Robust Model Fitting Using Higher Than Minimal Subset Sampling

Ruwan B. Tennakoon, Alireza Bab-Hadiashar, Zhenwei Cao, Reza Hoseinnezhad and David Suter

Abstract—Identifying the underlying model in a set of data contaminated by noise and outliers is a fundamental task in computer vision. The cost function associated with such tasks is often highly complex, hence in most cases only an approximate solution is obtained by evaluating the cost function on discrete locations in the parameter (hypothesis) space. To be successful at least one hypothesis has to be in the vicinity of the solution. Due to noise hypotheses generated by minimal subsets can be far from the underlying model, even when the samples are from the said structure. In this paper we investigate the feasibility of using higher than minimal subset sampling for hypothesis generation. Our empirical studies showed that increasing the sample size beyond minimal size (p), in particular up to $p+2$, will significantly increase the probability of generating a hypothesis closer to the true model when subsets are selected from inliers. On the other hand, the probability of selecting an all inlier sample rapidly decreases with the sample size, making direct extension of existing methods unfeasible. Hence, we propose a new computationally tractable method for robust model fitting that uses higher than minimal subsets. Here, one starts from an arbitrary hypothesis (which does not need to be in the vicinity of the solution) and moves until either a structure in data is found or the process is re-initialized. The method also has the ability to identify when the algorithm has reached a hypothesis with adequate accuracy and stops appropriately, thereby saving computational time. The experimental analysis carried out using synthetic and real data shows that the proposed method is both accurate and efficient compared to the state-of-the-art robust model fitting techniques.

Index Terms—Model fitting, Robust Statistics, hypothesis generation, data segmentation, higher than minimal subset sampling.

1 Introduction

The task of identifying the underlying model in a set of data contaminated with both noise and outliers is a highly researched area in computer vision. This task has many applications, including motion segmentation [1], [2], range image segmentation [3], [4], medical image analysis [5] and visual tracking [6]. In computer vision problems, the data often comprise multiple structures that result in pseudo-outliers (correct measurements of another structure away from the structure of interest) in addition to gross-outliers [7] that are produced by errors in the data generation process.

There are a large number of robust model-fitting techniques that can be used in recovering the underlying models in the presence of both gross and pseudo-outliers, and many of these techniques involve optimization of highly complex cost functions. A commonly used approach is to discretise the parameter space using sampling and evaluate the cost function on these discrete points to find the optimum (*hypothesize and verify strategy*). The assumption here is that at least one of the hypotheses selected will be sufficiently close to the true structure that is to be recovered.

In hypothesize and verify approach, the hypotheses are generated by sampling subsets of p data points and estimating the model represented by those data points. Here p refers to the number of parameters needed to represent the model and using p as the sample size is known as minimal subset sampling (MSS) [8]. In the presence of outliers and multiple structures, the chance of generating a hypothesis close to a true structure using random sampling is small. Recently several methods have been proposed to bias the sampling process towards selecting points from the same structure in consecutive steps [9], [10]. Estimating how many samples that need to be selected in order to guarantee success with a high probability is not trivial. The main assumption made in setting the number of samples is that one sample with only inliers (clean sample) will be adequate to generate a hypothesis close to the true structure. However, as shown in Fig. 1, in the presence of noise even a clean sample may result in a hypothesis that is far from the true model, particularly if the span of the sample data points, in one dimension, is not much larger than the scale of noise [8]. For this reason, most implementations generate a higher number of samples than necessary, which in applications involving high-dimensional model fitting, can make them computationally inefficient. More importantly, there is usually no measure to indicate the success, at a given number of samples.

Methods such as LO-RANSAC [11] try to improve the closeness of an initial hypothesis to the true model by local search. However, this only works when the initial

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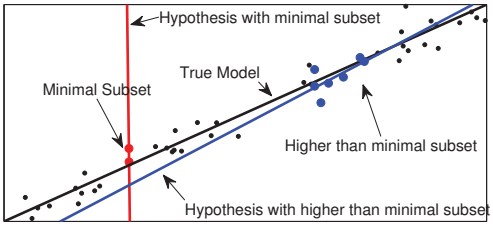


Fig. 1. Minimal subset sampling vs. higher than minimal subset sampling. The data do not contain outliers [8]. The figure represents an extreme case where the span of the data samples is made deliberately small.

guess is in the vicinity of the true structure. Pham et al. [8] proposed higher than minimal subset sampling to generate better hypotheses instead of refining the inaccurate ones. As shown in Fig. 1 using higher than minimal subset sampling for hypothesis generation has a greater chance of generating a hypothesis closer to the true model, given that all the points in the sample are inliers (this claim will be considered in more detail in the next section). It is important to note here, that selecting an all-inlier sample in the presence of multiple structures and gross outliers, becomes increasingly difficult even when the sample size is increased by a little (due to the multiplication of probabilities). This makes direct extension of MSS sampling methods to higher than minimal subset sampling computationally inefficient. To address this, we first investigated (Section 2) the benefit of increasing the sample size and found that while increasing the sample size beyond the minimal size (p) significantly increases the probability of generating a hypothesis closer to the true model, the significance of improvements diminishes after $p+2$. Next, we extend the minimal subset sampling method of [12] and propose a computationally efficient model fitting method to find and verify supported hypothesis in a given data set.

The rest of this paper is organized as follows. Section 2 discuss the implications of using higher than minimal subset sampling and prior work in that direction. Section 3 describes the proposed method in detail and Section 4 presents experimental results involving synthetic and real data, and comparisons with state-of-the-art model-fitting techniques. Section 6 concludes the paper.

2 Higher Than Minimal Sampling

2.1 Previous work

There are two approaches in the literature that use higher than minimal subsets to solve the model-fitting problem.

The first approach is to use higher than minimal subset samples to generate affinities between those points and represent them using a hyper-graph, which is then partitioned to obtain clusters in the data. Agarwal et al. [13] proposed a two-step algorithm to cluster the higher order affinities. In the first step, they constructed a hyper-graph with $h = p+1$ vertices per edge. This hyper-graph was then approximated with a pairwise graph using the clique averaging technique and the resulting pairwise graph was segmented using a spectral partitioning algorithm. A method that partitioned the hyper-graph directly without converting it to a pairwise graph was introduced by Liu et al. [14]. Their approach requires the hyper-graph and the weights to be calculated at the start which was very expensive in terms of computations and memory. Hairong et al. [15] proposed a computationally efficient hyper-graph clustering method that used a hypothesize and verify strategy to approximately construct the hyper-graph, called the random consensus graph, which is then converted to a pairwise graph that approximately retains the affinity information. It is then partitioned using a slightly modified version of the robust ensemble clustering approach proposed in [14]. Since this algorithm relies on a RANSAC like method to construct the consensus information, it inherits the problems that come with RANSAC: such as identifying structures with multiple noise levels.

The second approach is to use higher than minimal subset sampling to improve the quality of the hypothesis in a hypothesize and verify strategy. In LO-RANSAC method, Chum et al. [11] proposed a local optimization step that uses higher than minimal subset samples. However, this step would only work if an initial estimate in the vicinity of the true solution is provided using MSS. Pham et al. [8], used higher than minimal subsets obtained using random cluster models (RCM) to generate hypotheses and used those to initialize a metric labeling problem that clusters the data points and recovers the underlying model. However, their method relies on the spatial contiguity of structures in the dataset, which may not be true for some model-fitting problems. Due to the need to generate spatial relationships, this method is also computationally expensive.

2.2 Evidence to support the use of higher than minimal subset sampling

In robust model-fitting techniques that utilize the hypothesize and verify strategy, at least p points need to be sampled at a time to generate a valid hypothesis. The number of parameters p constitutes the necessary condition for the sample size to derive a unique hypothesis.

