Deterministic Fitting of Multiple Structures using Iterative MaxFS with Inlier Scale Estimation

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Abstract

We present an efficient deterministic hypothesis generation algorithm for robust fitting of multiple structures based on the maximum feasible subsystem (MaxFS) framework. Despite its advantage, a global optimization method such as MaxFS has two main limitations for geometric model fitting. First, its performance is much influenced by the user-specified inlier scale. Second, it is computationally inefficient for large data. The presented algorithm, called iterative MaxFS with inlier scale (IMaxFS-ISE), iteratively estimates model parameters and inlier scale and also overcomes the second limitation by reducing data for the MaxFS problem. The IMaxFS-ISE algorithm generates hypotheses only with top-n ranked subsets based on matching scores and data fitting residuals. This reduction of data for the MaxFS problem makes the algorithm computationally realistic. A sequential "fitting-and-removing" procedure is repeated until overall energy function does not decrease. Experimental results demonstrate that our method can generate more reliable and consistent hypotheses than random sampling-based methods for estimating multiple structures from data with many outliers.

1. Introduction

A common problem encountered in computer vision is the model fitting with data that may be contaminated with noise and outliers. The "hypothesize-and-verify" framework is the core of many robust geometric fitting methods. The Random Sample Consensus (RANSAC) algorithm [3] is a widely used robust estimation technique, and most of the state-of-the-art methods are based on random sampling. They involve iterative loop of two steps: random hypotheses generation and verification. A minimal subset of the input data points is randomly sampled and used to hypothesize model parameters. In the verification step, the hypotheses are evaluated against all the data and their support is determined.

There are two main drawbacks to random sampling-based techniques. The first problem is that it is difficult in general to determine the number of iterations to achieve desired confidence without a priori knowledge such as inlier ratio and inlier scale. The true inlier ratio and true inlier scale is usually unknown in most realistic applications. When the number of iterations computed is limited, therefore, the estimated solution may not be reliable. The existence of multiple structures makes the problem more difficult since the inliers belonging to other structures are regarded as outliers (pseudo-outliers).

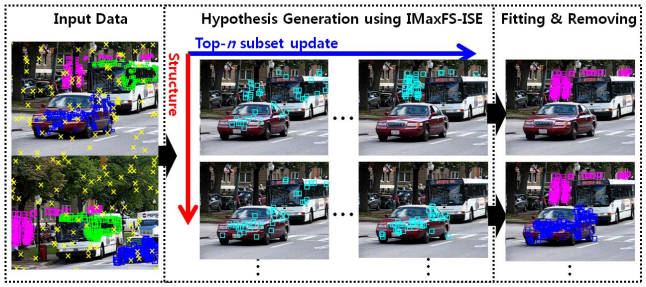


Figure 1: Overview of the presented approach on fundamental matrix estimation.

The second problem is the inconsistency of results, which is related to the first problem. If the number of iterations is insufficient, the random sampling-based techniques provide varying results for the same data and parameter settings. Despite their robustness, the random sampling-based methods provide no guarantee of consistency in their solutions due to the randomized nature [2].

Many advanced random-sampling methods have the same limitations of unreliability and inconsistency. There have been approaches to improving the efficiency of random hypothesis generation for the estimation of single structure [4, 6, 7, 8, 9, 10]. They have been developed to increase the frequency of hitting all-inlier samples.

To deal with multiple-structure data, guided sampling techniques have been developed [11, 12, 13, 14, 15]. They generate a series of tentative hypotheses from minimal subsets of the data in advance and carry out guided sampling based on preference analysis. The performance of these methods can be poor when outlier ratio is considerably high and thus the quality of initial hypothesis is less than desirable. Other multiple-structure model fitting methods

also start with random hypothesis generation [16, 17, 18, 5, 19, 14, 20].

Due to the non-deterministic nature of random sampling, the quality of the hypotheses generated by all the methods mentioned above depends on the proportion of pseudo-outliers and gross outliers. Thus, reliable and consistent performance may not be expected when a priori knowledge is not provided. The recent methods such as [21, 22, 23, 24] remove the dependency on inlier scale for the random sampling-based approach. Nevertheless, they cannot overcome the inherent limitation of random sampling.

Deterministic optimization has recently been actively investigated for model fitting problems in computer vision [2, 25, 26, 27, 28]. Despite the guarantee for globally optimal solution, the main limitation of the global optimization algorithms lies in their computational inefficiency. The presence of image features from multiple structures makes their computational cost even higher. Besides, there has been no deterministic method that estimates inlier scale estimation for model fitting problems.

