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A synthetic DNA based approach to design of adaptive systems

Y. Jin^{*}, G.E. Zouein, S.C.-Y. Lu (1)

IMPACT Laboratory, Department of Aerospace and Mechanical Engineering, University of Southern California, 3650 McClintock Avenue, OHE430, Los Angeles 90089-1453, USA

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ABSTRACT

Development of large engineered systems involves large amount of investments. Yet the value of these systems decreases significantly as requirements and environments change. For mission critical systems the capability of adapting to unpredictable situations is the key for success. While the importance of system adaptability has been recognized, little research has been done for “design for adaptability”. We take a “naturalistic design” approach to developing adaptive “lifelike” systems by exploiting natural “design” processes and mimicking its DNA based way of capturing, representing and applying “design” information pertaining to needed functions and changing operational situations. The concepts and examples of this approach are discussed.

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1. Introduction

The development of most engineered systems, such as new generation of copy machines, usually involves large amount of investments. Yet the value of these systems may decrease significantly as the requirements and operation environments change over time. The out-of-date systems are often discarded because upgrading them may cost more than buying new ones. For the systems of special missions, such as space exploration vehicles and military robots, the systems' capability of adapting to the situations of unpredictable events, e.g., malfunctions and being incapacitated by enemy fires, is often the key for accomplishing the planned missions. While it has been recognized that system adaptability is required by both economical and mission-critical needs, there has been little research that explores and develops theories and methods for designing adaptive systems partly because of limitations of traditional component-based framing of engineering design problems.

In our research on design of adaptive systems, we take a naturalistic *biological synthesis* approach. Our basic ideas are: (1) natural systems including animals and plants are highly adaptive to their changing environments. The *principles and mechanisms* of these biological systems provide both inspirations and insights for our research on adaptive systems; (2) common to all biological systems, *cellular structure* is indispensable for these systems to grow, reproduce, and adapt, thus we need a *cellular* or *cell-based* product definition framework; and (3) how dynamically capture, represent and apply design information pertaining to needed functions and changing environments is the key for survivability and adaptability; they in nature are performed through biological DNAs.

A true adaptive system must be able to recognize endogenous (system) and exogenous (environment) changes and possess mechanisms to self-design, self-build/grow, and self-repair in

response to these changes. Realization of these mechanisms requires that the “*design*” of the system must be carried by the system in a similar way as real life forms carry their genome via DNA. We call such design information *system genome* (*sGenome*), and its information carrier *design DNA* (*dDNA*). We envision that the *dDNA* of an adaptive system can be altered either purposefully through self-design or by accident, resulting in either catastrophic loss of functions or creation of new functions. We further consider that a new *sGenome*, thus a new adaptive system, can be created by composing a set of given *dDNAs*. Successful *dDNA* compositions can lead to new functional systems. It can be seen that *dDNA* is the basis for self-design, growing, repairing, and adapting.

All life forms are constructed by cells. We consider that for an adaptive system to have the similar capabilities, they need to employ a *cellular system structure*. A biological cell has three basic functions, namely, *cell growth and metabolism*, *cell creation* (or cell division), and *protein synthesis*. Determining *what* functions a *synthetic cell* should perform and *how* they should be performed is a fundamental research question. The answers to this question will emerge along the course of this research. At present, we hypothesize that a synthetic cell in a *cellular adaptive system*, called CAS, should be able to *store and apply* (or *convert*) *energy*, *process information*, and *perform functions* designated by its corresponding *dDNA*. We further hypothesize that the functions specifiable by a *dDNA* include (1) changes of the cell's form or structure, (2) activation of implemented behaviors, and (3) interactions with other synthetic cells.

Our long-term goal is to develop a *synthetic DNA* based design methodology to attain high level adaptability of engineered systems. As the first step toward this goal, in this paper we introduce a *dDNA based design and product representation framework* that maps biological concepts and processes into mechanical products and processes. Our initial research questions are (1) to what extent can we apply the concepts and processes of biological systems to the development of mechanical systems? (2) What are the characteristics that determine the adaptability of such

* Corresponding author.

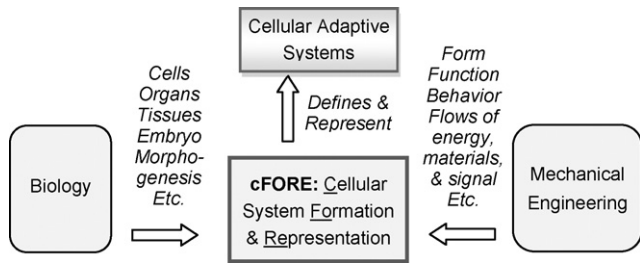


Fig. 1. cFORE representation model schematic.

