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Fast-Match: 001 Fast and Robust Feature Matching on Large 002 Images

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011 **Abstract.** Consumer digital cameras and camera phones produce im-
012 ages that often exceed 10 megapixels. Yet computing and matching local
013 features in images of this size can easily take more than twenty seconds
014 using fast matching algorithms. This is much too slow for interactive ap-
015 plications and much too expensive for large scale image operations. We
016 introduce *Fast-Match*, an algorithm designed to swiftly match large im-
017 ages without compromising on matching precision or recall. *Fast-Match*
018 derives its speed from only computing features in those parts of the image
019 that can be confidently matched. We show that *Fast-Match* is an order
020 of magnitude faster than *Ratio-Match*, yet often doubles the precision
021 on difficult to match image pairs at equal recall. In addition we prove
022 that when one image is known in advance, *Fast-Match* can achieve linear
023 performance $O(n)$ in the number of feature points n .

024 1 Introduction

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026 Whenever we match local image features we are faced with a choice between per-
027 formance and precision. On one hand SIFT features proposed by Lowe [1] have
028 shown again and again to compare favorably to other local image descriptors,
029 especially under unconstrained conditions such as perspective change with non-
030 planar scenes [2–4]. On the other, SIFT keypoints and descriptors are slow to
031 compute, the main *raison d'être* for the introduction of various alternative local
032 image features. In many applications of computer vision we would like the in-
033 crease the computational performance in order to work on larger images, bigger
034 image sets, at faster frame rates or with more limited hardware, but we cannot
035 give up the additional precision that SIFT affords us over other local features
036 without negative effects for our application.

037 In this paper we introduce a matching algorithm designed to match features
038 between two images only in image areas that are likely to correspond. This
039 approach is much faster than traditional methods because there is no need to
040 compute descriptors for areas in the image that are not matched. We provide
041 two variations of the algorithm: The *general* variation functions as a traditional
042 matching algorithm and matches two unknown images albeit faster and more
043 robustly than conventional methods. The *retrieval* variation on the other hand
044 assumes that we know one of the images we intend to match beforehand; under

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045 this assumption, it can be a magnitude faster than existing matching methods
 046 without compromising on accuracy. We will unimaginatively refer to the pro-
 047 posed algorithm as *Fast-Match* in this paper and make clear from the context
 048 whether this refers to the *retrieval* or *general* variation.

049 The problem that *Fast-Match* attempts to solve is two-fold. By matching only
 050 image areas that are likely to correspond we hope to improve accuracy by entirely
 051 ignoring parts of the images that would otherwise likely be a source of incorrect
 052 correspondences. At the same time, this enables us to improve computational
 053 speed by not having to compute keypoints and descriptors for large parts of the
 054 images and at the same time reducing the amount of feature points we need to
 055 match. Both problems have been addressed in part by past work.

056 *Fast-Match* makes use of an angular assumption to efficiently find new matches
 057 in the geometric neighbourhood of already confirmed matches. However this con-
 058 straint is only applied *locally* to increase the number of matches, making *Fast-*
 059 *Match* robust to outliers. In addition *Fast-Match* does not rely on an initial set
 060 of matches and derives much of its speed from the fact that not even an initial
 061 set of local image features is required.

062 This paper is structured as follows: Section 2 discuss related work. Section 3
 063 introduces the *Fast-Match* algorithm. Section 4 outlines the experimental setup.
 064 In Section 5 we discuss the results before concluding in Section 6.

065

066 2 Related work

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068 As noted, the cost of computing SIFT keypoints and descriptors is addressed by
 069 other local image features such as SURF [5], BRIEF [6], or BRISK [7], just to
 070 mention a few. Similarly efforts have been made to improve SIFT itself such as
 071 PCA-SIFT [8] and GLOH [2]. Both apply PCA to reduce descriptor lengths and
 072 improve distinctiveness, but neither have been shown to consistently outperform
 073 SIFT [2, 9].

