Model-Based Organ Segmentation: Recent Methods

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General Exam Paper

2009
Problem Statement

• Learn how to segment new, unseen CT images from a set of training CT images with ground truth organs marked.

• Goal: Minimize the training errors while generalizing to the new CT images
Problem Organ: The Liver
Why Difficult? (Shape Variations)
Why Difficult? (Similar Appearances)
Why Difficult? (Appearance Changes)
Why Difficult? (Position Changes)
Active Shape Model Based Framework

Training phase

Input

3D point correspondence

Training CT Volumes

Known point correspondences

Learning Statistical Shape Models

Learned Statistical Shape Model

Learning Boundary Intensity Model

Learned Boundary Intensity Model

Learning Organ Detection

Organ Detector

Testing phase

A Testing CT Volume

Organ Detection

Detected Bounding Box

Shape Model Initialization

Initial Shape

Boundary Refinement

Final Shape

…
Active Shape Models: Training

• Shapes are modeled in a training phase using a set of CT volumes whose ground truth segmentations are given.

• There are 4 steps to the training phase.

  1. Find 3D point correspondences on training meshes.
  2. Learn a statistical 3D shape model of the shapes.
  3. Learn a boundary intensity model for each vertex.
  4. Learn an organ detector that finds bounding boxes.
First find 3D point correspondences Among all the training models of The organ being modeled.
Next learn a statistical shape model of that organ.
Next learn a model of the boundary intensities.
Finally train a classifier to find the organ inside a bounding box.

- Given a bounding box and the CT slices inside it, a classifier learns to decide if *everything* inside the box is liver or not.

Where do you get the bounding box?
Active Shape Models: Testing

• There are 3 steps to the testing phase

1. **organ detection**: use the learned organ detector to detect the organ in the testing volume and return a bounding box

2. **shape model initialization**: initialize the learned statistical model based on the detected bounding box

3. **boundary refinement**: use the learned boundary intensity model to estimate the refinement to the model for this shape
Learned Statistical Shape Model

Test Organ

Find Bounding Box

Initialize Shape Model
Methods for Point Correspondences

1. Principal Component Analysis (PCA)

PCA takes in the points of each shape in the training set. It produces a set of basis vectors (the components).

Each shape can then be represented as a linear combination of these components.

\[ \tilde{x} = \bar{x} + \sum_{k=1}^{K} c_k b_k \]

where \( \bar{x} \) is the mean shape

The optimal K projection axes \( b_k \), \( k = 1 \) to \( K \) are the eigenvectors of the covariance matrix of the training set of points corresponding to the \( K \) largest eigenvalues.
Intuitive Meaning of Principal Components

eigenvector corresponding to highest eigenvalue

eigenvector corresponding to second eigenvalue
Eigenimages for Face Recognition

training images

mean image

linear approximations

3 eigenimages
3D Point Correspondence (MDL)

- **Goal:** Find 3D Point Correspondence
- **Idea:** Minimize MDL-based objective function
  - Evaluate the quality of the correspondence
    \[ F = \sum_{k=1}^{N} L_k \text{ with } L_k = \begin{cases} 1 + \log(\lambda_k/\lambda_{cut}), & \text{if } \lambda_k \geq \lambda_{cut} \\ \lambda_k/\lambda_{cut}, & \text{otherwise} \end{cases} \]
- The \( \lambda_k \)'s are the **eigenvalues** from PCA.
- **How:** Gradient descent
  - Manipulate correspondences by parameterization and re-parameterization.

Davies et al. [IEEE TMI’02]
• **Statistical Shape Models**
  – Principal Component Analysis (PCA)
  – Kernel PCA
  
  In either case the shape model consists of the PCA mean and basis. Any shape can be represented.

- **Boundary Intensity Models**
  - Gaussian distribution
  - AdaBoosted histogram classifiers
  - Heuristics

Cootes et al. [IEEE PAMI 01], Twining et al. [BMVC’01]
Cootes et al. [IEEE PAMI 01], Li [ICCV’05], Kainmuller et al. [MICCAI’07]
Organ Detection (MSL)

- **Goal**: Find the bounding box
  - The parameter space is 9D.
  - 3D positions, 3D scales and 3D orientations.

- **Idea**
  - Uniform and exhaustive search is unnecessary

- **How**: decompose the problem into three steps
  - position estimation, position-scale estimation and finally position-scale-orientation estimation.

