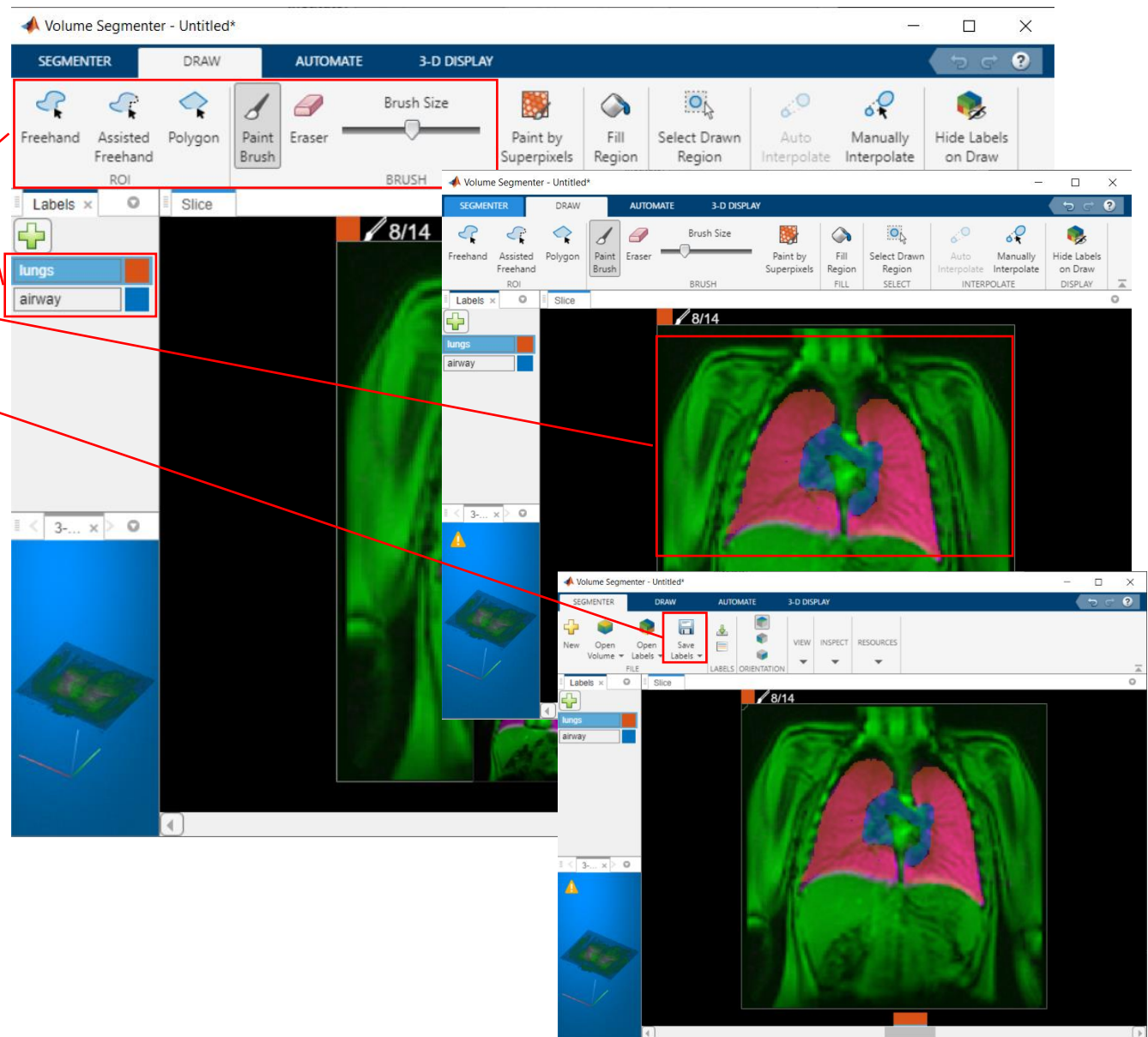
1-Create two labels for the lungs and airways.

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](#)

