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Quantitative modeling of gene networks of biological systems using fuzzy Petri nets and fuzzy sets

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Abstract Quantitative demonstrating of organic frameworks has turned into an essential computational methodology in the configuration of novel and investigation of existing natural frameworks. Be that as it may, active information that portrays the framework's elements should be known keeping in mind the end goal to get pertinent results with the routine displaying strategies. This information is frequently robust or even difficult to get. Here, we exhibit a model of quantitative fuzzy rational demonstrating approach that can adapt to obscure motor information and hence deliver applicable results despite the fact that dynamic information is fragmented or just dubiously characterized. Besides, the methodology can be utilized as a part of the blend with the current cutting edge quantitative demonstrating strategies just in specific parts of the framework, i.e., where the data are absent. The contextual analysis of the methodology suggested in this paper is performed on the model of nine-quality genes. We propose a kind of FPN model in light of fuzzy sets to manage the quantitative modeling of biological systems. The tests of our model appear that the model is practical and entirely powerful for information impersonation and thinking of fuzzy expert frameworks.

1. Introduction

As of late computational models show a crucial device which may be utilized for the configuration, enhancement and in *silico* verification of a new natural system previously its trial realization (Chen et al., 2012; Chen and Wang, 2006). Picking a fitting demonstrating procedure relies on the multifaceted nature of the watched GRN, wanted accuracy of final results and the accessibility of precise information, which portray the dynamical behaviors of any system. For the sake of standing quantitative techniques, the most part of the numerical reenactments should be taken into account of the arrangement of customary differential conditions. While depicting frameworks' progression precisely, this methodology requires exact data with a specific goal to deliver valuable simulation results

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(de Jong, 2002; Weiss, 1997; Gillespie, 2007; Cheng and Lu, 2012).

The flow of a discretionary GRN behavior can be generally portrayed with three unique procedures, i.e., transcription, translation and degradation of biological processes. Each procedure of the biological processes can be given no less than one substance response and its having a place kinetic rate also may be known as reaction kinetics. Kinetic rates can be now and again (precisely) controlled by utilizing different parameter forecast and estimation systems. On the off chance that test information for each process is accessible, these strategies can gauge missing Kinetic rate data, and can be utilized as a part of an ODE model (Moles et al., 2003; Lillacci and Khammash, 2010; Sun et al., 2012). Nonetheless, test data are frequently difficult to get. In these ones the parameter assessment methods can't be utilized and an alternate methodology is required.

Lately fuzzy Petri net has been built up as a new approach for the quantitative demonstrating of genes network (Du et al., 2005; Hamed et al., 2010). Fuzzy systems comprise linguistic terms (e.g. gene expression level is medium or high) and are direct to construct and additionally to make it easy to understand. At the point when kinetic rate data of the model are recognized the precision of fuzzy model demonstrating methodologies is equivalent to the current sureness methodologies, for example, ODE based models (Hamed and Ahson, 2011). Moreover, existing fuzzy methodologies can be utilized to acquire a qualitative reaction of the system's flow despite the fact that the kinetic rates are obscure. Uncertain data yet still present a noteworthy snag for acquiring the quantitative answer utilizing existing fuzzy modeling approaches (Hamed et al., 2010; Hamed and Ahson, 2011).

Existing fuzzy modeling approaches generally comprise the key occasion depictions e.g. gene activated or gene repressed in the gene networks (Windhager, 2013; Kitney and Freemont, 2012; Xia et al., 2012) but rather are all things considered not able to adapt to the quantitative reaction of the system, for example, gene concentration or degradation changes. Then again, Fuzzy models built to depict a gene network of biological systems (GRN), however are utilized as a qualitative diagram of the network (e.g. when genes are activated genes or repressed genes, how species regulated with each other, and so on.) (Suraj, 2013; Liu et al., 2016a,b).

To the best of our knowledge, it is the first time that an FPN reasoning process of fuzzy model in the learning representation precisely and formally is used to make quantitative inferences of a biological system. Here in this paper we exhibit another methodology that thoroughly takes advantage of fuzzy models to get the quantitative outcomes. The methodology can quantitatively portray the behavior of specific organic processes despite the fact that the kinetic rate data are uncertain or known just somewhat.