It is said that increasing the number of points in a sample beyond p (higher than minimal subset sampling - HMSS) will increase the quality of the hypothesis (closer to the true model), given that all the sampled points are from the structure of interest [8]. This assertion was examined by using a Monte Carlo simulation of a 2D line fitting. In this test, n data points representing a line in 2D space with Gaussian noise of $N(0, \sigma^2)$ were generated (no outliers) and all the possible tuples (each with h

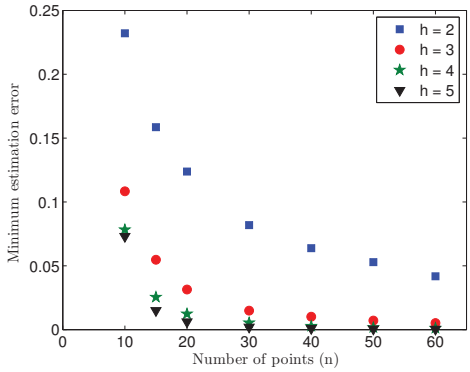


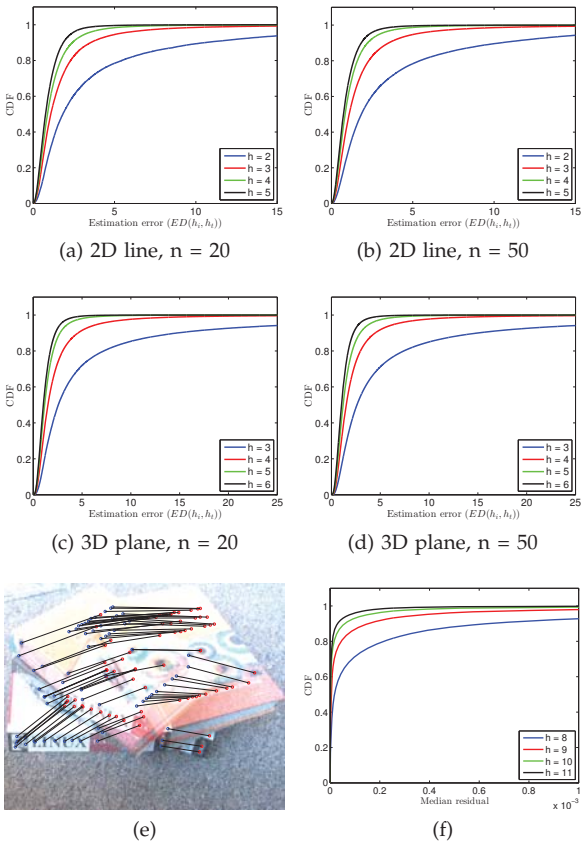
Fig. 2. The variation in minimum estimation error with number of data points n for different sample sizes (h). The figure shows the mean results of 100 experiments for each combination.

data points) were used to generate the hypotheses[1]. Next, to measure the closeness of a given hypothesis (h_i) to the original line (h_t) we used the following criterion: given that p_{h_i} and p_{h_t} are the two points on each line that is closest to the origin, the distance between these two lines is calculated as $||p_{h_i} - p_{h_t}||_2$. Since this distance measure is proportional to the scale of noise we normalize by σ to get the final measure $ED(h_i, h_t) = ||p_{h_i} - p_{h_t}||_2/\sigma$. The minimum of these estimation errors ($\min_{i=[1..\binom{n}{h}]} ED(h_i, h_t)$) indicates the closeness of the best hypothesis to the true model for a given number of points (n) and sample size (h). The average results of 100 such experiments for each n and h, are shown in Fig. 2.

The results show that the quality of the hypotheses generated increases with the sample size. However, the improvement becomes very small after a few additional points ($h = p + 2$), particularly for data structures with a high number of points ($n > 20$). Importantly, we observed similar patterns when the dimensionality of the data is varied.

To analyze the probability of generating a good hypothesis, given that the data are from the inlier set, we generated n data points from a 2D line model with noise $N(0, \sigma^2)$. For each dataset, the estimation errors ($ED(h_i, h_t)$) of all possible hypotheses generated with h points were computed. These estimation error values (repeated over 100 such experiments) were then used to draw the cumulative distribution function (CDF) of estimation errors, shown in Figures 3 (a) and (b). These results show that the probability of obtaining a good hypothesis (given that the data are inliers) increases with the sample size h. Similar to the previous results, the improvement is only significant up to a few additional points ($h = p+2$). The pattern remains similar when the dimensionality of the model is increased, as shown by

1. For $h = p = 2$, the hypothesis is generated by finding line connecting the two points. For $h > p$, the hypothesis is given by the least squares method.



(a) 2D line, n = 20 (b) 2D line, n = 50

(c) 3D plane, n = 20 (d) 3D plane, n = 50

(e) (f)

Fig. 3. The cumulative distribution function of estimation errors for 2D line (a), (b) and 3D plane (c), (d) fitting using different sample sizes (h). The data used for fundamental matrix estimation and the CDF of the median residuals are shown in (e), (f).

an equivalent 3D plane fitting experiment in Figures 3 (c) and (d).

To investigate the behavior on real data, we carried out a fundamental matrix estimation task. The points that belong to one group were segmented manually, as shown in Fig. 3(e) and the fundamental matrix was estimated using 10^5 random samples with sample size h. Since there is no information on the true model, the estimation error was calculated using median Sampson's distance from each hypothesis to the data points. The CDF of estimation error for different sample sizes is shown in Fig. 3(f) and similar observations can be made from these results.

The above results show that "Higher than Minimal Subset Sampling" increases the likelihood of the closeness of the generated hypothesis to the true model. However, in the presence of outliers, increasing the number of points in a sample will decrease the probability of selecting a clean sample exponentially. Therefore, identifying how many more points one should include, beyond the necessary condition, is not straightforward. The above presented Monte Carlo simulation and exper-

imental results show that the advantage of increasing the sample size beyond $h = p + 2$ would be limited. Even with the modest increase in sample size (by two), direct extension of RANSAC-like methods that use random sampling for higher than minimal subset sampling will be computationally inefficient due to the decreasing probability of selecting a clean sample. In addition, these methods provide no means of knowing that a good hypothesis has been reached, making it necessary to generate a predefined number of hypotheses even if a good hypothesis is obtained early. In the next section, we propose a new efficient method that carries out higher than minimal subset sampling.

3 Proposed Method

In this section we describe the proposed method for model fitting. The intention here is to cluster data points ($[x_i]_{i=1}^{n} \in \mathbb{R}^d$) into sub-groups, based on the existence of underlying models ($[\theta^{(j)}]_{j=0}^{n_c}$). Here n is the number of data points and n_c is the number of structures in the dataset with $j = 0$ assigned to outliers.

3.1 Cost function

The first task is to establish a cost function that quantifies the suitability of a given model to represent a structure in data. Here we select the Least k-th order statistics (LkOS) estimator, which is well known for its stability and high breakdown point [16]. The LkOS cost function is as follows:

$$F(\theta) = r^2_{i_{k,\theta}}(\theta) \tag{1}$$

where $r_i^2(\theta)$ is the i-th squared residual with respect to model θ and $i_{k,\theta}$ is the index of the k-th sorted square residual with respect to model θ. Here k refers to the minimum acceptable size of a structure in a given application and its effect on the methods performance is discussed in Section 5. It should be noted here that the value of k is almost always much larger than the dimensions of the parameter space ($k \gg p$).

Optimizing this cost function is highly complex. Hence, the parameter space is commonly discretized using randomly generated hypotheses and the cost function is evaluated at each of these points to find the best solution (hypothesize and verify). As was previously discussed, hypotheses generated using minimal subset sampling may not generate a hypothesis close enough to the true model. The intention in the proposed method is to generate more appropriate hypotheses using higher than minimal subset sampling. However, due to the multiplication of probabilities, it is not efficient to generate accurate hypotheses using random sampling of higher than minimal subsets. To find a way of conducting HMSS efficiently, we present a greedy algorithm that starts from a random location on the parameter space and takes steps proportional to the negative of the local gradient until either a solution that is with in the basin of attraction of a local minimum is found or the process is re-initialized.

The algorithm starts by generating a hypothesis (θ_0) via random sampling of h data points which are then used to generate the residuals $r^2(\theta_0)$. Next, these residuals are sorted and the h data points around the k-th sorted residual are used to generate a new set of parameters as follows:

$$\theta_{l+1} = LeastSquareFit\left([x_{i_{m,\theta_l}}]_{m=k-h+1}^{k}\right) \tag{2}$$

where θ_l is the parameters at iteration l and h is the sample size. This step (equation 2) is then repeated until the stopping criterion described in the next section is reached. The intuition behind the above choice and the behavior are explained in Section 3.3.

Following the analysis in Section 2.2, we have set $h = p + 2$. The above analysis showed that using higher than minimal samples significantly increases the probability of arriving at a more representative hypothesis for the structure when the selected points are all inliers. To visualize the operation of the above algorithm, the intermediate steps of the scheme in a simple 2D line fitting problem are shown in Fig. 4. The figure shows that the correct structure is recovered by going through only a few iterations, even when the starting samples are not members of that structure (outliers).

