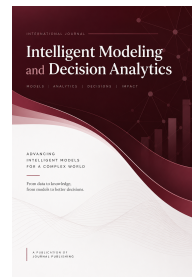


# Intelligent Modeling and Decision Analytics

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## Linear Diophantine Fuzzy Graph Connectedness for Uncertainty-Aware Kidney Segmentation in CT Images with LDF-TOPSIS Method Selection

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### ABSTRACT

We introduce a linear Diophantine fuzzy (LDF) graph model for the segmentation of kidneys and renal masses in computed tomography (CT) and use the same LDF framework for the selection of a segmentation method. A CT slice is represented by a superpixel graph whose vertices and edges carry LDF values: the membership and non-membership degrees describe photometric evidence, while the reference parameters, coupled by the Diophantine constraint, describe geodesic and boundary evidence. We prove that the construction satisfies the axioms of an LDF graph and that it reduces to the intuitionistic fuzzy case when no topological information is present. The segmentation is defined through LDF fuzzy connectedness, with the threshold determined by a stability criterion on the nested family of  $\varepsilon$ -clusters (LDF-FC). On thirteen test targets taken from public kidney CT collections, LDF-FC attained a mean Dice coefficient of 0.718 and a 95th percentile Hausdorff distance of 20.4 pixels, compared with 0.669 and 41.8 for the random walker and 0.603 and 40.1 for the intuitionistic variant. Under four noise models the method was significantly better than each of the eight competing methods (Wilcoxon signed-rank test,  $p < 0.03$ ). For the selection problem we propose an LDF-TOPSIS model with entropy weights in which the reference parameters encode the dispersion of the observed performance. The model ranked LDF-FC first (closeness coefficient 0.904), and the ranking was stable with respect to the reference parameters and the criteria weights.

### 1. Introduction

Computed tomography (CT) is the standard imaging modality for the detection, staging and follow-up of renal masses, and the delineation of the kidney and of a suspected lesion is the first quantitative step in diagnosis and treatment planning. Manual contouring is time-consuming and depends on the observer. Moreover, the image contains several sources of uncertainty: partial-volume effects at organ boundaries, low contrast between the kidney and the adjacent liver, spleen or bowel, internal heterogeneity of tumors (necrosis, hemorrhage, enhancing rim) and acquisition noise. Classical intensity-based techniques, such as Otsu thresholding [21], region growing, the watershed transform [33] and fuzzy c-means clustering [6], are sensitive to these effects, whereas deep networks such as U-Net [25] require large annotated training sets, which are rarely available in small clinical centers. Graph-based models, in which pixels or regions are vertices and their similarities are edge weights, provide an interpretable alternative [18, 9].

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The uncertainty in such graphs is classically described by fuzzy sets [37] and fuzzy graphs [26, 20]. Udupa and Samarasekera [32] showed that the max–min strength of paths in a fuzzy affinity graph (fuzzy connectedness) defines objects that are robust to gradual changes of intensity, and Bhattacharya and Suraweera [7] gave an efficient algorithm for the corresponding max–min closure. In previous work, Ibrišimović and co-authors applied fuzzy numbers [12], fuzzy-metric filtering [23, 22], phase-space and graph descriptors [14] and fuzzy-graph  $\varepsilon$ -clustering [13] to radiological images. These studies indicate that connectivity in a graph is a natural carrier of segmentation information. They also show, however, that a single membership degree cannot distinguish between two regions of similar intensity that are separated by a boundary and two regions that are not, which is precisely the situation in which a kidney segmentation extends into the liver.

Intuitionistic [3], Pythagorean [35] and  $q$ -rung orthopair [36] fuzzy sets introduce a non-membership degree, but the admissible region of the pair  $(\mu, \nu)$  is fixed in advance. Linear Diophantine fuzzy sets (LDFS), introduced by Riaz and Hashmi [24], remove this restriction by means of two reference parameters  $(a, b)$  satisfying  $a\mu + b\nu \leq 1$ , which allows the modeler to assign a separate weight to each degree. LDFS were extended to graphs [10, 4] and to planar graphs with edge strengths and dual graphs [17, 2], and they have been applied to medical decision problems [16].

To our knowledge, linear Diophantine fuzzy graphs have not been used to construct a segmentation of a medical image, and the LDF framework has not been used to select a segmentation method when accuracy, robustness, reproducibility and computational cost lead to different preferences. This gap is significant because both problems are decisions under uncertainty: one must decide whether two neighboring regions belong to the same organ, and which algorithm should be preferred when no method is best with respect to all criteria. The aim of this paper is twofold. First, we define a linear Diophantine fuzzy graph on the superpixels of a CT slice, in which  $(\mu, \nu)$  describe photometric evidence and  $(a, b)$  describe geodesic and boundary evidence, and we derive an LDF fuzzy connectness algorithm (LDF-FC) with an automatically selected stable  $\varepsilon$ -cluster. Second, we propose an LDF-TOPSIS model with Shannon entropy weights [11, 28, 5] for ranking segmentation methods, in which the dispersion of the observed performance is taken into account explicitly. The method is evaluated on renal CT images, including tumor cases from a public kidney CT collection [15], and compared with six classical methods and two fuzzy-graph variants under four noise models and perturbed seed positions.

## 2. Methodology

### 2.1 Preliminaries On Linear Diophantine Fuzzy Sets And Graphs

**Definition 1** (Riaz and Hashmi [24]). Let  $X$  be a nonempty set. A linear Diophantine fuzzy set on  $X$  is

$$\mathcal{L} = \{(x, \langle \mu(x), \nu(x) \rangle, \langle a(x), b(x) \rangle) : x \in X\}, \quad (1)$$

where  $\mu, \nu, a, b : X \rightarrow [0, 1]$  are the membership degree, the non-membership degree and the corresponding reference parameters, such that  $0 \leq a(x) + b(x) \leq 1$  and  $0 \leq a(x)\mu(x) + b(x)\nu(x) \leq 1$  for all  $x \in X$ . The score of an LDF number  $\ell = (\langle \mu, \nu \rangle, \langle a, b \rangle)$  is

$$S(\ell) = \frac{1}{2} [(\mu - \nu) + (a - b)] \in [-1, 1]. \quad (2)$$

**Definition 2** (Hanif *et al.*, [10]; Khan *et al.*, [17]). Let  $G^* = (V, E)$  be a simple graph. A linear Diophantine fuzzy graph on  $G^*$  is a pair  $G = (\mathcal{L}_V, \mathcal{L}_E)$ , where  $\mathcal{L}_V$  assigns an LDF number  $(\mu(v), \nu(v), a(v), b(v))$  to each  $v \in V$  and  $\mathcal{L}_E$  assigns an LDF number  $(\mu_E, \nu_E, \tau_E, \nu_E)$  to each  $uv \in E$ , such that

