Graphing Genes, Cells and Embryos

Stazione Zoologica Anton Dohrn, Naples (Italy)
May 17-20 2007

Program

Sabine Brauckmann and Gerd B. Müller: Introduction of the Workshop

Christiane Groeben Science joins the arts: The collection of watercolours and drawings of marine organisms at the Stazione Zoologica Anton Dohrn

From 2D Neurons to 4D Developmental Data
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Ariane Dröscher From the two-dimensional image of the Golghi apparatus to its three-dimensional model
Patrick Lemaire Virtual 3D embryos and their contribution to understanding developmental processes
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The Beauty of the Chick, or Embryology and Development
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Imaging and Modelling Evolution
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Denis Thieffry Genetic regulatory graphs as computational research tools

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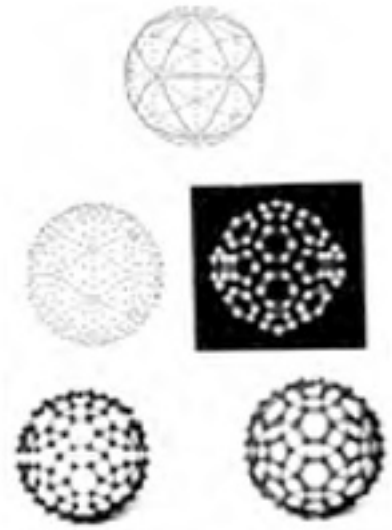
Imaging the virus of a shell: Modern architecture as an "anticipatory key" to understanding virus structure



By the early 1960s Aaron Klug and Donald Caspar had developed their "quasi-equivalence" theory regarding the formation of spherical viral shells. They had found inspiration for this theory in the visionary architect Buckminster Fuller's geodesic dome, a building model that emphasized efficiency, sturdiness, and straightforward assembly through the repetition of nearly identical subunits. Efficient construction, hardiness and simple (self) assembly seemed necessary for the success of a virus's protective covering, and so using Fuller's macro-world creations to help explain the architecture of viruses was entirely reasonable. In this paper I am interested in exploring how the architect's occupation with thinking through the issues of spatiality and natural physical laws and events (like gravity and weather) to build successful 3D structures could aid scientists who were trying to unlock the secrets of 3D biological objects that existed on an extremely microscopic scale. I will discuss the role of Fuller's ideas on Klug's and Caspar's theory of viral shell formation, especially as the virologists sought evidence and understanding of viruses in space through various experiments with imaging technologies and media: electron microscopy, crystallography, stereoscopy, 3D physical models, and Klug's own Fourier electron microscopy.

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Interpreting 4D developmental data

Reconstruction of developmental genetic regulatory networks (GRNs) requires unique computational tools that support the multicellular nature and changing topological relationships in those networks. The figure emphasizes the nested and dynamic spatial and temporal variations in the GRN controlling endomesoderm development in S. purpuratus.

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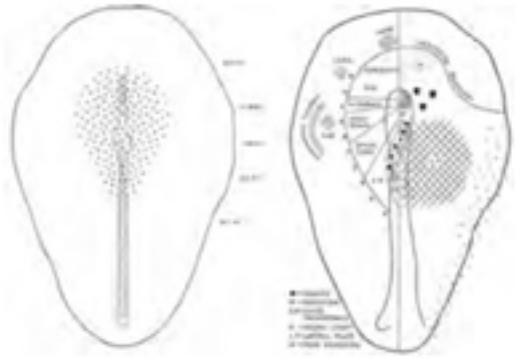
On fate and specification



Since the 1880s one depicted cell migration in images, later called fate maps, to visualize the presumptive fate of cells undergoing morphogenetic changes and phenotypic differentiation.
Until the 1940s one had accumu-lated a solid body of knowledge that was furnished by a gallery of images depicting the fate and specification of embryonic cells. However, many of these figures perpetuated optical illusions. Numerous review articles and even classical textbooks failed to distinguish between fate maps and specification maps. At best they represented optical hybrids of cell migration, layer movements and virtual mapping without recognizing the difference of embryonic layers and cell fates. Here I compare the 'classic' fate maps to the hand drawings of cell specification, published by female biologists in the 1930s. My objective is to visually elaborate the perceptive difference between 'fate' and 'specification'.

