DESIGN DEVELOPMENT BASED ON AN ANALOGY WITH DEVELOPMENTAL BIOLOGY

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Abstract. This paper introduces the commonality between diversity in the biological world and diversity in artifact design. It proposes a computational model of design development based on the analogy with the phenomena and principles of developmental biology. The model is feature based and is capable of varying design in logic, geometry, attribute and phase. Examples demonstrate this biological analogy and its benefits for design development.

1. Introduction

There are millions of species in the natural world. Moreover, within each species there exist subclasses. Even between individuals within a subclass, there are considerable variations. The natural biological world demonstrates its diversity. In order to be able to create diverse artifacts efficiently, it is useful to ask whether biological development may provide a possible source to inspire some ideas about the production of diversity during design development.

Design development is the aspect of a design process that places a greater emphasis on creating varied designs than on optimizing a parametric design. In this sense of producing variation, design development becomes a process to explore the potential diversity under a defined theme. Thus, design variation can be seen as one of the key issues in design development. Diversity of design variation is highly valued by modern designers and markets. Frequently it also contributes to the creativity of designs (Cross, 1994). A challenge facing designers is in a limited design cycle to develop diverse design alternatives. How it is possible to model a process capable of achieving such diversity?

Drawing an analogy with biology for novel design processes has proven to be a successful strategy for the development of novel processes. In this paper, we develop an analogy based on the processes and principles behind the production of diversity in the biological world.

Artifact design and the biology world are two remote areas, what is the commonality between them to draw an analogy. The commonality is with respect to the composition of parts and the whole object in both biology and design. A system of wholes and parts is a called complex system. According to the definition given by Simon *"*a complex system … is made up of a large number of parts that have many interactions. In such systems the whole is more

than the sum of the parts in the weak but important pragmatic sense that, given the properties of the parts and the laws of their interaction, it is not a trivial matter to infer the properties of the whole" (Simon, 1996). This becomes the common bridge between the two areas.

2. A Design-Oriented Model Based on Developmental Biology

We draw the following assumptions from concepts in developmental biology (Lewis, 1978; Jacob and Monod, 1961). In addition to the normal structural genes used in genetic algorithms (Mitchell, 1996) we introduce a variety of concepts and assumptions.

- A body consists of organs and sub organs; hierarchy is its structural characteristic.
- The expression of regulatory genes control structural genes.
- An organ is defined by its base point, attributes, and switch state.
- A bud point is the locus for a new organ in the current organ; the base point refers to the point from which the current organ starts, or reference point for the current organ.
- The switch state of an organ is determined by the overall switch states of its upstream organs or pathway.

We transfer the label body to design and organ to component. Based on the last four assumptions, the connection of two components in terms of geometry, logic and attribute are mathematically expressed as shown in the Appendix. Based on the first assumption and the expressions in the Appendix, the model expression for a design is established.

A design is treated as being composed of a number of components. If all those components are connected one by one according to the mathematical expressions of the connection of two components, the overall relations of the components in geometry, logic and attribute are expressed as three iteration equations, which describe the structure development process of a complex system.

3. Logic Hierarchy Iteration

As defined by equation (A.3) in the Appendix, each pathway represents an component's logical connection with all its upstream components. A group of pathways connecting all the components of a design is established as the following pathway iteration equation.

$$\begin{Bmatrix} L_1^{path} \\ L_2^{path} \\ \vdots \\ L_i^{path} \\ L_{i+1}^{path} \\ \vdots \end{Bmatrix} = [\lambda_L] \times [\kappa_L] \times \begin{bmatrix} l_{0,1} & \ddots & & \\ & & l_{(i-h),1} & \\ & & l_{(i-h),2} & \\ & & & \ddots \end{bmatrix} \times \begin{Bmatrix} 1 \\ L_1^{path} \\ \vdots \\ L_{i-h}^{path} \\ \vdots \end{Bmatrix} \quad (1)$$

h: *List number difference between two adjacent components.*

(i-h): *List number of an adjacent upstream component which is before and adjacent to component i.*

