Abstract

Finding shortest paths in a graph is relevant for numerous problems in computer vision and graphics, including image segmentation, shape matching, or the computation of geodesic distances on discrete surfaces. Traditionally, the concept of a shortest path is considered for graphs with scalar edge weights, which makes it possible to compute the length of a path by adding up the individual edge weights. Yet, graphs with scalar edge weights are severely limited in their expressivity, since oftentimes edges are used to encode significantly more complex interrelations. In this work we compensate for this modelling limitation and introduce the novel graph-theoretic concept of a shortest path in a graph with matrix-valued edges. To this end, we define a meaningful way for quantifying the path length for matrix-valued edges, and we propose a simple yet effective algorithm to compute the respective shortest path. While our formalism is universal and thus applicable to a wide range of settings in vision, graphics and beyond, we focus on demonstrating its merits in the context of 3D multi-shape analysis.

1. Introduction

Graphs are a fundamental data structure for representing relations between entities. A graph comprises of nodes and edges, where the nodes represent the entities, and edges connect nodes in order to represent their relations. By associating a scalar weight to each edge, one can compute the length of a path along a sequence of connected nodes by summing up individual edge weights. The widely-used graph-theoretic problem of finding shortest paths in a graph has a high relevance for numerous tasks in computer vision and graphics, including image segmentation [49], shape matching [38], computing similarities between shapes [28], or the computation of geodesic distances on surfaces [43, 36], among many others. While these are fundamentally different tasks, the respective shortest path formulations have in common that the weights associated to each edge in the graph are scalar-valued – yet, many problems related to computer vision and graphics rely on graphs with more complex relations between nodes, such as synchronisation methods [3, 44], which are for example relevant for multi-shape analysis. In synchronisation problems, the nodes of the graph represent objects (e.g. images, or 3D shapes), and the edges represent relative transformations between pairs of objects, such as permutation matrices for correspondence problems [8], or rigid-body transformations for alignment problems [7, 4].

Although the example of synchronisation methods illustrates that modelling more complex relations is highly relevant for processing and analysing visual data, we believe that we currently lack the algorithmic machinery in order to fully exploit the potentials of such complex data. As a first step towards addressing this issue, in this work we conceptualise the shortest path problem for graphs with matrix-valued edges. To this end, we address the fundamental question of how to – in a meaningful way – define the cost of
a path comprising of matrix-valued edges, as well as how to find the shortest path between two nodes. Experimentally, we demonstrate that such a formulation offers novel potentials in the context of 3D multi-shape analysis. Overall, our main contributions are:

- For the first time we conceptualise the shortest path problem for graphs with matrix-valued edges.
- For computationally finding shortest paths we introduce an exact search algorithm, which is based on a simple pruning strategy that guarantees to find the globally optimal shortest path.
- As a proof of concept, we show that our novel formalism is beneficial in the context of 3D multi-shape analysis, e.g., for finding intermediate shapes between pairs of shapes in a shape collection, to define a correspondence-free shape metric, or for shape morphing.

## 2. Related Work

In this section we summarise works that we consider most relevant to our approach.

**Graphs in visual computing.** Graphs are omnipresent in computer vision and graphics as they appear in an enormous variety of practical problems. For instance, Kurillo et al. [37] use graphs for multi-camera calibration, where the cameras are connected by edges whose weight represent the number of common points observed by pairs of cameras. In multiple object tracking, graph nodes are used to represent possible spatial locations of objects in different frames, which are connected by edges that represent possible spatial trajectories [33]. For geometric analysis, Sundar et al. [55] use skeleton graphs to compare 3D meshes using graph matching techniques. Wang et al. [59] propose a method based on graph neural networks for constructing 3D meshes from single RGB images. Overall, the diversity of these examples highlight the importance of graphs for addressing computational problems in visual computing.

**Shortest path algorithms.** Finding shortest paths in graphs is a popular graph-theoretic concept that is ubiquitous in many subdisciplines of computer science. Most commonly, a scalar weight is associated to each edge in the graph, so that the length of a path is computed by summing up the individual edge weights. The famous Dijkstra algorithm [18] provides an efficient way to find shortest paths in graphs with positive edge weights. The Bellman-Ford algorithm [5, 23] and the Floyd-Warshall algorithm [22] also allow for negative edge weights under the assumption that there are no cycles with negative weight. The A*-algorithm can improve the computational time in practice based on a heuristic function [26].

An alternative to summing up individual edge weights is the multiplication of edge weights. This is for example relevant for the ‘most reliable path’ problem, where the edge weights represent failure probabilities, and the purpose is to find the path between two nodes that has the lowest probability of failure. Roosta et al. [48] and Pan et al. [45] address this problem by transforming the edge weights logarithmically, so that multiplications become summations, and the problem amounts to an ordinary shortest path problems with additive path costs. Petrovic et al. [46] present algorithms where multiplications of the edge weights are used to determine the most reliable path. Similarly, Jain and Gopal [32] present an algorithm based on node removal techniques in order to reduce the computational effort compared to techniques based on Dijkstra or Floyd. While the mentioned works take into account multiplicative path lengths, they are only considered for the case of scalar edge weights. In contrast, in our work we consider matrix-valued edge weights, where we compute path lengths based on the composition of matrices (e.g. via matrix multiplication).

**Shortest paths in visual computing.** The concept of shortest paths also plays an important role in computer vision and graphics. For example, exact [15, 34, 43, 36] and approximate [2, 39] approaches have been considered to determine the shortest path over a polyhedral surface. Hilaga et al. [28] search for similarities between shapes by computing shortest paths to determine geodesic distances on the surface of every 3D shape.

Shortest paths have also been utilised for model-based 2D image segmentation [49]. Analogous approaches were proposed for 3D image segmentation, which, however, amounts to the significantly more difficult problem of finding a minimal surface [25]. Lähner et al. [38] use a shortest path formulation to determine a non-rigid 2D-to-3D shape matching, for which the product manifold between the 2D shape and the 3D shape forms the corresponding graph.

Berclaz et al. [6] use the shortest path algorithm for multiple object tracking, and Snavely et al. [52] use a modified version of the Dijkstra algorithm to determine structure from motion for large photo collections. The latter approach has led to impressive results, like the digital rebuilding of Rome [1]. Similar to our approach, Snavely et al. [52] use matrices to describe similarities between nodes. However, to compute shortest paths they summarise each matrix into a scalar value by computing the matrix trace, so that eventually they arrive at shortest path problem with scalar edge weights. While the discussed approaches emphasise that shortest paths play an important role in visual computing, existing works have the main limitation that they only consider scalar edge weights.

**Graphs with matrix-valued edges and beyond.** In order to represent complex interrelations between objects, oftentimes graphs with edges that go beyond simple scalar weights are utilised. One particular example are matrix-valued edges, which can for example represent relative spatial transformations, or correspondences between pairs of objects. Such graphs with matrix-valued edges are common
in synchronisation problems [3], where nodes represent objects (images, cameras, shapes, etc.) and the edges represent relative transformations between them (rigid-body motion, correspondences, etc.). The purpose of synchronisation is to establish cycle consistency in the set of pairwise relative transformations. One popular application of synchronisation is multi-view registration [50, 42], where edges model the rotation and translation between different views. Thunberg et al. [56] formulate the synchronisation problem over graphs with orthogonal matrices as a nonlinear least-squares problem. The algorithm was extended in [57] to also address translations. Similarly, Arrigoni et al. [4] present a method for synchronising graphs with matrices in SE(3), and Bernard et al. [7] show a method to align objects that are connected by invertible linear transformations. Synchronisation problems have also been utilised in various contexts for deep learning [31, 29, 24, 47].

Let us consider the function
\[ f: \mathcal{M} \rightarrow \mathbb{R}^+ \]
that maps a matrix to a non-negative real value. Among all possible paths from node \( s \) to node \( t \), we denote the path \( \pi_{st}^\star \) that gives rises to the lowest value of \( f \) as shortest path. We denote the composed matrices in the shortest path as \( M_{\pi_{st}^\star} \), so that the corresponding cost is \( f(M_{\pi_{st}^\star}) \), which we write as \( f(\pi_{st}^\star) \) by abuse of notation.

4. Algorithm

In the following we propose a search algorithm in order to find the shortest path between a source node \( s \in \mathcal{V} \) and all other nodes \( t \in \mathcal{V} \setminus \{s\} \). To this end, we introduce a generic framework that can handle arbitrary cost functions. For the sake of simplicity we assume that the graph is complete, i.e. \( \mathcal{E} = \mathcal{V} \times \mathcal{V} \). To guarantee the correctness of our algorithm, we have to ensure that adding an edge to the current path can only increase the path cost (analogously to the Dijkstra algorithm, in which scalar-valued edges cannot have negative costs). Formally, we require that the function \( f \) monotonically increases the path cost:

**Condition 1** (Monotonicity of path cost). The function \( f \) monotonically increases the path cost in the sense that \( f(M \circ X) \geq f(M) \) holds for all \( M \in \mathcal{M} \), \( X \in \mathcal{M} \).

In addition, we impose that \( f(I) = 0 \), i.e. the identity matrix has zero path cost. Condition 1 gives rise to the following straightforward yet important result:

**Lemma 1.** Consider \( k \geq 2 \). Let \( \pi_{sp}^\star \) be the shortest path from \( s \) to \( p \) among all paths with exactly \( k-1 \) edges, and \( \pi_{st}^\star \) the shortest path from \( s \) to \( t \) with at most \( k-1 \) edges. If \( f(\pi_{st}^\star) \leq f(\pi_{sp}^\star) \), then any path \( \pi \) that contains \( p \) at the \( k \)-th position cannot lead to a shorter path from \( s \) to \( t \) than \( \pi_{st}^\star \).

**Proof.** Consider the subpath \( \pi' \) of \( \pi \) from \( s \) to \( p \). Since \( \pi' \) comprises \( k-1 \) edges, \( f(\pi_{sp}^\star) \leq f(\pi_{sp}) \leq f(\pi', \pi) \), due to the optimality of \( \pi_{sp}^\star \). Further, as \( \pi' \) is a subpath of \( \pi \), from Condition 1 it follows that \( f(\pi') \leq f(\pi) \), so that \( f(\pi_{sp}^\star) \leq f(\pi) \).

This indicates that \( f(\pi_{sp}^\star) \) serves as lower bound for the cost of any path \( \pi \) from \( s \) to \( t \) that has \( p \) at the \( k \)-th position. Hence, we can prune paths with \( p \) at the \( k \)-th position from the search tree, whenever their cost is larger than the shortest path from \( s \) to \( p \) with at most \( k-1 \) edges, as illustrated in Fig. 2. To implement this, at a time we consider only paths comprising \( k \) edges, for which we keep track of all candidates of intermediate nodes \( p \) that can possibly lead to a shorter path between \( s \) and \( t \). Those candidates that can appear at the \( k \)-th position in the path from \( s \) to \( t \) are denoted by \( T_k(t) \). During our search, when considering paths from \( s \) to \( t \) comprising of exactly \( k \) edges, we only consider paths of the form \( \mathcal{A}(t) = \{(s, u_2, \ldots, u_k, t) : u_i \in T_i(t), i = 2, \ldots, k\} \).

Our algorithm is outlined in Alg. 1. It proceeds by iterating over \( k = 2, 3, \ldots \), where \( k \) denotes the number of
edges contained in a path. For a given number of edges $k$, we determine all candidate paths that could potentially be a shortest path between node $s$ and target node $t$, and store them in the set $\mathcal{A}(t)$. In case the set $\mathcal{A}(t)$ is empty for all $t$, we have evaluated all paths that are potential candidates for a shortest path, and we terminate. If the cost $f(\pi)$ of a path $\pi \in \mathcal{A}(t)$ from $s$ to $t$ is smaller than the cost $f(\pi^*_{st})$ of the current shortest path $\pi^*_{st}$ from $s$ to $t$, $\pi^*_{st}$ is updated.

In the case of a complete graph, there are $O(n!)$ candidates for the shortest path between source $s$ and a given target $t$, which need to be evaluated in the worst case. Yet, due to Lemma 1, we can reduce the average time complexity significantly in practice.

5. Application to Multi-Shape Analysis

We demonstrate the merits of our matrix-valued shortest path formalism and its universal applicability to a diverse range of tasks in multi-shape analysis. To this end, as a proof of concept we consider its application for the definition of a correspondence-free shape metric, for finding intermediate shapes between a given pair of shapes, and for shape morphing.

For the rest of the paper, we consider the specific choice $\mathcal{M} = \{X \in [0, 1]^{n \times n} : X1 = 1, X^T1 = 1\}$, i.e. the set of doubly-stochastic matrices, and we use matrix multiplication as composition operation $\circ$. Since the set of doubly-stochastic matrices forms a semigroup with matrix multiplication as group operation [21], $\mathcal{M}$ is closed under matrix multiplication, and contains the identity matrix $I$ as identity element. The doubly-stochastic matrix $M_{xy}$ connecting node $x$ to $y$ can be seen as a probabilistic correspondence between $n$ parts on $x$ and $n$ parts on $y$. Hence, we define all edge matrices in a symmetric manner, so that $M_{yx} = M_{xy}^T$. In order to quantify the cost of a path, we consider the “fuzzyness” of the composed probabilistic correspondence along a path. To this end, we set $f$ to the total entropy $H : [0, 1]^{n \times n} \rightarrow \mathbb{R}^+$, i.e.

$$H(X) = -\sum_{i, j} X_{ij} \log(X_{ij}),$$  

(1)

which is commonly used for this purpose [53]. We use the common convention that $0 \cdot \log(0) = 0$.

The following confirms that the function $H$ monotonically increases the path cost (as required in Condition 1):

**Lemma 2.** For $M, X$ being doubly-stochastic matrices it holds that $H(MX) \geq H(M)$.

**Proof.** The doubly stochastic matrix $X$ can be expressed as a convex combination of permutation matrices (Birkhoff’s theorem [11]), i.e. $X = \sum \alpha_i P_i$, where $P_i$ is a permutation matrix and $\alpha_i \geq 0$ with $\sum \alpha_i = 1$. Moreover, the function $H(\cdot)$ is concave over the domain $[0, 1]^{n \times n}$ [17], so that $H(MX) = H(\sum \alpha_i P_i) \geq \sum \alpha_i H(M P_i) = \sum \alpha_i H(M) = H(M)$, where the second-last equality follows since reordering the columns of the matrix $M$ by $P_i$ does not affect the value of $H(\cdot)$. Note that for the specific case of $X$ being binary, the inequality is tight, i.e. $H(MX) = H(M)$. \qed
Figure 3: **Closest shapes of SMAL toys [60].** The three closest shapes (left to right) of the four query shapes (gold) are shown. Shapes that belong to the same family as the query shape are shown in green. Our algorithm finds the most shapes from the same family. Note that each shape is scaled individually for visualisation purposes.

### 5.1. Probabilistic Multi-Matching Graph

Next, we explain how we construct our probabilistic multi-matching graph for a given collection \( S \) of 3D shapes. The \((n \times n)\)-dimensional doubly-stochastic matrices \( M_{xy} \) represents probabilistic correspondences between shapes \( x \in S \) and \( y \in S \). In contrast to commonly-used scalar edges, such matrix-valued edges constitute a powerful representation that can capture fine-grained information about correspondences between individual points of shapes. To obtain them, we first compute SHOT features for all vertices of each 3D shape [58]. Subsequently, in order to allow for shapes with a varying number of vertices, we cluster all vertices of one shape into \( n \) clusters using the k-means algorithm [40], where we choose \( n = 28 \) in all experiments. Then, we encode the SHOT feature distribution of all vertices within a cluster in terms of percentile statistics, which serves as a cluster-specific feature descriptor that summarises the characteristics of each cluster. Doing so allows us to compute the similarity matrix between the clusters of two 3D shapes, for which we consider a Gaussian kernel applied to the \( \ell_2 \)-norm of the difference between cluster feature descriptors, stored as \( n \times n \) matrix. In order to obtain the doubly-stochastic matrix \( M_{xy} \), we use the Sinkhorn matrix scaling algorithm [51]. Thus, each entry in \( M_{xy} \) can be interpreted as the probability to match a cluster of shape \( x \) to a cluster of shape \( y \). Overall, the probabilistic multi-matching graph \( \mathcal{G} = (S, E) \) is obtained by identifying each shape in \( S \) with a node, where all pairs of nodes are connected by an edge to which the respective probabilistic correspondence matrix is assigned. Further details regarding the probabilistic multi-matching graph generation are presented in the Appendix.