Furthermore, the proposed technique can be utilized as a part of a hybrid approach existing best in class quantitative demonstrating approaches just with the portions of the system, which may be vaguely characterized, i.e., where dynamic data are absent. We show the presented method on the foundation and examination of a FPN model of the nine-quality genes with activating and repressing processes.

It can be concluded that the experimental results of our FPN and fuzzy sets approach are feasible and acceptable. This illustrates that the FPN approach is able to perform as well as other methods for this task and other tasks, noting that the FPN approach could be a very good alternative to other methods of biological processes. The limitations of the study are those characteristics of methodology that impacted the interpretation of the findings from our quantitative modeling of gene networks of biological systems.

Section 2 depicts the use of FPN rationale with fuzzy set to organic frameworks computational. Foundation of a fuzzy concept of a biological network is introduced in Section 3. The concept of inhibition arc in FPN model is introduced in Section 4. Illustrative example of GRN with nine genes is introduced in Section 5. Implementation of a biological process of GRN with reasoning algorithm is introduced in Section 7. Reenactment comes about and their examination is introduced in Section 8.

2. FPN and fuzzy sets as a computational approach for GRN

Handling the data by utilization the capability of FPN model can be additionally indicated to as computing method for process a words. FPNs provide a dual use of formal and graphical tool, which consolidate the graphical capacities of PN and the abilities of fuzzy sets to build a model of fuzzy rules. In order to depict the end goal as a procedure with FPN model, all the fuzzy linguistic variables (i.e. I/O) must be characterized. Depending on our model the expert is required to accurately make a decision on the certainty factor (CF) of a transition FPN rule. In this case we can see the theory of fuzzy sets is more resilient in representing with unbelieves in representation of knowledge.

In FPN model the determination of the estimations of the output places (p_j) is computed with the assessment of if-then fuzzy transitions of the FPN model governs on the input fuzzy places and their membership function values.

FR (IF gene1 expression is *VeryHigh* and gene2 expression is *Medium* THEN target gene expression is *High*), indicates that the target gene expression is High. FPN can be utilized as a part of the mix with the conventional, i.e., crisp values. In any case, FPN estimations of input places of FPN model and the values of output places of FPN should be computed with a specific process to consolidate the fuzzy calculation of the inputs and outputs (see Fig. 1).

In a FPN, various kinds of fuzzy inference rules can be performed. The common kinds are:

A simple type of fuzzy production mechanism:

- $IF\ d_i \rightarrow d_j$ with respect to $(CF_j = f(t_j))$;

A composite type of conjunctive mechanism:

- $IF\ d_1\ AND\ d_2\ AND\ d_3 \ldots\ AND\ d_j \rightarrow d_j\ (CF_j = f(t_j))$;

A composite type of disjunctive mechanism:

- $IF\ d_1\ OR\ d_2\ OR\ d_3 \ldots\ OR\ d_j \rightarrow d_j\ (CF_j = f(t_j))$;

Information got from this modeling methodologies can assist us with the foundation of the FPN of the watched handle. For instance, despite the fact that some dynamic information may be obscure, we can utilize an ODE as a base model to