In this paper, we present a deterministic hypothesis generation algorithm for robust fitting of multiple structures. The goal of our method is to generate reliable and consistent hypotheses with reasonable efficiency based on the maximum feasible subsystem (MaxFS) framework. There are two limitations in using a MaxFS algorithm for hypothesis generation. First, its performance depends on the user-specified inlier scale. We present an algorithm, called *iterative MaxFS with inlier scale* (IMaxFS-ISE), that iteratively estimates model parameters and inlier scale. The second limitation is the computational inefficiency mentioned above. We circumvent this limitation by establishing MaxFS problems only with subsets of data but not the whole data. This reduction of data for the MaxFS problem makes our algorithm computationally tractable.

The whole algorithm consists of three major steps: 1) hypothesis generation, 2) labeling and 3) removing inliers. We repeat over these steps until all hypotheses are found.

The presented algorithm adopts a sequential "fitting-and-removing" procedure and consists of three major steps: 1) hypothesis generation, 2) labeling and 3) removing inliers. It repeats over these steps until all hypotheses are found. In our method, only one hypothesis is generated for each genuine structure. When a new hypothesis is added, hypothesis selection for each data are performed via the optimization of an energy function and the inliers for each hypothesis generated up to present are removed from whole data. This procedure is repeated until overall energy function is not decreased any more.

The hypothesis generation step itself consists of three steps. The first step is to calculate inlier probability for each set of data. In the second step, input data is sorted according to the inlier probability and the top-n ranked subset is updated. In the last step, the IMaxFS-ISE algorithm estimates the parameters of the hypothesis from the top-n ranked subset. These steps are repeated until the number of inliers is not changed.

Figure 1 provides an overview of our algorithm. In the input images shown on the left side, the yellow crosses indicate the gross outliers, and the other color markers denote three different structures. In the middle of Figure 1, the cyan squares indicate the top-n ranked subset and the images in each row show its update for each structure. The fitting results are shown on the right side of Figure 1.

Our main contribution is to develop a way of employing a MaxFS algorithm without prior knowledge of inlier ratio, inlier scale and the number of structures. This is unique in that the existing algorithms are predominantly based on random sampling and we believe that the presented method is a viable alternative to the random sampling algorithms. Our algorithm generates substantially more reliable hypotheses than the random sampling methods especially when (pseudo-)outlier ratio is high.

The rest of paper is organized as follows: Section 2 introduces our IMaxFS-ISE method. Section 3 describes the algorithm based on fitting-and-removing procedure. Section 4 shows the experimental results with real data, and we conclude in Section 5.

2. Iterative Maximum Feasible Subsystem with Inlier Scale Estimation

In this section, we describe the main optimization techniques that we employ in our method.

2.1. MaxFS Formulation for Geometric Fitting

The aim of a MaxFS framework is to find the largest cardinality set with constraints that are feasible [2, 26]. The objectives of the MaxFS and RANSAC are the same. However, the MaxFS guarantees a global solution unlike the RANSAC. The MaxFS problem admits the mixed integer linear programming (MILP) formulation. The MILP problem is known to be NP-hard. Hence, only relatively small problems can be solved practically. While the exact MILP formulation is useful for small models, it is not effective on large models due to its computational inefficiency [1].

We use the algebraic Direct Linear Transformation (DLT) to estimate hypothesis parameters [29]. The DLT-based geometric fitting problem can be formulated as a MaxFS problem. The set of input data $\mathcal{X}$ is partitioned into the inlier-set $\mathcal{X}^{\mathrm{I}}$ and the outlier-set $\mathcal{X}^{\mathrm{O}}$ with $\mathcal{X}^{\mathrm{I}} \subseteq \mathcal{X}$, $\mathcal{X}^{\mathrm{O}} \subseteq \mathcal{X}$, $\mathcal{X}^{\mathrm{I}} \cup \mathcal{X}^{\mathrm{O}} = \mathcal{X}$ and $\mathcal{X}^{\mathrm{I}} \cap \mathcal{X}^{\mathrm{O}} = \boldsymbol{\emptyset}$.

Algorithm 1. Iterative MaxFS with inlier scale estimation
$[\theta^*, s^*, I^{In*}]$ = IMaxFS-ISE($\mathcal{X}$, M, K)

Input: input data $\mathcal{X}$, M(for MaxFS), intial inlier scale s_0 and K value (for IKOSE)

Output: hypothesis parameter θ^*, inlier scale $s^*$and the number of maximum inliers I^{In*}

1: **Initialize** the inlier scale: s_0 (small value)

2: **Repeat**

3: **Estimate** parameter θ_t and the number of inliers $I^{In}{}_t$ in $\mathcal{X}$ using **MaxFS** with s_t (Sec. 2.1).

