

Joint 3D Shape Matching

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Abstract

In this paper we extend the global optimization-based approach of jointly matching a set of images to jointly matching a set of 3D meshes. The estimated correspondences simultaneously maximize pairwise feature affinities and cycle consistency across multiple models. We show that the low-rank matrix recovery problem can be efficiently applied to the 3D meshes as well. The fast alternating minimization algorithm helps to handle real world practical problems with thousands of features. Experimental results show that, unlike the state-of-the-art algorithm which rely on semi-definite programming, our algorithm provides an order of magnitude speed-up along with competitive performance. Along with the joint shape matching we propose an approach to apply a distortion term in pairwise matching, which helps in successfully matching the reflexive sub-parts of two models distinctively. In the end, we demonstrate the applicability of the algorithm to match a set of 3D meshes of the SCAPE benchmark database.

1 Introduction

Finding feature correspondences between two meshes is a new problem in computer vision with various applications such as structure from motion, model registration, shape analysis, to name a few. While previous efforts were mostly focused on matching a pair of images, many tasks require to find correspondences across multiple meshes in fact. A typical example is nonrigid structure from motion [4], where one can hardly reconstruct a nonrigid shape from two frames. Furthermore, recent work has shown that leveraging multi-way information can dramatically improve matching results compared to pairwise matching. The most important constraint for joint matching is the cycle consistency, i.e., the composition of matches along a loop of meshes should be identity, as illustrated in Figure 1. Given pairwise matches, one can possibly identify true or false matches by checking all cycles in the mesh collection. But there are many difficulties for this approach. For example, the input pairwise matches are often very noisy Figure 1. An illustration of consistent multi-mesh matching. With many false matches and missing matches, and the features detected from different meshes may only have a partial overlap even if the same feature detector is applied. Therefore, it is likely that very few consistent cycles can be found. Moreover, how to sample cycles is not straightforward due to the huge number of possibilities. Recent work on joint matching has shown that, if all feature correspondences within multiple meshes are denoted by a large binary matrix, the cycle consistency can be translated into the fact that such a matrix should be positive semi-definite and low-rank. Based on this observation, convex optimization-based algorithms were proposed, which achieved the state-of-the-art performances with theoretical guarantees. But these

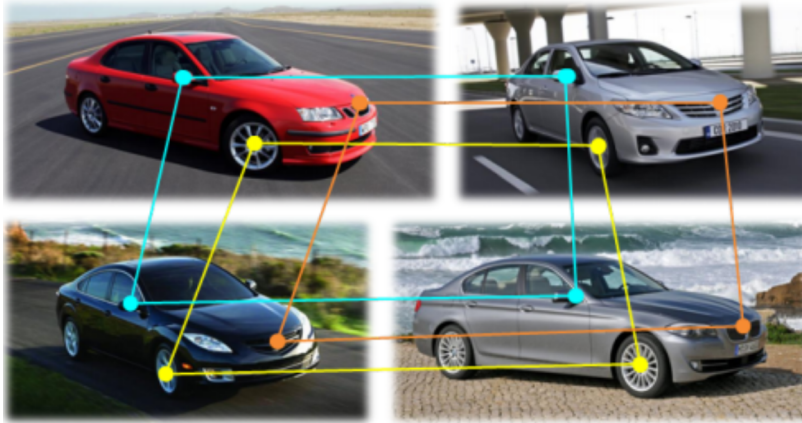


Figure 1: Illustration of Consistent Multi-Image Matching

algorithms rely on semi-definite programming (SDP) [9], which is not computationally efficient to handle image matching problems in practice.

