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ROBUST REGRESSION SAMPLE CONSENSUS ESTIMATOR MODEL: PERFORMED ON INLIERS

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Abstract-Robust regression play vital role in many fields specially image processing. Corner detection is the one of the important role in image process. Much corner detection is to develop day to day; such corner detection is based on robust regression. Sample Consensus (SAC) has been popular in regression problems with samples contaminated with outliers. It has been a milestone of many researches on robust estimators, but there are a few survey and performance analysis on them. According to SAC family to analyze the performance evaluation based on being accurate inliers (Maximum), being fast, and being robust. Performance evaluation performed online fitting with various data distributions. These papers analyze the performance of a more SAC family and also find a unique robust regression on the maximum number of inliers. Total Least Square (TLS) model fitting estimation was utilized the present performance in real data.

Keywords: RANSAC, fitting, robust regression, Regression.

I. INTRODUCTION

Robust regression is to develop day to day in computer vision and other related regression field. The theory of robust regression deals with deviations from the assumptions of the model and is concerned with the construction of regression procedures which are still reliable and reasonably efficient in a neighborhood of the model; see the books by Huber (1981), Hampel, Ronchetti, Rousseeuw, and Stahel (1986), Maronna, Martin, and Yohai (2006), and Dell'Aquila and Ronchetti (2006) for an overview. Robust regression are now some 40 years old. Indeed, one can consider Tukey (1960), Huber (1964), and Hampel (1968) the fundamental papers which laid the foundations of modern robust regression.

Robust regression control Type I error and also maintain adequate regression power. In contrast, claims that classic parametric tests are robust usually only consider a Type I error, not power. An overview of the robustness argument can be found in Sawilowsky (1990). The origin of the robustness argument can be traced back to several key articles and books, including Boneau (1960); Box (1953);

Lindquist (1953); and Glass, Peckham, and Sanders (1972). Countless studies have shown that even when classic parametric tests are robust to Type I errors, they are usually considerably less powerful than their modern robust counterparts [2]. The RANSAC families formulate regression with outliers as a minimization problem. This formulation is similar with least square method, which minimize sum of squared error values. Robust fitting algorithms are mostly based on sampling strategies, hypotheses are generated and their support is measured in the point cloud. Examples for this strategy are the least-median-of squares (LMS) [3].

The problem of estimation in the presence of high percentages of outliers. This type of problem occurs in all stages of automatic calibration, orientation and surface reconstruction, as automatic image matching procedures are error prone. Regression and probability theory are indispensable for handling uncertainty and estimating parameters under these conditions. There exists powerful robust estimation techniques. However, no unique techniques exists which is applicable in all situations [4].

The paper gives the demonstration on the ability (performance) of RANSAC family to correctly estimate parameters, mean and number of inliers to be taken. Even most of the robust regression method the percentage of outliers is far beyond 50% and the outliers hide the true solution. As an example we take the classical problem of straight line fitting. Experiments have been made with MATLAB a development package. Section 2 details the introduction of RANSAC families. Section 3 presents the performance of RANSAC families with comparisons and the paper is concluded in section 4.

II. ROBUST REGRESSION

Outliers are sample values that cause surprise in relation to the majority of the sample.

Outliers may be correct, but they should always be checked for transcription errors. They can play havoc with standard regression methods, and many robust and resistant methods have been developed since 1960 to be less sensitive to outliers. In computer vision widely using robust estimator specially RANSAC families. The following chart is to be



indicating that the unique model robust regression performed of RANSAC family.

A. Random Sample Consensus (RANSAC)

One of the most Robust attractive techniques is Random Sample Consensus (RANSAC) [5]. It randomly chooses a minimal set of observations and evaluates their likelihood until a good solution is found or a preset number of trials is reached. RANSAC is a technique which is best suited for estimated problems with a small number of parameters and a large percentage of outliers. It has regularly been applied matching, detection and registration.

The idea of the RANSAC algorithm is to repeatedly select a random subset S of the data, to determine a solution $p=F(S)$ and evaluate it with other data. RANSAC uses three parameters:

1. The number n of trials,
2. The threshold k for determining where a data point agrees with model in [6], and possibly.
3. The threshold t for the required number of inliers.

