

# **GROWTH AND DEVELOPMENT OF INHOMOGENEOUS STRUCTURES**

**Or Yogev and Erik K. Antonsson, Ph.D., P.E.**  
California Institute of Technology, Pasadena, CA 91125 USA

## **ABSTRACT**

This paper presents a new approach for the design synthesis of continuous inhomogeneous structures with an goal of mimicking the growth of biological structures in nature. The results presented here provide interesting insights into the concept of structural growth in biology, and motivate the combination of evolutionary techniques in future research, such that might provide the ability to explore a wide range of design configurations. In order to model biological growth an artificial model has been created composed of an external environment and a collection of cells. The environment represents the engineering requirements (loads and boundary conditions), while the cells represent small elements of volume of the structure. Each cell contains an artificial DNA sequence which serves as a set of rules that execute during the growth procedure. These rules form a recipe for the structure and are relatively simple. During the growth procedure, cells will be deformed, adhere to other cells, divide, and differentiate. The differentiating rule may cause a cell to change its mechanical properties ( $\sigma_y$ ,  $\nu$ ,  $E$ ), and by doing so introduce inhomogeneous properties in the structure. The rules form an alphabetic sequence and therefore are well-suited to be used in an evolutionary algorithm, where rules governing the growth and development of individuals are evolved instead of the more traditional evolution of parameters describing the complete individuals.

*Keywords: genetic algorithm, indirect encoding, evolution, development, growth, stresses, inhomogeneous structures, finite elements, artificial cells*

## **1 INTRODUCTION**

Inhomogeneous structures are widely found in nature. The most obvious examples are animal bones and plant stems. Both are highly inhomogeneous structures that are capable of supporting large loads. Bones are composed of two different types of materials: cortical bone which has nearly zero porosity and forms the long tubular shafts, and trabecular bone which resembles a sponge or closed-cell foam and fills the interior of the ends of long bones. The complexity of the bone structure makes it difficult to be replicated by engineering techniques.

The properties of these biological structures are derived from three attributes: the inhomogeneity of the structure, the shape of the structure, and the growth process. Animal bones and plant stems, like any other biological structure, grow through a process of cell division and adhesion until a complete structure is created. The environment plays an important role in affecting growth and development. Stresses on bone cells, for instance, affect osteocytes which are one type of bone cell that has mechanosensory receptors that can sense stresses and regulate bone growth and development. During growth, cells may differentiate according to various conditions, producing cells with different mechanical properties, resulting in an inhomogeneous structure.

Utilizing these ideas from biology and natural evolution, an evolutionary design synthesis environment has been created where artificial cells that sense stresses and other signals in the environment, grow and develop into adult individuals. Each cell has genetic information that encodes rules which are executed in response to this environment. Each artificial cell is based on a hexahedral three-dimensional linear finite element or "brick". The rules that control growth and development are encoded (generally)

as *if condition - then action* statements. The conditional part of each rule senses a signal or the environment (*e.g.*, stress or gravity or a concentration gradient). The action part of each rule causes changes to the cell, such as growth or deformation or division or differentiation. When cells differentiate, their mechanical properties change, including yield stress  $\sigma_y$ , Poisson's ratio  $\nu$ , and Young's modulus  $E$ . Cell differentiation introduces inhomogeneous properties in the structure.

During the growth and development procedure a three-dimensional finite element mesh is generated where each cell is one element in the mesh. The geometry and material properties of the structure are determined only from the rules, and the growth and development in response to the rules. With appropriate rules, structures can be created such that all the loads will be supported, and the maximum stress on each cell will be below the yield stress of its material.

## 2 PRIOR RELATED RESEARCH

Garcia and Gonzalez [1] present a way of evolving shapes of continuous structures while maintaining a fixed mesh grid. They show that the objective functions can be improved by 19% during evolution. Nadir, *et al.*, [2] show a way of optimizing structural truss topology by taking into account loading conditions and manufacturing costs. In both papers, the optimized results closely resemble the initial structure, which indicates that a local optimum has been found using the optimization scheme. Anathasuresh and Kota [3] demonstrate a way of synthesizing compliant two-dimensional MEMS devices by eliminating cells according to the evaluation of three parameters. The use of fixed-shape rectangular cells restricts the synthesis approach such that the final configuration must be re-sketched in order to become a valid engineering structure. These three papers present direct encoding approaches, where the structure (phenotype) is fully described by the genetic information (genotype). This approach limits the range of possible new design configurations that can be synthesized.