4: **If** $I^{In}{}_t > I_{th}{}^{In}$ (We set $I_{th}{}^{In}$ =10.)

5: **Estimate** inlier scale s_{t+1} using **IKOSE($\mathcal{X}$, K)** using Equation 3 (Sec.2.2).

6: **Else**

7: $s_{t+1} = s_t + \varepsilon$

8: **End if**

9: $\theta^* = \theta_t$, $I^{In*} = I_t^{In}$ and $s^* = s_t$

10: **Until** s_t converges

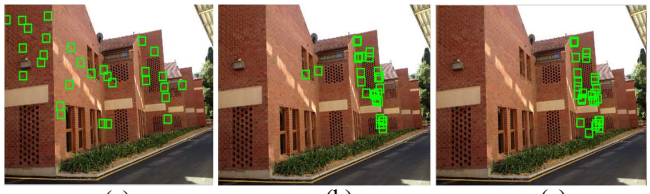
A maximum inlier scale s provides a bound for the algebraic residual $d_i = |\mathbf{a}_i^{\mathrm{T}}\boldsymbol{\Theta}|$ at point i, where $\mathbf{a}_i^{\mathrm{T}}$ is each row vector of $\mathbf{A}$ in the homogeneous equation $\mathbf{A\Theta=0}$:

$$d_i = |\mathbf{a}_i^{\mathrm{T}}\boldsymbol{\Theta}| \le s,\ s > 0. \tag{1}$$

A MaxFS formulation of Equation 1 is as follows:

$$\begin{aligned} \{\hat{\boldsymbol{\Theta}}^{MaxFS}, \hat{\mathbf{y}}\} = \underset{\boldsymbol{\Theta},\mathbf{y}}{\operatorname{argmin}} & \sum_{i=1}^{k} y_i \\ \text{subject to} \quad & |\mathbf{a}_i^{\mathrm{T}}\boldsymbol{\Theta}| \le s + M_i\, y_i, \quad \forall\, i \\ & \mathbf{c}^{\mathrm{T}}\boldsymbol{\Theta} = 1, \\ & \boldsymbol{\Theta} \in \Re^n,\ y_i \in \{0,1\},\ i = 1,\ldots,k, \end{aligned} \tag{2}$$

where M_i is a large positive number (Big-M value). The case where y_i=0 indicates that the i^{th} data is an inlier. If y_i=1, the i^{th} data is an outlier and the corresponding constraint is deactivated automatically. We use a linear constraint $\mathbf{c}^{\mathrm{T}}\Theta$=1, rather than the commonly used $\|\Theta\|$=1 where $\mathbf{c}$ is a problem dependent vector determined by a user [29]. Our MaxFS algorithm solves Equation 2 for input data $\mathcal{X}$ and the hypothesis $\hat{\boldsymbol{\Theta}}^{MaxFS}$ is generated from the maximum inlier-set.



(a) (b) (c)

Figure 2: Top-30 subset from the *unihouse* data: (a) initial subset, (b) updated subset after several iterations and (c) updated subset after final iteration

Figure 3: Top-n subsets after final iteration: (left) updated using only residuals for ranking and (right) updated using both residuals and matching scores

2.2. Iterative MaxFS with Inlier Scale Estimation (IMaxFS-ISE)

The MaxFS problem for geometric fitting can be exactly solved when true inlier scale is known. However, true inlier scale s is unknown in most practical situations and it is commonly set manually by a user. Recent work [24] has proposed a robust scale estimator called IKOSE which can accurately estimate the scale of inliers for heavily corrupted multiple-structure data. In our algorithm, we include a method for estimating the inlier scale from data in a similar iterative manner that has been shown in [24].

Given the true parameters of the Jth structure (θ^J), the inlier scale $\hat{s}_K^J$ and the inlier number of Jth structure v^J can be estimated by IKOSE as follows:

$$\hat{s}_K^J = \frac{|\tilde{r}_K^J|}{\Phi^{-1}(\frac{1}{2}(1+\kappa^J))}, \tag{3}$$

$$\kappa^J := K / v^J, \tag{4}$$

where $|\tilde{r}_K^J|$ is the kth sorted absolute residual given the parameters of the Jth structure (θ^J) and $\Phi^{-1}(\cdot)$ is the argument of the normal cumulative density function and v^J is the number of points satisfying $|r_i^J / \hat{s}_K{}^J| < 2.5$.