The number of iterations, n , is chosen high enough to ensure that the probability p (usually set to 0.99) that at least one of the sets of random samples does not include an outlier. Let u represent the probability that any selected data point is an inlier and $v=1-u$ the probability of observing an outlier. N iterations of the minimum number of points denoted m are required, where

$$p=1-(1-(1-u)^m)^n \quad \text{and} \quad n_{\min}(P_{\min, u, n})=\frac{\ln(1-p_{\min})}{\ln(1-(1-u)^m)}$$

B. Recursive RANSAC (RRANSAC)

The random sample consensus (RANSAC) algorithm is frequently used in computer vision to estimate the parameters of a signal in the presence of noisy and even spurious observations call gross errors. Instead of just one signal, we desire to estimate the parameters of multiple signals, where at each time step a set of observations of generated from the underlying signals and gross errors are received. RRANSAC develop the recursive RANSAC (RRANSAC) algorithm to solve the inherent data association problem and recursively estimate the parameters of multiple signals without prior knowledge of the number of true signals. The performance of RRANSAC with several existing algorithms, and also demonstrate the capabilities of RRANSAC in an aerial geolocation problem [7]. The general form of RRANSAC is denoted by $r_i[t]=\frac{1}{c}(r_i - r_v[t] + \epsilon_2[t])$

C. N Adjacent Points Sample Consensus (NAPSAC)

The most effective algorithms for model parameterization in the presence of high noise, such as RANSAC, MINPRAN and Least Median Squares, use random sampling of data points to instantiate model hypotheses. However, their performance degrades in higher dimensionality due to the exponentially decreasing probability of sampling a set of inliers. It is suggested that biasing this random selection towards clusters in multi-dimensional space may be preferable. Based on this premise, the NAPSAC (N Adjacent Points Sample Consensus) algorithm is derived and its performance in high dimensionality is shown to be superior to RANSAC on a hyper plane fitting problem [8].

D. M-estimator Sample Consensus (MSAC)

MASAC has two goals. The first is to develop a variety of robust methods for the computation of the Fundamental Matrix, the calibration-free representation of camera motion. The methods are drawn from the principal categories of robust estimators, viz. case deletion diagnostics, M-estimators and random sampling, and the paper develops the theory required to apply them to non-linear orthogonal regression problems. Although a considerable amount of interest has focused on the application of robust estimation in computer vision, the relative merits of the many individual methods are unknown, leaving the potential practitioner to guess at their value. The second goal is therefore to compare and judge the methods. Comparative tests are carried out using correspondences generated both synthetically in a regression controlled fashion and from feature matching in real imagery. In contrast with previously reported methods the goodness of fit to the synthetic observations is judged not in terms of the fit to the observations per se but in terms of fit to the ground truth. A variety of error measures are examined. The experiments allow a regression satisfying and quasi-optimal method to be synthesized, which is shown to be stable with up to 50 percent outlier contamination, and may still be used if there are more than 50 percent outliers. Performance bounds are established for the method, and a variety of robust methods to estimate the standard deviation of the error and covariance matrix of the parameters are examined. The results of the comparison have broad applicability to vision algorithms where the input data are corrupted not only by noise but also by gross outliers [9].

E. Locally Optimized RANSAC (LORANSAC)

A new enhancement of RANSAC, the locally optimized RANSAC (LO-RANSAC). It has been observed that, to find an optimal solution (with a given probability), the number of samples drawn in RANSAC is significantly higher than predicted from the mathematical model. This is due to the incorrect assumption, that a model with parameters computed from an outlier free sample is consistent with all inliers. The assumption rarely holds in practice. The locally optimized RANSAC makes no new assumptions about the data, on the contrary it makes the above-mentioned assumption valid by applying local optimization to the solution estimated from the random sample. The performance of the improved RANSAC is evaluated in a number of epipolar geometry and homographic estimation experiments. Compared with standard RANSAC, the speed-up achieved is two to three fold and the quality of the solution (measured by the number of inliers) is increased by 10-20%. The number of samples drawn is in good agreement with theoretical predictions [10].

