

User's Manual



¹²⁹Xe Image Processing Pipeline (XIPLINE): An Open-Source, Graphical User Interface Application for the Analysis of Hyperpolarized ¹²⁹Xe MRI

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Center for Pulmonary Imaging Research
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Table of Contents

1 Installation	4
2 Overview	5
3 Flip Angle and Frequency Calibration.....	10
3.1 Input.....	10
3.2 Adjusting Parameters.....	11
3.3 Save Results.....	12
4 Image Analysis	13
4.1 Inputs	13
4.2 Registration.....	17
4.3 Segmentation.....	Error! Bookmark not defined.
4.4 post-Processing	27
4.4 Results and Outputs.....	31
4.6 Patient Report	34
4.6 Viewing Window.....	35
5 Code Structure	36
5.1 Folders	36
5.2 Code Hierarchy	37
5.2 Implement Your Own Functions	38
6 Debugging	39
7 Report Issues	39

1 | Installation

- 1- Visit <https://github.com/aboodbdaiwi/XIPLINE> and watch video 1 for step-by-step instructions
- 2- You can launch the compiled application (**XIPLINE.exe**) independently, without requiring MATLAB.
- 3- For developers, please clone or download the folder to your local directory.
- 4- For customization, include the local folder in the MATLAB path and execute the **XIPLINE.mlapp** file using MATLAB version R2023b or newer.

2 | Overview

Main Menus:

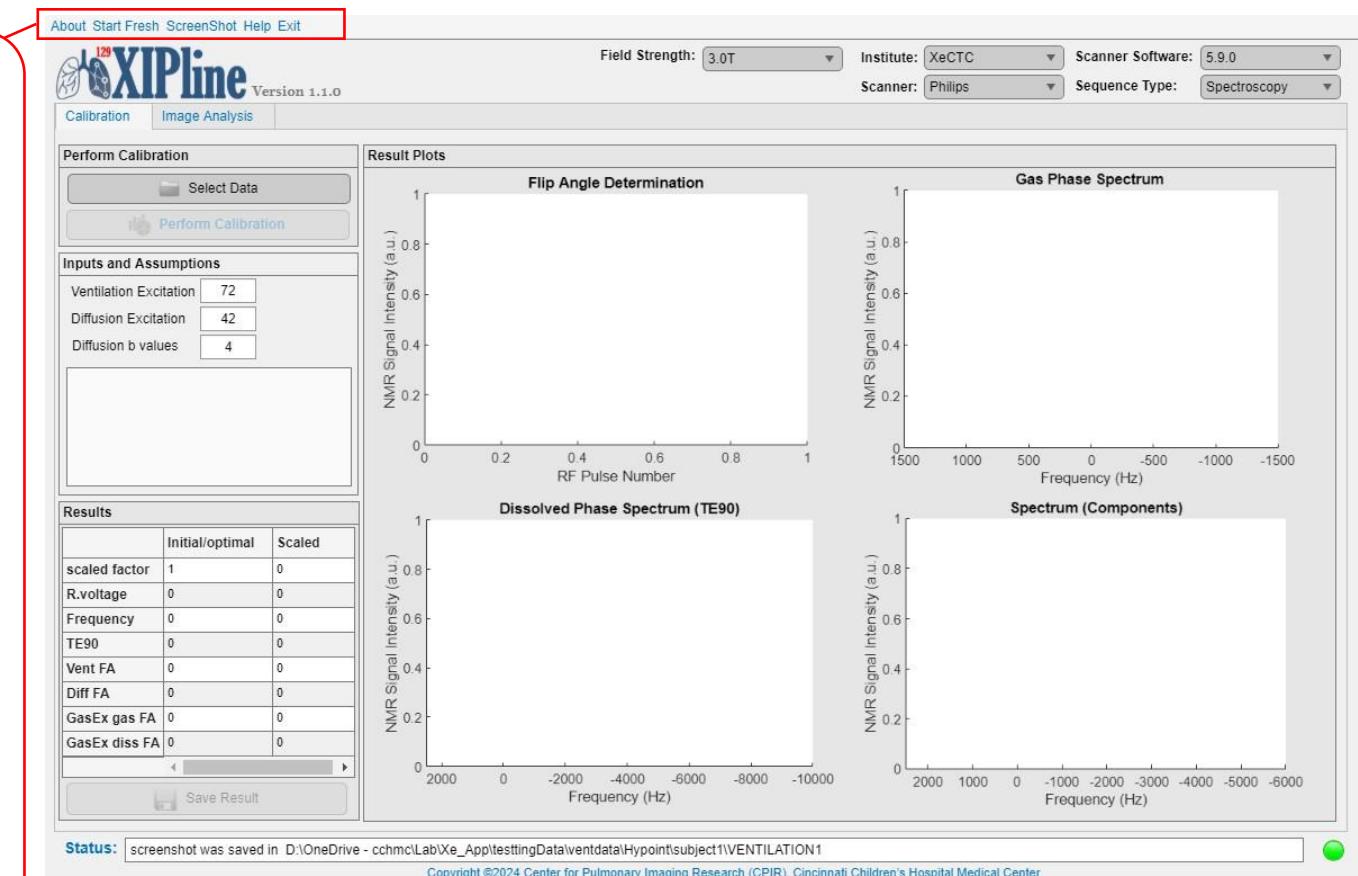
About: Provides an insightful overview of the application and its functionalities.

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 PNG file.

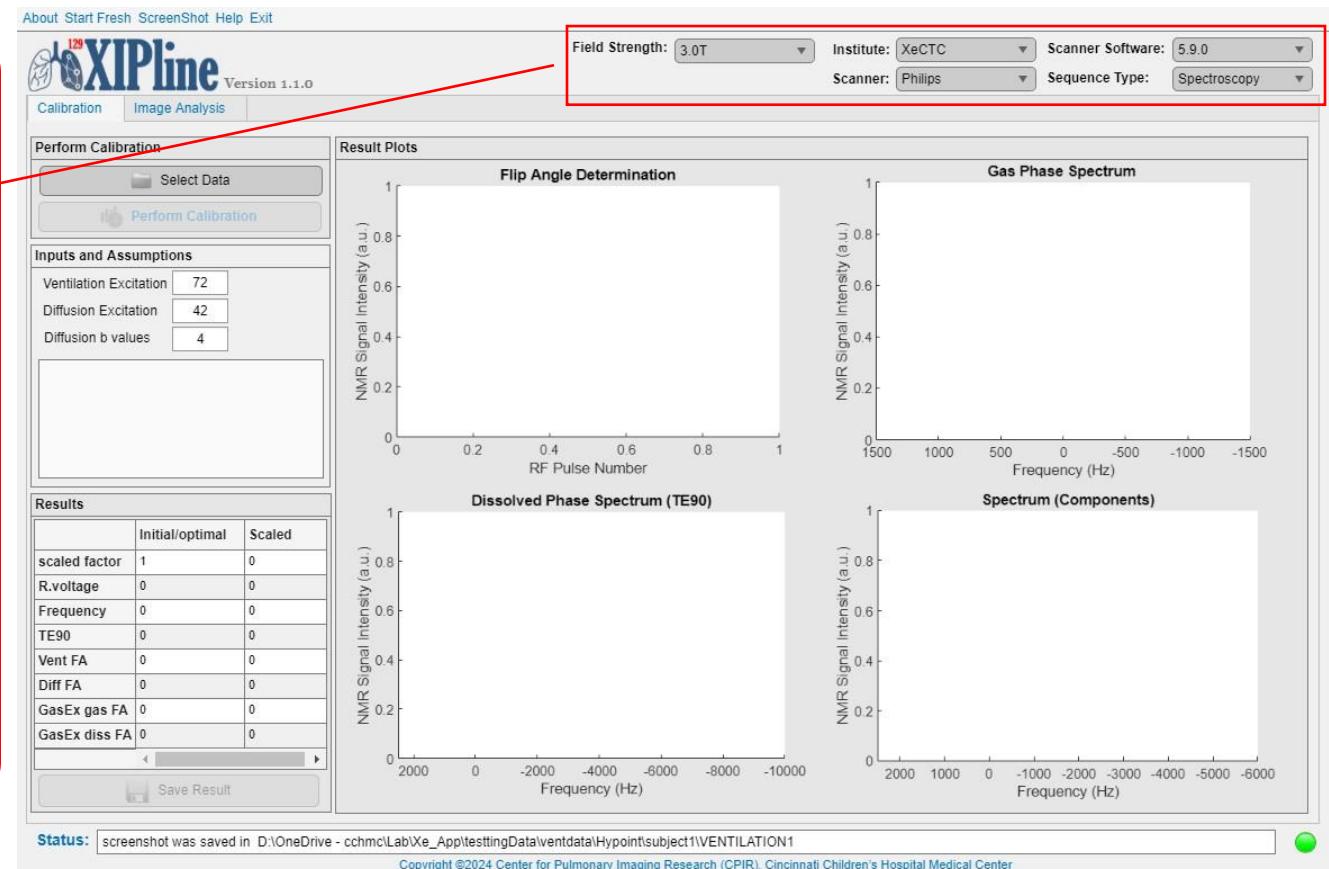
Help: Guides you to the comprehensive user manual, offering assistance and clarification.

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.

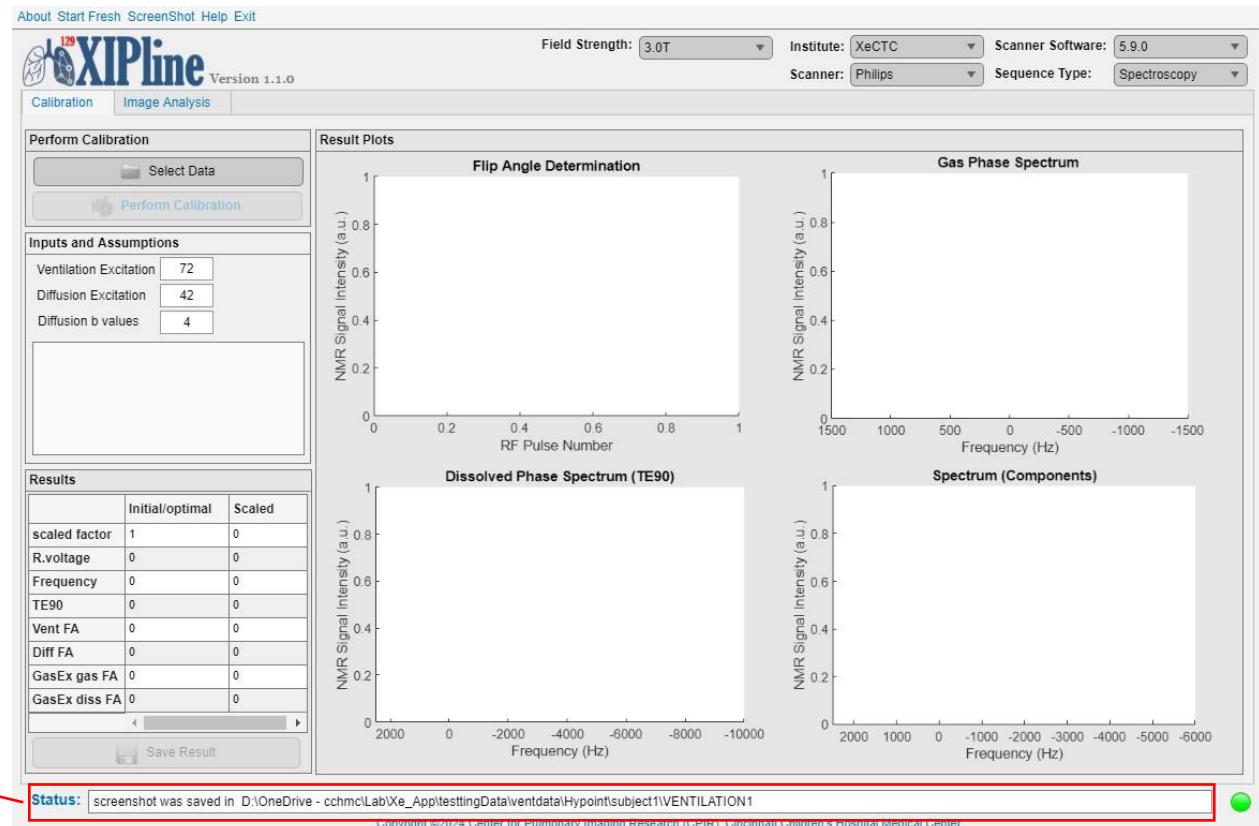
Image Analysis: Facilitates image reconstruction and conducts comprehensive post-processing analysis, enabling in-depth examination and evaluation.