### 5.2. Correspondence-Free Shape Metric

In this experiment we use our algorithm to define a metric on a given dataset \( S \) of 3D shapes. The distance between the shape \( x \in S \) and the shape \( y \in S \) is defined as the total entropy of the shortest path between them, i.e. \( H(M_{xy}) \), which we also write as \( H(\pi_{xy}) \) by abuse of notation. The following holds for \( H \):
Lemma 3. For our probabilistic multi-matching graph \( G = (S, E) \), the function \( H \) fulfills to following properties:

1. **Identity.** For all \( x \in S \), \( H(\pi^*_{xx}) = H(M_{xx}) = 0 \).
2. **Non-negativity.** For all \( x, y \in S \), \( H(\pi^*_{xy}) \geq 0 \).
3. **Symmetry.** For all \( x, y \in S \), \( H(\pi^*_{xy}) = H(\pi^*_{yx}) \).
4. **Triangle Inequality (under \( S \)).** For all \( x, y, z \in S \), \( H(\pi^*_{xy}) \leq H(\pi^*_{xz} \circ \pi^*_{yz}) \), where in this context the operation \( \circ \) denotes the concatenation of two paths.

**Proof.** 1. By definition, \( M_{xx} \) is the identity matrix \( I \), and \( H(I) = 0 \). Since there cannot be a shorter path with lower cost (due to 2.), the corresponding path \( (x) \) constitutes a shortest path from \( x \) to \( x \).

2. The total entropy maps doubly stochastic matrices to non-negative numbers, so \( H(M) \geq 0 \) for any \( M \in M \).

3. The commutativity of summation implies that the total entropy is symmetric in the sense that \( H(X) = H(X^T) \) for any \( X \in M \). Since by definition \( M_{xy} = M_{yx}^T \) for all \( x, y \in S \), the shortest path from \( y \) to \( x \) must be the same as the shortest path from \( y \) to \( x \) in reverse order. As such, \( H(\pi^*_{xy}) = H(M_{yx}) = H(M_{xu_1}M_{u_1u_2}...M_{u_ky}) = H(M_{yk}...M_{u_2u_1}M_{u_1x}) = H(M_{yx}) = H(\pi^*_{yx}) \).

4. Since \( H(\pi^*_{xz}) \) is the shortest path between node \( x \) and node \( z \), any other path between \( x \) and \( z \) via \( y \) cannot lead to a smaller cost. \( \square \)

**Results.** First, we run our algorithm to determine the distance between all pairs of 3D shapes. Given these distances, we obtain the \( k \) nearest neighbour shapes for a given query shape. In this experiment we consider the 41 toy animals of the SMAL dataset [60]. The dataset is categorised into five animal families (cats, dogs, cows, horses, hippos). For our evaluation, we interpret a nearest neighbour shape that belongs to the same animal family like the query shape as correct. We compare our metric with two baselines for computing nearest neighbours:

- **The Euclidean distance (Eucl)** between the vertices of shapes. In that case, vertex-to-vertex correspondences between the shapes need to be known. We emphasise that finding correspondences between a shape collection [9] is an extremely difficult problem, and thus this setting is rather unrealistic in many practical scenarios.

- **Hence,** we additionally consider the Euclidean distance after using the iterative closest point (ICP) algorithm [10, 16] for registering the randomly rotated shapes without known correspondences. This is a more realistic setting, since here we assume that we do neither know correspondences, nor the spatial alignment between shapes.

In Fig. 3 we show the three closest shapes of four different animals. It can be seen that our algorithm leads to the best results, i.e. it finds the most neighbour shapes from the same animal family. To quantitatively evaluate the performance of the three methods, we consider the proportion of correct nearest neighbours for the \( i \)-th animal and a given number of neighbours \( k \), denoted as \( g(i,k) \). The value of \( g(i,k) \) is evaluated for each of the three methods, where \( TP(i,k) \) denotes the total number of true positives of the \( i \)-th animal among the \( k \) nearest neighbour shapes obtained by the respective method. Further, \( m_i \) is the number of animals that belong to the category of the \( i \)-th animal, and \( k \) denotes the number of nearest neighbours that are considered. Fig. 4 shows that our method significantly outperforms both the Euclidean distance and ICP.

**5.3. Intermediate Shapes**

In this experiment we consider the task of finding intermediate shapes between two given shapes. This is closely related to shape interpolation [35, 27, 20, 19], which is typically based on the assumption that there exists a smooth deformation between two given shapes. The difference between an intermediate shape and shape interpolation is that intermediate shapes must be part of the shape collection. Hence, while interpolation can lead to implausible shapes, this cannot happen for intermediate shapes. Moreover, finding intermediate shapes within our shortest path setting does not require vertex-to-vertex correspondences between shapes, which is often necessary for interpolation methods that rely on explicit shape representations.