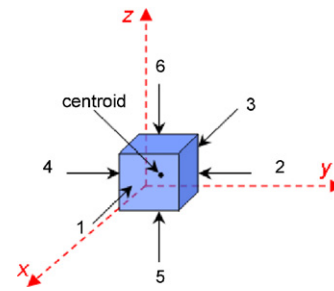


Fig. 2. Mechanical cell.

mechanical lifelike cellular adaptive systems? (3) What are the technological requirements for realizing such lifelike cellular adaptive systems, or CAS?

2. cFORE: cellular system formation and representation

Answering these questions requires a comprehensive representation framework that maps biological system concepts into mechanical systems. Fig. 1 illustrates our cellular system formation and representation (cFORE) scheme that is being developed to facilitate synthetic DNA-based adaptive system development.

As shown in Fig. 1, cFORE is developed through synthesizing system formation concepts from both fields of biology and mechanical engineering. After an extensive review of biology literature, we have identified 18 key biological concepts and processes that are integrated into the cFORE framework together with key design concepts found in mechanical engineering. In the following, we first present the definitions of a selected set of concepts and then discuss more about them in Section 3. Corresponding biology concepts are sometimes associated in parentheses when appropriate.

Definition 1 (Mechanical Cell).

A mechanical cell, *mCell*, see Fig. 2, is defined as: $mCell = \{Cu, (f), (\Phi), dDNA, Es, Ec, Mc\}$; *Cu*: control unit (nucleus), *dDNA*: design information, (Φ) : centroidal location, (f) : six sides, *Es* and *Ec*: energy storage and converter (mitochondria), *Mc*: material converter (lysosomes).

Defining *mCells* as cubes is for simplicity only. More sophisticated definitions will be introduced as our research progresses. At present, the cube based definition of *mCell* simplifies the phenotype information processing. The following definitions describe our genotype model of CAS.

Definition 2 (dDNA).

dDNA is a matrix representation containing system's genome: $dDNA =$

$$\begin{bmatrix}
 (\phi f)_{1,1} & \dots & (\phi f)_{1,n} & (\phi f)_{2,2} & \dots & (\phi f)_{2,n} & (\phi f)_{3,1} & \dots & (\phi f)_{3,n} \\
 (\phi f)_{1,1} & \dots & (\phi f)_{1,n} & (\phi f)_{2,2} & \dots & (\phi f)_{2,n} & (\phi f)_{3,1} & \dots & (\phi f)_{3,n} \\
 (\phi f)_{1,1} & \dots & (\phi f)_{1,n} & (\phi f)_{2,2} & \dots & (\phi f)_{2,n} & (\phi f)_{3,1} & \dots & (\phi f)_{3,n} \\
 (\phi f)_{1,1} & \dots & (\phi f)_{1,n} & (\phi f)_{2,2} & \dots & (\phi f)_{2,n} & (\phi f)_{3,1} & \dots & (\phi f)_{3,n} \\
 (\phi f)_{1,1} & \dots & (\phi f)_{1,n} & (\phi f)_{2,2} & \dots & (\phi f)_{2,n} & (\phi f)_{3,1} & \dots & (\phi f)_{3,n} \\
 (\phi f)_{1,1} & \dots & (\phi f)_{1,n} & (\phi f)_{2,2} & \dots & (\phi f)_{2,n} & (\phi f)_{3,1} & \dots & (\phi f)_{3,n} \\
 (\phi f)_{1,1} & \dots & (\phi f)_{1,n} & (\phi f)_{2,2} & \dots & (\phi f)_{2,n} & (\phi f)_{3,1} & \dots & (\phi f)_{3,n} \\
 \dots & & (\phi f)_{1,n} & (\phi f)_{2,2} & \dots & (\phi f)_{2,n} & (\phi f)_{3,1} & \dots & (\phi f)_{3,n} \\
 (\phi f)_{1,n} & \dots & \dots & \dots & \dots & (\phi f)_{3,1} & \dots & \dots & (\phi f)_{3,n}
 \end{bmatrix}, MIS$$

Organ Level
Organ Level
Organ Level

Energy Material Layer
Structural Layer
Interface Layer

where each item in the matrix is a *mCell Gene* with a *Function Layer* ID *m* and *Module* ID *n*.

