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A methodology for user directed search in evolutionary design

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Abstract A designer should be able to express their intentions with a design tool. This work describes a methodology that enables the architect to directly interact with the encoding of designs they find aesthetically pleasing. Broadening interaction beyond simple evaluation increases the amount of feedback and bias a user can apply to the search. Increased feedback will have the effect of directing the algorithm to more fruitful areas of the search space. We conduct trials on two interfaces for making localised changes to a design in order to evaluate if the user is capable of directing search. In addition, an examination of the locality of changes made by the users provides an insight into how they explore the search space. The results show that a suitably designed interface is capable of directing search and that the participants used different magnitudes of change during directed search.

Keywords Grammatical evolution · Interactivity · Interrupt intervene and resume

1 Introduction

In traditional interactive evolutionary computation (IEC) there is a disconnect between the user and the algorithm. User evaluation through selection is only indirectly responsible for the output. The designer must feel directly involved in the

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design process [3]. Take the example of a user evaluating bridge designs for an interactive evolutionary algorithm. Through selection they manage to find the perfect bridge, except that the handrail is out of place. The user knows it is possible to move the handrail to the correct place and wants to alter the design. If evaluation is the only means of making this change then the user must select bridges where the handrail is in the correct place and hope the algorithm intuits their wishes correctly. Interrupt, intervene and resume (IIR) is a desirable quality for an evolutionary design system [3] as it allows the user to directly manipulate the design while remaining within the evolutionary framework. Incorporating the immediate wishes of the designer into the process is necessary if evolutionary algorithms are to be used for design.

Grammatical evolution (GE) has shown itself to be a suitable representation for evolving architectural designs when combined with shape generating grammars [34, 38, 39]. For IIR to work with GE it must be possible to map changes to the phenotype back to the genotype. The mapping used by GE complicates this process. It is possible the user could make changes that are not expressible in the grammar and so a reverse mapping would be impossible. The user can export the design to a suitable CAD format and make further changes but then the design cannot be evolved.

An alternative approach that permits IIR when a mapping process is involved is to change the phenotype by *directly altering* the genotype. This work presents two novel interfaces that enable the user to directly manipulate the chromosome and instantly examine the resulting change. The immediate feedback presented to the users allows them to observe the possible impact of genotypic changes and choose their preference accordingly. The interface is not intended to replace evaluation in IEC but to increase user input through direct intervention and enhance existing interactive evolutionary design tools. The primary contribution of this work is that it provides a focused version of selection driven search that incorporates the intentions of the user into the evolutionary design process.

Locality—how well neighbouring genotypes correspond to neighbouring phenotypes - has been described as a key element in Evolutionary Computation [28]. In standard GE mutation there are two component behaviours. Nodal mutation alters a part of the genome that encodes for a leaf node of a derivation tree and structural mutation encodes for an internal node on a derivation tree. It has been previously demonstrated that nodal and structural mutation had a perceivable difference in the locality of their changes [6, 7]. Nodal mutation generated changes of high locality while structural mutation generated changes of low locality.

By giving the user the ability to selectively apply each operator the user can choose to move a small or a large distance from the current individual. Choosing which operator to apply allows the user to bias the search toward exploring a specific area of the search space, which has been shown by Whigham [51] to improve evolutionary search. User interaction with the search is increased by directly mutating individuals they find appealing. The approach taken in this work makes the assumption that when users want to see similar variations of their preferred designs. The experiments described in this work evaluate different user interfaces to the evolutionary algorithm. The intention of the experiments is to explore if the interface can aid the evolutionary design process.

The intention of this work is to examine if an IIR methodology combined with a suitable interface is capable of directing search. To this end, empirical experiments test whether the user can manipulate a given design to match a specified target. Previous research in this area is discussed in Sect. 2 An overview of grammatical evolution and the mapping process is given in Sect. 3 The initial interactivity experiment and static user interface are described in Sect. 4 The results from the first experiment led to a novel implementation of the animated interface. A new series of experiments were carried out on the animated interface, which are described in Sect. 5 Finally, the conclusions and future work are discussed in Sect. 6.

2 Related research

This work combines the use of grammars for architectural design with an investigation into different approaches for interactive evolutionary computation. Accordingly, the related research is split into two taxonomies.

2.1 Grammars for architectural design

Grammars are a simple way of describing a generative encoding that allow for syntactical correctness, compression and domain knowledge embedding [22]. A grammar defines everything that can be said in a language. A correctly formed grammar ensures that every completely mapped individual is valid. As well as ensuring syntactic correctness, grammars allow domain knowledge to be embedded in the system. By constraining the system to particular constructions or by calling predefined functions, the user can manipulate how the individuals generated by the grammar will behave.

The use of grammars to generate shapes was originally conceived by Stiny [45]. The shape grammar formalism developed by Stiny uses three types of rules, a start rule, at least one transformation rule and a termination rule. The transformation rules are applied to the start rule to generate shapes until a termination rule is reached. Shape grammars have had several successful applications for generating designs. Koning and Eizenberg [26] generated prairie houses in the style of Frank Lloyd Wright by starting at the central fireplace and building around it with variations on his tradition design. A shape grammar for describing and generating coffee maker designs was set out in [1] and there have been several shape grammars for capturing the aesthetic signature of classic designs such as the work by Pugliese and Cagan [41] on Harley Davidson motorcycles and the work by McCormack et al. [31] on Buick cars.

While shape grammars have a great expressive power, there is an inherent difficulty with implementing shape grammars on a computer. The computer must be able to recognise emergent shapes so that transformational rules may be applied to them. Computer vision algorithms are required to categorise these emergent shapes. The problem is explained in greater detail in [17]. There are three components required to implement shape grammars on a computer. An interpreter is required to apply shape grammar rules, a parser to deduce if a shape is in the shape grammar, and an inference program that given a set of shapes would infer the rules that created them.

O'Neill et al. [38] used context free grammars (CFG) in conjunction with grammatical evolution to generate two dimensional shapes. An objective fitness function and a specific target was used to automatically evolve designs. This work was furthered in O'Neill et al. [39] to make three dimensional designs for a smoking shelter. The output was rendered using Blender [44] and a user interface was provided for interactive fitness evaluation. The results attained were limited by the fact that many designs in the grammar were not connected to each other. Hemberg et al. [23] combined GE with a variation on Lindenmayer systems [40] to create abstract architectural designs. Evolution was guided by the user and by objective shape rules such as symmetry and smoothness. The user could also add repellors and attractors to manipulate the overall shape that was generated.

Machado et al. [29] used a graph based evolutionary approach combined with context free design grammars to evolve images. Context Free Art [11] is an image generation software package that uses context free design grammars to generate shapes and patterns. In this work the genotype was a well formed context free grammar that was represented as a graph. The graph used nodes to encode for non-terminals and the edges were annotated with the parameter values being passed to the non-terminals. The experiments used both objective and subjective fitness tests.

McDermott et al. [34] compared shape grammars with CFGs for design generation. It was shown that CFGs are easier to manipulate and eliminate much of the ambiguity present in shape grammar mappings-terminals. There have been several applications that have used CFGs for design generation. The work by Wonka et al. [52] used a context free grammar based approach for rapidly generating feasible architecture. By separating the generation process into split and set grammars they could generate varied architectural structures that still had aspects of regularity. Set grammars specify the overall layout of a design while split grammars break up an object into smaller interchangeable components. The results generated by the split grammar would then be used as components by the set grammar.

Coia and Ross [10] combined a context free grammar with CityEngine [15] for generating three dimensional buildings. The grammar applied rules such as extrude, rotate, split scale and insert, to a starting component to generate connected yet varied designs. The buildings were evolved using objective aesthetic constraints such as the number of unique face normals, overall surface area and overall height.

In an effort to create more coherent designs and also to avoid problems of infinite recursion in a grammar, higher order functions (HOF) were introduced. Currying higher order functions, i.e., setting a function argument to a fixed value, allows recursion to be used without having to worry about non terminating recursive calls Yu [53]. McDermott et al. [33] incorporated this approach into a CFG. Combining higher order functions and lambda abstraction meant that the problem of connectedness in a generated design was addressed and it also allowed for more modularity, regularity and hierarchy in the resulting designs.

The designs generated in this work use a context free grammar that incorporates both higher order functions and lambda functions to generate the designs. This means that there is a non-trivial mapping process between the genotype and the phenotype as discussed in greater detail in Sect. 3.2 The next section describes methods for user interaction with an evolutionary algorithm similar to the methods implemented in this work.

2.2 Interactive evolutionary computation

Human interaction was originally introduced to the evolutionary process for problems where no objective fitness function could be found. One of the earliest applications was the generation of images by Dawkins [13]. Interactive fitness functions have allowed EC to be applied to problems that have aesthetic considerations such as music and computer graphics, This allows EAs to function as an exploratory tool as opposed to being limited to optimisation.