$L^{path}{}_i$: *Pathway is a logical connection from the top upstream component to the current component.*

$l_{i,j}$: *Bud point gene as one kind of regulatory gene controlling the jth bud point of component i.*

$[k_L]$: *Hierarchical logic parameter matrix partly represents component's initial structural order.*

$[\lambda_L]$: *Environment factor matrix influences the logic hierarchy, which is unit matrix at beginning, could be varied according to environment variation.*

This hierarchical pathway iteration equation describes the logic hierarchy for the growth of components. The iteration matrix connects all pathways together. The environment influences the initial complex system $[k_L]$ in two ways, which are the mutation of regulatory genes $\{l_{i,j}\}$and the bifurcation of environment factor $[\lambda_L]$. Through this function, the pathways for all components $\{L^{path}\}$ are able to be iterated sequentially. This is the logic expression for the hierarchical control of regulatory genes (Lewis, 1978; Nuesslein-Volhard and Wieschaus, 1980).

4. Geometry Hierarchy Iteration

The geometrical relation between two connected components is expressed as equation (A.2) in the Appendix. The hierarchical geometrical relations for all components of a design are expressed in the following geometry iteration equation:

$$\begin{Bmatrix} p_{1,0} \\ p_{2,0} \\ \vdots \\ p_{i,0} \\ p_{(i+1),0} \\ \vdots \end{Bmatrix} = [\lambda_L] \times [\kappa_L] \times \begin{Bmatrix} p_{0,0} \\ p_{1,0} + p_{1,1} \\ \vdots \\ p_{(i-h),0} + p_{(i-h),1} \\ p_{(i-h),0} + p_{(i-h),2} \\ \vdots \end{Bmatrix} \quad (2)$$

$p_{i,0}$: *Base point of component i in absolute coordinates.*

$p_{i,j}$: *Bud point j in arbitrary coordinates with reference to the base point of component i,.*

This hierarchical geometry iteration equation describes the geometrical hierarchy of components' variation, and connects the geometry of all components together. The environment influences the geometry interpretation $\{p_{i,0}\}$ of components also in two ways, which are the mutation of structural genes $\{p_{i,j}\}$ and the bifurcation of environment factor $[\lambda_L]$. This geometry iteration expression describes how the geometrical variation of the upstream component is responded to by its downstream components.

5. Attribute Hierarchy Iteration

Based on the attribute equation (A.4) of two components in the Appendix, the attribute of all components for a design could be expressed by the attribute iteration equation:

$$\begin{Bmatrix} A_1 \\ A_2 \\ \vdots \\ A_i \\ A_{i+1} \\ \vdots \end{Bmatrix} = [\lambda_L] \times [\kappa_L] \times \begin{bmatrix} \lambda_{U_{1,0}} \times \frac{a_1}{1} & \lambda_{U_{2,1}} \times \frac{a_2}{a_1} & \ddots & & \\ & & & \lambda_{U_{i,(i-h)}} \times \frac{a_i}{a_{i-h}} & \\ & & & \lambda_{U_{(i+1),(i-h)}} \times \frac{a_{i+1}}{a_{i-h}} & \\ & & & & \ddots \end{bmatrix} \times \begin{Bmatrix} 1 \\ A_1 \\ \vdots \\ A_{i-h} \\ \vdots \end{Bmatrix} \tag{3}$$

A_i: *Attribute after the interpretation of attribute structural genes.*

$\lambda_{Ui,(i-h)}$: *Attribute unity influence between component i and component (i-h).*

a_i: *Attribute structural genes after attribute constraint interpretation.*

This attribute iteration equation describes the attribute hierarchy of components, and links the attributes of all components together. The environment influences the attribute interpretation $\{A_i\}$ of components also in two ways, which are the mutation of structural genes $\{a_i\}$ and both the bifurcation of environment factor $[\lambda_L]$ and unity environment factor $\lambda_{Ui,(i-h)}$. This attribute iteration expression describes how the attribute variation of the upstream component affects its downstream components.