A realized *dDNA* matrix is a complete description of a specific system or product, which we call *system genome* or *sGenome*. Note that the *mCell Genes* with the same *m* and *n* are having different

locations, i.e., (x, y, z) 's. Therefore, the number of rows of each column in a *dDNA* may not be the same and depends on a product's genotype-phenotype mappings. A *sGenome* contains information regarding, from global to local, cellular function layers (germ layers), modules (organs), cellular locations (Φ) , cellular functions (f) , and self-growth *mCell instruction set* (MIS) (transcribed protein sets).

Definition 3 (mCell Gene).

mCell Gene, *G_c*, is defined as:

$$G_c = (\phi f) = \langle x, y, z, (f_1 \dots f_{n1})_1, (f_1 \dots f_{n2})_2, (f_1 \dots f_{n3})_3, (f_1 \dots f_{n4})_4, (f_1 \dots f_{n5})_5, (f_1 \dots f_{n6})_6 \rangle$$

where (x, y, z) : geometric location; $(f_1, f_n)_i$: functions of face *i* (*i* = 1–6) of *mCell*; *m*: function layer ID; *n*: module ID.

Depending on the method used to implement *dDNA* and *sGenome*, *G_c*'s and consequently the process of design evolution may take different forms. Fig. 3 illustrates the *mCell Gene* of a binary [0, 1] implementation of *dDNA*, assuming only 2 bits are needed to describe *x, y, z*, and all the functions for each cellular face.

Based on the *mCell Gene* definition, we can introduce several layers of structural genes by drawing inspiration from the concepts of germ layer formation [1] and those of biological functional systems.

We introduce the concept of *Function Layers* (germ layers). More specifically, a CAS is defined to have three function layers: *Energy-Material Layer* (inner germ layer), *Structural Layer* (middle layer), and *Interface Layer* (outer layer).

Definition 4 (Function Layer Gene).

A *Function Layer* (germ layer) gene *G_{FL}* is defined as,

$$G_{FL} = \langle (G_o)_{k,1}, (G_o)_{k,2}, \dots, (G_o)_{k,n} \rangle; \quad k = 1 \dots 3$$

where *G_o*: module gene; *k* indicates 1 = FL-energy-material, 2 = FL-structure, and 3 = FL-interface.

Definition 5 (Module Gene).

A module (organ) gene is defined as,

$$G_o = \langle G_{c1}, G_{c2}, \dots, G_{cN} \rangle$$

where *G_{ci}* is a *mCell Gene*.

A complete *sGenome* encoded in *dDNA* defined in Definition 2 provides a blue print of a designed system. For such a system to be realized or implemented by *mCells*, the *sGenome* information must be interpreted and applied by *mCells*. In biology, the genetic information stored in DNA is transcribed by RNA and taken to the ribosome for protein production from a set of 20 amino acids [1]. The proteins are then used by cells as instructions to carry out particular actions in order to express the desired gene. The three basic categories of proteins are *structural proteins*, *enzymes*, and *signaling proteins*. Based on these biological concepts, in our model

Φ (location)			f (function of each face)					
<i>x</i>	<i>y</i>	<i>z</i>	<i>F</i> ₁	<i>F</i> ₂	<i>F</i> ₃	<i>F</i> ₄	<i>F</i> ₅	<i>F</i> ₆
0	1	1	1	1	1	0	0	0
0	1	1	1	1	1	0	0	0
0	1	1	1	1	1	0	0	0
0	1	1	1	1	1	0	0	0
0	1	1	1	1	1	0	0	0
0	1	1	1	1	1	0	0	0
0	1	1	1	1	1	0	0	0
0	1	1	1	1	1	0	0	0

Fig. 3. An example of *mCell gene*.

we introduce *instructions* (proteins) and *cellular actions* (amino acids) for *dDNA* transcription. We define *mCell Instruction Set*, or *MIS*, as a pre-transcribed set of cellular instructions defined by the designer of the system. In doing so MIS unifies RNA, proteins (structural, enzymes), ribosome and amino acids into one concept.

