

# Hausdorff morphs with fewer components

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## Abstract

We introduce two geometry-based morphing techniques that build upon the existing Voronoi and mixed morphs. These morphs are Hausdorff morphs, meaning they linearly interpolate the Hausdorff distance between the two polygons. Our new morphs are also Hausdorff morphs, and additionally reduce the number of components in intermediate shapes. In an experimental analysis we record data on the area, perimeter and total angular change throughout the morph, and the number of holes and components. Our new morphs perform better in these aspects than their original counterparts and the new component-reduced mixed morph also appears to introduce fewer visual artifacts in the intermediate polygons.

## 1 Introduction

Shape morphing, also called shape interpolation, is the process of gradually transforming a source shape to a target shape over time. Good morphs produce intermediate shapes that preserve the input shapes' appearances.

We focus on abstract morphing between 2D shapes. Abstract morphs do not concern themselves with (semantic) reasons to transform certain parts of the source shape to the target shape. This type of morphing can be used to morph between complex shapes that do not have any clear correspondence.

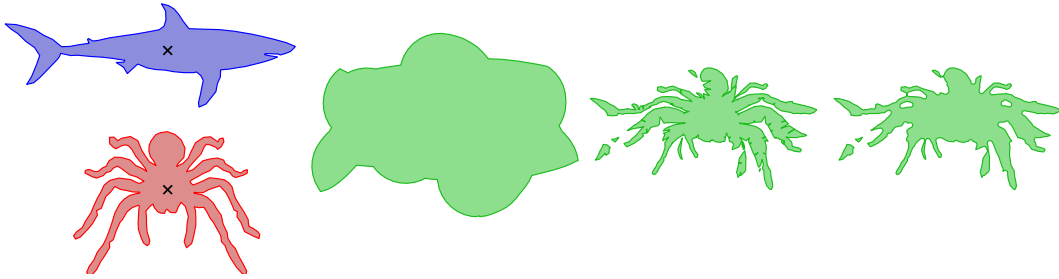
To capture a morph is gradual, we may use distance measures between shapes: ideally, the distance to the source shape should linearly increase, while the distance to the target shape should linearly decrease. A morph is a *Hausdorff morph*, when it satisfies this property using the Hausdorff metric [5]. The *dilation morph* [5] is such a Hausdorff morph, though the resulting intermediate shapes tend to lack characteristic features of either input shapes; see Figure 1. The *Voronoi morph* [3] is also a Hausdorff morph; compared to the dilation morph, it greatly reduces the area of intermediate shapes and also retains more characteristic features. This morph does however add superfluous components and noise: extra details that are not present in the input shapes; see Figure 1. The above two morphs combine into a *mixed morph* [3], which reduces, but does not eliminate these issues. We introduce the *Component-Reduced Voronoi morph* (CRV morph): a Hausdorff morph based on improving the Voronoi morph by reducing the number of extra components in intermediate shapes. We also describe the *Mixed Component-Reduced Voronoi morph* (MCRV morph), by combining our CRV morph with the dilation morph, resulting in intermediate shapes with considerably less noise and fewer superfluous components.

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■ **Figure 1** From left to right: two input shapes, with the origin of the plane indicated with a cross; intermediate shapes of the dilation [5], Voronoi [3] and mixed [3] morphs at  $\alpha = 1/2$ .

### 1.1 Preliminaries

**Hausdorff distance.** For two non-empty sets  $A$  and  $B$ , the Hausdorff distance is defined as

$$d_H(A, B) := \max\left(\sup_{a \in A} \inf_{b \in B} d(a, b), \sup_{b \in B} \inf_{a \in A} d(b, a)\right)$$

where  $d$  denotes the Euclidean distance.  $d_H(A, B)$  is a bottleneck metric that can be described as the largest distance from all points in  $A$  and  $B$  to their closest point on the other shape.

**Morphs.** We regard morphs as a function from the interval  $[0, 1]$ . The parameter  $\alpha$  operating on this interval can be viewed as time. The function operates on two shapes  $A$  and  $B$ , and outputs another shape  $C_\alpha$ , where  $C_0 = A$  and  $C_1 = B$ . The output shape is referred to as an *intermediate shape*.

