Interactive visualization and analysis of morphological skeletons of brain vasculature networks with VessMorphoVis

Supplementary Document

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March 27, 2020

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1 File formats

1.1 ASCII file format

The ASCII file format (.vmv) of the vasculature has the following structure.

1. Any line that starts with # is simply a comment.

2. At the beginning of the file we enumerate the parameters of the vertices and strands between $PARAM_BEGIN and $PARAM_END clauses.

   ```
   $PARAM_BEGIN
   NUM_VERTS
   NUM_STRANDS
   NUM_ATTRIB_PER_VERT
   $PARAM_END
   ```

3. The vertex list is instered between `$VERT_LIST_BEGIN` and `$VERT_LIST_END` clauses, where each item in the list has the following structure:

   - Vertex index (ESSENTIAL)
   - X-coordinate (ESSENTIAL
   - Y-coordinate (ESSENTIAL)
   - Y-coordinate (ESSENTIAL)
   - Z-coordinate (ESSENTIAL)
   - Radius (ESSENTIAL)
   - Other attribute 1 (Optional)
   - Other attribute 2 (Optional)

   For example:

   ```
   $VERT_LIST_BEGIN
   1 1.0 2.0 3.0 1.0 1.0
   2 5.0 3.0 4.0 2.0 3.0
   $VERT_LIST_END
   ```

4. The strands lists are insteretd between `$STRANDS_LIST_BEGIN` and `$STRANDS_LIST_END` clauses where each item has the following structure:

   - Strand index

- List of indices that correspond to those of the vertices specified in the defined vertex list

For example:

```
$STRANDS_LIST_BEGIN
1 3 6 2 4 5 8
2 3 4 7 2 6 10
3 77 4 7 2 8 8
$STRANDS_LIST_END
```

1.2 HDF5 file format

The Blue Brain Project uses an internal file format based on HDF5 to store morphologies of vasculature files. HDF5 is a binary format. It has the advantage of being scalable, efficient and supported in many languages. As the vasculature network can be seen as a graph, the file stores a dataset of edges between each sections and another one with the 3D coordinate of the sections themselves (as they are constituted by a succesion of 3D points). Finally a third dataset stores the type of each section (vein, artery, venule, etc.).

2 Supplementary figures

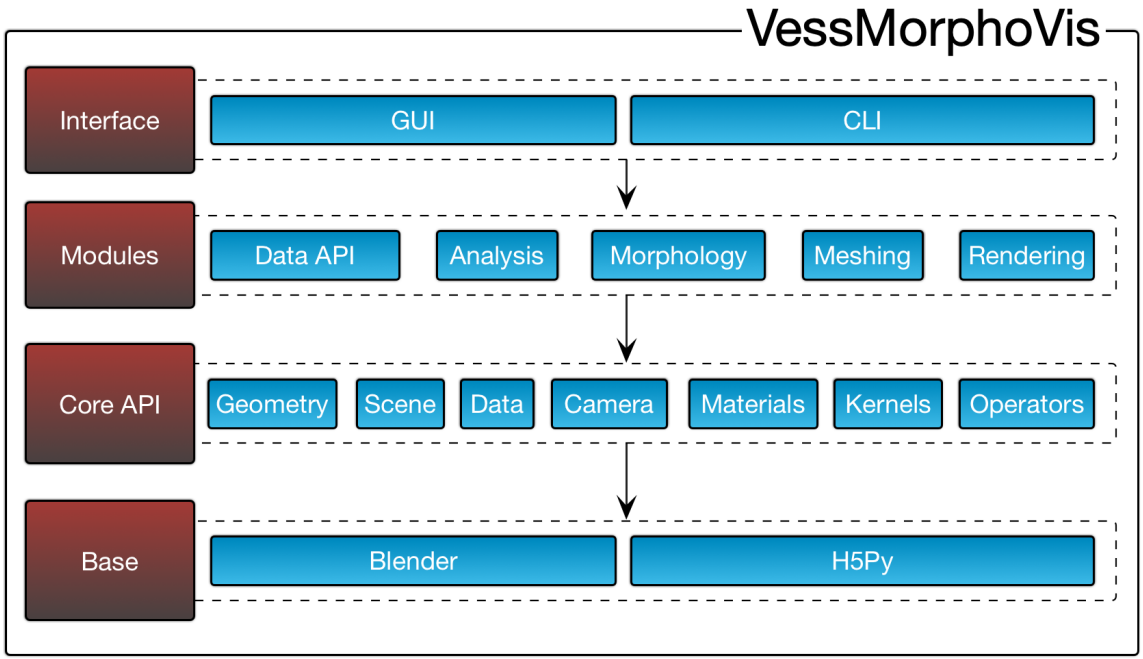

Figure S1: *VessMorphoVis* system architecture.

