Regional appearance modeling for deformable model-based image segmentation

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Directeur
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3D Anatomical Human project

• Overview\textsuperscript{1}:
  • improving virtual representations of human body
  • realistic functional 3D models
  • methodology demonstrated on lower limbs

• Implementing techniques to reproduce:
  • shape
  • physiological processes
  of lower limb structures

\textsuperscript{1} [1] http://3dah.miralab.ch
3D Anatomical Human: research

Multi-sequence images acquisition → 3D models and motion extraction → Soft tissues modeling and characterization

Motion analysis → Motion modeling

collected and produced data

Knowledge management → Ontology → Visualization and interaction
Segmentation: overview

MR images

Segmentation

structures of interest
Segmentation: approaches

- **Manual segmentation**\(^1\):  
  - high fidelity, despite expert variability  
  - lots of work  
  - ground truth

- **Region growing/classification/thresholding**\(^2\):  
  - simplest method, using level(s)  
  - no assumption about shape  
  - use of pre-processing

- **Atlas-guided approaches**:  
  - a priori on shape and/or position  
  - mesh\(^3\) and image\(^4\) atlases  
  - mesh atlas = deformable models

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Deformable models: overview

Internal (shape) forces + External (appearance) forces

smooth surface

close to apparent structure boundaries
Deformable models: approaches

- **Continuous Models**
  - Explicit Representation
    - Finite Differences
      - Finite-Elements
    - Deformable Templates
- Implicit Representation
  - Level-Sets
  - Algebraic Curves

- **Discrete Models**
  - Discrete Meshes
  - Particle Systems
  - Point Set
    - Simplex Mesh
    - Spring-Mass Models
    - Point Distribution Model
2-simplex meshes

- Main features:
  - discrete representation
  - dual of triangular meshes
  - local shape defined at each vertex

- Topology:
  - each vertex has 3 neighbors
  - each vertex and face is oriented

- Mesh quality:
  - decimation
  - refinement

Internal (shape) forces

- During mesh deformation, they ensure:
  - surface to be smooth, or close to a given shape
  - less sensitivity to noise (regularization effect)

- Simplex meshes:
  - simplex angle regularity constraint\(^1\) (smoothing)
  - shape memory constraint\(^1\) (convergence to initial shape)

- PCA-based methods\(^2,3\):
  - alignment of \( P \) training shapes with point correspondence\(^4\)
  - construction of a Statistical Shape Model\(^5\) (SSM) by reducing the dimensionality of the training set
  - multiresolution scheme\(^6\) (coarse-to-fine)

References:

External (appearance) forces

- During deformation, they attract the mesh to image-based features

  \[
  \text{appearance prior} \quad \text{external forces}
  \]

  \[
  \text{boundaries} \quad \text{gradient image}^1
  \]

  \[
  \text{regions} \quad \text{histograms}^2, \text{texture}^3
  \]

  \[
  \text{a priori} \quad \text{intensity profiles}^4
  \]

- Intensity profiles:
  - local information about the intensity evolution

- PCA-based methods

Limitations of appearance methods based on PCA

- Need for an accurate point-wise registration
- Need for a large number of datasets
- *Monomodality* = one single Gaussian distribution
  - wrong hypothesis in presence of pathologies
  - shape not necessarily correlated with appearance

- Drawback: Gaussian distribution with large covariance

**solution**: several Gaussian distributions with lower covariance
Our proposed approach

• Appearance prior **based on intensity profiles:**
  • discriminant features
  • good tradeoff between global and local features

• Profiles **classified for each mesh**, not for each vertex:
  • no accurate pointwise registration
  • no shape/appearance correlation

• Tests:
  • CT images of livers
  • MR images of lower limbs structures
Our proposed approach

• **Multimodal profiles:**
  - each profile may belong to several profile classes
  - more Gaussian distributions with lower covariance  

```plaintext
• 
```

```plaintext
| monomodal profiles | multimodal profiles |
```

---

more discriminant
Outline

1. Introduction

2. Multimodal Prior Appearance Model (MPAM)

3. MPAM-based External Forces

4. Results from Liver Database

5. Analysis of Lower Limb Structures

6. Conclusion
Multimodal Prior Appearance Model (MPAM)

1. Mesh
2. Image

Profile extraction → EM¹ → NEM² → Fusion of profiles

Registration & Prior Model

Unsupervised clustering

- Advantages: no assumption about the classification, automatic
  \[\text{hyperparameter } K \text{ (number of clusters)}\]
- Statistical method to separate data points into clusters

