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A Generalization of Gene Network Representation on the Hypercube

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Abstract

This article emphasizes the relation between Boolean input variables and Boolean states since the complexity of such connectivity increases enormously. Graphically, genetic systems up to 4-dimensional states of the implementation on hypercubes are accessible because the visibility of genetic systems up to 4-dimension on a hypercube is not laborious. The state connection on a hypercube is inflexible and only possible if the input variables are higher or more significant, for example, $N \geq 6$. We have explored similar relations in this manuscript for higher dimensions. An algorithm is developed in the form of a matrix such that the connections of higher dimensional genetic networks are understandable on the hypercube. We have obtained the resultant output matrix based on the linear fractional maps, which are indispensable to understanding the system's behavior.

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1. Introduction

Biological and physiological systems display a wealth of complex dynamics. Previous work has demonstrated how comparatively simple theoretical models are responsible for complex dynamics. The originator of such dynamics is transcription factors. Transcription factors are in action around the clock, manufactured, and ruined protein.[1] Moreover, transcription factors and thresholds have some features due to cells that need to be understood correctly. For example, when transcription factors cross the threshold, the behavior of transcription factors will change such that the active mode of protein production will be turned off the inactive mode will turn on, or vice versa.[2,3]

However, developing tools from dynamical systems and pure/applied mathematics are necessary to shed light on the mechanisms underlying protein-protein interactions.[4] Although significant signs of progress have been created,[5] an extensive understanding of the most naturally occurring biological throbs has yet to be achieved despite these favorable outcomes. The story started in 1960 by Jacob and Monod;[6] they elucidated how genetic networks could be formulated to lead to multi-stability and oscillation.

Discrete genetic network systems have a vast area to address.[7] Even experimental data are available to make an impact in discrete forms, such as the concept introduced in early 1969. The dynamics of such a system are composed of two sets of information, logical function interactions, and representations of gene-like states. Real-world problems are addressed based on discrete systems that are entirely deterministic.[8] However, its dynamics are found by the updates of each nodal information. A crucial drawback of such systems is nonother than the information gap between two consecutive states.[9]

Relationships between gene proteins are ubiquitous in modeling gene regulatory networks.[10] Living organisms are specified on the regulatory networks of interaction, where genes and proteins are indispensable for their existence.[11] Functional evaluations of the gene are addressed in.[12] Mathematical models of networks such as gene-DNA or protein-protein must be explained precisely, although complex networks are available.[13] Due to inadequate knowledge of a

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biochemical reaction, the genetic switch control[14] or feedback regulation of E.coli[15] is only partially understood.

In this study, we consider equations called glass networks based on the originator's original work. Genetic networks of dimension N were proposed in 1973, where logical interactions are embedded. Fixed points, cycles, cycling attractors, and other standard findings such as eigenvalues and eigenvectors have been explored. In late 1970, a 5-dimensional hypercube representation was proposed in the literature. In that representation, a four-dimensional hypercube has some open edges; via those edges, another 4-dimensional hypercube is connected.

However, we believe they did not recognize which node, *i.e.*, the state-space of that inner and outer hypercube, is attached. A 10-dimensional system has been proposed to study ring circuits.[16] They addressed several aspects of applications but not the hypercube presentation. Before this manuscript, no one had even thought about it. It is a significant point that led us to address it here and fills the gap between all these decades. The study arranges the article in the following ways; We gave a glimpse of the discrete version of the proposed model just after the theoretical description and studied the synchronous behavior of the system Eq. (2). Subsequently, interaction of genetic differential equations Eq. (1) is introduced, followed by logical interactions. Pragmatic coverage follows, such as the logical interaction of genetic differential equations Eq. (1). Then, we focus on the generalization and explore the unique way to represent that on a hypercube. This representation is a topologically equivalent representation of the state space on the hypercube. Finally, we depicted our findings in a two-dimensional space. We have presented a similarly higher-dimensional system and gained insight into the previous results. Such a procedure captures any dimensional representation as a two-dimensional presentation. This virgin dimensional system can be pictured as existing connections.

