PROMEDS: AN ADAPTIVE ROBUST FUNDAMENTAL MATRIX ESTIMATION APPROACH (ADDITIONAL RESULTS)

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1. INTRODUCTION

This document contains additional results obtained for [1]. In such document results were provided for synthetic data that was used to test several robust algorithms for fundamental matrix estimation. Provided results consisted on epipole error between estimated epipoles and ground truth epipoles obtained from ground truth fundamental matrices to obtain a measure of accuracy, and secondly, also the number of iterations needed for convergence into a solution was measured in order to obtain a relative measure of computational cost between each fundamental matrix estimation method.

Obtained results on synthetic data allowed to determine the behavior of our implementation (i.e. PROMedS) with greater accuracy, however, this document also provides detailed results on real data to validate the behavior of our implementation in a more realistic scenario.

To validate our algorithm with real data, we used datasets from Middlebury's stereo web size [2], where ground truth disparity is available for a set of images with up to 1 pixel of precision. Such ground truth disparity was used to estimate ground truth fundamental matrix for each dataset, however, because precision of disparity is up to 1 pixel, this method is not as accurate as



Fig. 1. Left: Average epipolar error [5] for several fundamental matrix estimation algorithms. Outliers contain Gaussian noise with $\sigma = 5$ pixels, inliers do not have noise. Right: Same as left but outliers contain Gaussian noise with $\sigma = 5$ pixels and inliers Gaussian noise with $\sigma = 0.25$ pixels, which can be seen as a more realistic measure. Non-robust methods are shown with dashed lines and robust methods are shown with solid lines. Figures shows that PROMedS and Mixed PROMedS is capable to adapt to the amount of inlier noise.

the one used in [1] over synthetic data where a pair of randomly generated pinhole cameras is used to directly estimate the ground truth of the fundamental matrix.

To validate our algorithm on Middlebury's datasets, we used a harris corner detector [3] on each pair of images to determine the points of interest on a pair of images with up to 1 pixel of precision. Those points of interests were used to obtain possible matches between the pair of images using Normalized Cross Correlation (NCC). For each match an NCC score ranging between -1 (i.e. worse match) and 1 (i.e. best match) was obtained. These matching scores were provided as input along with the matched point coordinates on PROSAC and PROMedS methods.

A set of robust (e.g. RANSAC, MSAC, LMedS, PROSAC and PROMedS) and non robust (e.g. 8-points algorithm, 7-points algorithm, weighted algorithm) algorithms [4] were used for each dataset in Middlebury's site using the method described above to retrieve point matches. The process was repeated several times and results were averaged on robust methods such as RANSAC because they provide results up to a certain confidence by picking points in a random manner, which can produce slightly different results on each run of the algorithm.

Because images on Middlebury's site are rectified, we do not provide the epipole distance since epipoles would be located at infinity (or as close as machine precision allows us to). Hence, measuring distance to such locations becomes meaningless mostly because of machine precision. Instead, to compare fundamental matrices we provide an epipolar comparison measure which is comparable to providing averaged measures of distances of projected image points towards their respective epipolar lines. The method is further described in [5]. Figure 1 shows the epipolar comparison for the synthetic data that we used in [1]. We provide such figure to compare later the performance of each algorithm on real data using Middlebury's datasets.

2. RESULTS ON REAL DATA

Below we provide a table containing epipolar comparison results for datasets in Middlebury's site for all the algorithms that we have taken into consideration. The table shows that results are within the values that we expected, and we can see that both PROMedS and Mixed PROMedS performs very similar to PROSAC, mostly because the accuracy of the matches and the ground truth is limited to 1 pixel. However, PROMedS proves to be advantageous respect to PROSAC in the fact that no threshold is needed to determine which points are inliers, since such threshold is computed automatically. This improvement can be helpful since the threshold for methods such as RANSAC, MSAC or PROSAC might need to be adjusted in a problem specific manner. Besides, synthetic data shows that in case that matches are provided with sub-pixel accuracy, both PROMedS and Mixed PROMedS would yield a more precise solution with a similar computational cost than PROSAC, which is considerably faster respect to other robust methods as was shown in [1].

As a final note, the table below also shows that non-robust methods produced better than expected results on the images that we have tested. This fact indicates that Harris corner detector is a suitable way of finding good matches to estimate fundamental matrices with a small amount of outliers, otherwise non-robust algorithms would have performed worse.

