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A FRAMEWORK OF THE GENETIC-ENGINEERING-BASED DESIGN THEORY AND METHODOLOGY FOR PRODUCT INNOVATION

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Abstract

Product innovation is by no means without a formal foundation. Products are always developed based on existing or similar products from low level to high level. The development process of products is very similar to the evolution process of living beings in nature. The genetic information of living beings is stored in the chromosomes contained in their cells and the evolution of living beings is based on variation of their chromosomes. Since the evolution of living beings is very slow, genetic engineering has been developed to reform consciously the chromosomes for living beings to accentuate good characters or to clone living beings according to their chromosomes. In a similar manner, the innovation of manufacturing products can also be implemented actively using similar reforming methods. This paper applies genetic-engineering techniques to develop a framework of such a design theory and methodology for product innovation. This design method is totally different from the conventional one and innovates products via artificial differentiation of products' chromosomes. It provides a logically structured process, which can reduce blindness to innovation and can even clone a product with the aid of advanced CAD/CAM technology.

Keywords: Genetic engineering, gene engineering, product innovation, design theory and methodology

1 Introduction

The fast growing global economy today demands that manufacturers must respond quickly and effectively to consumers' ever growing needs for better products at lower costs. As a result, companies around the world always find themselves seeking new and innovative products for survival. Traditionally, product innovation has proceeded by trial and error. With long-term efforts for searching innovation, some innovative methods have been developed, such as Brainstorming [1], Synectics [2], Checklist method [3], Morphological Analysis [4] and TRIZ [5,6]. Although these methods are more effective than the trial and error method, they do not always lead problem-solvers to innovative solutions since they do not provide a logically structured process with an appropriate knowledge base. Designers need an effective method to take them step by step, and rapidly, from clarifying the problem to creating an original, unexpected and creative solution or design.

In fact, product innovation is by no means without a formal foundation. Products are always developed based on existing or similar products from a lower level to a higher level. The development process of products is very similar to the evolution process of living beings in nature. The genetic information of living beings is stored in the chromosomes contained in their cells and the evolution of living beings is based on variation of their chromosomes. Since the evolution of living beings is very slow, genetic engineering [7,8] has been developed to reform consciously the chromosomes for living beings to accentuate good characteristics or to clone living beings according to their chromosomes. Genetic engineering is a set of techniques for isolating，modifying，multiplying and recombining genes from different organisms [8]. In a similar manner, manufacturing products also possess genetic information and their innovation can also be actively implemented using similar reforming methods even though such products have no physical chromosomes. This paper applies genetic-engineering techniques to develop a framework of such a design theory and methodology for product innovation. It is totally different from the conventional one and innovates products via artificial differentiation of products' chromosomes. It provides a logically structured process, which can reduce blindness to innovation and can even clone a product with the aid of advanced CAD/CAM technology.

2 Contents and data structure of products' virtual chromosomes

Since manufacturing products have no physical chromosomes, their virtual or analogous chromosomes need to be disclosed first so that genetic engineering techniques can be applied. Its contents must be determined according to its functions. Two functions are essential, i.e., the products should be able to be created or cloned according to their virtual chromosomes and secondly evolved by the differentiation of their virtual chromosomes. Therefore, the contents of a product's virtual chromosome include both genetic information and evolutionary information.

The former is needed to clone the product and includes all the information for reproducing the product, such as the lists of parts and units, the shapes, dimensions, materials，technical specification and manufacturing process of each part, and the topological relationships and assembly relationships among parts and units. It is much more than the information contained in the Bill of Materials (BOM). The BOM is used for production management and contains the information only about the hierarchical relationships among units, sub-assemblies, parts, blanks and raw materials, and lacks the information about the product's structure, manufacture, assembly, etc. A product cannot be cloned only according to its BOM.

The latter is all the information that is ever used as the genetic information in the chromosome of previous generations from the very beginning to present or grafted artificially from advanced products, and can make the product's chromosome possible to be differentiated for propagating offspring with performance that is different and may be better than its parents. For example, Steel is used for a part's material now; but Copper, Aluminum, and Plastics have been used for this kind of part in the past already. Thus, Steel is the genetic information. Copper, Aluminum, Plastics and the newly grafted materials, for instance, Titanium, whose properties are better than that of Steel, are the evolutionary information. To evolve or innovate a product, the virtual chromosome of the product should also contain all the evolutionary information from the very beginning, like the chromosomes of living beings in nature.