Zheng et al. [ICCV’07]
Two ASM-based Systems

<table>
<thead>
<tr>
<th>Kainmuller et al. [MICCAI’07]</th>
<th>Ling et al. [CVPR’08]</th>
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</thead>
<tbody>
<tr>
<td><strong>Statistical Shape Models</strong></td>
<td></td>
</tr>
<tr>
<td>– PCA</td>
<td>– PCA, hierarchical shape pyramids</td>
</tr>
<tr>
<td>– 43 CT volumes</td>
<td>– 75 volumes</td>
</tr>
<tr>
<td><strong>Boundary Intensity Model</strong></td>
<td></td>
</tr>
<tr>
<td>– Heuristics</td>
<td>– A boundary classifier</td>
</tr>
<tr>
<td><strong>Liver Detection</strong></td>
<td></td>
</tr>
<tr>
<td>– Lungs detection and DICOM info</td>
<td>– MSL (marginal space learning)</td>
</tr>
<tr>
<td><strong>Performance</strong></td>
<td></td>
</tr>
<tr>
<td>– Ranked first in a recent liver segmentation competition.</td>
<td>– 5 fold cross validation</td>
</tr>
<tr>
<td>– 10 testing volumes</td>
<td>– 1.59 mm (the average symmetric surface distance)</td>
</tr>
<tr>
<td>– 1.1mm (the average symmetric surface distance)</td>
<td>– 1.38 mm (the median)</td>
</tr>
<tr>
<td>– 15 minutes.</td>
<td>– 12 seconds.</td>
</tr>
</tbody>
</table>
Experimental Setting

• Datasets:
  – 4 types of organs (livers, left kidneys, right kidneys, spleens)
  – 15-20 subjects

• Leave-one-out cross validation

• Measure the reconstruction error

• Metrics: Euclidean and Hausdorff distance
MDL-2DPCA

- MDL-based objective function

\[
F = \sum_{k=1}^{N} L_k \quad \text{with} \quad L_k = \begin{cases} 
1 + \log(\lambda_k / \lambda_{\text{cut}}), & \text{if } \lambda_k \geq \lambda_{\text{cut}} \\
\lambda_k / \lambda_{\text{cut}}, & \text{otherwise}
\end{cases}
\]

- Idea: Generalize the objective function to 2DPCA space
  - Replace eigenvalues from PCA with those from 2DPCA
  - How: Gradient descent

- Comparisons: original MDL vs. MDL-2DPCA

* Chen and Shapiro [EMBC’09]
2DPCA

• When we use normal PCA, our representation of a shape is a vector
  
  \((x_1, y_1, z_1, x_2, y_2, z_2, ..., x_K, y_K, z_K)^T\)

• When we use 2DPCA, our representation of a shape is a 2D matrix (or tensor)
  
  \[
  \begin{bmatrix}
  x_1 & y_1 & z_1 \\
  x_2 & y_2 & z_2 \\
  x_K & y_K & z_K \\
  \end{bmatrix}
  \]

• And so are the components.
Results (3D Point Correspondences)

- Livers
  - Original MDL
  - MDL-2DPCA

- Left Kidneys

- Right Kidneys

- Spleens

Reconstruction error vs. # eigenvectors
Tensor-based SSM

• Idea: Tensor-based dimension reduction methods
  – 2DPCA
  – Parafac model
  – Tucker decomposition

• Comparisons: PCA vs. Tensor-based dimension reduction

* Chen and Shapiro [EMBC’09]
Results (Statistical Shape Models)

- Parafac
- PCA
- Tucker
- 2DPCA

Livers

Left Kidneys

Right Kidneys

Spleens
Organ Detection (Boosting Approach)

• **Idea:** Classify whether an image block contains an organ of interest

• **How:**
  – Partition slices into non-overlapping 32x32 blocks
  – Global features: gray-tone histogram of the image slice and its slice index
  – Local features: the position of a block, the mean and variance of its intensity values, and its intensity histogram.
  – 20,000 SVM linear classifiers + Adaboosting

• **Comparisons:** Manual vs. Adaboosting
## Results (Organ Detection)

<table>
<thead>
<tr>
<th></th>
<th>Positive (predicted)</th>
<th>Negative (predicted)</th>
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<tbody>
<tr>
<td><strong>Livers (Training)</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Positive (actual)</td>
<td>96.23%</td>
<td>3.77%</td>
</tr>
<tr>
<td>Negative (actual)</td>
<td>4.57%</td>
<td>95.43%</td>
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<td>Positive (actual)</td>
<td>91.23%</td>
<td>8.77%</td>
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<td>Negative (actual)</td>
<td>6.57%</td>
<td>93.43%</td>
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</table>
True Positive: Green,
False Negative: Red,
False Positive: Blue,
True Negative: Cyan
Graph Cuts Based Boundary Refinement

- The goal of the s-t cuts paper is to incorporate additional shape information (e.g., size) to find the boundary/shape of an organ of interest (e.g., kidney) in an image.

- Idea: Adding hard constraints to min s-t cuts
- Min s-t cuts with side constraints
  - NP-hard in general cases
  - Approximation algorithm: standard rounding algorithm
- Comparisons: with constraints vs. without constraints

Chen and Shapiro [ICPR’08]
Results (Boundary Refinement)

Initial Contour

Slice 1

Slice 2

without

with
What have we got?

• A great design.
• Several conference papers.
• No complete system, just pieces, some pieces never really done.
• Would be a space for a course or longer project.
• Livers came from here: http://sliver07.org/
• Here is a newer one: https://www.virtualskeleton.ch/ShapeChallenge/Start2014
• LOTS of data challenges here: https://grand-challenge.org/all_challenges/