2. Theoretical model

The genes are responsible for producing proteins. However, only a few genes act in such exertion.[17] It is well established through the literature that transcription factors regulate the activity of genes in such a network. Piecewise linear differential equations are used to formulate genetic networks of n genes.[18,19] We are interested in the following system (*i.e.*) Eq. (1), where xi for i = 1 . . . 4 represents the gene. The mathematical setup is followed by,[19] and the assumptions and variable transformations are the same as in.[20]

$$\begin{aligned}
\frac{dx_1}{dt} &= 2(\bar{X}_2\bar{X}_4 + X_2\bar{X}_3\bar{X}_4 + X_2X_3X_4) - 1 - x_1\\
\frac{dx_2}{dt} &= 2(\bar{X}_1\bar{X}_3 + X_1\bar{X}_4) - 1 - x_2\\
\frac{dx_3}{dt} &= 2(\bar{X}_1X_2 + X_1X_2X_4) - 1 - x_3\\
\frac{dx_4}{dt} &= 2(X_1\bar{X}_2 + \bar{X}_1X_2\bar{X}_3 + X_1X_2\bar{X}_3) - 1 - x_4
\end{aligned} \tag{1}$$

where X ī = 1−Xi for each i = 1, ...,4 and Bi = 2Xi(t+1)−1 in Eq. (1) is used to maintain the threshold at the intersections of the Euclidian space. To understand the system and its behavior, we first simulated the system and observed the time series, *i.e.* , the Fig. 1. We have projected its dynamics in the Fig. 2. These results give us a rigorous picture of the structure of the dynamics of the genetic network. A table with the descriptions of existing variables is shown in Table 1, which contains key information on the state space, logical variables, and other mathematical notations that are relevant to such modeling.

A verbal description might be helpful to extract information from the phase plane *i.e.*, Fig. 2 solution of the system Eq. (1). We can analyze the behavior of system Eq. (1). Here in Table 2 first column, the logical variable X1 follows a dynamic similar to a compliment circuit. When the logical variable X2 is off again, it behaves like an XNOR circuit for an on-state. However, Table 2 second column shows that the logical variable X2 follows the circuit compliment regardless of the On or Off state of the logical variable X1. The dynamics

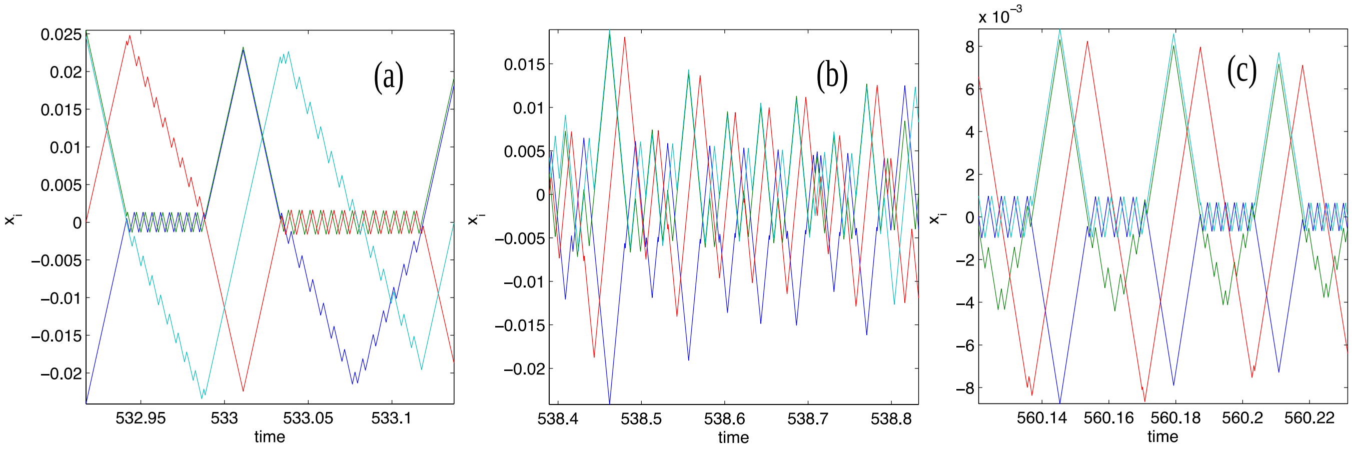

Fig. 1 Time trace of the Eq. (1) for 100 iterations at different time frame.

