

# Optimizing Query Perturbations to Enhance Shape Retrieval

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**Abstract.** 3D Shape retrieval algorithms use shape descriptors to identify shapes in a database that are the most similar to a given key shape, called the query. Many shape descriptors are known but none is perfect. Therefore, the common approach in building 3D Shape retrieval tools is to combine several descriptors with some fusion rule. This article proposes an orthogonal approach. The query is improved with a Genetic Algorithm. The latter makes evolve a population of perturbed copies of the query, called clones. The best clone is the closest to its closest shapes in the database, for a given shape descriptor. Experimental results show that improving the query also improves the precision and completeness of shape retrieval output. This article shows evidence for several shape descriptors. Moreover, the method is simple and massively parallel.

**Keywords:** Computer vision · 3D Shape matching and recognition · Shape Retrieval · Shape Descriptors · Cloning · Genetic Algorithms.

## 1 Introduction

Shape Retrieval computes which shapes in a database resemble the most to a given key shape  $Q$ , called the query [41]. Shapes are polyhedra with triangular faces. Output should be accurate (no false positive) and complete (no omitted solution). Basically, the shape retrieval algorithm computes off-line a shape descriptor, intuitively a signature or a feature vector, for each shape in the database. They do not depend on queries. It also computes on-line the shape descriptor of the query  $Q$ . Each shape descriptor induces a dissimilarity measure, or distance for short. For example, if the shape descriptor is an histogram, the dissimilarity measure can be the Chi-squared distance, the Kullback-Leibler divergence, the Hellinger distance, etc. Then, the algorithm computes this induced distance between  $Q$  and each shape in the database. Finally, the algorithm outputs the  $m$  (we use  $m = 11$ ) shapes with the smallest dissimilarity to the query  $Q$ .

Several shape descriptors have already been proposed in the literature, but none achieves satisfying retrieval results with all kinds of shapes [8, 10, 12, 14, 19, 20]. The classical approach to solve this issue is to combine several shape descriptors using some fusion rules [1, 4, 6, 25, 27].

This article proposes to solve the problem by improving the query shape itself. Our approach is therefore orthogonal to the classical approaches, which use only one query at a time, and (a fusion of) many shape descriptors.

To improve the query, we propose a genetic algorithm (GA) [21, 23, 33, 36] called GA-SR: Genetic Algorithm for 3D Shape Retrieval. GA-SR makes evolve a population of perturbed copies of the query shape. Perturbed copies are called clones. The fittest clone  $Q^*$  is the clone the closest to its  $m$  closest shapes  $M(Q^*, D)$  in the database, for a given shape descriptor and its induced distance  $D$ . The  $m$  closest shapes to  $Q$  are the  $m$  closest shapes to the fittest clone.

All shapes in the database, query  $Q$  and its clones are (generically non convex) polyhedra with triangular faces.  $Q$  and all its clones share the same topology, *i.e.*, the same incidence relations between vertices, edges and faces. The sole difference between  $Q$  and any one of its clones is that the 3D coordinates of some vertices of  $Q$  are weakly perturbed. The perturbation is small enough, in order for the query and its clones to have similar appearance for the human eye.

Improving the query also improves the precision (no false positive) and completeness (no forgotten solution) of shape retrieval, regardless of the used shape descriptor and its induced dissimilarity measure. This article shows evidences for several shape descriptors: VND (Vertex Normal Descriptor), DMC (Discrete Mean Curvature), LSD (Local Shape Descriptor), and TD (Temperature Distribution).

Shapes in the database are usually classified into several classes or clusters to facilitate the work of classical shape retrieval methods [1, 5, 6]. In opposite, GA-SR does not need to know the class of shapes in the database. This information is only needed for measuring and comparing performances of GA-SR [19, 23, 26, 27, 32, 38, 42].

The rest of this paper is organized as follows. Section 2 presents the background. Section 3 details GA-SR. Section 4 presents experimental results. Section 5 concludes.

## 2 Background and principles

### 2.1 Improvement of shape retrieval

Several efforts have already been conducted to improve shape retrieval [37, 43, 50]. Most of improvement methods are based on fusion of shape descriptors and their related dissimilarity measures. Chahooki et al. [6] proposed a method to fuse contour and region-based features for improving the retrieval precision. Akgül et al. proposed a fusion-based learning algorithm [1], which combines dissimilarity measures operating on different shape features. It computes their optimal combination by minimizing the empirical ranking risk criterion. Other fusion methods exist [7, 27].