F. Maximum Likelihood Sample Consensus (MLE SAC)

LORANSAC estimating multiple view relations from point correspondences. The method comprises two parts. The first is a new robust estimator MLESAC which is a generalization of the RANSAC estimator. It adopts the same sampling strategy as RANSAC to generate putative solutions, but chooses the solution that maximizes the likelihood rather than just the number of inliers. The second part of the algorithm is a general purpose method for automatically parameterizing these relations, using the output of MLESAC. A difficulty



with multi view image relations is that there are often nonlinear constraints between the parameters, making optimization a difficult task. The parameterization method overcomes the difficulty of nonlinear constraints and conducts a constrained optimization. The method is general and its use is illustrated for the estimation of fundamental matrices, image-image holographies, and quadratic transformations. Results are given for both synthetic and real images. It is demonstrated that the method gives results equal or superior to those of previous approaches [11]. This method is dubbed MLESAC (maximum likelihood consensus). For real systems it is sometimes helpful to put a prior on \hat{E} , the expected proportion of inliers.

G. Z-HangSAC

Zhang et al. (1997) proposed a sample consensus estimator, namely ZhangSAC and it is a novel technique for effectively calibrating a binocular stereo rig using the information from both scenes and classical calibration objects. The calibration provided by the classical methods is only valid for the space near the position of the calibration object. This technique tries to make the best use of the rigidity of the geometry between two cameras. The idea is to first estimate precisely the epipolar geometry which is valid for a wide range in space from all available matches, extracted from both the environment and the calibration objects. This allows us to conduct projective reconstruction. Using the prior knowledge of the calibration object and finally able to calibrate the stereo rig in a Euclidean space. The camera calibration method employs abstract concepts like the image of the absolute conic and circular points. It is restricted on homographic, research in computer vision, signal processing, multimedia computing and human machine.

H. PROSAC

Chum and Matas (2005) was developed a robust matching method PROgressive SAMple Consensus (PROSAC), it has exploits the linear ordering defined on the set of correspondences by a similarity function used in establishing tentative correspondences. Unlike RANSAC, which treats all correspondence equally and draws random samples uniformly from the full set, PROSAC samples are drawn from progressively larger sets of top-ranked correspondences.

The structure of the PROSAC algorithm is similar to RANSAC. First, hypotheses are generated by random sampling. The samples, unlike in RANSAC, are not drawn from all data, but from a subset of the data with the highest quality. In fact, PROSAC is designed to draw the same samples as RANSAC, only in a different order. The t^{th} sample in PROSAC and it is denoted by

$$\mathcal{M}_t = \{u_{g(t)}\} \cup \mathcal{M}_t^1 \tag{1}$$

where $g(t)$ is a growth function defined as $g(t) = \min\{n\}$ and \mathcal{M}_t^1 is a set containing $m-1$ points drawn at random from the set $U_{g(t)-1}$. In practice, the PROSAC approach often achieves significant computational savings, since good hypotheses are generated early on in the sampling process. Two important points must be noted. First, though PROSAC often succeeds in dramatically reducing the number of hypotheses required, this is data-dependent, and also hinges on the availability of a reasonable similarity function to rank correspondences.

Secondly, it is observe that in many cases, correspondences with high similarity scores often lie on the same spatial structure and are potentially in a degenerate configuration.

I. AMLESAC

Anton et al. (2005) introduced A Maximum Likelihood Estimator SAMple Consensus (AMLESAC) robust estimator, which is a noise adaptive variant of the renowned MLESAC estimator. It adopts the same sampling strategy and seeks the solution to maximize the likelihood rather than some heuristic measure, but unlike MLESAC, it simultaneously estimates the outlier share τ and inliers noise level σ . The effective optimization for computation speed-up is also introduced. The proposed algorithm searches for the parameter vector θ with highest likelihood on input data x with assumption that input data is a mixture of inliers measured with error that obey the Gaussian distribution and uniform distributed outliers.