- Basic approaches:
  - K-Means\(^1\)
  - Fuzzy C-Means\(^2\) (FCM)
  - Expectation-Maximization\(^3\) (EM)
  - Neighborhood EM\(^4\) (NEM):
    - derived from EM
    - spatial info is considered

EM classification of profiles

• Initialization: using Fuzzy C-Means (initialized with random centers)

• Coping with missing data due to incomplete profiles

• Singularities when inverting covariance matrix $\Sigma_k$:
  • coarse sampling of a high dimensional space (i.e. curse of dimensionality)
  • highly correlated data

• Three regularization methods\(^1\):
  • PCA-based regularization
  • diagonal regularization
  • trace-based regularization

Finding the number of clusters
Model order selection

• Objective: optimal tradeoff between under and overfitting (i.e. goodness of fit)

• Criteria:
  • FCM-based: *cluster validity indices* (e.g. \(v_{PC}^1, v_{PE}^1, v_{FVQ}^2\))
  • EM-based: *model order selection criteria* (e.g. \(AIC^3, AIC_C^4, BIC^5\))

• OSI criterion\(^6\): optimal tradeoff between overlap\(^7\) and separation\(^7\)

Model order selection

- A good criterion must:
  - find a reasonable number of modes (avoiding under/overfitting)
  - be robust to different datasets (STD on K must be minimum)

- Tested criteria: AIC, AICc, BIC, FVQ and OSI criterion

- To compare criteria:
  - profiles extracted from 35 ground truth liver meshes
  - profile length from/to [2,4,6,8,10,12] mm inward/outward
  - EM launched from $K_{\text{min}} = 2$ to $K_{\text{max}} = 20$

- Expected result: $3 \leq K \leq 6$
  - inner structures: parenchyma and non-parenchyma
  - outer structures: air, bones, soft tissue (more discriminant)

- classical criteria affected by under/overfitting
  \{ AIC-AICc-BIC: $\bar{K} > 11$, FVQ: $\bar{K} = 2$ \}

- OSI criterion seems to be a good tradeoff
  \{ OSI: $3 < \bar{K} < 4$ \}

- mode = intensity profile class = appearance region
Including spatial correlation

- **Objective:**
  - take neighborhood information into account
  - improve the fusion of appearance regions

- **Criterion:** Neighborhood EM\(^1\) (NEM)

- **Heuristic to set \(\beta_n\) automatically\(^2\)

\[
L(\theta) = L(\theta) + \beta_n \sum_{k=1}^{K} \sum_{i=1}^{N} \sum_{j=1}^{N} (\gamma_i^k \gamma_j^k v_{ij})
\]

Including spatial correlation

Fusion of modes

- **Objective:**
  - merge modes that are similar between datasets
  - reduce the complexity of the prior

- **Similarity measure between any pair of modes:**
  - threshold on the Jaccard index $J$ in the interval $[0-1]$
  - ratio of intersection/union of the regions spanned by the modes

![Graph showing the fusion of modes](image)
Projection to a reference mesh

• Objective: store the appearance information from $P$ datasets

• Reference mesh construction using Guimond’s method$^1$:
  
  • mesh-to-image registration based on deformable models$^2$

• mesh-to-mesh registration based on currents$^3$

Projection to a reference mesh

- Transfer of appearance information:
  - reference mesh must be the finest mesh w.r.t. resolution
  - interpolation based on closest points
  - neighbors are also considered

\[ N = 4530 \text{ vertices} \quad \text{and} \quad N = 11760 \text{ vertices} \]

\[ \rightarrow \text{sparse posterior probabilities = few non-negligible modes} \]
Examples of MPAM construction

- Data:
  - datasets: 7 livers (from CT images) and 4 tibias (from MR images)
  - profiles: outward, 10 samples every mm, $N \approx 4000$ vertices
Examples of MPAM construction

projection to $M_{liv}$

projection to $M_{tib}$

mode fusion

$J = 1.0$

$K = 28$

$J = 0.6$

$K = 11$

$J = 1.0$

$K = 10$

$J = 0.5$

$K = 5$
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Clustering for segmentation

