NOVEL CONCEPT OF MODELLING EMBRYOLOGY FOR STRUCTURING AN ARTIFICIAL NEURAL NETWORK

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Abstract. The organisation of an Artificial Neural Network (e.g., the organisation in layers, the number of cells per layer, the degree of connectivity between the cells) has a big influence on its abilities (e.g., learning ability). In our work we present a novel method to organise the nodes and links of an Artificial Neural Network in a biologically motivated manner using virtual embryology. For this purpose we developed a virtual embryogenesis, which mimics processes observable in biology. In our system a virtual embryo consists of individual cells, controlled by a genome. These cells can develop to nodes in the ANN during the embryogenetic process. The embryo is implemented as a spatially discrete and temporally discrete multi-agent model. The cells in our model interact with each other via virtual physics and via virtual chemistry. With the work at hand, we show that patterns developing in our virtual embryogenesis are comparable to patterns found during natural embryogenesis. We plan to combine the described virtual embryology with Evolutionary Algorithms to optimise the genome of the embryo. We expect the described model of virtual embryology (in combination with Evolutionary Algorithms) to lead to novel, evolutionary shaped net structures of Artificial Neural Networks.

1 Introduction

The morphological structure of an Artificial Neural Network (ANN) is very important for its functionality. Basic structural features of ANNs can determine the basic capabilities of the network [9] [4]. Several approaches to tune ANNs were published recently: One common approach is to fully link a network of cells, and then use a Genetic Algorithm to find optimal values for weighting these connections [12]. ANN controlled agents (e.g., autonomous robots) using such systems do not learn during runtime, but are customised for their environment by Artificial Evolution. Such concepts are very effective but become more and more time consuming with increasing numbers of cells due to the quadratic scaling of the number of connections.

In other approaches the structure of ANNs is manually predefined [4]. This allows to rely on a set of well-defined and hand-designed networks with well known features. A learning algorithm (e.g., reinforcement learning) tunes these weights of the connections during runtime. The advantage of such systems is the easy combination of several well defined network-structures for finding solutions to one given problem. The disadvantage of such systems is the low ability of the network to adapt to unknown situations or problems that were not taken into account during the network design. This ability of networks is especially needed in adaptive controllers for real-world robotics or for comparison with biological systems. In nature we find that structures of neural nets develop during embryogenesis. The outcome of this developmental process is shaped by natural selection. During lifetime the connections between cells are tuned by learning [11]. Biologically inspired controllers are able to adapt to new situations in an evolutionary way by changing its network structure and by learning processes. The organisational mechanisms working in embryos are easy to evolve and enable a fast and effective artificial evolutionary development of controllers (e.g., for the purpose of robot control) [5].

In the work at hand, we present a novel method to organise the nodes and links of an ANN in a biological motivated manner using a novel method of virtual embryology. Our concept of virtual embryogenesis, which we present here, is mimicking processes observable in biology during the developmental phase of most multicellular life-forms, like *Drosophila m.* [8] or other species [14][6][1]. Our approach also synthesises general concepts of biological embryogenesis and of artificial embryogenesis [21][2]. These very complex processes are strongly abstracted in our virtual embryogenesis. These simplifications are important, to enable a later optimisation of the resulting ANN, by using artificial evolutionary processes (see figure 1). Due to this requirement, the fast calculation of single embryologic processes is necessary. Especially for projects dealing with evolution in autonomous robotic systems (e.g., see [19][18]) the fast simulation of embryologic processes on systems with limited hardware resources is required.

2 Concept

Our virtual embryo consists of individual cells. These cells can develop to nodes in the ANN during the embryologic process. In our model, cells can duplicate, die, specialise, emit chemical substances (morphogenes), or build links to other cells. These links represent the connections between the nodes of the resulting ANN. Due to growth processes (duplication processes of other cells), which is an importand aspect that we implemented in our

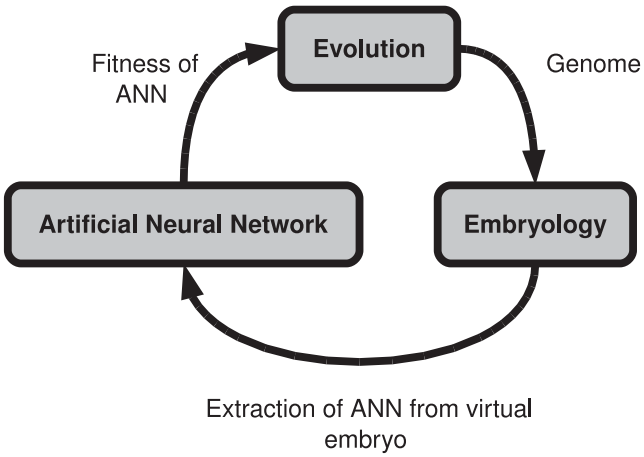


Figure 1: Process of optimisation of an ANN using artificial embryology and artificial evolutionary processes. For details please see 6.