Assume we are given two shapes  $A$  and  $B$  in the plane that is scaled so that  $d_H(A, B) = 1$ . A morph that outputs  $C_\alpha$  is called a *Hausdorff morph* if it satisfies the *Hausdorff property*:  $d_H(A, C_\alpha) = \alpha$  and  $d_H(B, C_\alpha) = (1 - \alpha)$ , for all  $\alpha \in [0, 1]$ . For shapes that do not have a Hausdorff distance of 1, we can easily scale the plane uniformly to achieve a Hausdorff distance of 1; as the considered morphs are scale-invariant, this does not affect results.

We define a *component* of a shape  $S$ , as a disjoint non-empty subset, such that two components of  $S$  are always positively separated.  $S$  is equal to the union of all its components.

**Dilation morph.** The *dilation morph* [5] is defined as

$$S_\alpha(A, B) := (A \oplus D_\alpha) \cap (B \oplus D_{1-\alpha}),$$

where  $\oplus$  denotes the Minkowski sum defined as  $\{a + b \mid a \in A, b \in B\}$ , and  $D_\alpha$  is a disc of radius  $\alpha$ . This operation is also called *dilation*. This morph produces the maximal shape to support the Hausdorff property. Therefore, any Hausdorff morph is a subset of  $S_\alpha$ .

**Voronoi morph.** The *Voronoi morph* [3] moves points in the source shape to their closest point on the target shape by a fraction of  $\alpha$  and moves every point in the target shape to their closest point in the source shape by a fraction of  $1 - \alpha$ . The union of these two sets results in the intermediate shape at a given  $\alpha$ . Formally, it is defined as

$$T_\alpha(A, B) := \{a + \alpha(c(a, B) - a) \mid a \in A\} \cup \{b + (1 - \alpha)(c(b, A) - b) \mid b \in B\},$$

where  $c(p, X)$  denotes the point on a shape  $X$  that is closest to a point  $p$ . If a point is equidistant to multiple points in the other shape, all options are included. To compute

this morph, the Voronoi diagram  $V(A)$  of the vertices, open edges the polygonal region of  $A$ , partitions  $B$  into regions; the Voronoi cells of  $V(A)$ . *Slices* of  $B$  are defined as disjoint non-empty subsets of  $B$ , such that two slices in one region of the partitioning by  $V(A)$  are always positively separated. Note that two slices in adjacent regions may not be positively separated. Symmetrically,  $A$  is partitioned into slices by  $V(B)$ .

**Mixed morph.** The *mixed morph* [3] is defined as

$$M_{\alpha,\varphi}(A, B) := ((T_\alpha(A, B) \oplus D_\varphi) \ominus D_\varphi) \cap S_\alpha,$$

where  $\ominus$  denotes the Minkowski difference, defined as  $A \ominus B := (A^c \oplus B)^c$ , where  $A^c$  is the complement of  $A$ . It first *dilates*  $T_\alpha$  by taking the Minkowski sum with a small disc. After that, it *erodes* the shape by taking the Minkowski difference with a disc of the same radius, causing small gaps and holes to close while keeping the rest of the shape intact. To make sure it is also a Hausdorff morph, the intersection with  $S_\alpha$  is taken.

## 2 Component-Reduced Voronoi Morph

We introduce the *Component-Reduced Voronoi morph* (CRV morph), which benefits from the advantages of the Voronoi morph, while reducing the number of components. This morph identifies which slices converge to extra components in the Voronoi morph, and tries to move them along with *neighboring* slices. Two slices of a shape  $S$  are neighboring if they are not positively separated. Every slice in the Voronoi morph has a *target*. This target is the site of the Voronoi cell by which the slice is partitioned. This site can be a vertex, edge or polygonal region of the other shape. Every slice is scaled and translated towards its target during the morph. In the CRV morph, the target of a slice can be set to the target of a neighboring slice. In that case, the slice is *redirected*. When two neighboring slices have the same target due to redirection, they will always be part of the same component during the morph. We call the targets of redirected slices *alternative targets*. Slices cannot always move along with a neighboring slice; the alternative target has to be valid. An alternative target is valid when the Hausdorff distance between the slice and target is smaller than  $d_H(A, B)$ , and it satisfies one of the following conditions: (1) it is the primary target of a neighboring slice that is part of a larger component, or (2) it is the alternative target of a neighboring slice that is redirected along with a larger component.