Improving pre-existing shape descriptors also improves shape retrieval output. For example, Bronstein and Kokkinos [3] present a scale-invariant version of the heat kernel descriptor previously proposed by Sun et al. [42]. Ling and Jacobs [28] aim to make the shape context descriptor by Sun et al. invariant to articulation: they replace the Euclidean distance by the inner (also called geodesic) distance to build a shape context descriptor. Other methods [51] for improving shape retrieval associate the database with a graph whose nodes are the database shapes. Therefore, the distance between shapes is defined as the length of the geodesic path in the graph associated to the database. A learning method permits to improve dissimilarity measure using graph transduction.

The concept of perturbation has been used as a successful strategy to improve many algorithms [15, 16, 22, 29, 46, 49].

For example, Thompson and Flynn [46] extract the iris from an image by finding circular boundaries that approximate the circle surrounding the iris. A perturbation is performed by changing the values of one or more parameters of the method.

Stochastic arithmetic is another field which uses random perturbations to improve the robustness of numerical computations [49].

In Computational Geometry, small random perturbations of geometric data remove all degeneracies such as, in 2D, three collinear points or four co-cyclic points [15, 16, 22]. Perturbation greatly simplifies geometric algorithms, because only a small number of generic cases needs to be considered, while the number of degenerate cases increases exponentially with the geometric dimension of the problem.

In Stochastic Resonance, perturbation enhances the transmission of information and the detection of low signals [11, 40].

In Machine Learning, several works [13, 24] recently showed that noisy computations improve associative memories.

More recently, a face recognition system [30] is enhanced by using landmark perturbation technique that sweeps more landmarks, which improves faces comparison.

Yin et al. [52] establish connections between evolutionary algorithms and stochastic approximations.

In this wake, Vaira and Kurasova [48] use a genetic algorithm based on random insertion heuristics for the vehicle routing problem with constraints.

Ernest et al. [17] use GA and Genetic Fuzzy trees to compute deterministic fuzzy controllers, for autonomous training and control of squadron of unmanned combat aerial vehicles.

GAs have been used for solving complex optimization problems [34, 35]. GAs have been also used as a powerful strategy to improve the precision in Information Retrieval Systems [18] and in Web Retrieved Documents [45].

GAs have been also used in Computer Vision and Graphics for measuring similarity of visual data, and in CBIR (Content-Based Image Retrieval). Syam and Rao [44] propose a GA-based similarity measure for CBIR: the GA integrates distinct image features in order to find images that are most similar to a given

query image. Aparna [2] proposes a GA-based CBIR method to merge similarity scores: it computes the adequate weight associated with each similarity measure. Chan and King [7] combine different shape features: a GA computes suitable weights for considered features.

Several fitness functions have been used for information retrieval involving GAs. Thada and Jaglan [45] give a comparative study of similarity coefficients used to find the best fitness function, in order to find the most relevant text documents for a set of given keywords. Fan et al [18] computes the best fitness function with a GA for information retrieval.

## 2.2 Shape descriptors

Shape descriptor represents an essential ingredient for measuring the similarity of shapes. For a polyhedral shape with vertices  $V$ , it consists in calculating a signature for some of its vertices. It can be for all vertices in  $V$ , or for a strict subset of  $V$  referred to by feature vertices.

Several researches have been conducted to propose discriminant shape descriptors [8, 10, 12, 14, 20].

We have considered several shape descriptors selected from different categories, such as Vertex Normal-based Descriptor VND [47], Local Shape Descriptor LSD [26], Temperature Distribution TD [19], and a Discrete Mean Curvature DMC [32]. The GA-SR methods based on these descriptors are referred as GA-VND, GA-LSD, GA-TD, and GA-DMC, respectively. We have selected these descriptors for their simplicity and efficiency. GA-SR improves all these shape descriptors, in terms of recall-precision curves. Other descriptors can be used.

**The Vertex Normal-based Descriptor (VND)** The VND [47] descriptor is simple and fast. It considers the normal vector at vertices. The normal vector  $\vec{N}$  at a vertex  $v$  is the average of normal vectors in the 1-star of the vertex:

$$\vec{N}(v) = \frac{1}{l} \sum \alpha_f \vec{N}_f \quad (1)$$

where  $l$  is the number of faces surrounding the vertex  $v$ , and  $\alpha_f$  is the ratio area of the face  $f$  to the total area of the 1-star. The normal vector  $\vec{N}_f$  of a face  $f$  with three points  $p_1, p_2$  and  $p_3$ , is given by:

$$\vec{N}_f = (p_2 - p_1) \times (p_3 - p_1) \quad (2)$$

$p_i = (x_i, y_i, z_i)$ ,  $i = 1, 2, 3$ , and  $\times$  stands for the cross product. The orientation of  $\vec{N}_f$  does not matter. Let  $F$  be the subset of feature vertices  $n(F) = 3000$ . Then the descriptor VND of a vertex  $v$  in  $F$  is given by:

$$VND(v) = \frac{\|\vec{N}(v)\|_2}{\sum_{v' \in F} \|\vec{N}(v')\|_2} \quad (3)$$

**Discrete Mean Curvature (DMC)** The Discrete Mean Curvature [32] of a vertex  $v$  is given by:

$$DMC(v) = \frac{1}{4} \sum_{i=1}^d l_i (\pi - \beta_i) \quad (4)$$

where  $d$  is the degree of vertex  $v$ ,  $\beta_i$  the internal dihedral angle (in radians) between two consecutive faces around the vertex  $v$ , and  $l_i$  the length of the edge common to those faces.

