IGAP: Interactive Genetic Algorithm Peer to Peer

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ABSTRACT

We present IGAP, a peer to peer interactive genetic algorithm which reflects the real world methodology followed in team design. We apply our methodology to floorplanning. Through collaboration users are able to visualize designs done by peers on the network, while using case injection to allow them to bias their populations and the fitness function to adapt to subjective preferences.

Categories and Subject Descriptors: I.2.8 [Artificial Intelligence]: Problem Solving, Control Methods, and Search

General Terms: Algorithms, Design, Human Factors

Keywords: Interactive genetic algorithm, collaboration, floorplanning, peer to peer network

1. INTRODUCTION

Design is a fundamental, purposeful, pervasive and ubiquitous activity and can be defined as the process of creating new structures characterized by new parameters, aimed at satisfying predefined technical requirements. It consists of several phases, which differ in details such as the depth of design, kind of input data, design strategy, procedures, methodology and results [6]. Usually the first stage of any design process is the preliminary or the conceptual design phase, followed by detailed design, evaluation and iterative redesign [2]. Computers have been used extensively for all these stages of design except the creative conceptual design phase. We are interested in supporting the creative conceptual design phase by not only saving and disseminating the initial ideas of designers, but also by providing the support for initial design ideas to serve as the seeds on which new designs are founded. Interactive genetic algorithms (IGAs) have been proposed as user guided innovation pumps [3]. We present IGAP, a peer to peer IGA, that allows designers to exploit and guide evolutionary computation to breed new design ideas quickly, while supporting a team collaborative aspect, consisting of the sharing of ideas among designers by visualizing and case injection of peer individuals into a designer's population.

We use floorplanning as a case study for IGAP. Floorplanning as it relates to architecture and building engineering is the art and science of laying out relationships between rooms and spaces within an enclosed area subject to engineering and design constraints. It is driven by a sense of aesthetics and functionality in the mind of the designer and end-user. IGAP combines both measures in its fitness function and allows the designer to simply and efficiently explore the space of simple floorplans, while also simulating the work and process flow in a design studio by emulating the collaborative atmosphere [1]. The IGAP framework is shown in Figure 1.

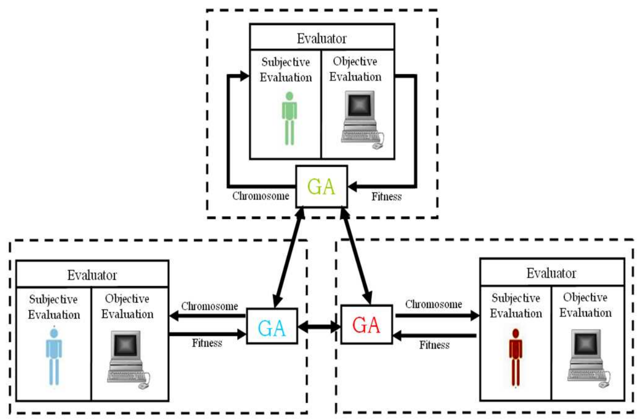

Figure 1: IGAP Framework

2. COLLABORATIVE METHODOLOGY

Evolution is guided individually by having the user evaluate a small subset of the population, optionally viewing the entire population by scrolling down, and selecting the individual the user likes the best. The fitness of every other individual in the population is interpolated based on similarity to the user selected best [1]. Individuals are also evaluated objectively based on architectural guidelines [1, 5].

Collaborative evolution is implemented with a peer to peer network. We treat each user participating in evolution as a node, handling incoming requests from other nodes (peers) and requesting information from peers. By using a peer to peer network, control is decentralized and each node is free to chose who to connect to and if necessary who to exclude from its set of peers.

The collaborative interface is shown in Figure 2. The rooms are color coded as red (living area), yellow (bedrooms), green (eating areas - kitchen and/or dining rooms), firebrick (bathrooms), and white (empty spaces). During collaborative evolution, a subset of peer-evolved designs is displayed to the right of the user's population. We limit the number of peer individuals to nine, organized in a 3x3 grid, similar to how we present the user's own population, in order to be consistent. For more than one peer, we cannot display all the individuals belonging to the subset of each peer, since we only display nine. We do make sure that the user selected best individuals from each peer are displayed on the peers subset. We save the user selected best from generation to generation, and we always make it part of the subset displayed the next time the IGA requires user input. We select the rest of the individuals that make up the peers subset by taking a random subset from a collective pool of all individuals that make up peers' subsets. By selecting a random subset, we believe that over many generations, all of the participants will get approximately the same amount of their designs displayed on the screens of collaborators.

The benefit of viewing the best individuals from peers is limited, unless the user is able to take promising individuals from peers and mold them to their liking. We support this by allowing the user to inject individuals from the subset of peers into the user's own population. The user can select an individual from a peer to be added to the user's own gene pool by clicking on the "Add to Genome" button. The user can also select a best individual from the subset of individuals from peers, in which case the user selected best is automatically injected into the population, and used for fitness interpolation. We require the user to select a best individual, but it does not have to be from the user's own population - the user selected best can come from peers.

