

Coronary Artery Tracking with Rule-based Gap Closing

Masterstudium:
Medizinische Informatik

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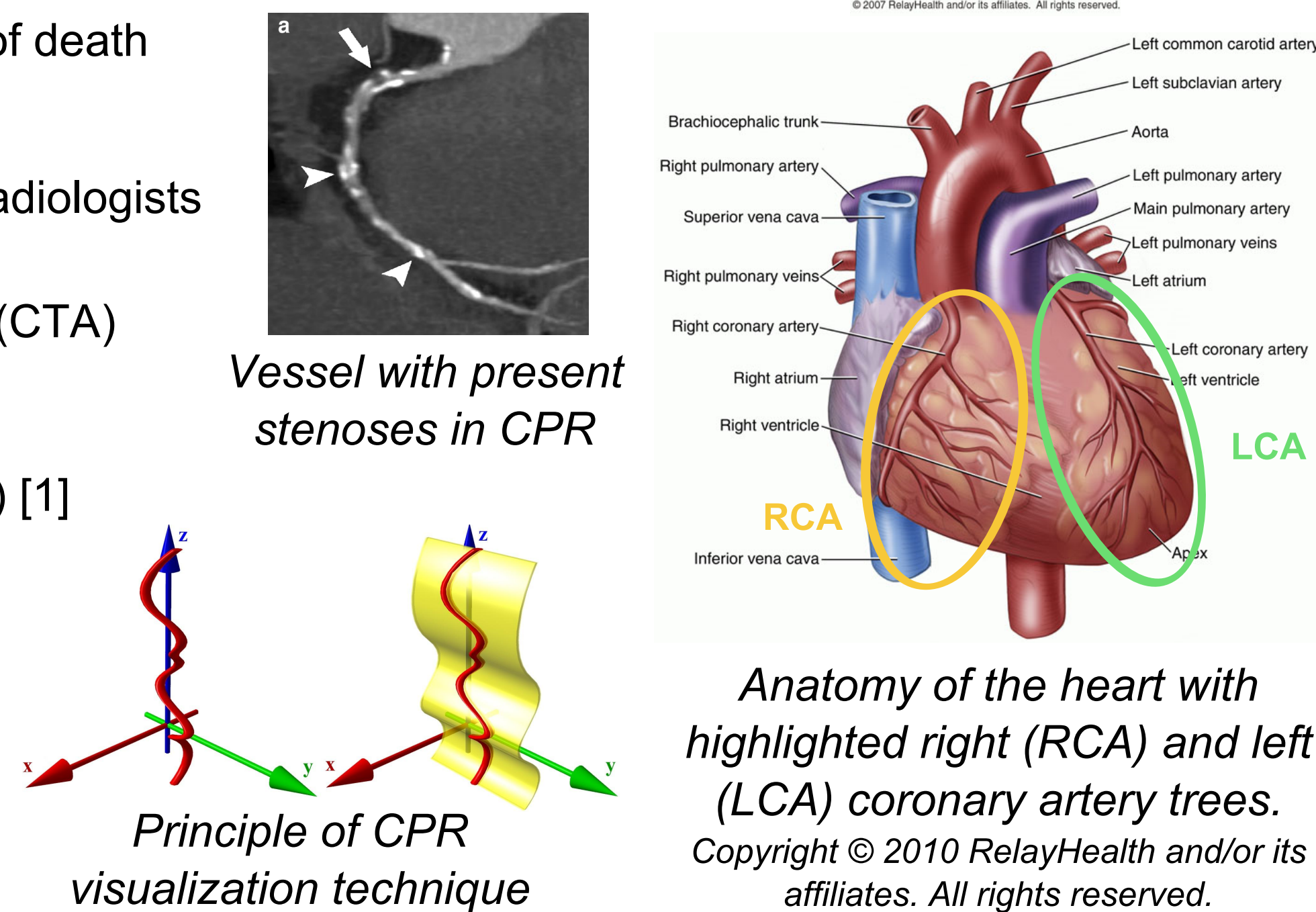
Motivation

