

000 Fast-Match: Fast and robust feature matching on 001 large images

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

023 1 Introduction

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

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

2 ACCV-14 submission ID ***

045 without compromising on accuracy. We will unimaginatively refer to the proposed algorithm as *Fast-Match* in this paper and make clear from the context
 046 whether this refers to the *retrieval* or *general* variation.
 047

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

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

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

065 2 Related work

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

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

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
 095 teams, 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 im-
 111 proving 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 *tar-*
 115 *get images*. A commonly used example is *RANSAC* applied to feature matching
 116 where matches are chosen from a pool of candidates according to how well they
 117 approximate a global epipolar geometry [20–22]. Similar global angular and dis-
 118 tance constraints can be used to filter a set of matches as shown in [23, 24]. Finally
 119 the problem of feature matching can be modelled as a graph matching problem
 120 where each feature is a vertex, and edge values correspond to a geometric re-
 121 lation between two features as demonstrated in [25–27]. For cases that require
 122 more flexibility such as scenes with moving elements and non-planar perspective
 123 change Pairwise constraints provide an alternative to the more rigid global con-
 124 straints. Introduced by Leordeanu and Herbert [28], pairwise constraints work by
 125 applying a geometric constraint across matches on a pairwise basis, attempting
 126 to minimize the pairwise error. This approach has later been adopted by Pang et
 127 al. but made scale invariant and more efficient by using a voting scheme [29, 30].
 128 Similarly we can cluster matches together based on a geometric constraint and
 129 treat each cluster as a separate case [31, 32]. An interesting application of this
 130 principle is demonstrated by Chen et al. who iteratively use a Hough transform
 131 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

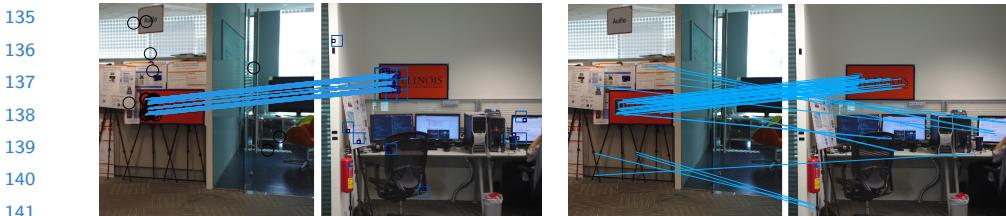


Fig. 1: The 50 best matches by the proposed *Fast-Match* algorithm (left) and the *Ratio-Match* algorithm [1] (right). The lines between the image pairs denote a match as proposed by the algorithm. For *Fast-Match* the zones of the right image where local features were computed has been marked with a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

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.
 182

184 Algorithm 1 Fast-Match

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}

200
 201 **3.2 Initiating Seeds**

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 204 Depending on the scenario, several strategies can be used to obtain a set of
 205 initial seed matches. For the case of matching a pair of two images we can get a
 206 rough group of seed matches by matching the thumbnails of the two images with
 207 for example *Ratio-Match*. However if we were matching images in a series, such
 208 as frames from a movie we could instead make use of a subset of the matches
 209 from the last frame to seed *Fast-Match* on the next. In practice we have found
 210 it efficient to resize both images to thumbnails of 300×300 pixels and use ratio
 211 match to obtain a set of matches and ratios that we then threshold with the
 212 confidence threshold τ to obtain the initial seed matches.
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214 **3.3 Collecting Matches and Computing Confidence**

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

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

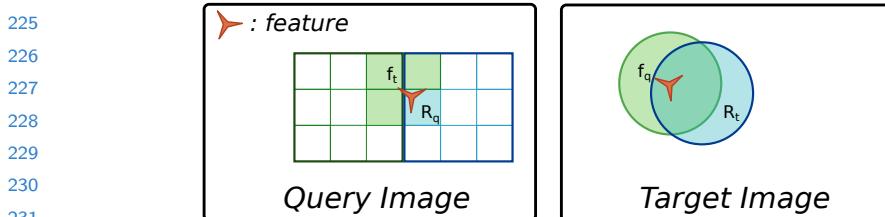


Fig. 2: Exploration of features based on match. The areas shaded blue are the areas that were searched to obtain the match. The areas shaded green are candidate areas for obtaining more matches.

of f_q in the *target image* then the ratio r is defined as follows:

$$r = \frac{d(f_q, f_t)}{d(f_q, f_b)}.$$

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

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

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

270 **3.4 Exploring for Matches**

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271
 272 In each iteration we compute a new set of seed matches, i.e. positions that
 273 might yield more matches in the image. For each region R_i evaluated during the
 274 collection step we now have a set of matches M_i and a set of confidence levels C_i
 275 that we can use to predict whether the neighbourhood of R_i is worth exploring.