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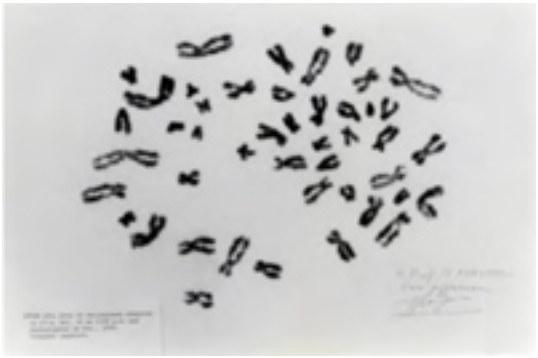
Visualising human chromosomes, 1950-1970



Work on human chromosomes in the 1950-70s was inextricably linked to changing practices of visualisation and display. Studying these practices in more detail we gain access to a research tradition in genetics that, at least at first sight, appears as markedly different from the molecular approach in biology that developed rapidly at the same time. The recount of human chromosomes in 1956 that gave rise to a flurry of work in the field was based on new techniques of fixing and spreading chromosomes on the microscope slide. Breaking with earlier traditions of drawing chromosomes viewed under the microscope with the camera lucida, the new images were produced through photography. These images exercised a unique fascination and circulated widely. For further analysis in the laboratory as well as in the clinic the chromosomes on the photographs were cut out, measured and displayed according to rules negotiated among scientists to achieve recognizable and comparable images. New banding techniques with fluorescent markers developed in the late 1960s abolished the work of measuring the chromosomes and instead introduced new ways of visual analysis, soon aided by the use of computers. In my paper I intend to explore these various transitions in representational practices and the issues involved for the production and circulation of knowledge on chromosomes.

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From the 2D image of the Golghi apparatus to its 3D model

For more than 60 years since its discovery in 1898 the Golgi apparatus has been almost exclusively a morphological research object. Yet, it turned out to be a highly pleiomorphic structure and its visualisation procured more puzzle than enlightenment.
In the 1950s electron micrographs produced still another rather different image. The networks, rods, and granules of the era of light microscopy became a complex stack of flattened cisternae, big vacuoles and small vesicles in the era of electron microscopy. In the 1960s still another challenge waited. Hilton H. Mollenhauer, W. Gordon Whaley and their collaborators from the Plant Research Institute of the University of Texas not only tried to identify the Golgi apparatus in plant cells but also to elaborate a three-dimensional picture in order to better grasp its nature and its dynamic role in cell physiology.

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Observation and judgement. Why did a prism matter in microscopical drawing?

Comparing historical examples (17th, 19th, 20th, 21st centuries) in which observation and visualization strategies were tightly related to the microscopist as a judging instance, I shall underscore the amazing continuity of the camera lucida principle as an imaging technology in microscopy since the early nineteenth century, and put up for discussion its validity in contemporary microscopy.

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Picturing RNA

While the double helix of DNA has become on iconic image, representations of RNA have not reached such status, in part because RNA structures are more varied. This paper will explore the scientific research as well as the aesthetics behind images of RNA. It will trace the changes in these images over time, changes which resulted from more structural information, the increasing sophistication of graphics programs, and shifting "styles" in scientific imaging.

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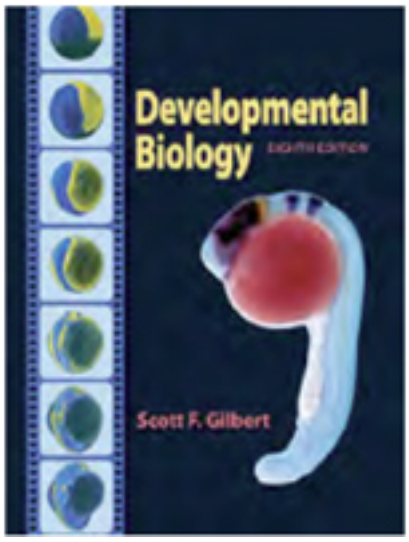
"The textbook account": How textbooks represent developmental phenomena



The embryology textbook has evolved in several ways. The revolution in developmental biology content has paralleled and has been assisted by the twin revolutions in printing (from mechanical to computer; from black-and-white to full color) and alternative communication.
In order to enrich and provide alternative access, books can now have embedded websites, DVDs, and other devises. Whereas textbook authors in the 1980s would await the mail to deliver hard copies of blackand- white images, today's author will receive by email a computergenerated jpg that is as original as the piece of data. Whereas publishers in the 1980s would provide transparencies to its professional users, these publishers now provide digital libraries of figures and movies. These changes may completely alter the ways by which students learn embryology.