074 Efforts to reduce the computational costs of finding nearest neighbours to
 075 feature points have largely focused on metric trees. Naïvely the set of near-
 076 est neighbours between features in two images can computed by brute force in
 077 $O(n^2)$, where n is the total number of feature points in the two images (a typical
 078 three megapixel image may contain anywhere from 500 to 5000 feature points).
 079 When SIFT was originally published Lowe, proposed using the Best-Bin-First
 080 method to approximately search for nearest neighbours [10, 11]. This reduces
 081 the computational complexity to $O(n \log n)$, but even approximate metric trees
 082 are hard pressed to compete with brute force due to the high dimensionality
 083 of SIFT and the constant costs incurred with constructing and searching in a
 084 metric tree. Later work by Muja and Lowe [12] focused on improving approxi-
 085 mate nearest neighbour searches by using several KD-Trees simultaneously while
 086 optimizing the tree structure using K-Means to cluster similar features. Recent
 087 work on knn-graphs shows a lot of promise for high dimensional cases [13]. We
 088 later review these improvements and their effect on efficiently matching large
 089 scale images.

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090 A wealth of matching methods have focused instead on increasing the efficiency of local feature matching. *Fast-Match* builds upon the foundation of
 091 *Ratio-Match* introduced originally by Deriche et al. [14] and Baumberg [15] even
 092 though Lowe is usually credited for introducing it [1]. They both propose using
 093 the ratio of the similarity of the best to second best match of a given point to evaluate
 094 how unique it is. Their finding has later been tested by several independent teams,
 095 all concluding that thresholding based on this ratio is generally superior
 096 to thresholding based on similarity or returning all nearest neighbours [1–3,16].
 097

098 Brown and Lowe [17] extend ratio match to deal with a set of images by using
 099 not the ratio of the best and second best match, but the average ratio of the best
 100 and the average of second best matches across a set of images. Rabin et al. [16]
 101 try to enhance descriptor matching by looking at the statistical distribution
 102 of local features in the matched images, and only return a match when such a
 103 correspondence would not occur by mere chance. Finally, Arnfred et al. generalize
 104 *Ratio-Match* to make use of both of the matched images to provide a more
 105 accurate evaluation of the uniqueness of a match [18].

106 Another inspiration for the design of *Fast-Match* is *Patch-Match* as introduced
 107 by Barnes et al. [19]. Like *Fast-Match*, *Patch-Match* is an iterative algorithm
 108 for fast image matching, but unlike *Fast-Match*, which uses sparse local
 109 image features, *Patch-Match* is designed for dense image features. It works by
 110 randomly creating a set of matches from both images and then iteratively improving
 111 it.

112 For sparse local image features many solutions have combined *Ratio-Match*
 113 with various geometric constraints to improve matching. These constraints are
 114 based on assumptions regarding the transformation between the *query* and *target images*.
 115 A commonly used example is *RANSAC* applied to feature matching where matches
 116 are chosen from a pool of candidates according to how well they approximate a global
 117 epipolar geometry [20–22]. Similar global angular and distance constraints can be
 118 used to filter a set of matches as shown in [23,24]. Finally the problem of feature
 119 matching can be modelled as a graph matching problem where each feature is a vertex,
 120 and edge values correspond to a geometric relation between two features as demonstrated
 121 in [25–27]. For cases that require more flexibility such as scenes with moving elements and non-planar perspective
 122 change Pairwise constraints provide an alternative to the more rigid global
 123 constraints. Introduced by Leordeanu and Herbert [28], pairwise constraints work by
 124 applying a geometric constraint across matches on a pairwise basis, attempting
 125 to minimize the pairwise error. This approach has later been adopted by Pang et
 126 al. but made scale invariant and more efficient by using a voting scheme [29,30].
 127 Similarly we can cluster matches together based on a geometric constraint and
 128 treat each cluster as a separate case [31,32]. An interesting application of this
 129 principle is demonstrated by Chen et al. who iteratively use a Hough transform
 130 to cluster matches using angular constraints [33].

132 While geometric constraints have been shown to work well, they are often
 133 susceptible to outliers and tend to be computationally demanding. All of the
 134 above geometric methods require a set of initial matches usually provided by



Fig. 1: The 50 best matches by the proposed *Fast-Match* algorithm (left) and the *Ratio-Match* algorithm [1] (right). The lines between the image pairs denote a match as proposed by the algorithm. For *Fast-Match* the areas where local features were computed are marked with blue squares in the right image.

