GENETIC ALGORITHM BASED STEREO IMAGE CORRESPONDENCE USING MULTI-OBJECTIVE FITNESS FUNCTION FOR REMOTELY SENSED IMAGES

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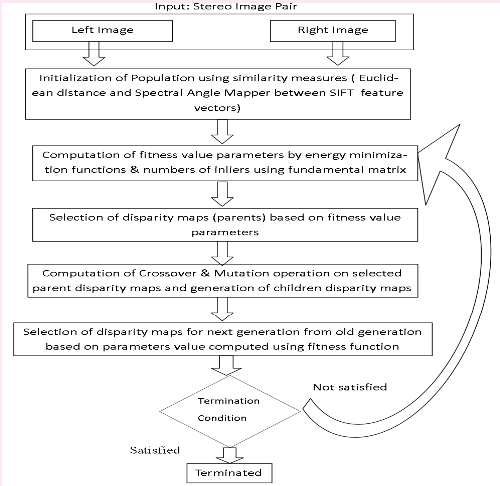
Introduction

- Accurate dense disparity map is the basic requirement for 3D reconstruction.
- Aim is the improved number of inliers in remotely sensed stereo images despite of noise, occlusion, geometric and radiometric distortion
- A novel dense stereo image correspondence method using genetic algorithm with multi-objective fitness function is proposed

Objectives

- To overcome the problems of remotely sensed stereo images, the genetic algorithm steps such as initialization of the population, fitness function, crossover and mutation operation are customized
- To make genetic algorithm suitable for stereo matching the constraints related to stereo image pair is encoded

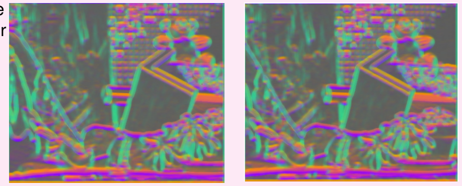
Methodology



Pixel wise SIFT feature descriptor extraction

- Pixel wise SIFT descriptor is extracted to characterize local image structures and encode contextual information by analyzing each pixel with respect to the neighboring pixel in terms of intensity variation, gradient variation, histogram of magnitude, gradient, and direction

For visualization purpose 128D SIFT feature vector is projected to 3D color space



Disparity space generation using feature matching

$$D(x,y,k) = \min\{ \sum_{\substack{-w \le i,j \le w \\ d_{min} \le d \le d_{max}}} \Psi(F_L(x+i, y+j), F_R(x+i, y-d+j))\}$$

- As a similarity measure Ψ, we use Spectral Angle Mapper and Euclidean Distance

$$\theta = cos^{-1}\frac{\sum_{i=1}^{n} t_i r_i}{\sqrt{\sum_{i=1}^{n} t_i^2}\sqrt{\sum_{i=1}^{n} r_i^2}} \qquad ed(t,r) = \sqrt{\sum_{i=1}^{n}(t_i - r_i)^2}$$

Multi-objective Fitness Function

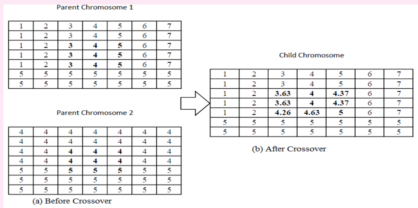
1. Minimization of energy representing the compatibility between corresponding pixels in the stereo image pair and the continuity in the generated disparity map

$$E = \sum_{x,y} |(F_L(x,y) - (F_R(x + d_{x,y}, y))| + \sum_{x,y} (|(d_{x,y} - d_{x+1,y})| + |(d_{x,y} - d_{x,y+1})|$$

2. Maximization of the number of matching points or inliers which is computed using the fundamental matrix, respecting the epipolar constraint of stereo matching

Crossover Operator

- one child chromosome is created by taking a weighted average of two parent chromosomes.



$$child = parent1 + scale * (parent2 - parent1)$$

Mutation Operator

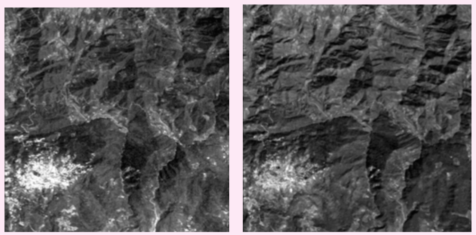
$$leftDiff = d(x,y-1) - d(x,y) \qquad rightDiff = d(x,y+1) - d(x,y)$$

$$d(x,y) = -0.5 + \frac{leftDiff}{leftDiff + rightDiff}; \quad if\ leftDiff \le rightDiff$$

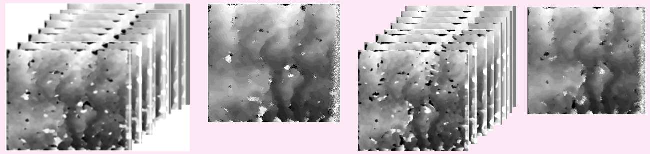
$$d(x,y) = -0.5 + \frac{rightDiff}{leftDiff + rightDiff}; \quad else$$

Results and Analysis

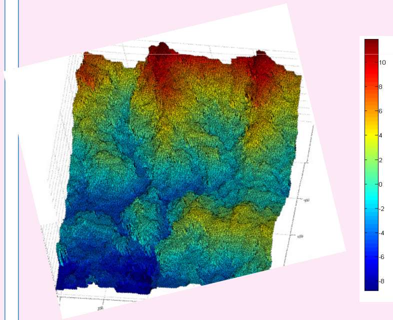
The test stereo image pair is captured by IRS 1C having spatial resolution of 5.8 m in Panchromatic. Its size is 254 X 254 pixels. Substantial illumination difference and geometric distortion among the image pair is present.



- Disparity space and sample chromosome computed from disparity space using Spectral Angle Mapper Euclidean distance



- 3D surface plot of test stereo image pair



Proportions of inliers in initial population	Proportions of inliers in final disparity map
66% to 71 %	76.68 %

Conclusion

- The dense disparity map obtained by our proposed novel stereo image correspondence method using genetic algorithm with multi-objective fitness function is useful for accurate 3D reconstruction
- Our proposed method improves the number of inliers by solving various issues of stereo image pair
- Various operations of genetic algorithm are designed in such a way that it can solve the complex real-world optimization problem of stereo correspondence.
- Our genetic algorithm achieves faster convergence due to the improved initialization of population.
- Various constraints related to stereo image pair is encoded in the multi-objective fitness functions which guided the genetic algorithm towards the optimum disparity map.

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