276 There are many possible heuristics for predicting possible regions including
 277 local and global epipolar assumptions and partial graph isomorphisms. However,
 278 for the sake of simplicity and speed we have chosen a straightforward approach
 279 based on weak angular assumptions, as illustrated in Figure 2. Assuming that the
 280 *target image* has been cached either in advance or before the matching step, the
 281 blue shaded areas show R_q and R_t for a given seed match. In the *target image* we
 282 collect all features in a given radius while we compute features in the rectangular
 283 R_q in the *query image*. For performance reasons we compute all features in the
 284 blue square but match only the features inside the shaded area. Next a match
 285 is found in the collection step between f_q and f_t . Based on the position of f_q in
 286 R_q we select three areas with potential for more matches. The center of each is
 287 matched with the center position f_t to produce three seed matches for the next
 288 iteration. In Figure 1 we illustrate this process in the *Fast-Match* image pair.
 289 The *query image* to the right in the figure has a small blue square for each region
 290 that has been used while matching the two images.

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

300 **3.5 Computational Complexity**

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301
 302 The difference between the *general* and *retrieval* variation of *Fast-Match* consists
 303 in whether we compute the features in the *target image* (*general*) or if we presume
 304 the features are computed offline (*retrieval*). Computing the features is linear in
 305 the number of feature points, while finding $d(f_q, f_b)$ for all n features in the
 306 *target image* can be done in $O(n \log n)$ using metric trees.

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

313 We will show that the number of possible seed matches is on average linear
 314 in the number of image features, and we also provide an upper bound for the

315 probability that it is not. We assume that outside of true correspondences, fea-
 316 tures have better or at least equally good matches in terms of confidence in the
 317 image they come from. More rigorously put: For any feature in the target image
 318 f_t let f_1, f_2, \dots be the best, second best, etc matching feature from either image
 319 which is not a true correspondence. Let A_{ti} be the event that f_i is found in the
 320 *query image*, then $\mathbb{P}(A_{ti}) \leq 0.5$ and A_{ti} is independent from A_{tj} when $i \neq j$.

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

$$324 X_t = |\{f_q \mid f_q \in F_{query}, d(f_q, f_t) < d(f_q, f_b)\}| \quad (1)$$

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

327 In the worst case, each feature in the *target image* has a true correspondence
 328 in the *query image* and $\mathbb{P}(A_{ti} = 0.5)$, in which case we find can find $\mathbb{P}(X_t =$
 329 $n) = \mathbb{P}(A_{ti})^n = 0.5^n$, as well as the expected value $\mathbb{E}(X_t) = \sum_{i=1}^{\infty} i 0.5^i = 2$, and
 330 the variance $Var(X_t) = \sum_{i=1}^{\infty} 0.5^i (i - 2)^2 = 6$.

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

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

$$341 \mathbb{P} \left(\left| \frac{S_n}{n} - \mathbb{E}(X_t) \right| \geq kn \right) \leq \frac{Var \left(\frac{S_n}{n} \right)}{kn^2} = \frac{6}{k^2 n^3} \quad (2)$$

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

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

353 4 Experimental Setup

354 We evaluate *Fast-Match* over 3024 image pairs featuring various 3D objects at
 355 different angles to measure precision and recall, as well as two pairs of images

360 with high pixel counts to measure performance in terms of speed. We compare
 361 the algorithm to the standard *Ratio-Match* [1] as well as the newer *Mirror-*
 362 *Match* [18]. These two algorithms were selected because they are magnitudes
 363 faster than the fastest geometric algorithms while at the same time providing
 364 robust matches.

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366 4.1 Evaluation of Fast-Match on 3D Objects

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

375



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

390

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

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

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

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405 under 3 different lighting conditions as provided by the dataset. We include all
 406 objects in the database for which photos at 5 degree angle intervals are available
 407 except for the “Rooster” and “Sponge” objects due to image irregularities.
 408

409 4.2 Configuration of *Fast-Match*

410
 411 The central parameters of *Fast-Match* are the confidence threshold τ for selecting
 412 seed matches and the final confidence threshold applied to the total set of
 413 matches. For the experiments on the 3D Objects we let $\tau = 0.9$ and created
 414 precision/recall plots by varying the confidence threshold over the final set of
 415 matches.

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

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 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
 432 results 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.

436 At low angular differences all algorithms show similar performance at low re-
 437 call, however *Fast-Match* is superior to *Ratio-Match* and *Mirror-Match* at higher
 438 recall, more than doubling the precision at similar recall levels. This picture re-
 439 mains the same at higher angular differences, but with a higher performance
 440 gap between *Fast-Match* and the other algorithms at low recall while more than
 441 doubling precision at higher recalls. For image pairs with angular differences of
 442 more than 40° the performance of all algorithms declines, with *Fast-Match* still
 443 coming out on top.

