

Visualization of evolutionary computation processes from a population perspective

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Abstract. The authors investigate a visualization framework for genetic algorithm, to express the evolutionary processes. Our framework differs from most existing methods in that it visualizes evolutionary processes from a population viewpoint, rather than chromosomal or problem spaces. A simple sexual selection model is used for demonstration purposes. We propose four visualization methods that are based on the framework. Those tools show how evolutionary trends and population characteristics are visually depicted. The framework is both user-friendly and extendable to other problems and models that address population changes over time.

Keywords: Genetic algorithm, information visualization, evolutionary computation

1. Introduction

After more than three decades of development, genetic algorithm (GA) researchers are still facing several frustrating issues, including parameter control, appropriate variation operator choice, and the prevention of premature convergence. Many of these unresolved issues are the result of poor insight into evolutionary processes; understanding how GA work is challenging due to the many potential relationships and interactions and that can occur between genes within a chromosome and between the chromosomes themselves. Even problems involving small populations and simple gene encoding can easily result in complex evolutionary dynamics; such dynamics are the central focus of many GA research projects.

Despite their robustness, developing GA to address specific problems can be time-consuming. Many test runs are required, with solutions for each run being compared to others in an attempt to understand how the GA in question goes about searching for solutions. Generally speaking, the most labor-intensive aspect of these projects is identifying an appropriate set of parameter values or operators, while keeping in mind that it is nearly impossible to find a mechanism that is adequate for all problems. This is made more challenging by the lack of information about GA evolutionary processes. The most common method for

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analyzing how GA evolves is monitoring chromosome fitness values, and creating fitness-versus-time graphs. However, such straightforward graphs can only provide a limited amount of information.

Information visualization is gaining research attention. According to its proponents, information is more easily understood when abstract concepts are mapped onto concrete, physical representations. Human cognition also plays a potential role in identifying hidden information patterns and trends. The approach is thought to be particularly useful in situations involving large amounts of information and complex relationships [19,23].

Information visualization is recognized as an effective means for understanding GA mechanisms [3,5,6,8,10,21]. Among the various studies that have used visualization techniques to facilitate GA development, a critical issue has been choosing a good viewpoint. Recently, a growing number of investigators have visualized the evolutionary process from the viewpoint of fitness, genes, or chromosomes. However, few researchers have adequately considered evolutionary trends and relationships between generations. No one has yet discovered an effective means of representing how an entire population behaves or changes across generations.

Our goal in this study is to propose a GA visualization framework based on a population viewpoint. Using a simple model – sexual selection – as an example for demonstration purposes, we will describe four visualization methods and offer explanations for how each one facilitates GA understanding. The three most significant aspects of this visualization framework are its representation for populations, ease-of-use, and extendibility to other models (e.g., multi-agent, ecological, and classifier systems).

In the following section we will offer a survey of current research in GA visualization (categorizing models in terms of their visualization viewpoints) and introduce the sexual selection model to be used for demonstration purposes. In the third section we will describe our visualization framework and the four visualization methods that are based on this framework. A summary of the results of the four visualization methods and a discussion of the framework's most important properties are presented in the fourth section. Conclusions and suggestions for future research are offered in final section.

2. Related works

2.1. Genetic algorithm visualization

Shine et al. [21] have categorized GA visualization approaches according to application purpose. They note that visualization is useful for exploring GA search spaces, analyzing convergence behavior, fine-tuning GA, and helping users achieve comprehensive views of fitness landscapes and evolutionary process dynamics. Similarly, Emma et al. [13] have created three broad visualization categories for GA: a) identifying population features, b) visualizing spaces that are searched by GA, and c) visualizing a problem's entire search space.

We prefer categorizing existing GA visualization approaches based on information granularity. GA runs produce huge amounts of information, which can be categorized according to their granularity. While each granularity reflects a significant part of information concerning GA evolution, it is impossible to get a complete understanding of all information granularities from a single type of visualization. Thus there exist visualization techniques from various kinds of viewpoints, which can be categorized in terms of fitness, genes, chromosomes, and problem space.

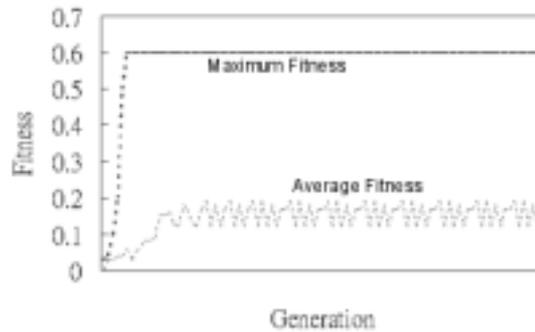


Fig. 1. Example of a fitness-versus-generation graph.

2.1.1. From a fitness viewpoint

Most GA users concentrate on changes in fitness values during evolutionary processes. Fitness is an important aspect of GA that affects not only the ability to find good solutions, but also search process efficiency. Therefore, it is intuitive to measure GA performance in terms of best and average chromosomes fitness values, as demonstrated in Fig. 1. It should be noted that in addition to two-dimensional representations, three-dimensional representations that trace population fitness values across generations are possible due to the development of advanced visualization techniques.

The large number of chromosomes in a population makes it virtually impossible to display all of their fitness values. Therefore, displays are usually restricted to the best chromosome fitness and average population fitness for each generation. GA convergence is determined by change in fitness; when population fitness stops increasing, it is usually assumed that convergence has occurred. However, visualization from this viewpoint has a major limitation in that only the best and average fitness values are displayed for each generation. Detailed information regarding population composition and change is not possible from this viewpoint.

2.1.2. From a gene viewpoint

Besides fitness values, specific gene frequencies are also monitored during evolution. Genes at different chromosomal positions differ in terms of importance. A gene-centered analysis identifies gene values that will improve the chances of chromosome survival, therefore greatly enhancing GA performance. Ackly et al. [1] monitored three genes during various evolutionary stages, with change rates indicating their varying degrees of importance. Similarly, Collins [9] and Routen et al. [20] have suggested using allele-loci frequency matrices to indicate the relative frequencies of individual alleles. Bedau et al. [2] have described what they refer to as “allele-wave visualization,” which uses “activity wave diagrams” to measure allele activity over time.