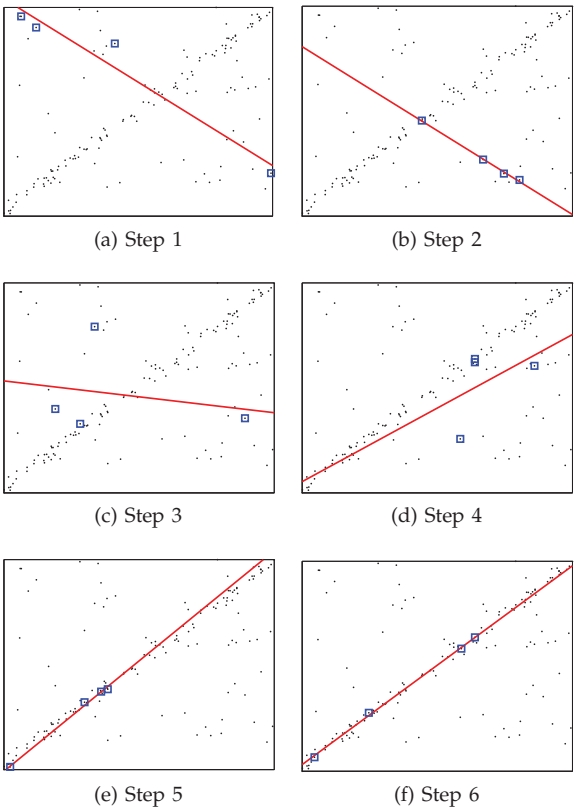
3.2 Stopping criterion

The next main challenge is to identify a method to stop the algorithm once it has reached a good estimate that is likely to be a true structure (having at least k points as inliers). Once the algorithm arrives at a vicinity of a local minima representing a structure in data, the first k sorted points should be from that structure. As the proposed algorithm picks the points for the next iteration around the k-th sorted index, they too would be from the same structure. This leads to a situation where the consecutive samples are from the same structure. This property is utilized here to devise a stopping criterion by which we can detect if the algorithm has found a structure in data.

The stopping criterion is as follows:

$$F_{stop} = \left(r^2_{i_{k,\theta_l}}(\theta_l) < \frac{1}{h}\sum_{j=k-h+1}^{k} \underbrace{r^2_{i_{j,\theta_{(l-1)}}}(\theta_l)}_{\text{(a)}}\right) \wedge \left(r^2_{i_{k,\theta_l}}(\theta_l) < \frac{1}{h}\sum_{j=k-h+1}^{k} \underbrace{r^2_{i_{j,\theta_{(l-2)}}}(\theta_l)}_{\text{(b)}}\right) \tag{3}$$

Here (a) and (b) are the residuals of the sampled points in iterations $l-1$ and $l-2$ with respect to the current parameters θ_l. This criterion checks the data points associated with the two previous samples to see if the average residuals of those points (with respect to the current parameters) are still lower than the inclusion



(a) Step 1 (b) Step 2 (c) Step 3 (d) Step 4 (e) Step 5 (f) Step 6

Fig. 4. The intermediate steps of the proposed method in a simple 2D line fitting example for $h = 4$. The model represented by the current hyper-edge is plotted to make the steps clear. Note that the vertices of the starting point (Step 1) are not members of the structure and the algorithm does not move away from the underlying structure after it is found (Step 6).

threshold associated with having k points (assuming that a structure has at least k points implies that data points with residuals less than $r^2_{i_{k,\theta_l}}(\theta_l)$ are inliers). This indicates that the samples selected in the last three iterations are likely to be from the same structure hence the algorithm has converged.

A challenging problem in multi structural data segmentation is the existence of some local minima due to accidental alignment of outliers and true structures. A common solution, also used by competing methods ([17], [15], [8]) is to reinitialize the hypothesis generation a number of times. Where this number is determined by the user. To quantify the number of required re-initializations, in our method this process is carried out until there is no further improvement in the cost function in consecutive runs and the algorithm is then stopped automatically. In our experiments, it was observed that the number of random initializations required was always smaller than ten across different types of problems, which was far less than the number of random samples needed by the RANSAC-based methods.

For problems with multiple structures, once a reliable local minimum is returned, the core data points that correspond with that minimum are segmented out and the process is repeated until all the structures are recovered. In this implementation, we selected the Modified Selective Statistical Estimator (MSSE) [18] to segment points due to its low computational cost, high level of consistency, and small bias in applications involving close data structures [19]. This step is aimed at removing the majority of points associated with already identified models to prevent the algorithm from returning the same structure in subsequent iterations. This may be particularly relevant to problems with one structure with a significantly lower level of noise compared to other structures. It should be noted that MSSE does not require any additional information (such as noise level) for the segmentation and if such information is available, a separate segmentation strategy utilizing those information would result in a better segmentation. The more one knows a priori, the better the outcome will be.

After all valid hypotheses are found, the final segmentation is carried out by calculating the residuals of all the points with respect to each model and assigning points to their closest model. The inliers of each model are then identified using the MSSE. The complete algorithm of the proposed higher than minimal subset sampling based model-fitting method is given in Algorithm 1.

3.3 How does the proposed method find a structure?

To analyze the local convergence of the proposed method, we first show that the parameter update of the proposed HMSS is similar to that of a generalized Newton method [20].

The cost function for HMSS can be written as:

$$\hat{F}(\theta) = \sum_{m=0}^{m=h-1} r^2_{i_{(k-m),\theta}} \tag{4}$$

where $i_{k,\theta}$ is the index of the k-th sorted square residual with respect to model θ, $r_{i_{m,\theta}} = \theta^T x_{i_{m,\theta}} - y_{i_{m,\theta}}$ and $k \gg h \geq p$. We show the proposed HMSS steps are similar to Newton method steps for finding the roots of the cost function derivatives:

$$H(\theta) = \frac{\partial \hat{F}}{\partial \theta} = 0. \tag{5}$$

In [12], it is shown that although the index i of the k-th sorted residual cost function in equation (5) depends on the parameter estimates, there is a finite neighborhood (D_H) around the estimate in which the sorted indices next to the kth residual do not change[2]. Inside this neighborhood, the cost function has a quadratic relationship to the model parameters. Therefore, the cost function and its derivatives are continuous and twice differentiable.

2. Only exception is when two residuals are exactly the same, in which case, the remedy is to merge those as one.

Algorithm 1 Step-by-step algorithm of proposed higher than minimal subset sampling based model-fitting methods

Inputs: Data Points ($X \in [x_i]_{i=1}^{N}$), minimum cluster size (k), Number of clusters (n_c)

$l_{max} \leftarrow 50$, $t_{max} \leftarrow 10$, $h \leftarrow p+2$
$l \leftarrow 0$, $t \leftarrow 1$, $j \leftarrow 1$, $[\hat{F}_{min}^{(j)}]_{j=1}^{n_c} \leftarrow \infty$
repeat
  repeat
    Select a random h-tuple from the data points.
    Generate model θ_0 using the h-tuple.
    repeat
      $[r^2(\theta_l), i_{\theta_l}]$ =SortedRes(X, θ_l) .
      Calculate the cost function $\hat{F}(\theta_l)$.
      $\theta_{l+1} \leftarrow$ LSFit$\left([x_{i_{m,\theta_l}}]_{m=k-h+1}^{k}\right)$
      Evaluate equation (3)
      if F_{stop} **then**
        break;
      end if
    until $(l{+}{+} < l_{max})$
    if $\hat{F}(\theta_l) < \hat{F}_{min}^{(j)}(t-1)$ **then**
      $\hat{F}_{min}^{(j)}(t) \leftarrow \hat{F}(\theta_l)$
      $\theta_{best}^{(j)} \leftarrow \theta_l$
    end if
    if $\hat{F}_{min}^{(j)}(t) = \hat{F}_{min}^{(j)}(t-1) = \hat{F}_{min}^{(j)}(t-2)$ **then**
      break;
    end if
  until $t{+}{+} < t_{max}$
  $[outliers]$ =GetOutliers$(X, \theta_{best}^{(j)})$.
  $X \leftarrow X(outliers)$
until $j{+}{+} < n_c$
Cluster data using $[\theta_{best}^{(j)}]_{n=1}^{n_c}$.

