Simvascular: Optimizing 3D and Comparing 3D models

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Abstract: Patient-specific blood flow modeling was pioneered in the late 1990's to investigate and predict the progression of cardiovascular disease, and in recent years, has proven to be a powerful tool in clinical research [3]. In the 2000's, researchers needed to purchase very expensive and robust specialized commercial tools for arterial model construction and blood flow simulation. Recently, a team of researchers at Stanford and UC Berkeley has promoted research in this area by creating an open source software pipeline called SimVascular. SimVascular provides a framework to reconstruct an arterial model from MRI or CT data, and then perform blood flow simulations on the reconstructed model. Despite being the leading computational tool for arterial modeling and blood flow simulation, it still takes an experienced user multiple hours to create an arterial geometry in SimVascular. This presentation will discuss our efforts to: (1) Lead the development of open source one-click conversion of image data into accurate 3D arterial models, (2) compare the open source models to previously created commercial models, and (3) make available a large number of open source arterial models that are ready for blood flow simulation and disease investigation. Through these efforts the group hopes to demonstrate the validity of the open source components of Simvascular. And ultimately, the goal of the Simvascular project is to allow for the proliferation of accurate arterial models and simulations into the hands of medical professionals.
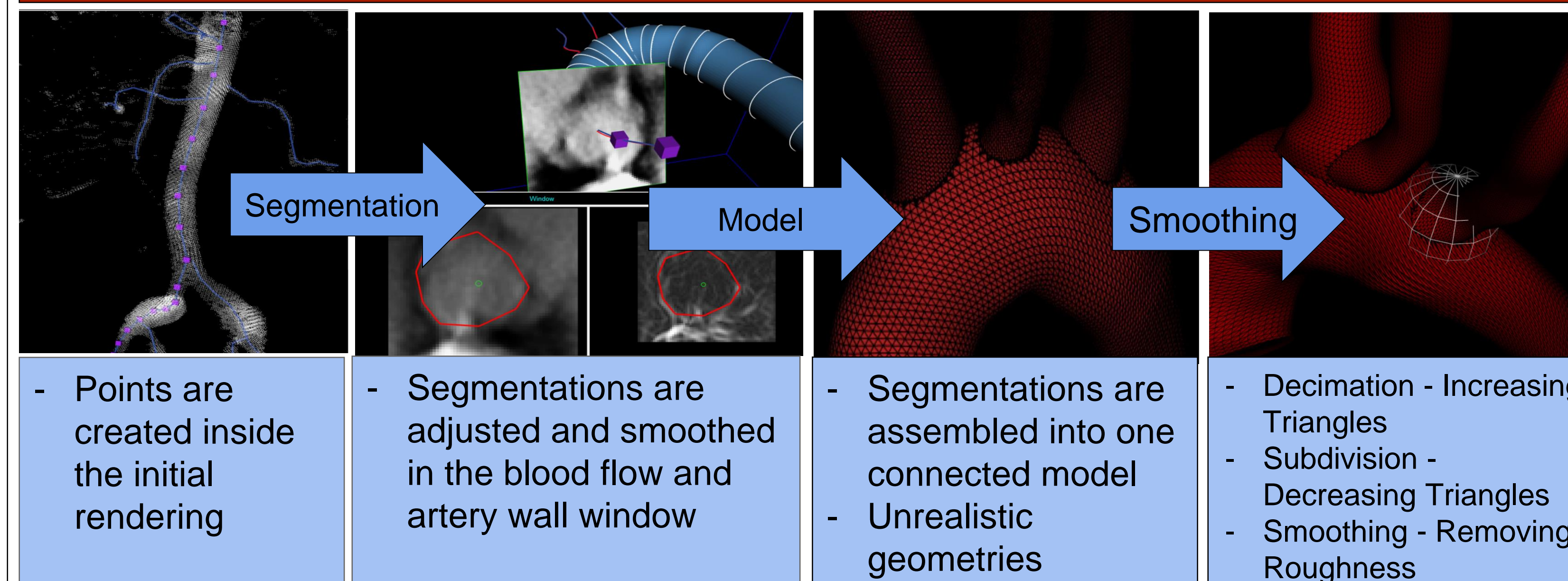
Motivation

