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An algebraic topology approach of multidimensional data management based on membrane computing

Cristian Kevorchian

Abstract. Using membrane computing formalism introduced by Gh. Paun [GhP98], and following results from [GiOl01] we propose an algebraic-topological point of view of membrane computing applied to multidimensional data management. The computational mechanism is based on q-analysis [Ke86] and [Ai71].

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1. Preliminaries

Intuitive, the membrane computing is based on *nesting* idea. There are a lot of methods to represent membrane structure. From these we can mention following ways: tree, diagrams, string matching parenthesis [GiOl01]. This approach provide a limited analogy with biological structure, because the direct interaction between different level of membrane structure are practically null unrepresented. The life of membrane structure is provided by the inside elements dynamic. Biological structures as cell nucleus,which include chromosome, are assimilated as 0-dimensional geometric structure,the cell membrane is a 1-dimensional structure and tissue as a cell family as 2-dimensional structure, etc. The computation process at the membrane structure level means:

- nesting and unnesting objects of membrane structure regions;
- nest the locally object in a region;
- create new region, through a nesting process, at the membrane structure level

Through q-analysis we can study the computational process as a nesting process, based on level of connectivity. In our approach through the computing process,the components of the membrane structure will be renested based on q-analysis

2. Combinatorial structure

Let a finite set $\mathcal{V}=\{v^i, i = 1..k\}$ and a collection $\mathcal{K}$ of its subsets organized as a membrane structure: $\mathcal{MS}=\{[v^{11}..v^{1i_1}], ...[v^{k1}..v^{ki_k}], i_1, ..i_k \in \{1..\text{k}\}$, a skin with k elementary membrane. Will note every (p+1) elementary membrane with σ_p and will approach as a p-simplex.
Let a partial ordering relation $\prec$ on $\mathcal{MS}$, $\sigma_p \prec \sigma_q$ where σ_p is a subsequent of σ_q. $(\mathcal{MS}, \prec)$ is a simplicial complex if and only if :
a) each elementary membrane $[v^i]$ is a element of skin $\mathcal{MS}$ as a σ_0
b) if $\sigma_p \in \mathcal{MS}$ and $\sigma_p \prec \sigma_q$ then $\sigma_q \in \mathcal{MS}$
The dimension of $\mathcal{MS}$ is provided by the largest dimension of its simplex and noted

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with $dim(\mathcal{MS})$. The membrane structure dynamics is based on simplex connection, named *chain connection*.
Our approach provide a geometrical representation of the skin,$\mathcal{MS}$ in terms of connected convex polyhedra. We will try to implement a computational process through the membrane dynamic. Using this procedure will obtain a new skin version as computation results. Now we'll analyze the simplicial complex connectivity.
Let two simplex σ_p,$\sigma_q \in \mathcal{MS}$ will say that are linked through a chain if there is a simplex sequence:

$$\sigma_{\alpha_1}, \sigma_{\alpha_2}, ..., \sigma_{\alpha_h}$$

a) σ_{α_1} is a face of σ_p
b) σ_{α_h} is a face of σ_q
c) σ_{α_i} and σ_{α_i+1} has a common face σ_{p_i} , for $i = 1, 2, ..., (h-1)$ Will say that such chain of connection is (h-1) length and we shall say that the chain is a q-connectivity if:

$$q = min(\alpha_1, \beta_1, \beta_2, ..., \beta_{h-1}, \alpha_h)$$

Let γ_q a relation on simplicial complex $\mathcal{MS}$:

$$* \text{ is q-connected to } *$$

It is easy to see that:
1) if $\sigma_p \in \mathcal{MS}$ then $(\sigma_p, \sigma_p) \in \gamma_q$
2) if $(\sigma_l, \sigma_p) \in \gamma_q$ then $(\sigma_p, \sigma_l) \in \gamma_q$
3) if $(\sigma_l, \sigma_m) \in \gamma_q$ and $(\sigma_m, \sigma_p) \in \gamma_q$ then $(\sigma_l, \sigma_p) \in \gamma_q$

γ_q is a equivalence relation and will note with Q_q the cardinally of set $\mathcal{MS}/\gamma_q$

