John-Tagore Tevet

NATURE OF THE STRUCTURE

Contents

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Research group S.E.R.R., Tallinn
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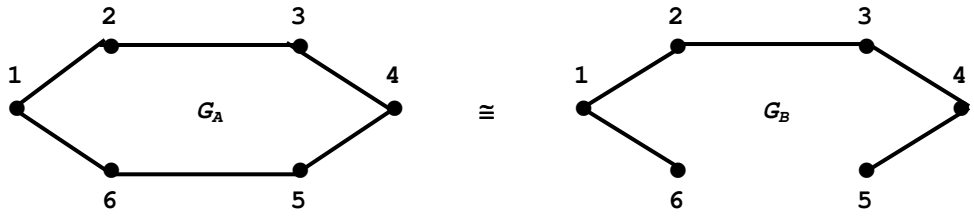
Introduction

There exist three formations that consist of elements (components, particles,) and relationships (connections) between them. These are *system, structure* and *graph.*

System is an association of empirical elements (components) and relationships where the significant meaning have it *function* and *structure.* These are principal features of all the systems.

Structure is the *ordering, organizational or constructional* side of systemic objects. Structure is generally defined as a permanently associated status of its elements. Unfortunately, the term "structure" has become a blurred adjective, or speaking only on the structure of a particular object. The attempts of explaining a common concept of structure can be noticed only in Continental European reference books [14, 18]. However, also over there are discrepancies. There existing different views, whether the structure is permanent or mostly permanent, whether is it an inexplicable relationship or the relationships between the elements. At the same, have come to an agreement that the *structure is an inseparable attribute of all the really existing objects.* In connection with multi-aspect of systemic objects (i.e. different possibilities to decomposing a system into components) is the system multi-structural. It is alleged that the structure is an abstraction of the system, where its elements and relationships have lost of its empirical meanings, but retain their differences in the form of ***positions*** in the structure. To end be understand that the essence of structure is related to the *invariance* and its *explanation attribute* is a ***graph***.

The essence of a position is trivial. Let graphs G_A and G_B present the structure of objects ***A*** and ***B***:



All the elements of ***A*** have a common position. The elements 5 and 6 of ***B*** have an *"end position"*, the elements 2 and 3 a *"middle position"* and elements 1 and 4 an *"intervening position"*. Positions have also the relationships between elements.

On the aspect of structure constitutes a graph only the initial data for recognition the structure, i.e. graph is only a list of adjacent elements or an adjacent matrix. *Isomorphic graphs* have the *equivalent structures*. Structure is a *complete invariant for the isomorphic graphs*. All the structural properties are expressed in the graphs, and properties of the graphs are the structural properties. The structure is reasonable to represent in a manner that represents all the relationships and positions and enables distinguish one structure from another. One structure differs from another by their *binary relations* between elements and by their *positions.* Position is an equivalence class that in the aspect of group theory to transitivity domain of automorphisms or the *orbit* called. The difference here lies only in the detection technique.

For recognition the structure designed a ***structural model*** *(model of structure, structure's model).* Pictorially says, structural model is a complemented and decomposed adjacent matrix that represent all the binary relations and positions [22, 25, 34, 37]. The structure of many empirical objects, such as *chemical compounds, ecological communities, genetic formations, communication networks*, etc are presentable in the form of a graph where the structural models enable to study and explore these from the structural view-point.

In this paper has tried the nature of structure and its application to set forth shortly, simply and pictorially.

1. GRAPH OF STRUCTURE and STRUCTURE OF GRAPH

1.1. Structural equivalence and isomorphism

Indeed, structure is presentable in the form of a graph and the graph has a certain structure. Let's we start from a hypothetical but workable principle that the structure ***S*** is an *identifiable (measurable) attribute* of graph ***G***:

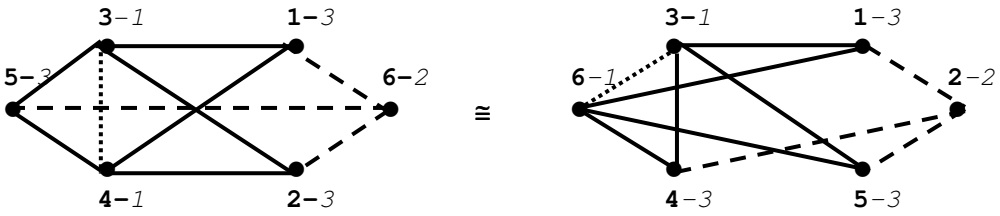
$$S = \mathfrak{F}(G).$$

Let to identify the *binary relations* (vertex pairs ***ij***) their *intersection of surroundings* $N_i \cap N_j$ as a sub-graph or ***binary graph*** g_{ij}. Corresponding algorithm ***SIA*** fixes for each binary graph g_{ij} its *invariant* or ***binary sign*** $\pm d.n.m._{ij}$, where ***+d*** is *collateral-* and ***–d*** *custom distance*, ***n*** *– number of vertices* and ***m*** *– number of edges* in this binary graph. The ordered system of binary signs – ***structure model*** **SM** – identifies the relationships between the elements, as well as positions [16, 28].

The *position of an element* in the structure is determined with the *binary relations with other elements*. The *position of an element-pair* in the structure is determined with these *positions of the elements* and with the *binary relation between* these. In the aspect of group theory is position an *orbit* [25, 34, 37].

The possibilities for complementary identification the relationships between vertices exist some (Prop. 1.1). Talking about the structure is preferred in place of the word *vertex* to use the *element*, and in place of *edge* to use *connection (relation)*.

Example 1.1. Graphs G_A and G_B, their binary signs and structure models $\mathbf{SM}_A$ and $\mathbf{SM}_B$:



A:–2.5.7; B:–2.5.6;
C:+2.3.3; D:+2.5.7; E:+3.6.10.

A:–2.5.7; B:–2.5.6;
C:+2.3.3; D:+2.5.7; E:+3.6.10.

							u_i	k	s_i
1	1	2	3	3	3				
3	4	6	1	2	5	i	ABCDE		123
0	D	–B	C	C	C	3	01310	1	103
	0	–B	C	C	C	4	01310	1	103
		0	E	E	E	6	02003	2	003
			0	–A	–A	1	20201	3	210
				0	–A	2	20201	3	210
					0	5	20201	3	210

							u_i	k	s_i
1	1	2	3	3	3				
3	6	2	1	4	5	i	ABCDE		123
0	D	–B	C	C	C	3	01310	1	103
	0	–B	C	C	C	6	01310	1	103
		0	E	E	E	2	02003	2	003
			0	–A	–A	1	20201	3	210
				0	–A	4	20201	3	210
					0	5	20201	3	210

Explanations:

a) The column u_i of model consists of the ***frequency vectors***, which for the element ***i*** show its relations with other elements. On the basis of vectors u_i are arranged the positions in model.

b) The column s_i of model consists of the ***position vectors*** that represent the connections of element ***i*** with elements in corresponding positions ***k***. If on the framework of frequency vectors arises differences of position vectors, then by lasts does a complementary partition into classes.

c) Different graphs G_A and G_B have equivalent structure models $\mathbf{SM_A} \approx \mathbf{SM_B}$! This means that the structures are ***equivalent*** and the graphs ***isomorphic*** $G_A \cong G_B$.

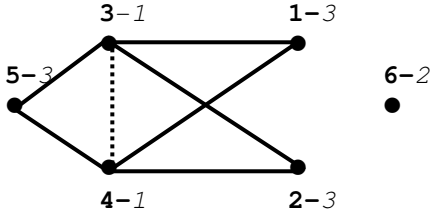
d) The structural elements are divided to ***three positions*** *(equivalence classes, orbits)* ΩV_k and element pairs to ***five positions*** ΩR_n, where the adjacent elements or "edges" divided to *three binary(+)positions (full line, a dotted, dashed-line)* that coincides with binary signs ***C, D, E*** correspondingly.

Here it may be noted that the first primitive "distance matrix" was presented already in 1973 by S. Toida [41], as isomorphism identification attribute. Indeed, the distance matrix can detect the isomorphism or "non-isomorphism" for quite many graphs, but it is by no means reliable.

The binary signs $\pm d.n.m._{ij}$ have a *meaning*, these have a *semiotic character.* This is essential for studying the nature of the structure. The first member of minus sign, i.e. of the binary(–)sign, represents the *shortest paths (distance) –d* between the elements ***i*** and ***j***, where it is fixed by all the different paths (chains). The second member of binary(–)sign represents the number of elements ***n*** and ***m*** the number of connections (edges) in corresponding binary graph g_{ij}. *Disconnected elements* are represented with the binary sign *–u.2.0.* The first member of the plus sign, i.e. binary(+)sign, represents the *collateral distance* ***+d***, i.e., *belonging the element pairs (and their connection) to the girth (circle) with length +d+1.* An exemption forms the *binary sign of branching, +1.2.1*, which show the distance *d=1.*

Example 1.2. ***Binary graph*** $g_{3.4}$ of element pair 3-4 ***(D: +2.5.7)*** of G_A (Example 1.1), its binary signs and structure model $SM_{3.4}$:

A:–2.4.5; B:–u.2.0; ***C:+2.3.3; D:+2.5.7.***

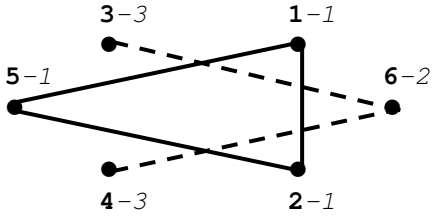


1	1	2	3	3	3		u_i	k	s_i
3	4	6	1	2	5	i	ABCD		123
0	D	–B	C	C	C	3	0131	1	103
	0	–B	C	C	C	4	0131	1	103
		0	–B	–B	–B	6	0500	2	000
			0	–A	–A	1	2120	3	200
				0	–A	2	2120	3	200
					0	5	2120	3	200

By dealing with the structure of a graph ***G*** is a desirable to show also its ***complement*** $\neg G$, because it opens up the structure as a whole.

Example 1.3. The *complement* $\neg G_A$ of graph G_A (Example 1.1) and its structure model:

A:–2.3.2; B:–u.2.0; ***C:+1.2.1; D:+2.3.3.***



1	1	1	2	3	3		u_i	k	s_i
1	2	5	6	3	4	i	ABCD		123
0	D	D	–B	–B	–B	1	0302	1	200
	0	D	–B	–B	–B	2	0302	1	200
		0	–B	–B	–B	5	0302	1	200
			0	C	C	6	0320	2	002
				0	–A	3	1310	3	010
					0	4	1310	3	010

Explanations:

- **a)** The ***element positions*** ΩV_k of G_A and its complement $\neg G_A$ *coincides* (as the positions are arranged by new frequency vectors* u_i then there exist a correspondence between positions, in present case *1→3, 2→2, 3→1*).
- **b)** *Coincides also the* ***binary positions*** ΩR_n, which are in the complement $\neg G_A$ with opposed signs, for each *binary*(+)*position ("edge"-position")* corresponds a *binary*(–)*position ("non-edge" position")*, and *vice versa.*

It is useful look to other ***co-graphs***, such as *sign-* and *adjacent graphs*. To these we arrive by dealing with structural changes.

It is obvious that a large part of the binary signs *are not complete invariants* of element pairs. Some of large symmetric structures require a ***perfection*** of binary signs. There are several ways [27, 29, 37].

Propositions 1.1. Perfection of binary signs:

P1.1.1. Using the complementary binary signs dnm_{ij}^{m} of the ***high degree m*** binary graphs g_{ij}^{m}, i.e. binary graphs, that remain between elements ***i*** and ***j*** of ***G*** after removing the preliminary binary graph g_{ij}.

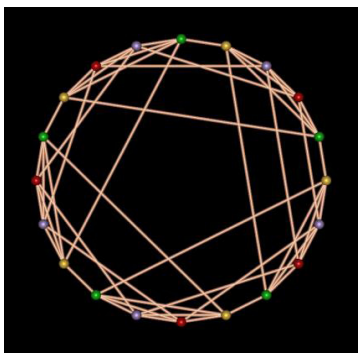
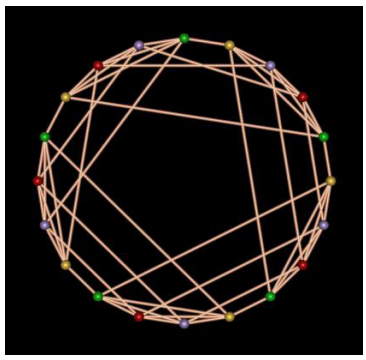
P1.1.2. Using the complementary binary signs of ***local structure models*** $\mathbf{SM}_{ij}$ of binary graphs g_{ij}.

P1.1.3. Using the complementary binary signs of ***sign structures*** GS_p, that consist of element pairs with a certain class of pair signs, independently from their positions,

P1.1.4. Using complementary binary signs of the ***product of adjacency matrix*** $E\times E\times E\times\ldots=E^n$ where up to certain degree ***n*** the ***values*** of elements e^n_{ij} as well as the number ***p*** of their ***differences*** become larger, and then make a halt.

The preliminary binary signs their meanings do not lose, these remains characterize belonging the elements and connections to the paths and girths that is needed by treatment of the structure. Perfected binary sign constitutes a quintuplet $\pm d.n.m.e^n_{ij}$, where the last represents the perfecting.

Example 1.4. Two "very similar" poly-symmetric graphs Pra_A and Pra_B (designed especially for isomorphism testing) their common and adjusted binary signs, structure models and isomorphism testing:

Common basic binary signs of Pra_A and Pra_B:

A:-3.8.10; B:-3.6.7; C:-2.4.4; D:-2.3.2; ***E:+2.4.6; F:+3.8.16.***

Adjusted by matrix product $E^{n=5}$ binary signs and structure model **SM** of graph Pra_A:

Marking the basic pair signs	0	-A	-B	-C		-D	E		F
Productive pair signs e^5	180	125	110	165	160	80	231	233	210
Adjusted pair signs	0	-A	-B	-C1	-C2	-D	E1	E2	F

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	i	ABCCDEEF	k
0	E2	E1	E1	F	C2	C1	C1	F	C2	C1	C1	D	A	B	B	D	A	B	B	1	24422212	1
	0	E1	E1	C2	F	C1	C1	C2	F	C1	C1	A	D	B	B	A	D	B	B	2	24422212	1
		0	E2	C1	C1	F	C2	C1	C1	F	C2	B	B	D	A	B	B	D	A	3	24422212	1
			0	C1	C1	C2	F	C1	C1	C2	F	B	B	A	D	B	B	A	D	4	24422212	1
				0	E2	E1	E1	D	A	B	B	F	C2	C1	C1	A	D	B	B	5	24422212	1
					0	E1	E1	A	D	B	B	C2	F	C1	C1	D	A	B	B	6	24222212	1
						0	E2	B	B	D	A	C1	C1	F	C2	B	B	A	D	7	24222212	1
							0	B	B	A	D	C1	C1	C2	F	B	B	D	A	8	24222212	1
								0	E2	E1	E1	A	D	B	B	F	C2	C1	C1	9	24222212	1
									0	E1	E1	D	A	B	B	C2	F	C1	C1	10	24222212	1
										0	E2	B	B	A	D	C1	C1	F	C2	11	24222212	1
											0	B	B	D	A	C1	C1	C2	F	12	24222212	1
												0	E2	E1	E1	C2	F	C1	C1	13	24222212	1
													0	E1	E1	F	C2	C1	C1	14	24222212	1
														0	E2	C1	C1	C2	F	15	24222212	1
															0	C1	C1	F	C2	16	24222212	1
																0	E2	E1	E1	17	24222212	1
																	0	E1	E1	18	24222212	1
																		0	E2	19	24222212	1
																			0	20	24222212	1

Adjusted by matrix product $E^{n=7}$ binary signs and structure model **SM** of graph Pra_B:

