Documentation

of the Pipeline for measuring Vessel Elasticity in a Sequence of retinal IR-Images
By Viktor Dinkel, 13/09/2017

1. Software Requirements

- ImageJ with specific Plug-Ins
- Working Python Environment with all the different packages (see Source code for imported packages)

Optional:

- Apache XAMPP (or something similar like WAMP) for a Web- and MySQL-Server. This is optional but necessary if using the Database features of the Pipeline as well as the web-based results browser
- MySQL Workbench connects to the database and allows comfortable data inspection/manipulation

2. SetUp of the Pipeline

ImageJ for image stabilization

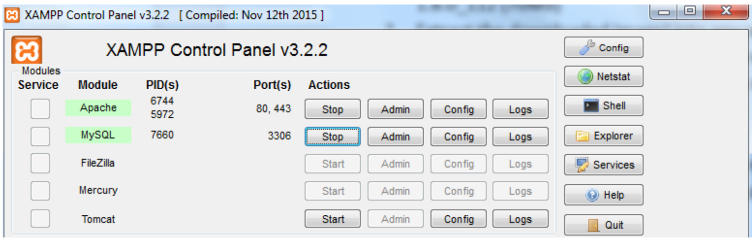
1. Get ImageJ from the Website: https://imagej.nih.gov/ij/download.html
   This Plug-In was developed and tested on this downloaded version: bundled with 64-bit Java 1.8.0_112 (70MB)
2. Extract the downloaded ImageJ into any working directory
3. Copy the contents of this folder directly into (your-ImageJ-directory)/plugins/
4. Run/Restart ImageJ, under the *Plugins* section should be the entry *disc stabilization*

Working Python Environment

This requires a 2.7 Python environment. There is no list of required packages, so the setup should be done with Anaconda or something similar with a package manager. The pulseWavePropagation code should simply be imported in any Environment.

Apache XAMPP

Download at https://www.apachefriends.org/download.html with the PHP version 5.6 for the corresponding platform. The installation routine is automated and no specific settings need to be done, just leave everything as default. After the installation is done, run the XAMPP Control Panel and start the Apache as well as the MySQL modules as shown here:



XAMPP Control Panel v3.2.2 [Compiled: Nov 12th 2015]