J. GASAC

Volker and Olaf (2006) proposed Genetic Algorithm SAMpling Consensus (GASAC), and it is a robust estimator based on an evolutionary optimization technique. GASAC is based on genetic algorithm, whose procedure is quite different from RANSAC. It manages a subset of data as a gene, which can generate a hypothesis. Each gene receives penalty by loss of its generated hypothesis. The penalty causes less opportunity in evolving the new gene pool from the current genes. A population G consists of several individuals, who are characterized by an individual chromosome. Such chromosome g corresponds to a duple of m elements, which are called genes. The representation of the existing problem by a chromosome is trivial, if for n homologous points X_i , the index i is directly defined as gene

$$g_k \in \{1, 2, \dots, n\} \text{ for } k = 1, 2, \dots, m \tag{2}$$

where a gene may occur only once within the chromosome. The fitness of a chromosome decides on its ability to prevail within the gene pool. The computation requires a linear method for the appropriate projective transformation with minimal parameters algorithm for the epipolar and 6-point-algorithm for the trifocal geometry. Then, the geometrical image error is determined for all points and a robust cost function is used to measure the fitness.

K. U-MLESAC

Choi and Kim (2008) proposed user independent parameter estimator, U-MLESAC, which is based on MLESAC. It is executed by four steps sampling data, estimating parameters, estimating variables of the error model, and evaluating the parameters according to ML criterion. In contrast MLESAC, U-MLESAC estimates variance of the error model. It also calculates the proper number of iteration according to its terminal criterion. Its terminal criterion is to guarantee that two events happen simultaneously all sampled data belong to inliers and have small noise enough to satisfy error tolerance. The number of iteration can be derived from probabilities of each event. Accuracy and running time can be adjusted by two conditions, failure rate and error tolerance.

U-MLESAC calculates the necessary number of iteration using two conditions, (i) Sampled data are all inliers (ii) they



are within desired error tolerance β . The error function is Gauss error function which is used to calculate a value of Gaussian cumulative distribution function. Coefficient k has physical meaning which is probability that sampled data belong to the error bound β . U-MLESAC can control trade-off between accuracy and running time using two variables α and β .

L. GroupSAC

Ni et al. (2009) introduced Group Sample Consensus (GroupSAC). It is a novel variant of the RANSAC algorithm called GroupSAC. It is much more efficient, in particular when dealing with problems with low inliers ratios. This algorithm assumes that there exists some grouping in the data, based on a new binomial mixture model rather than the simple binomial model as used in RANSAC. Group SAC draw samples from increasing number of groups but is still able to achieve the same random sampling as in standard RANSAC, i.e., each minimum sample set has the same chance being sampled, when the computation budget is exhausted.

More specifically, Group SAC goes through all possible configurations in the order of their cardinalities. Let k be the total number of groups among all the data points, and all the configurations can be divided into $R = \min(m, K)$ subsets $\{C_k\}$, $k=1, \dots, R$, such that

$$C_k = \{G_n \mid |G_n|=k\} \quad (3)$$

Group SAC starts sampling from C_1 until it finally reaches C_R . For each subset C_k , Group SAC goes through each configuration G_u by drawing minimum sample sets from it. By the end of the R^{th} stage, all the configurations will have had their opportunity to be selected. The Group SAC algorithm can be slightly modified to integrate the additional ordering based on the group sizes.

M. LO-MLESAC

Tian et al. (2009) introduced enhancement of MLESAC, the Locally Optimized MLESAC (LO-MLESAC). The LO-MLESAC adopts the same sample strategy and likelihood theory as the previous approach and an additional generalization model optimization step is applied to the models with the best quality.

The MLESAC, the probability density is also used for the classify inliers and outliers and it is satisfies the inequality as follows,

$$\gamma \left(\frac{1}{\sqrt{2\pi}\sigma} \exp\left(-\frac{e^2_i}{2\sigma^2}\right) \right) > (1 - \gamma) \frac{1}{w} \quad (4)$$

The idle number of outer iterations depends on algorithms confidence level $p(\cdot)$ and the inliers ratio γ :

$$I_{\max} = \frac{\log(1-p(\cdot))}{\log(\gamma^m)} \quad (5)$$

The LO-MLESAC algorithm can be summarized as follows.

