An innovative employment of the NetLogo AIDS model in developing a new chain code for compression

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Abstract. In this paper, we utilize the NetLogo HIV model in constructing an environment for bi-level image encoding and employ it in compression. Our model considers converting an image into a virtual environment that comprises female agents testing positive and negative for HIV. Female agents are scattered according to the allocation of the pixels in the original images to be tested. The simulation considers introducing male agents that test positive for HIV, the purpose of which is to track their movements while infecting other HIV- female agents. The progressions of the HIV+ male agents within the simulation take advantage of the relative encoding approach previously used by other image processing and agent-based modeling researchers. That is to say, the simulation allows generating a high proportion of similar movement forms that are similarly encoded regardless of the movements of agents. This is followed up by applying Huffman coding to the obtained chains of movement strings for further reduction. The ultimate results reveal that our product could outperform existing benchmarks using all the images we employed in testing.

Keywords: AIDS · NetLogo · agent-based model · chain code · compression · Huffman coding

1 Introduction

The accelerated expansion of computerized information such as digital documents, and data generated from social media, the Internet of Things (IoT), and Smart Cities (SC), has enlarged the demand for exploring new approaches to encode existing information and decrease its initial size. Among the approaches utilized to encode the data is called 'chain coding' that was first introduced by Freeman in 1961 [18]. His approach considers going along the borders of an image or contour to encode information based on 4 or 8 coding directions. Since then, the Freeman approach was subjective to further developments and enhancements, and researchers are still using it as a foundational method to

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design chain coding applications of unique characteristics. For example, Bons and Kegel [6] introduced a new mechanism called the 'Differential Chain Code' (DCC) that encodes based on the differences between adjacent pixels. Hwang et al. [20] improved the DCC by introducing an operator to eliminate the number of codes. Chain coding is widely used for many purposes such as biometric applications [5], character recognition [28], geometric fusion [1], and compression [13, 37].

The literature on image processing has highlighted several developments of chain coding mechanisms. For example, Bribiesca [7] designed the vertex chain code that allows encoding shapes based on the boundary information and uses one of three characters to represent each code. Similarly, Liu and Srinath [25] explored many chain coding techniques to be used in detecting corner information in images. Siddiqi and Vincent [32] present a group of characteristics that belong to bi-level images that represent textual information and used histograms obtained from chain codes for text recognition. Karczmarek et al. [23] examined a chain coding application that considers organizing particular sets of pixels into chunks that describe their surroundings. Many of the chain coding techniques in the literature are associated with other coding techniques such as Huffman or Arithmetic coding (e.g. [22, 24, 27, 36, 39, 40]). These are used to further compress the chains of codes resulting from the application of a particular chain coding method.

One variation of chain coding is encoding the directions based on how relative they are to their adjacent ones and not the actual directions themselves. This variation started with Liu and Žalik chain code [26] that uses the relative angles between neighboring codes. His method employs eight codes and applies Huffman coding to reduce the number of bits used for character representation. Likewise, Zahir and Dhou [38] created a chain code that considers the relative directions between codes and assigns characters to each code regardless of the paths. Additionally, they had a formula to group, eliminate, and combine characters the purpose of which is to reduce the chain length used for representation and to develop a mechanism that allows lossless and lossy compression. Similarly, Zhao et al. [41] introduced a chain code that consists of six directions and is distortion-free when an image is rotated. The authors concluded that their method offered a theoretical foundation to build a 'bead weaving machine'. Although these previous studies provided efficient chain coding mechanisms, the main issue is that they do not seem to allow simultaneous encoding of multiple parts of an image via the introduction of agents.

A new trend in chain coding is the involvement of agent-based modeling simulations to encode image information. Agent-based modeling is an automated approach that is aimed at simulating the interplay between many entities called agents, over a period of time. It is employed by researchers from various domains including marketing, biology, computing, and social sciences (Examples: [2–4, 30]). A well-known platform to develop agent-based modeling simulations is called 'NetLogo' [34]. It is a programming environment that is embedded with a diverse set of models to be harnessed by numerous research domains. Many

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NetLogo models such as the ants, paths, Kermack–McKendrick, and bacteria food hunt models inspired the development of new chain coding applications that include integrating behaviors such as the ones that exist in ants, rabbits, dolphins, beavers, and predator-prey systems [9–11, 13, 15, 17, 29] within agent-based modeling simulations. The purpose of integrating these behaviors is to identify agents that can encode image information and use the new strings for image representation and compression.

