An Algorithm for Segmentation and Detection of Changes in Signals Using Diffusion Equations

Aline R. Gesualdi[1,2], Marcelo P. de Albuquerque[2], Márcio P. de Albuquerque[2], Marcello L. R. de Campos[1]

[1]Universidade Federal do Rio de Janeiro, Rio de Janeiro RJ, Brazil

[2]Centro Brasileiro de Pesquisas Físicas, Rio de Janeiro RJ, Brazil

Abstract— **We will present, in details, an algorithm for the Stabilized Inverse Diffusion Equation (SIDE) technique introduced in [4]. The algorithm will be evaluated in two different application areas of interest, which are: signal detection and image segmentation. SIDEs are a family of semi-discrete evolution equations which stably sharpen edges and suppress noise. This characteristic makes SIDEs an efficient tool in noise reduction problems. This paper will focus on the detection of 1-D signals and on the segmentation of ultrasound and mammography images. Results will be presented.**

I. Introduction

THE objective of this paper is to present an algorithm for the implementation of SIDE technique introduced in [4], [5], that is applicable to 1-D and 2-D signals. Pollak and Willsky's work presented SIDEs as a family of semi-discrete evolution equations which stably sharpen edges and suppress noise. The implementation of SIDEs naturally results in a recursive region merging algorithm. We'll use SIDE algorithm in the detection of abrupt changes in 1-D signals, and in the segmentation of mammography and ultrasound images.

Scale has recently emerged as an important characteristic in signal and image analysis, and has played an increasingly important role in the solutions to many new problems. Any technique that incorporates a scale parameter - either directly in the computation procedure, or implicitly as a part of the image model - controls the smoothness of the estimate and/or sizes of the segmented regions. SIDEs are motivated by the interest in using scale evolutions specified by partial differential equations (PDE's), and may be viewed as a conceptually limiting case of Perona-Malik diffusions [5]. In this section we introduce the concepts of the Stabilized Inverse Diffusion Equations.

A. SIDEs: The Definition

Pollak and Willsky described a convenient mechanical analogy for the visualization of the evolution equations, illustrated in Figure 1.

Suppose that $\mathbf{u} \in \Re^N$ is a one-dimensional (1-D) sequence, and interpret $\mathbf{u}(t) = (u_1(t), \ldots, u_N(t))^T$ in (1) as a vector of vertical positions of the N particles of masses $M_1, \ldots, M_N$, depicted in Figure 1. The particles are forced to move along N vertical lines. Each particle is connected by springs to its two neighbors (except the first and last particles, which are only connected to one neighbor).

Aline R. Gesualdi and Marcello L. R. de Campos are with the Laboratório de Processamento de Sinais, Departamento de Engenharia Elétrica, COPPE/UFRJ, Rio de Janeiro - RJ, Brazil, CP 68504, 21945-970. Aline R. Gesualdi, Marcelo P. Albuquerque and Márcio P. Albuquerque are with the Centro Brasileiro de Pesquisas Físicas, Coordenação de Atividades Técnicas, Rio de Janeiro, RJ, Brazil, Phone: +55 21 2586 7426110 Fax: +55 21 2586 7426. E-mails: aline@cbpf.br, campos@lps.ufrj.br, marcelo@cbpf.br, mpa@cbpf.br.

The movement of the particles is made by the "force function" $F(v)$ and it's non-conservative, *i.e.*, stops after a small period of time Δt and restarts with zero velocity.

$$\dot{u}_n = \frac{1}{m_n}(F(u_{n+1} - u_n) - F(u_n - u_{n-1})),$$
$$n = 1, 2, \ldots, N \tag{1}$$

with the conventions $u_0 = u_1$ and $u_{N+1} = u_N$ imposed by the absence of springs to the left of the first particle and to the right of the last particle. m_n is refereed to as "the mass of the nth particle".