N. BetaSAC

Antoine et al. (2010) established Beta Sample Consensus (BetaSAC) and it is a strategy for RANSAC sampling with reference to the beta distribution. In the context of sample selection, this method builds a hypothesis set incrementally, selecting data points conditional on the previous data selected for the set. Such a sampling is shown to provide more

suitable samples in terms of inliers ratio but also of consistency and potential to lead to accurate parameters estimation.

BetaSAC differs essentially by the selection random variable $X(t; s)$. In standard RANSAC, the selection is uniform even for $t \leq T_N$. In PROSAC, $d(k)$ stands for the k^{th} data point in a sorting. This sorting is performed once and for all, based on an inliers prior associated to each data point. $g(t)$ is a growth function which limits a uniform selection in a progressively larger set of top ranked data points. Group SAC makes a uniform selection in a configuration defined as a union of predefined data groups

$$G(t) = \{G_i\}, i=1 \dots k. \quad (6)$$

BetaSAC is characterized by its random variable $XBetaSAC(t; s)$, where s is the partial minimal hypothesis set, being built at iteration t . $XBetaSAC(t; s)$ is the result of the selection of the k^{th} data point in a sorting depending on s , where k is a value in $\{1, \dots, N\}$ drawn by the random variable $B_{i(t)/n}$. The use of BetaSAC requires the definition of a scoring function q . It tries two different functions. The first, $q_{\text{matching}}(d)$ is simply the matching score of the correspondence d . The second scoring function is $q_{\text{affine}}(d, s)$. This is the function used in PROSAC framework is defined as

$$q_{\text{affine}}(d, s) = \begin{cases} q_{\text{matching}}(d), & \text{if } |s| = 0 \\ -(\|\alpha - \gamma\delta\|^2), & \text{otherwise} \end{cases} \quad (7)$$

O. INAPSAC

Muthukrishnan and Radha (2012) proposed Improved N Adjacent Point of Sample Consensus (INAPSAC) it is an improvement of NAPSAC with higher dimension. Especially the inliers identification scheme is based on proximity in 3 dimension spheres. If the initial point, X_0 , lies on the manifold, then the rest of the points sampled adjacently will theoretically have a significantly higher probability of being inliers. If there are not enough points within the hyper sphere to estimate the manifold, then that sample is considered a failure.

P. AMSAC

Wang et al. (2013) proposed an Adaptive M-estimator Sample Consensus (AMSAC). Based on AIKOSE, developed a novel robust estimator called AMSAC. It can adaptively compute the inliers scale without requiring a manually tuned threshold. The cost function of AMSAC is written as follows,

$$\mathfrak{R}_{AMSAC} = \sum_{i=1}^n \rho(r_i)^2 \quad (8)$$

$$\rho(r^2) = \begin{cases} r^2, & r^2 < 2.5\hat{S} \\ 2.5\hat{S}, & \text{otherwise} \end{cases} \quad (9)$$

where \hat{S} is obtained by Adaptive Iterative K^{th} Ordered Scale Estimator (AIKOSE). Thus the AMSAC estimator can be written as follows,

$$\theta_{AMSAC} = \arg \min_{\theta} \mathfrak{R}_{AMSAC} \quad (10)$$

Q. ANTSAC

Sebastian et al. (2014) introduced a generic RANSAC variant using principle of Ant Colony Algorithms (ANTSAC). This algorithm is present a new variant of the well-known



RANdom Sample Consensus (RANSAC) algorithm for robust estimation of model parameters. The idea of this method is based on a kind of volatile memory which is similar to the pheromone evaporation in the ant colony optimization algorithm. Therefore, it is called improved RANSAC like algorithm ANTSAC. ANTSAC is computationally efficient and convincingly easy to implement. It turns out that ANTSAC significantly outperforms RANSAC regarding the number of inliers after a given number of iterations. The advantage of ANTSAC increases with the complexity of the problem, i.e., with the number of model parameters, as well as with the relative number of outliers. ANTSAC is entirely generic, such that no further domain knowledge is required, as it is for many other RANSAC extensions. Nevertheless, it shows that it is competitive to state-of-the-art methods even in domain specific scenarios.

