



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 | Installation

- 1- Visit https://github.com/aboodbdaiwi/HP129Xe_Analysis_App.
- 2- Clone or download the folder to your local directory.
- 3- Download the MATLAB runtime compatible with the application's MATLAB version (R2022b) from here: <https://www.mathworks.com/products/compiler/matlab-runtime.html>
- 4- You can launch the compiled application (**HPXeAnalysisApp.exe**) independently, without requiring MATLAB.
- 5- For customization, include the local folder in the MATLAB path and execute the **HPXeAnalysis.mlapp** file using MATLAB version R2022b or newer.



2 | Overview

Main Menu:

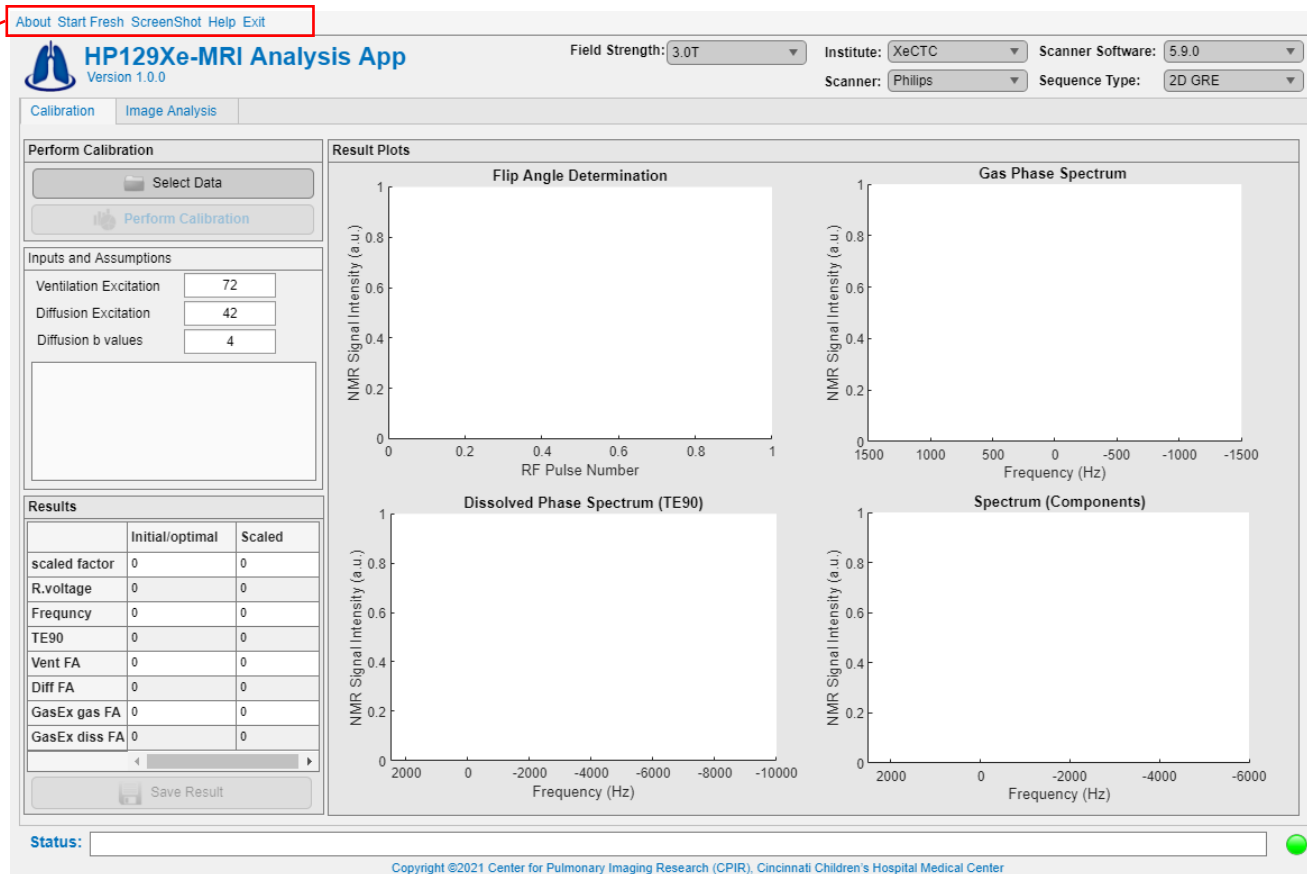
About: Provides an insightful overview of the application and its functionalities.

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

Field Strength: 3.0T Institute: XeCTC Scanner Software: 5.9.0
Scanner: Philips Sequence Type: 2D GRE

Calibration Image Analysis

Perform Calibration

Select Data

Perform Calibration

Inputs and Assumptions

Ventilation Excitation 72

Diffusion Excitation 42

Diffusion b values 4

Results

	Initial/optimal	Scaled
scaled factor	0	0
R.voltage	0	0
Frequency	0	0
TE90	0	0
Vent FA	0	0
Diff FA	0	0
GasEx gas FA	0	0
GasEx diss FA	0	0

Save Result

Result Plots

Flip Angle Determination

Gas Phase Spectrum

Dissolved Phase Spectrum (TE90)

Spectrum (Components)

Status:

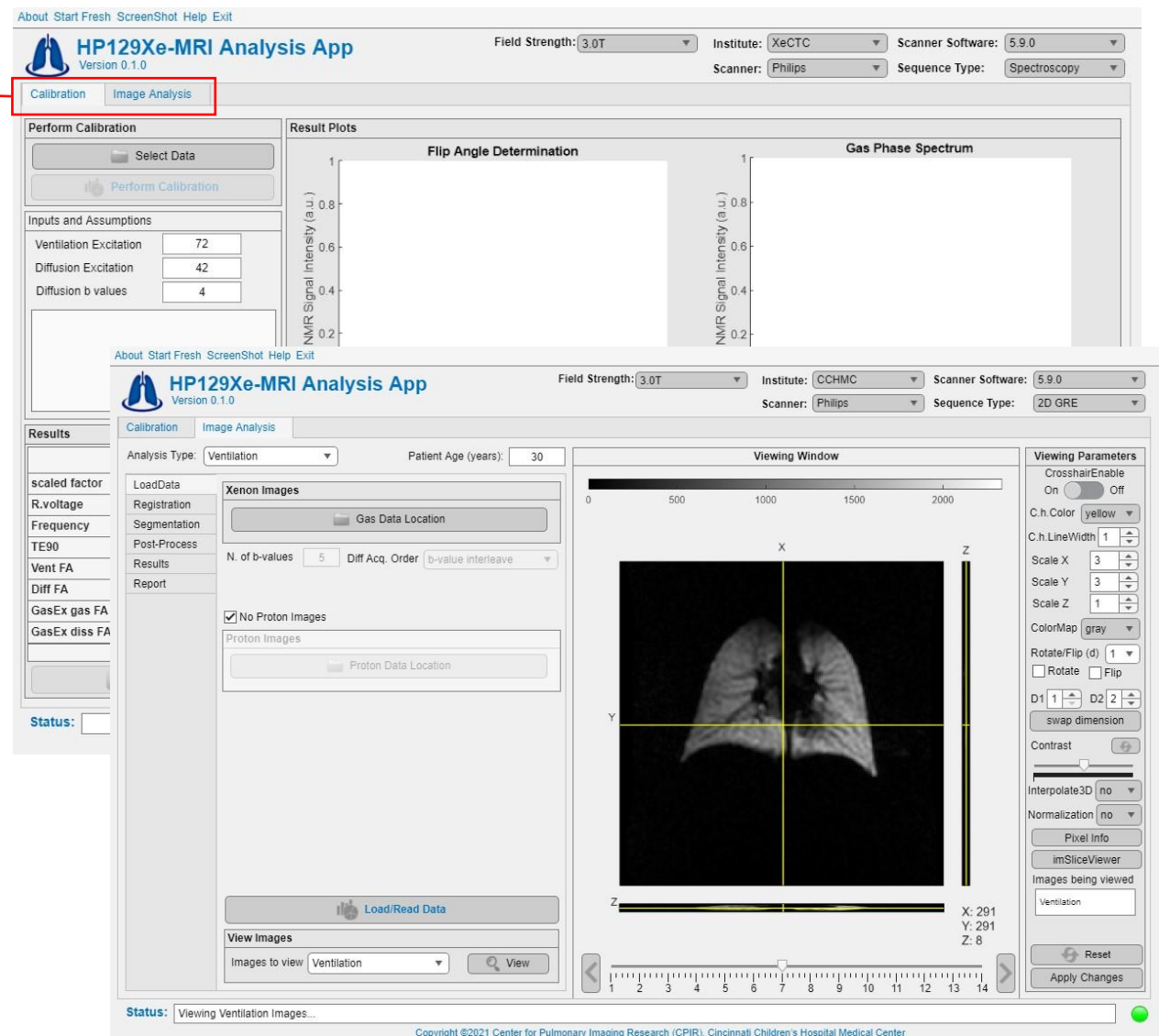
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Main Tabs:

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.

