

VMR Model Upload Pipeline

General overview

The first step is to download the VMR_Projects onto your own local machine. This contains files and scripts that are used to process the models locally before uploading them to the server for them to be viewed online.

The dataset Google Sheets can be found here:

While it's not necessary, it's best to follow the order of sections written when uploading models and/or simulation results.

1. Fill out svprojects dataset
2. Creating SimVascular project
3. Fill out svresults dataset (ONLY IF THERE ARE RESULTS TO BE UPLOADED)
4. Organizing SimVascular Results (ONLY IF THERE ARE RESULTS TO BE UPLOADED)
5. Create image
6. Record clinical data
7. Generate PDF
8. Uploading models and/or simulations to the Tetra server

A few phrases in this document will be highlighted in different colors.

A warning to look out for

Directory on the local side

Directory on the server side

Look at the LocalFileStructure.pdf and ServerFileStructure.pdf for detailed information on how the directories on the local side and on the server side are organized.

Fill out svprojects dataset

Necessary programs

- None

Necessary scripts/files

- dataset Google Sheets (specifically the dataset - svprojects tab)
- Information about the model to fill out the spreadsheet

Access the dataset Google Sheets here:

<https://docs.google.com/spreadsheets/d/1bacrtBCv49oEgHzC-uGS2iN-7NygEnquKo6EKo74pC0/edit?usp=sharing>

Save the copy in your own google drive by selecting **File** and **Make a Copy** and make future changes from your own local version.

	C	D	E	F	G	H	I	J
	Image Number	Sex	Age	Species	Ethnicity	Animal	Anatomy	Disease
1	0008	Male	6.00	Human	-	-	Aorta	Healthy
2	0009	Male	11.00	Human	-	-	Aorta	Healthy
3	0010	Female	11.00	Human	-	-	Aorta	Healthy
4	0011	Female	23.00	Human	-	-	Aorta	Healthy
5	0012	Male	26.00	Human	-	-	Aorta	Healthy
6	0013	Male	13.00	Human	-	-	Aorta	Coarctat
7	0014	Male	5.00	Human	-	-	Aorta	Coarctat
8	0015	Male	11.00	Human	-	-	Aorta	Coarctat

Fill out the dataset for the model for each of the columns. Capitalization and punctuation are important here, as the values in the columns will directly show on the VMR. Make sure when manually entering data that the values are identical (without misspelling and standardized throughout). For entered values that are displayed in the VMR filter bar (specified in *globalVar.js* in the function *getFilterTitles()*), they must be compatible with the ID attribute in HTML (i.e. don't use commas).

When adding a new row for a new model, always append the new model's row at the end of the dataset (add to the bottom of the dataset) to preserve the order of the models. The link for sharing models depends on this order.

A description of each column in the dataset is given below:

Category	Description	Entry Method
Name	The name of the model under the VMR naming convention. This is how it will show up on the website. See VMR Model Naming Convention for more details.	Will automatically generate if everything else is filled out.
Legacy Name	The name of the model that was used during the study/paper/model generation. If there is no legacy name enter “-”.	Manually type
Image Number	The 4-digit code corresponds to each unique medical image (.vti file) added to the repository. The image number will increment by 1 for each	If non-unique image number, then need to manually type it,

	<p>new model.</p> <p>If the model was made from a medical image already existing on the VMR then enter the same image number of the reused medical image.</p>	or else will automatically generate value through COUNTUNIQUE() - https://support.google.com/docs/answer/3093405?hl=en
Sex	The sex of the patient. Select between " Male ", and " Female ". Use “-” for models where the sex is not reported	Selection bubble
Age	The age of the patient in years rounded to two decimal places. If the age is not reported, then enter “-”.	Manually type
Species	The species of the patient. Select between " Human " or " Animal ".	Selection bubble
Ethnicity	The ethnicity of the patient (ex. Hispanic , Caucasian). If the ethnicity is not reported, or if the patient is not human then enter “-”.	Manually type
Animal	If the patient is an animal, then enter the specific animal (ex. Rabbit , Mouse). If the patient is human, then enter “-”.	Manually type
Anatomy	The anatomy of the model. Select between Aorta , Abdominal Aorta , Cerebral , Coronary , Pulmonary , Pulmonary Fontan , Pulmonary Glenn . If there is a new anatomy to be added see the <i>Adding new anatomies/disease/procedures</i> section.	Selection bubble
Disease	The disease of the model. Select between Abdominal Aortic Aneurysm , Aortoiliac Occlusive Disease , Alagille Syndrome , Aortic Dissection , Coronary Artery Disease , Coarctation of Aorta , Hypoplastic Left Heart Syndrome , Kawasaki Disease , Marfan Syndrome , Pulmonary Arterial Hypertension , Pulmonary Atresia , Single Ventricle Defect , Saphenous Vein Graft Disease , Tricuspid Atresia , Tetralogy of Fallot , Williams Syndrome . If there is no disease, then select Healthy . If there is a new disease to be added see the <i>Adding new anatomies/disease/procedures</i> section.	Selection bubble
Procedure	The surgical procedure the model has gone	Manually type

	<p>through (ex. Aortic Reconstruction, Coronary Artery Bypass Graft). If the patient did not go through a procedure then enter “None”. If a patient has gone through multiple procedures, list all the procedures and separate them using an underscore “_”.</p>	
Images	A flag to show if the SimVascular project folder contains medical images (.vti files) in the image sub-folder. Enter 1 if there are images, and 0 if there aren't images.	Manually type
Paths	A flag to show if the SimVascular project folder contains path files (.pth files) in the path sub-folder. Enter 1 if there are paths, and 0 if there aren't paths.	Manually type
Segmentations	A flag to show if the SimVascular project folder contains segmentation files (.ctgr files) in the segmentation sub-folder. Enter 1 if there are segmentations, and 0 if there aren't segmentations.	Manually type
Models	A flag to show if the SimVascular project folder contains model files in the models sub-folder. Enter 1 if there are models, and 0 if there aren't models.	Manually type
Meshes	A flag to show if the SimVascular project folder contains mesh files in the meshes sub-folder. Enter 1 if there are meshes, and 0 if there aren't meshes.	Manually type
Simulations	A flag to show if the SimVascular Project folder contains simulation files in the simulations sub-folder. Enter 1 if there are simulation files, and 0 if there aren't simulation files. These simulation files are files that are required to set up a CFD simulation (boundary conditions etc). Once a simulation is run, the actual results are stored separately as <i>simulation results</i> .	Manually type
Notes	<p>Details about the model that will be displayed on VMR. Add “\n” within the string of text to add newline breaks in the website display. If there are papers associated with a model, make sure to add the line:</p> <pre>\nSee \$url("http://www.doi.org/10.1007/s10237-018-0111 4-0", "paper")</pre>	Manually Type

	<p>Note: make sure to follow this exact format. For example, writing “url("path," "label”) with an extra space between (and “ will not render correctly.</p> <p>Change the highlighted URL of the DOI to the appropriate URL for the paper associated with the model.</p>	
DOI	The DOI (digital object identifier) of the paper(s) that reference the model. If there are multiple papers, separate each DOI with a comma. If there are no papers, then enter “-”.	Manually Type
Citation	The citation for the paper(s) referencing the model. If there are multiple citations, separate them with a newline (shift + enter on Google Sheets). See model 0102_H_PULM_H for a reference.	Manually Type
Image Manufacturer	The image manufacturer for the medical image (ex. SIEMENS, GE MEDICAL SYSTEMS). If the image manufacturer is unknown, enter “-”.	Manually Type
Image Type	The file type for the image (ex. vti).	Manually Type
Image Source	The institution where the images originated from, usually a hospital or university. If the image source is unknown, enter “-”.	Manually Type
Image Modality	The modality of the image (ex. MR or CT scan). If the image modality is unknown, enter “-”. If an image has multiple potential modalities, list all the modalities and separate them using an underscore “_”.	Manually Type
Results	A flag to show if there are simulation results for a model. Enter 1 if there are simulation results, and 0 if there aren't simulation results. These simulation results are the files with pressure values, velocity values, etc. generated once a CFD simulation is run. This is different from the files that are required to set up a CFD simulation (boundary conditions etc) which are referred to as simulation files.	Manually Type
Date Added	The date the model is officially added to the VMR. Format dd MON yyyy (ex. 21 JUL 2023).	Manually Type
Order Uploaded	An integer count representing the order the model	Manually Type

	was uploaded. This is mostly just useful if you have sorted the csv based on a different column (such as alphabetical ordering by name) and want to revert back to the original order.	
Model Creator	The creator of the SimVascular model. Write their first and last name, and keep names consistent throughout the dataset, considering if the model creator has already been mentioned in other models. If the model creator is unknown, enter “-”.	Manually Type

Creating SimVascular project

Necessary programs

- SimVascular

Necessary scripts/files

- Image (.vti file)
- VMR License File

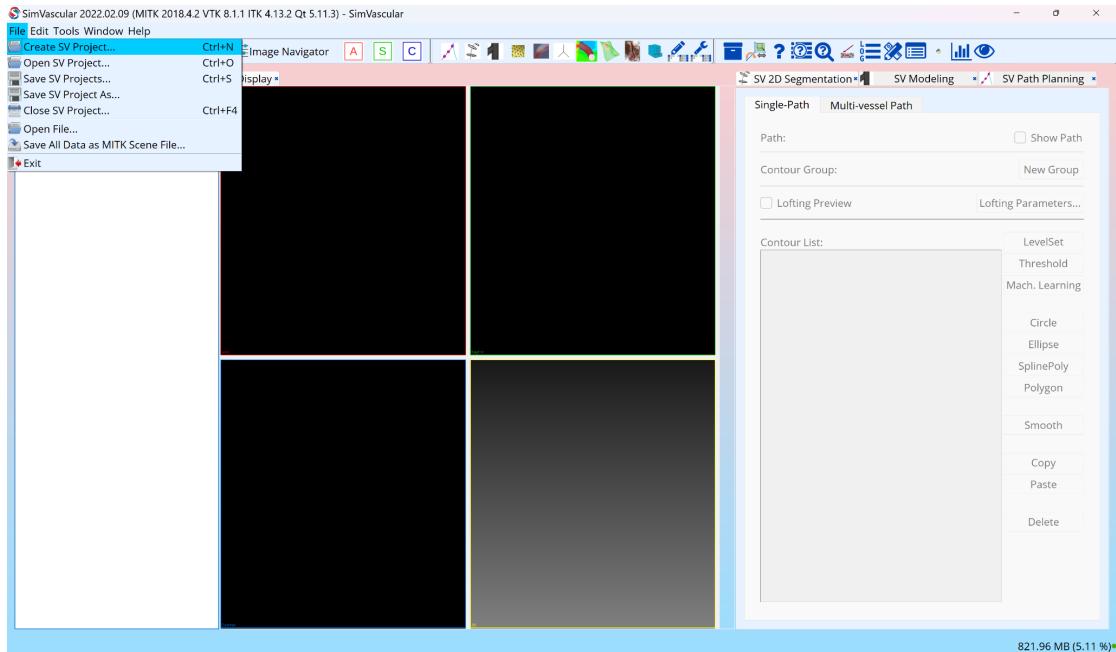
Optional scripts/files if available

- Path files (.pth)
- Segmentation files (.ctgr)
- Model files
- Mesh files
- Simulations files

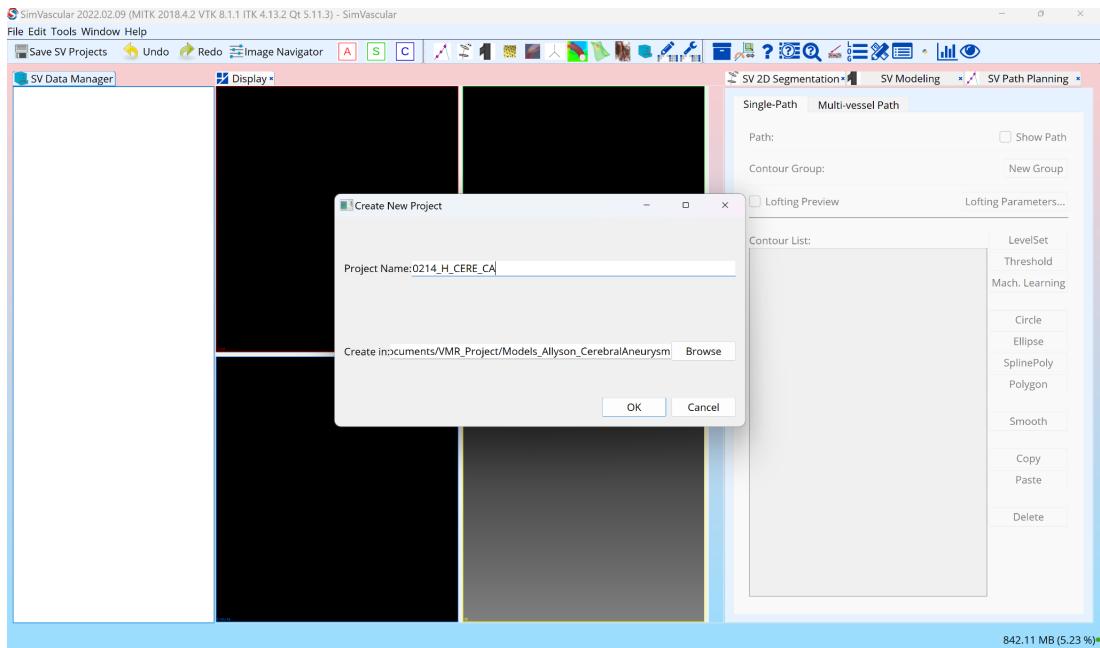
Sometimes, the data isn't given as a SimVascular project folder, or maybe it is a SimVascular project folder but from an outdated version of SimVascular. In these cases, a new SimVascular project is created with the proper name so that the file structure is automatically generated. **This documentation is based on the May 2023 version of SimVascular. All the models on the VMR have the SimVascular Project file structure created from that version.**

Name	Date modified	Type	Size
Images	6/6/2023 4:12 PM	File folder	
Meshes	3/30/2023 6:41 PM	File folder	
Models	6/6/2023 4:12 PM	File folder	
Paths	3/30/2023 6:41 PM	File folder	
ROMSimulations	3/30/2023 6:41 PM	File folder	
Segmentations	3/30/2023 6:41 PM	File folder	
Simulations	3/30/2023 6:41 PM	File folder	
svFSI	3/30/2023 6:41 PM	File folder	
simvascular	6/6/2023 4:12 PM	PROJ File	1 KB

1. Open up SimVascular and click File and Create SV Project



2. Name the project based on the VMR naming convention and save it in VMR_Projects



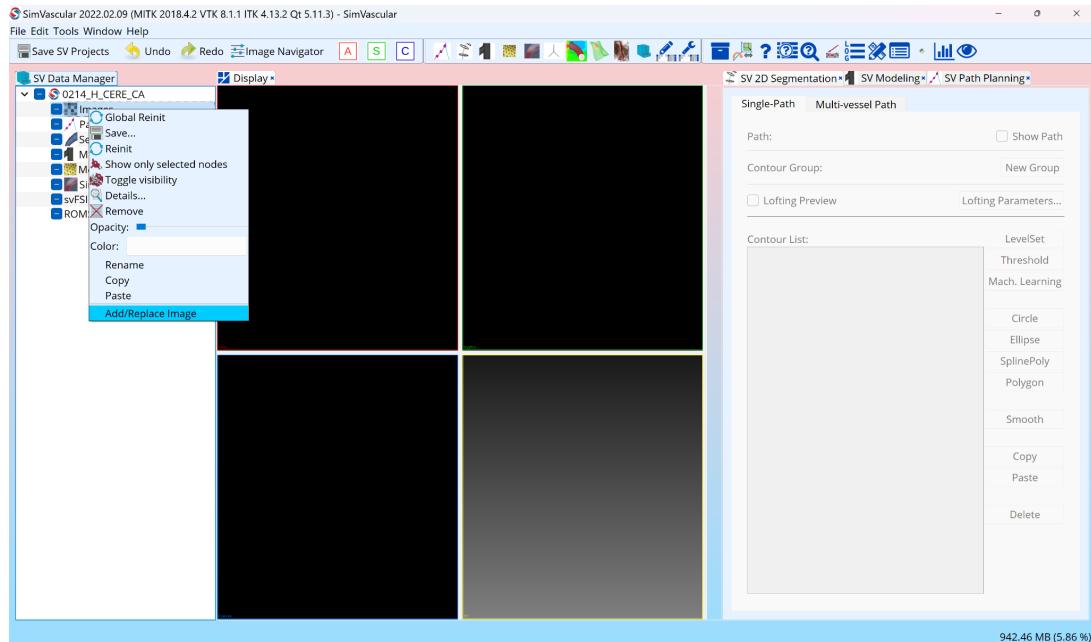
I like to organize the projects in a folder describing the creator and disease like **Models_Allison_CerebralAneurysm**, then within the folder have three sub-folders, **Raw Models** (all the original files that I was given), **SV Results** (files for simulation results, see *Organizing SimVascular results* section), and **Treated Models** (the actual SimVascular projects). This is all personal preference and just how I organized things, feel free to do what works best for you.