The primary problem with user interaction is the "fitness bottleneck" [4]. An algorithm can evaluate individuals in parallel and is limited only by the speed and number of the processors. Humans, conversely, can only process small amounts of input that is limited by their perceptual abilities and can only assign fitness to individuals serially. Miller [36] showed that humans have difficulty handling more than approximately seven quantized measurements of information. This is true regardless of sensory modality. The result is that user input slows the process of the EA due to the limited number of evaluations that they can perform.

How the user interacts with the algorithm is of paramount importance. There are many different implementations that vary the level of interaction and the amount of information provided to the user. In his survey paper Takagi [47] splits IEC into several different categories, each based on the level of interaction. Approaches that allow direct participation in the evolutionary process through means other than evaluation are categorised as active user intervention (AUI) [47]. The interfaces described in this work are based on the AUI approach. Several successful AUI methodologies have been used to increase user participation and are discussed below.

2.2.1 Online knowledge embedding

Online knowledge embedding (OLKE) [46] provides a mechanism for directing the algorithm through hints, ideas or intentions. The user highlights components of a design that they think have high fitness and the genes relating to these components are then fixed, which reduces the search space. An example of this is the tracking a criminal suspect through face-space with a genetic algorithm [9]. The main advantage of using IEC for this task was that it relied on human recognition instead of human recall. Identikit images that are normally used for criminal investigations were evaluated by the user. There were 10 discrete values for rating the likeness. If a user felt that they had matched a particular feature they could set it so it would stay fixed for the rest of the run. OLKE is only possible if each component of the output maps directly to a particular gene.

Hart [19] developed an evolutionary art that used a novel form of tree alignment to create better genetic dissolves. The user was given fine grained control of the mutation operator and was allowed to select or mask different types of mutation. They could also adjust the relative probability of mutation and bias the mutation rate depending on tree depth. This work is notable for letting the user apply their own intuition on the operator.

SBART [49], a 2D picture generator, enables the user to break parts of the population into different sub-populations. Each sub population evolves separately from their neighbours. Individuals may be saved and introduced into different populations, thus allowing individuals to be treated as "digital amber" [42], a metaphor for how the genetic code of an individual organism is preserved in the computer after a run is terminated, and whereby it may be reintroduced into future populations or reused in a different run entirely.

The approach of grouping and categorizing interesting individuals was also used in the evolutionary art tool NEvAr [30]. During the exploration stage of the selection process the chosen individuals are saved in a separate gallery. The user may then categorise the individuals as images that should be discarded, images that may be useful, images that should be further refined, and images that are artworks that fully satisfy the user's aesthetic criteria.

2.2.2 Visualised IEC

Visualised IEC (VIEC) collapses a multi-dimensional search space into a 2D representation. The individuals are then mapped to the 2D space and presented to the user. The user is able to observe the distribution and fitness of the population and direct the search to particular parts of the search space, thus combining both evolutionary and human search techniques. VIEC has been shown to dramatically improve convergence. Hayashida and Takagi [20] used self organising maps (SOM) to collapse an n-D Schaffer function into a 2-D representation and Hayashida and Takagi [21] compared different methods for mapping an n-D function to a 2-D representation. The problem with VIEC is that a meaningful mapping from n-D to 2-D space must be performed and the topological relationships must remain intact.

2.2.3 Human based genetic algorithm

Human based genetic algorithms (HBGA) enable the user to apply low level genetic operators such as mutation, initialisation, selection and crossover to the population [27]. Using humans is useful in problems such as evolving natural language statements, where it is hard to design efficient computational operators. HBGA requires that an individual in the population can be understood by the user and that the operators perform in a manner intuitive to the user.

Hyper-interactive evolutionary computation (HIEC) extends HBGA by giving the users access all the genetic operators [5]. HIEC treats the operators as a tool set for the user. Additional operators such as duplicate, delete are available to the users. The approach taken in this thesis is similar to HBGA in that the users choose when and where to apply mutation operators. The difference is that the users are presented with the consequences of applying an operator and they select the change they want. One early example of this is the mutasynth sound generation tool by Dahlstedt [12]. In conjunction with selection, the user manually mutates and freezes sets of genes to focus the search on preferred individuals.

The approaches described in this work are similar to HBGA and HIEC in that they allow the user to apply mutation operators. There are also aspects of OLKE as the user is allowed to focus search on a specific individual of interest. This section gave an overview of the related research under two taxonomies, grammars for architectural design and interactive evolutionary computing. The next section gives a detailed description of grammatical evolution, the evolutionary algorithm used in the experiments.

3 Grammatical evolution

Grammatical evolution [14, 37] is a grammar based form of genetic programming [35] that uses evolutionary processes to automatically generate programs. GE uses a mapping process to create output called the genotype to phenotype mapping. The genotype to phenotype mapping is a terminology that has been adapted from the field of biology. A genotype is an encoding upon which the evolutionary operators of mutation and recombination act. A biological example of a genotype would be human DNA. Changes to the genotype are translated into changes to the phenotype. A phenotype is an observable characteristic of an individual. An example of this in humans would be eye-color or height. Evaluation of the fitness is performed on the phenotype. This biological concept was introduced to the field of EC as a method for separating the search and solution space [2] and as a metaphor for describing the representations and mapping processes.

GE generates strings in a context free language by using a list of numeric values (called a chromosome) to select the production choices for non-terminals. The chromosome is made up of codons. Each codon in the chromosome is used to select a production rule from a BNF grammar. The numeric values of each codon can be stored as either binary or integer values. The choice of genotype representation has an effect on the algorithm, as shown by Hugosson et al. [25], but this is not examined as integer representations are used exclusively in the investigations of this work. Once all the non-terminals in a derivation have been mapped to terminals an output string in that language has been generated. The output string is the phenotypic form of the individual. The phenotype is a computer program that may then be executed and evaluated by the fitness function.

3.1 A component-based view of mutation in GE

As mutation is applied to the genotype and not the phenotype, single mutation events combined with the mapping process can result in different magnitudes of change to the phenotype, i.e., mutation events have different *locality*. Locality refers to how well neighboring genotypes correspond to neighboring phenotypes, i.e., a small change to the genotype results in a small change to the phenotype and vice

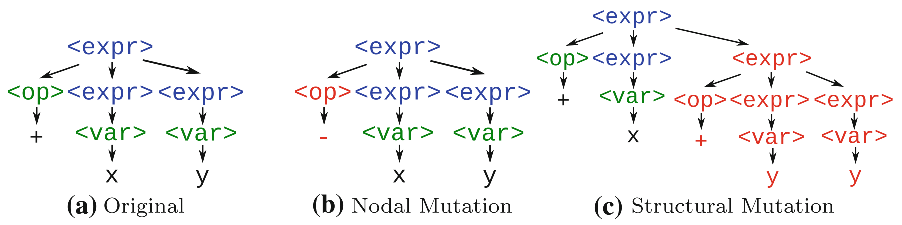


Fig. 1 Nodal (*green*) and structural (*blue*) nodes of a derivation tree. Nodal mutation changes a leaf node while structural mutation changes an internal node (Color figure online)

versa. A mapping has *locality* if the neighbourhood is preserved under that mapping [43]. In order to perform the classification of different types of mutation event, a derivation tree of the individual must first be created.

Standard GE mutation can be divided into two types of events, those that are structural in nature and those that are nodal. *Nodal mutation* changes a single leaf of the derivation tree. The structure of the derivation tree remains unchanged. A nodal codon encodes for a rule that only has terminal productions. *Structural mutation* changes one or more internal nodes of the derivation tree (and zero or more leaves) and can result in a change to the structure of the derivation tree. A structural codon encodes for a rule with non-terminal productions and zero or more terminal productions. An example of a nodal and structural mutation is given in Fig. 1b, c.

Previous work investigating locality in GE mutation [6–8] showed that structural and nodal mutation had different effects on locality during the mapping process and on the resulting output. Nodal mutation generates high locality changes and structural mutation generates low locality changes. As the user is exclusively applying mutation, we shall investigate how the different locality of events are used to navigate the search space.