If a slice has a valid alternative target, it will be redirected, making the alternative target the new target of the slice. When a slice has multiple valid alternative targets, it will be redirected to the alternative target to which the directed Hausdorff distance is smallest. Assuming the final targets are given, we formally define our new morph  $U_\alpha$  as:

$$U_\alpha(A, B) := \{a + \alpha(c(a, t_s) - a) \mid a \in A, t_s \in B\} \cup \{b + (1 - \alpha)(c(b, t_s) - b) \mid b \in B, t_s \in A\},$$

where  $c(p, t_s)$  is the closest point on the final target  $t_s$  of the slice in which point  $p$  is located. If a slice has no valid alternative targets, its target remains the closest point on  $B$ . Note that if no slices are redirected,  $U_\alpha(A, B) = T_\alpha(A, B)$ .

Alternative targets are valid only if their Hausdorff distance is smaller than that of the two input shapes. This means that redirected targets never determine the Hausdorff distance between an intermediate shape and the input shapes. Therefore,  $U_\alpha$  is a Hausdorff morph:

► **Theorem 1.** *Let  $A$  and  $B$  be two compact sets in the plane with  $d_H(A, B) = 1$ . Then for any  $0 \leq \alpha \leq 1$ , we have  $d_H(A, U_\alpha) = \alpha$  and  $d_H(B, U_\alpha) = 1 - \alpha$ .*

## 2.1 Mixed Component-Reduced Voronoi morph

We also define the *Mixed Component-Reduced Voronoi morph* (MCRV morph)  $U_{\alpha,\varphi}^m$ , to reduce noise on the boundary of intermediate shapes in the CRV morph as

$$U_{\alpha,\varphi}^m(A, B) := ((U_\alpha(A, B) \oplus D_\varphi) \ominus D_\varphi) \cap S_\alpha,$$

where  $\ominus$  denotes the Minkowski difference, defined as  $A \ominus B := (A^c \oplus B)^c$ , where  $A^c$  is the complement of  $A$ .  $D_\varphi$  denotes a disc of radius  $\varphi$ . This means that  $U_{\alpha,0}^m = U_\alpha$ . To make sure  $U_{\alpha,\varphi}^m$  is a Hausdorff morph, the intersection with  $S_\alpha$  is taken.

## 2.2 Algorithm

The algorithm to compute the CRV morph uses the algorithm to compute the Voronoi morph as the first step. To compute  $U_\alpha$  we assume  $A$  and  $B$  are (sets of) solid polygons that may contain holes. The basic algorithm on these input sets works as follows:

1. Compute  $T_\alpha$  at  $\alpha = 1/2$  as described in de Kogel et al. [3]. This results in a set of slices, with each slice transformed and scaled halfway to their target.
2. Determine which slices belong to which components in the halfway Voronoi morph for both input shapes separately.
3. For each input shape construct a graph  $G$  where each slice is a vertex and two neighboring slices are connected by an edge. For each slice, determine the closest neighboring component in  $G$ , using any graph searching algorithm.
4. For both shapes  $A$  and  $B$ , sort all slices separately based on two ascending sort keys. The primary sort key is the area of the component they belong to and the secondary key is the shortest-path distance from the slice itself in  $G$  to the closest slice in  $G$  that is part of an adjacent component in the initial shape.
5. For each slice  $s$ , in order of the previously sorted slices, determine which neighbors in the original shape are valid alternative targets based on the described criteria. The valid alternative target that is closest, in terms of the directed Hausdorff distance from slice  $s$  to the target, will be set as the new target. If slice  $s$  has no valid alternative targets, the primary target remains. If slice  $s$  is redirected, it is marked a follower of its neighboring slice  $l$  that  $s$  is redirected along with. If  $l$  is redirected, the target of slice  $s$  is set to the new target of  $l$ , if the Hausdorff distance allows for it. If the Hausdorff distance does not allow  $s$  to also be redirected again, the target of  $s$  slice is reset to its primary target.
6. Each slice in  $A$  is scaled and translated to its target in  $B$ . If the target is an interior component of the other shape, the slice will be stationary throughout the morph. If the target is a vertex, the slice will be uniformly scaled towards that vertex by a fraction of  $\alpha$ . If the target is an edge, the slice will scale perpendicular to the supporting line of that edge by a factor of  $\alpha$ . Slices in  $B$  are scaled towards their targets in  $A$  in the same manner, except that they are scaled by a factor of  $1 - \alpha$ .
7. Combine slices of  $A$  and  $B$  into one multipolygon.