The generalized Newton method for solving this can be defined as follows [20]:

$$\theta_{l+1} = \theta_l - V_l^{-1} H(\theta_l) \tag{6}$$

where $V_l \in \partial H(\theta_l)$. For the cost function (5) we can derive the following:

$$H(\theta) = 2\sum_{m=0}^{h-1} x_{i_{(k-m),\theta_l}}(\theta^T x_{i_{(k-m),\theta_l}} - y_{i_{(k-m),\theta_l}}) = 2J^\top r \tag{7}$$

$$H'(\theta) = 2\sum_{m=0}^{h-1} x_{i_{(k-m),\theta_l}} x_{i_{(k-m),\theta_l}}^\top = 2J^\top J \tag{8}$$

where $J^\top = [x_{i_{k,\theta_l}}, \cdots, x_{i_{(k-h-1),\theta_l}}] = \mathcal{X}^\top$ and $r^\top = [(\theta_l^\top x_{i_{k,\theta_l}} - y_{i_{k,\theta_l}}), \cdots, (\theta_l^\top x_{i_{k-h-1,\theta_l}} - y_{i_{(k-h-1),\theta_l}})]$. Equations (6), (7) and (8) can be simplified into:

$$\theta_{l+1} = \left[\mathcal{X}^\top \mathcal{X}\right]^{-1} \mathcal{X}^\top \mathcal{Y} \tag{9}$$

which is equal to the proposed HMSS parameter update in equation (2). Therefore similar to the Newton method, since the cost function is quadratic the extremum is found in one step. The above derivation is only valid for a given order of residuals around the k-th point.

In practice, as shown in Fig. 4, when θ_l is far from a true structure (and therefore does not have k support) the update choses points that does not belong to that (wrong) hypothesis, hence, θ_{l+1} moves away from θ_l. Although this may appear as choosing an arbitrary hypothesis, the residuals have characteristics that are exploited by the proposed move. Firstly, it is known (see [21], [22], [9] for instance) that residuals of data structures with respect to an arbitrary hypothesis have a high probability of clustering together in the sorted residual space. Secondly, we are choosing the next sample around the k-th residual point. This means those points are not arbitrary away from the current (wrong) hypothesis but those must have just missed the threshold of forming a structure in the data (otherwise this would have been a correct hypothesis). This makes those likely to be around the intersection of the current hypothesis with one of those clusters. When the hypothesis θ_l is in the vicinity of a true hypothesis and has k support, the HMSS step choses the best subset based on the given order. The algorithm takes these steps repeatedly and as soon as two sequential subsets remained inliers to the new hypothesis, it is deemed to have converged to a solution.

4 Experimental Analysis

We evaluated the proposed method using both synthetic and real data experiments. The results of the proposed method were then compared in terms of both accuracy and computational time with RCM [8], which uses higher than minimal subset sampling as well as the following state-of-the-art model fitting techniques: QP-MF [17], MultiGS [9], LO-RANSAC [11] and RGC [15].

The code for the proposed algorithm was developed in MATLAB and the codes provided by the authors were used to generate the results for competing methods with parameters either set as instructed by those authors or tuned to give the best results. It should be noted that the RCM, MultiGS and LO-RANSAC methods have some part of their code implemented in C (MEX) and the QP-MF method uses the MOSEK quadratic solver whereas the proposed method is implemented in MATLAB by simple scripts.

The experiments were run on a HP Z400 workstation with an Intel Xeon W3550 processor. For each instance, the experiments were repeated 100 times and the averages of the results are reported.

The accuracy of all methods was evaluated using the commonly used clustering accuracy measure [17], [15] given as:

$$CA = \frac{\sum_{i=0}^{n_c} n_{tp,i}}{\sum_{i=0}^{n_c} n_i} \tag{10}$$

where $n_{tp,i}$ is the number of true positives in group i and n_i is the total number of points in that group.

The MultiGS and LO-RANSAC are methods that only cancentrate on hypothesis generation and can be combined with any clustering method to generate the

clustering accuracy measure. In this paper, we have used consensus information (similar to RANSAC) as the clustering method for those techniques, noting that it requires scale of noise as an input. This parameter was manually set to the true inlier noise in our synthetic data experiments. Hence, the clustering accuracy for those methods reflects the best possible value and in practice, lower accuracies can be expected.

Since the MultiGS and LO-RANSAC methods do not have any explicit stopping criteria, in our experiments, the sampling times of these methods are limited to the average run time required by the proposed method in each problem.

4.1 2D line fitting

First, we evaluated our algorithm in detecting lines in a 2D point set contaminated with both noise and gross outliers using the standard regression model. The data points were generated by combining four intersecting lines, with each line containing n_i points with Gaussian noise $N(0, \sigma_i^2)$. Furthermore, uniformly distributed $n_0 = 100$ gross outliers were added. An example of a point set ($[n_i]_{i=0}^4 = 100, \sigma = 0.025$) is shown in Fig. 5(a). The structures returned by the proposed method are also shown.

We examined the performance of the algorithm for varying levels of inlier noise in the interval $\sigma_i \in [0.001, 0.05]$. The number of data points was fixed at $[n_i]_{i=0}^4 = 100$. The clustering accuracies are shown in Fig. 5(b) together with those of competing methods.

The results show that the proposed method produces the best accuracy, specially for higher noise levels, closely followed by MultiGS and LO-RANSAC. It should be noted here that the threshold value for clustering in MultiGS and LO-RANSAC was manually set to the true value, giving these methods an unrealistic advantage over the proposed method which uses MSSE for clustering (automatically estimating the scale of noise). The model complexity penalty (β) is an external parameter that is needed by the RCM method and during our experiments we found that in order to recover the correct model, this parameter needs to be manually tuned for each noise level. Fig. 5(e) shows the variation of the clustering accuracy with β for each noise level. The RCM clustering accuracy in Fig. 5(b) is the best achieved for a given noise level across all tested parameter values. None of the other methods required parameter tuning for each step.

Fig. 5(c) shows the total computation time for each method. The results show that the proposed method is the fastest of the tested methods and is more than an order of magnitude faster than RCM.

Next, the number of total data points was varied in the range 250-2500 while the noise was fixed at $\sigma_i = 0.01$. The total computation times are shown in Fig. 5(d). The results show that the proposed method is very efficient in terms of computation time with a slight linear increase in time with the number of points. As expected clustering accuracy remained constant.

Through these experiments the parameter k for the proposed method was fixed at $k = 0.1 * N$, where N is the total number of points. During the experiments we have observed that the model fitting accuracy will not change significantly with k so long as there are no structures with less than k points.

4.2 3D plane fitting

In the second set of experiments we detected planes in a 3D point set contaminated with both noise and gross outliers using standard regression model. The data points were generated by combining four planes, with each plane containing n_i points with Gaussian noise $N(0, \sigma_i)$. Furthermore, uniformly distributed n_0 gross outliers were also added. An example of a points set ($[n_i]_{i=0}^4 = 100, \sigma = 0.5$) is shown in Fig. 6(a) with the clusters returned by the proposed method.

We assessed the performance of the proposed algorithm for varying levels of inlier noise in the interval $\sigma_i \in [0.1, 5.0]$. The number of data points was fixed at $[n_i]_{i=0}^4 = 100$. The clustering accuracy and the total computation time of the proposed method are shown in Figures 6(b) and 6(c) respectively, together with those of the competing methods. The proposed method again produced the best clustering accuracy with the lowest computation time, and the improvement over MultiGS and LO-RANSAC is much larger than that of the 2D line fitting case.

As shown in Fig. 6(e), the clustering accuracy for MultiGS and LO-RANSAC does not exceed that of the proposed method (for high noise values) even when the sampling times for those methods are increased to 10 to 25 times that of the proposed method.

In the next experiment, the number of total data points was varied in the range 250-2500 while the noise level was fixed at $\sigma_i = 0.2$. The results shown in Fig. 6(d), indicate that the proposed method is very efficient in terms of computation time with slight linear increase in time with number of points, whereas the computation time of MultiGS increased exponentially with the size of the data. Fig. 6(f) shows the variation of Clustering Accuracy with the scale of noise for the proposed algorithm with h set to p and $p + 2$. This shows that using higher than minimal subsets improve the results significantly over those using minimal subsets.

