RANSAC for (Quasi-)Degenerate data (QDEGSAC)

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Abstract

The computation of relations from a number of potential matches is a major task in computer vision. Often RANSAC is employed for the robust computation of relations such as the fundamental matrix. For (quasi-)degenerate data however, it often fails to compute the correct relation. The computed relation is always consistent with the data but RANSAC does not verify that it is unique. The paper proposes a framework that estimates the correct relation with the same robustness as RANSAC even for (quasi-)degenerate data. The approach is based on a hierarchical RANSAC over the number of constraints provided by the data. In contrast to all previously presented algorithms for (quasi-)degenerate data our technique does not require problem specific tests or models to deal with degenerate configurations. Accordingly it can be applied for the estimation of any relation on any data and is not limited to a special type of relation as previous approaches. The results are equivalent to the results achieved by state of the art approaches that employ knowledge about degeneracies.

1 Introduction

The computation of a relation given sets of potential matches is necessary for many computer vision applications. It is applied for example computing fundamental matrices out of 2D-2D correspondences, projection matrices from 2D-3D correspondences, and 3D homographies from 3D-3D correspondences. The presented framework is not limited to these applications and can also be applied to the estimation of geometric entities like quadrics from 3D points and conics from 2D points. In such estimation problems it is not possible to provide a set of perfect correspondences due to noise in the image data and mismatches caused by ambiguities in the feature descriptions. Accordingly the computation of the relation always has to deal with perturbed data and mismatches called outliers.

The most common technique to deal with outliers in

Figure 1. Two views of the tray scene where most matches are on the plane (tray). Only a few matches are on the candlestick (light gray lines).

the matches is to employ the RANSAC algorithm [2, 7]. It solves the two problems of computing a relation that best fits the data and classifying the data as inliers (correct matches) and outliers. The classification is done by employing a cost function together with a threshold. The relation is selected as the one with the highest number of inliers or the largest robust likelihood [2, 9].

If only degenerate data are given it is not possible to compute the correct relation. Degeneracy means that the data do not provide enough constraints to compute the relation uniquely, but up to a family of relations that all explain the data. For example, for the computation of a fundamental matrix, matches that are on a plane are degenerate data [3] since they only provide constraints to compute a homography. Furthermore the data are often quasi-degenerate which means most data do not provide sufficient constraints to compute the relation uniquely (degenerate data) and only a small fraction of the data provides the remaining constraints. In order to compute the correct relation this small portion of the data has to be incorporated. Hence for quasi-degenerate data the relation can always be uniquely defined, but as explained in Section 3 the RANSAC algorithm has a low probability to compute the correct relation for quasi-degenerate data. Quasi-degenerate data for the fundamental matrix computation can be seen in Figure 1.

The next section reviews the existing techniques for the estimation of relations from (quasi-)degenerate data. Afterwards, Section 3 introduces and reviews the properties of RANSAC in more detail along with the notation used

throughout the paper. In Section 4 we propose a framework to robustly detect degenerate or quasi-degenerate data fully automatically. It selects the appropriate model for the given data without requiring any knowledge about the degeneracies. For quasi-degenerate data it computes the correct relation by using the small portion of the data that provide the remaining constraints in addition to the constraints provided by the degenerate fraction of the data. Accordingly it can be applied to a wide variety of estimation problems. We apply the framework to various estimation problems in computer vision, namely fundamental matrix estimation, projection matrix estimation, 3D homography estimation, and quadric fitting in Section 5. Since the framework is not limited to computer vision it can be employed for all other linear estimation problems.

2   Previous work

Estimating relations on data that contain matches as well as mismatches is a problem in most applications in computer vision. The most popular technique to deal with it is RANSAC introduced by Fishler and Bolles [2]. RANSAC is reviewed in more detail in Section 3.

The problem of degenerate data for the fundamental matrix computation was addressed by Kanatani [4]. Torr introduced a robust extension in [8, 9]. He proposed to employ model selection to overcome the limitations of RANSAC with degenerate data. The goal is to compute the model that explains the given data best by employing knowledge about the degeneracies in the presence of outliers. Torr addressed the case of 2D-2D point correspondences. If these matches are coplanar only a homography can be determined uniquely. The technique proposed by Torr computed a homography and a fundamental matrix for the data. For each of the relations a cost function is applied that measures the robust likelihood of the mapping for the correspondences. Additional penalties are applied for a lower number of constraints provided by a correspondence. For quasi-degenerate data the model selection typically votes for the homography since the cost for it is usually lower than the cost for the fundamental matrix as a result of the small number of off-plane inliers. These non-degenerate inliers are outliers to the homography but their small ratio in the data only slightly increases the cost for the homography. Hence due to the better cost of the homography and the fact that each element determines two degrees of freedom it is still cheaper for quasi-degenerate data than the correct fundamental matrix that has higher penalty for the lower number of constraints determined by each match. Additionally the RANSAC for the fundamental matrix has a low probability to compute the correct epipolar geometry [1] as explained in the next section. The model selection requires two RANSAC's and two nonlinear optimizations of the ro-

bust likelihood one for each relation.