Although the level of importance of individual genes can be highlighted by visualization from a gene viewpoint, their configuration (i.e., information on building blocks/schema considered important for GAs) is hard to be presented and analyzed, since the searching for schema involve information about chromosomal relationships.

2.1.3. From a chromosome viewpoint

Chromosomes are considered basic GA units; GA operators (e.g., crossover, mutation, and reproduction) are viewed in terms of chromosomal interactions. Routen et al. [20] used graphs to compare similarities among various generations of chromosomes compared to a base chromosome. Wu et al. [25,

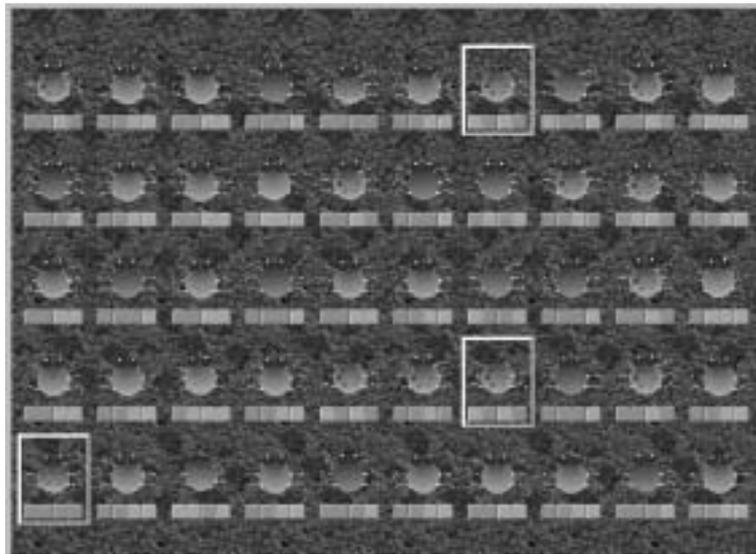


Fig. 2. Genetic algorithm (GA) simulations with detailed operator actions.

26] proposed using a VIS system to display family histories of individual chromosomes for the purpose of identifying crossover and mutation locations.

Furthermore, visualization has long been accepted as a helpful teaching approach [12]. GA visualization from the viewpoint of chromosomes is a useful tool for helping GA users to learn basic GA concepts. In [27], Wu created a tutorial tool for teaching GA evolution using a small population of insects, each with a unique individual feature (e.g., color or eye size). As shown in Fig. 2, the tool can be used to illustrate crossover and mutation concepts.

2.1.4. From a problem space viewpoint

Many researchers have adopted this type of visualization. As the gene encoding (i.e., solution representation) is defined, corresponding problem space is also established. All GA operators can be viewed as to search for a higher point (better solution) in this space, and chromosomes can be viewed as vectors. However, since the number of genes in a single chromosome generally exceeds three, visualizing a problem space requires that vectors be mapped onto two- or three-dimensional spaces [24].

The issue of visualizing multidimensional data in GA has received much attention. Spears [22] published an overview of multidimensional visualization techniques that are applicable to GAs. Collins et al. [5] visualized binary chromosomes by sammon mapping, but their study is limited by the computational complexity of sammon mapping and the lack of uniformity among mapping errors. Shine et al. [21] mapped one point in multidimensional space to another point in two-dimensional space by computing a quadcode from the vector specifying the point in multidimensional space. The quadcode specifies the location of the point in the two-dimensional array that is used as the display. In [6], a “search space matrix” was used to transform chromosome sets with many dimensions into chromosome sets with fewer dimensions.

From the viewpoint of problem space, GA visualization facilitates an understanding of how problem space is explored, and highlights both explored and unexplored regions for further analysis or fine-tuning. However, most methods for mapping multidimensional spaces onto a two-dimensional space are approximate, with only part of the problem space (or a projection) being displayed. This means that important information may be lost during the mapping process.

2.1.5. An integrated GA visualization tool

To overcome the barriers to getting a single-viewpoint understanding of a GA problem, some researchers have proposed integrating several visualization tools. Pohlheim et al.'s [18] combined set of standard techniques for observing GA status during evolution allows for the visualization of alleles and individual fitness, distances between individuals, and certain statistics about subpopulations. Collins [7] has created a visualization framework called "HENSON" to support GA visualization. In addition to reducing the costs associated with producing visualization, HENSON supports various perspectives—including fitness, genes, chromosomes, and search space. Emma et al.'s [13] GAVEL tool can be used to examine how crossover and mutation operations assemble the final result. This tool also supports easy visualization of important evolutionary features from the perspectives of genes, chromosomes, and search space. In addition to allowing GA visualization from different information granularities, these integrated tools also emphasize "hands-on" interactivity, which is considered an important issue in information visualization. This function facilitates to fine-tune GAs [6]. However, some researchers have argued that the fine-tuned GA may be only adjusted to solve some specific problem [13].

Very few visualization techniques allow for a GA population viewpoint. Although the PGA program [17] includes a tool that displays an entire population in text form, the amount of information produced by large populations is too much for users to easily comprehend. Even if users could absorb the information, they would still face the problem of identifying relationships between populations from different generations.

In this paper we are offering a framework for observing evolution from a population perspective, with information presented as a single point rather than as an allele-loci frequency matrix [13] or in text format [17]. The twin focuses of this framework are overall population change and relationships between generations during GA runs; combined, these permit users to observe evolutionary trends and dynamics. The visualization framework is based on two-dimensional chart, arguably the easiest format for comprehension purposes.

2.2. Sexual selection model

The sexual selection process usually involves females choosing mates on the basis of specific traits; males expressing those traits are more likely to be chosen and to pass on their genetic information to the next generation [16]. Mark Kirkpatrick has constructed a sexual selection model containing two loci, each with two alleles [15]. The model involves a mixed sex population in which each individual has one T gene and one P gene. In male chromosomes the T gene indicates the presence or absence of a particular trait and the P gene is unused. In female chromosomes the P gene indicates the carrier's preference for males with particular traits and the T gene is unused. In each generation a certain number of males carrying a particular trait are killed off before they can reproduce. Each female selects a surviving male, and together they produce two children (one of each sex). As shown in Fig. 3, Kirkpatrick's model dictates that regardless of a population's initial composition, it will eventually establish an equilibrium. In 1991, Collins et al. [4] simulated Kirkpatrick's model with a computer and reproduced the predicted equilibrium curve.