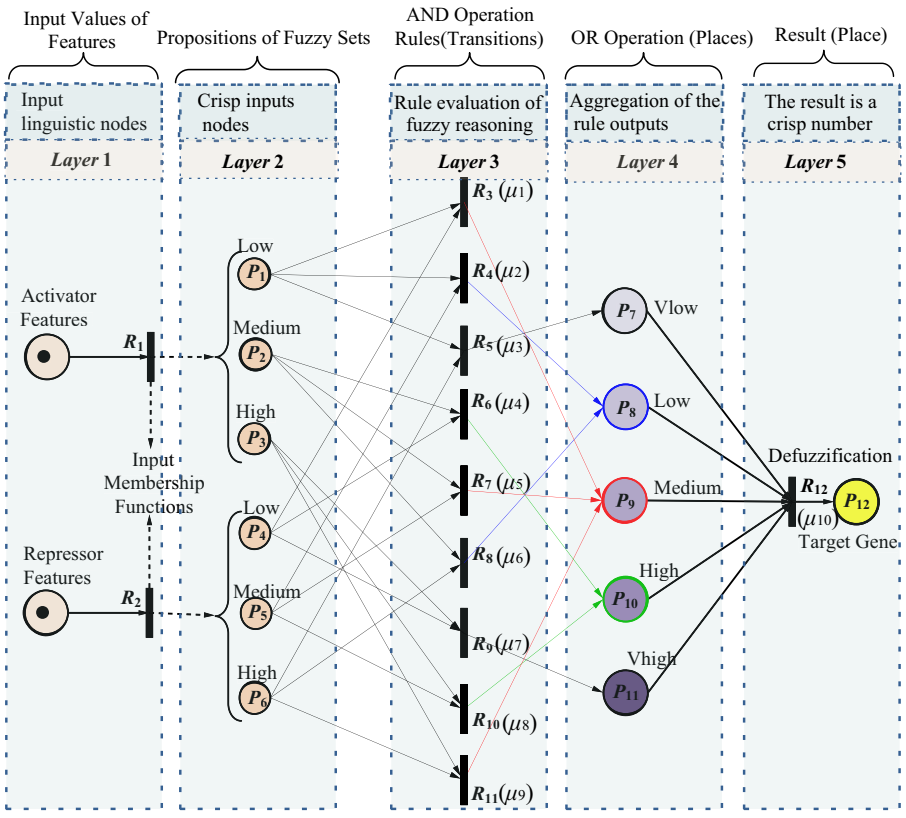

Figure 1 Handling the data with FPN. Activator features and Repressor features are fuzzified with MF to their conforming fuzzy set values of transitions rules. The transitions rules product output fuzzy linguistic variables *Vlow*, *Low*, *Medium*, *High* and *Vhigh* which are defuzzified and matches to their values.

decide I/O furthermore and to make an unpleasant estimation on the relations among the I/O.

3. Fuzzy concept of a gene networks

Current condition of the biological network is typically portrayed with the level of genes level or concentrations of watched chemical types. Fuzzy depiction of the present state can be then again characterized by linguistic variables which are defuzzified to get the outputs.

The formal depiction of a fuzzy variable is resolved with its MF, which characterizes the MF value from (0 to 1) for each input output variable. Most MFs have a triangular shape (see Fig. 2). The fuzzy MF of the different genes, i.e. changes in gene concentrations is depicted in Fig.2. It is depicted with five fuzzy sets, named as *Very low*, *Low*, *Medium*, *High*, *and Very high*.

Our method will be utilized to quantitatively depict the framework status changes created by the responses in watched GRNs. In each place truth degree value (i.e. $\alpha(p_i) = D_i$), will be characterized with the level in a specific period and their relating MF values (e.g. the concentrations of a gene protein can extend from 0 to 1 nM, however the concentrations from 0 to 0.25 nM can be referred to as very low, concentrations from 0 to 0.5Mn can be referred to as low, concentrations from 025 to 0.75 nM can be referred to medium, concentrations start from 0.5 to 1 Mn will referred to as high, and concentrations start from 0.75 to 1 Mn will referred to as very high; see Fig. 2.

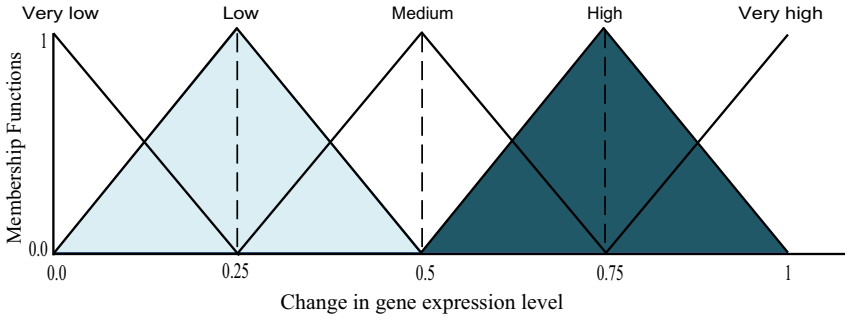

Figure 2 The fuzzy membership function of gene expression.

The final result of our FPN model will be characterized as outright changes of the concentrations brought on by the procedures that portray watched chemical processes. FPN can be utilized to quantitatively depict gene networks of biological system processes with vague or incomplete data. So as to make the approach perfect with other demonstrating techniques that as it were work with crisp values two main processes of FPN fuzzification and defuzzification are utilized as a part of the model as I/O.