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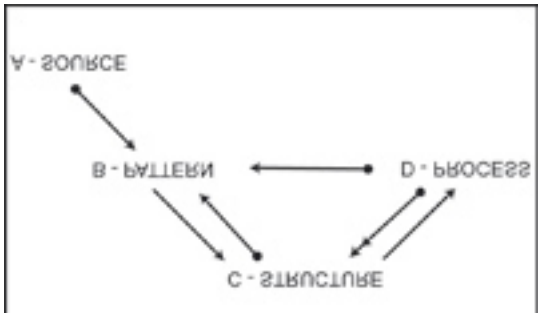
Visualization and visual modelling in biology and beyond



Visualization is ubiquitous in our culture. It should not surprise us to find that visual practices are also widespread in the sciences. I shall examine a range of uses of visual images in 19th and 20th century biological science and show how some of these rely

on representational techniques drawn both from other sciences and from beyond the sciences. I shall argue that similarities displayed by these cases show how the function of images changes and that these changes reflect changing demands on human cognitive capacities. As to the preeminence of visualization in the biological sciences, I shall consider whether they are different in this respect from other sciences.

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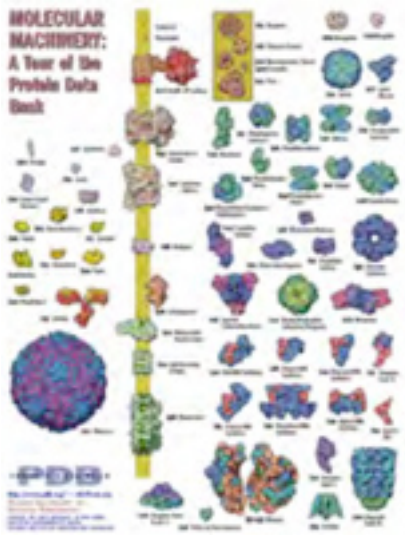
Visual methods from atoms to cells



Illustrations for use in education and public outreach often require a different set of graphical tools that those used for visualization in research. For the past 10 years, I have developed an approach for the presentation of illustrations that span the scale range from nanometers to micrometers, depicting subjects ranging from the atomic structure of biomolecules to the molecular ultrastructure of cells. The goal of this work is to create a consistent illustrative scheme for use over the entire range, which allows incorporation of diverse data from different spatial resolutions. My current approach uses non-photorealistic rendering, composed of flat colors and graphical outlines, of spacefilling representations.

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Science joins the arts: The collection of watercolours and drawings of marine organisms at the Stazione Zoologica Anton Dohrn

Communication of scientific results depends much on the author's ability to convey his findings through words and images. Research institutions have different and more diversified needs to diffuse knowledge. They may offer assistance to patrons or organise services in the wake of their institutional policies. At a time when photography only started to become a scientific tool, the Naples Zoological Station institutionalised the contribution of artists to scientific illustrations of marine organisms.

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Tactile teaching: Using physical models to explore protein structure/function

It is now possible to create accurate physical models of proteins based on atomic coordinates using rapid prototyping technologies. These models function as "thinking tools" in the hands of students and researchers alike. The models provide a concrete scaffold from which researchers can discuss their work with others, and students can build their initial understanding of the molecular world. These physical models are synergistic with computer-generated, virtual images of proteins; the use of physical models stimulates more sophisticated questions that can often be successfully investigated using computer visualization tools.

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Virtual 3D embryos and their contribution to understanding developmental processes.