<a>Home	Name	Date modified	Type
> <a>Brian - Personal			
<a>Desktop	<a>Raw Models	7/18/2023 2:08 PM	File folder
<a>Downloads	<a>SV Results	7/21/2023 4:35 PM	File folder
<a>Documents	<a>Treated Models	7/24/2023 5:32 PM	File folder

<a>Home	Name	Date modified	Type
> <a>Brian - Personal			
<a>Desktop	<a>0199_H_CERE_CA	7/21/2023 3:26 PM	File folder
<a>Downloads	<a>0200_H_CERE_CA	7/21/2023 3:26 PM	File folder
	<a>0201_H_CERE_CA	7/21/2023 3:26 PM	File folder
	<a>0202_H_CERE_CA	7/21/2023 3:26 PM	File folder

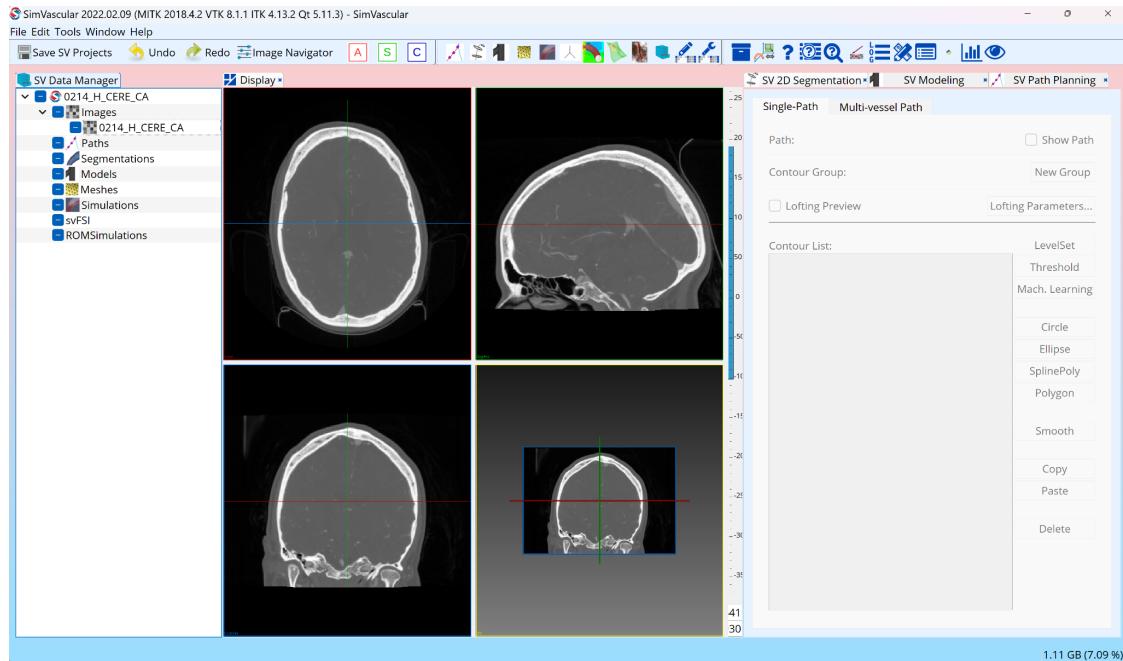
Within **Treated Models** are all the newly created SimVascular projects.

- Once the SimVascular project is created, the first thing to do is to add the medical image. Right-click on **Images** and selected the **Add/Replace Image** option.

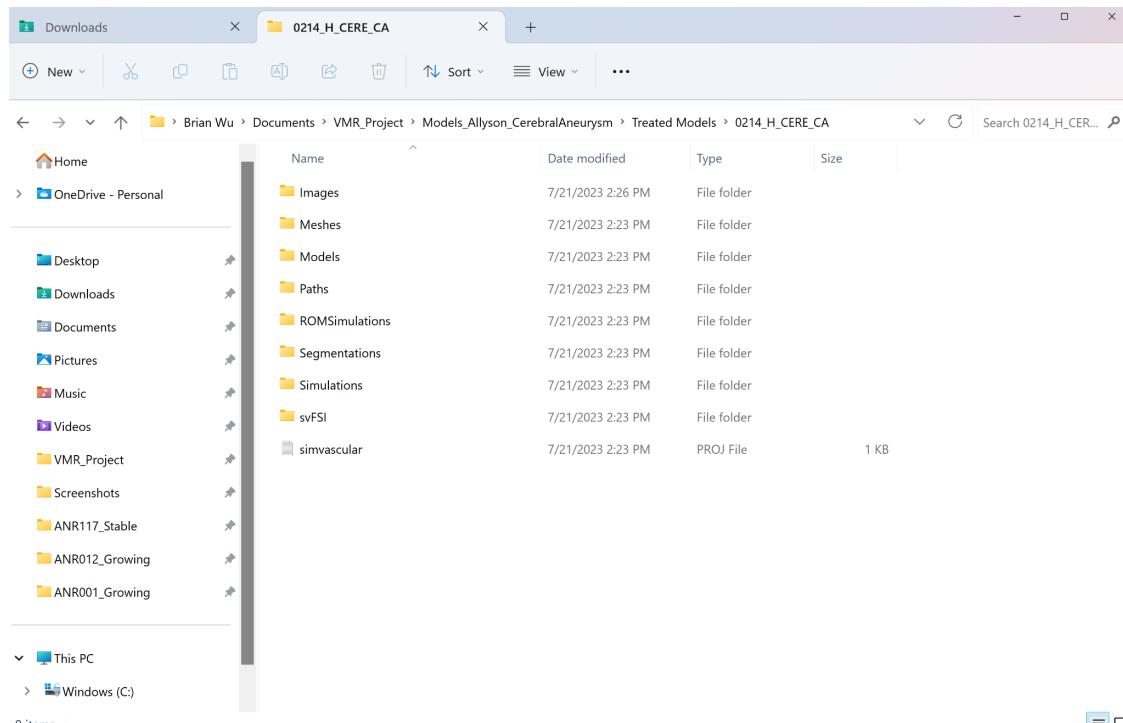


- Select the medical image file (.vti) associated with the model. SimVascular will then ask whether to save the image in the project as a .vti file. Select **Yes**.
- SimVascular will ask whether to scale the image. Select **No**.
- SimVascular will ask to name the image and give the image the same name as the project (ex. **0214_H_CERE_CA**).

7. The SimVascular page will look like this.



When accessing the folder of the SimVascular project through file explorer, you will see the following structure: **folders for Images, Meshes, Models, Paths, ROMSimulations, Segmentations, Simulations, svFSI, and a simvascular project file**.



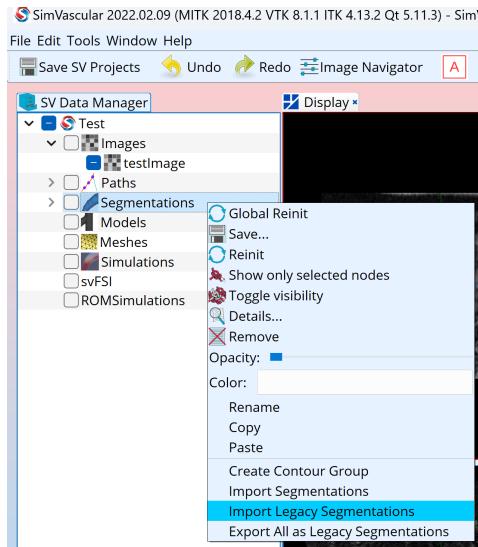
Currently, all the folders should be empty except for the images folder. The next step will be to copy any of the extra files you have into their respective folders that have been generated. (ex. **.pth files** into the **Paths folder**, **model files** into the **Models folder**).

Reload the SimVascular project and check to see that the copied files have been loaded (i.e. You should see paths being loaded if you had copied path files).

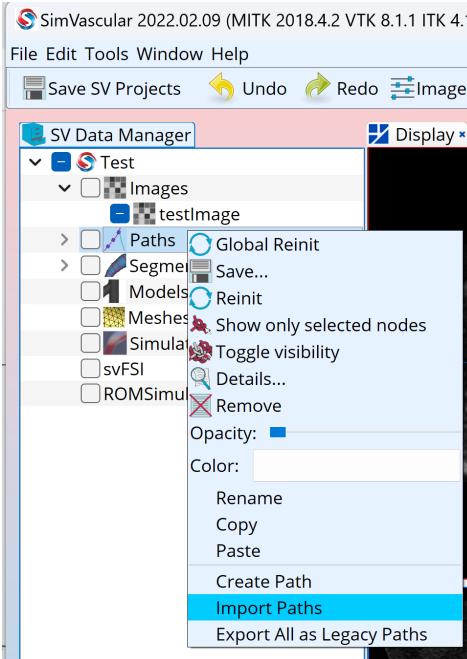
8. If you're having trouble loading in the segmentations by just copying and pasting, it could be that they are in a legacy format from an older version of SimVascular. This is the case if the Segmentations folder doesn't have .ctgr files and instead contains a TCL File called "**group_contents**" and various general files.

Name	Date modified	Type	Size
group_contents	7/26/2023 4:16 PM	TCL File	4 KB
LPA	7/26/2023 4:16 PM	File	69 KB
LPA1	7/26/2023 4:16 PM	File	12 KB
LPA2	7/26/2023 4:16 PM	File	14 KB

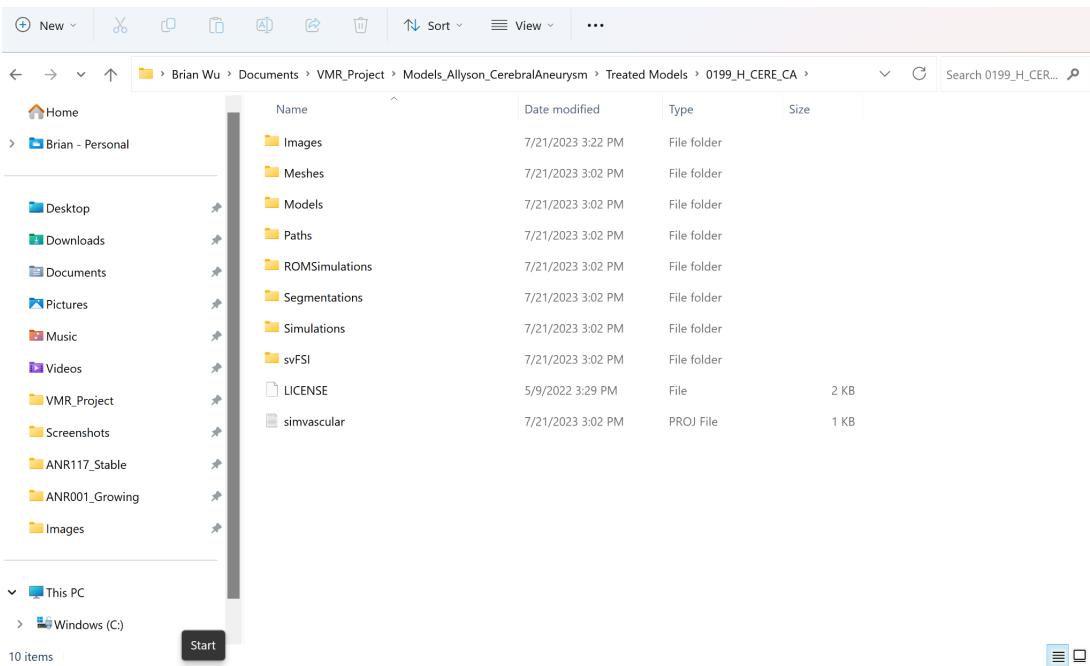
To remedy this, right-click on **Segmentations** in SimVascular and select **Import Legacy Segmentations** and navigate to where the legacy segmentation files are located.



Similarly, if you're having trouble loading the copied path files, try right-clicking on **Paths** and then selecting **Import Paths**, and then navigating to where the path files are located.



9. The final step is to copy the SimVascular **Licence** into the project folder.



Fill out svresults dataset

This step is only necessary if the models you are uploading also have simulation results available. If the model you are uploading does not have any results skip to the Create image section.

