

The Infection Algorithm: An Artificial Epidemic Approach for Dense Stereo Matching

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Abstract. We present a new bio-inspired approach applied to a problem of stereo images matching. This approach is based on an artificial epidemic process, that we call “the infection algorithm.” The problem at hand is a basic one in computer vision for 3D scene reconstruction. It has many complex aspects and is known as an extremely difficult one. The aim is to match the contents of two images in order to obtain 3D informations which allow the generation of simulated projections from a viewpoint that is different from the ones of the initial photographs. This process is known as view synthesis. The algorithm we propose exploits the image contents in order to only produce the necessary 3D depth information, while saving computational time. It is based on a set of distributed rules, that propagate like an artificial epidemy over the images. Experiments on a pair of real images are presented, and realistic reprojected images have been generated.

1 Introduction

The problem of matching the contents of a stereoscopic system is a classical (and extremely difficult!) problem in computer vision. Image matching has been shown recently to be NP-complete [14]. Stereo image matching has multiple practical applications, including robot navigation, object recognition, and more recently, realistic scene visualization or image-based rendering. Many approach exist today that attempts to solve this problem. These approaches are now classified in terms of local and global methods. Local methods are typically block matching, gradient based optimization, and feature matching, while global approaches are dynamic programming, intrinsic curves, graph cuts, nonlinear diffusion, belief propagation, and correspondenceless methods, see [2].

The matching of two images can be formulated as a constrained optimization problem. It is however necessary to deal with a huge search space and with

a) *Left image.*b) *Right image.*

Fig. 1. A stereo pair taken at the EvoVisión laboratory, notice several classical problems: occlusion, textureless areas, sensor saturation, and optical constraints.

some aspects that are hard to model, such as the occlusion of parts on the scene, regions with a regular pattern, or even regions with similar textures. Classical techniques are limited and fail, due to the complexity and nature of the problem. This is the main reason why artificial life and evolutionary methods are considered now in this framework, see: [11] and [6].

Our work aims to improve the speed and the quality of a stereo matching, while considering simultaneously local and global information. The local information is obtained from the correlation or objective function used to match the contents of both images, and from the constraints which are used to improve the matching process. The objective function and constraints are considered as local because they only depend on a local neighborhood. The global information is encapsulated within the algorithm that we will describe in section 3.

Artificial life obviously does not try to reproduce natural life, but to create systems that generate characteristics, responses or behaviors, similar to the ones observed in natural systems. One of the favorite topics of this domain is the study of emergence of complex behaviors from a set of elemental components acting according to simple rules.

This paper is organized as follows. The next section describes the nature of the matching problem, the objective function and constraints we consider. Section 3 introduces the proposed algorithm, with the main goal of saving on the number of calculations while maintaining the quality of the virtual reprojected image. Finally, a set of images and graphs illustrate the behavior and performances of the infection algorithm.

2 Statement of the Problem

Computational stereo or the correspondence problem refers to the problem of determining three-dimensional structure of a scene from two or more images taken from different viewpoints. The fundamental assumption used by stereo algorithms is that a single three-dimensional physical point projects onto a unique pair of image points for two cameras. On the other hand, if it is possible to

locate the image projected points on two observing cameras that correspond to the same physical point in space, then it is possible to calculate its precise 3D position. However, the problem becomes intractable for several reasons so that there exists no closed form solution to this problem. Stereo matching is an ill-posed problem with inherent ambiguities, due to ambiguous matches produced by occlusions, specularities, or lack of texture. Therefore, a variety of constraints and assumptions are commonly exploited to make the problem tractable. Figure 1 shows a classical pair of images illustrating the usual difficulties of computational stereo. The movement between both images is typically a translation plus a small rotation. The wooden house and the calibration grid are clearly visible in both images. However, the wooden puppet only appears in the right image, while the file organizer behind the box with the children face only appears on the left image.

These are examples of visibility constraints : due to obstructions in the workplace, all points of interest that lie within the field of view are not always projected on both cameras. Thus, the visibility of a feature of an object from a particular viewpoint depends if it is occluded by either some part of the object itself (self-occlusion), or by other objects in the environment. This problem is due to the opaqueness of the objects. Additionally, if the feature lies outside the field-of-view of the sensor it is not visible. Hence, matching is impossible for these previous cases. Moreover, matching large homogeneous (textureless) areas is also an ill-posed problem, since there is no way to decide which point corresponds to which other point over the entire area (no characteristic feature, ambiguity). This is clearly the case for the *EvoVisión* house as well as for the calibration grid of the test stereo pair.