We will show the foundation of a quantitative FPN approach on the four genes called repressilator (see Fig. 3) however, we want to show a simple example of FPN mode for two processes of activating and repressing (see Fig. 4) and then how we can map the relationship from biological concept to knowledge FPN. Despite the fact that the proposed method can be utilized to portray the entire model, we will apply it with the gene regulatory network with nine genes and 8 edges (see Fig. 5).

4. The concept of inhibition arc in FPN model

In (Hamed et al., 2010) provide a good mechanism for machine learning using FPN. The formula is dependent on the definition of Triangular norms (t-and s-norms) as computational models of the logical connectives. A transition t_i fires depending on its value of firing (i.e. the conditions for firing a transition) z exceeds its threshold λ_i.

$$z = T_{i=1}^{n}[(\lambda_i \rightarrow \alpha(p_i))sw_i]$$

where "→" denoted a fuzzy implication. The goal of this type of arc is to model the concept of inhibitory gene. The net places of the two-valued while carrying a nonzero number of tokens prevent the associated transitions from firing. On firing a transition t_i, the token at its input place is computed by

$$\alpha(p_{i(t+1)}) = \alpha(p_{i(t)})tz'$$

where t without bracket denotes 't' norm.

$$tz' = 1 - z$$

However, firing or processing of the transition t_i, the token or value of its output place $\alpha(p_i) = y_j$ is determined by

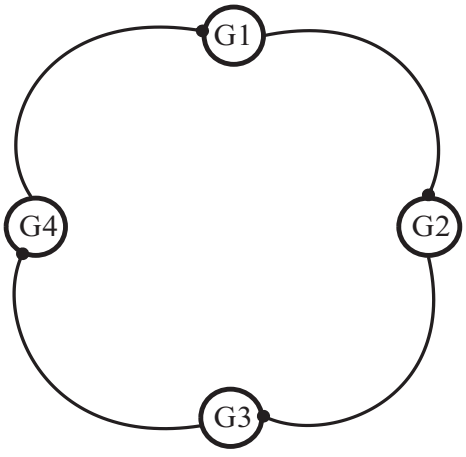

Figure 3 An example of Circular repression network of the four-genes.

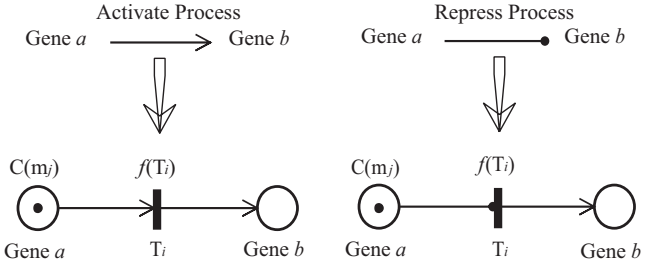

Figure 4 Gene relationships and their fuzzy Petri nets models.

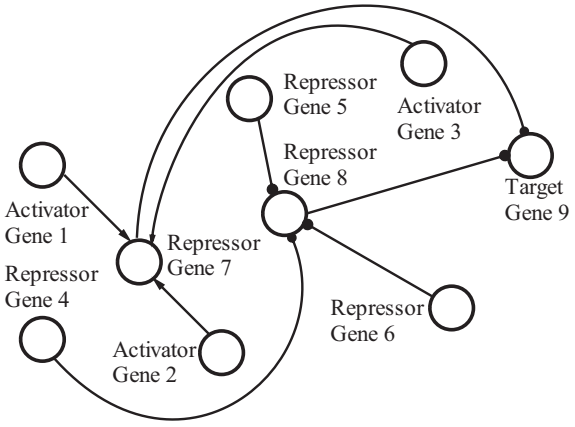

Figure 5 An example of gene regulatory network with nine genes and 8 edges.

$$(y_{i(t+1)}) = (y_{i(t)})sz$$

Regarding the model of the FPN the inhibitory is achieved by respecting to the complement of the token of the inhibitory source see Fig. 4 this concept $\overline{x_i}$, participates to the following formula to describe the value of firing z.

$$z = T_{j\neq i}^{n}\{[(\lambda_j \rightarrow \alpha(p_j))sw_j]\}t[(\lambda_i \rightarrow \overline{\alpha(p_i)})sw_i]$$

then

$$z = z^{+}tz^{-}$$

where

$$z^{-} = [(\lambda_i \rightarrow \overline{\alpha(p_i)})sw_i](\text{Inhibitory component})$$

and

$$z^{+} = T_{j\neq i}^{n}[(\lambda_j \rightarrow \alpha(p_j))sw_j](\text{Excitatory component})$$

We can see the value of $w_i = 0$ in our model and $\lambda_i = 1$, this mean inhibitory value effect z^{-} and will equally straightly $\overline{\alpha(p_i)}$ hence $\alpha(p_i) = 1$ this mean prohibits the rule or transition from enabling or firing.