- Limitation of the EM algorithm: **Gaussian assumption**
  - EM lacks of robustness when changing mesh resolution

- **Spectral clustering**\(^1,2,3\):
  - no Gaussian assumption (manifold assumption)
  - performs on a lower dimensional space
  - increases the robustness of the classification

Clustering for segmentation

- **A good clustering** does not guarantee a **good segmentation**:  
  - modes with large variance may not be discriminant enough
  - neighboring structure boundaries may not be present

- **Boosted clustering**:  
  - to make sure MPAM is suitable for segmentation purposes  
  - encourages modes with lower covariance  
  - vertices may not have any mode (considered as outliers)

objective: optimize the classification to meet a localization criterion
Localization criterion

Current profile

Similarity measure

Reference profile at vertex $p_i$
Localization criterion

- **Objective:** test if a profile mode determines the boundary at each vertex.

- **Intensity similarity measures:**
  - linear criterion
  - sum of absolute differences
  - Mahalanobis distance

- **External force based on MPAM:**
  
  \[
  f_{ext}(p(x_i)) = \beta(p(x_i)' - p(x_i))
  \]

  - localization criterion: \(\alpha_i \leq \text{threshold}\)

  \(\beta\) global weight on external forces

Clustering for segmentation

- Objective: create an appearance prior for segmentation purposes
Spectral clustering

- Similarity function:\n  - determines how similar two profiles are
  - is defined by the Gaussian kernel function
  - accounts for the connectivity between profiles

- Similarity graph:\n  - fully connected graph
  - $\epsilon$-neighborhood graph
  - $k$-nearest neighbor graph

  \{ may require large computation resources
  \} create sparse matrices

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Spectral clustering

- Top eigenvector extraction: Singular Value Decomposition (SVD) on sparse matrices (Krylov methods\textsuperscript{1})

- Model order selection: using the eigengap heuristic\textsuperscript{2}

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Boosted clustering

- Single pass boosted clustering

\[ \text{mesh} \quad \text{image} \quad \text{intensity profiles} \quad \text{Spectral clustering} \quad \alpha_i \quad \text{kept profiles} \quad \text{rejected profiles} \quad \text{Save GMM} \]

\[ \text{while decrease of kept profiles} \geq 0.01\% \]

\[ \text{Update } \mu \text{ and } \Sigma \]

\[ \text{only 30\%-60\% of kept profiles} \]
Boosted clustering

- Single pass boosted clustering
  - only 30%-60% of kept profiles

- Cascading boosted clustering
  - ≈ 60%-70% of kept profiles

Mesh

Image

Intensity profiles

Spectral clustering

$\alpha_i$

Rejected profiles

Kept profiles

Save GMM

Update $\mu$ and $\Sigma$

while decrease of kept profiles $\geq 0.01\%$

while increase of kept profiles $\geq 1\%$
Boosted clustering

- Single pass boosted clustering
  - only 30%-60% of kept profiles

- Cascading boosted clustering
  - ≈ 60%-70% of kept profiles

- Cascading boosted clustering with hierarchical approach
  - ≈ 75%-99% of kept profiles

while decrease of kept profiles ≥ 0.01 %
while increase of kept profiles ≥ 1 %
while $K_{ite} \leq K_{max}$
Boosted clustering

Cascading boosted clustering with hierarchical approach

K = 3
Initialization

K = 3
Ite #1: 58% kept profiles

K = 5
Ite #2: 67% kept profiles

K = 7
Ite #3: 77% kept profiles

K = 9
Ite #4: 85% kept profiles

K = 12
Ite #5: 92% kept profiles
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Data

- Database of 35 liver meshes from:
  - 3Dircadb1 (provided by IRCAD)
  - SLIVER07 (provided by MICCAI 2007)

- Creation of a mean mesh (from 16) using registration based on currents

- Reference mesh sampled in 4 resolutions using decimation/refinement

- The 4 resolutions of reference mesh are registered to the 35 livers

\[ \begin{align*}
N &= 3856 \text{ vertices} \\
N &= 7586 \text{ vertices} \\
N &= 11760 \text{ vertices} \\
N &= 35280 \text{ vertices}
\end{align*} \]
Spectral clustering