Kirkpatrick's model and Collins and Jefferson's simulation present population information in terms of how genes are distributed. In other words, the model observes evolution from a population perspective that is overlooked in most existing visualization approaches. However, evolution is only understood in static terms in these investigations, with predictions and simulations restricted to resultant sexual selection behavior—that is, the final population distribution. The evolutionary process (i.e., how the result emerged) is not presented.

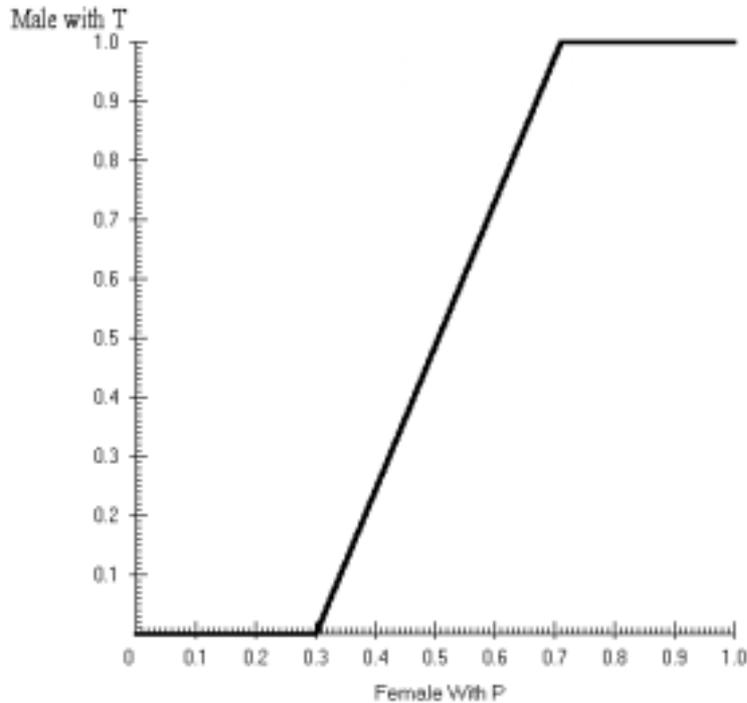


Fig. 3. Kirkpatrick's predicted equilibrium.

3. Model description

3.1. Visualization framework

The visualization framework presented in this section uses a two-dimensional plane to present population information. As shown in Fig. 4, the X-axis represents the proportion of males with a particular trait and the Y-axis the proportion of females preferring males with that particular trait.

This plane differs from traditional problem spaces in that a single point represents the population of one generation, whereas single points in traditional problem spaces represent single chromosomes. In our framework, population information (i.e., male-female distributions) can be shown clearly without any loss because each individual has only two genes, one of which is unused. More importantly, inter-generational relationships can be expressed in terms of distance and the relative positions of individual points. Evolutionary dynamics are expressed two ways: overall trends (relationships between generations) and detailed information (male and female distributions in single generations).

3.2. Four visualization methods

3.2.1. Evolutionary Distance Map

The Evolutionary Distance Map (EDM) measures the distance from a population's convergent position to the origin of coordinate on the plane. If two initial populations converge to the same position, they are said to have the same evolutionary distance (e.g., points A and B and points C and D in Fig. 5).

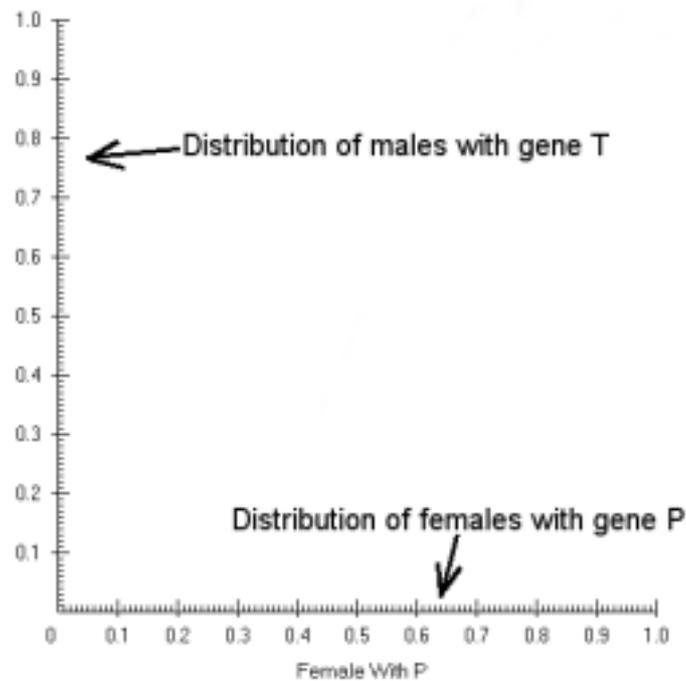


Fig. 4. Visualization framework.

The evolutionary distance of each population (representing as a point on the plane) in an EDM is represented using a gray scale; lighter colors imply longer evolutionary distances. By adding color to all points according to their evolutionary distances, convergence behavior becomes clear. Furthermore, color comparisons make it easier to determine the potential of any two points converging to the same position.

3.2.2. Convergent Line

The Convergent Line (CL) method emphasizes the relationship between a starting point and its convergence point, in contrast to EDM's focus on presenting a convergent position as a property of starting points. The CL, the line connecting the starting and convergent points are drawn in gray scale, with starting points the lightest and convergent points the darkest (Fig. 6). In CL, line direction represents the relative position between the starting and convergence points and length represents the distance between them. The relative position between a starting and convergence point indicates population change, while distance indicates the degree of that change.

