

# Program

## September 19th

8.30-12.30

**GERD B. MÜLLER** (*UNIVERSITY OF VIENNA AND KONRAD LORENZ INSTITUTE*)

### **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*)

### **Tree-thinking: from character evolution to model organism choice**

This unit will explain the central importance of phylogenetics for evo-devo. I will pay specific attention to the practical application of phylogenetic data and methods in modern evo-devo research. I will assume a basic familiarity with the central concepts of phylogenetics. Some of the topics covered are the relationship between gene and species trees, methods of ancestral state reconstruction, the challenges of phylogenomics, molecular clock estimates of divergence times, and the use of phylogenies in informing the choice of model organisms.

13.30-16.30

### **Practical exercise in tree-building, preparation of journal clubs**

## September 20th

8.30-12.30

**ANDREAS HEJNOL** (*SARS INTL. CENTER FOR MARINE MOLECULAR BIOLOGY, BERGEN*)

### **Comparative developmental biology and the evolution of animal organ systems**

Studying the development of a broad range of animals yields insights into the evolution of animal organ systems such as the nervous system, digestive tract, sensory and excretory organs. The application of advanced methods to study development at the morphological and molecular level is reviving the study of embryology in a broad range of animal taxa. Examples from different taxa and different organ systems will be used to explain the principles of this comparative approach, illustrating the importance of a phylogenetic framework and broad taxon sampling.

**GRAHAM BUDD** (*UNIVERSITY OF UPPSALA*)

### **Origin and evolution of morphological characters**

One of the most poorly explored aspects of evolutionary theory is the extent to which constraints generated within phenotypical complexes play a directive role in the evolution of the phenotype-genotype system. An overly atomistic view of the genotype-phenotype map would suggest that the phenotype is essentially at the mercy of genotypic change. Known cases of phenotypic transformation, however, suggest that evolution of either cannot be considered properly without reference to the other. Routes to a truly system-based approach to organismal evolution will be discussed, and an outline of the sort of experiments that might be interesting to perform to test it will be discussed. The significance of such an approach in bringing together classical but estranged aspects of evolutionary theory will also be touched on.

13.30-16.30

### **Journal Clubs (in small groups, moderated by teachers)**

## September 21st

8.30-12.30

**PATRICIA BELDADE** (*GULBENKIAN INSTITUTE, LISBON*)

### **Cis-regulatory evolution and pattern formation**

I will focus on the genetic basis of variation and diversification, with emphasis on cis-regulatory evolution. Heritable phenotypic variation is the raw material of evolution by natural selection, and understanding its generation is a crucial issue in contemporary evolutionary biology. What are the specific sequences (e.g. regulatory versus coding) that contribute to evolutionarily relevant variation? In what way do these affect development to generate different phenotypes? What is the relationship between the genes that contribute to large-effect versus subtle-effect variation, and to intra-specific variation versus inter-specific differences in phenotype? I will use both classical examples and the very recent literature to illustrate key principles and current ideas on the genetic basis of variation and diversity.

**JOHANNES JAEGER** (*CENTER FOR GENOMIC REGULATION – CRG, BARCELONA*)

### **The evolution of developmental gene regulatory networks**

We will discuss qualitative and quantitative approaches to the comparative study of developmental gene regulatory networks. Qualitative methods such as comparative description of gene expression patterns and methods of functional perturbation (such as RNAi) have yielded many important and intriguing insights into the evolutionary conservation or divergence of gene regulation. However, both of these methods are limited in their ability to keep track of the numerous interactions that constitute evolving gene networks. We illustrate how quantitative measurements of gene expression combined with mathematical modelling can transcend these limitations and yield a more integrated view of the evolution of development.

13.30-16.30

### **Exercise in evolutionary simulation, preparation of group projects.**

## September 22nd

8.30-12.30

**STUART A. NEWMAN** (*NEW YORK MEDICAL COLLEGE*)

### **The role of physics in the origination and development of biological form**

The clusters of cells leading to the first complex multicellular animals were subject to a characteristic set of physical determinants that pertain to all chemically and mechanically active matter. Understanding the physical forces, processes and effects that acted on these pre-metazoan organisms helps explain why animals are built the way they are. In particular, the morphological motifs of animal body plans and organs: multilayered, hollow, elongated, segmented, involuted and appendaged tissue masses, are predictable outcomes of the physics of 'mesoscale' materials. These physical effects were mobilized by ancient gene products, the developmental-genetic 'toolkit,' that first arose in unicellular lineages. A comparative review of developmental mechanisms will show that 'dynamical patterning modules' (DPMs), consisting of toolkit molecules and the physical processes they mobilize, remain conserved determinants of embryogenesis in modern animals. The ability of the DPM framework to resolve long-standing problems in evolutionary and developmental biology such as the causes of macroevolutionary change, the nature of morphogenetic fields and the basis of the phylogenetic developmental pattern known as the 'embryonic hourglass', will be discussed.

**CHRISTIAN BRAENDLE** (*CNRS AND UNIVERSITY OF NICE – SOPHIA ANTIPOLIS*)

### **Environment, evolution and the genotype-phenotype map**

Understanding how a genotype translates into a phenotype is one of the most central challenges in biology. Phenotypes can rarely be simply inferred from their underlying genotypes, and vice versa, because the mapping of genotypes into phenotypes is usually a non-linear process, shaped by highly complex genetic and environmental interactions. A single genotype may also generate multiple phenotypes, and conversely, multiple genotypes may generate the same phenotype. That such properties of the genotype-phenotype map are relevant for our understanding of the evolutionary process has been emphasized for a long time. It is, however, only relatively recently that the causal relationships between genotype and phenotype have received increased attention from evolutionary biologists. My lectures will focus on how environmental variation modulates the translation of genotype into phenotype by studying how developmental systems respond to ecologically relevant environmental variation, how such responses evolve, and in turn, what evolutionary consequences they may have. I will emphasize quantitative developmental genetic approaches making use of model organisms and natural genetic variation within and among closely related species. In particular, I will focus on the two fundamental developmental responses to the environment: phenotypic plasticity versus phenotypic robustness.

13.30-16.30

### **'Grant Panel' review and discussions of projects.**