

## EXCERPTS FROM REJOINDER

From [T.-J. Chin, J. Yu and D. Suter, Accelerated Hypothesis Generation for Multi-Structure Data via Preference Analysis, IEEE Trans. Pattern Anal. Mach. Intell. (PAMI)].

Due to its tendency to generate degenerate samples, it is recommend to combine PROSAC with... the algorithms proposed in [6,9]. It is not clear if the proposed Multi-GS algorithm shares the same vulnerability... I suggest to conduct further experiments on the robustness of the proposed sampling strategy against degenerate configurations... The results could easily be fitted.. by denoting after the number of all-inlier samples drawn by Multi-GS the percentage of non-degenerate samples among those all-inlier samples as well as the number of non-degenerate samples expected when drawing that exact number of all-inlier samples.

As suggested we have conducted further experiments to examine the performance of Multi-GS under degeneracies. We provide further elaborations here. First we create multiple instances of data based on the Dino-Books image pair; see Section 5.3.1. The inliers are separated into two sets: Set A (off-plane inliers) and Set B (dominant-plane inliers). The number of Set A inliers are varied, producing a series of ratios of on-plane inliers to total inliers

$$\gamma = \frac{|\text{Set B}|}{|\text{Set A}| + |\text{Set B}|}.$$

For each ratio 50 data instances are generated, and on each data instance each method is run for 10s. The median results across the 50 repetitions are presented in Fig. 9(b).

Degeneracies are detected, as suggested by Reviewer 2, by checking using ground truth knowledge whether more than 6 members of a minimal subset belong to the same plane. Note that in our case the Set A inliers are also from a plane; see Section 5.3.1. Since the number of Set A inliers added  $|\text{Set A}|$  can exceed 7 (but  $|\text{Set A}|$  is always less than  $|\text{Set B}|$ ), a minimal subset that has more than 6 members from Set A is also counted as denegate.

Given that minimal subset  $\mathcal{S}$  contains all inliers, the probability that  $\mathcal{S}$  is degenerate is

$$P_{\text{degen}|\text{all-inlier}} = \begin{cases} \sum_{i=7}^8 \binom{8}{i} \gamma^i (1 - \gamma)^{8-i} & \text{if } |\text{Set A}| < 7 \\ \sum_{i=7}^8 \binom{8}{i} \gamma^i (1 - \gamma)^{8-i} + \sum_{i=7}^{\min(8, |\text{Set A}|)} \binom{8}{i} (1 - \gamma)^i \gamma^{8-i} & \text{otherwise} \end{cases}$$

Note that this probability depends on the actual number of Set A inliers (randomly) added to reach the particular tested ratio  $\gamma$ . Thus, given that Multi-GS has sampled  $M$  all-inlier minimal subsets, the expected number of non-degenerate hypotheses among these is  $M(1 - P_{\text{degen}|\text{all-inlier}})$ . This value is shown as the cyan dashed line in Fig. 9(b).

The results do show that Multi-GS has a tendency to sample from the dominant plane, indicating a PROSAC-like vulnerability. However, the results show that Multi-GS is still able to generate significantly large numbers of non-degenerate hypotheses across a wide range of  $\gamma$ . This is not surprising, since in absolute terms Multi-GS can retrieve a much larger number of all-inlier minimal subsets (compare this to pure random sampling in Fig. 9(b)). Thus in a practical sense, Multi-GS is still an excellent choice in the presence of degeneracies.

We also remark that in the prior work [6,9] referred to by Reviewer 2, degeneracies are not handled in the hypothesis sampling process, i.e. the sampling does *not* explicitly search

for non-degenerate models. Instead a separate mechanism is used to detect degenerate hypotheses (e.g. robust rank detection in [9]) before invoking a correction routine (e.g. plane-and-parallax algorithm in [6]) to recover the fundamental matrix from the degenerate hypotheses. Such routines can be easily plugged into Multi-GS to recover non-degenerate hypotheses from the degenerate all-inlier minimal subsets.