3.2.3. Dynamic Evolution Map

EDM and CL facilitate convergent behavior observations, but their static representations are considered a drawback due to the characteristic of change that is inherent to evolutionary processes. Dynamic Evolution Map (DEM) shows changes in population proportions as point movements along a plane; by showing multiple points simultaneously, DEMs facilitate comparative observations. Color is assigned according to an individual point's position along the plane (i.e., relative to origin, X-axis, or Y-axis of

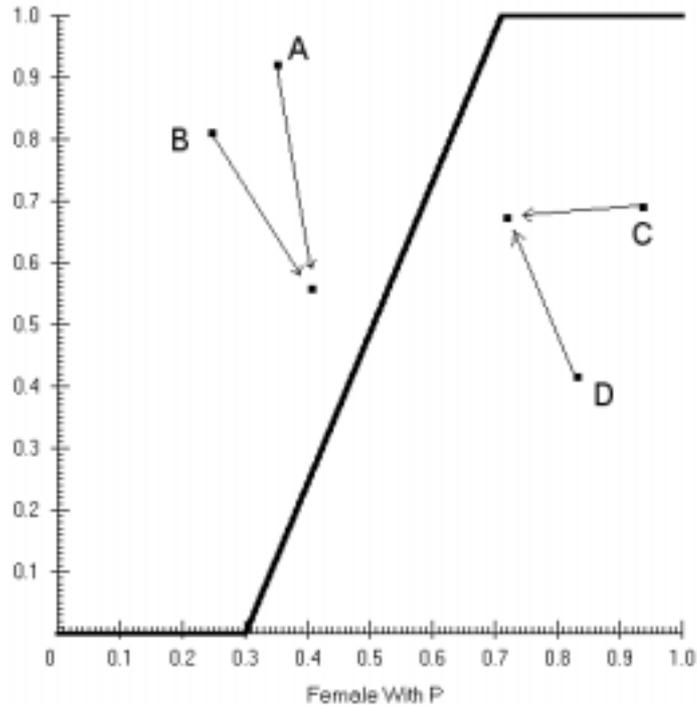


Fig. 5. Evolutionary distance map.

the coordinate). An example of how color is assigned according to Y-axis values is presented in Fig. 7. DEMs can be used to monitor overall trends (by showing all points along a plane) as well as individual movement (in the form of a single point or a small number of points).

3.2.4. Energy Contour Maps

Energy Contour Map (ECM) presents evolutionary dynamics using a three-dimensional contour format. Height represents energy of corresponding point on the plane – for instance, if a population goes through point A before going through point B during a GA run, A is said to have higher energy than B. According to this principle, a high-energy position means that a population's distribution tends to change, and a low-energy position means that a population tends to be stable. Position energy is calculated according to the number of times it is traversed—the higher the number of traverses, the lower the energy. Let T_{xy} be the number of times that point (x, y) is traversed, and T_{\max} the maximum of T_{xy} for every (x, y) on the plane. The energy at position (x, y) is therefore defined as E_{xy} :

$$E_{xy} = T_{\max} - T_{xy} \quad (1)$$

4. Visualization results

A list of the GA parameters used for simulating Kirkpatrick's model is presented in Table 1. These parameters are picked according to Collins and Jefferson's simulation [4]. After dividing the X-axis and

Table 1
GA parameters used in our simulation of Kirkpatrick's model

Population size	500
Generation	1000
Crossover rate	1.0
Mutation rate	0.0001

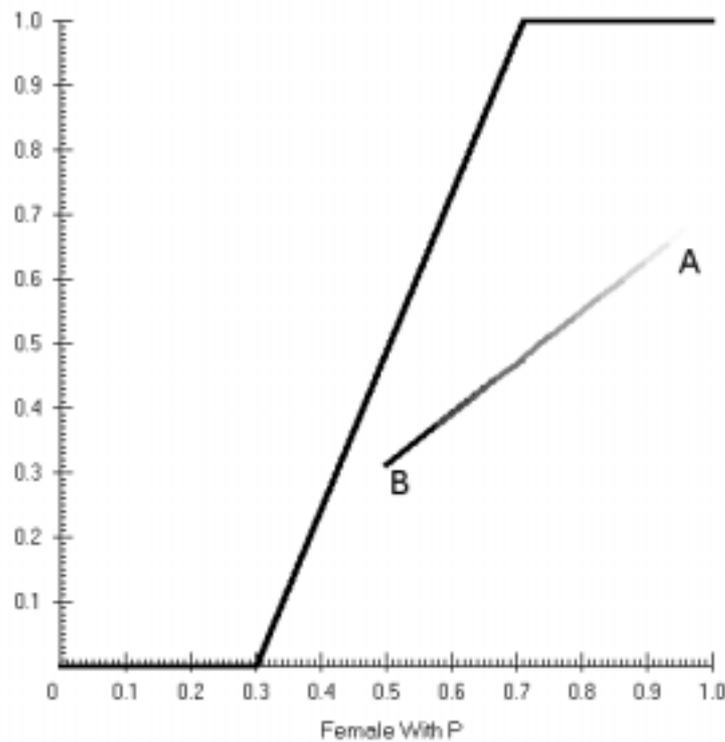


Fig. 6. Convergent line concept.

Y-axis into 100 parts each, 10,000 starting points were chosen along the plane. Evolution was simulated for 1,000 generations from each starting point, and convergence points were marked. Figure 8 shows the 10,000 convergence points resulting from the 10,000 runs; they clearly cover the equilibrium line, as predicted by Kirkpatrick's model.

4.1. Results from the four visualization methods

4.1.1. Evolutionary Distance Map

The EDM obtained with these parameter settings is shown in Fig. 9. The following observations were made:

- 1) Convergence points were dominated by females. Points along the plane were more likely to have the same color if their X-values were similar, regardless of their Y-values.