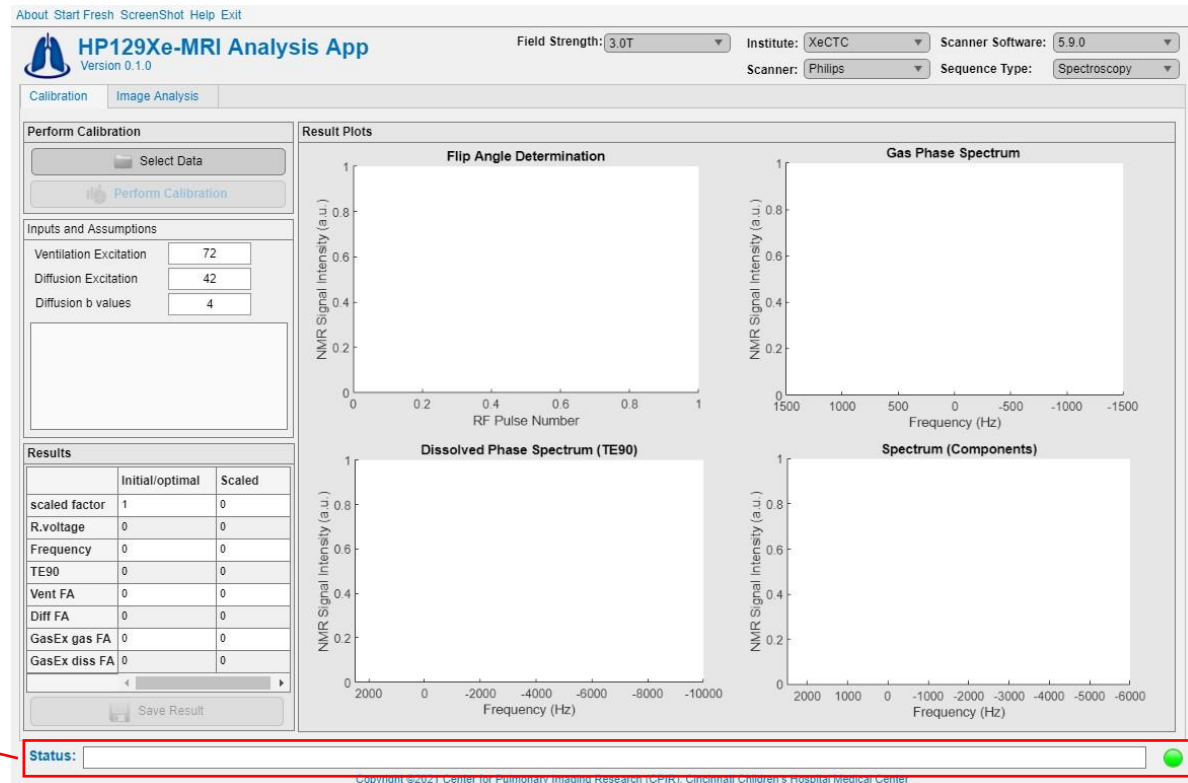
Note: These two tabs operate independently from each other, maintaining separate sets of parameters. There is no parameter sharing between them, ensuring complete autonomy and flexibility.





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.

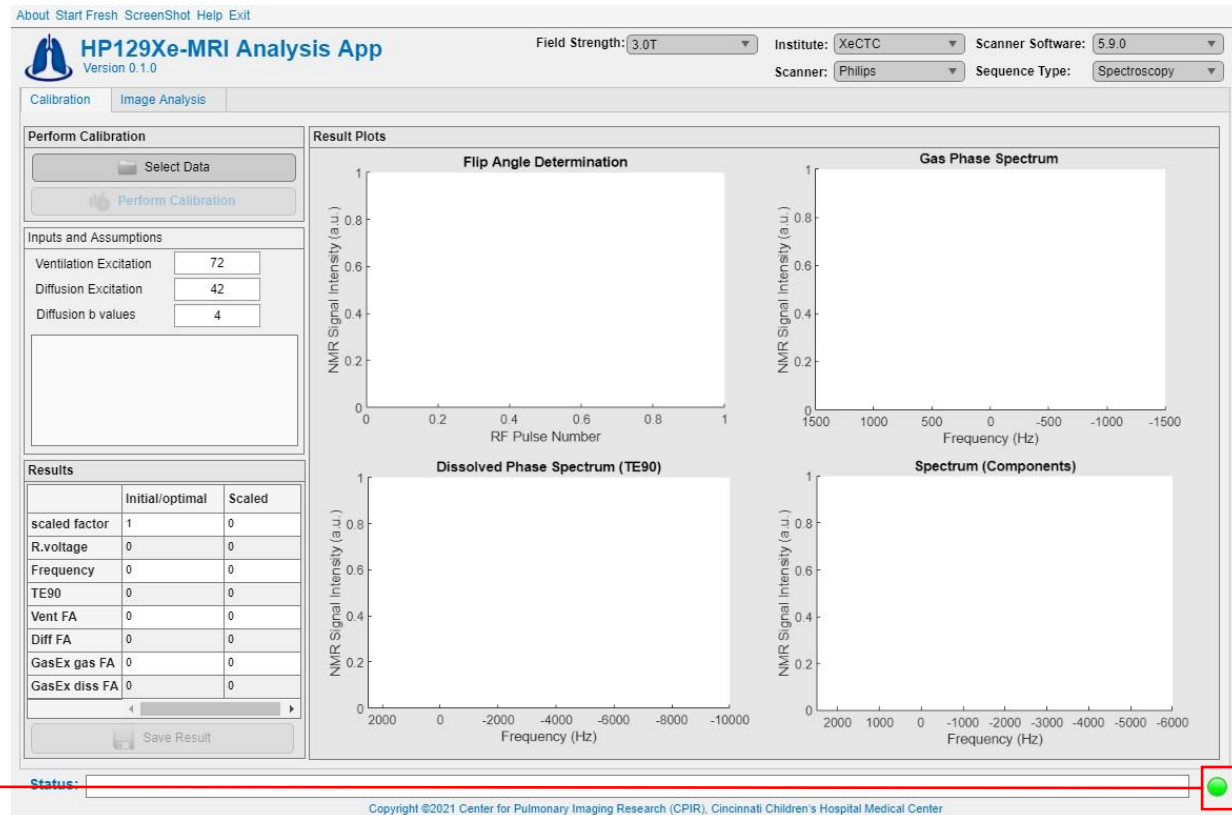




Lamp:

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.





3 | Flip Angle and Frequency Calibration

3.1 | 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 the results. The determined optimal flip angles and frequency parameters are subsequently entered prior to image acquisition.

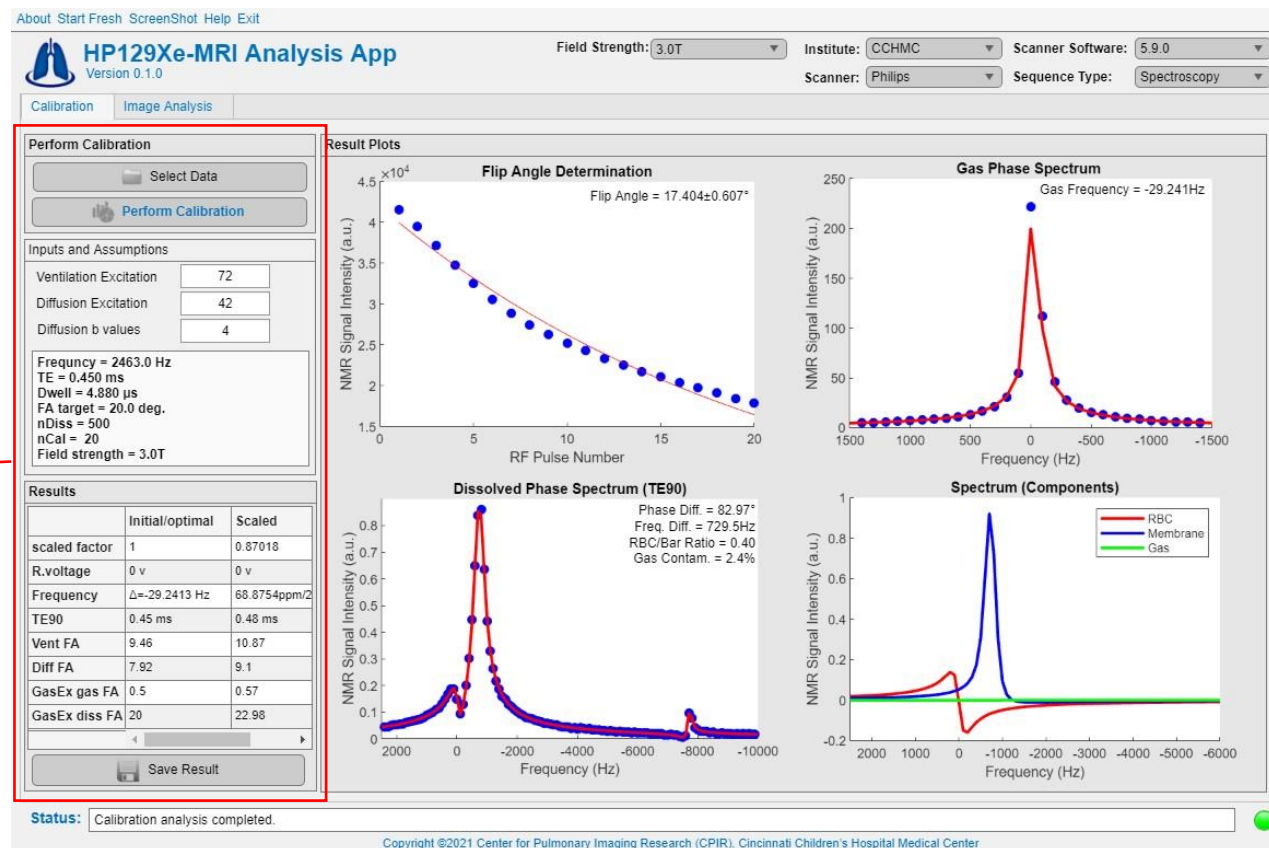


Table 2.1: Supported data type for Calibration analysis

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

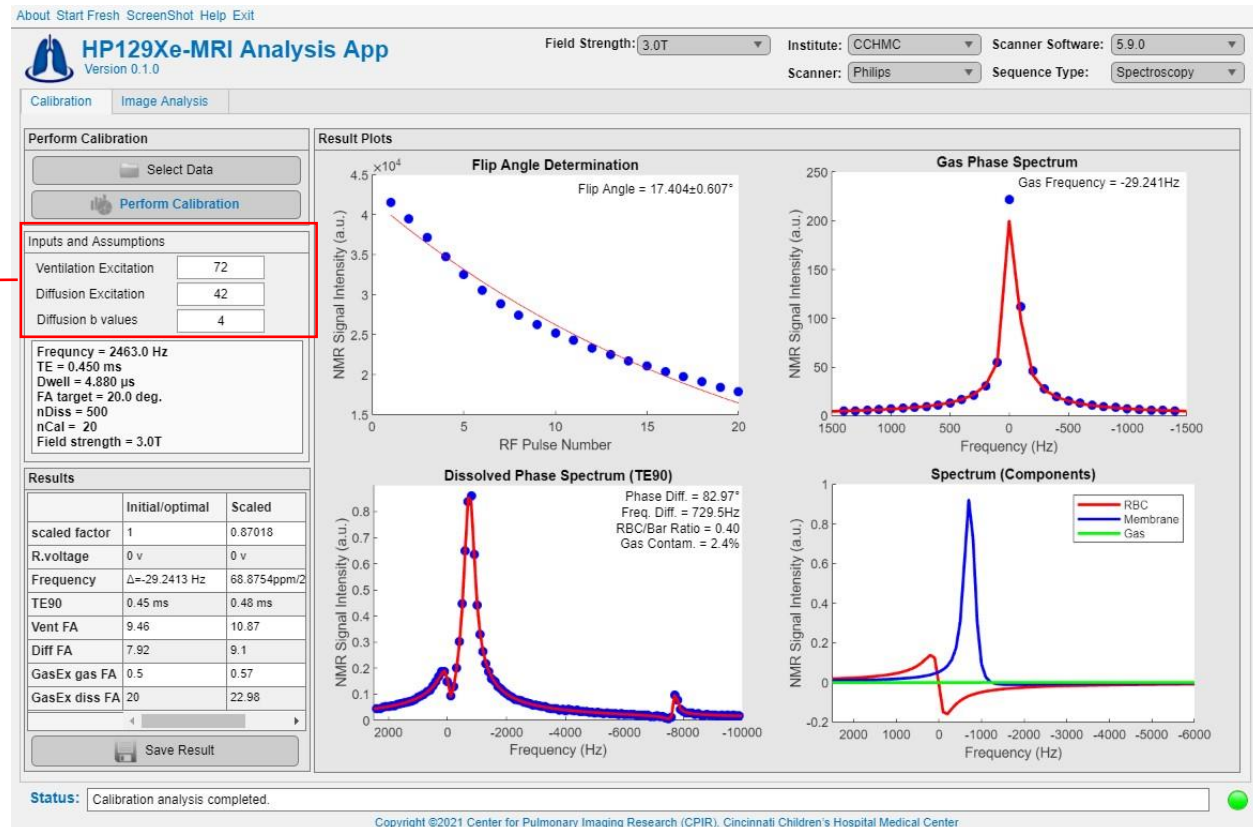
* The data that needs to be selected!