The first RANSAC approach for computing the epipolar geometry that can deal with quasi-planar data was recently introduced by Chum et al. [1]. They employ a criterion to detect degenerate samples during the RANSAC for the fundamental matrix computation by exploiting the knowledge that coplanar points are a degenerate configuration. It was done by examining samples that lead to an epipolar geometry with a higher number of inliers than all previous samples. Such a relation is expected to be a better relation than all previous ones. Then the sample is tested for degeneracy. If it contains too many degenerate inliers, it is extended to contain a sufficient number of non-degenerate inliers if those are available. For non-degenerate data the approach [1] computes the correct epipolar geometry and for degenerate data it chooses the appropriate model. For the fundamental matrix computation this approach represents the state of the art. Note that it requires an explicit test for dealing with the planar degeneracy. Later we will show that our technique provides equivalent results without requiring a specific test for the degeneracy which makes our approach generally applicable to linear model fitting problems with unknown degeneracies.

Tang et al. [6] proposed a tensor voting based approach that poses the problem of estimating the fundamental matrix as one of finding the most salient hyperplane in an eight-dimensional space. It detects (quasi-)degenerate data without prior knowledge but does not produce a fundamental matrix for these cases.

To summarize, the difference between the existing techniques and the proposed algorithm is that existing techniques except [6] require explicit models for the degenerate cases to avoid the computation of ambiguous relations. In contrast to those approaches, our technique does not require any specific knowledge of the degenerate and quasi-degenerate data. It detects cases of degenerate data automatically and chooses the appropriate model. All previous techniques can only be applied to explicitly modeled (quasi-)degeneracies whereas the proposed technique is generally applicable. The proposed technique will be explained in detail in the next section.

3   RANSAC

In the following we briefly summarize RANSAC and explain its behavior for (quasi-)degenerate data as this is important to show the properties of our proposed technique. RANSAC is employed to estimate an n-parametric relation T on the data $\{p\}$. Simultaneously it classifies the data $\{p\}$ into inliers $\{in\}$ and outliers $\{out\}$. It selects m random elements from $\{p\}$ and computes a candidate relation T_c from this random sample. The minimal number $m = \lceil \frac{n}{r} \rceil$ of elements required to compute the relation depends on the

number of constraints r provided by each element and the number n of parameters of the relation.

To achieve a better performance RANSAC often employs linear estimation of the relation T. For a linear estimation we have an linear inlier function f_{in} given by

$$f_{in}(t, w) = \|A_w t\| \text{ with } w \in \{p\} \qquad (1)$$

where the unit vector t represents the relation T and A_w is the matrix containing the data from the match w. The matrix A_w has r linearly independent rows because each match w provides r linearly independent constraints. An inlier to relation T is a data point w for which $f_{in}(t, w) < c_t$. In general a linear equation system is defined from the inlier function f_{in} and data $\{p\}$ by

$$\underbrace{A_w}_{A} t = 0 \text{ with } w \in \{p\}, \qquad (2)$$

where the data matrix $A \in \mathbf{R}^{r|\{p\}| \times (n+1)}$ consists of all sub matrices $A_w \in \mathbf{R}^{r \times (n+1)}$ induced by the matches $w \in \{p\}$. Hence the rows of the data matrix A contain the linear inlier test given by the inlier function f_{in}. The relation t is determined as the nullspace $\mathcal{N}$ of the data matrix A. Hence the data matrix should have a rank r_{A} of at most n to obtain a non trivial solution of (2). Accordingly the dimension r_{n} of the nullspace (codimension) is at least one. For noise free degenerate data the rank r_{A} is reduced to $r_d < n$ as a smaller number of independent constraints is provided by the data and the computed candidate t_c becomes ambiguous. Then the candidate relation T_c is a member of an r_{n} dimensional subspace $\mathcal{N}$ which can be represented by the matrix $N \in \mathbf{R}^{(n+1) \times r_{\text{n}}}$ containing the righthand singular vectors which are a base of the nullspace $\mathcal{N}$.

