

## SWIFT: Sparse Withdrawal of Inliers in a First Trial

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Detecting multiple model instances simultaneously is an active area of research. Early approaches in identifying multiple model instances estimated models sequentially using a single-model fitting method [2]. More recent studies try to find all the model instances and their parameters simultaneously. Generally, the research in this area is focused on two main aspects: (i) the study of the sampling process, whereby subsets of the data points are selected with the purpose of simultaneously instantiating the underlying model instances[4], and (ii) the clustering process which is used for grouping the data points, and the estimation of the underlying model parameters[1]. In this paper, our focus is mainly on the sampling step. In fact, our sampling method can be used as the front end to any unsupervised clustering method. Rather than focusing on the strategy of maximizing the probability of sampling inliers, our goal is to minimize the number of samples needed to instantiate all underlying model instances. More specifically, the proposed method named Sparse Withdrawal of Inliers in a First Trial (SWIFT) answers the following question:

“Given a large population of points with multiple instances of a structure and gross outliers, what is the minimum number of points  $r$  to be sampled randomly from this population in one grab, in order to make sure with probability  $P$  that there are at least  $\varepsilon$  samples on each structure instance?” Here,  $\varepsilon$  is greater than or equal to the number of samples needed to determine the number of degrees of freedom of the structure.

To derive the SWIFT sampling scheme, we start by dealing with the worst case scenario where in a population of  $N$  observations, the size of all model instances presumed to be equal to the minimum model size  $\theta$  and no gross outlier exists in the dataset. Thus, the maximum possible classes would be  $C = N/\theta$ . By this assumption, the objective of the SWIFT method can be expressed as the problem of finding  $r$  such that, for a given value  $\delta > 0$ , the probability of selecting at least  $\varepsilon$  points in each of  $C$  model instances is at least  $1 - \delta$ . Thus  $P$  can be written as:

$$P(\cap_{i=1}^C (d_i \geq \varepsilon)) \geq 1 - \sum_{i=1}^C P(d_i \leq \varepsilon - 1) = 1 - C\Delta = 1 - \delta \quad (1)$$

provided  $P[\cap_{i=1}^C (d_i = x_i)] = \frac{\prod_{i=1}^C \binom{\theta}{x_i}}{\binom{C\theta}{r}}$ ,  $\sum_{i=1}^C d_i = r$  and  $C\Delta = \delta$ .

The solution of the above problem is related to the question of finding upper bounds for the tail probabilities of the multivariate hypergeometric distribution. The usual approach is to use some kind of asymptotic expansion of the multivariate hypergeometric probability, or to approximate it by a multinomial probability. The difference between solution of the inequality (1) and the settings that have been considered previously is that (i) we are interested in constructing a non-asymptotic approach that will work for various parameter settings and (ii) we are interested in the solution of the inverse problem of finding  $r$  rather than estimating the probability in the left-hand side of the inequality (1). We show that the total probability of selecting not less than  $\varepsilon$  points in each of the model instance can be bounded above using de Morgan’s laws.

We prove that equation (2) is an upper-bound to equation (1) and can be used to obtain the value of  $r$  required for SWIFT sampling. Considering that equation (1) is a non-decreasing function when  $C$  is reasonably small,  $r$  can simply be computed by using a binary search through all possible values.

$$\Delta = P(d_1 \leq \varepsilon - 1) \leq P(d_1 = 0) \sum_{k=0}^{\varepsilon-1} \binom{C\theta}{k} \left( \frac{\theta}{N - r - \theta + k} \right)^k \quad (2)$$

where  $P(d_1 = 0) \leq \prod_{j=0}^{\theta-1} \frac{C\theta - Cj}{C\theta} = (1 - \frac{r}{C\theta})^\theta \leq e^{-r/C}$

To verify the accuracy of the estimated bounds, we compared the values of our approximation against the theoretical values. We chose different

population sizes with different embedded model instances. The result of theoretical and estimated values of  $r$  are plotted against different desired probability values in Figure 1. As expected, our approximations closely follow the theoretical values.

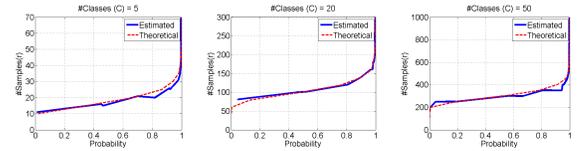


Figure 1: Comparison of estimated  $r$  averaged over 200 independent trials versus the theoretical value of  $r$  when  $N = \{100, 1000, 10000\}$  and  $\varepsilon = 2$ . From left to right:  $C = \{5, 20, 50\}$ .

SWIFT can be used in virtually any scenario where multiple structures need to be detected in a large population. Detecting planes in 3D space is one of the applications studied in this paper. Figure 2 shows the result of detecting planes in point cloud data using the two-level SWIFT algorithm.

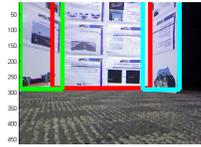


Figure 2: Detecting planes in 3D point cloud data collected using a Kinect. The population size is  $N = 167,028$  and  $\theta = 30,000$ . By setting  $P = 0.9$ , on the 1<sup>st</sup> level  $\varepsilon = 3$  then  $r = 43$  and on the 2<sup>nd</sup> level  $\varepsilon = 100$  then  $r = 714$ .

Moreover, we compare SWIFT with other existing methods in terms of sparseness and precision/recall. Since one of the primary goals of SWIFT is sparse sampling, we compared the sample size computed by SWIFT against the number of sampled points in other existing methods. Figure 3 shows the result of comparing the computed number of sample points in SWIFT, the method in [3], and the sequential-RANSAC.

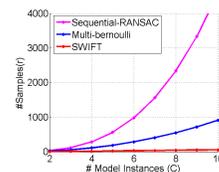


Figure 3: Comparing the averaged number of samples  $r$  over 200 trials in sequential RANSAC, the proposed method in [3], and the SWIFT sampling when  $N = \{100, 1000, 10000\}$ ,  $\varepsilon = 2$  and  $P = 0.9$ .

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