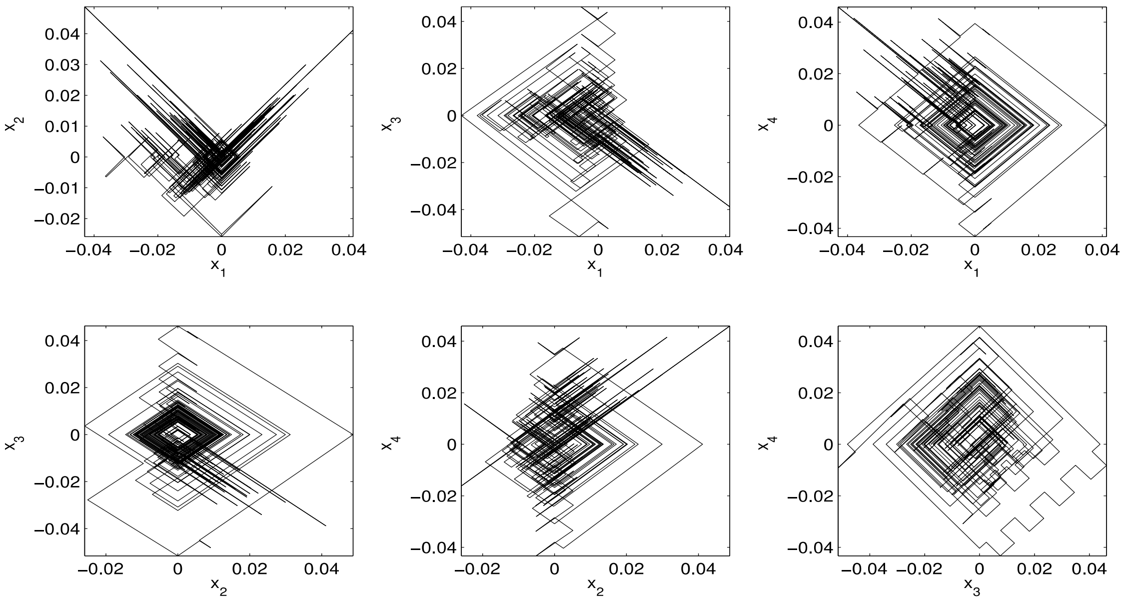

Fig. 2 Phase space projections of Eq. (1) of 500 iterations at different times in each pair of variables.

of x3 can be captured from the logical variable X3, *i.e.*, Table 2 third column. The real gene x3 follows the circuit TRANSFER when logical state X1 is off and follows the AND circuit for on the state. Both effects are captured in our simulation. However, the most problematic behavior is none other than x4. Logical interactions are in Table 2 fourth column. It follows the circuit INHIBITION when X1 is off and NAND when X1 is on. This is just one way to look at the dynamics. We can choose other logical variables, such as X2, X3, or X4 to express the dynamics. Regardless of our choices, we must end up with this unique dynamic, as we found in our numerical simulation of the system Eq. (1).

It is customary to understand this complex structure by dissecting the truth table, *i.e.*, Table 1.

3. Discrete switching

Genetical and neural networks exhibit elegant dynamics distinguished by interactions between significant nonlinear dynamical components distributed in space. Genetic details reside within each cell in our body. Such information accumulates in the inner part of the nucleus, known as deoxyribonucleic acid (DNA). DNA is a polymer made of nucleotides. Nucleotides fasten in the formation of the filament of DNA.

Table 1. Logical interactions of system Eq. (1), known as a truth table.

X_1 X_2 X_3 X_4 (t)	X_1 X_2 X_3 X_4 (t+1)
0 0 0 0	1 1 0 0
0 0 0 1	0 1 0 0
0 0 1 0	1 0 0 0
0 0 1 1	0 0 0 0
0 1 0 0	1 1 1 1
0 1 0 1	0 1 1 1
0 1 1 0	0 0 1 0
0 1 1 1	1 0 1 0
1 0 0 0	1 1 0 1
1 0 0 1	0 0 0 1
1 0 1 0	1 1 0 1
1 0 1 1	0 0 0 1
1 1 0 0	1 1 0 1
1 1 0 1	0 0 1 1
1 1 1 0	0 1 0 0
1 1 1 1	1 0 1 0

Table 2. Lower dimensional logical interactions between genes.

Logical structure of X_1, which depends on $X_2X_3X_4$		Logical structure of X_2, which based on $X_1X_3X_4$		Logical structure of X_3, which based on $X_1X_2X_4$		Logical structure of X_4, which depends on $X_1X_2X_3$	
$X_2X_3X_4$ (t)	X_1(t + 1)	$X_1X_3X_4$ (t)	X_2(t + 1)	$X_1X_2X_4$ (t)	X_3(t + 1)	$X_1X_2X_3$ (t)	X_4(t + 1)
0 0 0	1	0 0 0	1	0 0 0	0	0 0 0	0
0 0 1	0	0 0 1	1	0 0 1	0	0 0 1	0
0 1 0	1	0 1 0	0	0 1 0	1	0 1 0	1
0 1 1	0	0 1 1	0	0 1 1	1	0 1 1	0
1 0 0	1	1 0 0	1	1 0 0	0	1 0 0	1
1 0 1	0	1 0 1	0	1 0 1	0	1 0 1	1
1 1 0	0	1 1 0	1	1 1 0	0	1 1 0	1
1 1 1	1	1 1 1	0	1 1 1	1	1 1 1	0