After the computation of the candidate relation T_c, RANSAC applies it to all given data $\{p\}$ and classifies by thresholding (1) the data in inliers $\{in_c\}$ and outliers $\{out_c\}$. The random sampling is repeated until a sufficient number of samples has been evaluated. The number of required samples S is adaptively determined by exploiting the fraction $\epsilon = \frac{|\{in_c\}|}{|\{p\}|}$ of inliers in the data of the best currently known relation and the desired probability η that a good candidate relation has already been computed. The standard approach consists of stopping the RANSAC when the number of samples S is at least

$$S = \frac{\log(1 - \eta)}{\log(1 - \epsilon^m)}, \qquad (3)$$

where m is the number of elements in the sample. Afterwards the best candidate relation, the one with the most inliers is delivered as relation T_{RANSAC} which best fits the given data. Furthermore it gives the classification of the potential matches $\{p\}$ as inliers $\{in\}$ and outliers $\{out\}$.

In the following for (quasi-)degenerate data we will distinguish between two disjoint sets of inliers. Degenerate inliers are those inliers that are in degenerate configuration. These degenerate inliers do not determine all degrees of freedom of the relation uniquely. Hence the rank of the provided data matrix A_{deg} is always less than n. The set of inliers that are not in degenerate configuration is denoted as non-degenerate inliers. By adding the non-degenerate inliers the relation is uniquely determined. For the fundamental matrix degenerate inliers are all matches that are coplanar and non-degenerate inliers are the off-plane inliers.

| | $\epsilon = 0.9$ | | | | $\epsilon = 0.8$ | | | |
| | $\epsilon_d = 0.85$ | | $\epsilon_d = 0.88$ | | $\epsilon_d = 0.75$ | | $\epsilon_d = 0.78$ | |
	P_{nd}	P_s	P_{nd}	P_s	P_{nd}	P_s	P_{nd}	P_s
F	3%	36%	0.5%	5%	1.4%	47%	0.3%	8%
P	2.1%	19%	0.4%	3%	1.3%	26%	0.2%	4%
H	1.6%	54%	0.7%	9%	1.4%	66%	0.3%	13%
Q	3.6%	12%	0.3%	2%	1.13%	18%	0.2%	3%

Table 1. Probability for a non-degenerate sample P_{nd} and a successful estimation P_s for a RANSAC for quasi-degenerate data (F = fundamental matrix (8-point), P = projection matrix, H=3D homography, Q = quadric).

Samples containing only degenerate inliers give a high number of inliers for (quasi-)degenerate data without providing a sufficient number of constraints to compute all degrees of freedom of the candidate relation T_c. The remaining constraints are determined by the outliers in the sample or the noise in the degenerate inliers. So the robust nullspace[1] $\mathcal{N}$ has dimension $r_n > 1$. Accordingly all these samples contain all degenerate inliers and up to $\left\lceil \frac{r_{\text{n}}-1}{r} \right\rceil$ outliers, where $\left\lceil \frac{r_{\text{n}}-1}{r} \right\rceil$ is the number of elements that can be arbitrarily chosen to fix the remaining $r_{\text{n}}-1$ constraints, e.g. two for the fundamental matrix. The probability $P_{d,s}$ of a sample not providing a sufficient number of constraints is

$$P_{d,s} = 1 - P_{nd}\left(\left\lceil \frac{r_{\text{n}}-1}{r} \right\rceil\right), \qquad (4)$$

where $P_{nd}\left(\left\lceil \frac{r_{\text{n}}-1}{r} \right\rceil\right)$ is the probability to choose $\left\lceil \frac{r_{\text{n}}-1}{r} \right\rceil$ non-degenerate inliers. It is given by:

$$P_{nd}\left(\left\lceil \frac{r_{\text{n}}-1}{r} \right\rceil\right) = \sum_{j=0}^{m-\left\lceil \frac{r_{\text{n}}-1}{r} \right\rceil} \binom{m}{j} \epsilon_d^j (\epsilon - \epsilon_d)^{m-j}, \qquad (5)$$

where ϵ is the inlier fraction in $\{p\}$ and ϵ_d is the fraction of degenerate inliers in $\{p\}$. Accordingly the probability of

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[1]For a sample the data matrix A_{in} is the data matrix induced by only the inliers in the sample. Then the robust nullspace is the space that has the nullvectors belonging to singular values $\sigma_i < \epsilon$ with $i = 1, \ldots, r_{\text{d}}$ of the data matrix A_{in} as base.

RANSAC to succeed is $P_s = 1 - (1 - P_{nd})^S$ with S from (3). Examples of the probabilities P_{nd} and P_s are shown in Table 1 for common estimation problems. Table 1 illustrates the need for an estimation that is robust with respect to (quasi-)degenerate data, since for quasi-degenerate data the probability P_s of RANSAC to compute a correct solution is small.