**Local Shape Distribution (LSD)** The LSD descriptor [26] extracts  $n$  random vertices ( $n = 3000$ ), and characterizes each sample vertex  $v$  in terms of Euclidean distances to all other points belonging to its neighborhood. The neighborhood is a spherical region centered at point  $v$ . The LSD descriptor associates to each region a histogram of Euclidean distances between the point  $v$  and points in its neighborhood.

To compute the similarity between two shapes  $A$  and  $B$ , a complete bipartite graph  $g$  is built as follows: the first set of vertices of  $g$  is given by the regions of  $A$ , the second set is given by the regions of  $B$ . The cost of an edge  $(a, b)$  between two regions in  $g$  is the Chi-squared distance between the  $a$  histogram and the  $b$  histogram. By definition, the distance between  $A$  and  $B$  is the smallest cost of perfect matchings in  $g$ . This method does not only compute a distance between two shapes  $A$  and  $B$ , but it also matches regions in  $A$  with regions in  $B$ .

**The Temperature Distribution (TD)** The temperature distribution [42] simulates the heat diffusion process on the surface of a model, which starts at a vertex, and goes through other vertices over time.

The temperature distribution descriptor [19] of a vertex is represented as the average of temperatures measured on all vertices in the surface of the model, after applying a unit heat at that vertex. The average temperature for a vertex  $v$ , at heat dissipation time  $t$ , is given by:

$$TD(v) = \frac{1}{n-1} \sum_{w, w \neq v} \sum_i e^{-\lambda_i t} \phi_i(v) \cdot \phi_i(w) \quad (5)$$

where  $n$  is the number of vertices (usually  $n \approx 3400$ ),  $t = 50$  is a constant, and  $\lambda_i$  is the  $i^{th}$  eigenvalue (sorted in decreasing order) of the Laplacian of the underlying graph of the mesh, and  $\phi_i$  its  $i^{th}$  eigenvector. In practice, only few eigenvectors are used, four in our experiments.

The distribution of the average temperature values is then represented by means of a histogram. The distance between two shapes is the  $L_2$ -norm computed from their histograms.

TD descriptor is invariant to isometric transformations like pose changes, and robust against noise and geometric textures like bumps. However, TD is improved by GA-SR.

### 2.3 Shape similarity and statistical distances

There are many statistical distances to calculate dissimilarity between two shapes represented as distributions (histograms): Kullback-Leibler divergence, Hellinger distance, Bhattacharyya distance, Chi-squared distance,  $L_n$  norm, etc. In this work, we have used some of these distances to measure the dissimilarity of shapes based on each of the used descriptors. We have used Chi-squared distance [39] for VND, LSD and DMC, and  $L_2$ -norm for TD [9], in accordance to their experiments. Note that the number of drawers of histograms of compared shapes is  $b \approx \sqrt{n}$  ( $b \approx 50$ ). In the rest of this paper,  $D(A, B)$  refers to the distance between two shapes  $A$  and  $B$ .

## 3 GA-SR: Genetic Algorithm for Shape Retrieval

### 3.1 Notations and definitions

All shapes *i.e.*, the query, its clones, and shapes in the database, are polyhedra with triangular faces. A polyhedron is represented with a geometric part  $V$  and a topologic part  $F$ .  $V$  is an array of the 3D coordinates of vertices of the polyhedron:  $V_i = (x_i, y_i, z_i) \in \mathbb{R}^3$ . Coordinates are floating point numbers.  $F$  is an array of triangular faces:  $F_k = (a_k \in \mathbb{N}, b_k \in \mathbb{N}, c_k \in \mathbb{N})$ , where  $a_k, b_k, c_k$  are the indices in array  $V$  of the vertices composing face  $F_k$ .  $a_k, b_k, c_k$  are typically ordered counterclockwise, seen from outside the polyhedron. For convenience, a scaling normalization is applied to all polyhedra, so that the sum of all triangles areas equals one (one square meter, say).

