3D+t Statistical Shape Model of the Heart for X-ray Projection Imaging

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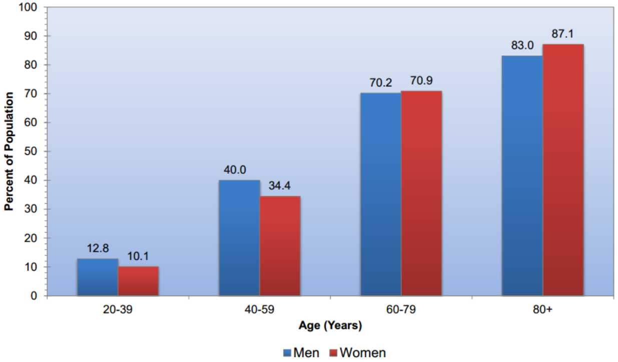
Heart disease

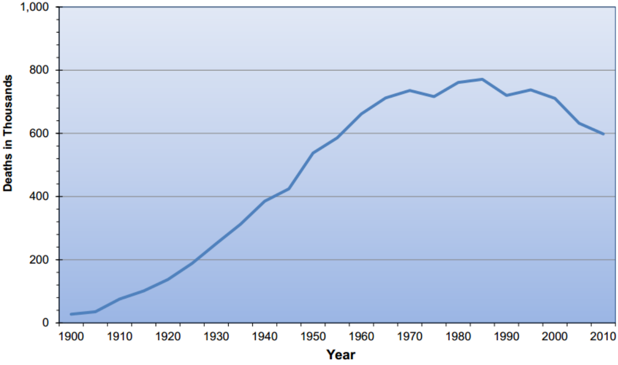
Figure: Prevalence of cardiovascular disease in the US [1].



[1] Go et al., "Heart disease and stroke statistics–2013 update: a report from the American Heart Association."

Heart disease

Figure: Deaths due to heart disease in the US [2].



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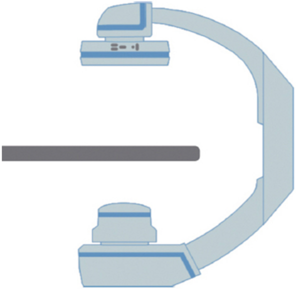

- C-arm CT dominant in interventional angiography
  - → Acquisition times of $\approx 5\,s$
- Motion compensation:
  - → 4D reconstruction
  - → Improved guidance
- Performance evaluation
  - → Exhaustive testing
  - → Normal and pathologic cases
- X-rays: somewhat "unhealthy"
  - → No ground-truth for real data

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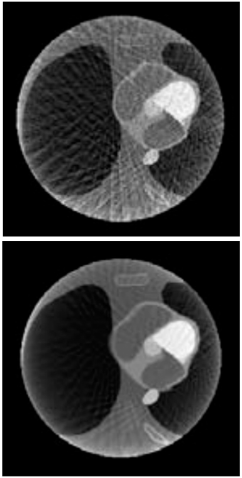

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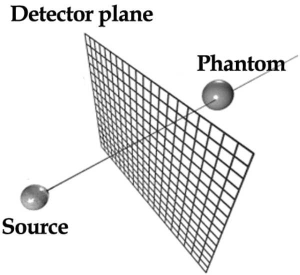

- Need for artificial data
  - → Simulation frameworks
  - → Numerical phantoms
- Enable comparison:
  - → Framework: CONRAD
- XCAT
  - → 3D from Visible Human
  - → Motion from **one** CT set
  - → Developed for ET
  - → Licensing fee

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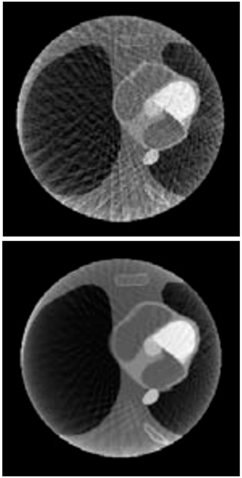

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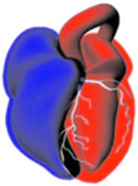
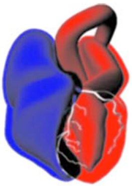


End-diastole



End-systole

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Goals

A new phantom should be:

- available
- dynamic (temporal variation)
- versatile (inter-subject variation)
- clinically relevant

Dynamic statistical shape model of the heart.

Goals

A new phantom should be:

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- dynamic (temporal variation)
- versatile (inter-subject variation)
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Dynamic statistical shape model of the heart.

Contents

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Problem statement

Learn valid behavior from training set
Many shapes from diverse anatomies. [3]

Point correspondence **must** be established/preserved.