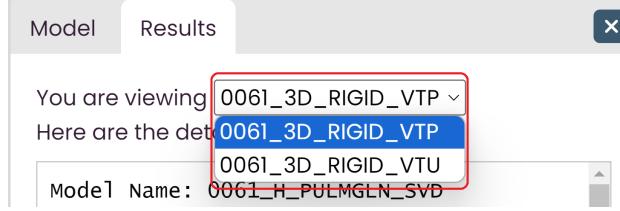
Necessary programs

- None

Necessary scripts/files

- dataset Google Sheets (specifically the dataset - svresults tab)
- Information about the model's simulation results to fill out the spreadsheet

Fill out the dataset for the model for each of the columns. A description of each column is given below:

Category	Description	Entry Method
Model Name	The name of the model that the simulation results are for.	Selection bubble
Full Simulation File Name	The full file name, which corresponds to the name of the file when users download that result.	Automatically generated
Model Image Number	The 4-digit number that represents the model image	Automatically generated
Short Simulation File Name	Shortened version of the full file name. When appended to the model image number, you get the shortened name that users see in the dropdown menu they use to toggle between different simulation results in the VMR. 	Automatically generated
Legacy Simulation File Name	The old name for the simulation results files. If there is no legacy name enter “-”.	Manually type
Simulation Fidelity	Describes whether the simulation results are 0D , 1D , or 3D models	Selection bubble
Simulation Method	Describes whether the simulation results were calculated with a Rigid Wall or with a flexible wall and solved for an FSI (Fluid Structure Interaction) simulation.	Selection bubble
Simulation Condition	Describes any context of the boundary conditions used for simulations, for example, were the simulations run at rest , exercise , or hyperemic states. If not specified enter “-”.	Selection bubble
Results Type	Describes whether the simulation results have values over multiple time points (Time-Resolved) or if there is one averaged value across all the time points (Average-Valued).	Selection bubble

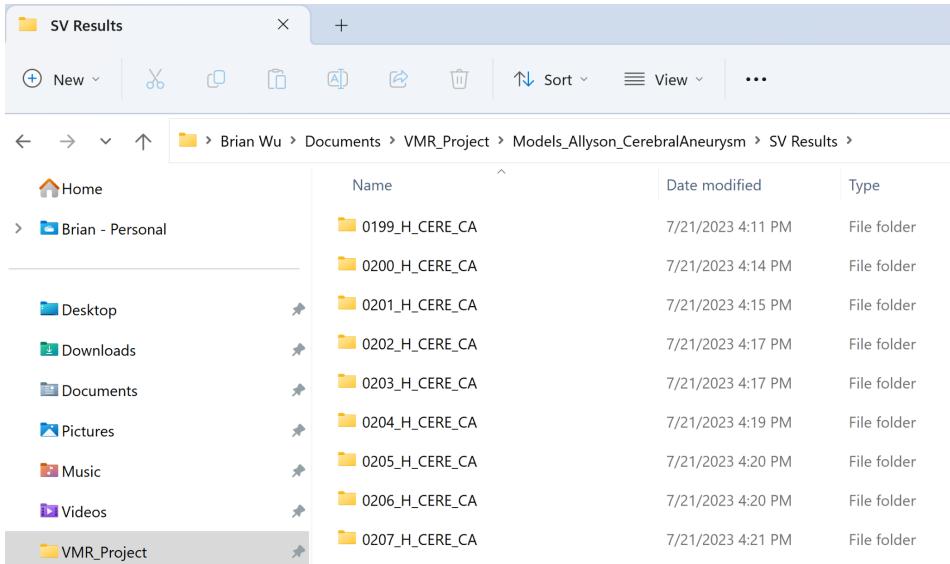
Simulation Creator	The name of the creator of the simulation. Write their first and last name, and keep names consistent throughout the dataset, considering if the model creator has already been mentioned in other models. If unknown, enter “-”.	Selection bubble
Notes	<p>Details about the simulation results that will be displayed on VMR. Add “\n” within the string of text for adding newline breaks in the website display. If there are papers associated with a model, make sure to add the line:</p> <pre>\nSee \url("http://www.doi.org/10.1007/s10237-018-0111 4-0", "paper") for more details.</pre> <p>Change the highlighted URL of the DOI to the appropriate URL for the paper associated with the model.</p>	Manually Type

1. Download the **svresults** tab from **dataset Google Sheets** as a .csv file by selecting **File, Download, and Comma Separated Values (.csv)**
2. Rename the file from “**dataset - svresults.csv**” to “**dataset-svresults.csv**” and move it into the **vmr-dataset** directory. (Super annoying why Google Sheets includes spaces in names. For our Python scripts and website JavaScript to work, all our file names are standardized to not contain spaces... oh well what can you do.)

Organizing SimVascular results

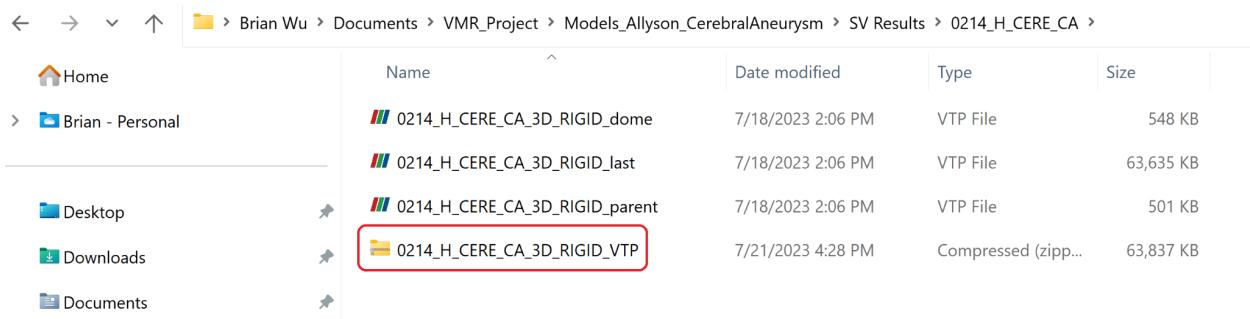
This step is only necessary if the models you are uploading also have simulation results available. If the model you are uploading does not have any results skip to the Create image section.

1. After filling out the **svprojects** and **svresults** tabs in the dataset Google Sheets create a folder with the generated model name in **VMR_Project**.



I like to organize the SV Results in a folder describing the creator like **Models_Allyson_CerebralAneurysm**, then in another sub-folder called **SV Results**, but this is just personal preference you can organize it in whatever way suits you the best.

2. Within each folder with the model name, I have the .vtp or .vtu files renamed based on the generated name from the **svresults** tab of the dataset Google Sheets, and I also zip the files and rename it to the generated name.



Another example of an SV Results folder with multiple zip files with the naming structure.

Name	Date modified	Type	Size
0139_H_CORO_KD_3D_FSI	7/28/2023 12:45 PM	VTP File	228,674 KB
0139_H_CORO_KD_3D_FSI	7/28/2023 12:48 PM	VTU File	892,756 KB
0139_H_CORO_KD_3D_FSI_VTP	7/28/2023 12:45 PM	Compressed (zipped)	228,197 KB
0139_H_CORO_KD_3D_FSI_VTU	7/28/2023 12:46 PM	Compressed (zipped)	882,444 KB
0139_H_CORO_KD_3D_RIGID	7/28/2023 12:46 PM	VTP File	104,648 KB
0139_H_CORO_KD_3D_RIGID	7/28/2023 12:48 PM	VTU File	769,935 KB
0139_H_CORO_KD_3D_RIGID_VTP	7/28/2023 12:47 PM	Compressed (zipped)	104,025 KB
0139_H_CORO_KD_3D_RIGID_VTU	7/28/2023 12:45 PM	Compressed (zipped)	759,912 KB

Create image

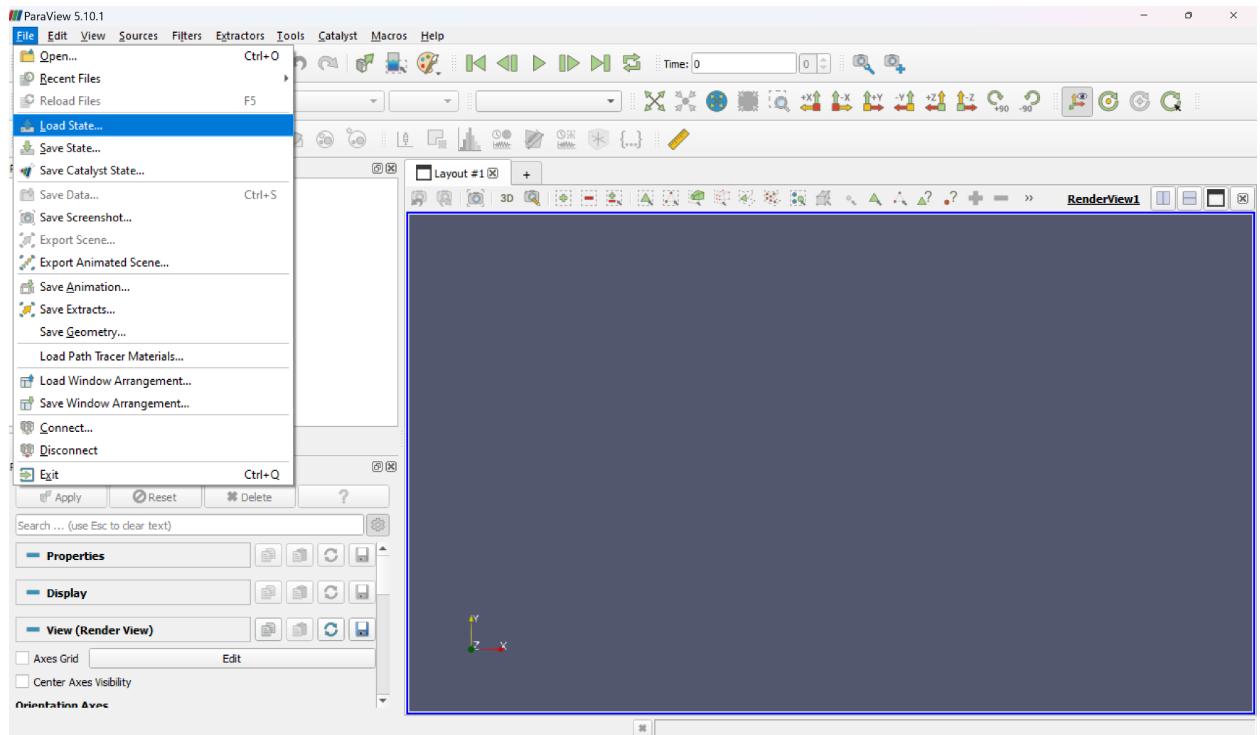
Necessary programs

- Paraview (<https://www.paraview.org/>)

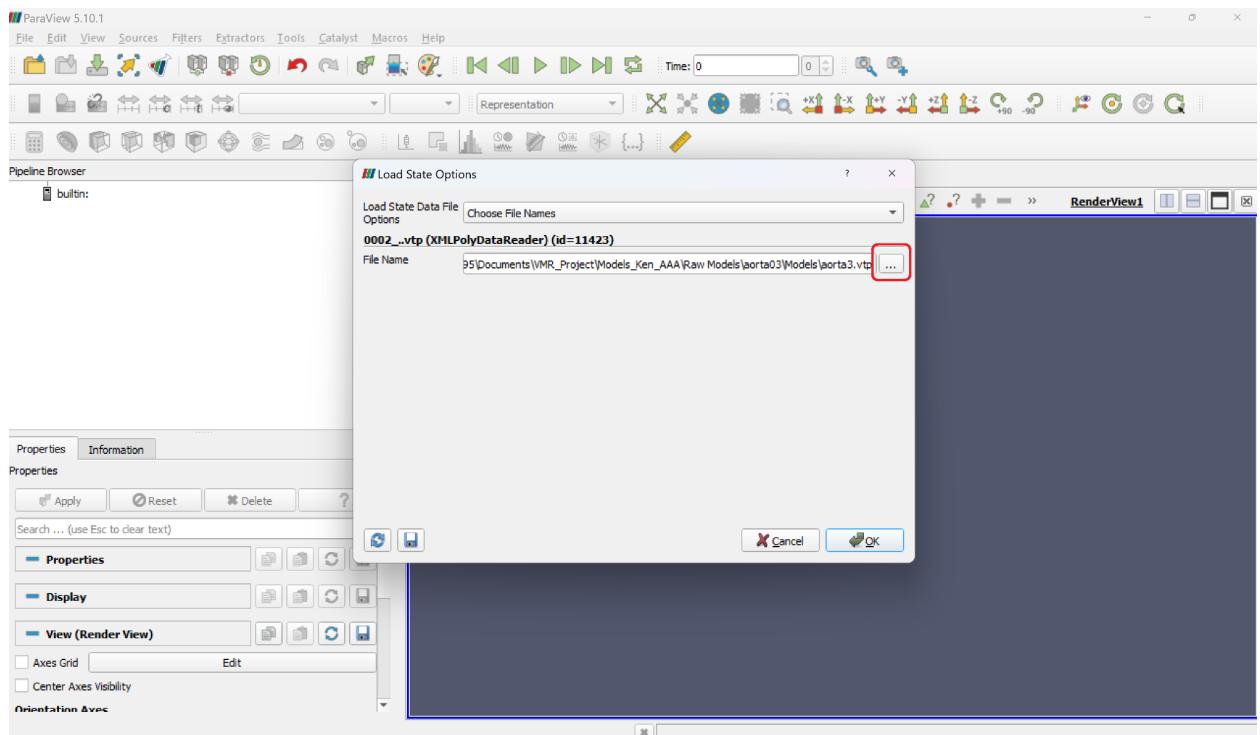
Necessary scripts/files

- model.pvsm (this file pre-loads specific visual settings when viewing in Paraview)
- Either a .vti or .vtu file of the model

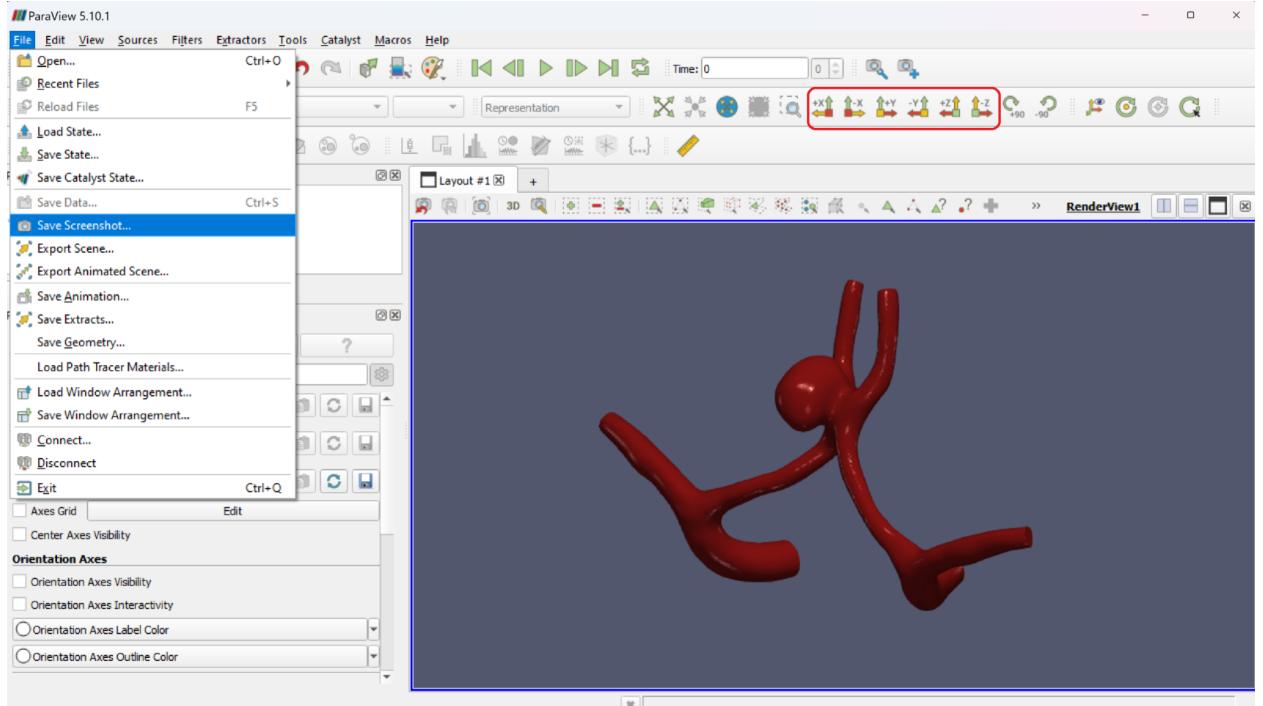
1. Open Paraview and click File then Load State



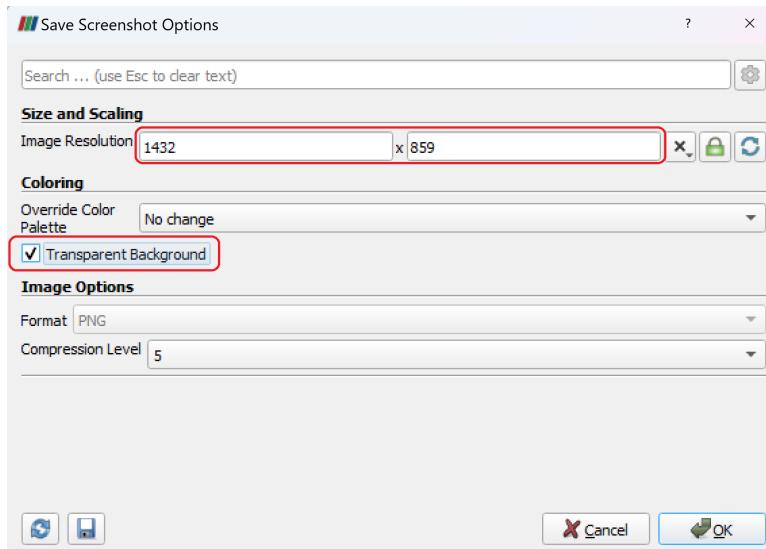
2. Locate where the **model.pvsm** file is stored and select it
3. When prompted for the Load State Options, make sure the **Choose File Names** option is selected then click the ... and navigate to the location of the .vti or .vtu file of the model and select it.



