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Segmentation of Tubular Structures in Presence of Other Objects

(Research Report)

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Overview

Motivation: Peripheral CT-A Data Processing

Challenge: Vessel Segmentation

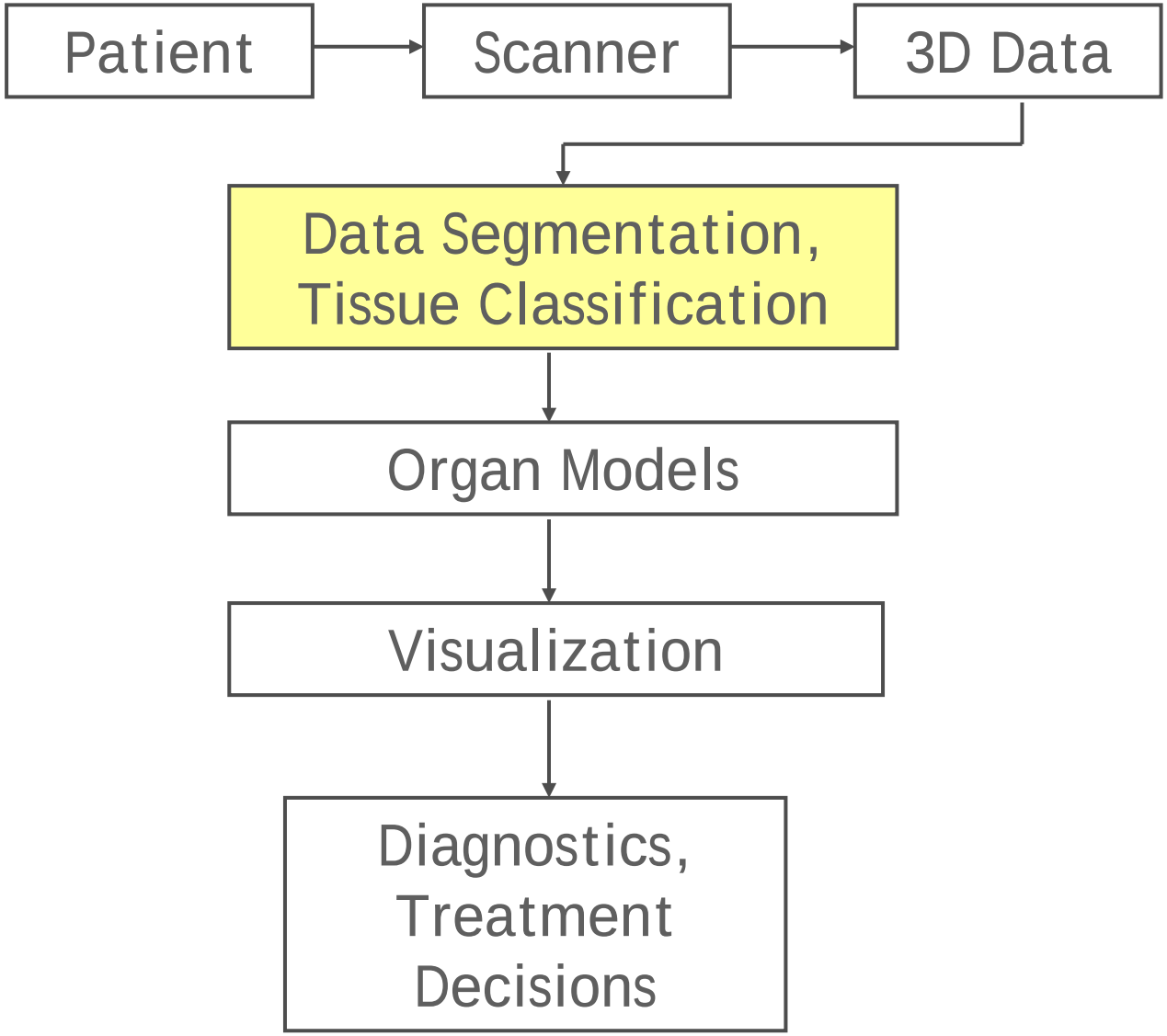
Approach: Modified Tubular Segmentation

Results & Discussion

Motivation

- Angiography: vessel visualization
- Diagnostics & treatment purposes
- Imaging: helical CT scanner
- Contrast agent enhancement
- Fast, minimally invasive, cheap
- Data:
  - acquisition in 40 secs
  - 3D modality
  - ~1400 axial slices (512x512 each)
  - Element size 0.5x0.5x1.0mm

Medical Data Processing



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CT-A Data Properties

- Vessels and bone denser as soft tissue
- Cortical bone denser as vessels
- Trabecular bone and vessels have similar densities
- Vessel density varies significantly
- Pathologies (calcifications, occlusions, ...)

Goal of CT-A Data Processing

- Visualization:
  - Of thick or isolated vessels - solved
  - Of thin vessels (near bones) – this talk
- Visualization with current techniques = get a model
- Model of a vessel:
  - Presence
  - Centerline & Orientation
  - Diameter/Radius

$\Big\} \Longrightarrow$ Tubular Model

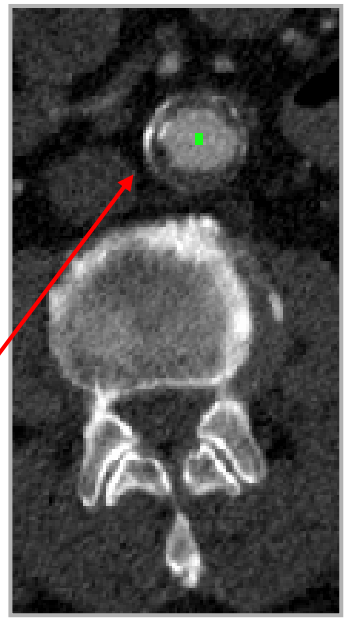