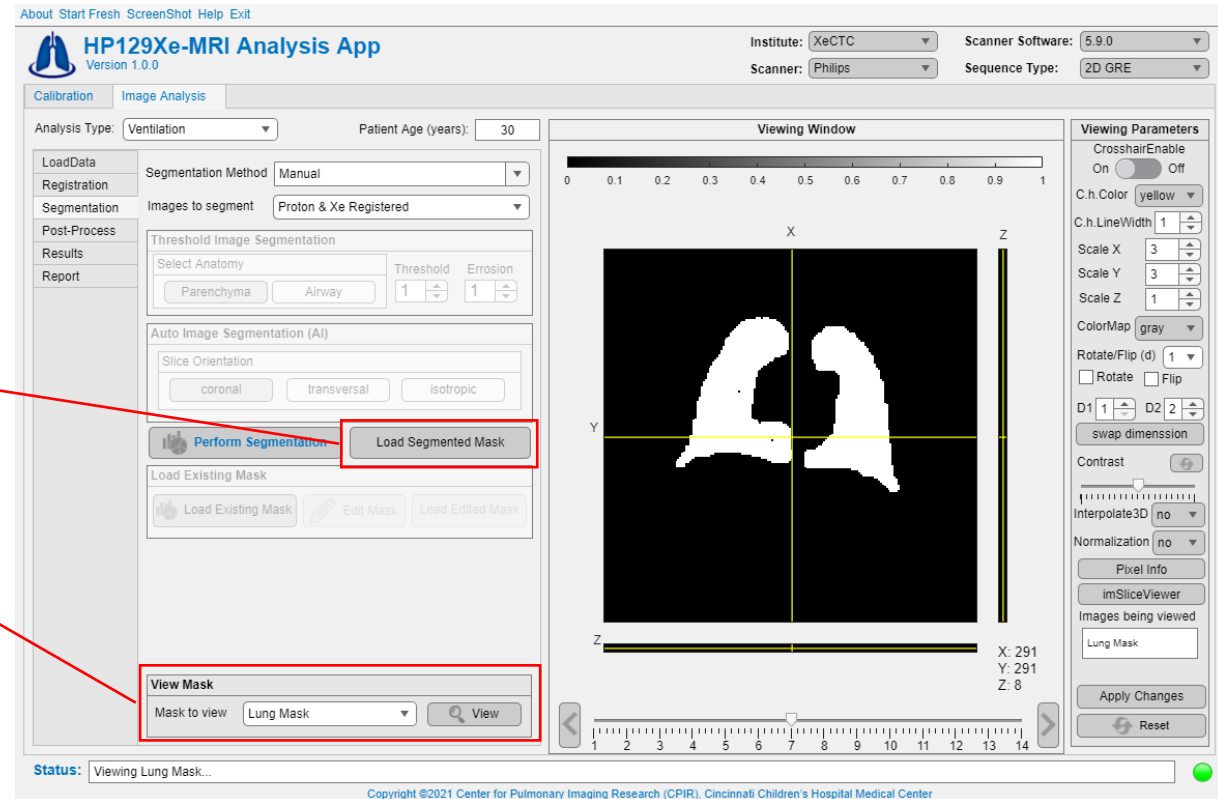




Manual Segmentation:

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:

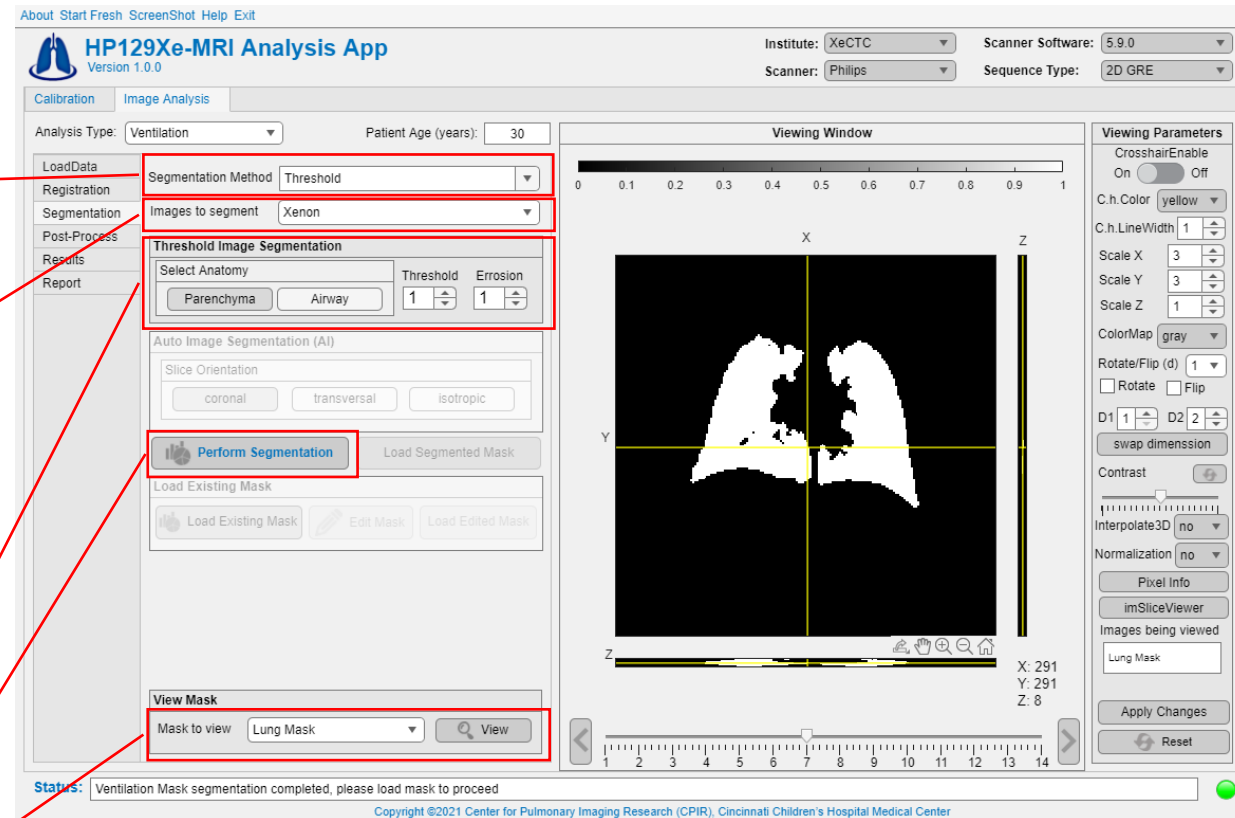
1-Select "Threshold Segmentation" from the dropdown menu.

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.

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





Threshold Segmentation:

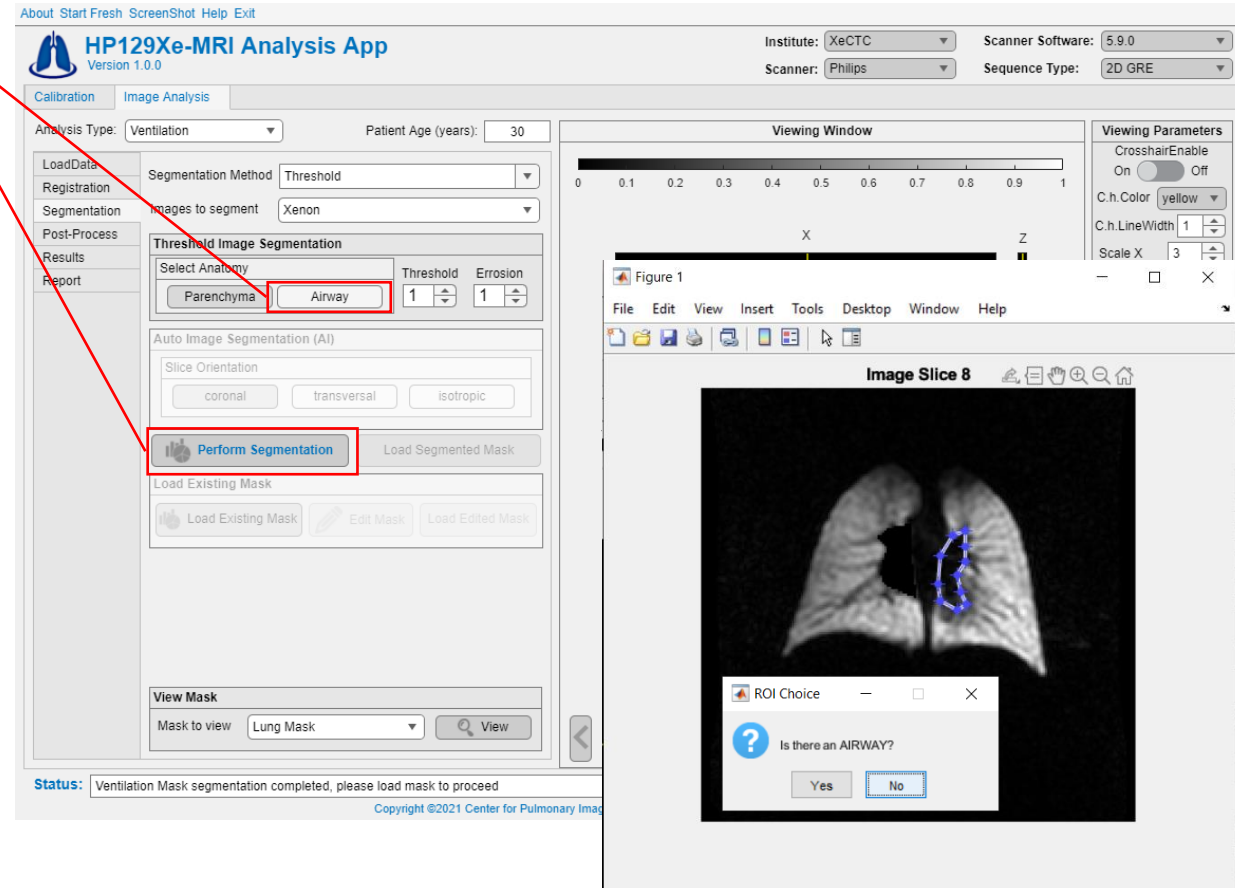
1-Select "Airway"

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.





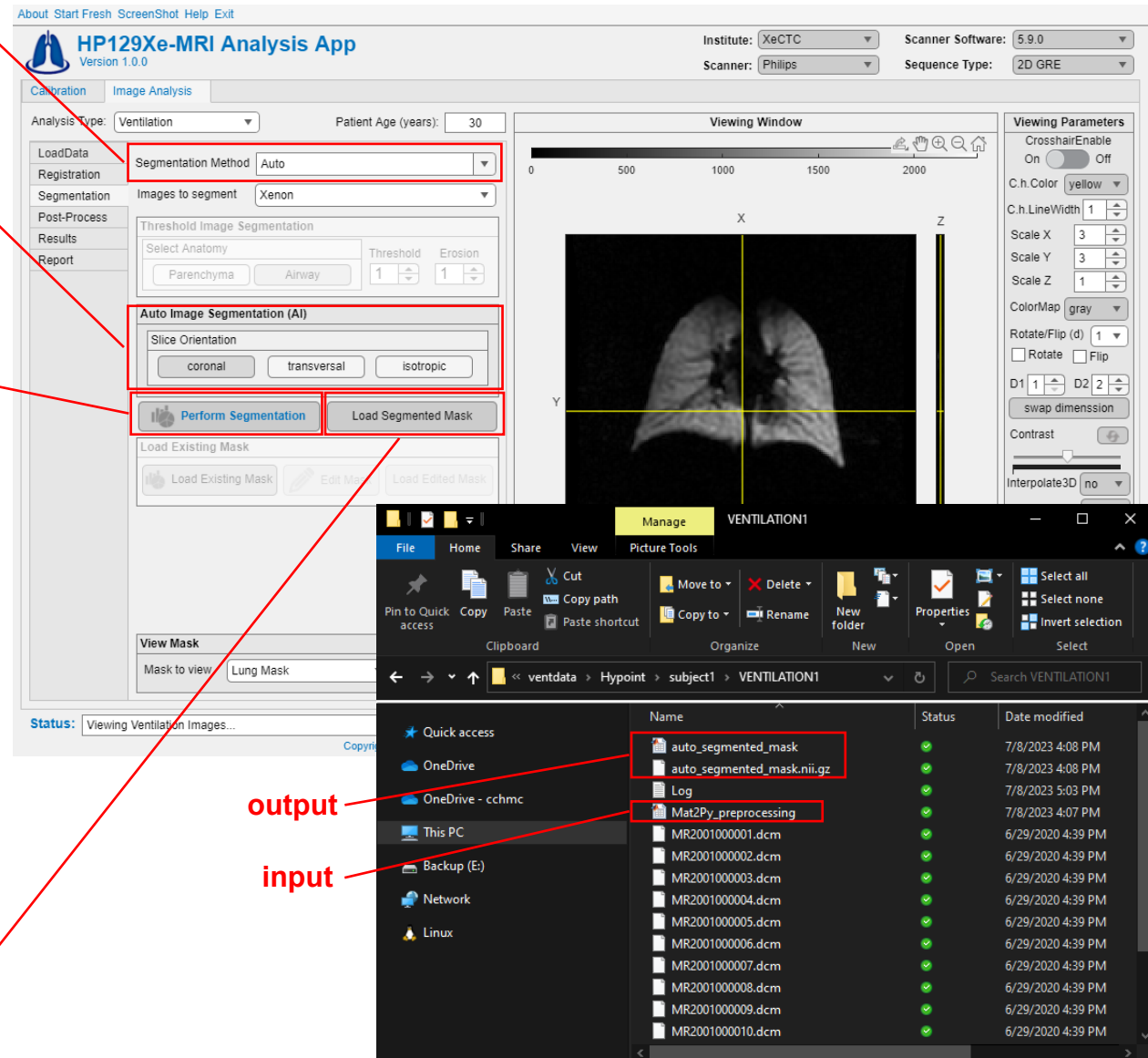
Auto Segmentation:

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

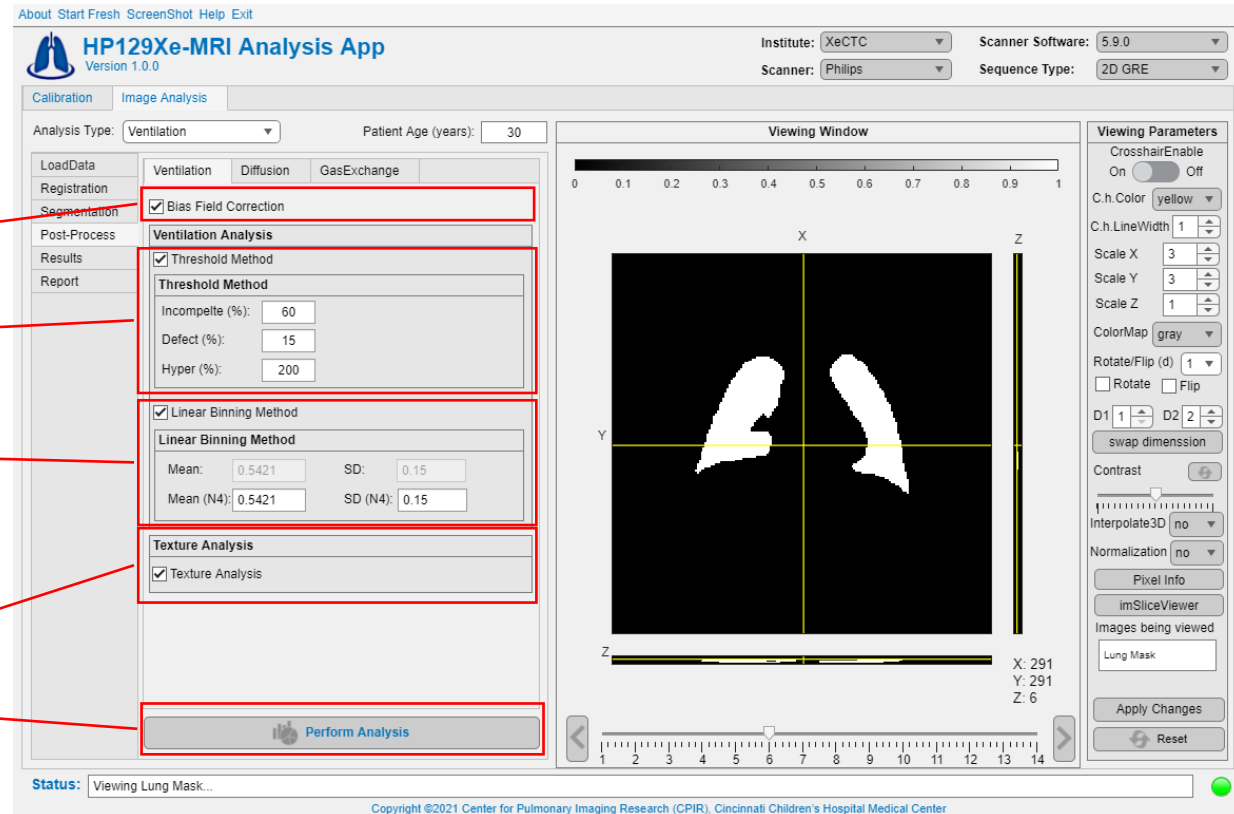
1- Choose "Bias Field Correction" if required.

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.

The screenshot shows the HP129Xe-MRI Analysis App interface. The 'Image Analysis' tab is active. The 'Analysis Type' is set to 'Diffusion'. The 'Patient Age (years)' is 30. The 'b-values' field is highlighted with a red box and labeled '1'. The 'ADC Analysis' section is highlighted with a red box and labeled '2'. The 'ADC Linear Binning Method' section is highlighted with a red box and labeled '3'. The 'Morphometry Analysis' section is highlighted with a red box and labeled '4'. The 'Perform Analysis' button is highlighted with a red box and labeled '5'. The 'Viewing Window' shows a cross-sectional image of the lungs. The 'Viewing Parameters' panel on the right includes settings for Crosshair/Enable, C.h. Color, C.h. LineWidth, Scale X, Scale Y, Scale Z, ColorMap, Rotate/Flip (d), Rotate, Flip, D1, D2, swap dimension, Contrast, Interpolate3D, and Normalization.



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.