4.3 Two-view motion segmentation

Two-view motion segmentation is the task of identifying the points corresponding to each object in two views of a dynamic scene that contains multiple independently moving objects. Provided that the point matches between the two views are given as , each motion can be modeled using the fundamental matrix $F \in \mathbb{R}^{3\times3}$ as [23]:

$$X_1^\top F X_2 = 0 \tag{11}$$

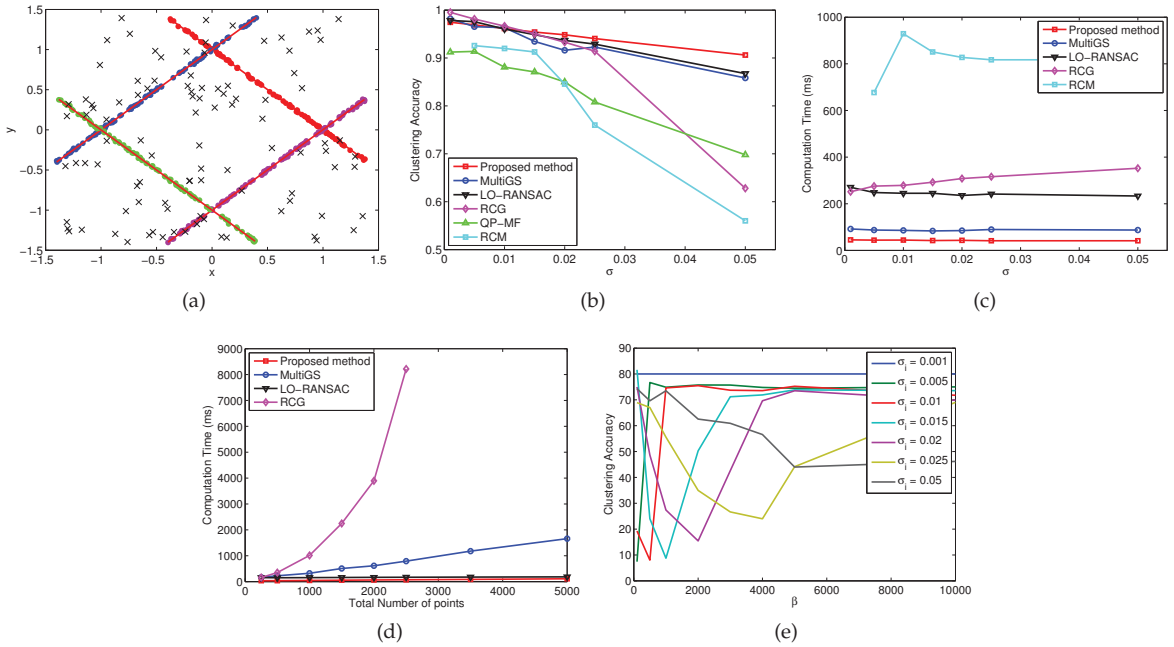


Fig. 5. (a) Example dataset used in the line fitting experiments together with the structures returned by the proposed method. (b) Variation of the clustering accuracy with the scale of noise for different algorithms. (c-d) Variation of the computation time with the scale of noise and the total number of points for different algorithms. (e) The effect of parameter β of RCM on clustering accuracy for data with varying scale of noise.

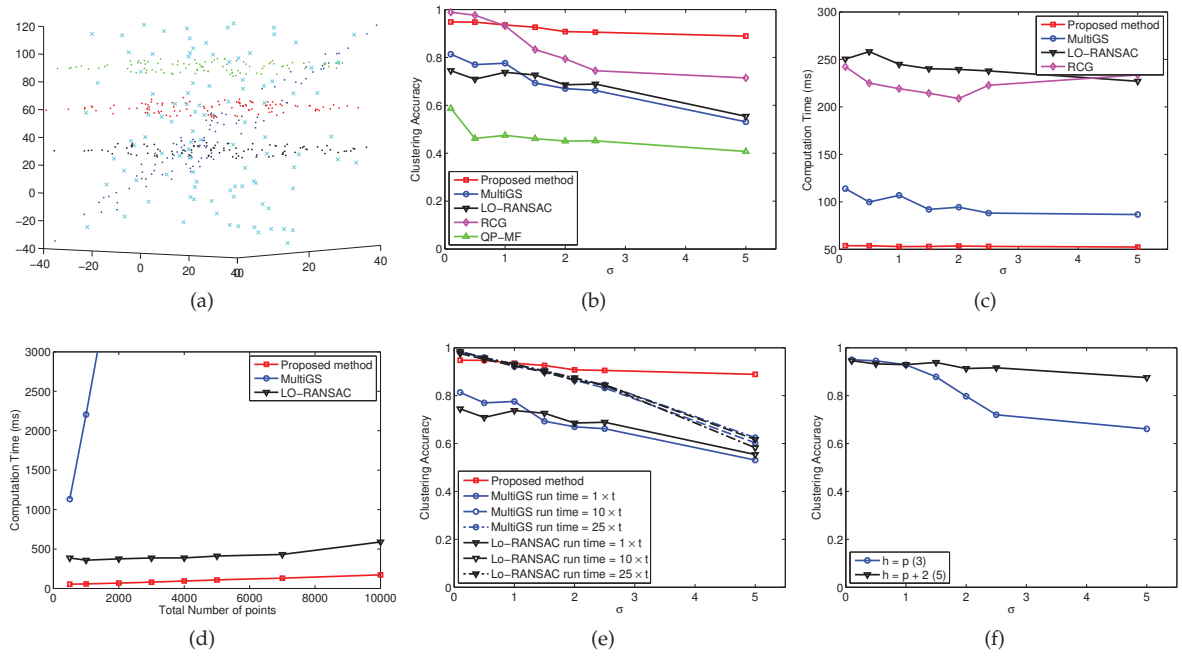


Fig. 6. (a) Example dataset used in the plane fitting experiments together with the structures returned by the proposed method. (b) Variation of the clustering accuracy with the scale of noise for different algorithms. (c-d) Variation of the computation time with the scale of noise and the total number of points for different algorithms. (e) The clustering accuracy variation for MultiGS and LO-RANSAC when the sampling times for those methods are increased to 10 and 25 times that of the proposed method. (f) The Clustering Accuracy variation with scale of noise for the proposed algorithm with h set to p and $p + 2$.

The distance from a given model to a point pair can be measured using the Sampson distance [24].

First, we used the "box-book-mag" image pair from [25] to evaluate the performance of the proposed and competing methods. The "box-book-mag" has two images of three independently moving objects together with feature correspondences. The performance of each algorithm was evaluated using clustering accuracy and computation time.

The clustering accuracy of the proposed method was observed while limiting the number of allowed random initializations to a specific value. The results are presented in Fig. 7(a), and show the proposed method achieves high accuracy without the need for many random re-initializations. Then, we set the sampling times of the MultiGS and LO-RANSAC to the time taken by the proposed method at each step and recorded their accuracy. The results, plotted on the same figure, show that these algorithms take longer to achieve the same level of accuracy as the proposed method. For comparison, we also included the results given by RCM. The results show that the proposed method is fast and can achieve better accuracy. Figures 7(b) and 7(c) show the inlier and outlier points identified by the proposed method, respectively.

The clustering results of the proposed method for the remaining sequences in dataset [25] is shown in Fig. 8. The results show that the proposed method has successfully identified the structures present in data with multiple structures and gross outliers.

4.4 Multi-homography detection

Assume that the point matches between two views of a static scene with multiple planar surfaces are given as $[X_1, X_2]$. Multi-homography detection aims to detect point matches arising from the same planar surface using a homography matrix $H \in \mathbb{R}^{3\times3}$ that relates the matching points via $X_1 \sim HX_2$. The distance from a data point to a given model can be measured using the Sampson's distance.

Similar to [8] we test the performance of the proposed method on the AdeladeRMF dataset [26]. The clustering accuracy of the proposed method together with RCM and multiGS is given in Table 1. Here, the sampling time of MultiGS method was set to ten times that of the proposed method.

The results show that the proposed method achieved high accuracy in a very short time compared to other methods. It should be noted here that the proposed method was not able to detect the two smallest (in terms of number of points) structures in *Johnsonb* dataset. This is due to the small number of points in each of those structures, which was 20 and 15 respectively. RCM was also not able to detect these structures reliably. The analysis of [19] showed that if the scale of inlier noise is not known a priori, its estimation requires more than 20 data points to limit the effects of the finite sample bias.

TABLE 1
Multi-homography detection results. The time is given in milliseconds.

	RCM		MultiGS		Proposed Method	
	CA	Time	CA	Time	CA	Time
Johnsona	0.91	1300	0.69	5023	**0.94**	**473**
Johnsonb	**0.89**	2150	0.73	6958	0.85	**663**
Ladysymon	0.91	1010	0.89	2371	**0.94**	**219**
Neem	0.92	1020	0.74	3565	**0.93**	**327**
Oldclassicswing	**0.98**	950	0.92	2699	0.97	**252**
Sene	0.98	1220	**0.99**	2590	0.98	**237**

To provide a qualitative measure of the performance of those methods, clustering results of the proposed method and RCM are compared with the ground truth in Fig. 9. The first column shows that both methods were able to achieve good results on *Unionhouse* having five structures. However, the proposed method was able to detect all six structures in the *BonHall* image (some incorrect classification of outliers as inliers can be seen) whereas RCM was not able to detect one of those structures. Due to the use of spatial consistency, RCM results are affected if the same structure is separated by either outliers or another structure as seen in images of *ElderHall, BarSmith* and *Napiera* buildings. The proposed method does not assume the existence of spatial contiguity and was therefore able to achieve good clustering in those cases.

