Coronary Artery Tracking with Rule-based Gap Closing
Andreas Grünauer

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

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

Future work:
• In-depth evaluation of potential paths during vessel segment tracking
• Calibration of connection rules

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]

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.)

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)
• OV (89.5%)

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

Conclusion

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

References: