An Evolutionary Approach to Aesthetically Pleasing Space Filling

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Introduction
It is sometimes desirable to generate patterns that rather than being infinitely repeatable or placed arbitrarily on a rectangular canvas are specifically tailored to fill a more complex shape. This work focuses on this problem as proposed by CERCIA partner Delcam.

Delcam’s software package JewelSmith [3] provides a CAD environment for the design of jewellery. This software currently lacks a sophisticated method of automated pattern generation and this work attempts to use natural computation techniques to evolve aesthetically pleasing patterns of circles that are based on the geometry of the shape they are filling.

Bounding Patterns by a Space
An algorithm augments the patterns of circles such that they neither overlap each other nor stray from the boundary of the shape. This algorithm iteratively rotates a candidate circle about the previous circle until it fits within the space without overlap. If a full rotation is completed the circle is made smaller and iterated around the circle again. This continues until the circle fits or aborts the drawing command if it gets too small. This process is very computationally demanding and is a major shortcoming of the system.

Finding Midlines
Delcam specified that work should be done to determine lines of interesting variation through shapes which they called ‘midlines’. Midlines should bisect a shape in an interesting but not necessarily symmetrical way and are purely an aesthetic tool, although they are calculated from the geometry of the shape.

Midlines are found by the system through geometric analysis of the shape. First a line in the direction of maximum variation is determined for the shape. Then each point on this line is shifted to the midpoint of a line perpendicular to it stretching to the out edge of the shape. This new augmented line is used as the midline. When patterns are drawn the size of each circle is determined by its distance from the midline. Figure 1 shows several shapes with their midlines in red as found by the system.

Genetic Representation of the Pattern
The patterns are represented by a sequence of commands inspired by the work done by the ImageBreeder [4] project. These commands are as follows:
• Draw ( ) – Draw a circle at the current point
• Turn (t) – Rotate about the current point t degrees
• Repeat (r, c) – Repeat r times the following c commands
• Make Module (c) – Treat the next c commands as a module
• Make Hub ( ) – Set the current location as a geographic hub
• Do (i) – Do the set of commands specified in module i
• Go (i) – Go to (geographically) hub i

A genome is made up of an array of classes; a separate class represents each command.

Crossover and mutation operators act on the genome at the discretion of the user, altering both the structure of genome and the parameters which are bound to each command.

A GUI inspired by the common approach to evolutionary art interfaces [1,2] allows the user to view the population and select individuals for breeding and mutation.

Results
The following is a selection of patterns generated by a single user which demonstrates both the strengths and weaknesses of the system.

Discussion
The system allows for the development of circle based patterns which are both interesting and aesthetically pleasing. In this respect it is a success. However, shortcomings abound and the system needs considerable further development to be of practical use. The system does not lend itself to filling the shape very effectively despite making interesting patterns and those that do fill the space tend to be rather chaotic. The amount of computational time required to fit a pattern to a shape means that it takes a prohibitively long period of time to display large genomes (of more than around 50 commands). Experimentation has shown that for a shape to be filled and for complex patterns to emerge genome lengths of over 100 are necessary. It is also clear that the mutation operators are not powerful enough and do not effectively traverse the local search space with their alterations to the genome seeming too minor. A refinement of the genetic operators and an effort to improve the efficiency of the space filling algorithm should be key focuses for future work.

References