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:

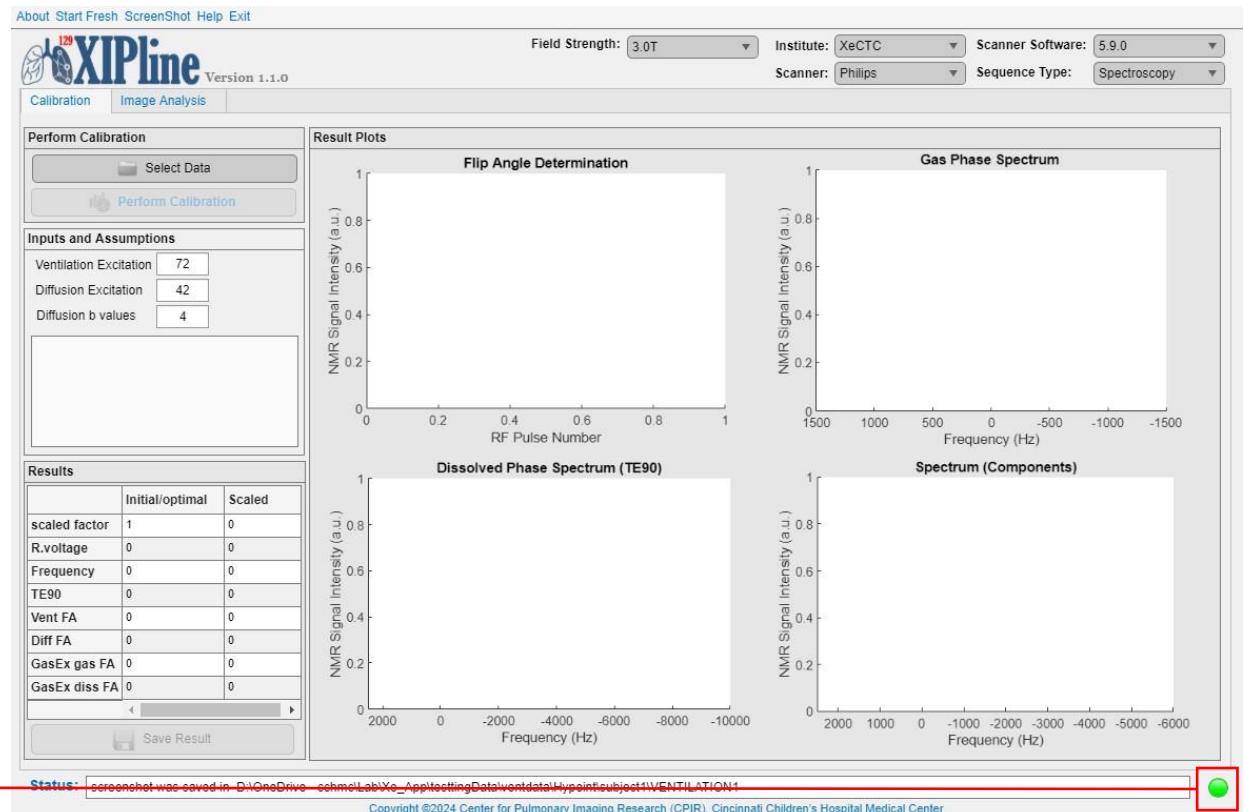
The status window presents a text box that provides real-time updates on tasks and displays error messages when necessary. It serves as a valuable tool for tracking progress and promptly addressing any issues that may arise.



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.



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.

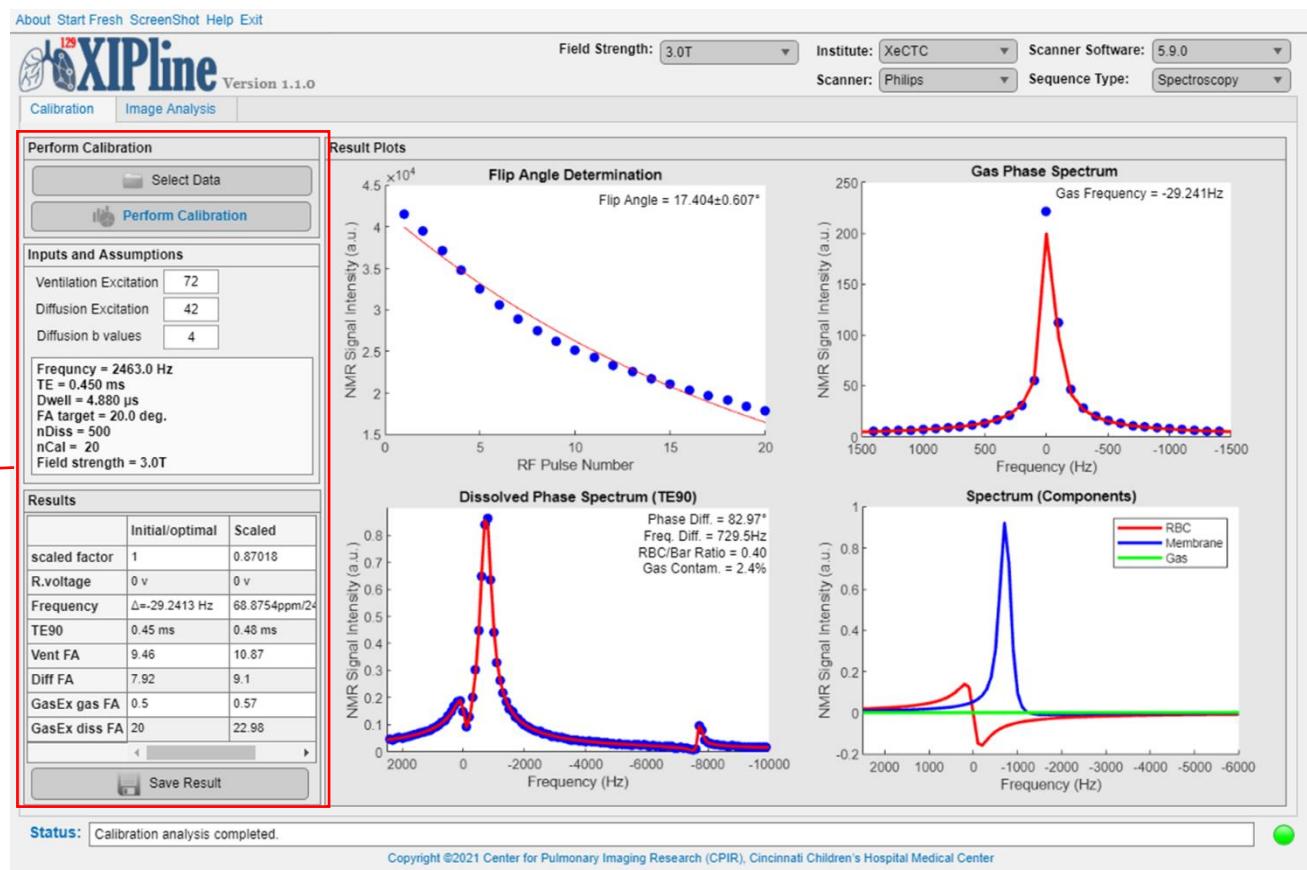


Table 2.1: Supported data type for Calibration analysis

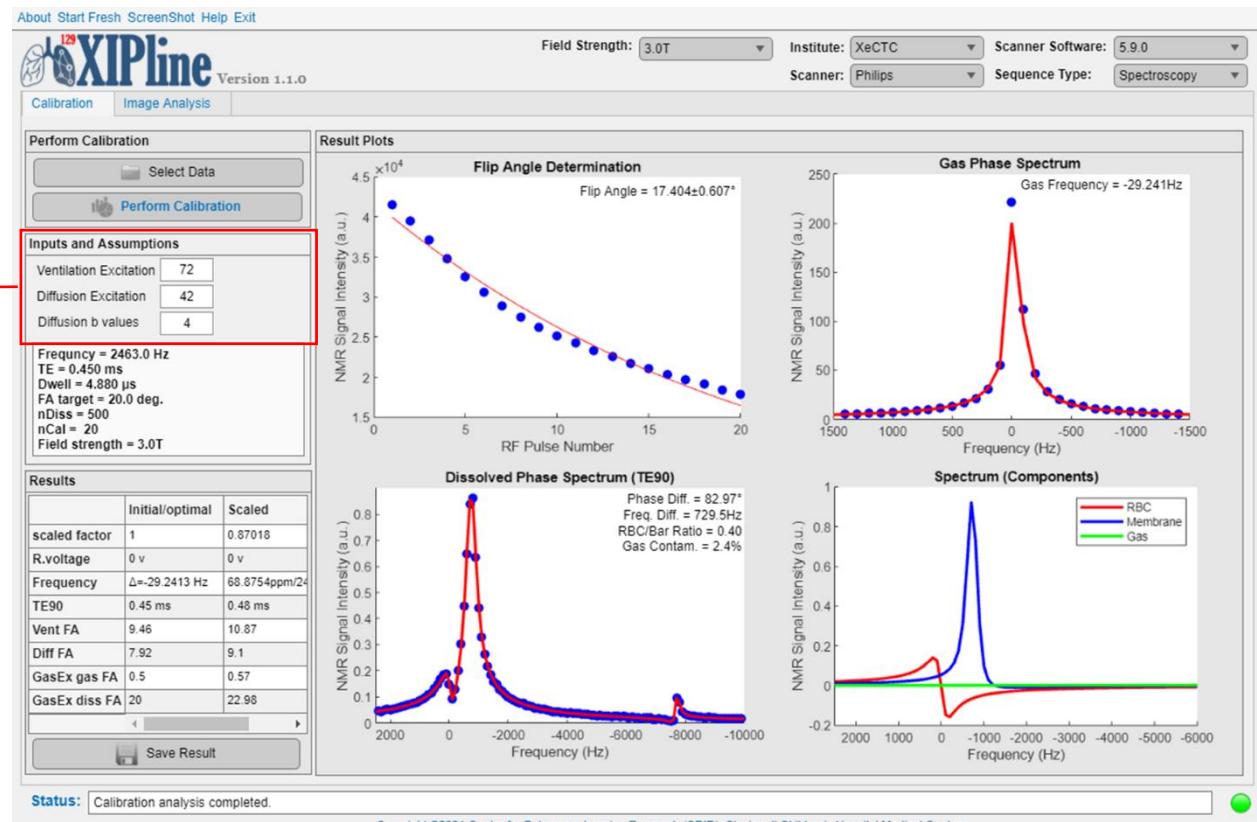
Scanner	Philips	Siemens	GE	ISMRMD
Data Type	.data*/.list	.dat*	.7*	.h5* or .mrd*

* The data that needs to be selected!

3.2 | Adjusting Parameters

Perform Calibration Analysis:

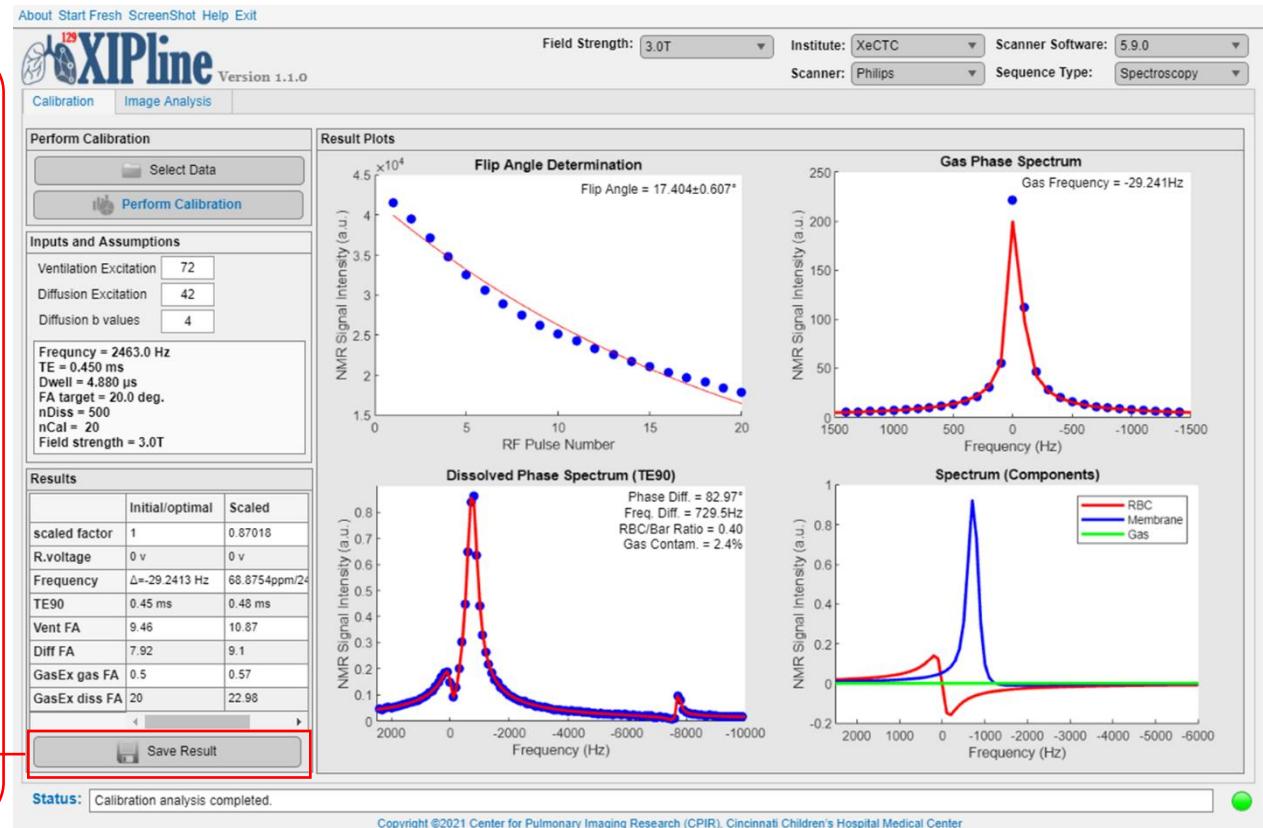
The calibration analysis allows for flexibility in adjusting parameters both before and after the analysis. These input parameters possess a dynamic property, meaning that any changes made to their values will automatically update the calculations. This enables effortless refinement and adaptation of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