5. Illustrative example of GRN with nine genes

The genome, including the arrangement of all genes in a living being alongside their level values, is treated to be an exchanging system. Such systems relate genes or gene products (for example, protein) from one to other as a chart, where the genes and relations among them relate to atoms and their existing

interrelationships. A coordinated edge keeps running starting with one gene to next gene. Consider the diagram portrayed in Fig. 5. Scientifically, a network is represented to a chart or graph consisting of a set of genes (i.e. places) and edges that associate two components in genes.

6. Fuzzy reasoning algorithm

As per the elements of FPN model of genes network, we can portray the reasoning process of fuzzy model in the learning representation precisely and formally. Before explaining the algorithm, some definitions are given below:

(1) Operator $\oplus$: $K1 \oplus K2 = K3$ where $K1$, $K2$, and $K3$ are all $m \times n$- dimensional matrices,
(2) Operator $\otimes$: $K1 \otimes K2 = K3$ where $K1$, $K2$, and $K3$ are $(m \times p)$, $(p \times n)$, $(m \times n)$-dimensional matrices, respectively, such that $d_{ij} = \max\{k1, k2\}$, $1 \leqslant k \leqslant p$ where α is the truth vector. $\alpha = (\alpha_1, \alpha_2, \ldots, \alpha_n)^T$, truth degree vector.
(3) Operator $\circ$: $K1 \circ K2 = K3$ where $K1$, $K2$, and $K3$ are all $m \times n$-dimensional matrices with $k1ij$, $k2ij$, and $k3ij$ being their elements respectively, and $k3_{ij} = k1_{ij} \times k2_{ij}$.
(4) *Operator* $\rightarrow$: $K1 \rightarrow K2 = K3$ where $K1$, $K2$, and $K3$ are all $m \times n$-dimensional matrices with $k1ij$, $k2ij$, and $k3ij$ being their elements respectively, and $d_{ij} = 1$, if $k1_{ij} \geqslant k2_{ij}$, $k3_{ij} = 0$ if $k1_{ij} < k2_{ij}$, $i = 1, 2, \ldots, m$, $j = 1, 2, \ldots, n$.

Depending on our algorithm the complete and functional steps are as follows:

The Input: The truth value of y_s of each d_s where $y_s \in [0.1]$.

The Output: The truth value of each proposition (i.e. d_j). The structure of our model represented as (transitions, set of places as a set of genes with two processes of activating and repressing), and the output of the target place are given as target gene.

Give k a chance to indicate the reasoning steps, then the fuzzy algorithm of the fuzzy model is.

Step 1: Set k = 1, where k denotes the iteration.

Step 2: Check which place will be enabled the variable D^k which indicates that

$$D^{(k)} = (d_i)^{(k)}_{m\times 1} = \overrightarrow{M_{k-1}} \rightarrow \overrightarrow{Th},$$

Step 3: Calculate the truth degree vector of fuzzy tokens of input places, if the value of $D^{(k)}$ is a nonzero; else, go to step 7

$$\alpha(p_i) = (\mathrm{I}^{\circ}\mathrm{LW})^T, \overrightarrow{M_{k-1}}$$

where $\mathrm{w} =, [\mathrm{LW1}, \mathrm{LW2}, \ldots, \mathrm{LWn}]_{m\times n}$

Step 4: Determine the vector $E^{(k)}$ that refer to the transitions fired of output places $\alpha(p_i)$

$$T_j = (t_j)^{(k)}_{1\times n} = (E_{1\times m} \times I) \rightarrow ((D^{(k_m)})^T \times I)$$

Step 5: with T_j in case the matrix is a nonzero, then the value of vector Y_i is determined by the following function; otherwise, go to step 7

$$Y_i = ((T_j^{\circ}\alpha(p_i), \vec{U})$$

Step 6: After these steps we need to calculate the new marking

$$\overrightarrow{M_k}$$

$$\overrightarrow{M_K} = \overrightarrow{M_{k-1}} \oplus (GW, Y_j)$$

If $\overrightarrow{M_K} = \overrightarrow{M_{k-1}}$ this referees to no more processes; otherwise let $k1 = k1 + 1$, and go to step 2.

