

LTSD: A Highly Efficient Symmetry-Based Robust Estimator

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Abstract

Although the least median of squares (LMedS) method and the least trimmed squares (LTS) method are said to have a high breakdown point (50%), they can break down at unexpectedly lower percentages of outliers when those outliers are clustered. In this paper, we investigate the breakdown of LMedS and the LTS when a large percentage of clustered outliers exist in the data. We introduce the concept of symmetry distance (SD) and propose an improved method, called the least trimmed symmetry distance (LTSD). The experimental results show the LTSD gives better results than the LMedS method and the LTS method particularly when there is a large percentage of clustered outliers and/or a large standard variance in the inlier population.

1. Introduction

To fit a model to noisy data (with large numbers of outliers) is a common task within the computer vision. Since it is unavoidable that data will be contaminated we require that all algorithms be robust for accurate estimation [2]. Robust regression methods can tolerate gross errors (outliers) [1][5].

The most common form of regression analysis is the least squares (LS) method, which can achieve optimum results when data are corrupted by Gaussian distributed noise. However, this method is extremely sensitive to outliers (gross errors) and will break down when outliers exist in the data.

Robust estimators with high breakdown point have been developed during the past three decades [1][7][8][16]. The least median of squares (LMedS) estimator and the least trimmed squares (LTS) estimator are the two most popular methods. The LMedS method and the LTS method are based the idea that the correct fit will correspond to the one with the least median of residuals (for LMedS) or the least sum of trimmed squared residuals (for LTS). This is true if the data are not contaminated or are contaminated by outliers which are not highly clustered. When large numbers of clustered outliers exist in the data, both LMedS and LTS may not fit the data correctly. The reason is that both LMedS and LTS only consider the residuals of the data points while they neglect other important characteristics of the model. Due to the affects of clustered outliers, the correct fit does not necessarily correspond to the fit with the least median of squared residual (for LMedS) or the least trimmed squared residuals (for LTS).

Symmetry is very common and important in our world [19-32]. When we will fit circles, ellipses, or any symmetric object; one of the most basic features is symmetry. We introduce symmetry into robust model fitting, producing a method that works better than LMedS and LTS under a large number of clustered outliers.

2. Robust estimators

The classical linear model can be described in the followed form:

$$y_i = x_{i1}\theta_1 + \dots + x_{ip}\theta_p + e_i \quad (i = 1, \dots, n) \quad (2.1)$$

the error term e_i is usually assumed to be normally distributed with mean zero and standard deviation σ .

The ordinary least squares method [3] estimates $\hat{\theta}$ by

$$\min_{\hat{\theta}} \sum_{i=1}^n r_i^2 \quad (2.2)$$

where the residual $r_i = y_i - x_{i1}\hat{\theta}_1 - \dots - x_{ip}\hat{\theta}_p$.

Although the LS method has low computational cost and high efficiency, it is very sensitive to outliers. In fact, only one single outlier can affect the result to a large degree. In order to reduce the influence of outliers, a number of robust estimators have been developed. Among these estimators, the maximum-likelihood-type estimators, i.e. the M-estimators, are best known [4][5].

2.1 M-estimators

The essence of the M-estimator is to replace the squared residuals r_i^2 by another function of the residuals:

$$\min_{\hat{\theta}} \sum_{i=1}^n \rho(r_i) \quad (2.3)$$

where ρ is a symmetric, positive-definite function with a unique minimum at zero.

Different choices of $\rho(r_i)$ will yield different M estimators. Unfortunately, it has been proved that M estimators have a breakdown point of at most $1/(p+1)$, where p represents the dimension of parameter vector [1][6]. This means that the breakdown point will diminish when the dimension of parameter vector increases.

2.2 The repeated median method

Before the repeated median estimator, it was controversial that if it was possible to find a robust estimator with a high breakdown point. In 1982, Siegel

proposed the repeated median (RM) estimator with a high breakdown point of 50%[7].

The repeated median method can be summarized as follows: For any p observations, $(x_{i1}, y_{i1}), \dots, (x_{ip}, y_{ip})$.