The relation T_c computed from these samples is an arbitrary element of a family of possible solutions for the degenerate data and fits the degenerate inliers perfectly resulting in a high number of inliers without providing the correct relation T_c. Hence the adaptive termination from (3) stops the sampling too early to have a probability η for the computation of a correct candidate relation T_c.

4 RANSAC for (quasi-)degenerate data (QDEGSAC)

The previous section showed that for (quasi-)degenerate data the standard RANSAC approach is highly unlikely to compute the correct relation. The model selection technique proposed by Torr [8, 9] exploited explicit knowledge about the degeneracies of the fundamental matrix computation without overcoming the problem caused by quasi-degenerate data. The degeneracy test proposed by Chum et al. [1] relies on the availability of a special test for degeneracy to handle quasi-degenerate data correctly. As discussed in Section 2 the rank of the data matrix A can be used to detect degenerate data if they are noise free. The computation of the rank is inaccurate since it is sensitive to noise in the data. The disturbance results in small singular values. Hence it is still possible to estimate the rank by using an appropriate threshold on the singular values. If a sample contains degenerate inliers and outliers the latter increase the rank of the data matrix. That means the rank of the data matrix appears to be equal to the expected rank for the non-degenerate case. So the ambiguity can not be detected by analyzing the singular values of the data matrix.

In this section we propose a new framework, QDEGSAC that employs RANSAC to compute the correct solution including model selection for the given data. The advantage of the novel framework is that it does not require any specific knowledge about the degeneracy, in particular no test is required to detect degenerate samples. Accordingly it can be applied to a wide variety of estimation problems not only to those where the degeneracies are known.

Our framework can be interpreted as a robust measurement of the rank r_A of the data matrix A. It detects automatically and robustly the higher codimension for (quasi-)degenerate data. For degenerate data it selects the right model to represent the data. If the data are quasi-degenerate the novel technique efficiently searches for additional inliers among the initial set of outliers to provide the highest

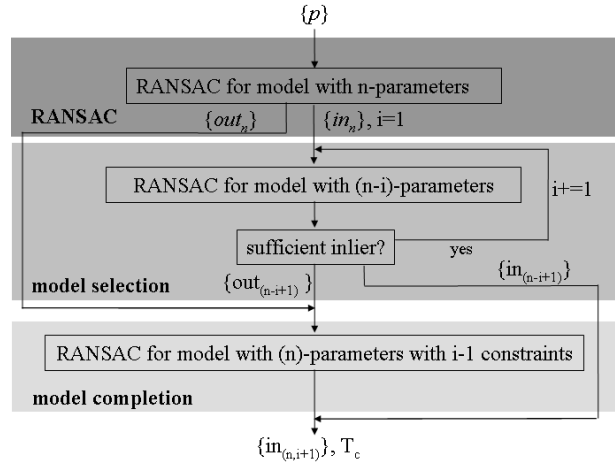possible rank r_A of the data matrix A.

Figure 2. Overview of the QDEGSAC.

The proposed framework consists of three phases as shown in Figure 2. The first RANSAC estimates the full model assuming that the data are not degenerate. The classification of the data into inliers $\{in_n\}$ and outliers $\{out_n\}$ of this process is used for the next two phases. A test for the number of constraints provided by the inliers $\{in_n\}$ is performed. This step is denoted as model selection in Figure 2. The model selection is the robust rank detection in the framework. Afterwards the model completion tests the outliers of the previous phases for non-degenerate inliers to compute the correct relation. In the following we will discuss the details of each phase.

RANSAC A general RANSAC(n) is performed to compute the desired relation T with n-degrees of freedom. Depending on the number n of degrees of freedom of the relation T it will take at least $m = \left\lceil \frac{n}{r} \right\rceil$ elements to compute the n degrees of freedom. The required number of elements m depends on the number r of constraints that are provided by each element. From those samples the data matrix A_s is constructed and used to compute the relation. The RANSAC(n) delivers a relation $T_{RANSAC,n}$ employing n constraints and a classification of the set of potential matches $\{p\}$ in inliers $\{in_n\}$ and outliers $\{out_n\}$. These sets are tested in the following two phases.

For only degenerate data in the sample the codimension r_n is greater than one. This is a result of the insufficient number of constraints provided by the data. In case of quasi-degenerate data in the sample the codimension r_n is one. For degenerate data and outliers in the sample the codimension is also one as the outliers provide the remaining constraints. All samples that contain only degenerate data or degenerate data and outliers commit a high number of inliers as explained earlier. Accordingly the relation $T_{RANSAC,n}$ delivered by the RANSAC(n) does not have probability η to be the correct relation. So often not all degrees of freedom of the relation $T_{RANSAC,n}$ are fixed

through constraints provided by inliers, since those constraints result from noise in the degenerate inliers or from outliers. Please note for non-degenerate data RANSAC(n) will deliver the correct relation T as the codimension r_n is one with a probability depending on the confidence threshold η. The idea of the proposed framework is to detect robustly the case where the codimension r_n is larger than one.