Since a product's chromosome contains so much information, its data structure is very complicated and can be in the form of multi dimensional networks as shown in Figure 1. Its characteristics can be summarized as: (1) its data structure is basically hierarchical, (2) its data structure is multi dimensional, and (3) there are inter-relationships among data or information. In Figure 1, the genetic information includes one piece of information in each node and the evolutionary information covers all the other pieces of information in each node. The product's chromosome contains so much information and is so complicated in data structure that it has to be stored and edited by database software. Some genetic and evolution information in a product's chromosome can be acquired from the design and manufacturing documentation of products, related design handbooks, technical standards, technical specifications, technical regulations, technical documents, or the designers' brains, while others have not been collected and sorted out, and need to be explored. As a result, the content and data structure of products' virtual chromosomes can be reverse deduced, based on careful analyses of the evolution course of products' design and manufacturing.

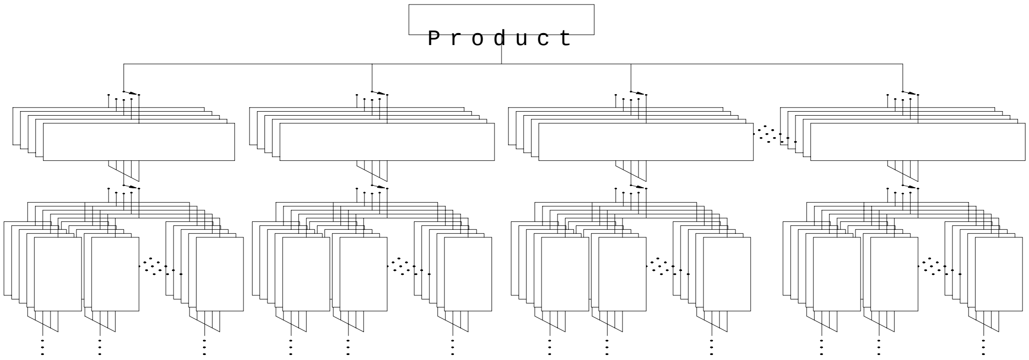
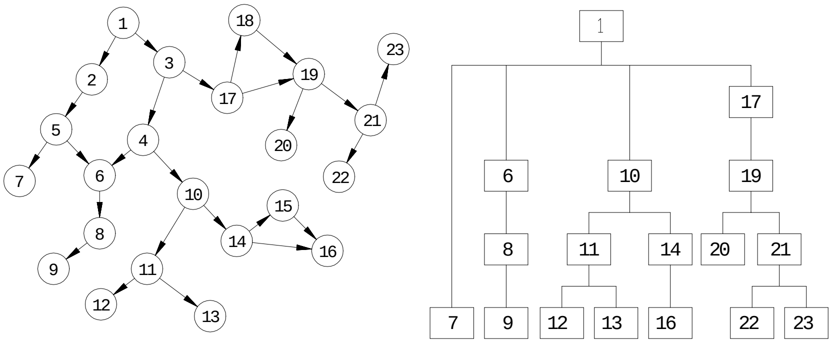


Figure 1. Schematic diagram of data structure of a product's virtual chromosome

3 Virtual genes and virtual genome maps

The chromosomes of living creatures contain many genes, and each gene either singly or in combination with others determine a particular characteristic of living creatures, such as eye color. A genome map is a map showing the relationships among genes and the locations of genes in the chromosome. Scientists have identified genome maps of human beings for reforming their chromosomes. In a similar manner, some evolutionary information in a product's virtual chromosome, which affects a certain aspect of a product's performances, are regarded as a virtual gene. For instance, the revolving accuracy of the spindle in a lathe is dependent on the type, structure, installation and maintenance of its bearing system, which can be regarded as a virtual gene. To improve a special aspect of a product's performances, the related virtual genes and their locations in the product's chromosome should be identified.