The approaches outlined above, using direct encoding and a pre-determined cell shape, lead to a limited exploration of new design configurations. Nature on the other hand utilizes a significantly different approach for developing new designs with high performance properties. Biological structures are grown in accordance with a set of rules encoded in a DNA sequence. Over many years this DNA sequence has been evolved in a way that the new configurations display improved performance. The approach presented here mimics the idea of *rules* in order to synthesize new structures. By the creation of an artificial environment, and artificial cells which contain a sequence of rules for growth and development, the execution of a relatively simple genome can give rise to complex, inhomogeneous three-dimensional structures. The environment has a crucial influence on cells.

Vander Sloten and Van Cleynenbreugel [4] showed that mechanical stresses have significant influence on the growth of bone cells. Other forms of environment can be temperature, chemical concentration *etc.*, where a protein is able to sense the environment and execute rules causing cells to grow and develop into a final configuration.

Recently a new technique called micro-molding has been used to create three dimensionally multi-layered micro-structures [5], which begins to provide the capability to mimic inhomogeneous materials developed by natural growth procedures. Unlike injection molding where the mold defines the boundary of the structure this method gives the ability to create structures which don't have a well defined boundary but rather adhere drops of material until a complete structure is created. This procedure is very similar to the growth of a biological structure, which begins from a single cell and as time evolved the complete shape of the structure is generated.

## 3 ARTIFICIAL CELLS

The artificial cell introduced here, represents an extended three-dimensional linear hexahedral finite element containing 8 nodes and 8 linear shape functions (producing 6 planar faces). By applying external loads on its nodes, stresses and displacements inside the cell can be calculated using a standard finite element scheme. In addition to its finite element properties, each cell can sense three types of quantities (Table 1). Although no diffusion processes are modeled in the cell, these three quantities are recog-

Table 1: Cell signals

ID	Description
<i>a</i>	Maximum principal stress normalized with the yield stress
<i>b</i>	Middle principal stress normalized with the yield stress
<i>c</i>	Minimum principal stress normalized with the yield stress
<i>d</i>	Principal vector correspond to the maximum principal stress
<i>e</i>	Principal vector correspond to the middle principal stress
<i>f</i>	Principal vector correspond to the minimum principal stress
<i>g</i>	Cell volume
<i>h</i>	Morphogen direction
<i>i</i>	Morphogen radiation intensity

nized by each cell, to mimic the ability of biological cells to sense distances, stresses, gravity, *etc.* The first quantity refers to the point inside the cell with the maximum principal stress. The stress tensor at this point will have three principal stresses which span from the maximum stress to the minimum stress. These three stresses are normalized by the yield stress of the material  $\sigma_y$ , and are identified in the genome with the letters *a*, *b*, *c*. In addition there are three principal directions which correspond to the directions of the three principal stresses, and are identified in the genome with the letters *d*, *e*, *f*.

The second quantity sensed by each cell is the level of a morphogen. In biology, a morphogen is a signaling chemical which governs the pattern of tissue development and the positions of the various specialized cell types within a tissue. A morphogen diffuses from a localized source and forms a concentration gradient across a developing tissue. Morphogens play a significant role in the growth and development of organisms.

In the model presented here there are two kinds of morphogens, one is a morphogen corresponding to a point load in space that is to be supported; the other is a morphogen corresponding to the ground. The ground is modeled as a volume where cells can be attached. Once a cell has penetrated the ground its nodes are clamped and it becomes a supporting cell for the structure. Cells are free to divide below (or inside of) the ground such that roots can be produced. Each morphogen radiates through space following an exponentially decaying function. This radiation diffuses through the cell's walls such that each cell can sense the local strength of the morphogen (normalized to a reference value), and the direction to its source. These two quantities are identified in the genome with the letters *h* and *i* respectively.

### 3.1 Execution of the rules

Each cell contains a genome which serves as an artificial genetic code common to all cells within the structure. This code is executed during the growth and development procedure. The code is composed of words (rules) and each word is composed of genes. During the growth procedure the rules encoded in the genetic code are executed, and a structure composed of hexahedral cells is created. The connectivity relations between these cells and their corresponding nodes is fully defined such that a complete finite element mesh of the structure is created.

### 3.2 Control mechanisms

In order to maintain a valid mesh during the growth procedure, two shape optimization tools are used. One relates to the condition number of the nodes [6] and the other tests and reshapes tangled cells [7]. After each time step, each cell is tested by both these tools. The condition number is determined for internal nodes, and a conjugate gradient method is used to relocate the node such that the condition number is minimized while its adjacent nodes are fixed. The second tool tests for tangled cells and untangles them.