In this paper, we make use of MatchALS [16], a novel algorithm for multi image matching, and use it for 3D model meshes. The inputs to our algorithm are original similarities between feature descriptors which we used Heat Kernel Signature as. The outputs are feature correspondences between all pairs of images. Unlike many previous methods starting from quantized pairwise matches, we postpone the decision until we optimize for both pairwise affinities and multi-mesh consistency. Instead of using Semi Definite Programming (SDP) relaxation, we formulate the problem as a low-rank matrix recovery problem and employ the nuclear-norm relaxation for rank minimization. We show that the positive semi-definiteness of a desired solution can be spontaneously fulfilled. Moreover, we derive a fast alternating minimization algorithm to globally solve the problem in the low-dimensional variable space. Besides validating our method on both simulated and real benchmark data sets, we also demonstrate the applicability of the proposed method combined with Re-weighted Random Walk (*RRWM*) [7] graph matching to match meshes with different models. We introduce a random walk view on the problem and propose a robust graph matching algorithm against outliers and deformation. Matching between two graphs is formulated as node selection on an association graph whose nodes represent candidate correspondences between the two graphs. The solution is obtained by simulating random walks with re-weighting jumps enforcing the matching constraints on the association graph. This algorithm achieves noise-robust graph matching by iteratively updating and exploiting the confidences of candidate correspondences. In a practical sense, this *RRWM* Distortion term is of particular importance since the real-world matching problem is made difficult by the presence of noise and outliers. Extensive and comparative experiments demonstrate that it outperforms the state-of-the-art graph matching algorithms especially in the presence of outliers and deformation.

2 Preliminaries and notation

Suppose we have n models and p_i features from each model i . The objective is to find feature correspondences between all pairs of models. Before introducing the proposed method, we first give a brief introduction to pairwise matching techniques and the definition of cycle consistency.

2.1 Pairwise matching

To match an image pair (i,j), one can compute similarities for all pairs of feature points from two images and store them in a matrix $S_{ij} \in R^{p_i \times p_j}$. We represent the feature correspondences for mesh pair (i,j) by a partial permutation matrix $X_{ij} \in 0, 1^{p_i \times p_j}$, which satisfies the doubly stochastic constraints:

$$0 \leq X_{ij} \mathbf{1} \leq 1, \quad 0 \leq X_{ij}^T \mathbf{1} \leq 1 \quad (1)$$

To find X_{ij} , we can maximize the inner product between X_{ij} and S_{ij} subject to the constraints in (1) resulting in a linear assignment problem, which has been well studied and can be efficiently solved by the Hungarian algorithm. In image matching, spatial rigidity is usually preferred, i.e., the relative location between two features in an mesh should be similar to that between their correspondences in the other mesh. This problem is well known as graph matching and formulated as a quadratic assignment problem (QAP). While QAP is NP-hard [2], many efficient algorithms have been proposed to solve it approximately, e.g. Those solvers basically relax the binary constraint on the permutation matrix, solve the optimization, and output the confidence of a candidate match being correct. We refer readers to the related literature for details. Here we aim to emphasize that the outputs of graph matching solvers are basically optimized affinity scores of candidate matches, which consider both feature similarity and spatial rigidity. We will use these scores (saved in S_{ij}) as our input in some cases.

2.2 Cycle Consistency

For any three models (i,j,z), cycle consistency can be described as

$$X_{ij} = X_{iz} X_{zj}, \quad (2)$$

and can be extended to the case with more than three models. The cycle consistency can be described more concisely by introducing a virtual “universe” that is defined as the set of unique features that appear in the image collection [13]. Each point in the universe may be observed by several images and the corresponding image points should be matched. In this way, consistent matching should satisfy $X_{ij} = A_i A_j^T$, where $A_i \in \{0, 1\}^{p_i \times k}$ denotes the map from Image i to the universe, k is the number of points in the universe, and $k \geq p_i$ for all i .

Suppose the correspondences for all $m = \sum_{i=1}^n p_i$ features in the image collection is denoted by $X \in \{0, 1\}^{m \times m}$ and all A_i s are concatenated as rows in a matrix $A \in \{0, 1\}^{m \times k}$. Then one can write X as

$$X = \begin{pmatrix} X_{11} & X_{12} & \dots & X_{1n} \\ X_{21} & X_{22} & \dots & X_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ X_{n1} & X_{n2} & \dots & X_{nn} \end{pmatrix}, \quad (3)$$

$$X = AA^T \quad (4)$$

From (4), it is clear to see that desired X should be both positive semi-definite and low rank, which effectively impose cycle consistency without checking all cycles of pairwise matches.

$$X \succeq 0, \quad \text{rank}(X) \leq k \quad (5)$$

3 Joint Matching via Rank Minimization

Given the affinity scores $\{S_{ij} | 1 \leq i, j \leq n\}$ for all models, we aim to find globally consistent matches X . Affinity scores can be computed from either feature similarities or graph matching solvers according to specific scenarios, For our experiments we use Heat Kernel Signature (HKS) feature descriptor to define the affinity score matrices.

3.1 Cost Function

To formulate the cost function, we treat the problem as a low rank matrix recovery problem. The inner product between X_{ij} and S_{ij} is maximized for all i, j as multiple linear assignment problems. Alongside, to enforce cycle consistency, the rank of X is minimized. We make following two relaxations on X to optimize the solution:

- X is treated as a real matrix $X \in [0, 1]^{m \times m}$ instead of a binary matrix. Experimental results show that the solution values can be stably quantized by a threshold of 0.5.
- Rank of X is replaced by nuclear norm $\|X\|_*$ (sum of singular values), which is a tight convex relaxation proven to be very effective in various low-rank problems such as matrix completion [6].

The estimated X should be sparse since at most one value in each row of X_{ij} can be nonzero. To induce sparsity, we minimize the sum of values in X . Combining all three terms, we obtain the following cost function:

$$\begin{aligned} f(X) &= - \sum_{i=1}^n \sum_{j=1}^n \langle S_{ij}, X_{ij} \rangle + \alpha \langle 1, X \rangle + \lambda \|X\|_*, \\ &= - \langle S - \alpha 1, X \rangle + \lambda \|X\|_*, \end{aligned} \quad (6)$$

where $\langle \cdot, \cdot \rangle$ denotes the inner product, $S \in R^{m \times m}$ is a collection of S_{ij} s, α is the weight of sparsity, λ controls the weight of the nuclear norm.

Besides the doubly stochastic constraints in (1), additional constraints shall be imposed on X after relaxation:

$$X_{ii} = I_{p_i}, 1 \leq i \leq n, \quad (7)$$

$$X_{ij} = X_{ji}^T, 1 \leq i, j \leq n, i \neq j, \quad (8)$$

$$0 \leq X \leq 1, \quad (9)$$

Finally, we obtain the following optimization problem:

$$\begin{aligned} \min_X & \langle W, X \rangle + \lambda \|X\|_*, \\ \text{s.t.} & X \in C, \end{aligned} \quad (10)$$

where $W = \alpha 1 - S$ and C denotes a set of matrices satisfying the constraints given in (1), (7), (8), and (9).

4 Fast Alternating Minimization

The state-of-the-art methods to solve the convex nuclear norm minimization in (10) are proximal method [14] or ADMM [3] based on iterative single value thresholding [5]. However, singular value decomposition (SVD) needs to be performed in each iteration, which is extremely expensive even for a medium-sized problem.

Similar low-rank optimization was solved in [16] for 2D images more efficiently via a change of variables $X = AB^T$, where $A, B \in R^{m \times k}$ are new variables with a smaller dimension $k < m$.

We use the following lowrank factorization-based formulation implemented for 2D images in [16] and extend it to 3D mesh based models:

$$\begin{aligned} \min_{A,B} \langle W, AB^T \rangle + \lambda \|AB^T\|_*, \\ \text{s.t. } AB^T \in C, \end{aligned} \quad (11)$$

Now rewriting the nuclear norm minimization problem as SDP [15],

$$\|X\|_* = \min_{A,B: AB^T=X} \frac{1}{2} (\|A\|_F^2 + \|B\|_F^2) \quad (12)$$

Finally the following formulation is obtained:

$$\begin{aligned} \min_{A,B} \langle W, AB^T \rangle + \frac{\lambda}{2} \|A\|_F^2 + \frac{\lambda}{2} \|B\|_F^2, \\ \text{s.t. } AB^T \in C, \end{aligned} \quad (13)$$

The selection of matrix dimension k is critical to the success of change of variables, while it directly affects the computational complexity.