As mentioned previously, there is much evolutionary information in a product's chromosome. Some of the evolutionary information displays dependences on other information, which can be used to draw a Causality Network as shown in Figure 2(a). For instance, the genetic information in Node 12 will be changed if the genetic information in Node 11 is changed. The arrowhead between the two nodes is used to indicate that, for instance, Node 11 is a cause or parent node and Node 12 is an effect or child node. The method for identifying both the genes and the genome maps can be derived based on the network, and goes through: (1) searching cellular genes, (2) searching combined genes from cellular genes, (3) searching larger combined genes from the searched combined genes, (4) stopping searching when it reaches the node that has no parent node. Taking Figure 2(a) as an example, its genome map can be obtained using the method, as shown in Figure 2(b) where each rectangle is a gene or combined gene and the number in a rectangle is the number of its parent node.



a) b)

Figure 2. Causality network and virtual genome map

4 Mapping between virtual genes and performances of a product

The purpose of reconstructing a product's chromosome is to eliminate some defects of the product. The genes, which affect the defects of the product, have to be identified first and then the gene engineering can be applied to reconstruct the product's chromosome. Each rectangle in the genome maps is a gene that affects certain performance of a product. After the genes and the genome maps are identified, mapping networks between genes and performances of a product can then be produced based on the knowledge about the product's design and manufacture. Figure 3 shows a simple mapping network, where Performance 1, for example, is affected by both Gene 1 and Gene 3. The product performances in the mapping networks are determined by product designers and/or customers, and can be supplemented continuously.

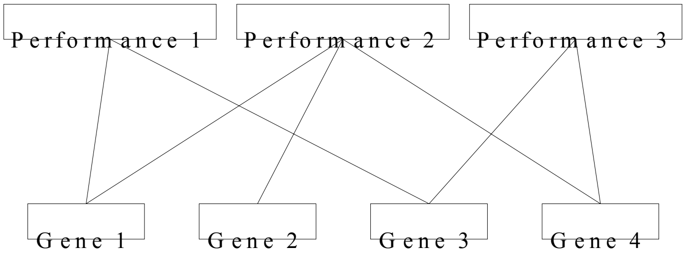


Figure 3. Mapping networks between genes and performances of a product

5 A framework of the genetic-engineering-based design theory and methodology for product innovation

A framework of the design theory and methodology for product innovation has been developed using genetic-engineering techniques. Its workflow and elements are shown in Figure 4 and illustrated as follows:

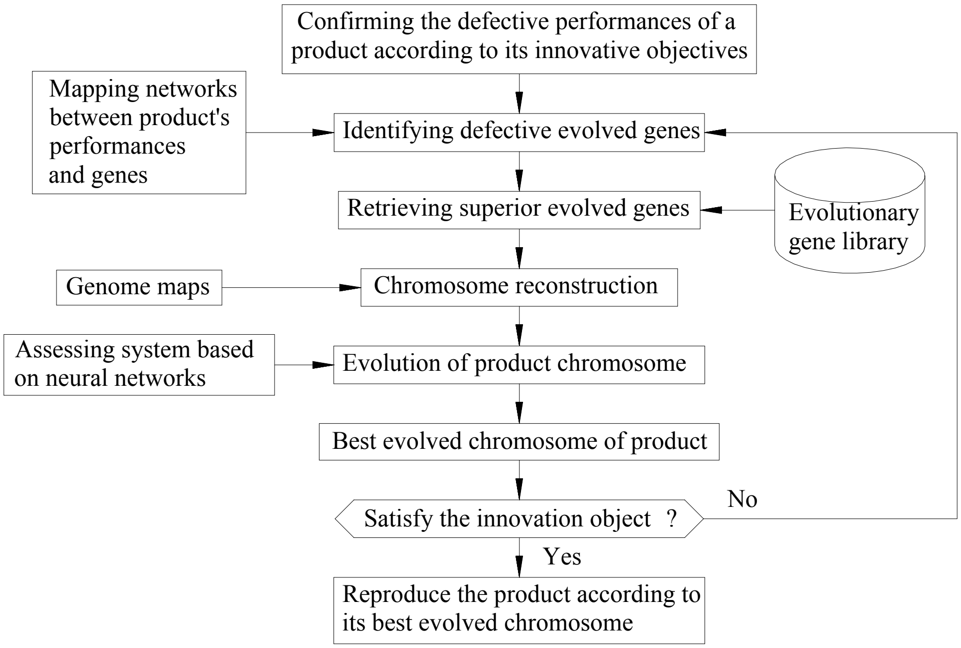


Figure 4. Workflow of the genetic-engineering-based design method

5.1 Confirming the defective performances of a product according to its innovative objectives

A defective performance of a product is defined as the performance that cannot satisfy the innovative objectives of the product. Before innovating products, it is necessary for designers to know the defective performances of the original product according to its innovative objectives, because problems or defective performances are not always clearly defined and all the relevant information is not always known by the designers. A problem defined well is already half solved. For innovation, there are many requirements and constraints that are coupled with each other. The approach for confirming them can go through (1) to collect all the necessary information using Innovative Situation Questionnaire (ISQ) [9], (2) to search a primary problem and break it down into many smaller problems, which are structured as contradictions, using Problem Formulation (PF) [9], and (3) to confirm defective performances (i.e., resolving one of these secondary problems will resolve the primary problem without coupling) using Axiomatic Design [10,11] principles. The ISQ and the PF have been developed for the application of TRIZ, and can be applied for confirming the defective performances.