| Left view | Right view | | Results | | | | | | | | |
|-----------|------------|------------------------|----------|----------|-----------|------------|----------|----------|-----------|------------------|------------|
| | | | 8-points | 7-points | Weighted | RANSAC | LMedS | MSAC | PROSAC | Mixed PROMedS | PROMedS |
| X | X | Epipolar Comparison | 0.000143 | 8.08E-05 | 0.0001937 | 0.282246 | 0.00151 | 0.060121 | 4.70E-13 | 1.26E-07 | 1.26E-07 |
| | | Average Iterations | 1 | 1 | 1 | 53.8421 | 6.3 | 53.3 | 1 | 1 | 1 |
| | | Epipolar Comparison | 0.000304 | 0.000593 | 0.0940685 | 0.00798459 | 0.002028 | 0.013228 | 0.0006524 | 0.00114708 | 0.00114708 |
| | | Average Iterations | 1 | 1 | 1 | 60.15 | 11.75 | 61.6 | 2.45 | 2.55 | 2.55 |
| <u>J</u> | all a | Epipolar Comparison | 7.64E-05 | 0.000295 | 4.02E-11 | 0.00334458 | 0.001414 | 0.003232 | 1.54E-10 | 5.37E-05 | 5.37E-05 |
| | | Average Iterations | 1 | 1 | 1 | 40.35 | 5.3 | 41.2 | 2 | 2 | 2 |
| | | Epipolar Comparison | 7.61E-05 | 0.000242 | 0.0093526 | 0.00263517 | 0.001668 | 0.007603 | 1.69E-14 | 7.69E-13 | 7.69E-13 |
| | | Average Iterations | 1 | 1 | 1 | 44.05 | 5.2 | 50.6842 | 1 | 1 | 1 |

| Left view | Right view | | Results | | | | | | | | |
|--|----------------|------------------------|----------|----------|-----------|------------|----------|----------|------------|------------------|-------------|
| | | | 8-points | 7-points | Weighted | RANSAC | LMedS | MSAC | PROSAC | Mixed PROMedS | PROMedS |
| No. |) ² | Epipolar Comparison | 0.00014 | 0.000314 | 4.88E-07 | 0.0070172 | 0.003233 | 0.068791 | 1.34E-12 | 3.20E-06 | 3.20E-06 |
| | | Average Iterations | 1 | 1 | 1 | 56.4211 | 6 | 53.6842 | 1 | 1 | 1 |
| | | Epipolar Comparison | 0.000233 | 0.000723 | 0.0006109 | 0.00566262 | 0.001594 | 0.009964 | 0.0002556 | 0.00038587 | 0.00038566 |
| | | Average Iterations | 1 | 1 | 1 | 50.05 | 6.15 | 61.8421 | 1.1 | 1.05 | 1.05 |
| | | Epipolar Comparison | 0.00019 | 0.000164 | 0.110219 | 0.0101254 | 0.001325 | 0.007235 | 4.55E-14 | 3.15E-13 | 3.15E-13 |
| | | Average Iterations | 1 | 1 | 1 | 71.45 | 11.55 | 65.3 | 1 | 1 | 1 |
| i an | | Epipolar Comparison | 0.00018 | 0.000387 | 0.670721 | 0.00955604 | 0.001323 | 0.015838 | 2.03E-12 | 3.01E-07 | 3.01E-07 |
| | | Average Iterations | 1 | 1 | 1 | 59.4 | 8.15 | 69.05 | 1 | 1 | 1 |
| 2 | | Epipolar Comparison | 0.00044 | 0.000599 | 1.80E-10 | 0.0460938 | 0.001784 | 0.005793 | 0.0749057 | 0.00960341 | 0.00960341 |
| | | Average Iterations | 1 | 1 | 1 | 31.75 | 4.35 | 33.8 | 1 | 1.5 | 1.5 |
| | | Epipolar Comparison | 6.83E-05 | 0.000282 | 1.23E-10 | 0.00899173 | 0.002361 | 0.004761 | 1.92E-14 | 5.80E-13 | 5.80E-13 |
| | | Average Iterations | 1 | 1 | 1 | 61.3 | 8 | 50.4 | 1 | 1 | 1 |
| | | Epipolar Comparison | 0.000108 | 0.000139 | 4.33E-10 | 0.00466707 | 0.001627 | 0.092428 | 1.19E-15 | 3.09E-13 | 3.09E-13 |
| | | Average Iterations | 1 | 1 | 1 | 52.3 | 7 | 40.9 | 1 | 1 | 1 |
| | 20 | Epipolar Comparison | 0.000151 | 0.000254 | 0.0625038 | 0.00616827 | 0.002169 | 0.008138 | 3.12E-13 | 4.53E-10 | 4.53E-10 |
| | | Average Iterations | 1 | 1 | 1 | 48.8889 | 4.85 | 41.7 | 1 | 1 | 1 |
| | | Epipolar Comparison | 0.00022 | 0.000553 | 0.0972519 | 0.00823292 | 0.002666 | 0.009533 | 8.73E-05 | 0.00021278 | 0.000212783 |
| | | Average Iterations | 1 | 1 | 1 | 60.95 | 7.25 | 78.85 | 5.75 | 5.1 | 5.1 |
| Y. | | Epipolar Comparison | 8.26E-05 | 7.36E-05 | 0.13465 | 0.0128632 | 0.001378 | 0.010174 | 2.60E-14 | 1.67E-11 | 1.67E-11 |
| | | Average Iterations | 1 | 1 | 1 | 70.9444 | 12.95 | 74.2632 | 1 | 1 | 1 |
| | K | Epipolar Comparison | 7.99E-05 | 2.68E-05 | 0.0179136 | 0.00268068 | 0.001729 | 0.01119 | 0.0072105 | 0.00737287 | 0.00737287 |
| | | Average Iterations | 1 | 1 | 1 | 66.2 | 9.45 | 70.85 | 1 | 2 | 2 |
| | | Epipolar Comparison | 0.000412 | 0.068618 | 0.0418575 | 0.00349842 | 0.002388 | 0.002679 | 0.00335111 | 0.0253062 | 0.0253062 |
| | | Average Iterations | 1 | 1 | 1 | 68.2 | 8.05 | 67.05 | 7.55 | 2.65 | 2.65 |