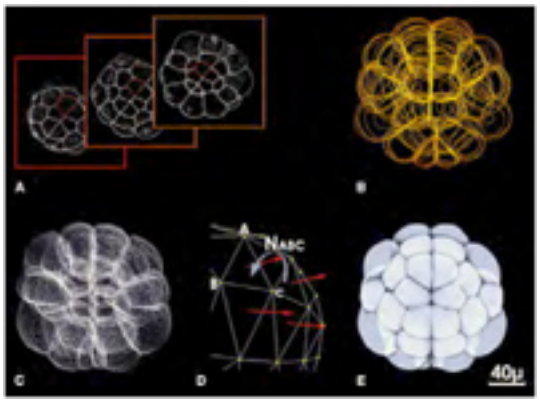

Figure 1. Reconstruction of 3D Embryo Models

(A) Examples of 2D confocal sections taken at different z values through a late 32-cell stage Ciona embryo fixed and stained with rhodamine-phalloidin.
(B) Animal view of the combined splines drawn around each cell contour on successive confocal images of a stack.
(C) Wire frame view of the reconstructed embryo.
(D) Schematic representation of the normal vectors associated to each triangle in the models. The direction of the normal for a triangle is determined by the order of the vertices.
(E) Embryo model displayed with a translucent texture.

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Evolving representations of gene regulation and cell signalling pathways and networks 1960-2007

Systems biology rests on the networks of gene regulation and cell-signalling which have been characterized during the previous decades. These

two networks have a different origin and history: the first abruptly originated at the beginning of the 1960s; the second was progressively described in the 1970s and 1980s. Their partial convergence was a subsequent phenomenon. What I will try to do is to compare the roots of these two descriptions, and the way these representations have evolved. The importance of these models within biology as well as to attract nonbiologists towards biology cannot be denied. The representation of these networks cannot be distinguished from their conceptual role. Their description is therefore a privileged way to outline the main characteristics of modern biology, as well as its recent transformations.

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Diagrams and theoretical content

Diagrams are often used to represent models in the biological sciences. What are the advantages and limitations of this representational format? What aspects of diagrammatic representation make this format especially well suited for use in the biological sciences?

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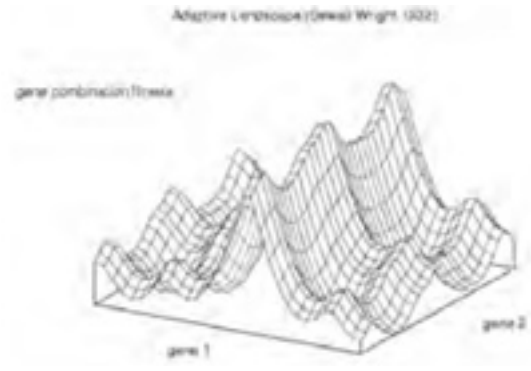
The rise and fall of the adaptive landscape



The aim of this talk is to provide a historical overview of the adaptive landscape metaphor, and to discuss some of the implications of the use of metaphorical language in biology.

I will address four main questions:
- What is an adaptive landscape?
- Where does the metaphor come from, and how has it influenced evolutionary theory?
- What are some of the key assumptions of the adaptive landscape metaphor?
- Are they warranted?

Sewall Wright (1931) developed a metaphor of an "adaptive landscape" to characterize the relative fitness of individuals, or, sometimes, whole populations. Wright's landscape was meant to illustrate the argument(s) of his "shifting balance" theory of evolution. A number of core assumptions found their way into the biological literature through this metaphor. I will argue that many of these assumptions are questionable, and ought to be discarded.

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From bifurcating trees to a cycle graph: The ring of life

Traditionally, biologist have represented the evolutionary relationships of all organisms by a

bifurcating phylogenetic tree. But recent analysis of completely sequenced genomes using conditioned reconstruction, a newly develop gene content method, suggest that a cycle graph or ring rather than a tree is a better representation of the evolutionary relationships between prokaryotes and eukaryotes. Conditioned reconstruction is the first phylogenetic reconstruction method to provide unequivocal evidence about the origin of the eukaryotes.

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Envisioning a New Science: Representing heredity in early genetics research, 1900-1919

This paper aims to consider both the representational traditions and graphical innovations employed as a new science of genetics was forged in the first two decades of the twentieth century. Through comparative analysis of representational strategies employed in several early genetics research programs, including those overseen by William Castle, Herbert Spencer Jennings, and T. H. Morgan, this paper will explore the representational strategies employed by these and other researchers as they aimed to define the science of genetics. The analysis will focus in particular on the contested meanings of heredity, genetics, and associated theoretical concepts in light of their visual representations in the early twentieth century, and the consensus that emerged in these practices and conceptions by the end of World War I.

