Medical Image Analysis
Statistical Shape Modeling

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Lecture Overview

- Statistical Shape Modeling
  - Motivation behind SSM of human organs
  - Mathematical tools
  - Shape representation
  - Establishment of point-to-point correspondence
  - Shape alignment
  - Point distribution models
  - Modeling of shape variability
  - Model evaluation
  - Exercise / Tutorial

- Statistical Shape Modeling for Segmentation!
  - Topic to be covered in the next session
Motivation Behind SSM of Human Organs

- Natural anatomical variability and distinctive patterns
- Knowledge of different patterns allows for improved medical technologies
- Population-based studies are key to identify the dissimilarities
- We do not look the same, neither our organs do!!!
Motivation Behind SSM of Human Organs

- Organ shapes vary according to several parameters
  - Ethnicity
  - Age
  - Gender
  - Lifestyle
  - Physical activity
  - ...

- Our goal is to identify these differences using mathematical tools and representations
Motivation Behind SSM of Human Organs

Prior knowledge (what we know in advance) vs Observation (what we see)

- Observation
- Prior

Patient-specific SSM Standard atlas (think of a template)
Motivation Behind SSM of Human Organs
Potential Applications

Example 1: Orthopaedic Implant Design
Why are we interested in human shapes?

Example 2: hearing aid design

Additional problem: Ear canals change shape when people chew
Why are we interested in human shapes?

Example 3: anatomy-physiology correlation

Corpus Callosum

Cognitive abilities
Statistical distribution of shape

How?!
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- **Statistical Shape Modeling for Segmentation!**
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Principal component analysis (PCA) is a method used to **reduce the dimensionality** of a linear system.

PCA projects the original data onto a lower-dimensional space.

PCA embeds the data in a more compact representation.

Let us first define PCA as a mathematical tool, and then see how we can apply it to SSM of anatomical structures.
Mathematical Tools
Principal Component Analysis

- Assume that you have 2-D data points
- In this example, data points are scattered along a principal direction
- PCA yields the main direction (and secondary directions), and creates an orthogonal coordinate system that maximizes the variance of the points in each direction
- Points can be referenced along the main component (axis) using a parameter $b$
- How?
Let \( M \) hold the coordinates of \( N \) (in this example 3) data points

\[
M = \begin{pmatrix}
x_1 & x_2 & x_3 \\
y_1 & y_2 & y_3
\end{pmatrix} = \begin{pmatrix}
X_1 & X_2 & X_3
\end{pmatrix}
\]

The principal axes of the variation of the points are represented by eigen-vectors and eigen-values of the covariance matrix of \( M \)

The covariance matrix is defined by

\[
Cov(M) = \frac{1}{N - 1} \sum_{i=1, \ldots, N} (X_i - \bar{X})(X_i - \bar{X})^T
\]
One approach is to run eigen-analysis on the covariance matrix

\[
\text{Covariance matrix} = \Gamma \Lambda \Gamma^T
\]

Spectral decomposition (or Jordan decomposition):
Given a symmetric matrix \( A \), we can decompose it as the product of three matrices: \( A = \Gamma \Lambda \Gamma^T \)
Mathematical Tools
Principal Component Analysis

Memory/computations issues when dimensionality of each sample is too large (why?)
High Dimensionality…

Sometimes the dimensionality of the samples is too large (e.g., too many points in a mesh)
This translates into a HUGE covariance matrix
Let’s say we have n observations of size p,
\[ X = (x_1, \ldots, x_p) \]
This gives us covariance matrix C of size \( p \times p \)
\[
C = \frac{1}{n} \sum_{i=1}^{n} dx_i dx_i^t \quad \quad dx_i = x_i - \bar{x}
\]
\[
D = (dx_i^t | \ldots | dx_n^t)
\]
High Dimensionality…

\[ C = \frac{1}{n} D D^t \]

\[ D = (dx^t_i \mid ... \mid dx^t_n) \]

\[ T = \frac{1}{n} D^t D \]

\[ T \Psi_i = \gamma_i \Psi_i \]

A smaller matrix T can be computed instead:

Dimension of T is now n x n !!

Eigenvectors-values of T is computable

After some simple algebra:

Eigenvector/values of C

\[ \Phi_i = \frac{1}{\sqrt{\gamma_i n}} D \Psi_i \]

\[ \lambda_i = \gamma_i \]

But..
we get only n-1 eigenvector/values

\[ \rightarrow \text{Intractable computation} \]
Another possibility is to use **Singular Value Decomposition (SVD)** on the original matrix $M$!
Mathematical Tools
Principal Component Analysis

- SVD diagonalizes the covariance matrix of the original data
- It directly yields the eigen-vectors and eigen-values of Cov(M)

\[ M = U W V^T \]

- Eigen-vectors
- Diagonal matrix of eigen-values

\[ M = \begin{bmatrix} U & W & V^T \end{bmatrix} \]
PCA assumes that the original data follows a Gaussian distribution (even if in reality it does not)

PCA results in an **orthogonal** lower-dimensional system. i.e., the principal axes are perpendicular

PCA is a **linear** method

There also exist several linear and non-linear dimensionality reduction techniques such as factor analysis Isomap, multidimensional scaling (MDS), etc.
Mathematical Tools
Principal Component Analysis

- Let us now see how can we use this statistical learning method and apply it to model anatomical shape variability
- Several preprocessing steps are required to make the data ready for statistical modeling
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- **Statistical Shape Modeling for Segmentation!**
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Different imaging modalities offer different ways to view and process anatomical structures.