3.2 Higher-order function grammar

Hornby [24] states that hierarchy, regularity and modularity are desirable qualities in a representation for design. McDermott et al. [33] and Yu [53] showed that grammars were capable of encoding such qualities through the use of higher-order functions (HOF). Higher-order programming requires that functions can be passed to other functions as arguments (first-class functions) and that anonymous functions can be created (lambda expressions). Lambda expressions allow the grammar to define unique functions for the program which then act as modules. Lambda expressions also allow for currying, where a pre-existing function is called except some of the arguments to that function are fixed. Passing functions to other functions allows for a level of hierarchy in the structure of the program. Both of these functions combine to generate structures that contain repetition and similarity, also known as regularity. An example of a program that uses such a grammar is now given.

```
#path generating function
circle_path(scalar, radius, midpoint, axis):
    When given a scalar value it will return a 3D coordinate on a circular path.
    The axis is the plane that remains constant for the circle coordinates

#connecting function
connect_3(starting_node, axis):
    Generates two additional nodes equidistant from the original and then connects them.
    The axis is the plane that remains constant for the circle coordinates

#connecting function
drop_perpendicular(node):
    When given a node it will add a node where the z-plane is zero and connect the nodes

#higher order function
map(scalar_point_function, scalar_list):
    Uses a list of scalar values and a function to create a list of nodes on a path

#higher order function
function_map(function_list, node_list):
    Higher order function that applies each function in the function list to the node list
```

Algorithm 1: A simplified function set from the higher order function grammar. It consists of a path generating function, two connecting functions and two higher-order functions.

A simplified example of the functional set of the grammar used in this experiment is given in Algorithm 1. The geometric objects are created by combining path functions and connecting functions. Path functions are given scalar values and return nodes on a path. Connecting functions are given nodes and then generate additional nodes and connect them together.

```
function_map([lambda x: connect3(x ,’y’),
                lambda x: drop_perpendicular(x)],
                map(lambda t : circle_path(t, 50, (0,0,0), ’z’),
                    [0,1,2,3,4,5])
```

Algorithm 2: An example program generated by the grammar. `function_map()` calls `drop_perpendicular()` and `connect3()` on the node list generated by `map()` and `circle_path()`.

Variations of the principles in the following example were used to create the bridge designs that were used in the experiments. An example of a program is shown in Algorithm 2. The program uses the map function in conjunction with a scalar list to generate a list of nodes that follow a circular path 2(a). Two of the arguments to `circle_path()` have been fixed or “curried”, the axis is set to z-axis and the circle radius is set to 50. The map function then applies the functions `Connect3()` and `drop_perpendicular()` to the set of nodes generated by `circle_path()`. `Connect3()` adds triangles to the nodes, as shown in Fig. 2b, and has the axis argument curried so that it is set to the y-axis for all of the triangles. Finally `drop_perpendicular()` add a vertical line as shown in Fig. 2c. The next section describes how the distances between bridge designs was measured objectively.

4 Application of nodal and structural mutation using a static interface

This experiment primarily examines if user application of mutation operators can direct the evolutionary algorithm during search. The secondary goal of the

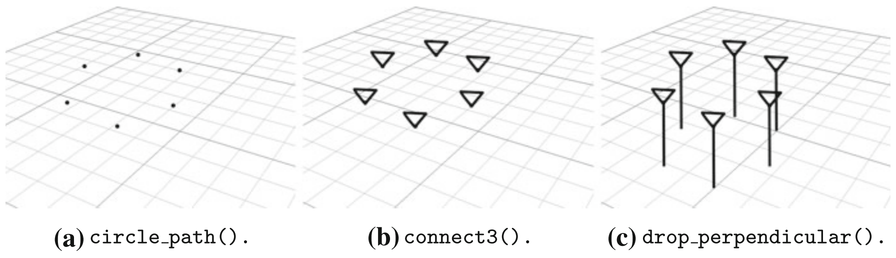


Fig. 2 The output design generated by the program example

experiment is to compare whether separating mutation events allows the user to navigate the search space more effectively by varying the locality of their search. The experiment compares user performance at directing search using integer mutation against a combination of nodal and structural mutation. A static interface consisting of generated is used as this is the traditional method for interactivity experiments involving visual stimulus.

The subjective nature of aesthetics makes interactive evolutionary design a difficult area to quantify. Normally a user is allowed to explore the search space until they discover an appealing design [30]. This approach is problematic as there is no way of distinguishing if the algorithm provided any benefit to the search or whether it just presented randomly generated designs to the user. In addition, there is also the problem that the interest a user has for a design is completely subjective and prevents any additional analysis of the results.

In an effort to generate measurable results, the experiment specifies a target design and the goal for the user is to match that target. The user's results are then compared against a control group of randomly generated selections. The user is asked to match three targets using two different techniques. Although this is quite different to the design process, it is analogous to the user combining an interesting design with a design they had observed previously during the evolutionary process, i.e., finding a path from the current design to one that incorporates features of the previously generated design. Setting an objective makes the task quantifiable but it does not simplify the task. The user must change the correct codons before they are mapped to obtain the desired output. This is a non-trivial task given the complex mapping processes in GE. The experiment described in the next section examines if the user can direct search to match a target using such an approach.

4.1 Experimental design

The grammar used in this experiment is a shape generating grammar that outputs bridges using the higher order function techniques as described in Sect. 3.2 The interface used in this experiment is shown in Fig. 3. There is a target bridge on the right hand side and nine bridges to select from on the left hand side. When the user selects a bridge 8 mutated variations are generated and their choice is saved in a green box in the top left frame, so that they may generate more mutations from it. The user can keep selecting bridges until they think they have matched the target or have

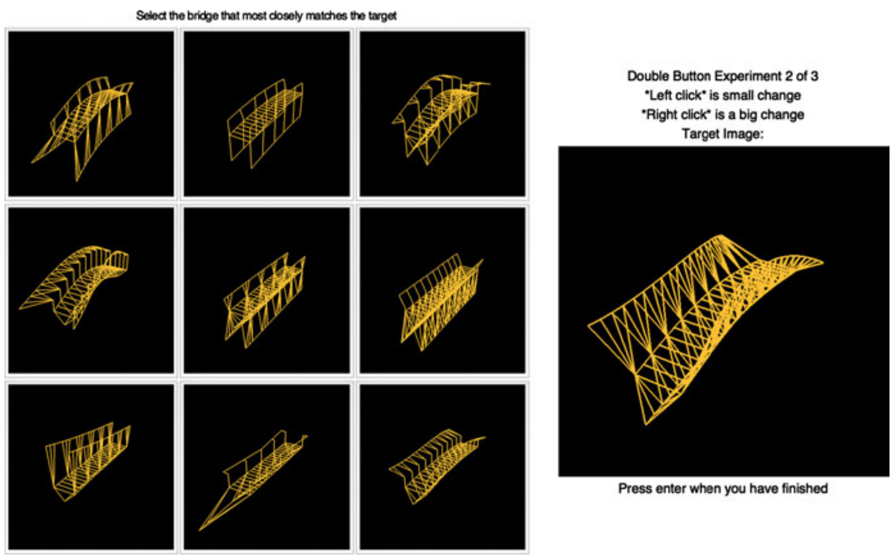

Select the bridge that most closely matches the target
Double Button Experiment 2 of 3
Left click is small change
Right click is a big change
Target Image:
Press enter when you have finished

Fig. 3 A screen-shot of the interactive GUI. The target is on the *right* and the results from the previous mutation choice are in the 9 frames on the *left*

reached the 5-minute time limit. A Euclidean distance measure, was used to calculate the distance of the user generated results from the target. The graph distance provided an objective measure to calculate how close the user got to the target. A more detailed description of the graph distance is given in Sect. 4.2 Twenty four volunteers participated in this experiment and the experiment itself was approved by the Ethics Committee in UCD (Reference number: LS-E-11-05-Byrne-ONeill).

There is no crossover used in this experiment. All variants are created exclusively by mutation events. The mutation operators select a codon from within the coding region of the genome and increment it by one. As a codon is only used when choosing the production of a rule, incrementing it by one means that it will always encode for a new production, thus ensuring a genomic change in the individual. It also means that the Hamming distance between mutation events is exactly one.

To avoid confusion it was decided to simplify the allowed user input. The user is limited to either the left mouse button (LMB) exclusively, or both the left and right mouse button (RMB). When the input is exclusively LMB, standard integer mutation is applied. When the user has a choice of both buttons, the LMB corresponds to a nodal mutation and the RMB corresponds to a structural mutation. The intention of this decision is to examine if more fine grained control can have an effect on how the users traverse the search space. The targets the user was required to match are shown in Fig. 4. They were created by generating a random genotype which was then mapped using the same bridge grammar that the static interface was based upon. Randomly generating the targets removes any human bias from the target selection process.