As the probability of finding M using the RANSAC algorithm raises with the number of iterations, the Tangential Inliers Probation (TIP) becomes more obvious, but is already noticeable after just a few iterations. To exploit this information during the iterative process need an appropriate memory to store the TIP information for each sample. Additionally, it is also have to modify the selection process in such a way that the TIP is respected profitably. In this approach both requirements are solved through techniques based on the Ant Colony Optimization (ACO) algorithm.

The pheromone level for each sample can be expressed as the probability

$$P(s, t) = \frac{T_s^{\alpha}}{\sum_{s^1 \in S} T^{(s^1)^{\alpha}}} \quad (11)$$

Combining a pheromone memory and probabilistic picking, the ANTSAC algorithm no longer is a pure Monte Carlo method like classic RANSAC, but rather a meta-heuristic search strategy, where the TIP gives some kind of search direction.

R. SSAC

Muthukrishnan and Ravi (2016) discovered S- estimator Sample Consensus (SSAC) it is based on residual scale of M estimation. M estimation is not a function of the overall data because it uses the median as the weights, and it uses S-estimator based residual standard deviation instead of median. According to Salibian and Yohai (2006), the S-estimator is defined by, $\hat{\beta} = \min \beta \hat{\sigma}_s(e_1, e_2, \dots, e_n)$ with determining minimum robust scale estimator $\hat{\sigma}_s$.

The matrix can be written as

$$(X' \phi_i X)^{-1} X' \phi_i Y \quad (12)$$

where ϕ_i is a $n \times n$ matrix with its diagonal elements are the iteratively reweighted. Equation (5.12) is known as iteratively reweighted least squares (IRLS) equation. Solution for this equation gives an estimator for $\hat{\beta}$. This is given by

$$\hat{\beta} = (X' \phi_i X)^{-1} X' \phi_i Y$$

The computational algorithm of SSAC, which is used in the place of sample selection, is as follows:

S. LO-SSAC

Muthukrishnan and Ravi established (2016) locally optimized SSAC (LO-SSAC) it likes LO-RANSAC, LO-MLESAC, an enhancement of SSAC. The mathematical aspects of SSAC procedure is described in [12]. To speed up the process of detecting the maximum of number of inliers, the LO-SSAC is proposed. The IRLS (Iterative Re-weighted Least Square) function,

$$w_i(u_i) = \begin{cases} \left[1 - \left(\frac{u_i}{c}\right)^2\right]^2 & , |u_i| \leq c \\ 0 & , |u_i| > c \end{cases} \quad (14)$$

where $u_i = \frac{e_i}{\sigma_s}$ and $c = 1.547$.

The average number of best sample is

$$\sum_i^k \frac{1}{x} \leq \int_1^k \frac{1}{x} dx + 1 = \log k + 1 \quad (15)$$

It is finite and upper bound as the number of correspondences is discrete. This theoretical bound was confirmed experimentally, the average number of local optimizations over and execution of SSAC.

T. RD-RANSAC

Ravi (2017) proposed a method for detection of outliers which a Robust Distance to be used RANSAC (RD-RANSAC). A novel idea on how to make RANSAC repeatable is presented, which will find the optimum set in nearly run for multi-model. Robust methods are capable of discriminating correspondence outliers, thus, obtaining better results. Our proposed method is an improvement of RANSAC which takes into account additional information of the quality of the matches to largely reduce the computational cost of the pair wise distance estimation by Rousseeuw's Minimum Covariance Determinant (MCD). However, even in quite large samples, the chi-square approximation to the distance of the sample data from the MCD centre with respect to the MCD shape is poor. RANSAC can only estimate one model for a particularly data set. The two or more model exists; RANSAC may fail to find either one. The problem is hard as the number of outlier is usually large, possibly larger than 50%, thus powerful estimation techniques are need. Experiments with up to 80% outlier prove the efficiency of RANSAC. RANSAC is not always able to find the optimum set even for moderately contaminated sets and it usually performs badly when the number of inliers is less. However this work proposes a new robust method for pair wise distance estimation to combine the benefits of RANSAC algorithm, namely improved quality, reduced computational time and less parameter to adjust and powerful estimation techniques up to more than 80% outlier prove the efficiency.