- Cardiovascular disease is the leading cause of death worldwide
  - Caused or enhanced by disruptions of blood flow
- In 2000's researchers required expensive commercial tools for arterial modeling
- Simvascular was created to reconstruct an arterial model from MRI and CT image data
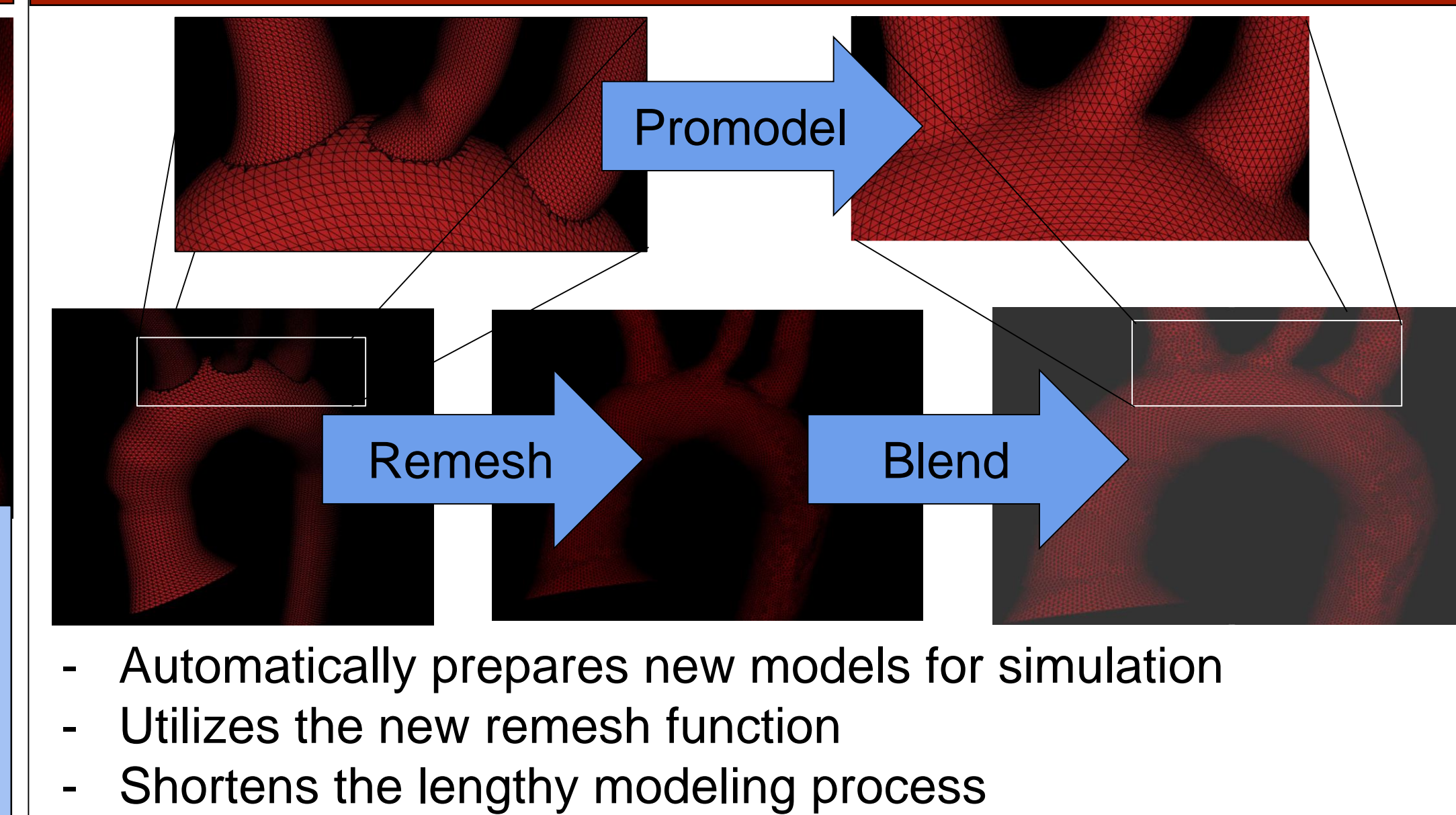- Currently has open source components that need to be compared to previously commercial components