? Data-driven segmentation (incl. manual)

! Registration-based segmentation

[3] How "many" and how "diverse"?

Problem statement

Learn valid behavior from training set
Many shapes from diverse anatomies.[3]

Point correspondence **must** be established/preserved.

- **?** Data-driven segmentation (incl. manual)
- **!** Registration-based segmentation

[3] How "many" and how "diverse"?

General idea

Propagate landmarks from atlas to new images.[4,5]

What is needed?

- Landmarked atlas segmentation
- Registration pipeline

What atlas? What pipeline?

[4] Frangi et al., "Automatic construction of multiple-object three-dimensional statistical shape models: Application to cardiac modeling".

[5] Ordas et al., "A statistical shape model of the heart and its application to model-based segmentation".

Atlas segmentation

1. Manual segmentation in ITK Snap
2. Mesh generation (coarsening and smoothing)

Data set used:

- 45 y/o female, 78% phase
- $512 \times 512 \times 241$ pixels
- $0.29 \times 0.29 \times 0.5\,mm$ spacing

Atlas segmentation

Figure: Axial slice

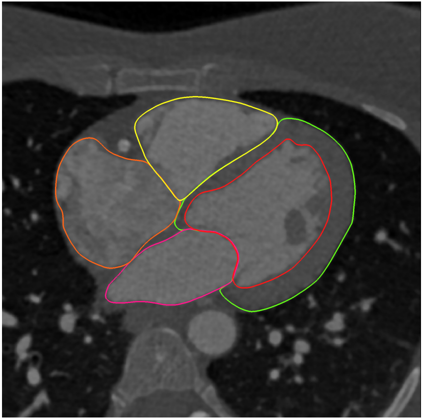
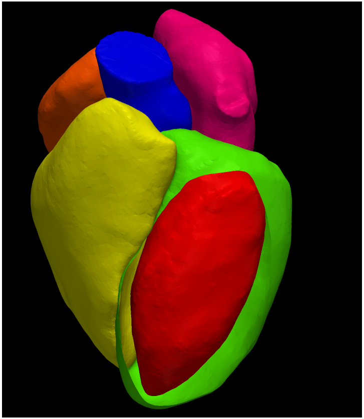


Figure: Surface rendering



Registration

Comparison of two pipelines:

Demons-based

Rigid:

- similarity transform
- mean-squares

Non-rigid: multi-resolution

- Thirion's Demons
- optical flow

Spline-based

Rigid:

- similarity transform
- mutual information

Non-rigid: multi-resolution

- B-spline transforms
- mutual information

Similarity transforms

- Rotation $R \in \mathbb{R}^{n \times n}$
- Translation $\boldsymbol{t} \in \mathbb{R}^n$
- Isotropic scaling σ, such that $\det(R) = \sigma^n$

Similarity transform

$$\mathcal{T}(\boldsymbol{x}) = R\boldsymbol{x} + \boldsymbol{t}$$

$\boldsymbol{x}$: a physical location

Thirion's Demons

Homologous points map to similar intensity

Calculate displacements using optical flow

Initialize $\boldsymbol{D}_0(\boldsymbol{x})$, then update:

Thirion's Demons

$$\boldsymbol{D}_i(\boldsymbol{x}) \propto -(m(\boldsymbol{x}) - f(\boldsymbol{x}))\nabla f(\boldsymbol{x})$$

f, m are the fixed and moving image

- Smooth $\boldsymbol{D}_i(\boldsymbol{x})$ between iterations with Gaussian

Mutual information

Reduce uncertainty in X by knowing Y

No explicit form of dependency needed

Mutual information

$$\int\int p_{fm}\left(f(\boldsymbol{x}), m(\boldsymbol{y})\right) \log\left(\frac{p_{fm}\left(f(\boldsymbol{x}), m(\boldsymbol{y})\right)}{p_f\left(f(\boldsymbol{x})\right)\, p_m\left(m(\boldsymbol{y})\right)}\right) \mathrm{d}\boldsymbol{x}\mathrm{d}\boldsymbol{y}$$

f, m are the fixed and moving image

p_f and p_m, and p_{fm} are the marginal and joint histograms

MI: intuitive examples

Independence

$$p(X,Y) = p(X)\,p(Y) \;\rightarrow\; \log\left(\frac{p(X,Y)}{p(X)\,p(Y)}\right) = 0$$