- Cooperation: Model $\leftrightarrow$ Segmentation
- Naïve segmentation approach: match a tubular template

Segmentation of Tubes in 3D data

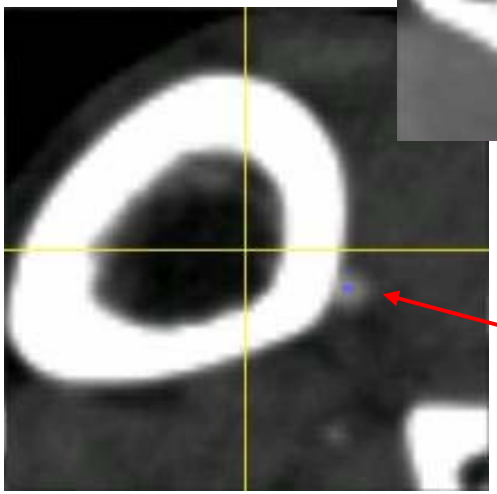
- Well-studied problem in literature
- Often easy, then
  - Thresholding, Region growing
  - Snakes, Active contours
  - Skeletonization
- Modeling based on tubular shape, tubularity defined as
  - High density change in two directions
  - Low density change in third third direction
  - Eigenvalue analysis

Vessels in Peripheral CT-A Data

- Bone and vessels lie very close
- Data blurred (partial volume effect)
- Vessel size vary (r = 1–30 voxels)



Aorta (r=20)



Tibial Artery (r=1.5)

Femoro-Popliteal Artery (r=5)

Problems in PeriphCTA Processing

- **Thresholding/region growing**: density uncertainity, noise
- **Snakes**: too many false edges, noise
- **Watersheds**: region merging/classification problematic
- **Hessian matrix+eigenvalues**: fails if both darker and brigher objects are close, response depends on contrast, no radius info
- **Anatomic atlases**: inter-patient anatomic variability too high
- **DoG filter:** only for larger objects, orientation info requires PCA computation
- **Distance field based skeletonization:** requires good pre_segmentation
- **Too many structures with quasi-tubular shape**