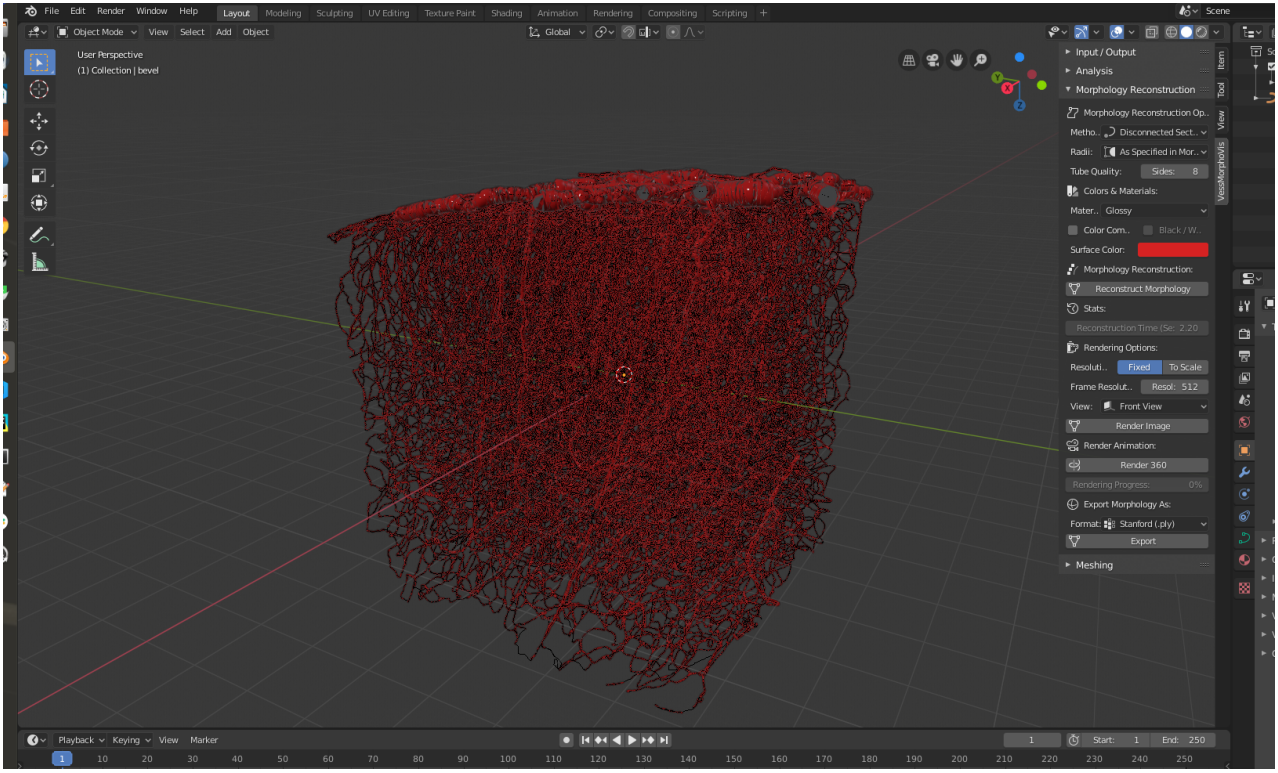

Figure S2: Loading and reconstructing a large vasculature morphology in Blender with VessMorphoVis.

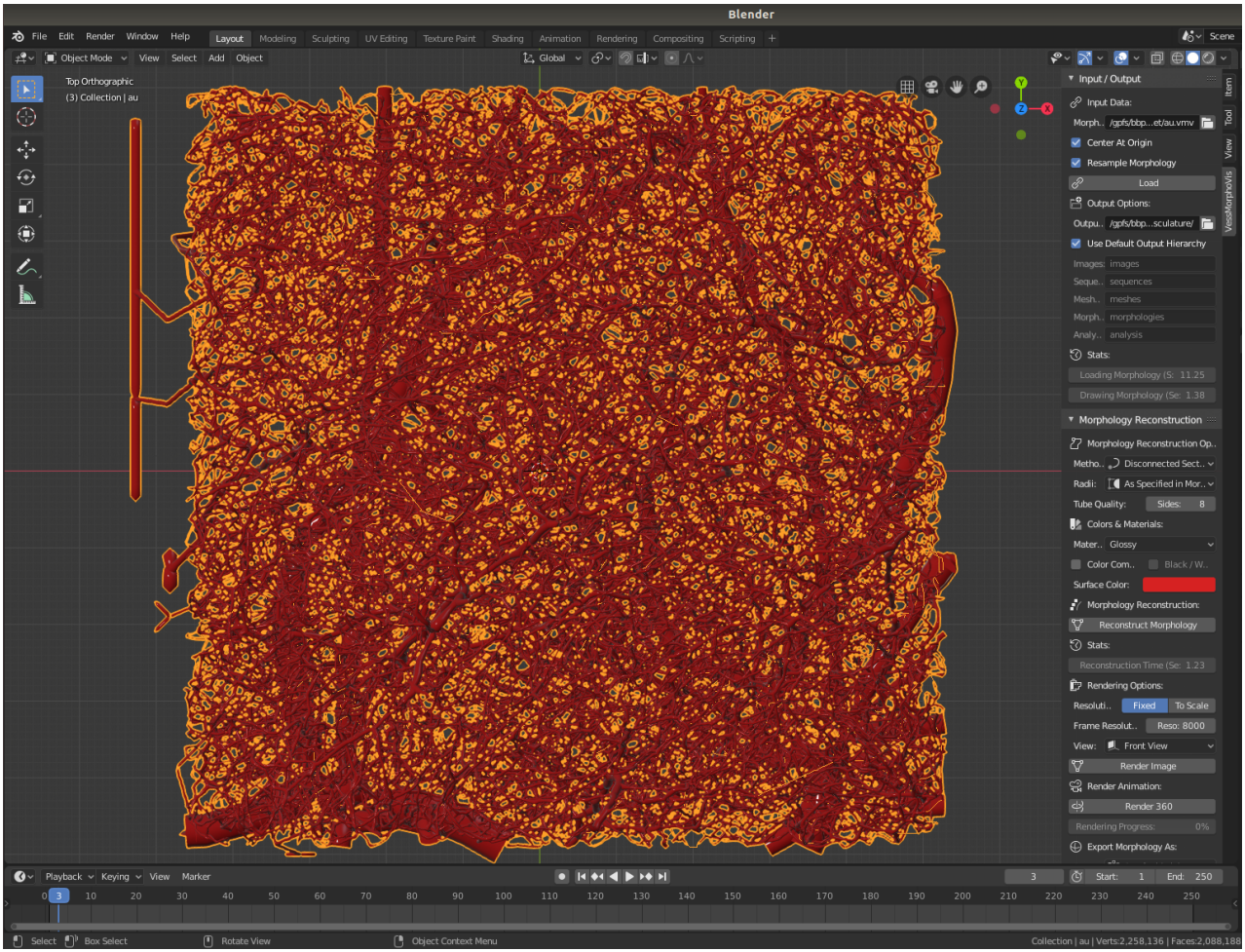

Figure S3: Visual analysis of the dataset loaded in Figure S2. The morphology skeleton has been resampled to remove the artifacts due overlapping samples.