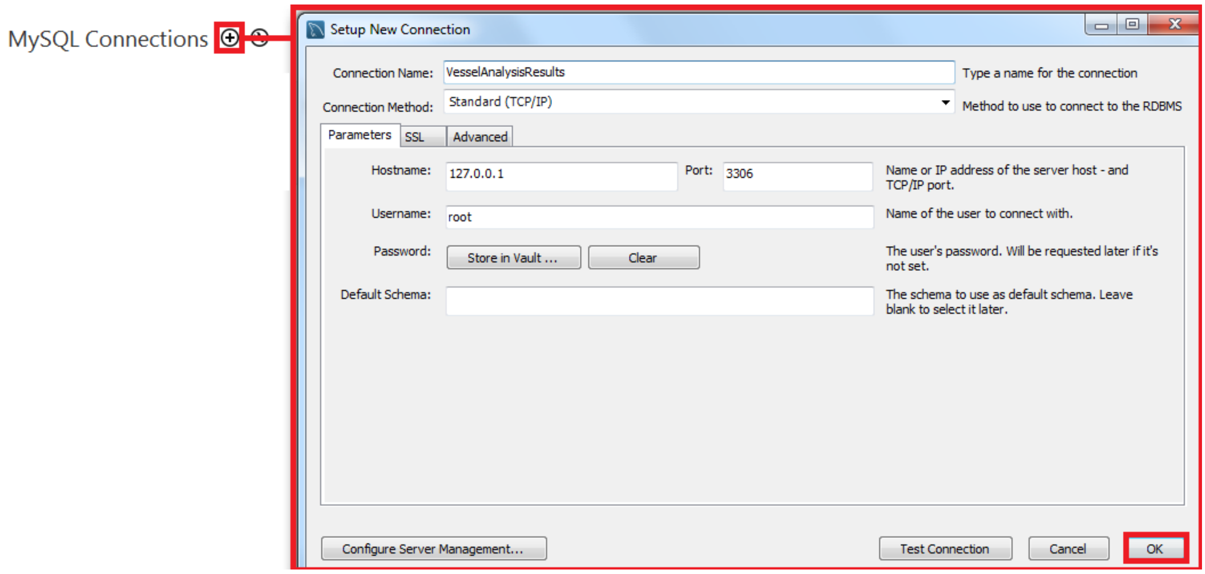
XAMPP Control Panel v3.2.2

Modules Service	Module	PID(s)	Port(s)	Actions			
□	Apache	6744 5972	80, 443	Stop	Admin	Config	Logs
□	MySQL	7660	3306	Stop	Admin	Config	Logs
□	FileZilla			Start	Admin	Config	Logs
□	Mercury			Start	Admin	Config	Logs
□	Tomcat			Start	Admin	Config	Logs

The launch of the XAMPP Control Panel and start of the modules has to be done after every restart of the machine (unless auto start was configured, see Config).

MySQL Database

Can be downloaded here https://dev.mysql.com/downloads/workbench/ and installed with all the default options. After installing and starting it, a new MySQL connection has to be created:



MySQL Connections ⊕ ⊙

Setup New Connection

Connection Name: VesselAnalysisResults — Type a name for the connection

Connection Method: Standard (TCP/IP) — Method to use to connect to the RDBMS

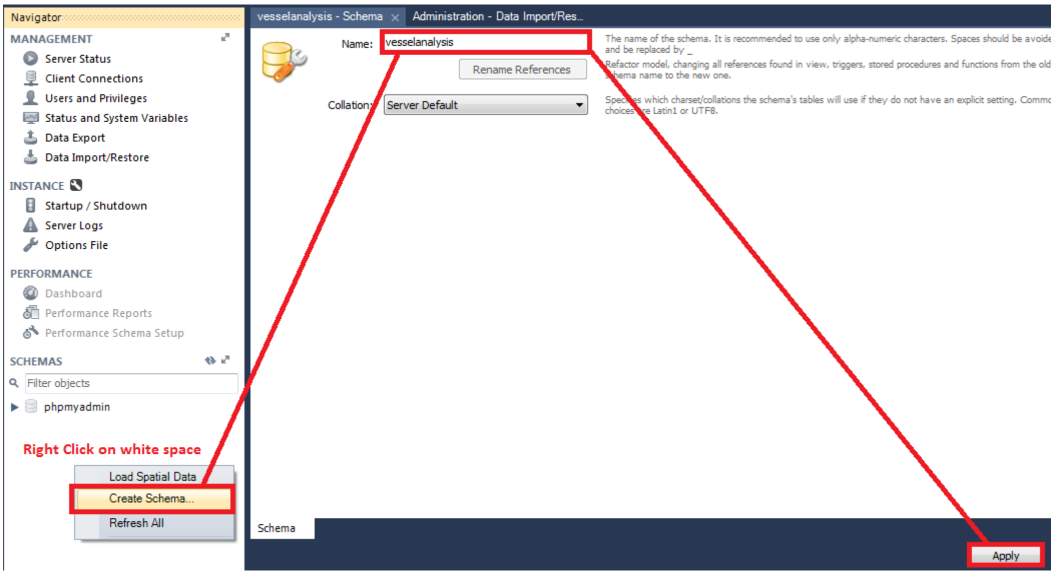
Hostname: 127.0.0.1 Port: 3306 — Name or IP address of the server host - and TCP/IP port.

Username: root — Name of the user to connect with.

Password: Store in Vault ... Clear — The user's password. Will be requested later if it's not set.

Default Schema: — The schema to use as default schema. Leave blank to select it later.