Two such filaments attach to configure a double-helical appearance, constituting the fully developed DNA. Several nucleotides are available, but only four include DNA.[21] The genetic information is distinctive to each organism and settles down in a precise sequence of nucleotides that assemble its DNA.[22] This sequence is known as a gene. Each functional unit (*i.e.*, gene) comprises the significant commands to produce the cell's protein. This protein is essential for the existence of the cell.[23] Mathematically, we are interested in modeling simplified genetic networks.[24] The Boolean equation, Eq. (2), is a representative of the logical structure of our simplified model example Eq. (1) as

$$\begin{aligned} X_1^{t+1} &= \bar{X}_2^t\bar{X}_4^t + X_2^t\bar{X}_3^t\bar{X}_4^t + X_2^tX_3^tX_4^t \\ X_2^{t+1} &= \bar{X}_1^t\bar{X}_3^t + X_1^t\bar{X}_4^t \\ X_3^{t+1} &= \bar{X}_1^tX_2^t + X_1^tX_2^tX_4^t \\ X_4^{t+1} &= X_1^t\bar{X}_2^t + \bar{X}_1^tX_2^t\bar{X}_3^t + X_1^tX_2^t\bar{X}_3^t \end{aligned} \tag{2}$$

where the (t + 1) represents the future activities of the stage. Obtaining the synchronous switching system Eq. (1) is customary. An appropriate display of the state space is depicted on a hypercube in Fig. 3. Collecting all possible transitions on a hypercube is known as the state transition diagram. Since we already assume no self-input, we further assume that a single variable will be allowed to pass its thresholds. Based on the second assumption, it is possible to map the trajectories of the differential equation onto a Boolean hypercube known as an N− cube.[25]

This second assumption is significant regarding the computational aspects of handling such models. Glass networks can be presented through symbolic dynamics, representing symbols sequentially. This sequence of characters can capture qualitative dynamics. Boolean variables are used to describe these symbolic dynamics. Furthermore, symbolic dynamics usually dissect the phase space into subspaces or compartments. A series of studies were accomplished that assigned symbols to each space.

The solution trajectory of the system evolves in an N-dimensional hypercube. Consider the current Boolean state Γ_2^1 from where trajectory initiates to Γ_2^2, the Boolean state toward which the trajectory is directed. There might be situations when Γ_2^1 and Γ_2^2 exist in the same orthant. In that case, the difference between the orthant is null, meaning Γ_2^1 approaches the fixed point in Γ_2^1.

This behavior eventually ends in a stable, steady state. If the distance between Γ_2^1 and Γ_2^2 is one, then trajectories that originated in Γ_2^1 are directed toward Γ_2^2 through the common boundary. Such as system Eq. (2) cases known as asynchronous switching; see Table 6 for details The Hamming distance may have a value greater than 1, and the trajectory from Γ_2^1 is directed to Γ_2^2. As a result of this discussion, transitions can be displayed as a directed graph on an N− cube. Moreover, we expressed the case for the system Eq. (2) for synchronous switching, *i.e.*, Table 1. Such updates (both asynchronous and synchronous) are evident in Fig. 3.

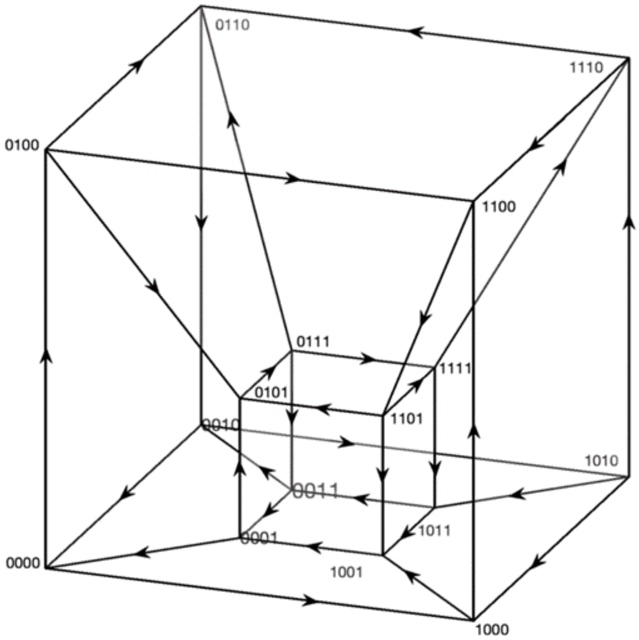

Fig. 3 A hypercube as a representative of states of the network in table 1 and its possible connections.