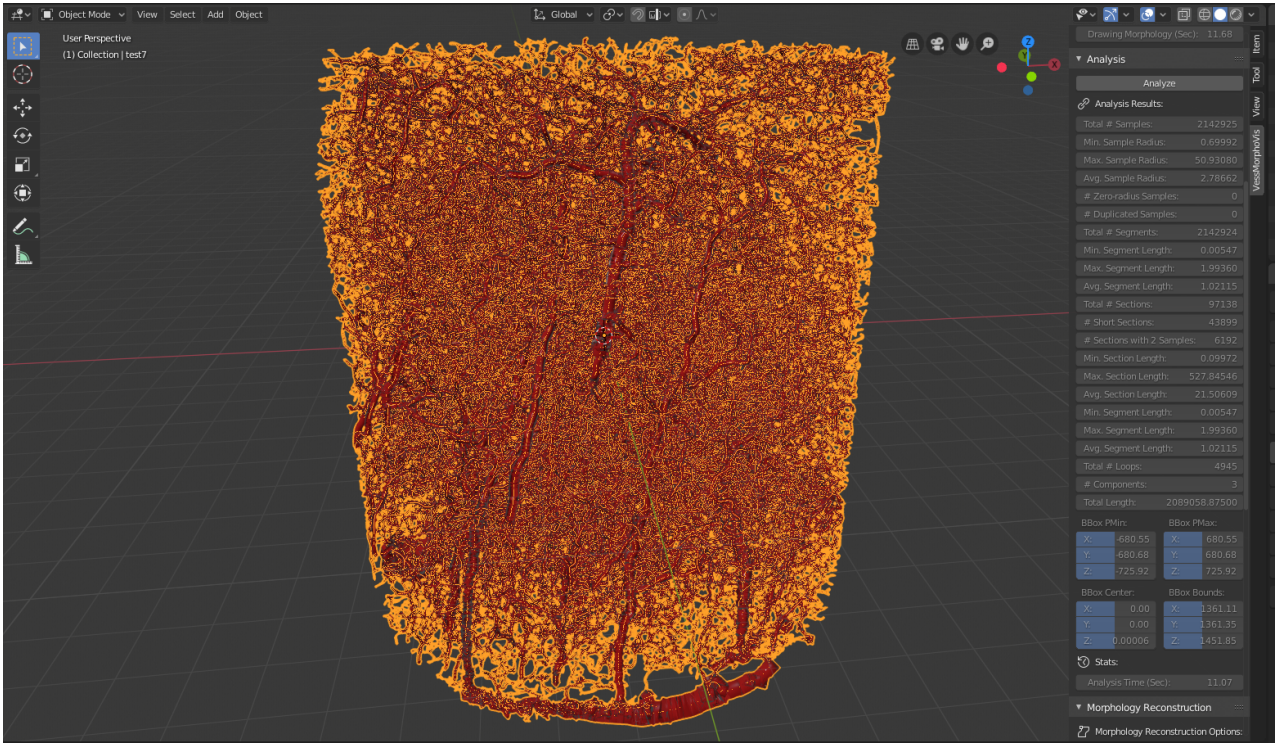

Figure S4: The analysis panel shows a fact sheet containing the analysis results of a vascular morphology consisting of ∼2.1 million samples. The analysis of the entire graph was performed in 11 seconds.

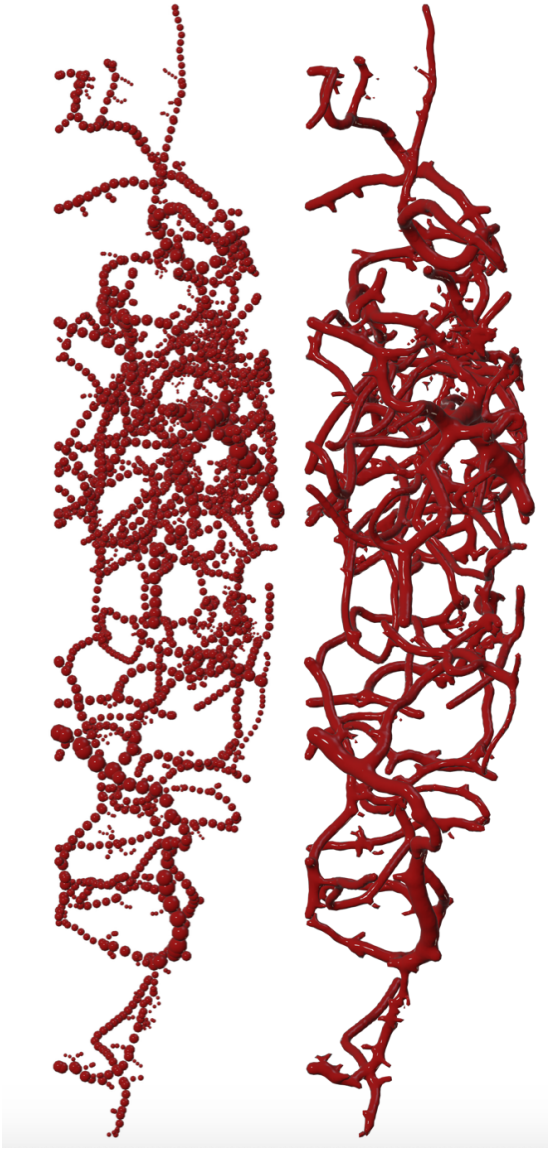

Figure S5: Using the samples builder to visualize the individual samples of the morphology might be cluttering compared to visualizing its connectivity for large morphologies.