| Left view | Right view | | Results | | | | | | | | |
|-------------|------------|------------------------|----------|----------|-----------|------------|----------|----------|-----------|------------------|------------|
| | | | 8-points | 7-points | Weighted | RANSAC | LMedS | MSAC | PROSAC | Mixed PROMedS | PROMedS |
| R. | | Epipolar Comparison | 0.000166 | 0.000756 | 0.029632 | 0.0452571 | 0.002202 | 0.045124 | 1.25E-13 | 3.24E-13 | 3.24E-13 |
| | | Average Iterations | 1 | 1 | 1 | 66.2105 | 7.95 | 69.8947 | 1 | 1 | 1 |
| R. | | Epipolar Comparison | 0.00029 | 0.000301 | 0.293753 | 0.0321614 | 0.001818 | 0.028508 | 0.0264204 | 0.281359 | N/A |
| | | Average Iterations | 1 | 1 | 1 | 60.875 | 6.75 | 55.6316 | 4090 | 2.84211 | N/A |
| | | Epipolar Comparison | 0.000302 | 0.004712 | 0.009796 | 0.00247314 | 0.002077 | 0.010426 | 3.22E-13 | 5.20E-13 | 5.20E-13 |
| | | Average Iterations | 1 | 1 | 1 | 71.75 | 7.85 | 61.75 | 1 | 1 | 1 |
| | FIL. | Epipolar Comparison | 0.000185 | 0.000473 | 0.0169212 | 0.00400592 | 0.001893 | 0.010873 | 2.15E-14 | 6.49E-12 | 6.49E-12 |
| | | Average Iterations | 1 | 1 | 1 | 54.6316 | 9.25 | 72.8421 | 1 | 1 | 1 |
| RI 1 | | Epipolar Comparison | 6.80E-05 | 0.000115 | 0.123192 | 0.00355844 | 0.001888 | 0.019594 | 2.80E-13 | 1.12E-07 | 1.12E-07 |
| | | Average Iterations | 1 | 1 | 1 | 63.05 | 9.05 | 64.8 | 1 | 1 | 1 |
| | 9 | Epipolar Comparison | 0.000475 | 0.000783 | 0.0374644 | 0.0040418 | 0.001704 | 0.007966 | 0.0059007 | 0.00424948 | 0.00424948 |
| | | Average Iterations | 1 | 1 | 1 | 65.1 | 11.4 | 66.7 | 1 | 2.3 | 2.3 |
| A. | T. | Epipolar Comparison | 0.000162 | 0.000145 | 2.16E-11 | 0.00217666 | 0.002095 | 0.007364 | 4.08E-12 | 2.31E-06 | 2.31E-06 |
| | | Average Iterations | 1 | 1 | 1 | 40.45 | 7.8 | 47.8421 | 1 | 1 | 1 |
| | | Epipolar Comparison | 7.42E-05 | 0.000169 | 1.76E-11 | 0.00560477 | 0.002031 | 0.037647 | 3.80E-14 | 7.42E-11 | 7.42E-11 |
| | | Average Iterations | 1 | 1 | 1 | 52.05 | 10.45 | 59.6 | 1 | 1 | 1 |
| | | Epipolar Comparison | 8.43E-05 | 8.53E-05 | 4.72E-08 | 0.00735677 | 0.002192 | 0.006172 | 5.18E-12 | 1.06E-07 | 1.06E-07 |
| | | Average Iterations | 1 | 1 | 1 | 51.5789 | 6.3 | 57.65 | 1 | 1 | 1 |
| | | Epipolar Comparison | 0.000348 | 0.000792 | 0.0007263 | 0.00239541 | 0.001857 | 0.012669 | 1.43E-10 | 0.00913111 | 0.00913111 |
| | | Average Iterations | 1 | 1 | 1 | 50.8333 | 6.15 | 61.6667 | 3.35 | 3.55 | 3.55 |

3. REFERENCES

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