The parameter vector $\hat{\theta} = (\hat{\theta}_1, \dots, \hat{\theta}_p)^t$ can be calculated from the given data points. The j th coordinate of this vector is denoted by $\theta_j(i_1, \dots, i_p)$. Then the repeated median estimator is defined as

$$\hat{\theta} = \underset{i_1}{\text{med}}(\dots(\underset{i_{p-1}}{\text{med}}(\underset{i_p}{\text{med}} \theta_j(i_1, \dots, i_p)))\dots) \quad (2.4)$$

The time complexity of the repeated median estimator is $O(n^p \log^p n)$, which prevents its application to even relatively simple tasks such as conic fitting.

2.3 The least median of squares method

In 1984 Rousseeuw proposed the least median of squares (LMedS). The LMedS family has excellent global robustness and a claimed high breakdown point (50%). In a relatively short time, the LMedS estimator has been widely applied in computer vision problems.

The LMedS method is based on the simple idea whereby one replaces the sum in least sum of squares by a median. Mathematically, the LMedS is given by

$$\min_{\hat{\theta}} \text{med}_i r_i^2 \quad (2.5)$$

The solution of the LMedS can only be given by an exhaustive search. In order to reduce the time complexity of the LMedS method to a feasible value, the Monte Carlo type technique is adopted.

If a p -subset consists of p good observations without contamination by outliers, the p -subset is "clean". One performs, m times, random selections of p -tuples so that the probability P that at least one of the m p -tuples is "clean" is almost 1. Let ε be the fraction of outliers contained in the whole set of points. The probability P can be expressed as follows:

$$P = 1 - (1 - (1 - \varepsilon)^p)^m \quad (2.6)$$

In order to find the best solution corresponding to the p -tuple which yields the approximately minimized value, P is required to be near 1. Accordingly, one can determine m for given values of ε , p and P by

$$m = \frac{\log(1 - P)}{\log[1 - (1 - \varepsilon)^p]} \quad (2.7)$$

If there are 50 percent of data contaminated by outliers, i.e. $\varepsilon = 0.5$, and we require $P = 0.99$, then, for circle fitting ($p=3$), we get $m=35$; for ellipses fitting ($p=5$), we get $m=145$.

2.4 The least trimmed squares method

The least trimmed squares (LTS) method has better statistical efficiency and local stability than the LMedS [8][1]. The LTS estimator is given by:

$$\min_{\hat{\theta}} \sum_{i=1}^h (r^2)_{i:n} \quad (2.8)$$

where $(r^2)_{1:n} \leq \dots \leq (r^2)_{n:n}$ are the ordered squared residuals, h is the trimming constant - which can be set to a value in the range from $n/2$ to n . Thus there will be

h data points, out of n , used to estimate the parameters. LTS also employs the random sampling technique.

Generally speaking, there are two possible ways to yield the h -subsets:

1. Directly yield a random h -subset from the data points n .

2 Firstly generate a random p -subset. If the rank of this p -subset is less than p , randomly add data points until the rank is equal to p . Next, use this subset to compute parameters $\hat{\theta}_j$ ($j=1, \dots, p$) and residuals r_i ($i=1, \dots, n$). Sort the residuals into $|r(\pi(1))| \leq \dots \leq |r(\pi(h))| \leq \dots \leq |r(\pi(n))|$, and h -subset is set to: $H = \{\pi(1), \dots, \pi(h)\}$.

Usually, a h -subset generated by method (1) more likely includes outliers than if it is generated by method (2).

2.5 Breakdown of LMedS And LTS

Consider the contaminated distribution [18][2]:

$$F = (1 - \varepsilon)F_0 + \varepsilon H \quad (2.9)$$

where F_0 is an inlier distribution, and H is an outlier distribution. When the standard variance of F_0 is small ($\ll 1$) and that of H is large or H is uniform distributed, the estimated parameters with the least median of the squared residuals (for LMedS) or the least sum of trimmed squared residuals (for LTS) will correspond to the correct fit. However, when the standard variance of F_0 is big, and H is clustered distributed with high density, the case above is not always true again. Let us see an example:

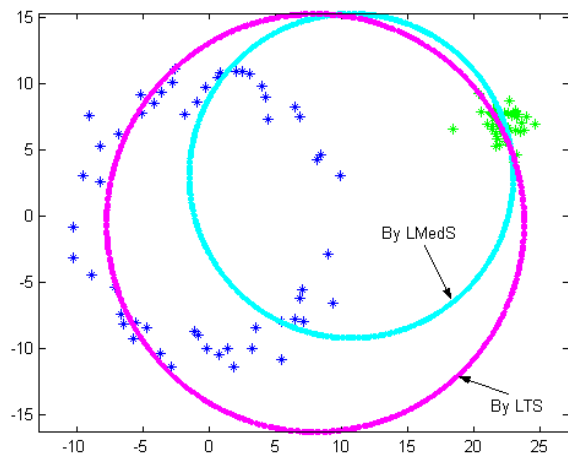


Fig.1 An example where the LMedS and LTS methods fail to fit a circle under clustered outliers residuals.

In figure 1, a total 100 data were generated. The inliers F_0 had 55 data points with radius 10.0 and a center at (0.0,0.0). F_0 has one unit variance. 45 clustered outliers were added possessing a spherical bivariate normal distribution with one unit standard variance and a mean of (22,7). As shown in figure 1, both LMedS and LTS failed to fit the circle: LMedS resulted in a fit with a radius of 12.2430 and center at (10.7113, 3.0125); the results obtained by LTS were that radius equalled 15.7822 and center was at (8.0017, -0.5369).

Let us check the median of the residuals (for LMedS) and the sum of the trimmed squared residuals (for LTS) and we will find that fits that minimize these criterion do not always reflect the true case when clustered outliers exist in the data. The median of residuals of the true fit is 1.5169. However the median of residuals of the final result by the LMedS method is 1.2493. In fact, during the searching procedure, the LMS estimator missed the “good” fit and choose a fit with even smaller median – as it was designed to do!

The reason that LTS failed is similar. LTS finds the fit with the smallest trimmed squared residuals. For the estimate it produced, the sum of trimmed squared residuals is 13.0237. However, that statistics for the true fit is 30.6820!

From the discussion above, we now see the reason that LMedS and LTS failed to fit the circle is they pay attention only to choosing the fit with the least median of residuals or the least sum of trimmed squared of residuals, omitting other characteristics of the data. Thus the resulting fits lost the most basic and common feature of circle—symmetry.

3. The symmetry distance

Symmetry exists almost everywhere in the world. A square, a cube, a sphere, and a lot of geometric patterns show symmetry. Architecture usually adopts symmetry. Symmetry is also an important parameter in physical and chemical processes and is an important criterion in medical diagnosis. Even we human beings show symmetry, (for instance, our faces and bodies are roughly symmetrical between right and left). Symmetric data should suggest symmetric models and data that is symmetrically distributed should be preferred as the inlier data (as opposed to the outlier. Considerable efforts have been focused on the detection of symmetry in images in regard to mirror symmetries [22][23] and in regard to circular symmetries [24][25]. Kirby etc. used the symmetric features of images for image compression [26]. Zabrodsky treated symmetry as a continuous feature and applied it in finding the orientation of symmetric objects [21]. Skewed symmetries in 3D structures have been extensively studied [28][29][30]. Symmetry has also been treated as a feature in cluster analysis [27]. We demonstrate here that symmetry can also be used as a feature to enhance the performance of robust estimators when fitting models with symmetric structure.

3.1 Definition of symmetry

There are many kinds of symmetry existing in the world. Generally speaking, symmetry can be classified into the followed basic types [20][21].

1. Mirror-symmetry: if an object is invariant under a reflection about a line (for 2D) or a plane (for 3D).
2. C_n -symmetry: if an object is invariant under rotation of $\frac{2\pi}{n}$ radians about its center (for 2D) or a line passing through its center (for 3D).

3. D_n -symmetry: if an object has both mirror-symmetry and C_n -symmetry.

4. Circular-symmetry: If an object has C_∞ -symmetry.

3.2 The symmetry distance

The exact mathematical definition of symmetry [31][32] is insufficient to describe and quantify symmetry found both in the natural world and in the visual world.