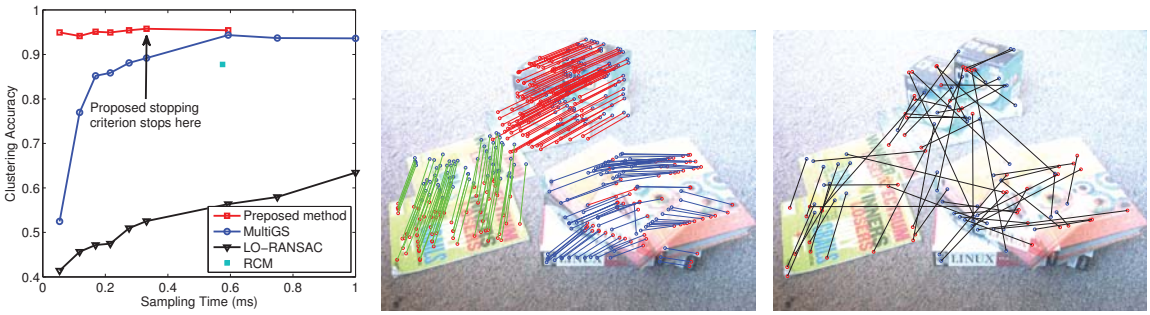
In these experiments, the parameter k of the proposed method was set to a value between 20 to 40 based on the number of points in each dataset.

4.5 3D-motion segmentation of rigid bodies

The objective of 3D motion segmentation is to identify multiple moving objects using point trajectories through a video sequence. If the projections (to the image plane) of N points tracked through F frames are available, $[x_{f\alpha}]_{\alpha=1\ldots N}^{f=1\ldots F} \in \mathbb{R}^2$ then [27] has shown that the point trajectories $P_\alpha = [x_{1\alpha}, y_{1\alpha}, x_{2\alpha}, \ldots x_{F\alpha}, y_{F\alpha}]^\top \in \mathbb{R}^{2F}$ that belong to a single rigid moving object are contained within a subspace of $rank \leqslant 4$, under the affine camera projection model. Hence, the problem of 3D motion segmentation can be reduced to a subspace clustering problem.

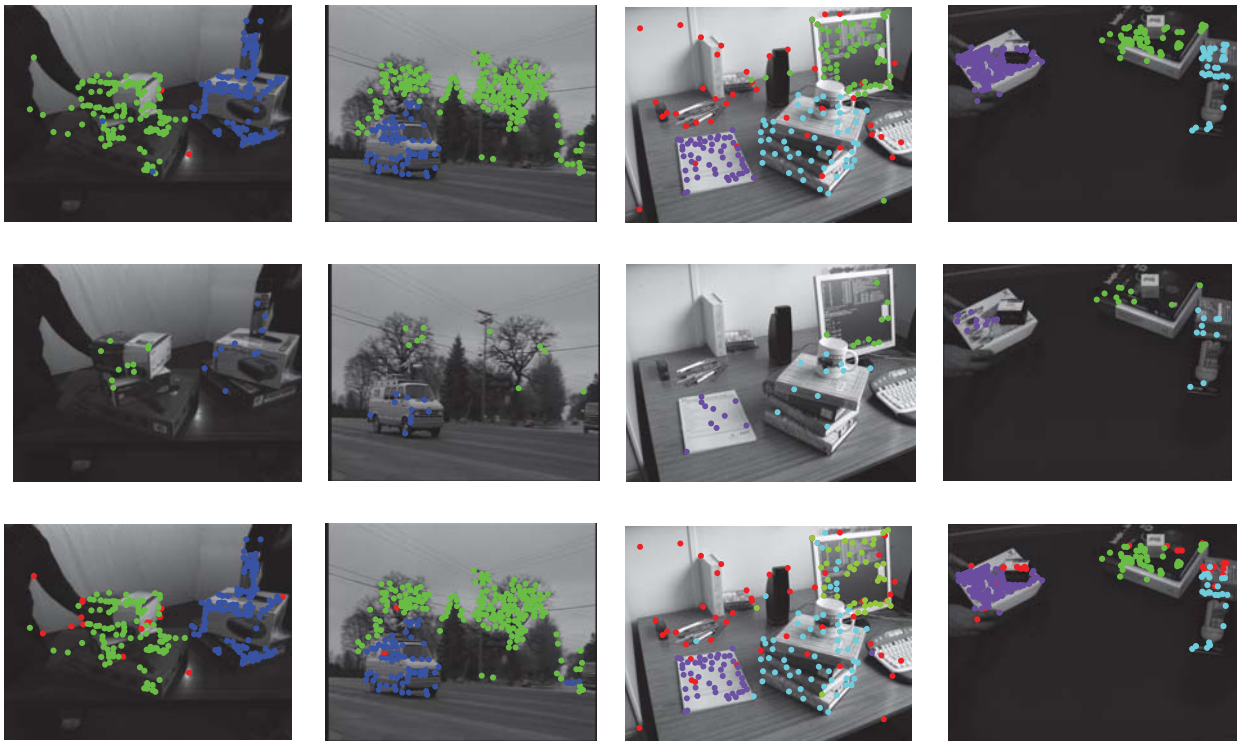
We utilized the commonly used "checkerboard" image sequence in the Hopkins 155 dataset [28] to evaluate our algorithm. This dataset contains trajectory information of 104 video sequences that are categorized into two main groups depending on the number of motions in each sequence (two or three motions).

One of the characteristics in subspace segmentation is that the dimension of the subspaces may vary between two and four, depending on the nature of the motions. The proposed method, which was not specifically developed to solve this problem (similar to most competing techniques) is not capable of identifying the number of



(a) (b) (c)

Fig. 7. (a) Variation of clustering accuracy with sampling time (b) Inliers identified by the proposed method (c) Outliers identified by the proposed method.



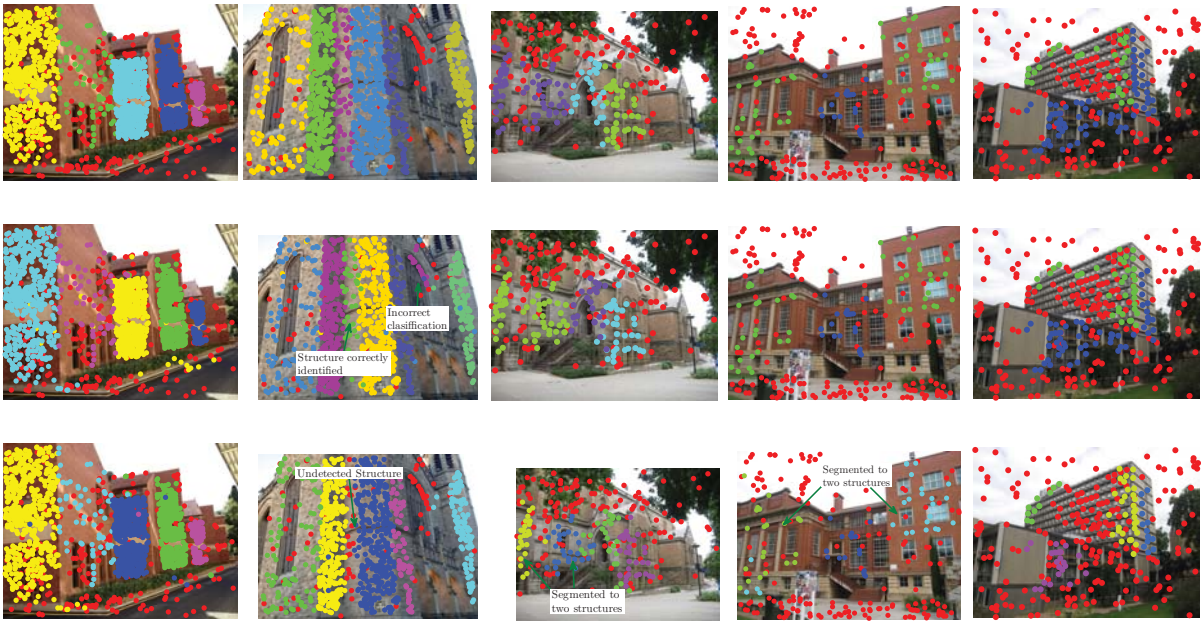
(a) boxes (a) deliveryvan (a) desk (a) lightbulb

Fig. 8. Two-view motion segmentation results for image sequences in dataset [25]. Line 1 shows the ground truth whereas lines 2 and 3 show the final HMSS samples selected and the clustering results of the proposed method. The outliers are marked in red.

dimensions of a given motion and requires this information as an input. In our implementation we have taken two approaches. In the first approach (PM T1), we set the dimensions of the subspaces to four and in the second we set the dimensions to three or four based on the average ground truth knowledge (not set for each sequence but to the whole sequence i.e. the subspace dimensions for all checkerboard three object sequences were set to [3, 4, 4]). The second approach (PM T2) is intended to demonstrate the accuracy of the method in cases where an estimate of the subspace dimensions is available.