We sort components from small to large in order to ensure that larger components can move along with smaller components if that smaller component is redirected to the target of an even larger component. Within each component, slices are sorted based on the distance to a neighboring component in terms of slices, to allow slices with no directly neighboring components to move along with neighboring slices that can be redirected.

$U_{\alpha,\varphi}^m$  can simply be computed when  $U_\alpha$  is constructed by dilating and eroding  $U_\alpha$  with a disc of radius  $\varphi$ , and intersecting the result with  $S_\alpha$ .

The Voronoi morph can construct any intermediate shape in  $O(n^2 \log n)$  time [3]. Our morph additionally relies on a sorting algorithm and a shortest path algorithm on a graph with  $n$  edges: both can be found in standard books [2]. The all-pairs shortest path in graph can be computed in  $O(V^3)$ . We have at most  $O(n^2)$  slices, resulting from the intersections between a polygon and the Voronoi diagram of the other polygon. Therefore, an intermediate shape can be constructed in  $O(n^6)$  time. In practice such a worst case scenario is very unlikely to occur. For the shapes used in our experiments (see Section 3), computing one intermediate shape took approximately five seconds on commodity hardware.

### 3 Experiments

We compare the Voronoi, CRV, mixed and MCRV morphs experimentally on two data sets: animal outlines from [1] and country outlines from [4]. The animal dataset contains a collection of nine outlines of animals, averaging 143 vertices, that all comprise one component. The country dataset contains 13 country outlines, averaging 1548 vertices and 12 components. We compute the four morphs for all animal pairs and all country pairs from these sets. The input shapes are scaled to have the same area and translated to have a common centroid.

For all experiments we record the perimeter, area, total angular change (sum of all enclosed boundary loops' angular changes), and the number of components and holes. We record this for  $\alpha$  values starting at zero and increasing in steps of  $1/8$ . For the perimeter and area we record the ratio between the value and a linear interpolation. The number of components and holes are discrete and directly recorded at every value of  $\alpha$  except for zero and one.

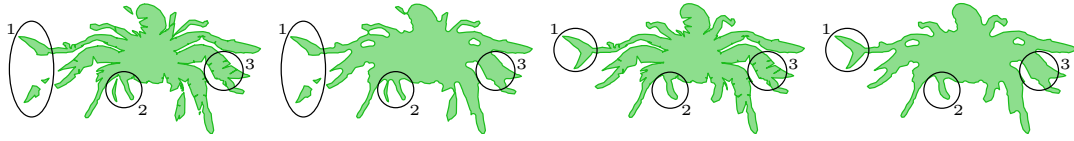
### 4 Results

Figures 2 and 6 show visual examples of the four morphing techniques.

The CRV morph can effectively reduce the number of extra components created in the Voronoi morph. Table 1 shows the average number of components created in the animal data set during the CRV morph to be more than three times less than that in the Voronoi morph. In Figure 2 we see that the CRV morph removes all extra components created in the Voronoi shark-spider morph. The mixed morph can also reduce the number of components, but as indicated by label 2 in Figure 2, this type of component reduction can still result in superfluous details that are not present in the CRV morph.

In terms of area, perimeter and total angular change, Figures 3, 4 and 5 indicate that the CRV and MCRV morphs perform slightly better or similar to their Voronoi and mixed morphs counterparts. In terms of holes the CRV morph performs worse than the Voronoi morph, but most of these holes are resolved in the MCRV morph which only has slightly more holes than the Mixed morph. The number of components and holes are recorded as the average over all  $\alpha$  values except 0 and 1.

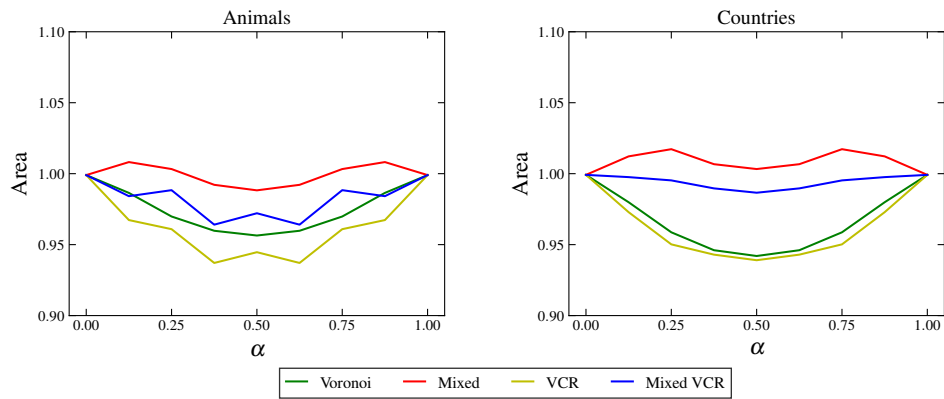
## 4:6 Hausdorff morphs with fewer components