$$\begin{aligned} \mu_E(uv) &\leq \min\{\mu(u), \mu(v)\}, & \nu_E(uv) &\leq \max\{\nu(u), \nu(v)\}, \\ \tau_E(uv) &\leq \min\{a(u), a(v)\}, & \nu_E(uv) &\leq \max\{b(u), b(v)\}, \end{aligned} \quad (3)$$

together with  $\tau_E + \nu_E \leq 1$  and  $\tau_E \mu_E + \nu_E \nu_E \leq 1$ . The strength of an edge [17] is the quadruple

$$I(uv) = \left( \frac{\mu_E(uv)}{\min\{\mu(u), \mu(v)\}}, \frac{\nu_E(uv)}{\max\{\nu(u), \nu(v)\}}, \frac{\tau_E(uv)}{\min\{a(u), a(v)\}}, \frac{\nu_E(uv)}{\max\{b(u), b(v)\}} \right). \quad (4)$$

**Definition 3** (Rosenfeld [26]; Udupa and Samarasekera [32]). Let  $\kappa : E \rightarrow [0, 1]$ . The strength of a path  $P = (v_0, \dots, v_n)$  is  $\kappa(P) = \min_{1 \leq i \leq n} \kappa(v_{i-1}v_i)$ , and the connectedness of  $x, y \in V$  is  $\mu^\infty(x, y) = \max\{\kappa(P) : P \text{ is a path from } x \text{ to } y\}$ . For  $S \subseteq V$  we put  $\mu^\infty(S, y) = \max_{s \in S} \mu^\infty(s, y)$ .

## 2.2 Superpixel Linear Diophantine Fuzzy Graph Of A CT Slice

Let  $I : \Omega \rightarrow [0, 1]$  be a CT slice, normalized by its 0.5 and 99.5 intensity percentiles and smoothed by an edge-preserving bilateral filter [31]. The domain  $\Omega$  is partitioned into SLIC superpixels [1] of mean area 25 pixels. Each superpixel is a vertex  $v$  with mean intensity  $m_v$  and centroid  $c_v$ , and two vertices are adjacent if the corresponding regions have a common boundary. For an edge  $uv$  we denote by  $\hat{g}_{uv} \in [0, 1]$  the mean Sobel gradient along the common boundary, divided by the 95th percentile of these values and truncated to  $[0, 1]$ . The user marks one or two object seeds, and the corresponding vertices  $S_o$  define the object prototypes  $\{o_k\}$ . The vertices meeting the image border and the vertices with photometric membership below 0.05 form the initial background seed set  $S_b$ ; the 10th, 50th and 90th percentiles of their intensities are the background prototypes  $\{q_j\}$ .

In LDF models the two reference parameters correspond to two different criteria [24, 17]. Accordingly, we let the pair  $(\mu, \nu)$  describe photometric evidence and the pair  $(a, b)$  describe topological evidence. For  $\sigma = 0.35 \text{ sd}(m)$  we define

$$\mu(v) = \max_k e^{-\frac{(m_v - o_k)^2}{2\sigma^2}}, \quad \nu(v) = \max_j e^{-\frac{(m_v - q_j)^2}{2\sigma^2}}. \quad (5)$$

Let  $D(v)$  denote the shortest-path distance from  $S_o$  to  $v$  in the superpixel graph with edge lengths  $\ell_{uv} = \|c_u - c_v\| (1 + 5|m_u - m_v|/\text{sd}(m) + 5\hat{g}_{uv})$ , and let  $\gamma(v) = \exp(-D(v)/\delta)$ , where  $\delta$  equals thirty mean superpixel diameters. Thus  $\gamma(v)$  is close to 1 if  $v$  can be reached from the seeds without crossing intensity changes or boundaries, and  $\gamma(v)$  is small for a vertex of similar intensity that lies behind a boundary (for instance, the liver next to the kidney). For  $\lambda \in [0, 1]$  we set

$$a(v) = \lambda \gamma(v), \quad b(v) = (1 - \lambda) (1 - \gamma(v)). \quad (6)$$

For an edge  $uv$  let  $s_{uv} = \exp(-(m_u - m_v)^2/2\sigma_e^2)$  with  $\sigma_e = 0.1 \text{ sd}(m)$ , and define

$$\begin{aligned} \mu_E &= \min\{\mu(u), \mu(v)\} s_{uv}, & \nu_E &= \max\{\nu(u), \nu(v)\} (1 - s_{uv}), \\ \tau_E &= \min\{a(u), a(v)\} (1 - \hat{g}_{uv}), & \nu_E &= \max\{b(u), b(v)\} \hat{g}_{uv}. \end{aligned} \quad (7)$$

The pair  $(\mu_E, \nu_E)$  describes photometric similarity of the endpoints, and the pair  $(\tau_E, \nu_E)$  describes their geodesic proximity to the seeds and the boundary between them. The latter information has no counterpart in an ordinary or intuitionistic fuzzy graph.

**Proposition 1.** The structure  $G = (\mathcal{L}_V, \mathcal{L}_E)$  defined by Eqs. (5)–(7) is a linear Diophantine fuzzy graph.

*Proof.* Since  $s_{uv}, \hat{g}_{uv} \in [0, 1]$ , the inequalities in Eq. (3) are satisfied. For every vertex we have  $a + b = \lambda \gamma + (1 - \lambda)(1 - \gamma) \leq \max\{\lambda, 1 - \lambda\} \leq 1$ , hence  $a\mu + b\nu \leq a + b \leq 1$ . For every edge,  $\tau_E \leq \lambda$  and  $\nu_E \leq 1 - \lambda$ , so  $\tau_E + \nu_E \leq 1$  and  $\tau_E \mu_E + \nu_E \nu_E \leq 1$ . ■

As edge affinity we use the score in Eq. (2), mapped affinely onto  $[0, 1]$ :

$$\kappa_{\text{LDF}}(uv) = \frac{1}{2} + \frac{1}{4} [(\mu_E - \nu_E) + (\tau_E - \nu_E)]. \quad (8)$$

For comparison we consider two special cases on the same graph: the fuzzy-graph affinity  $\kappa_{\text{FG}} = \min\{\mu(u), \mu(v)\} s_{uv}$  in the sense of Rosenfeld, with vertex evidence  $2\mu - 1$ , and the intuitionistic

affinity  $\kappa_{\text{IF}} = \frac{1}{2}[1 + (\mu_E - \nu_E)]$ , with vertex evidence  $\mu - \nu$ . All other steps, including the choice of  $\varepsilon$  described below, are identical for the three variants, so that any difference between them is due to the fuzzy structure only.