3.2 | 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.

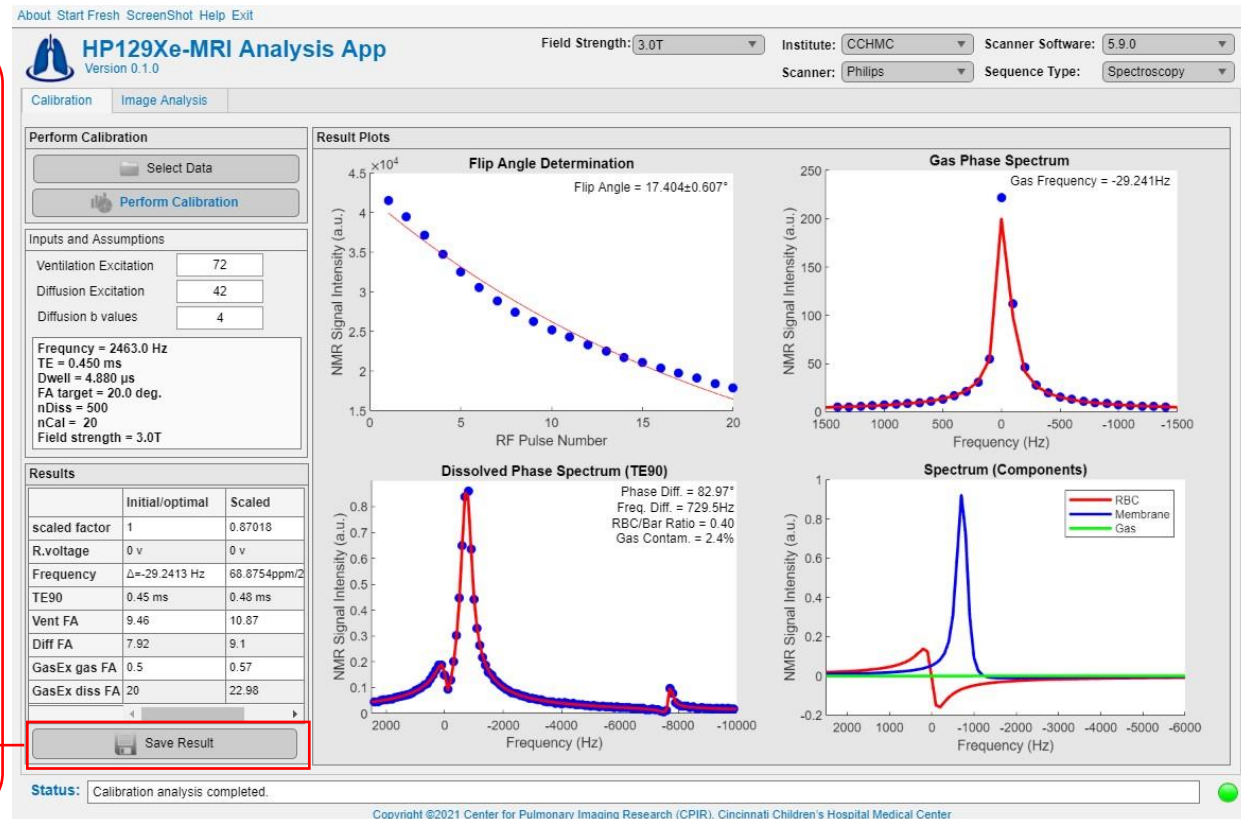




3.3 | Save Results

Save Results:

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



4 | Image Analysis

4.1 | Inputs

Load Data:

- 1- Select scan and sequence type.
- 2- Choose Analysis Type: Select the desired type of analysis from the available options.
- 3- Gas Data Selection: Choose the data file/s for analysis. If raw data is selected, reconstruction functions will be invoked to process the data.
- 4- Proton Data Selection: If proton data is available, select the corresponding data. Otherwise, check the "No Proton Images" box.
- 5- Load Data: Load the selected data for further processing and analysis.
- 6- Image Selection: Select the specific type of images to view.

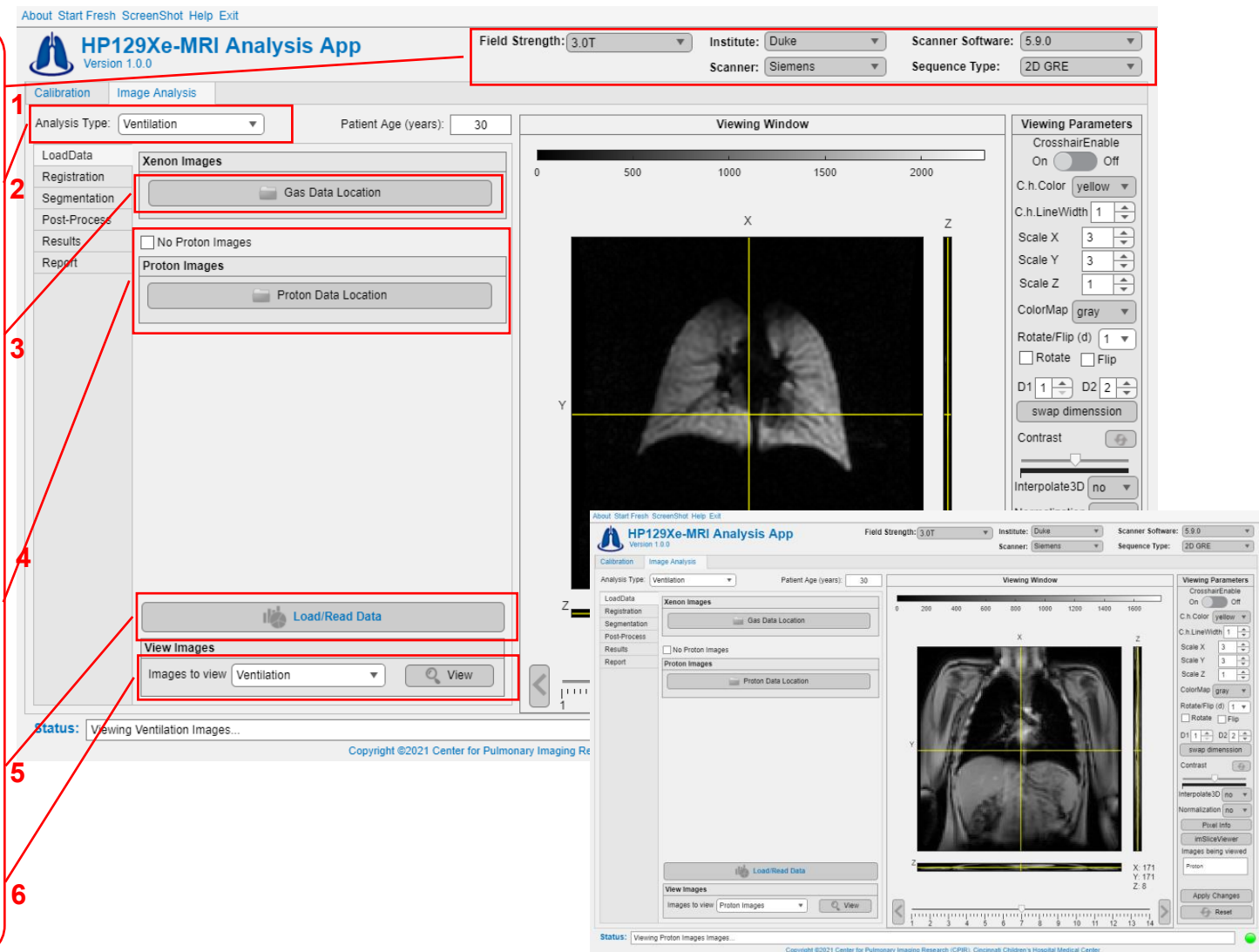




Table 3.1: Supported data type for image analysis

Data Type	DICOM (.dcm)		MATLAB (.mat)		Nifti (.nii or .nii.gz)		Raw data																	
	single	multiple	single	multiple	single	multiple	Philips						Siemens						GE					
							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	no	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, NC: Non-Cartesian

Table 3.2 Supported data formats.