4. You will see the model with a red glossy texture. Center the image. If there is a paper associated with the model then try to recreate the orientation of the model shown in the paper by using the mouse to click and drag. The axis-aligning buttons near the upper right can help quickly center the model. Next, select **File** and then **Save Screenshot**.

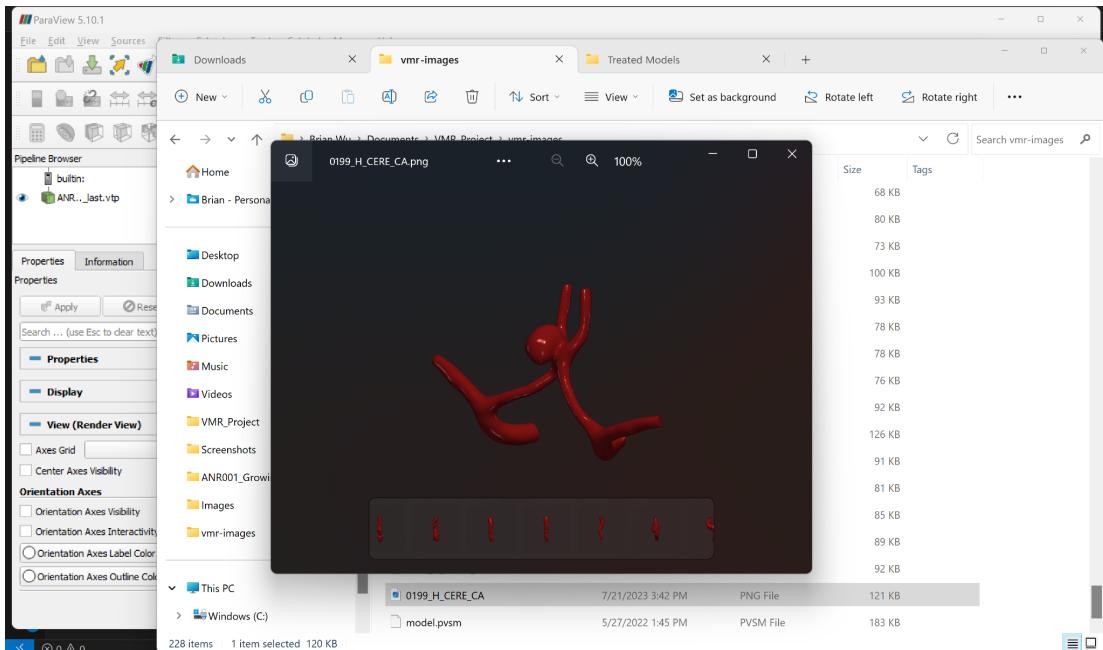


5. Save the image as a **.png file** in the **vmr-images** folder and name the image the same name as the model. When prompted for the Save Screenshot Options, set the image resolution to **1432 x 859** and make sure **Transparent Background** is selected.



6. You have now created a **.png** image for the model with the VMR texture and a transparent background. This image is used on the website and also the PDF generated

for each model (see *Generate PDF* section).



Record clinical data

Necessary programs

- Excel or any other text editor to create .csv files

Necessary scripts/files

- Information about relevant patient clinical data

- Create a .csv file with the first row as the labels and the second row as the specific patient data. The first three columns must be **name**, **sex**, and **age**. Where **name** is the name of the model, and **sex** and **age** are the sex and age of the patient. If the sex or age is not known then enter “-”. After those first three columns, the next columns can be whatever specific available patient clinical data is available for the model. Sometimes there isn't any extra available data, and if that is the case, then don't include any more columns.

	A	B	C	D	E	F	G	H	I	J	K	L	M
1	name	sex	age	Aneurysm Location	Diabetes Mellitus	Hypertension	Hyperlipidemia	Smoking	Family History of Cerebral Aneurysm				
2	0199_H_CERE_CA	Male	61	Anterior Communicating Artery	No	No	Yes	No	No				
3													

The details within this clinical data file will be read and generated into a table in the PDF containing details about the model (see *Generate PDF* section). If you want to have a

section of text to explain a portion of the table on the PDF then include a **notes** column where you can write up descriptions.

A	B	C	D	E	F	G	H	I	J	K
name	sex	age	notes	BSA (m^2)	HR (bpm)	BP (mmHg)	CO (L/min)	EF (%)	CAA Sizes (Z-scores)	
			Summary of patient data. BSA: Body surface area. HR: Heart rate. BP: Blood pressure (systolic/diastolic). CO: Cardiac output. EF: Ejection fraction. LAD: Left anterior descending artery. LCX: Left circumflex artery. RCA: Right coronary artery. LM: Left main coronary artery. CAA: Coronary artery aneurysm.							
KD1	N/A	N/A		0.95	78	106/48	3.8	51	LAD: 0.6, LCX: 1.1, RC	

Clinical Data

General Patient Data

Age (yrs)	N/A
Sex	N/A

Specific Patient Data

Summary of patient data.
BSA: Body surface area. HR: Heart rate. BP: Blood pressure (systolic/diastolic).
CO: Cardiac output. EF: Ejection fraction.
LAD: Left anterior descending artery. LCX: Left circumflex artery.
RCA: Right coronary artery. LM: Left main coronary artery.
CAA: Coronary artery aneurysm.

BSA (m ²)	0.95
HR (bpm)	78
BP (mmHg)	106/48
CO (L/min)	3.8
EF (%)	51
CAA Sizes (Z-scores)	LAD: 0.6, LCX: 1.1, RCA: -0.2

- Save the file as **ModelName_ClinicalData.csv** (ex.

0199_H_CERE_CA_ClinicalData.csv) in the **vmr-clinical_data folder**. Make sure you save the file as a .csv file, not an Excel file, or else the PDF generation script won't be able to read the file and properly generate the PDF.

Generate PDF

Necessary programs

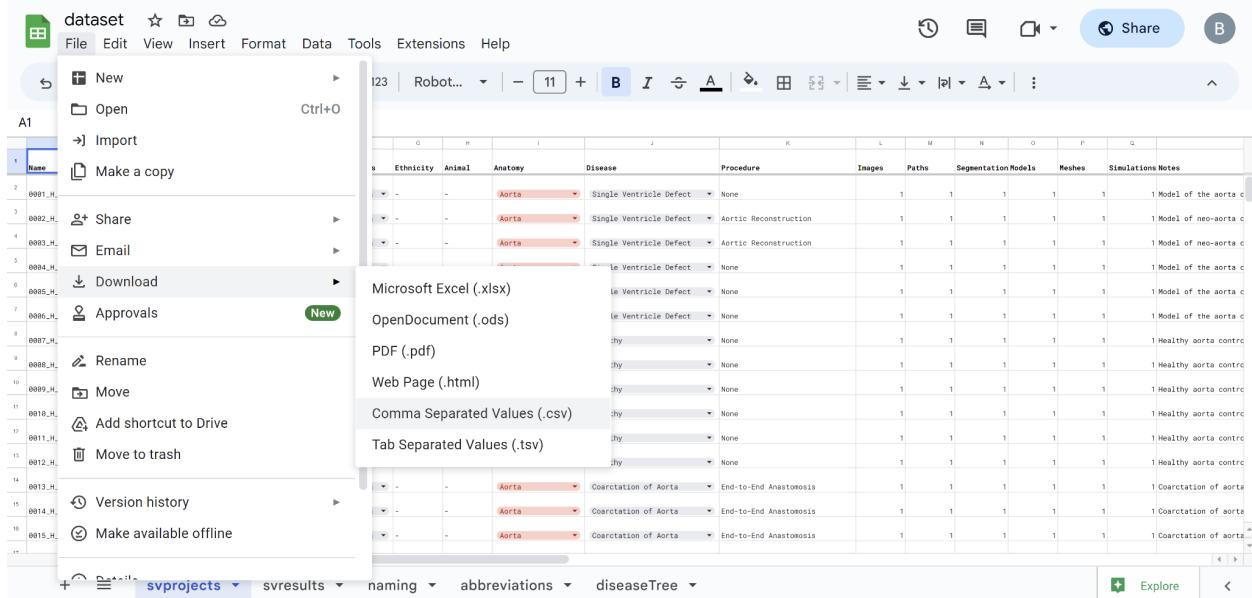
- An IDE to run Python scripts (ex. VS Code, PyCharm, etc.)
- A text editor (ex. Notepad++)

Necessary scripts/files

- generate_pdf.py
- vmr-clinical_data folder
 - model_ClinicalData.csv (all the model clinical data .csv files)
- vmr-images folder
 - model.png (all the model images)
- BackgroundAnatomy.csv
- BackgroundDisease.csv
- BackgroundProcedure.csv

- dataset-svprojects.csv (downloaded from dataset Google Sheets)

3. Download the **svprojects** tab from **dataset Google Sheets** as a .csv file by selecting **File, Download, and Comma Separated Values (.csv)**



- Rename the file from “dataset - svprojects.csv” to “dataset-svprojects.csv” and move it into the **vmr-dataset** directory. (Super annoying why Google Sheets includes spaces in names. For our Python scripts and website javascript to work all our file names are standardized to not contain spaces... oh well what can you do.)
- Open up **dataset-svprojects.csv** in a text editor like Notepad++ and scroll to the end and delete all the extra rows of commas.

