The Challenges and Advantages with a Parallel Implementation of Feature Matching

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Abstract: The number of cores per cpu is predicted to double every second year. Therefore, the opportunity to parallelise currently used algorithms in computer vision and image processing needs to be addressed sooner rather than later. A parallel feature matching approach is proposed and evaluated in Matlab®. The key idea is to use different interest point detectors so that each core can work on its own subset independently of the others. However, since the image pairs are the same, the homography will be essentially the same and can therefore be distributed by the process that first finds a solution. Nevertheless, the speedup is not linear and reasons why is discussed.

1 INTRODUCTION

An efficient parallel implementation of feature matching is proposed and discussed. Especially it will be shown how the different steps of matching can be implemented and that the problem itself, when solved in parallel, not only can be computed faster, but in part also becomes simpler.

Research in such areas as image processing, computer vision and pattern recognition, still mainly focus on sequential algorithms even though parallelism have been at hand for many years. Today, most laptops have two or more cores and desktop computers have even more. Not surprisingly, even some cell phones have more than one core nowadays. Moreover, multithreading makes it possible to run more than one program per core. It has been suggested that the number of cores will double every two years (Vajda, 2011) and therefore the communities in the aforementioned research areas have to, sooner rather than later, deal with parallel implementations of the most commonly used algorithms. Among these are certainly feature matching, including interest key point detection, matching, outlier removal using some variant of Random sample consensus (RANSAC) (Fischler and Bolles, 1981) and homography computation. Besides this, what is the fastest method for a sequential approach may not necessarily be the fastest in parallel and methods that were considered too slow in the past might be used in the future when making use of the multicore capacity.

It will be shown how feature matching can be implemented to benefit from the available parallelism and it will be shown how different types of interest points can be extracted in parallel together with the respective matching. Moreover, a parallel implementation of RANSAC is presented that works on each set of matches. Whenever, one of the processes finds a good solution, it is shared among the other processes so that the whole procedure will theoretically be just as fast as the one finding the solution first.

2 FEATURE MATCHING

Feature matching is important for applications like image stitching (Szeliski, 2006) and registration (Zitova and Flusser, 2003). The feature vector is usually a visual descriptor of the area around key points in the image. Many different descriptors have been proposed in literature and severals overviews have been published (Gauglitz et al., 2011). In the performed tests a Fourier based descriptor was used (Hast, 2014). However, the implementation discussed could use any kind of descriptor. More importantly is the fact that different different interest point detectors can be used and not only one, as usually is the case. Some of them will be mentioned in the following section as they will be used for the parallel implementation.

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2.1 Interest Point Detectors

The detector proposed by Harris and Stephens (Harris and Stephens, 1988) is based on the so called *structure tensor*, $\mathcal{S}$ of an image I, which is defined as

$$\mathcal{S} = \begin{bmatrix} I_x^2 & I_x I_y \\ I_x I_y & I_y^2 \end{bmatrix} \quad (1)$$

where I_x and I_y are image derivatives in the x and y directions, respectively.

In order to detect corners it was proposed to compute the response using the trace and determinant of the matrix as

$$\mathcal{R} = det(\mathcal{S}) - k \cdot tr^2(\mathcal{S}) \quad (2)$$

where k is a constant, typically set to 0.04. However, the formulation by Noble (Noble, 1989) will be used herein since it has no such *ad hoc* constant and is therefore, in some sense, more general. Noble proposed to use

$$\mathcal{R}_H = det(\mathcal{S})/(tr(\mathcal{S}) + \varepsilon) \quad (3)$$

where ε is a small constant used to avoid division by zero.

A Gaussian window is generally used to compute isotropic responses, i.e. each one of the elements in the tensor in equation 1 are all filtered separately using a Gaussian kernel. This was an improvement compared to the early detector by Moravec (Moravec, 1980), which used a square window, yielding non isotropic responses. This Gaussian convolution is omitted in the equations above for clarity.

Furthermore, the trace $\mathcal{R}_t = tr(\mathcal{S})$ can also be used for interest point detection and will find edges rather than corners. The Hessian matrix used for SURF by Bay et al. (Bay et al., 2008), on the other hand will find blobs and is defined as

$$\mathcal{H} = \begin{bmatrix} I_{xx} & I_{xy} \\ I_{xy} & I_{yy} \end{bmatrix} \quad (4)$$

They proposed to use the determinant of $\mathcal{H}$

$$\mathcal{R}_+ = det(\mathcal{H}) = I_{xx} I_{yy} - I_{xy}^2 \quad (5)$$

By changing the sign of $\mathcal{R}_+$ so that $\mathcal{R}_- = -\mathcal{R}_+$ a blob detector that will find dark blobs instead of bright blobs is obtained. Once again, the trace $\mathcal{R}_{t+} = tr(\mathcal{H})$can also be used for interest point detection. Moreover, the inverted sign $\mathcal{R}_{t-} = -\mathcal{R}_{t+}$ can be used for the Hessian. The trace of the structure tensor cannot be inverted as the sign does not matter, since it contains squares of derivatives.