4.1 Algorithm

We extend the following algorithm described in [16] for 2D Images to 3D models. The algorithm applies ADMM to solve (13). The augmented Lagrangian of (13) is as follows:

$$\mathcal{L}_\mu(X, A, B, Y) = \langle W, X \rangle + \frac{\lambda}{2} \|A\|_F^2 + \frac{\lambda}{2} \|B\|_F^2 + \langle Y, X - AB^T \rangle + \frac{\mu}{2} \|X - AB^T\|_F^2, \quad (14)$$

where Y is the dual variable and μ is a parameter controlling the step size in optimization. The ADMM alternately updates each primal variable by minimizing \mathcal{L}_μ and updates the dual variable via gradient ascent while fixing all other variables.

Result: Globally consistent matches X
randomly initialize A and B , $Y = 0$;
 $W = \alpha 1 - S$;

while *not converged* **do**

$$\begin{aligned} A &\leftarrow \left(X + \frac{1}{\mu} Y\right) B \left(B^T B + \frac{\lambda}{\mu} I\right)^{\tau}; \\ B &\leftarrow \left(X + \frac{1}{\mu} Y\right) A \left(A^T A + \frac{\lambda}{\mu} I\right)^{\tau}; \\ X &\leftarrow P_c \left(AB^T - \frac{1}{\mu} (W + Y)\right); \\ Y &\leftarrow Y^k + \mu (X - AB^T); \end{aligned}$$

end

quantize X with a threshold equal to 0.5;

Algorithm 1: Matching via Alternating Least Squares (MatchALS)

5 RRWM

Introduction to problem: Graph matching is an essential problem in computer vision and machine learning. In this paper, we implemented a random walk view on the problem and use a robust graph matching algorithm [7] against outliers and deformation. Matching between two graphs is formulated as node selection on an association graph whose nodes represent candidate correspondences between the two graphs. The solution is obtained by simulating random walks with re-weighting jumps enforcing the matching constraints on the association graph. Our algorithm achieves noise-robust graph matching by iteratively updating and exploiting the confidences of candidate correspondences. In a practical sense, our work is of particular importance since the real-world matching problem is made difficult by the presence of noise and outliers. Extensive and comparative experiments demonstrate that it outperforms the state-of-the-art graph matching algorithms especially in the presence of outliers and deformation.

Recent resurgence of combinatorial optimization approaches to feature matching has changed the situation and firmly settled graph matching formulations based on Integer Quadratic Programming (IQP), which is a generalization of the classical graph matching problems. IQP explicitly takes into consideration both unary and pair-wise terms reflecting the compatibilities in local appearance as well as the pair-wise geometric relationships between the matching features. Since IQP is known to be NP-hard, approximate solutions are required. This provides a novel interpretation of graph matching in a random walk view and relates it to the IQP formulation. Introducing an association graph constructed with nodes as candidate correspondences and edges as pair-wise compatibilities between candidate correspondences, we show that the search for correspondences between the given two graphs can be cast as a node ranking [11] and selection problem in the association graph. For this ranking, we introduce an *affinity-preserving random walk* and derive a ranking based on its quasi-stationary distribution, and prove its equivalence to the spectral relaxation for the IQP formulation. Then, in this random walk view, we adopt the personalization strategy of Web ranking algorithms [8] and propose the *re-weighted random walk algorithm* by re-weighting jumps for the graph matching constraints. It achieves noise-robust graph matching by simultaneously updating and exploiting the confidences of candidate correspondences. In a practical sense, our work is of particular importance since the real-world matching problem is made difficult by the presence of deformation and outliers.