A query and all its clones have the same topologic part  $F$ . However, the geometric parts are different. Let  $Q = \text{shape}(V, F)$  be the query shape. Let  $Q' = \text{shape}(V', F)$  be a clone of  $Q$ . The geometric part  $V'$  of  $Q'$  is defined as:

$$V' := V + P, \quad \|P\|_\infty \leq \epsilon, \quad \|P\|_0 = \mu = \lceil \rho n \rceil \quad (6)$$

where  $P_i = (x_i, y_i, z_i) \in [-\epsilon, \epsilon]^3$  is a perturbation vector,  $\epsilon \in \mathbb{R}^+$  the noise threshold,  $n$  the number of vertices.  $P$  is the unknown of our problem.

$\|P\|_\infty \leq \epsilon$  is imposed to guarantee the perturbation is small. This constraint is compatible with GA cross-over. Typically,  $\epsilon$  is between 0.002 (2 millimeters) and 0.06 (6 centimeters). The optimal values of  $\epsilon$  for VND, TD, DMC, and LSD are respectively 0.0074, 0.0022, 0.0562, and 0,0005.

Moreover, we impose that  $P$  is sparse. Let  $\rho$  be the probability for a vertex to be  $\epsilon$ -perturbed. In practice,  $\rho = 1/4$ . The number of perturbed vertices is  $\mu = \lceil \rho n \rceil$ , with  $n$  the number of vertices. The number of perturbed vertices is the same for all clones of a query. This constraint is sometimes written  $\|v\|_0 = \mu$ , where  $\|\cdot\|_0$  is a pseudonorm *i.e.*,  $\|v\|_0$  is the number of non zero coordinates of  $v$ .

Clones are not re-normalized. It is assumed that the perturbation size is less than the Least Feature Size of shapes, so perturbations do not introduce self-intersections or other geometric inconsistencies.

Let  $M(Q, D)$  or  $M(Q)$  be the set of the  $m = 11$  shapes in the database which are the closest to  $Q$ , according to the dissimilarity measure  $D$ .

Let  $q$  be a shape, typically a clone of  $Q$  or  $Q$  itself. Its fitness  $f(q)$  or  $f(q, D)$  is the averaged distance between  $q$  and shapes in  $M(q, D)$  defined as:

$$f(q, D) := (1/m) \sum_{b \in M(q, D)} D(q, b) \quad (7)$$

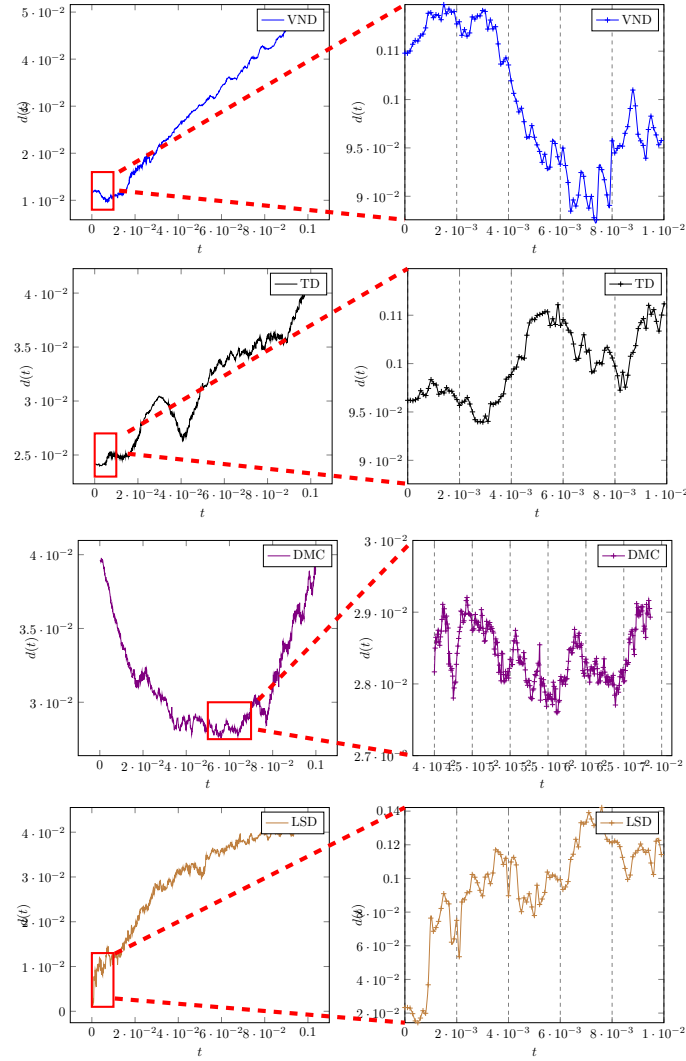
We are looking for the perturbation  $P$  such that the clone  $q = \text{shape}(V + P, F)$  is the closest to its  $m$  most similar shapes in the database, *i.e.*, such that  $f(q, D)$  is minimal. For convenience, pose  $g(P) := f(\text{shape}(V + P, F), D)$ . Then the problem becomes: find the optimal or a good enough perturbation  $X$  which minimizes  $g(X)$  with  $\|X\|_\infty \leq \epsilon$ ,  $\|X\|_0 = \mu$ :

$$X^* = \text{argmin } g(X), \quad \|X\|_\infty \leq \epsilon, \quad \|X\|_0 = \mu \quad (8)$$