The advantages of utilizing agent-based modeling simulations to encode image information as opposed to classical approaches are threefold: (a) agent-based modeling approaches allow incorporating biological behaviors to guide the process of information encoding. Examples of existing behaviors that were successfully embedded are the pheromone of ants and the echolocation dolphins [10, 29]; (b) employing an agent-based modeling simulation allows assigning multiple agents to encode information instead of being encoded from a single location; (c) agent-based modeling simulations give a researcher the flexibility to explore many parameters and introduce new variations, which can be tested on particular datasets. Utilizing agent-based modeling allows exploring a variety of virtual environments that have been explored by researchers from various domains (e.g. [8, 12, 14, 16]). We believe that these features distinguish agent-based modeling simulations and make them attractive to be employed in various data processing applications.

Although there are few existing agent-based models that were successfully applied in encoding image information, and using the generated representations in compression, further research is needed to investigate new behaviors and biological abstractions. In the present article, we develop a new chain code that is stimulated by the NetLogo HIV model [35] with some modifications and simplifications. The focus of the new model is to build an environment that consists of HIV positively and negatively infected female agents that map to the original distribution of pixels. Additionally, our model introduces HIV-infected male agents that are considered dynamic and move around to infect other HIV-negative female agents in the environment. Furthermore, the model assumes that some female agents can reproduce other HIV-infected male agents that also work on image encoding. The newly generated HIV-positive male agents and the ones that originally exist in the system work on encoding information, while their movements are tracked by the algorithm. The final chains are compressed using Huffman coding, and the results are compared with existing benchmarks used by image processing researchers.

2 Method

The existing method comprises a number of steps that involve the environment creation, agent movements, and other encountered scenarios:

- Step 1: The conversion of an image to a contour representation and the construction of the virtual environment based on the allocation of the pixels

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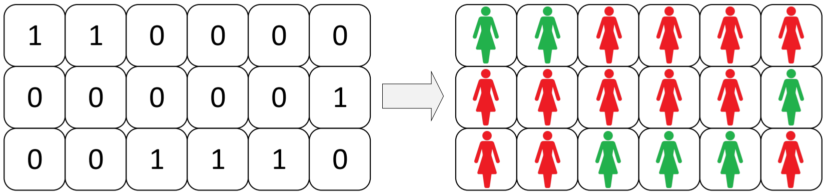
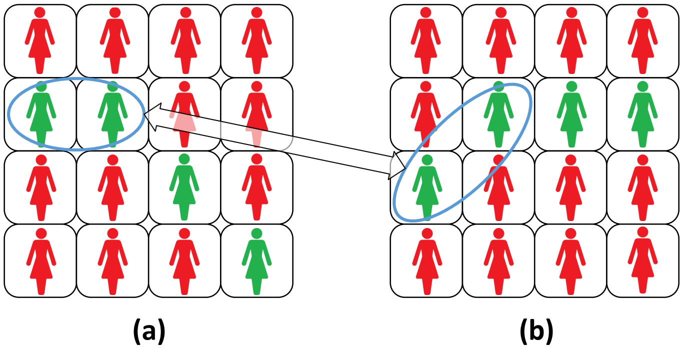
in the original image. The virtual environment can be imagined as a two-dimensional grid consisting of cells where each cell corresponds to a pixel. While building the virtual environment, each pixel marked with ‘1’ in the actual image is mapped to a cell with an HIV- female in the grid. On the other hand, each pixel marked with ‘0’ is mapped to a cell with HIV+ female. At the end of this step, the virtual environment will have HIV- and HIV+ female agents (Fig. 1). It is essential to mention that all the female agents within the system are stationary. In other words, they do not change their locations during the life of the simulation.



1	1	0	0	0	0
0	0	0	0	0	1
0	0	1	1	1	0

Fig. 1. An example showing the conversion of a sample image to a virtual environment

- Step 2: The inclusion of HIV+ male agents within the environment the purpose of which is to move around and transmit HIV to HIV- females via sexual contacts. These agents highly resemble the one employed in the NetLogo HIV model [35] in terms of their movements and tendency to transmit HIV within a limited human community.



