Active Appearance Model Based Segmentation
Cardiac MR and Transthoracic Echo Images and Image Sequences

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Medical Imaging and Analysis

- X-ray
- CT
- MR
- PET
- SPECT
- Ultrasound

- Medical imaging revolutionized diagnosing, treatment, and surgical interventions.
- Medical image analysis is still mostly performed visually, off-line, and has a qualitative character.
- Highly automated quantitative analysis is needed
Active Appearance Model Based Segmentation

- Goals:
  - Development of a robust segmentation technique based on shape and appearance
  - Single approach to variety of medical image analysis problems via machine learning
  - Native analysis in 2D, 2D+time, 3D, 4D
  - Validation in large groups of subjects
  - Application to cardiac MR, cardiac echo, liver tumor resection surgery planning, …
  - Direct computer-aided diagnosis of disease status

Medical Areas of Interest

- Quantitative assessment of left-ventricular (LV) and right-ventricular (RV) function
- Quantitative analysis of stress echocardiographic images
- Quantitative LV analysis is possible in MR - MASS package (Leiden University) based on optimal graph searching
- Fails in non-standard cases, no reliable RV segmentation exists
- No reliable Echo segmentation exists
Modeling of Shape

Point Distribution Models

- represent the shape borders of objects as a collection of corresponding points
- demo of basic steps ...
Compute the average shape

$$\bar{x} = \frac{1}{s} \sum_{i=1}^{s} x_i$$

Computing the modes of variation.

– Compute a covariance matrix

$$S = \frac{1}{s - 1} \sum_{i=1}^{s} (x_i - \bar{x})(x_i - \bar{x})^T$$

• Modes of covariance matrix variation can be determined via eigen-decomposition of the covariance matrix.

$$Sp_i = \lambda_i p_i$$

$$P = (p^1 p^2 p^3 \cdots p^{2N})$$

Principal Component Analysis creates a more compact basis function from a multi-dimensional set of data where the mean is at the origin.

The result is a PDM model of shapes

$$x \approx \bar{x} + Pb$$
Modeling Appearance

- The appearance of an object can be described by its shape and texture
- Shape is represented by landmark points
- Texture is represented by pixel intensities

Warping the images to the mean shape
The mean shape and mean gray-level

Active Appearance Models

- each example can be expressed by two vectors

\[
\begin{align*}
    b_s & \approx P_s^R (x - \bar{x}) \\
    b_g & \approx P_s^T (g - \bar{g}) \\
\end{align*}
\]

- \(b_s\) and \(b_g\) can be concatenated and PCA applied

\[
    b = \begin{pmatrix}
        Wb_s \\
        b_g
    \end{pmatrix}
\]

- apply a PCA to all concatenated b-vectors
Matching AAM’s

- Matching an AAM to an image requires:
  - a criterion function $e$:
    - the RMS error of the ‘difference image’ between the model and the underlying image patch
  - a minimization procedure (Levenberg Marquardt / simplex)
  - derivatives of the criterion function with respect to all ‘optimizable’ parameters
    - can be estimated using multiple linear regression
    - examples of derivative images
Results

Problems

- Appearance matching may lock on incorrect features and get stuck in a local minimum
- This is a problem for quantitative analysis
Arguments for a hybrid model

- Conventional AAM better suited for appearance matching than for accurate border detection - local structures and boundary information are not specifically considered
- Local border properties are considered in Active Shape Models
- Hybrid ASM/AAM matching

Hybrid ASM/AAM

- ASM’s shape/pose de-coupled from AAM in each iteration
- ASM and AAM matching steps are performed independently
- Resulting AAM and ASM shape/pose parameters are combined using weighted averaging after each iteration
- The refined AAM reflects the combined shape and current appearance
Combined AAM & ASM Fitting

- Hough Transform determines LV centers
- AAM matching till convergence
- ASM/AAM matching till convergence (typically 3-5 iterations)
- AAM matching initialized with mean appearance and most recent shape
- Several initial orientations used to achieve sufficiently good match.
RMS Error Function