3. Q-analysis and complexity of membrane structure

Through Q-analyze of the complex attached to membrane structure we can obtain an array (Q_q), $q \in 0, 1, .., dim(\mathcal{MS})$, where Q_q is the number of q-connected membrane components. Array Q can be considered as a *global indicator* of simplicial complex K, but didn't provide a unique characterization of attached simplicial complex to membrane structure. Two different membrane structure can be characterized by same Q array. More details about analysis can be obtained through the study of chains connectivity:

$$\Psi(\mathcal{MS}) = \frac{2}{(n+1)(n+2)} \sum_{q=0}^{n} (q+1)Q_q, \text{ where } n = dim(\mathcal{MS})$$

Let two membrane structure $\mathcal{MS}_1$ and $\mathcal{MS}_2$:

$$\mathcal{MS}_1 \equiv \mathcal{MS}_2 \text{ iff } \Psi(\mathcal{MS}_1) = \Psi(\mathcal{MS}_2)$$

the results of Q-analysis for two different membrane structure are the same iff numerical evaluation of $\Psi(\mathcal{MS}_1)$ and $\Psi(\mathcal{MS}_2)$ are equal. The local properties of individual simplex is very important in the analysis of membrane's structure. The measure of this indicator is *eccentricity of simplex* [Ko00]:

$$ecc(\sigma) = \frac{\hat{q} - \overline{q}}{\hat{q} - 1}$$

where $\hat{q}$ is the diagonal element of the row corresponding to σ in the "shared face matrix"[MSo00], SF=$\Lambda\Lambda^T - \Omega$, Λ is incidence matrix, Ω is a unit matrix. $\overline{q}$ is the largest non diagonal value of σ entrance. The eccentricity attached to a simplex is infinity iff this simplex is disconnected from all other simplex of the complex.
Each $Q_q, q \in \{0, 1, ..., dim(\mathcal{MS})\}$ belongs to the first structural vector Q that means

the number of q-connectivity components in membrane structure $\mathcal{MS}$. Each of such components can put together several simplexes. The vector Q didn't focus on this issue. We can use a $\overline{Q}$ named *second structural vector of the membrane structure* defined as :

$$\overline{Q}_q = 1 - \frac{Q_q}{n_q}$$

where n_q is the total number of d-simplexes($d \geq q$) belongs to Q_q connectivity components from the dimensional level q. $\overline{Q}$ vector can be interpreted as a modified measure of membrane connectivity degree at the level $q, q \in \{0, 1, ..., dim(\mathcal{MS})\}$ and improve membrane components dynamics. The ratio $\frac{Q_q}{n_q}$ defines the number of connectivity components per one simplex with $\sigma, dim(\sigma) \geq q$ We can obtain a new form of the skin:

$$\mathcal{MS}=\{[K_1], ...[K_k]\}, \text{ where } Q_0 = k$$

We'll identify the membrane structure with the component $Q_0 = 1$ as a simplicial complex.Let $K_Y(X, \lambda)$ the attached complex with $dim(K) = n$. This theoretical environment lead us to design a computational procedure[GiOl01] for skin transformation. The algebraic transformation of membrane structure can be written as a family of rules. The rules can be implemented in specialized language as MGS(***M***odèle ***G***énerale de ***S***imulation(de système dinamique)) The general form of the rule is: "*pattern* $\Rightarrow$ *expression*". The "pattern" of the rule match a membrane of a region on which the transformation is applied and expression provide the structure which will replace the element provided by pattern. Our computing procedure was done in MAPLE 8.

4. The Model

Let the following membrane structure :

$$MS = [[x_1, x_3], [x_1, x_2, x_4], [x_1, x_2, x_3, x_4, x_5], [x_2, x_4, x_5]]$$

Let the relation λ, with $\lambda \subseteq Y \times X$ where $X = \{x_1, x_2, ..., x_5\}$ and $Y = \{y_1, y_2, ..., y_4\}$ where $y_1, y_2, ..., y_4$ are simplex generated by membrane structure regions. $K_X(Y; \lambda^{-1})$ the simplicial complex provided by the relation λ^{-1} attached to membrane structure. $\Lambda = (\lambda_{i,j})$ is the incidence matrix, with 4 lines and 5 columns:

λ	x_1	x_2	x_3	x_4	x_5
y_1	1	0	1	0	0
y_2	1	1	0	1	0
y_3	1	1	1	1	1
y_4	0	1	0	1	1

The $K_Y(X, \lambda)$ complex is given by the evaluation of "shared face matrix", $\Lambda\Lambda^T - \Omega$, where Ω is a 4×4 1's matrix :

y_1	y_2	y_3	y_4	
1	0	1	-1	y_1
	2	2	1	y_2
		4	2	y_3
			2	y_4

and provide us the following structure vector for $K_Y(X, \lambda)$:

$$\text{Q}=(\overset{4}{1},\overset{3}{1},\overset{2}{1},\overset{1}{1},\overset{0}{1})$$

and the analysis result is a triangular matrix array. The -1 value means that y_1 and y_4 are not connected.
The Q_q analysis values are based on following data :

q=4	$q_4 = 1$	y_3
q=3	$q_3 = 1$	y_3
q=2	$q_2 = 3$	y_3, y_2, y_4
q=1	$q_1 = 4$	y_1, y_2, y_3, y_4
q=0	$q_0 = 1$	all

Based on Q-analysis we can transform membrane structure as following structure:

$$\overline{\mathcal{MS}} = [y_3, y_3, [y_3, y_2, y_4], [y_1, y_2, y_3, y_4], [y_1, y_2, y_3, y_4]]$$

x_1	x_2	x_3	x_4	x_5	
2	1	1	1	0	x_1
	2	0	2	1	x_2
		1	0	0	x_3
			2	1	x_4
				1	x_5

From evaluating of the above matrix $\Lambda^T\Lambda - \Omega$ we obtain the pattern for the complex $K_X(Y, \lambda^{-1})$ where

$$Q = (\overset{2}{2},\overset{1}{1},\overset{0}{1})$$

and for $K_X(Y, \lambda^{-1})$ we obtain:

q=2	$Q_2 = 2$	x_1, x_2, x_4
q=1	$Q_1 = 1$	all
q=0	$Q_0 = 1$	all

The membrane structure provided by transforming process is:

$$\widetilde{\mathcal{MS}} = [[[x_2, x_4], x1], [x_1, x_2, x_3, x_4, x_5], [x_1, x_2, x_3, x_4, x_5]]$$

The components of second structural vector are: Practically, the components of $\overline{Q}$

$$\begin{array}{ll} \text{q=2} & \overline{Q}_2 = 1 - (\frac{Q_2}{3}) = 0.66 \\ \text{q=1} & \overline{Q}_1 = 1 - (\frac{Q_1}{6}) = 0.17 \\ \text{q=0} & \overline{Q}_0 = 1 - (\frac{Q_0}{6}) = 0.17 \end{array}$$

show us the conectivity degree of membrane structure q-level and it adjust the membrane dynamics in a cantitatve structure(composition) of conectivity components.

5. An membrane approach of spatial data

The interaction operation from Vianu's abstraction[V96] can be interpreted as a statement **if** $\langle$ *body* is true $\rangle$ **then** $\langle$ *head* is true $\rangle$, where $head \leftarrow body_1, body_2, ..., body_n$
We can create two types of rules for working with membrane structure:

- membrane enumeration({})
- membrane grouping {{}, {}}

We must mention that we will work with nonrecursive and range-restricted rules(rules with same variables in head and body).

Example 5.1. *The below example will illustrate the concepts:*
- *p(X,{Y,Z,T})*
- $p(X,\{Y\}) \rightarrow q(\{X,Y,Z\})$

For every substitution $\theta = \{x/X\}$ *is created a fact* $p(x, \pi_Y \sigma_{X\theta} S)$ *where* π_Y *is a multiset projection defined by Vianu [V96] and mentioned by us in bellow section. Let facts q(a,b,c),q(a,b,d) and q(a,f,e) obtain* ***p(a,{b,b,f})***

We can generalize this result to a 2-dimensional data. Is a natural analogy between *tiling structure*(a square of $2^n \times 2^n$ size by tiles square 1×1) described in [DaVo98] and a 2-dimensional data structure. Let a finite set $U = \{t_0, t_1, ..., t_n\}$ of tiles as universe of membrane structure and the relations ***here*** and ***out*** from evolution of membrane structure defined in *section 3*. We say about t_i and t_j that are inside(horizontal) compatible iff holds ***here***(t_i, t_j) and outside(vertical) compatible iff holds ***out***(t_i, t_j). Let a 2-dimensional data structure(a square of size $2^n \times 2^n$ as:

$$q : \{1, ..., 2^n\} \times \{1, ..., 2^n\} \longrightarrow t_0, ..., t_n \tag{1}$$