Reference Distributions			
Vent Mean:	0.51	Vent SD:	0.19
Dissolved Mean:	0.0075	Dissolved SD:	0.00125
Barrier Mean:	0.0049	Barrier SD:	0.0015
RBC Mean:	0.0026	RBC SD:	0.001
RBCBarr Mean:	0.53	RBCBarr SD:	0.18
RBCOsc Mean:	8.96	RBCOsc SD:	10.56

Perform Analysis

Status: screenshot was saved in D:\OneDrive - cchmc\Lab\Xe_App\testingData\ventdata\Hypointsubject1\VENTILATION1

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Ventilation

[About](#) [Start Fresh](#) [ScreenShot](#) [Help](#) [Exit](#)



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

Viewing Window

0 0.1 0.2 0.3 0.4 0.5 0.6 0.7

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

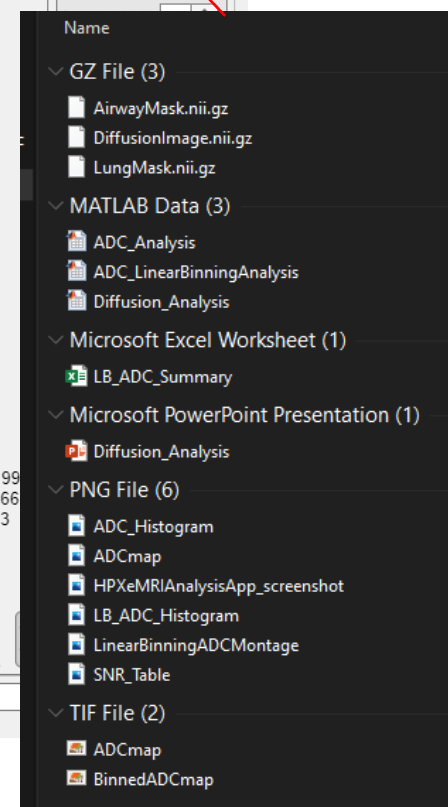
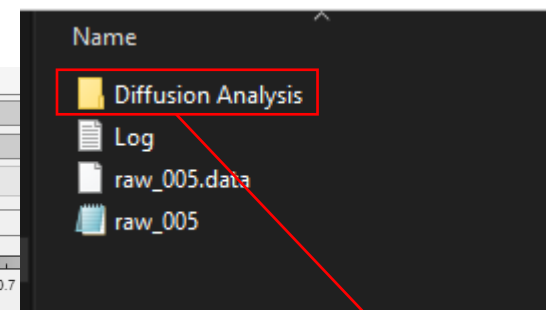
Mean Histogram Map

X: 99 Y: 66 Z: 3

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

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Gas Exchange

About Start Fresh ScreenShot Help Exit

HP129Xe-MRI Analysis App
Version 1.0.0

Institute: CCHMC Scanner Software: 5.9.0
Scanner: Philips Sequence Type: 3D Radial

Analysis Type: GasExchange Patient Age (years): 30

LoadData Registration Segmentation Post-Process Results Report

Ventilation Diffusion GasExchange

Ventilation Summary
Mean: 0.792±0.116 Histogram Map
Low Bin1 Bin2 Bin3 Bin4 Bin5 Bin6 High
0 0.09 2.3 16.77 62 18.84

Dissolved Summary
Mean: 0.01024±0.00098 Histogram Map
Low Bin1 Bin2 Bin3 Bin4 Bin5 Bin6 High
0 0 0.16 8.86 27.7 63.28

Barrier Summary
Mean: 0.00924±0.00093 Histogram Map
Low Bin1 Bin2 Bin3 Bin4 Bin5 Bin6 Bin7 Bin8 High
0 0 0 0.1 10.76 36.71 51.88 0.54

RBC Summary
Mean: 0.00417±0.00069 Histogram Map
Low Bin1 Bin2 Bin3 Bin4 Bin5 Bin6 High
0 0 0.02 22.85 51.61 25.52

RBC:Barrier Summary
Mean: 0.45432±0.07896 Histogram Map
Low Bin1 Bin2 Bin3 Bin4 Bin5 Bin6 High
0 5.21 78.81 15.41 0.57 0

RBC Oscillation Summary
Mean: 7.1558±11.325 Histogram Map
Low Bin1 Bin2 Bin3 Bin4 Bin5 Bin6 Bin7 Bin8 High
2.24 25.84 28.93 26.23 15.44 1.33 0 0

Status: GasExchange analysis completed

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Viewing Window
0 0.5 1 1.5 2 2.5 3 3.5 4 4.5 x10¹⁰

Viewing Parameters
CrosshairEnable On Off
C.h. Color yellow
C.h. LineWidth 1
Scale X 3
Scale Y 3
Scale Z 1
ColorMap gray
Rotate/Flip (d) 1
Rotate Flip
D1 1 D2 2
swap dimension
Contrast
Interpolate3D no
Normalization no
Pixel Info

Name
Gax Exchange Analysis
20230627_155953_CPIR_Gas_Exchange.lab
20230627_155953_CPIR_Gas_Exchange
20230627_155953_CPIR_Gas_Exchange
Log
ProtonRegistered
raw_405.data
raw_405

GZ File (8)
BarrierImage.nii.gz
ProtonImage.nii.gz
RBCImage.nii.gz
DissolvedImage.nii.gz
ProtonMask.nii.gz
VentImage.nii.gz
GasImage.nii.gz
ProtonMaskRegistered.nii.gz

MATLAB Data (1)
GasExchangeAnalysis

MATLAB Figure (9)
CorrDissolvedMontage
DissolvedNMR
Registrationfig
CorrVentMontage
GasMontage
SigDynamics
DissolvedMontage
ProtonMaskMontage
VentMontage

Microsoft PowerPoint Presentation (1)
GasExchange_Analysis

PNG File (8)
Barrier_Histogram
OscWorkFlow_Fig
RBC_Oscillation_Histogram
Dissolved_Histogram
RBC_Barrier_Histogram
Ventilation_Histogram
HPXeMRIAnalysisApp_screenshot
RBC_Histogram

TIF File (6)
BinnedBarrierUptake
BinnedRBCOscillation
BinnedDissolved
BinnedRBCTransfer
BinnedRBCBarrier
BinnedVent

Patient Report

- 1-Complete the patient report information.
- 2-Generate the report.