![RMS Error Function Graph](image)

~1 sec

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Fully Automated Segmentation of Cardiac MR Images

Original images - varying patient position, large field of view

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Complete Hybrid ASM/AAM Segmentation

Conventional AAM  Hybrid AAM

Experimental Methods

- Training set 102 images (11 patients and 23 normals); testing set 60 images (9 patients and 11 healthy subjects), completely disjoint
- Patients suffered from various pathologies such as hypertrophic obstructive cardiomyopathy, myocardial infarction or LV aneurysm.
- Three end-diastolic, mid-ventricular slices were selected per sample.
- Independent standard was manually traced
Validation Indices

- Border positioning errors (signed average, RMS, max)
- Area measurements (LV, RV, EPI)
- Computer-determined results compared with observer-defined independent standard
- Regression analysis used for area measurements
- Bland-Altman statistic used to compare area measures

Results

- Method never failed in the testing set
- All contours were visually pleasing
- No manual initialization
- No manual correction

- Signed border positioning errors
  < 0.2±2.2 pixel
Results

Original

Manual

Hybrid AAM
Results

Area Comparisons

- N=54
- Slopes not different from 1
  - for LV, RV (p=NS), p=0.03 for EPI
- Intercepts not different from 0
  - for LV, RV, EPI (p=NS)
Log-log Bland Altman

- Minimal bias
  - LV: -0.4%
  - RV: -0.6%
  - EPI: -0.2%
- 95% measurements within
  - LV: -8 — +8%
  - RV: -17 — +19%
  - EPI: -8 — +8%
- RV results worse than LV and EPI - caused by
  - ambiguities in training set
  - task difficulty

AAM vs. Hybrid AAM

- Our multistage hybrid AAM method significantly outperformed the conventional AAM approach at the significance level of p<0.001 as assessed by comparison of unsigned border positioning errors in the testing set.

- Demo of a 2D + time
Experiments and Results

- 129 unselected infarct patients (72 training + 57 testing)
- Endocardial percent area error \(-3.1 \pm 10.3\%\)
- Mean signed area ejection fraction errors \(0.6 \pm 5.5\%\)
Three-dimensional AAM

Problems of extension to 3D:

- Point Correspondence
  - Even if landmark points are easily identifiable, specifying uniquely corresponding points in-between landmarks is difficult in 3D.
- Aligning Shapes Three Dimensionally
- Three Dimensional Warping

3-D Point Correspondence
3D AAM Training

- Procrustes alignment and tetrahedral representation
- 3D PDM (using PCA)
- 3D warping
- 3D appearance model (PCA)
- 3D AAM – combined shape and appearance (PCA)

→ no algorithmic difference from 2D
→ increased computational complexity

Shape Aligning in 3-D

- Shape alignment in 2-D AAMs utilized Procrustes Analysis.
- 3-D Procrustes Analysis requires a quaternion representation of pose.
  - Rotation is represented as a unit vector and rotational twist
  - Euclidian Rotations may result in singularities known as gimbal-lock.
- Shape alignment uses procedure by Besl et al.
Three-dimensional AAM

- In general it is an extension of 2D + time
- Point correspondence remains a problem
- Model construction:
  - Instead of Delaney triangulation, LV is explicitly defined by hand as a set of tetrahedrons – doing it once for training set
  - Quaternion representation used for 3D objects (common in computer graphics)
  - 3D warping implemented using Barycentric coordinates (center of gravity of triangles)

3D AAM Segmentation Process
Results

Leave-one-out study of 53 volumetric MR images comparing automated and manual volumes.

Endocardial volume  Epicardial volume  Myocardial mass
3D-AAM …

unsolved problems

- Model lacks resolution in the z-direction affecting the ability of the model to extend to the apex and base in many segmentations
- Point correspondence still a difficult problem in developing new models.
- The model is dependent on the set of samples.