The injected individuals replace the bottom 10% of the population as done in [4]. If the number of injected individuals is less than 10% of the population, then we insert numerous copies of the injected individuals, until the total sum of the injected individuals is 10%. In case-injected GAs (CIGARs) typically a case base is kept of solutions to previously solved problems, and based on problem similarity, individuals similar to the best individuals in the current population are periodically injected, replacing the worst individuals [4]. In our algorithm, the designer plays the role of determining how many, when, and which individuals to inject at any step during the collaborative evolutionary process. If the injected individuals make a positive contribution to the overall population, then they will continue to reproduce and live on, while injected individuals which do not improve the population performance will eventually die off. Hence, the user is not penalized for injecting subpar individuals.

3. DISCUSSION AND FUTURE WORK

Figure 3 shows floorplans evolved individually and collaboratively. Banerjee et al. showed that using IGAP resulted in more original floorplans than those evolved individually [1]. Through collaboration users are able to evolve floorplans which reflect the expertise and preferences of the collective peer group. Users are exposed to diverse high fitness individuals, which can be used to bias search spaces.

Our preliminary observations have been that designs evolved collaboratively between peers tend to be more diverse and more unique. On the other hand, designs evolved individually tend to converge to a single design, lacking the high fitness diversity seen when evolving with peers. In other words, individual evolution tends to produce a lot of similar looking solutions that have moderately high fitness, while the collaborative evolution leads to a diverse pool of some very high fitness solutions and some very low fitness ones. Preliminary studies of creative content seem to show that the high fitness collaborative solutions are more "creative" than the corresponding high fitness solutions from the individual evolution runs [1].

Our methodology shows much promise and lays a good foundation for future research. We are interested in conducting further user studies, allowing the subjects to grade and assess the practicality of the resulting designs and the collaborative evolutionary approach. We will also be assessing how well our results generalize to other design domains.

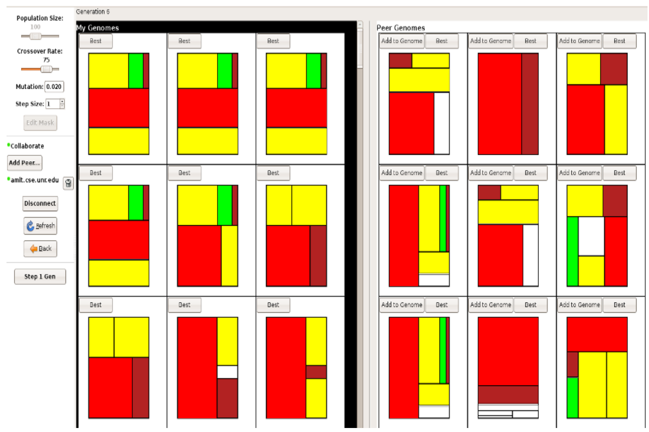

Figure 2: The Collaborative IGA Interface

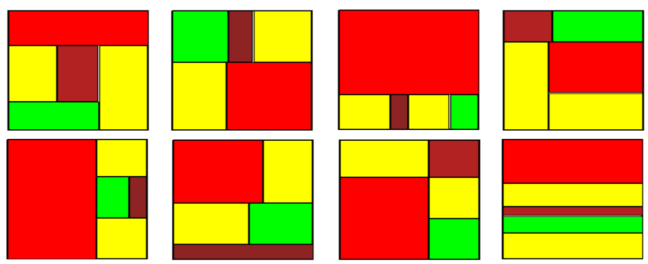

Figure 3: Floorplans evolved individually (top four) vs. collaboratively (bottom four).

4. ACKNOWLEDGMENTS

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5. REFERENCES

[1] A. Banerjee, J. C. Quiroz, and S. J. Louis. A model of creative design using collaborative interactive genetic algorithms. In *Proceedings of the Third International Conference on Design Computing and Cognition. DCC08*, 2008.

[2] P. J. Bentley and J. P. Wakefield. Conceptual evolutionary design by genetic algorithms. *Engineering Design and Automation Journal*, 3:119–131, 1997.

[3] D. E. Goldberg. *The Design of Innovation.* Springer, 1 edition, June 2002.

[4] S. Louis and C. Miles. Playing to learn: case-injected genetic algorithms for learning to play computer games. *Evolutionary Computation, IEEE Transactions on*, 9:669–681, 2005.

[5] E. Neufert, P. Neufert, B. Baiche, and N. Walliman. *Architects' Data.* Wiley-Blackwell, 2002.

[6] G. Renner and A. Ekárt. Genetic algorithms in computer aided design. *Computer-Aided Design*, 35:709–726, 2003.