The user was allowed two trial runs to familiarise themselves with the static interface and the different effects of the mutation operators. Finally, after completion of the trial the user was asked to complete six experiments. The first

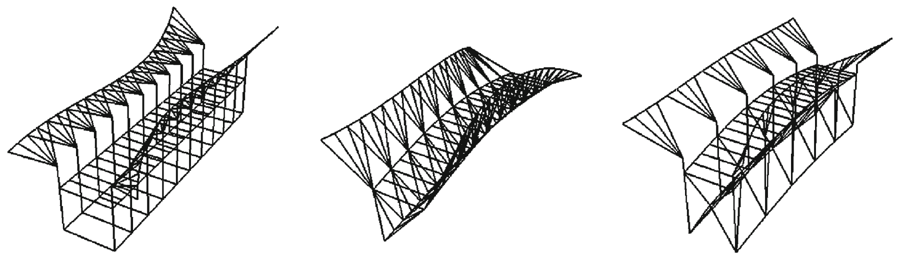

(a) Target 1. **(b)** Target 2. **(c)** Target 3.

Fig. 4 The targets that the users had to match

three of the experiments used integer mutation to match three targets and the next three experiments used nodal and structural mutation to match the same three targets. A fixed random seed was used for each experiment so that all participants would be presented with the same initial designs. The user had a time limit of 5 min to complete each task. The time of each selection and the individual selected were recorded. Once the user had completed the experiment they were asked to fill out a short survey that asked them which features they used to compare similarity.

The user was presented with every selection they had made upon completion of the experiment and was asked to select the design that most closely matched the target. In order to see if the improvement over time was due to the choices of users, a sample of random mutation events was generated for comparison. The random sample was created by allowing a Mersenne twister random number generator make selections using the same static interface that participants had used.

Given a sample of randomly generated mutation events μ_0, and the results of user application of mutation operators, μ_1 and μ_2, where μ_1 allowed the user to apply integer mutation and where μ_2 allowed the user to apply nodal and structural mutation, the following hypothesis is stated.

H_0: There will be no statistically significant difference between the random sample and either operator, $\mu_0 = \mu_1 = \mu_2$

H_1: There is a statistically significant difference in performance for a particular operator,$\mu_0 \neq \mu_1 || \mu_0 \neq \mu_2 || \mu_1 \neq \mu_2$

α: The significance level of the Wilcoxon rank-sum is 0.05.

4.2 Euclidean graph distance

The output of the evolutionary design software generated graph representations of designs. The graphs consisted of nodes and edges in a three dimensional space. Euclidean graph distance uses a Euclidean distance measure to compare the nodes of the output designs. Euclidean distance is defined as the straight-line distance between two nodes on the same plane. The distance, *d*, is given by the formula:

$$d((x_1, y_1, z_1), (x_2, y_2, z_2)) = \sqrt{(x_1 - x_2)^2 + (y_1 - y_2)^2 + (z_1 - z_2)^2}.$$

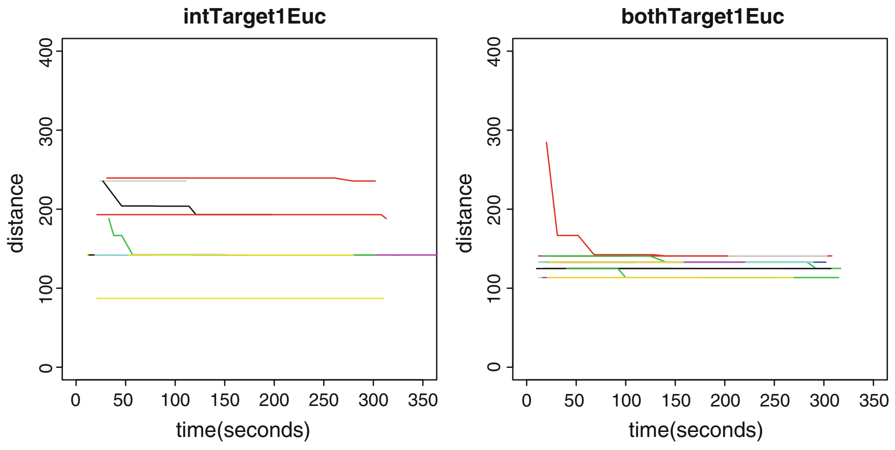
The graph with the most nodes is selected for iteration. The distance is then calculated by iterating though each node in the larger graph and comparing it with the the nearest node in the smaller graph. The distance between these nodes is then added to the total distance between designs. The euclidean graph distance fulfils the metric axiom of non-negativity, $d(a, b) \geq 0$.

The output graphs consist of nodes and the edges between them but the Euclidean distance formula only compares nodes in space. The edges between nodes must be taken into consideration so that $d(a, b) = 0$ if and only if $a = b$. Exhaustively checking how the nodes were connected proved to be computationally expensive. Instead, while computing the distance between node pairs, the number of outgoing edges for each pair is also compared. Any difference in the number of outgoing edges is added to the total fitness. As the fitness is being minimised this results in a worse fitness.

Two graphs, *a* and *b*, are considered identical if the distance for every node in graph *a* and its nearest respective node in graph *b* is zero and the number of edges for each node pair is identical. While Euclidean graph distance does not fulfill all of the axioms required by a metric this does not prevent it from being a useful measure in practice [18, 32]. The next section describes how the metric is used to evaluate the performance of the participants when using an interface to match a given target. The next section describes the first interface experiment carried out in this work.

4.3 Results

The results for the distance metrics are shown in Fig. 5. The Figures show the time taken by the user (in seconds) on the x-axis and the distance from the target on the



(a) Integer mutation. **(b)** Nodal / structural mutation.

Fig. 5 The best fitness Euclidean distance for target 1, the *x axis* is the time taken and the *y axis* is the distance from the target. There is no significant improvement in distance during the course of the run

y-axis. The smaller the value on the y-axis, the more closely the result matched the target. The graphs show the best result obtained from the users. As shown in the graphs, there is little or no improvement over time. This result was further confirmed by comparing the user input against the sample of random selections. A Wilcoxon rank-sum was performed and no significant difference was found between the user data and the randomly generated data. This result supports the null hypothesis. Only the results for the first target image are shown as the other target graphs show similar results.

These results appear to support the null hypothesis, that the user is unable to direct search using interactive operators and selection. This is a highly contentious conclusion to draw as many years of interactive evolutionary computation studies have generated results that reach the opposite conclusion [19, 30, 48]. If this is not the case then there are two possible causes for the results.

4.3.1 Choice of metrics

How a human evaluates the similarity of two designs is a subjective measurement. The survey showed that users often based how similar they found bridges on individual features or parts of the design, such as the handrail or the curve of the walkway. While no metric is perfect and human selection is subjective, Euclidean graph distance should have recorded some improvement over time.

4.3.2 Methodology

The experiment was constructed to present the evolved population to the user and to facilitate precise logging of input. Pilot studies were completed to ensure the static interface was usable and that certain concerns were addressed such as saving previous designs and allowing a single design to be repeatedly mutated. While these aspects of the static interface are important they are essentially technical concerns. What is not addressed is how to best facilitate the user's exploration of the search space.

A user made 17 selections on average during the 5 min they had to match a target. Although mutations could occur on the same codon, the user could theoretically move a maximum Hamming distance of 17 from their original selection. An average of 48 codons were used to encode a design so a Hamming distance of 17 could allow for significant change to the individual. The lack of progress during search arose from the fact that each selection presented the user with 8 more images. As the participant is presented with only 136 designs (on average) during the course of a run, the result is that they only observe a small part of the search space. To assume that a significant improvement could be made in this short distance was optimistic.

The target bridges were created by randomly generating genotypes and using these to select individuals from the search space. Little thought was given to how "far" the target individuals were from the starting node. Nor was it known if the targets were reachable from the starting node. The approach taken in this experiment was intended to reduce human bias but it may have inadvertently made the task too difficult for the user.

The user did not know what change to expect between a nodal and a structural mutation, which meant that the users intention of “big” and “small” changes may not be evident in the generated individuals. What constitutes a small or a large change depends on the user’s personal preference. The nodal mutation events presented a unique problem to the user as the resulting mutations looked identical to the user. Some nodal changes fell below the threshold of a Just Noticeable Difference (JND). JND is a concept from cognitive psychology first described by Ernst Heinrich Weber [50]. JND is the smallest difference between two stimuli that is still capable of being perceived. The lack of what the user perceived as new variations also hindered them in completing the task.

The grammar also complicated what was already a difficult task. Several participants complained of identical bridges being generated. Although most of these cases were a result of the JND described above, distance comparisons performed afterwards showed that some individuals were identical. Despite every mutation incrementing a used codon, sometimes the grammar generated anonymous functions that required codons for components that were not expressed in the output. An example of this would be codon values being used to define a curve and only half the curve being used in the final bridge design. Neutral mutations were removed in the following experiment by applying the euclidean graph distance formula to the mutated individuals. If the distance is zero then the mutated individual is removed from the population.

Due to the reasons discussed above a new approach was developed for allowing user interaction with the evolutionary algorithm. The new animated interface is discussed in the next section.