Model selection To determine the codimension a series of RANSACs is performed to estimate relations $T_{RANSAC,dim}$ with a smaller number of constraints $dim < n$. It starts with a RANSAC($n-1$) that lowers the number of constraints n employed for computation by one. That means it determines the relation $T_{RANSAC,n-1}$ by employing the closest rank $n-1$ approximation for the data matrix A_s of each sample. Accordingly RANSAC($n-1$) also uses a smaller number of elements $\tilde{m} = \left\lceil \frac{n-1}{r} \right\rceil \leq m$ in each sample than RANSAC(n) does. The input set for RANSAC($n-1$) is the set of inliers $\{in_n\}$ of the first RANSAC(n). It determines for those inliers $\{in_n\}$ if they can be represented by all relations in the nullspace of the resulting equations.

The evaluation for each potential match in $\{in_n\}$ employs the inlier criterion of RANSAC(n) to check if it is an inlier to all relations in the nullspace. The following theorem gives a necessary and sufficient condition to test this.

Theorem 1 (Inlier to all relations in nullspace) *Given a data matrix A its r_n-dimensional robust nullspace defines a set of relations $\mathcal{N}$. If an inlier w is an inlier to all relations N_j with $j = 1, \ldots, r_\mathrm{n}$ in an orthogonal base of $\mathcal{N}$ with cost $\|A_w N_i\| = c_i$ then its cost is bound by $\sqrt{\sum_{i=1}^{r_\mathrm{n}} c_i^2}$ for all relations $t \in \mathcal{N}$.*

proof: Each relation t in the robust nullspace of A can be written as a linear combination of the base vectors N_j with $j = 1, \ldots, r_\mathrm{n}$. The transformation t is defined by $t = Nn$ where N is the matrix containing the base vectors N_j and n is the unit vector that contains the weights for the base vectors. Then the maximal possible cost $\|A_w t\|$ is the maximum eigenvalue of A_w because $\|t\|$ is one. The cost c_w of the inlier w to a relation $t \in \mathcal{N}$ is

$$c_w^2 = n^T N^T A_w^T A_w N n \leq \sum_{i=1}^{r_\mathrm{n}} c_i^2,$$

because $N^T A_w^T A_w N$ is positive semi-definite its maximal eigenvalue is positive and bound by its trace. The trace is given by $\sum_{i=1}^{r_\mathrm{n}} N_i^T A_w^T A_w N_i = \sum_{i=1}^{r_\mathrm{n}} c_i^2$. $\square$

Theorem 1 shows that the squared algebraic error is bound by the sum of squared algebraic errors observed for the relations in the base of the nullspace $\mathcal{N}$. This means we can decide for each match w if it is an inlier to all relations $t \in \mathcal{N}$ by only computing r_n errors. In practice the c_i are often similar, i.e. c_w^2 is practically bound by $\max_i c_i^2$ and

not by $\sum_{i=1}^{r_\mathrm{n}} c_i^2$. The geometric error behaves similar to the algebraic error for normalized data. So it can also be used for the decision. For the experiments in Section 5 the results of the geometric and the algebraic error were equivalent.

RANSAC($n-1$) tests for all inliers $\{in_n\}$ of the relation $T_{RANSAC,n}$ if they are also inliers to all relations in the robust nullspace of the data matrix A. So if a relation $T_{RANSAC,n-1}$ with fewer parameters receives sufficient support, indicated by the number of inliers $\{in_{n-1}\}$ divided by the number of inliers $\{in_n\}$ of the originally computed relation $T_{RANSAC,n}$, then it follows that the data did not provide a sufficient number of constraints to determine the n degrees of freedom of $T_{RANSAC,n}$. If the relation does not have sufficient support in the inliers $\{in_n\}$, the data $\{in_n\}$ provided n constraints. The process of reducing the number of constraints exploited to compute the relation $T_{RANSAC,n-1}$ is continued until the relation $T_{RANSAC,n-i}$ does not have a sufficient support in the inliers $\{in_n\}$. Sufficient is determined by t_{red} as ratio of the inliers $\{in_{n-i}\}$ of RANSAC($n-i$) to the inliers $\{in_n\}$ of the first RANSAC(n). As we will see later, the technique is not sensitive to the ratio t_{red} and it can be safely chosen in a range of $50\% - 80\%$ without significant impact.

