

# A unified hypothesis generation framework for multi-structure model fitting



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## ABSTRACT

Generating promising hypotheses plays a critical role in the success of multi-structure model fitting methods. However, conventional multi-structure hypothesis generation strategies do not exploit the information derived from the results of model selection to guide the subsequent hypothesis generation process. This leads to the problem that these hypothesis generation strategies are often computationally expensive for generating promising hypotheses, especially for heavily contaminated multi-structure data. To address this problem, we first propose a guided sampling strategy to accelerate promising hypothesis generation process by using information derived from the results of model selection on the fly. Then we present a Unified Hypothesis Generation (UHG) framework, which effectively combines the conventional multi-structure hypothesis generation strategy with the proposed guided sampling strategy by using a Markov Chain Monte Carlo process based on a cooling schedule. Experimental results on public databases demonstrate that the proposed UHG achieves significant superiority over several state-of-the-art sampling methods in terms of accuracy and efficiency, especially on multi-structure data.

## 1. Introduction

Robust model fitting is a fundamental technique in computer vision, which has widespread applications, such as action potential classification [1], fundamental matrix estimation [2], motion segmentation [3], face clustering [4], image denoising [5]. The task of robust model fitting is to estimate the parameters of model instances in data. More specifically, given a geometric model, robust model fitting methods estimate the parameters and the number of model instances from the input data.

Fig. 1 illustrates the line fitting problem: given an input data with one or several lines generated by using a line model  $y = kx + b$ , robust model fitting methods need to estimate the model parameters  $[k, b]$  and the number of lines in the input data. Fig. 1(a) shows the input data including a model instance (i.e., a line) and Fig. 1(b) shows the input data including three model instances (i.e., three lines). The data points with Gaussian noise  $\sigma = 0.02$  “lying” on some lines are called the inliers of the lines. In contrast, the data points not belonging to any line are called gross outliers. The inliers of one line usually are pseudo-outliers of the other lines. A model instance is also called “a structure” [6–8]. A single-structure data refers to the data containing only one structure while a multi-structure data has multiple structures in the data. Of course, the model is not restricted to a line, and it can be any other geometric model such as circle, homography matrix, fundamental

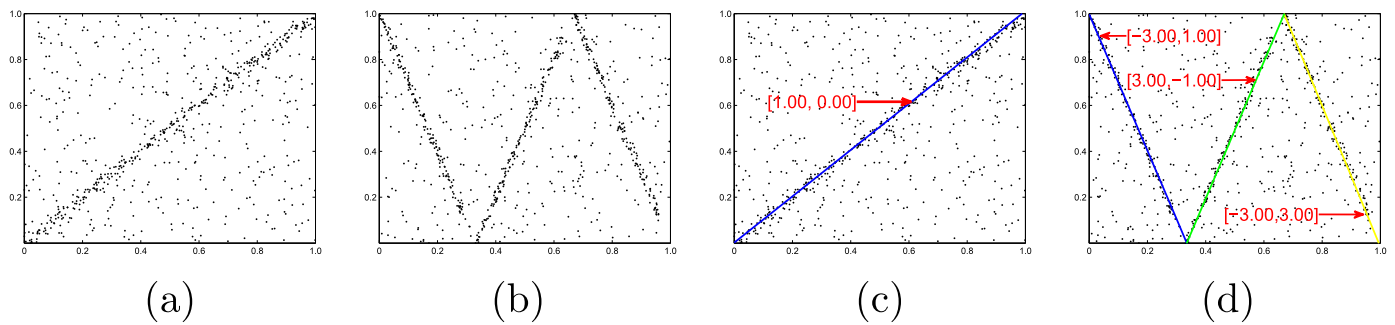
matrix, etc.

Most robust model fitting methods (e.g., [6,9]) are mainly composed of two steps: hypothesis generation and model selection. Hypothesis generation is also called sampling, because the most important step of hypothesis generation is sampling effective data from input data. In order to increase the probability of sampling all-inlier (i.e., inliers from the same structure) subsets, most hypothesis generation methods (e.g., [9,7,8]) sample minimal subsets for generating hypotheses. The minimal subsets contain the minimum number  $p$  of data points required to estimate a geometric model (e.g.,  $p=2$  for line fitting,  $p=4$  for homography matrix estimation). Some hypothesis generation strategies (such as [10–12]), which only consider the single-structure case, are called single-structure hypothesis generation strategies. While some other hypothesis generation strategies (e.g., [7,8]), which work for both single-structure and multi-structure data, are called multi-structure hypothesis generation strategies.