5 An animated search interface for interactive evolutionary architectural design

It became clear from the experiment in Sect. 4 that allowing the user to apply the mutation operators is not enough, the user has to be able to interact with the algorithm in a meaningful way and be able to process a much greater area of the search space. After analysing the results and user feedback gathered from the previous experiment, the interface was re-implemented in an attempt to allow the user to explore the search space more effectively. Whether the metrics adequately reflect similarity and locality is also examined. The problems and their respective solutions are shown in Table 1. The underlying principle of mutation driven search remains the same but instead of the user choosing an operator, all possible mutations of Hamming distance one were applied to an individual. Each codon was mutated in turn, the result was rendered and then the codon was restored to its original value. The productions for each codon generated a collection of nodal and structural mutation events to choose from. This process is shown in Fig. 6. By making no assumption about operator choice and instead presenting the user with every

Table 1 Problems addressed by the new interface

Problem	Solution
Magnitude of change unknown	Show all changes in advance
Limited user evaluations	Local search is animated for quicker evaluation
No measure of target difficulty	Each target increases in Hamming distance
No alternative paths allowed	"undo" button added
Difference below JND	Mutations animated to highlight changes
Identical Individuals	Removed by comparing Euclidean graph distance

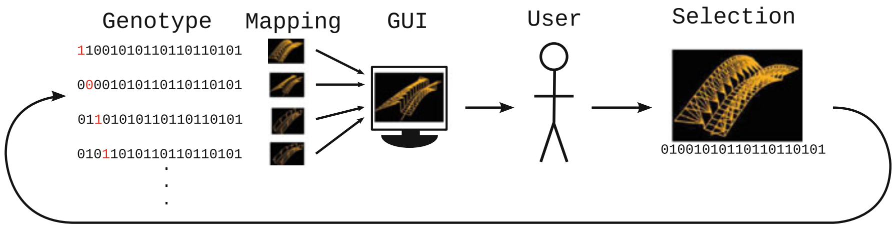
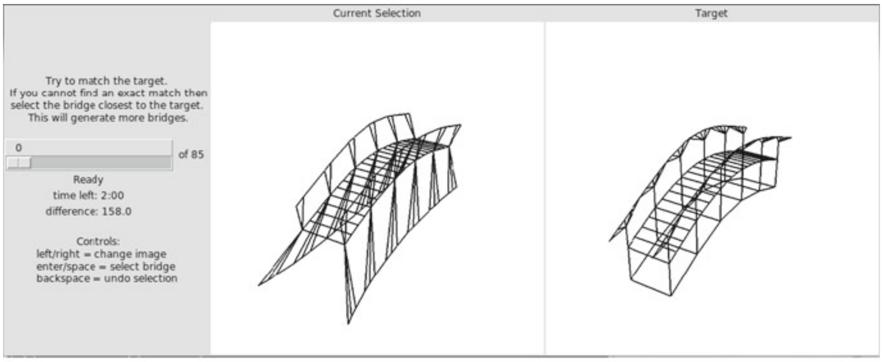


Fig. 6 Generating Hamming distance 1 individuals for user selection. The value of each codon is altered and the result is saved. The codon is then restored to the original value before moving on to the next codon

available option, it is now possible to examine how they navigate the search space based on their selections.

Presenting an entire population of mutation events to the user simultaneously is not feasible. The animated interface instead uses a single window for exploring the population. The interface is shown in Fig. 7. The current user selection is on the left and the target is the image on the right. The leftmost panel states the instructions, user controls, time remaining and the distance from the target (stated as the difference). The user scans through the mutation events using the left and right arrow keys and the selects the mutation change they want and that now becomes the basis for generating the next population. By presenting the phenotypic effects of a mutation change to the genome the user is not required to understand the relationship between the codons and their mapping to the phenotype. The interface displays the consequences of different mutation events and the user then selects the change that most closely matches their preference.

The user viewed the individuals by moving the slider or holding down the left and right arrow keys. The refresh rate for the window is ten frames per second. As the frame rate is at a level where the frames can be perceived individually, the user is capable of perceiving the bridges distinctly. A greater frame rate could result in the user skipping over bridges due to persistence of vision. Codon changes were made sequentially so a codon's productions are grouped in their presentation to the user. Overlaying groups of changes in the same window allowed the user to pick up smaller JND changes by viewing them in rapid succession.



Current Selection

Target

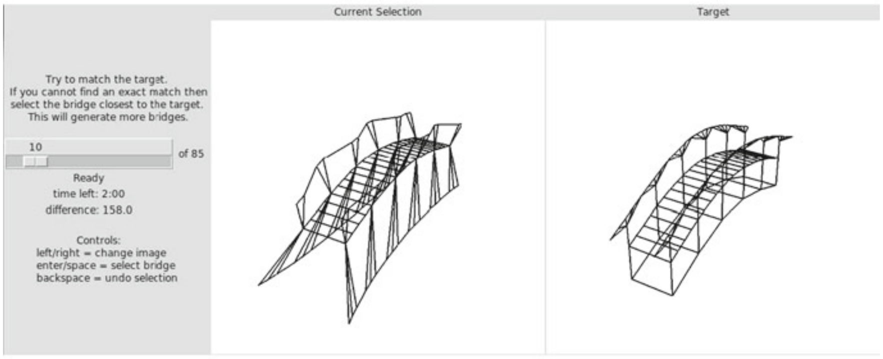
Try to match the target.
If you cannot find an exact match then
select the bridge closest to the target.
This will generate more bridges.

0 of 85

Ready
time left: 2:00
difference: 158.0

Controls:
left/right = change image
enter/space = select bridge
backspace = undo selection

(a) The target is on the right and the starting individual is in the middle frame.



Current Selection

Target

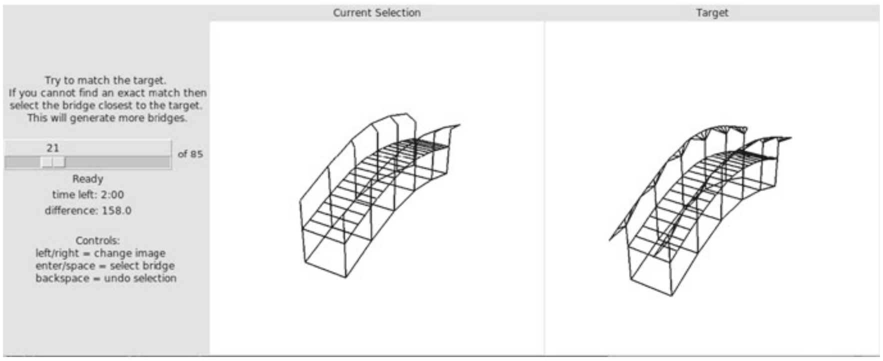
Try to match the target.
If you cannot find an exact match then
select the bridge closest to the target.
This will generate more bridges.

10 of 85

Ready
time left: 2:00
difference: 158.0

Controls:
left/right = change image
enter/space = select bridge
backspace = undo selection

(b) A nodal mutation of the starting individual. The handrail is altered slightly by the mutation event.



Current Selection

Target

Try to match the target.
If you cannot find an exact match then
select the bridge closest to the target.
This will generate more bridges.

21 of 85

Ready
time left: 2:00
difference: 158.0

Controls:
left/right = change image
enter/space = select bridge
backspace = undo selection

(c) A structural mutation of the starting individual. The supporting struts and the handrail design are altered by a single mutation event.

Fig. 7 New animated interface. The target is on the right and the current individual is in the middle frame. The user instructions and a slider that shows the current position in the population is on the left

5.1 Experimental setup

The subjective nature of aesthetics makes evolutionary design search a difficult area to quantify. To generate measurable results a target design is specified and the user must then attempt to match it. The experiment asked the user to match ten different targets. The random seed was fixed so that the animated interface always started from the same individual. The targets were mutated variants of the starting individual and they increased in difficulty as the Hamming distance was greater for each successive target.

The targets are shown in the order they were presented to the user in Fig. 8. The Hamming distance, the number of nodal and structural mutations and the Euclidean graph distance from the starting graph for each target is shown in Table 2. In an effort to generate a range of target difficulties, each target had a Hamming distance greater than or equal to the target that preceded it. Although this is not an absolute measure of difficulty it does mean that more input is required from the user to obtain a perfect match.

Each participant had 2 min in which to try to match the target. The experiment was set on a timer to end as soon as 2 min had been reached. This meant that all experiments could be compared equally. They were free to make as many selections within this time frame and they could undo selections if they wished. At the end of target exercise the user was asked a short survey asking them which features they used to compare similarity. Twenty five volunteers participated in this experiment and the experiment itself was approved by the Ethics Committee in UCD (reference number: LS-E-11-129-Byrne-ONeill).