### 3.2 Sensitivity to perturbations and discretization artifacts

Shape descriptors are very sensitive to noise, *i.e.*, small random perturbations and artifacts due to discretization. This sensitivity, which can be seen as a shortcoming of shape descriptors, is illustrated in Fig. 1: it shows for several shape descriptors the distance curves between a model David1 and clones of a model David2. David1 and David2 are two statues of David, in different poses. Let  $V_2, F_2$  be the geometry and the faces of David2. Let  $P_2$  be the normalized direction of some perturbation vector :  $\|P_2\|_\infty = 1$  for simplicity. Each curve in Figure 1 shows the curve  $d(t) = D(\text{David1}, \text{shape}(V_2 + tP_2, F_2))$ , with  $t$  sampled in  $[0., 0.1]$ .  $t$  is on the horizontal axis, and  $d(t)$  on the vertical axis.  $d(0)$  is not zero: it is the distance between David1 and David2. It depends on the used descriptor.  $d(t)$  quickly falls below  $d(0)$  for tiny values of  $t$  in  $[0, 0.006]$ , then slowly increases until  $t = 0.01$  or  $0.07$  depending on the used shape descriptor, and finally quickly increases. For  $t \in (0., 0.01]$  or  $(0., 0.07]$  depending on the used shape descriptor, all  $d(t)$  are below  $d(0)$  for this random perturbation direction  $P_2$ . These distance curves are rough or noisy. This is due to discretization artifacts. When it is possible, increasing  $n$ , the number of samples or feature vertices, and thus increasing the ratio  $n/b$  yield to smoother curves. Anyway, this noise does not jeopardize GA-SR, so it is useless to try to reduce it.

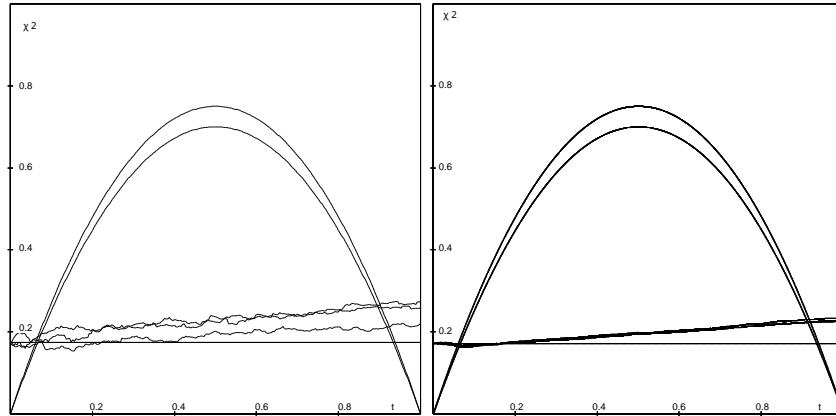
These features can be reproduced and more easily understood in the much simpler context of 1D shapes, see Fig. 2. A 1D shape is a continuous and derivable function from  $[0, 1]$  to  $[0, 1]$ , for convenience. For discretization, the interval  $[0, 1]$  is divided into  $n$  intervals, with  $n = 250$  or  $5000$  in Fig. 2. Each function  $f$  is discretized with a vector  $F$  such that  $F[i] = f(i/n)$ ,  $i \in [0, n]$ . The distance between two 1D shapes  $f_1$  with vector  $F_1$  and  $f_2$  with vector  $F_2$  is the Chi-squared distance between their histograms  $H(F_1)$  and  $H(F_2)$  with  $b = 50$  buckets per histogram (this is the value used in references). The example in Fig. 2 uses 1D shapes  $f_1(x) = L(a_1, x)$  and  $f_2(x) = L(a_2, x)$ , where  $L(a, x) = ax(1 - x)$  is the Logistic map, and  $a_1 = 0.7$  and  $a_2 = 0.75$ . Visually,  $f_1$  and  $f_2$ , or their respective vectors  $F_1$  and  $F_2$ , are very close, but the Chi-squared distance between their histograms is 0.16 or 0.17 (the possible maximal value in 1). Fig. 2 shows that