The screenshot shows the 'dataset-svprojects.csv' file in Notepad++. The file content consists of numerous lines of data, primarily about cerebral aneurysms, separated by commas. At the bottom of the file, there are several blank lines, each preceded by a horizontal dotted line, which represent the extra rows of commas mentioned in the instructions.

```

404 0202_H_CERE_CA_ANR102_Stable,0202,Female,53.00,Human,-,-,Cerebral,Cerebral Aneurysm,None,1,0,0,0,0,0,Categorized as a stable aneurysm (no increase in s
405 0203_H_CERE_CA_ANR004_Growing,0203,Female,65.00,Human,-,-,Cerebral,Cerebral Aneurysm,None,1,0,0,1,1,1,Categorized as a growing aneurysm (increased in s
406 0204_H_CERE_CA_ANR117_Stable,0204,Female,65.00,Human,-,-,Cerebral,Cerebral Aneurysm,None,1,0,0,1,1,1,Categorized as a stable aneurysm (no increase in s
407 0205_H_CERE_CA_ANR005_Growing,0205,Female,71.00,Human,-,-,Cerebral,Cerebral Aneurysm,None,1,0,0,0,0,0,Categorized as a growing aneurysm (increased in s
408 0206_H_CERE_CA_ANR112_Stable,0206,Female,59.00,Human,-,-,Cerebral,Cerebral Aneurysm,None,1,0,0,0,0,0,Categorized as a stable aneurysm (no increase in s
409 0207_H_CERE_CA_ANR006_Growing,0207,Female,61.00,Human,-,-,Cerebral,Cerebral Aneurysm,None,1,0,0,1,1,1,Categorized as a growing aneurysm (increased in s
410 0208_H_CERE_CA_ANR106_Stable,0208,Female,71.00,Human,-,-,Cerebral,Cerebral Aneurysm,None,1,0,0,1,1,1,Categorized as a stable aneurysm (no increase in s
411 0209_H_CERE_CA_ANR008_Growing,0209,Female,48.00,Human,-,-,Cerebral,Cerebral Aneurysm,None,1,0,0,1,0,0,Categorized as a growing aneurysm (increased in s
412 0210_H_CERE_CA_ANR108_Stable,0210,Male,50.00,Human,-,-,Cerebral,Cerebral Aneurysm,None,1,0,0,1,1,1,Categorized as a stable aneurysm (no increase in s
413 0211_H_CERE_CA_ANR009_Growing,0211,Female,68.00,Human,-,-,Cerebral,Cerebral Aneurysm,None,1,0,0,0,0,0,Categorized as a growing aneurysm (increased in s
414 0212_H_CERE_CA_ANR109_Stable,0212,Female,75.00,Human,-,-,Cerebral,Cerebral Aneurysm,None,1,0,0,0,0,0,Categorized as a stable aneurysm (no increase in s
415 0213_H_CERE_CA_ANR011_Growing,0213,Female,74.00,Human,-,-,Cerebral,Cerebral Aneurysm,None,1,0,0,0,0,0,Categorized as a growing aneurysm (increased in s
416 0214_H_CERE_CA_ANR111_Stable,0214,Female,41.00,Human,-,-,Cerebral,Cerebral Aneurysm,None,1,0,0,0,0,0,Categorized as a stable aneurysm (no increase in s
417 0215_H_CERE_CA_ANR012_Growing,0215,Female,66.00,Human,-,-,Cerebral,Cerebral Aneurysm,None,1,0,0,1,0,0,Categorized as a growing aneurysm (increased in s
418 0216_H_CERE_CA_ANR113_Stable,0216,Female,67.00,Human,-,-,Cerebral,Cerebral Aneurysm,None,1,0,0,1,0,0,Categorized as a stable aneurysm (no increase in s
419 0217_H_CERE_CA_ANR017_Growing,0217,Female,60.00,Human,-,-,Cerebral,Cerebral Aneurysm,None,1,0,0,1,0,0,Categorized as a growing aneurysm (increased in s
420 0218_H_CERE_CA_ANR118_Stable,0218,Female,64.00,Human,-,-,Cerebral,Cerebral Aneurysm,None,1,0,0,1,0,0,Categorized as a stable aneurysm (no increase in s
421 0219_H_CERE_CA_ANR016_Growing,0219,Female,80.00,Human,-,-,Cerebral,Cerebral Aneurysm,None,1,0,0,1,0,0,Categorized as a growing aneurysm (increased in s
422 0220_H_CERE_CA_ANR114_Stable,0220,Female,60.00,Human,-,-,Cerebral,Cerebral Aneurysm,None,1,0,0,1,0,0,Categorized as a stable aneurysm (no increase in s
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```

Normal text file

length : 161,681 lines : 1,178

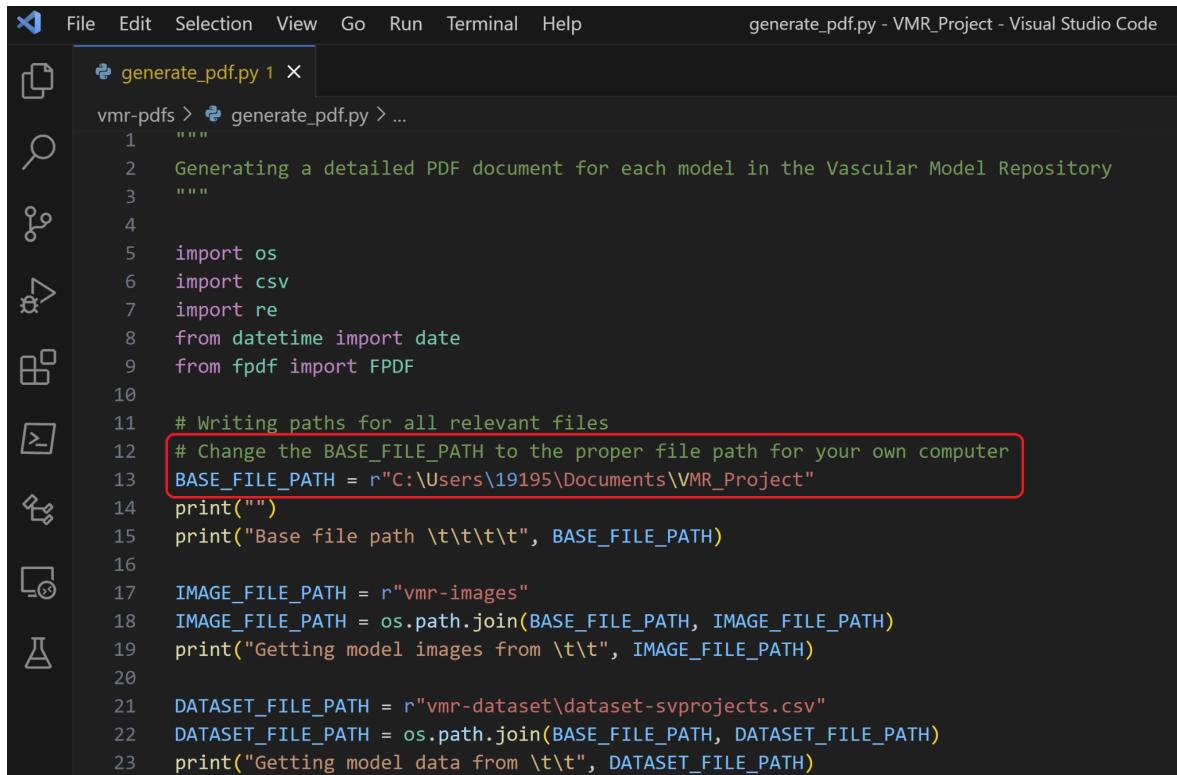
Ln : 522 Col : 29 Sel : 2,998 | 100

Windows (CR LF) UTF-8

INS

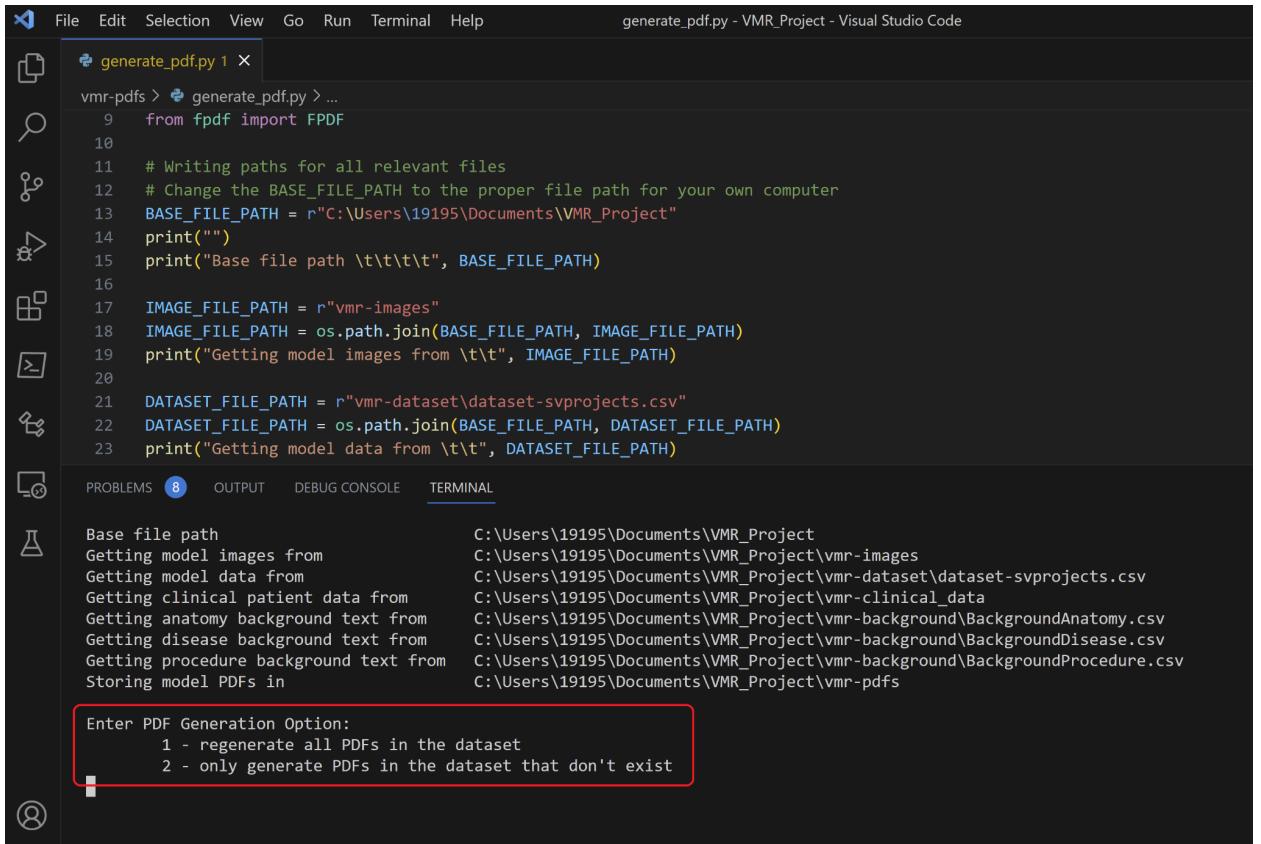
All the rows of commas are an unfortunate consequence of including selection bubbles in the dataset Google Sheets to make entering the data easier. It reads unselected data selection bubbles as empty elements.

6. Open up **generate_pdf.py** in an IDE of your choice (I'm using Visual Studio Code). Change the **BASE_FILE_PATH** to reflect the file path to the **VMR_Project** directory on your own computer.



```
File Edit Selection View Go Run Terminal Help generate_pdf.py - VMR_Project - Visual Studio Code
+ generate_pdf.py 1 ×
vmr-pdfs > + generate_pdf.py > ...
1 """
2     Generating a detailed PDF document for each model in the Vascular Model Repository
3 """
4
5 import os
6 import csv
7 import re
8 from datetime import date
9 from fpdf import FPDF
10
11 # Writing paths for all relevant files
12 # Change the BASE_FILE_PATH to the proper file path for your own computer
13 BASE_FILE_PATH = r"C:\Users\19195\Documents\VMR_Project"
14 print("")
15 print("Base file path \t\t\t", BASE_FILE_PATH)
16
17 IMAGE_FILE_PATH = r"vmr-images"
18 IMAGE_FILE_PATH = os.path.join(BASE_FILE_PATH, IMAGE_FILE_PATH)
19 print("Getting model images from \t\t", IMAGE_FILE_PATH)
20
21 DATASET_FILE_PATH = r"vmr-dataset\dataset-svprojects.csv"
22 DATASET_FILE_PATH = os.path.join(BASE_FILE_PATH, DATASET_FILE_PATH)
23 print("Getting model data from \t\t", DATASET_FILE_PATH)
```

7. Once you run **generate_pdf.py**, it will prompt you to either regenerate PDFs for all the models in the dataset or to only generate PDFs for models in the dataset that don't yet have PDFs in the **vmr-pdfs** folder.



```
File Edit Selection View Go Run Terminal Help
generate_pdf.py - VMR_Project - Visual Studio Code
generate_pdf.py 1
vmr-pdfs > generate_pdf.py > ...
  9  from fpdf import FPDF
 10
 11 # Writing paths for all relevant files
 12 # Change the BASE_FILE_PATH to the proper file path for your own computer
 13 BASE_FILE_PATH = r"C:\Users\19195\Documents\VMR_Project"
 14 print("")
 15 print("Base file path \t\t\t", BASE_FILE_PATH)
 16
 17 IMAGE_FILE_PATH = r"vmr-images"
 18 IMAGE_FILE_PATH = os.path.join(BASE_FILE_PATH, IMAGE_FILE_PATH)
 19 print("Getting model images from \t\t", IMAGE_FILE_PATH)
 20
 21 DATASET_FILE_PATH = r"vmr-dataset\dataset-svprojects.csv"
 22 DATASET_FILE_PATH = os.path.join(BASE_FILE_PATH, DATASET_FILE_PATH)
 23 print("Getting model data from \t\t", DATASET_FILE_PATH)

PROBLEMS 8 OUTPUT DEBUG CONSOLE TERMINAL

Base file path          C:\Users\19195\Documents\VMR_Project
Getting model images from C:\Users\19195\Documents\VMR_Project\vmr-images
Getting model data from  C:\Users\19195\Documents\VMR_Project\vmr-dataset\dataset-svprojects.csv
Getting clinical patient data from C:\Users\19195\Documents\VMR_Project\vmr-clinical_data
Getting anatomy background text from C:\Users\19195\Documents\VMR_Project\vmr-background\BackgroundAnatomy.csv
Getting disease background text from C:\Users\19195\Documents\VMR_Project\vmr-background\BackgroundDisease.csv
Getting procedure background text from C:\Users\19195\Documents\VMR_Project\vmr-background\BackgroundProcedure.csv
Storing model PDFs in    C:\Users\19195\Documents\VMR_Project\vmr-pdfs

Enter PDF Generation Option:
  1 - regenerate all PDFs in the dataset
  2 - only generate PDFs in the dataset that don't exist
```

If some change was made across the dataset for all the models, then regenerate all the PDFs. **Warning: regenerating all the PDFs will take a few minutes, so only choose this option if necessary.**

8. After the PDFs are generated, review each document to make sure all parts of the document have been properly generated. If there is a part that is incomplete, most likely one of the input documents wasn't properly updated or misplaced.

Vascular Model Repository

Specifications Document

From 0214_H_CERE_CA.png



From dataset-svprojects.csv

0214_H_CERE_CA

Legacy Name: ANR111_Stable

Model added: 21 Jul 2023

Species	Human
Anatomy	Cerebral
Disease	Cerebral Aneurysm
Procedure	None

Last updated: 24 Jul 2023

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Clinical Significance and Background

From [BackgroundAnatomy.csv](#)

Cerebral

The cerebral arteries are involved in providing blood to the brain and the spine. They provide about 20% of the blood to the brain while the carotid arteries provide the other 80%. The two vertebral arteries start at the subclavian arteries near the collarbone and run up the left and right sides of the spinal column in the neck. At the base of the skull, the two vertebral arteries then merge into one artery called the basilar artery which is the main supply of blood to the brain stem and also supplies blood to the brain itself through the Circle of Willis.

Cerebral Aneurysm

From [BackgroundDisease.csv](#)

A cerebral aneurysm, also known as a brain aneurysm, is a weakened or thin spot on an artery in the brain that bulges and fills with blood. If left untreated, it can rupture, leading to a hemorrhage, potentially causing serious health issues such as hemorrhagic stroke, brain damage, coma, or even death. While some small aneurysms may not cause immediate problems, they have the potential to rupture and cause bleeding within the brain or surrounding areas. Symptoms of an unruptured aneurysm may include pain behind the eye, numbness, weakness, vision changes, and more. When an aneurysm ruptures, it presents with a sudden and severe headache, double vision, nausea, stiff neck, and other alarming symptoms. Immediate medical attention is crucial if any of these symptoms occur.

Cerebral aneurysms can be classified into three types: saccular, fusiform, and mycotic. The saccular aneurysm is the most common form and is typically found on arteries at the base of the brain. They can be categorized by size as small (less than 11 mm), large (11-25 mm), or giant (greater than 25 mm).

Clinical Data

From [0214_H_CERE_CA_ClinicalData.csv](#)

General Patient Data

Age (yrs)	41
Sex	Female

Specific Patient Data

Aneurysm Location	Left Cavernous ICA
-------------------	--------------------

Last updated: 24 Jul 2023

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Diabetes Mellitus	No
Hypertension	No
Hyperlipidemia	No
Smoking	Yes
Family History of Cerebral Aneurysm	No

Notes

Categorized as a stable aneurysm (no increase in size by at least 1mm in two or more dimensions between checkups). Aneurysm located in the left cavernous ICA. Paired with growing aneurysm 0213_H_CERE_CA. See below for information on the image data.

Image Type: VTI
Image Source: Stanford Health database

Publications

There are no publications associated with the featured model.

From dataset-svprojects.csv

Last updated: 24 Jul 2023

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Uploading models and/or simulation results to Tetra server

Before you begin the final process of uploading the models and information to the server, please make sure you have updated the following files:

- dataset-abbreviations.csv in **vmr-dataset**
- dataset-diseaseTree.csv in **vmr-dataset**
- dataset-svprojects.csv in **vmr-dataset**
- dataset-svresults.csv in **vmr-dataset**
- Image of the model(s) in **vmr-images**
- Clinical data of the model(s) in **vmr-clinical_data**
- PDF of the model(s) in **vmr-pdfs**
- SimVascular project of the model
 - Images folder
 - Meshes folder
 - Models folder
 - Paths folder
 - ROMSimulations folder
 - Segmentations folder
 - Simulations folder
 - svFSI folder
 - LICENSE file
 - simvascular.proj file

Transferring and managing files between local and remote servers are done through Linux commands. Here are some of the common commands that will be used and some documentation if you are not familiar with them:

- **scp** (secure copy)
<https://www.geeksforgeeks.org/scp-command-in-linux-with-examples/#>
- **vim** (text editor) <https://www.geeksforgeeks.org/getting-started-with-vim-editor-in-linux/>
- **find** (finding and deleting certain files)
<https://www.geeksforgeeks.org/find-command-in-linux-with-examples/#>
- **zip** (zipping files) <https://www.geeksforgeeks.org/zip-command-in-linux-with-examples/>

1. From your local terminal, navigate to **VMR_Project**.
2. Copy over the **SimVascular results folder** into the **/var/www/vascularmodel/svresults** directory on the Tetra server using the **scp** command (within these folders includes the actual .vt and .vtu files and most importantly the zipped versions of these files).

```
19195@LAPTOP-JJ1VN399 MINGW64 ~/Documents/VMR_PProject/Models_Allyson_CerebralAneurysm/SV_Results
$ scp -r 0220_H_CERE_CA bwu@simvascular.stanford.edu:/var/www/vascularmodel/svresults
bwu@simvascular.stanford.edu's password:
0220_H_CERE_CA_3D_RIGID_dome.vtp                                100%   169KB   5.9MB/s  00:00
0220_H_CERE_CA_3D_RIGID_last.vtp                               100%   59MB   33.4MB/s  00:01
0220_H_CERE_CA_3D_RIGID_parent.vtp                             100%  304KB   13.2MB/s  00:00
```

If there are no simulation results then skip this step.

3. Copy over the **SimVascular project(s) folder** into the **/var/www/vascularmodel/svprojects** directory on the Tetra server using the **scp** command.