The type of force function of interest to us here is illustrated in Figure 2. Because of the discontinuity at the origin of the force function, there is a question of how one defines solutions of (1) for such a force function. Indeed, if (1) evolves toward a point of discontinuity of its RHS, the value of the RHS of (1) apparently depends on the direction from which the point is approached [because $F(0^+) \neq F(0^-)$], making further evolution nonunique. Therefore, in terms of our spring-mass model of Figure 1, once the vertical positions $\mathbf{u}_i$ and $\mathbf{u}_{i+1}$ of two or more neighboring particles becomes equal, the springs connecting them are replaced by a rigid link. In other words, the particles are simply merged into a single particle which is twice as heavy, yielding the following modification of(1):

$$\dot{u}_{n_i} = \frac{1}{m_{n_i}}(F(u_{n_i+1} - u_{n_i}) - F(u_{n_i} - u_{n_i-1}))$$
$$u_{n_i} = u_{n_i+1} = \ldots = u_{n_i+m_{n_i}-1},$$
$$\text{onde } i = 1, \ldots, p \tag{2}$$
$$1 = n_1 < n_2 < \ldots < n_{p-1} < n_p \leq N,$$
$$n_{i+1} = n_i + m_{n_i}$$

The compound particle described by the vertical position u_{n_i} and mass m_{n_i} consists of m_{n_i} unit-mass particles $u_{n_i}, u_{n_i+1}, \ldots, u_{n_i+m_{n_i}-1}$ that have been merged.
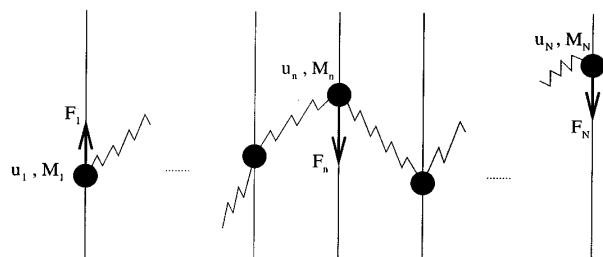

Fig. 1. A spring-mass model.

Choosing a SIDE force function best suited for a particular application is an open question. The evolution of SIDEs automatically produces a multiscale segmentation of the original signal.

II. CHANGE DETECTION PROBLEMS SOLVED BY SIDES

In the signal detection theory, the "transmitter" and the "receiver" know, *a priori*, the set of symbols and the waveform associated with each symbol. What the receiver does not know in advance is which symbols have been transmitted during a given interval. Since the received waveform is usually distorted and masked by noise, the receiver will occasionally make errors in determining which symbol was present in an observation interval.

There are many applications in which we have to make a choice or decision based on observations. In digital communication systems, for example, the receiver has to make a decision as to which one of M possible signals is actually present based on noisy observations. In each case the solution involves making a decision based on observations of data that are random variables. The theory behind the solutions to these problems have been developed by statisticians and fall under the general area of statistics known as statistical inference, decision theory, or hypothesis testing.

In classical hypothesis testing, decisions are based on the likelihood function, whereas in the theoretical approach, the *a priori* probabilities and costs associated with various decisions will also be included in the decision rule. The likelihood function used in SIDE evolution is the expected edges of the received signal.

In this section we use SIDE definition in order to build an algorithm to solve edge detection or binary classification problems. In the case of a binary communication system, the receiver knows that either a "1" or "0" is transmitted every T seconds and that a "1" is represented by a positive pulse and a "0" is represented by a negative pulse.

Given an observation $\mathbf{u} = (u_1, \ldots, u_N)^T$, where $N = \frac{T}{k}$ and k is the number of periods of the input signal ($k = 7$ in this example), as the input signal corrupted by an additive noise. The goal is to label each sample as coming from one of the two classes, *i.e.* to produce a binary signal $\mathbf{h}$ whose entries are zeros and ones. We call any such binary signal $\mathbf{h}$ a *hypothesis*. The SIDE algorithm for signal detection, can be summarized as follows:

i. Initially assume the finest segmentation: each sample is a separate region, *i.e.* $m_n = 1$ for $n = 1, \ldots, N$;

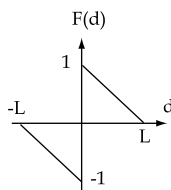ii. Define the stopping criterion: number of level crossings α;

iii. Evolve equation (2), with $F(v) = sgn(v)$, until the values in two or more neighboring regions become equal;

iv. Merge the neighboring regions whose values are equal;

v. Go to step iii until the number of edges is lower or equal α.