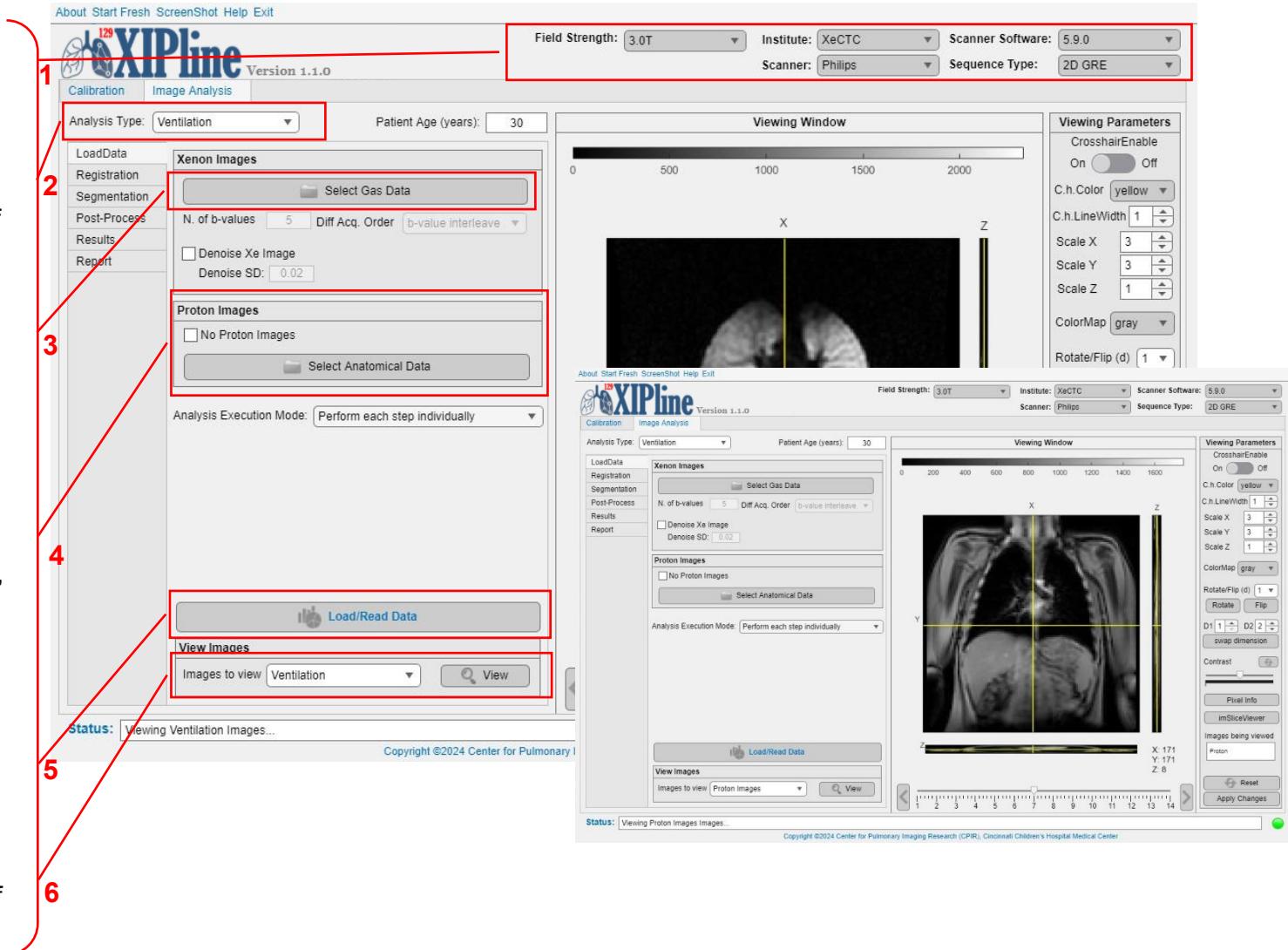


Table 3.1 Supported data formats.

Imaging Type	Supported Data Type				
	General Image Formats	Raw Data			
		Philips	Siemens	GE	ISMRMD
Calibration	-	.data/.list	.dat	.7	.h5 or .mrd
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 (2D Cartesian only)	.dat (2D Cartesian only)	.7 (2D Cartesian only)	.h5 or .mrd (2D Cartesian 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 (2D Cartesian only)	.dat (2D Cartesian only)	.7 (2D Cartesian only)	.h5 or .mrd (2D Cartesian only)
Gas Exchange	.mat (single): Not recommended.	.data/.list/.sin (3D radial only)	.dat (3D radial only)	-	.h5 or .mrd (3D radial only)
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 (2D Cartesian or 3D radial only)	.dat (2D Cartesian or 3D radial only)	-	.mrd or .h5 (2D Cartesian or 3D radial only)

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

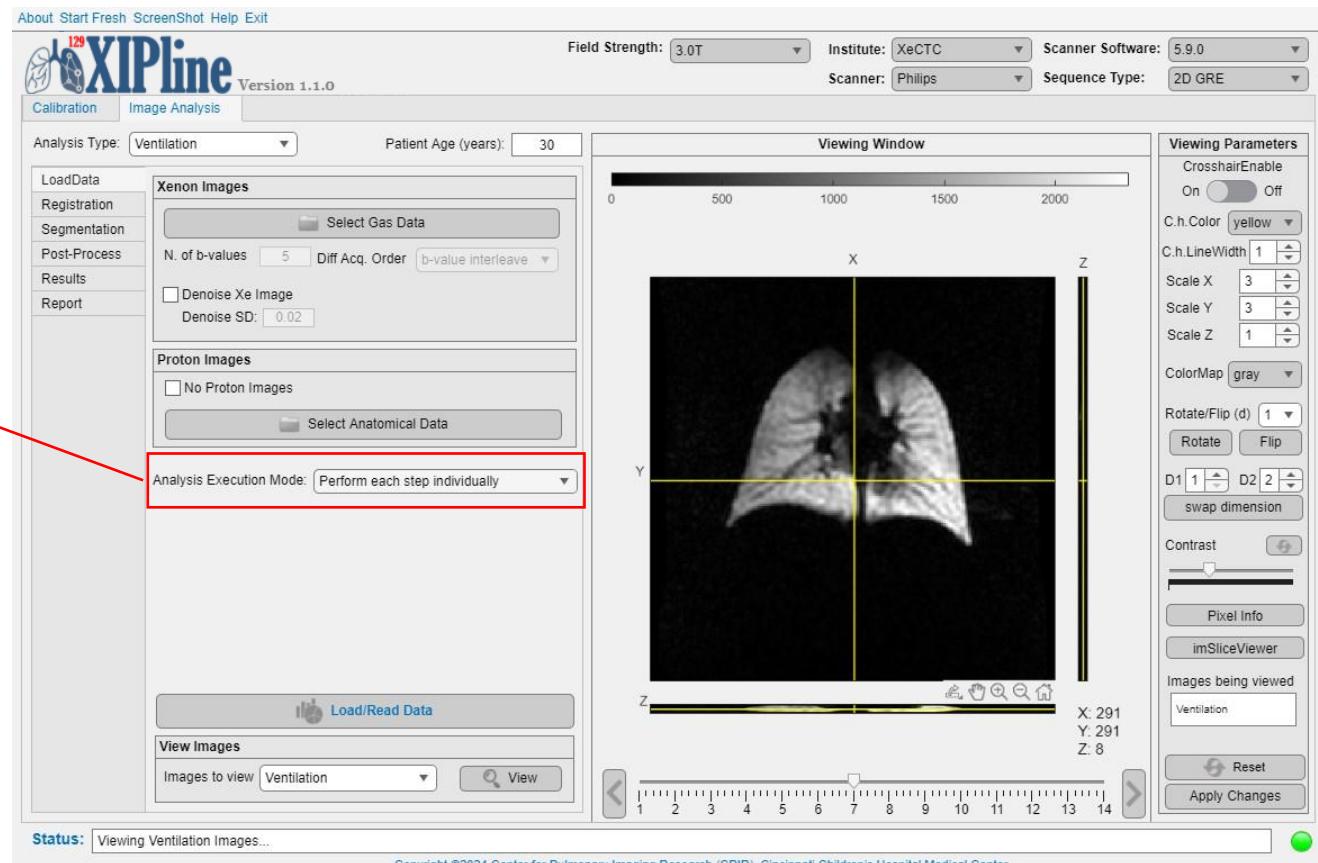
```
UncorrectedVentImage
VentImage
GasImage
DissolvedImage
CorrDissolvedImage
AppendedDissolvedNMRFit
RBC2Bar_struct
RBCOsc_High_Image
RBCOsc_Low_Image
RBCOsc_Normalization
ActTE90
DisFlipAngle
PixelShift
DissolvedNMR
SigDynamics
```

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

```
ProtonImage
file_name
HDataLocation
H_RecMatrix
ProtonMax
```

Load Data:

This choice provides the flexibility to execute each step individually, such as loading data or performing registration. Users can also opt to perform all steps collectively. However, it's essential for the user to configure the desired settings for each step before clicking the "Load/Read Data" button.



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:

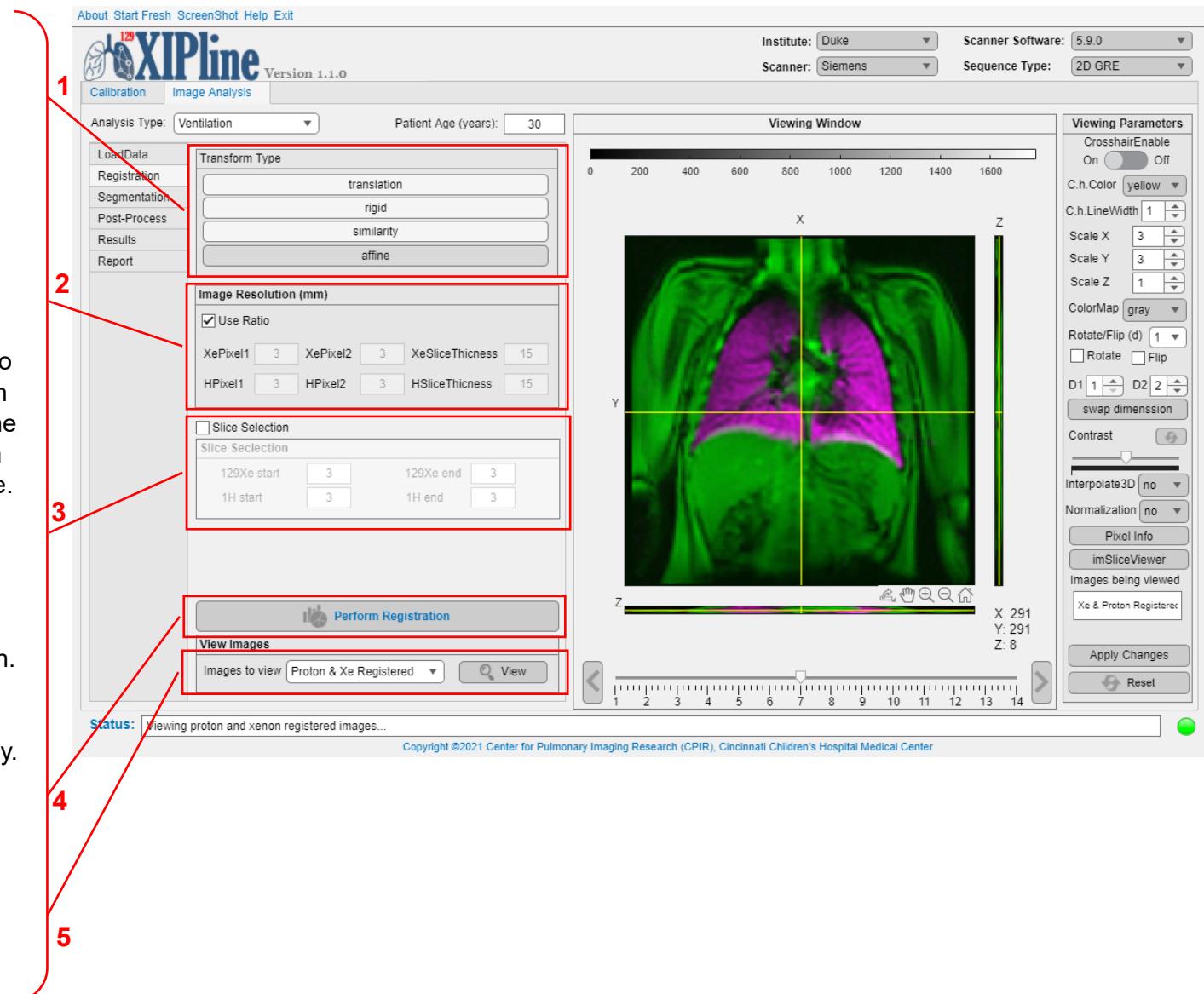
In case the slices of the images do not align, you can specify the starting and ending slices of the matched region. Linear interpolation will be employed to adjust the number of slices accordingly.