In addition to the structure order of components, the interpretation process from genotype to phenotype is also affected by the physical constraints of components, such as the distance and relative position among components.

$$f_L(\lambda_L(s) \times k_L, L) \tag{4}$$

$$f_P(\lambda_P(s) \times k_P, P) \tag{5}$$

$$f_A(\lambda_A(s) \times k_A, A) \tag{6}$$

f_L, f_P, f_A : *Constraints for the genes in logic, geometry and attribute.*
$\lambda_L(s), \lambda_P(s), \lambda_A(s)$: *Environmental influence factors for the phases in logic, geometry and attribute.*
k_L, k_P, k_A : *Initial phases of a complex system in logic, geometry and attribute.*
L, P, A : *Genes in logic, geometry and attribute.*

6. Design Application

We develop an example of a "NotIt" building design to show the potential of the analogy. There are two meanings for "NotIt" building design. One is that the design is not a real building design, but an abstract design to demonstrate a design method. Another meaning is that the design presents some aspects of artificial intelligence or artificial life. Although the outcomes are not necessarily different from the normal design, the important point is that the means to achieve it are like the development of living organs, whose development is a function of the organs before and after, and how they interact harmoniously.

This design model is a feature-based model, because in addition to the geometry information, it includes the information of attributes, logic and phase of components. Figure 1 shows the basic design as *Design A*. In this NotIt building design, the environmental influence upon genes { *L,P,A* } and environment phase variation { $\lambda_L, \lambda_P, \lambda_A$ } are illustrated in the remaining designs.

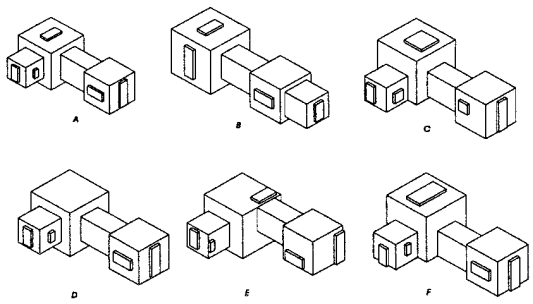

Figure 1. Diverse design variation

Design B is a drastic hierarchy variation of *Design A* produced by swapping the left wing room with the door of right wing room, which is manipulated by changing the phase bifurcation matrix λ_L.

Design C illustrates a gradual phase transition, in which the rooflight's shape of the lobby is changed from rectangle into square, the rooflight's size is an attribute gene, but its shape is determined by its phase (or the ratio of shape k_A)

and environment influence factor λ_A.

Design D shows the mutation of a regulatory gene related to the existence state of the rooflight of the lobby, as a result, it disappears. The mutation of regulatory gene *L* causes a macro design variation.

Design E shows the mutation of structural genes, in which the mutation of geometry structural genes for windows, doors, corridor and rooms is interpreted as the variation of their geometrical locations. The structural gene's mutations {*P, A*} are related to micro level gene drifting and result in a smaller design difference like color and micro position variation.

Design F shows a size and geometry variation. In this model, such variation implies micro evolution rather than macro evolution across design series, which is the mutation of structural genes in attribute and geometry (Gould, 1989). This mechanism is used to optimize design variables such as the size and relative location of components from initial to what is required as shown by *Design F* in Figure 1, in which the size of components and location are evolved to a desirable condition.

The following simulations of the NotIt building design demonstrate a number of biological characteristics that are valuable for the computer-aided design of diversity.

Diverse Speciation for Series Design: Speciation is the process of biological species formation, and depends upon two factors, which evidently affect the macro difference of a complex system These are phase variation and the mutation of regulatory genes. Figure 2 demonstrates the phase bifurcation of the NotIt building.