Basic pair signs	*0*	*–A*	*–B*		*–C*			*–D*	***E***		***F***
Productive signs e^7	*4410*	*3437*	*3276*	*3277*	*4081*	*4088*	*4011*	*3010*	*4831*	*4803*	*4445*
Adjust. pair signs	*0*	*–A*	*–B1*	*–B2*	*–C1*	*–C2*	*–C3*	*–D*	***E1***	***E2***	***F***

|1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**	**18**	**19**	**20|**	***i***	*ABBCCCD**EEF***	***k***
|0	***E1***	***E2***	***E1***	***F***	*C1*	*C2*	*C3*	***F***	*C3*	*C2*	*C1*	*D*	*B2*	*B1*	*A*	*D*	*A*	*B1*	*B2|*	**1**	*2222222**212***	*1*
	0	***E1***	***E2***	*C3*	***F***	*C1*	*C2*	*C1*	***F***	*C3*	*C2*	*A*	*D*	*B2*	*B1*	*B2*	*D*	*A*	*B1|*	**2**	*2222222**212***	*1*
		0	***E1***	*C2*	*C3*	***F***	*C1*	*C2*	*C1*	***F***	*C3*	*B1*	*A*	*D*	*B2*	*B1*	*B2*	*D*	*A|*	**3**	*2222222**212***	*1*
			0	*C1*	*C2*	*C3*	***F***	*C3*	*C2*	*C1*	***F***	*B2*	*B1*	*A*	*D*	*A*	*B1*	*B2*	*D|*	**4**	*2222222**212***	*1*
				0	***E1***	***E2***	***E1***	*D*	*A*	*B1*	*B2*	***F***	*C1*	*C2*	*C3*	*A*	*D*	*B2*	*B1|*	**5**	*2222222**212***	*1*
					0	***E1***	***E2***	*B2*	*D*	*A*	*B1*	*C3*	***F***	*C1*	*C2*	*B1*	*A*	*D*	*B2|*	**6**	*2222222**212***	*1*
						0	***E1***	*B1*	*B2*	*D*	*A*	*C2*	*C3*	***F***	*C1*	*B2*	*B1*	*A*	*D|*	**7**	*2222222**212***	*1*
							0	*A*	*B1*	*B2*	*D*	*C1*	*C2*	*C3*	***F***	*D*	*B2*	*B1*	*A|*	**8**	*2222222**212***	*1*
								0	***E1***	***E2***	***E1***	*A*	*B1*	*B2*	*D*	***F***	*C3*	*C2*	*C1|*	**9**	*2222222**212***	*1*
									0	***E1***	***E2***	*D*	*A*	*B1*	*B2*	*C1*	***F***	*C3*	*C2|*	**10**	*2222222**212***	*1*
										0	***E1***	*B2*	*D*	*A*	*B1*	*C2*	*C1*	***F***	*C3|*	**11**	*2222222**212***	*1*
											0	*B1*	*B2*	*D*	*A*	*C3*	*C2*	*C1*	***F|***	**12**	*2222222**212***	*1*
												0	***E1***	***E2***	***E1***	*C3*	***F***	*C1*	*C2|*	**13**	*2222222**212***	*1*
													0	***E1***	***E2***	*C2*	*C3*	***F***	*C1|*	**14**	*2222222**212***	*1*
														0	***E1***	*C1*	*C2*	*C3*	***F|***	**15**	*2222222**212***	*1*
															0	***F***	*C1*	*C2*	*C3|*	**16**	*2222222**212***	*1*
																0	***E1***	***E2***	***E1|***	**17**	*2222222**212***	*1*
																	0	***E1***	***E2|***	**18**	*2222222**212***	*1*
																		0	***E1|***	**19**	*2222222**212***	*1*
																			0|	**20**	*2222222**212***	*1*

Explanations:

- **a)** Graph Pra_A has *five* binary(−)positions by *–A, −C2,* and *−D* with power 20 and two pair positions by *−B* and *−C1* with power 40.
- **b)** Graph Pra_B has *seven* binary(−)positions whit power 20.
- **c)** Thus, the structure models of Pra_A and Pra_B are ***non equivalent*** and graphs ***non isomorphic.***.
- **d)** Both graphs have *three* pair(+)positions ***E1, E2*** and ***F*** with power 20.
- **e)** The ***complement*** $PrauC_A$ of $Prau_A$ has pair signs *–A:-2.14.68, -B:-2.12.47,* ***C:+2.10.35, D:+2.10.36, E:+2.11.44, F:+2.12.48***.

The structure model **SM** is the *canonical description* of structure (graph) with exactness up to *binary signs, positions, isomorphism and others* structural attributes. The problem of *canonical representation of the graphs* was set by Lazlo Babai in 1977th [1]. The presentation modes are proposed much [4, 9]. Unfortunately, they do not contain almost information about the structure.

Proposition 1.2. If the structure models of graphs G and H are *equivalent* $\mathbf{SM}_G \approx \mathbf{SM}_H$ then the graphs are *isomorphic* $G \cong H$, [22, 25, 26, 34, 36].

The isomorphism problem is to design an algorithm that recognizes the isomorphism of two objects. The ***graph isomorphism problem*** came into prominence in 1857, when Arthur Cayley reported his research on organic isomers. Two graphs called isomorphic, if they differ only in the labeling of their vertices. An isomorphic mapping from graph G_A to graph G_B is a bijection $\varphi: V_A \to V_B$:

$$v_1 \quad v_2 \quad \ldots v_i \quad \ldots \quad v_n$$
$$\varphi(v_1)\ \varphi(v_2)\ \ldots\ \varphi(v_i)\ \ldots\ \varphi(v_n)$$

A naive algorithm for isomorphism detection obviously exist – try all the possible permutations of the rows and columns of adjacency matrix of G_B until it coincides with adjacency matrix of G_A. However, this is an impossible task to perform for all practical purposes, since the number of permutations that one may need to check can go up to ***n!*** Nearly in all existing heuristic algorithms of isomorphism recognition to attempt in various ways avoid such situation, and only in a few algorithms detects it with exactness up to vertex substitutions.

For example, in the algorithm [3] are used incomplete structure models, but isomorphism detection takes place on the level of vertex substitutions. In some algorithms do not suffice to detect the vertex

substitutions, but enable to measure the "similarity" of structures [15]. The formation of the structure models and detection their equivalence goes in such a way where it would be inappropriate to talk about the great complexity of the algorithm.

Proposition 1.3. For recognition the equivalence of structure models $\mathbf{SM}_A$ and $\mathbf{SM}_B$ is necessary and sufficient:

- **a)** to detect the coincidence of the *sequences of binary signs* $\{\pm d.n.q._{ij}\}_A$ and $\{\pm d.n.q._{ij}\}_B$;
- **b)** to detect the coincidence of the *frequency vectors* $\{u_i\}_A$ and $\{u_i\}_B$;
- **c)** to detect the coincidence of the *position vectors* $\{s_i\}_A$ and $\{s_i\}_B$.

Probably do not need the fact that isomorphic graphs have the same structure, which expressed in the form of structural equivalence of models, here anew explanation. However, repeat:

1) Isomorphism is a one-to-one correspondence between elements.
2) Isomorphism detection does not detect the structure, but the structure model detects the structure with exactness up to isomorphism.
3) Equivalence of structure models is a coincidence on the level of binary signs, binary- and element positions.
4) Detecting the positions by binary signs is more simple than detecting the orbits on the ground of the group ***AutG***.

1.2. Structural properties

Essential structural properties are ***regularity*** and ***symmetry*** Regularity and symmetry of structure are very rare conditions, but for that reason are more intriguing. With the symmetry of the graphs arise confusions. Some call to symmetric the simple graphs, because the edges are not directed. Others call symmetric the transitive of vertices or edges graphs, which meant the transitivity domain of automorphisms in ***AutG***. With the latter must be consent.

To the assumption of symmetry is ***regularity***, but not vice versa. Regularities are several, and they are easily readable out from structure model **SM** [35]. We define these.

Definitions 1.1. Kinds of regularity:

D1.1.1. Structure (graph), where by each element i the number v of binary(+)signs $+dnm_{ij}$ is constant is ***v-degree-regular***.

D1.1.2. Degree-regular structure (graph), where by each element i the number of partial signs $-d$ of binary(–)signs $-dnm_{ij}$ are constant is ***d-distance-regular***

D1.1.3. Degree-regular structure (graph), where by each element i the number of partial signs $+d$ of binary(+)signs $+dnm_{ij}$ are constant is ***(d+1)-girth-regular***.

D1.1.4. Degree-regular structure (graph), where each element i belong to a clique with the power $n<|V|$ is ***n-clique-regular***, where $|V|$ is the number of structural elements.

D1.1.5. Degree-regular structure (graph), where each pair of adjacent elements holds $a\geq 0$ common neighbors and each nonadjacent pair holds $b\geq 1$ common neighbors is ***strongly-regular***.

Propositions 1.4. Properties of regularity:

P1.4.1. Each element v_i of a *clique- (or girth-) regular* structure belongs to $a\geq 1$ cliques (girths) and each edge to e_{ij} to $b\geq 1$ cliques (girths).

P1.4.2. The cliques of *clique-regular* structure are ***components, connected*** or ***intersected.*** The intersections can be in the aspect of elements or connections.

P1.4.3. If structure consists of ***m component n-cliques*** then its ***complement*** is an ***m-partite complete graph***, i.e. is an ***n-m-clique*** – and *vice versa*.

Size	Graph	Its complement
m	Number of component cliques	Number of parts
n	Power of these cliques	Power of parts

P1.4.4. Complement of m-partite structure is in case of equal parts ***n n-clique-regular,*** with m non-intersected n-cliques**.**

P1.4.5. The ***n-m-clique*** contains $s=n^m$ (ordinary)cliques with power m, this is ***m-clique-regular***, i.e. bi-clique is *2-clique-regular,* tri-clique *3-clique-regular* etc.

P1.4.6. All the ***n-m-cliques*** are ***strongly regular***, but not contrary.

P1.4.7. *Connected complement* of strongly regular structure is strongly regular**.**

Symmetry is a structural property that expressed as recurrence of similar elements (particles) in the space or time [14, 18]. Indeed, what greater is a position then greater the structural symmetry. ***Symmetry of the structure*** depends on the number and size of positions [32, 34, 37]. We define it.

Definitions 1.2. Kinds of symmetry:

D1.2.1. *Complete* structure (graph) has *one* element- ΩV_k and *one* binary position ΩR_n and it is ***completely symmetric.***

D1.2.2. *Transitive* structure (graph), as it in graph theory called, has *one* element position ΩV_k and it is ***element symmetric***.

D1.2.3. *Element symmetric* structure (graph), that has *one* binary(+)position („edge position") ΩR_n^+ and *one* binary(–)position („non-edge position") ΩR_n^- is ***bisymmetric*** (see Example 1.5).

D1.2.4. *Element symmetric* structure (graph), that has *one* binary(+)position ΩR_n^+ and *several* binary(–)positions ΩR_n^- is (+)***symmetric*** or ***edge symmetric*** (for example Hamilton graph et al).

D1.2.5. *Element symmetric* structure (graph), that has *several* binary(+)- ΩR_n^+ and *several* binary(–)positions ΩR_n^- is ***poly-symmetric*** (see Example 1.4).

D1.2.6. Structure (graph), that *not element symmetric*, but has *one* binary(+)position ΩR_n^+ is ***semi-symmetric*** (see Example 1.6)**.**

D1.2.7. Structure (graph), that *not element symmetric*, i.e. that has *more than one* element positions, with *at least* one of these positions ΩV_k has *at least* two elements is ***partially symmetric*** (see Examples 1.1 – 1.3, 2.1, 2.2).

D1.2.8. Structure (graph), where the number K of element positions ΩV_k equals to the number $|V|$ of elements (vertices) is ***0-symmetric*** or ***completely asymmetric*** (see Example 1.13).

Symmetry and regularity is quite strongly related to with each other.

Propositions 1.5. On the relationships between symmetry and regularity:

P1.5.1. *Element symmetric (transitive)* structure is ***girth-*** or ***clique-regular.***

P1.5.2. *Complement* of an *edge symmetric* ***girth-regular*** structure is ***clique-regular*** and *vice versa*.

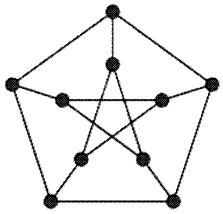
P1.5.3. Connected *bisymmetric* structure is ***strongly regular, 2-distance-regular*** and ***girth-*** or ***clique-regular.***

P1.5.4. Strong regularity of ***bisymmetric*** structure is unavoidable, because it is *2-distance-regular* and by existence only two binary signs $-d.n_1.m$ and $+d.n_2.m$ where $-d=2$ sow n_1-2 the ***number of common adjacent elements***.

P1.5.5. If all the m component cliques are *with equal power* n, then structure and its component are ***bisymmetric*** (i.e. all the *m-n-cliques are bisymmetric*)**.**

We begin the explanations with the Petersen graph, because it has essential symmetry properties that are presented in various propositions.

Example 1.5. Petersen graph ***Pet***, the binary signs and structure model for Petersen graph and its complement ***PetC*** (the numbering starts here from the upper element and goes clockwise):



A:-2.3.2; ***B:+4.10.15.***

1	1	1	1	1	1	1	1	1	1		u_i	
1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	***i***	***AB***	***k***
0	***B***	*-A*	*-A*	***B***	***B***	*-A*	*-A*	*-A*	*-A*	**1**	***63***	1
	0	***B***	*-A*	*-A*	*-A*	***B***	*-A*	*-A*	*-A*	**2**	***63***	1
		0	***B***	*-A*	*-A*	*-A*	***B***	*-A*	*-A*	**3**	***63***	1
			0	***B***	*-A*	*-A*	*-A*	***B***	*-A*	**4**	***63***	1
				0	*-A*	*-A*	*-A*	*-A*	***B***	**5**	***63***	1
					0	*-A*	***B***	***B***	*-A*	**6**	***63***	1
						0	*-A*	***B***	***B***	**7**	***63***	1
							0	*-A*	***B***	**8**	***63***	1
								0	*-A*	**9**	***63***	1
									0	**10**	***63***	1

A:-2.6.12; ***B:+2.5.8.***

1	1	1	1	1	1	1	1	1	1	u_i
1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	***AB***
0	*-A*	***B***	***B***	*-A*	*-A*	***B***	***B***	***B***	***B***	***36***
	0	*-A*	***B***	***B***	***B***	*-A*	***B***	***B***	***B***	***36***
		0	*-A*	***B***	***B***	***B***	*-A*	***B***	***B***	***36***
			0	*-A*	***B***	***B***	***B***	*-A*	***B***	***36***
				0	***B***	***B***	***B***	***B***	*-A*	***36***
					0	***B***	*-A*	*-A*	***B***	***36***
						0	***B***	*-A*	*-A*	***36***
							0	***B***	*-A*	***36***
								0	***B***	***36***
									0	***36***

Explanations to show that it is possible to read out from the structure model:

a) Petersen graph ***Pet*** is ***bisymmetric*** (i.e. has two binary positions). This has *one greatest substructure* $\boldsymbol{GS}^{sub}_{n=+B}$ (reflected as its 15 possible isomorphic greatest subgraphs) and *one smallest superstructure* $\boldsymbol{GS}^{sup}_{n=-A}$ (reflected as its 30 possible isomorphic smallest super-graphs).

b) From bisymmetry concludes ***strong regularity*** of ***Pet.***

c) Graph ***Pet*** is ***5-girth-regular***, there exist twelve *5-girths*, in present case: (1)**:** 1-2-3-4-5-1**,** (2)**:** 6-8-10-7-9-6**,** (3)**:** 1-2-3-8-6-1**,** (4)**:** 1-2-7-10-5-1**,** (5)**:** 1-5-4-9-6-1**,** (6)**:** 2-3-4-9-7-2**,** (7)**:** 3-4-5-10-8-3**,** (8)**:** 1-2-7-9-6-1**,** (9)**:** 1-5-10-8-6-1**,** (10)**:** 2-3-8-10-7-2**,** (11)**:** 3-4-9-6-8-3**,** and (12)**:** 4-5-10-7-9-4. Each element belongs to six girths, each edge belongs to four girths.

d) Binary sign ***+4.10.15*** means, that the element pair belongs to an assemblage of 5-girths, which consists of 10 elements and 15 connections (edges) – it is the *complete invariant* of Petersen graph, such sign do not have other structures.

e) The ***complement*** of Petersen graph ***PetC*** is ***4-clique-regular.*** Explicit clique sign do not exist, but *binary graph* of binary sign ***+2.5.8*** contains the *4*-clique. For example, the local structure model of binary graph with sign ***+2.5.8*** for elements 1 and 3 contains the signs of *4*-clique, ***+2.4.6***, that shows the existence of *4*-clique 1,3,9,10:

-A: -2.4.5; ***B: +2.3.3;*** ***C: +2.4.6;*** ***D: +2.5.8.***

1	3	9	10	7	***i***	***ABCD***	***k***	123
0	***D***	***C***	***C***	***B***	**1**	***0121***	1	**121**
	0	***C***	***C***	***B***	**3**	***0121***	1	**121**
		0	***C***	*-A*	**9**	***1030***	2	**21**0
			0	*-A*	**10**	***1030***	2	**21**0
				0	**7**	***2200***	3	**2**00

f) And so exists in the complement five intersected *4*-cliques, in present case with elements: (1)**:** 1,3,9,10**;** (2)**:** 2,4,6,10**;** (3)**:** 1,4,7,8**;** (4)**:** 2,5,8,9**;** and (5)**:** 3,5,6,7. Each element belongs to two cliques, each edge belongs to one clique.