4. Registration Process:

Initiate the registration process for multimodal 3D medical images.

5. Image Selection:

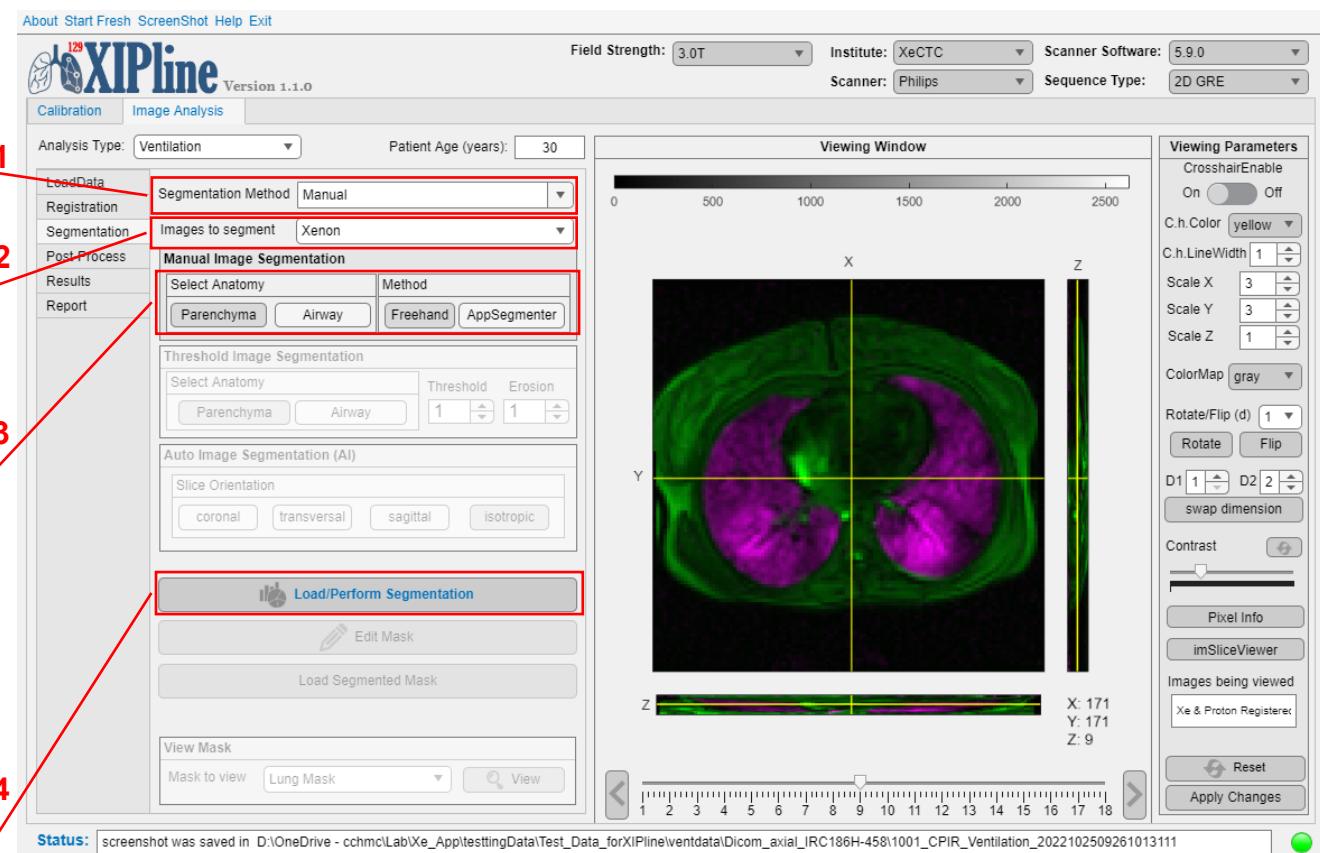
Select image type to view.



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-Select lung anatomy to segment. Also, select the manual segmentation method. Freehand is the only method that's available when running the compiled application. However, both methods are available when running the application in developer mode.
- 4-Initiate the segmentation process.



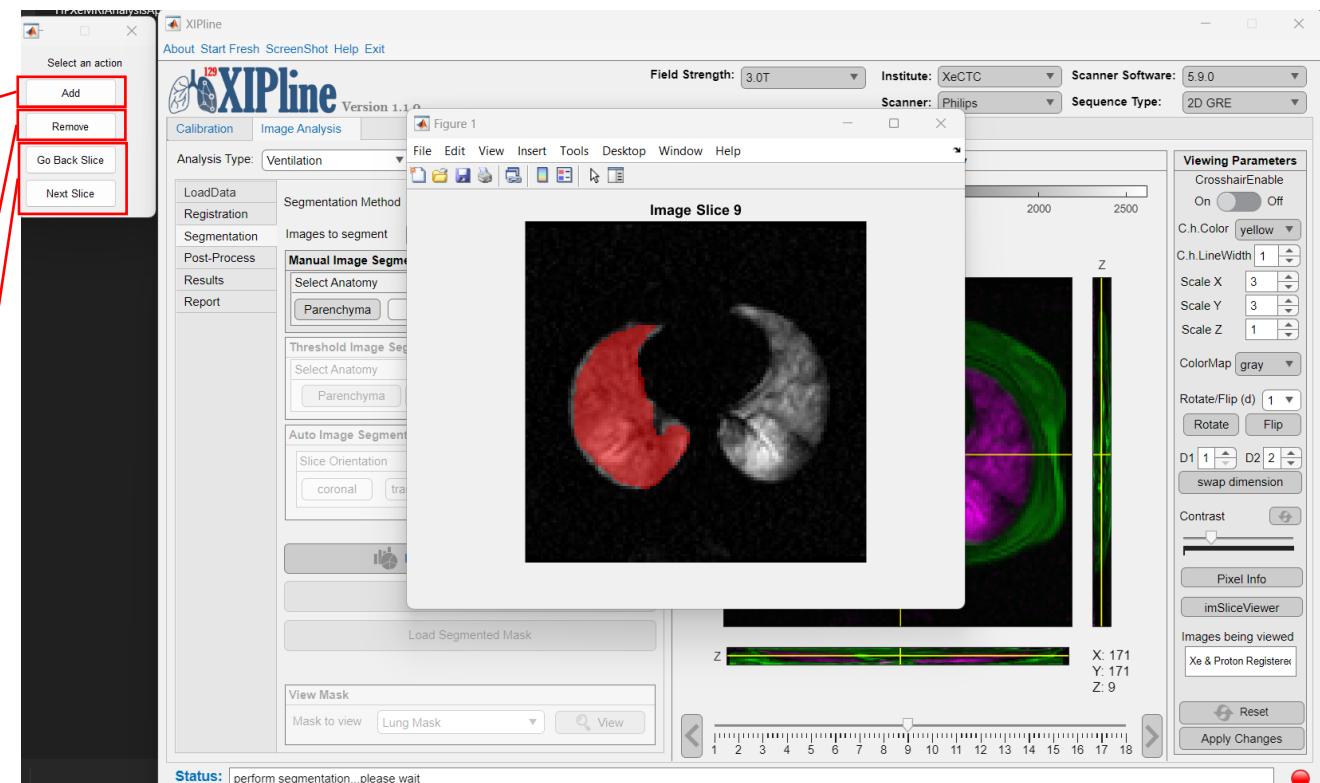
Manual Segmentation:

(Freehand)

1-click 'add' to add segmentation. Select a point and click and hold the mouse and start drawing. Once you close the boundaries of the drawn ROI let go the hold.

2-click 'remove' to remove segmentation. Same process as above.

3-go back or move forward.



Manual Segmentation:

(AppSegmenter)

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

2-Select lung anatomy to segment. Also, select the manual segmentation method. Freehand is the only method that's available when running the compiled application. However, both methods are available when running the application in developer mode.

3-Initiate the segmentation process.

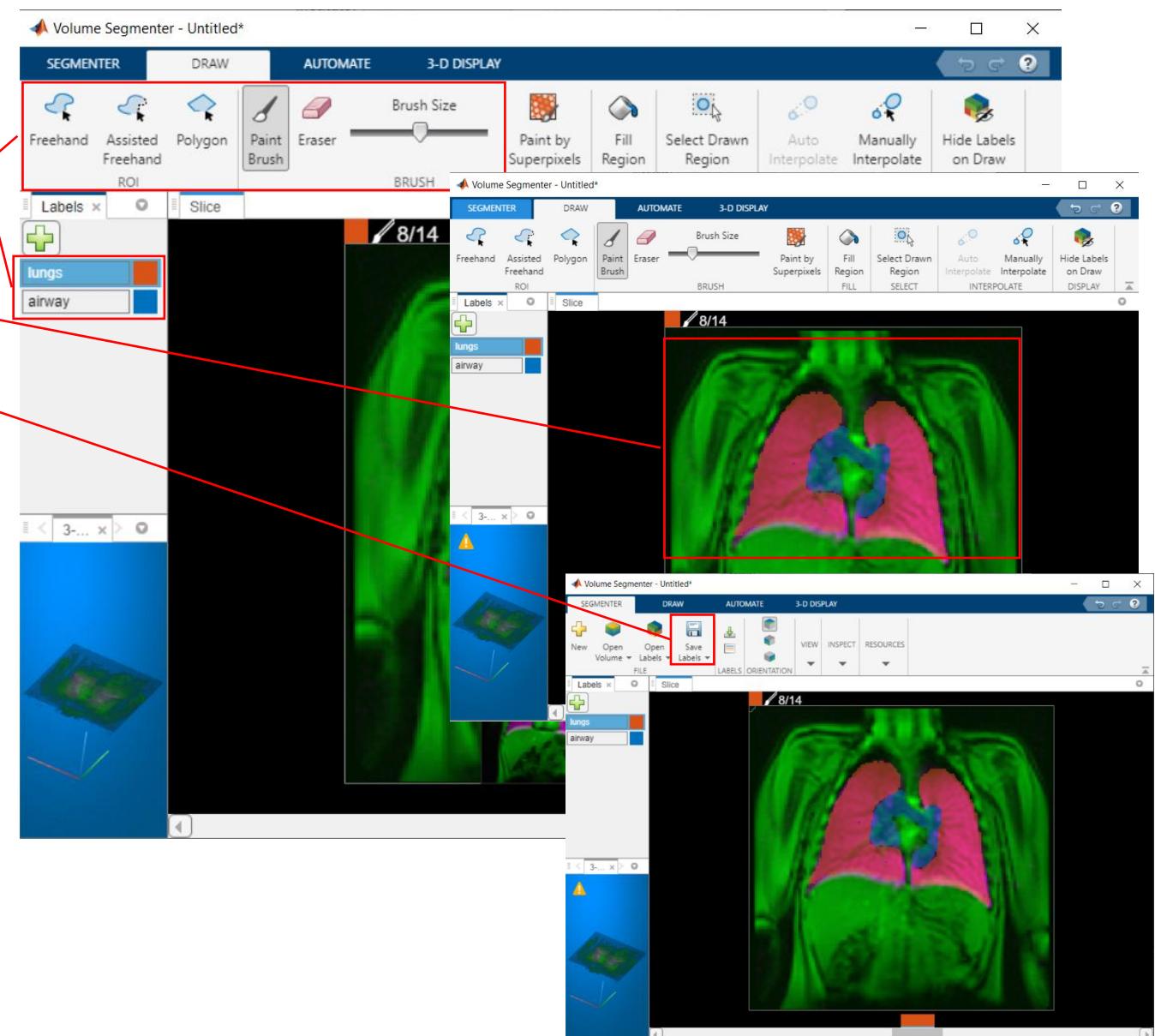
Manual segmentation utilizes [MATLAB's built-in App Volume Segmenter](#) which offers many advanced segmentation tools.