Su et al. [27] proposed a non-metric distance measure based on the concept of “point symmetry”. Given n points x_i , $i=1, \dots, N$ and a reference vector C (e.g. the centroid of the data), the point symmetry distance between a point x_j and C is defined as follows:

$$d_s(x_j, C) = \min_{\substack{i=1, \dots, N \\ \text{and } i \neq j}} \frac{\|(x_j - C) + (x_i - C)\|}{\|x_j - C\| + \|x_i - C\|} \quad (3.1)$$

From (3.1) we can see that the point symmetry distance is non-negative definition. When $x_i = (2C - x_j)$ exists, $d_s(x_j, C) = 0$.

However, according (3.1), one point could be used repeatedly as the “balancing point” with respect to the center. This does not seem to properly capture the notion of symmetry. In order to avoid one point being used as a “symmetric point” more than one time by other points, we refine the point symmetry distance between a point x_j and C as follows:

$$D_s(x_j, C) = \min_{\substack{i=1, \dots, N \\ \text{and } i \neq j \\ \text{and } i \notin \mathfrak{R}}} \frac{\|(x_j - C) + (x_i - C)\|}{\|x_j - C\| + \|x_i - C\|} \quad (3.2)$$

where \mathfrak{R} is a set of points that have been used as “symmetric point”. We propose a non-metric Symmetry Distance (SD):

$$SD(x, C) = \frac{1}{n} \sum_{i=1}^n D_s(x_i, C) \quad (3.4)$$

When the SD of a pattern is equal to 0.0, the pattern is perfectly symmetric; when the SD of a pattern is very big, the pattern has little symmetry.

4. The proposed method

In this paper, we present a novel robust method, we call LTSD, employing symmetry distance. We consider symmetry distance as its criteria. The steps of the LTSD method is described as follows:

Step 1. Initialise h with $[(n+p+1)/2] \leq h \leq n$ and the repetition count rt .

Step 2. Randomly choose p -subset, and extend to a h -subset H_1 by the method (2) in subsection 2.4

Step 3. Compute $\hat{\theta}_1$ by the LS method based on H_1 .

Compute symmetry distance SD_1 based on $\hat{\theta}_1$ and H_1 using (3.2) in section 3 and using the centre of the fit (circle or ellipse) as the reference vector C . Decrement rt and if rt is smaller than 0, go to step 4, otherwise, go to step 2. We calculate the parameters $\hat{\theta}$ based on a h -

subset instead of a p-subset in order to improve the statistical efficiency.

Step 4. Output $\hat{\theta}$ with the lowest SD.

5. Experimental results

In this section, we will show several examples using the proposed method to fit a model with symmetrical structures. Circle fitting and ellipses fitting have been very popular topics in the computer vision field. One of the obvious characteristics of circles and ellipses is that they are symmetric. We first present an example of circle fitting, to provide insights into the proposed method. We then present a relatively more complicated example of ellipses fitting. The results are compared with those of the LMedS method and the LTS method.

5.1 Circle fitting.

As shown in figure 1, 45 percent of clustered outliers were added to the original data. Because the LMedS and the LTS only paid attention to the residuals of the data points, their results were affected by the standard variance of the inliers and density of the clustered outliers. Therefore, they failed to fit the circle under a high percentage of clustered outliers. However, the proposed method pays attention not only to the residuals of the data, but also the symmetry of the object, this makes it find the right model (see figure 2.)

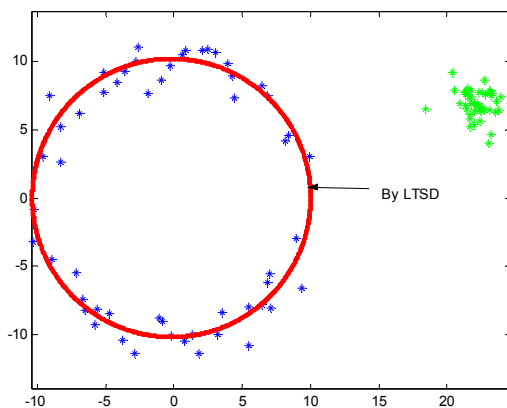


Fig. 2 Using the symmetry feature of the circle, the proposed the method found the approximately right results.