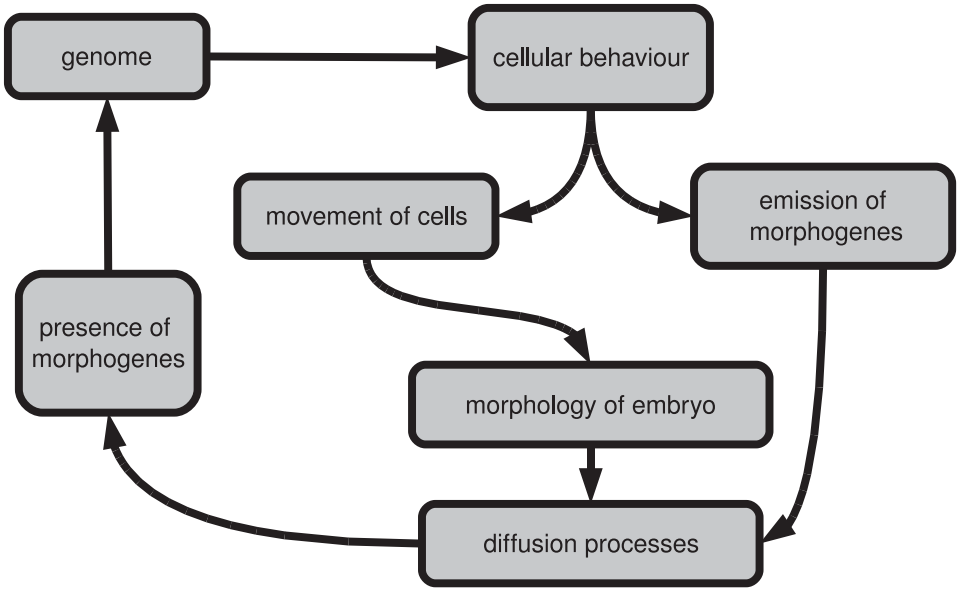


Figure 2: Network of feedbacks within the developing embryo. Boxes indicate subunits of the system controlling the growth of the embryo. Arrows indicate influences of one subunite on another.

model, a cell can be "pushed around" in space. A cell has no ability for active movement. The cells' actions are defined by the genome of a cell, which consists of a collection of genes, which can be triggered by virtual morphogenes. One possible effect of gene-activation can be the production of another morphogene. This way a network of feedbacks emerges (see figure 2). The resulting selforganised process governs the growth of the embryo. When the embryologic process is finished, the developed network is analysed and translated into a datastructure, which is compatible to a standard ANN-interpreter.

3 Implementation

3.1 Diffusion processes

In our model, the embryo is implemented as a multi-agent model, in which a single cell is represented by an agent. The space in our model is discrete. Each spatial unit (patch) can be occupied by a cell. These cells interact with each other via virtual physics and via virtual chemistry. Morphogenes are emitted by cells and diffuse throughout the embryo [3]. The concentration $c_{m,x,y,t}$ of a morphogene m at the position x,y at time step t is calculated according to

$$c_{m,x,y,t} = min(c_{max,m}, cn_{m,x,y,t-1} - d_m), \tag{1}$$

whereby $c_{max,m}$ is the maximum concentration of a morphogene m, $cn_{m,x,y,t}$ is the maximum concentration of the morphogene m in the cell at the position x,y and in all neighbouring cells ("Von Neumann" neighbourhood), at the

Cell reaction	Description
Emission of morphogene	A cell emits a morphogene into the embryo.
Cell duplication	The cell duplicates, which leads to a change of the embryo, due to virtual physics. For details see subsection 3.3.
Cell death	The cell dies, which leads to a change of the embryo, due to virtual physics. For details see subsetion 3.3.
Changes in responsiveness	Changes the cells responsiveness towards a certain morphogene. By changing this values the cell is able to differentiate.
Changes of internal values	Internal values represent the predisposition for certain functions.
Linking to neighbours	Builds a neural connection (dendrite) to a neighbouring cell.