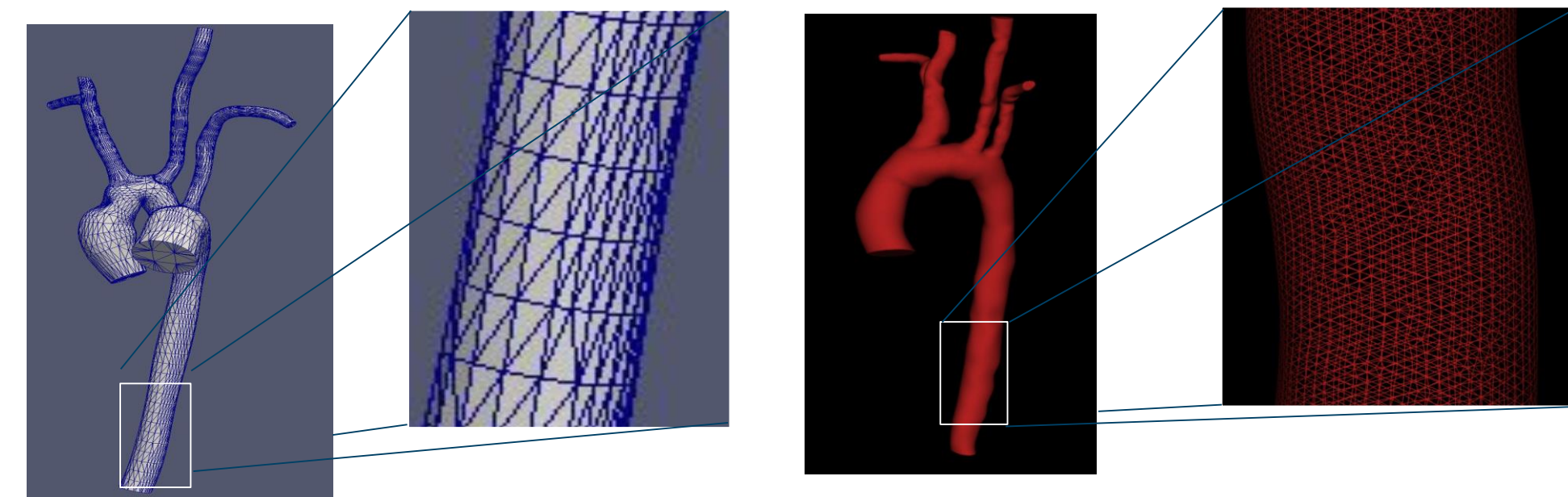[1] Plaque formation

Model Creation

Segmentation → Model → Smoothing

- Points are created inside the initial rendering
- Segmentations are adjusted and smoothed in the blood flow and artery wall window
- Segmentations are assembled into one connected model
- Unrealistic geometries
- Decimation - Increasing Triangles
- Subdivision - Decreasing Triangles
- Smoothing - Removing Roughness

Promodel

Remesh → Blend → Promodel

- Automatically prepares new models for simulation
- Utilizes the new remesh function
- Shortens the lengthy modeling process

Comparing Models

- Parasolid: Commercial
  - Analytic modeling
- Polydata: Open Source
  - Points form triangles

Average Hausdorff distance
- Maximum distance between two surfaces $d(\mathcal{S},\mathcal{S}') = \max_{p \in \mathcal{S}} d(p,\mathcal{S}').$

$$d_s(\mathcal{S},\mathcal{S}') = \text{Mean}\left[d(\mathcal{S},\mathcal{S}'), d(\mathcal{S}',\mathcal{S})\right].$$