Click on the newly created connection and it should successfully connect to the database. Now the Schema needs to be created in order to import the tables into it:



Name: vesselanalysis

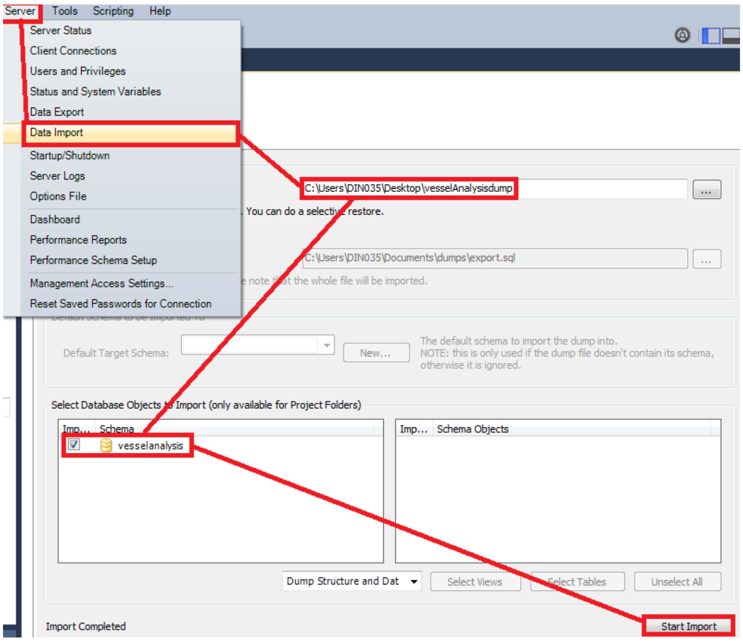
The name of the schema. It is recommended to use only alpha-numeric characters. Spaces should be avoide and be replaced by _

Refactor model, changing all references found in view, triggers, stored procedures and functions from the old schema name to the new one.

Collation: Server Default

Specifies which charset/collations the schema's tables will use if they do not have an explicit setting. Commo choices are Latin1 or UTF8.

Click *apply* and *finish* in the prompts, where the SQL-statement of creating the Schema is displayed again. In the final step, we want to import the tables with all the results which are contained in the vesselAnalysisDump.



C:\Users\DIN035\Desktop\vesselAnalysisdump

. You can do a selective restore.

C:\Users\DIN035\Documents\dumps\export.sql

e note that the whole file will be imported.

Default Target Schema:

The default schema to import the dump into.
NOTE: this is only used if the dump file doesn't contain its schema, otherwise it is ignored.

Select Database Objects to Import (only available for Project Folders)

☑ vesselanalysis

Dump Structure and Dat

Import Completed

In order to delete all containing results, sequences and individuals, these statements can be used:

```
delete from vesselanalysis.individuals WHERE 1;
delete from vesselanalysis.results WHERE 1;
delete from vesselanalysis.sequence WHERE 1;
```

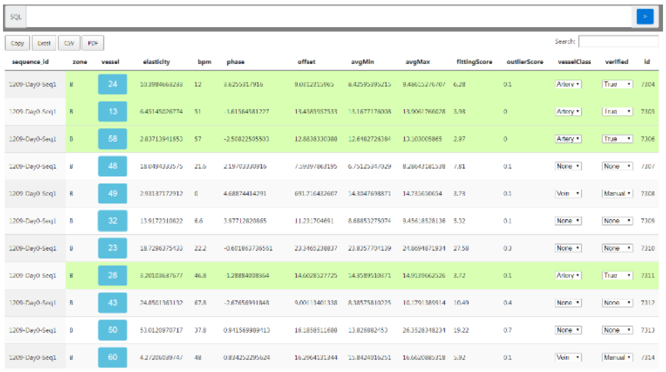
Now the database with the necessary Schema is up and running and the Python-Pipeline can connect to it and insert/retrieve the vessel analysis results.

Web based results browser

Assuming XAMPP was installed in the default dir C:\xampp:

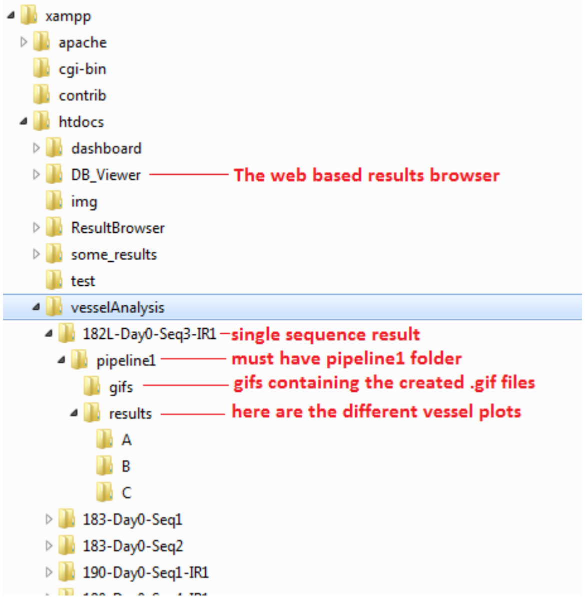
1. Copy the folder *DB*_Viewer into the directory *C:\xampp\htdocs\*
2. Create a new folder *C:\xampp\htdocs\vesselAnalysis\*
3. Open your browser and enter this into the URL (requires running Apache and MySQL modules):
   http://localhost/DB_Viewer/results.html

This should display the results browser and all the results from the results table. If the database is empty, then an error will occur. A reload of the page (and a database with results in it) will fix the displayed error.



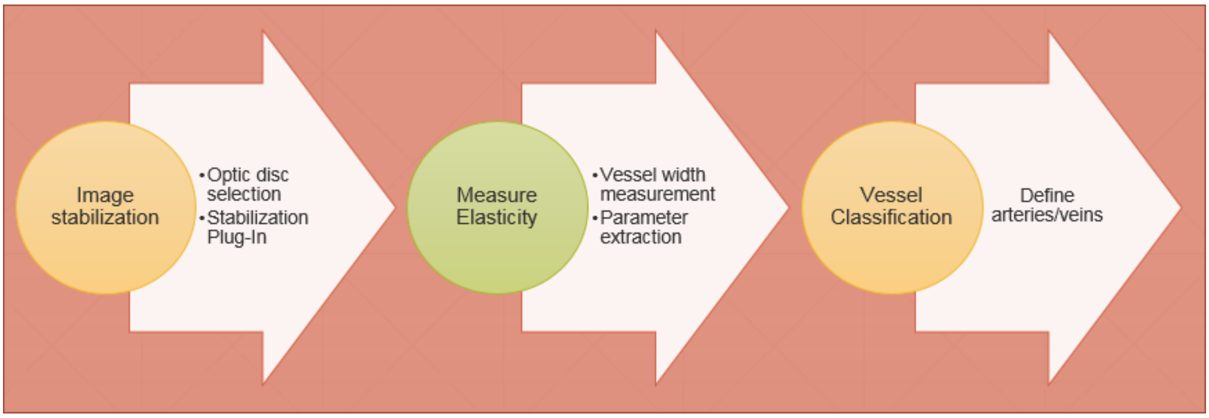
sequence_id	zone	vessel	elasticity	bpm	phase	offset	avgMin	avgMax	fittingScore	outlierScore	vesselClass	verified	id
1209-Day0-Seq1	B	24	10.3984663233	12	3.6255317916	9.0312315965	8.42595395215	9.48615276707	6.28	0.1	Artery	True	7304
1209-Day0-Seq1	B	13	6.45145026774	51	-1.61564581227	13.4585957533	13.1677176008	13.9061766028	5.98	0	Artery	True	7305
1209-Day0-Seq1	B	58	2.83713941653	57	-2.50822505503	12.8838330388	12.6482726384	13.103005865	2.97	0	Artery	True	7306
1209-Day0-Seq1	B	48	18.0494333575	21.6	2.19703330916	7.59397863195	6.75125347029	8.28643181538	7.81	0.1	None	None	7307
1209-Day0-Seq1	B	49	2.93137172912	0	4.68874414291	691.716432607	14.3047698871	14.735650654	3.73	0.1	Vein	Manual	7308
1209-Day0-Seq1	B	32	13.9172310822	6.6	3.97712820865	11.231704691	8.68853275074	9.45618528136	5.32	0.1	None	None	7309
1209-Day0-Seq1	B	23	18.7296375433	22.2	-0.601863736561	23.3465238837	23.8357704139	24.8694871934	27.58	0.3	None	None	7310
1209-Day0-Seq1	B	28	3.20103637677	46.8	1.28884008364	14.6028527725	14.3589510871	14.9139662526	3.72	0.1	Artery	True	7311
1209-Day0-Seq1	B	43	24.8501363132	67.8	-2.67656991848	9.00113401338	8.38575810225	10.1791389914	10.49	0.4	None	None	7312
1209-Day0-Seq1	B	50	53.0120970717	37.8	0.941569989413	16.1858511688	13.826882453	26.3528348234	19.22	0.7	None	None	7313
1209-Day0-Seq1	B	60	4.27206039747	48	0.834252295624	16.2964131344	15.8424016251	16.6620885318	5.92	0.1	Vein	Manual	7314