We consider two settings for this experiment: (i) In the first setting, we find the shortest path between two given shapes that has a fixed number of edges \( k \). By doing so, we can exactly specify the number of desired intermediate shapes, so that this setting is relevant whenever we are interested in a fixed number of intermediate shapes. Results for shortest paths among all paths with a fixed number of edges are shown in Fig. 5. (ii) In the second setting, we consider the shortest path among all possible paths, rather than paths with a fixed number of edges. Here, the number of obtained intermediate shapes is directly determined.
by the dataset. As such, there is also the possibility that the
direct path leads to the lowest cost, and thus there may not
always exist intermediate shapes between a pair of shapes.
Respective results are shown in Figs. 6 and 7. We can even
find reasonable intermediate shapes when the topologies be-
tween shapes vary drastically, as demonstrated in Fig. 7.

5.4. Shape Morphing

A use case for intermediate shapes between two shapes is
shape morphing. To do so, given a source and a target
shape, we first find all intermediate shapes along the short-
est path between the source and the target. Subsequently,
we perform a piecewise linear interpolation between pairs

![Figure 5: Shortest paths comprising $k=3$ edges. We find reasonable intermediate shapes (second and third column), between the source (left) and the target shape (right), i.e. between a standing cat and a running dog (top row, Non-Rigid World dataset [12]), as well as between a rounded armchair and a square armchair (bottom row, ShapeNet [14]).](image)

![Figure 6: Intermediate shape between two different shapes. By finding the shortest path from a source to a target shape, our algorithm is able to find a reasonable intermediate shape between a standing cat and an attacking lion, a jumping centaur and a running lion, as well as a jumping dog and a standing lion (Non-Rigid World dataset [12]).](image)

| Source | Intermediate | Target |
|--------|--------------|--------|
| ![Cat](image) | ![Intermediate](image) | ![Dog](image) |
| ![Armchair](image) | ![Intermediate](image) | ![Armchair](image) |

| Dataset       | #Shapes | Time (SP) [s] | Time (CERT) [s] |
|---------------|---------|---------------|-----------------|
| SMAL          | 41      | 1.6           | 154             |
| ShapeNet Chairs | 51      | 3.8           | 35.2            |
| TOSCA (‘Michael’) | 20      | 0.33          | 1.6             |
| Non-Rigid World | 78      | 147.45        | 147.45†         |

Table 1: Runtimes of our algorithm for finding the globally optimal shortest paths between all node pairs (SP), and for certifying their global optimality (CERT).

of shapes along this shortest path. In contrast, a naive linear
interpolation between the source and target leads to severe
artefacts, which are particularly prominent if both shapes
differ significantly. We illustrate results in Fig. 8 for mor-
phing two human body shapes with large poses differences.
Animated results can be found in the Appendix. Although
more involved interpolation methods could also be used
(both in conjunction with our method, and for direct source-
to-target morphing), here we use a simple linear interpola-
tion to highlight potential problems due to a direct morph-
ing, which is effectively circumvented using our method.

6. Discussion & Future Work

While we believe that our work offers a strong potential
for numerous applications, even beyond multi-shape analy-
isis, interesting open research questions are remaining.

**Computational cost.** Our proposed shortest path prob-
lem does (in general) not exhibit the optimal substructure
property, i.e. a subpath of a shortest path may not neces-
sarily be a shortest path. As such, generalising existing
shortest paths paradigms (e.g. Dijkstra) to our setting would
generally not guarantee the global optimality of so-obtained
‘shortest’ paths. While Alg. 1 finds globally optimal short-
est paths, it has an exponential worst-case time complex-
ity. For moderately-sized graphs ($\leq 51$ nodes), we can find
Figure 7: **Intermediate shapes for different topologies.** Our method can find reasonable intermediate shapes between various types of chairs from ShapeNet [14], even if their topology varies drastically.