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.

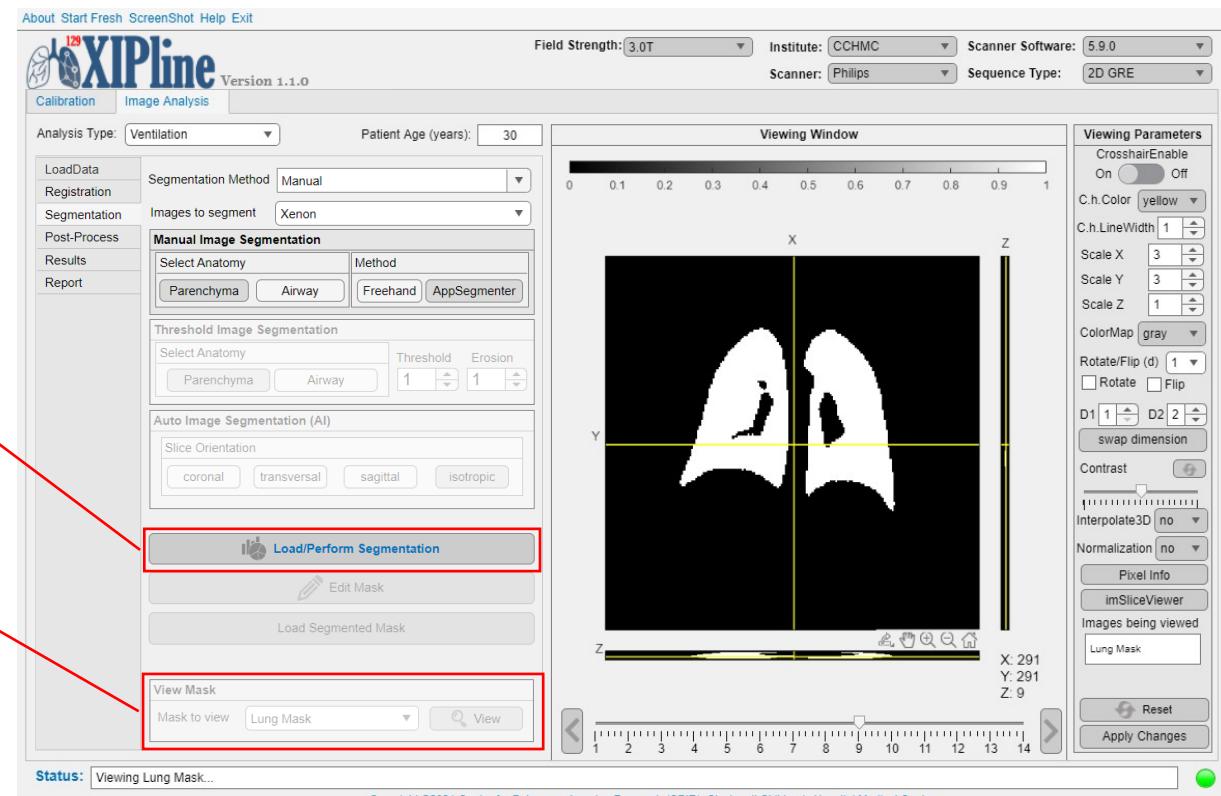
Note: There are several segmentation tools available, including thresholding and the option to add your own functions. Feel free to explore and find the most suitable tool for your needs. [MATLAB's built-in App Volume Segmente](#)



Manual Segmentation:

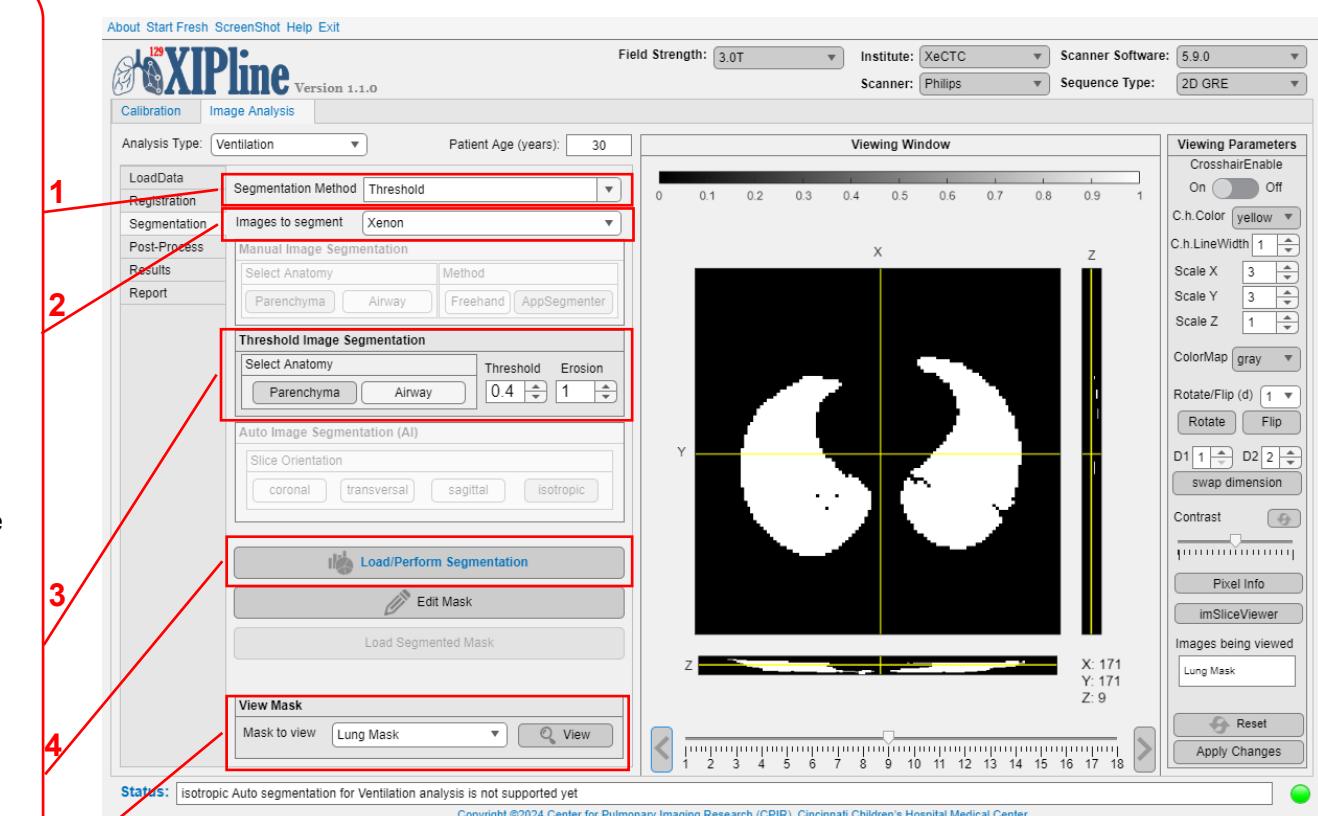
1-Once you have saved the mask, click on "Load Segmented Mask" to automatically upload the mask.

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:

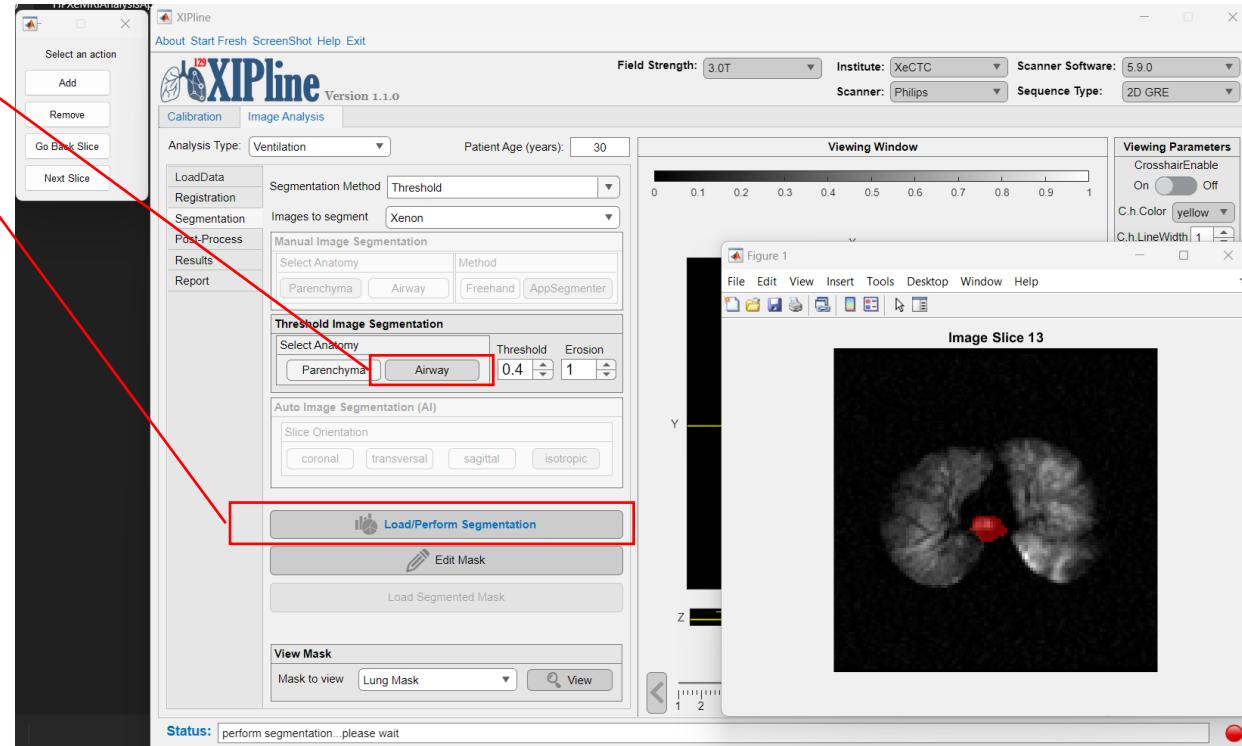
- 1-Select "Airway"
- 2- Initiate the segmentation process. The airway mask can only be drawn manually.

Begin drawing the boundaries of the airways by click and hold the mouse and moving the mouse.

Add or remove segmentation using the option box on top left.

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

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



Set-up Auto Segmentation:

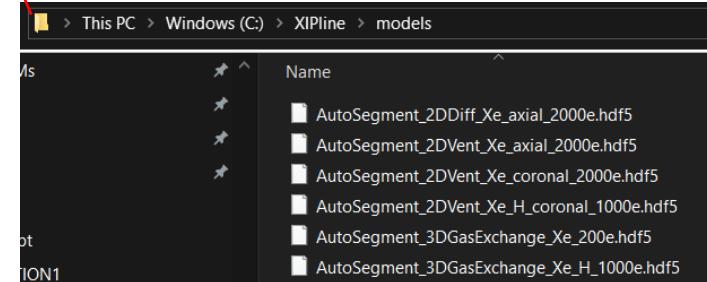
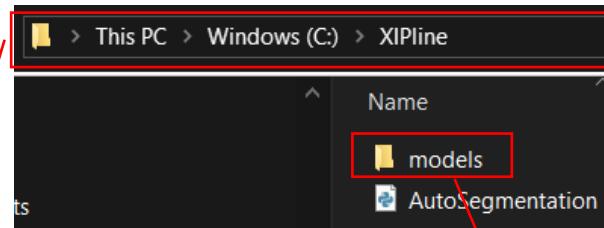
1- create this path:
C:\XIPlane\models then copy AutoSegmentation.py script in **C:\XIPlane** and the pretrained models (see the github page) in **C:\XIPlane\models**. Refer to the GitHub instructions for downloading these models.

2-Install [Python](#) 3.10
 create a text file with the name "python_path" and add the path to the pythonw.exe file in the first line in the text file.

(only one time for setting it up).