In order to click on the blue vessel numbers and display the plots as well as the width measurement gifs, the results of the vessel analysis pipeline have to be copied manually into the created directory *C:\xampp\htdocs\vesselAnalysis\*. This is the structure which is necessary for that:



```
xampp
  apache
  cgi-bin
  contrib
  htdocs
    dashboard
    DB_Viewer ——— The web based results browser
    img
    ResultBrowser
    some_results
    test
    vesselAnalysis
      182L-Day0-Seq3-IR1 —single sequence result
        pipeline1 ——— must have pipeline1 folder
          gifs ——— gifs containing the created .gif files
          results ——— here are the different vessel plots
            A
            B
            C
      183-Day0-Seq1
      183-Day0-Seq2
      190-Day0-Seq1-IR1
```

3. How to use the pipeline



Create a folder (*analysis folder*) where you copy all the separate sequence folders, which you want to analyse.

Image stabilization

1. Open ImageJ
2. Click *Plugins -> disc stabilization*
3. Select the first image of the sequence, which has to be stabilized
4. A frame opens up, click and drag a rectangle around the optic disc and click *ok*
5. A new folder pipeline1 is created in the same directory, where the image was selected. This folder contains the stabilized images as well as the disc parameters, which are used in the further processing during the pipeline
6. Repeat steps 2-4 for all sequences inside the *analysis folder*

Measure Elasticity

1. Set the *pathWithSequences* value as your path for the *analysis folder* like this:
   pathWithSequences = "C:\\Users\\DIN035\\Documents\\Project\\ ViktorDinkel\\SequencesToAnalyse\\"
2. Set the value of the variable *pipeline_step* in the file *IR_VesselSegmentation.py* to *2* like this:
   pipeline_step = 2
3. Run the IR_VesselSegmentation.py once. This will analyse all the folders inside your *analysis folder* and export the results to the database. If you don't want to use the database, then change the value in the config as follows:

   Config.py -> GetConfigForMeasurement -> AnalysisSteps -> 'exportToDB': False

All the results are saved in the corresponding \pipeline1\results\ folder of a sequence. The measurements are in the file classifiedVesselData.npy and measurements.npy (in the corresponding zones B and C) and can be loaded in the python code with the commands

```
np.load(<pathToTheFile>+'measurements.npy')
np.load(<pathToTheFile>+'measurements.npy').item()
```

The vessels are not classified or verified yet.

Vessel Classification

1. Set the value of the variable *pipeline_step* in the file *IR_VesselSegmentation.py* to *3* like this:
   pipeline_step = 3
2. Run the pipeline once for each sequence (automatically iterates over the sequences for each new start of the pipeline)
   a. Select with the left mouse click a vessel spline to be artery
   b. Right mouse click selects the vessel spline as vein
   c. Middle mouse click resets the classification of selected spline
3. After the selection is done, close the opened figure window with the red cross in the top right corner, in order to continue with the pipeline and export of the vessel classification to the database

For this step, the database is required as the results are exported to it (updates the vesselClass in the database). In case the database is not used, then the function *DBActions.py -> updateVesselData* can be modified in order to process the selected arteries/veins in a custom way.

Furthermore, finished vessel classifications are stored in the *finished.npy* file and are skipped for further vessel classifications. If a reset is required (for re-classification), then the easiest way is to delete the file *finished.npy* although this also means, that all sequences within the folder, which have been classified, will have to be classified again if the code is run. A custom workaround can be programmed by manipulating the loaded *finished.npy* in the vessel classification step (adding/removing sequences).

This vessel classification step automatically sets the verified status of vessels, which have an outlier score <= 0.1 and were classified as arteries, to *True*.