2.1 Correlation as an Objective Function

A correlation measure can be used as a similarity criterion between image windows of fixed size. The input is a stereo pair of images, I_l (left) and I_r (right). The process of correlation can be thought as a search process in which the correlation gives the measure used to identify the corresponding pixels on both images. This process attempts to maximize the similarity criterion within a search region. Let p_l and p_r be pixels in the left and right image, $2W + 1$ the width (in pixels) of the correlation window, $R(p_l)$ the search region in the right image associated with p_l , and $\phi(I_l, I_r)$ a function of both image windows. The ϕ function is defined as the Zero-mean Normalized Cross-Correlation (ZNCC) in order to match the contents of both images. This function is used to match points in two images, as it is invariant to local linear radio-metric changes.

$$\phi(I_l, I_r) = \frac{\sum_{i,j} [(I_l(x+i,y+j) - \overline{I_l(x,y)})(I_r(x'+i,y'+j) - \overline{I_r(x',y')})]}{\sqrt{\sum_{i,j} (I_l(x+i,y+j) - \overline{I_l(x,y)})^2 \sum_{i,j} (I_r(x'+i,y'+j) - \overline{I_r(x',y')})^2}} \quad (1)$$

2.2 Constraints on Dense Stereo Matching

Stereo matching is a very difficult search process. In order to minimize false matches, some matching constraints must be set. The constraints we have considered in our algorithm are the following.

- Epipolar geometry. Given a feature point p_l in the left image, the corresponding feature point p_r must lie on the corresponding epipolar line. This constraint reduces the search space from two-dimensions to one-dimension. Unlike all other constraints, the epipolar constraint would never fail and could be applied reliably once the epipolar geometry is known (stereo calibrated system).
- Ordering. If $p_l \leftrightarrow p_r$ and $p'_l \leftrightarrow p'_r$ and if p_l is on the left of p_r then p'_l should also lie on the left of p'_r and reversely. That is the ordering of features is preserved.
- Orientation. We use as a constraint not only the grey value of a pixel but also the orientation of the epipolar line on which the pixel lies.

3 Artificial Epidemics for Dense Stereo Matching

The motivation to use what we called the infection algorithm has two main origins. First, when we observe a scene, we do not observe everything in front of us. Instead of it, we focus our attention to some parts which keeps our interest on the scene. Hence, we believe that many of the attention process are handled by guessing, while we are developing our activities (which also may be the source of optical illusions). The process of information guess from characteristic points can be implemented via a matching propagation. This point also has some intuitive connections with disease spread in a population.

Invasion of disease into a population is a natural phenomenon. This phenomenon can be noticed in any species populations, and has been a concern for human beings for centuries. The problem has been deeply studied during the last fifty years, with the aim of obtaining ideas about how a given disease will spread into a population, and also to decide how to vaccinate the people in order to stop the propagation of the disease. Although there have been several approaches to the study of disease propagation, researchers agree that the first attempt to formulate a mathematical model is due to Lowell Reed and Wade Hapton in the 1920s [1], and the model was called SIR (Susceptible/Infective/Recovered) model. In this model a population is divided into three classes according to their status in relation to the disease of interest: *susceptible*, meaning they are free of the disease but can catch it, *infective*, meaning they have the disease and can pass it to others, and *recovered*, meaning they have recovered from the disease and cannot longer pass it on. Some probability values per unit of time are employed to calculate transitions from a given state to another one. Contact patterns between individuals from the population are also required for modeling the phenomenon.

The model has been later revised and several researchers have studied exact solutions for this timely called *epidemic models* [5]. Given the features of epidemic models, some authors have employed them to study different behaviors in computer networks and parallel machines. For instance, in [9] an epidemic based protocol is applied for implementing computer models on Parallel Machines. Ganesh [4] presents an epidemic based protocol for decentralized collection of information in a distributed network. Very recently, a new kind of models aimed at describing interaction through social, technological and biological networks has been presented, and also employed for the study of the spread of disease. These models have been called *small-world networks*, and try to study how information traverses a network featuring some properties [17]. The concept of small-world network is being recently applied to study the effect of epidemic algorithms [10]. But epidemic algorithms can also be seen from another point of view. Given that the model employs transition rules from the different states that each individual from the population may have during the epidemic process, other authors have studied and modeled the disease spread in population by means of cellular automata [8], which is another very well-known algorithm inspired by nature.

Cellular automata (CA) are fundamental computational models of spatial phenomena, in which space is represented by a discrete lattice of cells. Each cell concurrently interacts with its neighborhood which, in traditional CA, is limited to the cells nearest neighbors. Cellular automata are considered as one of the best representatives of parallel algorithms inspired by nature [15].

