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An Improved RANSAC based on the Scale Variation Homogeneity[1]

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Abstract: For random sample consensus (RANSAC) method, high levels of contamination may slow down its convergence and impede the acquisition of the optimal model. In this paper, an improved RANSAC algorithm based on SIFT matches is proposed, which could provide robust performance in high levels of contamination and with low computational complexity. The improved RANSAC algorithm is particularly tailored to planar homography, by appropriately exploring feature scales. Firstly, a new feature scale constraint, i.e., the scale variation homogeneity (SVH), is proposed by exploiting the fact that the feature scale ratio of a correct match is approximate to the actual scale variation of two matched images. As a result, the potential correct and false matches can be effectively determined by SVH. Secondly, each model is scored by the number of partial identified false matches instead of all correct matches, which will speed up the evaluation process. Finally, fast converge can be obtained by adaptive selection of the test set for determining termination criterion according to the levels of contamination. Experimental results have demonstrated that the proposed SVH-RANSAC algorithm can perform very well even in the scenario of 90% contamination level. The number of iterations could be decreased by at least 35% and computational complexity for the evaluation procedure could be decreased by at least 2.5% compared with the LO^{+}-RANSAC.

Index-terms Scale variation homogeneity; scale ratio; RANSAC; SIFT matches

1. Introduction

Any two images of the same planar surface can be related by a homography, where a two-dimensional model can be constructed. Homography estimation is the algorithm to estimate the optimal model parameters based on the input matches. In practice, the input matches are inevitably

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