Ratio-Match which acts as a lower bound on their running time. In practice even fast graph matching methods such as the covering trees method proposed by Yarkony et al. are two or three magnitudes slower than *Ratio-Match* [26].

3 Matching Fast and Slow

In this section we will introduce the fundamentals of *Fast-Match* and motivate the design choices as we go. The algorithm consists of 3 components; finding seeds, finding matches, and exploring for other places where matches might be.

3.1 Considerations

If we set out to design a truly fast matching algorithm, we cannot rely just on optimizing the matching step once the descriptors from both images have been found and computed. Finding and computing descriptors can easily account for 80% of the time spent matching for bigger images (cf. Figure 5). For this reason *Fast-Match* is designed to only compute features for the part of the image we hope to match.

The *Fast-Match* algorithm is demonstrated in Algorithm 1. Given a *query image* and a *target image* that we intend to match and a confidence threshold τ , we obtain a set of seed matches from the two images. For each seed match we look at the matched position in the *query* and *target images* and find a set of matches. We save these matches and their confidence scores; for those that pass the confidence threshold τ , we obtain another set of seed matches. In this way we iterate until we have no more seed matches and return the matches and their confidence scores. In an intuitive sense τ serves as a parameter directing the thoroughness of the algorithm, i.e. how much time we spend matching, while the final precision and recall can be adjusted by thresholding the matches on their confidence scores at the end.

We a *general* and a *retrieval* variation of the algorithm. The latter assumes that we know one of the images that we intend to match ahead of time and

180 can do some off-line computations. For the *general* variation we make those
 181 computations on the fly instead and do not assume anything to be pre-computed.
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184 Algorithm 1 Fast-Match

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185 Require:  $I_{query}, I_{target}$  : images, maxiter  $\in \mathbb{N}$ ,  $\tau \in [0, 1]$ 
186  $M_{seed} \leftarrow \text{seed\_matches}(I_{query}, I_{target})$ 
187  $M_{final} \leftarrow \emptyset$ 
188  $C_{final} \leftarrow \emptyset$ 
189  $M_{seen} \leftarrow \emptyset$ 
190 while  $M_{seed} \neq \emptyset \wedge i < \text{maxiter}$  do
191      $M_{round} \leftarrow \text{get\_matches}(M_{seed})$ 
192      $C_{round} \leftarrow \text{get\_confidence}(M_{round})$ 
193      $M_{seed} \leftarrow \text{get\_seeds}(M_{round} \setminus M_{seen}, C_{round}, \tau)$ 
194      $M_{seen} \leftarrow M_{seen} \cup M_{seed}$ 
195      $M_{final} \leftarrow M_{final} \cup M_{round}$ 
196      $C_{final} \leftarrow C_{final} \cup C_{round}$ 
197 end while
198 return  $M_{final}, C_{final}$ 

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202 3.2 Initiating Seeds

203 Depending on the scenario, several strategies can be used to obtain a set of
 204 initial seed matches. For the case of matching a pair of two images we can get a
 205 rough group of seed matches by matching the thumbnails of the two images with
 206 for example *Ratio-Match*. However if we were matching images in a series, such
 207 as frames from a movie we could instead make use of a subset of the matches
 208 from the last frame to seed *Fast-Match* on the next. In practice we have found
 209 it efficient to resize both images to thumbnails of 300×300 pixels and use ratio
 210 match to obtain a set of matches and ratios that we then threshold with the
 211 confidence threshold τ to obtain the initial seed matches.
 212

214 3.3 Collecting Matches and Computing Confidence

215 If a seed match yields a connection between two points p_q in the *query image* and
 216 p_t in the *target image*, then we are interested in collecting all matches between
 217 the regions R_q and R_t centered around p_q and p_t respectively. From each region
 218 we can extract a set of feature points between which we try to find a set of
 219 matches M_{qt} and a set of confidence scores C_{qt} .