Not every strongly regular graph can be bisymmetric. Among the graphs with up to 20 elements exists 39 *bisymmetric* & *strongly regular* & *clique- or girth-regular* graphs, including the 27 simply constructed *n-m-cliques* and 12 "non-m-n-cliques", where belongs also Petersen graph. As a rule, the lists of strongly regular graphs are incomplete. By help of the structure models succeeded these lists to supplement [29].

It is deal with partial coincidence of bisymmetry and strong regularity. Bisymmetry includes also the disconnected structures and strong regularity can be exists in the case of mono-, poly-, and partial symmetry, although among the structures with up to 20 elements it not been observed. Here has treated only symmetric structures, i.e. graphs that have large positions. Structure, where each element represents a separate position $\boldsymbol{\Omega V}_k$ (hence every pair of elements has its own position) is *0-symmetric*, and their treatment goes by other ways.

The positions make the structure to *inner variety*. Variety can be expressed by the power of positions and their number in the form of *variety signs.*

Definitions 1.3. Variety signs:

D1.3.1. Vector with elements $|\Omega V|^m$, where $|\Omega V|$ is the power of an element position and m the number of positions with such power is ***sign of element variety SVV***.

D1.3.2. Vector with elements $|\Omega R|^m$, where $|\Omega R|$ is the power of a binary position and m the number of positions with such power is ***sign of binary variety SRV***.

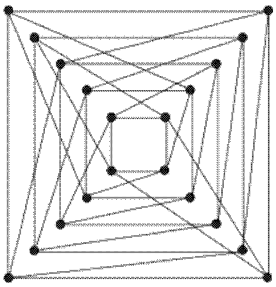
Variety signs of in the Example 1.1 showed structure *GS22(6.10.4)* (in [17] G189) are: $SVV= 1^1 2^1 3^1$, $SRV= 1^1 2^1 3^2 6^1$ where the sign of "edge variety" is $SEV=1^1 3^1 6^1$. The values of variety are computable on the basis of the variety signs by Shannon formula as the *information capacity.* For example by ***SRV*** obtained ***HR****=2.106.* The *regularity of binary positions* expressed in the form ***SR = 1 – HR*****: log|*R*|,** where $0 \le SR \le 1$. In present case ***SR****=0.46,* were *regularity of binary*(+)*positions* ***SE****=0.610* and *regularity of elements* ***SV****=0.478.* This is a specific form of regularity [33, 37].

Each position is "naturalizable" in the form of a *position structure* [33, 34, 37].

Definition 1.4. ***Position structure*** GS_n is a structure that consists of element pairs, which belong to a certain *binary position* ΩR_n. The number of position structure equal to the number of binary positions.

The position structures opens some various "hidden sides" of the structure, that sometimes also "mystical" seems. In principle, the position structures are inevitable, so as the cowering, cliques and others structural attributes, where their identification to a very practical and necessary deemed.

Example 1.6. *Bipartite and semi-symmetric* Folkman's graph ***Fol***, its binary signs, structure model and list of its position structures GS_n:



A:-4.14.21; B:-3.8.10; C:-2.6.8; D:-2.4.4; E:-2.3.2; ***F:+3.6.8.***

1	1	1	1	1	1	1	1	1	1	2	2	2	2	2	2	2	2	2	2	u_i	k	s_i
11	**12**	**13**	**14**	**15**	**16**	**17**	**18**	**19**	**20**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**i**	ABCDE**F**		12
0	-E	-E	-E	-E	-E	-E	-E	-E	-C	**F**	-B	-B	**F**	-B	**F**	-B	-B	-B	-F	**11**	061084	1	04
	0	-E	-E	-E	-E	-E	-E	-C	-E	-B	**F**	-B	-B	**F**	-B	-B	-B	**F**	**F**	**12**	061084	1	04
		0	-E	-E	-E	-E	-C	-E	-E	**F**	-B	**F**	-B	-B	-B	-B	**F**	**F**	**B**	**13**	061084	1	04
			0	-E	-E	-C	-E	-E	-E	-B	**F**	-B	**F**	-B	-B	**F**	**F**	-B	-B	**14**	061084	1	04
				0	-C	-E	-E	-E	-E	-B	-B	**F**	-B	**F**	**F**	**F**	-B	-B	-B	**15**	061084	1	04
					0	-E	-E	-E	-E	-B	-B	**F**	-B	**F**	**F**	**F**	-B	-B	-B	**16**	061084	1	04
						0	-E	-E	-E	-B	**F**	-B	**F**	-B	-B	**F**	**F**	-B	-B	**17**	061084	1	04
							0	-E	-E	**F**	-B	**F**	-B	-B	-B	-B	**F**	**F**	-B	**18**	061084	1	04
								0	-E	-B	**F**	-B	-B	**F**	-B	-B	-B	**F**	**F**	**19**	061084	1	04
									0	**F**	-B	-B	**F**	-B	**F**	-B	-B	-B	**F**	**20**	061084	1	04
										0	-A	-D	-D	-A	-D	-A	-D	-D	-D	**1**	360604	2	40
											0	-A	-D	-D	-A	-D	-D	-D	-D	**2**	360604	2	40
												0	-A	-D	-D	-D	-D	-D	-A	**3**	360604	2	40
													0	-A	-D	-D	-D	-A	-D	**4**	360604	2	40
														0	-D	-D	-A	-D	-D	**5**	360604	2	40
															0	-D	-A	-A	-D	**6**	360604	2	40
																0	-D	-A	-A	**7**	360604	2	40
																	0	-D	-A	**8**	360604	2	40
																		0	-D	**9**	360604	2	40
																			0	**10**	360604	2	40

Explanations:

a) Graph ***Fol*** decompose correspondingly its binary positions *–A, –B, –C, –D, –E and* ***F*** to six *position-structures*:

b) To binary position *–A* corresponds *position structure* $\boldsymbol{Fol}_{n:\,-A}$ is ***Petersen's graph*(!)**. This fact is showed also in partial model $\mathbf{SM}_{2.2}$, if there the sign *–A* replace with Petersen sign ***+4.10.15*** and *–D* replace with sign *–2.3.2* then it is equivalent with structure model of Petersen graph (see Example 1.5).

c) To binary position *–B* corresponds *position structure* $\boldsymbol{Fol}_{n=-B}$ turns out to *another semi-symmetric graph*, designed by V. Titov [40] that has also a position structure in the form of *Petersen graph*.

d) To binary position *–C* corresponds *position structure* $\boldsymbol{Fol}_{n=-C}$ is a graph with ten *components* of *2-cliques*.

e) To binary position *–D* corresponds *position structure* $\boldsymbol{Fol}_{n=-D}$ is the *complement of Petersen graph* (!).

f) To binary position *–E* corresponds *position structure* $\boldsymbol{Fol}_{n=-E}$ is the *complement of position structure* $\boldsymbol{Fol}_{n=-C}$, i.e. *2-quinta clique*.

g) To binary position ***+F*** corresponds *position structure* $\boldsymbol{Fol}_{n=+F}$ is naturally *Folkman graph* self.

The importance of position structures lies in the explaining structural properties, but these also recognize the identical particles of various structures. For example, could be argued that the semi-symmetrical graphs with 20 elements represent a kind of "genetic group" that contains position structures in the form of Petersen graphs. Also, all the graphs of *n*-polygons are proven to be the widespread position structures. Such relationships between the position structures appear in various ways. If the structure is partited, or contain components, cliques, girths, etc., then appear the corresponding attributes in position structures in another forms [33, 34, 37].

Propositions 1.6. Properties of position structures:

P1.6.1. Position structures $\boldsymbol{GS}_n$ open the different "hidden" sides and particles of its initial structure ***GS***.

P1.6.2. Position structure is *element symmetric*, i.e. its elements belong to the same position $\boldsymbol{\Omega V}_{k=1}$.

P1.6.3. To the binary(+)position $\boldsymbol{\Omega R}_n^{+}$ corresponds a position(+)structure $\boldsymbol{GS}_n^{+}$ is a *partial structure* of ***GS***; to the binary(–)position $\boldsymbol{\Omega R}_n^{-}$ corresponds a position(–)structure $\boldsymbol{GS}_n^{-}$ is a *partial structure of complement* $\neg\boldsymbol{GS}$.

P1.6.4. To each binary(+)position $\boldsymbol{\Omega R}_n^{+}$ of structure ***GS*** corresponds the binary(–)position of complement $\neg\boldsymbol{GS}$ where their *position structures coincides*, $\boldsymbol{GS}_n^{+} \equiv \neg\boldsymbol{GS}_n^{-}$.

P1.6.5. Some position structure $\boldsymbol{GS}_n$ can be *appear isomorphic with initial structure,* ***GS***, $\boldsymbol{GS}_n \cong \boldsymbol{GS}$ (for example, an position structure of the cube is also cube).

P1.6.6. *Different position structures* $\boldsymbol{GS}_n$ of initial structure ***GS*** or *position structures of different structures* can be *isomorphic* or *coincides*.

Under the looking are also the position structures of position structures, i.e. second and high degree position structures.

Propositions 1.7. Properties of high degree position structures:

P1.7.1. Second or high degree position structure can be *isomorphic or coincides with a lower degree position structure or initial structure. Coincidence* of a position structure and initial structure constitutes a *reconstruction* of initial structure.

P1.7.2. High degree position structures *no open more complementary "hidden sides"*, these begin to repeat.

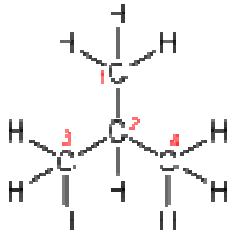
P1.7.3. Formation of high degree position structure is a *convergent process,* it finished with a crop up or reconstruction a low degree or initial structure

1.3. Structure of the natural objects

Structural model of the ***chemical compound*** is a detailed submission of the classical structural formula, i.e. of a graph that represents this formula.

This is the so-called *systemic approach* to the study of chemical compounds where different chemical elements (atoms) as a rule, are divided into different *positions* as *subsystems*. In case of more complex compounds, however, may also the same elements (atoms) belong to different positions (for example, ethanol, butane, propane, etc.). The main idea of such systemic approach consists in treatment of the whole on the basis of positions and the relationships between them. Structural models open up the possibility for additional investigation of chemical compounds. The structural models of some polymers and organic matters tend to be very large. Here is limited with moderates.

Example 1.7. Structural formula of *isobutan* C_4H_{10}, its binary signs and structure model:

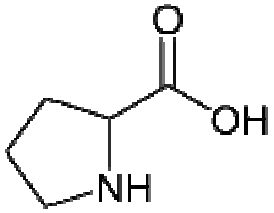


A:-4.5.4; B:-3.4.3; C:-2.3.2;
D:+1.2.1.

2| 1 3 4|11| 5 6 7 8 9 10 12 13 14| **i**	u_i		s_i
C| **C C C**| **H**| **H H H H H H H H H**| ***a***	*ABCD*	***k***	1234
0| ***D D D***| ***D***| *-C -C -C -C -C -C -C -C -C*| **C** 2	*0094*	*1*	0**3**10
| *0*	*-C -C*| *-C*| ***D D D*** *-B -B -B -B -B -B*| **C** 1	*0634*	*2*	**1**003
0	*-C*| *-C*| *-B -B -B* ***D D D*** *-B -B -B*| **C** 3	*0634*	*2*	**1**003
0| *-C*| *-C*| *-B -B -B -B -B -B* ***D D D***| **C** 4	*0634*	*2*	**1**003
0| *-B*| *-B*| *-B -B -B -B -B -B -B -B -B*| **H** 11	*0931*	*3*	**1**000
| *0*	*-C -C*| *-A*| *-A -A -A -A -A -A*| **H** 5	*6331*	*4*	0**1**00
0	*-C*| *-A*| *-A -A -A -A -A -A*| **H** 6	*6331*	*4*	0**1**00
0| *-A*| *-A*| *-A -A -A -A -A -A*| **H** 7	*6331*	*4*	0**1**00
0| *-C*| *-C*| *-A -A -A -A -A -A*| **H** 8	*6331*	*4*	0**1**00
0| *-C*| *-A*| *-A -A -A -A -A -A*| **H** 9	*6331*	*4*	0**1**00
0| *-A*| *-A*| *-A -A -A -A -A -A*| **H** 10	*6331*	*4*	0**1**00
0| *-C*| *-C*| *-A -A -A -A -A -A*| **H** 12	*6331*	*4*	0**1**00
0| *-C*| *-A*| *-A -A -A -A -A -A*| **H** 13	*6331*	*4*	0**1**00
0| *-A*| *-A*| *-A -A -A -A -A -A*| **H** 14	*6331*	*4*	0**1**00

Explanation: Decomposition of the elements C and H to four positions should not cause questions.

Example 1.8. Structural formula, binary signs and structure model of the amino acid *proline* $C_5H_9NO_2$:



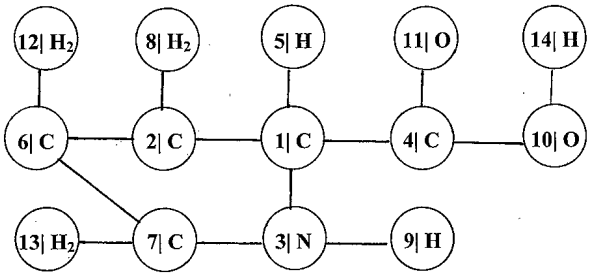
A:-6.7.6; B:-5.6.5; C:-4.5.4; D:-3.4.3; E:-2.3.2;
F:+1.2.1; G:+4.5.5.