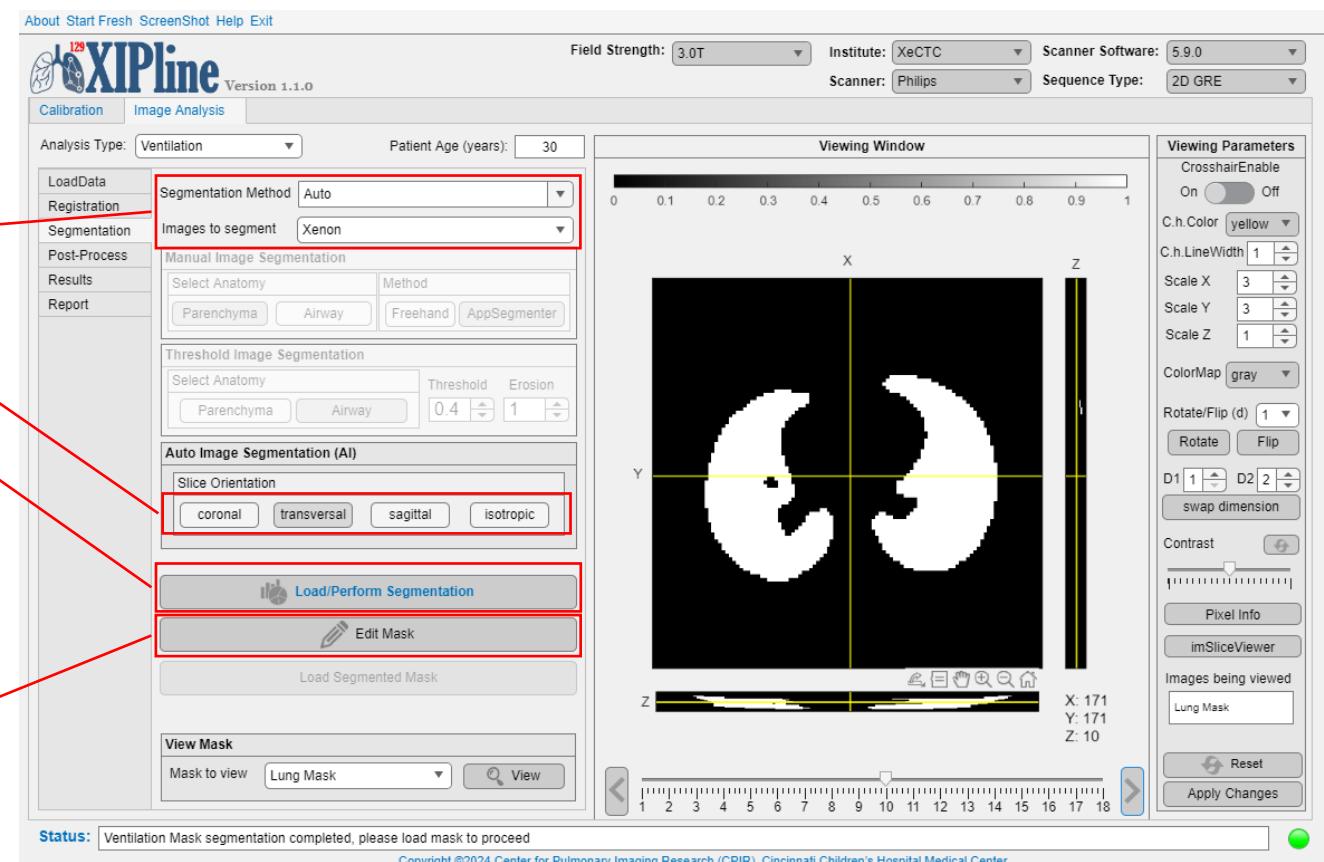
```
% add the local path to pythonw.exe file
C:\Users\bda5ik\AppData\Local\Programs\Python\Python310\pythonw.exe')

First time run will take a few minutes to install the necessary libraries. When the installation is completed, a text file with the name "python_requirement_satisfied" will appear in the XIPlane folder.
```



Auto Segmentation:

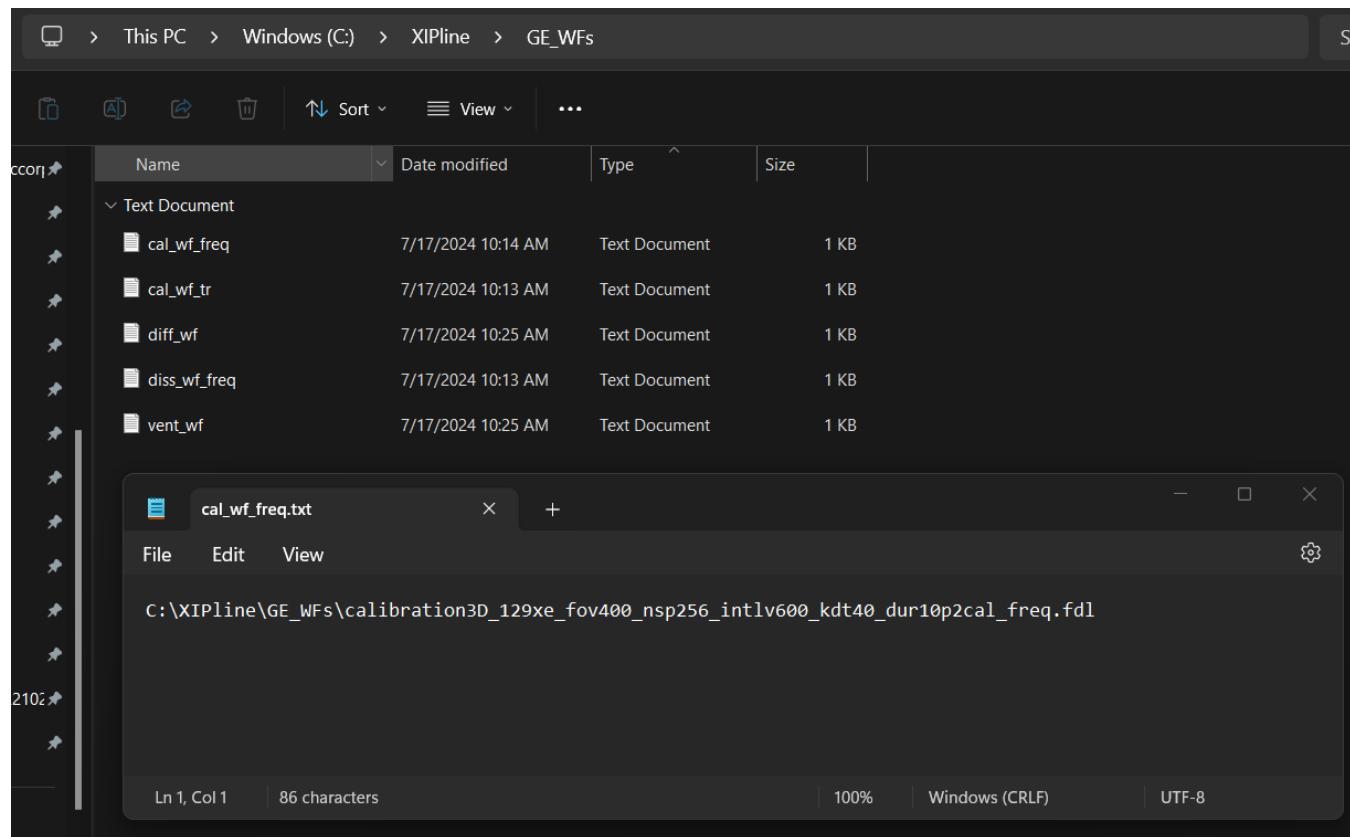
- 1-Choose "Auto" from the dropdown menu and xenon image to segment.
- 2-Select the slice orientation.
- 3-Initiate the segmentation process. This will take a few seconds. Mask will be automatically saved in the local folder and in MATLAB workspace for the subsequent analysis steps.
- 4- If the mask 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

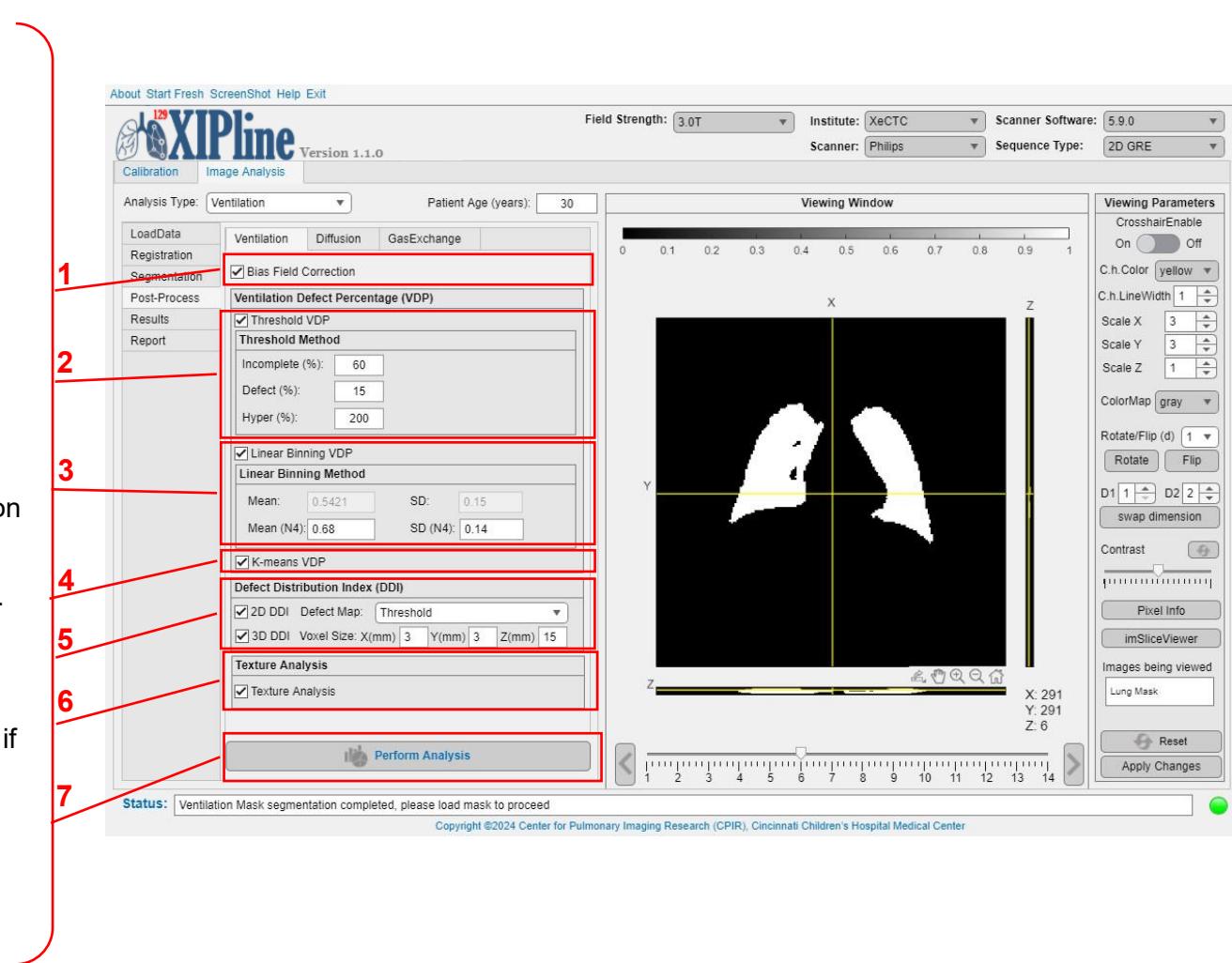
For GE data, the path to the waveform files needs to be added to text files in the XIPlane folder.

- 1- Create a folder with the name “GE_WFs”.
- 2- Create text files with the following names: cal_wf_freq, cal_wf_tr, vent_wf, diff_wf, diss_wf_freq
- 3- Add the path to each WF file in each file



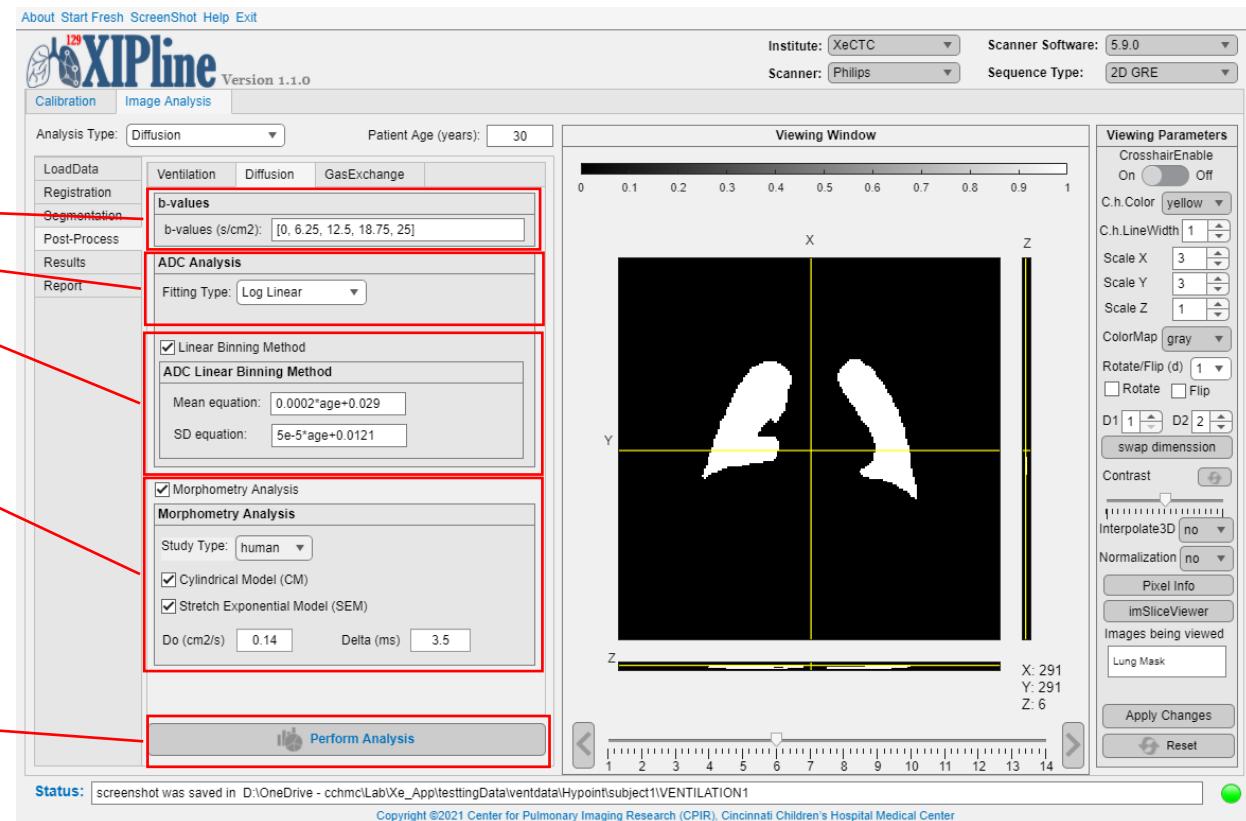
Post-Processing: Ventilation

- 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-check k-means if desired.
- 5-select 2D, 3D DDI, if desired (recommended)
- 6-Select "Texture Analysis" if desired.
- 7-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.