**Proposition 2.** Let  $\phi : [0, 1] \rightarrow [0, \infty)$  be strictly increasing. Then the connectedness computed with the affinity  $\phi \circ \kappa$  equals  $\phi \circ \mu^\infty$ , where  $\mu^\infty$  is computed with  $\kappa$ . In particular, if  $\tau_E - \nu_E$  is constant on  $E$ , then LDF-FC and IF-FC produce the same family of  $\varepsilon$ -clusters, up to a relabeling of the levels.

*Proof.* A strictly increasing map commutes with min and max over finite sets, which gives the first claim. If  $\tau_E - \nu_E = c$  on  $E$ , then  $\kappa_{\text{LDF}} = \frac{1}{2}\kappa_{\text{IF}} + \frac{1}{4}(1 + c)$ , which is a strictly increasing affine function of  $\kappa_{\text{IF}}$ . ■

Proposition 2 shows that the LDF model contains the intuitionistic model as a special case, and that the two can differ only through the variation of  $\tau_E - \nu_E$  on the graph.

### 2.3 LDF Fuzzy Connectedness And Stable $\varepsilon$ -Clusters

For  $\varepsilon \in (0, 1]$  the LDF  $\varepsilon$ -cluster of the seed set  $S_o$  is  $C_\varepsilon = \{v \in V : \mu^\infty(S_o, v) \geq \varepsilon\}$ .

**Lemma 1.** Let  $G_\varepsilon = (V, E_\varepsilon)$  with  $E_\varepsilon = \{e \in E : \kappa(e) \geq \varepsilon\}$ . Then  $C_\varepsilon$  is the union of the connected components of  $G_\varepsilon$  that intersect  $S_o$ , and  $\varepsilon_1 \geq \varepsilon_2$  implies  $C_{\varepsilon_1} \subseteq C_{\varepsilon_2}$ .

*Proof.* We have  $\mu^\infty(S_o, v) \geq \varepsilon$  if and only if there exist  $s \in S_o$  and a path from  $s$  to  $v$  whose edges all satisfy  $\kappa(e) \geq \varepsilon$ , that is, a path in  $G_\varepsilon$ . Since  $E_{\varepsilon_1} \subseteq E_{\varepsilon_2}$  for  $\varepsilon_1 \geq \varepsilon_2$ , the inclusion follows. ■

By Lemma 1, the clusters  $C_\varepsilon$  coincide with the fuzzy-graph  $\varepsilon$ -clusters of Ibrišimović *et al.*, [13], now computed with the LDF affinity, and they form a nested family. It remains to choose  $\varepsilon$ . Let  $\varepsilon_1 > \varepsilon_2 > \dots$  be the distinct values of  $\mu^\infty(S_o, \cdot)$  and  $A_k = |C_{\varepsilon_k}|$  the area of the corresponding cluster in pixels. We select the level that precedes the largest relative growth of the cluster,

$$\varepsilon^* = \varepsilon_{k^*}, \quad k^* = \arg \max_{k: A_{\min} \leq A_k \leq A_{\max}} \frac{A_{k+1} - A_k}{A_k}, \quad (9)$$

where  $A_{\min} = 0.003|\Omega|$  and  $A_{\max} = 0.25|\Omega|$ . The rule is motivated by the fact that, when the cluster passes into a neighboring organ, the whole organ is added at once, and the area grows abruptly. In addition, every vertex with clearly negative score,  $S(v) < -0.4$ , is added to  $S_b$ , so that the vertex evidence, and not only the edge evidence, enters the decision. Finally, following the principle of relative fuzzy connectedness [32], a vertex is assigned to the object if it belongs to  $C_{\varepsilon^*}$  and is more strongly connected to the object seeds than to the background seeds:

$$\mathcal{O} = \{v \in C_{\varepsilon^*} : \mu^\infty(S_o, v) > \mu^\infty(S_b, v)\}. \quad (10)$$

The labels are then transferred to pixels, holes are filled, and the components containing the seeds are retained. Both maps  $\mu^\infty(S_o, \cdot)$  and  $\mu^\infty(S_b, \cdot)$  are computed by a max–min version of Dijkstra's algorithm in  $O(|E| \log |V|)$  time [7]. The procedure is summarized in Algorithm 1.

#### Algorithm 1

##### LDF-FC segmentation of a CT slice

**Input:** slice  $I$ , object seed points, parameter  $\lambda$ ; **Output:** binary mask  $\mathcal{O}$

- 1: Normalize  $I$  and apply bilateral smoothing; compute SLIC superpixels, adjacency and boundary gradients
- 2: Map the seed points to  $S_o$ ; compute  $\{o_k\}$ , the initial set  $S_b$ ,  $\{q_j\}$  and the geodesic proximity  $\gamma$
- 3: Compute the vertex LDF values by Eqs. (5)–(6) and the edge LDF values by Eq. (7)
- 4: Compute the affinity  $\kappa_{\text{LDF}}$  by Eq. (8) and add the vertices with  $S(v) < -0.4$  to  $S_b$
- 5: Compute  $\mu^\infty(S_o, \cdot)$  and  $\mu^\infty(S_b, \cdot)$  by max–min Dijkstra propagation
- 6: Determine  $\varepsilon^*$  by Eq. (9) and the object vertices by Eq. (10)
- 7: Transfer the labels to pixels, fill holes and keep the components containing the seeds

## 2.4 Data And Reference Delineations

We used seventeen targets (kidneys or renal masses) on axial abdominal CT slices (Table 1). Eight tumor slices were taken from the publicly available CT kidney collection of Islam *et al.*, [15]; the target is the kidney containing the tumor or the renal mass itself. Five normal kidneys come from three slices obtained from The Cancer Imaging Archive [30]: a non-contrast slice with one kidney, a non-contrast slice with both kidneys and a contrast-enhanced slice with both kidneys. The remaining two targets are the kidneys of a non-contrast slice studied by Ibrišimović *et al.*, [12, 13]. Before the experiments, the targets were divided into a *development set* of four targets (the latter two kidneys and two additional tumor slices of the public collection), used only for the choice of parameters, and a *test set* of thirteen targets, on which all reported results are computed.