LTSD is more stable, when there is a large variance of inliers, than LMedS and LTS. When the variance of inliers is large, LMedS and LTS will fail to fit the model by their criteria. LTSD, because it considers both the residuals and the symmetry if the data, can still correctly estimate the model. If we change the variance σ of the inliers (F_0), while the 45% clustered outliers are drawn from a spherical bivariate normal distribution with one unit standard variance and mean (22,7), then we can get table 1. As shown in table 1, when the variance of inliers σ was small (e.g. 0.4), all three methods got the correct results. However, when σ was increased to 0.7,

LTS first failed to fit the circle. In this case, both LTSD and LMedS correctly fitted the circle. When σ was 1.0 or 1.3, only LTSD correctly found the circle; LMedS and LTS both failed to fit the circle.

	σ	Xc (0.0)	Yc (0.0)	R (10.0)
LTSD	0.4	-0.3083	0.1879	9.9479
LTS		-0.2055	0.1366	9.8954
LMedS		-0.2098	0.1342	9.9248
LTSD	0.7	-0.0699	0.0142	10.3030
LTS		7.4093	-19.2381	29.8931
LMedS		-0.0965	0.1501	10.1212
LTSD	1.0	-0.2510	-0.2106	9.8444
LTS		13.6641	21.8484	17.3485
LMedS		14.9724	7.4475	7.4507
LTSD	1.3	0.8147	-0.0503	9.8923
LTS		2.3155	11.7841	19.9118
LMedS		13.9648	9.2348	8.2795

Table 1. Comparison of the estimated parameters by LTSD, LTS, and LMedS in circle fitting under 55% inliers with different variance σ (and all having 45% clustered outliers).

5.2 Ellipses fitting.

Ellipses often occur in geometric shapes. Round objects and circles may be projected into ellipses in the perspective projection model. Thus ellipses are frequently used in computer vision for model matching. A general conic equation can be written as follows:

$$ax^2 + bxy + cy^2 + dx + ey + f = 0$$

(a,b,c,d,e,f) are the parameters needed to find from the given data. When $b^2 < 4ac$, the equation above corresponds to ellipses.

The ellipse can also be represented by its more intuitive geometric parameters:

$$\frac{(x \cos \theta + y \sin \theta - x_c \cos \theta - y_c \sin \theta)^2}{A^2} + \frac{(-x \sin \theta + y \cos \theta + x_c \sin \theta - y_c \cos \theta)^2}{B^2} = 1$$

where (x_c, y_c) is the center of the ellipse, $\{A,B\}$ are the major and minor axes, and θ is the orientation of the ellipse.

The relation between (a,b,c,d,e,f) and (x_c, y_c, A, B, θ) is

$$\begin{cases} x_c = \frac{be - 2cd}{4ac - b^2} \\ y_c = \frac{bd - 2ae}{4ac - b^2} \\ \{A, B\} = 2 \sqrt{\frac{-2f}{a + c \pm f \sqrt{b^2 + \left(\frac{a-c}{f}\right)^2}}} \\ \theta = \frac{1}{2} \tan^{-1} \frac{b}{a-c} \end{cases}$$

We found it is convenient to find (a,b,c,d,e,f) first by the given data and then convert to (x_c, y_c, A, B, θ) . 200 data were generated with 50% clustered outliers. The outliers were compacted within a region of radius 5 and center at (20.0, 5.0). The inliers had a standard variance 0.8, major axis 10.0, minor axis 8.0, and center (0.0,0.0).

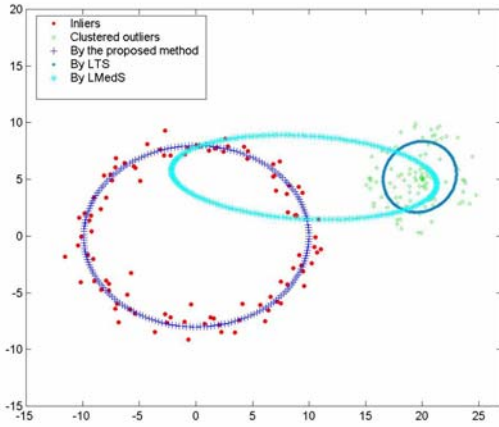


Fig. 3 Comparison of the results obtained by the proposed method, LTS and LMedS in ellipses fitting under 50% clustered outliers.

	x_c	y_c	A	B	$\theta(\text{deg})$
True value	0.0	0.0	10.0	8.0	0.0
The proposed method	0.032	-0.020	9.948	7.978	0.307
The LTS method	19.786	5.162	3.328	3.035	34.129
The LMedS method	9.560	5.208	11.757	3.679	-3.307

Table 2. Comparison of the estimated parameters by the proposed method, LTS, and LMedS in ellipses fitting under 50% clustered outliers.