Note that the hypothesis is uniquely defined by the set of its edges (α). This is the only information the receiver has to know in advance, there is no need to estimate the probability density function of the signal. In case of binary communication systems, we know de duration of the symbols and so of the received signal. We can then estimate the numbers of zero crossings.

We first tested the algorithm on a unit step function corrupted by additive white Gaussian noise whose standard deviation is equal to the amplitude of the step, and which is depicted in Figure 3.
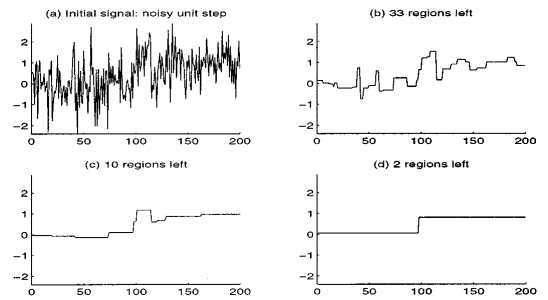

Fig. 3. (a)The original signal; (b)The resulting SIDE detection.

Note that the remaining edge in Figure 3(b) is located between samples 80 and 81, which is quite close to the position of the original edges (between samples 79 and 80).

Our second example, depicted in Figure 4, shows a binary communication signal corrupted by additive noise, with amplitude ten times higher than the original signal. Note that the amplitudes of the final signal (Figure 4(b)) are quite different from those of the initial condition (Figure 4(a)). The stopping criterion for the evolution is $\alpha = 6$, *i.e.* when there are only seven regions left. The detected signal (Figure 4(c)) is very close to the original one (Figure 4(a)), showing that the correct detection was made.
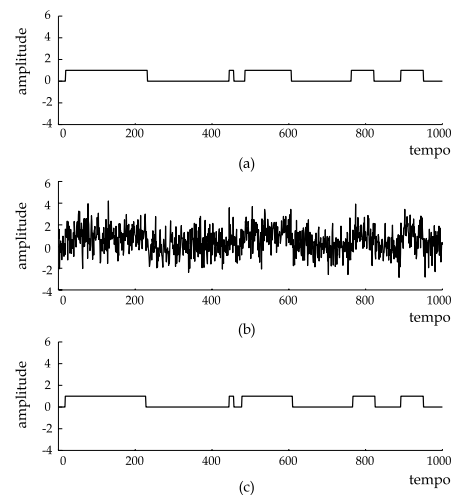

Fig. 4. (a)The original (transmitted) signal; (b)The received signal; (c)The resulting SIDE signal.

Fig. 2. Force function for a stabilized inverse diffusion equation ($F(v) = sgn(v) - \frac{v}{L}$, for $L > \max(\mathbf{u}^0)$).

III. Image Segmentation with Stabilized Inverse Diffusion Equations

In the previous section we showed the SIDE algorithm used in the detection of changes in 1-D signals. In this section we will evaluate an SIDE algorithm in problems of segmentation of images.

To segment an image means to partition the domain of its definition into several regions in such a way that the image is homogeneous within each region and changes abruptly among regions [5]. Image segmentation is closely related to restoration, that is, the problem of estimating an image based on its degraded observation. The solution to one of these problems makes the other simpler, *i.e.* segmentation is easier once a good estimate of the image has been computed. It is therefore natural that many segmentation algorithms are related to restoration techniques, and in fact some methods combine the two, producing estimates of both the edge locations and image intensity [7], [8].

In describing any restoration or segmentation technique, the notion of scale is very important. SIDE technique incorporates a scale parameter, directly in the computation procedure, which controls the smoothness of the estimate and sizes of the segmented regions.

Given an image or a set of images resulting from a medical image procedure - such as ultrasound or mammography - it is necessary to extract certain objects of interest. Mammography images, for example, are used to detect a number of abnormalities, the two main ones being calcifications and masses. On the other hand, ultrasound images are used to detect cysts. However, ultrasound does not have as good spatial resolution as mammography.

