

Poster guide

Andrzej Gecow gecow@twarda.pan.pl

Brief

ESEB 05 20.36

The title is:

Complexity of ontogeny as the main cause of regularities in ontogeny evolution

Please follow the color to trace a theme.

Complexity - **Threshold of network complexity** is shown below.

Regularities are an old classic but not correctly resolved theme. **Current views** on their causes **are false**.

I have found their causes in the evolution of complex networks, not in the gene language as commonly assumed.

Our assumptions: Ontogeny is a complex network of conditional transformations subjected to adaptive evolution. Stages of ontogeny are related to functional order.

These 3 main assumptions (here color-coded) are developed below:

Model of adaptive evolution of phenotype y defines **adaptive condition** which accepts or eliminates changes and **size L of change** as number of changed properties. The result is the **Small change tendency**.

Model of ontogeny as complex network and its assumed changeability (before **elimination**): addition and removal with equal probability at any **stage**. The result is a **threshold of network complexity**.

Depth D - a sequential measure of **functional order** is defined. It describes **ontogeny stages** and defines the "terminal". **Historical order H** is defined as a **stage of network growth** in which the transformation was added.

Resulting (accepted) changeability in **complex ontogeny**. The **Small change tendency** using **elimination** gives together: **Terminal Additions with pressing back** and **Terminal Modification**, also **Similarity of historical and functional order**. **This regularities are strong, thus should be expected in nature.**

Extended

Title and current views

Complexity of ontogeny as the main cause of regularities in ontogeny evolution

The **complexity** is a real parameter. There is shown below **Threshold of network complexity**.

The **regularities** in ontogeny evolution **are old classical but not dead themes**, in anabioze awaiting the time of their explanation. They were an attempts towards evolutionary understanding old **von Baer's observation**. The biology of the 20th century had not managed to solve this problem and now it is mostly forgotten.

I have found their mechanisms in the evolution of complex networks but not in the gene language where they have been commonly searched for.

There are **two basic regularities** :

1 - Terminal Additions and Compression of early stages, known as „**Pressing back**” – Weismann's (1902) conception **with the fatal first old explanation: inheritance of acquired characters...**The second explanation was offered by Gould (1977) in his *K*- and *r*-strategy scenario using de Beer's suggestion of heterochrony importance (because they are expression of gene mutations), **but this hypothesis is also unsuccessful**. Our explanation based on **functional order** does not see **heterochronies**, they **appear not to be important** in the explanation (like other properties of the gene language).

Regularity **Terminal Additions** was **displaced** by (we obtain them **together** (co-occurring)):

2 - Terminal Modifications and Conservation of early stages (Naef 1917)

Current explanation of Terminal Modifications is profoundly false.

Change initiations occur with equal probability throughout the whole ontogeny, but they cause changes in all the later (subsequent) part of ontogeny. **That's all! Lack of consideration of size of change** in phenotype (let's denote it by **L**) and **elimination** most of changes due to their large **size** (and changes initiated in **earlier stages** have greater **size** - Darwin's remark). Since de Beer (1940) **it is commonly taken view**.

De Beer's view is based on one of two tacit false assumptions:

1 ontogeny is a **linear chain** of events, thus **L** does not depend on the **ontogeny stage** of change initiation (**one L**).

2 **size L of change** in the phenotype does not strongly correlate with the chance of its **elimination**.

These both alternatives are **wrong**.

Our assumptions

1. Ontogeny is a complex network of conditional transformations (not only a pure linear chain as in de Beer's thinking). This means it is a directed network similar to Kauffman's Boolean network. (Complexity is the Schmalhausen's suggestion)

2. It is subjected to adaptive evolution, therefore not all changes are allowed and maladaptive changes are eliminated. Assumed and resulting (accepted) change distributions will differ – these differences are the searched regularities (tendencies).

3. Stages of ontogeny are related to functional order. Stages of ontogeny are sequential like time, but the functional order is not sequential. We define a sequential measure of functional order named "Depth D", but this also is not exactly equivalent to ontogeny stages, only statistically similar (and this is enough for our purposes).

Please follow colors in the poster, to trace a theme referring to the color-coded assumption.

Model of adaptive evolution of phenotype y

describes phenotype as a set of m properties.

- 1. Each property has s variants,**
- 2. each variant has the same probability.**

The **fitness b** is defined as result of comparing the phenotype y to an ideal y^* - that is a number of properties of the phenotype which have the same variant as those of the "ideal".

This allowed us to define **adaptive condition a** which **eliminates** a change if fitness b decrease, otherwise it accepts a change which forms the adaptive evolution.

The **size L of change** is defined as the number of changed properties.

These assumptions and definitions allowed us to calculate $P(a|L,b)$ - probability of change acceptance if we fix size L and fitness b .

Remark, that for living object, the fitness b is very high.

The main result of this model is the "**Small change tendency**" (marked with yellow color) - **for the relevant high fitness b , only very small changes are acceptable.** It helps us to understand the mechanisms of regularities.