```
19195@LAPTOP-JJ1VN399 MINGW64 ~/Documents/VMR_PROJECT/Models_Alyson_CerebralAneurysm/Treated Models
$ scp -r 0220_H_CERE_CA bwu@simvascular.stanford.edu:/var/www/vascularmodel/svprojects
bwu@simvascular.stanford.edu's password:
0220_H_CERE_CA.vti                                100%   49MB  30.0MB/s  00:01
0220_H_CERE_CA.vti.hdr                            100%   638    179 4KB/s  00:00
```

4. Copy the **dataset-abbreviations.csv**, **dataset-diseaseTree.csv**, **dataset-svprojects.csv**, and **dataset-svresults.csv** into the **/var/www/vascularmodel/dataset** directory on the Tetra server (if some files haven't changed from the last time you uploaded models then there is no need to upload it to the server)

```
19195@LAPTOP-JJ1VN399 MINGW64 ~/Documents/VMR_PROJECT/vmr-dataset
$ scp dataset-abbreviations.csv bwu@simvascular.stanford.edu:/var/www/vascularmodel/dataset
bwu@simvascular.stanford.edu's password:
dataset-abbreviations.csv                           100% 1137    88.9KB/s  00:00
```

```
19195@LAPTOP-JJ1VN399 MINGW64 ~/Documents/VMR_PROJECT/vmr-dataset
$ scp dataset-diseaseTree.csv bwu@simvascular.stanford.edu:/var/www/vascularmodel/dataset
bwu@simvascular.stanford.edu's password:
dataset-diseaseTree.csv                           100%  625    67.2KB/s  00:00
```

```
19195@LAPTOP-JJ1VN399 MINGW64 ~/Documents/VMR_PROJECT/vmr-dataset
$ scp dataset-svprojects.csv bwu@simvascular.stanford.edu:/var/www/vascularmodel/dataset
bwu@simvascular.stanford.edu's password:
dataset-svprojects.csv                           100% 136KB   6.8MB/s  00:00
```

```
19195@LAPTOP-JJ1VN399 MINGW64 ~/Documents/VMR_PROJECT/vmr-dataset
$ scp dataset-svresults.csv bwu@simvascular.stanford.edu:/var/www/vascularmodel/dataset
bwu@simvascular.stanford.edu's password:
dataset-svresults.csv                           100%  63KB   3.4MB/s  00:00
```

You will have a different login name (instead of `bwu@simvascular.stanford.edu`) and a different password for the Tetra server.

5. Copy over the local **vmr-images** directory into the server-side **/var/www/vascularmodel/img** directory. You can also choose to just copy over the newly created files if none of the previous files have changed. I'm just lazy and find copying over the entire directory easier. Just make sure the directory you copy over isn't corrupted or is missing files. Note the directory to be copied to is the **/img** directory. Note the “-r” flag is used to not just copy the directory but also recursively copy all the contents of the directory.

```
19195@LAPTOP-JJ1VN399 MINGW64 ~/Documents/VMR_PROJECT
$ scp -r vmr-images bwu@simvascular.stanford.edu:/var/www/vascularmodel/img
bwu@simvascular.stanford.edu's password:
0001_H_AO_SVD.png                                100%   84KB   5.6MB/s  00:00
0002_H_AO_SVD.png                                100%   74KB   3.6MB/s  00:00
0003_H_AO_SVD.png                                100%   85KB   7.9MB/s  00:00
```

6. Copy over the local **vmr-clinical_data** directory into the server-side **/var/www/vascularmodel** directory. You can also choose to just copy over the newly created files if none of the previous files have changed. I'm just lazy and find copying over the entire directory easier. Just make sure the directory you copy over isn't corrupted or is missing files. Note the “-r” flag is used to not just copy the directory but

also recursively copy all the contents of the directory.

```
19195@IAPTOP-111VN399 MTNGW64 ~/Documents/VMR_Project
$ scp -r vmr-clinical_data bwu@simvascular.stanford.edu:/var/www/vascularmodel
bwu@simvascular.stanford.edu's password:
0001_H_AO_SVD_ClinicalData.csv          100%   195    24.9KB/s  00:00
0002_H_AO_SVD_ClinicalData.csv          100%   193    45.4KB/s  00:00
0003_H_AO_SVD_ClinicalData.csv          100%   136    41.7KB/s  00:00
0004_H_AO_SVD_ClinicalData.csv          100%   197    70.1KB/s  00:00
```

7. Copy over the local **vmr-pdfs** directory into the server-side **/var/www/vascularmodel** directory. You can also choose to just copy over the newly created files if none of the previous files have changed. I'm just lazy and find copying over the entire directory easier. Just make sure the directory you copy over isn't corrupted or is missing files.
Note the “**-r**” flag is used to not just copy the directory but also recursively copy all the contents of the directory.

```
19195@IAPTOP-111VN399 MTNGW64 ~/Documents/VMR_Project
$ scp -r vmr-pdfs bwu@simvascular.stanford.edu:/var/www/vascularmodel
bwu@simvascular.stanford.edu's password:
0001_H_AO_SVD.pdf           100%    93KB   4.7MB/s  00:00
0002_H_AO_SVD.pdf           100%   85KB  208.6KB/s  00:00
0003_H_AO_SVD.pdf           100%   95KB   1.4MB/s  00:00
```

8. Log into the Tetra server and navigate to the **/var/www/vascularmodel/vmr-clinical_data** directory and run the **move_clinical_data.py** script to move all the clinical data csv files to their respective model folders. This will copy over ALL the csv files again, which guarantees that the model files on the server will always have the latest versions of the csv files that were just uploaded from the local side.

```
$ pwd
/var/www/vascularmodel/vmr-clinical_data
$ python move_clinical_data.py

Copying Clinical Data csv from /var/www/vascularmodel/vmr-clinical_data

Copied 0058_H_PULMFON_PAT
Copied 0007_H_AO_H
```

9. Navigate to the **/var/www/vascularmodel/vmr-pdfs** directory and run the **move_pdf.py** script to move all the pdf files to their respective. This will copy over ALL the PDF files again, which guarantees that the model files on the server will always have the latest versions of the csv files that were just uploaded from the local side.

```
$ pwd
/var/www/vascularmodel/vmr-pdfs
$ python move_pdf.py

Copying PDFs from /var/www/vascularmodel/vmr-pdfs

Copied 0209_H_CERE_CA
Copied 0158_H_AO_H
```

10. If you navigate to **/var/www/vascularmodel/svprojects** and enter one of the model folders and list the contents, you should now see the clinical data csv file and the PDF

file along with the original SimVascular folders and the LICENSE file.

```
$ pwd
/var/www/vascularmodel/svprojects/0220_H_CERE_CA
$ ls
0220_H_CERE_CA_clinicalData.csv    LICENSE      Paths          Simulations
0220_H_CERE_CA.pdf                  Meshes       ROMSimulations simvascular.proj
Images                                Models       Segmentations svFSI
$ ...
```

- Within **/var/www/vascularmodel/svprojects** it should have a directory for every model and a zipped file for all the previous models. The newly added models should not have any zip files yet.

0008_H_AO_H.zip	0044_H_ABAO_AAA.zip	0075_H_AO_H.zip	0109_H_PULM_H.zip	0140_H_CORO_KD.zip	0159_H_AO_H.zip	0193_H_ABAO_AAA.zip
0009_H_AO_H.zip	0045_H_ABAO_AAA.zip	0075_H_CORO_CAD.zip	0110_H_PULM_H.zip	0141_H_AO_H.zip	0159_H_AO_H.zip	0194_H_ABAO_AAA.zip
0010_H_AO_H.zip	0045_H_ABAO_AAA.zip	0076_H_AO_H.zip	0110_H_PULM_H.zip	0141_H_CORO_KD.zip	0159_H_CORO_SVGD.zip	0194_H_ABAO_AAA.zip
0011_H_AO_H.zip	0046_H_ABAO_AIOD.zip	0076_H_AO_H.zip	0110_H_PULM_H.zip	0142_H_AO_H.zip	0160_H_AO_H.zip	0195_H_ABAO_AAA.zip
0011_H_AO_H.zip	0047_H_ABAO_AIOD.zip	0076_H_CORO_CAD.zip	0111_H_PULM_H.zip	0142_H_AO_H.zip	0160_H_AO_H.zip	0196_H_ABAO_AAA.zip
0012_H_AO_H.zip	0047_H_ABAO_ATOD.zip	0076_H_PULM_H.zip	0112_H_PULM_H.zip	0142_H_AO_H.zip	0161_H_PULMFON_SVD.zip	0197_H_ABAO_H.zip
0012_H_AO_H.zip	0048_H_ABAO_ATOD.zip	0077_H_PULM_H.zip	0112_H_PULM_H.zip	0142_H_CORO_KD.zip	0161_H_PULMFON_SVD.zip	0197_H_ABAO_H.zip
0013_H_AO_COA.zip	0048_H_ABAO_ATOD.zip	0077_H_PULM_H.zip	0113_H_PULM_H.zip	0142_H_CORO_KD.zip	0162_H_PULMFON_SVD.zip	0198_H_ABAO_AAA.zip
0014_H_AO_COA.zip	0049_H_ABAO_ATOD.zip	0078_H_PULM_H.zip	0113_H_PULM_H.zip	0143_H_AO_H.zip	0163_H_PULMFON_SVD.zip	0198_H_ABAO_AAA.zip
0014_H_AO_COA.zip	0049_H_ABAO_ATOD.zip	0079_H_PULM_H.zip	0114_H_PULM_ALGS.zip	0143_H_CORO_KD.zip	0163_H_PULMFON_SVD.zip	0199_H_CERE_CA.zip
0015_H_AO_COA.zip	0050_H_CERE_H.zip	0079_H_PULM_H.zip	0115_H_PULM_ALGS.zip	0143_H_CORO_KD.zip	0164_H_PULMFON_SVD.zip	0199_H_CERE_CA.zip
0016_H_AO_COA.zip	0051_H_CERE_H.zip	0080_H_PULM_H.zip	0115_H_PULM_ALGS.zip	0144_H_AO_H.zip	0165_H_PULMFON_SVD.zip	0200_H_CERE_CA.zip
0016_H_AO_COA.zip	0051_H_CERE_H.zip	0080_H_PULM_PAH.zip	0116_H_PULM_ALGS.zip	0144_H_AO_H.zip	0166_H_PULMFON_SVD.zip	0201_H_CERE_CA.zip
0017_H_AO_COA.zip	0052_H_CERE_H.zip	0081_H_PULM_H.zip	0116_H_PULM_ALGS.zip	0144_H_CORO_KD.zip	0166_H_PULMFON_SVD.zip	0201_H_CERE_CA.zip
0017_H_AO_COA.zip	0052_H_CERE_H.zip	0082_H_PULM_H.zip	0117_H_PULM_ALGS.zip	0145_H_AO_H.zip	0166_H_PULMFON_SVD.zip	0202_H_CERE_CA.zip
0018_H_AO_COA.zip	0053_H_CERE_H.zip	0082_H_PULM_H.zip	0118_H_PULM_WS.zip	0145_H_AO_H.zip	0167_H_PULMFON_SVD.zip	0202_H_CERE_CA.zip
0018_H_AO_COA.zip	0053_H_CERE_H.zip	0083_H_PULM_PAH.zip	0118_H_PULM_WS.zip	0145_H_CORO_KD.zip	0168_H_PULMFON_SVD.zip	0203_H_CERE_CA.zip
0019_H_AO_COA.zip	0054_H_PULMFON_TAT.zip	0083_H_PULM_PAH.zip	0119_H_PULM_WS.zip	0146_H_AO_H.zip	0168_H_PULMFON_SVD.zip	0204_H_CERE_CA.zip
0019_H_AO_COA.zip	0054_H_PULMFON_TAT.zip	0084_H_PULM_H.zip	0119_H_PULM_WS.zip	0146_H_AO_H.zip	0169_H_CORO_KD.zip	0204_H_CERE_CA.zip
0020_H_AO_COA.zip	0055_H_PULMFON_HLHS.zip	0084_H_PULM_H.zip	0120_H_PULM_ALGS.zip	0146_H_CORO_SVGD.zip	0169_H_CORO_KD.zip	0205_H_CERE_CA.zip
0020_H_AO_COA.zip	0056_H_PULMFON_TAT.zip	0085_H_PULM_PAH.zip	0121_H_PULM_ALGS.zip	0146_H_CORO_SVGD.zip	0170_H_CORO_KD.zip	0205_H_CERE_CA.zip
0021_H_AO_COA.zip	0056_H_PULMFON_TAT.zip	0086_H_PULM_PAH.zip	0122_H_PULM_ALGS.zip	0147_H_AO_H.zip	0171_H_AO_H.zip	0206_H_CERE_CA.zip
0022_H_AO_MFS.zip	0057_H_PULMFON_TAT.zip	0087_H_PULM_PAH.zip	0122_H_PULM_ALGS.zip	0147_H_CORO_SVGD.zip	0171_H_CORO_KD.zip	0207_H_CERE_CA.zip
0022_H_AO_MFS.zip	0058_H_PULMFON_PAT.zip	0087_H_PULM_PAH.zip	0123_H_PULM_ALGS.zip	0147_H_CORO_SVGD.zip	0172_H_CORO_KD.zip	0207_H_CERE_CA.zip
0023_H_AO_MFS.zip	0058_H_PULMFON_PAT.zip	0088_H_PULM_PAH.zip	0123_H_PULM_ALGS.zip	0148_H_AO_H.zip	0172_H_CORO_KD.zip	0208_H_CERE_CA.zip
0024_H_AO_H.zip	0059_H_PULMFON_TAT.zip	0088_H_PULM_PAH.zip	0124_H_PULM_WS.zip	0148_H_AO_H.zip	0173_H_CORO_KD.zip	0209_H_CERE_CA.zip
0024_H_AO_H.zip	0059_H_PULMFON_TAT.zip	0089_H_PULM_ALGS.zip	0124_H_PULM_WS.zip	0148_H_CORO_SVGD.zip	0173_H_CORO_KD.zip	0209_H_CERE_CA.zip
0025_H_AO_MFS.zip	0060_H_PULMGLN_SVD.zip	0089_H_PULM_ALGS.zip	0125_H_PULM_WS.zip	0149_H_AO_H.zip	0174_H_CORO_KD.zip	0210_H_CERE_CA.zip
0025_H_AO_MFS.zip	0061_H_PULMGLN_SVD.zip	0090_H_PULM_ALGS.zip	0126_H_PULM_PAH.zip	0149_H_AO_H.zip	0175_H_CORO_KD.zip	0210_H_CERE_CA.zip
0026_H_AO_MFS.zip	0062_H_PULMGLN_SVD.zip	0091_H_PULM_TOF.zip	0127_H_PULM_PAH.zip	0149_H_CORO_SVGD.zip	0176_H_CORO_KD.zip	0211_H_CERE_CA.zip
0027_H_AO_MFS.zip	0062_H_PULMGLN_SVD.zip	0092_H_PULM_PAH.zip	0127_H_PULM_PAH.zip	0150_H_AO_H.zip	0176_H_CORO_KD.zip	0212_H_CERE_CA.zip
0027_H_AO_MFS.zip	0063_H_PULMGLN_SVD.zip	0092_H_PULM_PAH.zip	0128_H_PULM_PAH.zip	0150_H_AO_H.zip	0177_H_CORO_KD.zip	0212_H_CERE_CA.zip
0028_H_ABAO_H.zip	0063_H_PULMGLN_SVD.zip	0093_A_AO_H.zip	0128_H_PULM_PAH.zip	0150_H_CORO_SVGD.zip	0177_H_CORO_KD.zip	0213_H_CERE_CA.zip
0028_H_ABAO_H.zip	0064_H_PULMFON_SVD.zip	0093_A_AO_H.zip	0129_H_PULM_PAH.zip	0150_H_CORO_SVGD.zip	0178_H_CORO_KD.zip	0213_H_CERE_CA.zip
0029_H_ABAO_H.zip	0064_H_PULMFON_SVD.zip	0094_A_AO_H.zip	0129_H_PULM_PAH.zip	0151_H_AO_H.zip	0178_H_CORO_KD.zip	0214_H_CERE_CA.zip
0029_H_ABAO_H.zip	0065_H_PULMFON_SVD.zip	0094_A_AO_H.zip	0130_H_PULM_PAH.zip	0151_H_AO_H.zip	0179_H_ABAO_AAA.zip	0214_H_CERE_CA.zip
0030_H_ABAO_H.zip	0065_H_PULMFON_SVD.zip	0095_A_AO_H.zip	0130_H_PULM_PAH.zip	0151_H_CORO_SVGD.zip	0179_H_ABAO_AAA.zip	0215_H_CERE_CA.zip
0030_H_ABAO_H.zip	0066_H_PULMFON_SVD.zip	0095_A_AO_H.zip	0131_H_PULM_PAH.zip	0151_H_CORO_SVGD.zip	0180_H_ABAO_AAA.zip	0215_H_CERE_CA.zip
0031_H_ABAO_AAA.zip	0067_H_AO_H.zip	0096_H_AO_COA.zip	0132_H_PULM_PAH.zip	0152_H_AO_H.zip	0181_H_ABAO_AAA.zip	No zip files for the newest uploaded models
0032_H_ABAO_AAA.zip	0067_H_AO_H.zip	0097_A_AO_COA.zip	0132_H_PULM_PAH.zip	0152_H_AO_H.zip	0181_H_ABAO_AAA.zip	No zip files for the newest uploaded models
0032_H_ABAO_AAA.zip	0067_H_CORO_KD.zip	0097_A_AO_COA.zip	0133_H_PULM_PAH.zip	0152_H_CORO_SVGD.zip	0182_H_ABAO_AAA.zip	No zip files for the newest uploaded models
0033_H_ABAO_AAA.zip	0067_H_CORO_KD.zip	0098_A_AO_COA.zip	0133_H_PULM_PAH.zip	0153_H_AO_H.zip	0182_H_ABAO_AAA.zip	No zip files for the newest uploaded models
0034_H_ABAO_AAA.zip	0068_H_CORO_KD.zip	0098_A_AO_COA.zip	0134_H_PULM_PAH.zip	0153_H_AO_H.zip	0183_H_ABAO_AAA.zip	No zip files for the newest uploaded models
0034_H_ABAO_AAA.zip	0068_H_CORO_KD.zip	0099_A_AO_COA.zip	0134_H_PULM_PAH.zip	0153_H_CORO_SVGD.zip	0183_H_ABAO_AAA.zip	No zip files for the newest uploaded models
0035_H_ABAO_AAA.zip	0069_H_CORO_KD.zip	0099_A_AO_COA.zip	0135_H_PULM_PAH.zip	0153_H_CORO_SVGD.zip	0184_H_ABAO_AAA.zip	No zip files for the newest uploaded models
0035_H_ABAO_AAA.zip	0069_H_CORO_KD.zip	0100_A_AO_COA.zip	0135_H_PULM_PAH.zip	0154_H_AO_H.zip	0184_H_ABAO_AAA.zip	No zip files for the newest uploaded models
0036_H_ABAO_AAA.zip	0070_H_AO_H.zip	0101_A_AO_COA.zip	0136_H_CORO_KD.zip	0154_H_AO_H.zip	0185_H_ABAO_AAA.zip	No zip files for the newest uploaded models
			0136_H_CORO_KD.zip	0154_H_CORO_SVGD.zip	0185_H_ABAO_AAA.zip	No zip files for the newest uploaded models

Zip the new files using the following command:

```
$ zip -r 0216_H_CERE_CA.zip 0216_H_CERE_CA
adding: 0216_H_CERE_CA/ (stored 0%)
adding: 0216_H_CERE_CA/svFSI/ (stored 0%)
adding: 0216_H_CERE_CA/Segmentations/ (stored 0%)
```

If none of the previously uploaded models had any changes to their files then skip to step 13. (I'll admit this part of the pipeline is quite manual and tedious, I did not get to automate this section with a bash script, but it shouldn't be too hard to implement just be careful).

- In some cases, one or more previous models' SimVascular files/clinical data csv files/PDF files will have been updated (most often the PDF is what has changed due to new formatting or updating a background text, etc.). The zip file for the model is no longer up to date and you have to remove the old file and re-zip it.

```
$ rm -r 0155_H_AO_H.zip
$
```

```
$ zip -r 0155_H_AO_H.zip 0155_H_AO_H  
adding: 0155_H_AO_H/ (stored 0%)  
adding: 0155_H_AO_H/0155_H_AO_H.pdf (deflated 4%)  
adding: 0155_H_AO_H/Segmentations/ (stored 0%)
```

If EVERY single model needs a new zip file (ex. The general format for PDFs has changed and now each model has a newer version of the PDF) use the following command to delete all the zip files in the directory. **USE WITH CAUTION THERE IS NO UNDO AFTER YOU DELETE A FILE.**

```
$ find . -name "*.zip" -type f -delete
```

Before running the whole command, you can run it without the -delete flag to list all the files it would delete. It can be a good idea to always double-check what files you would be potentially deleting forever.

```
$ find . -name "*.zip" -type f
```

Once all the zip files for every model are deleted, run the bash script **create_all_zips.sh** to automatically generate zip files for every model.

```
$ bash create_all_zips.sh  
adding: 0001_H_AO_SVD/ (stored 0%)  
adding: 0001_H_AO_SVD/flow-files/ (stored 0%)  
adding: 0001_H_AO_SVD/flow-files/inflow_1d.flow (deflated 71%)  
adding: 0001_H_AO_SVD/flow-files/inflow_3d.flow (deflated 72%)
```

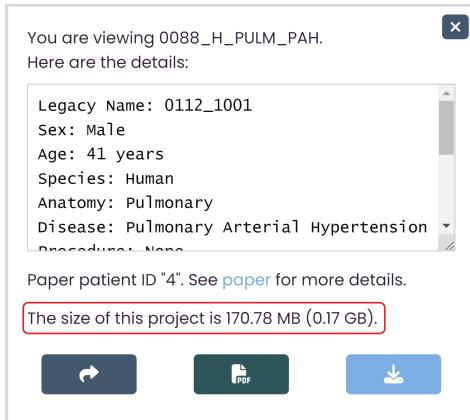
Zipping all the model files over again actually takes quite a bit of time so be warned (~1.5 hours to zip 220 models). Make sure your computer doesn't shut off halfway.

13. Once all the models are zipped and the simulation results are uploaded properly navigate to **/var/www/vascularmodel** and run the **generate_file_sizes.py** script.

```
$ ls  
additionaldata      filtertutorial.html    README  
additionaldata.html gallerytutorial.html  scss  
contacts.html       generate_file_sizes.py share.html  
contributors.html   img                  sharingtutorial.html  
css                 index.html           statistics.html  
dataset              js                  svprojects  
dataset.html         LICENSE             svresults  
documentation.html md_docs            tutorial.html  
extra_data          minututorial.html  vmr-clinical_data  
FAQs.html          partials            vmr-pdfs  
$ python generate_file_sizes.py  
$ |
```

This updates the **file_sizes.csv** in **/var/www/vascularmodel/dataset** which is read to

display the download sizes of the files on the VMR website.



14. You should now be able to see all the new files live on the website! If you don't see the new models immediately, try clearing the cache of the web browser (or open up the VMR in incognito mode which doesn't use a cache).

Adding new anatomies/diseases/procedures

New anatomies

1. Go to the **naming** tab of the **dataset Google Sheets**. Add the new anatomy and a reasonable acronym under the **Anatomy Identifier** section. Try to use an acronym seen commonly in literature. Make the acronym fully uppercase for consistency.

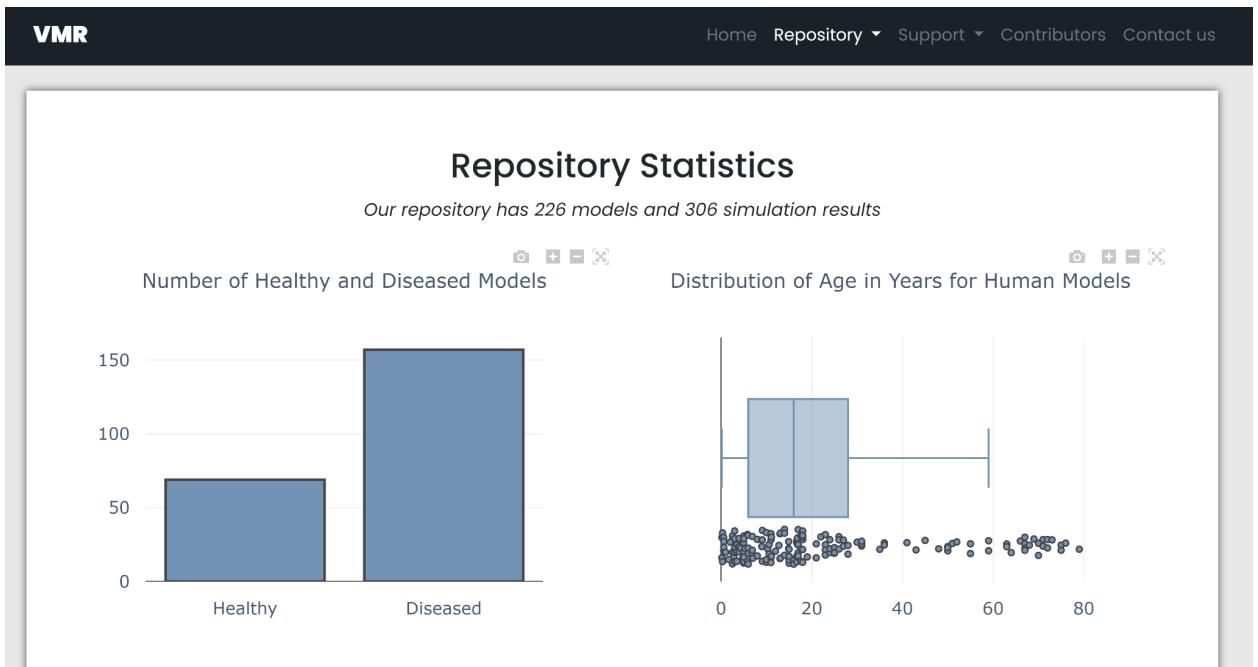
A screenshot of a Google Sheets document titled "dataset". The "naming" tab is active. The table has the following structure:

	A	B	C	D	E	F	G	H	I	J
1	Species Identifier		Anatomy Identifier			Disease Identifier			Number of Padded Zeros	
2	H	Human		AO	Aorta		H	Healthy		0000
3	A	Animal		ABAO	Abdominal Aorta		AAA	Abdominal Aortic Aneurysm		
4				CERE	Cerebral		AIOD	Aortoiliac Occlusive Disease		
5				CORO	Coronary		ALGS	Alagille Syndrome		
6				HEPA	Hepatic		AOD	Aortic Dissection		
7				PULM	Pulmonary		CA	Cerebral Aneurysm		
8				PULMFON	Pulmonary Fontan		CAD	Coronary Artery Disease		
9				PULMGLN	Pulmonary Glenn		COA	Coarctation of Aorta		
10							HLHS	Hypoplastic Left Heart Syndrome		
11							KD	Kawasaki Disease		
12							MFS	Marfan Syndrome		
13							PAH	Pulmonary Arterial Hypertension		
14							PAT	Pulmonary Atresia		
15							SVD	Single Ventricle Defect		
16							SVGD	Saphenous Vein Graft Disease		
17							TAT	Tricuspid Atresia		
18							TOF	Tetralogy of Fallot		
19							WS	Williams Syndrome		
20										

2. Go to the **abbreviations** tab of the **dataset Google Sheets**. Add the anatomy name as well as the same anatomy abbreviation used in the naming tab. Make sure that your spelling under LongName is exactly the same as that under the models in the dataset.

	A	B	C	D	E	F	G
1	Species ShortName	Species LongName	Anatomy ShortName	Anatomy LongName	Disease ShortName	Disease LongName	Method ShortName
2	H	Human	AO	Aorta	H	Healthy	RIGID
3	A	Animal	ABAO	Abdominal Aorta	AAA	Abdominal Aortic Aneurysm	FSI
4			CERE	Cerebral	AIOD	Aortoliac Occlusive Disease	
5			CORO	Coronary	ALGS	Alagille Syndrome	
6			HEPA	Hepatic	AOD	Aortic Dissection	
7			PULM	Pulmonary	Ane	Aneurysm	
8			PULMFON	Pulmonary Fontan	CA	Cerebral Aneurysm	
9			PULMGLN	Pulmonary Glenn	CAD	Coronary Artery Disease	
10					COA	Coarctation of Aorta	
11					CHD	Congenital Heart Disease	
12					HLHS	Hypoplastic Left Heart Syndrome	
13					KD	Kawasaki Disease	
14					MFS	Marfan Syndrome	
15					PAD	Pulmonary Artery Disease	
16					PAH	Pulmonary Arterial Hypertension	
17					PAT	Pulmonary Atresia	
18					Ste	Sclerosis	
19					SVD	Single Ventricle Defect	
20					SVGD	Saphenous Vein Graft Disease	
21					TAT	Tricuspid Atresia	
22					TOF	Tetralogy of Fallot	
23					WS	Williams Syndrome	

This abbreviations tab is used for updating the statistics page of the VMR, as charts dynamically adjust with monitor width. For mobile phones, the full name of the label becomes this specified abbreviation.



3. Download the **abbreviations** tab from **dataset Google Sheets** as a .csv file by selecting **File, Download, and Comma Separated Values (.csv)**.
4. Rename the file from "**dataset - abbreviations.csv**" to "**dataset-abbreviations.csv**" and move it into the **vmr-dataset** directory (Super annoying why Google Sheets includes spaces in names. For our Python scripts and website javascript to work all our file names are standardized to not contain spaces... oh well what can you do.)

5. Open up a terminal and navigate to the **vmr-dataset** directory where you just moved **dataset-abbreviations.csv** to and copy it into the Tetra Server using this command:

```
19195@LAPTOP-JJ1VN399 MINGW64 ~/Documents/VMR_PROJECT/vmr-dataset
$ scp dataset-abbreviations.csv bwu@simvascular.stanford.edu:/var/www/vascularmodel/dataset
bwu@simvascular.stanford.edu's password:
dataset-abbreviations.csv                                         100% 1137     88.9KB/s   00:00
```

You will have a different login name (instead of `bwu@simvascular.stanford.edu`) and a different password for the Tetra Server.

6. Open **BackgroundAnatomy.csv** in the **vmr-background** directory and create an entry for the new anatomy as well as a short background overview of the anatomy.

A	B
1 Anatomy	Background
2 Aorta	The largest blood vessel and the primary artery of the human body, the aorta is responsible for carrying oxygenated blood pumped from the heart to the rest of the body. The aorta is divided into four
3 Abdominal Aorta	ascending aorta, the aortic arch, the thoracic aorta, and the abdominal aorta.
4 Coronary	main coronary arteries are the left main and right coronary arteries, and they wrap around the outside of the heart.
5 Hepatic Artery	Hepatic artery (HA) is soft oxygenated blood vessel that supplies oxygen-rich blood to the liver, duodenum, and pancreas. Hence the risk of vessels embolization is least as compared to intraperitoneal infusion. Due to oxygen enrichment in HA it is more advisable for stem cell transplantation. In addition it is a routinely used technique for arterial chemo-embolization of liver tumor and hence can be utilized for stem cell infusion.
6 Pulmonary	HA is mainly accessed through trans-radial, trans-femoral, and trans-bronchial and have also demonstrated safety and efficacy of stem cell transplantation through HA in patient with hepatic cirrhosis (Khan et al., 2008). This was further supported by other clinical studies (Lyra et al., 2010). Despite highly efficient and direct site of stem cells repopulation in liver, access of HA might pose the risk of occlusion, fibrosis due to hypertension, and embolization of cells.
7 Pulmonary Fontan	Pulmonary circulation involves blood flowing from the right ventricle of the heart into the pulmonary arteries. From the pulmonary arteries, the blood then reaches the lungs, performs a gas
8 Pulmonary Glenn	exchange, and then returns to the left atrium via the pulmonary veins. The pulmonary veins are the blood vessels responsible for transporting deoxygenated blood to the lungs to perform respiration. A normal pulmonary anatomy involves the main pulmonary artery (MPA) trunk leaving the right ventricle and bifurcating into the left and right pulmonary arteries.
9 Cerebral	The pulmonary arteries are the blood vessels responsible for transporting deoxygenated blood to the lungs to perform respiration. A normal pulmonary anatomy involves the main pulmonary artery bifurcating into the left and right pulmonary arteries. The cerebral arteries are involved in providing blood to the brain and the spine. They provide about 20% of the blood to the brain while the carotid arteries provide the other 80%. The two vertebral arteries start at the subclavian arteries and join to form the basilar artery, which then divides into the posterior cerebral arteries.

These blurbs are used when automatically generating PDFs for each model. When I write up a background text, I write up the background paragraphs in the **BackgroundAll.docx** file first and then just copy it into the csv files. It's a lot easier to edit and keep track of the writing.

New diseases

1. Go to the **naming** tab of the **dataset Google Sheets**. Add the new disease and a reasonable acronym under the **Disease Identifier** section. Try to use an acronym seen commonly in literature. Make the acronym fully uppercase for consistency.

dataset

	B	C	D	E	F	G	H	I	J	K	L
1	fier		Anatomy Identifier				Disease Identifier		Number of Padded Zeros	SvnProjects wit	
2	Human	AO	Aorta	H	Healthy			0000		0001_H_AO_S1	
3	Animal	ABAO	Abdominal Aorta	AAA	Abdominal Aortic Aneurysm					0002_H_AO_S1	
4		CERE	Cerebral	AIOD	Aortoiliac Occlusive Disease					0003_H_AO_S1	
5		CORO	Coronary	ALGS	Alagille Syndrome					0004_H_AO_S1	
6		PULM	Pulmonary	AOD	Aortic Dissection					0005_H_AO_S1	
7		PULMFON	Pulmonary Fontan	CA	Cerebral Aneurysm					0006_H_AO_S1	
8		PULMGLN	Pulmonary Glenn	CAD	Coronary Artery Disease					0007_H_AO_H	
9				COA	Coarctation of Aorta					0008_H_AO_H	
10				HLHS	Hypoplastic Left Heart Syndrome					0009_H_AO_H	
11				KD	Kawasaki Disease					0010_H_AO_H	
12				MFS	Marfan Syndrome					0011_H_AO_H	
13				PAH	Pulmonary Arterial Hypertension					0012_H_AO_H	
14				PAT	Pulmonary Atresia					0013_H_AO_C1	
15				SVD	Single Ventricle Defect					0014_H_AO_C1	
16				SVGD	Saphenous Vein Graft Disease					0015_H_AO_C1	
17				TAT	Tricuspid Atresia					0016_H_AO_C1	
18				TOF	Tetralogy of Fallot					0017_H_AO_C1	
19				WS	Williams Syndrome					0018_H_AO_C1	
20										0019_H_AO_C1	
21										0020_H_AO_C1	
22										0021_H_AO_M1	
23										0022_H_AO_M1	
24										0023_H_AO_M1	

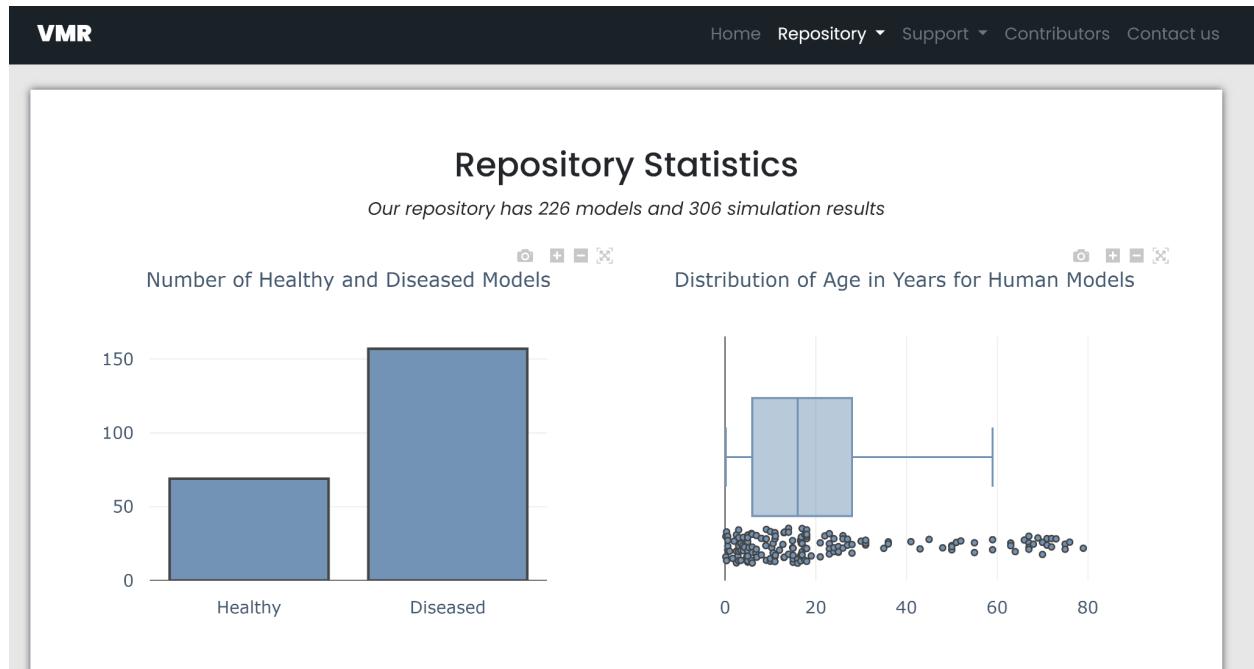
2. Go to the **abbreviations** tab of the dataset Google Sheets. Add the disease name as well as the same disease abbreviation used in the naming tab.

dataset

	B	C	D	E	F	G	H
1	Species LongName	Anatomy ShortName	Anatomy LongName	Disease ShortName	Disease LongName	Method ShortName	Method LongName
2	Human	AO	Aorta	H	Healthy	RIGID	Rigid Wall
3	Animal	ABAO	Abdominal Aorta	AAA	Abdominal Aortic Aneurysm	FSI	Fluid-Structure Interact
4		CERE	Cerebral	AIOD	Aortoiliac Occlusive Disease		
5		CORO	Coronary	ALGS	Alagille Syndrome		
6		PULM	Pulmonary	AOD	Aortic Dissection		
7		PULMFON	Pulmonary Fontan	Ane	Aneurysm		
8		PULMGLN	Pulmonary Glenn	CA	Cerebral Aneurysm		
9				CAD	Coronary Artery Disease		
10				COA	Coarctation of Aorta		
11				CHD	Congenital Heart Disease		
12				HLHS	Hypoplastic Left Heart Syndrome		
13				KD	Kawasaki Disease		
14				MFS	Marfan Syndrome		
15				PAD	Pulmonary Artery Disease		
16				PAH	Pulmonary Arterial Hypertension		
17				PAT	Pulmonary Atresia		
18				Ste	Stenosis		
19				SVD	Single Ventricle Defect		
20				SVGD	Saphenous Vein Graft Disease		
21				TAT	Tricuspid Atresia		
22				TOF	Tetralogy of Fallot		
23				WS	Williams Syndrome		
24							

This abbreviations tab is used for updating the statistics page of the VMR, as charts dynamically adjust with monitor width. For mobile phones, the full name of the label

becomes this specified abbreviation.



3. Go to the **diseaseTree** tab of the **dataset Google Sheets**. If applicable, add the new disease under the proper parent group (ex. **Cerebral Aneurysm** is within the **Aneurysm** parent group). Make sure any model with that label would always fit under the parent group (ex: every single **Kawasaki Disease** model can also be considered a **Coronary Artery Disease** model, but not every single **Coronary Artery Disease** can be a **Stenosis** so it's not in that category)

The screenshot shows a Google Sheets document with the 'diseaseTree' tab selected. The table has columns labeled A through F. Row 1 contains the column headers. Rows 2 through 5 show specific disease entries. The cell containing 'Cerebral Aneurysm' in row 5, column D is highlighted in yellow.

	A	B	C	D	E	F
1	Coronary Artery Disease	Single Ventricle Defect	Pulmonary Artery Disease	Aneurysm	Stenosis	Congenital Heart Disease
2	Saphenous Vein Graft Disease	Hypoplastic Left Heart Syndrome	Alagille Syndrome	Abdominal Aortic Aneurysm	Aortoiliac Occlusive Disease	Single Ventricle Defect
3	Kawasaki Disease	Pulmonary Atresia	Williams Syndrome	Kawasaki Disease	Coarctation of Aorta	Tetralogy of Fallot
4		Tricuspid Atresia	Pulmonary Arterial Hypertension	Marfan Syndrome	Pulmonary Arterial Hypertension	Coarctation of Aorta
5				Cerebral Aneurysm	Saphenous Vein Graft Disease	Alagille Syndrome
6						Williams Syndrome
7						
8						
9						
10						
11						
12						
13						
14						
15						
16						
17						
18						
19						
20						
21						
22						
23						
24						

4. Note that some diseases may fall into multiple groups. List the disease under *all* relevant

groups (ex. **Alagille Syndrome** falls under **Pulmonary Artery Disease** and **Congenital Heart Disease**). Spelling here is again important. Ensure values here are consistent with model labels throughout the dataset.

5. Download BOTH the **abbreviations** tab and the **diseaseTree** tab from **dataset Google Sheets** as a .csv file by selecting **File**, **Download**, and **Comma Separated Values (.csv)**.
6. Rename the file from “**dataset - abbreviations.csv**” to “**dataset-abbreviations.csv**” and “**dataset - diseaseTree.csv**” to “**dataset-diseaseTree.csv**” and move both into the **vmr-dataset** directory (Super annoying why Google Sheets includes spaces in names. For our Python scripts and website javascript to work all our file names are standardized to not contain spaces... oh well what can you do.)
7. Open up a terminal and navigate to the **vmr-dataset** directory where you just moved **dataset-abbreviations.csv** and **dataset-diseaseTree.csv** to and copy it into the Tetra Server using these commands:

```
19195@LAPTOP-JJ1VN399 MINGW64 ~/Documents/VMR_PROJECT/vmr-dataset
$ scp dataset-abbreviations.csv bwu@simvascular.stanford.edu:/var/www/vascularmodel/dataset
bwu@simvascular.stanford.edu's password:
dataset-abbreviations.csv                                         100% 1137     88.9KB/s  00:00

19195@LAPTOP-JJ1VN399 MINGW64 ~/Documents/VMR_PROJECT/vmr-dataset
$ scp dataset-diseaseTree.csv bwu@simvascular.stanford.edu:/var/www/vascularmodel/dataset
bwu@simvascular.stanford.edu's password:
dataset-diseaseTree.csv                                         100% 625      67.2KB/s  00:00
```

You will have a different login name (instead of `bwu@simvascular.stanford.edu`) and a different password for the Tetra Server.

8. Open **BackgroundDisease.csv** in the **vmr-background** directory and create an entry for the new disease as well as a short background overview of the disease.

The screenshot shows a Microsoft Word document titled "BackgroundDisease". The table has two columns, A and B. Column A lists diseases, and Column B contains their descriptions. The descriptions are formatted with some text highlighted in yellow.

A	B
4 Aneurysm	An aneurysm is a bulge in a blood vessel caused by a weakness in the blood vessel wall, usually where it branches. As blood passes through the weakened blood vessel, the b
5 Aortoiliac Occlusive Disease	A buildup of fatty deposits in your arteries is called atherosclerosis. When these fatty deposits accumulate and narrow or block the iliac arteries, arteries that bring blood to
6 Cerebral Aneurysm	A cerebral aneurysm, also known as a brain aneurysm, is a weakened or thin spot on an artery in the brain that bulges and fills with blood. If left untreated, it can rupture, le
7 Coarctation of Aorta	Coarctation of the aorta is a birth defect in which a part of the aorta is narrower than usual. If the narrowing is severe enough and if it is not diagnosed, the baby may ha
8 Congenital Heart Disease	Congenital heart disease is one or more problems with the structure of the heart that exist since birth. Congenital means that you are born with the condition. Congenital he
9 Coronary Artery Disease	Coronary artery disease (CAD) is a type of heart disease where the arteries of the heart cannot deliver enough oxygen-rich blood to the heart. It is often caused by cholesterol
10 Kawasaki Disease	Kawasaki disease (KD), also known as Kawasaki syndrome, is an acute febrile illness of unknown cause that primarily affects children younger than 5 years of age. The disease
11 Marfan Syndrome	Marfan syndrome is an inherited disorder that affects connective tissue, also known as the fibers that support and anchor your organs and other structures in your body. Ma
12 Myocardial Infarction	A myocardial infarction, more commonly known as a heart attack, happens when one or more areas of the heart muscle do not get enough oxygen. This happens when blood
13 Pulmonary Arterial Hypertension	Pulmonary hypertension is a type of high blood pressure that affects the arteries in the lungs and the right side of the heart. In one form of pulmonary hypertension, called p
14 Single Ventricle Defect	A single ventricle defect (SVD) is a type of heart defect that a child is born with. It occurs when one of the two pumping chambers in the heart, called ventricles, is not large e

These blurbs are used when automatically generating PDFs for each model. When I write up a background text, I write up the background paragraphs in the **BackgroundAll.docx** file first and then just copy it into the csv files. It's a lot easier to edit and keep track of the writing.

New procedures

1. Open **BackgroundProcedures.csv** in the **vmr-background** directory and create an entry for the new disease as well as a short background overview of the disease. These blurbs are used when automatically generating PDFs for each model. When I write up a background text, I write up the background paragraphs in the **BackgroundAll.docx** file first and then just copy it into the csv files. It's a lot easier to edit and keep track of the writing.