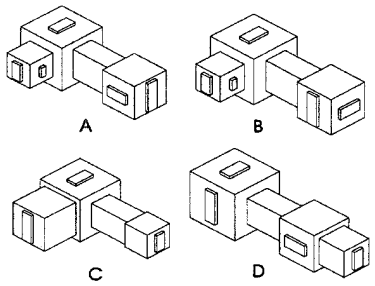

Figure 2. Phase bifurcation for series design

In this figure, compared with *Design A, Design B* has swapped the window with the door of the same room. *Design C* has swapped the left wing room with the right wing room. *Design D* has swapped the left wing room with the door of the right wing room.

Harmony, Relevancy and Independence for Design Consistency: Harmony, relevance and independence is demonstrated through the variation of one component in logic, attribute, or geometry resulting in its down stream components' corresponding variation. One issue in computer-aided design is the consistency of design variations, which means the arrangement and adjustment of one component in a design should automatically lead to the variation of its relevant components (Kalay, 1989, Peraza, 1990). Figure 3 demonstrates the issue of resultant design inconsistency, in which one room disappearing does not cause its sub windows and door to disappear, *Design A,* or the shrinkage of one room should have been responded to by its related rooms, sub-windows and sub-door, *Design B*.

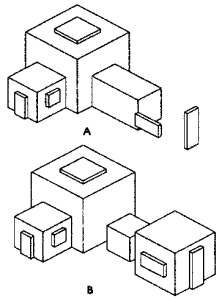

Figure 3. Examples of inconsistency in design

This model, derived from development biology, offers an intelligent and automatic mechanism for solving the problem of design consistency.

Logic harmony variation: The logic hierarchy for a complex design system defines how components are connected. The existence of the lower level components is a function of the upper level components. For instance, in Figure 4 the variation of regulatory genes results in the different existence outcomes.

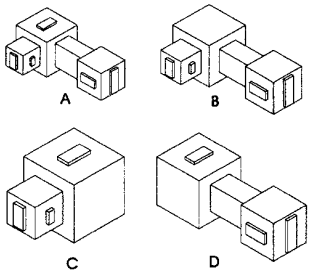

Figure 4. The effect of regulatory genes' mutation

Compared with *Design A, Design B* is a consequence of the mutation of the regulatory gene for the window of the lobby. *Design C* is a consequence of turning off the regulatory gene for the right wing room, its sub window and door disappear. *Design D* is a consequence of switching off the regulatory gene for the left wing room, its sub window and door disappear.

Attribute harmony variation: Attribute variation of one component results in the harmonious variation of the attributes of its lower level components. For instance, in Figure 5, compared with *Design A, Design B* has increased the size attribute factor of the right wing room. As a result, its sub door and window are correspondingly enlarged. *Design C* has increased the size attribute factor of the left wing room, as a result, its sub door and window are correspondingly enlarged. *Design D* has increased the size attribute factor of the corridor. Thus, its downstream room and sub door and window are correspondingly enlarged.

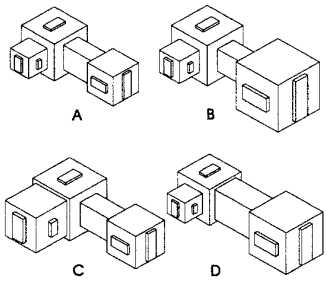

Figure 5. Scale attribute harmony variation

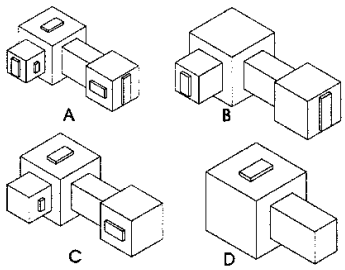

Figure 6. The effect of relevant gene mutation

Relevant variation: In addition to the hierarchical variation, in development biology, one gene mutation can result in a number of components' variations at different locations in different branches or pathways. The *Designs B, C* and *D* in Figure 6 demonstrate that the mutations of relevant genes cause the disappearance of windows, doors and rooms at different hierarchical branches.