Figure: No misalignment

Figure: 10° rotation

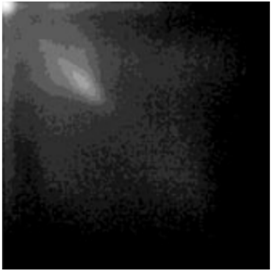
MI: intuitive examples

Independence

$$p\left(X,Y\right)=p\left(X\right)\,p\left(Y\right)\;\rightarrow\;\log\left(\frac{p\left(X,Y\right)}{p\left(X\right)\,p\left(Y\right)}\right)=0$$

Figure: No misalignment

Figure: 10° rotation



B-Spline transforms

Smooth transforms defined on control grid

Weighted sum of points in finite support region

1D B-Spline

$$\mathcal{T}(\boldsymbol{x}) = \sum_{n=0}^{d} B_n(u)\Phi_{k+n},$$

$u = \frac{x}{n_x} - \lfloor \frac{x}{n_x} \rfloor \in [0, 1] \quad k = \lfloor \frac{x}{n_x} \rfloor - 1$

$B_n(u)$: B-Spline basis function ($:=$ weights)

Φ_i: control points in grid

Registration: Reminder

Demons-based

Rigid:

- similarity transform
- mean-squares

Non-rigid: *multi-resolution*

- Thirion's Demons

$\rightarrow\ 1\,h\,49\,min$

Spline-based

Rigid:

- similarity transform
- mutual information

Non-rigid: *multi-resolution*

- B-spline transforms
- mutual information

$\rightarrow\ 2\,h\,21\,min$

Evaluation

Procedure

- Fix registration parameters
- Register to data at all cardiac phases

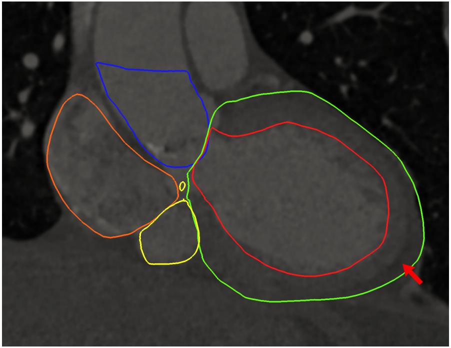
Quality assessment

Representative female and male patient data

- Visual evaluation
- Expert ranking

Visual evaluation: End-Diastole

Figure: Female, B-splines: Coronal view



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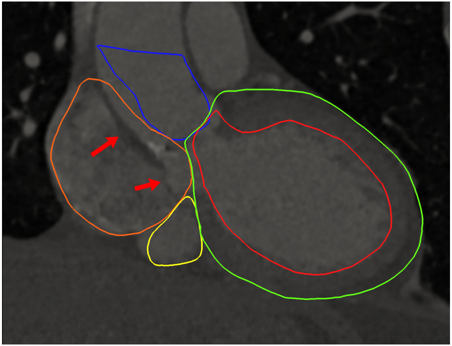

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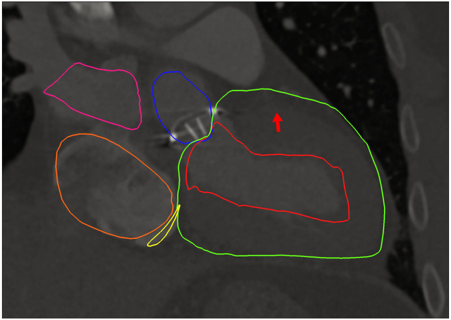

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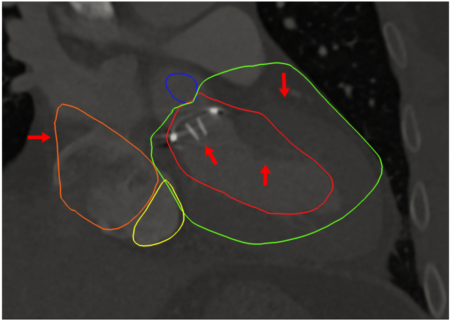


Visual evaluation: Discussion

Demons

+ Short computation time (GPU)
- Marginally separated structures
- Low-contrast boundaries
- "Minimal regularization": Gaussian smoothing

Visual evaluation: Discussion

B-Spline

+ Support region: "regularization"
+ Better agreement with data

$\pm$ Many tunable parameters

$\pm$ Marginally separated structures

\- Complexity

Expert ranking

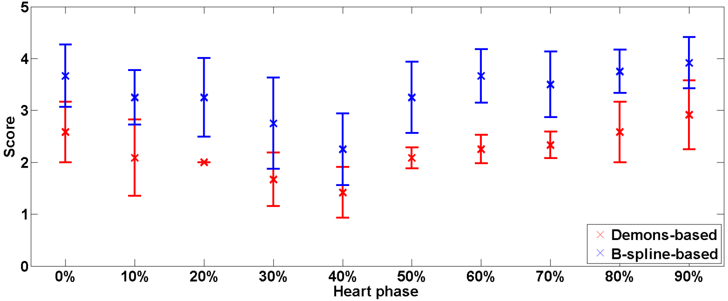
Procedure

Comparison and rating of 20 images at all cardiac phases, each.