Problem:

- Coronary artery (CA) diseases are among the leading causes of death in the industrial countries
- Increased demand of robust methods to support diagnosis of radiologists
- Detailed assessment of CA vessels by use of CT angiography (CTA) in extended diagnosis
- Visualization techniques like Curved Planar Reformation (CPR) [1] are based on extracted centerline of the blood vessel lumen

Goal:

- Accurate and complete centerline extraction of the CA trees
- Use advantages of existing methods



Basic Approaches

Method of Zambal et al. [2]:

- Top-down approach
 - Identify roots of CA tree by local symmetry feature
 - Tracking of CA trees by iterative matching of cylindrical shape models
- + Very accurate centerline
- Vessels terminate prematurely in areas of low contrast

Method of Bauer et al. [3]:

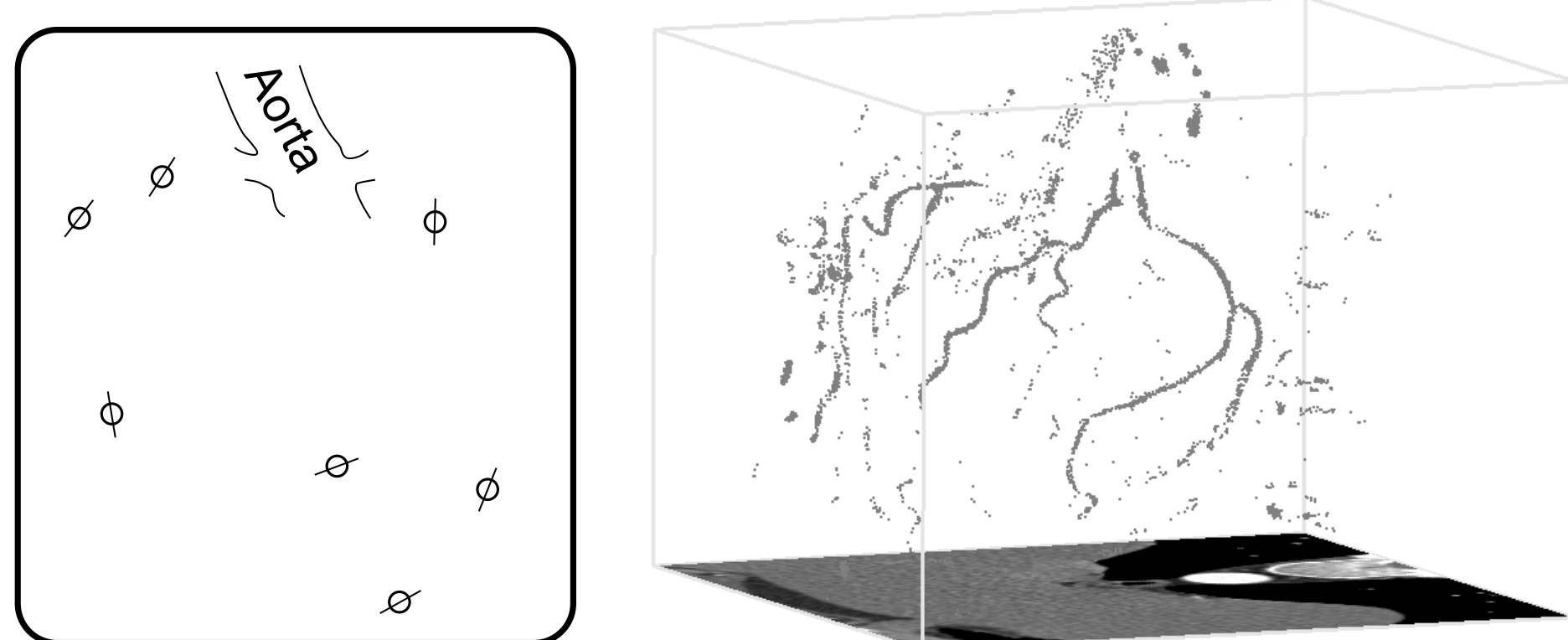
- Bottom-up approach
 - Extract centerlines using gradient vector fields
 - Link centerlines based on distance and orientation to each other
- + High overlap due to linking over areas of low contrast
- Lower accuracy than Zambal et al. [2]