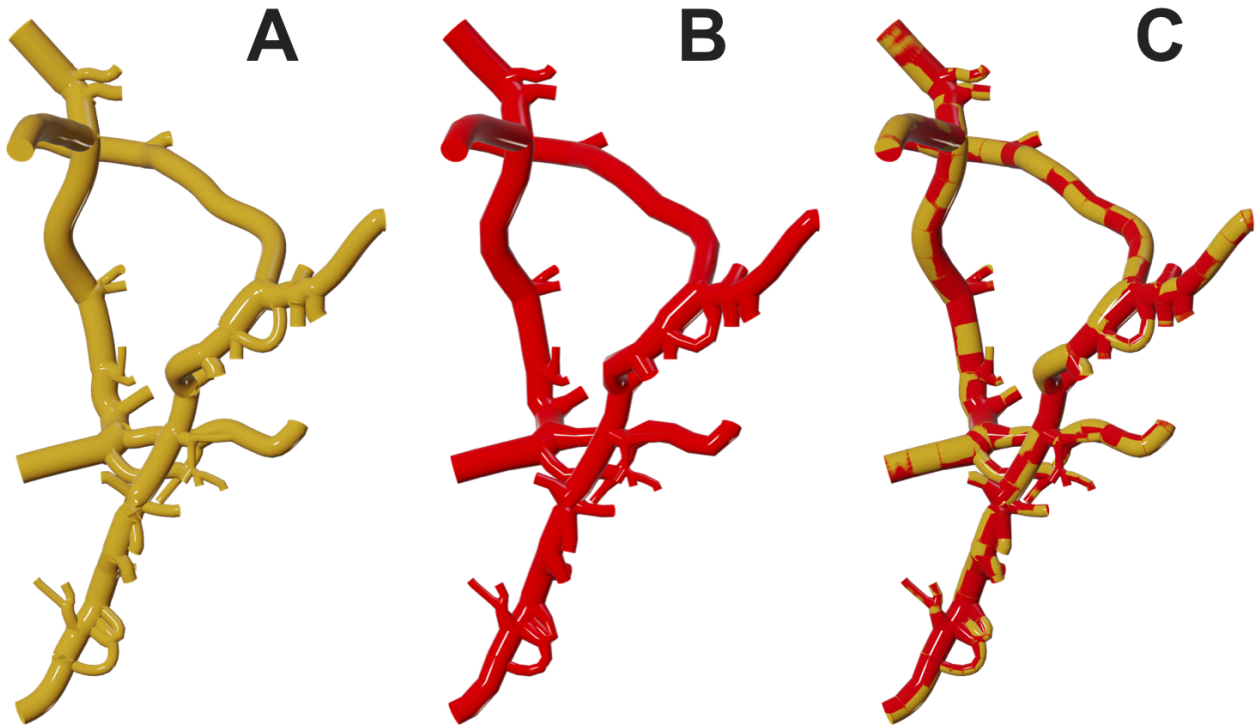

Figure S6: Validating morphology resampling. The original morphology skeleton in (A) used to validate the resampled one in (B) by creating a combined rendering of the two morphologies on top of each other where we can visually see the differences between the two skeletons.

