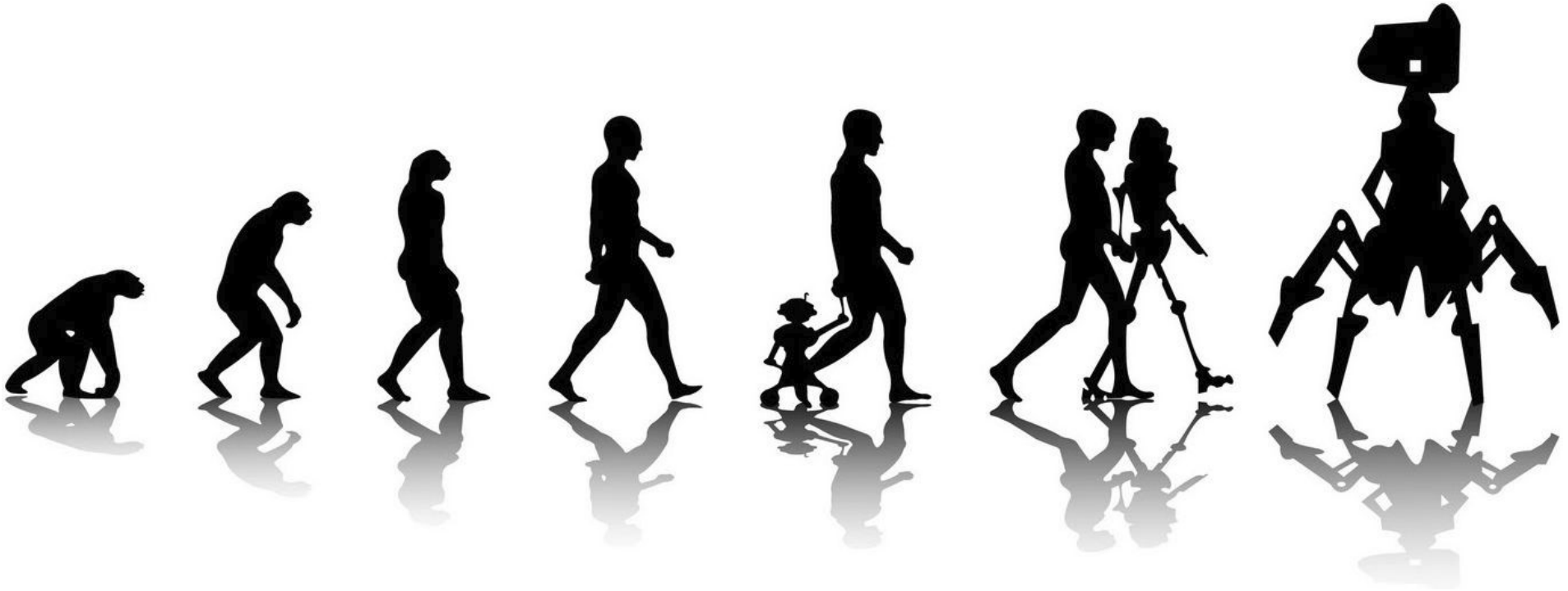


Modern Robotics: Evolutionary Robotics

COSC 4560 / COSC 5560

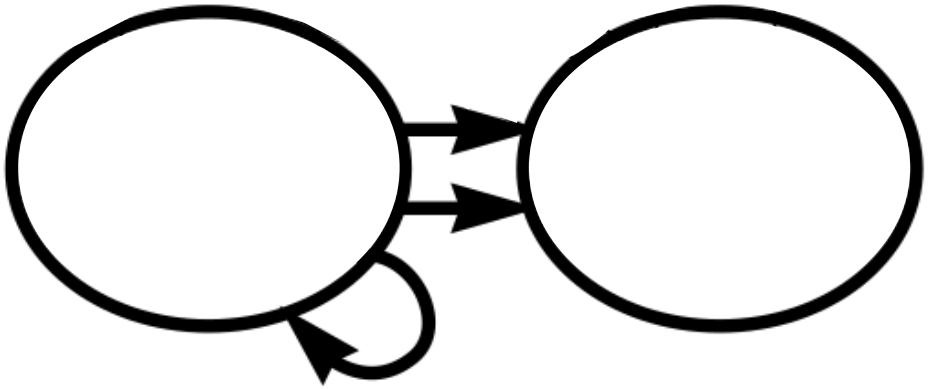
Professor Cheney

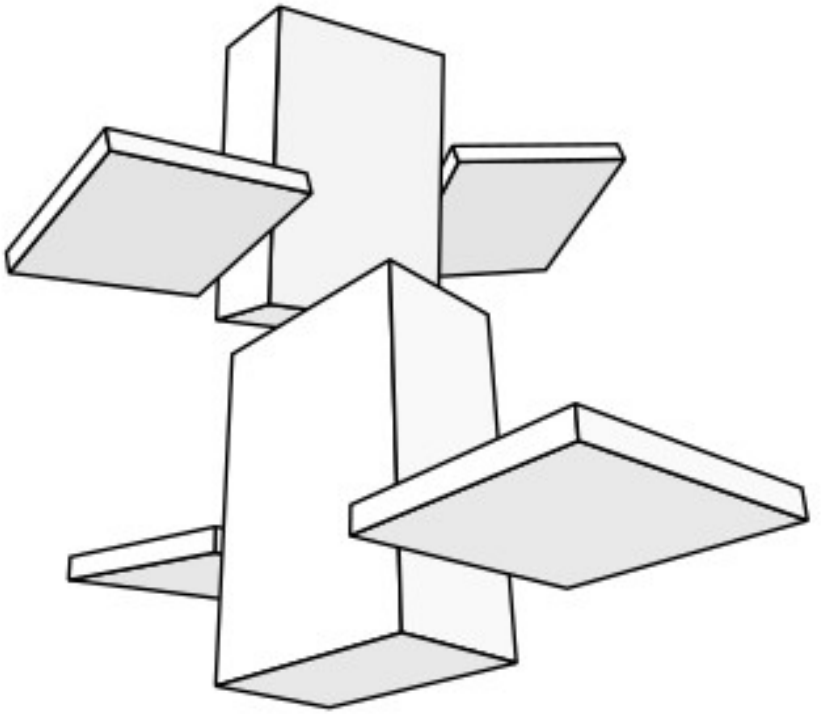
2/14/18

Artificial Embryogeny

Indirect Encodings

Figure 4a: The phenotype morphology generated from the evolved genotype shown in figure 3.





Direct vs. Generative Encodings

Direct Encoding: each genotypic element specifies an independent phenotypic element

Genotype	Phenotype
leg 1: 2’ leg 2: 2’ leg 3: 2’ leg 4: 2’	

Direct vs. Generative Encodings

Direct Encoding: each genotypic element specifies an independent phenotypic element

Genotype	Phenotype	Genotype'	Phenotype'
leg 1: 2’ leg 2: 2’ leg 3: 2’ leg 4: 2’		leg 1: 2’ leg 2: 2’ leg 3: 1’ leg 4: .5’	

Direct vs. Generative Encodings

Direct Encoding: each genotypic element specifies an independent phenotypic element

Genotype	Phenotype	Genotype'	Phenotype'
leg 1: 2’ leg 2: 2’ leg 3: 2’ leg 4: 2’		leg 1: 2’ leg 2: 2’ leg 3: 1’ leg 4: .5’	 

Direct vs. Generative Encodings

Direct Encoding: each genotypic element specifies an independent phenotypic element

Genotype	Phenotype	Genotype'	Phenotype'
leg 1: 2’ leg 2: 2’ leg 3: 2’ leg 4: 2’		leg 1: 2’ leg 2: 2’ leg 3: 1’ leg 4: .5’	 

Generative Encoding: genotypic elements can influence many phenotypic elements

Genotype	Phenotype
4x leg: 2’	

Direct vs. Generative Encodings

Direct Encoding: each genotypic element specifies an independent phenotypic element

Genotype	Phenotype	Genotype'	Phenotype'
leg 1: 2’ leg 2: 2’ leg 3: 2’ leg 4: 2’		leg 1: 2’ leg 2: 2’ leg 3: 1’ leg 4: .5’	 

Generative Encoding: genotypic elements can influence many phenotypic elements

Genotype	Phenotype	Genotype'	Phenotype'
4x leg: 2’		4x leg: 1’	

In humans…

Encoding length: 3 billion base pairs

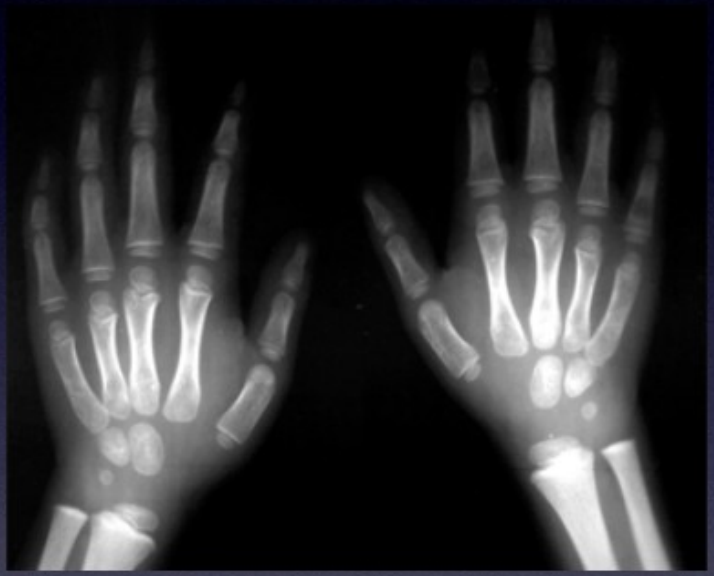
Number of cells encoded: ~10 trillion cells

Number of neurons in the brain: 100 billion

Generative Encodings

Desirable properties

- Coordinated mutational effects
- Scalability
  - Low dimensional search, highly complex phenotype
- Structural Organization
  - Regularity...with and without variation
  - Modularity
  - Hierarchy



Regularity

reuse of information

compressibility

irregularity

less compressible

irregular

less compressible

Lipson (2007)

What's the best generative encoding?

What are some options for generative encodings?

Grammatical Approaches

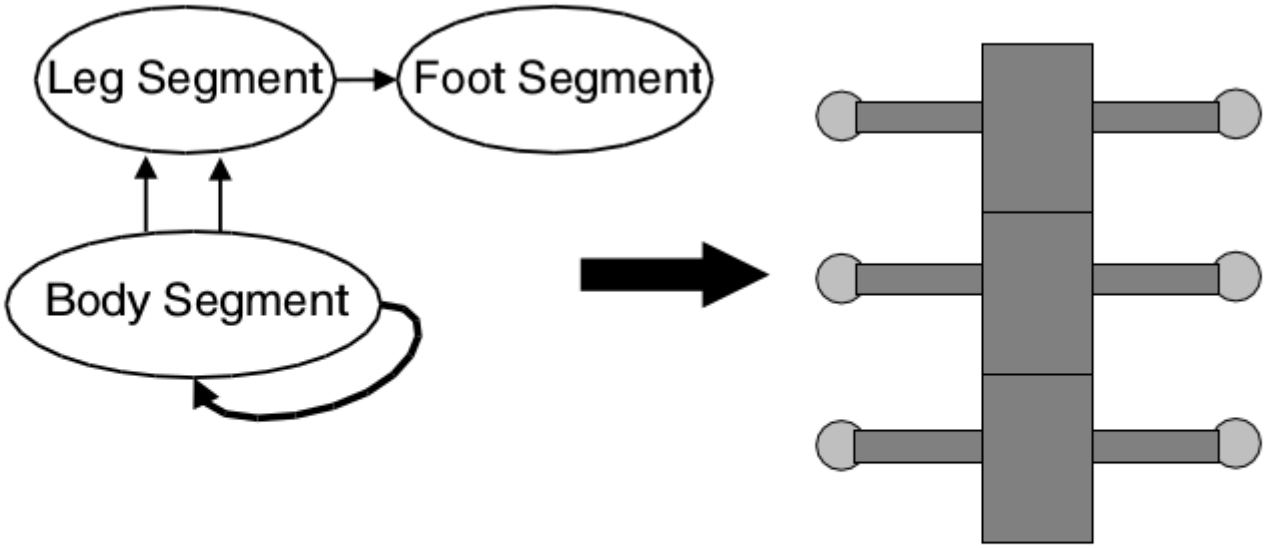


Figure 2. Development of body morphology [72]. The graph on the left specifies how the morphology on the right develops. The body segments repeat because of the recurrent loop on the body-segment instruction node, which allows the reuse of genetic code. The number of repetitions is determined by an evolved parameter in the loop, which is not shown. The final structure is a centipede-like creature with six legs and feet on each leg. Sims' work has inspired many AE researchers to explore body-brain evolution in simulated 3D environments.

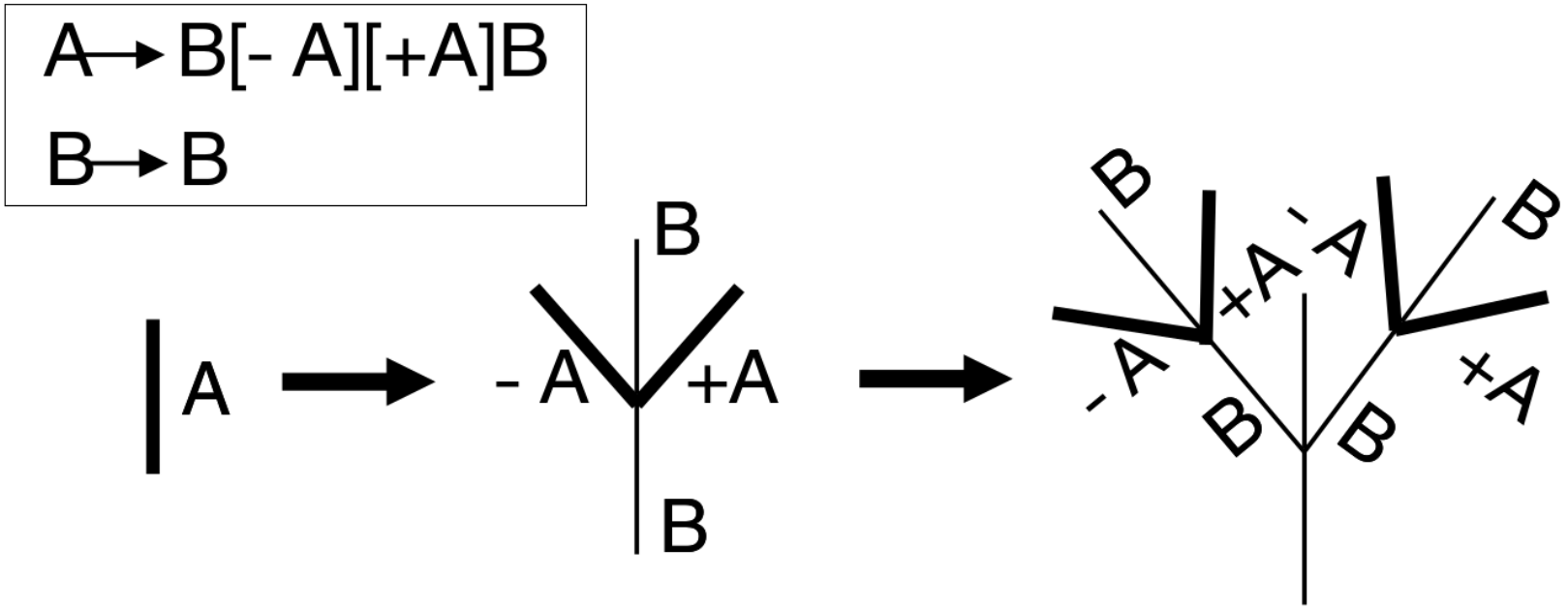


Figure 1. Grammatical approach example (L-systems) [50]. The two rewrite rules (inset) describe the growth of a treelike morphology. The symbol *A*, shown as a thick line in the tree, is the only symbol that is rewritten in this grammar. The symbol *B*, which does not expand, becomes a thin branch, and − and + determine relative angles of branches expanded from *A* symbols. This example illustrates how a few simple generative rules can encode a large structure with many components.

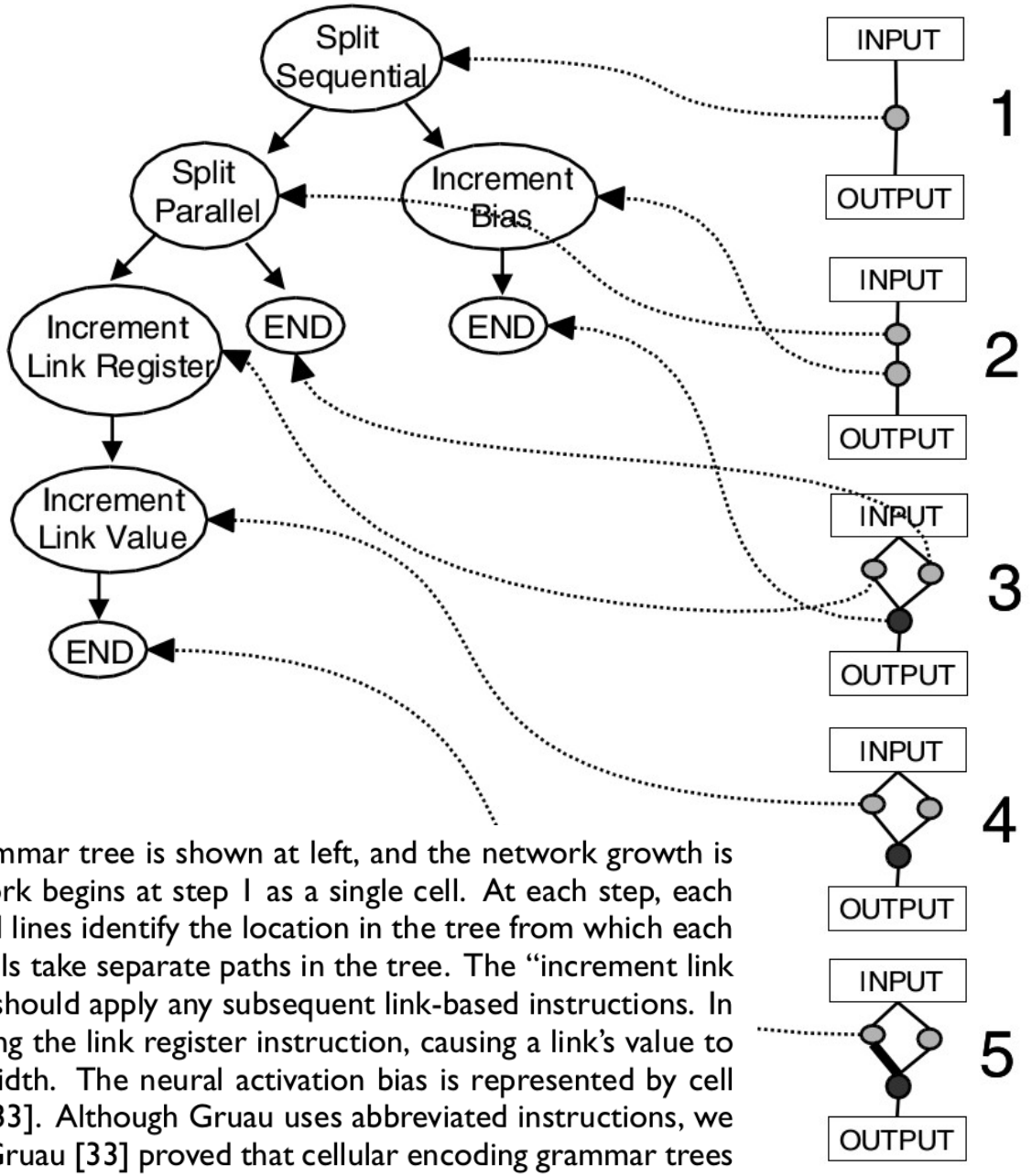


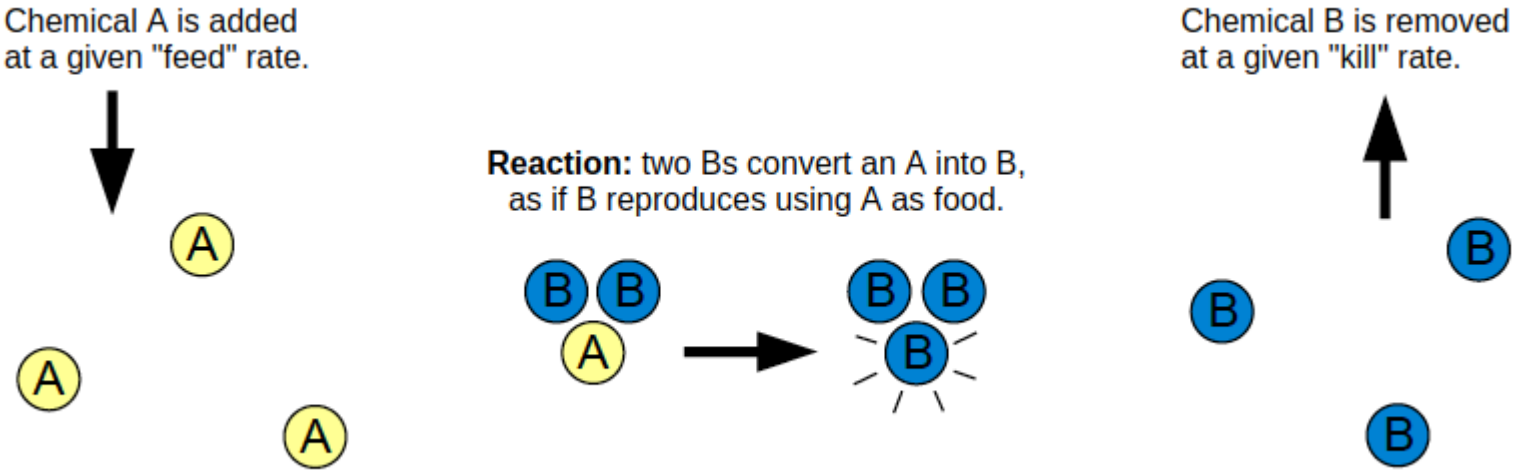
Figure 3. Cellular encoding (CE) example [33, 34]. The grammar tree is shown at left, and the network growth is shown from top to bottom in five steps at right. The network begins at step 1 as a single cell. At each step, each network cell is reading from its own part of the tree. Dotted lines identify the location in the tree from which each cell is reading at each step. When a cell splits, its children cells take separate paths in the tree. The "increment link register" instruction is the way a cell knows to which link it should apply any subsequent link-based instructions. In the example, such an instruction occurs immediately following the link register instruction, causing a link's value to increase, represented in the network by a thickening line width. The neural activation bias is represented by cell darkness. This example is based on others given by Gruau [33]. Although Gruau uses abbreviated instructions, we spell them out entirely to make the example easy to follow. Gruau [33] proved that cellular encoding grammar trees can describe any network topology.

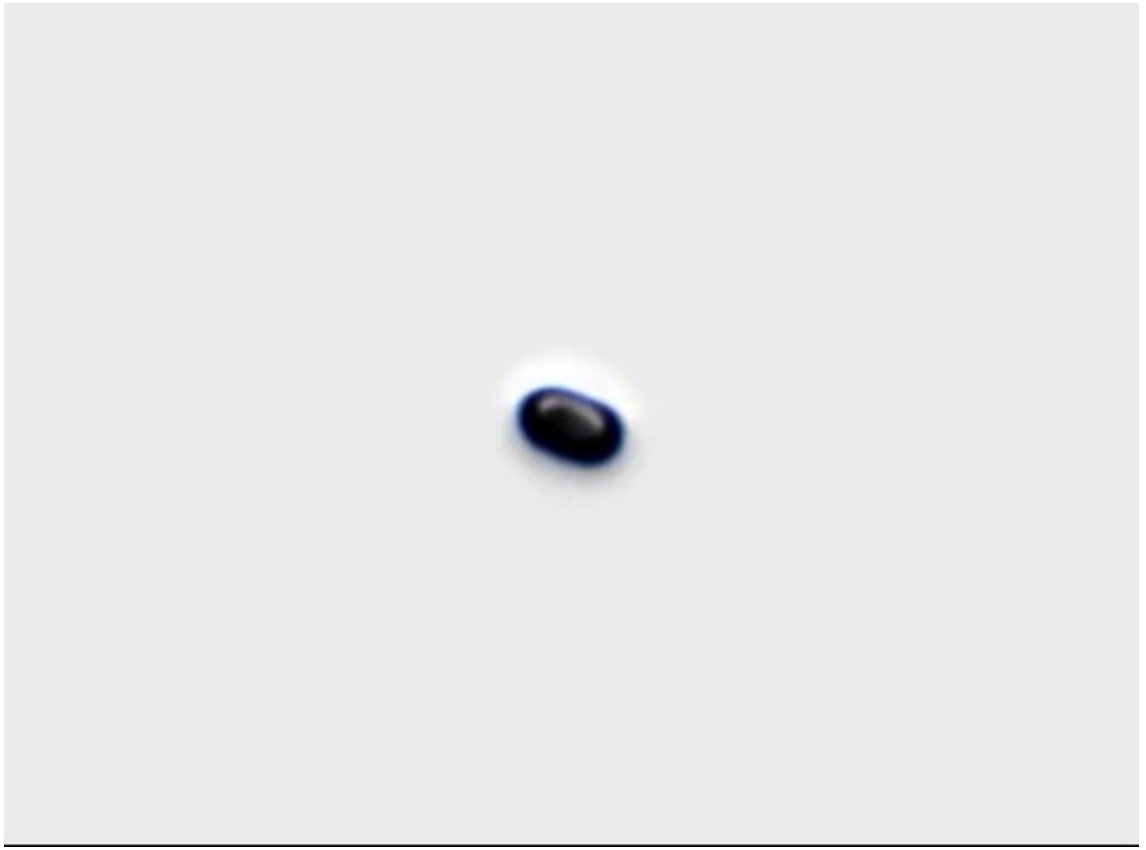
Cell Chemistry Approaches

Reaction-Diffusion Tutorial

Karl Sims

A simulation of two virtual chemicals reacting and diffusing on a 2D grid using the Gray-Scott model



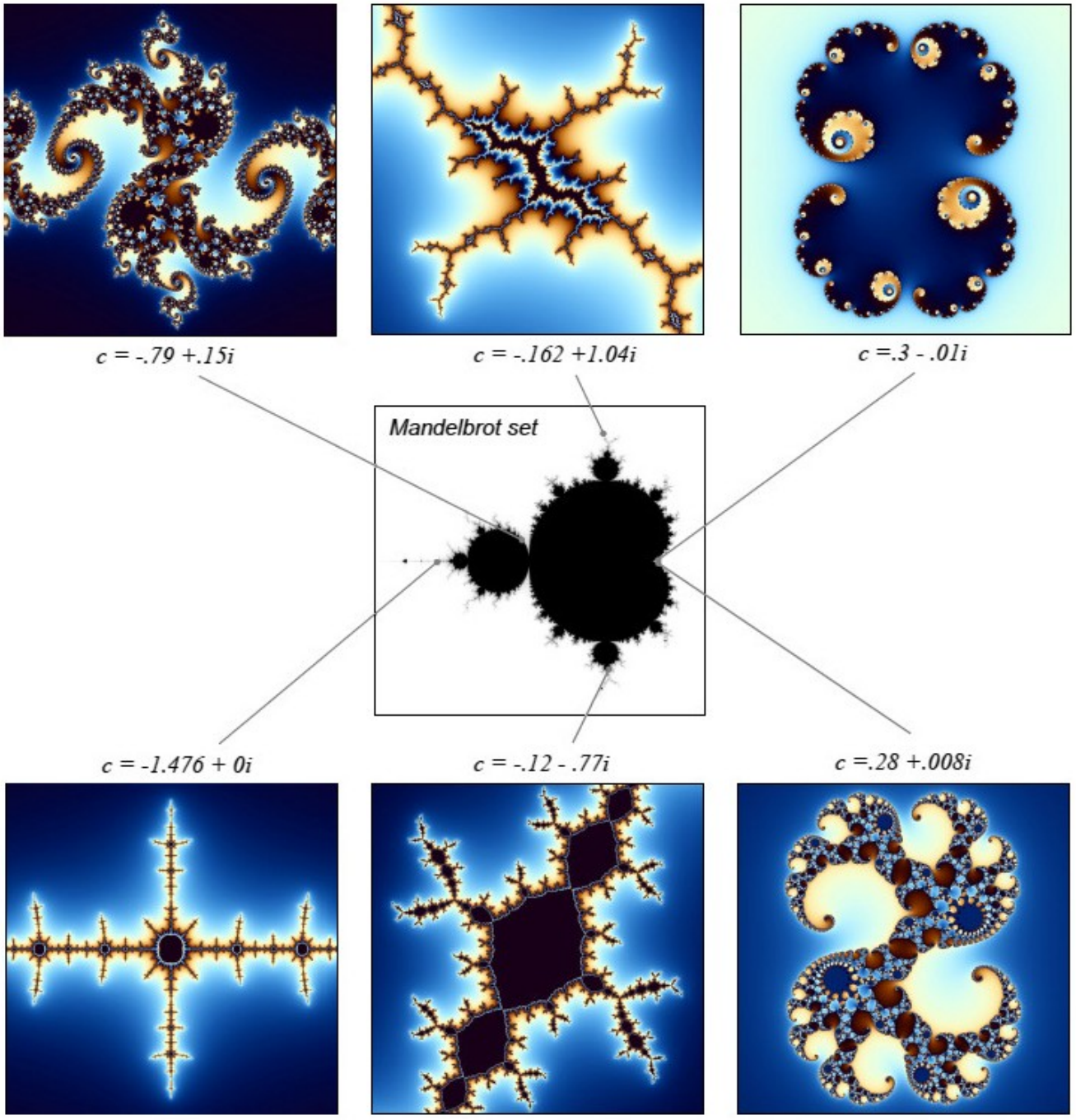


Gray-Scott Reaction-Diffusion System in 3D Using an Alternating Direction Implicit Method

All results generated by the CUDA implementation.
Every 20th frame rendered with POV-Ray.

All scenes have N = 64, dt = 1.2,
and show the v-field.

Left video shows iso-surface,
Right video shows volumetric field.


c = -.79 +.15i
c = -.162 +1.04i
c =.3 - .01i
Mandelbrot set
c = -1.476 + 0i
c = -.12 - .77i
c =.28 +.008i

Start with a circle of radius 2

Start with a circle of radius 2

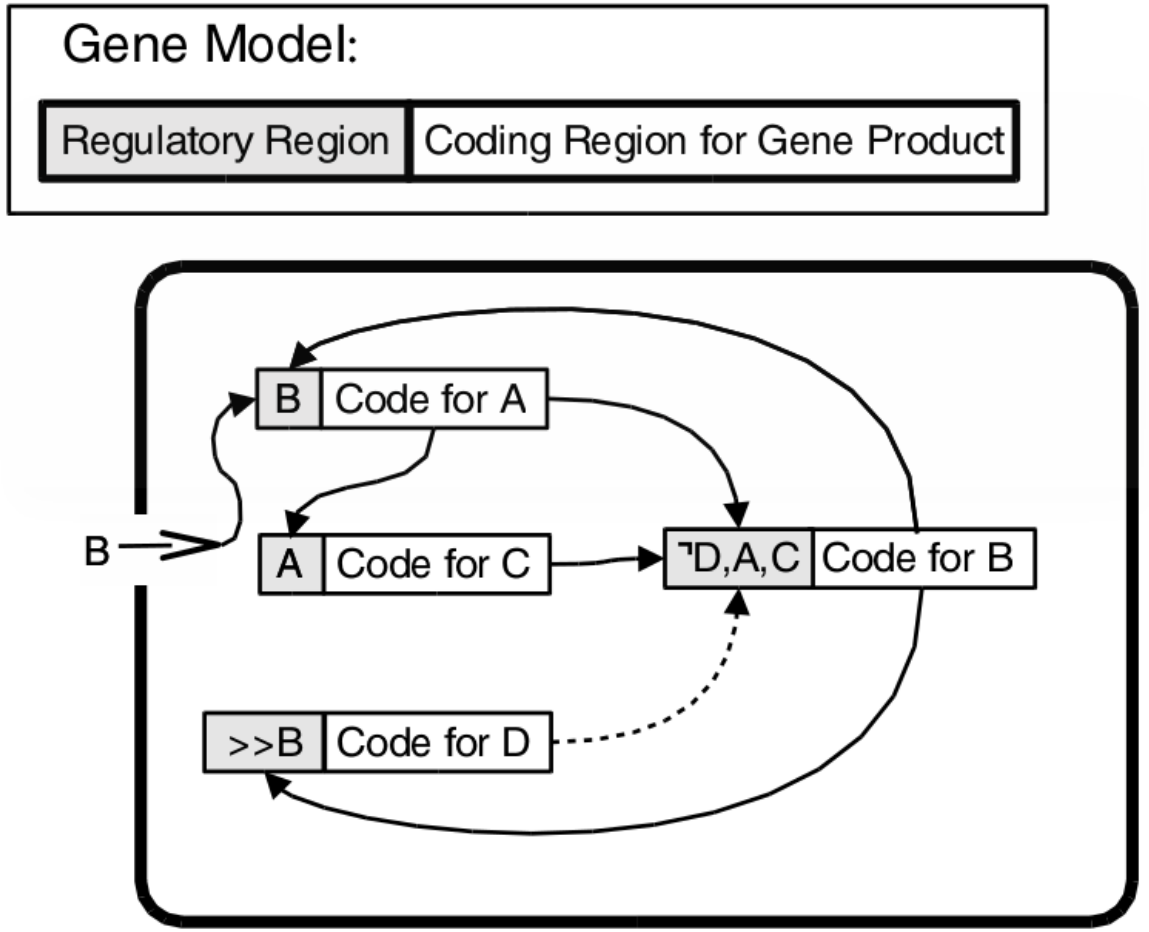
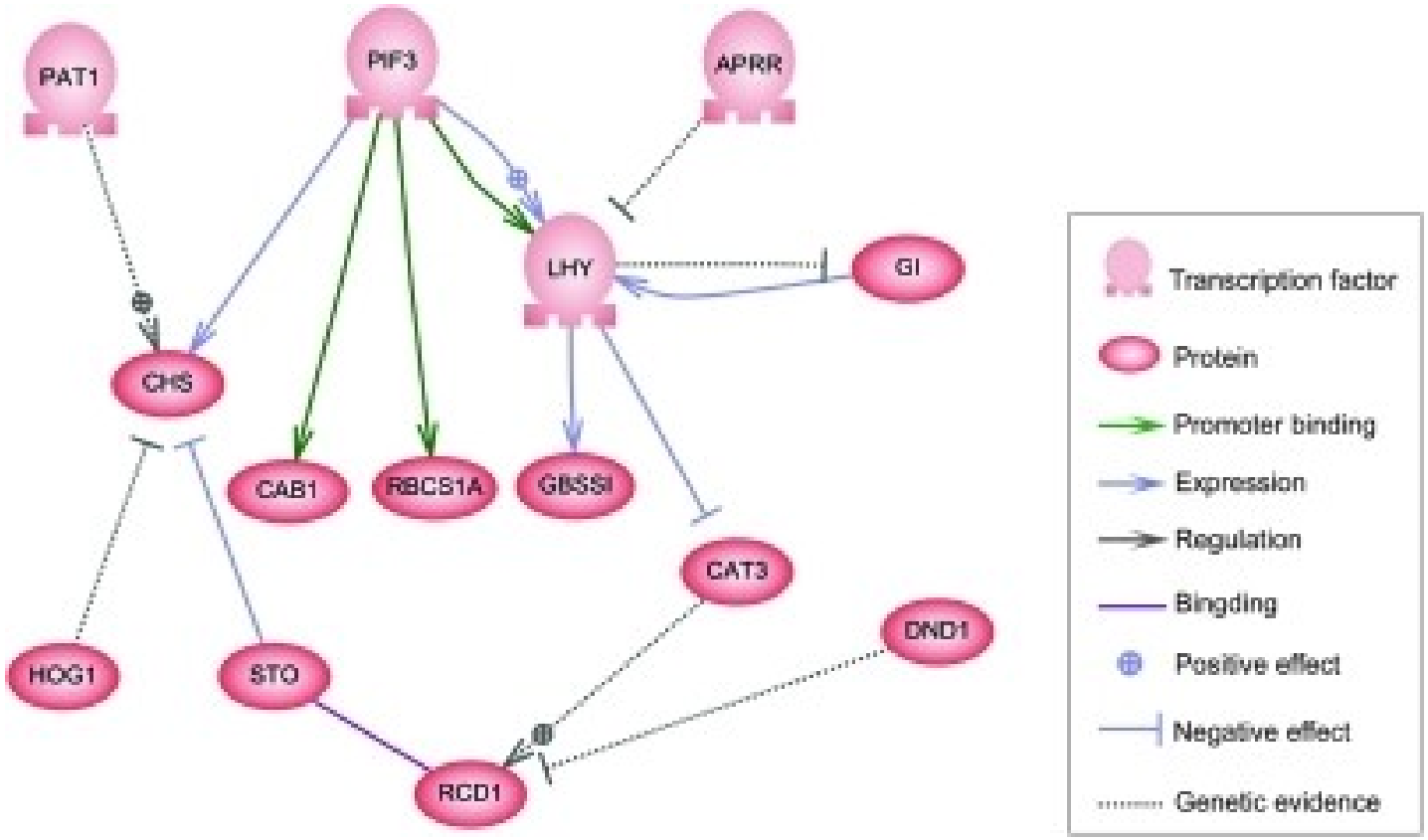
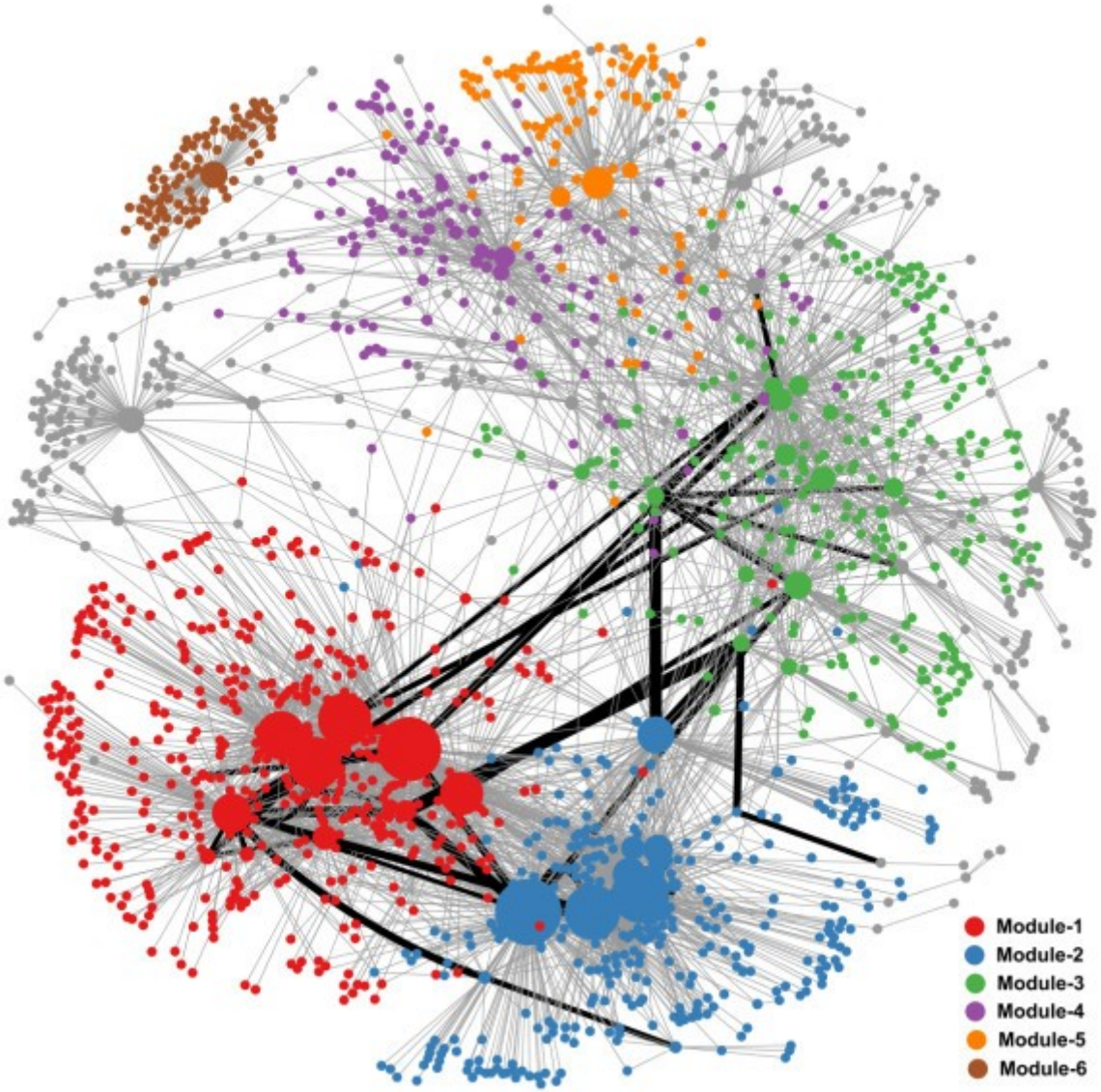


Figure 4. Genetic regulatory network example. Each gene is modeled as a regulatory region and a coding region that codes a particular product (e.g., a protein in a natural cell). A simple network showing how different gene products of some genes regulate other genes is shown inside a cell, depicted as a rounded rectangle. The network describes a system that produces a number of products and then turns off when enough of product *B* is produced. The symbol "≫" means a large amount. The diagram shows that the entire network becomes activated when product *B* enters the cell from an external source. *B* causes *A* to be produced, which in turn causes *C* to be produced by another gene. *A* and *C*, without *D* in the cell, cause more *B* to be created, which in turn feeds back into the production of *A*, further strengthening the cycle. Eventually, when a great deal of *B* is present, *D* is finally produced, stopping the generation of *B* and ending the feedback cycle. The GRN shows that interesting dynamics can result from the regulatory interactions of different genes. In an AE model, gene products might, for example, cause axons to grow or reduce neural thresholds.


PAT1
PIF3
APRR
LHY
GI
CHS
CAB1
RBCS1A
GBSSI
CAT3
DND1
HOG1
STO
RCD1
Transcription factor
Protein
Promoter binding
Expression
Regulation
Bingding
Positive effect
Negative effect
Genetic evidence


Module-1
Module-2
Module-3
Module-4
Module-5
Module-6

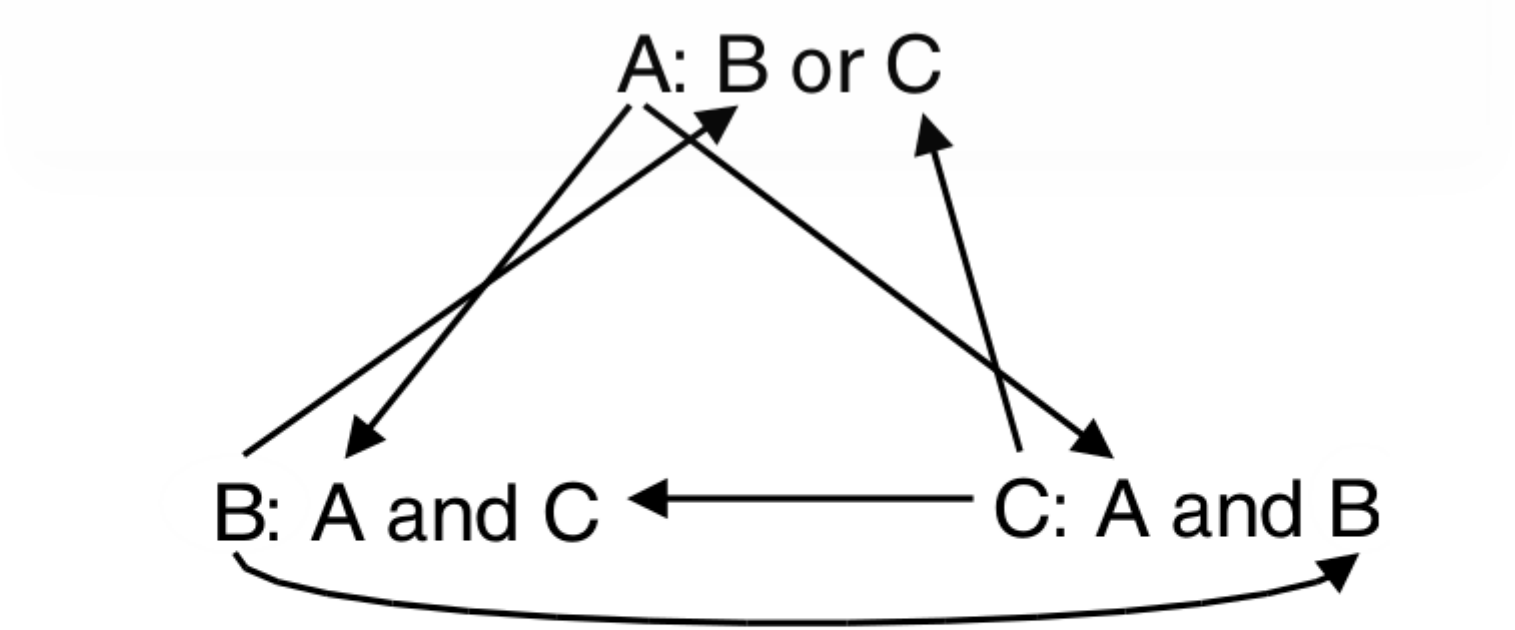


Figure 5. Random Boolean network (RBN) example. The state of the network is given by the Boolean values of *A*, *B*, and *C*. At each time step, the state values are updated based on their values in the previous time step. In the approach of Dellaert and Beer [22], the current state of a cell is given by the current state of its RBN. Individual bits in the state signal events like cell splitting or creating connections between cells. RBNs were introduced by Kauffman [44] to simulate the protein expression patterns in cells in a developing embryo. RBNs are computationally less expensive than full-blown GRN implementations (Figure 4), while exhibiting similar dynamics.

Dimensions of Development

1. **Cell Fate**: The *fate* of a cell is the eventual role it will come to play during development. For example, a cell may become a neuron or a muscle cell. There are several ways that cell fates are determined in nature. Since cells in AE systems must eventually play a role in the mature phenotype, it is important to consider the means through which those roles can be determined.

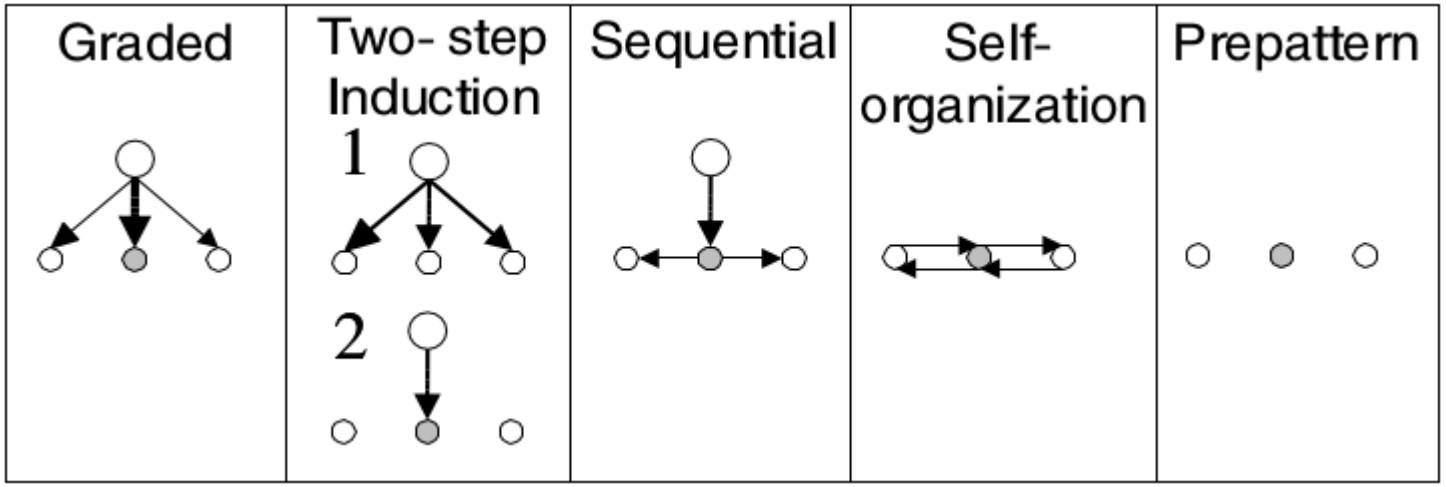
2. **Targeting**: The ways that cells can develop connections to target locations is an important aspect of development. Connectivity contributes to the overall functionality of complex systems, particularly neural networks. AE system design can benefit from an analysis of the ways that connections develop in nature.

3. **Heterochrony**: The timing and ordering of events in the embryogeny of a lineage of organisms can change over generations. Such changes can result in different final results, sometimes leading to important innovations in natural organisms. AE researchers may consider whether their encodings allow similar flexibility.

4. **Canalization**: Biological genomes are tolerant to mutations. Several mechanisms allow developing components to adjust to changes caused by mutations in connected components. These mechanisms can be employed in AE systems.

5. **Complexification**: Over the course of biological evolution, new genes are occasionally added to genomes, increasing the complexity of the phenotype. Complexification has led to major innovations in body-plan organization. By implementing a mechanism for handling variable length genomes, AE can also utilize complexification.

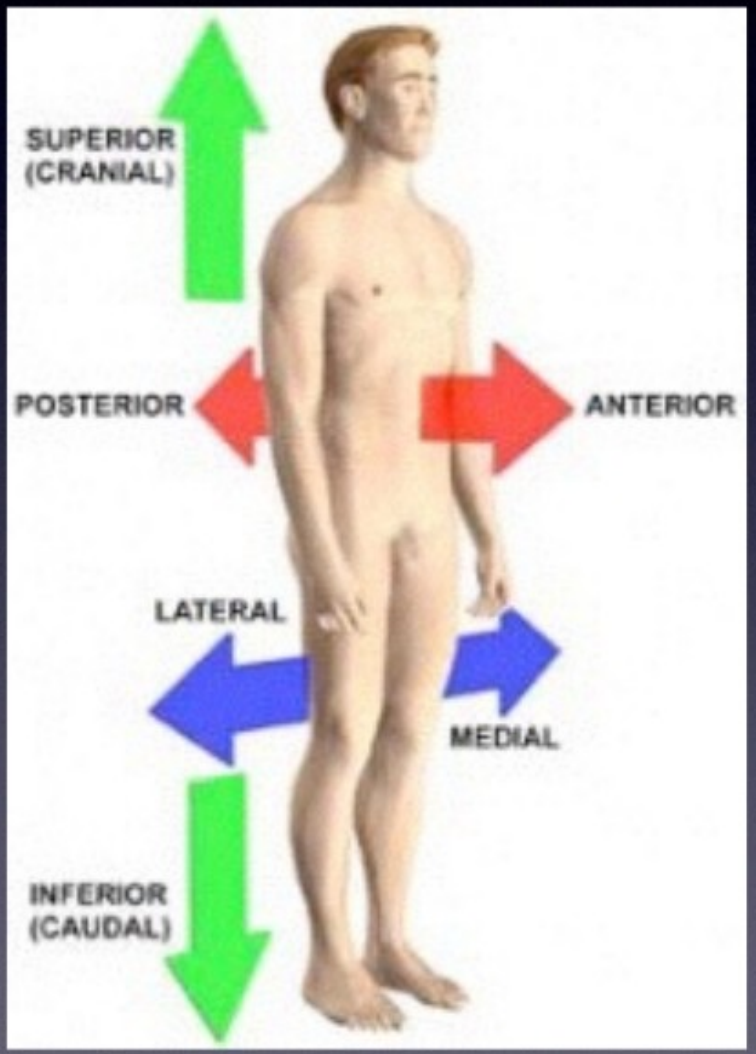
Cell Fate



- **Graded Induction**: A signal is released from an organizer in a graded pattern. The precursor cell receiving the most signals assumes fate *A*, while those receiving fewer signals assume fate *B*.
- **Two Step Induction**: The organizer first releases a uniform signal to all the precursor cells to let them know that they form a precursor group. A secondary signal is subsequently released to a subset of the group in order to further distinguish fates.
- **Sequential**: The signal from the organizer reaches only a single precursor cell, which assumes fate *A*. It then sends secondary signals to adjacent precursor cells, giving them secondary identities.
- **Self-organization**: The precursor cells signal each other and the dynamic properties of the network of signals assigns fates, without any organizer cell necessary.
- **Prepattern**: Gene expression alone, deriving from each precursor cell's lineage, is responsible for fates. Signals are not utilized, that is, the state of the parent cell fully specifies the states its progeny.

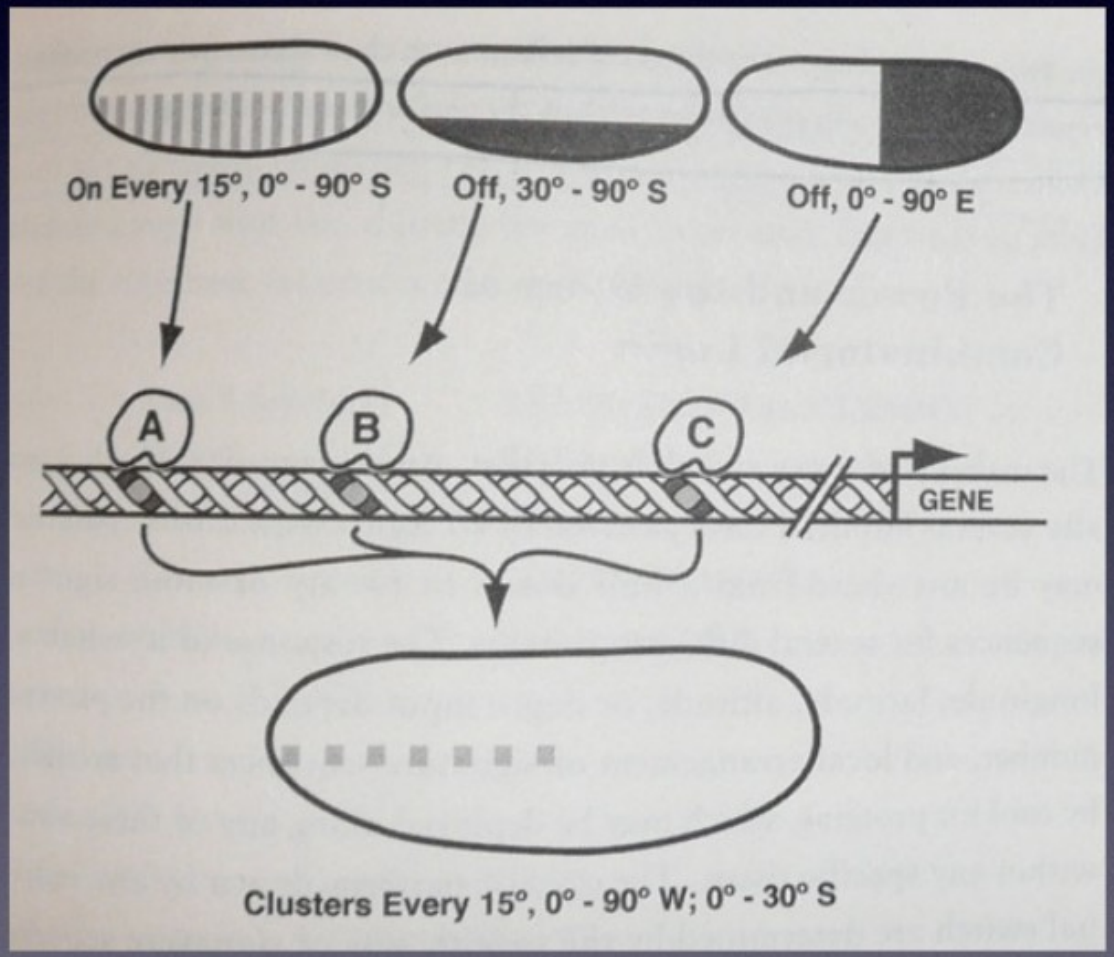
How nature builds complexity

- Generative encoding...
- ...where cell fate is a function of geometric position

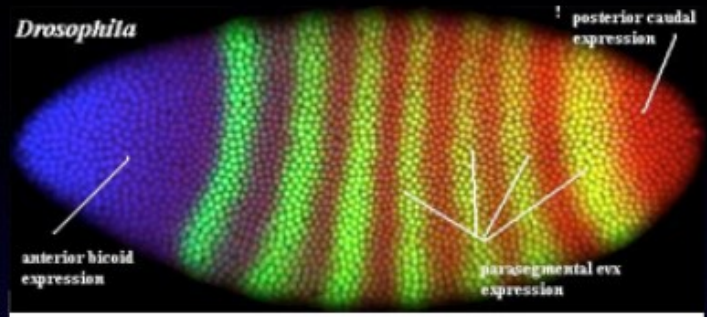


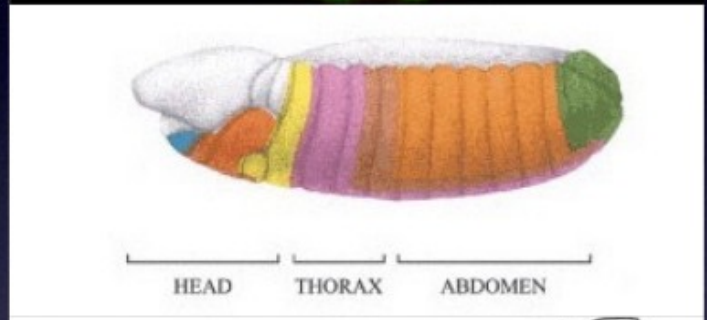
How nature builds complexity

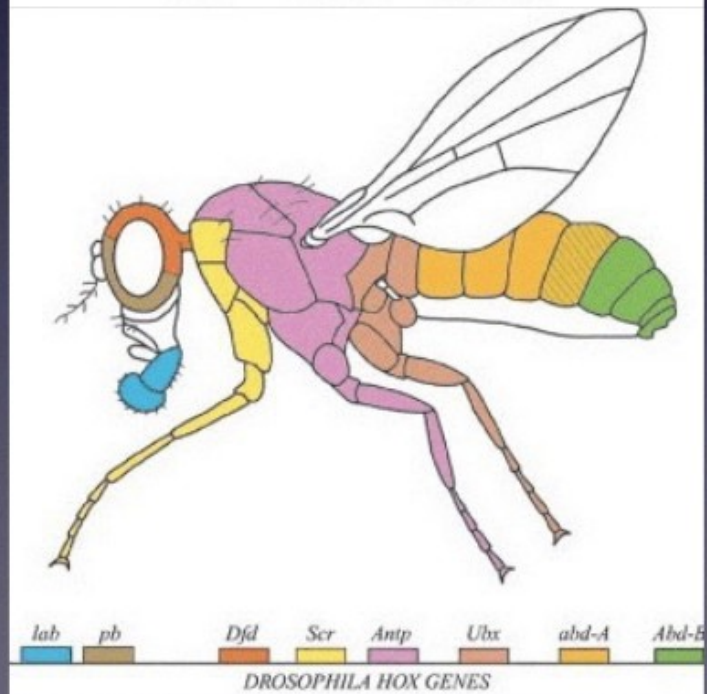
Development involves producing complex coordinate frames

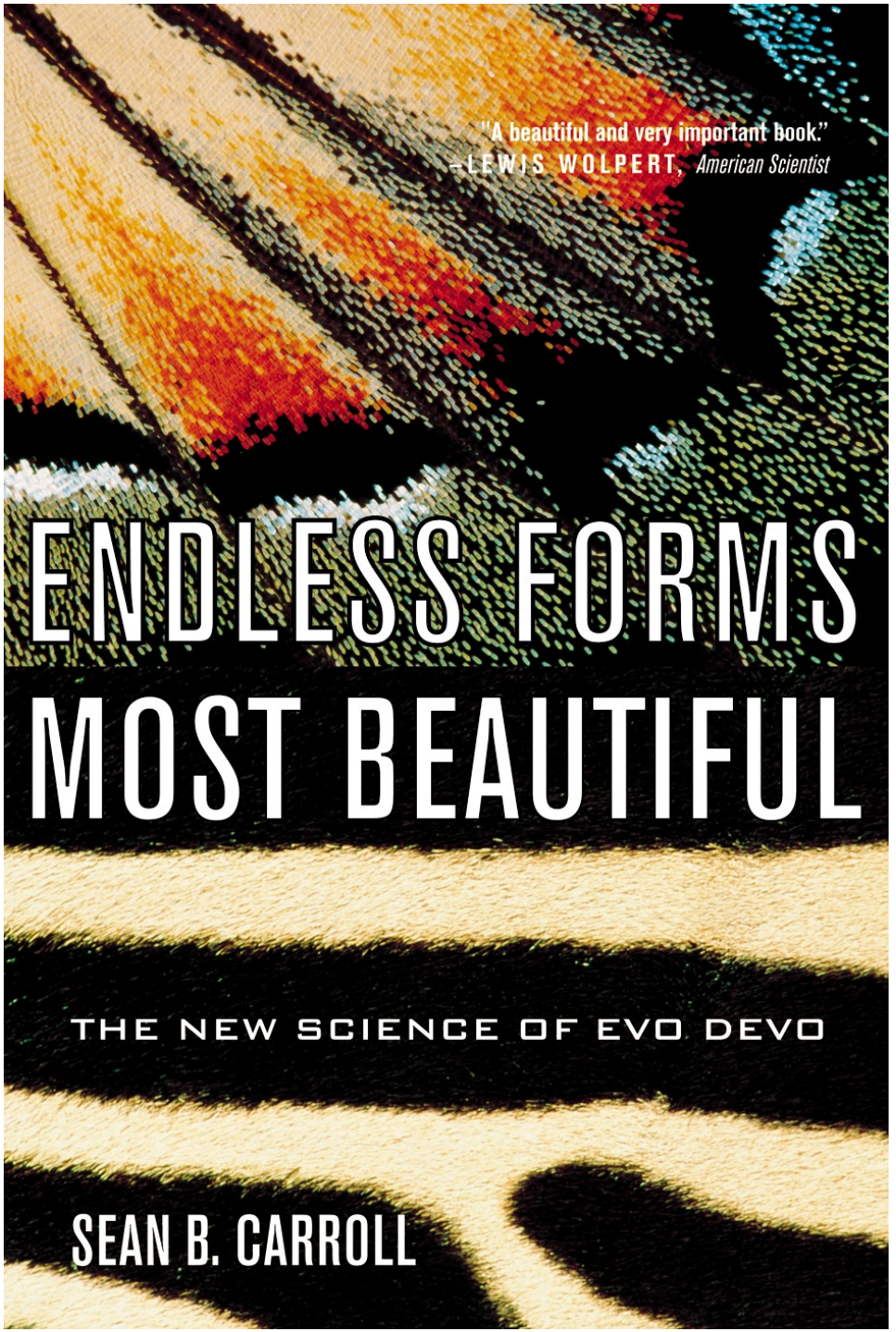


Sean Carroll: Endless Forms Most Beautiful (2005)

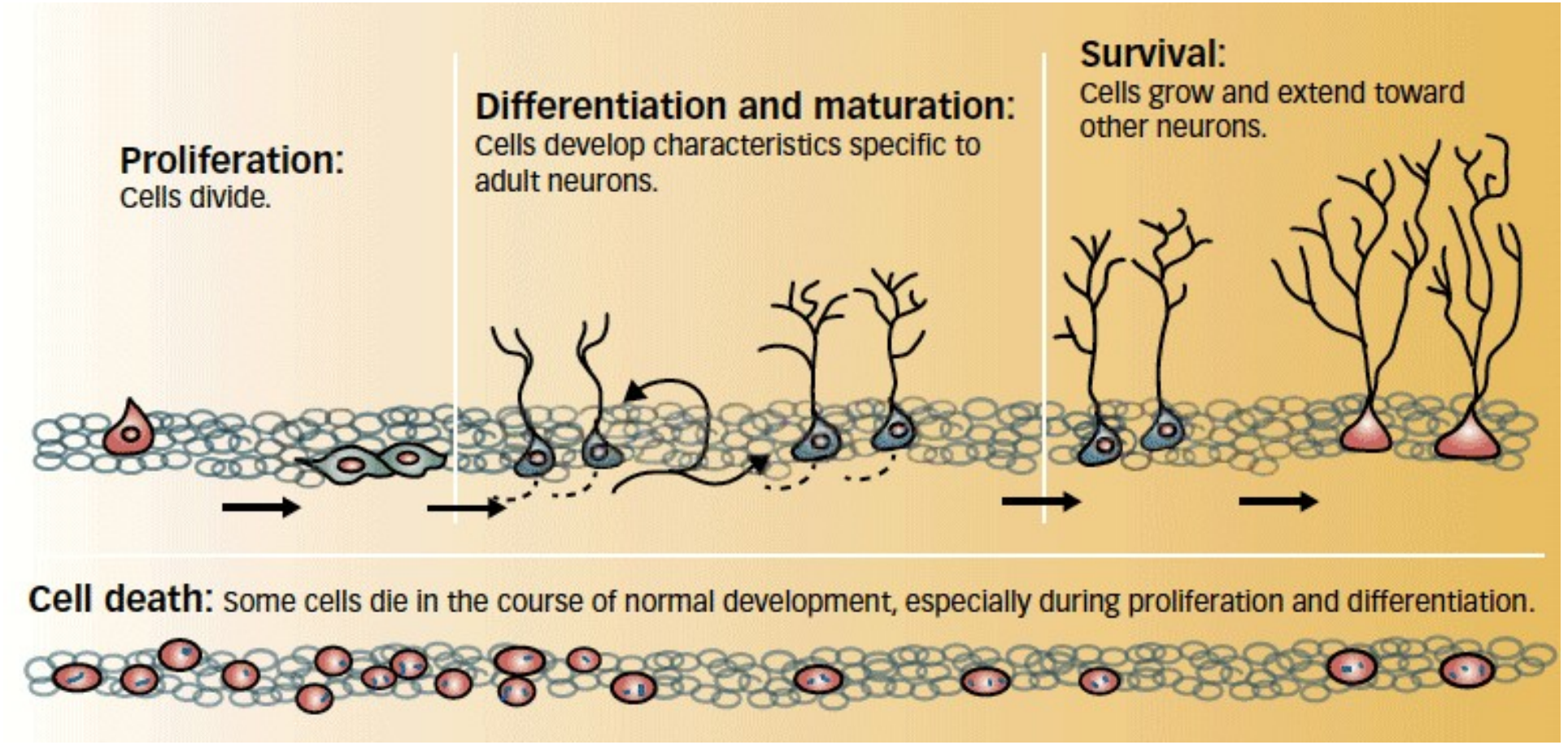




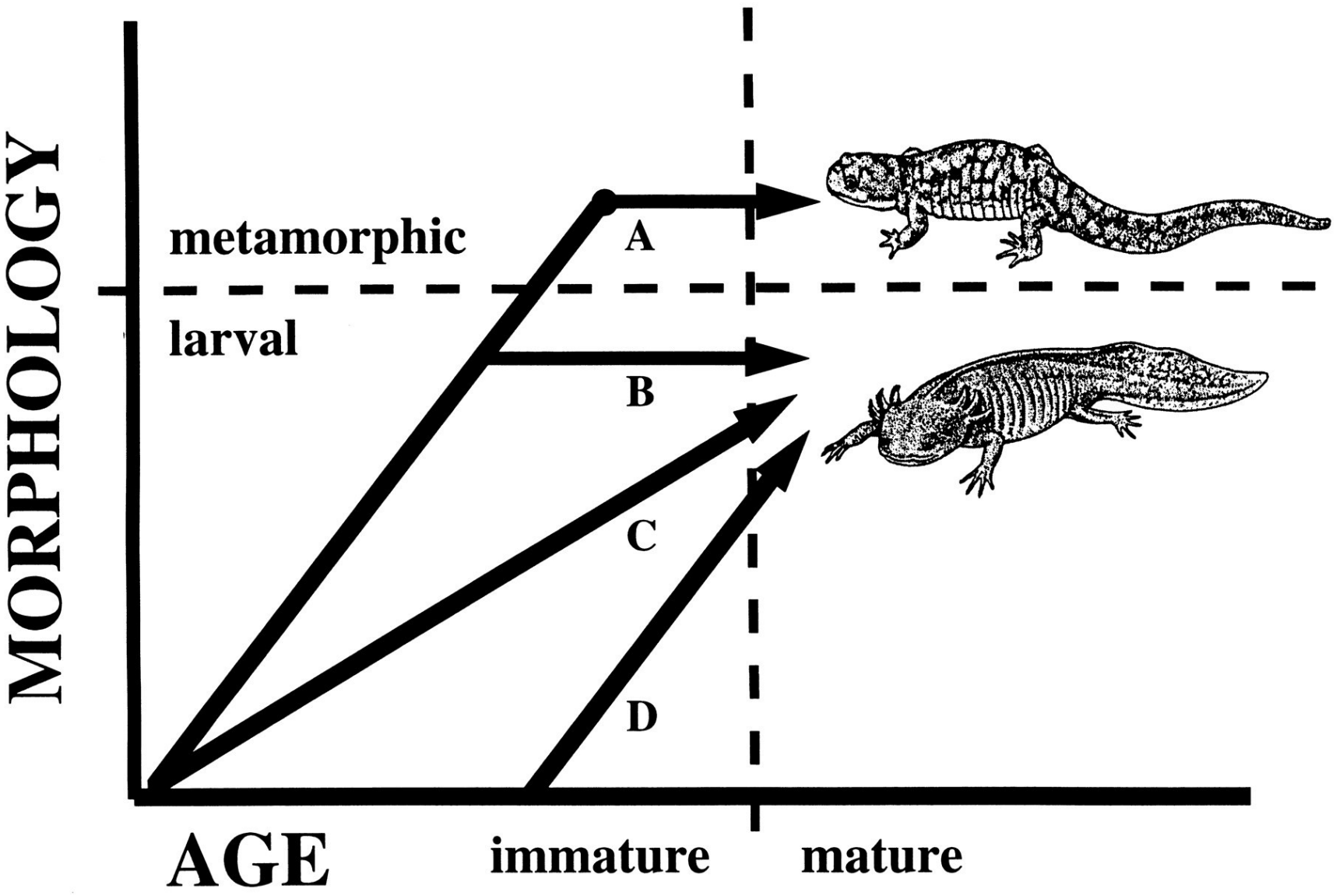



"A beautiful and very important book."
–LEWIS WOLPERT, American Scientist
ENDLESS FORMS
MOST BEAUTIFUL
THE NEW SCIENCE OF EVO DEVO
SEAN B. CARROLL

Targeting


Proliferation:
Cells divide.
Differentiation and maturation:
Cells develop characteristics specific to adult neurons.
Survival:
Cells grow and extend toward other neurons.
Cell death: Some cells die in the course of normal development, especially during proliferation and differentiation.

Heterochrony


MORPHOLOGY
metamorphic
larval
A
B
C
D
AGE
immature
mature

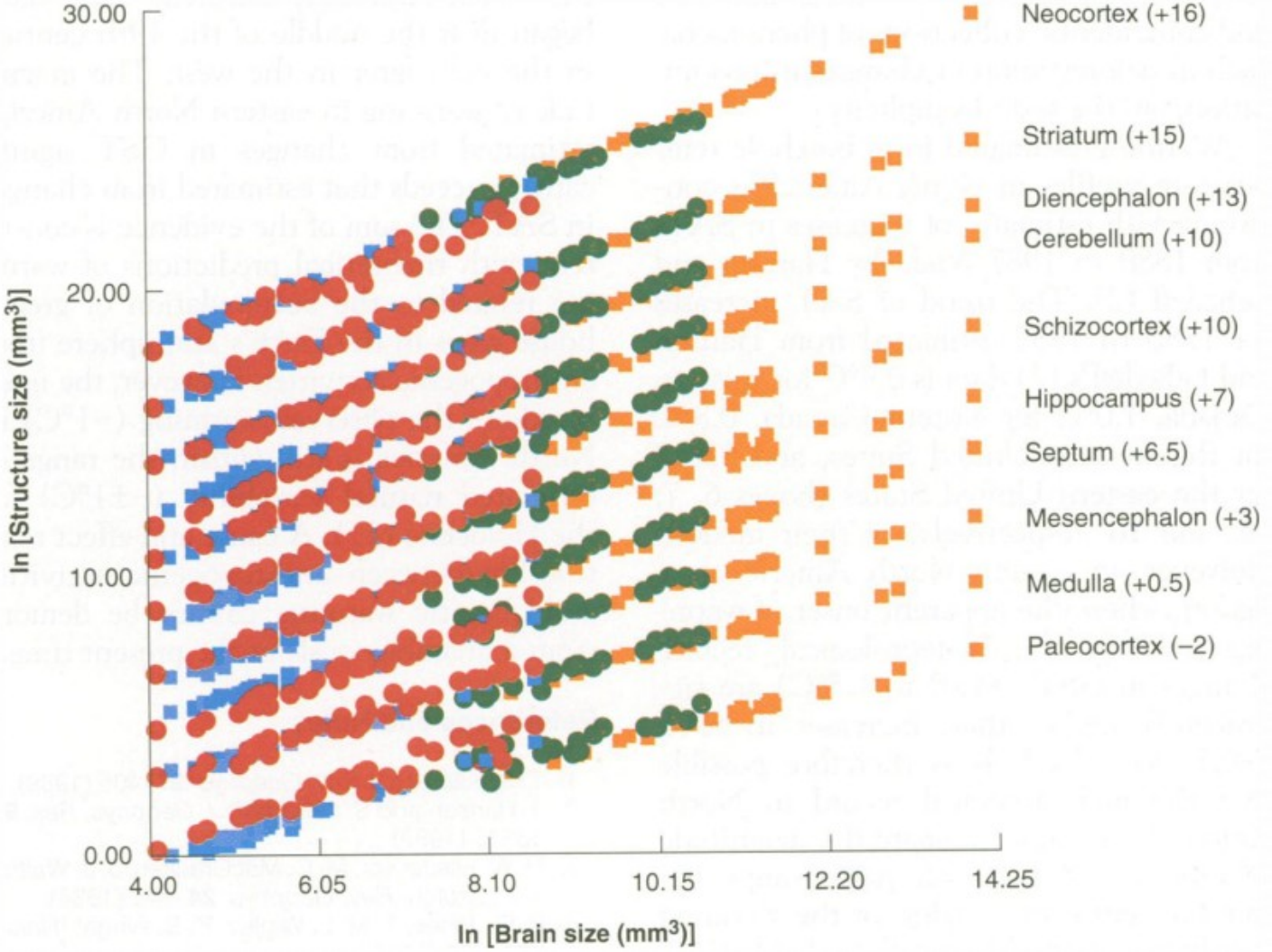
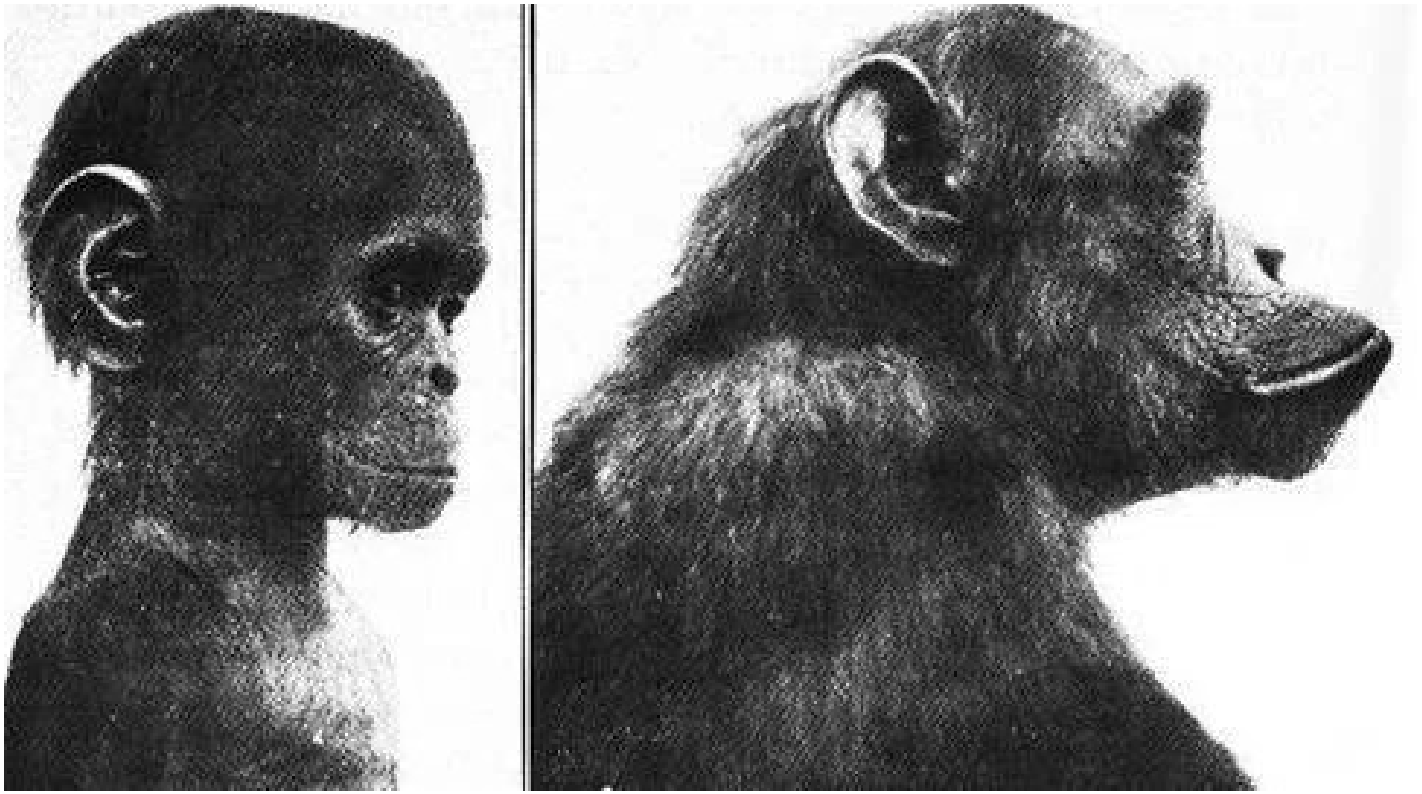
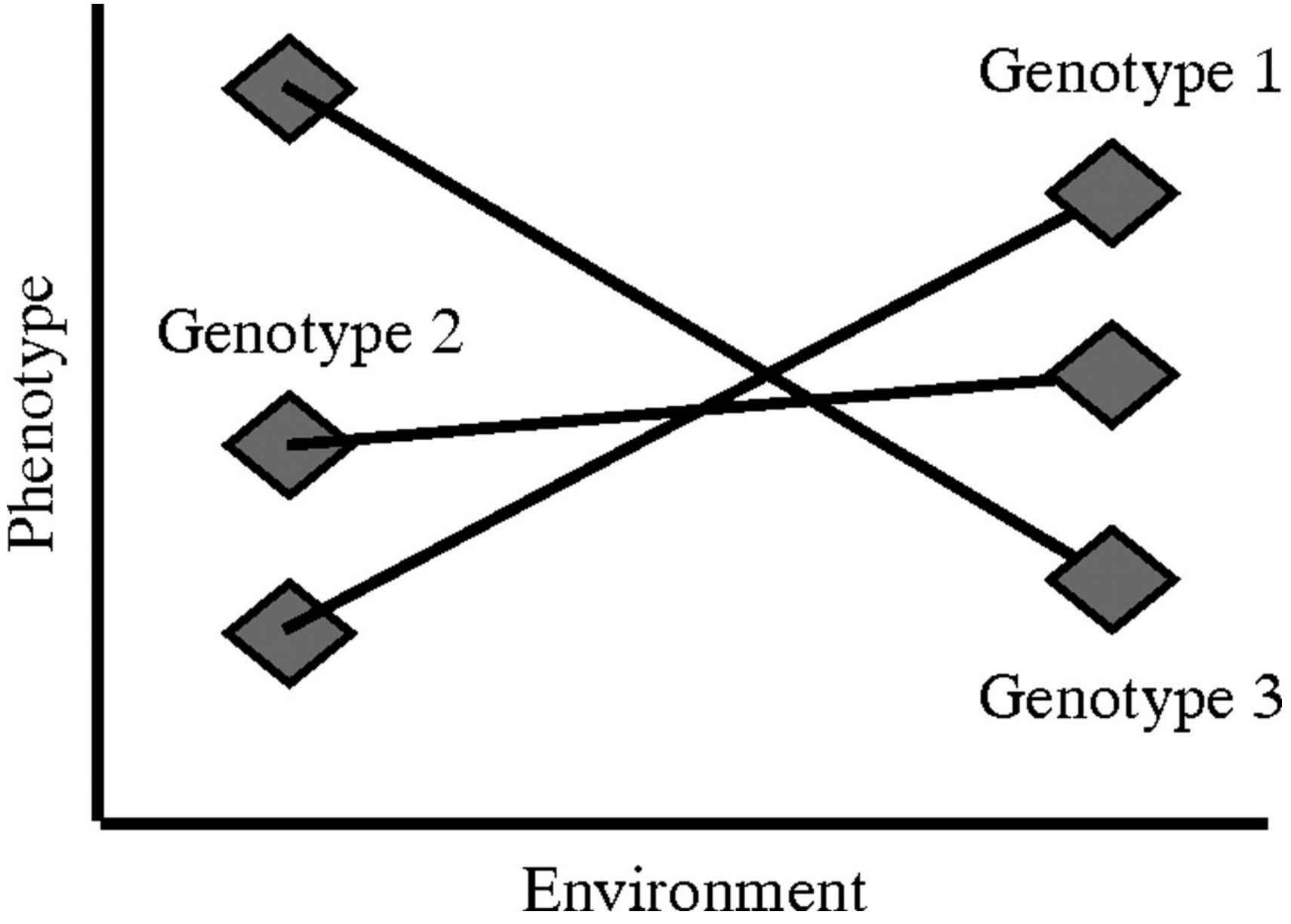


Fig. 1. Sizes of 10 measured brain subdivisions from 131 species plotted as a function of total brain size (orange squares, simians; green circles, prosimians; red circles, insectivores; and blue squares, bats). This method of representation emphasizes the linearity of the relation between brain sizes and structure sizes across mammalian groups on logarithmic scales. Each scatterplot of data points corresponds to a brain subdivision. Arbitrary constants (in parentheses after each subdivision name) were added to separate the plots visually; their normal overlap can be seen in Fig. 2A. Table 1 lists the slopes and intercepts of each regression equation for each structure.

e.g. paedomorphism



Canalization


Genotype 1
Genotype 2
Genotype 3
Phenotype
Environment

Complexification

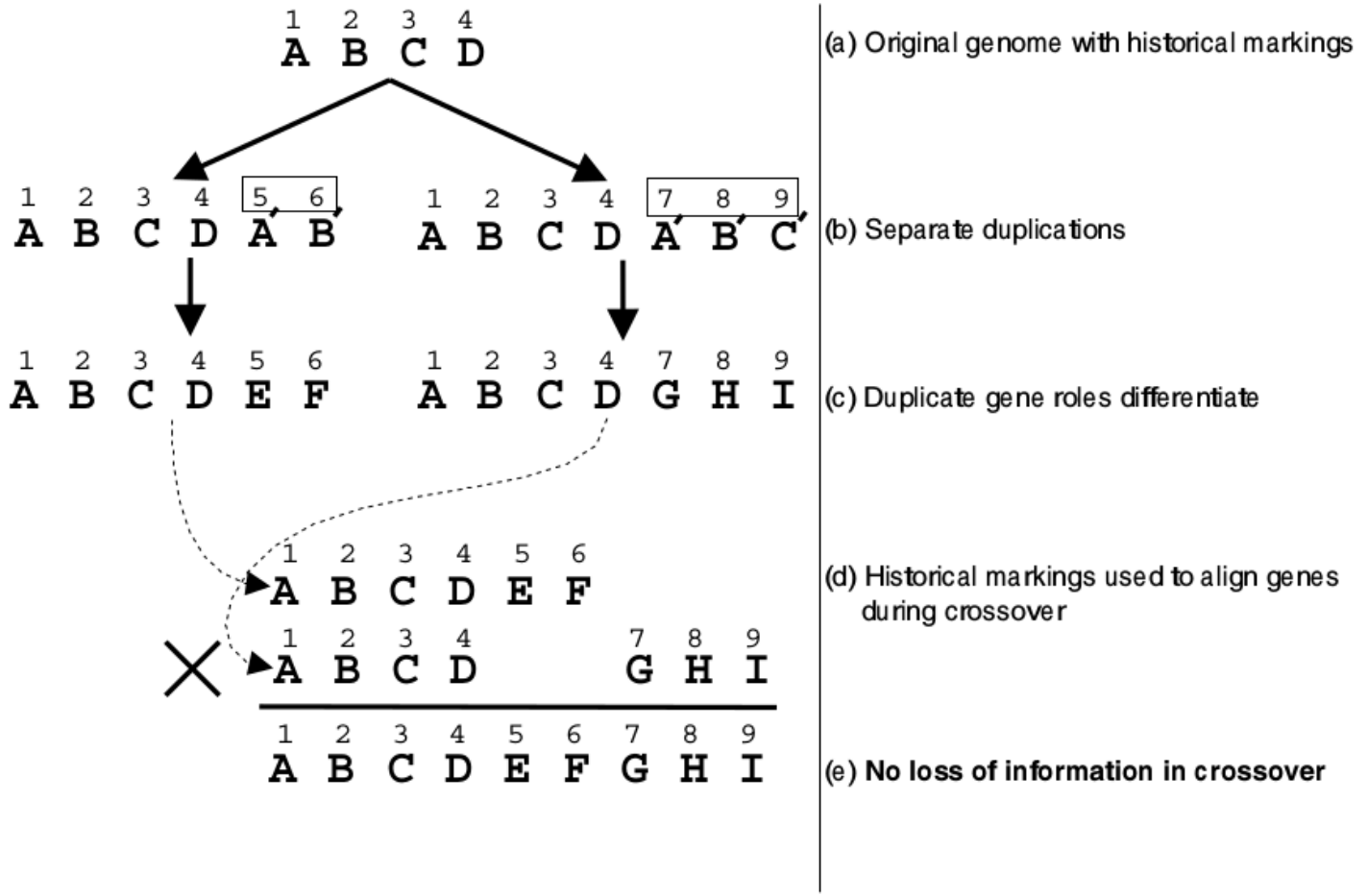


Figure 10. Solving the variable-length genome problem with historical markings. Historical markings are numbers assigned to each gene that represent the order in which new genes appeared over evolution. (a) The original genome contains four genes—*A*, *B*, *C*, and *D*, assigned historical markings 1 through 4. (b) When new genes appear through duplication, they are assigned numbers in the order in which they appear. Assuming the duplication on the left happened before the one on the right, the new genes—*A′* and *B′*, and *A′*, *B′*, and *C′*—are assigned the numbers 5 through 9. (c) As the products of the duplicate genes differentiate, their historical markings continue to serve as a record of their origins. (d) During crossover, those genes that have matching historical markings are aligned, while those that are disjoint are purposely not aligned. (e) The result is that any kind of crossover can preserve the information and relationships between all the genes in variable length genomes by utilizing the historical markings. Historical markings are an abstraction of synapsis, the process used in nature to match up alleles of the same trait during crossover [63, 70].