Noise removal in images using isotropic finite-differences

Typical partial differential equation (PDE) based techniques for image processing regard the original image as the initial state of a parabolic process, and extract filtered versions from its temporal evolution. Conventional numerical schemes for the solution of PDEs are however directionally biased, i.e. anisotropic[1]. They therefore may not be well suited for noise-removal applications. We show noise removal in images, based on Perona–Malik equation[2], using a conventional scheme, and a scheme based on isotropic finite differences[1,3].

A PDE[2], extensively used for image processing applications, is

$$\frac{\partial \phi}{\partial t} = \nabla \cdot (c \nabla \phi), \tag{1}$$

where $\phi(x, y)$ is the image, c the diffusion coefficient. c is chosen to retain the 'features' and dissipate the 'noise'. c, for example, can be given by

$$c = \frac{1}{1 + (\| \nabla \phi \| / K)^2}, \tag{2}$$

where K is a constant.

In eq. (1), isotropic finite differences are evaluated at the mid-points $(i+\frac{1}{2}, j)$ and $(i, j+\frac{1}{2})$ using the values at (i, j), and at the points (i, j) using the values at the mid-points[3], to give the isotropic scheme. Conventional central differences are used for the conventional scheme. Integration in t is carried out using the Euler scheme.

The directionally biased nature of the conventional numerical scheme can be seen by considering the exact solution of (1),

$$\phi_0 = \begin{cases} 1 & \text{if } r < r_0 \\ 0 & \text{otherwise} \end{cases}, \tag{3}$$

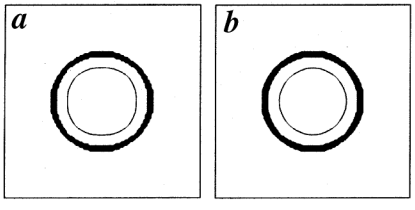

Figure 1. A simulation showing the directional bias of the conventional scheme. Computed error at $t = 0.5 \times 10^{-3}$ given by the noise removal simulation based on (***a***) the conventional scheme, and based on (***b***) the isotropic scheme. 101×101 grid ($h = 0.01$). $r_0 = 0.25$, $K = 1$.

with c given by (2), and carrying out the noise-removal simulation from the initial condition ϕ_0. Figure 1 shows the contours of the error, $\phi - \phi_0$, where ϕ is the computed solution. The numerical solution is expected to be smeared near the discontinuity; we however also note that the contours in the conventional scheme simulation show a directional bias.

The directionally biased nature of the numerical scheme can lead to degradation in the noise-removal simulation. This is shown by adding a random noise to (3), Figure 2 *a*, and carrying out the noise-

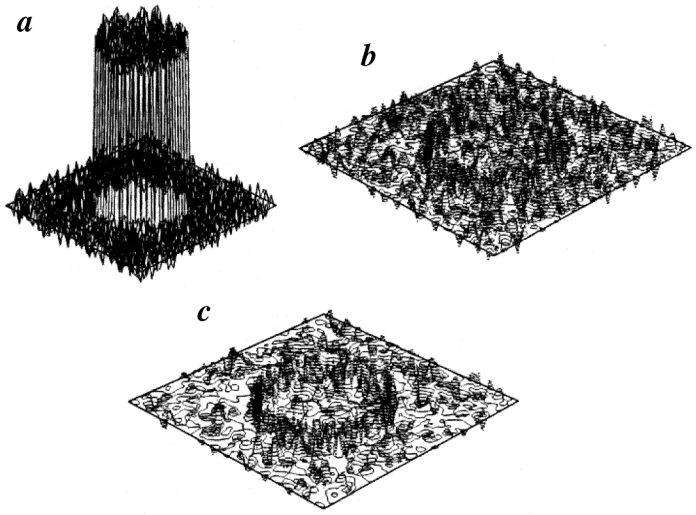

Figure 2. (***a***) An image with noise. The error in the image, at $t = 0.5 \times 10^{-3}$, using the noise removal simulation based on (***b***) the conventional scheme, and based on (***c***) the isotropic scheme.

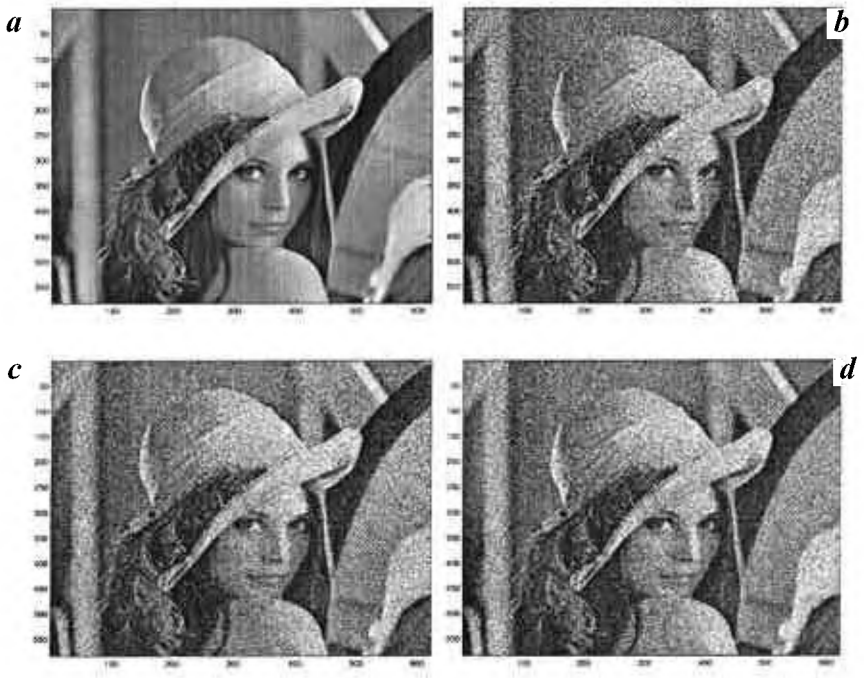

Figure 3. (***a***) The original image, and (***b***) the image with added noise. Processed images, at $t = 5 \times 10^{-5}$, with noise removal based on (***c***) the conventional scheme, and based on (***d***) the isotropic scheme.

removal simulation. Figure 2 *b*, *c* shows the error in the processed image by the two schemes. Isotropic scheme is seen to give a better noise removal.

We also show a picture, taken from the web, Figure 3 *a*. A random noise is added to the picture, Figure 3 *b*. In order to run the noise-removal simulation, the integer pixel values, obtained using MATLAB, are converted to real values which are then divided by a factor 'FTOINT'. After the noise removal simulation, the real values are multiplied by FTOINT, and then converted to integer for plotting. Figure 3 *c*, *d* are pictures from the noise-removal simulation by the two schemes.

1. Kumar, A., *J. Comp. Phys.*, 2004, **201**, 109–118.
2. Perona, P. and Malik, J., *IEEE Trans. Pattern Analysis Machine Intelligence*, 1990, **12**, 629–639.
3. Kumar, A., Isotropic numerical schemes for image processing, Report PD CM 0402, C-MMACS, Bangalore, May 2004.

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Inheritance of wilt resistance in chickpea – A molecular marker analysis

The low productivity in chickpea is due to several biotic and abiotic factors. Among biotic factors, *Fusarium* wilt caused by *Fusarium oxysporum* f-sp *ciceris* is the major problem. A-1, the main variety under cultivation in Karnataka, being susceptible to wilt, the disease has spread to all the chickpea-growing regions of the state, severely affecting the productivity[1]. The screening of international germplasm has led to identification of stable sources of resistance to race 1 of *Fusarium oxysporum*, which is most prevalent in India. Genetic analysis has indicated that resistance to wilt race 1 is governed by (a) single gene[2–6], (b) two genes[7,8] and (c) three genes (H, H_2 and H_3)[9]. Partially recessive alleles in homozygous form at either of the first two loci and the dominant allele at the third locus delay wilting, but any two of these alleles together confer complete resistance[9].