Many two-stage model fitting methods (such as [9,14–18,3]), conducting hypothesis generation and model selection as two disjoint stages, have been proposed to simultaneously estimate multiple structures in data. These methods perform model selection after generating a set of hypotheses. However, such two-stage model fitting methods fail to work when the generated hypotheses do not contain one clean solution, where it is obtained when at least one all-inlier minimal subset is sampled for each model instance in data. To

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**Fig. 1.** Examples of line fitting: (a) and (b) Input data with one line and three lines, respectively. (c) and (d) The fitting results of (a) and (b) obtained by the model fitting method KF [13], respectively. The red numbers in  $[\cdot, \cdot]$  are the estimated model parameters. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article).

efficiently generate hypotheses for these fitting methods, several sampling strategies (e.g., [7,19]) have been proposed to generate promising hypotheses for multi-structure data. Nevertheless, there are still some problems unsolved. For example, Proximity [19] will break down if data fail to satisfy the assumption of spatial proximity; while MultiGS [7] cannot generate an accurate clean solution for multi-structure data heavily corrupted with outliers in a reasonable time,<sup>1</sup> due to expensive computational cost during the hypothesis generation process.

For these conventional multi-structure hypothesis generation strategies, hypothesis generation and model selection are two independent processes. As a matter of fact, one important observation is that the probabilities of generating promising hypotheses by these sampling strategies usually increase progressively as the iteration progresses. Thus, the process of generating promising hypotheses could be efficiently accelerated, if the information (derived from the results of model selection on the generated hypotheses) is properly applied to guide the subsequent process of hypothesis generation. We note that some hypothesis generation strategies (e.g., [10,20]) have been developed to guide their sampling processes by using the information derived from the results of model selection. However, these methods are hard to work properly for multi-structure data because they are mainly designed for single-structure data, and they can result in overfitting on multi-structure data (i.e., the inliers of one fitted hypothesis include the inliers of multiple structures).

In this paper, we propose a Unified Hypothesis Generation (UHG) framework that can efficiently generate promising hypotheses for multi-structure data. In UHG, we propose a guided sampling strategy (i.e., the local search), which effectively uses the information derived from the results of model selection to accelerate the process of promising hypothesis generation. To guide the sampling process of the proposed guided sampling strategy, UHG also employs a conventional multi-structure hypothesis generation strategy (i.e., the global search). Therefore, UHG effectively combines these two sampling strategies by using a Markov Chain Monte Carlo process based on a cooling schedule.

Fig. 2 illustrates an example result of the proposed UHG by employing the Proximity sampling [19] for global search, where the Proximity sampling is reviewed in Section 2. The *Barrsmith* image pair with two model instances are used for homography matrix estimation, shown in Fig. 2(a) and (b). The proposed UHG firstly performs model selection (Section 3.2.1) after newly generating a batch of hypotheses, where a snapshot of the detected model instances is shown in Fig. 2(c). The proposed guided sampling strategy in UHG then guides its subsequent sampling process (Section 3.2.2) by using the information

obtained from the inliers of the detected model instances, even though one true model instance is detected as two model instances initially (marked in both blue squares and carmine circles). This process significantly reduces the influence of outliers and thus increases the probabilities of generating promising hypotheses. The final model instances detected on the hypotheses generated by the proposed UHG within the given time are shown in Fig. 2(d), where two homography instances are accurately segmented.

The main contributions of this paper are two-fold: (1) We propose a guided sampling strategy to generate promising hypotheses for multi-structure data. The proposed sampling strategy guides the subsequent sampling process by using the information derived from the detected model instances that are updated by model selection on the fly. It effectively increases the probabilities of generating promising hypotheses. Moreover, we introduce two effective residual update schemes to efficiently perform model selection for the proposed sampling strategy after each new batch of hypotheses is generated. (2) We propose a Unified Hypothesis Generation (UHG) framework. Under this new framework, the conventional hypothesis generation strategy is successfully combined with the proposed sampling strategy by using a Markov Chain Monte Carlo (MCMC) process with a cooling schedule. Compared with conventional hypothesis generation strategies, UHG is much more efficiently in generating promising hypotheses for multi-structure data.

## 2. Related work

Sampling methods can be roughly grouped into random sampling and guided sampling methods. Random sampling [6] is a widely used sampling method, and has been adopted in many recently-proposed model fitting methods (e.g., [9,21]) due to its simplicity. The sampling processes of random sampling can be briefly described as: randomly sample a minimal subset with  $p$  data points from the input data and generate a hypothesis by using the sampled minimal subset. However, random sampling is not an efficient and effective sampling method. The probabilities of sampling all-inlier minimal subsets exponentially decrease when the dimension of the model grows or the inlier rate of input data reduces [7].

To improve the performance of random sampling, a number of guided sampling methods have been proposed. Compared with random sampling that assumes each data point has the same probability of being an inlier, the guided sampling methods compute sampling weight for each data point by using the domain knowledge (such as matching scores, spatial proximity, etc). Each data point probably has different sampling weight. The general sampling processes of guided sampling can be summarized as: first compute sampling weights for input data, then sample a minimal subset from input data according to the computed sampling weights and generate a hypothesis by using the sampled minimal subset. We review the related guided sampling methods according to different domain knowledge used as follows.

<sup>1</sup> The time to obtain an acceptable solution varies with problem complexity, and the “reasonable” time also varies depending on the type of tasks. Here, as in [8], five seconds and ten seconds are chosen as indicative “reasonable time” for homography and fundamental matrix estimation, respectively.

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