Volumetric CT … Liver + Tumor
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Image Analysis Part

LSPS - Image Analysis Part

Segmentation

CT Slice Stack

Liver segmentation

Vascular tree segmentation

Liver partitioning

Tumor segmentation

Radiological Knowledge

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Challenges

Partial Volume Effect

Proposed Solution … Sequential Segmentation

1. Middle lobe of right lung
2. Quadrate lobe liver
3. Left lobe of liver
4. Diaphragm
5. Heart
6. Upper lobe of the left lung

Impact of Diaphragm Segmentation

Ground Truth
Diaphragm
Elevation image describes dome shape
Conversion of a 3D problem to 2½ D
Landmark placement using 2D grid

2D reference curve
Key landmark point
Landmark point
**3D Shape Modeling**

Reference curve model: \( x = \bar{x} + P_x b_x \)

Elevation image model: \( h = \bar{h} + P_h b_h \)

- The shape models are linked via a warping function
- Fringe (extension of the shape)

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**3D Appearance Representation**

- Warping all layers to the mean reference curve shape and sample them into vectors
- Concatenating all the vectors into one intensity vector \( g \)
3D Appearance Modeling

- Normalizing the intensity vector \( \mathbf{g} \)
- Applying PCA to the normalized data

Model of 3D Appearance:
\[
\mathbf{g} = \bar{\mathbf{g}} + \mathbf{P}_g \mathbf{b}_g
\]

Building a 3D AAM

Concatenating appearance and shape models, one more PCA

\[
\mathbf{b} = \begin{bmatrix} \mathbf{W}_x \mathbf{b}_x \\ \mathbf{W}_h \mathbf{b}_h \\ \mathbf{b}_g \end{bmatrix} = \begin{bmatrix} \mathbf{W}_x \mathbf{P}_x^T (\mathbf{x} - \bar{\mathbf{x}}) \\ \mathbf{W}_h \mathbf{P}_h^T (\mathbf{h} - \bar{\mathbf{h}}) \\ \mathbf{P}_g^T (\mathbf{g} - \bar{\mathbf{g}}) \end{bmatrix}
\]

Complete 3D AAM:
\[
\mathbf{b} = \mathbf{P}_c \mathbf{c}
\]
Diaphragm Segmentation
A New 3D AAM Approach

3D AAM
- Parameters
- Texture Layers
- Elevation Image
- Reference Curve
- 3D Surface Model
- Comparison
- Optimization
- Volume Data
- 3D Texture Sampling

Preliminary Results in CT Data
- Training 20 cases
- Testing 8 cases
- 9 Texture layers
- Fringe (extrapolation)
- Mean model scaled by 1.15
- Reference plane position, scaling in height and model placement defined interactively

Signed surface positioning error (3D):
-0.16 ± 2.95 mm
After fitting the model, modal indices $b$ represent the departure from the mean $x \approx \hat{x} + Pb$.

- Can modal indices be used as disease-specific features?
  1) shape features distinguish normal/infarct/hypertrophic heart in 2D cardiac MR
  2) motion features in 2D+T echo

Cardiac MR - Infarct

Normal Post-Infarct

Modal indices of LV/RV shape
Cardiomyopathy

- Promising results for distinguishing hypertrophic cardiomyopathy

- Early detection of irreversible changes of RV function in congenital heart disease – project ongoing

Wall Motion from 2D+T Echo

- Modal indices of shape/motion from a fitted AAM used to test classification correctness vs. visual scoring.
- Classification correctness predicted using optimal feature selection and a leave-one-out approach, 129 clinical cases.
- Classification correctness:
  - Overall 92%
- Multivariate linear regression correlation of AAM coefficients and visual wall motion score
Conclusion

- AAM is a powerful technique with a wide application field to medical image data
- Hybrid ASM/AAM further improves segmentation performance
- New applications can be designed almost automatically by supplying new sets of manually-traced examples