Mayer *et al.*[10] developed an allele-specific associated primer (ASAP) CS-27_{700} which identifies already established locus (H_1) susceptible to race 1 of wilt pathogen. The marker was validated in a limited number of germplasm lines. However, there is a need to test this marker in different crosses and commonly used potential genotypes suitable for Indian conditions. In the present study an attempt has been made to validate the ASAP marker linked to H_1 in a cross between highly susceptible and resistant genotypes. An attempt was also made to understand the inheritance of wilt resistance coupled with segregation of associated marker.

JG-62, a highly susceptible, early-wilting genotype was crossed with WR-315, resistant to *Fusarium* wilt during *rabi* (2001) and advanced to F_5 generation by single seed descent (SSD) method using two seasons per year. The F_5 lines were tested for their reaction to wilt (race 1) in sick pots under net-house conditions[11]. A single spore isolate of pathogen *F. oxysporum* f-sp *ciceris* race 1 was obtained from International Crops Research Institute for Semi Arid Tropics (ICRISAT), Patancheru, and maintained on fresh potato dextrose agar (PDA). The inoculum was then increased in 100–150 g of corn-meal–sand (CMS) mixture in conical flasks and incubated for 21 days at room temperature[12]. The infested CMS was mixed thoroughly with an autoclaved soil mixture (clay loam, sand, FYM, 1 : 1 : 1 v/v) at (1 : 12 w/w) in earthern pots of 30 cm diameter. The seeds were surface-disinfected with 70% alcohol for 1 min and air-dried. The susceptible cultivar JG-62 was grown in all the pots (3–5 seeds/pot) and allowed to wilt. Seeds of the hundred F_5 genotypes were sown in these sick pots to study their wilt reaction. Three seeds/pot and two pots/genotype were maintained for each F_5 line. In each pot, one seed of JG-62 was also sown as reference. The pots were fertilized with 100 ml of Hoagland's solution every week[13]. The number of days taken from sowing to complete wilting was recorded for each genotype. Based on the number of days taken for complete wilt, the genotypes were classified as early-wilting (less than 25 days), late-wilting (25–55 days) and no wilting. Plants which remained healthy with no symptoms of wilting on the 55th day were considered as no wilting. The highly susceptible genotype JG-62 took less than 25 days for wilting in all the pots.

The hundred F_5 progenies, which were phenotyped for wilt reaction were used for validation of ASAP marker[10]. The DNA was extracted from all the progenies using CTAB method[14]. The DNA was used for polymerase chain reaction following the protocol of Mayer *et al.*[10]. The gels were scored for the presence or absence of specific marker (CS-27_{700}) linked to H-1 and tested for single locus goodness-of-fit for 1 : 1 segregation. The parental genotypes JG-62 and WR-315 showed polymorphism for the ASAP marker. Among the 100 F_5 progenies studied, 53 showed the presence of CS-27_{700} marker linked to H_1 and in the remaining the marker was absent (Figure 1). The goodness-of-fit for 1 : 1 segregation ratio showed single locus segregation of the linked marker (Table 1), thus supporting the contention that the parents differ at the locus linked to the marker.

Among 100 F_5 progenies studied under pot culture, 28 showed early-wilting, 43 showed late-wilting, while 29 showed no wilting (Table 2), segregating in the ratio

Table 1. Single locus goodness-of-fit for 1 : 1 ratio of presence and absence of ASAP marker (CS-27_{700}) in chickpea progenies

Locus	+	–	χ^2
CS-27_{700}	53	47	0.36

Table 2. Classification of F_5 progenies of chickpea for combination of wilt susceptibility and presence/absence of ASAP marker (CS-27_{700})

	+(Marker)	–(Marker)	Total
Early-wilting	28	0	28
Late-wilting	25	18	43
No wilting	0	29	29
Total	53	47	100