Many other detectors have been proposed in literature (Smith and Brady, 1997; Obdrzálek and Matas, 2006; Hast and Marchetti, 2014; Hast, 2015), as discussed in the aforementioned overviews. However the six rather different detectors discussed above ($\mathcal{R}_H, \mathcal{R}_t, \mathcal{R}_-, \mathcal{R}_+, \mathcal{R}_{t-}, \mathcal{R}_{t+}$) will be used for the proposed parallel implementation of feature matching.

2.2 Nearest Neighbour Search

By comparing the feature vectors extracted for key points in image $\mathcal{A}$ with the points in image $\mathcal{B}$, tentative correspondences are obtained. A distance measure is used to determine how similar these feature vectors are and the pair of features having the smallest distance is consequently considered as nearest neighbours. If there are few points and the feature vectors themselves are rather small, then an exhaustive search can be applied where each of the features in one set is compared to all of the features in the other set. This is often a rather time consuming approach that can be improved by some kind of partitioning method such as kd-trees (Friedman et al., 1977) or k-means clustering (Fukunage and Narendra, 1975) and a short overview of such approximating approaches is given by (Muja and Lowe, 2009). Nevertheless, a proof of concept is given herein using the exhaustive search and therefore the choice of approximate algorithms are left to the reader.

2.3 RANSAC

RANSAC is one of the most used algorithms for outlier removal, i.e. removing false positives among the tentative correspondeces, even though other approaches exist (Enqvist and Kahl, 2008). The main idea is to generate a hypothesis from random samples and then verifying it using all the data. In practice, it first starts by selecting the minimal number of points required to determine the model parameters, i.e. finding the homography (Brown and Lowe, 2007), which is the projective transformation between the images. Then the set is rescored using this transformation, in the way that the number of inliers that falls below a certain predefined tolerance ε, are counted. This means that when transformed, these points are being close enough to its corresponding match and are hence regarded as true inliers.

If the number of inliers is large enough or more commonly when the probability of finding a better model becomes lower than some threshold, then the algorithm terminates, otherwise it starts all over again. RANSAC generally treats all correspondences equally and draws random samples uniformly from the full set.

2.4 Parallel RANSAC

MultiRANSAC (M. Zuliani and Manjunath, 2005) is a parallel extension of the sequential RANSAC that allows to deal simultaneously with multiple models, which have the advantage of being able to cope with a high percentage of outliers. Nevertheless, running the algorithms on several cores is only proposed for further research. GASAC (Rodehorst and Hellwich, 2006) is another parallel algorithm using a genetic algorithm approach. Neither this approach is implemented for several processors, instead it is parallel in the sense that several evaluated solutions exists simultaneously.

There are very few attempts to parallelise RANSAC in literature as noted by Hidalgo et al. (Hidalgo-Paniagua et al., 2014), who make a comparative study of parallel versions using OpenMP and CUDA. The algorithm starts by clustering points and each thread is then working on a subset of the original set. The overhead for this type of approach is therefore the clustering of these subsets. They refer to what they claim to be the only other parallel implementation by Iser et al.(Iser et al., 2009). This approach lets several threads be divided into two groups which samples the two point sets, in each image, and updates a hash table to establish correspondences. Nevertheless, Fijany and Diotalevi (Fijany and Diotalevi, 2012) propose a variant of RANSAC that was implemented on a many-core architecture and is based on cooperative search, where a global broadcast is done, if and when a better partial solution is found. In this way the best solution is known to all processes that draw samples from the whole dataset, which resides in shared memory.

In conclusion, RANSAC is close to embarrassingly parallel, as each process can work on the whole data, drawing samples and scoring in parallel, and the only thing needed is to distribute the best result to all processors in order to keep track of the best homography. Alternatively, it can work on a clustered subset of the data, with the overhead of performing such clustering.