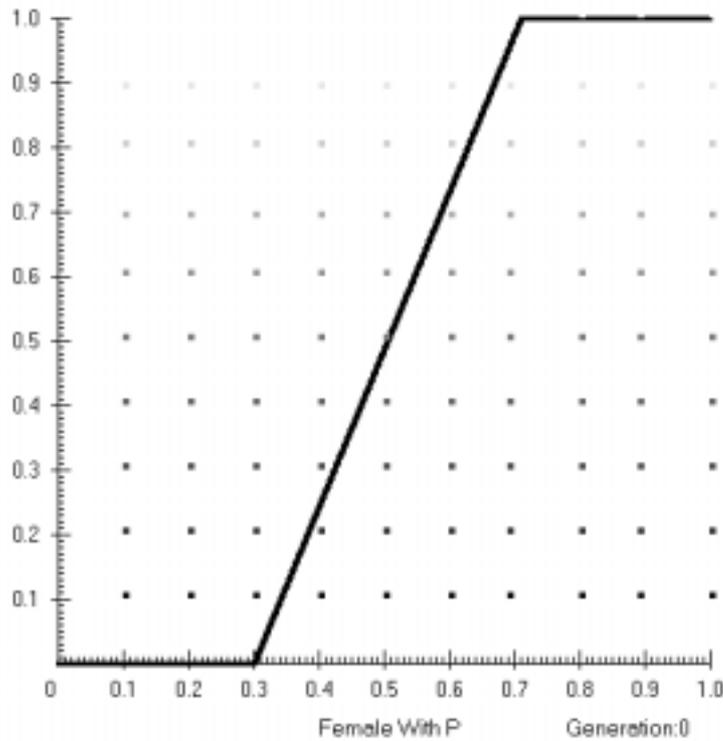


Fig. 7. Grayscale color assignment according to Y-axis values.

- 2) The closer that X-values approached 0, the darker the point. In other words, lower proportions of females with the P gene tended to result in fewer males with the T gene.

Although these observations can also be made from the results of non-visual methods, we believe that our approach allows for a faster view of richer data compared to the complex numeric information that is usually produced by these procedures.

4.1.2. Convergent Line

A representation of the CL produced by our visualization is shown in Fig. 10. The following observations were made:

- 1) The CLs tended to be orthogonal to the X-axis, that is, greater change occurred in male than in female proportions.
- 2) Population change can also be acquired from CL. The longer the distance of a point from Kirkpatrick's predicted equilibrium, the longer the CL; the longer the CL, the greater the change in population proportions. In Fig. 10, population distribution at the upper-left or lower-right corners of the plane changed more than points in other plane positions.

An important CL fact is that all lines cannot be shown on a single graph; some lines are covered by other lines, making them less visible as the number of lines increases. To make CL more useful, researchers need to observe the CLs of all points to identify important parts or patterns before observing them

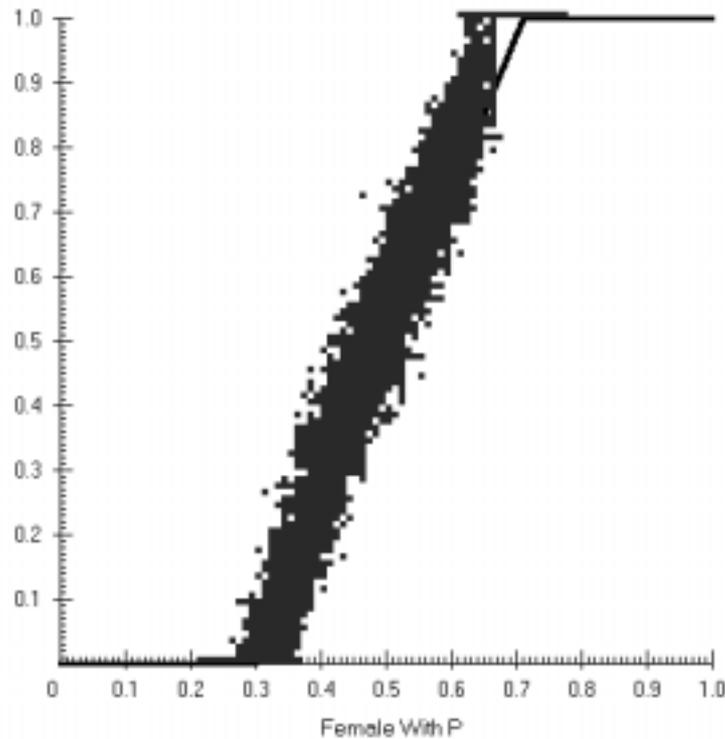


Fig. 8. Distribution of the 10,000 convergence points following a simulation of Kirkpatrick's model.

in specific areas to gather more detailed information. This “*overview+detail*” technique is commonly applied in many instances of information visualization.

4.2. Dynamic Evolution Map

For our DEM observations, we chose 100 starting points on the plane and marked each one in a gradation of gray according to its X-value. Evolutionary movement between generations 0 and 11 is shown in Figs 11 and 12.

In this case, evolutionary processes could be understood in detail because the EDM shows the position of each point generation by generation, thus facilitating cross-population comparisons. As stated in an earlier section, an important DEM advantage is that it presents dynamic information that provides a great amount of detail compared to more static presentations. However, we believe that the limitations of human long-term memory dictates that a combination of dynamic and static presentations may be the most efficient for users, with the former allowing for observations on trends of evolution and the latter providing information for more detailed analyses.

4.3. Energy Contour Map

We recorded the number of traversals across 10,000 starting points on the plane. Using Eq. (1) in Section 3 and plotting height as the energy of an individual point at that position, we produced the visual representation shown in Fig. 13.

