

# Programme: The Evolution of Developmental Processes

## Monday, September 28<sup>th</sup> — Introduction and Phylogenetics

9.00–12.30

**YOGI JÄGER** (*CENTRE FOR GENOMIC REGULATION, BARCELONA/WISSENSCHAFTSKOLLEG ZU BERLIN*)

### Introduction: the Process Perspective

Evo-devo strives to re-unite the study of development and evolution. I will introduce two philosophical notions that provide the foundations for this endeavour (and this course in particular). The first is process philosophy, which argues that processes are more fundamental than static things. Developmental and evolutionary processes are but two aspects of the same unifying underlying dynamic. The second is perspectivism, which argues that evolutionary phenomena (and reality in general) can be studied from many only partially overlapping angles, and that conceptual unity may be unattainable and, in fact, not even desirable. This prepares the way for a theory of evolving dynamical systems, which is complementary to traditional evolutionary genetics.

**GERD MÜLLER** (*UNIVERSITY OF VIENNA/THE KLI INSTITUTE, KLOSTERNEUBURG*)

### Introduction to Evo-devo and the Extended Synthesis in Evolutionary Theory

This unit will provide an overview of the conceptual background of evolutionary developmental biology, highlighting how new concepts, such as developmental constraint, facilitated variation, epigenetic innovation, or dynamical patterning, in concert with advances in other domains, contribute to an extended theoretical framework of evolutionary biology.

**RONALD JENNER** (*NATURAL HISTORY MUSEUM, LONDON*)

### The role of phylogenetics in evo-devo

Evo-devo is a fundamentally comparative discipline. Hence, phylogenetic data, methods and hypotheses are an integral part of most evo-devo research. My lecture will introduce you to important concepts that any end user of phylogenetic trees needs in order to judge their merit as interpretative frameworks. The afternoon lecture and practical exercise then provide the opportunity to apply phylogenetic methods yourself, and conduct a molecular phylogenetic analysis. The aim is to empower those who have little or no experience in phylogenetics to apply this to their own hard-won data.

13.30–16.30

### Phylogenetics Practical (Jenner)

16.30–dinner time

### (Voluntary) Poster Session for Participants

## Tuesday, September 29<sup>th</sup> — Regulatory Evolution

9.00–12.30

**ANDREW PEEL** (*UNIVERSITY OF LEEDS*)

### Developmental Dynamics and Evo-Devo

The same developmental genes are often involved in the formation of similar morphological traits in distantly related animals. This has led some to argue that these traits are homologous; i.e. shared due to their inheritance from an ancient, and perhaps surprisingly complex, common ancestor. However, homology at lower levels of biological complexity (e.g. genes/gene networks) is not necessary for, nor always sufficient to prove, homology at overlying levels of biological complexity (e.g. cellular morphology). For example, there has been significant divergence in the developmental mechanisms controlling the formation of homologous body segments in arthropods. Conversely, it seems likely that homologous genes, and perhaps even homologous gene networks, pattern non-homologous body segments in arthropods and vertebrates. Studies on the evolution of animal segmentation mechanisms provide increasingly detailed examples of how homology can become 'decoupled' at different levels of biological complexity. I will outline three questions that these complex data, and their interpretation, raise: 1) Is the concept of homology still useful? Or can we establish a more sophisticated intellectual framework within which to debate the origin and evolution of animal body plans? 2) By comparing development in an increasing, but still finite, number of extant animals, will we be able to reconstruct the body plans of long extinct ancestors? 3) What are the 'Principles of Evolutionary Developmental Biology' that will fill future textbooks?

**DAVID E. K. FERRIER** (*UNIVERSITY OF ST ANDREWS*)

### Homeobox Gene Clusters and the Interplay Between Genome Organization & Evo-Devo

The rejuvenation of modern evo-devo in large part stemmed from the discovery of the homeobox and the revolution of being able to compare the development of different species on a molecular basis. The Hox gene cluster, which is composed of some of the best-known homeobox genes, has been the focus and stimulus for much evo-devo research. It is now known to have evolved within the context of further homeobox gene clusters: Hox, ParaHox, NK, SuperHox and Mega-homeobox clusters. We will discuss what this wider context of homeobox gene organization can tell us about evo-devo. Why is there so much diversity in homeobox gene clustering across lineages and what are the constraints or biases acting on development and genome organization, if any? Is the phenomenon of Colinearity real or not? Are all genomes equal in their evolutionary behavior, and if not then what does this tell us about the evolution of development across the animal kingdom?

**ALISTAIR MCGREGOR** (*OXFORD BROOKES UNIVERSITY*)

### Evo-Devo & Evolutionary Genetics

'Micro-evo-devo' brings a developmental and phenotypic focus to population genetics on one hand, and population/quantitative genetic approaches to development and morphology on the other. It addresses how genotypic variation changes developmental programs to give rise to phenotypic differences, and describes the evolutionary forces involved. Its potential has long been recognized. However, the relative dearth of micro-evo-devo studies may risk pushing evo-devo to the periphery of the larger field of evolutionary biology. In my lecture, I will restate the case for micro-evo-devo and then explore how this synthesis helps to address three outstanding questions vital to understanding the evolution and development of organisms: (1) What is the contribution of standing genetic variation to species differences? (2) What is the genetic basis of changes in complex quantitative traits? (3) What evolutionary forces have shaped phenotypic diversification?