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

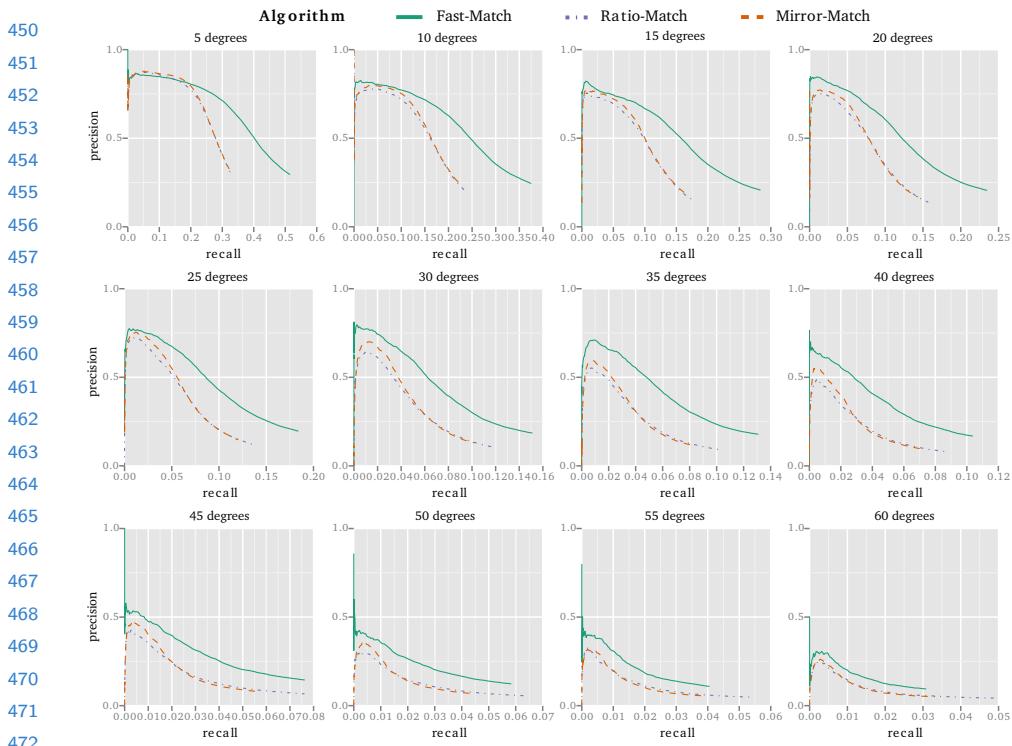


Fig. 4: Results for the 3D Objects dataset. Each plot contains data accumulated from 84 objects photographed under 3 different lighting conditions.

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

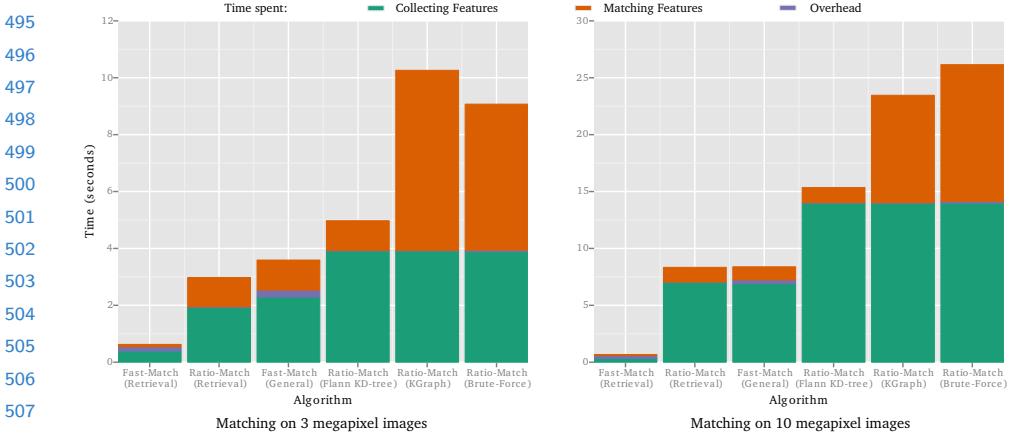


Fig. 5: The duration in seconds of different variations of *Fast-Match* and *Ratio-Match*. The top plot shows results for two 10 MPixel images two 3 Mpixel images is used for the comparison at the bottom. From the left, the first two results presume a precached image while the rest do not require knowing 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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