43075-01 Probabilistic Shape Modelling

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Introduction   26. February 2019
Deadline   **19. March 2019** (Discussion / presentation during exercise session)

Exercise 0: Before you begin

0.1 Forming groups

You should work on the exercises and projects in this course in groups of two students. We will discuss your answers to the questions during the exercise session on the 19. March (14.15 - 16.00). *Please send us the names of the persons in your group via email to ghazi.bouabene@unibas.ch no later than 05. March. Once we have all the names, we will send a schedule with the timeslots for the discussions.*

0.2 Setting up the environment

We strongly suggest that you start working with Scalismo as a library instead of using Scalismo-Lab. This will make your life much easier in the later parts of the course. We also advice you to use the latest version of Scalismo (v0.17) and Scalismo-ui (v0.13). We have prepared for each tutorial in ScalismoLab a corresponding tutorial that shows the concepts in "modern" scalismo. To set up your development environment, follow the steps indicated in the guide *Using Scalismo in an IDE*.

Scalismo tutorials: `https://unibas-gravis.github.io/scalismo-tutorial/`

Scalismo in an IDE: `https://unibas-gravis.github.io/scalismo-tutorial/ide.html`

Exercise 1 — Normal distributions, Gaussian processes and rigid Alignment

1. Femur project: first steps

The goal in this exercise is to perform the first two steps of the MOOC femur project:

1. Create your account on the SICAS Medical Imaging Repository (SMIR)

2. Download the femur data and rigidly align the femurs to the provided reference femur.

You need to create an account on the SMIR repository in order to be able to access the project data. Follow the instructions in Step 4.11: "Femur Project: First Steps" , section "Create you account on SMIR" in week 4 on FutureLearn. *Important: Please make sure to follow the instructions of the above mentioned section only. The rest of the material in this step is too advanced at this stage.*

1.1 Rigid Alignment of femur bones

Once your SMIR account created, you can proceed to downloading the femur data and rigidly align it to the reference, by following the instructions in step 5.11: "Femur project: data download and preparation" step in week 5 on FutureLearn.

2. Generalized Procrustes Alignment

The goal in this exercise is to implement the Generalized Procrustes Alignment method. As training data, manually create 10 random samples from the face model (bfm.h5). Use the mesh "paola.stl" as your initial mean. Visualize how the mean shape changes during each iteration. Compare the mean shape with the shapes in the population. Is the outcome what you expect?

3. Theory questions

3.1 Definition of shape

In the classical definition of shape, not only rotation and translation but also scaling is normalized.

- What can you say about the variability of different shapes that a model represents, when scaling is normalized? Is it larger or smaller than when you do not normalize scale? Explain.

- Assume we would also normalize with respect to a reflection along one of the coordinate axis? How is the variability of different shapes in the model affected in this case? Could you still detect differences in shapes of left and right hands?

3.2 Bivariate normal distribution

Given the following bi-variate normal distribution

$$N\left(\left(\begin{array}{c} 0 \\ 0 \end{array}\right), \left(\begin{array}{cc} 4 & 6 \\ 6 & 9 \end{array}\right)\right).$$

Plot some samples from this normal distribution (using a tool of your choice, such as Matlab, Python, R, Scala, ...). What can you observe? Can you explain what is happening?

3.3 Rank of a statistical shape model

Assume we are given 10 example surfaces in 2D in correspondence and we let each surface be defined on 1024 points. Assume further, that we represent each example s^i as a vector $\boldsymbol{s}^i = (s_x^1, s_y^1, \ldots, s_x^{1024}, s_y^{1024})$ and estimate the covariance matrix using the formula

$$\Sigma = \frac{1}{n-1} \sum_{i=1}^{n} (s^i - \overline{s})(s^i - \overline{s})^T$$

where $\overline{s}$ is the sample mean

$$\overline{s} = \frac{1}{n} \sum_{i=1}^{n} \boldsymbol{s}^i$$

What is the rank of the covariance matrix? Explain why.
Hint: In case you are not sure how to start, just create 10 random vectors $\boldsymbol{s}^i, i = 0, \ldots, 10$, compute the covariance matrix and observe how the rank changes when you increase the dimensionality.

3.4 Gaussian processes and multivariate normal distribution

Given a discrete Gaussian process $GP(\mu, k)$, with mean function $\mu : \tilde{\Omega} \to \mathbb{R}^3$ and covariance function $\mu : \tilde{\Omega} \times \tilde{\Omega} \to \mathbb{R}^{3 \times 3}$ defined on some discrete domain $\tilde{\Omega}$.
Assume your task is to develop a IO method, which can store the GP in a file and load it again from file. Would it be sufficient to store the mean vector $\boldsymbol{\mu}$ and covariance matrix and Σ, obtained by evaluating the mean and covariance functions at all the points of the domain $\tilde{\Omega}$? Why or why not?

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