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Eigenvalue analysis

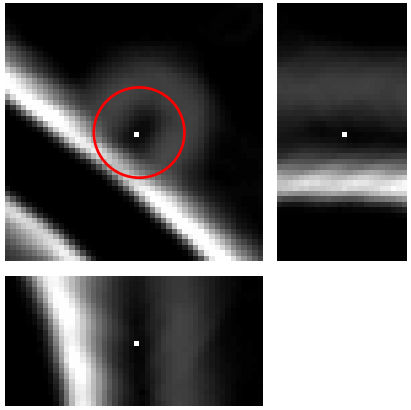
- Derives orientation of object
- Eigen decomposition:

$$\mathbf{A}\vec{x} = \lambda\vec{x}$$

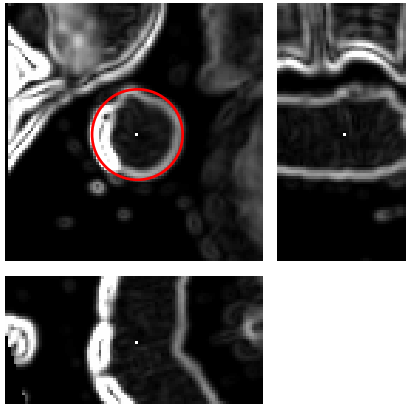
- Returns 3 independent vectors (orientation) and 3 scalars (variation in given direction)
- Used in:
  - PCA (Hotelling Transform)
  - Hessian-Matrix-based analysis
  - Structure Tensor, …
- Matrix $\mathbf{A}$: "2nd order element matrix" (2nd partial derivations, covariations, …)
- No precise radius information

Radius Estimation

- Maximum of GradMag averaged on cylindrical surface (3D)
- In along-axis-resampled data
- Requires precise centre and orientation
- Works for blurred or non-ideal contours



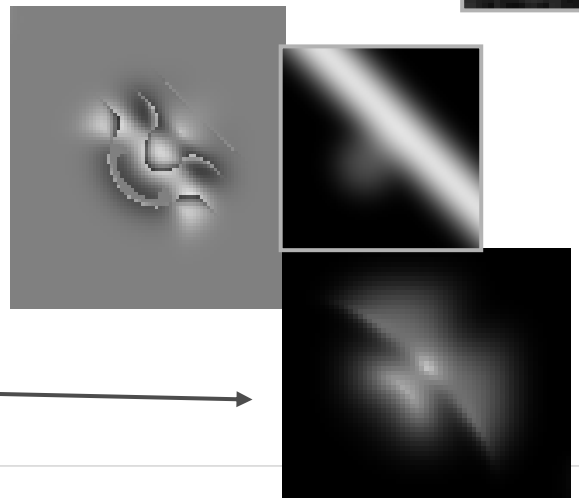
GradMag image,
r=2, trilinear int.