- Spectral clustering of profiles extending both sides

- Eigengap heuristic applied on the four resolutions of reference mesh

N = 3856 vertices  N = 7586 vertices  N = 11760 vertices  N = 35280 vertices

⇒ robustness of eigengap heuristic w.r.t resolution
Two features are expected from the algorithm:
- a high percentage of kept profiles per dataset (%)
- a similar behavior through the resolutions (% and K)

<table>
<thead>
<tr>
<th>Resolutions</th>
<th>%</th>
<th>K</th>
<th>%</th>
<th>K</th>
<th>%</th>
<th>K</th>
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<tr>
<td>3856</td>
<td>41</td>
<td>5</td>
<td>41</td>
<td>5</td>
<td>43</td>
<td>5</td>
</tr>
<tr>
<td>7586</td>
<td>43</td>
<td>5</td>
<td>43</td>
<td>5</td>
<td>53</td>
<td>11</td>
</tr>
<tr>
<td>11760</td>
<td>53</td>
<td>11</td>
<td>53</td>
<td>11</td>
<td></td>
<td></td>
</tr>
<tr>
<td>35280</td>
<td>91</td>
<td>41</td>
<td>91</td>
<td>41</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- %: average percentage of kept profiles per dataset
- K: average number of modes per dataset
- [SingPassBoost]: single pass boosted clustering
- [CascBoost]: cascading boosted clustering
- [CascBoostHier]: cascading boosted clustering with hierarchical approach

[CascBoostHier] features the best results for both % and K
Fusion of modes

- MPAM may reach a steady K value after the fusion of $K_{\text{min}}$ modes

  appearance around the same anatomical structure should be the same

- Plot of K when adding datasets to the MPAM for different J:
  
  $J = 1.0$ [––], $J = 0.8$ [– –], $J = 0.7$ [– –], $J = 0.6$ [– – –], $J = 0.5$ [– – – –]

  
  - N = 3856 vertices
  - N = 7586 vertices
  - N = 11760 vertices
  - N = 35280 vertices

  🎉 J = 0.5 features a rather steady state

  😞 likely to create modes with large variance
Segmentation: tradeoff on forces

- Objective: find a reasonable tradeoff between internal and external forces

- External forces from MPAM generated: using profiles from the 35 liver meshes, after [CascBoostHier] and without mode fusion ($J = 1.0$)

\[ \begin{align*}
\alpha &= 0.1, \quad \beta = 0.1, \quad \eta = 1 \\
\alpha &= 0.1, \quad \beta = 0.1, \quad \eta = 5 \\
\alpha &= 0.3, \quad \beta = 0.1, \quad \eta = 5 \\
\alpha &= 0.3, \quad \beta = 0.1, \quad \eta = 10
\end{align*} \]

initialization = ground truth liver meshes

Segmentation: external forces

- **Objective:** compare the external forces from both MPAM and PCAP
  - initialization = ground truth liver meshes
- **Setup:**
  - both: profiles from 31 liver meshes, no initialization, same \(\{\alpha, \beta, \eta\}\), several intensity similarity measures (maha, diff, line)
  - MPAM: [CascBoostHier], several thresholds on Jaccard index \(J\)
  - PCAP: several ratios on eigenvalues \(R\) (only with maha)

Segmentation of 4 liver images using their associated ground truth liver meshes

- original mesh
- MPAM, maha, \(J = 1.0\)
- PCAP, maha, \(R = 0.9\)

- original mesh
- MPAM, maha, \(J = 1.0\)
- PCAP, diff

[maha: Mahalanobis distance, diff: sum of absolute differences, line: linear criterion]
Segmentation: external forces