In this section we present an SIDE-based image segmentation algorithm, which can be used in both exams to help physicians to locate abnormalities. The scale space produced by SIDE has the advantage of grouping similar regions (tissues) and suppressing noise produced by the measurement. The SIDE semi-discrete scale space (*i.e.*, continuous in scale, or time, and discrete in space) presented in section I-A is used for 2-D signals. To extend the mechanical model of Figure 1 to images, we simply replace the sequence of vertical lines with a N-by-N square grid of such lines. A particle at location (i, j) is connected by springs to its four neighbors, except for the particles in the four corners, and those on the boundary of the square.

The partial differential equation (PDE) evolution presented in equation 2 automatically produces a multiscale segmentation of the original signal. The same PDE can be used for 2-D images, which is immediate upon re-writing equation 2:

$$\dot{u}_{n_i} = \frac{1}{m_{n_i}} \sum_{n_j \in \mathcal{A}_{\backslash_{\rangle}}} F(u_{n_j} - u_{n_i}), \tag{3}$$

where m_{n_i} is again the mass of the compound particle n_i (number of pixels in the region n_i). $\mathcal{A}_{\backslash_{\rangle}}$ is the set of indices of all neighbors of n_i, *i.e.*, of all the compound particles that are connected to n_i by springs.

Just as in 1-D, two neighboring regions n_1 and n_2 are merged by replacing them with one region n of mass $m_n = m_{n_1} + m_{n_2}$ and a set of neighbors $A_n = A_{n_1} \cup A_{n_2} (n_1, n_2)$. Viewed as a segmentation algorithm, this evolution can be summarized as:


```
begin
    Reading image u⁰
    Initializing variables:
    K = 0,04                          two neighbors are equal if | a − b | < K → a = b
    λ = 0,01                          scale step t or iteraction (initialization)
    Mass = ones(N × M)                initializing mass matrix with the same size of u⁰.
    Starting with the finnest segmentation.
    each pixel is a distinct region of mass equal to 1.
    Regions = N * M                   initial number of regions (number of pixels in u⁰)
    L = max(diff uₙⱼ) ∀nⱼ ∈ Aₙᵢ
    F(v) = sign(v) − v/L               force function definition F
    uₙ = u⁰
    while Regions > 2 do
        uₙₒⱼ = diff(uₙ)                evaluating columns difference
        for col = 1 to M do
            Finding neighbors in columns with values lower than K
            Grouping regions in uₙ if the previous condition is satisfied
            Updating Mass matrix and number of Regions
        od
        uₙₒᵢ = diff(uₙ)                calculating differences between image lines
        for row = 1 to N do
            Searching for neighbors in lines with values lower than K
            Grouping regions in uₙ if the previous condition is satisfied
            Updating Mass matrix and number of Regions
        od
        uₙₒₑ = F(uₙ)                   Applying force function.
        uₙ = uₙ + λ * uₙₒₑ./Mass       Next image of the evolution.
    od
end
```

Program 1 - Algorithm for 2-D signals.

The algorithm showed above applies SIDE theory in the reduction of noise in 2-D signals. The number of evolutions made by the algorithm will determine the number of remaining regions. In this paper we are interested in binary images, which means that the algorithm will be evaluated until there are only two regions left. The number of iterations, the constants K, $lambda$ and the force function F will depend on the noise added to the image. These constants play an important role in the convergence of the images, and their determination is based on a subjective analysis of images during evolution.

Figures 5 and 6 ilustrate the evolution process obtained in the segmentation of ultrasound and mammography images.