(a) (b)

Fig. 2. Assuming that the first codes (i.e. marked within the blue space) in each of the two sample image segments are similar, the algorithm generates similar codes for each segment regardless of the pixel distribution

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- Step 3: HIV+ male agents begin the search process and their inclination is to identify HIV- female agents. This design serves many purposes: (a) it allows the algorithm to track the needed movements and therefore, generate new chains to be used for representation; (b) it eliminates the movements that do not need to be counted within the string of movements; (c) HIV+ male agents can always consider HIV+ female agents, if necessary (i.e. no HIV- female agents in the neighborhood). Although these movements related to contacts with HIV+ female agents are sometimes necessary to be performed by the algorithm, they are not counted towards the final representation.
- Step 4: The search process involves the employment of a relative coding mechanism that encodes each direction according to the direction that precedes it. The possible encoding directions can be to the right, left, 45 degrees to the right, 45 degrees to the left, and straight movement. In this encoding mechanism, two directions can be different while still encoded similarly (Fig. 2). The advantage of employing a relative coding design lies in the fact that it can generate a large number of similar codes, which can eventually improve the compression ratio as previous studies have shown (e.g. [10, 13, 15]).

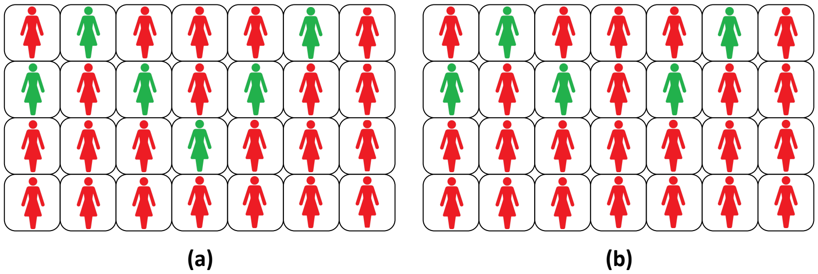

Fig. 3. (a) One connected chain; (b) Two chains and none of them is connected since each contains less than five HIV- female agents that are tied together

- Step 5: The present design assumes that the fifth encountered HIV- female agent within a connected chain has the ability to reproduce an HIV+ male agent to continue working on the encoding process. A connected chain in the present article is defined as five or more HIV- females that are tied together (e.g. Fig. 3).
- Step 6: The Huffman coding algorithm is applied to the final chains that represent the movements of HIV+ male agents for further reduction. The algorithm uses the movements of the agents and the initial coordinates for image reconstruction (i.e. decoding).

3 Results

To assess the effectiveness of the algorithm, we compared our results with standardized benchmarks that are used by image processing researchers: G3, G4, JBIG1, and JBIG2. To this end, we applied our algorithm on eight sample images taken from [42] and compared the size of the chain movements generated by our algorithm with the outcomes of the other algorithms we used for comparison. Table 1 shows the results of a comparison between our algorithm and other existing algorithms. It can be seen from the data in Table 1 that we could outperform all the standardized benchmarks using all the images we utilized in testing. That is to say, for the eight images, our algorithm generated 91052 bits, while G3, G4, JBIG1, and JBIG2 generated 269552, 155584, 112848, and 106904 bits, respectively.

Table 1. The number of bits generated from compressing the chains of movements as opposed to the number of bits generated by other standardized benchmarks: G3, G4, JBIG1, and JBIG2 for a sample of eight images [19, 21, 31, 33, 42]

Image	Original size	G3	G4	JBIG1	JBIG2	AIDS
Image 1	35328	10512	4528	4728	4712	**2188**
Image 2	141456	22160	7920	5720	5336	**3430**
Image 3	91008	15888	5792	5024	4888	**2617**
Image 4	414720	102208	81424	62208	58728	**56214**
Image 5	102408	26464	17376	15032	13896	**13718**
Image 6	325120	26704	11936	6312	6104	**3861**
Image 7	544640	45120	16768	7744	7312	**5418**
Image 8	250560	20496	9840	6080	5928	**3606**
Total	**1905240**	**269552**	**155584**	**112848**	**106904**	**91052**

4 Discussion and conclusion

In this investigation, the aim was to design, and implement an agent-based model of HIV transmission within a social society, to employ it in encoding bi-level image information, and to compress the new chains. The present study extends the previous research studies that explore different behaviors within agent-based modeling environments in encoding image information. The exploration reveals the effectiveness of the current model in encoding image information, and the experimental findings showed that we could outperform well-known standardized benchmarks in bi-level compression.

Our findings suggest that in general, agent-based modeling simulations can be effectively utilized in reducing the size of digital data and change its original representation. The outcomes from the AIDS study are strongly correlated with previous agent-based models that were utilized in image encoding. However, the current study adds a new dimension that shows how to design agent movements

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that stem from HIV transmission in a society. Furthermore, our investigation offers new insights on agent design and behaviors that can be incorporated for purposes other than building the model itself.

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