The new algorithm we present in this paper is called the *infection algorithm*. It possesses some properties borrowed from epidemic models: information is transmitted between individuals from the population based on some transition rules. Nevertheless, as we will see later, the number of different states that each individual from the population may feature is larger than in an epidemic model. On the other hand, the pattern of contacts among individuals is restricted to the close neighbors, instead of establishing complex networks of contacts. The algorithm is also inspired by cellular automata, because transition rules are employed to determine the next state of each individual from the population. But these transition rules not only uses the states of the individual and its neighbors, but also employ some external information, correlation and constraints, which are computed from the problem we are addressing. With this in mind, the infection algorithm is described in the following section.

4 The Infection Algorithm

The infection algorithm is based on the concept of natural virus for searching the correspondences between real stereo images. The purpose is to find all existing corresponding points in stereo images while saving the maximum number of calculations and maintaining the quality of the reconstructed data.

The search process is based on transition rules, similarly to cellular automata. Cellular automata are models of dynamic systems based on simple rules that



a) Image considering 155 initial points.



b) Image after 5 iterations.



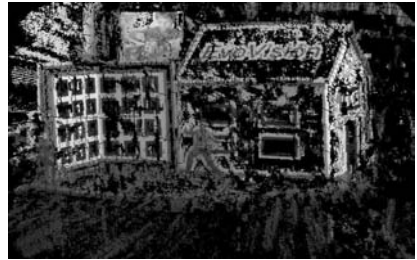
c) Image after 10 iterations.



d) Image after 30 iterations.



e) Image after 100 iterations.



f) Image after 200 iterations.



g) Final view of our algorithm.

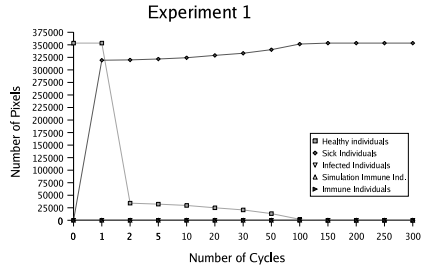


h) Final image with an exhaustive search.

Fig. 2. These 8 images show the evolution of our algorithm within a synthetic view. The new image represents a new viewpoint between the two original images. The last two images show the final step of our algorithm. We apply a median filter to achieve the new synthetic image g), as well as to obtain image h), which is product of an exhaustive search. We compared images g) and h): the quality is slightly better on g), while saving 47% of calculations.



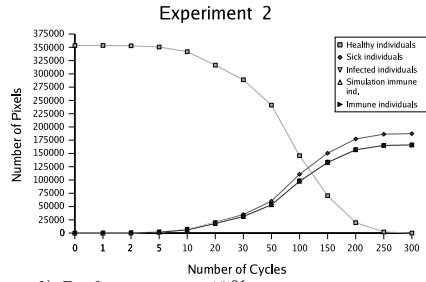
a) Final view with 0% savings.



b) Performance at 0%.



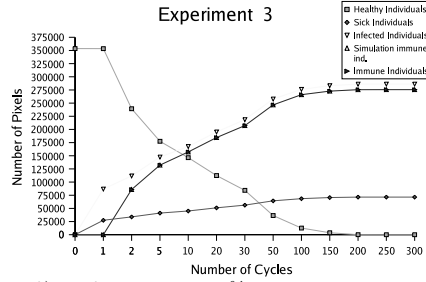
c) Final view with 47% savings.



d) Performance at 47%.



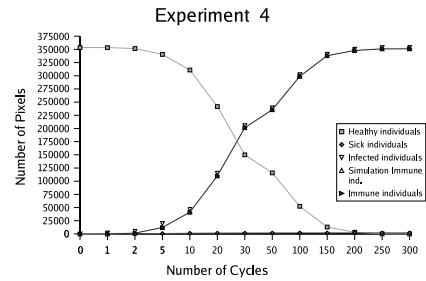
e) Final view with 80% savings.



f) Performance at 80%.



g) Final view using mainly the seeds.



h) Performance at 99%.

Fig. 3. These 4 images show the final results of our algorithm after modifying the rules in order to obtain different levels of savings on the number of computations. The quality of the virtual image is deteriorated, when the level of automatically allocated pixels is increased. However, the quality of the final image is relatively good due to the quality of the nucleus of infection.

interact to produce a global and complex behavior. Our automaton can be seen as a distributed sequence of discrete time steps governed by a fixed set of rules. The rule entries depends on the state of the pixel's neighborhood. The neighborhood structure considered here is a 25 neighbors lattice including the central cell: it is positioned inside a 7x7 window centered on the pixel of interest, with 9 close neighbors and 16 external ones.