4. Irregular choices may lead to deadlock position

The study discussion already focuses on getting to know that the hypercube presentation of the solution of piecewise linear differential equations is topologically equivalent to the real solution of differential equations. However, random choices of placement of nodes on a hypercube may lead to something unsuitable for further investigation of the connection of the existing nodes of the system. Due to the limitations of MATLAB, we know that MATLAB starts its indexing from 1. We have used the formula

(binary number)2 = (decimal number)10 + 1.

We must do this by counting the Hamming distance between each hypercube node. It is difficult to make a hypercube presentation of the five-dimensional problem. Tables of connections and graphical two-dimensional representation are available in the supplementary document. Once we further investigate, there is no way to crack it in terms of the hypercube.

This study resolves such issues for any dimensional system; to the best of our knowledge, it is open to address. Therefore, we are interested in the generalization of the Boolean states with the use of minimal existing information. This article's findings help improve the branch hypercube drawing branch in MATLAB Fig. can be generated in MATLAB using some commands for example, figure = [1 1 1 2 2 3 3 4 5 5 6 7]; t =

[2 4 8 3 7 4 6 5 6 8 7 8]; G = graph (s, t); plot (plot (G,’ Layout’ ,’ force’)). The previous comments in the command window in MATLAB can obtain a figure. However, we firmly believe that we obtain flaws in sophisticated software such as MATLAB. That also does not give us any information listed in Table 3. Please see the attachment of the supplement document for more understanding of the event.

Table 3. Successor states of the vertices in asynchronous switching of the system Eq. (1)

X_1 X_2 X_3 X_4 (t)	X_1 X_2 X_3 X_4 (t+1)	X_1 X_2 X_3 X_4 (t)	X_1 X_2 X_3 X_4 (t+1)
0 0 0 0	0 1 0 0 0 0 0 0	1 0 0 0	1 0 0 1 1 1 0 0
0 0 0 1	0 0 0 0 0 1 0 1	1 0 0 1	0 0 0 1
0 0 1 0	0 0 0 0 1 0 1 0	1 0 1 0	1 0 0 0 1 1 1 0 1 0 1 1
0 0 1 1	0 0 0 1 1 0 1 1	1 0 1 1	0 0 1 1 1 0 0 1
0 1 0 0	0 1 1 0 1 1 0 0 0 1 0 1	1 1 0 0	1 1 0 1
0 1 0 1	0 1 1 1	1 1 0 1	1 1 1 1 0 1 0 1
0 1 1 0	0 0 1 0	1 1 1 0	1 1 0 0 0 1 1 0

5. Idea of generalization of possible boolean states

Proteins are the most flexible macromolecules of the cell. The two greatest revolutions about protein occurred within the last three decades that have changed the course of action, biologists believe. These revolutions have affected how experiments are outlined.[26] The earliest revolution was the structural revolution. It authorizes the design of experiments that would never otherwise have been feasible. The subsequent revolution after the first one is the genomic revolution. The availability of the sequences of all genomes of organisms ranging from bacteria to human beings is still under rigorous intervention. People are working in different directions, but we restrict our analysis to a hypercube; the nodes of a hypercube represent genomic sequences, *i.e.*, genes involved in the system. We also found the representative allowable hypercube transition Fig. 4(a-c), later used as a general setup for any dimensional system.

Leveling the binary number using a decimal, as we did in the previous section. Following these trends, we can accurately generalize the idea of the connection of possible Boolean states with each node of the hypercube. We have labeled the orthant in decimal and Boolean numbers to represent it as a generalization of such a system. We have developed an indispensable connection matrix between the nodes; please visit Table 4. We believe that Fig. 5 will provide a profound intuition of the connection matrix representation on the hypercube. This analysis leads us to label the notion of marking the nodes in the hypercube for any dimension. We have tested it from a lower, *i.e.*, a minimum 2 to 25 extent in the form of a matrix.

6. Connection Matrix

A hypercube representation of five, six, and seven-dimensional systems is not apparent, so we presented that connection in Fig. 5 in the ambiance of the two-dimensional graph. Such a representation is unique to the notion of developing a generalized algorithm for any dimensional system. We obtain the conjecture of ties between the tables and the graphs. The possible output states for two, three, and four input Boolean variables are 22 = 4, 23 = 8, and 24 = 16.