Average Closest Distance
- The mean distance between each surface
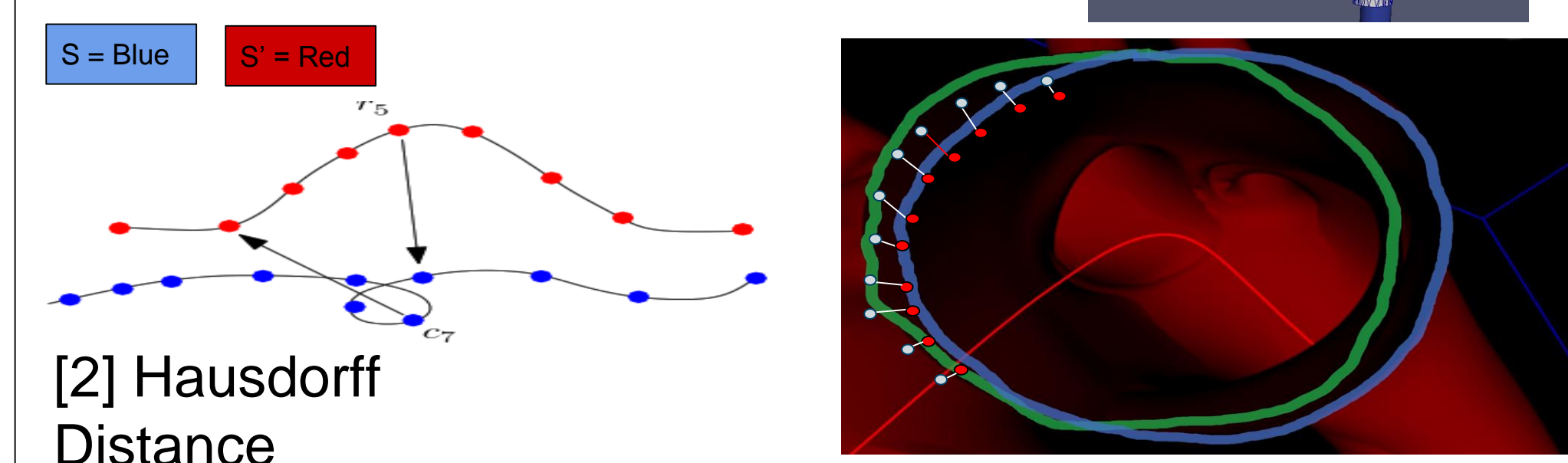
S = Blue   S = Red

[2] Hausdorff Distance

Results

Case 1: Compare Parasolid models of different triangle edge sizes
- Used as a control
- Same model

0.15 cm → 0.35 cm + 0.15 cm ← 0.35 cm

1.7cm
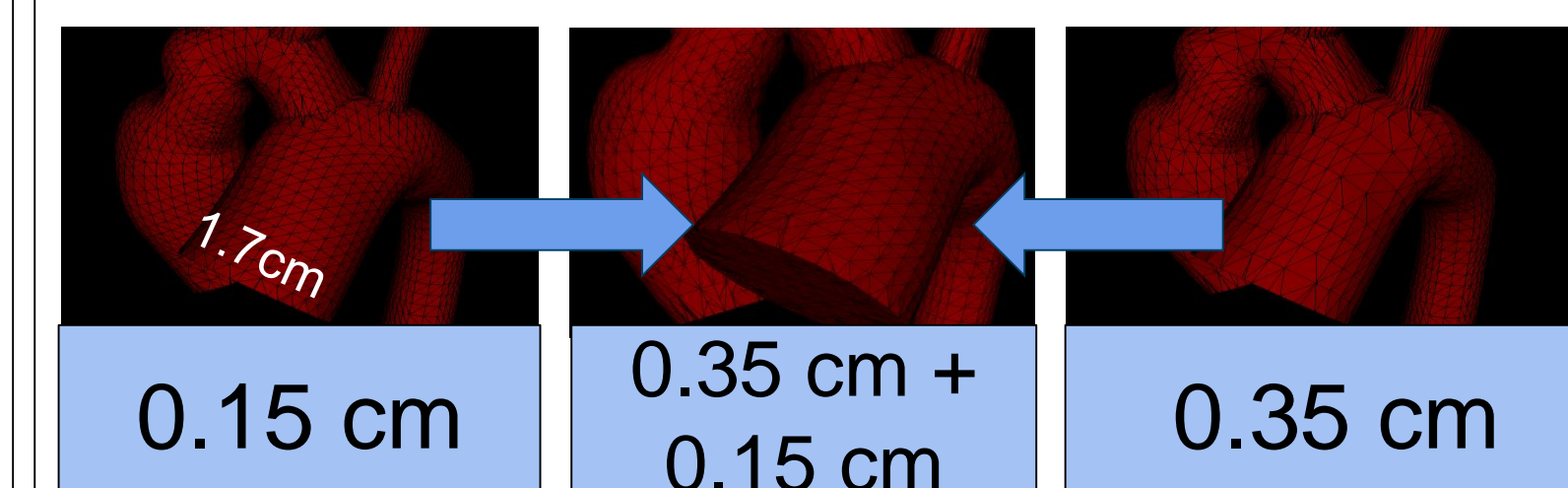
Case 2: Parasolid to Polydata created from same segmentations (Figure 1)
Case 3: Previous Polydata models, compared to Polydata models created from new segmentation (Figure 2 &3)
- Models are remeshed to the same edge size

Figure 2.