Figure 8: **Morphing the ‘Michael’ shape from the TOSCA dataset [13].** Frames of the shape morphing process at t=0 (source), t=0.4, t=0.6, t=0.75 and t=1 (target) are shown. For each time step, the left shape shows our morphing, whereas the right shape shows the morphing via naive linear interpolation. Overall, our morphing leads to significantly fewer artefacts.

shortest paths between all nodes within seconds, and we certify the global optimality within minutes (see Table 1). † For the larger Non-Rigid World dataset [12], where we included quadrupeds, the centaur and the Michael shape, we limit the maximal number of edges in a path to $k_{\text{max}}=3$.

**Edge matrix construction.** In our experiments we considered edge matrices obtained via percentile statistics summarising the SHOT feature distribution of vertex clusters. While we demonstrated various intriguing results, we found that e.g. inconsistent clusters may cause problems (see Appendix). Yet, this is neither a limitation of our shortest path formalism, nor of our algorithm, but rather stems from the specific choice of edge matrices. The exploration of improved graph construction methods is an interesting direction for future work. One way may be the integration of our method into end-to-end trainable deep neural networks, e.g. via differentiable programming, in order to learn task-specific optimal edge matrices directly from data. Additionally we expect that our method will inspire follow-up works that consider shortest paths for edges with even more elaborate attributes than matrices.

**7. Conclusion**

For the first time we have conceptualised the shortest path problem for graphs with matrix-valued edges. To this end, we introduced a generic modelling framework, along with a globally optimal search strategy for finding respective shortest paths. As a proof of concept, we studied matrix-valued shortest paths in the context of multi-shape analysis. We believe that our formalism has a strong potential for numerous other applications in vision, graphics, and beyond. Overall, we hope that our work will spark interest in developing more involved algorithmic machinery that is better capable of modelling and analysing the complex interrelations that occur in real-world visual computing problems.

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A. Appendix

In this document we present additional results and an in-depth explanation of our graph generation.

A.1. Additional Results

Shape morphing. We use the two settings (‘Michael’ and cat) from the TOSCA dataset [13] to show exemplary shape morphing results using an intermediate shape found using our matrix-valued shortest path paradigm. In Fig. 9, we show the intermediate shapes between the source and target shape that were used to compute our morphing. For the ‘Michael’ shape (see Fig. 8, as well as the animation in Fig. 11), we place the intermediate shape at t=0.5. In this case, we can observe a smooth morphing result.

For the cat (see Fig. 10, as well as the animation in Fig. 11), the intermediate shape is placed at t=0.8, because its pose lies much closer to the target shape than to the source shape. In this case, there is no intermediate shape in the dataset that fits to t=0.5, so that particularly during the first part of the morphing we can observe some minor artefacts using our method, whereas naive linear interpolation leads to more drastic artefacts (see the gif animation). This emphasises that shape morphing is highly data-dependent, in the sense that the denser the different pose changes are covered in a dataset, the better the morphing results.

| Source | Intermediate | Target |
|--------|--------------|--------|
| ![Source Shape](image1.png) | ![Intermediate Shape](image2.png) | ![Target Shape](image3.png) |
| ![Source Shape](image4.png) | ![Intermediate Shape](image5.png) | ![Target Shape](image6.png) |

Figure 9: Intermediate shapes used for our shape morphing. We use two example shapes of the TOSCA dataset [13] (‘Michael’ and cat) to morph the source (left) over the intermediate (middle) to the target shape (right).

Failure cases. Our edge matrices are obtained in terms of the similarity between clusters extracted from two 3D shapes. While in many cases doing so leads to sensible results, there are also some failure cases. We illustrate one such case in Fig. 12, where the found clusters are inconsistent. In turn, the respective edge matrices are not very meaningful, so that an implausible intermediate shape is obtained. We emphasise that this is neither a limitation of our shortest path formalism, nor of our shortest path algorithm, but rather due to a suboptimal feature engineering.

Our edge matrices inherit rotation-invariance from the SHOT features. Although rotation-invariance is a desirable property in many cases, in the context of shape morphing it may lead to undesirable results. For example, the intermediate shape between two standing ‘Victoria’ shapes of the TOSCA dataset leads to a shape in lying position, as shown in Fig. 13 – although in this case the intrinsic shape properties are indeed ‘intermediate’, when considering the extrinsic shape, e.g. as it would be used for shape morphing, the results appear unnatural. Again, this is not a limitation of our method, but rather due to the way how the edge matrices are constructed.