Based on such information, we can validate the possible output states. For example, if a system comprises four and six Boolean input variables, the possible output states are 16 and 64, respectively. Table 4 comprises the same number of nodes or states. Fig. 5 comprises exactly such nodes. If we focus on Table 4, we can extract information about the connection of five, four or even lower dimensional systems. For example, if we eliminate the last column of the left Table 4, we can extract

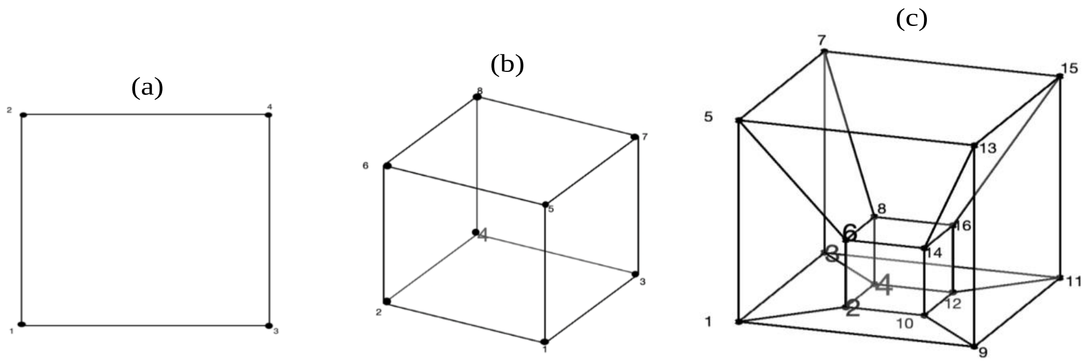

Fig. 4 A representative of a two-dimensional hypercube (left panel (a)), a three-dimensional hypercube (middle panel (b)), and a four-dimensional hypercube (right panel (c)) with the right orientation. This is the first attempt to generalize a similar system for any dimension.

a five-dimensional system's connection from that table with 32 nodal connections.

A precise representation of a five-dimensional hypercube is difficult. Nevertheless, each node of the hypercube has five connections, and the connection matrix represents all possible relations between the nodes, *i.e.*, Table 4 (once the last column of the matrix and the second portion of that table was eliminated) represents such connections where a horizontal line presents states, and the vertical line presents possible connections between the nodes.

We also used the following formula to make it a tracible mod(2dim + N, 2dim). A verbal description of the computation of the connection matrix of the five- dimensions is as follows: for example, we obtain numbers more significant than any number between 1 and 32. In that situation, we have used the above formula to obtain the decimal number within the possible range of 1, · · · , 32. Additionally, for dim = 5, once it exits the possible limits 25 = 32, it will build the connection between the lower decimal numbers to higher numbers. Consequently, the above formula is used to get the numbers accordingly. A similar treatment has been done to increase the consecutive dimension of possible numbers of increased Boolean variables, *i.e.*, dim= 6, 7, 8, · · ·.

While constructing the connection matrix, we investigated each column’ s hidden characteristics. We will describe such features in Tables 4 and Fig. 5. In the first column of Table 4, we unveil that the difference of consecutive numbers is 1, *i.e.*, 20 = 1. For the second column, the differences in the obtained insights of Boolean ties to build a connection matrix are depicted in the Fig. 5. The historical development of genetic networks is available.[27] A ten-dimensional system was studied in a ring circuit, and different aspects were explored.[16]

Table 4. Nodal Connections between each state in six dimensions.

x_1	x_2	x_3	x_4	x_5	$x_6(t)$
2	3	5	9	17	33
1	4	6	10	18	34
4	1	7	11	19	35
3	2	8	12	20	36
6	7	1	13	21	37
5	8	2	14	22	38
8	5	3	15	23	39
7	6	4	16	24	40
10	11	13	1	25	41
9	12	14	2	26	42
12	9	15	3	27	43
11	10	16	4	28	44
14	15	9	5	29	45
13	16	10	6	30	46
16	13	11	7	31	47
15	14	12	8	32	48
18	19	21	25	1	49
17	20	22	26	2	50
20	17	23	27	3	51
19	18	24	28	4	52
22	23	17	29	5	53
21	24	18	30	6	54
24	21	19	31	7	55
23	22	20	32	8	56
26	27	29	17	9	57
25	28	30	18	10	58
28	25	31	19	11	59
27	26	32	20	12	60
30	31	25	21	13	61
29	32	26	22	14	62
32	29	27	23	15	63
31	30	28	24	16	64