**Fig. 1.** The impact of perturbation parameter  $t$  (horizontal axis) applied on the clones of David2 model, using VND, TD and DMC descriptors in term of distance (vertical axis) to David1 model. Distances are computed between a model David1 and clones of David2. Values of graphs of the left column are picked with a step of 0.0001 in the interval  $[0,0.1]$ , and those of the right column are picked with the step in the intervals  $[0,0.01]$ ,  $[0,0.01]$ ,  $[0.04,0.07]$ , and  $[0,0.01]$ .



clones of  $F_2$  are closer to  $F_1$ . Each point  $(x, y)$  of a curve in Fig. 2 is  $(x = t, y = \chi^2(H(F_1), H(F_2(t))))$  and  $F_2(t) = F_2 + tP_2$ , where  $P_2$  is a random perturbation vector. Three random perturbation vectors  $P_2$  were tried. For all of them, some clone of  $F_2$  is better than the query  $F_2$ , *i.e.*, closer to  $F_1$ . With  $n = 5000$ , curves are smoother than with  $n = 250$ .



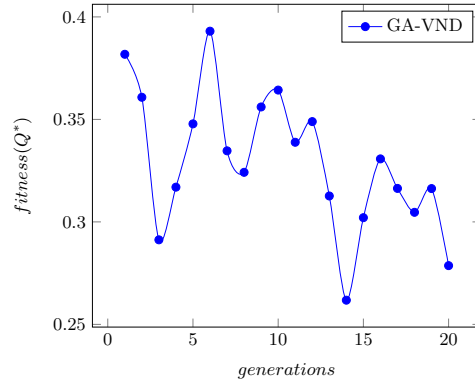
**Fig. 2.** Distance curves between  $F_1$  and clones of  $F_2$ . Left:  $n = 250$  samples. Right:  $n = 5000$  samples. The height of the horizontal line is 0.17, the Chi-squared distance between  $F_1$  and  $F_2$  histograms. Many clones of  $F_2$  are closer to  $F_1$  than  $F_2$  itself.

### 3.3 The genetic algorithm

GA-SR is a genetic algorithm. Let  $Q$  be the query, and  $D$  be the shape descriptor and its induced distance. GA-SR makes evolve a population  $P$  of  $K = 15$  clones during  $G = 20$  iterations, from generation  $P_0$  to  $P_G$ . The first population  $P_0$  contains  $Q$  and  $K - 1$  mutants. Next populations are generated with GA operators: crossover and mutation. Equation (7) defines the fitness of a clone  $q$ : the closest to the set  $M(q, D)$  of its most similar shapes in the database, the fittest. Figure 3 shows the evolution of the fitness value of the best clone at each generation of the GA. The best solution of the GA corresponds to the minimal fitness value, in this case at the fourteenth generation.

The genotype of a clone is an unsorted array of its  $\mu$  perturbed vertices:  $(i, x_i, y_i, z_i)$ , where  $i$  is the index of the perturbed vertex, and  $(x_i, y_i, z_i)$  the 3D coordinates of the vertex after perturbation. The tuple  $(i, x_i, y_i, z_i)$  is called a gene in the GA parlance. It is easy to obtain vertex coordinates of the clone from the vertex coordinates of the query and from the genotype.

Each clone in the first population  $P_0$  is generated with mutations of the query. Let  $V, F$  be the geometric and topologic parts of  $Q$ . The  $\mu$  genes of each



**Fig. 3.** Evolution of the fitness of the best clone among generations.

clone are generated as follows.  $\mu$  distinct vertex indices in  $1, \dots, n$  are picked at random. Let  $i$  be one of these integers. Let  $V_i = (x_i, y_i, z_i)$  be the 3D coordinates of vertex  $V_i$  of  $Q$ . The gene is  $(i, x_i + \epsilon R(), y_i + \epsilon R(), z_i + \epsilon R())$  where function  $R()$  returns a pseudorandom floating point value uniformly distributed in the interval  $[-1, 1]$ .

For each population  $P_g$ ,  $g = 0, \dots, G$ , the fitness function (see eq. 7) of every clone is computed. To renew the population, standard genetic operators are applied to selected parents to generate new clones: there is no elitism, so the curve in Fig. 3 is not monotonous. More precisely,  $K/2$  pairs of clones are selected using the fitness-proportionate selection rule (also called the roulette-wheel selection). Each selected pair generates two new clones with a standard crossover operation between the two genotypes. These two new clones replace their parents in the next generation.

The standard crossover between a first genotype  $G_1 = L_1R_1$  (L for left, R for right) and a second genotype  $G_2 = L_2R_2$  gives two genotypes  $L_1R_2$  and  $L_2R_1$ , where lengths of  $L_1, L_2$  are equal. Any classical crossover operator can be used. Some vertices may be perturbed several times, without hindering GA-SR.