Step 7: No more processes and then the game is over.

It is important to call attention to that the I/O factors utilized in the reasoning process can have diverse structures taking into account the fuzzy sets. The principal favorable position of the proposed method is that we can consider specific case and get which set of factors is most in understanding with genuine gene network in the learning representation what's more, thinking procedure.

7. Implementation of a biological process of GRN

A good example regarding gene network of biological processes is proposed to demonstrate the method of FPN algorithm. Hence, FPN and fuzzy sets are utilized here to represent the GRN in biological processes. Via the proposed model, GRN can be changed over into relationships between FPN places and FPN transitions (see Fig. 6), and after that the GRN caused by different situations can be specified.

Let d_i be nine genes (i.e. propositions), then the model existed in the system of the GRN are defined as shown below

D_1: IF d_1 AND d_2 AND d_3 THEN d_7, ((0.3, 0.7), (0.3, 0.6), (0.2, 0.7); 0.47, 0.29, 0.24; (0.96, 0); 1);
D_2: IFd_4 THEN d_8, ((0.2, 0.8); 1; (0.96, 0); 0.3);
D_3: IFd_5 THEN d_8, ((0.3, 0.6); 1; (0.90, 0); 0.3);
D_4: IFd_6 THEN d_8, ((0.2, 0.7); 1; (0.99, 0); 0.4);
D_5: IFd_7 THEN d_9, ((0.2, 0.8); 1; (0.99, 0); 0.6);
D_6: IFd_8 THEN d_9, ((0.2, 0.8); 1; (0.98, 0); 0.4).

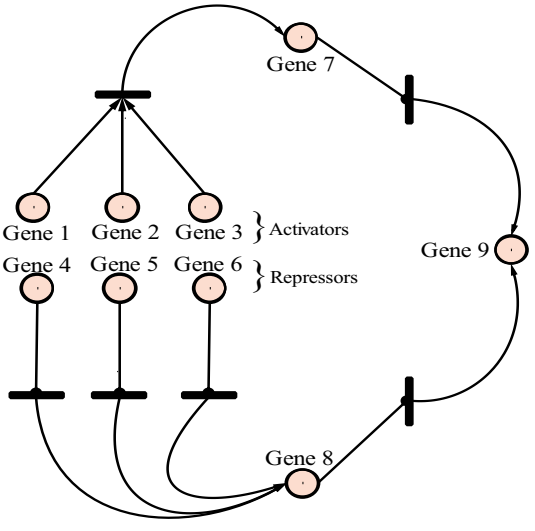

Figure 6 FPN model of Fig. 5 of gene regulatory network with nine genes and 8 edges.

The potential gene expression of the network gene concentration is dealt with as Petri net places, and causal connections among them are dealt with as transitions. In view of the transition standards presented, we can delineate above six proposition rules into a fuzzy set as appeared in Fig. 6. The places in the representation model and their relative propositions are displayed in Table 1. Genes p_1, p_2, p_3, p_4, p_5, and p_6 are starting genes from our network model in Fig. 2, the p_7 and p_8 intermediate places, and the place (i.e. target gene) p_9 is a terminating gene.

Depending on the degree of input place (i.e. $\alpha(p_i) = D_i$), we suppose that the values of the starting places for this system are as follows:

$$\vec{\alpha}(p_1) = (0.8, 0.1), \quad \vec{\alpha}(p_2) = (0.9, 0.05),$$
$$\vec{\alpha}(p_3) = (0.6, 0.35) \quad \vec{\alpha}(p_4) = (0.5, 0.4),$$
$$\vec{\alpha}(p_5) = (0.7, 0.2), \quad \vec{\alpha}(6) = (0.8, 0.15).$$