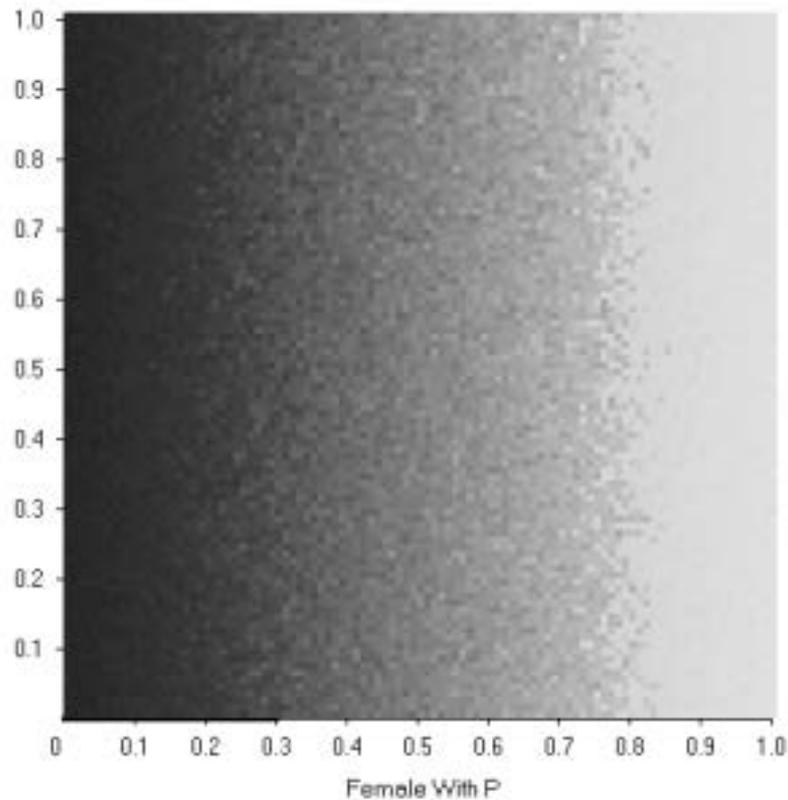


Fig. 9. EDM results.

Based on the assumption that the position with the lowest energy represents a convergence point, convergence is most likely to occur at the gulf found in the middle of the plane. This agrees with Kirkpatrick's prediction that convergence occurs along the equilibrium line. Furthermore, the appearance of any point along the plane makes it possible to a) calculate the energy of its position and neighborhood and b) predict its position in the following generation. These are considered two positive qualities for visual representations.

4.4. Visualization framework characteristics

4.4.1. Relationships among the four methods

A comparison of the four visualization methods is presented in Table 2, which lists the information used to create visualizations and the information obtained. The output is classified as either convergent behavior or the movement behavior of the points involved.

We want to emphasize the complementary characteristics of the four visualization methods—that is, they should not be considered as independent entities. Combined, EDM and CL can make information on convergent behavior more obvious and accessible in terms of both global (EDM) and local (CL) views. The advantages and disadvantages of the two methods are listed in Table 3. A similar comparison

Table 2
A Comparison of the four visualization methods

	Input	Output	Information type
EDM	Convergent position of points	Relative convergent behavior of all populations.	Convergent behavior (global).
CL	Lines between starting and converging points	Change rate of male and female distributions.	Convergent behavior (local).
DEM	Movement of points.	Dynamic information on evolution.	Movement behavior (dynamic).
ECM	Traversed position times.	Point moving trends.	Movement behavior (static).

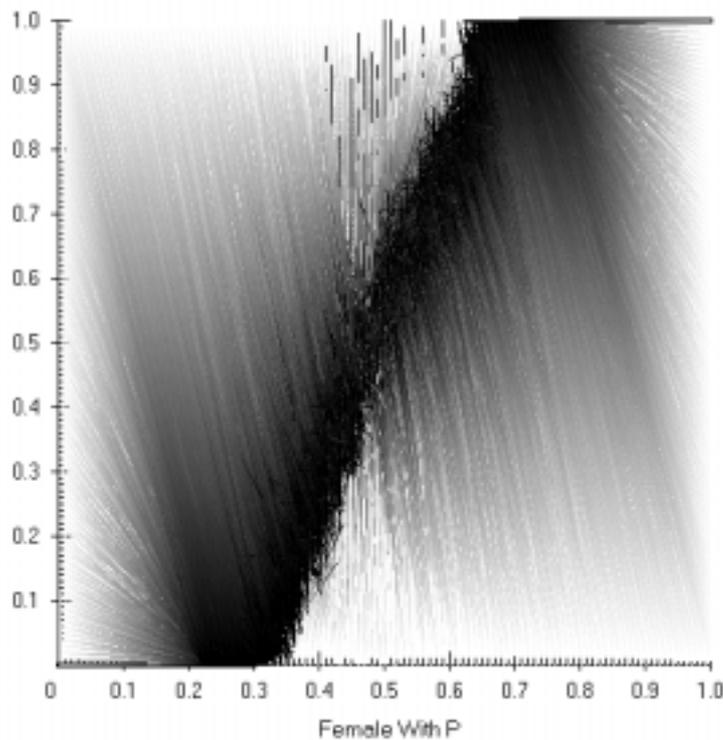


Fig. 10. Convergent Line results.

between the DEM and ECM methods, both of which focus on the movement of points along a plane, is shown in Table 4. The DEM-ECM combination matches our perceived need for point movement information that is both dynamic (good for pattern recognition and predictions) and static (good for pattern and prediction verification).

4.4.2. Trade-offs in usability versus expressiveness

Most GA visualization techniques have not gained acceptance from GA users because of perceived tradeoffs between usability and expressiveness [8]. While other researchers refer the usability as difficulty level of making visualization (programming environments) for GA, here we refer it as the difficulty level of using visualization tools. At the beginning of this project, we acknowledged that many users are put