5.1 Problem Formulation

The objective of graph matching is to determine the correct correspondences between two attributed graphs $G_P = (V_P, E_P, A_P)$ and $G_Q = (V_Q, E_Q, A_Q)$ where V represents a set of nodes, E , edges, and A , attributes. Each node $v_i^P \in V^P$ or edge $e_i^P \in E^P$ has an associated attribute vector $a_i^P \in A^P$ or $a_i^P j \in A^P$. In feature correspondence problems, a node attribute a_i^P usually describes a local appearance of feature i in model P , and an edge attribute $a_i^P j$ represents the geometric relationship between features i and j in the image P . For each pair of edges $e_i^P j \in E^P$ and $e_a^Q b \in E^Q$, there is an affinity or compatibility $W_{ia};jb = f(a_i^P, a_j^P, a_i^Q, a_b^Q, a_a^Q, a_b^Q)$ that measures the mutual consistency of attributes between the pairs of candidate correspondences (v_i^P, v_a^Q) and (v_j^P, v_b^Q) . Thus, using a matrix form W , a non-diagonal element $W_{ia};jb$ contains a pair-wise affinity between two correspondences (v_i^P, v_a^Q) and (v_j^P, v_b^Q) , and a diagonal term $W_{ia};ia$ represents a unary affinity of a correspondence (v_i^P, v_a^Q) . Representing the correspondence with an assignment or permutation matrix $X \in \{0, 1\}^{n^P n^Q}$ is common, such that $X_{ia} = 1$ implies that node v_i^P corresponds to node v_a^Q , e.g., feature i in the image P is matched to feature a in the image Q , and $X_{ia} = 0$ otherwise. In this paper, we denote $x \in \{0, 1\}^{n^P n^Q}$ as a column-wise vectorized replica of X . The graph matching problem can be formulated as an integer quadratic program (IQP), that is, finding the indicator vector x^* that maximizes the quadratic score function as follows.

$$x^* = \operatorname{argmax}(x^T W x) \quad (15)$$

$$s.t. x \in \{0, 1\}^{n^P n^Q}, \forall i \sum_{a=1}^{n_q} x_{ia} \leq 1, \forall a \sum_{i=1}^{n_p} x_{ia} \leq 1$$

where the two-way constraints refer to the one-to-one matching from G^P to G^Q . In general, no efficient algorithm exists that can guarantee the optimality bounds since the IQP is NP-hard, thus approximate solutions are required.

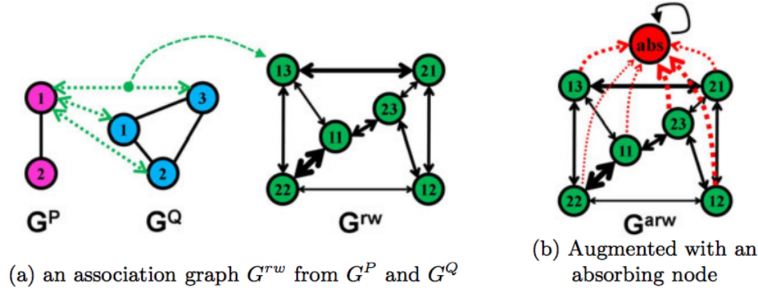


Figure 2: Association Graphs for Graph Matching by Random Walks

5.2 Algorithm

In the previous affinity-preserving random walks, the matching constraints are ignored and not reflected in the random walk process. Inducing the matching constraints only as a post-processing

discretization step like leads to a weak local optimum. How then can we reflect the two-way matching constraints in the affinity-preserving random walk? We adopts the personalization approach widely used in Web ranking methods, which strengthens the effects of reliable nodes in random walks. This is achieved by adopting a jump or teleport in the random walk: the random walker moves by traversing an edge with probability α or by performing a jump to some constrained nodes with probability $1 - \alpha$. α represents the bias between the two possible actions, i.e., following an edge or jumping. To address the lack of personalization or user's focus, Web ranking algorithms adopted this approach in topic-sensitive or query dependent variants. In our formulation, adopting the personalized jump, the probability distribution is updated using the following equation:

$$\left(x^{(n+1)T} x_{abs}^{(n+1)}\right) = \alpha \left(x^{(n)T} x_{abs}^{(n)}\right) P + (1 - \alpha) r^T \quad (16)$$

where a re-weighting jump vector r is added to the affinity-preserving random walk of. In this approach, we use the jumps for generating a biased random walk to the matching constraints.

