Geometry Constrained Feature Matching

Morten R. Hannemose, mohan@dtu.dk

April 1, 2022

02504 Computer vision course lectures,
DTU Compute, Kgs. Lyngby 2800, Denmark

Learning objectives

After this lecture you should be able to:

- explain and implement the eight point algorithm for estimating the fundamental matrix
- explain and implement estimation of the fundamental matrix with RANSAC
- choose the threshold for RANSAC using χ^2

Presentation topics

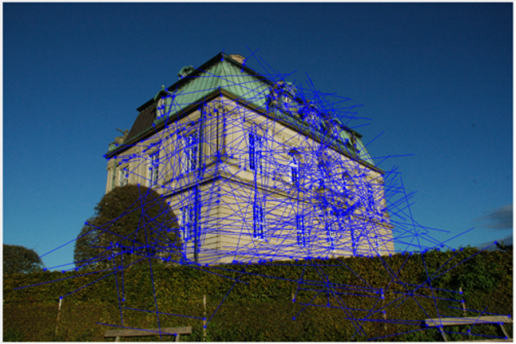
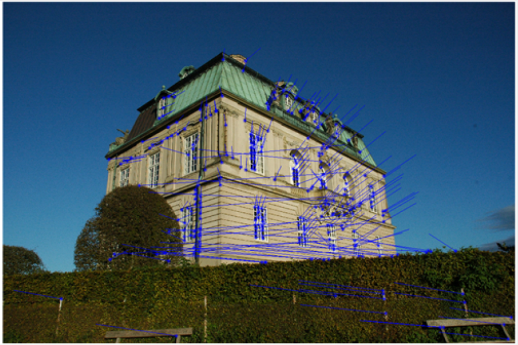
- Estimating the fundamental matrix
    - Linear algorithm
    - Incorporating RANSAC
- Thresholding for RANSAC

Setting the scene

- Stereo geometry
- (SIFT) Features
- RANSAC

Geometry constrained feature matching

Use multi view geometry to filter matches

Fundamental matrix – Recap

$\boldsymbol{R}$ and $\boldsymbol{t}$ describe the relative pose between the cameras.

$$\begin{aligned} \boldsymbol{E} &= [\boldsymbol{t}]_\times \boldsymbol{R} \\ \boldsymbol{F} &= \boldsymbol{K}_2^{-\top} \boldsymbol{E} \boldsymbol{K}_1^{-1} \\ 0 &= \boldsymbol{q}_2^\top \boldsymbol{F} \boldsymbol{q}_1 \end{aligned}$$

The fundamental matrix expresses that corresponding points lie on their epipolar lines.

Estimating the fundamental matrix

Fundamental matrix problem

The fundamental matrix is defined with the relation $\boldsymbol{q}_2^\top \boldsymbol{F} \boldsymbol{q}_1 = 0$.

Consider the points $\boldsymbol{q}_{1i}$ and $\boldsymbol{q}_{2i}$ projected into cameras one and two, respectively. The relation is then

$$\begin{aligned} 0 &= \boldsymbol{q}_{2i}^\top \boldsymbol{F} \boldsymbol{q}_{1i} \\ &= \begin{bmatrix} x_{2i} \\ y_{2i} \\ 1 \end{bmatrix}^\top \begin{bmatrix} F_{11} & F_{12} & F_{13} \\ F_{21} & F_{22} & F_{23} \\ F_{31} & F_{32} & F_{33} \end{bmatrix} \begin{bmatrix} x_{1i} \\ y_{1i} \\ 1 \end{bmatrix} \end{aligned}$$

Fundamental matrix problem

Rearrange the terms:

$$
\begin{aligned}
0 &= \boldsymbol{q}_{2i}^{\top} \boldsymbol{F} \boldsymbol{q}_{1i} \,, \\
0 &= \boldsymbol{B}^{(i)} \mathsf{flatten}(\boldsymbol{F}^{\top}) \,,
\end{aligned}
$$

where

$$
\begin{aligned}
\boldsymbol{B}^{(i)} &= \begin{bmatrix} x_{1i}x_{2i} & x_{1i}y_{2i} & x_{1i} & y_{1i}x_{2i} & y_{1i}y_{2i} & y_{1i} & x_{2i} & y_{2i} & 1 \end{bmatrix} \,, \\
\mathsf{vec}(\boldsymbol{F}) &= \begin{bmatrix} F_{11} & F_{21} & F_{31} & F_{12} & F_{22} & F_{32} & F_{13} & F_{23} & F_{33} \end{bmatrix}^{\top}
\end{aligned}
$$

Fundamental matrix solution

Define $\boldsymbol{B}$

$$\boldsymbol{B} = \begin{bmatrix} \boldsymbol{B}^{(1)} \\ \boldsymbol{B}^{(2)} \\ \vdots \\ \boldsymbol{B}^{(n)} \end{bmatrix}.$$

Subject to $||\text{flatten}(\boldsymbol{F}^\top)||_2 = 1$ the solution is the singular vector with the smallest singular value.

Degrees of freedom – Eight point algorithm

$\boldsymbol{F}$ has 9 numbers, and is scale invariant.

Each pair of corresponding point fixes a degree of freedom. Eight points is enough to estimate the fundamental matrix.

