Distance transform to seeds: computation and application

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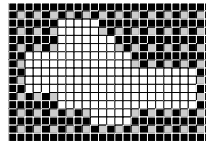lotufo@unicamp.br

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 gener-
alization 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 ap-
proaches, but the first linear time algorithm to com-
pute 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 impor-
tant, since the MA has sufficient information for
the reconstruction of the original shape (reversibil-
ity 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 dis-
tance 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 algo-
rithms proposed in the literature seldom make ref-
erence 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: $DT_{\overline{S}}$

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.
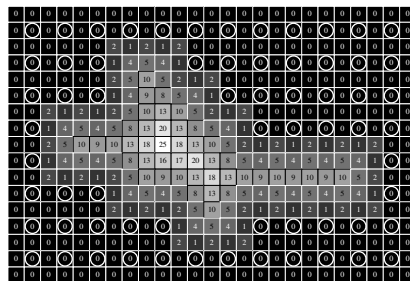
We give an example of the DTS in Figure 2.

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 skele-
tons: 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:

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

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.
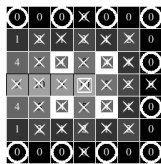

Figure 3. Maximal H-ball. A zoom on Figure 2. Circled points: seeds; squared diagonal star: center x; diagonal stars: Euclidean disk centered in x with radius 10, including points of the background; thick squared diagonal stars: $B_h^<(x, 10)$, a H-ball. The H-ball $B_h^<(x, 10)$ does not include its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

References

[1] D. Coeurjolly and A. Montanvert, *Optimal Separable Algorithms to Compute the Reverse Euclidean Distance Transformation and Discrete Medial Axis in Arbitrary Dimension*, IEEE Trans. on PAMI **29** (2007), no. 3, 437–448.

[2] M. Couprie and A. V. Saúde and G. Bertrand, *Euclidean homotopic skeleton based on critical kernels*, SIBGRAPI, 2006, pp. 307-314, DOI 10.1109/SIBGRAPI.2006.16, (to appear in print).

[3] O. Cuisenaire and B. Macq, *Fast Euclidean Distance Transformation by Propagation Using Multiple Neighborhoods*, Computer Vision and Image Understanding **76** (1999), no. 2, 163–172, DOI 10.1006/cviu.1999.0783.

[4] A. X. Falcão and J. Stolfi and R. A. Lotufo, *The Image Foresting Transform: Theory, Algorithms and Applications*, IEEE Trans. on PAMI **26** (2004), no. 1, 19-29.

[5] T. Hirata, *A unified linear-time algorithm for computing distance maps*, Information Processing Letters **58** (1996), no. 3, 129-133.

[6] A. Meijster and J. B. T. M. Roerdink and W. H. Hesselink, *A general algorithm for computing distance transforms in linear time*, 5th Mathematical morphology and its applications to image and signal processing, 2000, pp. 331-340.

[7] E. Rémy and E. Thiel, *Exact Medial Axis with Euclidean Distance*, Image and Vision Computing **23** (2005), no. 2, 167-175.

[8] A. V. Saúde and M. Couprie and R. A. Lotufo, *Exact Euclidean medial axis in higher resolution*, DGCI, 2006, pp. 605–616.