When true inlier scale is known, correct model

parameters can be estimated by solving the MaxFS problem. When true model parameters are known, on the other hand, accurate inlier scale can be estimated from IKOSE. To solve this problem, we propose an iterative scheme called IMaxFS-ISE method and it is summarized in Algorithm 1.

We set the initial inlier scale s_0 to a small value to guarantee that initial model parameter estimate is not badly biased. In the iteration procedure, the estimated inlier scale s_t increases with the iteration step t until it reaches the true inlier scale and the estimated model parameters reach the true model parameters.

3. Fitting and Removing Procedure for Multi-Structure Fitting

In this section, we describe our deterministic algorithm for robust fitting of multiple structures. It is summarized in Algorithm 2.

Algorithm 2. Fitting-and-Removing Procedure

Input: input data $\mathcal{X}_N$, M(for MaxFS), initial K value (for IKOSE) $K^{(0)}$ and the number of data points in subset n

Output: hypotheses parameter set $\Theta = \{\theta^*_l\}^L_{l=1}$ and S $= \{\sigma_l^*\}^L_{l=1}$

1: $\Theta = \emptyset$, S= $\emptyset$, $\mathcal{X}_{\mathcal{RD}} = \mathcal{X}_N$ and $l = 1$
2: **Repeat**
3: $h = 1$ and $K_l^{(h=1)} = K^{(0)}$
4: **Initialize** top-n ranked subset $\mathcal{X}_n^{(h=1)}$ from $\mathcal{X}_{RD}$
5: **Repeat**
6: **Estimate** hypothesis parameter using $[\theta_l^{h*}, s_l^{h*}, I^{In}{}_l^{h*}]$=**IMaxFS-ISE**($\mathcal{X}_n^{(h)}$, M, $K_l^{(h)}$) (Sec. 2.2).
7: **Estimate** inlier scale σ_l^{h*} using IKOSE($\mathcal{X}_N$, $K_l^{(h)}$)
8: **Calculate** inlier probability $P(x_i)$ (Sec.3.2)
9: **Update** top-n ranked subset $\mathcal{X}_n^{(h+1)}$ from $\mathcal{X}_{RD}$
10: $K_l^{(h+1)} = I^{In}{}_l^{h*}$
11: $h = h+1$
12: **Until** the number of inliers is not changed
13: $\Theta = \Theta \cup \{\theta_l^{h*}\}$ and S = S $\cup \{\sigma_l^{h*}\}$
14: **Obtain** labels f_l via α-expansion (Sec. 3.1)
15: **Generate** the reduced data $\mathcal{X}_{\mathcal{RD}}$ (Sec. 3.2)
16: $l = l+1$
17: **Until** $E(f_{l-1}) < E(f_l)$

3.1. Fitting-and-Removing Procedure

Our goal is to estimate the parameters $\Theta = \{\theta_l\}^L_{l=1}$ and the inlier scale $S = \{\sigma_l\}^L_{l=1}$ for multiple structures from input data $\mathcal{X}_N = \{x_i\}^N_{i=1}$. The parameters and inlier scale of the hypothesis for each structure is deterministically estimated using the IMaxFS-ISE. Moreover, only one reliable hypothesis is generated for each structure unlike random sampling-based methods which generate a large number of hypotheses. This facilitates the use of the "fitting-and-removing" procedure.

Our algorithm consists of three major steps: hypothesis generation, labeling and removing inliers. We repeat over these steps until the overall energy function does not decrease. At each iteration stage, a new hypothesis corresponding to a new structure is generated and added to Θ. After a new hypothesis is added, a set of labels $f = \{f_i\}^N_{i=1}$ assigns each data point x_i either to one of the structures or to an outlier by minimizing an objective function using the α-expansion optimization [20]. Our objective function is defined as follows:

$$E(f) = \sum_{i=1}^{N} D(x_i, f_i) + \sum_{<i,j>\in\mathcal{N}} V(f_i, f_j) + O(f) \cdot \quad (5)$$