Table 1: Possible reactions of a virtual cell in our model

time step t. The amount of the decrease of the morphogene concentration when diffusing from one cell to another is d_m. When a cell at position x, y emits a morphogene, its value for $c_{m,x,y,t}$ is set according to

$$c_{m,x,y,t} = c_{max,m}. \tag{2}$$

Please note, that no conservation of mass is implemented in our model. This simplification of real physical diffusion processes is necessary to achieve the required computational speed (mentioned in section 1). The results of this abstract diffusion model suffices for our needs to achieve the desired embryogenesis.

3.2 Genetics and cellular behaviour

In our model, a cell measures the concentrations of morphogenes every time step and reacts in a preprogrammed way. The concentration of a morphogene needed to trigger a reaction as well as the triggered type of reaction is specified in the genome of the cell. The genome N is a set of n genes G (see equation 3). Each gene is a tuple of numeric values (see equation 4). These values determine which cell-reaction r is triggered, if a defined morphogene s is present with a concentration higher than c_{min} and lower than c_{max} at the position of the cell in the embryo. All cells share the same genome, which does not change during the embryogenetic process.

$$N = \{G_1, \ldots, G_n\} \tag{3}$$

$$G_n = (s, c_{min}, c_{max}, r) \tag{4}$$

The reactions r of cells can be as follows: emission of a morphogene, cell duplication and cell death. They are described in detail in table 1.

The fact that our “genes“ are triggered by morphogenes is comparable to the mechanisms of gene expression and protein synthesis found in nature. Especially the concepts of second-messenger mechanisms [7] and transcription-coregulator mechanisms found in biological cells [17] were used in a very simplified way for our concept of virtual embryology.

3.3 Simulated physics

In case of cell duplication or cell death the positions of cells within the embryo have to be reorganised. We implemented this process by assuming that cells interact with each other physically via pushing. No other complex interactions (e.g., cellular cohesion) are simulated. If a cell (mother cell) duplicates, it determines the numbers of cells in the directions up, down, left and right. The cells have to be in a continuous row to be counted. In the direction where the number of cells is the smallest, the whole continuous row of cells is shifted by one position in the according direction. The new cell (daughter cell) is then placed on the new free position next to the mother cell (see figure 3A). This process simulates the movement of cells during the growth process. In case of a cell’s death, analogously to cell duplication, the free patch of the died cell is filled by shifting the whole row of cells towards the empty space (see figure 3A). In both, the movement of cells after cell duplication and the movement of cells after cell death, always the smallest possible number of cells is moved. This simulates the physical situation in a loose group of cells, where the physical inertia of subgroups of cells determines which cells have to move.

As well as there are morphogenes that can induce growth, other morphogenes can reduce growth. The balance between these two groups of morphogenes during the embryogenesis determines the size of the embryo (see figure 4). A big variety of shapes can emerge from this system, because growth factors can be emitted in different locations and in different timephases during embryology.