4	3	15	5	10	2	1	8 9	12	17	16	6 7	13 14	11			u_i	
C	**C**	**N**	**C**	**H**	**C**	**C**	**H** **H**	**H**	**O**	**O**	**H** **H**	**H**	**H**	**H**	**a**	**i**	*ABCDE**FG***	***k***
0	***G***	***G***	***F***	***F***	*−E*	*−E*	*−E* *−E*	*−E*	*−E*	*−E*	*−D* *−D*	*−D*	*−D*	*−D*	**C**	4	*0005722*	*1*
	*0***/***−E***	*−E*	*−E*	***G***	*−E*	***F*** ***F***	*−D*	*−D*	*−D*	*−E* *−E*	*−D*	*−D*	*−C*	**C**	3	*0015622*	*2*
	0	*−E*	*−E*	*−E*	***G***	*−D* *−D*	***F***	*−D*	*−D***/***−D* *−D*	*−E*	*−E*	*−C*	**N**	15	*0016612*	*3*
	0	*−E*	*−D*	*−D*	*−D* *−D*	*−D*	***F***	***F***	*−C* *−C*	*−C*	*−C*	*−E*	**C**	5	*0045430*	*4*
	0	*−D*	*−D*	*−D* *−D*	*−D*	*−D*	*−D*	*−C* *−C*	*−C*	*−C*	*−C*	**H**	10	*0057310*	*5*
	0	***G***	*−E* *−E*	*−D*	*−C*	*−C*	***F*** ***F***	*−E* *−E*	*−B*	**C**	2	*0123622*	*6*
	0	*−D* *−D*	*−E*	*−C*	*−C*	*−E* *−E*	***F*** ***F***	*−B*	**C**	1	*0124522*	*7*
	0 *E*	*−C*	*−C***/***−C*	*−D* *−D*	*−C* *−C*	*−B*	**H**	8	*0156310*	*8*
	0	*−C*	*−C*	*−C*	*−D* *−D*	*−C* *−C*	*−B*	**H**	9	*0156310*	*8*
	0	*−C*	*−C*	*−C* *−C*	*−D* *−D*	*−B*	**H**	12	*0166210*	*9*
	0	*−E*	*−B* *−B*	*−B* *−B*	***F***	**O**	17	*0453220*	*10*
	0	*−B* *−B*	*−B* *−B*	*−D*	**O**	16	*0454210*	*11*
	0 *−E*	*−D* *−D*	*−A*	**H**	6	*1236310*	*12*
	0	*−D* *−D*	*−A*	**H**	7	*1236310*	*12*
	0 *−E*	*−A*	**H**	13	*1245310*	*13*
	0	*−A*	**H**	14	*1245310*	*13*
	0	**H**	11	*4532110*	*14*

			s_i
a	***i***	***k***	*12345678901234*
C	4	*1*	0**1111**000000000
C	3	*2*	**1**0000**1**0**2**000000
N	15	*3*	**1**000000**1**0**1**00000
C	5	*4*	**1**00000000**11**000
H	10	*5*	**1**00000000000000
C	2	*6*	0**1**0000**1**0000**2**00
C	1	*7*	00**1**00**1**000000**2**0
H	8	*8*	0**1**000000000000
H	9	*8*	0**1**000000000000
H	12	*9*	00**1**000000000000
O	17	*10*	000**1**0000000000**1**
O	16	*11*	000**1**0000000000
H	6	*12*	00000**1**00000000
H	7	*12*	00000**1**00000000
H	13	*13*	000000**1**0000000
H	14	*13*	000000**1**0000000
H	11	*14*	00000000**1**0000

Structure model of proline also provides all the relationship between the elements. Its 17 elements are concentrated in 14 different positions. Presented separately position-vectors s_i constitutes an adjacent matrix of positions, which enable compose corresponding "position's graph".

Example 1.9. The *position's graph* of proline:



The structural model of this position graph ("positions model") we here no represents, we note only that this has 10 positions, in which joined former positions (2, 3), (6, 7), (8, 9) and (12, 13).

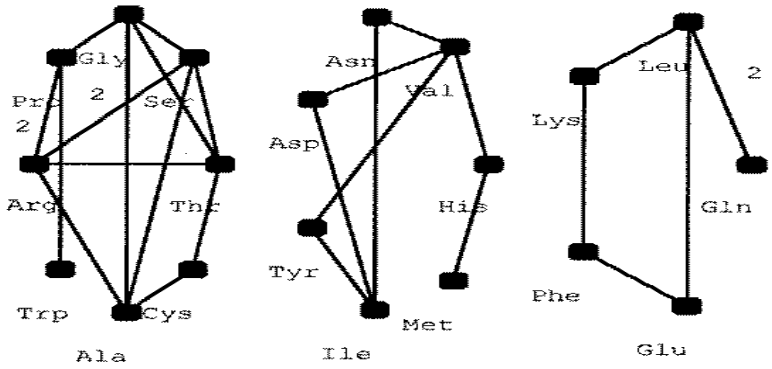
The structural model of chemical compound opens for chemist unfamiliar structural side, but this side does not advisable to ignore because the existence of structure is real. To this end, all of this is presented here.

Exists also such a thing as a “chemical graph theory”, which can be regarded as the mainstay of chemical compounds in the field of work by Arthur Cayley in 1874 (although if the term “graph” was not yet used). The end of the last century, thousands of articles on the subject, and in 1980 published a two-volume monograph of Nenad Trinaisti on *Chemical Graph Theory*. Proponents of this theory argue that it is giving valuable information about chemical phenomena, however, to the opponents seems it reasonable only in exceptional cases. I support the first. Moreover, the structural model is something perfect than a graph.

*

The ***genetic code*** in biology describes how genes that are composed of DNA are translated into proteins composed amino acids. The American bioinformatics William Seffens seems that genetic codes can be represented as *graphs* where the elements are *amino acids.* In his article, he justifies this view-point (). Here we limited with the treatment of graphs and structural model of the genetic code [19].

Example 1.10. The graph with three components of *Standard genetic code* (ID=1), its binary signs and structure model:



A: -4.7.9; B:-4.7.8; C:-3.6.8; D:-3.6.7; E:-3.5.5; F:-3.4.3;
G:-2.6.10; H:-2.5.6; I:-2.4.4; J:-2.3.2; K:-u.2.0;
L:+1.2.1; M:+2.3.3; N:+2.4.5; O:+3.4.4; P:+3.5.6; Q:+3.6.10.

L	**E**	**K**	**V**	**R**	**G**	**N**	**D**	**Y**	**Q**	**F**	**S**	**A**	**T**	**H**	**P**	**M**	**I**	**W**	**C**		**a**		
11	7	12	20	2	8	3	4	19	6	14	16	1	17	9	15	13	10	18	5	***i***		***deg***	***k***
0	***O***	***O***	-K	**-**K	-K	-K	-K	-K	***L***	-I	-K	-K	-K	-K	-K	-K	-K	-K	-K	11	**Leu**	*3*	*1*
0	-I	-K	-K	-K	-K	-K	-K	-J	***O***	-K	-K	-K	-K	-K	-K	-K	-K	-K	-K	7	**Glu**	*2*	*2*
0	-K	-K	-K	-K	-K	-K	-K	**-**J	***O***	-K	-K	-K	-K	-K	-K	-K	-K	-K	-K	12	**Lys**	*2*	*2*
0	-K	-K	***P***	***P***	***P***	**-**K	-K	-K	-K	-K	***L***	-K	-J	-H	-K	-K	-K			20	**Val**	*4*	*3*
0	-G	-K	-K	-K	**-**K	-K	***N***	***M***	***M***	-K	***Q***	-K	-K	-J	-I					2	**Arg**	*4*	*4*
0	-K	-K	-K	**-**K	-K	***N***	***M***	***M***	-K	***Q***	-K	-K	-J	-I						8	**Gly**	*4*	*4*
0	-I	-I	**-**K	-K	-K	-K	-K	-J	-K	-F	***P***	-K	-K							3	**Asn**	*2*	*5*
0	-I	-K	-K	-K	-K	-K	-J	-K	-F	***P***	-K	-K								4	**Asp**	*2*	*5*
0	-K	-K	-K	-K	-K	-J	-K	-F	**P**	-K	-K									19	**Tyr**	*2*	*5*
0	-E	-K	-K	-K	-K	-K	-K	-K	-K	-K										6	**Gln**	*1*	*6*
0	-K	-K	-K	-K	-K	-K	-K	-K	-K											14	**Phe**	*2*	*7*
0	***N***	***N***	-K	-I	-K	-K	-E	-I												16	**Ser**	*4*	*8*
0	-G	-K	-I	-K	-K	-E	***Q***													1	**Ala**	*4*	*9*
0	-K	-I	-K	-K	-E	***Q***														17	**Thr**	*4*	*9*
0	-K	***L***	-D	-K	-K															9	**His**	*2*	*10*
0	-K	-K	***L***	-C																15	**Pro**	*3*	*11*
0	-B	-K	-K																	13	**Met**	*1*	*12*
0	-K	-K																		10	**Ile**	*3*	*13*
0	-A																			18	**Trp**	*1*	*14*
0																				5	**Cys**	*2*	*15*

		u_i				s_i
i	***a***	*ABCDEFGHIJ*	*K*	***LMNOPQ***	***k***	123456789012345
11	**Leu**	*0000000010*	*15*	***100200***	*1*	020001000000000
7	**Glu**	*0000000011*	*15*	***000200***	*2*	100000100000000
12	**Lys**	*0000000011*	*15*	***000200***	*2*	100000100000000
20	**Val**	*0000000101*	*13*	***100030***	*3*	000030000100000
2	**Arg**	*0000001011*	*12*	***021001***	*4*	000000012010000
8	**Gly**	*0000001011*	*12*	***021001***	*4*	000000012010000
3	**Asn**	*0000010021*	*13*	***000020***	*5*	001000000000100
4	**Asp**	*0000010021*	*13*	***000020***	*5*	001000000000100
19	**Tyr**	*0000010021*	*13*	***000020***	*5*	001000000000100
6	**Gln**	*0000100002*	*15*	***100000***	*6*	100000000000000
14	**Phe**	*0000100010*	*15*	***000200***	*7*	020000000000000
16	**Ser**	*0000100020*	*12*	***004000***	*8*	000200002000000
1	**Ala**	*0000101010*	*12*	***021001***	*9*	000200010000001
17	**Thr**	*0000101010*	*12*	***021001***	*9*	000200010000001
9	**His**	*0001000003*	*13*	***200000***	*10*	001000000001000
15	**Pro**	*0010000030*	*12*	***100002***	*11*	000200000000010
13	**Met**	*0100030001*	*13*	***100000***	*12*	000000000100000
10	**Ile**	*0101000100*	*13*	***000030***	*13*	000030000000000
18	**Trp**	*1000300002*	*12*	***100000***	*14*	000000000010000
5	**Cys**	*1010000030*	*12*	***000002***	*15*	000000002000000

All three components are by Seffens represented as a common graph, because in case of alternative genetic codes exists relationships between the components. The numbers by relations indicate the number of edges (multigraph's existence). The cycles exist in standard genetic code with a length of 3 and 4. Disconnections with the other components represent binary sign *K:–u.2.0.* Twenty amino acids form the fifteen positions. We can see that the common positions ***k*** in the genetic code have the following amino acids

k=2) *glutamic acid* (Glu) ja *lysine* (Lys); ***k=4***) *arginine* (Arg) ja *glycine* (Gly);
k=5) *aspargine* (Asn), *aspartic acid* (Asp) ja *tyrosine* (Tyr); ***k=9***) *alahine* (Ala) ja *threonine* (Thr).

If is accepted the positions in genetic code, then should also be accept the relationships between positions (position vectors s_i), which constitutes the adjacent matrix of positions. The corresponding graph plotted from here does not make sense, but the structural model can be set up. Existing there double and triple connections can be ignore, because these characterize only the number of amino acids that having a common position.

Example 1.11: Binary signs and structure model of *position's relationships* of Standard genetic code:

A:–4.5.4; B:–3.4.3; C:–2.3.2; D:+u.2.0; ***E:+1.2.1; F:+2.3.3.***

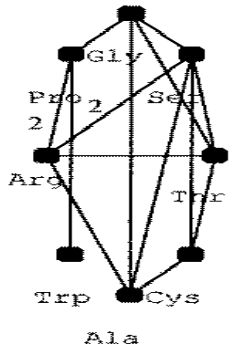
															u_i			
|	1	2|	4|	3|	9|	5	10|	6	7|	8|11|	12	13|	15|	14|	***k***	*ABC*	*D*	***EF***	***k****
|	*0*	***E***|	–D|	–D|	–D|	–D	–D|	***E***	–C|	–D|	–D|	–D	–D|	–D|	–D|	1	*001*	*11*	***20***	*1*
		0|	–D|	–D|	–D|	–D	–D|	–C	***E***|	–D|	–D|	–D	–D|	–D|	–D|	2	*001*	*11*	***20***	*1*
			0|	–D|	***F***|	–D	–D|	–D	–D|	***F***|	***E***|	–D	–D|	–C|	–C|	4	*002*	*9*	***12***	*2*
				0|	–D|	***E***	***E***|	–D	–D|	–D|	–D|	–C	–C|	–D|	–D|	3	*002*	*10*	***20***	*3*
					0|	–D	–D|	–D	–D|	***F***|	–C|	–D	–D|	***E***|	–B|	9	*011*	*9*	***12***	*4*
						0	–C|	–D	–D|	–D|	–B	***E***|	–D|	–D|			5	*011*	*10*	***20***	*5*
							0|	–D	–D|	–D|	***E***	–B|	–D|	–D|			10	*011*	*10*	***20***	*5*
								0	–B|	–D|	–D|	–D	–D|	–D|	–D|			6	*011*	*11*	***10***	*6*
									0|	–D|	–D|	–D	–D|	–D|	–D|			7	*011*	*11*	***10***	*6*
										0|	–C|	–D	–D|	–C|	–B|			8	*012*	*9*	***02***	*7*
											0|	–D	–D|	–B|	***E***|			11	*012*	*9*	***20***	*8*
												0	–A|	–D|	–D|			12	*111*	*10*	***10***	*9*
													0|	–D|	–D|			13	*111*	*10*	***10***	*9*
														0|	–A|			15	*112*	*9*	***10***	*10*
															0|			14	*121*	*9*	***10***	*11*

	s_i			
k|	12345678901	***k****	***a***	*
1|	**1**0000**1**00000	*1*	**Leu**	
2|	**1**0000**1**00000	*1*	**Glu, Lys**	*
4|	000**1**00**11**000	*2*	**Arg, Gly**	*
3|	0000**2**000000	*3*	**Val**	*
9|	0**1**0000**1**00**1**0	*4*	**Ala, Thr**	*
5|	00**1**00000**1**00	*5*	**Asn, Asp,**	*
10|	00**1**00000**1**00	*5*	**His, Tyr**	*
6|	**1**0000000000	*6*	**Gln**	*
7|	**1**0000000000	*6*	**Phe**	*
8|	0**1**0**1**0000000	*7*	**Ser**	*
11|	0**1**000000000**1**	*8*	**Pro**	*
12|	0000**1**000000	*9*	**Met**	*
13|	0000**1**000000	*9*	**Ile**	*
15|	000**1**0000000	*10*	**Cys**	*
14|	0000000**1**000	*11*	**Trp**	*

In the structure model of *position's relationships* are some previous positions ***k*** merged into new positions ***k****, the number of previous positions was 15, now 11. Also here represent the position vectors a new adjacent matrix, on which it could continue to operate. However we limited, because the genetic significances of the obtained results are not covered here.

Alternative genetic codes differ from standard code a greater or lesser extent. Different components of the codes can be isomorphic. For example, the second and third component of Euplotid Nuclear code (ID=10) is isomorphic with the corresponding components of Standard genetic code, etc. The differences expressed as a few different loop, a new relationship (edge) in component or between components.

Example 1.12. First component of *Euplotid Nuclear code* (ID=10), its binary signs and structure model:



A:-4.8.14; B:-3.7.13; C:-3.5.5; D:-2.6.11; E:-2.6.10; F:-2.5.8;
G:-2.4.4; H:-2.3.2;
I:+1.2.1; J:+2.3.3; K:+2.4.5; L:+2.5.7; M:+3.6.10.

| G	R|	S|	T	A|	P|	W|	C|		***a***	u_i		s_i
| 8	2|	16|	**17**	1|	15|	18|	5|	***i***		*ABCDEFGH**IJKLM***	***k***	123456
0	*-E*|	***K***|	***J***	***J***|	***M***|	*-H*|	*-F*|	8	**Gly**	*00001101**02101***	1	0**121**00
	0|	***K***|	***J***	***J***|	***M***|	*-H*|	*-F*|	2	**Arg**	*00001101**02101***	1	0**121**00
		0|	***L***	***L***|	*-G*|	*-C*|	***K***|	16	**Ser**	*00100010**00320***	2	**2**0**2**00**1**
			0	*-D*|	*-G*|	*-C*|	***J***|	17	**Thr**	*00110010**03010***	3	**21**0000**1**
				0|	*-G*|	*-C*|	***J***|	1	**Ala**	*00110010**03010***	3	**21**0000**1**
					0|	***I***|	*-B*|	15	**Pro**	*01000030**10002***	4	**2**0001**0**
						0|	*-A*|	18	**Trp**	*10300002**10000***	5	000**1**00
							0|	5	**Cys**	*11000200**02100***	6	0**12**000

Euplotid Nuclear code is an *adjacent superstructure* of Standard code (see chp. 2.2). Addition of the relation between Ser-Cys changes the structure, but the positions will be retained. W. Seffens has treated 15 genetic codes, which on the structural aspect forms a "space of genetic codes".