Definition 6 (*mCell Instruction Set, MIS (transcribed protein set)*):

MIS is defined as one of two types of instruction sets (proteins):
 $\langle mCellInstructionSet \rangle ::= \langle enzymes \rangle | \langle structuralInstructions \rangle | \langle communicationInstructions \rangle$

$\langle enzymes \rangle ::= \langle cellularFunctionExpressionInstructions \rangle | \langle formationInstructions \rangle$

$\langle cellularFunctionExpressionInstructions \rangle ::= \langle expressionActions \rangle | \langle generalActions \rangle$

$\langle formationInstructions \rangle ::= \langle formationActions \rangle | \langle generalActions \rangle$

$\langle structuralInstructions \rangle ::= \langle structuralActions \rangle | \langle generalActions \rangle$

$\langle communicationInstructions \rangle ::= \langle commActions \rangle | \langle generalActions \rangle$

In biology, amino acids are the basic structural building units of proteins. Similarly we define a group of cellular actions and group them into four sets.

Definition 7 (*Cellular Actions (amino acids)*).

A set of *cellular actions* is defined as:

$\langle cellularActions \rangle ::= \langle generalActions \rangle | \langle expressionActions \rangle | \langle formationActions \rangle | \langle structuralActions \rangle | \langle commActions \rangle$

$\langle generalActions \rangle ::= \langle (x,y,z), F1, F2, F3, F4, F5, F6, \& \rangle$: General actions that stores centroid location (x, y, z), mCell face information F1 through F6 and the “&” operation.

$\langle expressionActions \rangle ::= \langle f1 f2 \dots fn \rangle$: Expression amino acid that stores cellular functional expression instructions.

$\langle formationActions \rangle ::= \langle u d l r f b A D \# \rangle$: formation actions that store the formation actions. u, d, l, r, f, b, A, D, # stand for up, down, left, right, forward, backward, attach, detach and an integer value respectively.

$\langle structuralActions \rangle ::= \langle cs1, cs2, \dots \rangle$: Structural actions that stores construction actions.

$\langle commActions \rangle ::= \langle cm1, cm2, \dots \rangle$: Communication actions.

An example of an instruction (protein) composition of cellular actions is: $\langle formationInstructions \rangle = (2,1,6)DF3d1AF3(1,1,5)AF1$,

which states that the cell at centroid location (2,1,6) should detach face 3, move down 1 and attach at its face 3 the cell at centroid location (1,1,5) at its face 1.

Given a *sGenome* encoded in *dDNA* and its transcribing methods defined above, mCells will need mechanisms to apply these design information, instructions and to grow into the desired system. One key process governing the self-growth from an embryo to a mature system in biology is *morphogenesis*, which determines the shapes, sizes, and layouts of organs, tissues and overall body anatomy [1]. Essentially, morphogenesis is guided by a set of rules or principles followed by an embryo in its transformation into a complete system. Drawing insight from this concept we introduce a similar process for our CAS. A set of *Self-formation Governing Principles*, or *SGP* was developed to guide self-organization of *mCells* in forming a bio-inspired system. It has been recognized that all biological systems follow a “*minimization of energy principle*” when they undergo growth, development or preservation of life [2]. In cFORE, the SGP is defined as follows.

Definition 8 (*Self-formation Governing Principle, SGP (morphogenesis)*).

A SGP is defined as follows.

$\langle SGP \rangle ::= \langle layoutPrinciples \rangle | \langle developmentPrinciples \rangle | \langle layoutPrinciples \rangle | \langle developmentPrinciples \rangle | \langle layoutPrinciples \rangle ::= [System layout is determined by dDNA genes at FunctionLayer, Module, and mCell levels]$

$\langle developmentPrinciples \rangle ::= \langle functionLayerFormationPrinciple \rangle | \langle cellularActionPrinciple \rangle | \langle systemFormationPrinciple \rangle$

$\langle functionLayerFormationOrder \rangle ::= [Form Energy Material Layer first, if no such layer exists then form Structural Layer Form Structural Layer second, if no such layer exists then form Interface Layer Form Interface Layer, if no such layer exists then begin bonding formed layers together]$

$\langle cellularActionPrinciple \rangle ::= [Minimize energy needed to carry out cellular actions] | \langle systemFormationPrinciple \rangle ::= [Minimize total energy needed to carry out actions of all mCells].$

3. Simulation study and discussion

Given the cFORE framework, two questions must be addressed in order to realize our synthetic DNA based approach to developing adaptive systems. First, *dDNA* should support system design so that a specific *sGenome* can be composed either by designers or through computing. Second, adaptive systems must be able to *build themselves* from *mCells* based on a given *sGenome*. Our previous research on evolutionary design has shown preliminary viability of such a *dDNA* based approach [3]. Further research is being carried out to deal with this issue. To address the second question, we conducted a computer simulation study using the cFORE model. The goals of the study are (1) to verify the effectiveness of *dDNA* and *sGenome* representation and (2) to test the effectiveness of the SGP based self-growth of adaptive systems based on given synthetic DNA information.