5.2 Identifying defective evolved genes

The defective evolved genes that affect the defective performances can then be identified from the mapping networks between the product's performances and genes according to the defective performances determined in the first stage. Their locations in the chromosome can be recognized from the genome maps of the product.

5.3 Retrieving superior evolved genes

The superior evolved genes are used to replace corresponding defective evolved genes to improve the performance of a product and can be derived from successful products among the same and similar types of products in the world and the latest achievement in science and technology. The superior evolved genes should be recorded in a suitable data structure and stored in an evolutionary gene library along with the contradictions to be resolved. According to the innovative objective or the pair of functions forming contradictions, the code names and detailed information of the superior evolved genes that can resolve the contradictions can be retrieved from the evolutionary gene library.

5.4 Chromosome reconstruction

The reconstruction procedure will be first to endow the defective evolved genes with zero or much lower probability for being selected as genetic information, and then graft the superior evolved genes to the locations of corresponding defective evolved genes and endow them with higher probabilities. Although the defective evolved gene is still remained in the chromosome as evolutionary information, it has very little chance to be selected as genetic information during subsequent evolution process. This operation is just like cutting off the defective evolved gene. Sometimes, there are several superior evolved genes possibly used to replace the same defective evolved gene. These superior evolved genes should all be grafted in the location of corresponding defective evolved genes and endowed with different higher probabilities according to their effects on realizing the innovation objective. Except the defective evolved gene, the evolutionary information used earlier as genetic information in the same node should also be endowed with lower probability. But, the sum of the probabilities for all the evolutionary information and genetic information in the node should be equal to 100%. If the genetic information in a node is not a defective evolved gene, endow it with a probability of 100%, and other evolutionary information in the node can be endowed with zero probabilities.

5.5 Evolution of product chromosome

It is possible to have several superior evolved genes, defective evolved genes, or places where each type of defective evolved gene appears in the chromosome. Thus, there is a question: which genes in which places will be selected to be genetic information in the chromosome of an innovative product. The best choice can be obtained using Genetic Algorithms [12-14] based on the optimization model derived from the product's chromosome as shown in Figure 5. In the model, *n* nodes in the chromosome of a product ($G_1, G_2, \cdots, G_n$), where the genetic information needs to be selected from the evolutionary information in the same nodes for product innovation, are arranged into a string as a special type of chromosomes (we call it as an algorithmic chromosome) specially for using Genetic Algorithms. Under each node (we also call it as an algorithmic gene), all the pieces of evolutionary information with their endowed probabilities for being selected as genetic information are listed. The optimization process can be regarded as the evolution process of a product’s chromosome. Its survival-of-the-fittest mechanism is implemented by means of a neural-network-based assessment system of products’ performances [15-17].

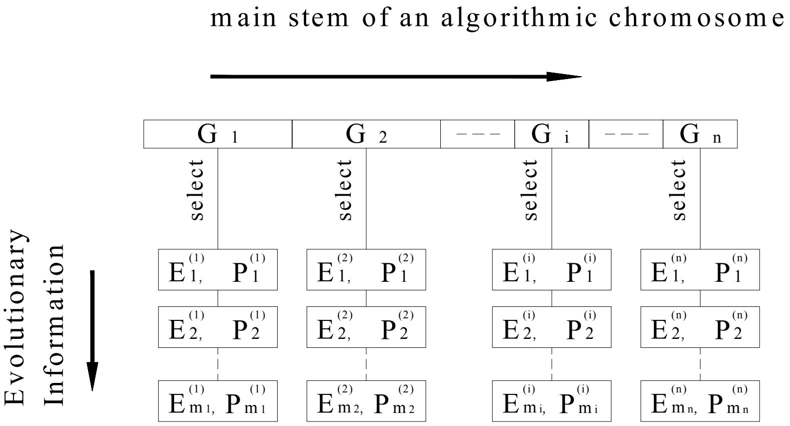


Figure 5. Chromosome of genetic algorithms for product innovation

5.5 Innovating the product according to its evolved virtual chromosome

According to the algorithmic chromosome, a best-evolved chromosome of the product can be obtained, on which the new product can be redesigned and manufactured based. If the best-evolved chromosome of product does not meet the innovative objectives satisfactorily, return to Step (2) to repeat the design procedure until the new product can satisfy the innovative objectives.