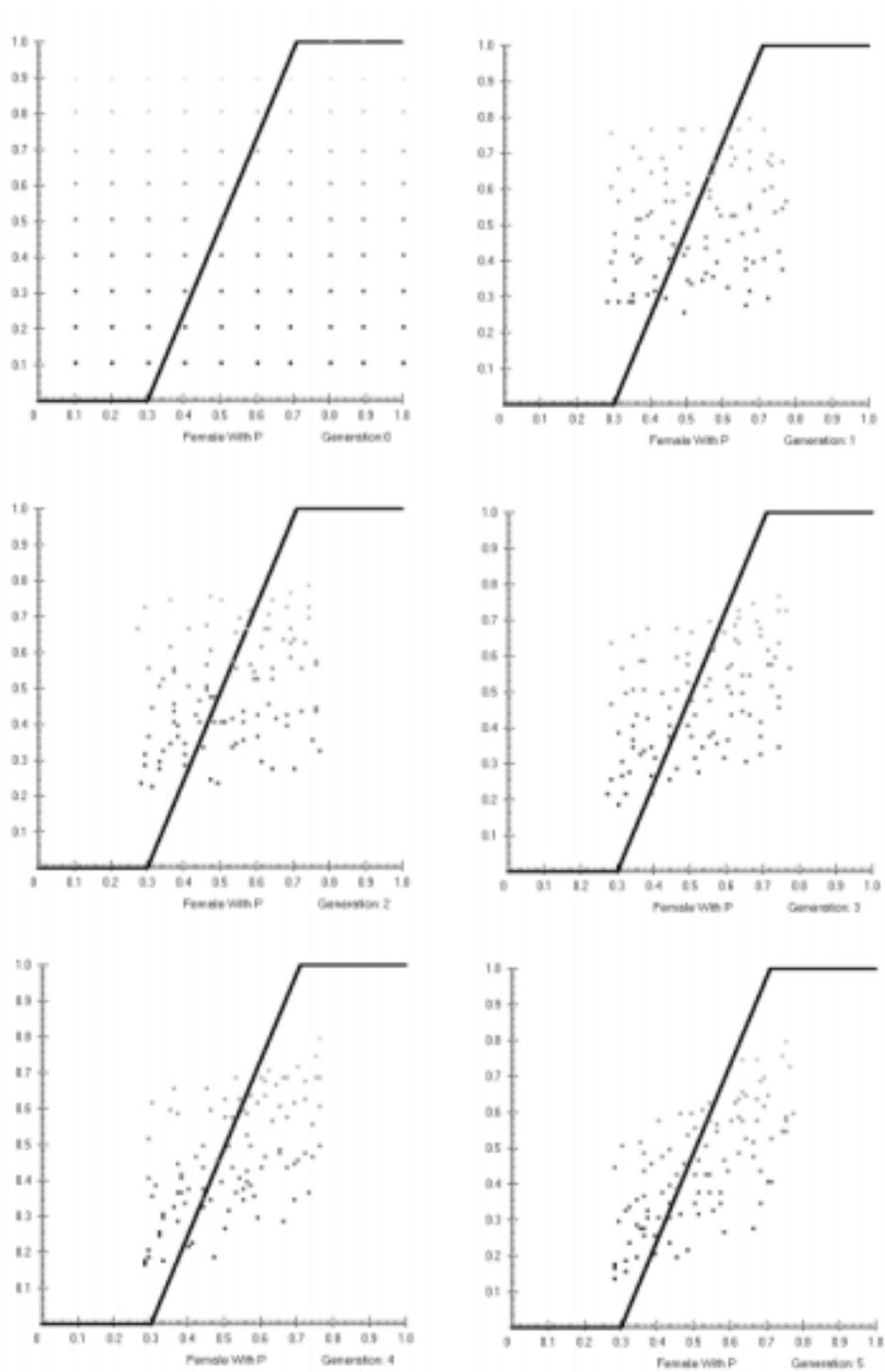


Fig. 11. DEM results (generations 0 to 5).

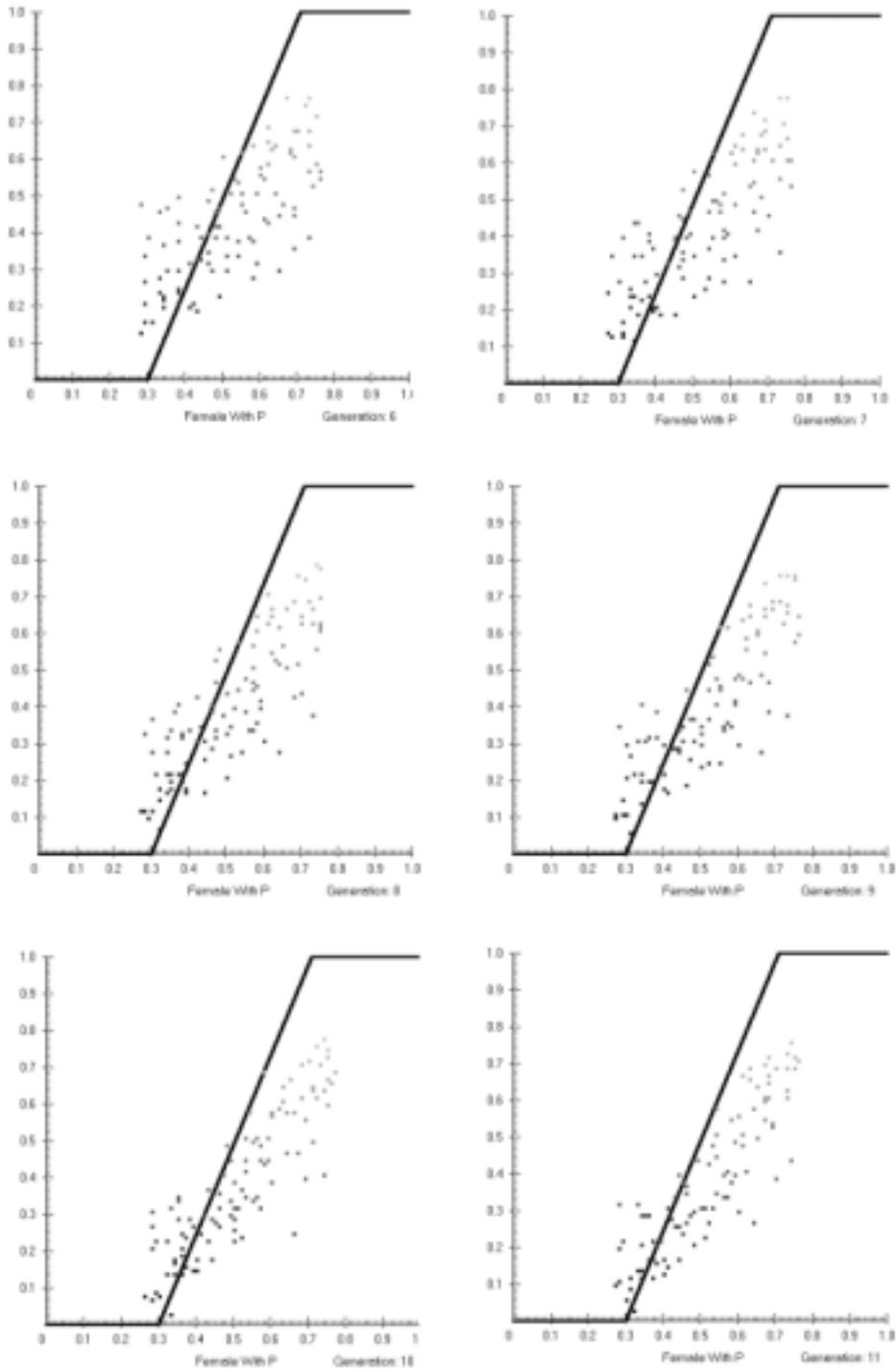


Fig. 12. DEM results (generations 6 to 11).

