

# Distance transform to seeds: computation and application

ANDRÉ VITAL SAÚDE<sup>1</sup>, MICHEL COUPRIE<sup>2</sup> and  
 ROBERTO DE ALENCAR LOTUFO<sup>3</sup>

<sup>1</sup> Universidade Federal de Lavras (UFLA), Brazil  
[saude@dcc.ufla.br](mailto:saude@dcc.ufla.br)

<sup>2</sup> Institut Gaspard-Monge, Laboratoire A2SI, Groupe  
 ESIEE, France  
[coupriem@esiee.fr](mailto:coupriem@esiee.fr)

<sup>3</sup> Universidade Estadual de Campinas (Unicamp), Brazil  
[lotufo@unicamp.br](mailto:lotufo@unicamp.br)

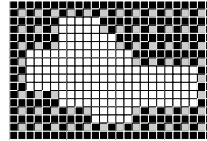


Figure 1. The distance transform to seeds maps distances from white (object) to gray (seeds) points.

## 1. Introduction

The *distance transform* (DT) is the mapping which gives for each point of an object, its distance to the nearest point in the complementary of the object. The *distance transform to seeds* (DTS) is a generalization of the DT. It maps to each point of the object, its distance to the nearest point in a selected set of seeds.

The DT has been studied since the sixties. Many algorithms have been proposed in different approaches, but the first linear time algorithm to compute the DT with the Euclidean metric has only been proposed in 1996 by Hirata [5].

In skeletonization, the notion of *medial axis* (MA), the set of centers of maximal balls, is very important, since the MA has sufficient information for the reconstruction of the original shape (reversibility property). A maximal ball is a ball included in the object and not completely covered by any other ball also included in the object. The computation of the MA depends on the computation of the DT. In a previous work [8], we have also defined the *exact Euclidean medial axis in higher resolution* (HMA). Based on the DT, we have provided an algorithm for the HMA in 2D and 3D, but not for  $nD$ .

In this paper we show how to use the separable distance transform algorithm to compute the distance transform to seeds, and we show how it is applied on the computation of skeletons in higher resolution, using the HMA.

## 2. Distance Transform to Seeds

We denote by  $DT_X$  the distance transform of  $X$ , and by  $DT_{\{X,S\}}$  the distance transform of  $X$  with respect to the seeds  $S$ . We illustrate the concept of the DTS in Figure 1.

A DTS where the set of seeds is the whole set of background points is in fact a DT. There is no doubt that algorithms that compute the DT can be

adapted to compute the DTS. Moreover, some DT algorithms by propagation [3, 4] are already defined as a DTS.

Nevertheless, the separable line scanning algorithms proposed in the literature seldom make reference to this problem. Those who work with the Euclidean distance are interested on adaptations of such algorithms, because the separable line scanning algorithms are the most efficient algorithms for the Euclidean DT.

Indeed, the Euclidean DTS can be computed by any DT algorithm in two steps:

1. compute the DT from each point not in the seeds set  $S$ , to the points in  $S$ :  $DT_{\bar{S}}$
2. set points not in  $X$  to zero

This is done in linear time by Hirata's algorithm. A variation of this algorithm can easily implement the two steps above in a single function.

We give an example of the DTS in Figure 2.

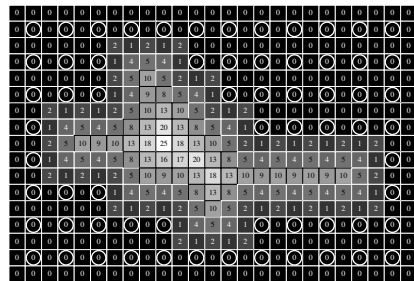


Figure 2. Distance transform to seeds. Object points have the distances to the nearest seed. Seeds are circled.

## 3. Application: Euclidean skeletons

The following characteristics are desired for skeletons: homotopy, centeredness, reversibility, and

thinness. To produce a skeleton with all those characteristics is very challenging, specially when working with skeletons centered with respect to the Euclidean distance. In this section we always refer to the Euclidean distance.