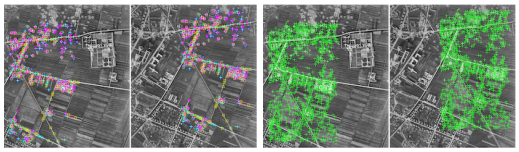
3 PARALLELISATION OF FEATURE MATCHING

In this paper a rather different approach is taken, even if some details are similar, as parallelisation is proposed not only for RANSAC, but also for interest point extraction. The idea is to let several processes extract interst points that by definition are different and thus, to some extent, the clustering for nearest neighbour search comes for free. This can be achieved by using the previously explained interest point detectors that generally finds different features, such as corners, dark and white blobs, and lines (or ridges). Another advantage is that only the strongest responses (interest points with high contrast (Lowe, 2004)) are useful, as low contrast points often are more sensitive to noise. This implies that it theoretically could be better to use the top n responses from k number of detectors than m number of points from any single detector, where $m = n \cdot k$. Then each process performs matching within its own set only. Especially, if an exhaustive search for true matches is used for comparing feature point neighbourhoods, it is an advantage to use several detectors (k) and fewer points within them (n), than using one detector and many points (m). Hence, the exhaustive search is delimited to be performed only on the points from each detector and the matching will therefore be faster. The number of comparisons will therefore be $k \cdot n^2$ instead of $m^2 = (n \cdot k)^2 = k \cdot (k \cdot n^2)$, which means that the total work done in the exhaustive search will be scaled down with a factor of k.

Furthermore, since these different detectors generally find different interest points, then RANSAC can be run in parallel, where each thread or process computes the homographies for each such set. If a true homography is found for one set then it should also be possible to use for the other sets. If this is the case, then a true solution is found and all sets can be combined to a single set and the homography can be computed for the resulting set. The advantage is that the sets the different processes are working on are smaller ($n < m$) than what would be the case if only one detector was used. Hence, n points are evaluated using the homography in each thread instead of m points. If, on the other hand kd-trees or similar are used to speed up the matching, the above reasoning must be changed accordingly. However, the overhead of making such trees might not be worth the extra work needed, as the matching is divided into k sets anyway and are therefore smaller from the start.

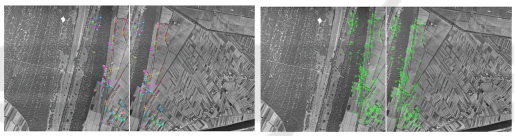
Whenever a process i finds a transformation giving more inliers than the maximum so far, the homography $\mathcal{H}_i$ is broadcasted to all other processes. They, in their turn probe for such messages and try out the homography on their set of matches. In this way, if some process finds a good homography it is shared and the other processes will test how well the model works on their data. One advantage is that if some processes are having trouble finding a good homography, they will automatically get help from those who are more successful. The result will be a more consistent result as they are helping each other. Another

advantage is that the total speed of the whole procedure will in principle be just as fast as the process that finds the best homography first, with the added overhead of distributing the homography and scoring it. In this paper the RANSAC used (Hast et al., 2013) for the suggested parallel implementation stops when two identical sets are found after local optimisation, re-estimation and pruning. Whenever this occurs, the homography is broadcasted to all processes, which in their turn scores their sets, computes the homography and then terminates.



Pisa, The Duomo

Pisa, The Duomo and the city centre



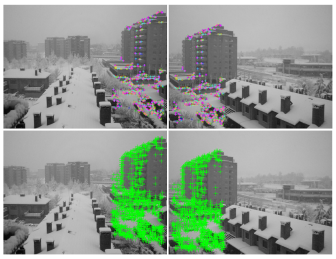
Pisa, Fields north of the river Arno

Figure 1: Illustration of corresponding pairs (inliers only) for a set of images. The six different detectors are visualised using individual colours and glyphs, while the case of one detector (DoH) using 6 times more key points is depicted using green '+'. ©MiBAC-ICCD, Aerofototeca Nazionale, fondo RAF.

4 RESULTS

A proof of concept was performed on a set of images shown in figure 1. Six cores were used to compute the aforementioned interest points and matched using a simple invariant matching procedure (Hast and Marchetti, 2013; Hast, 2014). A parallel version was compared to a ordinary sequential version in 1000 test runs. The results are shown in figure 1 and 2. In each pair of images, to the left, the resulting inliers are depicted using different glyphs in different colours: $\mathcal{R}_H(blue)$, $\mathcal{R}_L(green)$, $\mathcal{R}_{L-}(red)$, $\mathcal{R}_{L+}(cyan)$, $\mathcal{R}_{L-}(magenta)$, $\mathcal{R}_{L+}(yellow)$. The top 500 points were chosen from each detector, giving a total of 3000 points. When one detector only was used, depicted in the right image pairs with green '+', the top 3000 were chosen using $\mathcal{R}_H$, just for comparison.