*

It is appropriate to note that symmetry (i.e. existence the positions with more than one element) in natural structures is an extremely phenomenon. The structure of natural objects, such as communication and other networks, are usually 0-symmetric (i.e., each element is in a separate position and the same binary signs can exist only in the different positions) [34, 37]. Let us here make a "living example".

Since real ***communication networks*** are very large. Imagine here one a peculiar companionship ***Z*** consisting of *Adolf, Berta, Charles, Diana, Erik, Frieda, George, Helen, Ingvar and Jane*. They are mutually agreed that everyone communicates with the five, known to us, parlor companions. The latter circumstance had required of coordination, and someone had to do it.

Adolf – Berta, Charles, Diana, George, Jane;
Berta – Adolf, Charles, Helen, Ingvar, Jane;
Charles – Adolf, Berta, Diana, Erik, George;
Diana – Adolf, Charles, Erik, Frieda, Ingvar;
Erik – Charles, Diana, Frieda, Helen, Jane;
Frieda – Diana, Erik, George, Helen, Ingvar;
George – Adolf, Charles, Frieda, Helen, Jane;
Helen – Berta, Erik, Frieda, George, Ingvar;
Ingvar – Berta, Diana, Frieda, Helen, Jane;
Jane – Adolf, Berta, Erik, George, Ingvar.

This situation constitutes a *five-valence-regular structure* in which all the members seem to be in "equal position". To represent this situation, make the structure model of ***Z.***

Example 1.13. Structure model of situation ***Z***:

A:–2.6.10; B:–2.6.9; C:–2.5.8; D:–2.5.7; E:–2.5.6; F:–2.4.5; G:–2.4.4;
H:+2.3.3; I:+2.4.5; J:+2.5.7; K:+3.10.25.

1	2	3	4	5	6	7	8	9	10		u_i	
F	**A**	**D**	**H**	**C**	**B**	**I**	**J**	**E**	**G**	***name***	*ABCDEFG**HIJK***	***k***
0	*–G*	***I***	***J***	*–D*	*–F*	***I***	*–E*	***I***	***H***	**Frieda**	*0001111**1310***	1
	0	***H***	*–G*	***J***	***I***	*–D*	***I***	*–D*	***I***	**Adolf**	*0002002**1310***	2
		0	*–C*	***I***	*–D*	***H***	*–E*	***I***	*–D*	**Diana**	*0012100**2300***	3
			0	*–E*	***H***	***I***	*–B*	***H***	***H***	**Helen**	0110101**3110**	4
				0	***H***	*–G*	*–A*	***H***	***H***	**Charles**	*1001101**3110***	5
					0	***I***	***I***	*–E*	*–A*	**Berta**	*1001110**2300***	6
						0	***H***	*–A*	*–D*	**Ingvar**	*1002001**2300***	7
							0	***K***	***H***	**Jane**	*1100200**2201***	8
								0	*–B*	**Erik**	*1101100**2201***	9
									0	**George**	*1102000**4100***	10

Unfortunately, the structure ***Z*** is *0-symmetric*, there do not "equality", each member has its own private position. *Different position* means different connectivity, "relationships" with other members. Between ten members exists 11 different relationships, which is characterized by the binary signs (see frequency vectors $\boldsymbol{u}_i$). The problem lies here in the *grouping of strictly differentiated members*. This fact leads us back to the *sign structures* $\boldsymbol{GS_p}$ (see P1.1.3). In selection of the sign must be proceeds from:

1) Selected sign must be exits *in case of each structural element*.
2) To keep in mind the *meaning of sign*, because the sign structure be formed on the aspect of sign.

In principle is the companionship decomposable to eleven inseparable component sign structures $\boldsymbol{GS_p}$, and gives different groupings. This is inappropriate, and useful to go the other way.

Let to it is the rearranging the members by their "direct communication signs" ***HIJK*** of frequency-vectors in Example 1.13.

Example 1.14. Rearranged by ***HIJK*** structure model ***Z***:

1	2	4	5	3	6	7	8	9	10		u_i	
F	**A**	**H**	**C**	**D**	**B**	**I**	**J**	**E**	**G**	***name***	***k***	***HIJK***	**R**
0|-G|	***J***|-D|	***I***|-F|	***I***|-E|	***I***|	***H***|	**Frieda**	1	***1310***	**1**
0|-G|	***J***|	***H***|	***I***|-D|	***I***|-D|	***I***|	**Adolf**	2	***1310***	**1**
0|-E|	***-C***|	***H***|	***I***|-B|	***H***|	***H***|	**Helen**	4	***3110***	**2**
0|	***I***|	***H***|-G|-A|	***H***|	***H***|		**Charles**	5	***3110***	**2**
0|-D|	***H***|-E|	***I***|***-D***|				**Diana**	3	***2300***	**3**
0|	***I***|	***I***|-E|-A|				**Berta**	6	***2300***	**3**
0|	***H***|-A|-D|					**Ingvar**	7	***2300***	**3**
0|	***K***|	***H***|				**Jane**	8	***2201***	**4**
0|-B|							**Erik**	9	***2201***	**4**
0|							**George**	10	***4100***	**5**

The resulting grouping corresponds to the requirement of "direct communication signs", where the *ten positions* ***k*** reduces to *five groups*, with the members:

R_1= (*Frieda, Adolf*)**,** R_2**=** (*Helen, Charles*)**,** R_3= (*Diana, Berta, Ingvar*)**,**
R_4= (*Jane, Erik*) and R_5= (*George*)**.**

For finding the "similarity" of members can be use also *approximate or rounded-off* binary signs.

Example 1.15. Using the rounded-off binary signs:

Rounding-off: *a***=** [*A:-2.6.10; B:-2.6.9*], *b*= [*C:-2.5.8; D:-2.5.7; E:-2.5.6*],
c= [*F:-2.4.5; G:-2.4.4*], ***d*=** [***H: +2.3.3; I:+2.4.5; J: +2.5.7***], ***e*= (*K: +3.10.25*)**.
Rounded binary signs: *a*:*(A, B)* ≈ *–2.6*, *b*:*(C, D, E)* ≈ *–2.5*, *c*:*(F, G)* ≈ *–2.4*, ***d*:*(H, I, J)* ≈ *+2*** ja ***e*: *K* ≈ *+3*.**

1	2	3	4	5		a	b	c	***d***	***e***		u^*_i	
F	**A**	**D**	**H**	**C**	**B**	**I**	**J**	**E**	**G**	***name***	*AB*|*CDE*|*FG*| ***HIJ***| ***K***	***k***	*abcde*	***k****
0|-G|	***I***|	***J***|-D|	-F|	***I***|-E|	***I***|	***H***|		**Frieda**	*00*|*011*|*11*| ***131***| ***0***	1	*02250*	***1***
0|	***H***|-G|	***J***|	***I***|-D|	***I***|-D|	***I***|			**Adolf**	*00*|*020*|*02*| ***131***| ***0***	2	*02250*	***1***
0|-C|	***I***|-D|	***H***|-E|	***I***|-D|					**Diana**	*00*|*121*|*00*| ***230***| ***0***	3	*03050*	***2***
0|-E|	***H***|	***I***|-B|	***H***|	***H***|				**Helen**	*01*|*101*|*01*| ***311***| ***0***	4	*12150*	***3***
0|	***H***|-G|-A|	***H***|	***H***|					**Charles**	*10*|*011*|*01*| ***311***| ***0***	5	*12150*	***3***
0|	***I***|	***I***|-E|-A|						**Berta**	*10*|*011*|*10*| ***230***| ***0***	6	*12150*	***3***
0|	***H***|-A|-D|							**Ingvar**	*10*|*020*|*01*| ***230***| ***0***	7	*12150*	***3***
0|	***K***|	***H***|							**Jane**	*11*|*002*|*00*| ***220***| ***1***	8	*22041*	***4***
0|-B|										**Erik**	*11*|*011*|*00*| ***220***| ***1***	9	*22041*	***4***
0|										**George**	*11*|*020*|*00*| ***410***| ***0***	10	*22050*	***5***

The resulting grouping by rounded-off binary signs:

k**$_1$*= (*Frieda, Adolf*)**,** ***k**$_2$=** (*Diana*)**,** ***k**$_3$*= (*Helen, Charles, Berta, Ingvar*)**,**
***k**$_4$*= (*Jane, Erik*) and ***k**$_5$*= (*George*)**.**

We can see that there exist coincidences between the results of "direct communication signs" and rounding-off. The first way shall be considered as more distinct and therefore more reliable. The "rounding" of binary signs may prove to be quite arbitrary. Mention must be the *specific role of Jane and Erik* in this companionship, to their relationship ***K: +3.10.25*** includes all members and relationships, and they may be *coordinators.*

Such *0*-symmetric structures can be treats, investigate, and elements grouped in several ways:

1) Investigation of the selected sign structures GS_p.
2) Investigate on the basis of some selected binary signs formed the so-called complex sign structures.
3) Reordering the structural model by the given binary signs (Example 1.14).
4) For reducing the positions to use the connected or "rounded" binary signs (Example 1.15).

All of this requires a good knowledge of the subject and suitable choices the aspects for the investigation.

2. STRUCTURAL CHANGES

2.1. Elementary structural changes

Elementary structural changes expressed in two modes: 1) As a *greatest subgraph* G^{sub}, obtained by ***removing an edge*** $G\backslash e_{ij}$ of G; 2) As a *smallest supergraph* G^{sup}, obtained with ***adding an edge*** $G\cup e_{ij}$ to G. The number of G^{sub} equals to the number of edges and the number of G^{sup} to number of "non-edges.

Definition 2.1. Greatest subgraphs G^{sub} and smallest supergraphs G^{sup} called ***adjacent graphs*** G^{adj} of graph G.

Proposition 2.1. If the edge operations f in the framework of a binary position $\Omega R_n = \Omega(r_{ij1},\ldots,r_{ijq})_n$ *are separated* $\{(f_{ij})_1\vee\ldots\vee(f_{ij})_q\}_n$, then the adjacent graphs are ***isomorphic***, i.e. form an *isomorphism class* $\Gamma_n=\{(G^{adj}{}_n)_1\cong\ldots\cong(G^{adj}{}_n)_q\}$.

Now we must do the difference between *adjacent graph* G^{adj} and *adjacent structure* GS^{adj}. Structure can be *represented* by the arbitrary designed and labeled graphs of the isomorphism class Γ_n, because they structures are equivalent [22, 27, 34, 37].

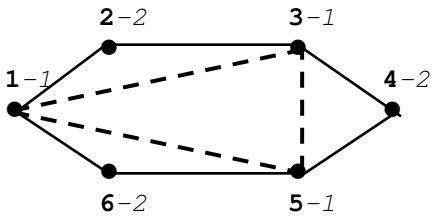
Proposition 2.2. Adjacent graphs G^{adj}, which belong to one isomorphism class Γ_n have equivalent *structure models* **SM** and represent the ***adjacent structure*** $GS^{adj}{}_n$. The number of adjacent structures equals to the number of binary positions ΩR_n.

Definition 2.2. Disjunctive edge operation $F_n=\{(f_{ij})_1\vee\ldots\vee(f_{ij})_q\}_n$, which changes the structure GS to its adjacent structure GS^{adj} called ***morphism*** F_n, $F_n: GS\rightarrow GS^{adj}$.

Morphisms are the principal instruments of elementary structural changes.

Proposition 2.3. Morphism $F_n: GS\rightarrow GS^{adj}{}_n$ has a ***morphism probability,*** $PF=\mathrm{card}|\Omega R_n|:\mathrm{card}|R|$, where $\mathrm{card}|\Omega R_n|$ is the power of binary position and card|R| the number of corresponding element-pairs in the structure GS, i.e. the number of edges or "non-edges" in the graph,

Example 2.1. Structure *GS.37(6.9.4)* (see [30, 37]) with two element positions and two "edge" positions, its graph, structure model, characteristics of changes and morphisms:



A:−2.4.5; B:−2.3.2;
C:+2.3.3; D:+2.4.5.

1	1	1	2	2	2		u_i	k	s_i
1	3	5	2	4	6	i	ABCD		12
0	D	D	C	−A	C	1	1022	1	22
	0	D	C	C	−A	3	1022	1	22
		0	−A	C	C	5	1022	1	22
			0	−B	−B	2	1220	2	20
				0	−B	4	1220	2	20
					0	6	1220	2	20

	$GS^{adj}{}_n$	1	2
GS.37	$GS^{sup}{}_{n-}$	29	30
	k.k'(p)	2.2 (−B)	1.2 (−A)
	$PF^{sup}{}_{n-}$	3/6	3/6
GS.37	$GS^{sub}{}_{n+}$	72	76
	k.k'(p)	1.1 (+D)	1.2 (+C)
	$PF^{sub}{}_{n+}$	3/9	6/9

Explanations:

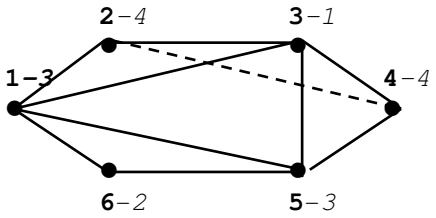
a) $GS^{sup}{}_{n-}$ and $GS^{sub}{}_{n+}$ denotes the *ordering numbers* of adjacent superstructures and adjacent substructures in the system of structures with six elements (see Example 2.5);

b) ***k,k'*** – index of partial model $\mathbf{SM}_{k,k'}$, where belong the binary position ***(p)***;

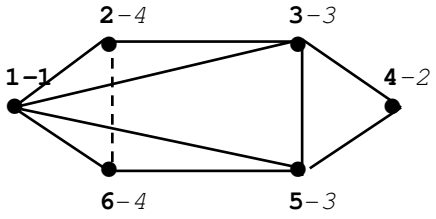
c) $\boldsymbol{PF_n}$ – *morphism probability*.

Example 2.2. Representing the ***adjacent superstructure*** $\boldsymbol{GS^{sup}{}_{n=-B}}$, (*GS.29,* [30, 37]) of structure *GS.37* (Example 2.1) *isomorphic graphs*, their *common binary signs* and *equivalent structure models* $\mathbf{SM_1} \equiv \mathbf{SM_2} \equiv \mathbf{SM_3}$ that obtained by *adding* the connections 2-4, 2-6 and 4-6 (dashed line) to binary(–)position *–B* of *GS.37*:

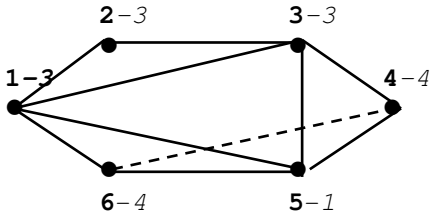
A:-2.5.8; B:-2.4.5; C;-2.3.2;
D:+2.3.3; E:+2.4.5.



