EN.601.461/661

Computer Vision

Assignment #3

Due date: October 1st 11:59PM

5 marks (10% per day late submission)

Instructions: Answer your questions on paper or electronic/printout document. Use a new sheet for each question (i.e. don't answer two questions on the same sheet). Scan/save your calculations as a pdf document or take pictures of your solution and submit it on Gradescope. You are encouraged to use a calculator or other software to help with math but you must include all the steps of the calculations in your submission.

1. DLT (2pt)
   Given the following points $\boldsymbol{x_i} \leftrightarrow \boldsymbol{x}_i'$ correspondences:
   1: $(0,0) \leftrightarrow (0.037, 0.086)$
   2: $(1,0) \leftrightarrow (0.49, -0.107)$
   3: $(1,1) \leftrightarrow (0.291, 0.401)$
   4: $(0,1) \leftrightarrow (-0.054, 0.548)$
   5: $(0.5, 0.5) \leftrightarrow (0.238, 0.174)$
   a. Calculate the DLT matrix A composed of all correspondences
   b. Calculate the SVD decomposition of A and show the solution for $\boldsymbol{h}$ (you can use Matlab or any other software). No need to show copies of the matrices U, D and V.
   c. Build the homography H from $\boldsymbol{h}$.
   d. Calculate the norm $\|A\boldsymbol{h}\|$

2. Log-likelihood (1pt)
   In question 1, supposed that the points $\boldsymbol{x_i}$ are the true coordinates and the points $\boldsymbol{x}_i'$ are noisy (error in one image).
   a. What is the reprojection error for H from 1.c?
   b. Instead of H above you found the following homography
   $$\hat{H} = \begin{bmatrix} 0.455800 & -0.137164 & 0.064297 \\ -0.187786 & 0.577227 & 0.065843 \\ 0.025337 & 0.135953 & 1.045104 \end{bmatrix}$$
   What is the reprojection error of $\hat{H}$?

3. RANSAC (2pt)
   You add a sixth correspondence to the data set $(2, 1) \leftrightarrow (0.951, -0.959)$. Use the following two sets of correspondences for RANSAC: $s_1 = \{1, 2, 3, 4\}, s_2 = \{3,4,5,6\}$.
   a. Use DLT to calculate the H_1 and H_2 for each s_i (you can reuse the A_i you had in question 1.)
   b. For each H_i, calculate the sets of inliers points S_i that are within threshold distance $t = 0.1$ of each model.