In a previous work, we have presented a homotopic Euclidean skeleton which is defined in the domain of abstract complexes [2]. Please refer to the reference [2] for further information on the advantages of computing homotopic skeletons in such domain. Abstract complexes are represented in the doubled resolution square grid. In order to preserve reversibility, the usual approach is to preserve the points of the MA, *i.e.*, the set of centers of maximal Euclidean balls inside the object. However, for the doubled resolution grid, we have defined the HMA [8], which allowed us to obtain a thinner but yet reversible Euclidean skeleton.

The definition of the HMA is similar to that of the MA. Consider that an object in  $\mathbb{Z}^n$  is represented in  $[\frac{1}{2}\mathbb{Z}]^n$  after transformed to the higher resolution. Consider that a ball in the higher resolution can be centered at any point of  $[\frac{1}{2}\mathbb{Z}]^n$ , but contains only points of  $\mathbb{Z}^n$ . Let us call such balls the  $H$ -balls. A  $H$ -ball with center  $x \in [\frac{1}{2}\mathbb{Z}]^n$ , and radius  $R \in \mathbb{N}$ , is denoted  $B_h^<(x, R)$ , and is defined by:

$$B_h^<(x, R) = \{y \in \mathbb{Z}^n, (2y - 2x)^2 < R\} \quad (1)$$

The factor 2 in  $2y$  and  $2x$  assures that the distances in  $[\frac{1}{2}\mathbb{Z}]^n$  are equal to distances in  $\mathbb{Z}^n$ . The HMA is the set of centers of maximal  $H$ -balls, where a maximal  $H$ -ball is a ball included in the object and not completely covered by any other  $H$ -ball included in the object. If the  $H$ -balls that compose the HMA are reconstructed, every object point in  $\mathbb{Z}^n$  is reconstructed, and the reversibility is guaranteed.

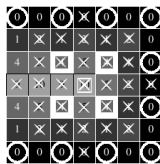


Figure 3. Maximal  $H$ -ball. A zoom on Figure 2. Circled points: seeds; squared diagonal star: center  $x$ ; diagonal stars: Euclidean disk centered in  $x$  with radius 10, including points of the background; thick squared diagonal stars:  $B_h^<(x, 10)$ , a  $H$ -ball. The  $H$ -ball  $B_h^<(x, 10)$  does not include its center  $x$ .

In [8] we have provided an algorithm to compute the HMA. The algorithm detects the radii of maximal  $H$ -balls using the DT of the object in higher resolution. We have proved that the values of the Euclidean DT are sufficient to determine the radii of maximal  $H$ -balls in 2D

and 3D, but they are not sufficient in  $n$ D. In addition, the algorithm proposed is based on [7] and, although efficient, it is not  $O(n)$ .

We can prove that if we take the object  $X$  in higher resolution, and the set  $S = \mathbb{Z}^n \setminus X$  as seeds (see Figure 2), the transform  $DT_{\{X, S\}}$  gives, for each point of the object, the radius of the maximal  $H$ -ball.

We can thus obtain an efficient algorithm for the  $n$ -dimensional HMA of an object  $X$  if we replace  $DT_X$  by  $DT_{\{X, \mathbb{Z}^n \setminus X\}}$  in the algorithm, where the HMA is represented in  $[\frac{1}{2}\mathbb{Z}]^n$ .

## 4. Conclusion

We have presented the application of Hirata algorithm to the computation of distance transforms to seeds. We have presented a special set of seeds, the set  $S = \mathbb{Z}^n \setminus X$ , which generalizes to  $n$ D the algorithm that computes the HMA on the  $[\frac{1}{2}\mathbb{Z}]^n$  grid. The original algorithm was valid only in 2D and 3D. In a full paper, we will combine the DTS with the approach proposed by Coeurjolly and Montanvert [1] in order to obtain a reversible subset of the HMA in linear time, which will allow us to compute, also in linear time, an Euclidean skeleton with all the desired characteristics listed in the beginning of this paper.

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