220 Lowe and others have shown that the distance between two SIFT descriptors
 221 is much less indicative of a true correspondence than the ratio between the best
 222 and second best match [1–3,16]. This ratio is more formally defined as follows: If
 223 we let f_q be a feature in the *query image* and f_t, f_b be the two nearest neighbours
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225 of f_q in the *target image* then the ratio r is defined as follows:

$$226 \\ 227 \quad r = \frac{d(f_q, f_t)}{d(f_q, f_b)}. \\ 228$$

229 Here $d(f_i, f_j)$ is the distance between the features f_i and f_j . For SIFT this is
 230 the Euclidean distance. The distance between two feature points is greater when
 231 the feature points resemble each other less. For this reason we have higher con-
 232 fidence in a match with a low r -value. Using r as a measure of match confidence
 233 presumes that we expect each feature in the *target image* to have at most one
 234 true correspondence in the *target image*. Intuitively if we try to find a match
 235 for a feature f_i in an image that does not have any true correspondences, then
 236 we would expect the two closest neighbours to be roughly equally well matched
 237 with f_i . For this reason we attribute high confidence to matches where the clos-
 238 est neighbour is dramatically closer to f_i than the second closest neighbour and
 239 discard the rest.

240 We are faced with a problem when applying this technique to obtain the set
 241 of confidence scores C_{qt} , since for any match in M_{qt} we only know the nearest
 242 neighbours amongst the features of R_q and R_t . To get around this problem we
 243 either assume to know one of the images beforehand (the *retrieval* variation) or
 244 – in case we cannot make that assumption – we compute the features of one of
 245 the images (the *general* variation). For a given match between features f_q and
 246 f_t we can now find the second closest neighbour f_b and calculate the
 247 confidence as $r = d(f_q, f_t)/d(f_q, f_b)$.

248 In the retrieval scenario where we know an image beforehand, we can further
 249 optimize this step. If we assume the *target image* is known in advance we can
 250 approximate the ratio by letting $\hat{r} = d(f_t, f_q)/d(f_t, f_b)$. Here the feature f_b is
 251 also part of the target image, which means we can pre-calculate $d(f_t, f_b)$ for
 252 all features in the cached *target image* before we start matching. When these
 253 distances are tied to their corresponding feature in the target image, it becomes
 254 trivial to calculate \hat{r} .

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257 3.4 Exploring for Matches

258 In each iteration we compute a new set of seed matches, i.e. positions that
 259 might yield more matches in the image. For each region R_i evaluated during the
 260 collection step we now have a set of matches M_i and a set of confidence levels C_i
 261 that we can use to predict whether the neighbourhood of R_i is worth exploring.

262 There are many possible heuristics for predicting possible regions including
 263 local and global epipolar assumptions and partial graph isomorphisms. However,
 264 for the sake of simplicity and speed we have chosen a straightforward approach
 265 based on weak angular assumptions, as illustrated in Figure 2. Assuming that the
 266 *target image* has been cached either in advance or before the matching step, the
 267 blue shaded areas show R_q and R_t for a given seed match. In the *target image* we
 268 collect all features in a given radius while we compute features in the rectangular
 269 R_q in the *query image*. For performance reasons we compute all features in the

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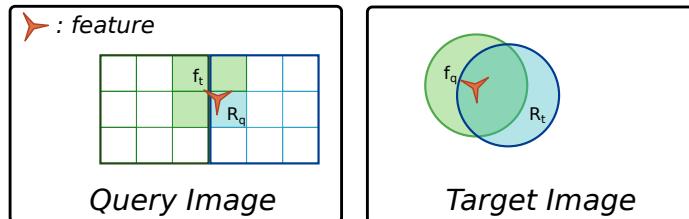


Fig. 2: Exploration of features based on a match. The areas shaded blue are the areas that were searched to obtain the match. The areas shaded green are candidate areas for obtaining more matches.

blue square but match only the features inside the shaded area. Next a match is found in the collection step between f_q and f_t . Based on the position of f_q in R_q we select three areas with potential for more matches. The center of each is matched with the center position f_t to produce three seed matches for the next iteration. In Figure 1 we illustrate this process in the *Fast-Match* image pair. The *query image* to the right in the figure has a small blue square for each region that has been used while matching the two images.