Since the public sources contain only image-level labels, reference masks were prepared for this study. Each target was outlined by a polygon with 12–20 vertices on a magnified view, and the polygon was refined by a morphological geodesic active contour [19] restricted to a band of four pixels around the polygon. If the refinement changed the area by more than 8%, the polygon was kept. All masks were visually checked by the author. One object seed was placed at the interior point nearest to the centroid of the reference region. For tumor targets a second seed was placed at the interior point whose intensity is closest to the opposite (15th or 85th) percentile of the intensities in the region; this corresponds to a second click on the heterogeneous part of a lesion.

## 2.5 Compared Methods And Experimental Protocol

LDF-FC was compared with six seeded classical methods and two fuzzy-graph variants. All methods received the same smoothed image and the same seed points. The classical methods are: three-class multi-Otsu thresholding [21] followed by extraction of the component containing the seeds; seeded region growing (tolerance 0.08); marker-controlled watershed on the Sobel gradient [33] (background markers at intensity distance greater than 0.25 from the seeds); the random walker [9] ( $\beta = 2000$ , marker distance 0.2); fuzzy c-means [6] with five clusters; and the pixel-level  $\varepsilon$ -clustering of Ibrišimović *et al.*, [13] ( $\varepsilon = 0.05$ ). The variants FG-FC and IF-FC of Section 2.2 use the same superpixel graph and the same rule in Eq. (9) as LDF-FC and differ from it only in the affinity. The main parameter of each method (given in parentheses above; for the graph methods  $\sigma$ ,  $\sigma_e$  and the superpixel size, and for LDF-FC also  $\lambda = 0.5$ ) was determined by a grid search on the development set, maximizing the mean DSC over the clean slice and two noisy versions, and was then kept fixed on the test set. The three graph methods use the same graph parameters.

To study robustness, each normalized slice was corrupted by the four noise models used by Ralević *et al.*, [23]: additive Gaussian noise ( $\sigma_n \in \{0.03, 0.06, 0.09\}$ ), salt-and-pepper noise (2% and 5% of the pixels), multiplicative speckle noise (standard deviation 0.10 and 0.20) and Poisson noise. Three independent realizations were generated for each setting, which gives 24 noisy versions of each target. The dependence on the user input was studied by five additional random displacements of every seed within a  $13 \times 13$  window inside the reference region. The quality of a segmentation was measured by the Dice similarity coefficient (DSC), the Jaccard index, precision, recall, the 95th percentile Hausdorff distance (HD95) and the average symmetric surface distance (ASSD), in accordance with Taha and Hanbury [29] and Seghier [27]; distances are expressed in pixels. The paired differences between LDF-FC and each competing method over all noisy trials were tested by the two-sided Wilcoxon signed-rank test [34]. All algorithms were implemented in Python 3.11 with scikit-image and SciPy and executed on a two-core CPU.

## 2.6 LDF-TOPSIS Model For Selecting A Segmentation Method

The choice of a segmentation method cannot be based on a single measure. We therefore formulate it as a multi-criteria decision problem with alternatives  $A_1, \dots, A_m$  (the nine methods) and criteria  $C_1$ : mean DSC on clean slices (benefit),  $C_2$ : mean HD95 (cost),  $C_3$ : mean DSC under noise (benefit),  $C_4$ : mean DSC with displaced seeds (benefit) and  $C_5$ : mean running time (cost). For every

alternative  $A_i$  and criterion  $C_j$  we record the mean  $x_{ij}$  and the standard deviation  $s_{ij}$  over targets and trials. The dispersion is not treated as a separate criterion; it enters the model through the reference parameters.

The weights are determined by the Shannon entropy method [28, 5]. Let  $z_{ij}$  be the min-max normalized values (reversed for cost criteria),  $p_{ij} = z_{ij} / \sum_i z_{ij}$ ,  $e_j = -\frac{1}{\ln m} \sum_i p_{ij} \ln p_{ij}$  and  $w_j = (1 - e_j) / \sum_k (1 - e_k)$ . Each entry of the decision matrix is represented by the LDF number

$$\mu_{ij} = g_{ij}, \quad \nu_{ij} = 1 - g_{ij}, \quad a_{ij} = \lambda(1 - \hat{s}_{ij}), \quad b_{ij} = (1 - \lambda)\hat{s}_{ij}, \quad (11)$$

where  $g_{ij} \in [0, 1]$  is the normalized goodness and  $\hat{s}_{ij} = s_{ij} / \max_i s_{ij}$  the normalized dispersion. Clearly  $a_{ij} + b_{ij} \leq 1$ . By this choice a high value obtained with large dispersion receives a smaller reference parameter of membership than an equal value obtained with small dispersion; an intuitionistic decision matrix cannot express this distinction. The positive and negative ideal solutions are  $\ell_j^+ = (\max_i \mu_{ij}, \min_i \nu_{ij}, \max_i a_{ij}, \min_i b_{ij})$  and  $\ell_j^- = (\min_i \mu_{ij}, \max_i \nu_{ij}, \min_i a_{ij}, \max_i b_{ij})$ . Using the weighted LDF Hamming distance of Riaz and Hashmi [24],

$$d(\ell_1, \ell_2) = \sum_j \frac{w_j}{4} (|a_1 \mu_1 - a_2 \mu_2| + |b_1 \nu_1 - b_2 \nu_2| + |a_1 - a_2| + |b_1 - b_2|), \quad (12)$$

we define the closeness coefficient  $CC_i = d_i^- / (d_i^+ + d_i^-)$ , where  $d_i^\pm = d(A_i, \ell^\pm)$  [11], and rank the alternatives by decreasing  $CC_i$ . The stability of the ranking is examined for  $\lambda \in \{0.5, 0.6, 0.7, 0.8\}$ , for equal weights, for the omission of each criterion, for the weighted LDF score  $\sum_j w_j S(\ell_{ij})$  of Eq. (2), and in comparison with an intuitionistic TOPSIS on the same pairs  $(\mu_{ij}, \nu_{ij})$ .

### 3. Results

#### 3.1 Data Summary And Development Set

The targets are listed in Table 1. The test set contains small normal kidneys (1 356–2 867 pixels) and large heterogeneous masses (up to 25 671 pixels), slices with and without contrast, and lesions with cystic, necrotic and enhancing parts.