1	2	3	3	4	4	u_i		s_i
3	**6**	**1**	**5**	**2**	**4**	**i**	*ABCDE*	*k*	1234
0	–*B*	***E***	***E***	***E***	***E***	**3**	*01004*	*1*	0022
	0	***D***	***D***	–*C*	–*C*	**6**	*01220*	*2*	0020
		0	***E***	***D***	–*A*	**1**	*10022*	*3*	**1111**
			0	–*A*	***D***	**5**	*10022*	*3*	**1111**
				0	***D****	**2**	*10121*	*4*	1011
					0	**4**	*10121*	*4*	1011



1	2	3	3	4	4	u_i		s_i
1	**4**	**3**	**5**	**2**	**6**	**i**	*ABCDE*	*k*	1234
0	–*B*	***E***	***E***	***E***	***E***	**1**	*01004*	*1*	0022
	0	***D***	***D***	–*C*	–*C*	**4**	*01220*	*2*	0020
		0	***E***	***D***	–*A*	**3**	*10022*	*3*	**1111**
			0	–*A*	***D***	**5**	*10022*	*3*	**1111**
				0	***D****	**2**	*10121*	*4*	1011
					0	**6**	*10121*	*4*	1011

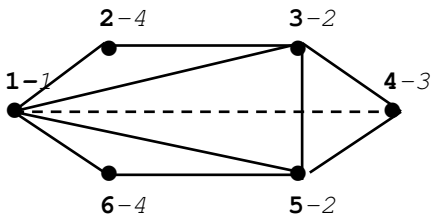


1	2	3	3	4	4	u_i		s_i
5	**2**	**1**	**3**	**4**	**6**	**i**	*ABCDE*	*k*	1234
0	–*B*	***E***	***E***	***E***	***E***	**5**	*01004*	*1*	0022
	0	***D***	***D***	–*C*	–*C*	**2**	*01220*	*2*	0020
		0	***E***	–*A*	***D***	**1**	*10022*	*3*	**1111**
			0	***D***	–*A*	**3**	*10022*	*3*	**1111**
				0	***D****	**4**	*10121*	*4*	1011
					0	**6**	*10121*	*4*	1011

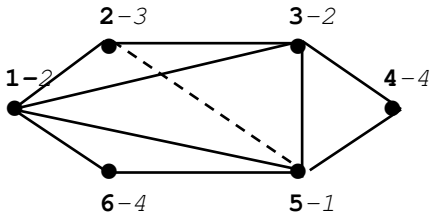
Explanation: Equivalent structure models differ from each other only numbered elements in different positions in the division.

Example 2.3. Representing the ***adjacent superstructure*** $\boldsymbol{GS^{sup}{}_{n=-A}}$, (*GS.30,* [30, 37]) of structure *GS.37* (Example 2.1) *isomorphic graphs*, their *common binary signs* and *equivalent structure models* $\mathbf{SM_1} \equiv \mathbf{SM_2} \equiv \mathbf{SM_3}$ that obtained by *adding* the connections 1-4, 2-5 and 3-6 (a dashed line) to binary(–)position *–A* of *GS.37*:

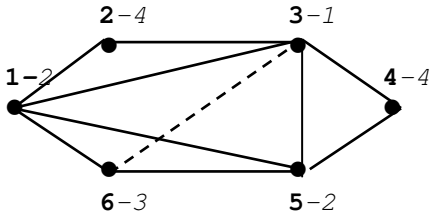
A:-2.4.5; B:-2.3.2;
C:+2.3.3; D:+2.4.5; E:+2.6.15.



1	2	2	3	4	4	u_i		s_i
1	**3**	**5**	**4**	**2**	**6**	**i**	*ABCDE*	**k**	1234
0	***E***	***E***	***D****	***C***	***C***	**1**	*00212*	*1*	0212
	0	***D***	***D***	***C***	–*A*	**3**	*10121*	*2*	**1111**
		0	***D***	–*A*	***C***	5	*10121*	*2*	**1111**
			0	–*A*	–*A*	**4**	*20030*	*3*	**12**00
				0	–*B*	**2**	*21200*	*4*	**11**00
					0	**6**	*21200*	*4*	**11**00



1	2 2	3	4 4		u_i		s_i
5	1 3	2	4 6	i	ABCDE	k	1234
0	E E	D*	C C	5	00212	1	0212
| 0	D	D	−A C	1	10121	2	1111
	0	D	C −A	3	10121	2	1111
	| 0	−A −A	2	20030	3	1200
		| 0 −B	4	21200	4	1100
			0	6	21200	4	1100

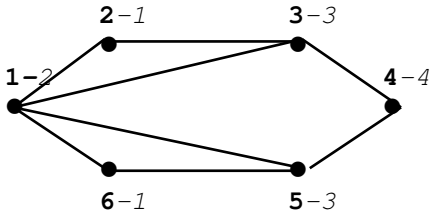


1	2 2	3	4 4		u_i		s_i
3	1 5	6	2 4	i	ABCDE	k	1234
0	E E	D*	C C	3	00212	1	0212
| 0	D	D	C −A	1	10121	2	1111
	0	D	−A C	5	10121	2	1111
	| 0	−A −A	6	20030	3	1200
		| 0 −B	2	21200	4	1100
			0	4	21200	4	1100

Explanation: The adjacent structures that are obtained by the same binary position ΩR_n are *equivalent*, but by different binary positions obtained adjacent structures are *non-equivalent.* It is valid also in case of *adjacent substructures.*

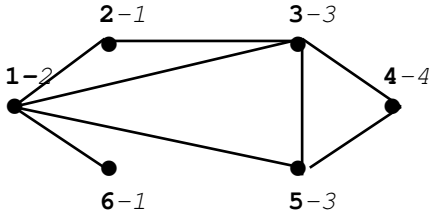
Example 2.4. The ***adjacent substructures*** $GS^{sub}_{n=+D}$, (*GS.72,* [30, 37]) and $GS^{sub}_{n=+C}$, (*GS.76*) of structure *GS.37* (Example 2.1) that obtained by *removing* the connection 3-5 from binary(+)position **+D** and *removing* the connection 5-6 from binary(+)position **+C** correspondingly. Their *non-isomorphic graphs, different binary signs* and *non-equivalent structure models* $\mathbf{SM}_A$ and $\mathbf{SM}_B$:

A:−2.4.4; B:−2.3.2;
C:+2.3.3; D:+3.4.4.



1 1	2	3 3	4			u_i		s_i
2 6	1	3 5	4	i	ABCD	k	1234
0 −B	C	C −B	−B	2	0320	1	0110
0	C	−B C	−B	6	0320	1	0110
| 0	C C	−A	1	1040	2	2020
| 0−A*	D	3	1121	3	1101
	0	D	5	1121	3	1101
		0	4	1202	4	0020

A:−3.5.6; B:−2.4.5; C:−2.3.2;
D:+1.2.1; E:+2.3.3; F:+2.4.5.



1	2	3	4	5	6			u_i		s_i
3	1	5	2	6	4	i	ABCDEF	k	123456
0	F	F	E	−C	E	3	001022	1	011101
0	E	E	D	−B	1	010121	2	101110
| 0	−B	−C	E	5	011021	3	110001
| 0	C*	−C	2	012020	4	110000
	0	−A	6	103100	5	010000
	0	4	111020	6	101000

Explanation: By different binary positions obtained adjacent structures are *non-equivalent.*

Proposition 2.4. Each structure *GS* is an adjacent substructure GS^{sub}_n or adjacent superstructure G^{sup}_n of some other structures.

2.2. Adjacent structures and Ulam Conjecture

Proposition 2.5. Morphism F is ***reversible –*** in each adjacent structure GS^{adj} of GS exist an "*reverse position*" ΩR^{rev}, whereat used *reverse morphism* F^{rev} ***reconstruct*** the initial structure GS, F^{rev}**:** $GS^{adj} \rightarrow GS$**.**

Let the structure on Example 2.2 is an initial structure GS that has an adjacent substructure $GS^{sub}{}_n$ in the forms of structure on Example 2.1. Then GS can be *reconstruct* by adding a connection to the *reverse position –B* of $GS^{sub}{}_n$ with morphism probability PF^{rev}=3/6.

The reversing of morphism is valid both in the case of adjacent sub- $GS^{sub}{}_{n+}$ and super-structures $Gs^{sup}{}_{n-}$. Indeed, structure GS can be reconstructed by each of its adjacent structure GS^{adj} separately. On the set $\{GS^{adj}{}_n\}$ of all the adjacents of GS there exists certain *set of opposite morphisms* $\{F'_n\}$, $n \in [1, N]$, such that each its disjunctive element $(F'_1: GS^{adj}{}_1 \rightarrow GS) \vee \ldots \vee (F'_N: GS^{adj}{}_N \rightarrow GS)$ *reconstructs the structure* GS *separately.*

Thus, to be precise, the morphisms exist between the binary positions of structures.

Proposition 2.6. If morphisms $F_n: GS \rightarrow GS^{adj}{}_n$ are applied to binary positions $\Omega R_1, \ldots, \Omega R_n, \ldots, \Omega R_N$ of GS disjunctivelly, $F_1 \vee \ldots \vee F_n \vee \ldots \vee F_N$, then GS is ***decomposed*** *(deconstructed)* to its *adjacent structures* $GS^{adj}{}_1, \ldots, GS^{adj}{}_n, \ldots, GS^{adj}{}_N$.

Non-decomposable structures do not exist.

Proposition 2.7. If structure GS is ***decomposed*** *(deconstructed)* to its ***adjacent substructures*** $GS^{sub}{}_1, \ldots, GS^{sub}{}_n, \ldots, GS^{sub}{}_N$, then their ***union*** $\cup(GS \backslash e_{ij})_n$, $n^+ \in [1, N^+]$, ***reconstruct*** *(recompose)* the structure GS.

This applies in particular for union of adjacency matrices $\cup(E \backslash e_{ij})_n = E$.

Proposition 2.8. If structure GS is ***decomposed*** *(deconstructed)* toi ts ***adjacent superstructures*** $GS^{sup}{}_1, \ldots, GS^{sup}{}_n, \ldots, GS^{sup}{}_N$, then their ***intersection*** $\cap(GS \cup e_{ij})_n$, $n^- \in [1, N^-]$, ***reconstruct*** *(recompose)* the structure GS.

Conclusion. Thus, the ***reconstructing (restoring) of structure is inevitable***, non-reconstructive structures do not exist.

The *reconstruction problem* is known as ***Ulam's Conjecture*** and constitutes the isomorphism relations between two graphs and their $(G \backslash v_i)$-subgraphs [43]. It is formulated as follows: "Let graph G has $p \geq 3$ vertices v_i and H has $p \geq 3$ vertices u_i. If for each i, the sub-graphs $G_i = G \backslash v_i$ and $H_i = H \backslash u_i$ are isomorphic, then the graphs G and H are isomorphic".

This problem has been over the past half century, one of under active consideration graph theoretical problem, but the ultimate solutions have only some graph classes. Why so? Evidently be interested on the question**:** contain the collection of sub-graphs $G \backslash v_i$ of G enough information about graph G itself? On the structural aspect is the *wording* of this conjecture *nonsense,* because, if given graphs G and H then on the ground of *structure models* we obtain the complete information about their isomorphism and isomorphism of their adjacent graphs.

Ulam's Conjecture treats the reconstruction on the aspect of removing of the vertices, but we treat it on the aspect of adding and removing of edges. This not changes the essence of reconstruction, because all remains to the frame of graphs (structures) and their adjacent graphs (-structures). Already old master W. T. Tutte emphasized that reconstruction-problem must be solve on the basis of isomorphism classes, that we also have followed [42].

2.3. Genesis of the structures

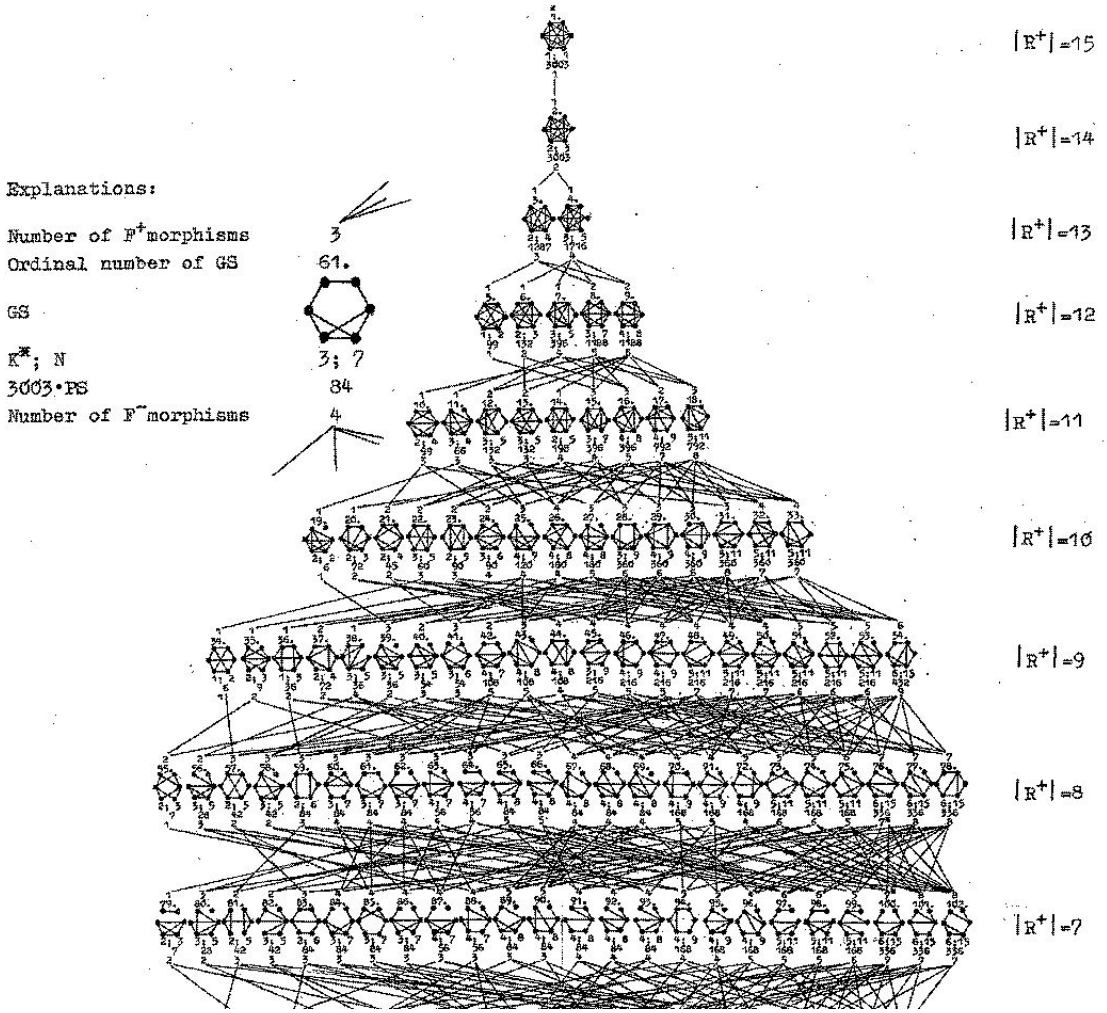
Genesis of the structures constitutes *generating of all adjacent structures of the structures with |V| elements*, i.e. adjacent structures of the adjacent structures or successors of the successors [22, 34, 37].

The idea of structural genesis is simple. Let the number of elements (vertices) of the genesis's condition is fixed. In the first step of genesis arises there a first relationship (edge). The second step is a bit more complex: there can arise a relationship with an element, which already has relationship with another element, but can also appears a relationship between elements that do not yet have relationship. The latter is more likely. Thus, after the second step the genesis is *branched* to two, i.e. appear two possible "successors".

In the third step the right genesis, i.e., the branching of possible successors only begins. With further addition of relationships, the *structure dense* and the *branching increase*, until it reaches the *middle-phase* of genesis. From the middle-phase the *branching begins to decline*, although *thickening continues*. Middle phase is the *bisector* of genesis, where for each *structure* in first half of genesis correspond its *complement* in the second half of the genesis. To the last step of genesis being the adding of last relationship to the very thicken (dense) structure, to achieve the *complete structure.*

Generating of the structures takes place by help of the structure models. It is presentable in the form of lattice, where the elements are structures ***GS*** and to relationships morphisms ***F***. In present case we have begin from complete structure.

Example 2.5. First half of the lattice of genesis the structures with six elements:



Explanations:

a) $|\mathbf{R}^+|$ denote the *structural level,* i.e. the number of relationships in the structures.
b) Each graph represents there its *isomorphism class* or *structure*.
c) Each structure in this lattice is an *adjacent structure* of some other structures.
d) In the Examples 1.1 – 1.3 and 2.1 – 2.4 showed structures are in this lattice represented by their ordering numbers
e) The *complements* of represented structures placed symmetrically in the second half of the lattice.