Table 2: Geometrical operation genes

ID	Name	$N^1$	Possible Parameters
A	Shear	1	$(d, e, f, h) \times$ fractional coefficient
B	Anisotropic growth	3	$(a, b, c, g, i) \times$ fractional coefficient
C	Isotropic growth	1	$(a, b, c, g, i) \times$ fractional coefficient

$^1N$  =Number of Parameters

Table 3: Cell-type operation genes

ID	Name	$N^1$	Possible Parameters
D	Cell division	1	$(d, e, f, i)$
K	Cell death	0	
F	Cell differentiation	1	$(1, 2..^1n)$

$^1N$  =Number of Parameters

$^1n$  =Number of different cells

## 4 GENES

Rules (or words) are composed of genes. All genes are identified with capital letters. There are three kinds of genes. The first kind are conditional genes (Table 4). These genes can place restrictions on other gene activity within a word and are related quantitatively to one of the signaling quantities. Currently there are two kinds of conditional (or veto) genes identified in the genome with the letters *W* and *V*. The first one suppresses the execution of a word if one of the signaling quantities in a cell is below a reference value. The second one suppresses the execution of a word if one of the signaling quantities in a cell is above a reference value.

The second and the third kind of genes are operation or transformation genes (Tables 2 and 3). The nature of the genes was chosen such that basic transformations of cells observed in nature can be implemented.

### 4.1 Geometrical operations

The first type of operations are geometrical, and there are three basic types of geometrical operation genes, illustrated in Figure 1. These operations occur on small regions that subdivide a structure during its growth procedure [8].

The first gene represents isotropic growth and is identified in the genome with the letter *C* (Table 2). This gene has two parameters: the first is a coefficient that represents a fractional part of the second parameter which can be one of the three signaling quantities. The product of the first parameter with the level of the signaling quantity identified by the second parameter defines the ratio of the new cell volume and the current volume.

The second operation gene is anisotropic growth and is identified in the genome with the letter *B*. This gene has six parameters divided into three groups; each group contain two parameters. The first parameter, as before, is a fractional part of the value of the second parameter, where the second parameter

Table 4: Veto (conditional) genes

ID	Name	$N^1$	Possible Parameters
V	Suppress if below	1	$(a, b, c, g, i) \times$ fractional coefficient
W	Suppress if above	1	$(a, b, c, g, i) \times$ fractional coefficient

$^1N$  =Number of Parameters

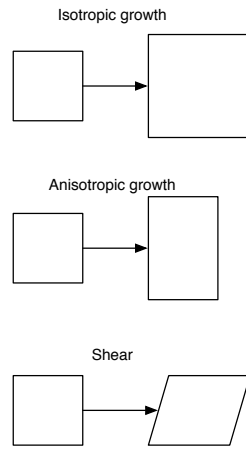


Figure 1: Geometrical operations

is one of the three signaling quantities. The product of each pair of parameters specifies the amount the cell should grow in each of the  $x$ ,  $y$ , and  $z$  directions, in that order.

The last geometrical operation gene corresponds to a shearing operation and is identified in the genome with the letter  $A$ . A cell can shear itself by an amount such that the deformed cell will shear toward a specified vector. This gene has six parameters divided into three groups; each group contains two parameters. The first parameter is a fractional coefficient indicating the amount cell shearing in the  $x$  direction toward the second parameter which is the  $x$  component of the vector representing the desired amount of shear. The pairs of parameters for  $y$  and  $z$  are defined in the same manner.

Each of the geometrical operations is implemented in the local coordinate system of the cell using the inverse iso-parametric mapping. The cell shape in the reference coordinate system is a perfect cube centered at the origin. By applying displacements in all three directions, and using the notion of deformation gradient, all three basic geometrical operations can be implemented.

## 4.2 Cell-type operations

The second type of operation relates to cell-type. Genes with this type of functionality are common in almost all biological cells, and play a significant role in growth of complex organisms. The model developed here has three types of cell-type operations. The first is cell division and is identified in the genome with the letter  $D$ . The cell division operation simply divides a cell into two cells in a direction dictated by the genome, while the total volume of the two daughter cells remains the same as the original cell. This operation is not instantaneous but rather occurs continuously, where at each time step a small portion of the new cell is grown and a new volumetric equilibrium is achieved.

The second cell-type operation is cell death and is identified in the genome with the letter  $K$ . The cell death operation kills a cell, removes it from the structure and updates all the connectivity relations with its (former) adjacent nodes and cells.

The third cell type operation is cell differentiation and is identified in the genome with the letter  $F$ . When the conditional test(s) determine that a cell should differentiate, this rule will alter the material properties of the cell.