With the fuzzy sets and Fig. 6, we can gain

$$I = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix} \quad O = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 1 \end{bmatrix}$$

$$GW = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0.3 & 0.3 & 0.4 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 1 \end{bmatrix}$$

$$\vec{U} = [(0.96, 0.1) \quad (0.96, 0.1) \quad (0.90, 0.0) \quad (0.99, 0.0) \quad (0.99, 0.1) \quad (0.98, 0.0)]$$

$$\text{LW} = [0.470 \quad 0.29 \quad 0.240 \quad 1.0 \quad 1.0 \quad 1.0 \quad 1.0 \quad 1.0 \quad 0.0]^T$$

$$\overrightarrow{Th} = [(0.31, 0.70)\ (0.30, 0.61)\ (0.20, 0.71)\ (0.20, 0.80)\ (0.30, 0.6)\ (0.21, 0.71)\ (0.20, 0.80)\ (0.20, 0.80)\ (1.0, 0.0)]^T$$

The initial marking vector of the first iteration is

$$\overrightarrow{M_0} = [(0.80, 0.10)\ (0.91, 0.05)\ (0.61, 0.35)\ (0.50, 0.40)\ (0.70, 0.21)\ (0.80, 0.15)\ (0.0, 10)\ (0.0, 10)\ (0.0, 10)]^T$$

On the off chance that we decipher the input and output thinking as arithmetical t-standard, then, as per the thinking calculation of our fuzzy PN model, we can process the accompanying.

Table 1 Places of the FPN model and with respect to their propositions and truth value.

Place (p_i)	Proposition (d_i)	Truth value (α_i)
$p1$	Activator gene 1 that increases gene 7 expression	(0.8, 0.1)
$p2$	Activator gene 2 that increases gene 7 expression	(1.0, 0.0)
$p3$	Activator gene 3 that increases gene 7 expression	(0.6, 0.35)
$p4$	Repressor gene 4 that decreases gene 8 expression	(0.5, 0.4)
$p5$	Repressor gene 5 that decreases gene 8 expression	(0.7, 0.2)
$p6$	Repressor gene 6 that decreases gene 8 expression	(0.8, 0.15)
$p7$	Repressor gene 7 that decreases gene 9 expression	(0.0, 1.0)
$p8$	Repressor gene 8 that decreases gene 9 expression	(0.0, 1.0)
$p9$	Target gene 9	(0.0, 1.0)

(1) Compute the empowered starting place vector $\alpha(p_i) = D_i$

$$D_1 = \overrightarrow{M_0} \rightarrow \overrightarrow{Th} = [1 \quad 1 \quad 1 \quad 1 \quad 1 \quad 1 \quad 0 \quad 0 \quad 0]^T$$

Depending on this vector, the process to compute the subsequent steps of the truth degree vector will proceed further.

(2) the fuzzy tokens of places are computed as a vector in this step as a set of genes (α(p1)):

$$\alpha(p_1) = (I^{\circ} W)^T, \vec{M_0})$$
$$= [(0.81, 0.115)\ (0.51, 0.40)\ (0.70, 0.20)\ (0.80, 0.15)\ (0.0, 10)\ (0.0, 10)].$$

Depending on our problem of gene network we suggest the following set of weighting vectors ω = (0.35, 0.52, 0.35) in the fuzzy model.

(3) After computing the value of each input place the second step to calculate the enabled transition vector T1

$$T_1 = (E \times I) \rightarrow (D^T \times I) = \text{Then } T_1 = [1 \quad 1 \quad 1 \quad 1 \quad 0 \quad 0].$$

(4) Then determine the output of the truth degree vector α (pi) = y1.

$$y_1 = [(T1^{\circ} \alpha(p_1) \otimes \vec{U})$$
$$= (0.768, 0.115)\ (0.48, 0.40)\ (0.63, 0.20)\ (0.791, 0.15)\ (0.0, 1.0)\ (0.0, 1.0)].$$

(5) After the first iteration is to compute the new marking $\vec{M}_1$

$$\vec{M}_1 = \vec{M_0} \otimes (\text{GW}, y_1)$$
$$= [(0.80, 0.10)(0.9, 0.50)(0.60, 0.350)(0.50, 0.40)(0.7, 0.2)(0.8, 0.15)(0.768, 0.115)(0.675, 0.219)(0, 1)]^T.$$