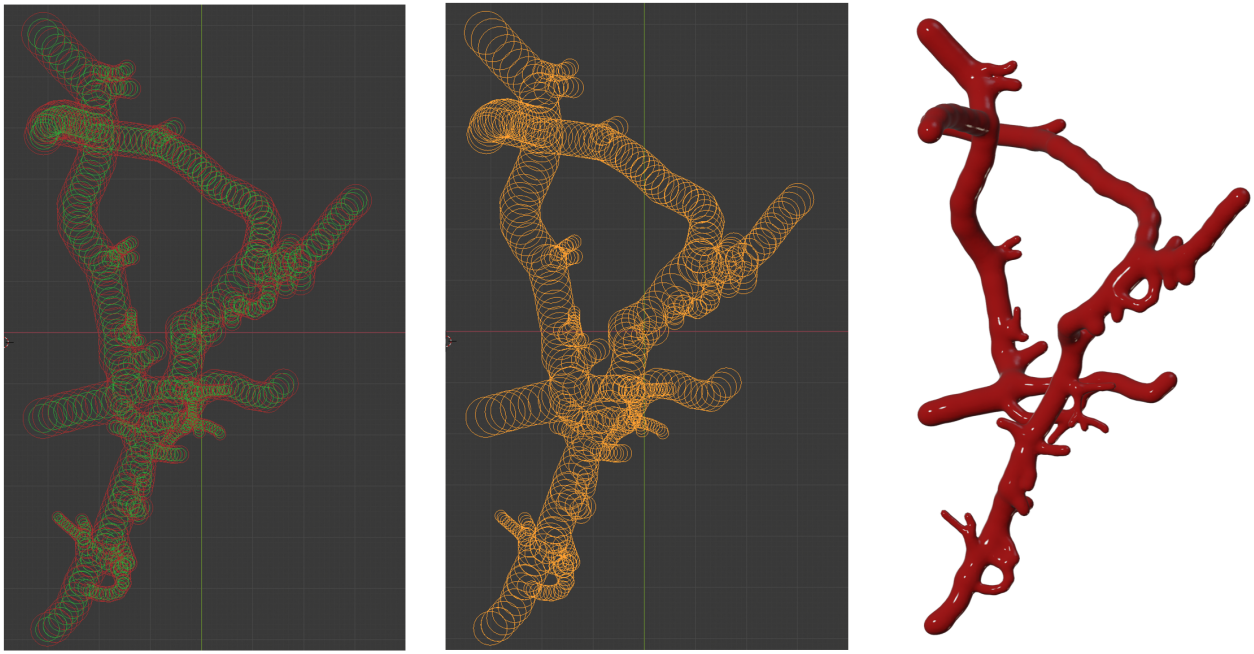

Figure S7: Meta balls meshing. The steps of building a meta object from a morphological skeleton and converting the final result into a manifold surface mesh.

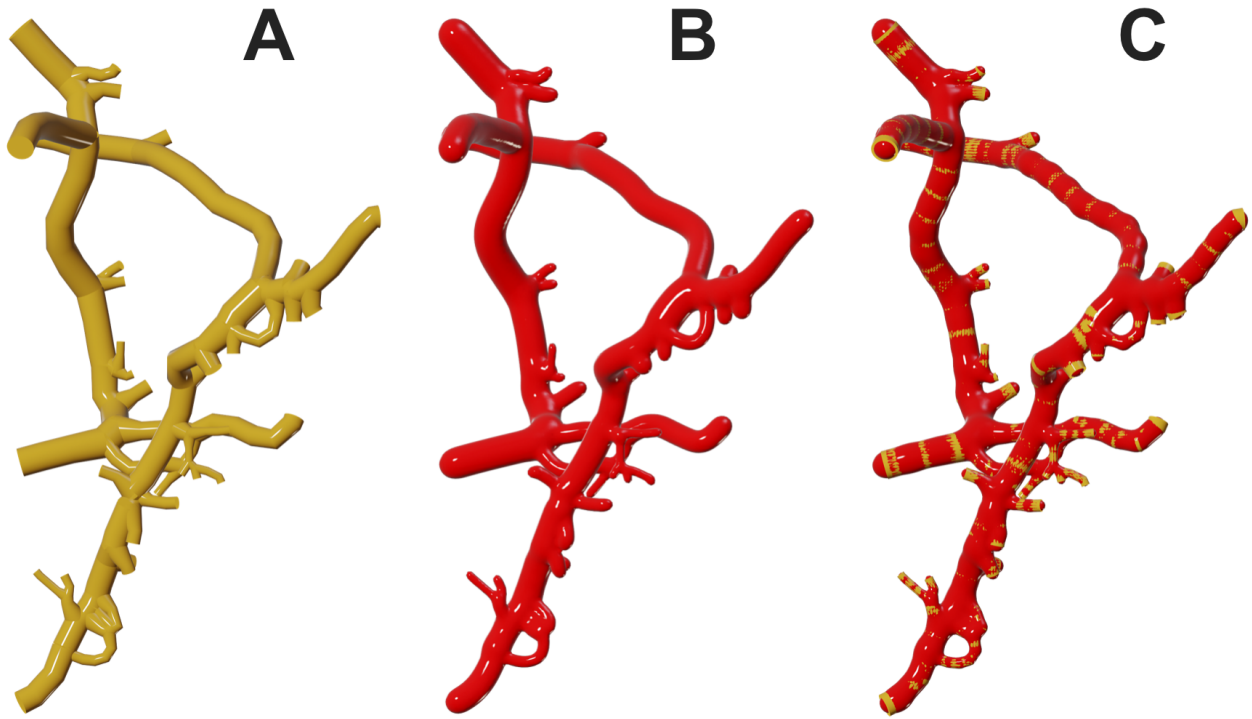

Figure S8: Validating reconstructed meshes from the MetaBalls implementation. The morphology skeleton in (A) is used to validate the reconstructed mesh in (B) by creating a combined rendering of both structures on top of each others to reveal the differences visually.