Given the weight matrix W , the reweight factor α , and the inflation factor β ;
Prevent conflicting walks by setting $W_{ia;jb} = 0$ for all conflicting match pairs ;
Set the maximum degree $d_{max} = \max_i \sum_{jb} W_{ia;jb}$;
Initialize the transition matrix $P = W/d_{max}$, the starting probability x as uniform ;
while x not converged **do**
 (Affinity-preserving random walking by edges) ;
 $\bar{x}^T = x^T P$;
 (Reweighting with two-way constraints) ;
 $y^T = \exp(\beta \bar{x} / \max \bar{x})$;
 while y not converged **do**
 normalize across rows by $y_a i = y_a i / \sum_{i=1}^I y_a i$;
 normalize across columns by $y_a i = y_a i / \sum_{q=1}^A y_a i$;
 end
 $y = y / \sum y_a i$;
 (Affinity-preserving random walking with reweighted jumps) ;
 $x^T = \alpha \bar{x}^T + (1 - \alpha) y^T$;
 $x = x / \sum x_a i$;
end
Discretize x by the matching constraints;

Algorithm 2: Reweighted Random Walk Graph Matching

6 Experimental Results

We evaluate the performance of the proposed method using SCAPE benchmark data [1]. We use the blended intrinsic maps described in [10] to evaluate the performance of MatchALS for 3D meshes with RRWM Distortion term added and compare the matching errors for different models. The size of universe is fixed as 100 points and in each mesh a random sample of the points are observed with a probability denoted by ρ_o . The number of meshes is denoted by n , which is generic in our code but for this simulation purposes it was kept to 4. Then, the ground-truth pairwise matches are established, and random corruptions are simulated by removing some true matches and adding some false matches to achieve an error rate of ρ_e . Finally, the corrupted permutation matrix is fed into our Algorithm as the input affinity scores.

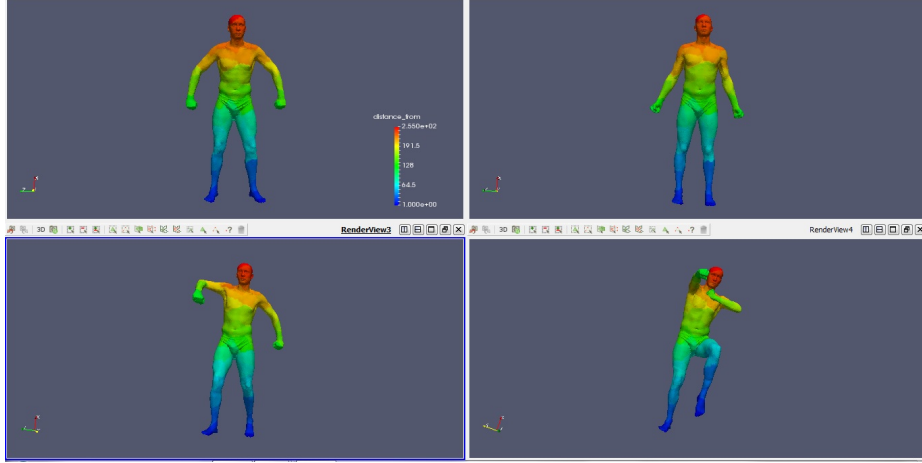


Figure 3: Results of MatchALS performed on 4 Meshes from SCAPE Benchmark Dataset

Figure 3 shows the results we obtained before we applied the RRWM distortion term. We observed 1-to-many feature correspondences prior to RRWM application, and this can be seen by the same color of Figure 3 meshes at the limbs which give false matches sometimes due to the inherent geometrical symmetry of the object.