Following Shen [4], we take the “spider and snake” design as our target adaptive system. With this system, in the situation where climbing or grasping is required, the *mCells* form themselves to a spider, and when fitting through a tight crevice or hole is required, they reconfigure to form a snake. Fig. 4 illustrates the four steps of dynamic system formation, starting from blastula stage and undifferentiated *mCells*, going through “acquiring” spider *dDNA* and forming a spider and “acquiring” snake *dDNA* and constructing a snake.

Our simulation system is built using a Java-based multi-agent simulation package, MASON. In the simulation, each *mCell* is treated as an agent. All *mCells* can move in two-dimensional space (x, y) and they can express their functions by showing colors. The *mCells* can communicate with each other and with a shared message board. A binary method, similar to that shown in Fig. 3, was used to implement *dDNA*. For example, the mCell gene for the top left leg of the spider shown in Fig. 5 is represented as [(10,70; 0,1,0,0) (30,70; 0,1,0,1) (50,70; 0,1,0,1)], where first two numbers indicate relative location and the remaining four binary digits are functional encoding. The *dDNAs* for Spider and Snake are pre-defined and can be seeded to each *mCell* through broadcasting. All *mCells* hold the same *dDNA* information at any given time.

The SGP (self-formation governing principles) were implemented by following a CPM algorithm indicated in Fig. 5. After *dDNA* is seeded into each *mCell*, the *mCells* will calculate their desired locations by

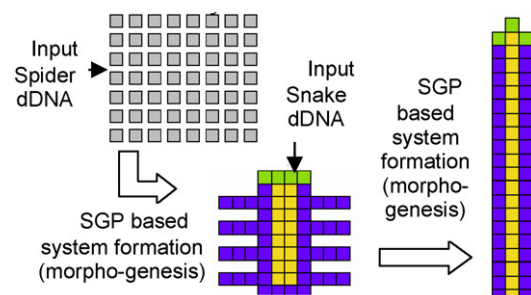


Fig. 4. A “Spider-Snake” adaptive system.

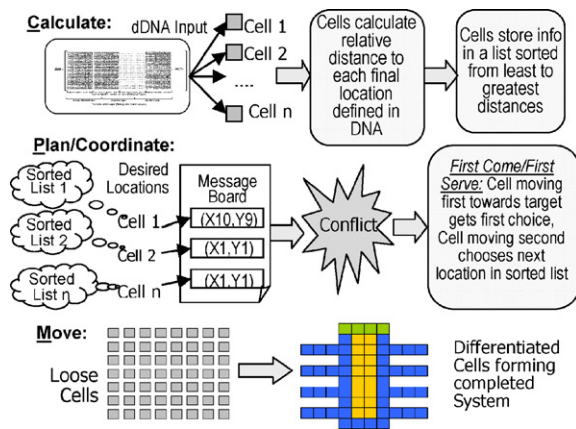


Fig. 5. A CPM (calculate, plan, move) algorithm.

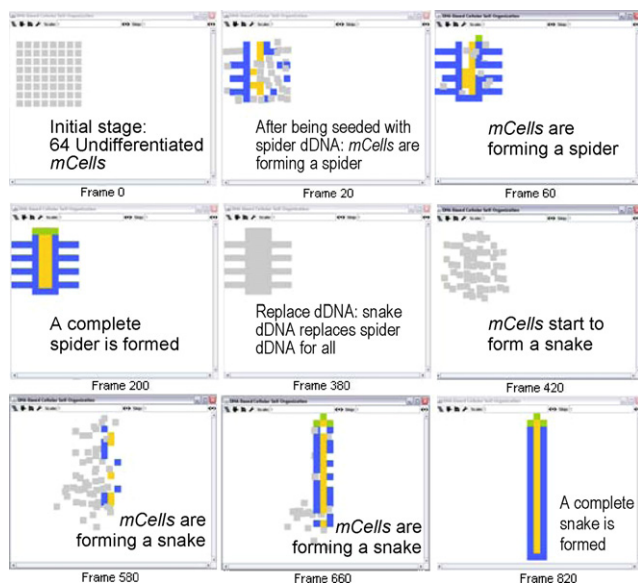


Fig. 6. Simulation result of Loose->Spider->Snake.