A.2. Details on Graph Generation

Next, we explain how we construct our probabilistic multi-matching graph for a given collection \( S \) of 3D shapes, where each shape in \( S \) represents a graph node. For each pair of shapes we compute a probabilistic correspondence matrix of size \( n \times n \). To obtain them, we first compute SHOT features for all vertices of each 3D shape [58]. Subsequently, in order to allow for shapes with varying number of vertices, we cluster all vertices of one shape into \( n \) clusters using the k-means algorithm [40], where we choose \( n = 28 \) in all experiments. Then, we describe the SHOT feature distribution of all vertices within a cluster in terms of percentile statistics, which then serves as a cluster-specific feature descriptor that summarises the characteristics of each cluster. For each cluster \( i \), and each of the shapes \( x \) and \( y \), we obtain the percentile statistics matrices \( P_i^{(x)} \) and \( P_i^{(y)} \) of size \( p \times f \), where \( p \) is the number of considered percentiles and \( f = 352 \) is the dimension of the SHOT feature descriptor. For every pair of clusters between shape \( x \) and \( y \), we consider the Frobenius norm of the difference between the per-cluster percentile statistics. To this end, we define the distance between the \( i \)-th cluster of shape \( x \) and the \( j \)-th cluster of shape \( y \) as

\[
d_{ij} = \| P_i^{(x)} - P_j^{(y)} \|_F. \tag{2}
\]

In order to transform the distances \( d_{ij} \) to similarity scores, we apply a Gaussian kernel, i.e.

\[
m_{ij} = \exp(-\frac{d_{ij}^2}{\sigma^2}). \tag{3}
\]

Eventually, we use the Sinkhorn matrix scaling algorithm [51] in order to obtain the doubly-stochastic matrix \( M_{xy} \). Here, each entry at position \((i, j)\) of the matrix \( M_{xy} \) can be interpreted as the probability to match the \( i \)-th cluster of shape \( x \) to the \( j \)-th cluster of shape \( y \). The choice of
Figure 10: **Morphing the cat shape from the TOSCA dataset [13].** Frames of the shape morphing process at t=0 (source), t=0.4, t=0.6, t=0.75 and t=1 (target) are shown. For each time step, the left shape shows our morphing, whereas the right shape shows the morphing via naive linear interpolation. We can see that our morphing gives more plausible results compared to naive linear interpolation.

Figure 11: Animation of shape morphing of the 'Michael' and cat shapes from the TOSCA dataset [13]. (supported PDF reader required to play animation)

Figure 12: **Inconsistent clusters lead to unreliable intermediate shapes.** Using the chairs of ShapeNet [14], some obtained intermediate shapes are not plausible (top row). This is not a limitation of our method per-se, but stems from inconsistent clusters (bottom row).

| Dataset             | #percentiles | p   | standard deviation | σ   |
|---------------------|--------------|-----|--------------------|-----|
| Non-Rigid World     | 300          | 2   |                    |     |
| TOSCA 'Michael'     | 3000         | 4.5 |                    |     |
| TOSCA 'Victoria'    | 150          | 0.7 |                    |     |
| TOSCA Cat           | 150          | 1   |                    |     |
| SMAL                | 300          | 3   |                    |     |
| ShapeNet Chairs     | 1000         | 2   |                    |     |

Table 2: Overview of chosen parameters.

the parameters $p$ and $σ$ is shown in Table 2, and the entire process of the graph generation is outlined in Fig. 14.
Figure 13: **Rotation invariance may lead to undesirable intermediate shapes.** The intermediate shape of two standing 'Victoria' shapes of the TOSCA dataset [13] results in a lying shape that is unsuitable for shape morphing. This can be avoided by considering rotation-variant features for constructing the edge matrices.
Figure 14: **Probabilistic multi-matching graph construction.** First, we compute SHOT features on the 3D shapes [58], and perform a k-means clustering [40]. We then summarise the distribution of the SHOT features in the clusters in terms of percentile statistics. We use the \( \ell_2 \)-norm to compute differences between the per-cluster percentile statistics, so that we obtain a distance matrix of size \( n \times n \). By applying a Gaussian kernel, distances are translated into similarity scores. Eventually, the Sinkhorn matrix scaling algorithm [51] is used to obtain doubly-stochastic matrices that can be interpreted as probabilities of matching pairs of clusters between shapes.