Decision P-trees and Random P-forests

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Goals of this work: (1) To implement decision trees and random forests in P systems
 (2) To implement a machine learning technique to obtain decision trees and random forests from given data through membrane and object rules

Previous Works

Decision Tree Models Induced by Membrane Systems (2015) J. Wang, J. Hu, M.J. Pérez-Jiménez, A.Riscos-Núñez ROMJIST Vol.18 No.3 pp 228-239

Wang <i>et al</i> .	Our approach	
Tree-like objects	 Trees defined by the membrane structure	
External Induction Algorithm	 Algorithm runs by P rules within an entropic manner	

A Decision Tree is a representation for a discrete-valued function

 $f: A_1 \times A_2 \times \cdots \times A_n \to B$



An example: protein-protein interactions prediction



(From "What are decision trees ?". Carl Kingsford & Steven L. Salzberg. Nature Biotechnology 26 No. 9, 1011 – 1013 (2008))

Implementing decision trees by membrane structures (I)



Objects alphabet

{ECno, ECyes, Sfno, Sfyes, SCLno,SCLyes, GDL5yes,GDL5no YES,NO}

Implementing decision trees by membrane structures (II)

а	Gene Pair	Interact?	Expression correlation	Shared localization?	Shared function?	Genomic distance
	A-B	Yes	0.77	Yes	No	1 kb
	A-C	Yes	0.91	Yes	Yes	10 kb
	C-D	No	0.1	No	No	1 Mb
	:					





Implementing decision trees by membrane structures (III)

а	Gene Pair	Interact?	Expression correlation	Shared localization?	Shared function?	Genomic distance
	A-B	Yes	0.77	Yes	No	1 kb
	A-C	Yes	0.91	Yes	Yes	10 kb
	C-D	No	0.1	No	No	1 Mb





Implementing decision trees by membrane structures (IV)

а	Gene Pair	Interact?	Expression correlation	Shared localization?	Shared function?	Genomic distance
	A-B	Yes	0.77	Yes	No	1 kb
	A-C	Yes	0.91	Yes	Yes	10 kb
	C-D	No	0.1	No	No	1 Mb
	:					





Implementing decision trees by membrane structures (V)

а	Gene Pair	Interact?	Expression correlation	Shared localization?	Shared function?	Genomic distance
	A-B	Yes	0.77	Yes	No	1 kb
	A-C	Yes	0.91	Yes	Yes	10 kb
	C-D	No	0.1	No	No	1 Mb









а	Gene Pair	Interact?	Expression correlation	Shared localization?	Shared function?	Genomic distance
	A-B	Yes	0.77	Yes	No	1 kb
	A-C	Yes	0.91	Yes	Yes	10 kb
	C-D	No	0.1	No	No	1 Mb





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	A-C	Yes	0.91	Yes	Yes	10 kb
	C-D	No	0.1	No	No	1 Mb
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	:					







Applying a machine learning technique inside a P system

Sample	X	Y	Z	Decision
1	High	High	High	Yes
2	High	High	High	Yes
3	Low	High	Low	Yes
4	Medium	High	High	Not

Applying a machine learning technique inside a P system

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3	Low	High	Low	Yes
4	Medium	High	High	Not

 X^1_{High} Y^1_{High} Z^1_{High} $Decision^1_{YES}$ X^2_{High} Y^2_{High} Z^2_{High} $Decision^2_{YES}$ X^3_{Low} Y^3_{High} Z^3_{Low} $Decision^3_{YES}$ X^4_{Medium} Y^4_{High} Z^4_{Low} $Decision^4_{NO}$

A generic algorithm to build decision trees from data					
Input: A finite set of supervised tuples E Output: A decision tree T Method: 1) Create an arbitrary root 2) If all the tuples belong to class C_j then <i>return</i> (root, C_j) else 1. <u>Select</u> an attribute X with values $x_1, x_2,, x_M$ 2. Make a partition of E according to the attribute value $E_1, E_2,, E_M : E = \bigcup_{i=1}^M E_i$ 3. Build decision trees for every subset: $T_1, T_2,, T_M$					
endMethod					
$x = x_1$ $X = x_2$ $X = x_M$					

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2	High	High	High	Yes
3	Low	High	Low	Yes
4	Medium	High	High	Not

 X_{High}^1 Y_{High}^1 Z_{High}^1 $Decision_{YES}^1$ X_{High}^2 Y_{High}^2 Z_{High}^2 $Decision_{YES}^2$ X_{Low}^3 Y_{High}^3 Z_{Low}^3 $Decision_{YES}^3$ X_{Medium}^4 Y_{High}^4 Z_{Low}^4 $Decision_{NO}^4$

A generic algorithm to build decision trees from data					
Input: A finite set of supervised tuples E Output: A decision tree T Method: 1) Create an arbitrary root					
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endMethod					

Suppose that the attribute for the node root is X, then we apply the following three rules (membrane creation)

 $\begin{array}{l} X_{High}^{1} \ Y_{High}^{1} \ Z_{High}^{1} \ Decision_{YES}^{1} \ X_{High}^{2} \ Y_{High}^{2} \ Z_{High}^{2} \ Decision_{YES}^{2} \rightarrow [\ Y_{High}^{1} \ Z_{High}^{1} \ Decision_{YES}^{1} \ Y_{High}^{2} \ Z_{High}^{2} \ Decision_{YES}^{2}]_{X_{High}} \end{array}$ $\begin{array}{l} X_{Low}^{3} \ Y_{High}^{3} \ Z_{Low}^{3} \ Decision_{YES}^{3} \rightarrow [\ Y_{High}^{3} \ Z_{Low}^{3} \ Decision_{YES}^{3}]_{X_{Low}} \end{array}$ $\begin{array}{l} X_{Medium}^{4} \ Y_{High}^{4} \ Z_{Low}^{4} \ Decision_{NO}^{4} \rightarrow [\ Y_{High}^{4} \ Z_{Low}^{4} \ Decision_{NO}^{4}]_{X_{Medium}} \end{array}$

Applying a machine learning technique inside a P system

How can the appropriate rules be selected ?

• External algorithm selects the rule and we apply a translation scheme from decision trees to P systems

Work in Progress

- Apply a P system working within an entropic manner
- Apply rules according to a functional criterium

 $f: M(V) \to R$

From decision trees to random forests



Random Forest algorithm

mtry: number of features for node splitting *ntree*: number of trees in the forest

From cell-like P systems to tissue-like P systems



Initially we have only one cell with cell-creation rules and all the input data

 $X_{v} Y_{w} \dots Z_{u} \rightarrow X_{v} Y_{w} \dots Z_{u}(X_{v} Y_{w})$

 $X_v Y_w \dots Z_u \to X_v Y_w \dots Z_u (Y_w Z_u)$

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Rules inside every P system at skin region (communication rules)



 $NO \rightarrow (NO)_i$





Majority rules $\#YES > \#NO \rightarrow YES_{out}$ $\#NO > \#YES \rightarrow NO_{out}$



THAT'S ALL THANK YOU !!!