Model of ontogeny and its assumed (before elimination) changeability

This is a model of a **general complex directed network** (similar to Kauffman's Boolean network); we named it „**aggregate of automata**".

On outputs of this network occurs a set of signals which we interpret as properties of a phenotype y .

Assumed changeability: addition "+" and removal "-" of a transformation (automaton) occurs with equal probability in any place in the network (aggregate) – it means: at any stage of ontogeny.

The main result of this model is the **threshold of network complexity**. If number of signal variants $s > 2$, then change initiated in some place of network statistically increases. If it does not fade out during the first few steps, then it explodes throughout the whole network. In effect, the size of changes can be only either very small or very large, but not medium. If network contains feedbacks then the frequency of moderate changes is exactly 0. Such situation appears in network exceeding certain size which depends on feedbacks presence. This is the real threshold of complexity.

There are shown four distributions $P(L)$ for different networks, complex or small and with or without feedbacks. $P(L)$ shows changeability not controlled by adaptive condition - before elimination. For complex network there are 2 peaks and near 0 in-between.

Note, that $s=2$ (Boolean network) gives the opposite effect, but we expect s to be much higher in the interpretation due to the assumption of equal probability of each variant.

Depth D, functional order & ontogeny stages

Functional order is not a sequential order. It is not easy to define a good sequential measure of functional order. It has been achieved experimentally. Definition of Depth D as a functional order measure is constructed, based on the probability to fade out of change at the outputs of our aggregate (network). It is not the shortest way, but something similar.

Ontogeny stages are similar to functional order and D, but not exactly the same – **heterochronies do not change the functional order**. This similarity is statistical but strong.

Depth D describes thus **ontogeny stages** and defines the term "**terminal**", but this is an approximation.

Volume (number of automata) of such particular depth D varies and depends on **stage of growth**, like in the triangle diagram. This diagram shows the growing aggregate (ontogeny). This growth is an effect of predominance of acceptance probability of addition over that of removal, because there are equal chances of addition and removal.

In each **stage of growth**, the number of automata increases by 128. An automaton “remembers” the stage of its addition to the network - this is the **historical order H**.

Resulting (accepted) changeability in a complex ontogeny

Generally

The **Small change tendency** using **elimination** gives together (co-occurring):

Terminal Additions with pressing back and **Terminal Modification**, as well as **Similarity of historical and functional order**.

Simulation results

Triangle diagram shows **Terminal addition and compression of early stages** by balance figures of dominance probability of acceptance of addition “+” or removal “-” $P(a|+,D)-P(a|-,D)$, and **pressing back** by balance on boundary of depth D.

To the right there are four main results of the simulations.

1. Statistical similarity of the historical and functional orders. Average stage of growth H of automata addition for automata on depth D.
2. P(D) shows assumed changeability, constant throughout the whole space of aggregate. Distributions for the accepted changeability are shifted to the left – Terminal Modifications. For accepted additions + and removals -, the distributions differ creating regularity Terminal Additions (terminal predominance of additions).
3. shows probability distribution of acceptance of any change at fixed D for different simulations (e.g., $s=4,8,16$). Values are normalized for easier comparison of the patterns. There is a strong maximum for early stages - Terminal Modifications.
4. difference of addition and removal acceptance probability gives Terminal Additions (terminal predominance of additions).

Please note that these regularities are very strong and grow with the parameter s which should be higher in the biological interpretation.

Conclusion

We have modeled evolution of a general complex network of conditions. Strong statistical regularities were obtained for such networks. Ontogeny is an evolving complex network of conditions and therefore such regularities are also expected there.

We have investigated mechanisms of these regularities. They are not related to genetics, where they were expected. The complexity and elimination are enough to cause them.

More in the paper: A. Gecow, From a “Fossil” Problem of Recapitulation Existence to Computer Simulation and Answer. Neural Network World 3/05, 189-201 ICS AS CR 2005
<http://www.cs.cas.cz/nnw/contents2005/number3.shtml>

Abstract

A study of grammar and a dictionary of language in which a novel is written are not enough to know what the novel is about and why it is so successful. A set of computer commands does not contain the text-editor rules. Similarly, details of gene mechanisms cannot explain why peacock has so colorful tail (only: how it is done) or why some regularities are observed in ontogeny evolution. Terminal addition and modifications, now disregarded, have been recognized long ago, but no mechanism deriving them from genetics was found and they do not appeared each time. We have found a mechanism creating those regularities in adaptive evolution of complex networks, but from the genetic language it borrows only the complexity of phenotype description. The abstract model and results of its computer simulation are presented. Now we should expect those regularities in more complex regulative type ontogenies as a regular statistical component interfering with other phenomena. Weismann's "terminal additions" become a very good quantitative first approximation, but the commonly accepted de Beer's explanation (and its implications) of Naef's "terminal modifications" become faulty. De Beer described ontogeny as a linear chain of events and ignored complexity which is the main cause of regularities and needs a full network description. Above a certain level of complexity, only very small or very large changes of network results appear and nothing in-between. Only these very small changes, initiated generally near the end of the process, can be accepted by the adaptability test.