First step is to have accurate segmentations of the images.

Then a surface model is generated from the segmentation mask (isosurface).

How is this surface represented?
Shape Representation

- Surface model can be represented and stored in different ways
  - Parametric surface (splines, etc.)
  - Combination of implicit functions (quadrics, etc.)
  - Oriented Bounding Box
  - Medial Representation
  - Surface mesh (surface points and connecting lines)
  - Point Cloud (non-connected surface points)
  - ...
Shape Representation
Point Clouds

- A set of points evenly distributed on the surface of the organ
- Each point is represented by its 2D or 3D coordinate vector
Shape Representation
Point Clouds

- Every surface point: \( p_i = \{x_i, y_i, z_i\} \)
- The surface is represented by concatenating the points

\[ S = \{p_1, p_2, \ldots, p_n\} \]

\[ \Rightarrow s_i = \{x_{i,1}, y_{i,1}, z_{i,1}, x_{i,2}, y_{i,2}, z_{i,2}, \ldots, x_{i,n}, y_{i,n}, z_{i,n}\} \]

- \( n \) = number of points that constitute the surface
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- **Statistical Shape Modeling II**
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Now assume we have two different objects of the same class (i.e., two femurs from two different patients).

Initially, isosurfacing results in point clouds with a different number of points.

We should establish anatomical correspondence between the points.
Among the different methods, one can list
- Mesh-based registration (e.g. iterative closest point)
- Image-based registration (e.g. non-rigid registration)
- ...

The idea is to use a reference mesh and morph it to match the other meshes, thus **keeping a consistent number of points**.

The topic of image registration will be reviewed in future sessions and is outside the scope of this lecture.
Alignment and correspondence

How to make *alignment*?
- Rigid registration

How to establish *correspondence*?
- Manually (landmarks selection)
- Automatically (non-rigid registration)
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The bone is described as a coordinate vector
This vector can be seen as a point in the space
But the space is not 2D, not 3D, not 4D, but… nD!!
So if the shape is described by n points, the dimension of the space is 3xn
(in this case: n=123.200, so the space dimension is 369.600!)
Adding shapes to the space

We can add other shapes to our space in order to describe their variability (our initial aim)

Shape1 = \([x_1, y_1, z_1, x_2, y_2, z_2, \ldots x_n, y_n, z_n]^T\)

Shape2 = \([x_1, y_1, z_1, x_2, y_2, z_2, \ldots x_n, y_n, z_n]^T\)

Shape3 = \([x_1, y_1, z_1, x_2, y_2, z_2, \ldots x_n, y_n, z_n]^T\)

369.600-dimensional space
Point Distribution Models (PDM)

- So far, we have:
  - A set of aligned shapes
  - Each shape has the same number of surface points
  - Surface points correspond anatomically and/or spatially
  - Each shape is represented by a vector of coordinates
    \[ s_i = \{x_{i,1}, y_{i,1}, z_{i,1}, x_{i,2}, y_{i,2}, z_{i,2}, \ldots, x_{i,n}, y_{i,n}, z_{i,n}\} \in \mathbb{R}^{3n} \]

- We can represent the set of shapes in a matrix by concatenating the \( m \) shape vectors \( s_i \)

\[
M = \begin{pmatrix}
    S1 \\
    S2 \\
    S3 \\
    Sm
\end{pmatrix}
\]
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We now come back to the matrix of shapes $M$ of dimension $3n \times m$ (usually huge in practice).

The following figure is an example of a set of landmarks taken on different resistors (aligned and normalized).

Each group of landmarks (in 2-D) can be thought of as the scattered points example shown earlier.

We should find the principal directions of variation of each landmark.
Modeling of Shape Variability

- Subtract mean from each instance of $M \rightarrow D = M - \text{mean}(M)$
- Apply SVD directly on matrix $D$

$$D = U W V^T$$

$U$ = eigen-vectors of $\text{Cov}(M)$
$\text{diag}(W) = \text{eigen-values of } \text{Cov}(M)$

$n = \text{number of points per mesh}$
$m = \text{number of training samples}$
Modeling of Shape Variability

- The eigen-vectors are a set of orthogonal axis, each corresponding to one of the main directions of variation.
- As shown earlier, each direction has a different scale.
- The scale is given by the eigen-values.
- The eigen-values represent the variance of the points in each direction (over each principal component).
- The eigen-values are usually stored in decreasing magnitude (the corresponding eigen-vectors are sorted accordingly).
What can we do with shapes in a reduced space?