Novel approach:

- Combination of the highly accurate tracking method of Zambal et al. [2] with segment linking similar to Bauer et al. [3]

Coronary Artery Tracking Framework

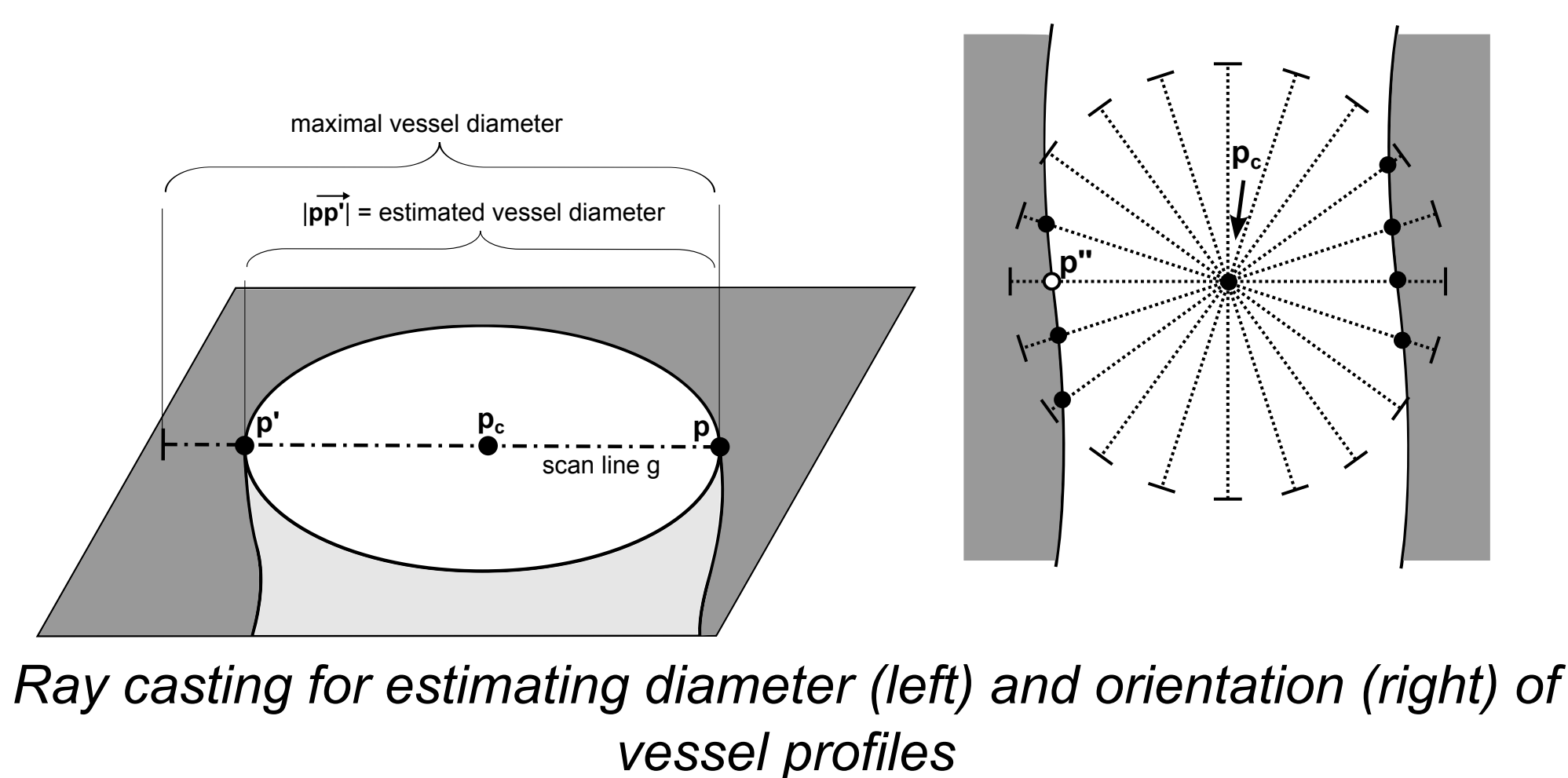
Phase I: Seed calculation



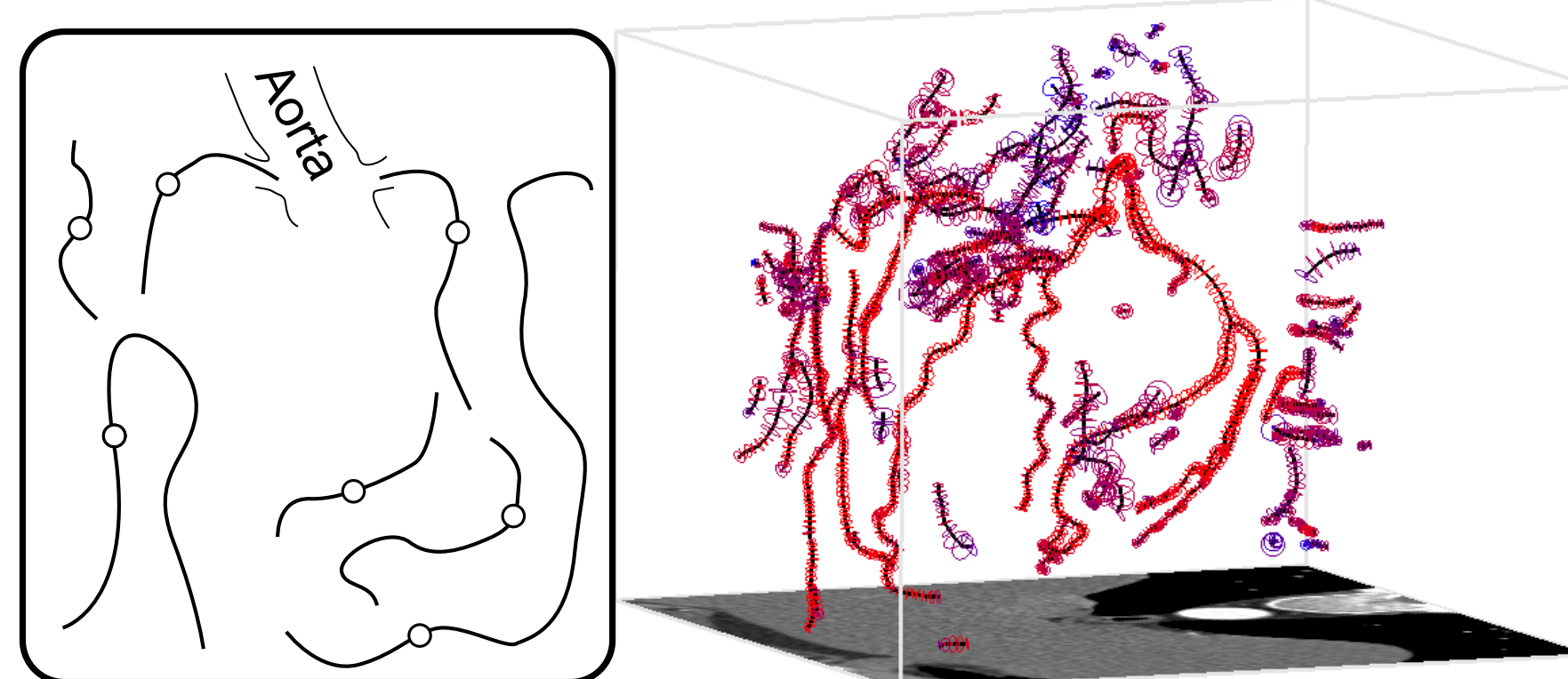
Output: Initial seeds for vessel segment tracking, schematic (left) and on CTA dataset (right).