The data cost $D(x_i, f_i)$ in Equation 5 is formulated as

$$D(x_i, f_i) = \begin{cases} r(x_i, \theta_{f_i}) & \text{if } f_i \in \{1,...,L\}, \\ \sigma_{l^*} & \text{if } f_i = 0, \end{cases} \quad (6)$$

$$l^* = \arg\min_l r(x_i, \theta_l), \quad (7)$$

where $r(x_i, \theta_{f_i})$ is the absolute residual of x_i after fitting the structure θ_{f_i} and σ_{l^*} is the inlier scale estimated from the structure θ_{l^*} which is the penalty for labeling x_i as an outlier. The smoothness cost $V(f_i, f_j)$ in Equation 5 penalizes $f_i \neq f_j$ in some manner. We construct a neighborhood graph from the Delaunay Triangulation on input data $\mathcal{X}_N$ as in [15, 20]. The label cost $O(f)$ is proportional to the number of structures l in Θ and penalize overly complex models. For the label cost weight, we select a maximum value to include all the true structures. We choose a very small weight (near zero) for the smoothness term since our method estimates a hypothesis with an inlier scale for one structure at a time.

After labeling is performed for the set of hypotheses Θ at an iteration stage, a reduced input data $\mathcal{X}_{\mathcal{RD}}$ is generated by removing all the estimated inliers from input data $\mathcal{X}_N$. At the next iteration stage, the hypothesis is generated from the reduced input data $\mathcal{X}_{\mathcal{RD}}$.

3.2. Hypothesis Generation using IMaxFS-ISE from Subset with Top-*n* Ranked Data

We now describe our hypothesis generation method based on the IMaxFS-ISE algorithm. It splits a large problem into smaller ones and thus makes the IMaxFS-ISE algorithm efficient.

Hypothesis generation consists of three steps. The first step is to calculate inlier probability $P(x_i)$ for x_i. In the second step, the inlier probability is used to sort the input data $\mathcal{X}_{\mathcal{RD}}$ and update the top-n ranked subset $\mathcal{X}_n^{(h+1)}$. The last step employs the IMaxFS-ISE algorithm to estimate the parameters of the hypothesis θ_l^{h*} on the top-n ranked subset. These steps are repeated until the number of inliers is not changed.

The initial subset $\mathcal{X}_n^{(0)}$ consists of n data with the highest matching scores among the input data $\mathcal{X}_{\mathcal{RD}}$. It will contain mostly inliers from the several structures but it is unknown where each inlier belongs. Given $\mathcal{X}_n^{(0)}$, the maximum inliers are estimated with the IMaxFS-ISE algorithm and they are used to generate initial hypothesis.

For a subset, a MaxFS method guarantees that the maximum inliers are found as long as the number of inliers is larger than the minimum number required for estimating model parameters. When the number of structures is large, the inliers from a single structure may be insufficient in the initial subset and the initial hypothesis can significantly deviate from the true structure. When this happens, our algorithm updates the subset using inlier probability until it includes enough inliers from a single structure. Figure 2 shows the initial top-n ranked subset, an updated subset after several iterations and the final subset.

Given a hypothesis θ_l^h, we compute the inlier probability of $x_i \in \mathcal{X}_{\mathcal{RD}}$ as follows:

$$P(x_i) \propto P(x_i \mid q)P(x_i \mid \theta_l^h) = q(x_i)\frac{1}{Z}\exp\left(\frac{-r(x_i,\theta_l^h)^2}{2\sigma_l^{h2}}\right), \quad (8)$$

where $q(x_i)$ is the normalized matching score for the input x_i, $r(x_i,\theta^h{}_l)$ is the absolute residual of x_i computed with the hypothesis θ_l^h generated for the lth structure in the hth iteration, σ_l^h is the inlier scale corresponding to the hypothesis θ_l^h, and Z is a normalization constant. After the IMaxFS-ISE step is finished in the hth iteration, σ_l^h is estimated from the whole dataset $\mathcal{X}_N$ using IKOSE. Note that σ_l^h is different from the inlier scale s_l^h which is estimated from the subset $\mathcal{X}_n^{(h)}$.