If a relation that cannot represent the inliers $\{in_n\}$ is found the appropriate model for the inliers $\{in_n\}$ has been computed in the previous step $i-1$. It has $n-i+1$ degrees of freedom and a codimension of $i-1$. The successive reduction of the number of constraints used to compute the relation determines how many constraints are delivered by the inliers $\{in_n\}$. At this point the model selection is finished and the model is the relation family that is orthogonal to the constraints provided by the inliers $\{in_n\}$.

The computational cost of each of the RANSACs except from the last one is smaller than the cost of the first RANSAC(n). It results from the fact that the set of potential matches is the set of inliers $\{in_n\}$ of the first RANSAC and the inlier fraction is comparably high for degenerate data. It follows from (3) that the number of steps as well as the number of evaluations needed to decide between outliers and inliers is lower than for the first RANSAC(n). So the computation is less than i-times the cost of the first RANSAC(n).

The computationally most expensive RANSAC is the RANSAC($n-i$) that can not find a relation that represents the inliers of RANSAC(n). It requires S_{n-i} iterations according to (3), with

$$S_{n-i} = \frac{\log(1-\eta)}{\log(1 - t_{red}^q)} \text{ with } q = \left\lceil \frac{n-i}{r} \right\rceil. \quad (6)$$

The threshold t_{red} influences the runtime of RANSAC($n-i$) as it is the minimum required inlier ratio. According to (6) the RANSAC($n-i$) needs a significant number of trials to prove that the inliers are not supported by a relation

computed by employing $n - i$ constraints.

Model completion After finishing the model selection for quasi-degenerate data it is still possible to find the correct n-parametric relation employing data that is not covered by the selected model. These data are usually only a small fraction of the data $\{p\}$. Accordingly the low probability to select those non-degenerate inliers often leads to an ambiguous relation $T_{RANSAC,n}$ during the RANSAC(n). The model selection provides a restrictive model which classifies the data $\{p\}$ into degenerate inliers $\{in_s\}$ and outliers $\{out_s\}$. The degenerate inliers $\{in_s\}$ provide a data matrix A_{deg}. The model completion uses the closest rank $n - i + 1$ approximation of A_{deg} and extends that with the A_w matrices coming from a RANSAC with samples of size $\lceil \frac{i-1}{r} \rceil$ from the outliers $\{out_s\}$.

To summarize, the novel framework first performs a RANSAC to find a transformation that explains the data. Afterwards the codimension of the data matrix from the inliers is estimated robustly. It determines a larger codimension for degenerate data even if outliers determine free constraints. Finally the framework inspects the data for inliers that provide the remaining constraints to compute the n-degrees of freedom of the relation T.

5   Experimental results

In this section we apply our novel framework to various estimation problems in computer vision. First the estimation of the epipolar geometry is shown for (quasi-)degenerate data. Afterwards, the estimation of the camera projection matrix, the estimation of 3D homographies as well as the estimation of quadrics for (quasi-)degenerate data are discussed.

The QDEGSAC technique was tested on three images of the tray scene, two of which are shown in Figure 1. The 365 potential point triplets were established with the wide baseline SIFT-feature matching technique of [5]. It contains 337 matches on the dominant plane (tray). Only 11 matches are off-plane on the candlestick. The latter matches have to be employed to compute the correct relations.

Fundamental matrix estimation   QDEGSAC uses a linear eight point algorithm for the estimation of the fundamental matrix [3]. For all experiments we assume an algebraic error comparable to an average distance of 1.5 pixel to the epipolar line in the image for inliers. The threshold t_{red} was set to 70% and η was set to 99%.

First we tested QDEGSAC on the tray scene shown in Figure 1, for which the predicted probability of computing the correct epipolar geometry with RANSAC is $P_{nd} = 1.7\%$ and the probability P_s of a successful RANSAC is $P_s = 12\%$. For the eight point algorithm the codimension is three for coplanar matches [3, page 281]. instead of one. Hence the computed relation has six linearly indepen-

(a)   (b)

Figure 3. (a) Correct epipolar geometry computed by QDEGSAC valid for all points. (b) Epipolar geometry computed by RANSAC only valid for points on the tray (plane).