In practice it is necessary that these squares overlap in order to detect features lying close to the edges. This incurs a bit of overhead which is minimized by only collecting features for groups of 9 squares. In order to avoid computing the same matches or features twice, quite a bit of care has to be expended making sure that results are properly cached. A matrix containing ‘bins’ of features can conveniently be used to store features from different image regions. Similarly a hash-set is suitable for keeping track of which regions have already been matched and which matches have already been found.

3.5 Computational Complexity

The difference between the *general* and *retrieval* variation of *Fast-Match* consists in whether we compute the features in the *target image* (general) or if we presume the features are computed offline (retrieval). Computing the features is linear in the number of feature points, while finding $d(f_q, f_b)$ for all n features in the *target image* can be done in $O(n \log n)$ using metric trees.

Once the features and their distances have been computed, the algorithm iteratively finds new seed matches based on previous sets of seed matches. For each seed match we collect new matches, calculate confidence scores, and obtain new seed matches. Each of these steps varies only with the local region size which is constant. As a consequence the running time is linear in the amount of possible seed matches.

We will show that the number of possible seed matches is on average linear in the number of image features, and we also provide an upper bound for the probability that it is not. We assume that outside of true correspondences, features have better or at least equally good matches in terms of confidence in the

315 image they come from. More rigorously put: For any feature in the target image
 316 f_t let f_1, f_2, \dots be the best, second best, etc matching feature from either image
 317 which is not a true correspondence. Let A_{ti} be the event that f_i is found in the
 318 *query image*, then $\mathbb{P}(A_{ti}) \leq 0.5$ and A_{ti} is independent from A_{tj} when $i \neq j$.

319 For a given feature in the *target image* f_t , its nearest neighbour in the *target*
 320 *image* f_b , and the set of features in the *query image* F_{query} , we can define the
 321 stochastic variable X_t as follows:

$$322 \quad X_t = |\{f_q \mid f_q \in F_{query}, d(f_q, f_t) < d(f_q, f_b)\}| \quad (1)$$

324 That is, X_t is the number of features in the query image closer to f_q than f_b .
 325 For each feature f_t , X_t is an i.i.d. stochastic variable.

326 In the worst case, each feature in the *target image* has a true correspondence
 327 in the *query image* and $\mathbb{P}(A_{ti} = 0.5)$, in which case we find can find $\mathbb{P}(X_t = n) = \mathbb{P}(A_{ti})^n = 0.5^n$, as well as the expected value $\mathbb{E}(X_t) = \sum_{i=1}^{\infty} i 0.5^i = 2$, and
 328 the variance $Var(X_t) = \sum_{i=1}^{\infty} 0.5^i (i - 2)^2 = 6$.

329 For $\tau = 1$ we accept a seed match when $d(f_t, f_q) \leq d(f_t, f_b)$. That means
 330 that for any feature in the *query image*, we accept at most X_t matches. To find
 331 the total amount of seed matches given n , we let $S_n = X_1 + \dots + X_n$, in which
 332 case $\mathbb{E}(S_n) = 2n$. This proves that the expected amount of seed matches is linear
 333 in the number of target features.

334 For the above case it is theoretically possible that for every one of the n
 335 features we end up considering kn seed matches for some constant k , i.e. a
 336 quadratic behaviour. Using Chebyshev's inequality we can provide an upper
 337 bound on the probability of this event:

$$340 \quad \mathbb{P}\left(\left|\frac{S_n}{n} - \mathbb{E}(X_t)\right| \geq kn\right) \leq \frac{Var\left(\frac{S_n}{n}\right)}{kn^2} = \frac{6}{kn^3} \quad (2)$$

341 It is clear that for any constant k we can pick a number of features n which
 342 render the likelihood of a quadratic behaviour infinitesimal. In essence the larger
 343 n becomes, the less likely *Fast-Match* is to exhibit super linear behaviour.

344 The noteworthy part of this result is that for the *retrieval* variation we can
 345 match two images in $O(n)$. Since there are no large constants involved this makes
 346 it possible to rapidly match very large images. In particular *Fast-Match* is suited
 347 for cases where we are looking to match several large *query images* to one *target*
 348 *image*. In this case we can compute the features and distances of the *target*
 349 *image* and then match each *query image* in linear time. In contrast the general
 350 variation still has a complexity of $O(n \log n)$ due to the necessity of calculating
 351 distances online.