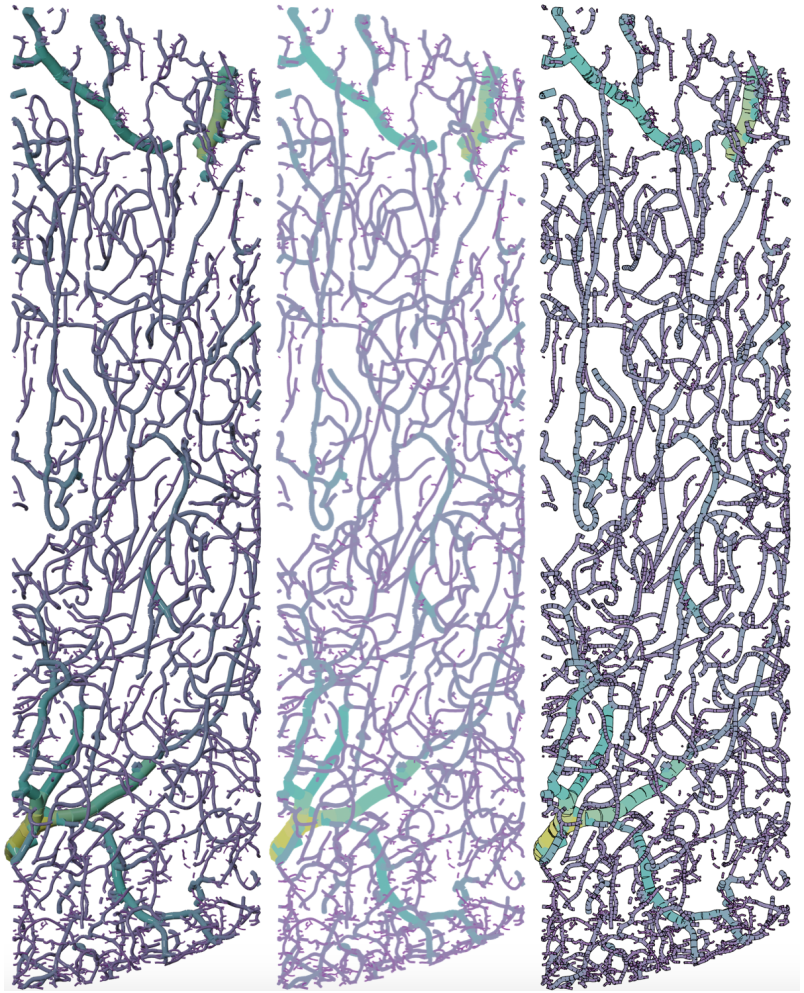

Figure S9: Using different shading styles with a radius-based colormap applied to every segment in the morphology.

3 Supplementary videos

3.1 Video V1

https://www.youtube.com/watch?v=LLDj0AM7_-k

3.2 Video V2

https://www.youtube.com/watch?v=nePn8HJ2sSM

3.3 Video V3

https://www.youtube.com/watch?v=QfOQPS5wZAM

3.4 Video V4

https://www.youtube.com/watch?v=GyXfHHpk2M8

3.5 Video V5

https://www.youtube.com/watch?v=cTqipOYKz7A

3.6 Video V6

https://www.youtube.com/watch?v=266C6hjy-lk

4 GUI panel and modules

4.1 Data handling

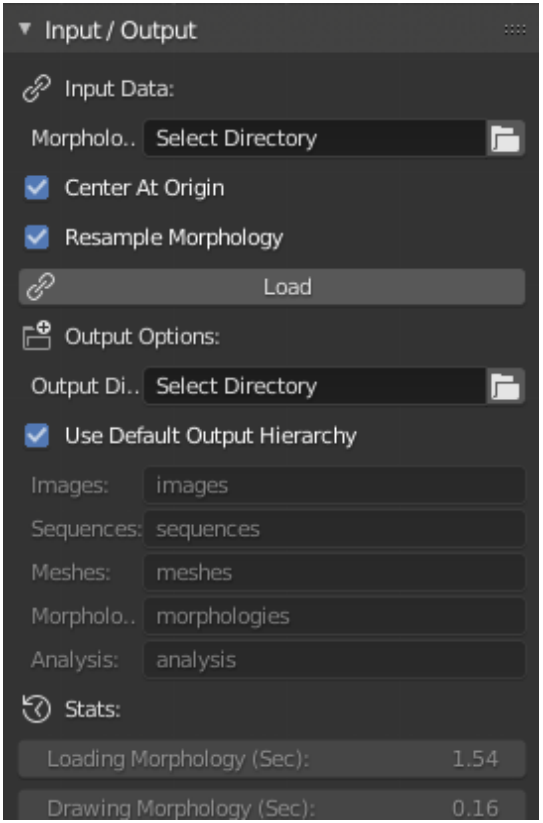

Figure S10: The data handling module is responsible for loading morphologies of different types, resampling them and setting the root output directory where all the results will be generated.