(a)   (b)
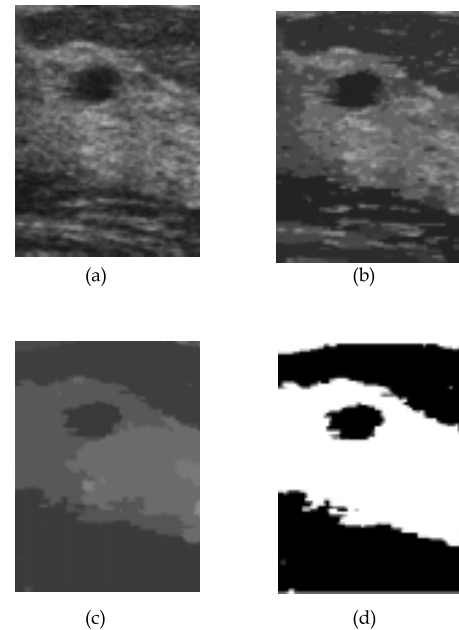
(c)   (d)

Fig. 5. Evolution of SIDE equation in ultrasound images.(a)original image, (b) 1000 regions image, (c) 4 regions image and (d) two regions image.

We can observe that the number of iterations needed for convergence varies from one image to another, as we can see in Figures 5 and 6. The number if iterations needed to segment the

ultrasound image is twice as big as the number needed for the mammography image. One of the aspects that we can observe is that during the evolution, different tissues are enhanced.

IV. CONCLUSIONS AND FUTURE RESEARCH

In this paper we present two algorithms that implement the SIDEs technique and demonstrate their successful application to signals and images with very high levels of noise, as well as to blurry signals. Our algorithms are based on a class of evolution equations for the processing of imagery and signals called stabilized inverse Diffusion Equations or SIDEs. These evolutions have their own unique qualitative characteristics that suggest a good noise reduction algorithms. Methods for choosing the force function F need some more investigation in order to stabilize regions in fewer steps. The algorithms presented can be otptimized in merging regions.

ACKNOWLEDGMENTS

REFERENCES

[1] Perona, P. and Malik, J, *Scale-space and edge detection using anisotropic diffusion*, IEEE Trans. Pattern Anal. Machine Intell., vol. 12, no. 7, bf 1990.

[2] Perona, P., Shiota, T. and Malik, J, *Anisotropic diffusion*, in Geometry-Driven Diffusion in Computer Vision, B. M. ter Haar Romeny, Ed. Norwell, MA: Kluwer, 1994.

[3] Brice, C. and Fennema, C., *Scene analysis using regions*, Artif. Intell., vol. 1, 1970.

[4] Pollak, I., Willsky, S. and Krim, H., *Image segmentation and edge enhancement with stabilized inverse diffusion equations*, IEEE Trans. on Image Processing, vol. 9, no. 2, 2000.

[5] Pollak, I., *Nonlinear Scale Space Analysis in Image Processing*, PhD Thesis, Massachusetts Institute of Technology, August, 1999.

[6] Geman, D. and Reynolds, G., *Constrained restoration and the recovery of discontinuities*, IEEE Trans. Pattern Anal. Machine Intell, vol. 14, no. 3, 1992.

[7] Mumford, D. and Shah, J., *Boundary detection by minimizing functionals*, InProc. CVPR, San Francisco, CA, 1985.

[8] G. Koepfler, C. Lopez, and J. M. Morel., *A multiscale algorithm for image segmentation by variational method*, SIAM J. Numer. Anal., 31(1), 1994.
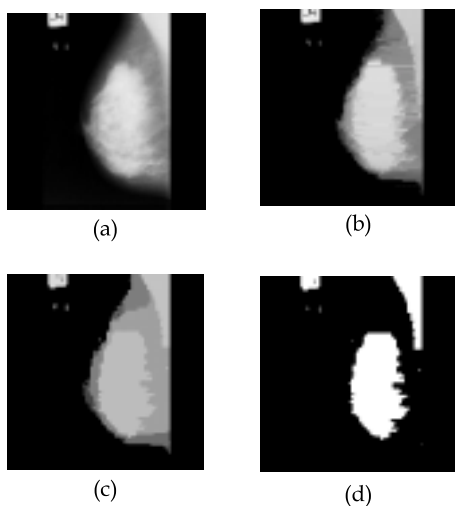

(a)

(b)

(c)

(d)

Fig. 6.   SIDE evolution in a mammography image. (a)original image, (b) 500 regions image, (c) 5 regions image and (d) two regions image.