The initialisation of the process is based on a set of seed – or nucleus of infection – distributed over the whole image, that attack their neighboring cells. The infection nucleus are generated on the left image with the O&H and K&R corner detectors [13]. The infection evolves over the image according to a set of rules that changes the state of a pixel depending on the state of its neighborhood. Four states are defined as follows.

1. **Healthy individuals** (Not-Explored). Nothing has been decided yet for the pixel.
2. **Sick individuals** (Explored). The pixel has been computed using constraints of dense stereo matching.
3. **Infected individuals** (Proposed). The value of the pixel is guessed on the basis of its neighborhood state. Some controversial information from various neighbors prevent to fix its status at the moment,
4. **Immune individuals** (Automatically allocated). All the information from the neighborhood are coherent and the guessed value has been confirmed.

Healthy individuals are the cells which have not been affected by the virus at time t (initial state). The Sick individuals are the cells which have been affected by the virus, and represent pixels which have been calculated or explored in order to find the correspondence on the right image. The proposed or infected individuals represent cells or pixels which we don't know yet if we need to calculate it, or automatically allocate it a correspondence or matching. Finally, the immune individuals are the most important state because they represent the automatic allocation of the corresponding pixels in the right image without the need of calculating the matching. The assignment is made only through the consideration of the set of local rules, which produces then a global behavior.

The algorithm works in the following way using the above information. First, we need to calculate the projection matrix and the fundamental matrix. We consider a calibrated system using a calibration grid from which we calculate a set of correspondences with a high-accurate corner detector, see Olague et al. [12]. The obtained information is used to calibrate rigorously the stereo system. It is important to mention that because the correspondence problem is focused on a calibrated system using real stereo images we work now for simplicity with a scene that is rigid. The camera is moving but not the scene. It is also important to mention that within the cells we create data structures composed of the following information: cell state, corresponding coordinates, and angle of the epipolar line. The whole virtual image is initialized to healthy state (Not-Explored). The lattice is examined cell by cell in a number of cycles.

The aim is to find the maximum number of existing correspondences according to the employed rules. These rules are defined and coded in a file according

to the nature of the problem. They determine the desired global behaviour, even if their application only involves local informations (state of the neighborhood). At each step, the algorithm scans the set of rule in order to make a decision based on local informations.

This structure is flexible: rules and neighborhood system directly tune the global behaviour of the system. For example it allows to obtain various infection percentages (that is directly related to the saving of computational cost) and various quality levels of stereo matching results.

Each central cell is analyzed in order to precisely define its state, as well as the state of its neighborhood. The algorithm searches the set of rules in order to apply the rules that match the current local state (state of central cell, number of external neighbors in each state, and precise state of the close neighbors). An action is then activated that produces a path and sequence around the initial nucleus. When the algorithm needs to execute a rule to evaluate a pixel, it calculates the corresponding epipolar line using the fundamental matrix information. The correlation window is defined and centered with respect to the epipolar line when the search process is started. The correlation is the main measurement that is used to identify which pixel on the right image corresponds to the studied pixel of the left image (of course, improvements may be drawn from employing both directions).

In the case of automatic allocation of the central cell, angle of the epipolar line, and orientation constraints of the explored neighbors are checked to be coherent with the corresponding values of the central cell. The algorithm then saves the coordinates of the corresponding pixel, otherwise the algorithm calculates the pixel. On the other hand, if the central cell is in the state “proposed”, the central cell is only marked as “infected.” Finally, when the search is finished, the algorithm saves a synthetic image, which is the projection of the scene between the two original images. This algorithm approaches then the problem of dense stereo matching. It is summarized as follows.

1. All pixels in the images are initiated to the state “not-explored”.
2. Then, pixels of maximum interest are extracted. They are in the state “explored” (nucleus of infection).
3. Transition rules are applied to any pixel in the images except if their state is “automatically allocated” or “explored.”
4. While there still exists pixels that are not “automatically allocated” or “explored,” go to step 3.

5 Experiments and Conclusions

Experiments are presented in figures 2 and 3. Figure 2 shows a virtual image which represents the match data reprojected on a new viewpoint. Figure 3 shows a set of experiments where the local rules were changed in order to modify the behaviour of the algorithm. The latter case represents a high percentage of automatically allocated pixels producing a good quality image.

We have derived a new bio-inspired algorithm, that we have for the moment applied to dense stereo matching. It has been proved efficient for the aim of computational saving without losing the quality of the virtual image. In the future we intend to extend this model in order to identify occluded regions and vantage viewpoints for stereovision. However it seems that the infection algorithm may be useful in other image applications, where local informations needs to be propagated in a coherent way, such as: monocular vision or “shape fom ...” problems, among others.

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