We compared our results with energy minimization and QP-MF[3]. For completeness we also included the results of the sparse subspace clustering (SSC) [1] method which does not rely on dimensionality information. The results are shown in Table 2. The proposed method with fixed subspace dimensions (dim = 4) achieved better results than the competing model-fitting techniques (QP-MF, RANSAC, Energy minimization) but these results are not as good as SSC. However, when some informa-

3. The results published in [17] are used in this comparison.



(a) Unionhouse (b) BonHall (c) ElderHallb (d) BarSmith (e) Napiera

Fig. 9. Qualitative results of multi-homography estimation. line 1 is the ground truth where as lines 2 and 3 are segmentation results of the proposed method and RCM respectively. The outliers are marked in red.

tion about the dimensionality of the subspaces was provided to the algorithm, our proposed algorithm achieved results comparable with the SSC.

To provide a qualitative measure of the performance the final segmentation results of several sequences in the Hopkins 155 dataset, where the proposed method was successful, are shown in Fig. 10. These results show that the proposed method has been successful in a range of problems with different types of motion. We have also included some cases where the proposed method was not successful (Fig. 11). Figures 11(a) and 11(b) show instances where a single motion has been segmented into two. This is because some motions are segmented in to multiple degenerate motions. Figures 11(c) and 11(d) show instances where a structure has very low number of points relative to the other structures and in these cases the proposed method would be expected to fail due to the finite sample bias in the inlier noise estimation.

5 Discussion

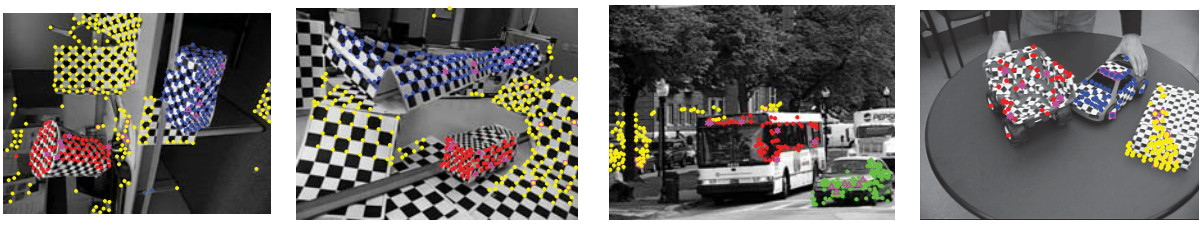
This paper presents an accurate and efficient method that can be used to detect underlying structures in data contaminated with noise and outliers. The proposed method is very general and requires only a very few input parameters compared to the competing methods.

One of the parameters required by the proposed method is the value of k, which defines the minimal acceptable size for a structure in a given application. Any robust model fitting method needs to establish the minimal acceptable structure size (either explicitly or implicitly), or else it may result in a trivial solution. For example if we are given a set of 2D points and asked to identify the lines in data without any additional constraint, there would be no basis to exclude the trivial solution because any two points will result in a perfect line. Hence in order to find a meaningful solution there must be some additional constraints such as the minimal acceptable size for a structure. Knowing the scale of noise is essential for accurate segmentation. While most competing methods require this as an input, the proposed method estimates the noise scale from data. The analysis of [19] showed that the estimation of the noise scale from data requires more than 20 data points to limit the effects of finite sample bias. As such, the proposed method is not suitable for finding structures with only a small number of data points (< 20).

The proposed method also assumes that the number of structures is known a prior. This is one of the weakness in the proposed method, however the problem of identifying the number of structures present and the scale of noise simultaneously is still a highly researched area with no good solutions. Remaining outliers can always be seen as members of a model with large noise values. Some model fitting methods that are based on energy minimization [29], [8] are devised to estimate the number of structures given the scale of noise. They achieve this by adding a model complexity term to the cost function that penalize additional structures in a given solution. However, these methods require an additional parameter that balances the data fidelity cost with the model complexity (number of structures in RCM). Our experiments on RCM showed that the output of these methods were heavily dependent on this parameter and required hand tunning to generate reliable results (see

TABLE 2
Percentage clustering Error of 3D motion segmentation.

	Reference	RANSAC	Enargy	QP-MF	SSC	PM T1	PM T2
2 Objects							
Mean	2.76	6.52	5.28	9.98	2.23	3.98	3.88
Median	0.49	1.75	1.83	1.38	0.00	0.00	0.00
3 Objects							
Mean	6.28	25.78	21.38	15.61	5.77	11.06	6.81
Median	5.06	26.01	21.14	8.82	0.95	1.20	1.04



(a) 1R2RC (b) 2R3RTCRT (c) cars10 (d) three-cars

Fig. 10. Segmentation result for several sequence in the Hopkins 155 dataset where the proposed method was successful. The sample used to generate the best hypothesis is also shown.

(a) 1R2RCT-A (b) 2RT3RCR (c) cars2-06 (d) cars2-07

Fig. 11. Segmentation result for several sequences in the Hopkins 155 dataset where the proposed method was not successful. The sample used to generate the best hypothesis is also shown.

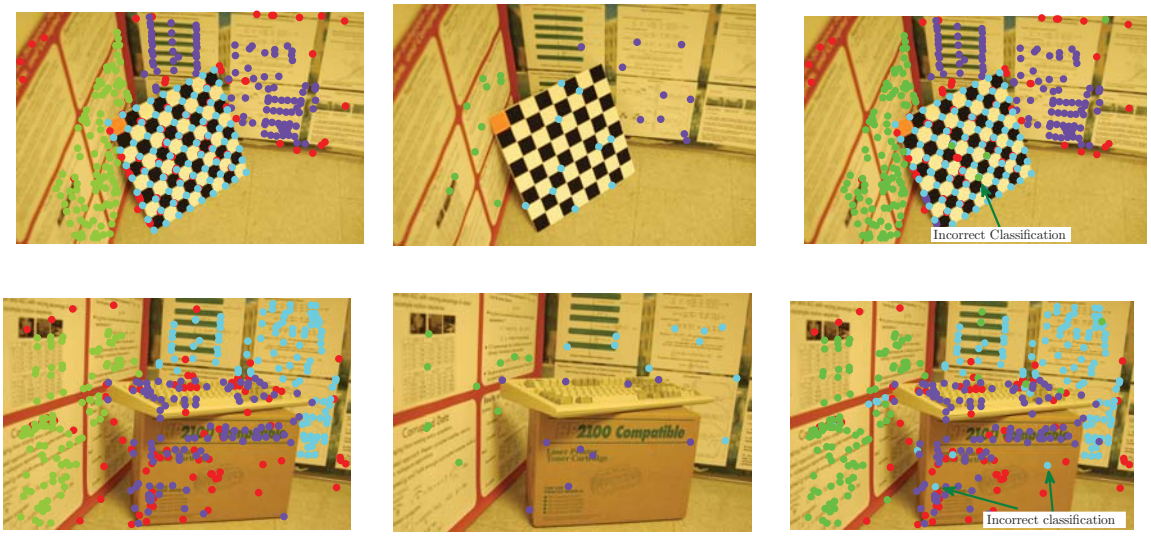
Fig. 5). The RCG method which is a hyper-graph-based method does not take the number of structures directly as an input. However, it may also result in multiple models representing the same structure and in order to remove these repetitions that method uses an additional pruning step that requires the knowledge of separation between the structures (another parameter).

The MSSE algorithm which is used to estimate the scale of noise, requires the constant threshold T as an input. T defines the inclusion percentage of inliers based on a normal distribution for noise which is a number around 2.5, i.e. $T = 2.5$ will include 99% of inliers.

The proposed method does not employ any additional information, such as the spatial contiguity, in the clustering. While this is advantageous in cases where the spatial contiguity is violated (see Fig. 9), in some problems where a structure has spatial contiguity, not using such priors will result in slight degradation in the clustering. This problem is elaborated in Fig. 12. The clean samples in the figure shows that the proposed algorithm has identified the underlying model correctly. However some points within one structure is clustered into another as these points are closer to that model. This problem can be eliminated by coupling the segmentation step with partial contiguity prior where applicable. However, we have not implemented such scheme in this paper as the main aim is to detect the a underlying models.