## 4.3 Cell adhesion

The final operation that is used in the model presented here, but not encoded in the genome, is cell adhesion. Under some conditions, cells will adhere to other cells. The condition for adhesion of two cells is a geometrical intersection between them. Cells will adhere to each other in a way that minimizes the strain energy that will be generated by the deformations required for two nearby faces to adhere.

All of the rules described above are listed in Tables 2, 3, and 4.

## 5 GENOME

The genome contains a number of words (or rules) separated by spaces. Each word comprises a number of genes that are executed by their order in the word. Each word begins with a priority gene. The priority gene begins with the letter *Z* followed by a number which represents the order (or priority) of execution of that word. The length of the word is unlimited. Generally words can be interpreted as an *if conditional then action* rule. The *if* part relates to signal(s) or the environment, and the *then* part is an operation. Since all of the signals are normalized with reference values, the operation will be executed if the signal is below or above a value. This value is composed of two parts. The first part represents a number within the range of 0 to 1. This range is divided into a fixed number of levels and the coefficient determines the reference level. The second parameter refers to the signal that is going to be compared (stress, volume or signaling quantity). For example, given the maximum principal stress on a cell, a cell operation might be executed if the normalized maximum principal stress on the cell is above a value equal to 0.5.

## 6 RESULTS

The model has been tested by establishing the following environment. Two signaling morphogens were placed in the environment. One represents the ground ( $20m \times 20m \times 5m$ ), and the other represents a load that was placed above the center of the ground with a force  $F = 15,000kN$  in the  $x$  direction (see Figure 2a). Two types of cells were used: one with the mechanical properties of steel ( $\sigma_y = 700MPa$ ), and the other with the properties of an alloy ( $\sigma_y = 140MPa$ ). The test genome code used here consisted of six words, and produces a single individual structure. The genome contained the following code:

*Z5C1h Z4A1i Z3V2aB5a5b5c Z2W1aB1a1b1c Z1W99gDidef Z1V1aW2aF2*

Each word begins with the letter *Z*. The order of execution of the genome starts from the first word on the left and proceeds to the last word on the right (from the highest *Z* value to the lowest).

The first word executes an isotropic growth (*C*) with an amount proportional to the level of the load morphogen. The second word executes a shearing operation which shears the cell toward the load morphogen in the amount of 10% at each time step. The third word starts with a veto gene (*V*) which suppresses all the other genes in the word if the maximum normalized stress is below 0.25, otherwise an isotropic growth with values proportional to the normalized principal stresses is executed. The fourth word also starts with a veto gene (*W*) that suppress the execution of the word if the maximum normalized principal stress is above 0.25, otherwise an isotropic shrink with values proportional to the normalized principal stresses is executed. The fifth word starts with a veto gene (*W*) that suppresses the word execution if the volume of the cell is less than twice the reference volume, otherwise cell division is executed in the direction of the face pointing closest to the load morphogen. The sixth word executes a rule that differentiates a cell (*i.e.*, changes it's material properties) if the maximum principal stress is in a certain range.

### 6.1 Images

In the images of the results, the color of each cell in the left image results represents the mechanical stresses on the cell. A green color represents low stress (well below the yield stress of the material) and red represents high stress (greater than the yield stress). A structure can support the load if all the cells are green.

The color of each cell in the right image represents the cell-type. There are two types of cells, one marked with gray color and the other one with brown.

When the growth and development begins, a structure is created from a single cell connected to ground, and grows only in response to the signaling morphogen from the load (see Figure 2a). The stresses in each cell are zero (green) since the structure hasn't reached the load. Once the structure reaches the load (see Figure 2b) stresses start to be distributed along the cells. Due to the nature of the simple four-word genome used here, cells grow inside the ground (Figure 2c), however, these cells are attached to ground, and therefore carry no load. The growing and developing procedure continues until