Average Distance Forward: New PolyData Models

Figure 1.

Average Hausdorff
Average Distance Forward
Average Distance Backwards

Average Distance Forward: Old Segmentations

Figure 3. Average Hausdorff Distance: New PolyData Models

Discussion

- Case 2 (Figure. 1) had average distance values around .027 cm, a small difference between Polydata and Parasolid models as compared to control, lofting method did not have a large effect.
- Case 3 (Figure 2 & 3) had average distance and hausdorff distances all larger than the average distance graph given in case 1.
- Using new tools in Simvascular, it is clear that the newer models match the image data more closely.

Conclusion

- 15 models were successfully created, deposited and ready for blood flow simulation.
- An automatic model preparation function was successfully created, moving closer to one step conversion of image data into models.
- A metric was created for the assessment of the average distance and hausdorff difference between two models.
- Using the same segmentations, creating models in Polydata or Parasolid format did not have a large effect on models.
- Further work needs to be done to automate the lengthy segmentation process.

References

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[2] Structural Bioinformatics Library, [Image]. Available http://sbl.inria.fr/doc/Conformational _ensemble_comparison-user-manual.html:
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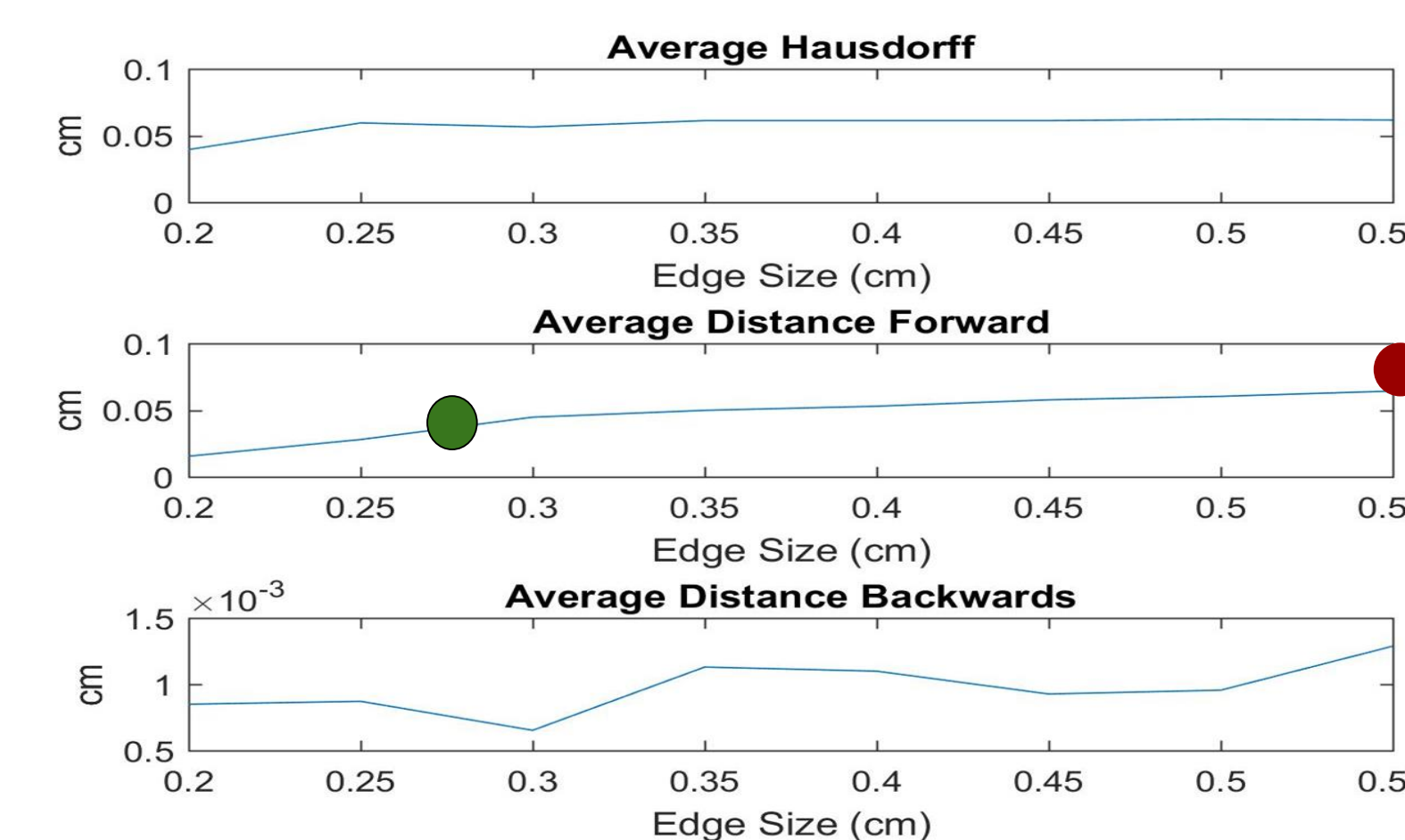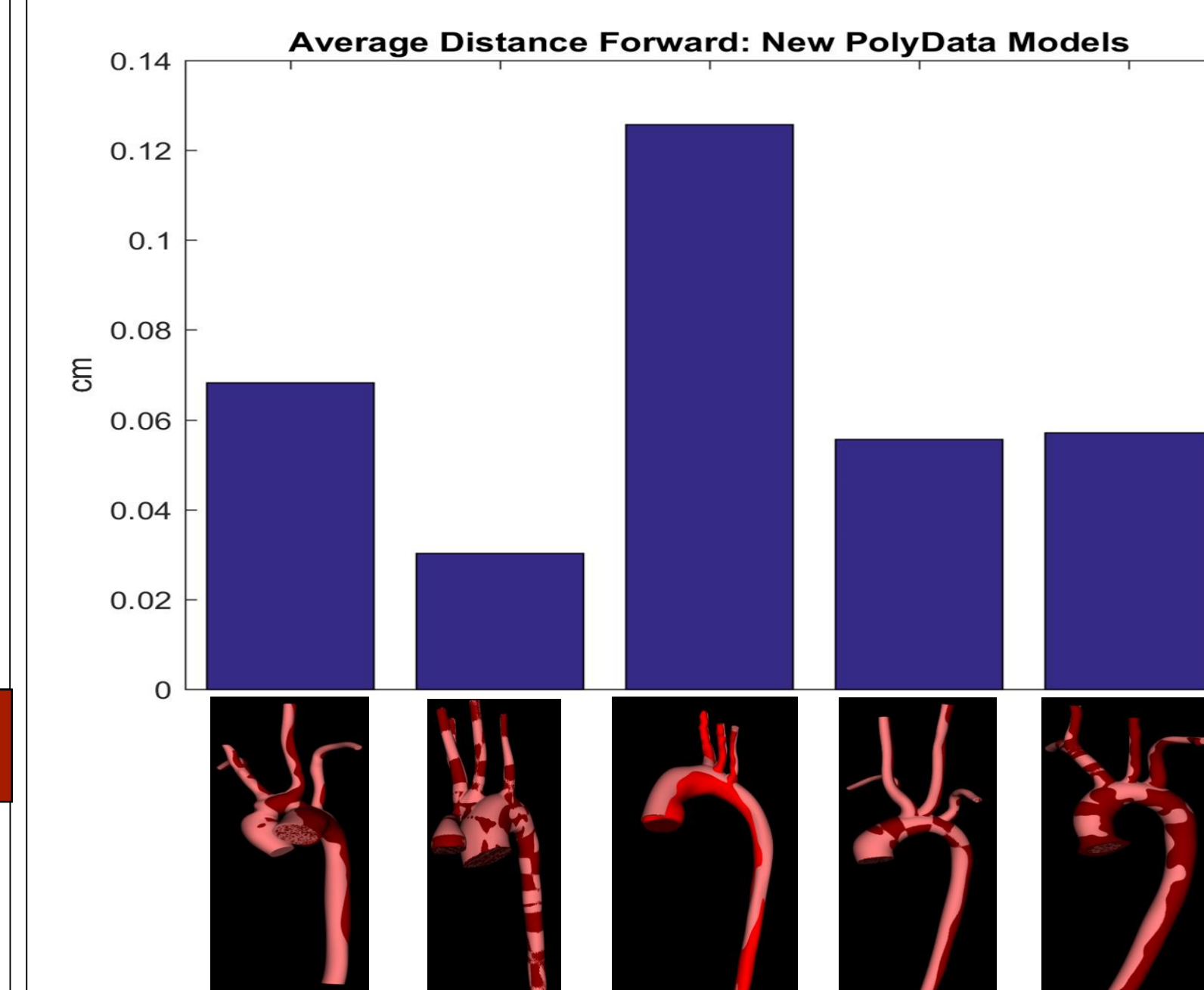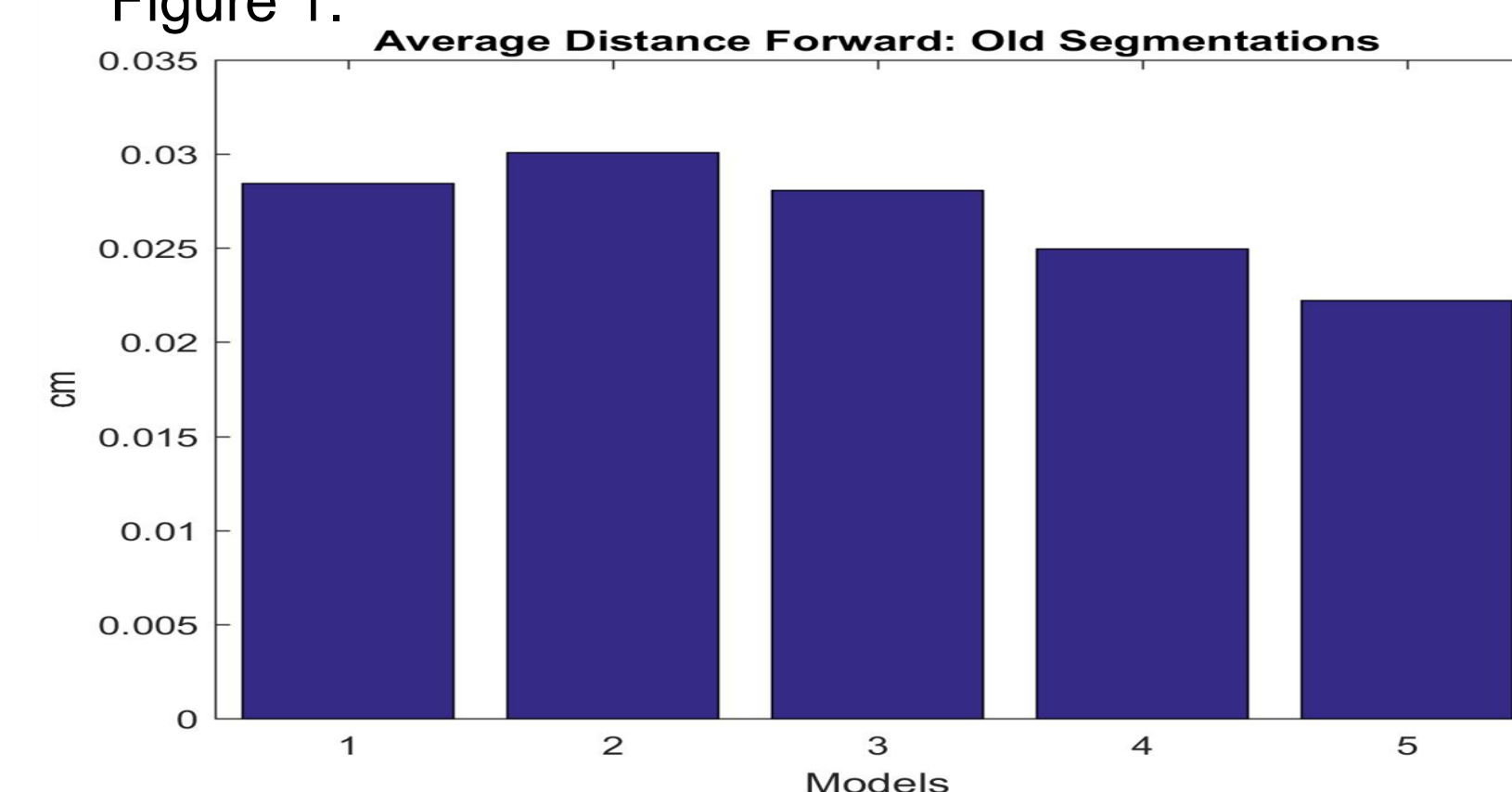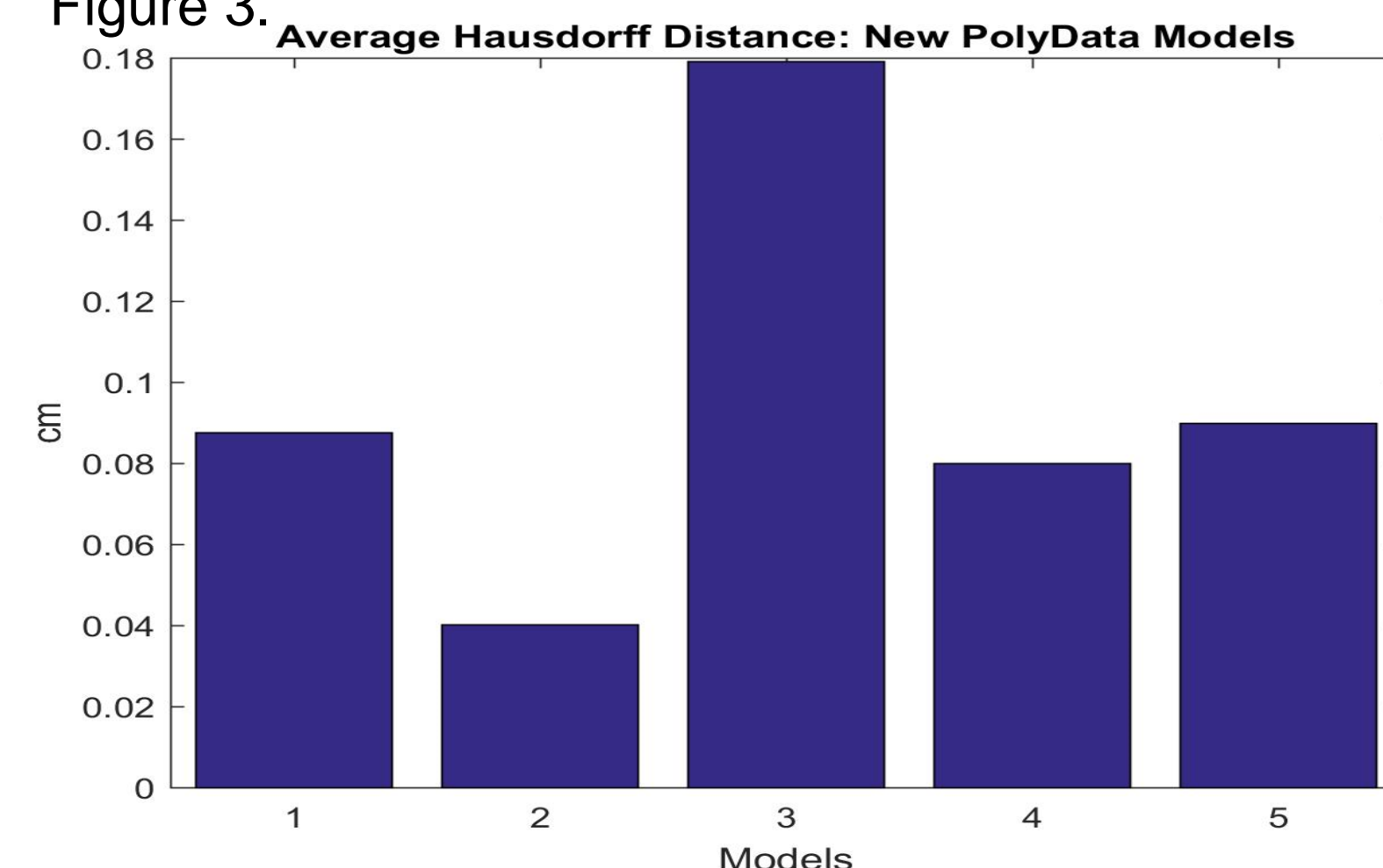
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