The use of both the inlier scale σ_l^h and the matching score $q(x_i)$ in Equation 8 results in more reliable subset than using only residuals for data ranking. When θ_l^h is badly biased, the inliers of other structures can be included in the top-n ranked subset instead of the outliers with small residuals since $P(x_i)$ is more influenced by $P(x_i \mid q)$ than $P(x_i \mid \theta_l^h)$. If θ_l^h is a good hypothesis, θ_l^{h+1} can be made better since the $\mathcal{X}_n^{(h+1)}$ includes more inliers. Moreover, the inliers in the

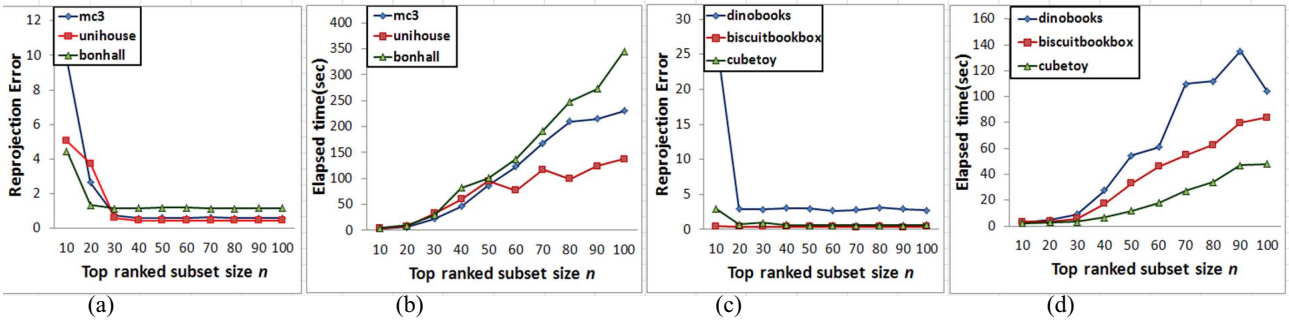


Figure 4: Re-projection errors and the elapsed time for computation for subset size n = 10~100

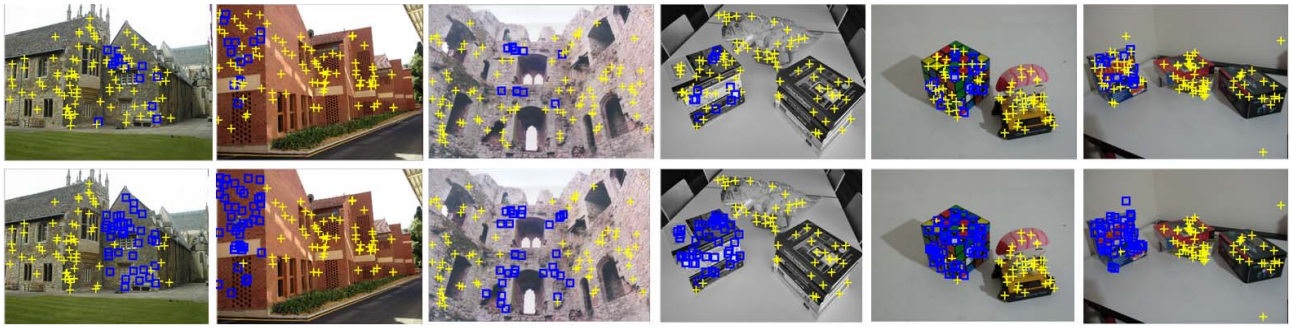
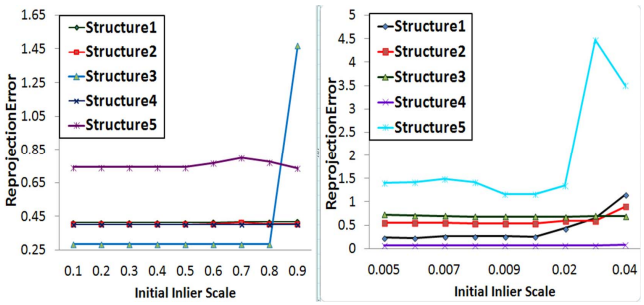
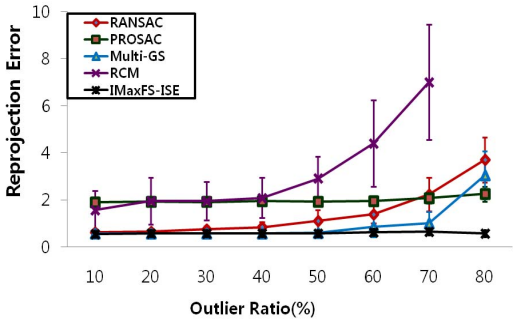


Figure 5: Inlier estimation with IMaxFS-ISE: (top row) results with initial inlier scale s_0 and (bottom row) results with final inlier scale (Blue squares indicate the estimated inliers and yellow crosses denote outliers.)



Figures 6: Re-projection errors with varying initial inlier scales from: (a) homography estimation and (b) affine fundamental matrix estimation



Figures 7: Re-projection errors with varying outlier rates (BCD data)

subset selected by considering the estimated inlier scale σ_l^h tend to be more spread out spatially over the structure. Figure 3 shows an example where inliers are widely distributed in space when the matching scores are used.