355 4 Experimental Setup

356 We evaluate *Fast-Match* over 3024 image pairs featuring various 3D objects at
 357 different angles to measure precision and recall, as well as two pairs of images
 358 with high pixel counts to measure performance in terms of speed. We compare

360 the algorithm to the standard *Ratio-Match* [1] as well as the newer *Mirror-
 361 Match* [18]. These two algorithms were selected because they are magnitudes
 362 faster than the fastest geometric algorithms while at the same time providing
 363 robust matches.

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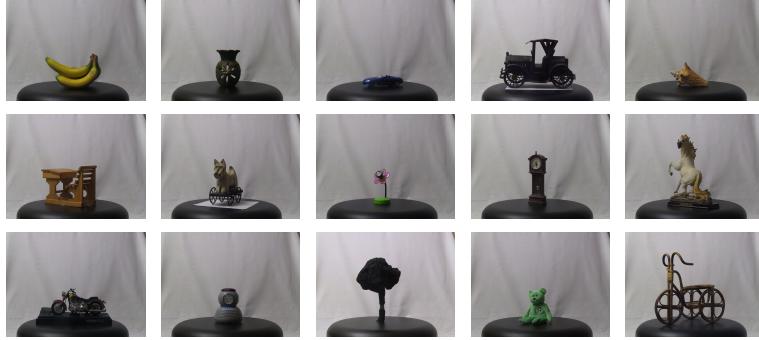
365 4.1 Evaluation of Fast-Match on 3D Objects

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367 The 3D Objects dataset by Moreels and Perona [3] allows us to experimentally
 368 compare matching algorithms over a large range of object and surface types
 369 rotated on a turnstile and photographed from every angle in increments of 5
 370 degrees. 15 objects from the dataset are shown in Figure 3. We use images of
 371 84 different objects photographed under three different lighting conditions at
 372 12 different angle intervals, conducting experiments with a total of 3024 image
 373 pairs. All photos a taken with a consumer camera in 3.1 mega pixel resolution.

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376 Fig. 3: 15 objects from the 3D Objects dataset by Moreels and Perona [3].

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To validate matches, Moreels and Perona propose a method using epipolar constraints [3, p.266]. According to their experiments, these constraints are able to identify true correspondences with an error rate of 2%. We use their proposed method to generate the ground truth for the evaluation of our framework.

To compute the total number of possible true correspondences, we take each feature in a *query image* and count how many of them have a feature in the *target image* which would satisfy the epipolar constraints. When using this dataset, features with no correspondences were not included in the set of features for testing, so as to avoid matching non-moving background and foreground objects.

We evaluate all matching algorithms from our framework on the 3D Objects dataset by matching images at different angular intervals. For each object we pick the *query* image as the image taken at 10 degrees rotation for calibration stability. We then match this image with the same object turned an additional Δ degrees, $\Delta \in \{5, 10, \dots, 60\}$. For every angle interval we compare images taken under 3 different lighting conditions as provided by the dataset. We include all

405 objects in the database for which photos at 5 degree angle intervals are available
 406 except for the “Rooster” and “Sponge” objects due to image irregularities.
 407

408 4.2 Configuration of *Fast-Match*

410 The central parameters of *Fast-Match* are the confidence threshold τ for select-
 411 ing seed matches and the final confidence threshold applied to the total set of
 412 matches. For the experiments on the 3D Objects we let $\tau = 0.9$ and created
 413 precision/recall plots by varying the confidence threshold over the final set of
 414 matches.
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416 To achieve a good balance between speed and robustness we let the region in
 417 which we extract features be a square with a side length of 90 pixels. On empirical
 418 tests we found that anything smaller would result in decreased performance while
 419 much bigger regions would decrease speed. The 90 pixel window is split in to
 420 nine smaller squares (see also Figure 2). When a seed match falls in any of these
 421 squares we match only the features within the smaller square. We let both the
 422 regions and the smaller squares overlap each other at all edges with 25 pixels in
 423 order to capture feature points lying close to an edge. For the image we have
 424 already cached we find all features within a radius of 50 pixels of the seed match.
 425