For example, *Design B* is the result of the gene mutation that controls relevant components on different hierarchy branches, leading to the disappearance of the windows in the lobby and two other rooms. *Design C* is the result of a gene mutation that results in the loss of the windows in two rooms. *Design D* is a gene mutation that results in the loss of two rooms and their sub windows and doors.

Independent variation: There is another case, in which the independent attribute variation of one component does not cause the same attribute variation of other components, but other components harmonize the variation in other ways. This can be seen in *Design B* and *Design D* in Figure 7, where the independent size attribute variation of the corridor is followed by the harmonious geometrical variation rather than size attribute variation of other components. Another example is the independent size attribute variation of the lobby, followed by the harmonious geometrical variation rather than size attribute variation of other components, *Design C*.

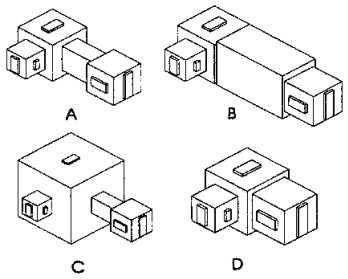

Figure 7. The effect of component scale attribute variation

7. Conclusion

Biology and design are two apparently remote areas. However, developmental biology is proving to be a useful analogical source for ideas about processes that produce diversity and consistency during design development in computer-aided architectural design. Computational models of processes drawn from developmental biology are proving to provide an integrative framework for a number of different requirements in designing for diversity. The ideas derived from developmental biology are an adjunct to the better known concepts used in genetic algorithms and genetic programming derived from neo-Darwinian evolution.

8. Acknowledgements

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APPENDIX

Developmental Biology Basis

Regulatory genes as master genes regulate other regulatory genes and structural genes, and structural genes are coded for protein synthesizing (Jacob et al, 1961). In other words, regulatory genes are control genes, and structural genes are responsible for the physical generation of cells. The value of regulatory genes is Boolean type, and the value of structural genes is real type. Therefore, the point and attributes of a cell are associated with structural genes. While its switch state relates to regulatory genes.

How to express the regulatory genes controlling structural genes? The way to connect regulatory genes with structural genes is to use Boolean variable to multiply real variable, such as, $\{l \times p\}$, or $\{l \times a\}$, in which l is a regulatory gene (or a Boolean switch), p and a are the position of a point and its attribute.

If $l = 0$, $\{l \times p\}$ *then the point p of a cell is closed, and its attribute is not opened either.*

If $l = 1$, $\{l \times p\}$ *then the point p of a cell in space exists, its attribute is active as well.*

If $l = 0$, $\{l \times a\}$ *then the attribute of a cell is closed, and its point is not active either.*

If $l = 1$, $\{l \times a\}$ *then the attribute of a cell exists, and its point is active as well; the*

Boolean switch l keeps a point and its attribute acting simultaneously.

A component is assumed to be a large number of cells with the same attribute, however, its position and existence are determined by its base cell.

Component

A component is defined by its base point, attribute and switch state as expressed in Equation A.1. Firstly, a component is composed by a great number of cells, but the base point of a base cell as a reference determines the positions of other cells. Secondly, the shape, size, and color of an component are classified as its attributes, which are contributed by a number of cells of the component. Thirdly, whether a component exists or not is determined not only by its own switch state, but also by the switch states of its upstream components, which means that if all the switch states of its upstream components are turned on, the component and its attributes exist.

$$O_i = L^{path}{}_i \times \{p_{i,0}, A_i\} = L^{path}{}_i \times \{p_{i,0}, \Sigma\, \alpha_i\} \qquad \text{(A.1)}$$

A_i : A*ttribute of component i.*

$L^{path}{}_i$ *Switch state of component i, which is determined by the switch state of its all upstream components.*

O_i : Component i of a design.