GradMag image,
r=22

Segmentation of Large Vessels

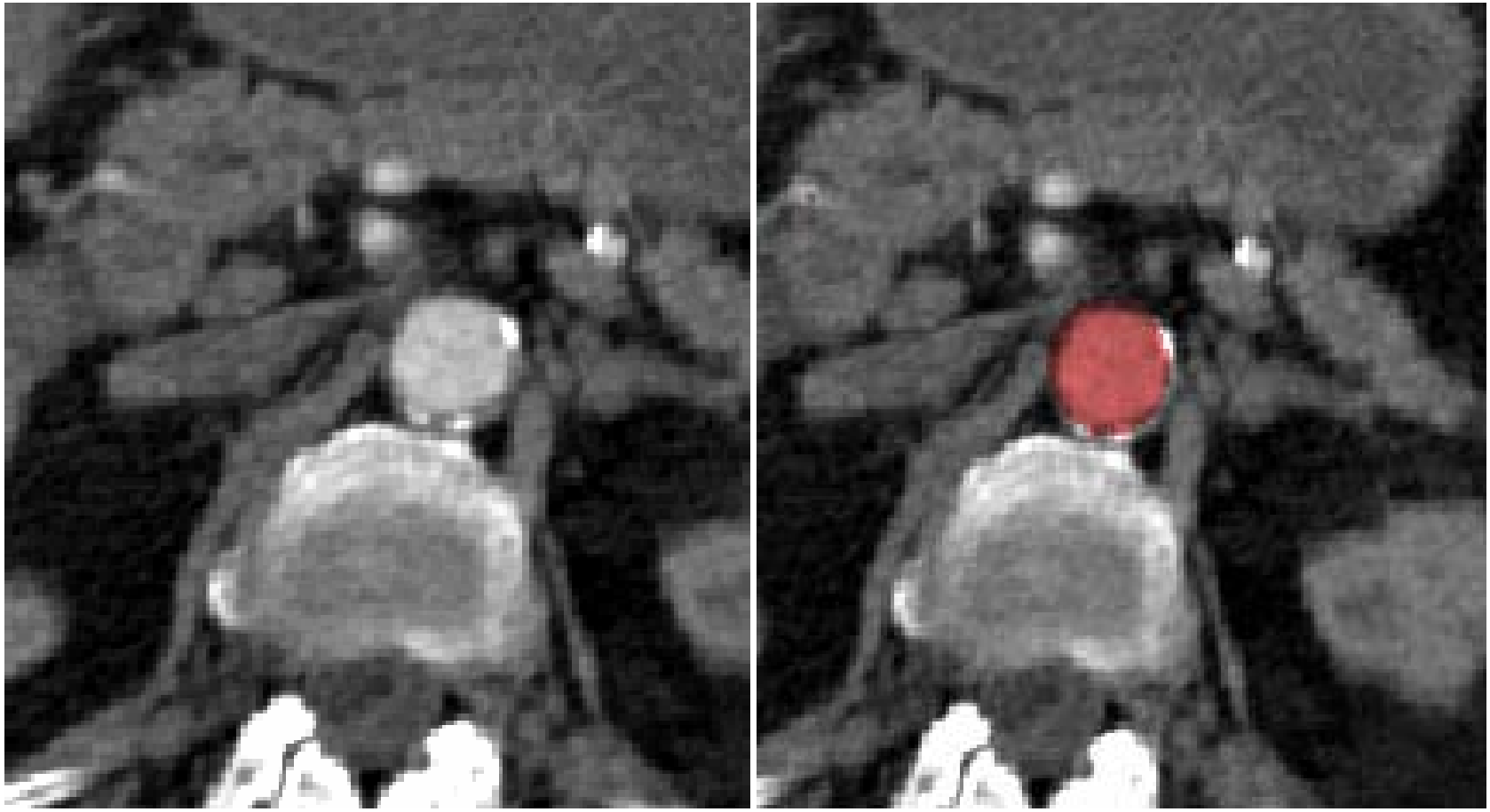
- Large: a lot of samples (>50 per slice)
- Tubular shape nicely recognizable
- Quite easy:
  - Orientation: DoG + PCA, Hessian Matrix, …
  - Center: PCA, CoG, maximum
  - Radius estimation: GradMag maximum
  - Tracking: “Shift along axis and recompute parameters”
- Center estimation fails for:
  - thin vessels, close to bone