**Table 1**

Segmentation targets used in the study (K: public CT kidney collection of Islam *et al.*, [15]; T: slices from The Cancer Imaging Archive [30]; CT1: slice used by Ibrišimović *et al.*, [12]; L/R: left/right kidney)

| Target                             | Split       | Content        | Area (px)    | Seeds | Phase        |
|------------------------------------|-------------|----------------|--------------|-------|--------------|
| CT1-L, CT1-R                       | development | normal kidneys | 3 777; 2 496 | 1     | non-contrast |
| K-D1725, K-D1425                   | development | renal masses   | 5 277; 3 855 | 2     | contrast     |
| K-T1, K-T450, K-T600, K-T900       | test        | renal masses   | 3 508–25 671 | 2     | contrast     |
| K-T1200, K-T1350, K-T1650, K-T1800 | test        | renal masses   | 4 369–7 049  | 2     | contrast     |
| T-A-L                              | test        | normal kidney  | 1 356        | 1     | non-contrast |
| T-B-L, T-B-R                       | test        | normal kidneys | 2 483; 2 867 | 1     | non-contrast |
| T-C-L, T-C-R                       | test        | normal kidneys | 2 717; 2 556 | 1     | contrast     |

With the selected parameters, the mean DSC on the clean development slices was 0.784 for FG-FC, 0.730 for region growing, 0.669 for the random walker, 0.662 for IF-FC and 0.654 for LDF-FC, and below 0.40 for Otsu thresholding, fuzzy c-means and pixel-level  $\varepsilon$ -clustering. Hence the development data did not favor LDF-FC, and the comparison on the test set is an out-of-sample comparison.

#### 3.2 Segmentation Accuracy On Clean Test Slices

Table 2 contains the mean values of the metrics over the thirteen test targets with the original seeds. LDF-FC has the largest DSC (0.718), Jaccard index (0.608) and precision (0.941), and the smallest boundary errors (HD95 = 20.4 px, ASSD = 9.0 px). Among the graph variants, the non-membership degree (IF-FC versus FG-FC) increases the DSC by 0.010, while the reference parameters (LDF-FC versus IF-FC) increase it by a further 0.115 and reduce HD95 by one half. This agrees with the role of

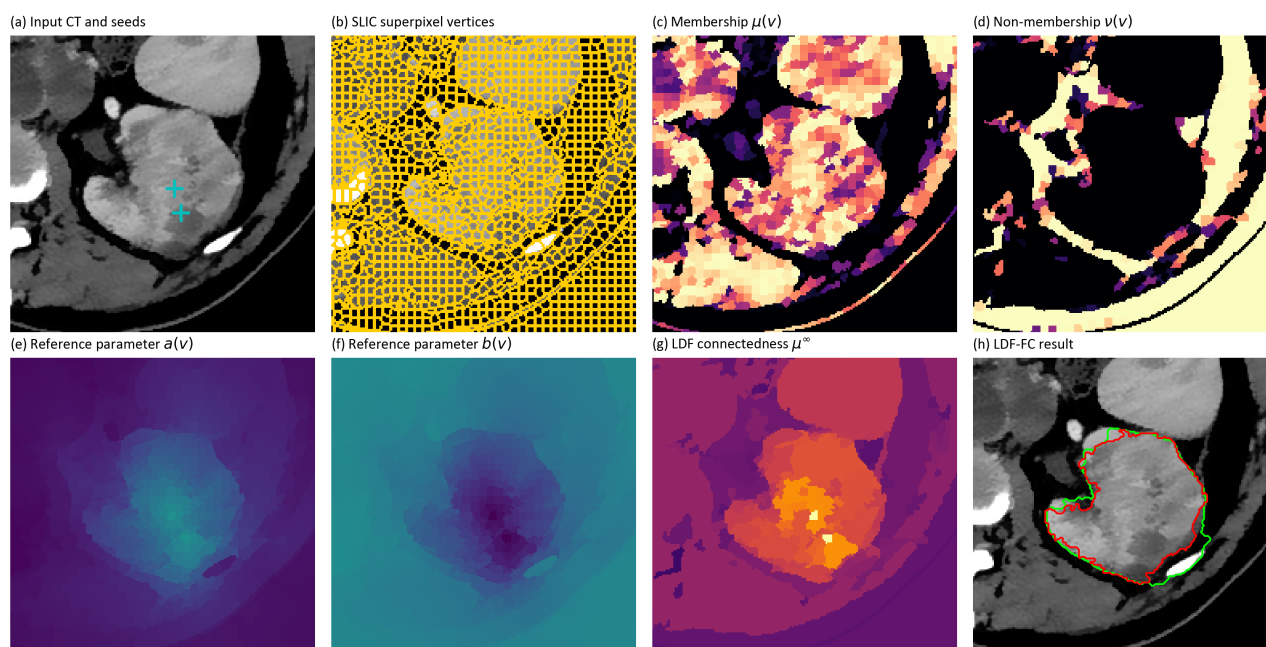
( $a$ ,  $b$ ) in the construction, namely to prevent the extension of the region into neighboring organs. The best classical method is the random walker (DSC 0.669); its precision (0.777) is lower, which indicates over-segmentation. The high recall of Otsu thresholding and  $\varepsilon$ -clustering (0.860 and 0.970) is a consequence of frequent extension into large parts of the abdomen, as seen from HD95 values above 110 px. LDF-FC was the best method on four of the thirteen targets, the random walker on three, and FG-FC and  $\varepsilon$ -clustering on two each.

**Table 2**

Mean segmentation quality on the thirteen clean test targets (best value in bold; HD95 and ASSD in pixels; time in seconds per slice)

| Method                    | DSC          | Jaccard      | Precision    | Recall       | HD95        | ASSD       | Time        |
|---------------------------|--------------|--------------|--------------|--------------|-------------|------------|-------------|
| Otsu                      | 0.500        | 0.389        | 0.519        | 0.860        | 111.9       | 52.8       | <b>0.03</b> |
| Region growing            | 0.617        | 0.488        | 0.750        | 0.697        | 48.6        | 17.4       | <b>0.03</b> |
| Watershed                 | 0.540        | 0.429        | 0.569        | 0.839        | 87.3        | 37.6       | 0.09        |
| Random walker             | 0.669        | 0.560        | 0.777        | 0.762        | 41.8        | 15.4       | 1.31        |
| FCM                       | 0.450        | 0.344        | 0.651        | 0.566        | 69.8        | 27.9       | 3.51        |
| $\varepsilon$ -clustering | 0.391        | 0.321        | 0.341        | <b>0.970</b> | 187.9       | 106.8      | 0.19        |
| FG-FC                     | 0.593        | 0.460        | 0.844        | 0.583        | 31.8        | 13.2       | 0.94        |
| IF-FC                     | 0.603        | 0.463        | 0.821        | 0.624        | 40.1        | 16.2       | 0.80        |
| LDF-FC (proposed)         | <b>0.718</b> | <b>0.608</b> | <b>0.941</b> | 0.653        | <b>20.4</b> | <b>9.0</b> | 1.01        |