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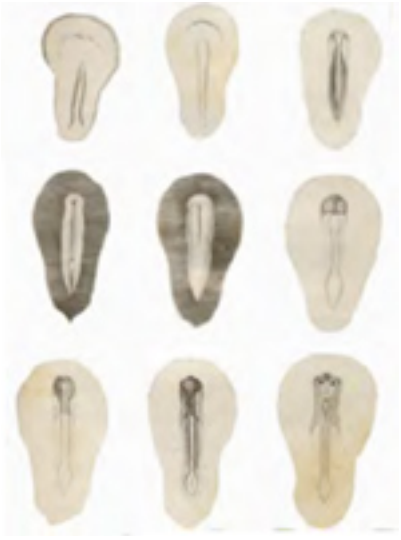
Pander, d'Alton and the representation of epigenesis



Christian Heinrich Pander (1794-1865), a Russian scientist of German culture, is known for his epoch-making work in embryology, as well as for his important contributions to palaeontology. Under the supervision of Ignaz Döllinger, he undertook in 1816 a complete study of the development of the chicken during the first five days of incubation. He was assisted by the famous draftman Eduard d'Alton (1772-1840). The three men worked together for several months in close collaboration, and the results were presented in Pander's doctoral Dissertatio in Latin. The plates engraved by d'Alton were printed the same year, with a German text. They are interesting, from a epistemic point of view, since they comprise no legend in themselves, but are covered by a tracing paper with schematic interpretation and legends. This mode of representation can be connected with Pander's conception of embryology as a gradual, epigenetic transformation (as opposed to preformation) with an intermediary stage, the formation of simple germ-layers.

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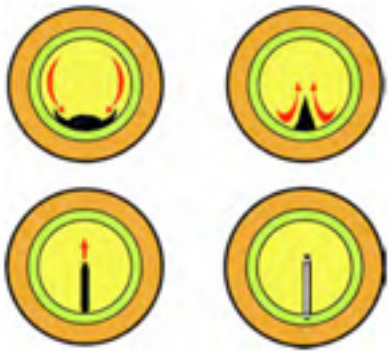
From fate maps to embryo: The magic of gastrulation



The event of gastrulation is considered by some to be a more important event in life than marriage, birth or death. During gastrulation cells first organise themselves into layers and communicate with one another, they move around the embryo to generate form and the embryo starts to fix its initial body pattern. Of many old questions which remain unanswered is to what extent cells acquire their distinct identity (fate) and then move to the correct locations, and to what extent they move before becoming specified. In either case, where are the instructions that direct cell movements to their destinations? In this talk I will explore these questions using a combination of experimental embryology and modern imaging technology (multi-photon time-lapse microscopy) to image the gastrulating chick embryo in 4-dimensions.

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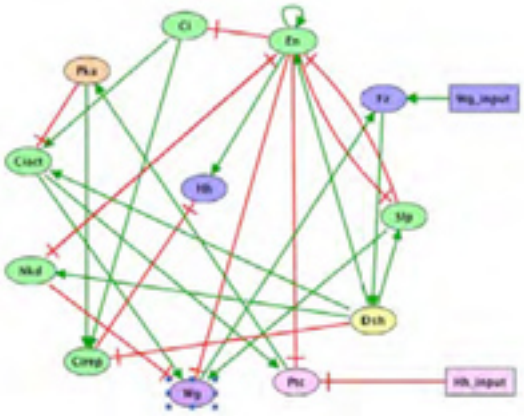
Genetic regulatory graphs as computational research tools



I will present an overview of the main graphical representations of biological regulatory networks (genetic and metabolic networks, signal transduction pathways, etc.) and contrast their different functions, from explanatory cartoons to computational devices.

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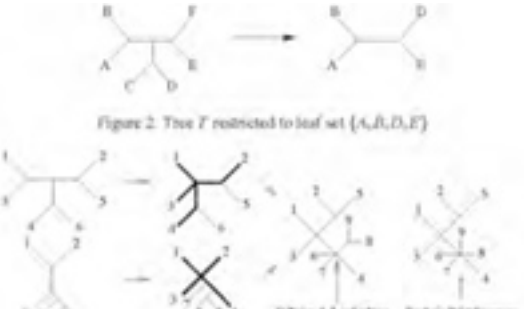
The landscape of life



Phylogenetic heuristics are one of the primary techniques for inferring evolutionary trees. In this talk, we discuss the landscape of tree solutions found during a phylogenetic search.