4.2 Analysis

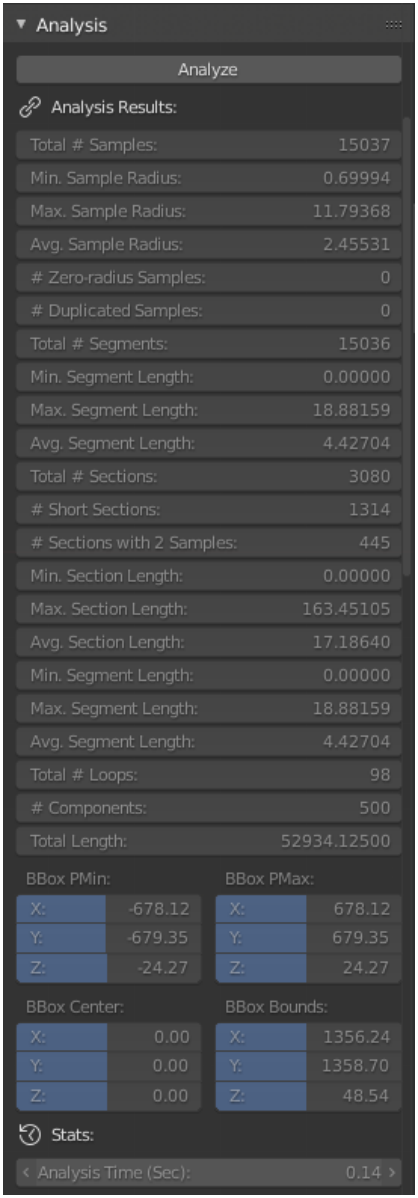

Figure S11: The analysis module contains a single button, when clicked, all the analysis results will be generated and displayed in a fact sheet on this panel.

4.3 Morphology reconstruction

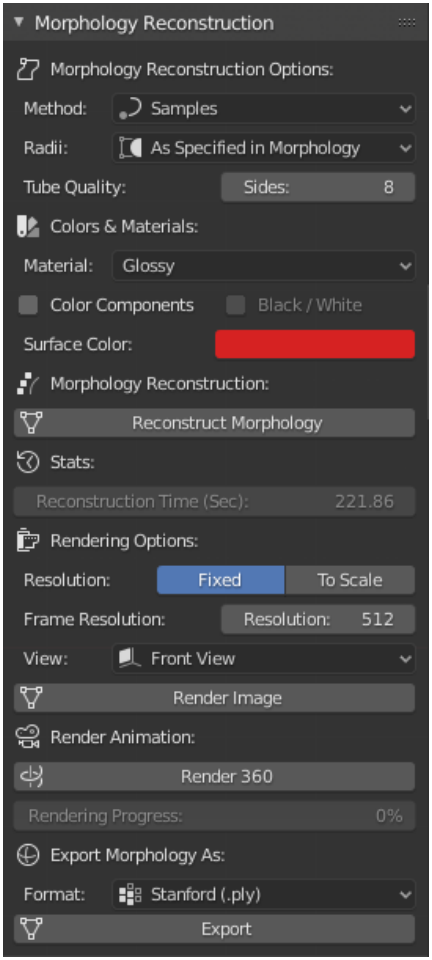

Figure S12: The morphology reconstruction options are exposed to the user within the morphology panel.

4.4 Mesh reconstruction

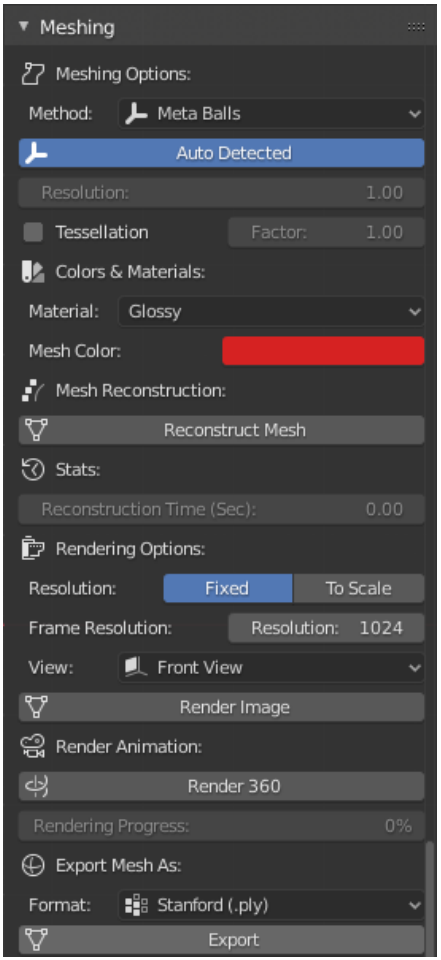

Figure S13: The mesh reconstruction options are exposed to the user within the morphology panel. Note the morphology parameters applied in the morphology panel, Figure S12 will be applied on the morphology skeleton before the meshing stage.