426 5 Results

428 Figure 4 shows the performance of the different matching methods in our pro-
 429 posed framework for 12 increasingly bigger angle differences. The results are
 430 shown in a precision-recall plot to make it easy to compare performance in terms
 431 of precision at similar levels of recall. For each plot we show the accumulated re-
 432 sults on all 3D objects, weighted by the number of possible true correspondences
 433 for the individual objects. This ensures that each object contributes equally to
 434 the final result, despite some objects resulting in disproportionately more matches
 435 than others.
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437 At low angular differences all algorithms show similar performance at low re-
 438 call, however *Fast-Match* is superior to *Ratio-Match* and *Mirror-Match* at higher
 439 recall, more than doubling the precision at similar recall levels. This picture re-
 440 mains the same at higher angular differences, but with a higher performance
 441 gap between *Fast-Match* and the other algorithms at low recall while more than
 442 doubling precision at higher recalls. For image pairs with angular differences of
 443 more than 40° the performance of all algorithms declines, with *Fast-Match* still
 444 coming out on top.

445 The high recall rates of *Fast-Match* are partially explained by the fact that
 446 we can allow our confidence thresholds to be more lenient when we already
 447 know that we are likely to find true correspondences in the regions that we are
 448 matching. However, lenient thresholds can easily impact the matching speed,
 449 so in practical situations we usually have to choose between matching fast and
 precisely, or more slowly with higher recall.

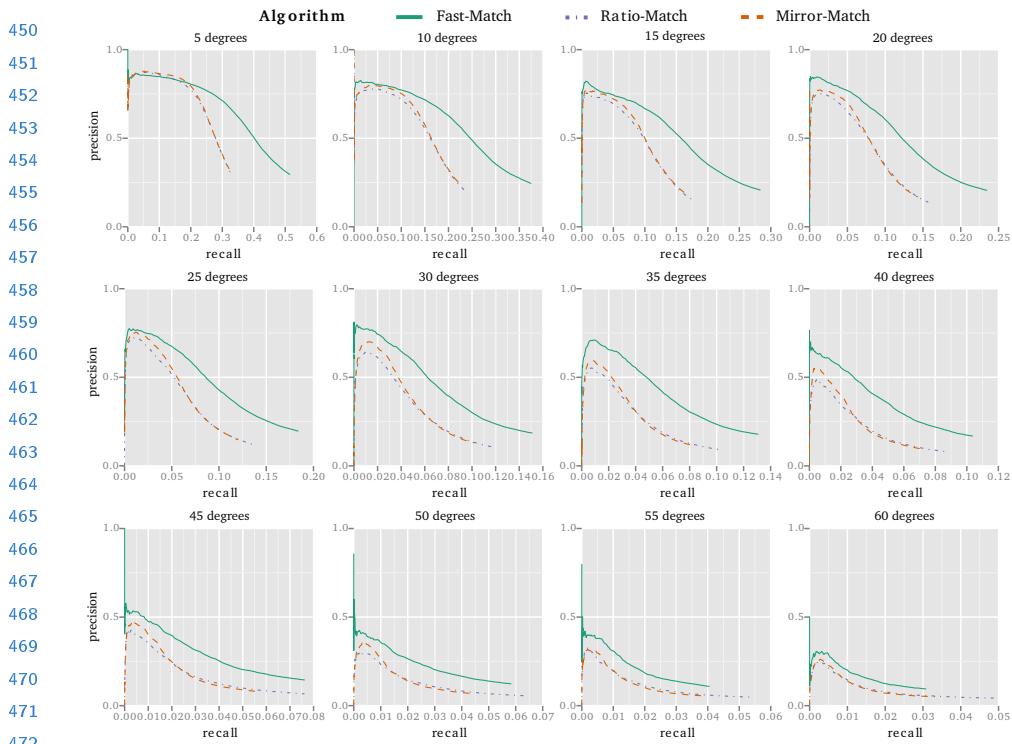


Fig. 4: Results for the 3D Objects dataset. Each plot contains data accumulated from 84 objects photographed under 3 different lighting conditions.