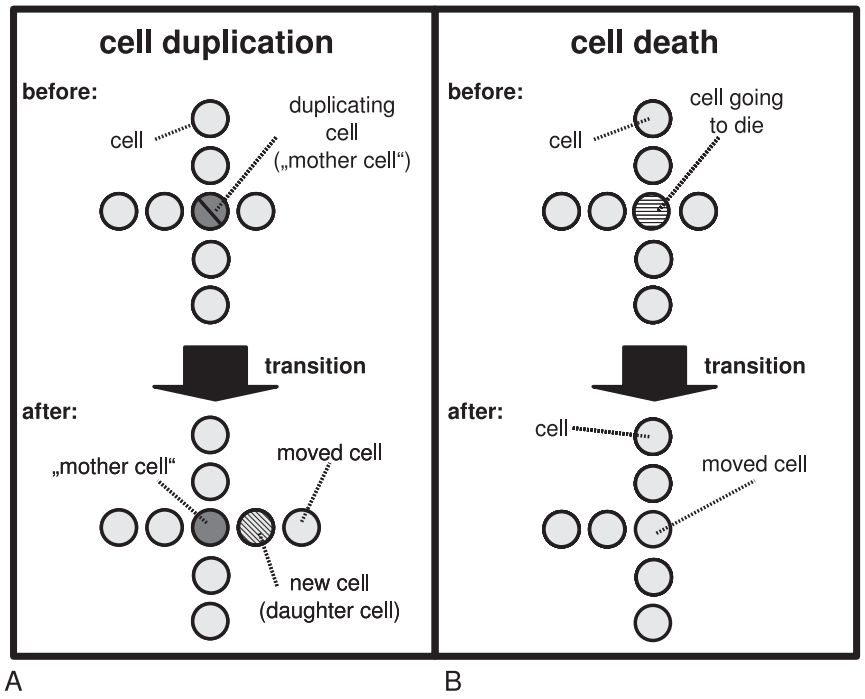


Figure 3: Movement of cells in the embryo during cell duplication and cell death processes. A: Modelling cell duplication: The daughter cell is placed in the direction where the number of other cells is lowest. B: Modelling cell death: Neighbouring cells are moved in from that direction where the number of cells is minimal.

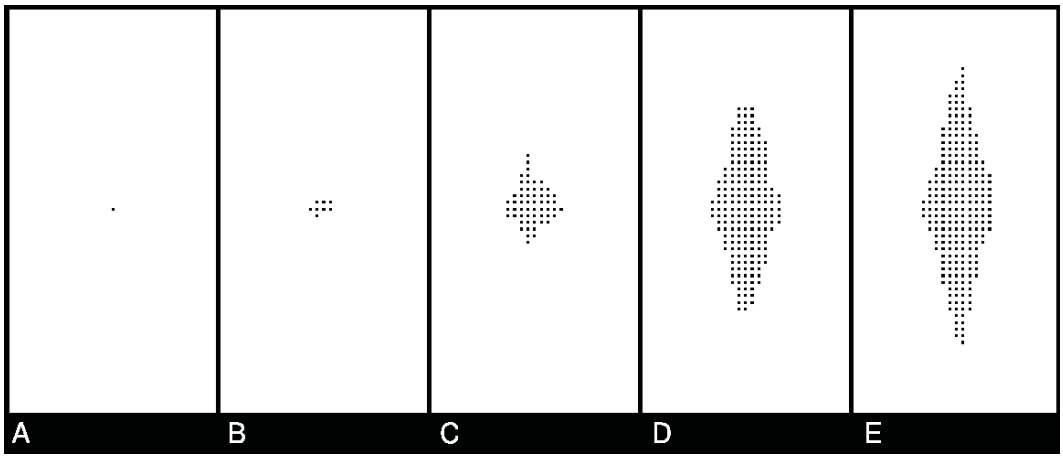


Figure 4: Screenshots of the growing embryo. The cells of the embryo are indicated by boxes. A: Starting condition with one single cell. B: Status of the embryo after 5 time steps. C. Status of the embryo after 10 time steps. D: Status of the embryo after 20 time steps. E: Final shape of the embryo.

3.4 Cell specialisation

Morphogenes can not only influence the growth of the embryo by inducing cell duplication or cell death, but they can also change internal status variables of cells (see figure 5). These values can code for the receptivity for another morphogene, the probability quality of linking to other cells (mentioned below), or for properties that are necessary for the function of the resulting neural net (e.g., if a cell is an input cell or an output cell). Usually, the processes of cell specialisation take longer than the development of the shape of the embryo during embryogenesis. Especially the shape of the embryo has a big influence on the interactions of different morphogenes, what goes along with results found in nature [16]. Some of the emerging processes can be interpreted as being a sort of "Turing processes" [20].

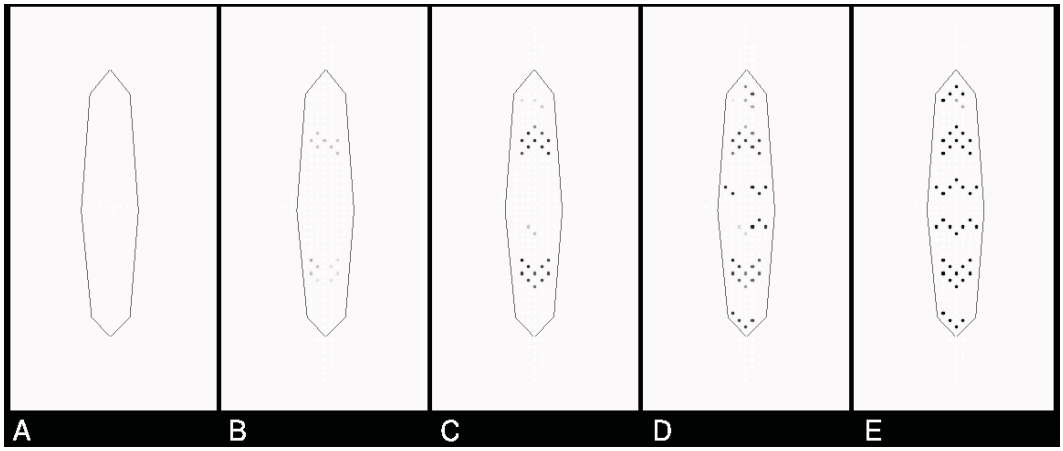


Figure 5: Screenshot of a virtual embryo during cell specialisation process. Specialised cells (high value of a given internal status variable) are indicated as gray dots, not specialised cells are not drawn. Lines indicate the boundaries of the virtual embryo. A: Starting condition, B: Status of the embryo after 25 time steps. C: Status after 30 time steps. D: Status after 40 time steps. E: Final status of the embryo.

3.5 Linkage

During our simulated embryogenesis, all cells can link with other cells (see figure 6). As mentioned above, those links represent the connections between the nodes of the neural network. The amount of links built by a cell, as well as the distance to the linked cells, depends on the interplay between the morphogenes and the genome (see figure 7). This way the degree of connectivity within a certain area of the embryo is determined by the embryologic process. If the cell is moved after linking, it stays still linked. This can lead to long-distance connections and enables a structuring of the resulting neural network (see figure 8). If a cell dies during the embryological process its links are deleted. Not all cells within the embryo have to be linked to other cells. Cells, that are not linked, are not without function, they can operate as morphological structuring cells in our model. These cells are needed for shaping the embryo due to growth or dying, as well as for shaping the gradients of morphogenes.

3.6 End of growth process

For the work at hand, the modelled embryo was allowed to grow and differentiate, until all growth and cell-differentiation had finished. That means that no more cell duplication events, cell death events, or cell linking events occurred. Also the distribution of growth factors within the embryo had to stay stable. If an embryo reaches this stable point of a complex equilibrium of development, it is defined as "finished". If the growth processes are not regulated well by the genome, the embryo can grow infinitely. In our simulation, the embryological process is stopped, if the number of cells reaches a certain point, to deal with such "pathologic" forms of embryos that grow infinitely. The resulted embryo is then rejected from further analysis.

3.7 Extracting ANNs from our virtual embryos

After the embryogenesis is finished, the embryo is analysed and the network topology is transferred into a structure, that is readable for a standard neural network interpreter. Cells that had only a morphological structuring function during the embryogenesis and have not linked during the embryogenetic process are excluded from the translation process to save computational time. These cells have no influence on the shape or function of the ANN after the embryogenesis has finished.

4 Results

Using our model of virtual embryogenesis we can simulate the development of an embryo from a simple hand-coded genome for the purpose of structuring an Artificial Neural Network (see figure 10). The final shape of

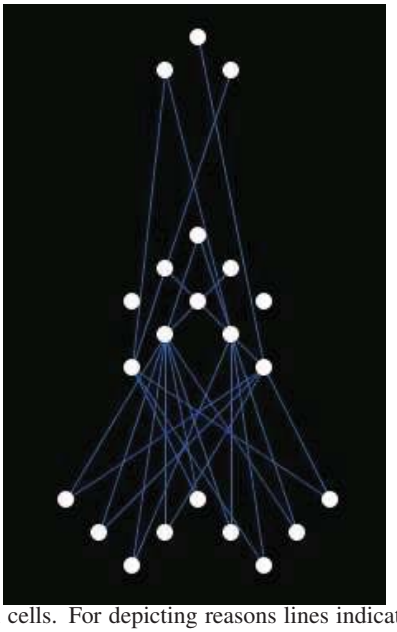


Figure 6: Example of links between cells. For depicting reasons lines indicating intercellular links are drawn into the embryo. The area of linked cells is depicted enlarged. Cells are indicated by white circles.

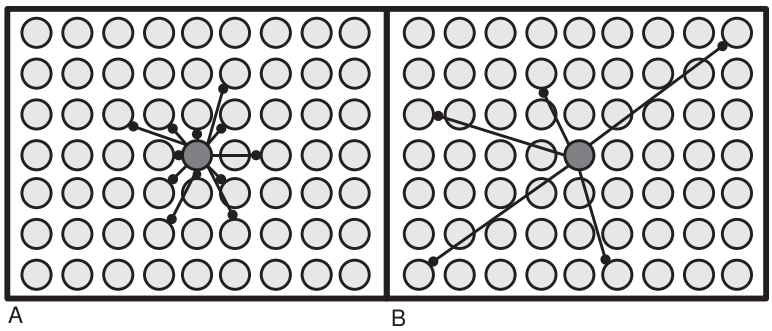


Figure 7: The process of linking cells: The degree of connectivity and the distance of cells selected for connection is determined by the genome, by the morphogene level and by the internal state of the cell. A: A focal cell links with its closest neighbours with a high density. B: A focal cell builds up a few long distance connections with cells further away.

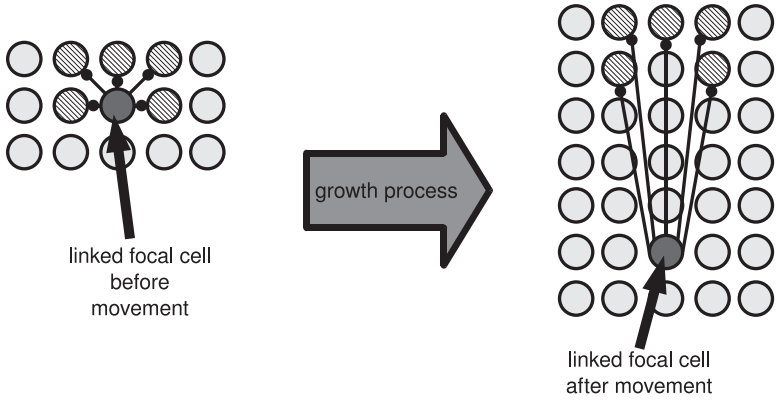
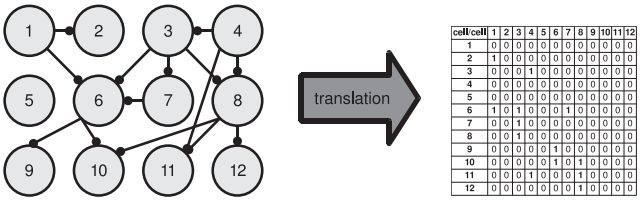


Figure 8: Scheme for the movement of linked cells. Once the focal cell is linked, the connections to other cells persistfor the rest of the embryologic process, even if the cell is moved within the embryo.

the embryo, the connectedness of the embryos' cells, as well as the internal specialisation of cells (see figure 10 D) are controlled by a system of feedbacks. These feedbacks arise from the ruleset described above (section 3), from the genome, from the spatial distribution of the cells within the embryo (see figure 10 A) and from the diffusion abilities of the morphogenes (see figure 10 B,C). The specialisation of cells within the embryo allows the development of different tissues, neural cells or structure cells, which have no neural function but morphological function. The resulting patterns found in simulations of our model are comparable with patterns found in nature during embryological development. In figure 10, we compare the self-organised segmentation processes in our



cell/cell	1	2	3	4	5	6	7	8	9	10	11	12
1	0	0	0	0	0	0	0	0	0	0	0	0
2	1	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	1	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0	0	0	0	0	0
6	1	0	1	0	0	0	1	0	0	0	0	0
7	0	0	1	0	0	0	0	0	0	0	0	0
8	0	0	1	0	0	0	0	0	0	0	0	0
9	0	0	0	0	0	1	0	0	0	0	0	0
10	0	0	0	0	0	1	0	1	0	0	0	0
11	0	0	0	1	0	0	0	1	0	0	0	0
12	0	0	0	0	0	0	0	1	0	0	0	0

Figure 9: Scheme for the translation of a cellular pattern into a tabular representation which is easily readable by a standard neural network interpreter. Please note that not all cells in the embryo have to be translated into the neural net. Cell number 5, for example, has no connection to other cells, for it had a purely morphological structuring function during embryogenesis. For details see subsection 3.5.

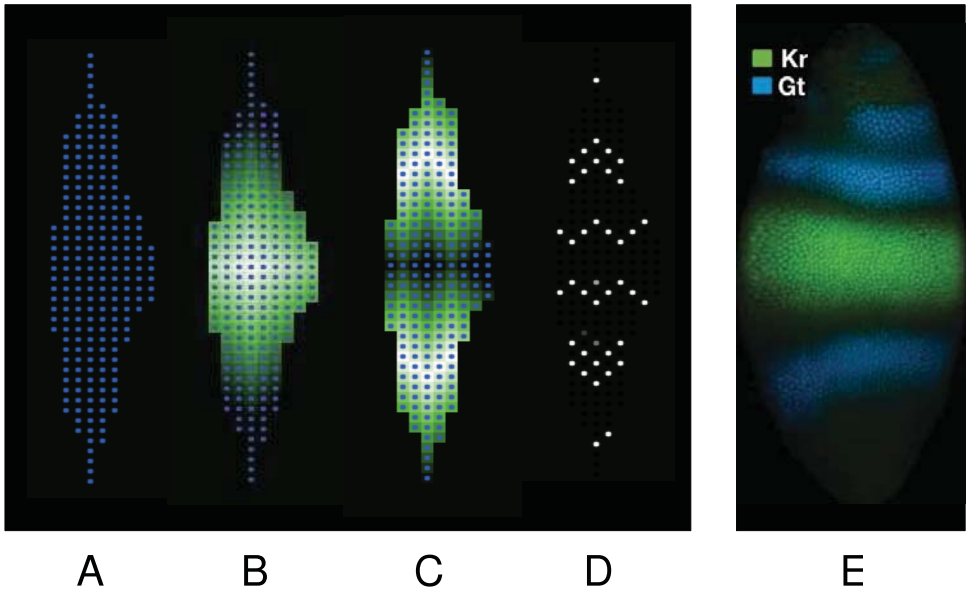


Figure 10: Comparison of virtual embryogenesis in our model and real-world embryogenesis: A: Virtual embryo, consisting of cells (dots); B: Morphogene gradient in embryo; C: Gradient of another morphogene, inducing cell differentiation. D: Embryo consisting of differentiated cells (white dots) and non-differentiated cells (invisible) ; E: Natural examples of gene expression: Activity domains of gap genes in larva (lateral view) of *Drosophila m.* (from [8]; 'Kr' and 'Gt' indicate gap genes.)

virtual embryo (figure 10A-D) with images from natural embryogenesis in *Drosophila m.* (figure 10E). Similar segmentation patterns are described also by Kalthoff [10].

5 Related work

First ideas about possible self-organisation processes shaping or structuring a living creature can be found in [20], where the authors describe the interaction of different antagonistic chemical substances diffusing through a medium. Early models of shape-giving processes are described in [6] [1]. In recent years many studies about mechanisms that are structuring an embryo have been published, dealing with the topics of genetic control mechanisms of embryogenesis as well as with physical mechanisms spatially organising an embryo (for a review please see [16]).

The topic of organising ANNs using genetic optimisation methods have been investigated recently in [13] which describes the coding of network topologies in a genome. Another study [15] shows the technique to arrange groups of cells to solve a "french flag test", using evolutionary methods. Such tests have become a common benchmark in the field of virtual embryogenesis [22].

6 Conclusion and Outlook

Our model of embryogenesis for the purpose of structuring artificial neural nets uses ideas from evolutionary developmental biology. Our approach produces results that are comparable with the products of natural developmental

processes. The virtual embryogenetic processes described in this article have the potential to structure groups of cells, on the level of body shape, as well as at the level of microstructure.

We plan to combine our virtual embryology with Artificial Evolution. The network of (neural) cells that develops during the embryologic process will be tested in a standard neural network interpreter. The fitness of a genome will be determined by the quality (e.g., learning ability) of the resulting "grown" neural net. This way we plan to evolve novel and efficient Artificial Neuronal Network structures (see figure 1). Additionally, we think we can learn more about the properties of basic processes that act during the biological evolution of brain structures (e.g., evolution of hierarchical brain-structures).

7 Acknowledgements

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