Table 3
A Comparison of the EDM and CL visualization methods

	Advantages	Disadvantages
EDM	1) Gives complete information in a single graph. 2) Makes it easy to find patterns.	1) Detailed information is not shown.
CL	1) Relationships between initial and final populations are highlighted. 2) Detailed information is provided on each population.	1) The number of lines in a single graph is limited, making it hard to give a global view.

Table 4
A Comparison of the DEM and ECM visualization methods

	Advantages	Disadvantages
DEM	1) Shows evolutionary information in detail. 2) Useful for comparing neighborhood points.	1) Limited due to the long-term limitations of human cognition.
ECM	1) Provides strong, reliable information for predictions.	1) Detailed information is skipped.

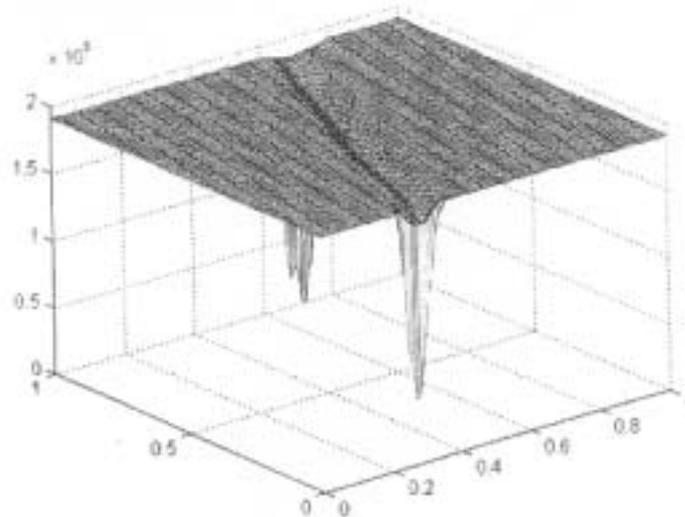


Fig. 13. ECM result.

off by the amount of time required to become familiar with existing GA visualization tools, restricting those tools' use to a relatively small number of researchers interested in GA problems or who already have considerable experience with information visualization concepts. We believe a strong point of our proposed framework is that the two-dimensional base presentation makes it easily to be established and understood.

4.4.3. Framework extension for more complex GA problems

The two-dimensional base presentation in this framework may be argued by its usefulness in problems with more dimensions/genes. In this paper, the framework is illustrated by a sexual selection model, whose population contains chromosomes with two genes. This doesn't mean that it is only applicable for GA problems with very small dimensions/genes. It is also applicable for problems with much more dimensions/genes by constructing a two-dimensional plane that is suitable or representative for the population distribution.

Common dimension reduction techniques are not applicable for the construction of our two-dimensional plane. Since most existing dimension reduction techniques used in GA map an n-dimensional chromosome into a point on the two-dimensional plane. However, in our framework, a single point on the plane doesn't represent the individual chromosome, but the whole population. It would be difficult to map a population on a two-dimensional plane without processing the population information.

According to the nature of problems, and their representations of chromosomes in GA, the two-dimensional plane can be constructed by two ways:

1) Constructing the plane to illustrate the population with respect to two specific genes:

In some GA problems, the importance of each gene in a chromosome is not equivalent. In such cases, it is important to know the individual importance of each gene, and the correlation between them. The two-dimensional plane can be constructed with respect to two specific genes, to reveal the relation between these two genes. The occurrence of convergence on the plane indicates that these two genes are strongly correlated.

2) Constructing the plane to illustrate the population with respect to two criteria:

In many traditional GA applications, it is possible to observe the population according to some criteria. These criteria are heavily problem dependent, and they are also partially determined by the presentation of chromosomes. Besides, for some GA variations, the population can be also observed with respect to some criteria. Here we provide two types of GA variations as examples, and discuss them in more detail.

a) Multi-objective Genetic Algorithm:

The multi-objective genetic algorithm (MOGA) was first introduced by Fonseca et al. [11]. It functions by seeking to optimize multiple objective functions, in contrast to traditional GA that optimizes only single objective function. In the MOGA, the users often want to know how the population evolves with respect to different objective functions, and the relation between them. Our framework provides a viable solution. For example, the two-dimensional plane can be constructed according to the population's two average fitness values of their corresponding objective functions, to observe the evolution with respect to the two objective functions.

b) Co-evolutionary Genetic Algorithm:

The Co-evolutionary Genetic Algorithm (CGA) explores the search space by utilizing a population which contains two or more species or sub-populations. Those species constantly interact and co-evolve. For example, Hillis proposed a computational model to find a network that correctly sorts lists of numbers [14]. In this model, there are two populations. One consisted of alternatives of sorting networks, and the other consisted of a set of lists to be sorted. The two populations interacted through inverse fitness evaluation. That is, a sorting network was evaluated by the percentage of lists that are correctly sorted, while the set of list was evaluated by the percentage of lists that are incorrectly sorted. In this case, the two-dimensional plane can be constructed according to the average fitness of the two sub-populations, to see how the overall population evolves with respect to each sub-population.

5. Conclusion

The huge amount of data produced by GA presents challenges for the visual presentation of information that is useful, that gives an overall picture instead of partial images, that filters out useless information,

and that facilitates recognition of specific phenomena. We believe these goals can be achieved through the use of a visualization framework that emphasizes a population perspective of evolutionary processes.

Our framework visualizes the evolutionary process of GA from a population perspective. Although it is illustrated by a sexual selection model whose population contains chromosomes with only two genes, it is also applicable for GA problems with much more dimensions/genes. Furthermore, it is also applicable to GA variations, such as Multi-objective GA and Cooperative GA. Future work includes applying our framework to different type of GA problems, and investigating the possibility of more sophisticated visualization techniques based on our two-dimensional population distribution plane.

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