The complete explanation of structural genesis is represented the following issues: 1) Genesis of structures with five elements in [34]; 2) Genesis of structures with six elements [37].

Genesis of the structures takes place as generation of the morphisms $\boldsymbol{F_n}$, so that in the framework of structures ***GS*** of each structural level $|\mathbf{R}^+|$ are formed their adjacent structures, i.e. the structural level of adjacent structures $\boldsymbol{GS^{adj}}$. In result of structural genesis is the ***system of structures*** $\mathfrak{G}$ obtained.

The first sample of non-isomorphic graphs with up to six vertices was represented by Frank Harary in 1969th [6]. Later, F. Harary and E. Palmer had calculated the number of non-isomorphic graphs (i.e. structures) up to 24 vertices [7]. R. Read and F. Wilson were in "Graph Atlas" also given the diagrams of graphs up to seven vertices [17]. But so far do not are discussed about the relationships between adjacent graphs, i.e. morphisms.

Example 2.6. General characteristics of some systems $\mathfrak{G}$ of structures with $|V|$ elements**:**

Number of elements $\|V\|$	Number of structures p	Among this connected p^*	Number of levels m	Number of morphisms q	Number of binarypositions q^*
3	4	2	4	3	6
4	11	6	7	14	28
5	34	21	11	72	144
6	156	112	16	572	1144
7	1044	853	22		
8	12346	11117	29		

Explanation:
The number $\boldsymbol{m}$ of structural levels $|\mathbf{R}^+|$ equals to the number of relationships in complete structure plus one. Can be do note, that in case $|V|=10$ the number of structures is 12005156, in case $|V|=20$ 645490122795799841856164683490742749440, etc.

Structure genesis is realizable in the way of successive formation the structure models. It is not possible that someone would have tried to do anything like on the base of combinatorics, algebra or other classical attributes.

Propositions 2.9. Some properties of structure systems $\mathfrak{G}^{|V|}$:

P2.9.1. If the number of structural levels $\boldsymbol{m}$ in system $\mathfrak{G}^{|V|}$ is *even number* (as in case $|V|=6$ and $|V|=7$), then is it lattice *bilateralllly symmetric* with regard its bisector, which separates the structures ***GS*** from their *complements* $\rceil\boldsymbol{GS}$.

P2.9.2. If the number of structural levels $\boldsymbol{m}$ in system $\mathfrak{G}^{|V|}$ is *odd number* (as in case $|V|=4$, $|V|=5$, $|V|=8$ and $|V|=9$), then the bisector is a structural level in which be found *structures* ***GS***, their *complements* $\rceil\boldsymbol{GS}$ and also *self-complemented* structures $\boldsymbol{GS}=\rceil\boldsymbol{GS}$.

P2.9.3. Algebraic properties: a) The class of morphisms **F** form an ***additive group A*** in the meaning of the composition ***F&F.*** b) The class of structures **GS** together with the class of morphisms **F** forms a ***category C***.

In structural genesis has important role *randomness.* This manifests in the form of *selection the adjacent structures*, i.e. elementary structural changes. The *probabilities* of this system are related with *internal*

diversity of structure, i.e. binary positions, and have essential meaning in the research of structure systems.

Propositions 2.10. Probabilistic characteristics of structure systems $\mathfrak{G}^{|V|}$:

P2.10.1. *Randomness* in the systems $\mathfrak{G}$ based on the *morphism probabilities* $\boldsymbol{PF_n}$.

P2.10.2. There exists *transition probability* $\boldsymbol{P_{ij}}$ at a structure $\boldsymbol{GS_i}$ to a non-adjacent structure $\boldsymbol{GS_j}$.

P2.10.3. Transition probabilities $\boldsymbol{P_{ij}}$ form the *stationary Markov chain* ***PM*** of structural genesis (see Example 2.8).

P2.10.4. *Existence probability* ***PS*** of the structure ***GS*** in system $\mathfrak{G}$ characterize its being among other structures on the structural level $|\mathbf{R}^+|$. This expressed in the form:

$$\boldsymbol{PS=_{n=1}\sum^{N-}PS^{sup}{}_n\times PF^{sub}{}_n=_{n=1}\sum^{N+}PS^{sub}{}_{n-}\times PF^{supp}{}_n,}$$

where $\boldsymbol{n}$ is the structural index of binary position, $\boldsymbol{PS^{sup}{}_n}$ existence probability of adjacent superstructure and $\boldsymbol{PF^{sub}{}_n}$ its morphism probability.

P.2.10.5. The *sum of existence probabilities* $\boldsymbol{PS_m}$ of structures in the structural level $|\mathbf{R}^+|$ equal to one, $\boldsymbol{\sum PS_m=1.}$

P2.10.6. Existence probabilities of *structure* and its *complement* are equal, $\boldsymbol{PS(GS)=PS(\neg GS)}$.

P2.10.7. Existence probabilities ***PS*** are *rational numbers*, where their *smallest common denominators* are directly related with the degree of genesis $|V|$.

P2.10.8. Distribution of probabilities ***PS*** in the structure level approaching to *logarithmic normal distribution.*

Exist some real systems whose working (functioning) can represent in the form *of successive changing their structure in the time.* It can be argued that all the *developmental, evolutionary and revolutionary* phenomena are related to structural changes [10, 11, 22]. Structure model enables to select its possible immediate (direct) states (conditions).

Successive structural changes are showed in the lattice of structure system $\mathfrak{G}^{|V|}$ as a *path*. It is modeled proceeding from a concrete structure $\boldsymbol{GS_0}$.

Definition 2.3. Successive morphisms $\boldsymbol{F_1\&F_2\&\ldots\&F_t}$ on the structures ***GS,***

$$\boldsymbol{{}^{F1:}GS_0\rightarrow {}^{F2:}GS_1\rightarrow {}^{F3:}GS_2\rightarrow\ldots {}^{Ft:}GS_{t-1}\rightarrow GS_t,}$$

forms a ***sequence of structural changes SF.***

Propositions 2.11. Properties of structural changes ***SF*:**

P2.11.1. Sequence ***SF*** can be ***random*** or ***teleological***, if the selection of morphisms takes place on the ground of certain requirements**.**

P2.11.2. Sequences between non-adjacent structures $\boldsymbol{GS_i}$ and $\boldsymbol{GS_j}$ in system $\mathfrak{G}^{|V|}$ constitute an ***assemblage of structural sequences***.

P2.11.3. Structural changes that take place on the basis of only $\boldsymbol{F^+}$morphisms or only $\boldsymbol{F^-}$morphisms constitute a ***"vertical sequence".***

P2.11,4. Sequence ***SF***, where the initial structure $\boldsymbol{GS_i}$ and finish structure $\boldsymbol{GS_j}$ belongs to the same structural level $\mathfrak{G}^{\mathbf{m}}$ is a ***"horizontal sequence".*** Such structural changes based on the *morphism pairs* $\boldsymbol{F^-\&F^+}$ (or $\boldsymbol{F^+\&F^-}$), that constitute "replacing of a relationship" in the structure ***GS*** (see Example 2.6).

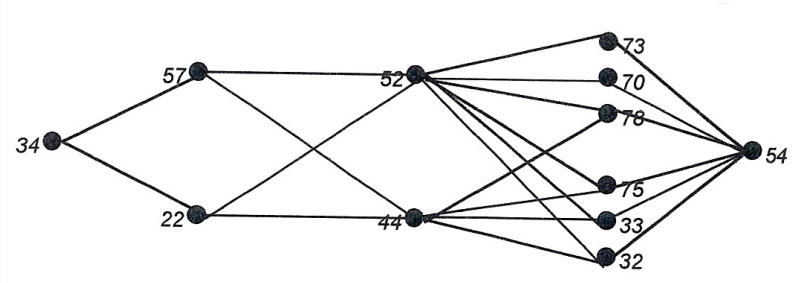
P2.11.5. Sequence ***SF***, where the values of structural characteristics change monotonically, is a ***monotonous sequence SFM*** on the apect of characteristics (see Example 2.8).

P2.11.6. A random, with *t* steps successsion, has ***sequence probability PSF*** in the form of product of morphism probabilities:

$$\boldsymbol{PSF=_{i=1}\prod^{t}PF_i=PF_1\times PF_2\times\ldots\times PF_t.}$$

Take a look to an *assemblage of horizontal sequences* between the symmetric structure ***GS.34*** (*SR=0.751, PS=6:3003*) and 0-symmetric structure ***GS.54*** (*SR=0, PS=432:*3003) in the structural level $\mathfrak{G}^{m=9}$.

Example 2.7. Assemblage of horizontal sequences between two structures**:**



Explanation:
The structures 22, 32, 33 belong to the structural level ***m***=8, structures 34, 44, 52, 54 to ***m***=9, structures 57, 70, 73, 75, 78 belong to the level ***m***=10.

Example 2.8. The *stationary Markov chain* $\boldsymbol{PM_{34,54}}$ of this assemblage of horizontal sequences**:**

GS	**34**	**22**	**57**	**44**	**52**	**32**	**33**	**75**	**78**	**70**	**73**	**54**
34	***0***	***1 20250***	***1 30375***	***2 8100***	***2 16200***	***3 2160***	***3 2160***	***3 2160***	***3 4320***	***3 2160***	***3 2160***	***4 1728***
22	***1 3375***	***0***	***2 4050***	***1 10125***	***2 20250***	***2 2700***	***2 2700***	***2 2700***	***2 5400***	***2 2700***	***2 2700***	***3 2160***
57	***1 3375***	***2 2700***	***0***	***1 6750***	***1 13500***	***2 1800***	***2 1800***	***2 1800***	***2 3600***	***2 1800***	***2 1800***	***3 1440***
44	***2 450***	***1 3375***	***1 3375***	***0***	***2 4725***	***1 6750***	***1 6750***	***1 6750***	***1 13500***	***3 405***	***3 405***	***2 3600***
52	***2 350***	***1 3375***	***1 3375***	***2 1800***	***0***	***1 3375***	***1 3375***	***1 3375***	***1 6750***	***1 6750***	***1 6750***	***2 3600***
32	***3 60***	***2 450***	***2 450***	***1 3375***	***1 3375***	***0***	***2 1125***	***2 1125***	***2 2025***	***2 2700***	***2 2700***	***1 6750***
33	***3 60***	***2 450***	***2 450***	***1 3375***	***1 3375***	***2 1125***	***0***	***2 1125***	***2 2025***	***2 2700***	***2 2700***	***1 6750***
75	***3 60***	***2 450***	***2 450***	***1 3375***	***1 3375***	***2 1125***	***2 1125***	***0***	***2 2025***	***2 2700***	***2 2700***	***1 6750***
78	***3 60***	***2 450***	***2 450***	***1 3375***	***1 3375***	***2 1125***	***2 1125***	***2 1125***	***0***	***2 2700***	***2 2700***	***1 3375***
70	***3 60***	***2 450***	***2 450***	***3 420***	***1 6750***	***2 2700***	***2 2700***	***2 2700***	***2 1350***	***0***	***2 1350***	***1 6750***
73	***3 60***	***2 450***	***2 450***	***3 420***	***1 6750***	***2 2700***	***2 2700***	***2 2700***	***2 1350***	***2 1350***	***0***	***1 6750***
54	***4 24***	***3 180***	***3 180***	***2 900***	***2 1800***	***1 3375***	***1 3375***	***1 3375***	***1 3375***	***1 3375***	***1 3375***	***0***

Explanations:

a) Numbers 1 to 4 show the number of steps ***t***, i.e. distance ***d.***

b) Numbers 24 to 30375 show the transition probabilities $\boldsymbol{P_{ij}}$**,** multiplied with 50625.

c) *Transition probability* $\boldsymbol{P_{ij}}$ from symmetric structure ***GS.34*** to *0*-symmetric ***GS.54*** $P_{34,54}$=1728**:**50625 is 1728**:**24=***72 times greater*** as in contrary direct, $P_{54,34}$=24**:**50625**!**

d) The difference of *existence probabilities* ***PS*** is also ***72 multiple***, where PS_{34}=*6:3003* and PS_{54}=*432:3003.*

In $\mathfrak{G}^{|V|=6}$ exists only one ***monotonous sequence SFM***, that thoughts all the structural levels.

The structural changes in the system $\mathfrak{G}^{|V|}$ can be describe also on the aspect of concepts of dynamical systems [8].

2.4. About structural genesis of the natural objects

There are natural objects in which their development, genesis, evolution is manifested in the form of changes in their structure. We take a look one of a sub phenomenon of *ecological genesis*, ***coenogenesis*** that mean the genesis of the plant community, i.e., its transformation and evolution.

As a pioneer of the application of discrete mathematics in investigation of biological systems should be regarded N. Rashevsky, who created in years 1954-1957 the foundations of so-called *topological biology*. In the years 1958-1978 develop R. Rosen the *relationic biology*, which later became known as *(M,R)-systems*. In the period 1967-1972 represents N. Rashevsky the *concepts of organismic sets* that by I. Baianu and M. Marinescu in years 1968-1980 developed as the *theory of organismic super category*.

It is widely believed that the biological system is to be considered as a large physico-chemical formation, where its behavior is depends from its structure, based on the laws of physics and chemistry. To this contradict the bio-semiotics, who wants to see a whole. Any system (as a whole), also biological is many-aspect, it can be treated on a given or an agreeable to the investigator aspect. Any case, it is related to the need to determine the sub-systems, elements and their relationships.

Development of plant communities, i.e. *coenogenesis* expressed in the changing of abundance and nomenclature of species. This is related with the change in coverage and the associated *competitive relationships*. In other words, the coenogenesis constitutes a *sequence of structural changes*.

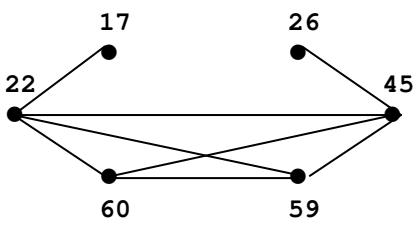
The given *simulation of coenogenesis* on the title is based on the observation data – topographical diagrams and descriptions of epilithic lichen synusiae made by ecologist Jüri Martin on various age moraines on the glaciers called after L. S. Berg in the Polar Urals. Thus, to be precise, it is a simulation of *lichogenesis*. The observations have been made hundreds where for the simulations were selected 92, These include 60 species of lichens, mosses and flowering plants as well. In each synusiae was a fixed 4 to 10 different species. The species are met in 92 synusiae squares 757 times forming 1120 pairs of species, that in their turn described by 3252 contacts among 4371 individual thalluses [10, 11].

The simulation is based on three principles, formulated by J. Martin :

1) Lichogenesis characterized by *competition between species* that are detected as direct *contacts or connections* between species.
2) Each *states* of lichogenesis are presented in the form of the *graphs*, obtained by analyzing of the 92 *topographic scheme* of synusiae (observation area 20x20 cm).
3) Under normal environmental conditions the lichogenesis manifests itself in the form of an *increase in the coverage of synusiae*.

The battle rages in the interests of living space and for characterization the development stages is useful to divide the states, on the basis of coverage's coefficient $\boldsymbol{c}$, $\boldsymbol{c}\in[\,0,\,1]$, to nine steps: $\boldsymbol{c}_{t=1}$:$(0<\boldsymbol{c}\le 0{,}05)$; $\boldsymbol{c}_{t=2}$:$(0{,}05<\boldsymbol{c}\le 0{,}1)$; $\boldsymbol{c}_{t=3}$:$(0{,}1<\boldsymbol{c}\le 0{,}17)$; $\boldsymbol{c}_{t=4}$:$(0{,}17<\boldsymbol{c}\le 0{,}6)$; $\boldsymbol{c}_{t=5}$:$(0{,}6<\boldsymbol{c}\le 0{,}7)$; $\boldsymbol{c}_{t=6}$:$(0{,}7<\boldsymbol{c}\le 0{,}8)$; $\boldsymbol{c}_{t=7}$:$(0{,}8<\boldsymbol{c}\le 0{,}87)$; $\boldsymbol{c}_{t=8}$:$(0{,}87<\boldsymbol{c}\le 0{,}95)$; $\boldsymbol{c}_{t=9}$:$(0{,}95<\boldsymbol{c}\le 1{,}0)$.