One important issue in IMaxFS-ISE is how to choose K. To include as many inliers as possible, K should be set to the largest possible value that does not yield breakdown. In our algorithm, $K_l^{(h+1)}$ is set to $I^{In}{}_l^{h*}$ which is the number of maximum inliers estimated from the previous IMaxFS-ISE procedure. On the other hand, we conservatively set the initial value $K^{(0)}$ to a small value, e.g., 10.

4. Experimental Results

We have implemented our algorithm in MATLAB using the LP/MILP solver GUROBI [30] which provides functions for the LP/MILP, and a desktop with Intel i5-2500 3.30GHz (4 cores) and 3GB RAM is used for experiments. We tested five methods including ours on several real datasets. For performance evaluation and comparison, we measured the actual elapsed computation time. Images and keypoint correspondences were acquired from the Oxford VGG dataset [31] and the Adelaide RMF dataset [34, 35]. We used manually labeled keypoint correspondences which were obtained by SIFT matching. If keypoint matching scores are not available, we assigned a proper matching score to each correspondence.

4.1. Analysis: IMaxFS-ISE

We performed the DLT-based IMaxFS-ISE to estimate planar homography and affine fundamental matrix for each data subset. For our IMaxFS-ISE algorithm, the Big-M value in Equation 2 was set to 10000 and both the initial $K^{(0)}$ value and I_{th}^{In} were set to the fixed value of 10.

To determine the parameters n (subset size) and s_0, we experimentally examined the effects of parameter n (subset size) on re-projection error. We investigated the effect of n in the range of [10 100] on data with different outlier rates. Figures 4 (a) and (b) show the re-projection errors and the computation time for homography estimation with the IMaxFS-ISE method, respectively. Only the results from three datasets are shown in the plots. Figures 4 (c) and (d) show the re-projection errors and the computation time for affine fundamental matrix estimation, respectively. It can be seen in Figure 4 that high accuracy is achieved for the subset size n from about 30 up and the computation time gradually increases with n. For the IMaxFS-ISE algorithm, we set n to 30 to attain both accuracy and computational efficiency.

We investigated the effect of initial inlier scale s_0 on re-projection error for five different structures in three datasets. Figures 6 (a) and (b) show the results for homography and affine fundamental matrix, respectively, and they demonstrate that our algorithm is stable for a wide range of the initial inlier scale s_0. If s_0 is too small, the computation time becomes too long since our method performs the MaxFS algorithm increasing the inlier scale gradually until $I^{In}{}_t > I_{th}^{In}$. We find that the s_0 values of 0.5 and 0.01 for the estimation of homograpy and fundamental matrix, respectively, are the good compromises between stability and computational efficiency for all the datasets we tested.

Figure 5 shows the inlier estimation with our IMaxFS-ISE algorithm at the initial and the final iteration stages. The top row shows the inliers estimated from IMaxFS-ISE at the first iteration and the bottom row shows the final results. The blue squares indicate the estimated inliers while the yellow crosses denote the outliers. In these experiments, we performed the IMaxFS-ISE algorithm on one subset with 100 data points for each dataset.

4.2. Comparison with random sampling approaches

Our algorithm is compared with four other methods based on random sampling: uniform random sampling (RANSAC) [32, 3], PROSAC [9], Multi-GS [11, 33] and the state-of-the-art algorithm RCM [15, 37]. We implemented the PROSAC algorithm in MATLAB. For performance evaluation, we measured elapsed computation

Table 1 Performance of various methods on homography estimation for the several real datasets.

Data	Outlier Ratio	Method	RANSAC	PROSAC	Multi-GS	RCM	IMaxFS-ISE
raglan	10%	**Elapsed time [sec]**	70	70	70	**8.352**	69.5471
		Mean	0.8565	1.3974	1.0313	0.8456	**0.8178**
		Std	0.0761	0.0649	0.0942	0.7225	**0**
		L	30014	**30577**	1410	9	11
mc3	10%	**Elapsed time [sec]**	25	25	25	**4.6127**	24.3706
		Mean	1.1645	1.241	1.5296	2.0281	**0.4598**
		Std	0.0927	0.079	0.232	0.2099	**0**
		L	**15052**	12815	985	5	7
library	70%	**Elapsed time [sec]**	20	20	20	**1.6123**	19.15
		Mean	1.1518	0.9468	0.9739	2.8468	**0.8658**
		Std	0.2193	0.0145	0.1706	3.4552	**0**
		L	**17749**	17604	2031	5	3
unihouse	30%	**Elapsed time [sec]**	20	20	20	**7.4608**	20.42
		Mean	1.5419	1.3743	1.8665	4.4215	**0.4621**
		Std	0.2855	0.0828	0.2641	2.6775	**0**
		L	8748	**10520**	789	4	6
bonhall	30%	**Elapsed time [sec]**	35	35	35	**6.1367**	36.22
		Mean	1.0982	**0.7331**	1.5117	1.8345	1.274
		Std	0.2076	0.0273	0.3292	2.7598	**0**
		L	**21056**	20390	1327	6	6