The formula that we can use to create new instances is:

\[ x = \bar{x} + \Phi b \]

where:
- \( x \) is the new shape vector
- \( \bar{x} \) is the average shape
- \( \Phi \) is the chosen eigenvector
- \( b \) is a parameter whose value is: \( -3\sqrt{\lambda_i} \leq b \leq +3\sqrt{\lambda_i} \)
  (\( \lambda \) is the corresponding eigenvalue)
Let’s summarize....
Summary Statistical Shape Modelling

1.- Point Distribution Model (PDM)

- Common reference space

- Find anatomical corresponding points amongst shapes
Summary Statistical Shape Modelling

- Common reference space

- Find anatomical corresponding points amongst shapes (Registration task)
**Summary Statistical Shape Modelling**

- Find anatomical corresponding points amongst shapes
- Model variability

**Principal modes of deformation**
Summary Statistical Shape Modelling

Model: \( x = \bar{x} + \phi b \)  \( \bar{x} = \frac{1}{N} \sum_{i=1}^{N} x_i \)  Mean Shape

Statistical Analysis via Principal Component Analysis (PCA)

Eigen-decomposition of matrix

\[ s = \frac{1}{N} \sum_{i=1}^{N} dx_i dx_i^T \quad dx_i = x_i - \bar{x} \]

provides eigenvectors/eigenvalues \((\lambda, \phi)\)

\[ S \phi_k = \phi_k \lambda_k \]  With k, the kth eigen-vector/value
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Commonly, three measures are used to evaluate a statistical shape model, namely
- Compactness
- Generalization
- Specificity

They are used to indicate how well the modeling process has been able to embed the original data into a lower dimensional space.
Model Evaluation
Compactness

- Compactness is a measure of how good the data reduction process is.
- In other words, a model that is compact enough, allows the generation of new shape instances using as few parameters (principal modes or components) as possible.
- It is represented by a curve showing how much of the total variance a certain number of modes of variation can capture.
Model Evaluation
Compactness

- \( t \) = number of modes used
- \( \lambda_i \) = eigen-values
- \( \lambda_{\text{total}} \) = total variance = all eigen-values summed together

\[
C(\lambda_t) = \frac{\lambda_t}{\lambda_{\text{total}}}
\]
Model Evaluation
Generalization

- Generalization is performed using leave-one-out (cross-validation) reconstruction experiments.
- It represents the ability of the model to generate new instances from the class.
- For every left-out instance, a new statistical model is computed from the remaining training instances.
- The parameters of the left-out instance are computed.

\[ b_{out} = \phi^{-1}(x_{out} - \bar{x}) \]
The parameters are used to reconstruct the instance

\[ \tilde{x} = \bar{x} + \phi b_{out} \]

The errors are measured and averaged over all training instances yielding the \textbf{generalization curve} of the model generalization

\[ \frac{1}{N} \sum_{i} (x_i - \tilde{x}_i)^2 \quad i: \text{sample reconstructed} \]

It is also dependent on the number of modes of variation (parameters used in the reconstruction process)
Model Evaluation

Generalization

Model Generalization

- Lumbar
- Thoracic
- Cervical
- Total

Generalization vs. number Of Modes
Specificity is an indicator of **how good the model is in generating instances similar to those presented in the training set**

It is measured by generating a large number of random instances using different number of modes, and for every new instance, compute the distance to the closest shape in the training set
An example of application to Orthopaedic Research
“What defines a good implant design?”

- Implant Fitting
- Implant Stability
- Bone Healing Impact
- Intervene as less as possible
  - Torsions are bad
  - Screws deformations
Example: Computer-Assisted Orthopedic Implant Design

Population-based implant design
Statistical shape space: axes define different patterns of shape variability

\[ \tilde{x} = x + \phi \alpha \]
Proposed methodology

Three-step method:

A. **Create statistical shape model** of a selected population
   
   This creates a new space to describe shape variability, where different axes describe specific patterns of shape variability.

B. **Perform automated implant fitting** on the modelled shape
   
   Partition the space between “good” and “bad” fittings
   
   => A fitting criteria is defined.

C. **Find correlations** between the fittings distribution and the bone shape variability
   
   Understand the partitioned space to change implant design.
Asian/Caucasian Distance Maps

Average distance
Asian

Caucasian

Max. distance
Asian

Caucasian

Range: 0 – 4 mm

Range: 0 – 7 mm
Segmented bones favour “good” fitting
Fitting criteria: error less than 1mm

Partitioned space
Negative values of 1st variation mode favour “good” fitting

Modify the implant to get the “good” fitting in the whole shape space
Expand the partitioned space!

In a 3D space, one can have nearly 57K fitting operations!
How to change the implant design? Understanding the partitioned space!

1st variation mode is the most responsible for the shape variability and fitting result!!

“good” area

“bad” area

Oblique line of tibia:
flatten the curvature of implant

Lateral surface of tibia:
twist the surface of implant

instance from “good” area

instance from “bad” area
New implant model

old implant  new implant
Comparison between implants

Modified implant expand the space of “good” fitted bones
New implant shape fits better majority of the population
With a new implant design there is an increase of 40% on the number of instances that satisfy the given fitting criterion.

Kozic et al. MedIA 2010
Kozic et al. ISBI 2009
Thanks for your attention! – Questions?