This is the eight point algorithm.

Degrees of freedom – Seven point algorithm

$[\boldsymbol{t}]_\times$ has rank 2, and thus $\boldsymbol{F}$ is also rank deficient, i.e. $\det(\boldsymbol{F}) = 0$.

Thus $\boldsymbol{F}$ has 7 degrees of freedom, and can be found from 7 matches.

$\boldsymbol{B}$ will have two singular vectors with singular value 0.
Denote these $\boldsymbol{F}'$ and $\boldsymbol{F}^\dagger$.

$\boldsymbol{F} = \alpha \boldsymbol{F}' + (1-\alpha)\boldsymbol{F}^\dagger$, where α is chosen such that $\det(\boldsymbol{F}) = 0$.

This is the seven point algorithm.

F can be estimated from eight point correspondences easily.

Possible to estimate from just seven.

Can be followed by non-linear optimization

Estimating the fundamental matrix with RANSAC

To use RANSAC, we need a way to measure distance from our model

What does $\boldsymbol{q}_{2i}^{\top}\boldsymbol{F}\boldsymbol{q}_{1i}$ equal if points are not corresponding?

Estimating the fundamental matrix with RANSAC

To use RANSAC, we need a way to measure distance from our model

What does $\boldsymbol{q}_{2i}^{\mathsf{T}}\boldsymbol{F}\boldsymbol{q}_{1i}$ equal if points are not corresponding?

$\boldsymbol{q}_{2i}^{\mathsf{T}}\boldsymbol{F}$ and $\boldsymbol{F}\boldsymbol{q}_{1i}$ are epipolar lines.

Distance from point to line

$$d = \begin{bmatrix} a & b & c \end{bmatrix} \begin{bmatrix} x & y & 1 \end{bmatrix}^{\mathsf{T}}$$

should have $a^2 + b^2 = 1$, but is not fulfilled for the epipolar lines.

Geometric distance

We can normalize the distance to both epipolar lines, using their first two coordinates.

The squared geometric distance is then given by

$$= \left(\boldsymbol{q}_{2i}^{\top}\boldsymbol{F}\boldsymbol{q}_{1i}\right)^2 \frac{1}{(\boldsymbol{q}_{2i}^{\top}\boldsymbol{F})_1^2 + (\boldsymbol{q}_{2i}^{\top}\boldsymbol{F})_2^2} \frac{1}{(\boldsymbol{F}\boldsymbol{q}_{1i})_1^2 + (\boldsymbol{F}\boldsymbol{q}_{1i})_2^2},$$

where $\boldsymbol{x}_i^2$ refers to the square of th i^{th} element of $\boldsymbol{x}$

Sampson's Distance

A similar distance is Sampson's distance.

$$d_{\mathsf{Samp}}(\boldsymbol{F}, \boldsymbol{q}_{1i}, \boldsymbol{q}_{2i}) = \frac{\left(\boldsymbol{q}_{2i}^\top \boldsymbol{F} \boldsymbol{q}_{1i}\right)^2}{(\boldsymbol{q}_{2i}^\top \boldsymbol{F})_1^2 + (\boldsymbol{q}_{2i}^\top \boldsymbol{F})_2^2 + (\boldsymbol{F} \boldsymbol{q}_{1i})_1^2 + (\boldsymbol{F} \boldsymbol{q}_{1i})_2^2}$$

Performs slightly better than the geometric distance in practice.

Is a squared distance.

Thresholding for RANSAC

Thresholding distances

- How to choose the threshold for RANSAC?

Thresholding distances

- How to choose the threshold for RANSAC?
- Introduce assumptions! 🙂
- Assume that the errors of inliers follow a normal distribution.

Dimensionality of the error

- Fundamental/essential matrix
  - The error is the distance to the epipolar line
  - This is an error in one dimension
- Homography
  - The error is the distance from mapped point to true point
  - This is an error in two dimensions
- Pose estimation/camera calibration
  - Again it is a distance between points
  - This is an error in two dimensions

This is called the codimension of the problem.

We denote this m.

Choosing the threshold

- Assume that the error of each sample follows an m-dimensional normal distribution with standard deviation σ
- The squared error is χ_m^2 distributed (by definition)
- Always work with squared distances
  - Not necessary to take square root when comparing distances

Choosing the threshold

- Assume that the error of each sample follows an m-dimensional normal distribution with standard deviation σ
- The squared error is χ_m^2 distributed (by definition)
- Always work with squared distances
  - Not necessary to take square root when comparing distances
- Choose a confidence interval e.g. 95%
  - i.e. we want our threshold to correctly identify 95% of all inliers.
- Look up the CDF for our χ_m^2 distribution.
- E.g. for a fundamental matrix and 95%, $\tau^2 = 3.84 \cdot \sigma^2$

Some values from the CDF of χ^2_m

$m \backslash 1-p$	90%	95%	99%
1	2.71	3.84	6.63
2	4.61	5.99	9.21

Learning objectives

After this lecture you should be able to:

- explain and implement the eight point algorithm for estimating the fundamental matrix
- explain and implement estimation of the fundamental matrix with RANSAC
- choose the threshold for RANSAC using χ^2

Exercise time!