dent constraints. Figure 3(b) shows one example of a wrong epipolar geometry computed by RANSAC(8) due to degenerate data. The epipolar geometry computed by QDEGSAC is shown in Figure 3(a).
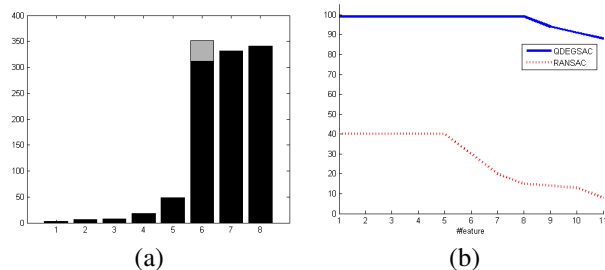

(a)   (b)

Figure 4. (a) Number of inliers (y-axis) for different numbers of employed constraints (x-axis), with $t_{red} = 0$. For six constraints the additional inliers found by QDEGSAC are stacked. (b) Number of classifications as inlier for off plane inliers for 100 QDEGSAC executions.

The QDEGSAC algorithm was executed one hundred times on the potential matches. For the 11 not coplanar matches the number of detections as inlier was counted and are shown in Figure 4(b) as well as the number of inliers for the models with different number of employed constraints. The evaluation shows that the QDEGSAC always found the correct solution in contrast to the traditional RANSAC that had success in 17% of the runs. Furthermore it always detected the six linear constraints provided by the degenerate inliers. Figure 4(a) shows that the framework is not sensitive to t_{red} which was set to zero for the chart. The range of t_{red} could be between 20% and 80% without influencing the result.

QDEGSAC needs for this scene about 4-7 trials in the first RANSAC(8). The RANSAC(7) and RANSAC(6) need together 4 trials according to the high inlier probability in $\{in_8\}$. The unsuccessful RANSAC(5) needs 26 samples according to (3) and $t_{red} = 70\%$. The RANSAC for model

completion needs up to 28 samples. For non-degenerate data the required overhead would have been 54 RANSAC samples for an unsuccessful RANSAC(7).
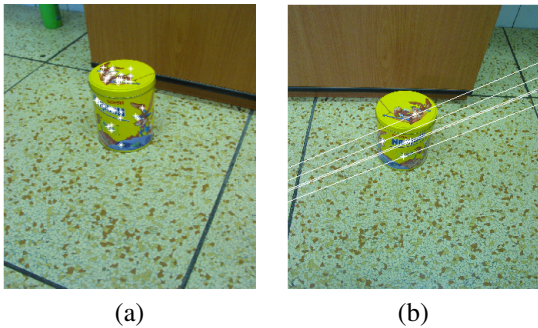

(a)   (b)

Figure 5. Example from [1] of a scene that mostly contains features on one plane (ground plane). (a) Off plane inliers used by QDEGSAC to compute the correct epipolar geometry shown in (b).

The problem of the estimation of the fundamental matrix from (quasi-)degenerate data has been addressed by Chum et al. [1] on the data shown in Figure 5(b). They determined the rate of detection for the off-plane inliers in one hundred runs. The detection rate of their algorithm is shown in Figure 6(b). The proposed QDEGSAC algorithm was tested on the same set of matches and the detection rate is also shown in Figure 6(b). The comparison shows that QDEGSAC achieves the same results as the technique from [1] without incorporating any knowledge about the degeneracy. The computed epipolar geometry for the box scene is shown in Figure 5(a)-(b).
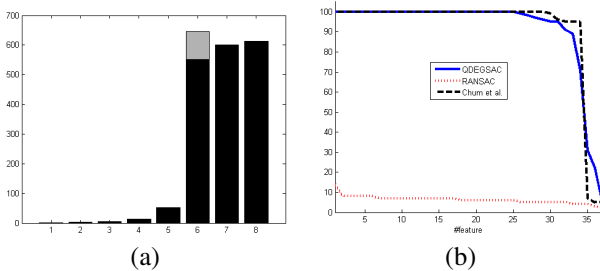

(a)   (b)

Figure 6. (a) Number of inliers (y-axis) for different numbers of employed constraints (x-axis). For six constraints the additional inliers of QDEGSAC are stacked. (b) Comparison for detection of the off plane inliers.

The model selection of Torr [8, 9] tests for coplanar matches for which a homography is computed. Otherwise the fundamental matrix is computed. For the decision the GRIC criterion [8] is employed. We computed the GRIC for both transformations on the tray scene. The GRIC $GRIC_F$

for the fundamental matrix was computed for the fundamental matrix computed by the first RANSAC(8) in the framework and was $GRIC_F = 250.27$ for the potential matches $\{p\}$. The $GRIC_F$ is only slightly decreased for the correct epipolar geometry as expected. The GRIC for the homography was $GRIC_H = 45.12$. Hence the model selection would always decide on a homography for the tray scene whereas our framework is able to compute the epipolar geometry without knowledge about the potential degeneracies. Therefore, while [8] works well for degenerate data, it can not deal with quasi-degenerate data.