$p_{i,0}$: *Base point of component i.*

$\Sigma\, \alpha_i$: *Attribute of component i contributed by a large number of cells.*

In equation (A.1), a component is abstractly expressed by its base point and attribute, activated by its switch state, although an component is composed by a large number of cells, and created by cells division in reality. The advantage of this expression, is that only the most important base point of an component (the first growing point for new component) is emphasized, which enables this research to focus on the component level rather than cell level, to explore how regulatory genes and structural genes manipulate components.

Connection between Two Components

To know how two components are connected is important to understand the connection of a group of components for a design. To do that another assumption is made, which is that the bud points of a component are the first points for the new components to develop. The regulatory genes are the connection between the bud point of a component and the base points of its next components. The following three equations illustrate how the regulatory genes, base points, bud points and attributes of two adjacent components are connected and are affected.

Geometrical connection of components: A component's base point is connected by the base point of its adjacent upstream component and the arbitrary coordinate of the bud point between two components as expressed in equation (A.2), and also illustrated in Figure A.1.

$$p_{i,0} = p_{(i-h),0} + p_{(i-h),j} \qquad \text{(A.2)}$$

$p_{i,0}$: *Base point for component i in absolute coordinate.*

$p_{i,j}$: *Bud point j in arbitrary coordinate with reference to the base point of component i.*

(i-h): *Adjacent upstream component which is before and adjacent to component i.*

h: *Difference of list number between two adjacent components.*

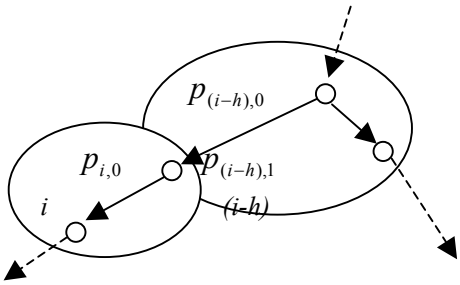

Figure A.1. The geometrical connection between two components

Equation (A.2) expresses the geometrical connection between two components indicating the base point of a component is able to be expressed by the base point of its adjacent upstream component and the bud point between the two base points.

Logical connection of components and pathway: A component exists because its switch state is turned on. This is determined by the switch state of its adjacent upstream component and the on and off state of the regulatory gene at the bud point of this adjacent component as expressed on the left-hand side of equation (A.3). The switch state of a component is also controlled by the regulatory genes of its all previous upstream components. This concept could be expressed by the pathway of a component, which is the logical connection from the top upstream component, through all its upstream components, to the current component. It is expressed by the logical "AND" operation of the regulatory genes of all upstream components at the relevant bud points as expressed on the right-hand side of equation (A.3).

$$L^{path}{}_i = L^{path}{}_{(i-h)} \times l_{(i-h),j} = l_{0,1} \times \ldots \times l_{(i-h),j} \tag{A.3}$$

$L^{path}{}_i$: *Pathway is a logic connection from the top upstream component to the current component.*

$l_{i,j}$: *Regulatory gene controls the jth bud point of component i.*

Attribute connection of components: The attribute variation of two adjacent components (upstream or downstream) is defined as.

$$A_i = \lambda_{u_{i,(i-h)}} \times \frac{a_i}{a_{(i-h)}} \times A_{(i-h)} = \lambda_{Ui,(i-h)} \times \ldots \times \lambda_{U2,1} \times \lambda_{U1,0} \times a_i \tag{A.4}$$

A_i: *Attribute of component i.*

a_i: *Attribute structural gene for component i.*

$\lambda_{Ui,(i-h)}$: *Attribute unity environment factor between component i and component (i-h).*

Equation (A.4) is the attribute connection between component i and its adjacent upstream component i-h. The attribute of component i is interpreted by its attribute structural gene, and is also affected by the attribute environment factors of all its upstream components.