A sample of random trials were generated to examine if the users were capable of using the animated interface to match the target. The same interface was used except selections were chosen randomly by a Mersenne twister random number generator. Twenty five random samples were generated for each of the targets. The distribution of the random selections for each target matched the user's click average and standard deviation, as shown in Table 2.

Given the distance results of a sample of randomly selected individuals from a given target, μ_0, and the distance results of the user selected individuals from a given target, μ_1, the following hypothesis is stated:

H_0 There will be no statistically significant difference between the random sample and the user generated results, $\mu_0 = \mu_1$

H_1 There is a statistically significant difference in distance from the target for the user generated results, $\mu_0 \neq \mu_1$

α The significance level of the Wilcoxon rank-sum is 0.05.

5.2 Results

The number of user selections (user clicks) and the number of images presented to the user (user evaluations) are shown in Table 2. In the previous experiment, the users selected 17 individuals and evaluated 136 designs on average in a five minute time period, the equivalent of 27 evaluations per minute. The user click and user

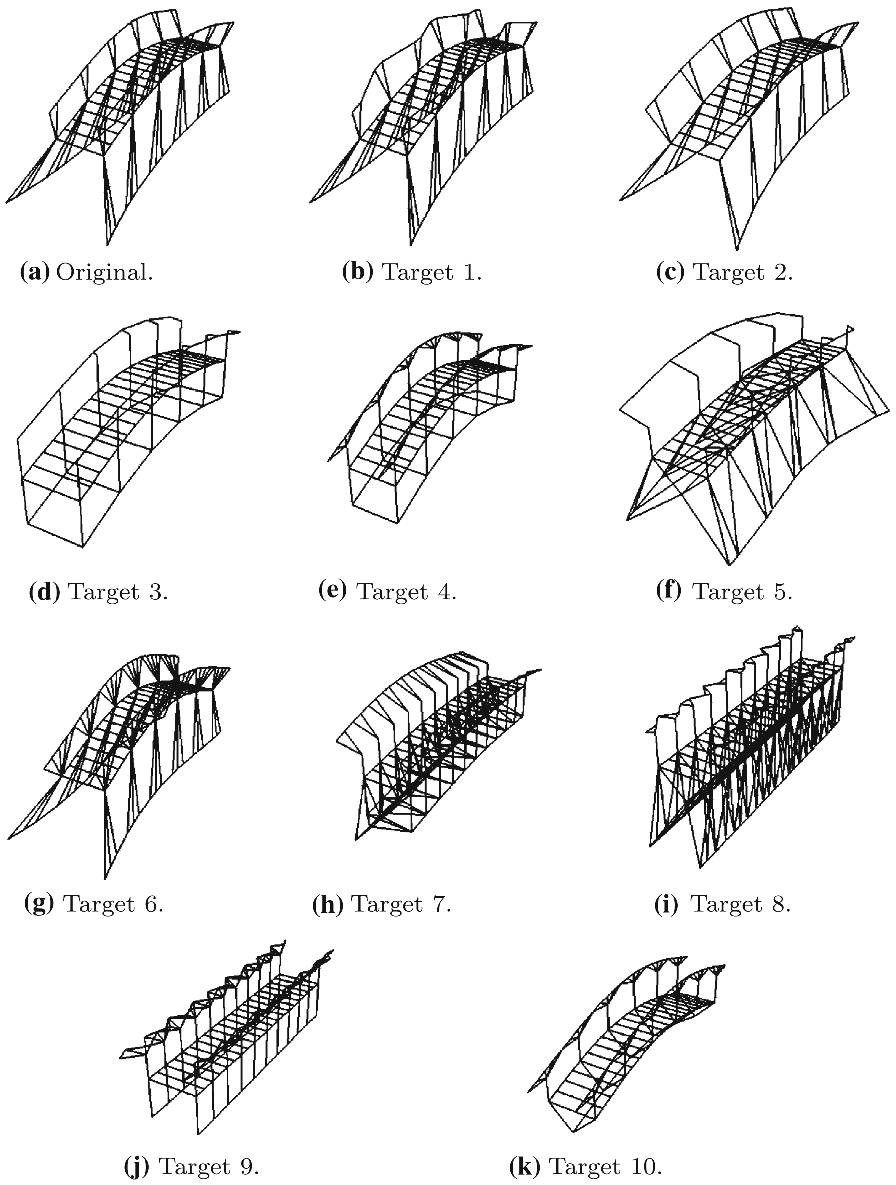


Fig. 8 The targets that the user had to match, the original individual that the user started with is in the *top left corner*

evaluation results show that the user made fewer selections with the new animated interface than in the previous experiment but they evaluated many more designs within a two minute time period. The highest number of evaluations was for target 5 where the user was presented on average with 325 images for evaluation, the equivalent 162 evaluations per minute.

Table 2 The distance and change types for each target

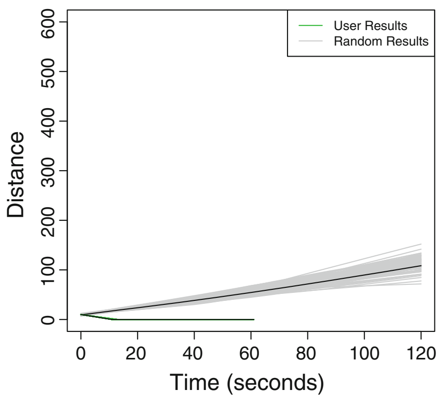
Target	Nodal: structural	Hamming: Euclidean	User clicks	User evaluations	User matched (%)	Random matched (%)
Target 1	1:0	1:10	1.0 ± 0.0	22.4 ± 34.9	100	4.0
Target 2	2:1	3:92	3.8 ± 2.1	190.3 ± 80.6	64.6	11.8
Target 3	2:2	3:184	2.7 ± 1.3	202.4 ± 61.6	64.9	12.1
Target 4	4:1	5:158	4.1 ± 2.2	245.2 ± 126.4	74.1	20.3
Target 5	5:1	6:214	3.3 ± 1.1	325.6 ± 130.2	36.6	31.8
Target 6	7:0	7:188	3.5 ± 1.3	196.0 ± 61.4	58.9	31.3
Target 7	6:2	8:465	3.5 ± 1.2	262.3 ± 83.2	57.6	15.9
Target 8	7:1	8:457	4.0 ± 1.9	364.7 ± 131.0	37.5	27.0
Target 9	7:2	9:273	4.8 ± 2.0	306.4 ± 86.1	28.2	36.4
Target 10	7:4	11:117	4.9 ± 2.0	282.4 ± 103.7	29.7	42.5

The percentage of user mutations (User Matched) and random sampling mutations (Random Matched) that matched the target codon changes are also shown in Table 2. With some exceptions, the percentage of matched codon mutations decreases as the Hamming distance increases. The opposite is true for random sampling: as more codons are changed there is an increased likelihood that a random mutation would match that of the target.

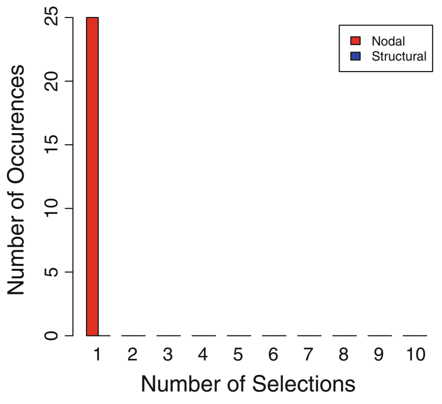
A Wilcoxon rank-sum test compared the final selections for the user and the random sampling. There was a statistically significant difference from the random sample with exceptions of target 5 and target 10. The result rejects the null hypothesis for 8 of the 10 targets. In these cases the results show a distinct improvement over time for the user generated results while the random samples either show no reduction of distance from the target or an increase in distance from the target. The results show that users could successfully use the animated interface to direct search.

Scatter plots were generated to examine if there was an improvement over time regarding Euclidean graph distance from the target. Each user selection generated a data point that recorded the time, distance from the target and the mutation type. A locally weighted scatter plot smoothing (LOESS) was performed on the results to plot a smooth curve of the average values. The set of data points was then bootstrapped [16]. The graphs on the left of Figs. 9, 10, 11, 12, 13, 14, 15, 16, 17, 18 compares the user distribution (green) with the random sampling (grey).

The type of mutation used for each selection was recorded with intention of examining if mutation operators of different locality were used at different points during the target matching process. The user was not informed of whether they were making a nodal or structural mutation. They made their selection based on the output of the mutation event. Bar charts showing the number of nodal mutations (red) compared to the number of structural mutation (blue) are shown in the graphs on the right of Figs. 9, 10, 11, 12, 13, 14, 15, 16, 17, 18. The X-axis is the number of selections made while the y-axis shows cumulative frequency for a particular type of mutation.