(6) With the next new iteration, k = 2

$$D_2 = [1,\ 1,\ 1,\ 1,\ 1,\ 1,\ 1,\ 1,\ 1,\ 1,\ 0]^T$$

$$T_2 = [1\quad 1\quad 1\quad 1\quad 1\quad 1]$$

$$Y_2 = [(0.768, 0.115)(0.480, 0.4)(0.63, 0.2)(0.792, 0.15)\ (0.760, 0.115)(0.661, 0.219)]^T.$$

$$\overrightarrow{M_2} = [(0.80, 0.10)(0.91, 0.05)(0.61, 0.35)(0.50, 0.40)\ (0.70, 0.21)(0.80, 0.15)(0.768, 0.115)\ (0.675, 0.219)(0.725, 0.149)]^T.$$

(7) For next iteration, k = 3

$$\overrightarrow{M_3} = [(0.80, 0.10)\ (0.91, 0.05)(0.61, 0.35)\ (0.50, 0.40)\ (0.70, 0.21)\ (0.80, 0.16)\ (0.83, 0.115)\ (0.715, 0.219)\ (0.83, 0.24)]^T.$$

Depending on the results of third iteration, $k = 3$ we saw that the $= \overrightarrow{M_2}$ and this refers that there are no more processes. The final result is [(0.80, 0.10) (0.91, 0.05) (0.61, 0.35) (0.50, 0.40) (0.70, 0.21) (0.80, 0.16) (0.83, 0.115) (0.715, 0.219) (0.83, 0.24)]^T, which includes the values of propositions of gene network. Therefore, we can acquire the thinking aftereffects of all the explanations in the considered circumstance. In this framework, the conclusion will be that the model may have the issue of gene 9 (i.e. *d*9) with its truth quality being (0.83, 0.24). This number means that the enrollment level of truth degree of gene 9 is 0.725, while the non-membership value is 0.149. Along these lines, by utilizing our model, the proposed FPN model is more adaptable in managing fuzzy data in the reasoning process.

Then again, it is conceivable to create diverse thinking calculations for shortcoming conclusion of the air ship generator taking into account distinctive blends of FPN model administrators and intuitionistic fuzzy t-standards. In this illustration, we considered the (Min and Max), the FPN model as deduction administrators to promote show the proposed FPN model. The thinking comes about determined are organized in Table 1. As shown, contingent upon the specific set of thinking administrators utilized, the got consequences of the data surmising might be distinctive, consequently prompting diverse choices. Be that as it may, in this illustration, it appears to be clear that the likelihood of the framework having the flaw of d9 is high.

In this case and from the above affectability examination, we can watch that appropriate determination of info/yield administrators playing a critical part in the information thinking since they may influence the thinking consequences of the master framework. To begin with, the information derivation administrators can be dictated by the leader through counseling authentic information in the event that they have led a comparable flaw examination some time recently. Second, the rationale thinking administrators can be doled out by the leader relying upon the issue considered. Since various sorts of total administrators can be yielded by utilizing an alternate sign of the weighting vector, the information/yield administrators can be picked agreeing to the different strategies recommended for OWA weight era in [46]. What's more, in the most pessimistic scenario, distinctive arrangements of learning thinking administrators can be used together so that the leader can take an extensive variety of situations into thought what's more, get more finish data for choice making.

8. Conclusion

Incomplete active data show a noteworthy hindrance in the quantitative demonstrating of organic systems. Despite the fact that a few data are absent, different parameter estimation procedures might be utilized for their assessment. These methods however regularly require substantial arrangements of test data, which are in some cases hard or even difficult to acquire. The proposed algorithm can manage uncertain, unclear, and vague data in a more adaptable and viable way. Thus, it can be utilized for systems based frameworks where data are inaccessible or problematic.

A novel approach of FPN is presented to quantitative modeling of gene networks following through fuzzy set. The FPN model system as presented in this paper determine the gene network behavior of specific organic processes despite the fact that the kinetic rate data are known just somewhat. Here in our approach that endeavors the properties of FPN and fuzzy sets empowers us to get quantitatively applicable reproduction comes about despite the fact that the main data are imperfect.

Since the proposed technique depends on the concept of fuzzy the dynamic data that are known, differences between the fuzzy and the customary model would increment with the quantity of procedures displayed by fuzzy model. Be that as it may, the approach would in any case have the capacity to deliver quantitative outcomes with natural importance. Numerical results appear that the FPN model is reasonable and very successful for information representation of intuitionistic fuzzy frameworks.

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