x_1	x_2	x_3.	x_4	x_5	$x_6(t)$
34	35	37	41	49	1
33	36	38	42	50	2
36	33	39	43	51	3
35	34	40	44	52	4
38	39	33	45	53	5
37	40	34	46	54	6
40	37	35	47	55	7
39	38	36	48	56	8
42	43	45	33	57	9
41	44	46	34	58	10
44	41	47	35	59	11
43	42	48	36	60	12
46	47	41	37	61	13
45	48	42	38	62	14
48	45	43	39	63	15
47	46	44	40	64	16
50	51	53	57	33	17
49	52	54	58	34	18
52	49	55	59	35	19
51	50	56	60	36	20
54	55	49	61	37	21
53	56	50	62	38	22
56	53	51	63	39	23
55	54	52	64	40	24
58	59	61	49	41	25
57	60	62	50	42	26
60	57	63	51	43	27
59	58	64	52	44	28
62	63	57	53	45	29
61	64	58	54	46	30
64	61	59	55	47	31
63	62	60	56	48	32

Moreover, a twelve-dimensional system is proposed.[6] Some core activities, such as eigenvalues and eigenvectors, can be extracted using this article's method.[28] A profound mathematical analysis of biochemical networks is ready and worth reading to learn how a couple of successive entities are 2, *i.e.*, 21 = 2. The subsequent column bears the same differences for three, four, five, and six dimensions 22 = 4, 23 = 8, 24 = 16, and 25 = 32. Finally, we disclose the hidden behavior of Boolean relations to construct a connection matrix.

7. Pictorial representation of connection matrix

As discussed earlier, we have five circles in each vertical column for a five-dimensional system. Please visit the supplementary attached file for figures and descriptions. Each node in such a system has five connections at a time. five, six, and seven different colors of, at best, 32,64, and 128 circles represent the number of nodes in such states. Moreover, we extract the following beautiful pattern of such a connection.[29] As the number of system dimensions increases, previous pictures emerge twice between the newly generated nodes. Following this footprint, it is possible to create photographs of beauty similar to that of the higher-dimensional system. However, it is less important because we obtain the mechanism of such a formulation.

The study claims that two-dimensional phase space might make any dimensional connection possible. This analysis chooses genes as individual states of the system.

We focus on a particular Fig. 5. Here, the system has six genes, and the connection of all genes between each state is piecewise linear.[30] Their relations are either represented from the top or the bottom. Five genes have a relationship similar to gene 6, but it has a zigzag cycle under the top or above the bottom connections of Fig. 5. Throughout the picture, we see links that appear twice. Other genes follow the same pattern, which is visible in this figure. Point to be noted that the lowest consecutive two-dimension might not follow such evidence. Nevertheless, their connection will be twice their immediate higher dimension, *i.e.*, dimension 3. These processes help us obtain every connection on the hypercube without explicitly representing them.

After this work, focusing on hypercube representation might be optional. Instead, we might obtain all possible connections on a two-dimensional graph. We have presented a seven-dimensional system in another figure (please look at the supplement file) for similar nodal connections of a real hypercube in a two-dimensional graph.

8. Results and Discussion

The study presents a 4−dimensional differential equation to determine the system's behaviors, investigate the discrete output, and validate the result with its piecewise linear differential equation.[30] Asynchronous behaviors that rarely find stable or unstable fixed points have been studied. We then turn the system into a connected piecewise system and investigate its dynamics in state space and on the hypercube.[31,32]

This study will be more relevant to understand synchronous Boolean network models, an unrealistic system representative of simplified real biological systems.[33,34] To investigate such a system, iteration is indispensable for the synchronous switching system Eq. (2). However, a biological system does not have such switching.[35] As a result, a

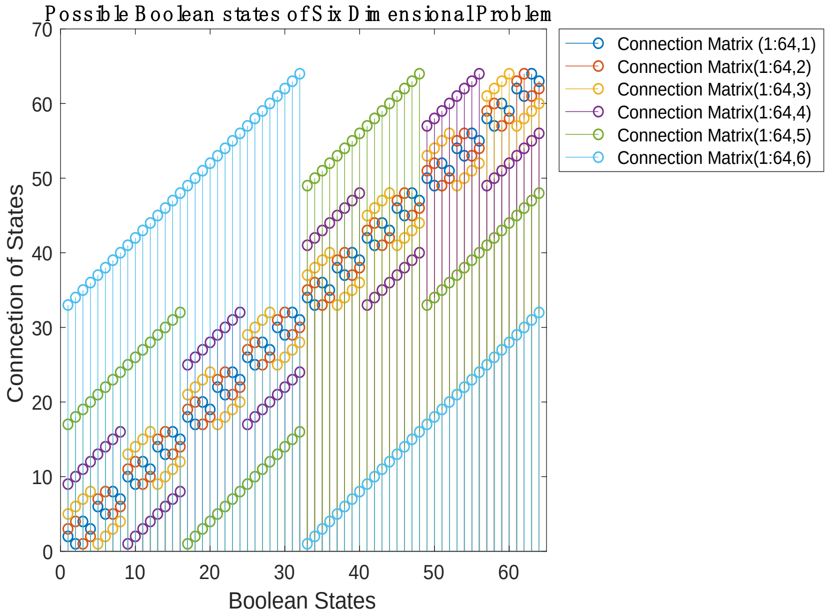

Fig. 5 A representative of a six-dimensional connection matrix.