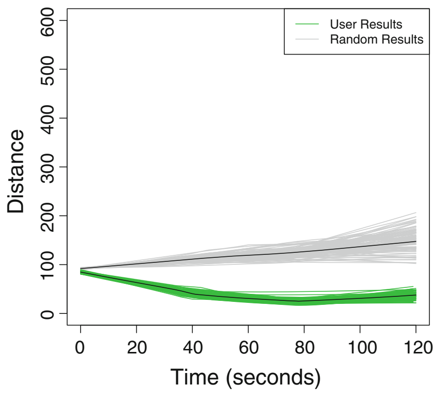


(a) LOESS and bootstrapping results.

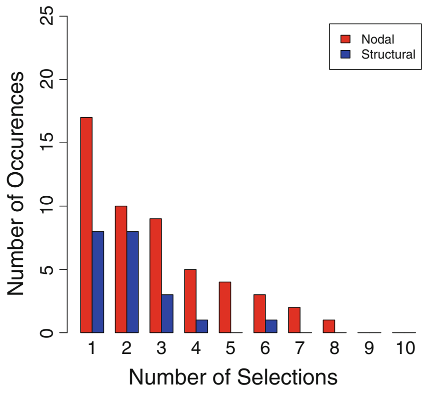


(b) Structural / nodal selections.

Fig. 9 Target 1 was used to introduce the user to the animated interface. As the target was a Hamming distance of one from the original, every participant successfully matched the target with one selection. The result shows that if a desired individual is in the immediate proximity of the current individual, the user is capable of finding it



(a) LOESS and bootstrapping results.

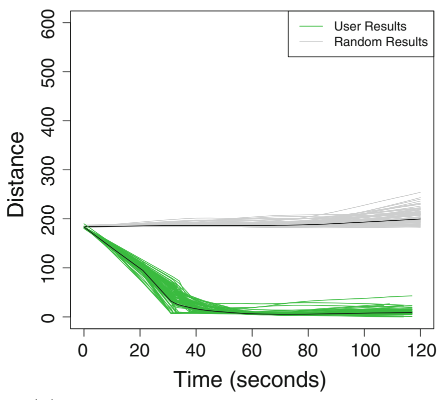


(b) Structural / nodal selections.

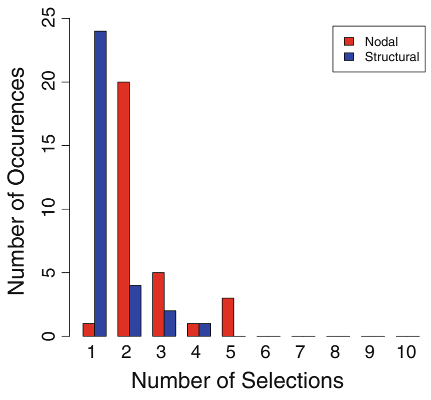
Fig. 10 Target 2 consisted of two nodal mutations and one structural mutation and was one of the three instances where there was more nodal selections initially than structural selections. This meant the users chose a high locality mutation event instead of a low locality event. As the Euclidean distance from the original caused by the mutation events was only 92, meaning that none of the mutation events had a greatly changed the individual

5.3 Discussion

The results discussed in Sect. 5.2 show that the users were able to direct search towards a target using the new animated interface, with the exception of target 5 and target 10. In the case of target 5, the users matched few of the mutated codons and so followed a different mutation path that ended up in a local optima. In the case of



(a) LOESS and bootstrapping results.

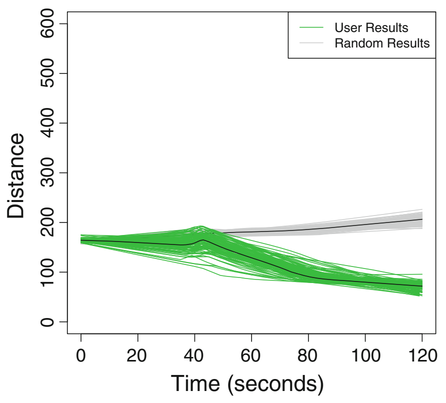


(b) Structural / nodal selections.

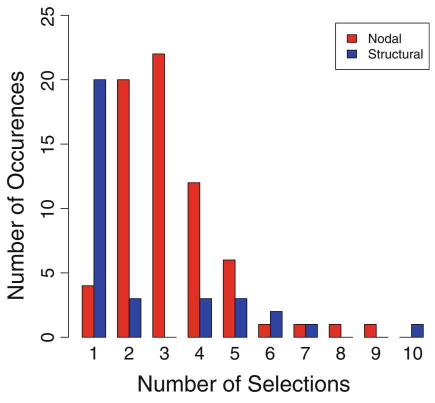
Fig. 11 Target 3 consisted of two nodal and two structural mutations. The participants overwhelmingly chose a structural mutation initially and then refined their selection with higher locality nodal mutations. This is shown in the LOESS results as a steep decrease in the distance followed by a plateau where there was little additional improvement

target 10, a large percentage of the expressed codons were mutated and so it presented too difficult a challenge to match all the changes within the allotted time.

This evidence supports the hypothesis that the user could use such an animated interface to mutate a design to incorporate features that they had previously seen in other designs generated by the evolutionary algorithm. The results obtained regarding the participants use of nodal and structural mutation show that users

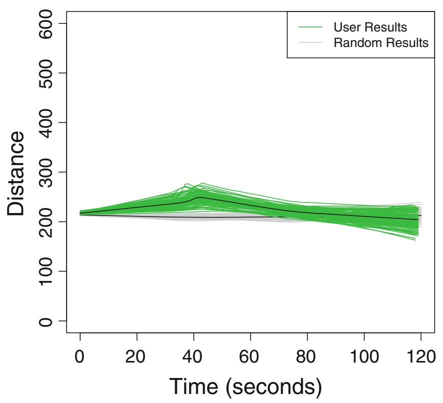


(a) LOESS and bootstrapping results.

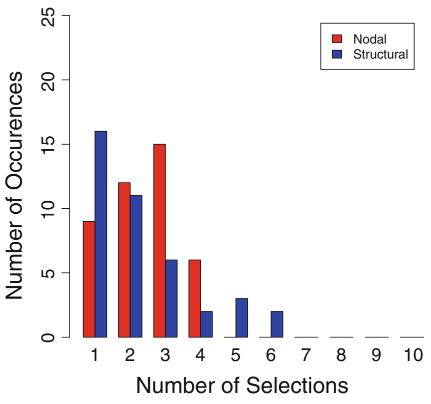


(b) Structural / nodal selections.

Fig. 12 Target 4 consists of four nodal mutations and one structural mutation. Participants overwhelmingly started with structural mutation and then applied nodal mutations. Despite the user's preference for a low locality event for their first selection, the fitness initially got worse according to the Euclidean distance. Additional selections made by the participants increased the fitness and there was significant improvement in distance by the end of the task



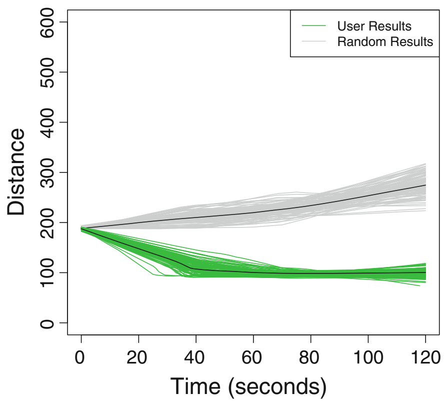
(a) LOESS and bootstrapping results.



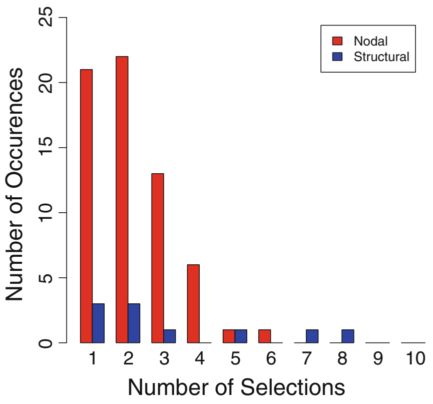
(b) Structural / nodal selections.

Fig. 13 Target 5 consists of five nodal mutations and one structural mutation. Although more structural mutations were applied in initially, the proportion of nodal and structural mutations remains consistent. The participants mutated the same codons used to create the target only 36 % of the time, resulting in a poor score. There is no improvement made by the participants for this experiment and their results are indistinguishable from random selection

started by predominantly applying a structural mutation and then moving to nodal mutation. The result means that the participants commenced their search by making large phenotypic changes and then fine tuning that solution with high locality mutation events. There were three exceptions to this including target 6 which consisted of nodal mutations exclusively.