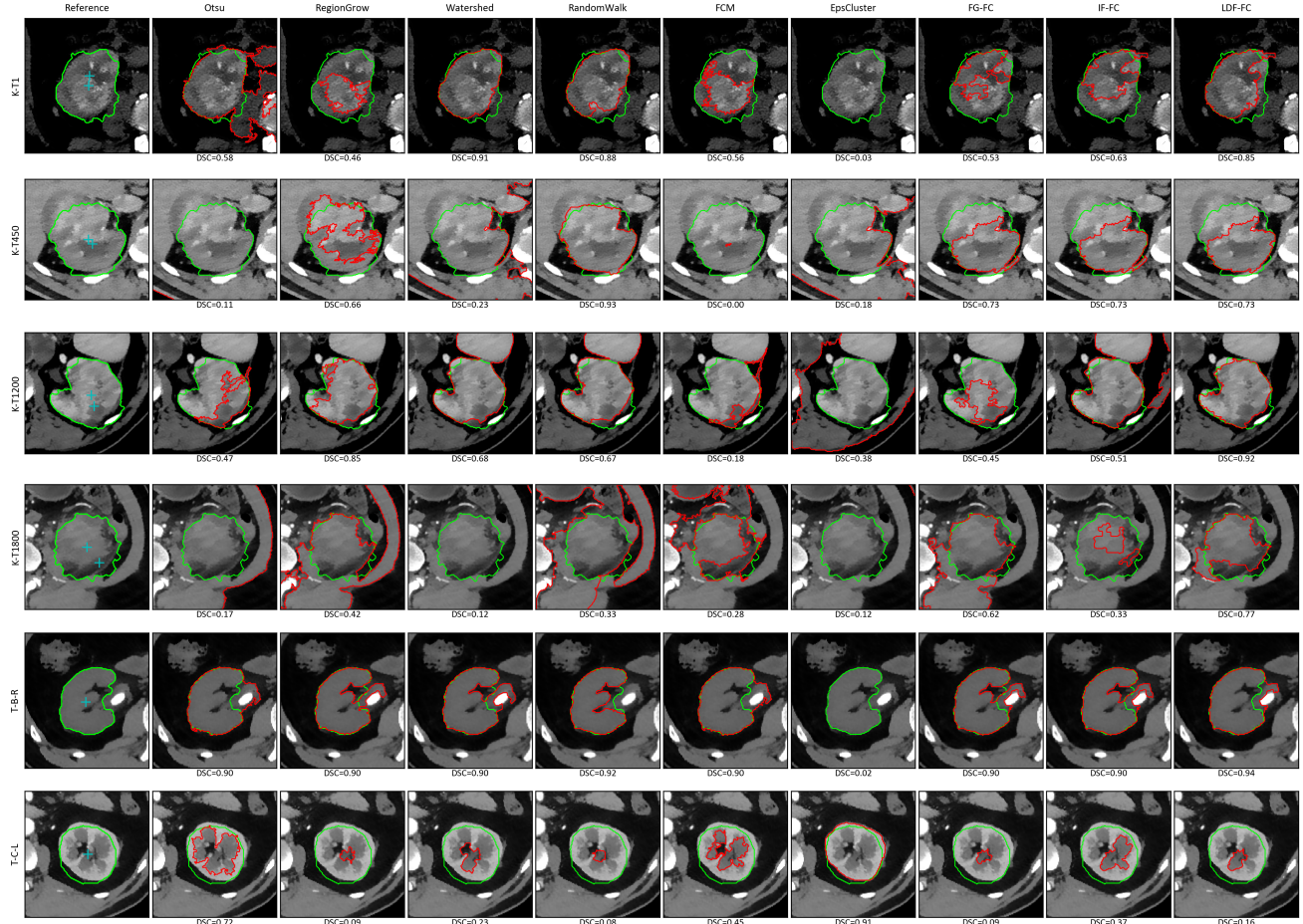
Figure 1 shows the intermediate quantities for the test target K-T1200, a contrast-enhanced kidney with a heterogeneous tumor in the lower pole. The membership  $\mu$  (c) is large both in the kidney and in the spleen above it, since the two organs have similar attenuation. The reference parameter  $a$  (e) is large only in a neighborhood of the seeds and decreases beyond the perirenal fat, and  $b$  (f) behaves in the opposite way. Consequently, the LDF connectedness (g) separates the kidney from the spleen by a distinct gap between levels, and the resulting contour (h) is close to the reference (DSC = 0.92; FG-FC and IF-FC give 0.45 and 0.51 on the same slice).



**Fig. 1.** LDF-FC on test target K-T1200: (a) smoothed slice with the two seeds, (b) superpixel vertices, (c)–(f) vertex LDF values  $\mu$ ,  $\nu$ ,  $a$ ,  $b$ , (g) LDF connectedness to the object seeds, (h) result (red) and reference (green)

Figure 2 compares the methods on six targets. The classical methods either extend into the surrounding tissue ( $\varepsilon$ -clustering and fuzzy c-means on K-T1200, region growing and the random walker

on K-T1800) or stop at internal boundaries of the tumor (region growing on K-T450). FG-FC and IF-FC give compact regions but often omit the part of the lesion with different attenuation. The last row shows a typical failure of seeded methods: on the contrast-enhanced kidney T-C-L the seed lies on the renal sinus, and most methods, LDF-FC included, segment the sinus fat instead of the parenchyma. Only  $\varepsilon$ -clustering and Otsu thresholding, which do not use spatial coherence around the seed, recover most of the kidney in this case.



**Fig. 2.** Qualitative comparison on six test targets (green: reference; red: segmentation; cyan crosses: seeds); the DSC of each result is given below the panel

