Improved Interface for Interactive Evolutionary Design

Henry Kwong and Christian Jacob

University of Calgary

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Abstract

This project is in the area of evolutionary design. Specifically it deals with providing a user-friendly interface to the EVOLVICA software system (Jacob 2000) that is used to evolve biomorph sketch figures and L-system (Lindenmayer system) flowers. In addition to creating an easier to use interface, I also experimented with the visualization of the genotype and phenotype of the biomorphs and L-systems.

By the end of the project, I had developed several GUI widgets in *Mathematica* (Wolfram 1996), some of which include data input forms, a point-and-click expression browser, and a graphical selection widget. In addition I made the phenotype visualization more dynamic and interactive by integrating a Mathematica add-on called Live Graphics 3-D (Kraus 2000). In the case of the biomorph system, I added 3-D phenotypic visualization to make the biomorphs appear more like real world objects. I also improved genotype visualization by representing the genotype in forms that are easier to read and recognize, such as standard L-system notations, and tree-based forms. For biomorph genomes, I presented the genome in a tabular form to make comparisons between genomes easier. The resulting systems have improved the ability of the user to observe the changes to the genotype and phenotype that take place through the evolution of L-system flowers and biomorphs.

Introduction

Evolutionary design is a relatively new area in the field of artificial intelligence (Bentley 1999). There are many researchers who have developed evolution programs to explore this new area of research. Such systems are designed to automate part of the innovation processes needed to design objects by mimicking the forces of evolution. EVOLVICA is one such evolutionary design system used to interactively breed computer programs, robot control programs, fractal L-systems, models of natural computation processes, and growth and development programs based on Lindenmayer systems (Jacob 1995a, Jacob 1995b, Jacob 1996, Jacob 1999, Jacob 2000).

In this paper I will describe the current state of EVOLVICA for evolving biomorph and L-systems, and then I will describe some shortcomings of EVOLVICA and my solutions to these shortcomings. Specifically I will discuss the limitations of the user interface, and the visualization of the genotype and phenotype. Some familiarity with general evolutionary computation concepts are assume in this paper.

Background

Biomorphs

Biomorphs are simple recursive two-dimensional line figures that were first introduced by R. Dawkins in order to demonstrate the creative potential of simple selection-mutation mechanisms (Dawkins 1986, Dawkins 1996). Inspired by Dawkins's biomorphs, Dr. Jacob developed an interactive evolution system for generating biomorphs (Jacob 2000). In this system, the genotype of a biomorph consists of a vector of 21 integers, where the first entry gives the recursion depth (from 1 to 4), and the remaining entries give, for each recursion depth, the colour, thickness, branching angle, number of branches, and length of each branch (see figure 1.1).