Imaging Type	Supported Data Type				
	General Image Formats	Raw Data			
		Philips	Siemens	GE	ISMRMD
Calibration	-	.data/.list	.dat	-	-
Ventilation	.dcm (single or multiple files). .mat (single): one 3D variable size (x,y,slices). .nii or .gz (single): one 3D variable size (x,y,slices).	.data/.list	-	-	.mrd or .h5 (2D GRE only)
Diffusion	.dcm (single or multiple files): have to specify the number of b-values and acquisition order. .mat (single): one 4D variable (x,y,slices,b-values) .nii or .gz (single): one 4D variable size (x,y,slices,b-values)	.data/.list	-	-	.mrd or .h5 (2D GRE only)
Gas Exchange	.mat (single): Not recommended.	.data/.list/.sin	-	-	-
Anatomical	.dcm (single or multiple files). .mat (single): one 3D variable size (x,y,slices). .nii or .gz (single): one 3D variable size (x,y,slices). See below for gas exchange data.	.data/.list .data/.lab/.sin	-	-	.mrd or .h5 (2D GRE only)



For gas exchange, the following list of variables are needed if .mat file is selected for gas data:

- UncorrectedVentImage
- VentImage
- GasImage
- DissolvedImage
- CorrDissolvedImage
- AppendedDissolvedNMRFit
- RBC2Bar_struct
- RBCOsc_High_Image
- RBCOsc_Low_Image
- RBCOsc_Normalization
- ActTE90
- DisFlipAngle
- PixelShift
- DissolvedNMR
- SigDynamics

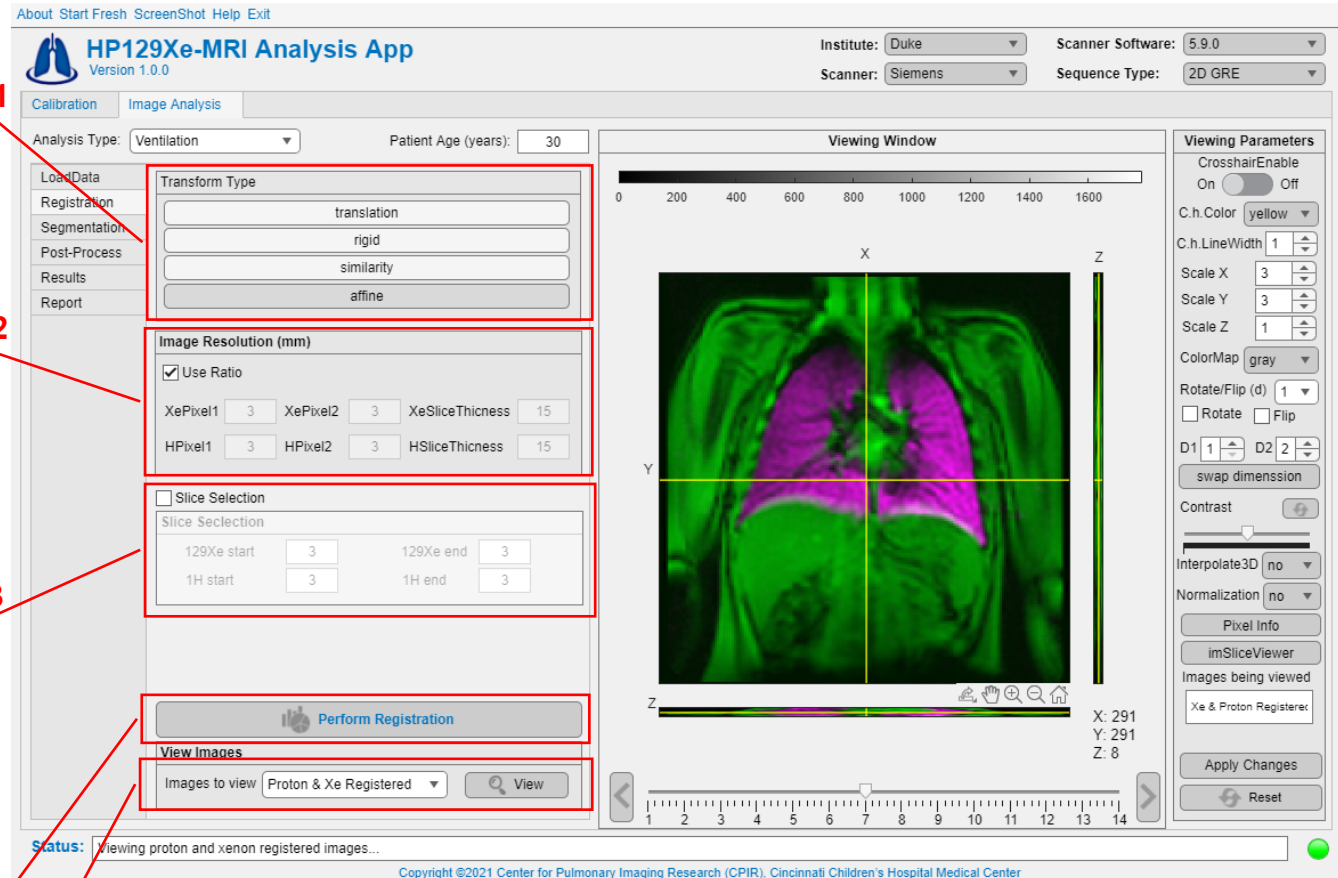
and the following list of variables are needed if .mat file is selected for proton data:

- ProtonImage
- file_name
- HDataLocation
- H_RecMatrix
- ProtonMax

4.2 | 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.

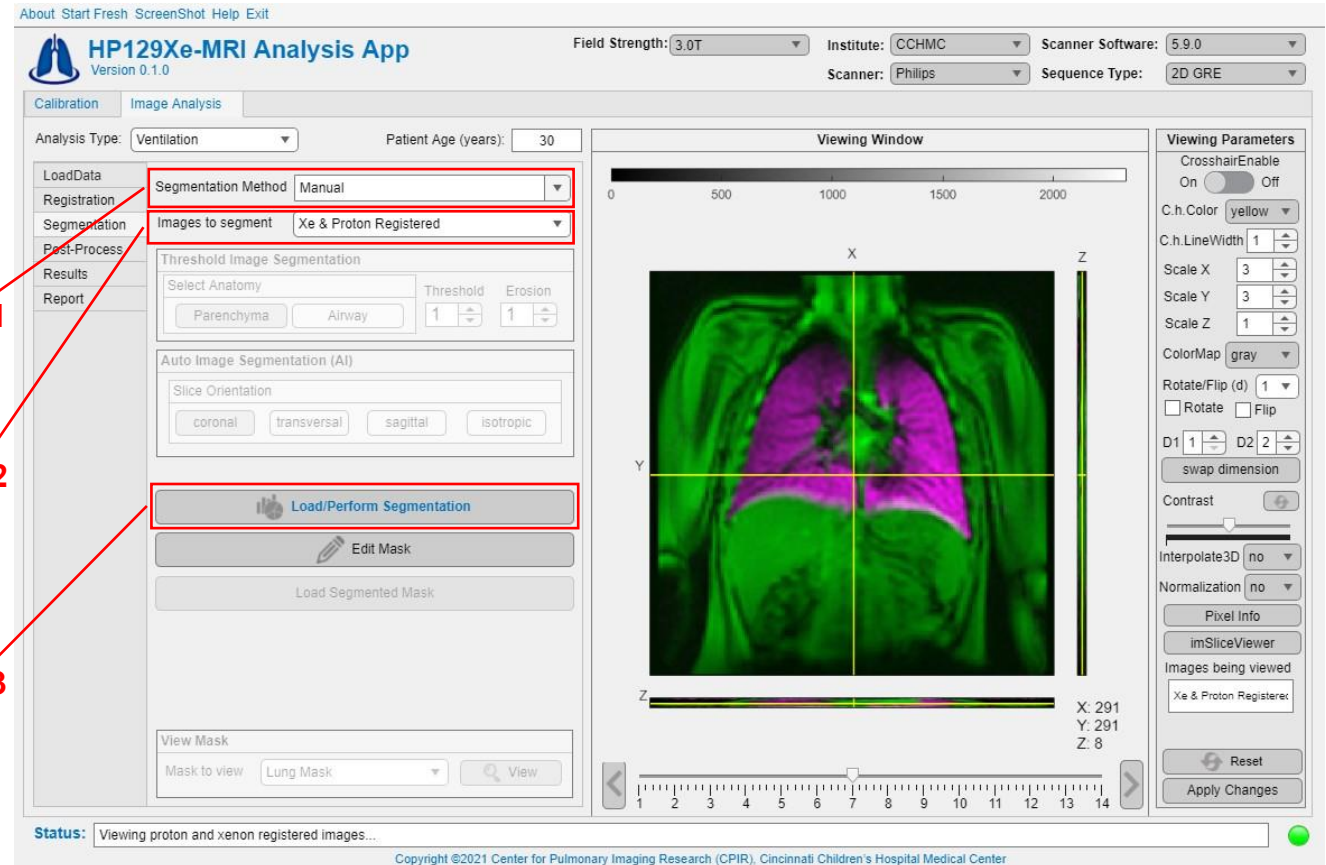




4.3 | Segmentation

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.





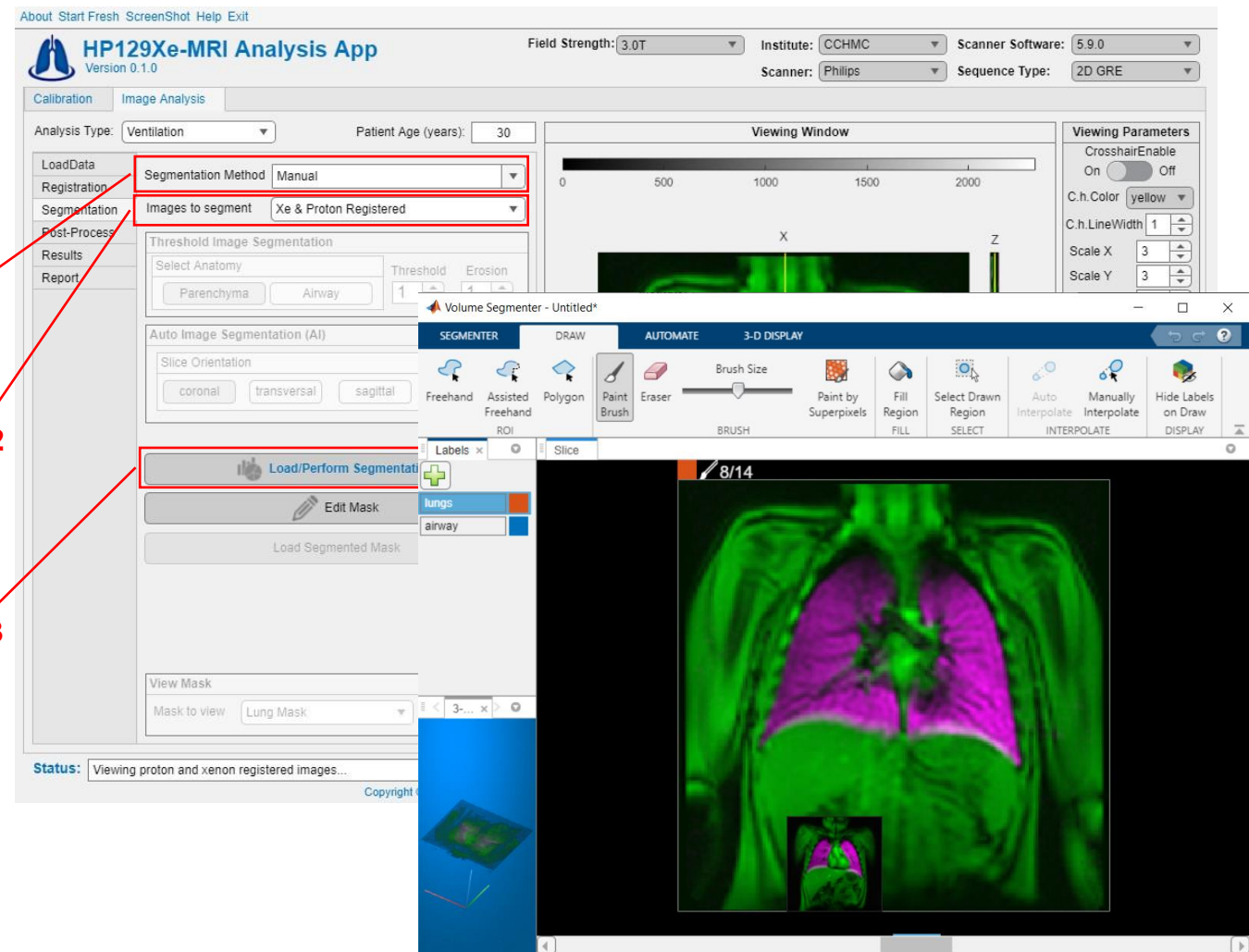
Manual Segmentation:

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 Segementer](#) which offers many advanced segmentation tools.





Manual Segmentation:

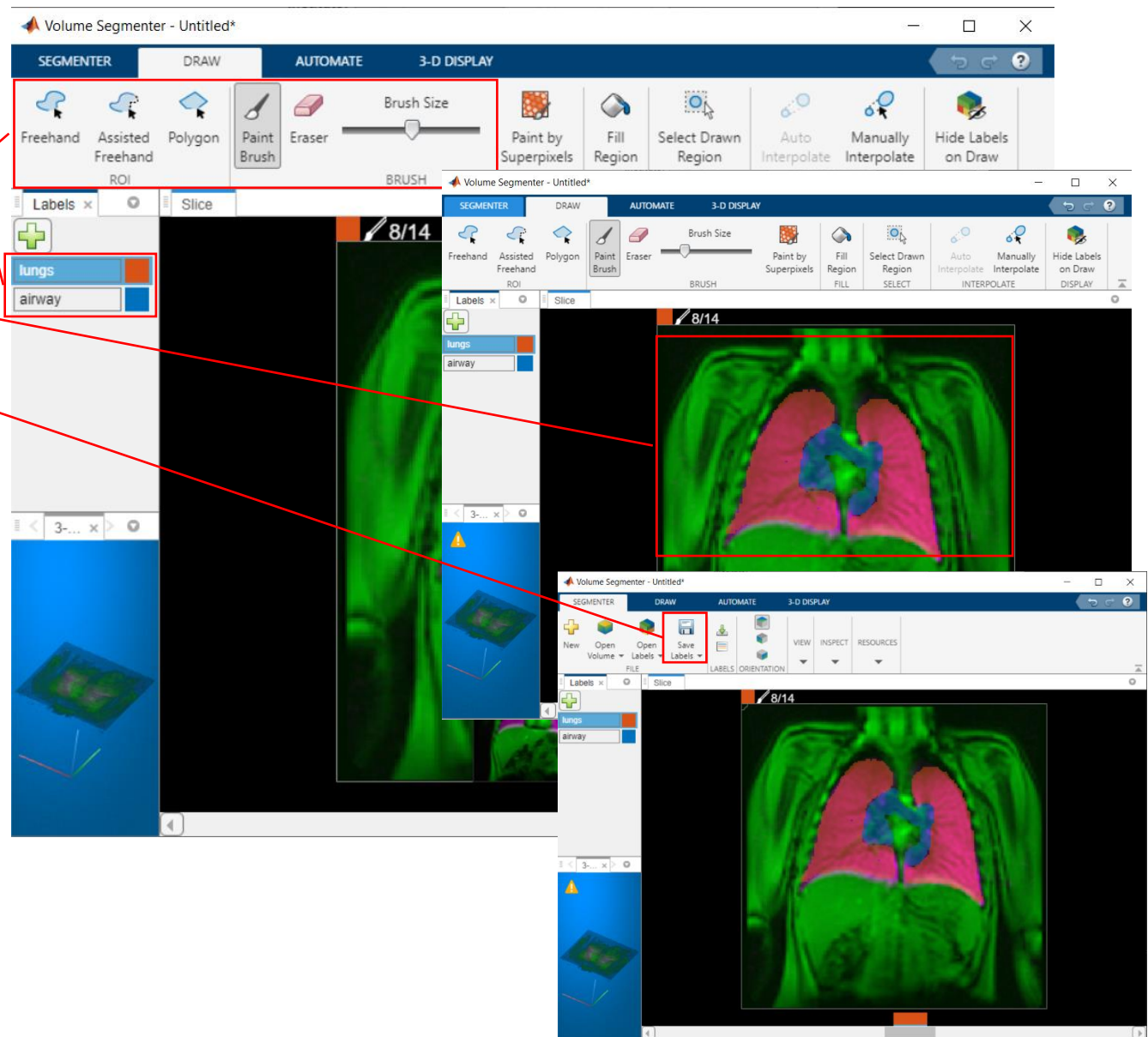
1-Create two labels for the lungs and airways.

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](#)

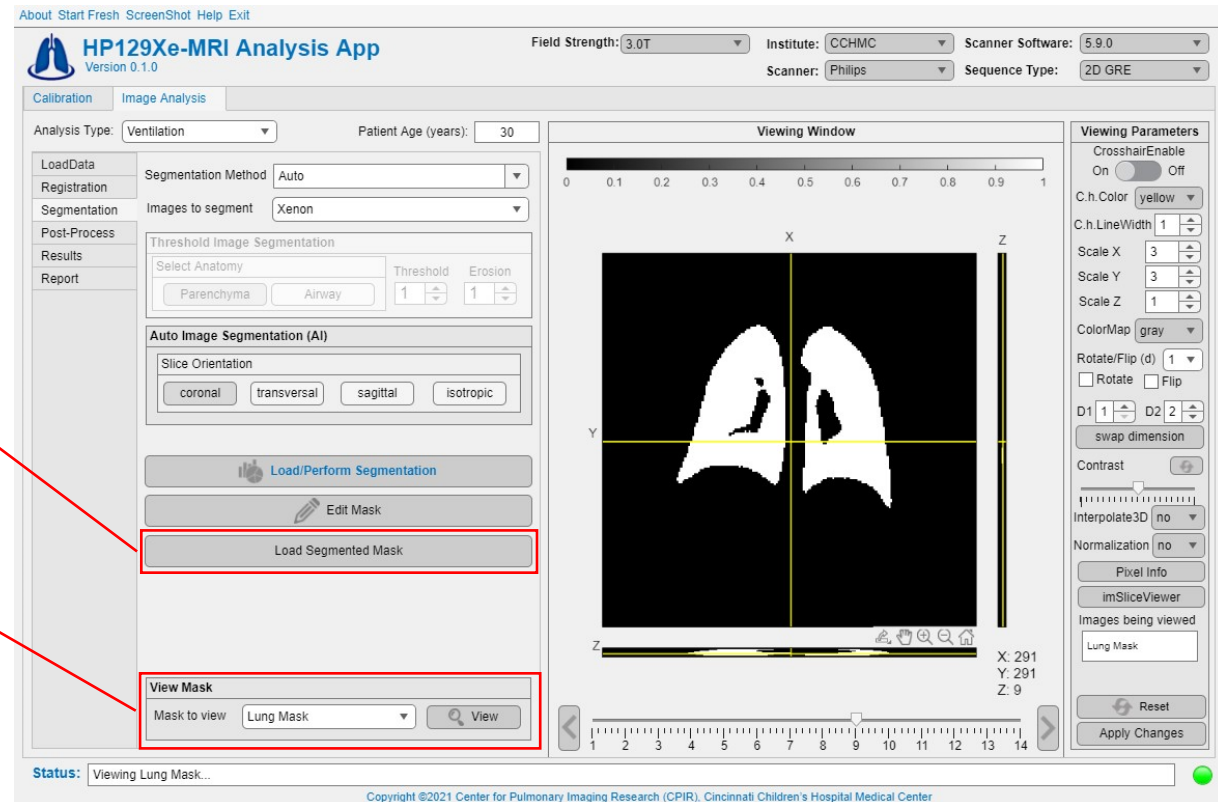




Manual Segmentation:

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:

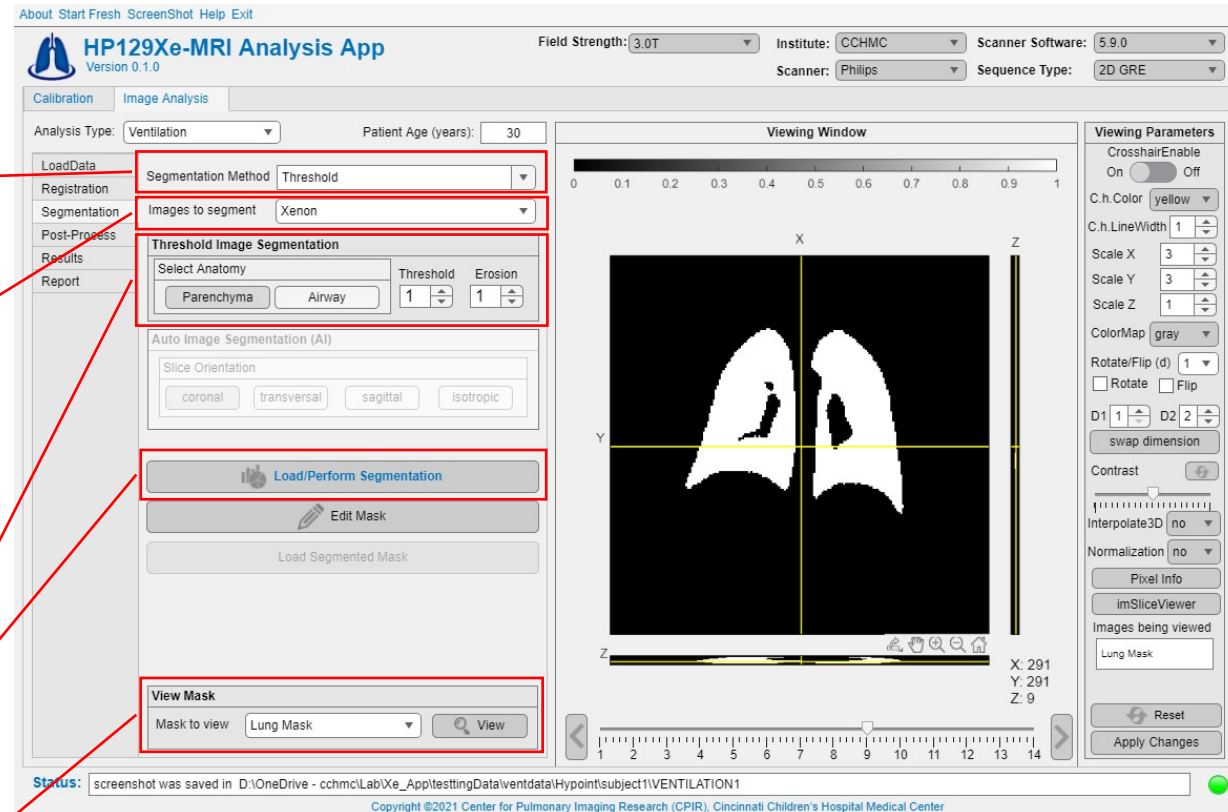
1-Select "Threshold Segmentation" from the dropdown menu.

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:

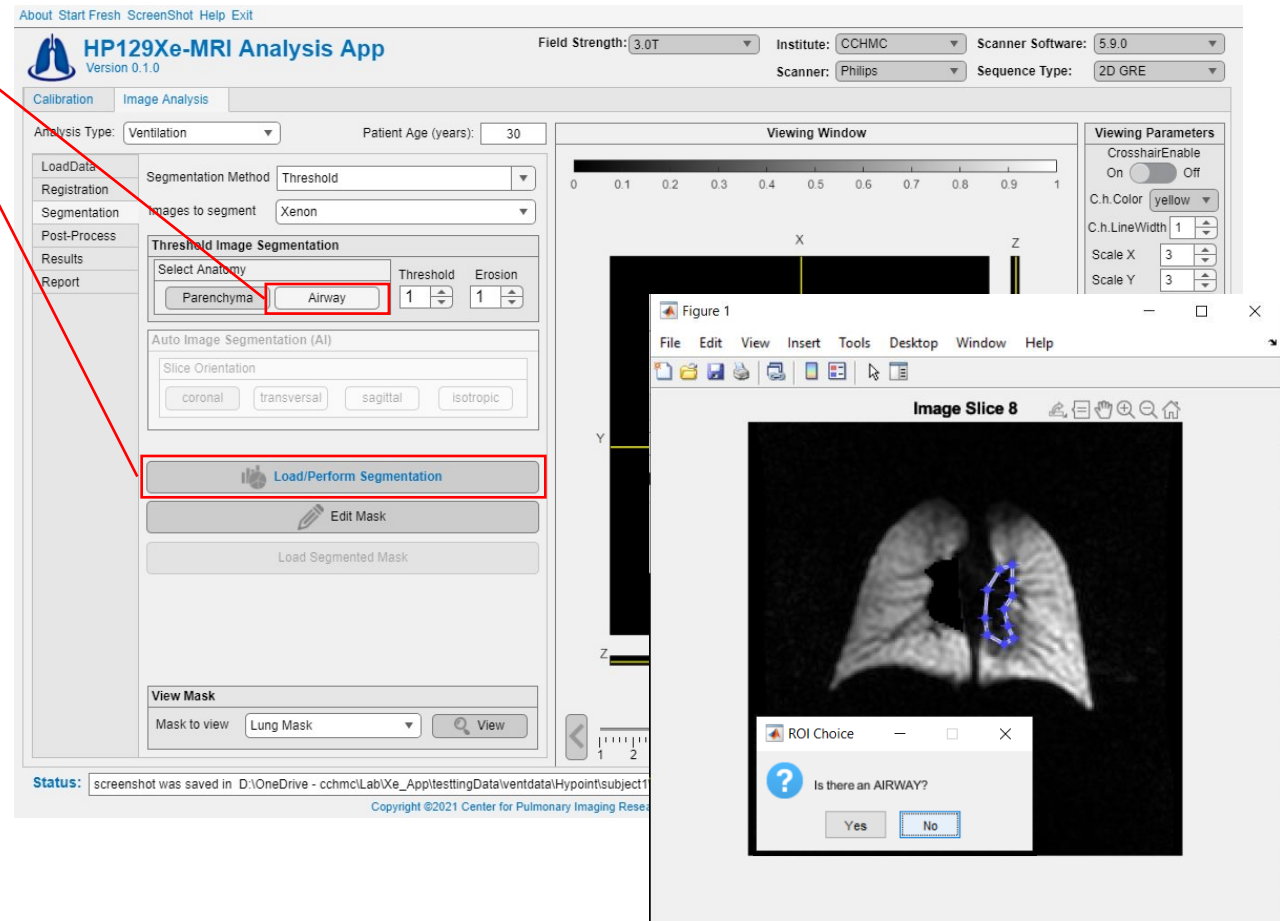
1-Select "Airway"

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.





Set-up Auto Segmentation:

1-If the pretrained models are not existed in the Segmentation folder, copy them into your local directory. Refer to the GitHub instructions for downloading these models

2-Install Python 3.10.

3- Create CPython

> Github > HP_Xe_Analysis_App > +Segmentation

Name

- AutoSegment_2DVent_Xe_axial_2000e.hdf5
- AutoSegment_2DVent_Xe_coronal_2000e.hdf5
- AutoSegment_2DVent_Xe_H_coronal_1000e.hdf5
- AutoSegment_3DGasExchange_Xe_200e.hdf5
- AutoSegment_3DGasExchange_Xe_H_1000e.hdf5

Python 3.10

In MATLAB, run the following commands (only one time for setting it up).

```
terminate(pyenv)
```

% add the local path

```
pyenv('Version','C:\Users\bda5ik\AppData\Local\Programs\Python\Python310\pythonw.exe'); %Call Python 3.10
```

% install the necessary packages

```
system('pip install numpy')
```

```
system('pip install keras')
```

```
system('pip install tensorflow')
```

```
system('pip install nibabel')
```

```
system('pip install scipy')
```

```
terminate(pyenv)
```



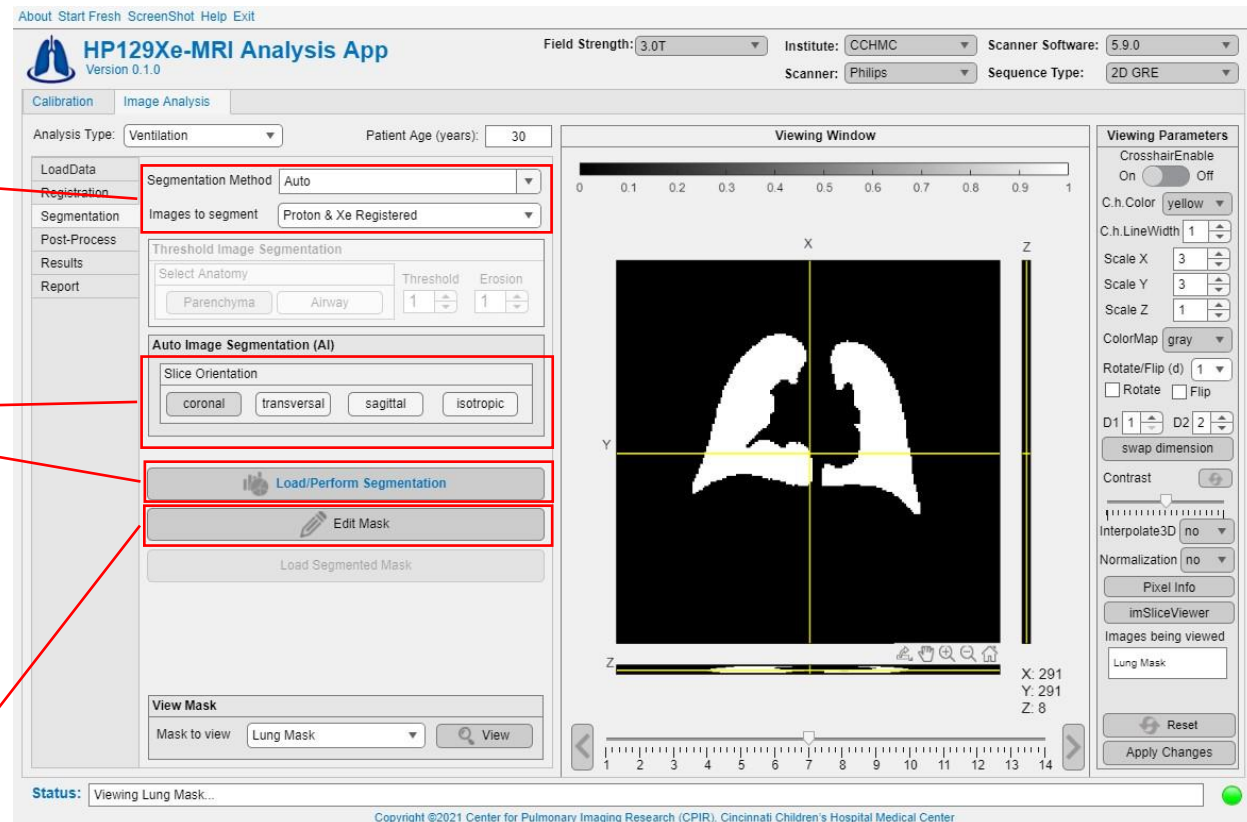
Auto Segmentation:

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

2-Select the slice orientation.

3-Initiate the segmentation process. This will take a few seconds. Mask will be automatically saved in the local folder and in MATLAB workspace for the subsequent analysis steps.

4- If the mask isn't optimal, click on "Edit Mask". This will launch the manual segmentation, explained above. Follow the same steps for manual segmentation.