Next we demonstrate the results obtained from running the MatchALS for 3D Meshes in Figure 4 using the RRWM Distortion term, and the results can be clearly seen to weed out the false positive matches in Figure 4. Precisely colored the same, the limbs are now of different colors, which signifies that RRWM allows one-to-many matches that appear due to inherent symmetry of models, to be filtered out in a very precise manner.

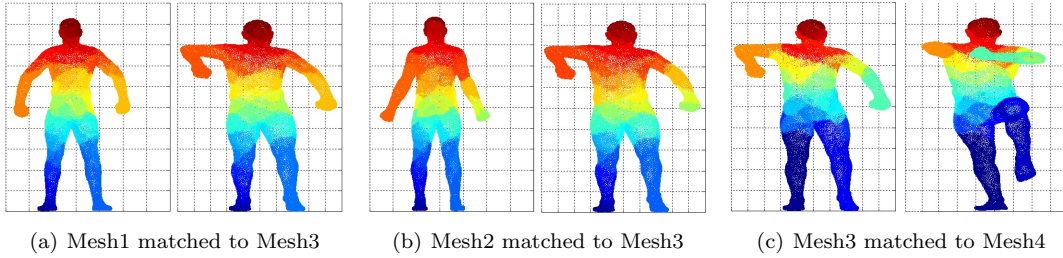


Figure 4: Results of MatchALS combined with RRWM

Figure 5 next shows the 1-to-1 correspondences we have achieved between one pair of meshes we matched and the run time for the simulation was **4.53 seconds**

Next we demonstrate the matching errors between the 4 meshes we obtained. For each pair of possible matching the evaluation was performed by calculating the average Geodesic Error. For the SCAPE Data-set [12] provides the ground truth vertex-to-vertex correspondence. To evaluate performance of our algorithm we map every vertex that has a ground truth correspondence. A geodesic distance between the predicted correspondence and the true correspondence is recorded. Then the error per sample is averaged to calculate the Average Geodesic Error of a mapping between

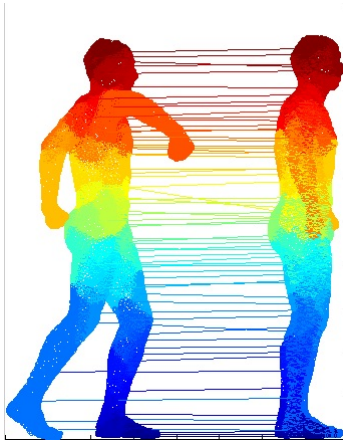


Figure 5: Illustration of 1 to 1 Mapping of feature correspondences in 2 Meshes

	Mesh1	Mesh2	Mesh3	Mesh4
Mesh1	0	1.904%	2.637%	13.909%
Mesh2	1.904%	0	6.824%	18.363%
Mesh3	2.637%	6.824%	0	8.236%
Mesh4	13.909%	18.636%	8.236%	0

Table 1: Average Geodesic Error for matching a pair of Meshes using MatchALS and RRWM

a pair of meshes. Table 1 shows the evaluation results of the pairwise matching of the 4 meshes we used to demonstrate our results.

7 Conclusion

In this paper, we extended the joint matching algorithm MatchALS for 2D images to 3D mesh matching. We use pairwise feature similarities, the heat kernel signature feature descriptor, as inputs and obtain accurate matches by an efficient algorithm (MatchALS) that globally optimizes for both feature affinities and cycle consistency of matches. The experiments not only validate the effectiveness of the proposed method but also demonstrate that joint matching is a promising approach to matching a collection of meshes obtained from crowd sourced 3D model collections. MatchALS is a powerful algorithm that can be extended to 3-D mesh models and the performance generated by the algorithm is almost the same as the state-of-the art algorithm but with exponential orders of increment in speed, as we ourselves observed in our simulation. Coupling the MatchALS with Re-weighted Random Walk Matching is something that has not been done before and our novel implementation of stitching the two algorithms has given very fruitful and promise-bearing results applicable to real world 3-D model matching applications. The results reveal that the matching accuracy in the challenging situations largely depends on the effective exploitation of the matching constraints.

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