<table>
<thead>
<tr>
<th>MPAM (ASSD [mm])</th>
<th>J</th>
<th>1.0</th>
<th>0.7</th>
<th>0.6</th>
<th>0.5</th>
<th>0.4</th>
<th>0.3</th>
<th>0.2</th>
<th>0.1</th>
</tr>
</thead>
<tbody>
<tr>
<td>maha</td>
<td>1.3</td>
<td>3.1</td>
<td>6.8</td>
<td>5.9</td>
<td>5.4</td>
<td>5.3</td>
<td>5.3</td>
<td>5.3</td>
<td>5.3</td>
</tr>
<tr>
<td>diff</td>
<td>1.9</td>
<td>2.0</td>
<td>2.4</td>
<td>2.6</td>
<td>2.7</td>
<td>2.6</td>
<td>2.6</td>
<td>2.6</td>
<td>2.6</td>
</tr>
<tr>
<td>line</td>
<td>2.5</td>
<td>1.9</td>
<td>2.9</td>
<td>3.2</td>
<td>3.2</td>
<td>3.2</td>
<td>3.2</td>
<td>3.2</td>
<td>3.2</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>PCAP (ASSD [mm])</th>
<th>R</th>
<th>1</th>
<th>0.98</th>
<th>0.95</th>
<th>0.9</th>
<th>0.8</th>
<th>0.6</th>
<th>0.4</th>
<th>0.2</th>
<th>0.1</th>
</tr>
</thead>
<tbody>
<tr>
<td>maha</td>
<td>5.8</td>
<td>3.8</td>
<td>3.5</td>
<td>3.4</td>
<td>3.5</td>
<td>3.8</td>
<td>3.9</td>
<td>3.9</td>
<td>3.9</td>
<td>3.9</td>
</tr>
</tbody>
</table>

[ASSD: Average Symmetric Surface Distance, J: Jaccard index, R: ratio on eigenvalues]
[maha: Mahalanobis distance, diff: sum of absolute differences, line: linear criterion]

[MPAM+maha] with J = 1.0 performs the best
[PCAP+maha] with R = 0.9 performs the best
MPAM outperforms PCAP
Segmentation from affine registration

- Initialization: registration of reference mesh towards 12 ground truth liver meshes using a similarity transformation

<table>
<thead>
<tr>
<th></th>
<th>[PCAP+diff]</th>
<th>[PCAP+line]</th>
<th>[PCAP+maha]</th>
<th>[MPAM+maha]</th>
</tr>
</thead>
<tbody>
<tr>
<td>ASSD [mm]</td>
<td>3.74 ± 1.56</td>
<td>4.14 ± 1.43</td>
<td>4.14 ± 1.07</td>
<td>2.24 ± 1.08</td>
</tr>
<tr>
<td>VOE [%]</td>
<td>20.5 ± 7.17</td>
<td>22.2 ± 5.76</td>
<td>22.7 ± 4.52</td>
<td>12.9 ± 5.04</td>
</tr>
</tbody>
</table>

[diff: sum of absolute differences, line: linear criterion, maha: Mahalanobis distance]
[ASSD: Average Symmetric Surface Distance, VOE: Volumetric Overlap Error]

MPAM outperforms PCAP, despite less modes (≈1250 vs 7586)
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- EPFL: EPFL, Switzerland
- UCL: University College London, United Kingdom
- IOR: Istituto Ortopedico Rizzoli di Bologna, Italy
- CRS4: CRS4, Italy
- INRIA: INRIA, France
- STAR: Vrije Universiteit Brussel, Belgium
- SMI: Aalborg University, Denmark

Collaborative works:

- Subject-specific models for kinematic simulations\textsuperscript{1}
  - UNIGE: Jérôme Schmid
  - EPFL: Anders Sandholm

- Bone segmentation using few training datasets\textsuperscript{2}
  - UNIGE: Jérôme Schmid

\textsuperscript{1} Schmid, Recent Advances in the 3D Physiological Human, 2009.  \textsuperscript{2} Chung, Visual Comput, 2010.
Motivation and overview

- 3D reconstruction method:
  - accurate
  - subject-specific
MRI acquisition

- **Subject**
  - female (24 years old)
  - written consent
  - medical-ethical committee

- **Six acquisitions:**
  - limited Field of View
  - registration step

- **Slice thickness:**
  - hip and knee (2mm)
  - long bones (10mm)
  - foot (4mm)
Interpenetration removal

• Meshes likely to penetrate each other

• Pairwise procedure:
  • distance map created for each model
  • If interpenetration, a force is applied
Tendons

- Detection in MR images:
  - maximum intensity ridge tracing method\(^1\)
  - manual placement of landmarks linked as tubular structures