Method:

- Estimate vessel profiles at each position in dataset
- Use ray casting based on gradients at vessel surface



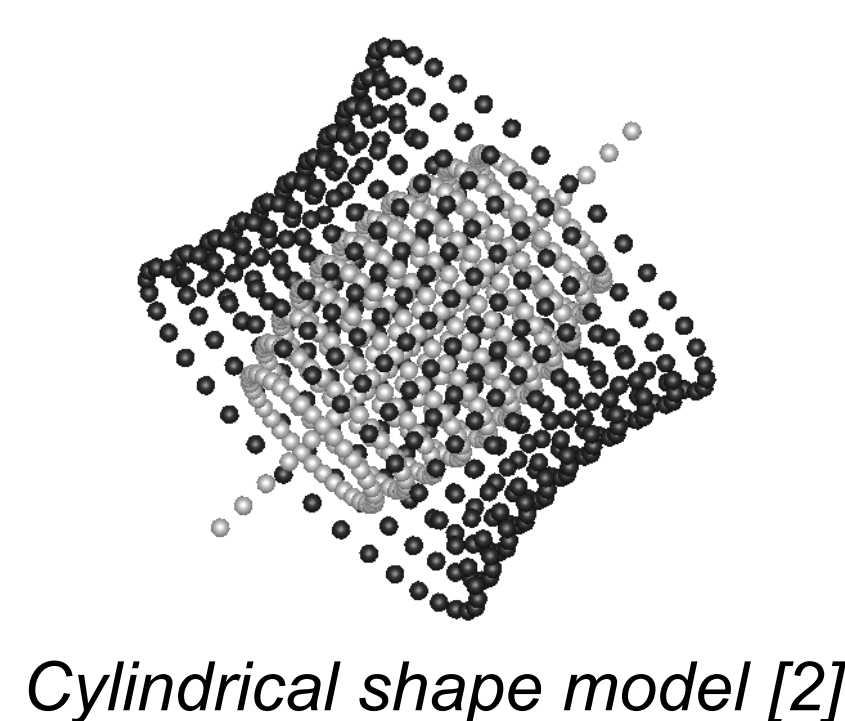
Phase II: Tracking of vessel segments



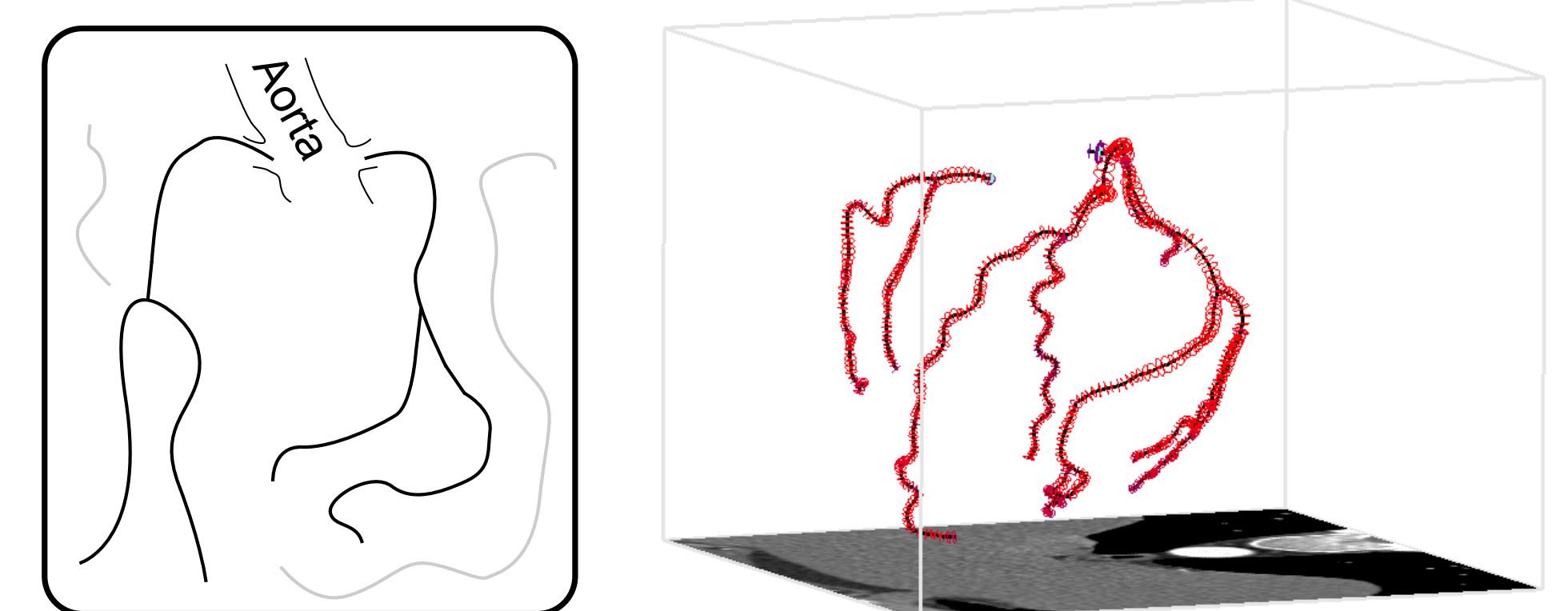
Output: Set of unconnected vessel segments, schematic (left) and on CTA dataset (right).