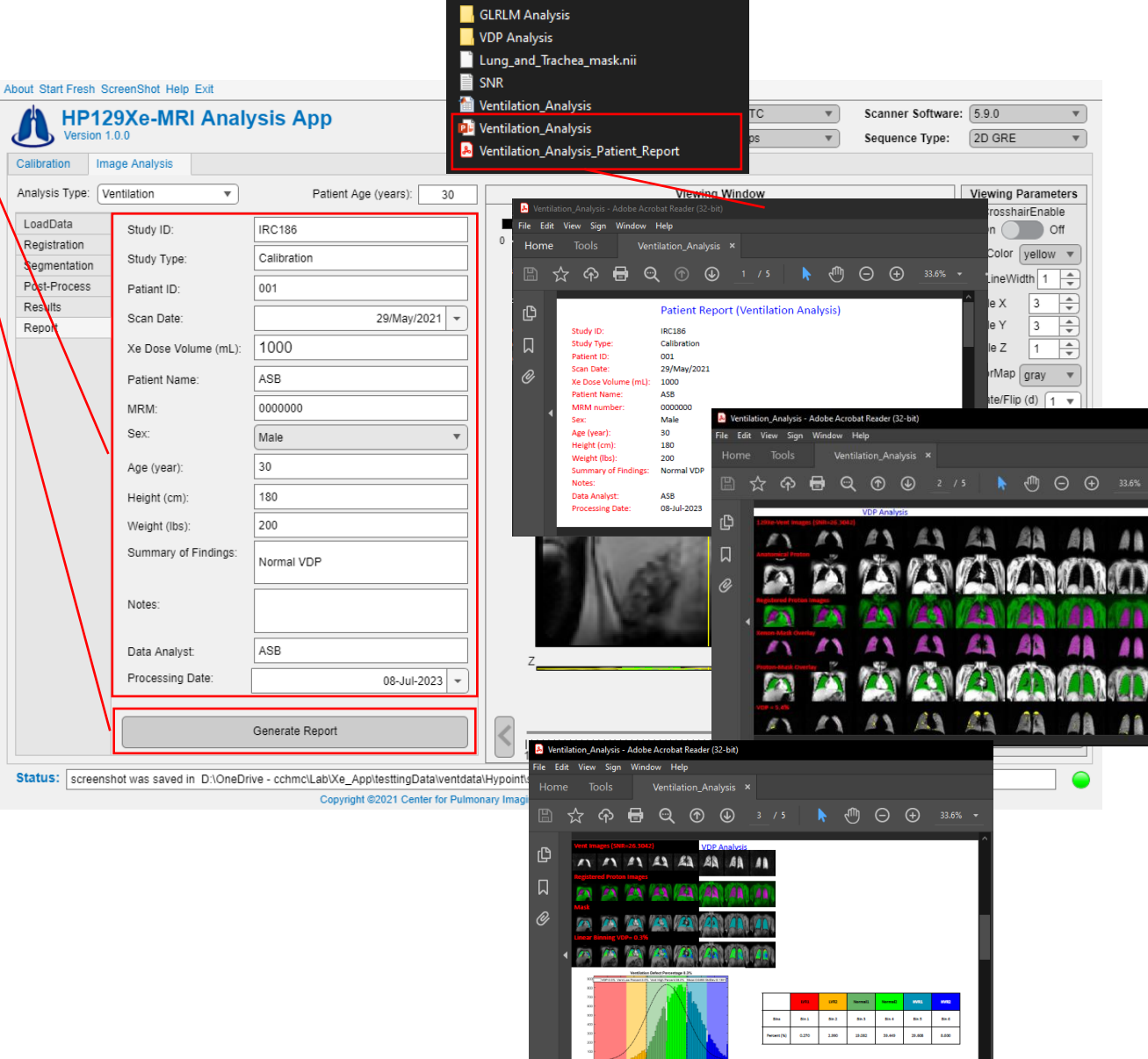
This will generate .ppt and .pdf files containing all patient information and a summary of the findings.