### 3.3 Robustness To Noise And To Seed Placement

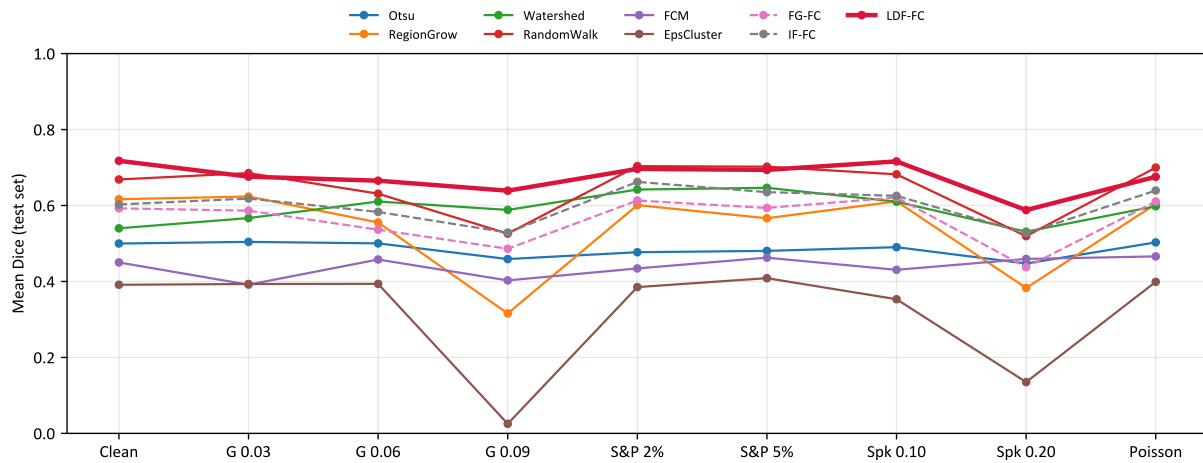
The mean DSC under noise is given in Table 3 and Figure 3. In four of the eight noise settings the largest value is attained by LDF-FC and in the other four by the random walker. The random walker is better for weak Gaussian, salt-and-pepper and Poisson noise, with differences from 0.008 to 0.024, and LDF-FC is better for medium and strong Gaussian noise and for both levels of speckle noise. The largest differences occur for strong Gaussian noise ( $\sigma_n = 0.09$ : 0.639, compared with 0.588 for the watershed and 0.526 for the random walker) and for strong speckle noise (0.588 compared with 0.531), that is, in the settings in which the intensity is least reliable and the topological evidence is most important. Region growing and  $\varepsilon$ -clustering deteriorate considerably under strong Gaussian noise (0.316 and 0.025). Over all noisy trials ( $n = 312$  per method) the DSC of LDF-FC is larger than that of each competing method; the paired Wilcoxon signed-rank test gives  $p < 10^{-5}$  for all methods except the random walker (mean difference 0.025,  $p = 0.027$ ).

For randomly displaced seeds the mean DSC of LDF-FC is 0.641, which is the largest value (region growing 0.622, random walker 0.613, IF-FC 0.604). The standard deviation of DSC over the six seed

**Table 3**

Mean DSC on the test set under noise (G: Gaussian,  $\sigma_n$ ; S&P: salt-and-pepper, fraction of pixels; Spk: speckle, standard deviation; three realizations each; best value in bold)

| Method                    | G 0.03       | G 0.06       | G 0.09       | S&P 0.02     | S&P 0.05     | Spk 0.10     | Spk 0.20     | Poisson      |
|---------------------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|
| Otsu                      | 0.504        | 0.500        | 0.459        | 0.477        | 0.481        | 0.490        | 0.447        | 0.503        |
| Region growing            | 0.624        | 0.555        | 0.316        | 0.601        | 0.566        | 0.611        | 0.383        | 0.604        |
| Watershed                 | 0.567        | 0.611        | 0.588        | 0.642        | 0.647        | 0.610        | 0.531        | 0.598        |
| Random walker             | <b>0.685</b> | 0.631        | 0.526        | <b>0.704</b> | <b>0.702</b> | 0.682        | 0.519        | <b>0.700</b> |
| FCM                       | 0.392        | 0.458        | 0.403        | 0.434        | 0.463        | 0.431        | 0.459        | 0.466        |
| $\varepsilon$ -clustering | 0.393        | 0.394        | 0.025        | 0.385        | 0.409        | 0.353        | 0.135        | 0.399        |
| FG-FC                     | 0.586        | 0.536        | 0.486        | 0.613        | 0.594        | 0.621        | 0.438        | 0.611        |
| IF-FC                     | 0.618        | 0.583        | 0.529        | 0.662        | 0.635        | 0.626        | 0.527        | 0.639        |
| LDF-FC (proposed)         | 0.676        | <b>0.665</b> | <b>0.639</b> | 0.696        | 0.694        | <b>0.716</b> | <b>0.588</b> | 0.676        |

**Fig. 3.** Mean DSC on the test set for the clean slices and the eight noise conditions

positions of a target is similar for the region-based seeded methods (0.110–0.123 for LDF-FC, IF-FC, FG-FC, region growing and the random walker) and smaller for Otsu thresholding and  $\varepsilon$ -clustering (0.027–0.028). The small dispersion of the latter two methods is due to the fact that they return almost the same, incorrect, region for every seed position. For this reason the dispersion is used in the decision model to modify the confidence in a performance value, and not as an independent criterion.

### 3.4 LDF-TOPSIS Selection Of A Segmentation Method

Table 4 contains the decision matrix, the entropy weights and the LDF-TOPSIS results for  $\lambda = 0.6$ . The largest weight is assigned to the DSC on clean slices ( $w_1 = 0.265$ ), followed by the DSC under noise (0.201), the DSC with displaced seeds (0.198), HD95 (0.178) and the running time (0.158). LDF-FC is ranked first ( $CC = 0.904$ ), followed by IF-FC (0.851), FG-FC (0.812), region growing (0.798) and the random walker (0.657); pixel-level  $\varepsilon$ -clustering is ranked last (0.210). LDF-FC has the smallest distance to the positive ideal solution ( $d^+ = 0.031$ ) and the largest distance to the negative ideal solution ( $d^- = 0.291$ ).

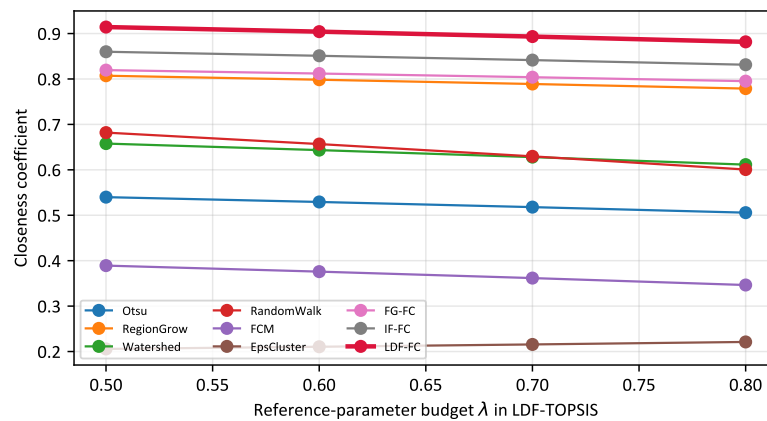
The ranking is stable. For  $\lambda \in \{0.5, 0.6, 0.7, 0.8\}$  the closeness coefficients change by at most 0.09, the first four positions (LDF-FC, IF-FC, FG-FC, region growing) remain unchanged, and the only change is the exchange of the random walker and the watershed for  $\lambda = 0.8$  (Figure 4). If one criterion is omitted, if equal weights are used, or if the alternatives are ranked by the weighted LDF score in Eq. (2), LDF-FC remains first and IF-FC second; in the last case region growing moves to the third position. In the intuitionistic TOPSIS on the same pairs ( $\mu_{ij}, \nu_{ij}$ ) the random walker moves from the fifth to the second position, since the large dispersion of its running time and of its accuracy over the targets is no longer taken into account. Thus the reference parameters allow us to express that a good mean