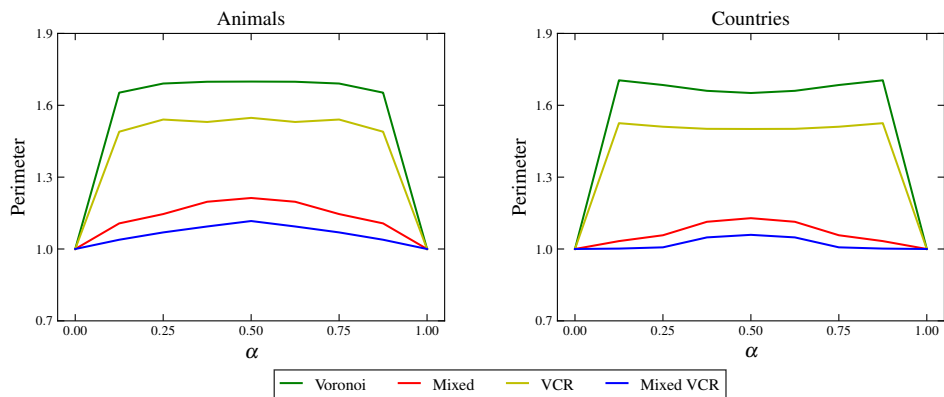
**Figure 2** Intermediate shapes at  $\alpha = 1/2$  when morphing between the outlines of a shark and spider shown in Figure 1. The images show the Voronoi, mixed, CRV and MCRV morphs from left to right. The labeled ellipses are highlighted parts of the shape in which details differ.

Category	Voronoi		Mixed		CRV		Mixed CRV	
	Mean	SD	Mean	SD	Mean	SD	Mean	SD
Components	11.262	4.686	4.210	2.480	3.710	2.263	3.016	2.024
Holes	0.282	0.589	0.337	0.663	1.690	1.787	0.508	0.770

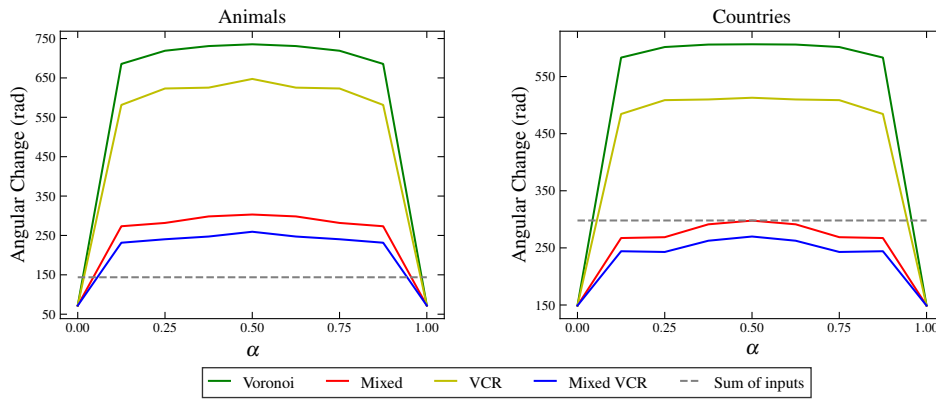
**Table 1** Component and hole count distributions for each morphing method for all tested values of  $\alpha$  except 0 and 1. Only the animal data set is included, as these shapes only have one component.



**Figure 3** Normalized average area for the animals and countries data set experiments.



**Figure 4** Normalized average perimeter for the animals and countries data set experiments.



■ **Figure 5** Average total angular change for the animals and countries data set experiments.



■ **Figure 6** Intermediate shapes for  $\alpha \in \{0, \frac{1}{4}, \frac{1}{2}, \frac{3}{4}, 1\}$  when morphing between outlines of Germany and Italy. The columns show the Voronoi, mixed, CRV and MCRV morphs from left to right.

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