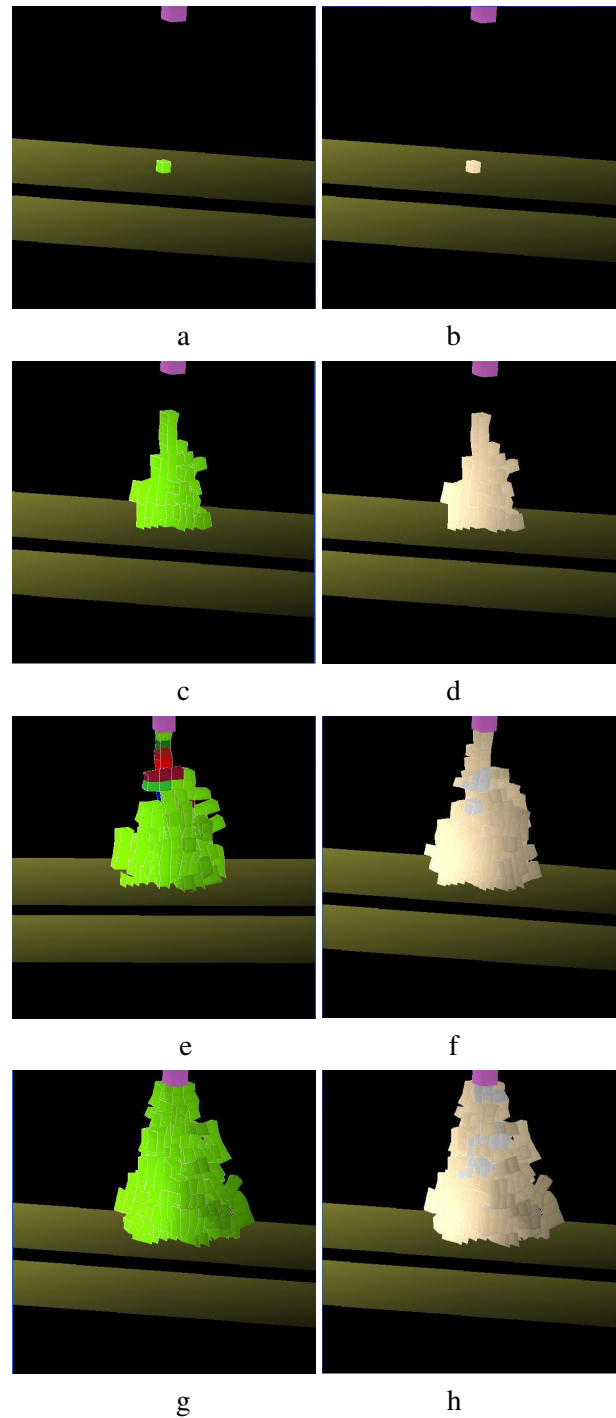


Figure 2: The growth and development of an inhomogeneous structure. The colors in the images on the left show the stress on the structure. Green is low stress. Red shows stresses greater than  $\sigma_y$ . The colors in the images on the right show the cell-type in the structure. Gray represents one cell-type and brown represents the other.

a,b) Initial state, two morphogens and a single cell ( $t = 0\text{sec}$ ).

c,d) Growth in response to the morphogens, zero stress ( $t = 10\text{sec}$ ), no cell differentiation.

e,f) Attachment of the structure to the load ( $t = 13\text{sec}$ ) stresses and cell differentiation appear.

g,h) Structure supporting the load, all stress below  $0.25\sigma_y$ , some regions have differentiated.

all cells are green (see Figure 2d - e). At this stage, the structure (individual) has reach maturity and the growth procedure stops.

## 7 CONCLUSION

A new method has been presented, utilizing a biological approach to growth and development of configurations of inhomogeneous structures. Recently, advanced manufacturing techniques have been developed that can integrate layers or small distinct volumes of dissimilar materials. The challenges of creating designs that can take advantage of these advanced materials require formal structured design synthesis techniques, such as the one presented here.

The illustrative example shown here uses a simple genome, which encodes six *rules* for growth and development, but it is able to grow and develop a structure that meets the engineering requirements (to support the load without exceeding the yield stress of the material). Due to the nature of the *rules*-based indirect encoding, small changes in the genome may result in significant changes in the resulting the individuals.

Similar mechanisms give rise to the wide range of biological structures observed in nature. Structural configurations synthesized in this way have many interesting properties, including symmetry, regularity, and in some cases modularity.

The next step in this research will be to use evolution algorithms to evolve genomes (rules), based on the engineering performance of the resulting structures. The advantages of this approach are that the information contained in the genome is small, but the range of different configurations that can be created is large, including multiple inhomogeneous materials integrated into a single functional structure. Additionally, a *rules*-based approach has the promise to be able to synthesize configurations that have regularity, symmetry and perhaps even modularity. The combination of evolutionary tools in the technique presented here has the promise to produce novel sets of design configurations which cannot be synthesized other design methods. Examination of the rules generated by such a design synthesis has the promise to provide insight into the nature of symmetric, regular and possibly modular designs.

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Contact: Prof. Erik K. Antonsson, Ph.D., P.E.  
California Institute of Technology  
Division of Engineering & Applied Science  
1200 East California Blvd.  
Pasadena, CA 91125-4400 U.S.A  
+1 626.583.4963 Fax  
<http://www.design.caltech.edu/>