As illustrated in figure 3 and Table 2, LTS and the LMedS were seriously affected by the clustered outliers. However, the proposed method worked well.

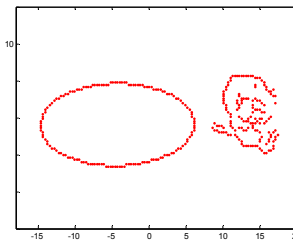
Next we use pad shown in figure 4. The edge image was obtained by using Canny operator with threshold 0.07. In total, 310 data points were in the edge image (fig. 4(b)). The clustered outliers, due to the flower, occupy 50% of the data. As shown in figure 4(c), both the LTSD and the LTS correctly found the edge of the mouse pad. However, the LMedS fails to detect the edge of the mouse pad. This is because he statistical efficiency of the LTS is better than the LMedS.

Figure 5 shows how to use the LTSD method to fit an ellipse to the rim of a cup. Fig. 5 (a) gives a real cup image. After applying the Prewitt operator, the edge of the cup is detected is shown in fig. 5 (b). We can see there is a high percentage (about 45%) of clustered outliers existing in the edge image, external to the rim of the cup (the ellipse we shall try to fit), mainly due to the figure on the cup. However, the rim of the cup has a

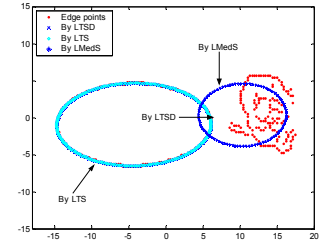
symmetric elliptical structure. Fig. 5 (c) shows that the LTSD method correctly finds the ellipse in the opening of the cup, while both the LTS and the LMedS fail to correctly fit the ellipse.



(a)



(b)

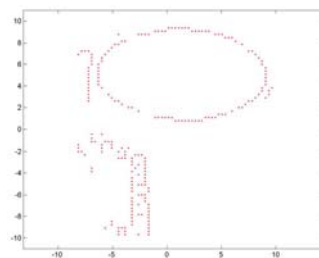


(c)

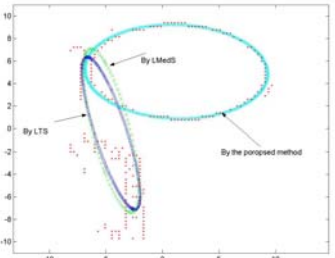
Fig. 4 Fitting a mouse pad: (a) a mouse pad with some flowers; (b) the edge image by using Canny operator; (c) the results obtained by the LTSD, LTS and LMedS methods.



(a)



(b)



(c)

Fig. 5 Fitting the ellipse in a cup: (a) cup image; (b) applying Prewitt operator; (c) comparative results obtained by the LTSD, LTS and LMedS methods

6. Conclusion

In this paper, we demonstrated that both the least median of squares method and the least trimmed squares methods to fail to fit a model under clustered outliers. We proposed a new method that incorporates symmetry distance into model fitting. This method can achieve

better performance than the least median of squares method and the least trimmed squares method especially when large percentages of clustered outliers exist in the data and the standard variance of inliers is large. The price paid for the improvement in fitting models is an increase of the computational complexity. Unfortunately, our method was especially designed for a symmetric model. For those models that do not have symmetric characteristics, or if symmetry in the data is lost through occlusion, the LTSD method is not a good choice. However, the LTSD approach does provide a feasible way to greatly improve the achievements of conventional estimators such as the LMedS and the LTS methods, especially, when data (with symmetry) contain inliers with large variance and are contaminated by large percentage of clustered outliers.

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