Using (1) we can write:
- $q(i, j)$ and $q(i, j+1)$ are "***here***" iff $t_{i,j}$ and $t_{i,j+1}$ are adjacent
- $q(i, j)$ and $q(i+1, j)$ are "***out***" iff $t_{i,j}$ and $t_{i+1,j}$ are adjacent

Let the universe $U = \{T_1, T_2, T_3, T_4\}$, based on this set we can generate the following supercell : $[T_1, T_2, T_3, T_4]$ and represent it through a table:

T_1	T_2
T_3	T_4

(2)

with every component a multiset as : $[[b, a, c, a], [c, a, b, b], [c, a, b, b], [a, a, a, c]]$ or we can represent as a hypertile of rank 2(formated from tiles a,b and c)[DaVo98] with following representation :

b	a	c	a
c	a	b	b
c	a	a	a
b	b	a	c

(3)

In addition to the predicates **here** and **out** will be interpreted with following relations define following binary predicates : $S_1, S_2, ...S_n$. The statement $S_i(T, t_0)$ is hold iff :
- H is a supercell with deg(T)=i
- H is a supercell with the tile t_0 in the top left corner

Let the 2-dimensional data structure:

H_1	H_2
H_3	H_4

(4)

The data structure (2) will lead us to define the predicate S_1

$$S_1([H_1, H_2, H_3, H_4], H_1) \rightarrow here(H_1, H_3), here(H_2, H_4), out(H_1, H_2), out(H_3, H_4). \tag{5}$$

Let following 2-dimensional data structure represented by following membrane structure:

$$[[A_1, A_2, A_3, A_4], [B_1, B_2, B_3, B_4], [C_1, C_2, C_3, C_4], [D_1, D_2, D_3, D_4]] \tag{6}$$

with rank $i+1$ and 9 data structure with rank i. The attached rules are:
$S_{i+1}([[A_1, A_2, A_3, A_4],\ [B_1, B_2, B_3, B_4],\ [C_1, C_2, C_3, C_4],\ [D_1, D_2, D_3, D_4]], T_0) \rightarrow$

$S_i([A_1, A_2, A_3, A_4], t_0)$, $S_i([A_2, B_2, A_4, B_3],\_)$... With rules family generated bellow we can obtain a query of 2-dimensional data structure.

6. Conclusion

The algebraic topology study of membrane structure has as the main target characterization of membrane dynamic, that means : store and move objects between regions of membrane structure,transform locally the object, transform locally the objects stored in a region, create, delete and rearrange the organization of membrane regions. We used the chain complex concept to obtain a accurate representation of the topological organization of a membrane structure. Our approach based on analogy between membrane computing with dynamics of membrane components neighborhood or with other words membrane structure dynamic.

References

[Ai71] T. Aizawa, Some Homology Theoretic Structures of Languages, *Systems, Computers, Controls*, **2**(5), 1971.

[GiOl01] J.-L. Giavitto, O. Michel, *The Topological Structures of Membrane Computing* Rapport de Recherche no. 70/2001, CNRS-Univeriste d'Evry Val d'Essonne.

[GhP98] Gh. Paun, *Computing with membranes*, TUCS Research report No.208, November 1998.

[Ke86] Hacic Cristian Kevorchian, *Semiotics and artificial intelligence an algebraic topological approach*, R.R.L. **XXIII**, Ed.Academiei 1986.

[Ko00] K.Y. Degtiarev, System analysis:mathematical modeling and approach to structural complexity measure using polyhedral dynamics approach, *Complexity International*, **7**, 2000,http://www.csu.edu.au/ci/vol07/degtia01/.

[MSo00] M. Sonis, G.J.D.Hewings, *Introduction to Input-Output Structural Q-analysis, REAL 00-T-1,http://www.uiuc.edu/unit/real*.

[V96] V. Vianu, *Database Theory Column* ACM SIGACT News, 27(2), 30-37, June 1996.

[WiEi00] I.H. Witten, Eibe Frank, *Data Mining*,Morgan Kaufmann Publishers, 2000.

(Cristian Kevorchian) University of Craiova,
Mathematics - Informatics Faculty, Computer Science Department
A.I. Cuza street 13, Craiova RO-200585, Romania
E-mail address: c_kevorchian@yahoo.com