Mutation is an important operator in evolutionary algorithms. Each generated clone is subject to a post-mutation: with probability 0.01, each gene  $(i, x_i, y_i, z_i)$  is changed to  $(j, x_j + \epsilon_x, y_j + \epsilon_y, z_j + \epsilon_z)$ , where  $j$  is selected randomly and  $\epsilon_x, \epsilon_y, \epsilon_z$  are pseudo random values uniformly distributed in  $[-\epsilon, \epsilon]$ .

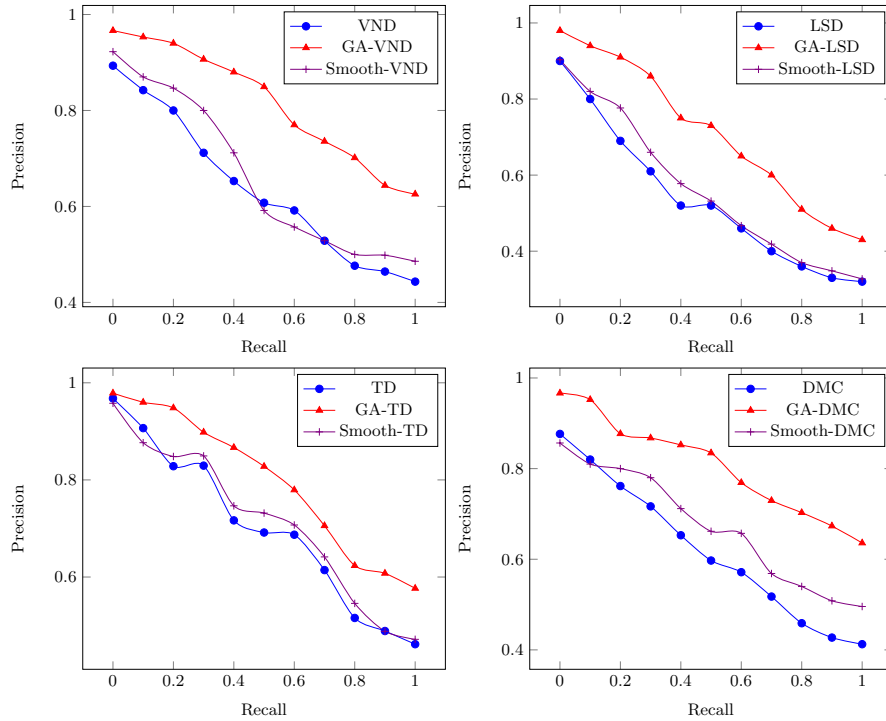
## 4 Experiments

### 4.1 Databases used

We used the databases TOSCA [53] and SHREC'11 [26]. TOSCA contains 148 3D models (eg. Cats, Centaurs, Dogs, Wolves, Horses, Lions, Gorillas, Sharks, Female and Male figures). The models are distributed into 10 categories including a variety of poses. SHREC'11 contains about 600 non-rigid 3D objects

classified into different groups of models, each of which contains approximately the same number of models. In both databases, 3D models are represented as triangular meshes stored in ASCII files in .off format (Object File Format). The name of each file implicitly gives the class (*e.g.*, Cats, Dogs, etc), which permits measurement of performances of retrieval algorithms.