13:30–16:30

**Journal Club (in small groups, moderated by teachers)**

## Wednesday, September 30<sup>th</sup> — Systems, Models & Fossils

9.00–12.30

**YOGI JÄGER** (CENTRE FOR GENOMIC REGULATION, BARCELONA/WISSENSCHAFTSKOLLEG ZU BERLIN)

### Biological Structuralism/Evolutionary Systems Biology/Dynamical Modelling

In this one-hour-long lecture, I will attempt the impossible task of introducing biological structuralism, evolutionary systems biology, and dynamical modelling; or at least their three principal questions: (1) How do developmental regulatory systems evolve? (2) How does the regulatory structure of biological systems in turn affect the rate and direction of evolutionary change (evolvability)? (3) And what kind of methods and concepts do you need to even start investigating this incredibly complex feedback between development and evolution?

**GIUSEPPE FUSCO** (UNIVERSITY OF PADOVA)

### Models and Descriptions in Evo-Devo

The way we conceptualise, describe, and represent objects (or phenomena) strongly affects the questions we ask and thus the answers we get. We will explore this subject in the context of evo-devo. Most models of morphological traits are based on suitable “geometric” variables (e.g. size and shape), but completely disregard the “biological” variables relevant for the (developmental) generation of biological form. One example of this is provided by classical algorithmic models of mollusc shell shapes, which are useful for exploring the “morphospace” of these forms, but cannot capture variation in the way molluscs build their shell. As a general rule, a descriptive model for a given form cannot be used to address questions about the underlying generative processes, either in development or in evolution, and evo-devo approaches must consider parameters of a generative “morphogenetic space” to explore evolutionary change. My lecture will not focus on any particular technique, but instead will highlight and discuss the necessity of developing an effective critical attitude toward descriptions, in their dialectic relationship with model construction and interpretation.

**GRAHAM BUDD** (UNIVERSITY OF UPPSALA)

### Constraining the Unconstrainable? Fossils and the Phenotype-Genotype Map

All evolutionary change took place in the extinct stem groups to living taxa and as a result must remain partly shrouded in mystery. Given that one of the principal results of the field of evo-devo has been to emphasise the complexity of the genotype-phenotype map, it follows that even if we can recover the routes *phenotypic* evolution has taken, to unearth the true correlative *genotypic* evolution will likely be highly problematic. This uncomfortable feature has led to a tendency in the literature to equate the (observed) results of genotypic evolution with the mechanism of the genotypic change driving (observed) phenotypic change – a move that I shall argue is invalid. If we are really to determine the patterns of causal evolution, we will need to know (1) how far we can reconstruct the pattern of phenotypic change in the past (with the fossil record); (2) to what extent there is true freedom in the genotype-phenotype map within such phenotypic variation; and (3) if there are experimental ways of addressing what this freedom might consist of. I shall attempt to address each of these broad questions in turn without promising a solution to their most intractable aspects.

13.30–dinner time

### Preparation of Project Presentations

## Thursday, October 1<sup>st</sup> — Eco-Evo-Devo

9.00–11.00

**CHRISTEN MIRTH** (*INSTITUTO GULBENKIAN DE CIENCIA, OEIRAS*)

### **Phenotypic Plasticity and the Evolution of Polyphenisms**

The environment moulds the development of virtually every organism. Sometimes differences in the rearing environment result in dramatically different phenotypes, or polyphenisms, from the same genotypes. A common example of this is nutritional differences giving rise to queen versus worker bees. Nevertheless, we understand very little about how these traits are regulated and how they evolve. Further, the role of phenotypic plasticity in evolution has been undervalued. In this module, we will explore three unanswered questions: (1) What are the mechanisms underlying phenotypic plasticity? (2) How do polyphenisms evolve? (3) How does plasticity contribute to the diversification of species?

**ABDOU KHILA** (*INSTITUT DE GÉNOMIQUE FONCTIONNELLE DE LYON*)

### **Integrating Evo-Devo with Ecology for a better Understanding of Phenotypic Evolution**

Evolutionary developmental biology (evo-devo) has provided invaluable contributions to our understanding of the mechanistic relationship between genotypic and phenotypic change. Similarly, evolutionary ecology has greatly advanced our understanding of the relationship between the phenotype and the environment. To fully understand the evolution of organismal diversity a thorough integration of these two fields is required. In this lecture, we will discuss the challenges that have been hindering such integration. We will then briefly discuss a few case studies showing how the implementation and combination of these approaches can advance our understanding of how the interaction between genotypes, phenotypes, and the environment drives the evolution of distinct morphologies. Finally, we will see how natural models (in this case water striders) can greatly help understand how the emergence of new genetic interactions can shape adaptive phenotypes during development and evolution, and why such phenotypes are favoured by natural selection.

11.30–12.30

### **Final Preparation of Project Presentations**

13.30–16.30

### **Project Presentations**

16.30–18.30

### **Closing Discussion**