4.4 | post-Processing

Post-Processing: Ventilation

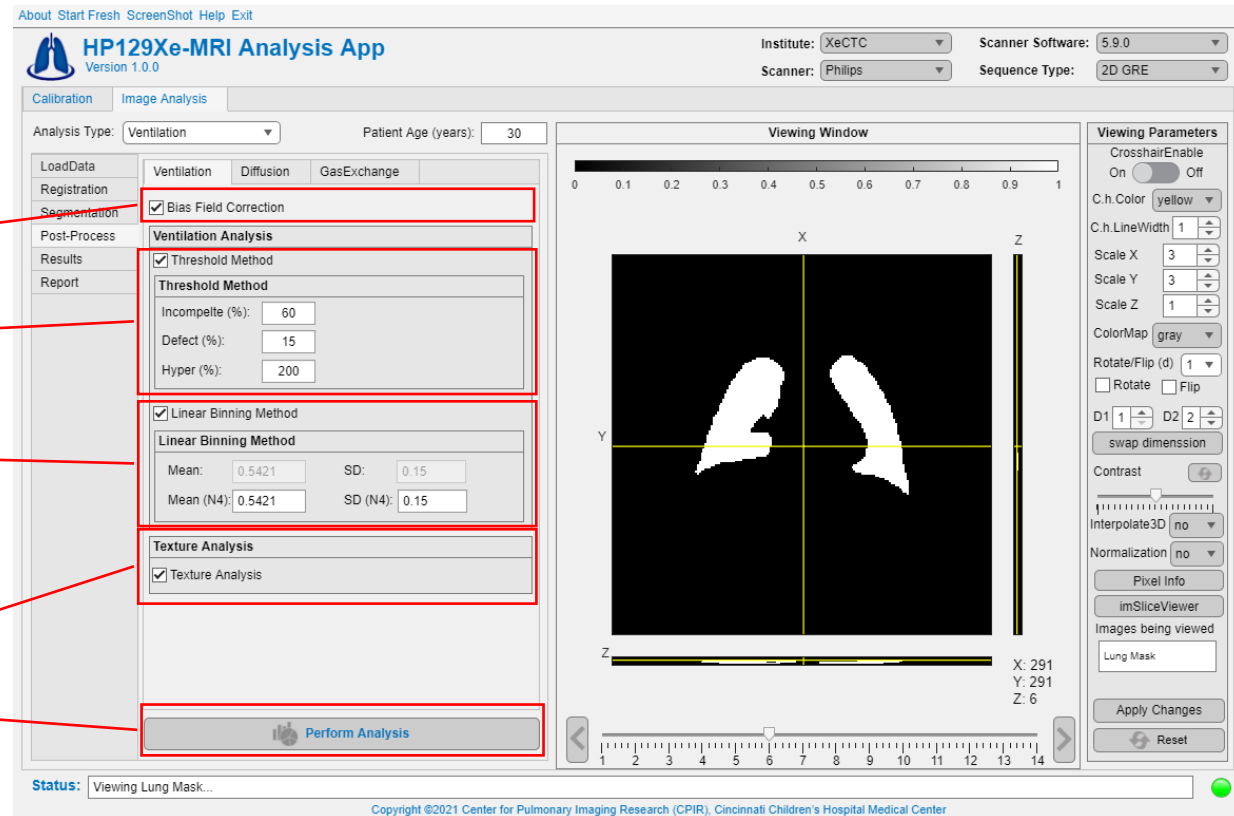
1- Choose "Bias Field Correction" if required.

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 displays the HP129Xe-MRI Analysis App interface. The 'Image Analysis' tab is active, and the 'Diffusion' sub-tab is selected. The 'Analysis Type' is set to 'Diffusion'. The 'Patient Age (years)' is 30. The 'b-values' field contains the values [0, 6.25, 12.5, 18.75, 25]. The 'ADC Analysis' section shows 'Fitting Type' set to 'Log Linear'. The 'ADC Linear Binning Method' section includes 'Mean equation: 0.0002*age+0.029' and 'SD equation: 5e-5*age+0.0121'. The 'Morphometry Analysis' section is checked, with 'Study Type' set to 'human', 'Cylindrical Model (CM)' checked, and 'Stretch Exponential Model (SEM)' checked. The 'Do (cm2/s)' is 0.14 and 'Delta (ms)' is 3.5. The 'Perform Analysis' button is highlighted. The 'Viewing Window' shows a 3D visualization of the lungs. The 'Viewing Parameters' panel on the right includes settings for 'CrosshairEnable', 'C.h. Color', 'C.h.LineWidth', 'Scale X', 'Scale Y', 'Scale Z', 'ColorMap', 'Rotate/Flip (d)', 'D1', 'D2', 'Contrast', 'Interpolate3D', and 'Normalization'. The status bar at the bottom indicates the screenshot was saved in D:\OneDrive - cchmc\Lab\Xe_App\testingData\ventdata\Hypointsubject1\VENTILATION1.



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.

HP129Xe-MRI Analysis App

Version 1.0.0

Institute: XeCTC Scanner Software: 5.9.0

Scanner: Philips Sequence Type: 3D Radial

Analysis Type: GasExchange Patient Age (years): 30

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\Hypoints\subject1\VENTILATION1

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4.4 | Results and Outputs

Ventilation

About Start Fresh ScreenShot Help Exit

HP129Xe-MRI Analysis App
Version 1.0.0

Institute: XeCTC
Scanner: Philips

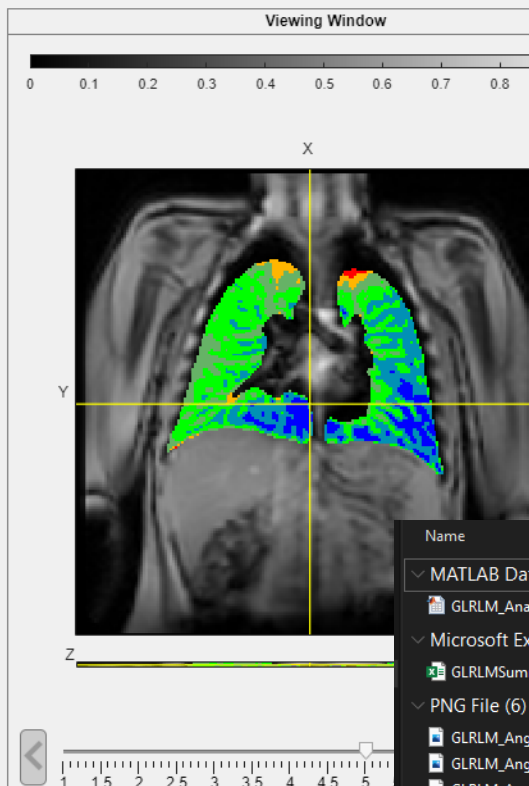
Calibration Image Analysis

Analysis Type: Ventilation Patient Age (years): 30

LoadData	Ventilation	Diffusion	GasExchange
Registration	Threshold Method Results		
Segmentation	VDP (%): 5.4227% VDP Map		
Post-Process	Normal (%): 1114.87±277.03 (94.5%) VDP Histogram		
Results	Incomplete (%): 515.75±106.82 (5.4%)		
Report	Complete (%): NaN±NaN (0.0%)		
	Hyper (%): 2241.80±49.87 (0.0%)		

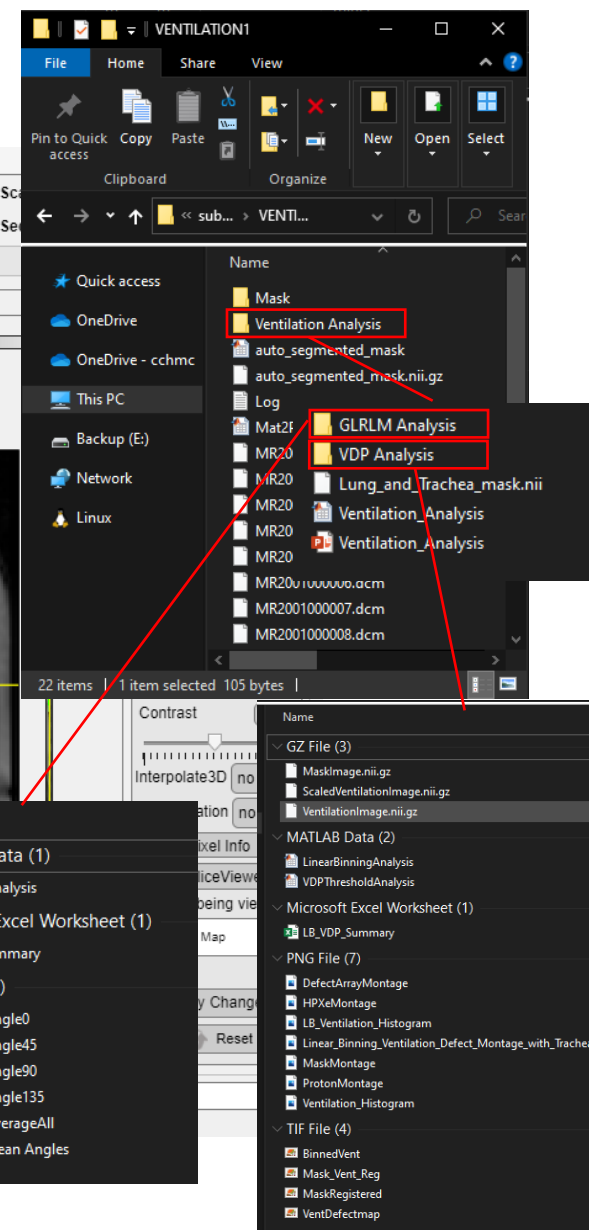
Linear Binning Method Results						
LB VDP (%): 0.27027%		LB VDP Map				
Mean: 0.64948±0.13905		LB VDP Histogram				
Bin1	Bin2	Bin3	Bin4	Bin5	Bin6	
0.27	2.99	19.08	39.45	29.61	8.6	High
Defects						

Texture Analysis (GLRLM) Results			
SRE:	0.30789	HGRE:	2534.4049
LRE:	19.5507	SRLGR:	0.018525
GLN:	225.6584	SRHGE:	2523.4149
RLN:	346.5259	LRLGE:	8.6749
RP:	1.1144	LRHGE:	2817.0225
LGRE:	0.33322	Mean GLRLM Map	



Status: Ventilation analysis completed

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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

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

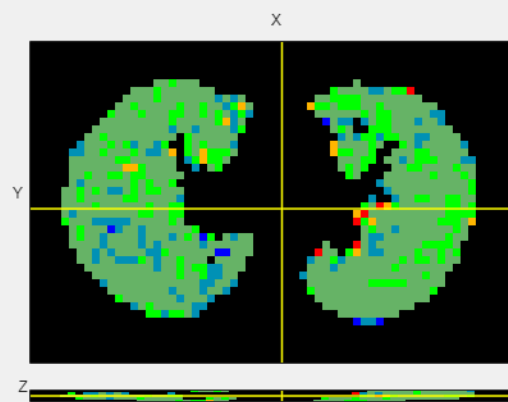
SEM Parameters Alpha: Heterogeneity index

Mean

Histogram

Map

0 0.1 0.2 0.3 0.4 0.5 0.6 0.7



X: 99
Y: 66
Z: 3

Status: Diffusion analysis completed

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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

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
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



4.6 | 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.