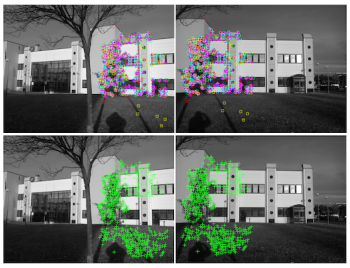
Venice, Palazzo Contarini del Bovolo



Bologna, Snowfall in Casalecchio di Reno

Florence, Ponte Vecchio

Rome, Colloseum



Pisa, CNR

Figure 2: Illustration of corresponding pairs (inliers only) for a set of images. The six different detectors are visualised using individual colours and glyphs, while the case of one detector (DoH) using 6 times more key points is depicted using green '+'. All images ©Anders Hast.

Table 1: Comparison between a parallel and sequential implementation of feature matching, showing inliers after matching and after RANSAC, as well as wall clock time and speedup (ratio).

image	Inliers matching		Inliers RANSAC		Time		Speedup
	parallel	sequential	parallel	sequential	parallel	sequential	ratio
Pisa 1	613	509	443	352	1,99	5,24	2,64
Pisa 2	1046	1211	932	1146	2,08	6,29	3.03
Pisa 3	453	454	273	330	3,63	5,74	1,58
Venice	1835	2139	1728	2078	7,74	18,36	2,37
Bologna	1160	1048	1008	908	3,28	10,65	3,25
Florence	1443	1090	1365	1014	4,75	6,75	1,42
Rome	702	985	532	893	4,54	6,43	1,42
Pisa	1172	848	944	542	5,14	35,96	7,00

In table 1 the results are shown for each image pair and the number of inliers, after matching and after RANSAC, measured wall clock time and speedup is reported for both the parallel and sequential implementation.

5 DISCUSSION

The results in table 1 reveals that the speedup varies noticeably for these few examples, when one could expect close to six times speedup. The implementation in Matlab® seem to have a rather high overhead when using the *smpd* command for launching the program on several cores. Another reason for the results might be that interest points are found in parallel and then a barrier waits for all processes to return their result. In the next step feature extraction and matching is done followed by a barrier. Finally the parallel RANSAC is called and the whole procedure ends when all processes terminates. The reason for the barriers is simply that different parallel functions were made so that the user easily can change each one of them. By incorporating all steps into one continuous process, the time to finish would be decreased, but the parallel program would be more complex. It is of course not enough to use only eight image pairs to draw decisive conclusions. However, the images are from two different types of applications (aerial photography and outdoor scenes) and the idea is just to give a proof of the concept. We strongly believe that an entire implementation in OpenMP or MPI, using C++ instead of Matlab would get better results. In any case, the results obtained show that a parallel approach is possible and will always be faster than a sequential approach.

In the performed test runs, six cores were available and used. However, there is nothing that prevents from using fewer or more cores. For the latter case more interest point detectors are necessary and several have, as mentioned, been proposed in literature. Alternatively one could use different σ for the gaussian in order to detect points of different sizes. One advantage is that more cores means less points to handle per core and only the strongest responses are used, which prevents from using noisy data. This is also clearly visible in the images as the different detectors finds points only in *interesting* areas where there are large changes in derivatives. It can be noted that many points lie close to each other, but at least in theory they are most of the time different. In any case it is an advantage that they find the strongest points and points that are resulting from noise are therefore reduced.

6 CONCLUSION AND FUTURE WORK

The main idea proposed is to use different interest point detectors for image matching and distributing each set to different cores or processes. Moreover, each core works on its own data and shares the homography to the other processes whenever a probable transformation is found. In this way several things can be done independently, such as obtaining interest points, descriptor extraction, matching and finally outlier removal. Another advantage is that the nearest neighbour search is automatically clustered into individual sets that are not dependent of each other, other than that they share the same transformation, and this will in itself reduce the computational cost with a factor corresponding to the number of cores. The drawback is that distributing data over several processes and communicating between them has its own cost and reduces the theoretical gain.

For future work it is proposed to incorporate all steps necessary, from interest point detection and matching to outlier removal, into one single procedure without any barriers. Furthermore, the implementation should benefit from using C++ together with OpenMP or MPI. It should also be examined

how the parallel algorithm could be distributed over more cores by using other kinds of interest point detectors and feature descriptors than the ones used in the experiments, such as SURF (Bay et al., 2008) and SIFT (Lowe, 2004).

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