Method:

- For each seed, track vessel segment in both directions without branching, until termination criterion is reached
- Use cylindrical shape model and histogram-based vessel evaluation function of Zambal et al. [2]



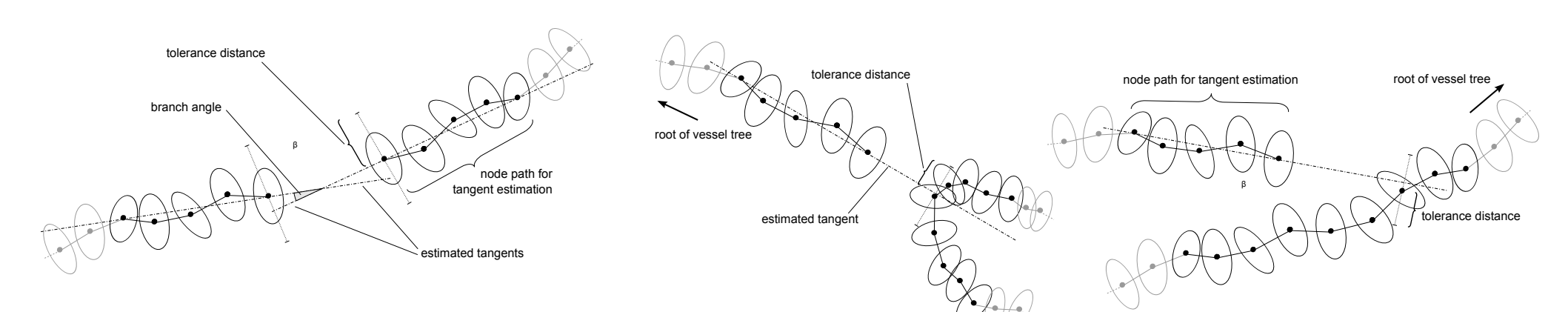
Phase III: Tree growing



Output: Vessel segments connected to full CA trees, schematic (left) and on CTA dataset (right).

Method:

- Connect vessel segments to create complete CA vessel trees, starting at user-defined root points
- Apply a set of connection rules on the tree, until no further vessel segment can be connected
- Connections are found according to rule parameters (segment distance, angle between estimated segment trajectories, etc.)