Projection matrix estimation The linear estimation of the projection matrix also suffers under 3D points lying on a 3D world plane. The techniques proposed in [1, 9] can be extended to detect coplanar points which is one of the known degenerate cases. In this section we apply the novel framework for the linear estimation of the projection matrix. The experiments used the tray scene from Figure 1.
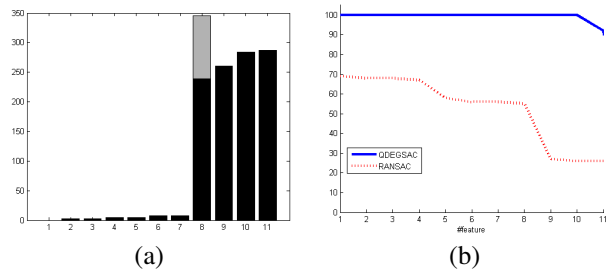

(a)   (b)

Figure 7. (a) Number of inlier (y-axis) as a function of the number of employed constraints (x-axis) for the computation of P. (b) Comparison of detection rates (y-axis) for QDEGSAC and RANSAC for the off plane inliers on the tray scene

The projection matrices of the first two cameras where deduced from the fundamental matrix estimated employing our novel frame work. The 3D points are triangulated from the first two images of the scene. These 3D points where used to estimate the projection matrix of the third view.

To evaluate the performance of the novel technique we perform 100 estimations on the 2D-3D matches and count the number of detections for the off plane inliers (on the candlestick). The detection rates are shown in Figure 7.

It can be seen that the estimation employing the new framework overcomes the problem of the traditional RANSAC. The off-plane inliers are always detected as inliers and the estimated projection matrix is always correct. The reprojection errors for QDEGSAC and traditional RANSAC are shown in Figure 8.

The new proposed framework always detects the greater codimension of the data matrix of four instead of one. The detection is robustly performed regardless of the projection matrix extracted in the first RANSAC. The tests with the

(a)   (b)

Figure 8. (a) reprojection error for the projection matrix estimated with QDEGSAC (b) reprojection error of a RANSAC solution.

projection matrix show that our proposed framework detects the case of degenerate data robustly and always computes the correct projection matrix in contrast to the traditional RANSAC which only computes it in 27% of the runs.

3D homography estimation The proposed framework is also applied to the linear estimation of a 3D homography that maps 3D points to 3D points. We apply it again to the tray scene from Figure 1 to establish two projectively skewed scenes. The first scene is triangulated from view one and view two, and the second scene was established from the second and the third view. The coplanar points are also a degenerate configuration for the computation of the 3D homography. The proposed framework showed a similar behavior for detection of off-plane inliers as for the estimation of the fundamental matrix and the projection matrix for one hundred runs of QDEGSAC. The graph for the measurements is not included due to the lack of space. The framework detects the eleven degrees of freedom provided by the degenerate inliers on the plane. Afterwards the four missing constraints provided by the non-degenerate inliers are used to compute the correct 3D homography. In one hundred runs the traditional RANSAC was successful in about 13% of the runs whereas QDEGSAC always computed the correct 3D homography.

Quadric estimation The previous paragraphs evaluated the novel framework on the estimation of relations frequently employed in computer vision applications. The linear estimation of quadrics from 3D points is also done with the framework. It is done for a quadric defined by two planes. Most potential matches are on one plane and only 2% of the potential matches $\{p\}$ are on the second plane. The latter have to be employed to determine the quadric uniquely. The given 1000 potential matches contain 88% degenerate inliers and 10% outliers. The degenerate and non-degenerate inliers are disturbed with Gaussian noise with a standard deviation 2% of the bounding box. We observe a similar behavior for the detection of non-degenerate inliers in one hundred QDEGSAC runs as for all previous experiments. The traditional RANSAC only computed the correct quadric once in one hundred runs

whereas QDEGSAC always computed the correct quadric. QDEGSAC always detected the reduced rank of six instead of nine of the data matrix.

6 Conclusion

We have introduced a new framework for the robust computation of a relation from (quasi-)degenerate data. The framework simultaneously classifies the data into inliers and outliers with regard to the relation. The novel technique evaluates the computed model in contrast to traditional RANSAC. For degenerate data an appropriate model is chosen. For quasi-degenerate data the small fraction of the data that provides the necessary additional constraints is identified. Accordingly the computation does not suffer from ambiguities. We also show the wide field of applications of the framework. Finally we compare our technique with the existing techniques for the special case of the fundamental matrix computation. This comparison showed that our approach performed as well as the state of the art while being more generally applicable.

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