Example 2.9. The graph of a state of lichogenesis, its binary signs and structure model:



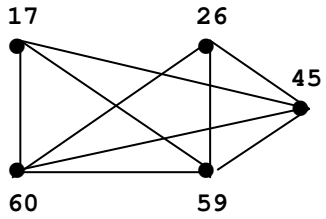
A:-3.4.3; B:-2.3.2; ***C:+1.2.1; D:+2.4.6.***

1	1	2	2	3	3	u_i	s_i		
22	45	59	60	17	26	i	ABCD	k	123
0	D	D	D	C	-B	22	0113	1	121
	0	D	D	-B	C	45	0113	1	121
		0	D	-B	-B	59	0203	2	210
			0	-B	-B	60	0203	2	210
				0	-A	17	1310	3	100
					0	26	1310	3	100

Explanation: The elements are enumerated by species, where 17 – *Lecanora polytropa*, 22 – *Lecanora atra*, 26 – *Umbilicaria cylindrica*, 45 – *Umbilicaria hyperborea*, 59 – *Rhizocarpon geographicum*, 60 – *Rhizocarpon hochstetteri*. The species are here divided into three and the relationships to seven positions.

For fixing the successors of conditions used here the maximum value of a *successor coefficient* δ, $\delta = 2\rho : (n_a + n_b)$, where ρ is the number coincides species in states a and b, and (n_a+n_b) the number of speciesc in those states.

Example 2.10. The graph of a successor state of preceding, its binary signs and structure model:



A:-2.5.9; ***B:+2.4.6;*** ***C:+2.5.9.***

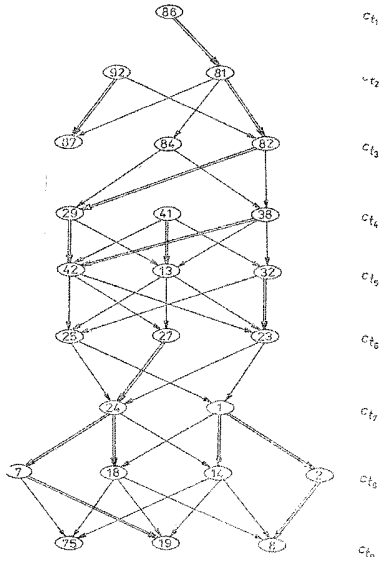
1	1	1	2	2	*i*	u_i		s_i
45	**59**	**60**	**17**	**26**	***i***	*ABC*	***k***	12
0	***C***	***C***	***B***	***B***	**45**	*022*	**1**	**22**
	0	***C***	***B***	***B***	**59**	*022*	**1**	**22**
		0	***B***	***B***	**60**	*022*	**1**	**22**
			0	*-A*	**17**	*130*	**2**	30
				0	**26**	*130*	2	30

Explanation: The increasing of coverage is associated with the increasing of the number of competing pair of species, and resulted disappear here the species 22. This was to be expected, because with species 45 had previously the same number of competitors, but on the level of individuals was competes more dense. The structure itself is thus simplified. Species 17 and 26 continue to hold their position. The species 59 and 60 have a common position with the 45. The species are here divided into two and the relationships to three positions.

Since in lichens synusiae, unlike higher plant communities, there are no seasonal fluctuations then we can the relationships between species consider reasonably stable. If one species ousted from synusiae, then it is unlikely that it gets back there because the vacant space occupied by the fastest-growing and competing-ability species.

Aside of coverage coefficient c is still under observation *structural complexity* η and *ecological variety* μ (*variety of life forms*: crustaceous and folious lichens, fruticose lichens, mosses etc). Ecological variety characterizes the *evolutionary stages* of the community. For the simplified representation of lichogenesis are selected 24 conditions, that embrace all the evolutional stages and the probable successions.

Example 2.11. The lattice L of lichogenitical conditions (structure models):



On the ground of lattice $\boldsymbol{L}$ and phase space $\boldsymbol{R}(\boldsymbol{c}_t, \boldsymbol{\eta}, \boldsymbol{\mu})$ obtained various data about *successions of lichogenetic states, behaviour of species, ecological niches, evolutionary stages* and other: For instance: Emergence of lichen species in synusiae is various. There exist species that appear in the early stages of lichogenesis, species that are always present, and species that appear only in recent stages of lichogenesis.

Using the *structural models* gives here new possibility:

1) Detection the successions (sequences) of lichogenetic states.
2) Detection the pairs of non-competed species.
3) Detection the species that have common positions.

*

If *coenogenesis* proceeds in direction from empty structure to the dense complete structure, then behind all the known facts proceeds the ***ontogeny*** (*genesis of an individuals*) to an opposite direction: from a concentrated (spore) condition in the direction of branching and thinning. The central states of ontogeny are ***origin, maturity,*** and ***cessation***.

The elements of coenogenetic simulation were empirical structures that follow the ecological laws. On the framework of *ontogeny hypothesis* we attempt to find among the formal structures such *successions* (*sequences*) that follow provisions of ontogeny [22].

We depart here from seven postulates:

1. *Moses' postulate (I Mos. 3, 19)*: "You're from the earth, and under the earth must again depart",
2. *Ludwig von Bertalanffy's postulate (1934)*: The essence of living phenomenon expressed on the level of its *organizing* (pro: *structure*).
3. *Norbert Wiener's I postulate (1948)*: The *complexity* of living system *increases monotonically*, reaching its peak in maturity, and it starts to fall apart.
4. *Norbert Wiener's II postulate (1948)*: During the life processes occurs a *monotonic decrease of entropy*.
5. *Teilhard de Chardin's I postulate (1955)*: The living matter is *granular*, between these exist *phenomenal-energetic relationships* that ensure the *fundamental integrity*, unity.
6. *Teilhard de Chardin's postulate II (1955)*: In the stage *arising (origin)* of living phenomena exist the maximum concentration phenomenal-energetic relationships, they breaking means the cessation of existence.
7. *(Une postulate a la s'est la vie)*: The probability of achieve (obtaining) the maturity stage is always less than the probability of cessation.

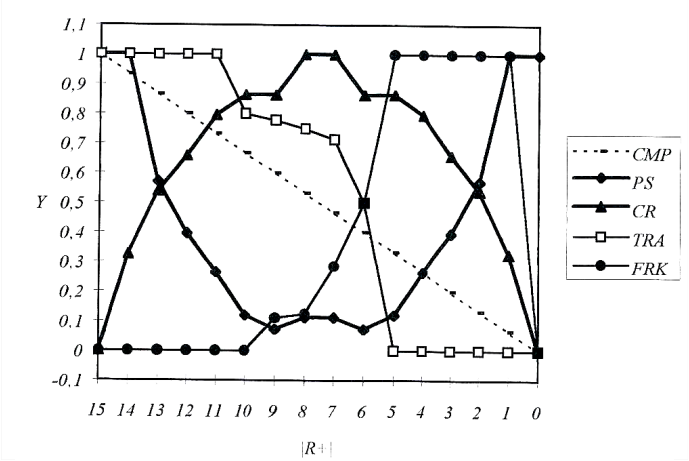
The Mose's postulate confirms the fact of *cessation of the arised* as also the possibility of *new arising of the ceased*. Both Ludwig von Bertalanffy [2] and Teihard de Chardin's I postulate confirm the *structural nature* of the living system. The second postulate of Teilhard de Chardin [20] can be interpreted as a correspondence between *complete structure and origination's state*, and correspondence between *empty structure and cessation*. First postulate of N. Wiener [46] defines the genesis of life as a *sequence of monotonous changing of the living structure*, and *monitors its changing of complexity*. His second postulate added a requirement of *decreasing of entropy*.

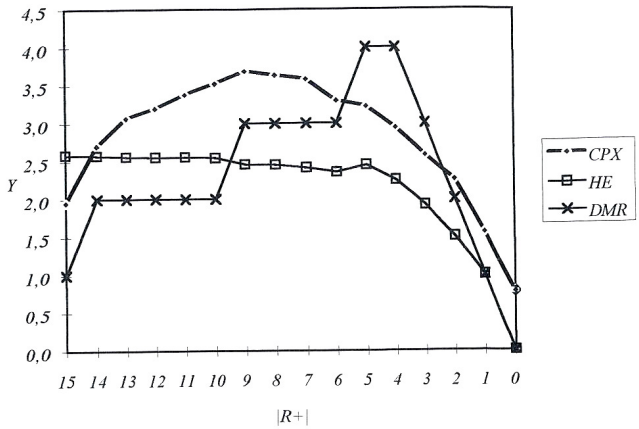
These requirements are tempting to interpret on the basis of *structural genesis* $\mathfrak{G}$, where:

A. The *states of living systems (ontogeny)* can be characterized by the *structures* and represented in the form of *structural models.*
B. Elementary *structural changes* can be presented as the *morphisms* between structures.
C. The *living process* can be presented as a *monotonous sequence (succession) of structures.*
D. The state of *origin (arising)* can be presented as a *complete structure.*
E. The state of *maturity* can be constitutes as a *structure with the maximum complexity.*
F. The state of *cessation* can be presented as an *empty structure*.
G. The structural parameters, such as *complexity, entropy, probability* and others, are *measurable.*

The requirements A to G are satisfied only in one monotonous sequence (succession) ***SFM*** in the lattice of $\mathfrak{G}^{|V|=6}$ (in the right edge), this is: $GS_1 \rightarrow GS_2 \rightarrow GS_4 \rightarrow GS_8 \rightarrow GS_{17} \rightarrow GS_{33} \rightarrow GS_{53} \rightarrow GS_{76} \rightarrow GS_{100} \rightarrow GS_{122} \rightarrow GS_{138} \rightarrow GS_{146} \rightarrow GS_{151} \rightarrow GS_{154} \rightarrow GS_{155} \rightarrow GS_{156}$. The parameters of this structural sequence (succession) be changed in the given order. This is a fact what allows it call to the ***ontogeny hypothesis (simulation)***.

Example 2.12. Diagrams of parameters of the monotonous sequence (succession) ***SFM***:





The horizontal axis characterizes the sequence by the number of connections (edges), but the vertical axis represents the normalized parameters (first diagram) or absolute values (second diagram). Some parameters: *CMP* – structural concentration or density of the state; *PS* – probability of the condition; *CR* – structural (Option I); *CPX* - Complexity (Option II); *HE* – entropy.

In the system $\mathfrak{G}$, the majority of such structures, which do not belong to living being. In case of larger structures the number of conditions and possible sequences enlarges exponentially. The larger the number of elements in the structure, the more complicated is the system. So Bertalanffy, Wiener and Teilhard de Chardin speak about the ***structure***, *its changes and the relationships between elements* in a very general manner, and do not specify their biological nature. Here is suitable to agree with the view-point of Teilhard de Chardin, that the structural elements are ***phenomenal*** and the relationships ***energetic*.** So, we can say that the talk is about a living *super-structure*, which here is taken to interpret. It is possible that the structural changes take place by the help of some "external influences".

Consider first the states of ***origin*** and ***cessation***. They are *opposites* (as *spore (germ)*) and a *corpse*), which on structural aspect are *complements* – the firs is strongly related and the other is empty. However, their structural elements remain the same, identical, indistinguishable and form an element position $\Omega V_{k=1}$. But, the recurrence of the same constitutes *symmetry*, where the structures of origin and cessation are bi-symmetrical.

The living process takes place by way gradual elimination the relationships between the elements. Up to ***ripeness*** condition take place the increasing of *structural (internal) diversity* or *complexity CR*. The elements have not "good" or "bad" positions, but they have *different positions* $\boldsymbol{\Omega V_k}$, that we cannot qualitatively characterize. The number of positions *k* will increase to the *ripeness* state and then decrease.

In arriving to *ripeness* state is the structural diversity in maximum that is the stage of prosperity and stability. It is expressed in the structure as a *maximum number of the positions*, each element has its own position. After this, the number of positions, that is, the structural complexity and diversity decrease.

It can be noted that in the second half of the life process begin to go through the "opposites" or *complements* of the conditions of the first half. Of course, in opposite ordering. But the process of removal the relations between elements continue to *cessation* state, i. e. to *empty structure.*

So as exist a relation between the origin and cessation, so is it also between *cessation* and *origin (arising) of a new*. Nature does not like empty spot, empty structure begins to re-filling (nothing laziness for astral body!). Begins the *process of reincarnation*, arise the relationships between the elements. This is a "complement" of ontogeny, an opposite direction, we call it *onto regenesis*, the nature of which remains hidden for us. But also the "onto-regenesis" can be disrupted before the arriving to a "new origin".

The presented speculative hypothesis is based only on the interpreting of outside properties, but the existence of structural changes in the process is not advisable to ignore.

Maybe someone will ever can be capable the conditional structures of ontogeny better to associate with the life processes.

Comparing the ideal ontogeny hypothesis and pragmatic coegenesis simulation can note the following:

1) The postulate of L. von Bertalanffy [2] about the structural essence of living phenomenon is universal.
2) The first postulate of Teihard de Chardin [20] about the "graining" ("granular") of living matter and existence the structure-forming "phenomenal-energetic" relationships between elements is valid also in case of plant communities. The first obtains in coegonesis the meaning of *species variety* and second the meaning of *competition*.
3) The second postulate of Teihard de Chardin [20] about origin of living as maximum concentration of "phenomenal-energetic" relationships be valid only in the level of individual organisms. In case of communities, the situation is reversed: in the formation stage the competition relationships are not yet exist (the structure is "sparse"). The "moderate large" concentration reached in stage of maturity (characterized as coenigenetic homeostasis), which is also the end stage. The maximum of competition's concentration can not be stable.
4) The first postulate of N. Wiener [46] about increasing the complexity up to maturity stage is valid also in case of communities. Decreasing of complexity can be happens only by some changes in the environment.
5) N. Wiener's postulate about decreasing in entropy can also apply for the communities.

Conclusion

Here is demonstrated that the ***nature of the structure*** is revealed on the base of the *relationships between the elements* and their *positions*. It is presentable in the form of *structural model*. The structure semiotic approach to investigation of essence of the structure can be to someone like or not like, but its propositions about structure and its changing works truely. In principle is all this provable with existing mathematical means – when someone has an interest. Unfortunately, the interests are concentrated by so-called trends.

Is the structure a matter about oneself? Exists an agreement that the structure is an inseparable attribute of all the really existing objects. Structure exists there where the relations between element pairs are recognizable. The relations are simple presentable in case of chemical compounds, genetic formations and some networks. In case of ecological and social communities must be previously to agree on the *aspect* of decomposition the object to its elements and their connections (relations). If is accepted the existence of structure, then is desirable accept also their attributes. For example, accept the positions and the relationships between these. Presumably, that such attributes for chemists, ecologists and others are the unaccustomed matters, but it is the *structural reality*.

"Nonessential" problems with the graphs are also other. For example, exist the problem of involution (multiplication) the adjacent matrices. On this base has been developed a spectral treatment of the graphs, *spectral graph theory*. Unfortunately, is not known what constitute the elements as binary signs, themselves, and to what degree must the matrices to raises. There is only alluded that these elements characterize the longest paths between the vertices. This is doubtful, since these also appear in the main diagonal, while the relationships between the vertices, occasionally turn out to be zero. Obviously, this nobody not interested. In present case the elements of certain degree adjacent matrices found the application for perfecting the binary signs for some symmetric graphs. In principle, the structure model can be based only on the elements of graduated adjacent matrices, if would known the meaning of those elements. In present case we cannot distinguish from each other even adjacent and non-adjacent pairs of elements. The binary signs are indispensable (required), the more that in case of strongly regular graphs, matrices exponentiation works only partially.

Already in 1976 were drawn attentions to the too one-sided approach to the graphs that impede the development of graph theory [13].

Hope, that this paper gives a sufficient overview about the nature of the structure

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