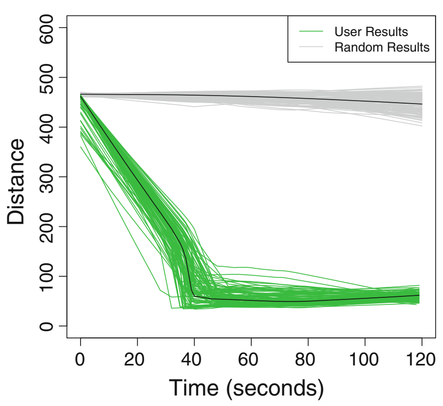


(a) LOESS and bootstrapping results.

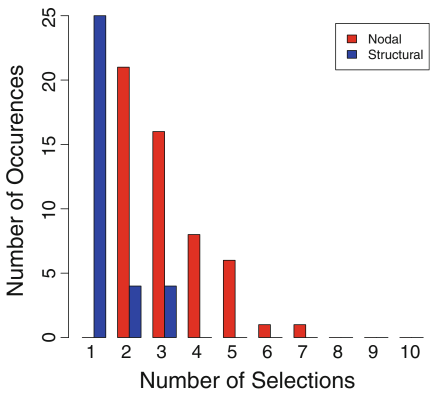


(b) Structural / nodal selections.

Fig. 14 Target 6 consists of seven nodal mutations and no structural mutations. This is the second of the three instances where there were more nodal mutations made initially than structural mutations. As all the changes that generated the target were nodal changes and 58.9 % of the user selections matched the mutated codons, it shows that the users were capable of following an evolutionary path similar to the one that created the target



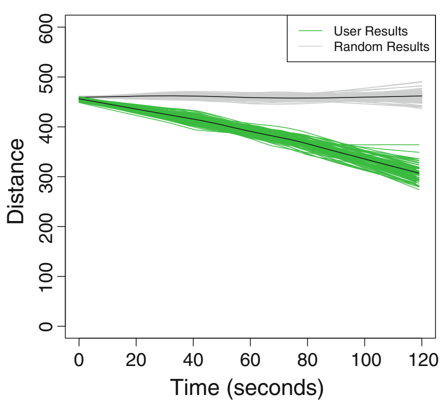
(a) LOESS and bootstrapping results.



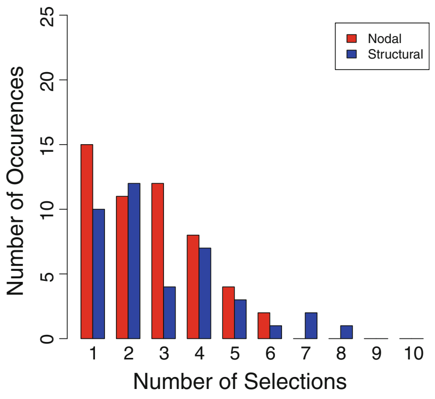
(b) Structural / nodal selections.

Fig. 15 Target 7 consists of six nodal mutations and two structural mutations. There is a large drop off in distance initially as users all selected the same structural codon for mutation. The low locality that results from changing the structural codon is evident in the Euclidean distance. Once the distance had been reduced the users used nodal mutations of higher locality vary the design, resulting in smaller fitness changes

A surprising result is that there was a definite improvement in Euclidean graph distance for targets 8 and 9 while the overall percentage of codons matched were low (37.5 and 28.2 % respectively). The result shows that it is possible to get close to matching a target without following the exact same mutation path. What this also means is that the user is following a different genotypic path to arrive at the same phenotypic output.

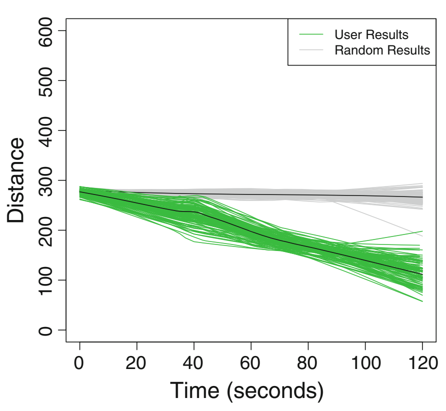


(a) LOESS and bootstrapping results.

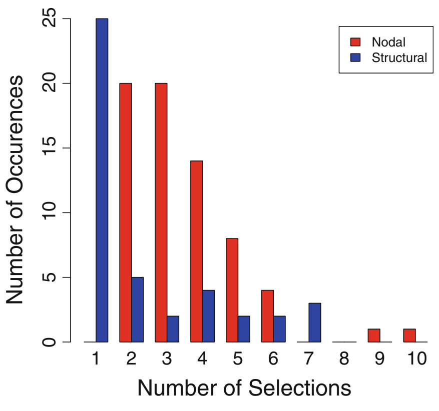


(b) Structural / nodal selections.

Fig. 16 Target 8 consists of seven nodal mutations and one structural mutation. It is the third instance where there were more nodal mutations initially than structural mutations. Overall there was a lower percentage of matched codons. This means that the users were not mutating the same codons that changed to generate the target but there was still a significant decrease in distance. The result suggests the users could match the phenotypic output but by following a different genotypic path

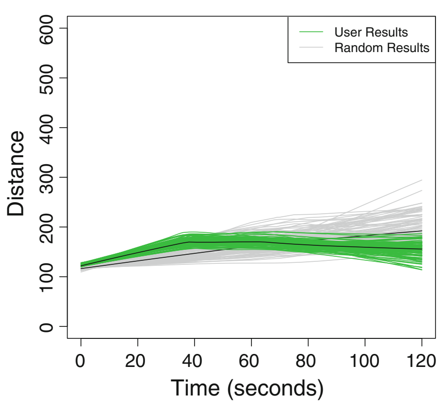


(a) LOESS and bootstrapping results.

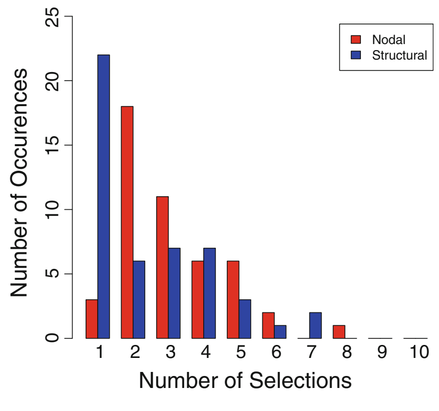


(b) Structural / nodal selections.

Fig. 17 Target 9 consists of seven nodal mutations and two structural mutations. The users all applied an initial structural mutation but it does not have the same level of improvement as seen in Fig. 15. Overall the users matched less codons than the randomly generated sample (28 and 36 % respectively). Despite this there still was still a significant reduction in distance. The variance of the results is much larger than on the other targets, indicating that several participants were unable to match the target. The results for the eighth and ninth targets support the hypothesis that different genotypic paths could lead to the same phenotypic output



(a) LOESS and bootstrapping results.



(b) Structural / nodal selections

Fig. 18 Target 10 consists of seven nodal mutations and four structural mutations. This was the largest Hamming distance and over one third of the expressed codons were mutated. As the user only made four selections on average it is unlikely the user would be able to match the target. There was no statistically significant difference between the user results and the randomly generated sample

6 Conclusion

In this work a novel animated interface was presented. The initial static experiments failed to show that the user was capable of directing search. A second animated interface was developed that allowed the user to perform a local search on a specific individual. The experiments showed that the user was able to use the animated interface to match a target by directly manipulating the genotypic representation. This result supports the hypothesis that the user is able to perform a directed local search toward a desired individual. Examining the user generated results showed that they moved from low locality operators to high locality operators to both explore and exploit the search space. As the user changes are made to the genotypic representation, the new individual can be reintroduced into the population and evolutionary algorithm can continue iterating. The intention of this work was to combine the interface with existing evolutionary design tools to explore the additional benefits of combining AUI with evaluation for evolutionary architectural design.

7 Future work

The objective nature of the target matching experiments constrained the participant while they interacted with the new interface. It is our intention to allow a more unrestricted usage of the interface in future experiments. The more qualitative aspects of the interface would be examined, such as the benefit the user thinks the interface provides, as well as how much they found it aided their search. The application of the animated interface in conjunction with evaluation may provide speed up convergence and should be investigated further. The interface combined with evaluation could be used for a real world design challenge with a control group using subjective selection exclusively. This would allow for the investigation of the benefit provided by the interface.

This approach was developed to handle the mapping process in GE but it should be applicable to any form of GP. We intend to make the animated interface as a stand-alone application so that it may be applied to different GP methodologies. The Euclidean graph distance is still at a early stage and future work will involve developing it into a full metric. We also plan on carrying out a study comparing similarity as measured by humans and the Euclidean graph distance.

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