6 An example

Since the length of a conference paper is limited, we take a simple type of mechanical product, Ball Bearings [18,19], as an example to illustrate briefly the product innovation using the genetic-engineering-based design method developed. Its detailed design process will be introduced in another paper.

According to the design method developed, the innovative objectives of ball bearings have to be first confirmed. Its innovative objectives were: carrying both larger radical and larger bi-directional thrust loads (A), adapting to varying working load, i.e. varying proportions of radical load to thrust loads (B), and lower cost (C). According to the innovative objectives, its defective performances can be obtained using the method introduced in Section 5.1. Then, the genes which need to be reformed can be identified from the mapping networks between ball bearings’ performances and genes as follows: (1) the method of filling balls, (2) the radius of its raceway’s groove in comparison with balls’ radii, (3) the geometry of raceway, (4) the method of adjusting the clearance between raceways and balls, (5) the number of ball rows, (6) the number of raceways, and (7) the numbers of outer ring and inner ring. These seven genes can form the main stem of an algorithm chromosome specially for using Genetic Algorithms. For each algorithmic gene, all the pieces of its evolutionary information and the grafted superior evolved genes retrieved from its evolutionary gene library were then listed with their endowed probabilities for being selected as genetic information. The probabilities were endowed based on the rules introduced in Section 5.4. The assessment system of ball bearings' performances was designed using artificial neural networks. The inputs of the neural-network-based assessment system of ball bearings' performances are the above seven algorithmic genes and its outputs are the above three innovative objectives (A, B, and C). The fitness of a chromosome is a function of these outputs, and can be expressed as follows:

$$F = k_1 A + k_2 B + k_3 C \qquad (1)$$

where k_1, k_2, and k_3 are constants and used to adjust the weights of A, B, and C. But, their sum should be equal to 100%. Genetic Algorithms were applied to evolve the algorithmic chromosome. After many generations, the algorithms converge to the best algorithmic chromosome. According to the best-evolved algorithmic chromosome, the chromosome of a new ball bearing can be obtained, on which a new ball bearing was redesigned based. Its structure is shown in Figure 6. This innovative ball bearing has one row of balls, a retaining cage, an outer ring, and a pair of separable inner rings. Since there is no need to use second row of balls or another ball bearing to carry the thrust load in another direction, its cost is lower. The cross sections of the grooves on both inner and outer rings have two symmetrical arcs, the centers of which are located on two diagonal contact lines respectively as shown in figure 6, and the radii of the arcs are larger than the radii of balls. The clearances between raceway and balls can be adjusted accurately by grinding the inner face in one of the two inner rings, so that the contact angle between balls and raceway will not be changed much when load is varying, and the bearing can thus adapt to a varying working load. Since the inner rings can be separated while the balls are filled, this ball bearing can thus contain more balls so that it can carries not only larger radical load but also larger bi-directional thrust loads. Therefore, this ball bearing can meet its innovative objectives satisfactorily.

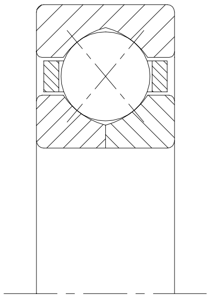


Figure 6. Innovated ball bearing

7 Conclusions

This paper applies genetic engineering techniques to develop a framework of a design theory and methodology for product innovation. This design method is totally different from the conventional one and innovates products via artificial differentiation of products' chromosomes. The key issues include formulating an approach for confirming the defective performances of a product; disclosing the contents and data structure of the products' virtual chromosome;

developing the methods for identifying products' virtual genes in their virtual chromosomes, creating virtual genome maps, and deriving mapping networks between products' performances and virtual genes; and developing the method of reconstructing product chromosomes for product innovation using genetic-engineering techniques. Therefore, it is not a simple application of genetic algorithms. It provides a logically structured method, which can reduce blindness to innovation and can even clone a product with the aid of advanced CAD/CAM technology. Although the chromosomes for different types of products are very similar to each other, the products in different fields should have their own chromosomes, genome maps, gene libraries and mapping networks between a product's performances and genes, just like the chromosomes of human beings and other living beings, which are very similar but cannot be exchanged. Therefore, more research on the application of the new design method for different products can be implemented based on the results.

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