6 Conclusion

In this paper we first studied the usefulness of using higher than minimal subsets for hypothesis generation in parametric model fitting. The synthetic data experiments showed that using higher than minimal subset samples for hypothesis generation increases the probability of generating a good hypothesis close to the true model, given that it is a clean sample. The experiments also showed that the probability increase is only significant up to few additional data points. However, the probability of selecting a clean sample decreases with the increase



(d) Ground truth (e) Clean sample (f) Results

Fig. 12. Two-view motion segmentation results for image sequences "*poster-checkerboard*" (line 1) and "*poster-keyboard*" (line 2) from [2].

of the sample size, making it improbable to extend the commonly used sampling methods to accommodate higher than minimal samples.

This paper presents a new approach to parametric model fitting that uses higher than minimal subset sampling to generate hypotheses.

The performance of the algorithm in terms of accuracy and computational efficiency was evaluated on several models-fitting problemsand were compared with state-of-the-art model fitting techniques. The comparisons showed that the proposed method is both highly accurate and computationally efficient.

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References

[1] E. Elhamifar and R. Vidal, "Sparse subspace clustering: Algorithm, theory, and applications," *IEEE Transactions on Pattern Analysis and Machine Intelligence*, vol. 35, no. 11, pp. 2765–2781, 2013.

[2] B. Poling and G. Lerman, "A new approach to two-view motion segmentation using global dimension minimization," *International Journal of Computer Vision*, vol. 108, no. 3, pp. 165–185, 2014.

[3] R. Hesami, A. Bab-Hadiashar, and R. HosseinNezhad, "Range segmentation of large building exteriors: A hierarchical robust approach," *Computer Vision and Image Understanding*, vol. 114, no. 4, pp. 475–490, 2010.

[4] C. Lara-Alvarez, L. Romero, J. Flores, and C. Gomez, "A simple sample consensus algorithm to find multiple models," in *Progress in Pattern Recognition, Image Analysis, Computer Vision, and Applications*, ser. Lecture Notes in Computer Science, E. Bayro-Corrochano and J.-O. Eklundh, Eds. Springer Berlin Heidelberg, 2009, vol. 5856, pp. 918–925.

[5] N. Hevia-Montiel, J. R. Jimenez-Alaniz, V. Medina-Banuelos, O. Yanez-Suarez, C. Rosso, Y. Samson, and S. Baillet, "Robust nonparametric segmentation of infarct lesion from diffusion-weighted MR images," in *29th Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2007. EMBS 2007.* IEEE, 2007, pp. 2102–2105.

[6] M. Lucena, J. M. Fuertes, N. P. de la Blanca, and M. J. Marín-Jiménez, "Tracking people in video sequences using multiple models," *Multimedia Tools and Applications*, vol. 49, no. 2, pp. 371–403, 2010.

[7] C. V. Stewart, "Bias in robust estimation caused by discontinuities and multiple structures," *IEEE Transactions on Pattern Analysis and Machine Intelligence*, vol. 19, no. 8, pp. 818–833, 1997.

[8] T. T. Pham, T.-J. Chin, J. Yu, and D. Suter, "The random cluster model for robust geometric fitting," in *2012 IEEE Conference on Computer Vision and Pattern Recognition (CVPR).* IEEE, 2012, pp. 710–717.

[9] T.-J. Chin, J. Yu, and D. Suter, "Accelerated hypothesis generation for multi-structure robust fitting," in *Computer Vision - ECCV 2010*, ser. Lecture Notes in Computer Science, K. Daniilidis, P. Maragos, and N. Paragios, Eds. Springer Berlin Heidelberg, 2010, vol. 6315, pp. 533–546.

[10] L. Fan and T. Pylvänäinen, "Adaptive sample consensus for efficient random optimization," in *Advances in Visual Computing*, ser. Lecture Notes in Computer Science, G. Bebis, R. Boyle, B. Parvin, D. Koracin, Y. Kuno, J. Wang, R. Pajarola, P. Lindstrom, A. Hinkenjann, M. Encarnação, C. T. Silva, and D. Coming, Eds. Springer Berlin Heidelberg, 2009, vol. 5876, pp. 252–263.

[11] O. Chum, J. Matas, and J. Kittler, "Locally optimized ransac," in *Pattern Recognition*. Springer, 2003, pp. 236–243.

[12] A. Bab-Hadiashar and R. Hoseinnezhad, "Bridging parameter and data spaces for fast robust estimation in computer vision," in *Digital Image Computing: Techniques and Applications, 2008. DICTA'08.* IEEE, 2008, pp. 1–8.

[13] S. Agarwal, J. Lim, L. Zelnik-Manor, P. Perona, D. Kriegman, and S. Belongie, "Beyond pairwise clustering," in *IEEE Computer Society Conference onComputer Vision and Pattern Recognition, Proceedings CVPR 2005.*, vol. 2. IEEE, 2005, pp. 838–845.

[14] H. Liu, L. J. Latecki, and S. Yan, "Robust clustering as ensembles of affinity relations," in *Advances in Neural Information Processing Systems*, 2010, pp. 1414–1422.

[15] L. Hairong and Y. Shuicheng, "Efficient structure detection via random consensus graph," in *IEEE Conference on Computer Vision and Pattern Recognition (CVPR), 2012*, 2012, pp. 574–581.

[16] P. J. Rousseeuw and A. M. Leroy, *Robust regression and outlier detection*. John Wiley & Sons, 2005, vol. 589.
[17] J. Yu, T.-J. Chin, and D. Suter, "A global optimization approach to robust multi-model fitting," in *2011 IEEE Conference on Computer Vision and Pattern Recognition (CVPR)*. IEEE, 2011, pp. 2041–2048.
[18] A. Bab-Hadiashar and D. Suter, "Robust segmentation of visual data using ranked unbiased scale estimate," *Robotica*, vol. 17, no. 6, pp. 649–660, 1999.
[19] R. Hoseinnezhad, A. Bab-Hadiashar, and D. Suter, "Finite sample bias of robust estimators in segmentation of closely spaced structures: A comparative study," *Journal of Mathematical Imaging and Vision*, vol. 37, no. 1, pp. 66–84, 2010.
[20] L. Qi and D. Sun, "A survey of some nonsmooth equations and smoothing newton methods," in *Progress in Optimization, volume 30 of Applied Optimization*. Kluwer Academic Publishers, 1999, pp. 121–146.
[21] R. Toldo and A. Fusiello, "Robust multiple structures estimation with j-linkage," in *Computer Vision–ECCV 2008*. Springer, 2008, pp. 537–547.
[22] H. Chen and P. Meer, "Robust regression with projection based m-estimators," in *Proceedings. Ninth IEEE International Conference on Computer Vision, 2003.* IEEE, 2003, pp. 878–885.
[23] P. H. Torr and D. W. Murray, "The development and comparison of robust methods for estimating the fundamental matrix," *International Journal of Computer Vision*, vol. 24, no. 3, pp. 271–300, 1997.
[24] R. Hartley and A. Zisserman, *Multiple view geometry in computer vision*. Cambridge university press, 2003.
[25] K. Schindler and D. Suter, "Two-view multibody structure-and-motion with outliers through model selection," *IEEE Transactions on Pattern Analysis and Machine Intelligence*, vol. 28, no. 6, pp. 983–995, 2006.
[26] H. S. Wong, T.-J. Chin, J. Yu, and D. Suter, "Dynamic and hierarchical multi-structure geometric model fitting," in *2011 IEEE International Conference on Computer Vision (ICCV)*, Nov 2011, pp. 1044–1051.
[27] Y. Sugaya and K. Kanatani, "Geometric structure of degeneracy for multi-body motion segmentation," in *Statistical Methods in Video Processing*, ser. Lecture Notes in Computer Science, D. Comaniciu, R. Mester, K. Kanatani, and D. Suter, Eds. Springer Berlin Heidelberg, 2004, vol. 3247, pp. 13–25.
[28] R. Tron and R. Vidal, "A benchmark for the comparison of 3-D motion segmentation algorithms," in *IEEE Conference on Computer Vision and Pattern Recognition, 2007. CVPR'07.* IEEE, 2007, pp. 1–8.
[29] A. Delong, A. Osokin, H. N. Isack, and Y. Boykov, "Fast approximate energy minimization with label costs," *International journal of computer vision*, vol. 96, no. 1, pp. 1–27, 2012.

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