- 3 experts
- Grades $\in [0, 5]$, 5 := best

Expert ranking: Results

Figure: Average grade at different heart phases



Expert ranking: Discussion

- B-Spline: 3.33 ± 0.51
- Demons: 2.19 ± 0.45

$\rightarrow$ B-Spline pipeline significantly better!

- Atlas segmentation is at 78% phase (end-diastole)

$\rightarrow$ Induces bias.

Expert ranking: Discussion

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Conclusions

- Reduce bias: create atlas from "mean heart"
- Automatic registration: parameters fixed
- Stability w.r.t. global contrast variations?
- Regularization, local adaptation,...

Training set generation: not time-sensitive
$\rightarrow$*Use of B-Spline pipeline favorable.*

Conclusions

- Reduce bias: create atlas from "mean heart"
- Automatic registration: parameters fixed
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Best case scenario

Figure: Atlas segmentation

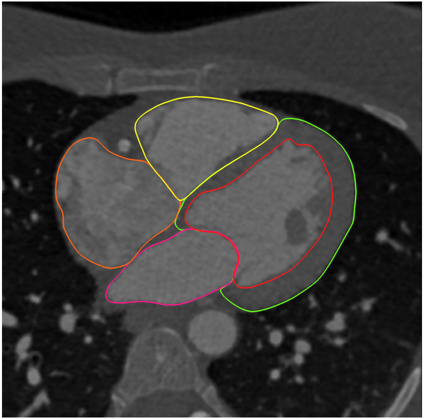
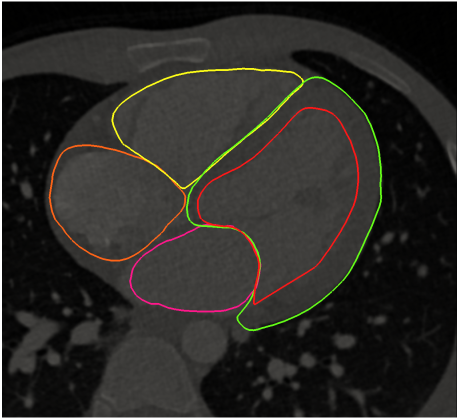


Figure: Female, end-diastole



Contents

Procedure

Statistical shape model generation

Four step process:

1. Obtain training shapes
2. Establish point correspondence
3. Align shapes
4. Extract principal modes of variation

Training set

20 ten phase CTA data sets

9 male patients:	23-92 y/o	$(59.56 \pm 25.10\,\text{years})$
11 female patients:	51-81 y/o	$(70.45 \pm 12.89\,\text{years})$

Ejection fractions: $52.13 \pm 9.11\%$

Alignment

Generalized Procrustes Analysis

Pose and scale is not part of shape.

- Analytic solution for two shapes
- Iterative procedure, else

Alignment: Procedure

1. Center and scale input samples X_i
2. Rotate all n shapes X_i to fit X_1
3. Calculate consensus shape Y
4. Until convergence:
   - Rotate and scale X_i to consensus Y
   - Reassure proper scaling
   - Calculate residual change

Alignment: Discussion

- Considerable amount of computation required
- Converges well

- 0.1% of initial residual $\rightarrow$ 6 iterations

PCA

Goals of Principal Component Analysis

- Extract most important information from the data
- Reduce dimensionality of the data
- Simplify description of shapes

PCA: Procedure

Procedure

1. Compute mean shape $\bar{X}$
2. Covariance matrix: $S = \sum_{i=1}^{n} (X_i - \bar{X})(X_i - \bar{X})^T$
3. Solve: $S\,\Phi_k = \lambda_k \Phi_k$
4. Pick largest c principal components Φ_k
   e.g. cumulative variance $r > 75, \cdots, 99\%$

Statistical shape model: $\{\bar{X}, \mathbf{\Phi}\}$

PCA: Procedure cont.

Statistical shape model: $\{\bar{X}, \Phi\}$

Shape description

$$X_i \approx \bar{X} + \sum_{k=1}^{c} \beta_{i,k} \Phi_k$$

Φ_k: $c < n$ principal modes of variation

β_k: principal components

PCA: Procedure cont.

Inter-subject and temporal variation.

Valid dynamic shapes from multi-phase data.