Results

• An atlas composed of meshes representing lower limb structures:
  • bones: 6 (thigh: 3 and leg: 3)
  • muscles: 34 (thigh: 21 and leg: 13)
  • tendons: a pair for each muscle

109 meshes
Overview
3D Anatomical Human project

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Motivation and overview

- In PCA-based methods, **numerous datasets** are required

  ![meaningful prior]

- Study the influence of **few training datasets** on segmentation results:

  - **shape**:
    - shape memory¹ (SMEM)
    - Statistical Shape Models² (SSM)

  - **appearance**:
    - mean intensity profiles (PROF)
    - PCA-based intensity profiles³ (PCAP)
    - multimodal intensity profiles (MPAM)

Data

- Six lower limb MRI datasets:

- Four levels of details for both femur and hip bones:
**Segmentation results**

![Leave-One-Out (LOO) cross validation](image)

<table>
<thead>
<tr>
<th></th>
<th>DICE(^1)</th>
<th>D3</th>
<th>D6</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Femur</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SMEM</td>
<td>92.38</td>
<td><strong>92.51</strong></td>
<td>90.51</td>
</tr>
<tr>
<td>SSM</td>
<td>90.57</td>
<td>90.52</td>
<td>90.71</td>
</tr>
<tr>
<td><strong>Hip</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SMEM</td>
<td>84.67</td>
<td><strong>91.45</strong></td>
<td>84.27</td>
</tr>
<tr>
<td>SSM</td>
<td>67.07</td>
<td>88.50</td>
<td>88.10</td>
</tr>
</tbody>
</table>

[PCAP: PCA-based intensity profiles, PROF: mean profiles, MPAM: multimodal profiles]

**For all combinations, using D3 gives better results than D6**

**PROF+SMEM performs the best for femur (D3) and hip (D3/D6) segmentation**

**MPAM+SSM performs the best for femur (D6) segmentation**

---

Discussion

- Using 3 datasets (D3) gives better results than 6 datasets (D6):
  - counter-intuitive: more datasets should be better
  - 3 additional datasets from D6 corrupted by artifacts

- Shape memory gives better results than Statistical Shape Models:
  - local approach to segment structures with few inter-subject variation
  - PCA is known to give better results with more datasets (>>> 6)

- MPAM/SSM gives the best results for femur segmentation with D6:
  - MPAM features a sensitivity to global MR intensity distribution
  - similarity measure should be optimized to cope with the noise

- In general, mean profiles give the best results:
  - NCC\(^1\) is used for both training set creation and segmentation
  - NCC\(^1\) is known to be robust to intensity change

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Main contributions

- **Multimodal Prior Appearance Model (MPAM):**
  - multimodality
  - no accurate pointwise registration
  - outperforms PCA-based appearance prior (PCAP) with less modes

- **OSI criterion:**
  - tradeoff between under/overfitting for the classification of profiles

- **Spectral clustering of intensity profiles:**
  - no Gaussian assumption
  - robust in different resolutions

- **Boosted clustering:**
  - optimization of profile classification for segmentation

- **Subject-specific anatomical models** for kinematic simulations:
  - complete pipeline from MR images to realistic 3D models
Other contributions

- **Covariance matrix regularization:**
  - to avoid singularities due to the covariance matrix inversion

- **Spatial regularization** during classification:
  - EM clustering: based on Neighborhood EM (NEM)
  - spectral clustering: based on a neighborhood weight

- **Fusion of modes:**
  - using the Jaccard index
  - to reduce the complexity of the MPAM
Publications

• Journal and book chapter:

• International conference:

• National conference:
Perspectives

- Segmentation using **MPAM combined with robust shape priors**:
  - *i.e.* through a statistical analysis of shape based on PCA

![Images of anatomical structures](Heimann, Med Image Anal, 2009)

- **Study of other appearance feature vectors**:
  - *e.g.* intensity blobs, texture descriptors, wavelets

Perspectives

- Improvement of the mode fusion:
  - *i.e.* improving segmentation while reducing the number of modes
  - including intensity normalization between images (*e.g.* MRI)
  - leading to an automatic labelling of a reconstructed mesh

- Segmentation of other anatomical structures:
  - from CT images: *e.g.* prostate, spleen, kidney and lungs
  - from other modalities (*e.g.* MRI)
Regional appearance modeling for deformable model-based image segmentation

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