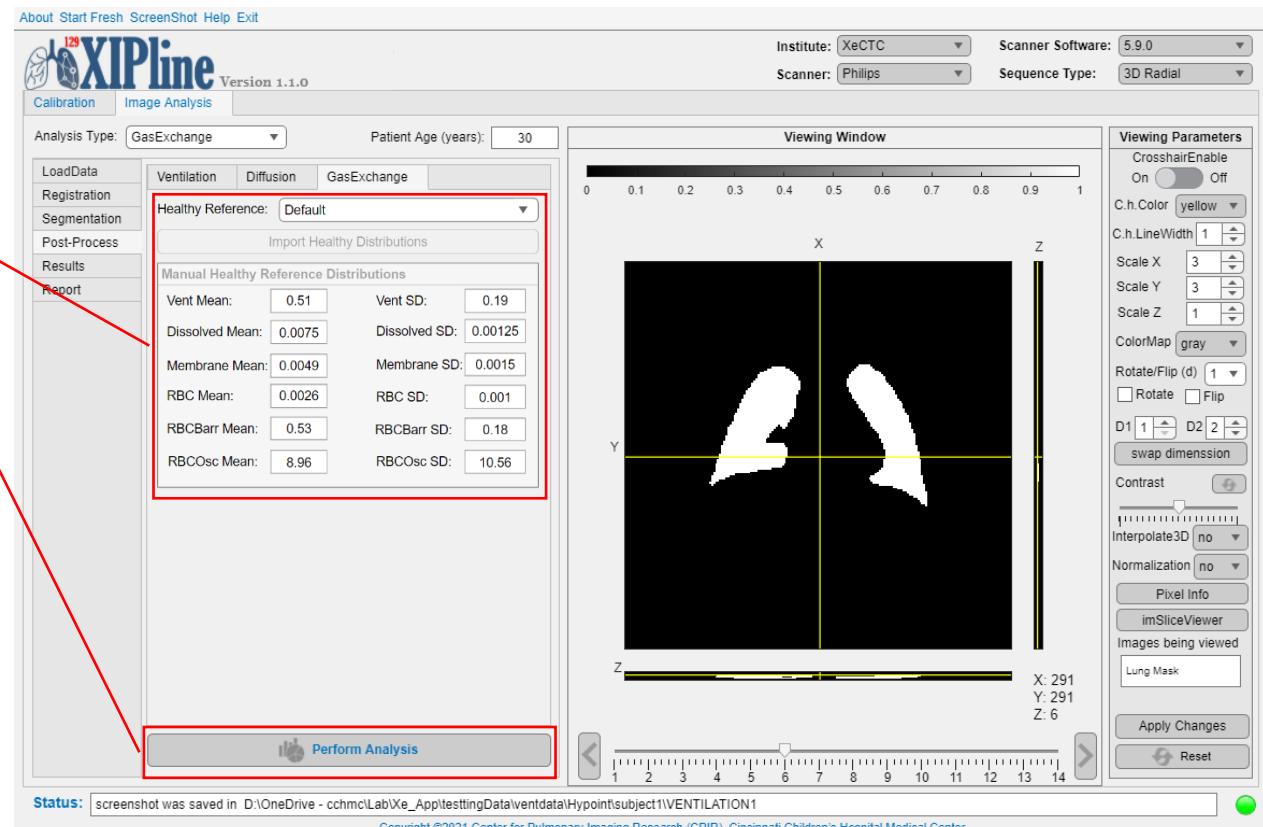


Post-Processing: Gas Exchange

1- Three options in the dropdown menu for selecting the healthy reference distributions: default, import, and manual. Default will select the healthy distributions based on gas exchange data from Cincinnati's Children's Hospital Center. The user can also import a healthy distribution file in (.mat) format; otherwise, manual values are provided, and users have the option to modify these values as needed.

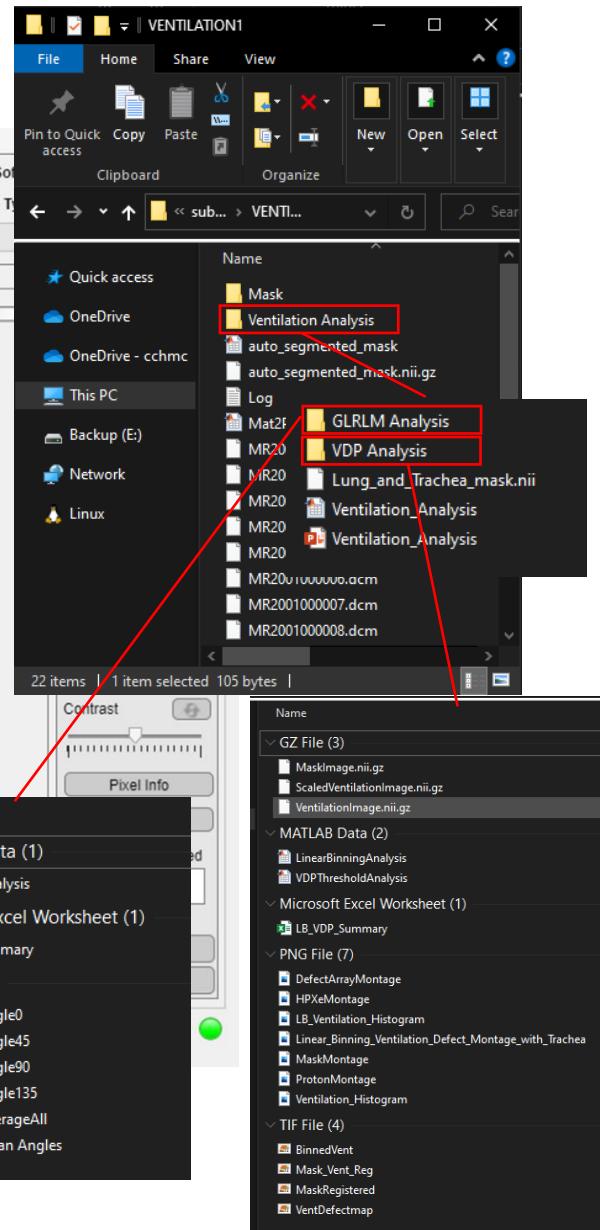
2-Initiate the analysis.

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.



4.4 | Results and Outputs

Ventilation



Diffusion

About Start Fresh ScreenShot Help Exit



Version 1.1.0

Calibration Image Analysis

Analysis Type: Diffusion

Patient Age (years): 25

Field Strength: 3.0T

Institute: CCHMC

Scanner: Philips

 LoadData
Registration
Segmentation
Post-Process
Results
Report

Ventilation Diffusion GasExchange

ADC Results

 Mean ADC (cm²/s)

0.032886±0.0095862

ADC Map

ADC Histogram

ADC Linear Binning Results

LB ADC Map LB ADC Histogram

Bin1 Bin2 Bin3 Bin4 Bin5 Bin6

1.016 5.495 53.544 34.286 4.423 1.236

Low High

Morphometry Analysis
Cylindrical Model (CM) Results

CM Parameters R: External Acinar duct radius

Mean 346±70 Histogram Map

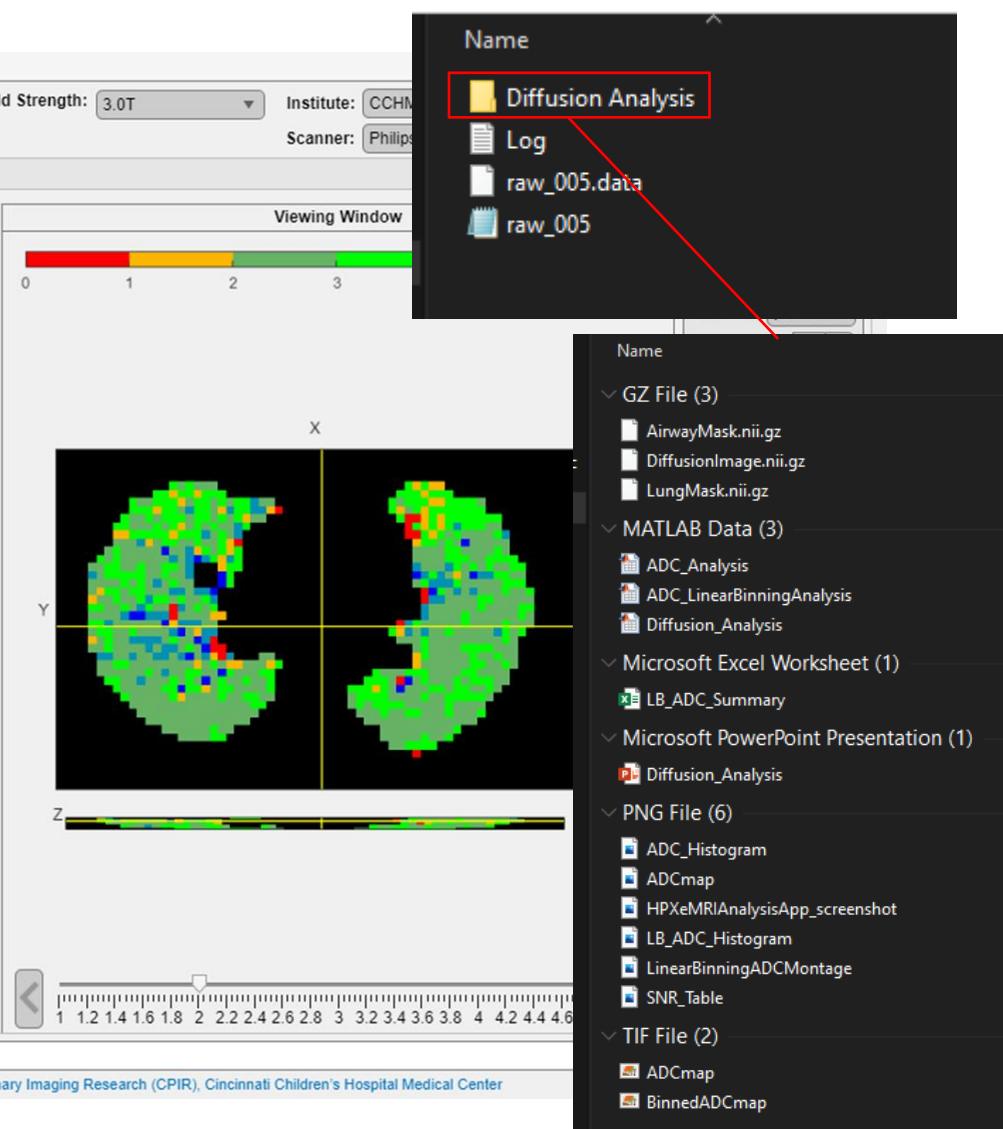
Stretch Exponential Model (SEM) Results

SEM Parameters LmD: Mean diffusive length scale

Mean 191±40 Histogram Map

Status: Diffusion analysis completed

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Gas Exchange

About Start Fresh ScreenShot Help Exit

XIPLine Version 1.1.0

Field Strength: 3.0T Institute: XeCTC Scanner Software: 5.9.0
 Scanner: Philips Sequence Type: 3D Radial

Calibration Image Analysis

Analysis Type: GasExchange Patient Age (years): 25

LoadData Registration Segmentation Post-Process Results Report

Ventilation Summary
 Mean: 0.706 ± 0.198 Histogram Map
 Low Bin1 Bin2 Bin3 Bin4 Bin5 Bin6 High
 5.72 7.65 24.39 48.32 12.23 1.69