following $\langle \text{layoutPrinciples} \rangle$, $\langle \text{functionLayerFormationOrder} \rangle$ and $\langle \text{cellularActionPrinciple} \rangle$. Desired locations are then posted to a message board for conflict resolution. A *First-Come-First-Serve* $\langle \text{systemFormationPrinciple} \rangle$ was adopted in the simulation for resolving conflicts. Alternatively, a minimum-system-energy principle could be employed.

MASON has the capability of producing video clips of simulated cell movements. Fig. 6 shows the result of one simulation run in which initial undifferentiated *mCells* receive spider *dDNA* and then form a spider through SGP based self-growth. After that snake *dDNA* is seeded, the *mCells* leave their spider identity and change into a snake defined by the given snake *dDNA*.

Summarizing the results of multiple simulation runs, we found that (1) system growth can be realized through a *dDNA* controlled and decentralized cellular self-organizing formation strategy; (2) as in biology, cellular self-organizing for self-growth of mechanical systems can be achieved through the use of *dDNA* and SGP (morphogenesis) principles, and cellular actions including $\langle \text{commActions} \rangle$; and (3) as in biology, altering a system's *dDNA* results in a new system with either modified or entirely new system level functionality. Mechanical system reconfiguration as a means of modifying or attaining new functionality is primarily a result of altering a system's *dDNA*. Moreover, the simulation design and results also pointed us to some important and otherwise unidentified issues.

3.1. Conflict resolution

Since each *mCell* applies $\langle \text{cellular ActionPrinciple} \rangle$ that demands minimization of cellular energy usage (i.e., travel distance in this simulation), it is likely that multiple *mCells* may

desire to fulfil the same cellular location. Hence the “first come first serve” conflict resolution technique was needed to overcome the arising conflicts between the *mCells*. This “conflict resolution” issue is unique to *mCells* because, unlike bio-cells, *mCells* cannot create new *mCells* through cell division (mitosis). Instead, new *mCells* must be created from outside of the system and then move to their identified target locations. We envision that different conflict resolution strategies will be required for different types of adaptive systems. We plan to explore more along this direction.

3.2. Cellular communication

Cellular communication is another important factor that affects the outcome of *dDNA* based self-growth process. Again, the chief issue is conflict between or among *mCells*. Cell division (mitosis) based bio-cell creation eliminates tremendous needs for cellular communications. In case of *mCells*, however, we envision that successful cellular communication is the key for effective *dDNA* and *mCell* based system formation. More inter-*mCell* communication mechanisms need to be explored in addition to the message board method.

3.3. Information of *dDNA*

As in biology, without DNA, the cells comprising the system would simply function as independent cells never expressing system level genes, resulting in systems of collections of cells with cell divisions occurring out of necessity rather than requirement. Testing this phenomenon in the mechanical world, we observe that the result of not seeding the *mCells* of the system with *dDNA* results in that very same collection of cells seen in biology. Contrary to biology though, which seeds each cell with DNA through cellular division, the *mCells* require individual seeding with the appropriate *dDNA*. As in biology, defects in *dDNA* will lead to undesired system. Therefore maintaining complete and healthy (gracefully degraded) *dDNA* information is important.

4. Concluding remarks

The environmental pressure on use of limiting resources and the increasing human desire of exploring untouched universe calls for highly adaptive systems that can self-create and self-grow. We argue that the traditional product development approach has its limitations due to separation of design and manufacturing and conventional *component* based system definition.

We take a synthetic DNA approach to developing such adaptive systems. Unlike other bio-mimetic engineering research works that mimic mechanical mechanisms of specific animals or plants [5,6], our approach uniquely attempts to mimic the “biological process” of creating, storing, and applying “design” information. Our *dDNA* based product representation captures both system and system formation information and can be embedded in any pieces of a system. The simulation based case studies demonstrated the effectiveness of our cFORE framework and led us to a better understanding of some of the key issues related to *dDNA* based product development. Our future work will address the above mentioned issues and will carry out more simulation/experiment studies on *dDNA* based system design, repair and innovation.

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