Three types of connection rules: end-to-end points (left), end-to-inner points (center), inner-to-end points (right)

Results

Evaluation Framework:

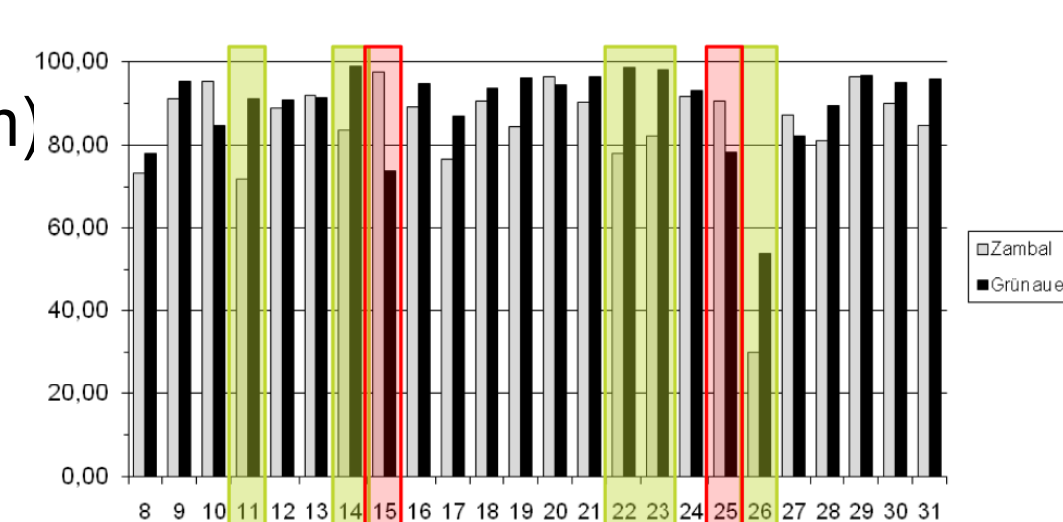
- "Rotterdam CA Algorithm Evaluation Framework" [4]
- 24 CTA datasets, each provided with four expert annotated centerlines

Measures:

- Ability to track the complete vessel (Overlap OV)
- Accuracy inside vessel (AI)

Results:

- Very precise AI (0.24 mm)
- High OV (89.5%)

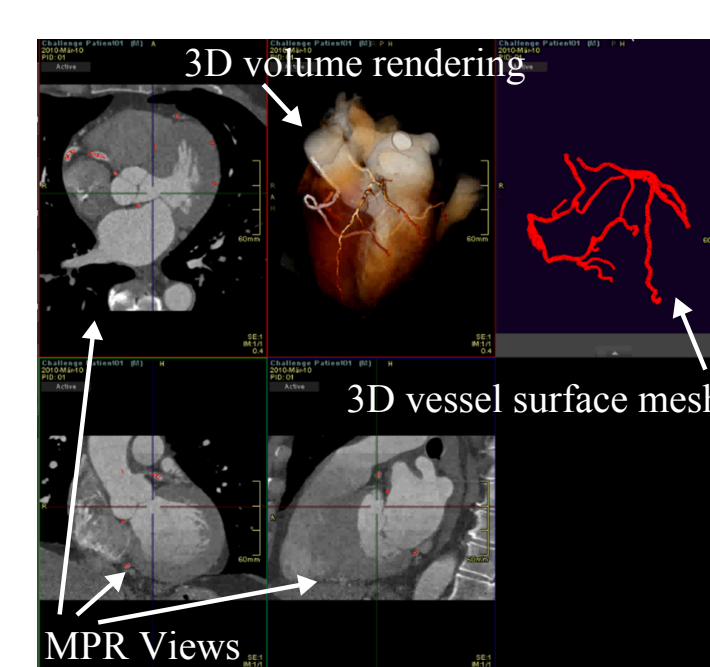


OV results compared to approach of Zambal et al.: significant improvements (green) and degradations (red) on 24 CTA test sets

Integration in clinical software

Functionality:

- (Semi)-automatic tracking of the CA trees at user-defined root-points
- Single-click tracking of vessels at manually placed seeds



GUI of the developed CA tracking plug-in



3D vol. rendering without segmentation (left), heart and blue colored CAs (center), transparent heart with opaque CAs (right)

Conclusion

- Novel approach achieves high overlap in combination with very high accuracy
- BUT: Balancing of tree growing rules is a critical task

Future work:

- In-depth evaluation of potential paths during vessel segment tracking
- Calibration of connection rules
- Automatic root-point selection