III. EXPERIMENTAL RESULTS

To developed simulation software to investigate it is based on SSAC, LO-SSAC and RD-RANSAC. The user specifies the number of points, the percentage of outliers, the straight line and the measuring precision used for generating the inlier data using TLS model. In addition, the user specifies the required minimum probability for success and the expected error rate, independent of the generation in order to investigate the effect of erroneous assumptions In this section presents the simulation study with result to compare the performance of RD-RANSAC, SSAC, LO-



SSAC, RANSAC and other RANSAC families. This simulation study is carried out for the different number of threshold such as 2 and for various samples sizes, $n=100$, $n=500$ and $n=1000$ with error (ϵ) 5%, 10% and 20%. The data is generated using TLS tools. The number of inliers are estimated using various RANSAC techniques, the results are summarized in the below table

Table 3.1 Inliers Identification under various RANSAC family procedures

Methods	$\epsilon=0.05$			$\epsilon=0.1$			$\epsilon=0.2$		
	Sample size (n)			Sample size (n)			Sample size (n)		
	100	500	1000	100	500	1000	100	500	1000
TLS	95	475	950	90	450	850	80	400	800
LMeDs	94	463	940	88	438	847	78	395	759
RANSAC	94	463	940	88	438	847	78	395	759
ZhangSAC	93	460	926	86	437	841	74	390	745
MLESAC	92	460	931	87	432	843	75	395	755
NAPSAC	93	462	927	87	432	841	76	366	751
R RANSAC-T	91	453	931	85	421	840	71	381	740
R RANSAC-S	91	453	931	85	421	840	71	381	740
FH-MAPSAC	90	452	931	84	427	839	74	385	752
LORANSAC	92	462	932	81	417	841	70	386	753
PROSAC	90	452	932	82	426	834	71	380	758
AMLESAC	91	441	930	81	415	836	72	388	756
GASAC	90	452	931	84	427	839	74	385	752
U-MLESAC	91	459	922	84	429	840	71	384	756
GroupSAC	92	460	911	81	430	841	70	380	758
Lo-MLESAC	91	467	930	85	427	838	69	388	744
BetaSAC	90	466	920	83	424	833	73	378	756
INAPSAC	93	463	928	87	433	842	78	386	752
AMSAC	92	471	934	80	431	840	74	382	748
ANTSAC	91	472	933	82	424	837	77	387	759
SSAC	94	467	942	89	440	848	80	397	763
LO-SSAC	94	466	942	89	441	848	80	397	764
MAPSAC	91	472	933	82	424	837	77	387	759
RD-RANSAC	94	467	942	89	441	848	80	397	764

It is observed from the table, error tolerance and the numbers of inliers are conflicting to each other, if error tolerance increases the number of inliers decreases. Further, it is noted that the TLS, RRANSAC, MLESAC and INAPSAC techniques produces the similar results. But SSAC, LO-SSAC and RD-RANSAC inliers identified similar to each other compared to others method. It is concluded that SSAC, LO-SSAC and RD-RANSAC out performs over the other SAC procedures in the different types of error situations.

IV. CONCLUSION

RANSAC and its descendants are summarized in three viewpoints: accuracy, computing time, and robustness. This paper also describes that completely different methods share the same idea. The results of this experiment were also analyzed in three viewpoints. The results presented a trade-off of accuracy/robustness and computing time. A meaningful research has been performed in RANSAC family, but it needs to investigate more. Balanced accuracy/robustness and computing time can be achieved from merging the previous works or the new breakthrough. Adaptation in variable data is a challenging problem because the previous works do not keep accuracy in low inlier ratio. MLESAC is the first breakthrough which reformulated original RANSAC in the probabilistic view. The new interpretation of the problem can lead another breakthrough. The problem can be incorporated with other problems such as model selection. With data with multiple models is a attractive problem for the current single result formulation. The new tool can stimulate this field such as genetic algorithm of GASAC. Survey and performance evaluation, including the recent works, contributes users to choose a proper method for their applications.

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