HP129Xe-MRI Analysis App
Version 1.0.0

Analysis Type: Ventilation Patient Age (years): 30

Study ID: IRC186
Study Type: Calibration
Patient ID: 001
Scan Date: 29/May/2021
Xe Dose Volume (mL): 1000
Patient Name: ASB
MRM: 0000000
Sex: Male
Age (year): 30
Height (cm): 180
Weight (lbs): 200
Summary of Findings: Normal VDP
Notes:
Data Analyst: ASB
Processing Date: 08-Jul-2023

Generate Report

Ventilation_Analysis_Patient_Report

Patient Report (Ventilation Analysis)


Study ID: IRC186
Study Type: Calibration
Patient ID: 001
Scan Date: 29/May/2021
Xe Dose Volume (mL): 1000
Patient Name: ASB
MRM number: 0000000
Sex: Male
Age (year): 30
Height (cm): 180
Weight (lbs): 200
Summary of Findings: Normal VDP
Notes:
Data Analyst: ASB
Processing Date: 08-Jul-2023

VDP Analysis

Linear blend images (100% VDP)

Area	Area 1	Area 2	Area 3	Area 4	Area 5	Area 6
Normal	0.000	0.000	0.000	0.000	0.000	0.000

4.6 | Viewing Window



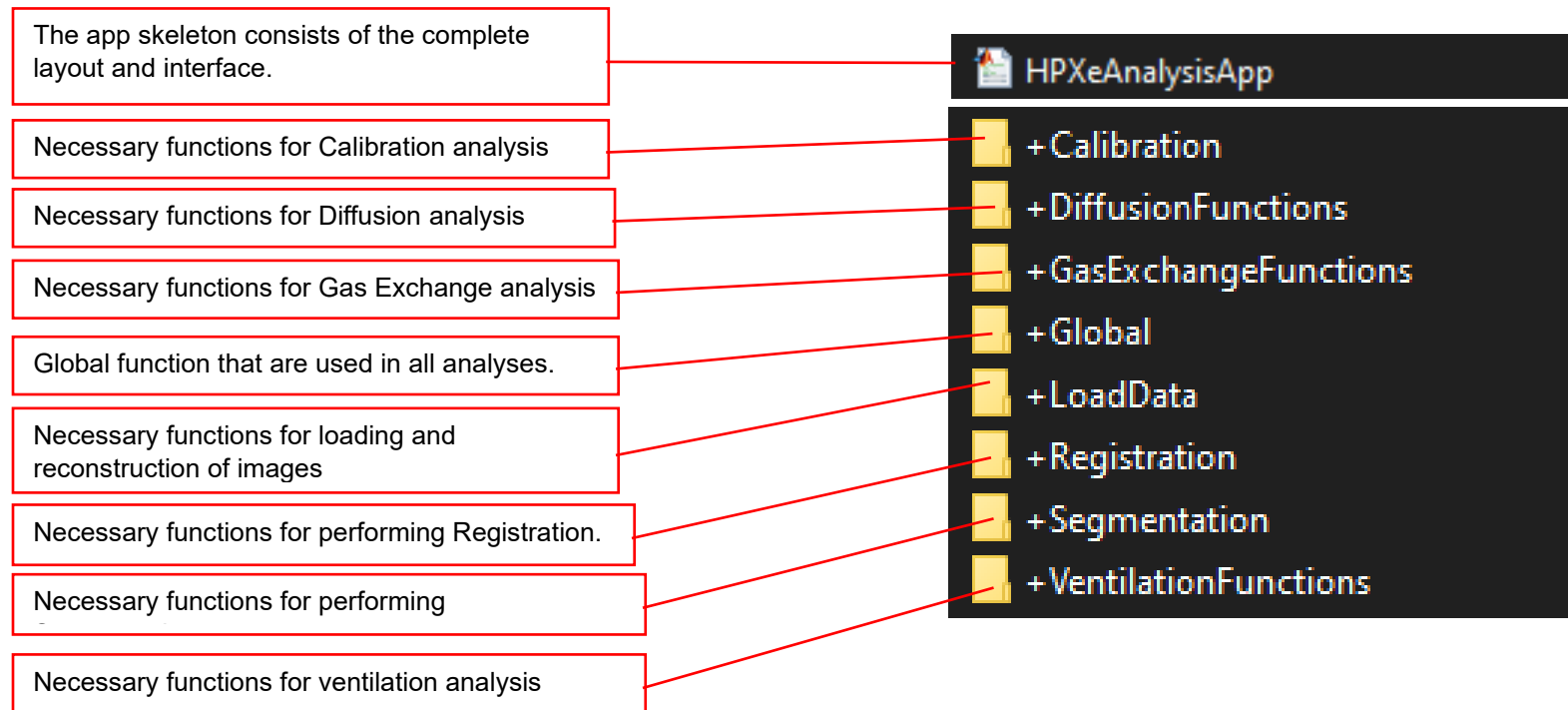
The screenshot displays the HP ¹²⁹Xe MRI Analysis App interface. The main viewing window shows a grayscale image of lungs with a yellow crosshair. The interface includes a top menu bar, a left sidebar with navigation options, and a right sidebar with viewing parameters. Red callout boxes provide instructions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

- Enable and disable crosshair:** Points to the 'CrosshairEnable' toggle 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.
- 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.
- 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.
- Browse between slices:** Points to the 'View Images' section in the left sidebar.



5 | Code Structure

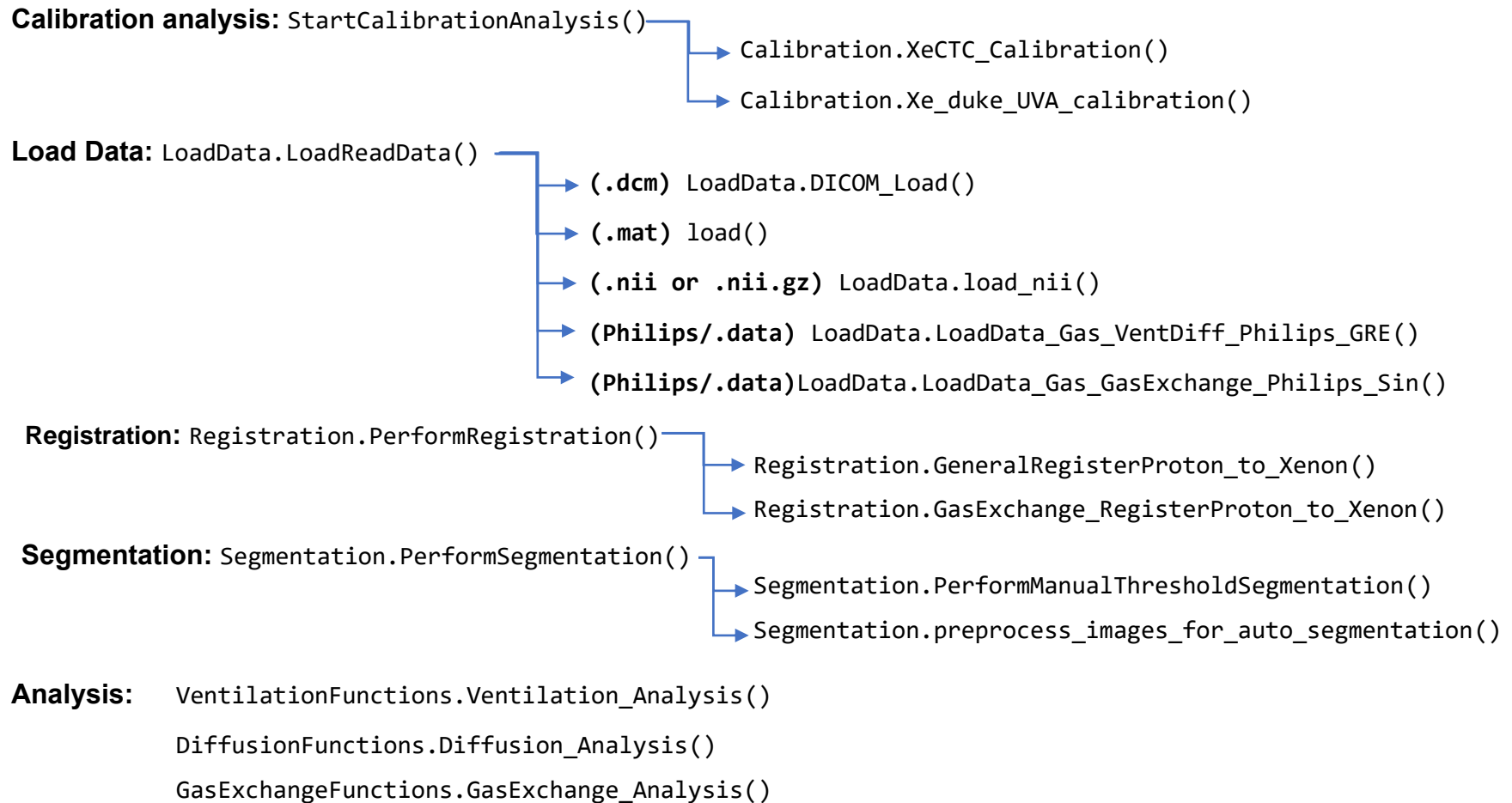
5.1 | Folders





5.2 | Code Hierarchy

Here are the main and submain functions:





5.2 | 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
```



6 | 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, adding new features, and testing, allowing users to evaluate new functions before integrating them into the application.

7 | Report Issues

If you encounter any problems, kindly create an issue on our GitHub account (https://github.com/aboodbdaiwi/HP129Xe_Analysis_App), and our team of authors will collaborate with you to address and resolve the issue promptly.