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

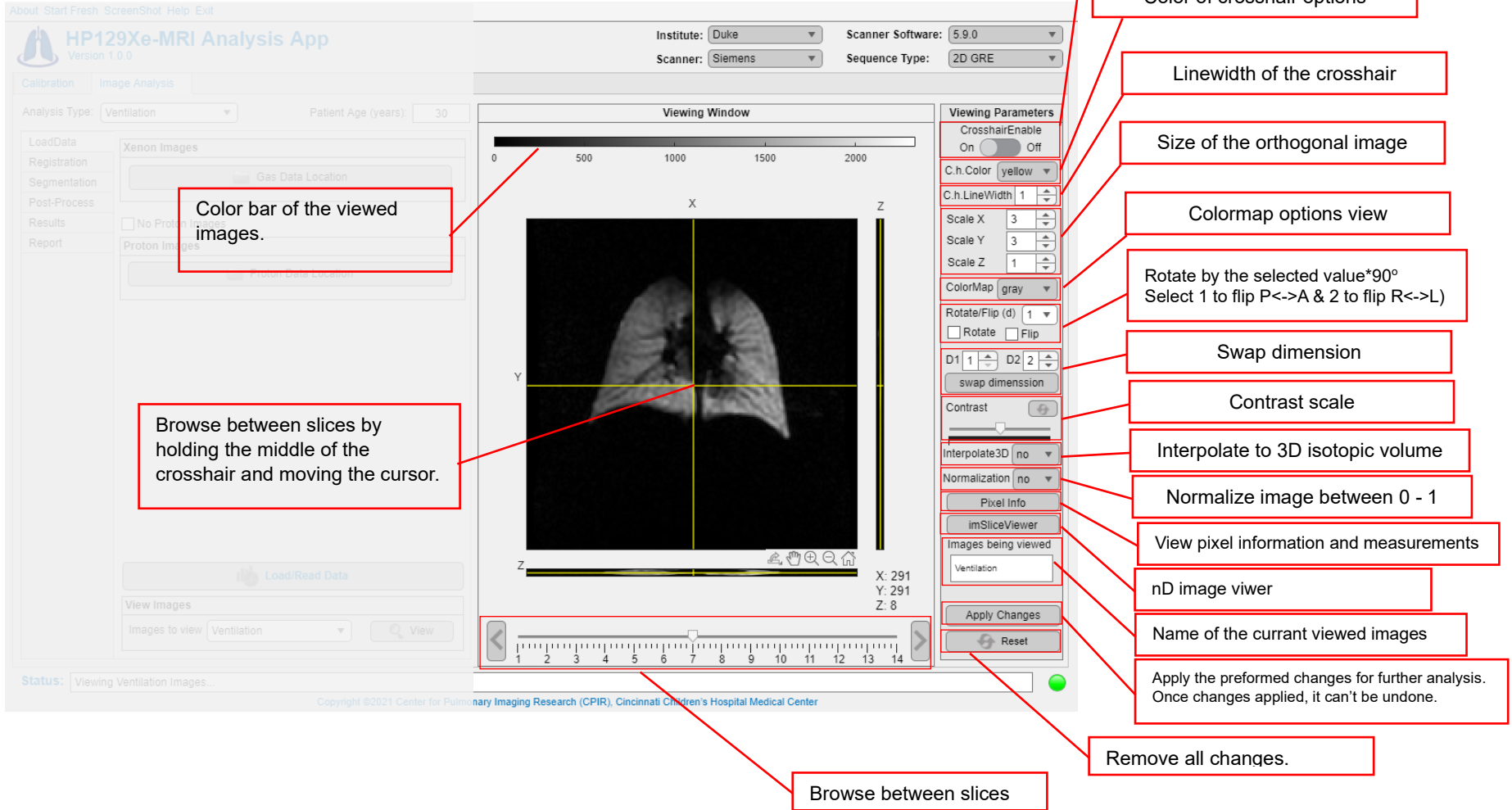
1-Complete the patient report information.

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



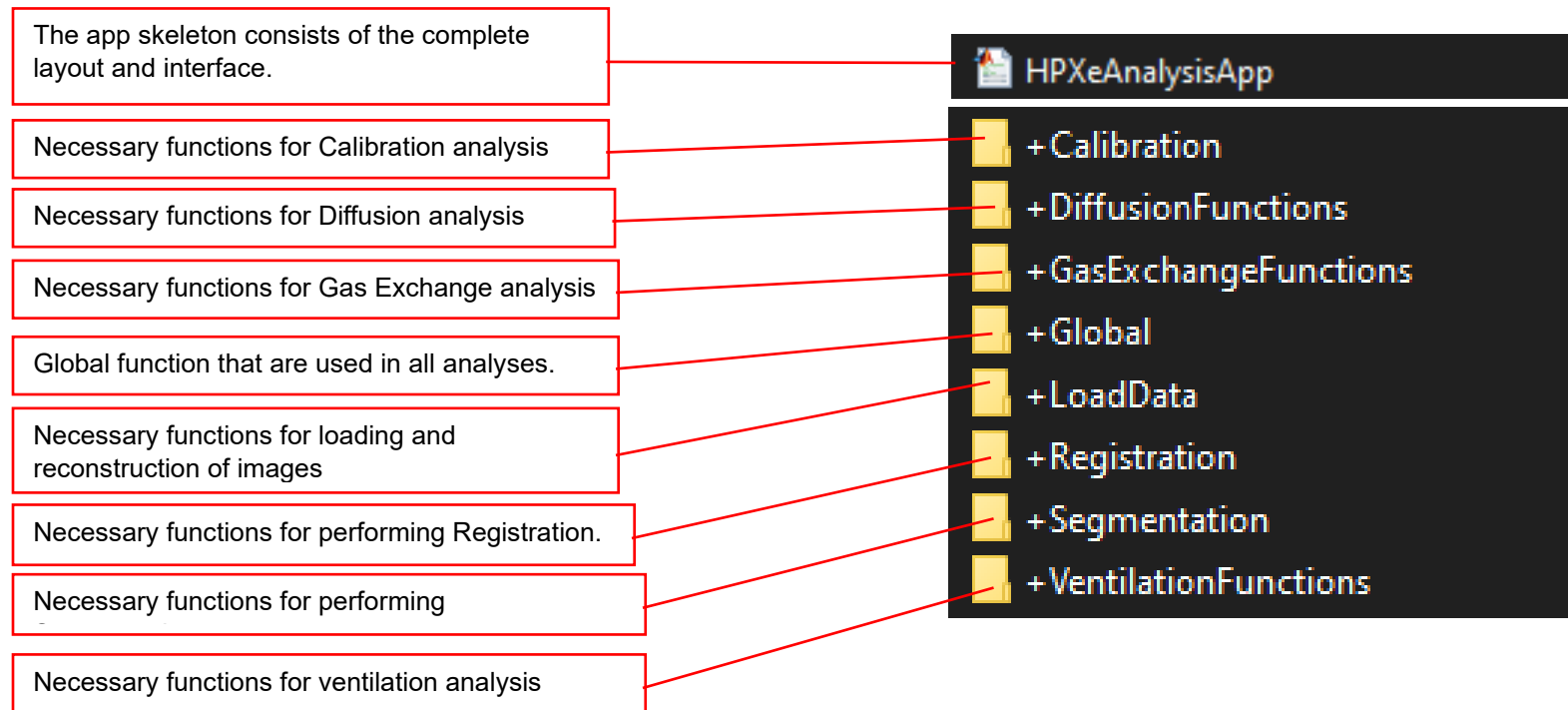
The screenshot displays the HP ¹²⁹Xe MRI Analysis App interface. The main viewing window shows a grayscale lung scan with a yellow crosshair. The interface includes a top menu bar, a left sidebar with navigation options, and a right sidebar with viewing parameters. Red callout boxes provide detailed instructions for various controls:

- Enable and disable crosshair:** Points to the 'CrosshairEnable' toggle switch in the 'Viewing Parameters' panel.
- Color of crosshair options:** Points to the 'C.h. Color' dropdown menu.
- Linewidth of the crosshair:** Points to the 'C.h. LineWidth' slider.
- Size of the orthogonal image:** Points to the 'Scale X', 'Scale Y', and 'Scale Z' sliders.
- Colormap options view:** Points to the 'ColorMap' dropdown menu.
- Rotate by the selected value*90° Select 1 to flip P<->A & 2 to flip R<->L):** Points to the 'Rotate/Flip (d)' dropdown menu.
- Swap dimension:** Points to the 'D1' and 'D2' dropdown menus and the 'swap dimension' button.
- Contrast scale:** Points to the 'Contrast' slider.
- Interpolate to 3D isotopic volume:** Points to the 'Interpolate3D' dropdown menu.
- Normalize image between 0 - 1:** Points to the 'Normalization' dropdown menu.
- View pixel information and measurements:** Points to the 'Pixel Info' button.
- nD image viewer:** Points to the 'imSliceViewer' button.
- Name of the current viewed images:** Points to the 'Images being viewed' text field.
- Apply the preformed changes for further analysis. Once changes applied, it can't be undone.** Points to the 'Apply Changes' button.
- Remove all changes.** Points to the 'Reset' button.
- Browse between slices:** Points to the 'Browse between slices' button at the bottom of the viewing window.
- Color bar of the viewed images:** Points to the color bar on the right side of the viewing window.
- Browse between slices by holding the middle of the crosshair and moving the cursor.** Points to the crosshair in the viewing window.



4 | Code Structure

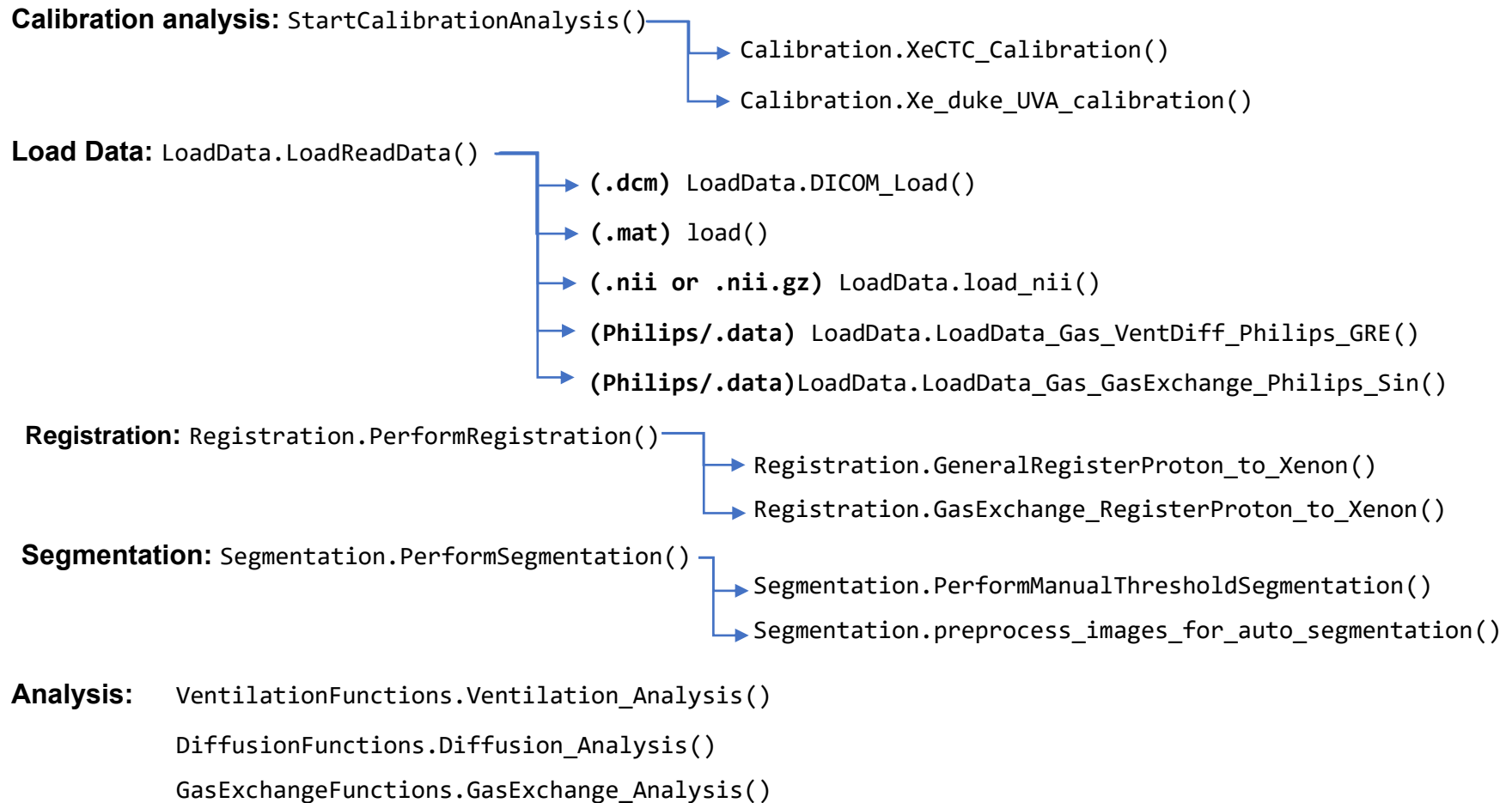
4.1 | Folders





4.2 | Code Hierarchy

Here are the main and submain functions:





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
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.