piecewise system is proposed and studied by various methods.[36] The dynamics of such a system can be depicted as a state transition diagram, an elegant way of representing its dynamics,[37] for a quick reference please see the Figs. 3 or 5 (as a two-dimensional representative).

The study presents best to fill that scientific knowledge gap about the representation of differential equation solutions on the hypercube.[38-39] An expression of three or four dimensions is available in such ambiance [40]. A spitting image of the five dimensions is unavailable, but half of the understanding is possible and reported early in 1980[41]. We have proposed a valuable method to move further to any higher dimension. We might wonder about our limitation in the development of infinite arithmetic.[42-44] However, significant insight is possible if someone wishes to test our results on the advanced tool. Each row of these metrics presents topological equivalents to state-space connections *i.e.*, Table 4. For example, consider Table 4 such that you have eliminated the last two columns and kept the first sixteen rows, which provides four-dimensional system connections. Consider the first row (left column), where all genes involved in the system are in the off state, and have connections with the following states 2 3 5 and 9. Please see Fig. 4(c) for a clear picture of the state space connections on the hypercube.[45] Finally, a generalized algorithm is developed. Due to the limitations of advanced tools such as supercomputers, we have tested the results for a network comprising 25 genes that might be useful to obtain a new direction and fill the gap in scientific knowledge.

9. Conclusion

We depict the unique way that led us to generalize it for any dimension. A compute code in MATLAB is available in the appendix and might be tested for any dimensional system.[46] We have explicitly presented the hypercube's six-dimensional connections utilizing metrics to set a pathway of generalization.[47] Lower dimensional cases are available in the supplement document appended with this article. Interested readers get insightful thoughts and understand the work explicitly if the original work seems difficult to them.

This article might benefit from problems of the higher dimension in computer, electrical, and software engineering.[48] Mathematicians and mathematical biologists can use it to determine eigenvalues of the higher dimensional system since the theory of linear fractional maps is well established. We have tested it for a couple of references. As a result, once we implement linear fractional maps for their similar dimensions, we need several metrics manipulations to determine the outcome in the matrix and the eigenvalues of those metrics. We already know that the system's complexity is enormous in Boolean states, and the variables associated with piecewise linear differential equations need further attention.[49-51] Considering the article's length, we did not incorporate the results here. Such work might be addressed in a subsequent manuscript since such a model is unavailable.

Profound theoretical development has yet to be achieved since we have tested our findings numerically and validated them through pictorial representations.[52] In the future, we could develop such theoretical stuff. At least in the form of lemmas, we will try to gain insight. It would be interesting if we could obtain some idea about the chaos behavior in this setup on the hypercube. Additionally, if the threshold is increased, this setup might need redefinition to tackle it. We didn't try it on in this present situation.

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Conflict of Interest

There is no conflict of interest.

Supporting Information

Applicable.

Appendix

The beauty of science and its limitations are precisely depicted in this section. Reviewers may write the following lines in MATLAB to obtain its flavor. Please run it on a computer that has incredible memories like supercomputers.

```
dim=input ('Dimension of the problem:' )
dim; V=[1:2^dim]'; A = zeros(2^dim,dim);
for i=1: dim % This loop is for the column of the Branch
Matrix
n = pow2(i-1); k = 0;
count = 1;
for j=1: 2^dim % This loop is for the rows of the Branch
Matrix
if n > k && count == 0
A(j,i) = V(j) + n; k = k+1;
```

```
if n == k   count = 1; k=1;    end
else
A(j,i) = V(j) - n; k = k+1;
if k == n          count = 0; k=1;          end
end
end
end
A;
```

Just think, the combinations of 3 billion characters such as A G T P are the representatives of genome sequences of individual human beings. Due to the limitations of available tools, we have tried the connection for 25 genes under the setup of the so-called Hypercube.

Higher than that dimension, *i.e.*, 25, I didn't get any results due to the deficiency of memories of computers. This is because of the generated matrix dimension that is just gigantic. It is also a representative of complexity and the flaw of innovation. The available cutting-edge technology is still insufficient due to the hidden complexity.

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