Hessian-Matrix-Eigenvalues

Structure-Tensor-Eigenvalues

Segmentation of Large Vessels



Segmentation of Small Vessels

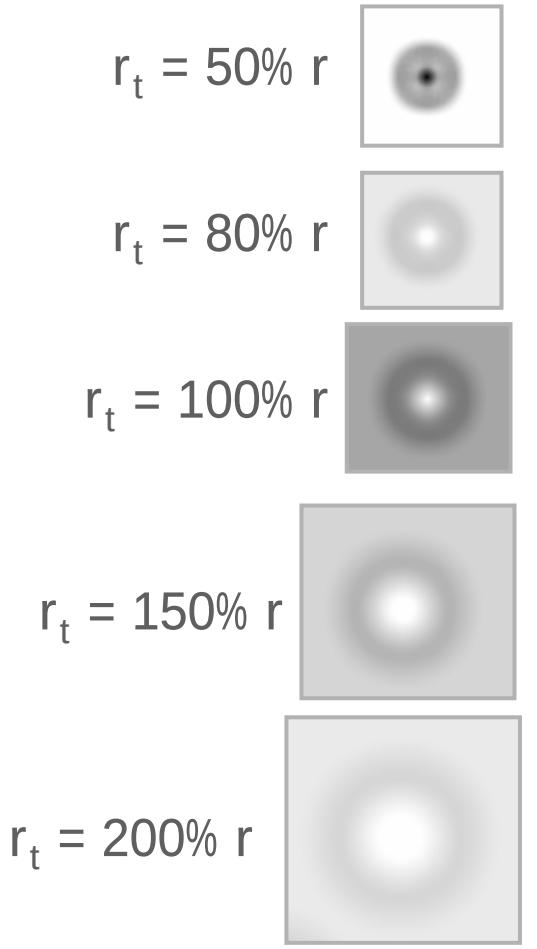
- Precise center computation needed
  - For radius computation
  - For precise modeling
  - For “shift along axis and recompute” algorithm
- Orientation info and approximate position available
  $\Rightarrow$ Template Matching feasible
- Algorithm: evaluate best position for vertical cylinder template (compute difference between template and data densities in given position)

Template Matching

- Parameters to estimate:
  - Vessel density
  - Surrounding tissue density (bones, soft tissue)
  - Vessel template radius
- Standard template matching – two rectangular volumes – axially not symetric
- Modified template matching:
  - Vessel density similar “inside the object”
  - Enough difference in density “outside the object”
  - Radius

Template Match. – Parameter Estimation

- Template vessel density D_V – use data from previous match
- Radius: use primary user-defined estimation
- Density for surrounding tissue not needed:
  - Check if “outside” is the density different enough
  - D_d – density diff (fore-/background)



$$f(\bar{x}_0) = \frac{1}{xyz}\sum_{x,y,z}\begin{cases} \left(D_V - D(x,y,z)\right)^2 & r(x,y,z) < r_t \\ \left(\dfrac{D_d - D_V - D(x,y,z)}{D_d}\right)^2 & r_{t2} > r(x,y,z) > r_t \end{cases}$$

Results

Old system, would require ~25min of manual segmentation

Proposed solution, would require <5min of manual interacton

Conclusions

- Global filters not usable $\Rightarrow$ local user interaction always needed
- Always compute result from multiple samples
- After precise segmentation, higher level models can be computed or applied

Limitations

- Requires user interaction (start point)
- Requires approximate estimation of the radius for:
  - σ in filters
  - size of search area in template matching
- No “native” stopping criteria
  - Wrong segmentation if underlying data change too much (radius)
  - Always computes results, even if nonsense
- Speed / response time (seconds)

Approach

- Eigenvector analysis gives good results for orientation
- **Structure Tensor:**

$$J(\bar{x}) = \int_V W() \begin{pmatrix} \frac{dG(\bar{x})}{dx}\frac{dG(\bar{x})}{dx} & \frac{dG(\bar{x})}{dx}\frac{dG(\bar{x})}{dy} & \dots \\ \dots & \frac{dG(\bar{x})}{dy}\frac{dG(\bar{x})}{dy} & \dots \\ \dots & \dots & \frac{dG(\bar{x})}{dz}\frac{dG(\bar{x})}{dz} \end{pmatrix} dV$$

Thank you for your attention

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http://www.viskom.oeaw.ac.at/~straka/AngioVis