**Table 4**

Decision matrix (criterion means over the test set), entropy weights and LDF-TOPSIS results for  $\lambda = 0.6$  (C1, C3, C4 are benefit criteria; C2, C5 are cost criteria)

| Method                    | C1 DSC | C2 HD95 | C3 DSC noise | C4 DSC seeds | C5 Time | $d^+$ | $d^-$ | $CC$  | Rank |
|---------------------------|--------|---------|--------------|--------------|---------|-------|-------|-------|------|
| Otsu                      | 0.500  | 111.9   | 0.483        | 0.489        | 0.03    | 0.152 | 0.170 | 0.529 | 7    |
| Region growing            | 0.617  | 48.6    | 0.533        | 0.622        | 0.03    | 0.065 | 0.257 | 0.798 | 4    |
| Watershed                 | 0.540  | 87.3    | 0.599        | 0.541        | 0.14    | 0.115 | 0.207 | 0.643 | 6    |
| Random walker             | 0.669  | 41.8    | 0.644        | 0.613        | 1.23    | 0.111 | 0.211 | 0.657 | 5    |
| FCM                       | 0.450  | 69.8    | 0.438        | 0.495        | 3.90    | 0.201 | 0.121 | 0.376 | 8    |
| $\varepsilon$ -clustering | 0.391  | 187.9   | 0.312        | 0.378        | 0.17    | 0.254 | 0.068 | 0.210 | 9    |
| FG-FC                     | 0.593  | 31.8    | 0.561        | 0.561        | 0.97    | 0.061 | 0.261 | 0.812 | 3    |
| IF-FC                     | 0.603  | 40.1    | 0.602        | 0.604        | 0.89    | 0.048 | 0.274 | 0.851 | 2    |
| LDF-FC                    | 0.718  | 20.4    | 0.669        | 0.641        | 0.97    | 0.031 | 0.291 | 0.904 | 1    |
| Weight $w_j$              | 0.265  | 0.178   | 0.201        | 0.198        | 0.158   |       |       |       |      |

value with large dispersion is less reliable than a slightly smaller value with small dispersion.



**Fig. 4.** Sensitivity of the LDF-TOPSIS closeness coefficients to the reference-parameter budget  $\lambda$

### 3.5 Discussion

We summarize the main observations. First, the linear Diophantine structure has a measurable effect: with photometric information only (FG-FC), or with photometric information and non-membership (IF-FC), the superpixel graph performs similarly to the classical seeded methods, while the reference parameters increase the DSC by more than 0.11 and reduce the boundary error by one half on data not used for tuning. By Proposition 2, this difference is caused exactly by the variation of  $\tau_E - \nu_E$  on the graph. Second, the improvement is largest when intensity is least informative, i.e. for heterogeneous tumors adjacent to organs of similar attenuation and for strongly corrupted slices. On the five normal TCIA kidneys, which are separated from the neighboring organs by perirenal fat, thresholding is already competitive (mean DSC 0.807, compared with 0.686 for LDF-FC). The difference is caused by the two contrast-enhanced kidneys, where the seed on the renal sinus (T-C-L) and the strong cortico-medullary contrast (T-C-R) violate the assumption of a photometrically homogeneous object; on the three non-contrast kidneys LDF-FC attains 0.91–0.94. Third, the result of the decision model depends on the way in which the dispersion of the evaluation is treated. If dispersion were an independent cost criterion, methods that fail consistently would be preferred. Representing it by the reference parameters keeps accuracy as the primary criterion and uses stability to adjust the confidence.

The study has several limitations. The data set is small (seventeen two-dimensional targets), and the JPEG images of the public collection do not preserve Hounsfield units; therefore the absolute values of DSC are lower than those reported for supervised three-dimensional networks trained on large

annotated collections [25]. The reference masks were prepared and checked by one observer, so inter-observer variability could not be assessed [27]. The method is semi-automatic and depends on the position of the seeds, as the case T-C-L shows; an automatic test whether a seed lies in the renal sinus, or an automatic proposal of seeds, would remove this type of failure. Finally, the development set contains only four targets, and on these targets FG-FC performed better than LDF-FC, which suggests that the relative performance of the variants may depend on the composition of the data.

#### 4. Conclusions

We introduced a linear Diophantine fuzzy graph on the superpixels of a CT slice, in which the membership pair describes photometric evidence and the reference pair describes geodesic and boundary evidence, and we proved that the construction satisfies the axioms of an LDF graph and contains the intuitionistic model as a special case. On this graph we defined the segmentation by LDF fuzzy connectedness and a stability rule on the nested family of  $\varepsilon$ -clusters. On thirteen test targets not used for the choice of parameters, LDF-FC attained the largest mean Dice coefficient (0.718) and precision (0.941) and the smallest boundary errors (HD95 = 20.4 px, ASSD = 9.0 px) among nine methods. It was also the most accurate method under medium and strong Gaussian noise, under speckle noise and with displaced seeds. The comparison with the fuzzy and intuitionistic variants shows that the improvement is due mainly to the reference parameters. For the selection of a method we proposed an LDF-TOPSIS model in which the dispersion of the observed performance determines the reference parameters. In this model LDF-FC was ranked first ( $CC = 0.904$ ), and the ranking was stable with respect to  $\lambda$  and to the weights of the criteria. These results answer the two questions posed in the introduction: an LDF graph yields a segmentation that is more robust than its fuzzy and intuitionistic counterparts, and the same framework provides a transparent selection among competing algorithms under uncertainty. Further work will concern three-dimensional data in Hounsfield units, comparison with reference delineations of several observers, automatic placement of seeds, and the use of the LDF decision model for combining the outputs of several segmentation methods.

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#### Conflicts of Interest

The author declares no conflicts of interest.

#### Data Availability

The CT images used in this study are publicly available from the CT kidney collection of Islam *et al.*, [15] and from The Cancer Imaging Archive [30]. The reference masks, seed coordinates and the Python implementation are available from the author upon reasonable request.

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