Figure 5 demonstrate the speed of *Fast-Match* on image sizes as is typically produced by modern consumer cameras and camera phones. In Figure 5 we compare the speed of the two variations of *Fast-Match* to different variations of *Ratio-Match* on two image pairs, one with two images of 10 megapixel and another where the same image pair has been scaled to 3 megapixels. For the larger images we see the clearest difference in performance. The retrieval variant of *Fast-Match* matches the image pairs in around one second while a retrieval variant of *Ratio-Match* with precomputed features spends eight seconds on the same task. This result is roughly equal to the time the general variation of *Fast-Match* spends matching the two images without any pre-computations. For the nearest neighbor search we note that for large images there are substantial speed gains to be had by choosing the right algorithm for finding nearest neighbors, with Muja et al.'s Flann matcher being vastly superior to brute force and KGraph.

For the 3 megapixel picture the pattern repeats itself, although with smaller margins separating *Fast-Match* and *Ratio-Match*. When images are smaller, computations like obtaining the initial seed matches are comparatively more costly.

Figure 1 shows the result from matching the pair of three megapixel images using *Fast-Match* and *Ratio-Match*. *Fast-Match* ends up only matching the part

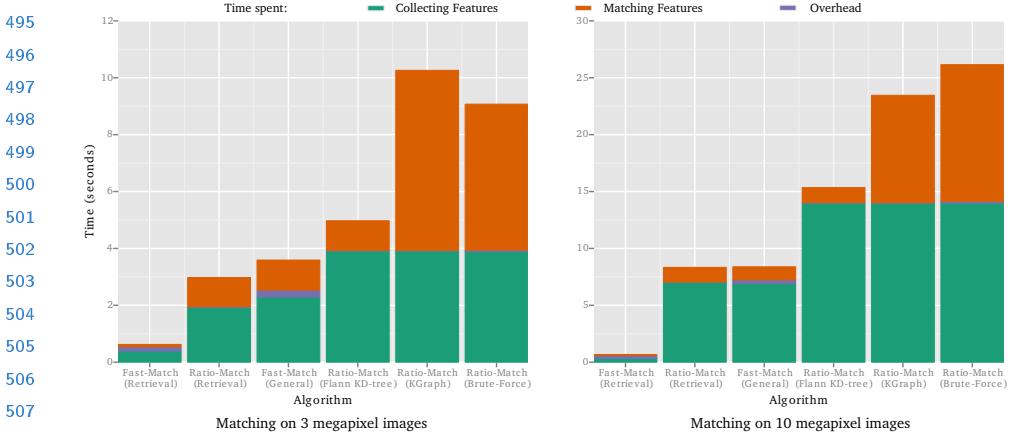


Fig. 5: Running times of different variations of *Fast-Match* and *Ratio-Match*. The top plot shows results for two 10 MPixel images two 3 Mpixel images is used for the comparison at the bottom. From the left, the first two results presume a precached image while the rest do not require knowing any inputs beforehand. The image pairs used be seen in Figure 1.

of the images that are likely to have correspondences. This highlights both a strength and a weakness of *Fast-Match*. It is this myopic matching approach that is responsible for *Fast-Match*' speed and precision; on the other hand, *Fast-Match* is not the best candidate for images that are almost identical, because its step by step approach incurs too much overhead to compete in speed with *Ratio-Match* in those cases.

6 Conclusion

We have introduced *Fast-Match* in two forms, a general and a retrieval variation. The retrieval variation assumes that we know one of the images that we are matching ahead of time in order to pre-cache feature points. The general variation has no assumptions and performs the pre-caching of feature points online instead. We have proven that while the general variation has a computational complexity of $O(n \log n)$ with n being the number of feature points, the retrieval variation will on average run in $O(n)$. From experiments on large images we have shown that *Fast-Match* can be a magnitude faster than *Ratio-Match* while providing comparable results. We further compared *Fast-Match* to *Ratio-Match* and *Mirror-Match* using images of rotated 3D objects to demonstrate that *Fast-Match* outperforms the other algorithms significantly over 3024 image pairs and in most cases doubles the matching precision at similar recall rates. *Fast-Match* is particularly applicable in cases where we are interested in matching one image to multiple large images, in which case we can quickly pre-cache the image and use this data for each of the other images.

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