Table 2 Performance of various methods on affine fundamental matrix estimation for the several real datasets.

Data	Outlier Ratio	Method	RANSAC	PROSAC	Multi-GS	RCM	IMaxFS-ISE
cubetoy	20%	**Elapsed time [sec]**	10	10	10	**1.0403**	7.244
		Mean	0.6211	0.7185	0.6159	0.8578	**0.6127**
		Std	0.0043	0.0493	0.0044	0.1155	**0**
		L	13263	**13586**	2067	3	2
carsbus	40%	**Elapsed time [sec]**	10	10	10	**3.8849**	9.5698
		Mean	**0.6772**	0.7058	0.6806	1.4978	0.7678
		Std	0.0016	0.0037	0.0191	0.453	**0**
		L	**6410**	6238	1171	3	3
dinobooks	70%	**Elapsed time [sec]**	20	20	20	**11.6536**	17.187
		Mean	3.044	3.5394	2.7171	5.3322	**2.7146**
		Std	0.3924	0.3497	0.4198	1.4298	**0**
		L	**9899**	9163	1453	2	3
4B	70%	**Elapsed time [sec]**	**15**	**15**	**15**	64.5312	16.941
		Mean	1.3576	1.2837	1.102	3.5178	**1.0818**
		Std	0.1606	0.0678	0.1605	2.1612	**0**
		L	**2504**	2500	668	1	6
5B	10%	**Elapsed time [sec]**	10	10	10	**4.4897**	12.152
		Mean	0.2872	0.9137	**0.2605**	1.4975	0.3195
		Std	0.0112	0.1273	0.0059	0.6388	**0**
		L	**1639**	1442	492	3	6

time and the number of generated hypotheses (L) and computed the re-projection errors (mean and standard deviation). The results for the five algorithms are summarized in Tables 1 and 2 with the best results boldfaced.

For each label/structure, the hypothesis that shows the minimum re-projection error is selected. Overall error was calculated by averaging re-projection errors for all the structures. For RANSAC, PROSAC and Multi-GS, 50 random sampling runs were carried out. The computation times (elapsed times) of these three algorithms were made similar to that of our method. Since our method and RCM run till completion of algorithm, the elapsed computation times for our method and RCM were not limited but measured. For RCM, the averages of computation times are measured.

Homography Estimation Table 1 summarizes the performance of five methods for estimating planar homography for five datasets. The results demonstrate that our method yields reliable and consistent results with reasonable computational efficiency especially when the (pseudo-)outlier ratio is high. Since our algorithm generates slightly more hypotheses than the number of structures, there is no need to reduce or merge the generated hypotheses.

Fundamental Matrix Estimation Table 2 shows the performance of the algorithms for estimating affine fundamental matrix for five datasets. The results show that our algorithm generates high-quality hypotheses with reasonable efficiency for the datasets with high outlier ratios and thus finds all the true structures stably from all the datasets. Note that the random sampling-based methods produce large variation in their results.

Figure 7 shows the re-projection errors produced by the five methods on the BCD data as outlier ratio increases. Our algorithm outperforms the other algorithms as outlier ratio is high. Since the probability of producing an all-inlier subset decreases with the random sampling-based approaches as the outlier ratio increases, the errors increase substantially. On the other hand, the hypothesis generated

by the IMaxFS-ISE algorithm is little influenced by the outlier ratio.

5. Conclusion

We present a novel deterministic approach to reliable and consistent hypothesis generation for multiple-structure model fitting. Instead of generating hypothesis based on random sampling, we make a deterministic optimization method computationally realistic by utilizing only top-*n* ranked subsets and providing a way of estimating inlier scale. The experiments show that without prior knowledge of inlier ratio, inlier scale and the number of structures, our method generates reliable and consistent hypotheses efficiently.

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