1. Shape models at phase p: $\{\bar{X}, \mathbf{\Phi}\}^{(p)}$
2. Principal components of shapes: $\boldsymbol{\beta}_i^{(p)}$
3. Build component vector:
   $\boldsymbol{\beta}_i = (\boldsymbol{\beta}_i^{(1)}, \cdots, \boldsymbol{\beta}_i^{(p)})$

PCA: Procedure cont.

PCA on component vectors: $\{\bar{\beta}, \boldsymbol{\rho}\}$

Compact interface for dynamic model generation

Dynamic model

$$(\varkappa^{(1)}, \cdots, \varkappa^{(p)}) = (\bar{X}^{(1)}, \cdots, \bar{X}^{(p)}) + (\boldsymbol{\Phi}^{(1)}, \cdots, \boldsymbol{\Phi}^{(p)})(\bar{\boldsymbol{\beta}} + \boldsymbol{\rho}\,\boldsymbol{\delta})$$

Interpolation for continuous representation.

Results: Generalization

Cross validation: leave-one-out test

Capability to represent unseen instances.

- Exclude shape from model
- Fit model to shape
- Compute error

90% variation: $5.00 \pm 0.93\,mm$

95% variation: $4.89 \pm 0.90\,mm$

Results: Specificity

Random shape sampling

Validity of new instances.

- Generate random component vectors
- Compute distance to nearest training shape

Static:	1000 samples	$7.18 \pm 0.45\, mm$
Dynamic:	100 samples	$7.30 \pm 0.97\, mm$

Results: Variability at diastole

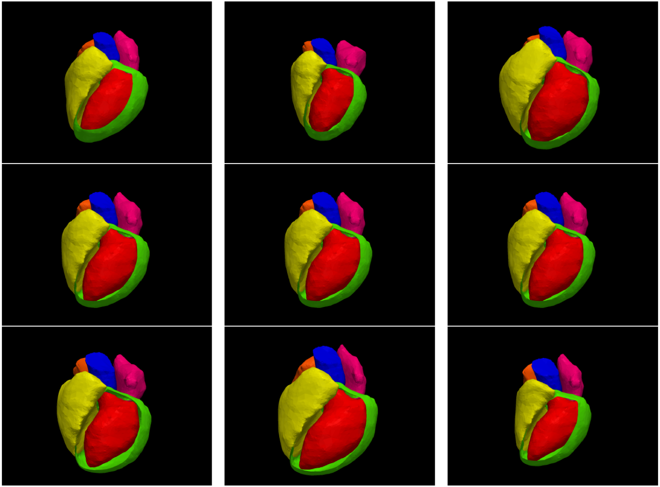


Figure: Decreasing variance μ from left to right: $\delta_b = -\mu_b/2$ top, $\delta_b = \mu_b/2$ bottom, and $\delta_b = 0$ mid.

Results: Projection imaging

Figure: Volume rendering

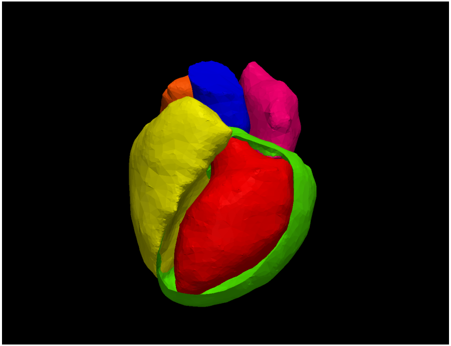
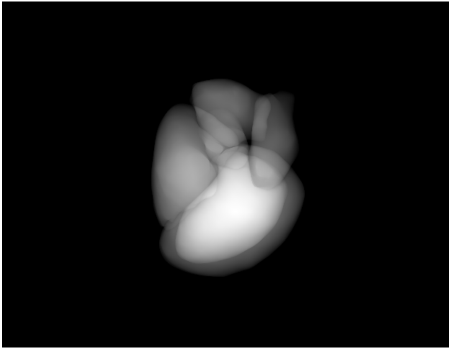


Figure: Projection image



Conclusions

- Large variation among few samples
- Deteriorates specificity

$\rightarrow$ Revisit training set generation

- Currently: anatomy at rest determines contraction

$\rightarrow$ Multi-linear PCA

To our knowledge the first open-source, dynamic statistical shape model of the heart. [6]

[6] Available at: `http://www5.cs.fau.de/conrad/`

Contents

Summary

We...

- compared two registration-based segmentation pipelines.
  MI-driven B-Splines superior
- developed a dynamic SSM of the heart.
  Open-source, freely available

All algorithms and sample projections are available.[7]

[7] http://www5.cs.fau.de/conrad/

Questions? Comments?