Dissolved Summary
 Mean: 0.00783 ± 0.00111 Histogram Map
 Low Bin1 Bin2 Bin3 Bin4 Bin5 Bin6 High
 0 18.41 60.73 20.29 0.57 0

Membrane Summary
 Mean: 0.00713 ± 0.00096 Histogram Map
 Low Bin1 Bin2 Bin3 Bin4 Bin5 Bin6 Bin7 Bin8 High
 0 13.86 65.24 20.76 0.15 0 0 0

RBC Summary
 Mean: 0.00298 ± 0.00078 Histogram Map
 Low Bin1 Bin2 Bin3 Bin4 Bin5 Bin6 High
 0.05 18.36 47.92 30.55 3.13 0

RBC:Membrane Summary
 Mean: 0.41677 ± 0.08227 Histogram Map
 Low Bin1 Bin2 Bin3 Bin4 Bin5 Bin6 High
 0 4.04 53.53 40.81 1.63 0

RBC Oscillation Summary
 Mean: -0.77915 ± 4.7025 Histogram Map
 Low Bin1 Bin2 Bin3 Bin4 Bin5 Bin6 Bin7 Bin8 High
 0.35 42.64 46.94 10.07 0 0 0 0

Viewing Window
 0 1 2 3 4 5 6

Viewing Parameters
 CrosshairEnable
 On

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

swap dimension Contrast

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

Status: GasExchange analysis completed

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4.6 | Patient Report

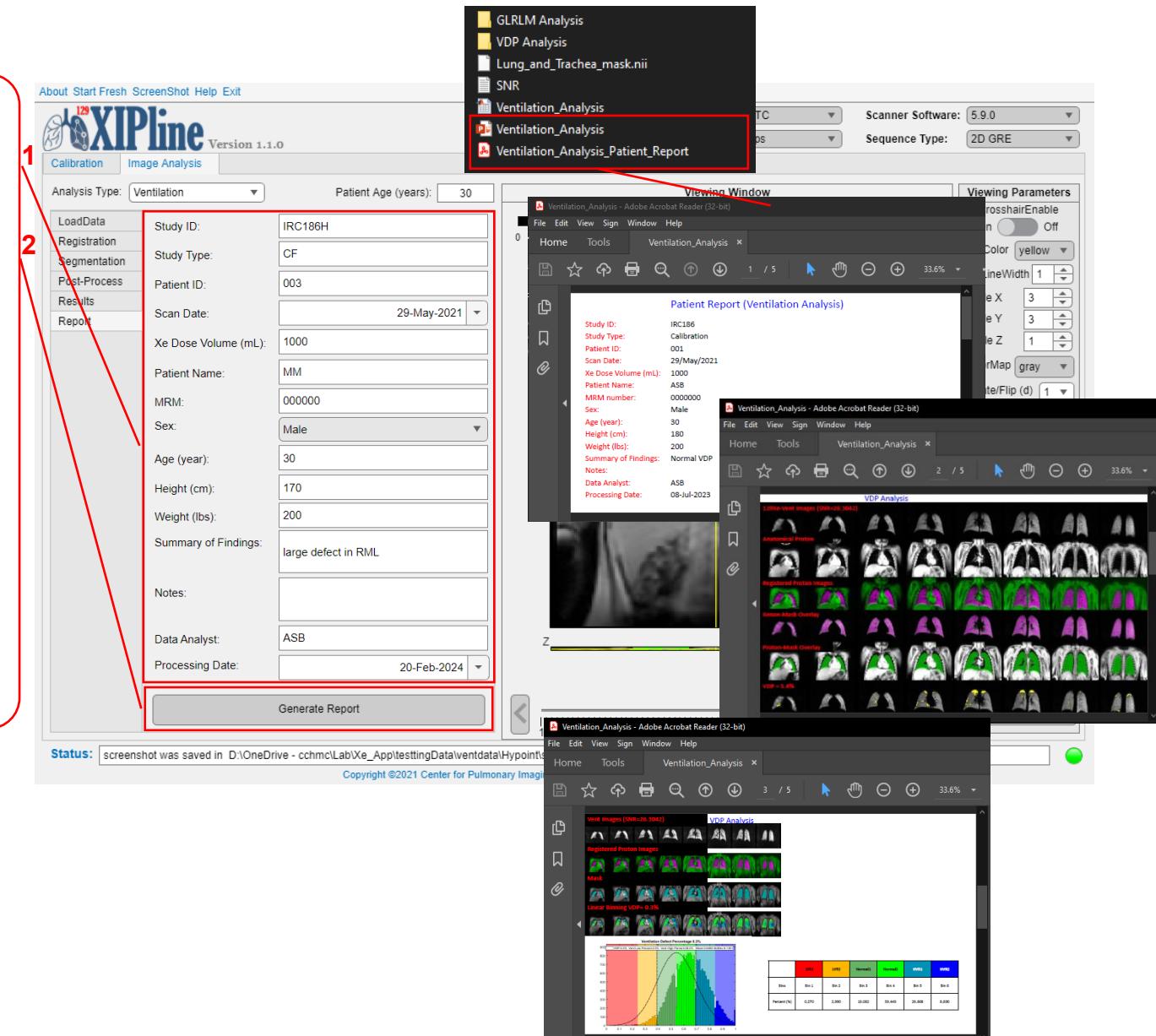
Patient Report

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.

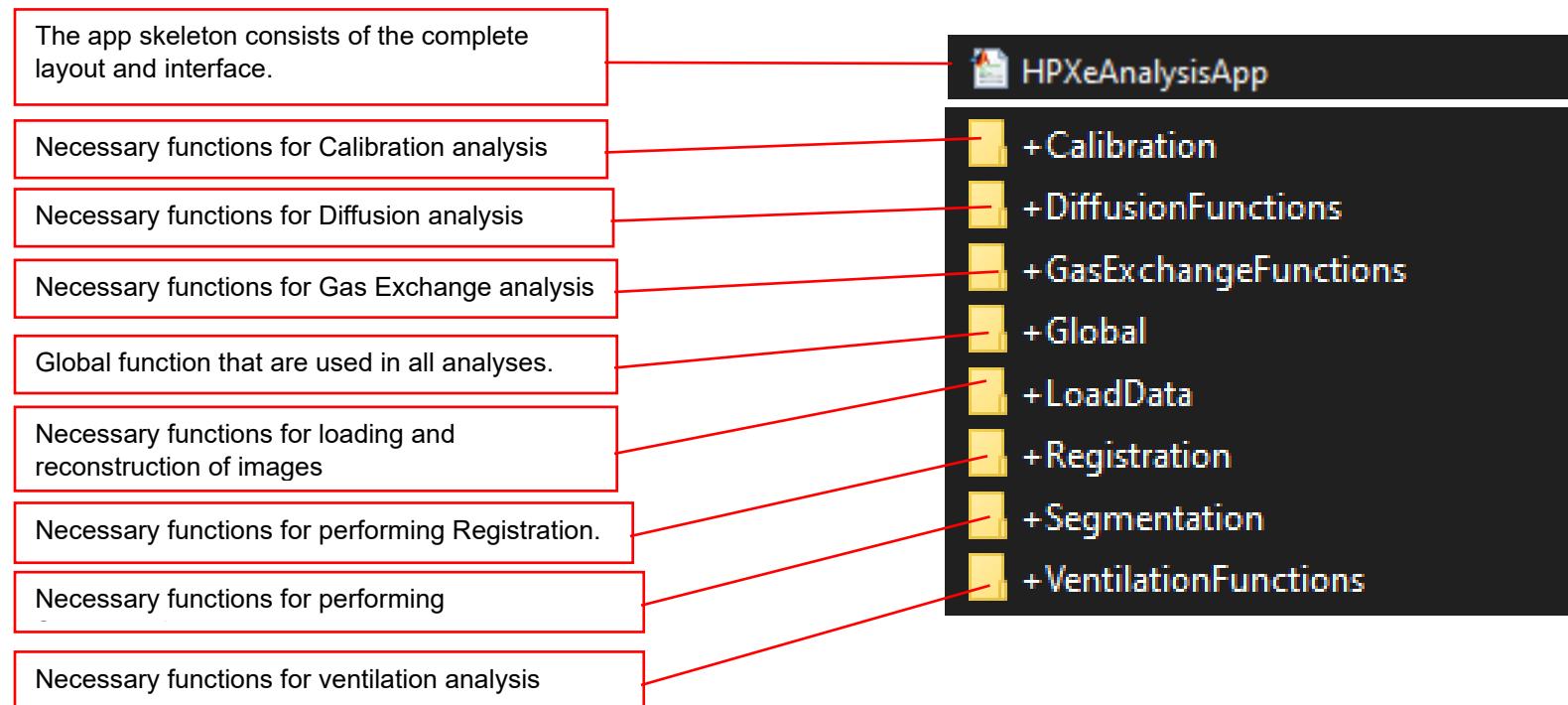


4.6 | Viewing Window



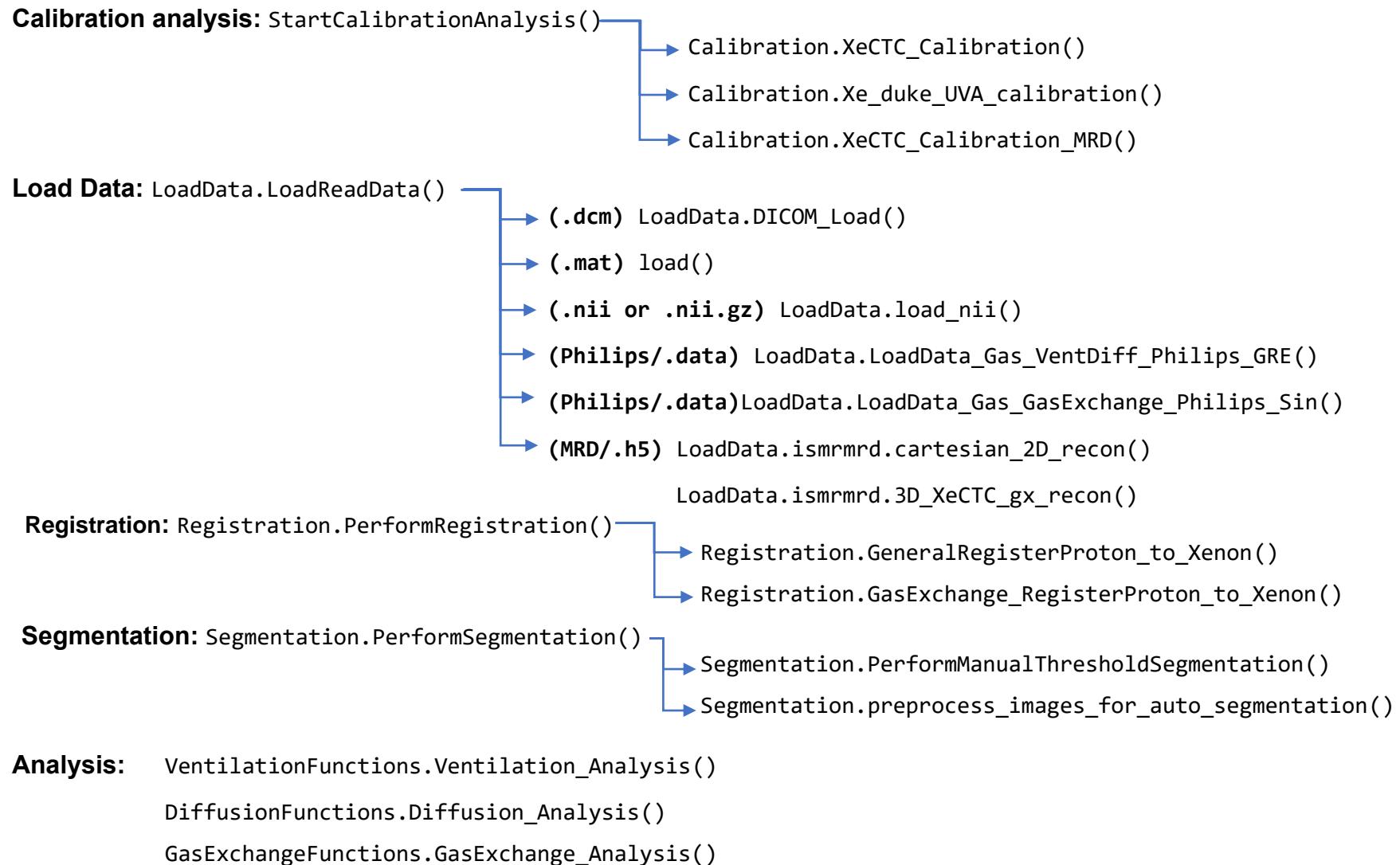
5 | Code Structure

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
```

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 (XIPLINE.m) 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/XIPLINE>), and our team of authors will collaborate with you to address and resolve the issue promptly.