## 4.2 Tests and results

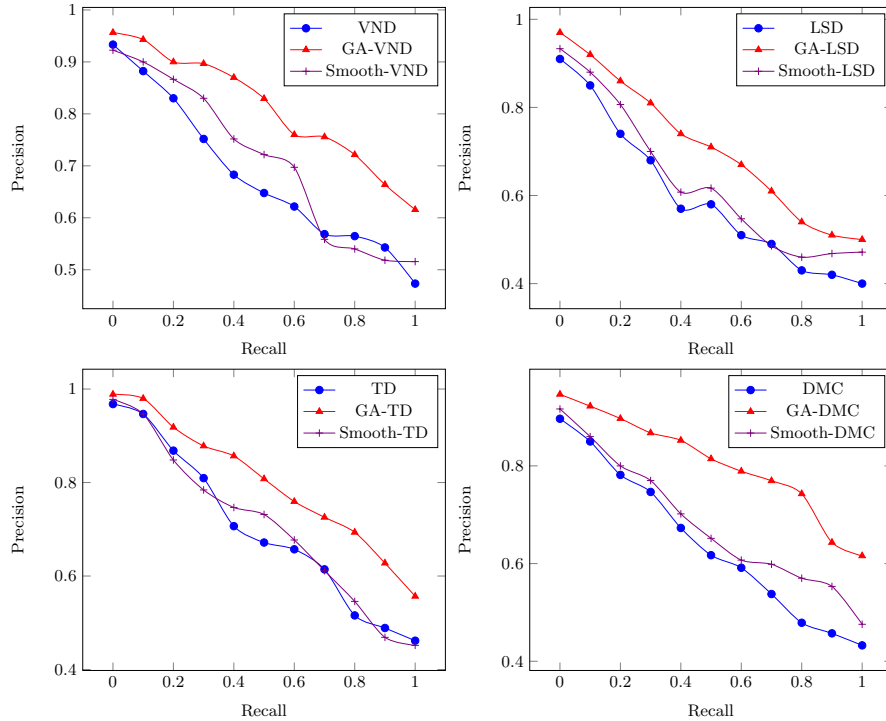


**Fig. 4.** Averaged 11-point precision-recall curves of random queries of the TOSCA database using original descriptors (blue), Smooth-based descriptors (violet) and the GA-based descriptor (red).

The output quality of shape retrieval algorithms is measured with precision-recall curves. They account both for precision and completeness. They are drawn with the 11-point interpolated average precision algorithm by Manning et al. [31]. It is the reason why we use  $m = 11$ . The higher the precision-recall curve, the better the retrieval.

Figures 4 for TOSCA and 5 for SHREC11 show the precision-recall curves of descriptors VND, LSD, DMC, and TD compared to their GA counterparts. Clearly, GA-SR significantly improves all these descriptors.

To show the effectiveness of our method, we compare it to the following existing methods: D2 [38], MDS–ZFDR [27], GPS [42], and GT [51]. Comparison



**Fig. 5.** Averaged 11-point precision-recall curves of random queries of the SHREC’11 database using original descriptors (blue), Smooth-based descriptors (violet) and the GA-based descriptor (red).

results are illustrated in plots of Figure 6. GA-SR shows better performance.

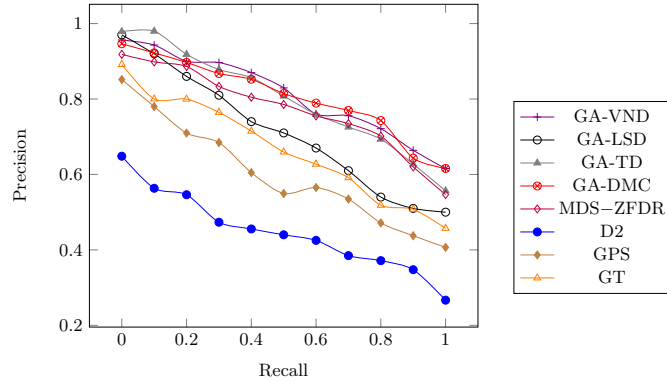
Smoothing of a query shape is another possible way to improve shape retrieval. To smooth a shape, all its vertices are smoothed (without any constraint regarding the order). Let  $v$  be a vertex, let  $g$  be the barycentre of its neighbors. Then  $v'$ , the corresponding smoothed vertex, is defined using (9).

$$v' := \text{smooth}(v) := \alpha v + (1 - \alpha)g \quad (9)$$

where  $\alpha$  is a parameter in  $[0, 1]$ . Then  $D'$ , the smoothed distance for  $D$  in VND, LSD, DMC, TD, is (10):

$$D' := D(\text{smooth}(A), \text{smooth}(B)) \quad (10)$$

where  $\text{smooth}(\cdot)$  is the smoothing operator. Smoothing reduces noise and irregularities, so intuitively, we expect smoothing to reduce distances:  $D'(A, B) \leq$



**Fig. 6.** Comparing results of GA-SR with other methods proposed in the literature. Curves are plotted according to results reported on the SHREC’11 database.

$D(A, B)$ . Smoothing is simple and fast, in particular faster than GA-SR. Figures 4 for TOSCA and 5 for SHREC’11 show the precision-recall curves for VND, LSD, DMC, TD, their smoothed counterparts, and their GA counterparts. Clearly, cloning achieves better retrieval results than smoothing.

Finally, GA-SR is compatible with fusion: let  $D_1, \dots, D_s$  be  $s$  shape descriptors and their induced distances. Then define their fusion distance  $D$  with:  $D(A, B) := \min(D_1(A, B), \dots, D_s(A, B))$  (or any other fusion rule), and use this distance  $D$  with GA-SR. We compared GA-SR and SR with this min-merged shape descriptor, and here too, GA-SR improves SR. No figure is provided for conciseness.

## 5 Conclusion

Shape descriptors are very sensitive to small perturbations. This shortcoming is also an opportunity for improving shape retrieval. GA-SR achieves better results than previous classical retrieval methods, and better results than smoothing. Other shape descriptors are easily taken into account. GA-SR is simple and massively parallel. It needs no machine learning, no deep learning, no supervision.

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