SECTION 11 THEORETICAL BIOLOGY

Section Leader P. Haccou

GENERAL INTRODUCTION

The section organises its activities around the grand unifying theory of biology: Darwinism. Organisms differ from the entities of physics and chemistry by the fact that they reproduce. That they do so only almost faithfully is the main cause of their present day diversity and complexity. Moreover, they are composed from parts in a hierarchical manner, leading to a combinatorial explosion of possibilities: the space of possible organisms is huge, and existing organisms occupy a nearly empty subset of this space. To understand its population, it is necessary to integrate studies of the principles by which organisms are built (development), their inner workings (function and so-called internal selection), the workings of the selective arena (population and community ecology), and the history of their descent (phylogeny). The section provides a single home for the IBL theoreticians active in these areas, thus creating a platform for the cross-fertilisation of disciplines, as well as of techniques, be they statistical, computational, or mathematical. Moreover, their independent affiliation allows the members of the section a great diversity of collaboration with the empirically oriented sections of the IBL, or outside the IBL if theoretical developments so demand. Historically, the section concentrated mainly on the phenotypic level, a strategy justified by the contorted and (in certain aspects) weak link between the genotypic and the phenotypic levels, and the apparent domination of the selective regime in determining many features of great biological interest, as corroborated by the predictive power of the theory. The theories of physiologically structured populations and of adaptive dynamics are internationally recognised successes. In more recent years the interface towards the genetic level is attracting more attention, with i.a. activities in the area of evo-devo and RNA function.

Research themes:

1. Bio-Informatics and Self-Organising Systems
2. Innovations and Constraints in Evolution
3. Ecological Dynamics and ESS Theory
4. Adaptive Dynamics

1. Bio-Informatics and Self-Organising Systems (dr. A.P. Gultyaev)

This project aims to contribute to the field of Bio-informatics by data-mining and the simulation of complex systems, and to the theory of self-organising complex systems. In the theme there is a distinct accent on intracellular processes, in particular those relating to the secondary and tertiary structure of RNA in relation to its function and evolution.

In 2007, structure-function relationships and evolution of RNA molecules in various biological systems have been further analyzed. In particular:

A systematic analysis of conseved RNA structures encoded in the influenza genome is launched. Preliminary results show that the folding of virus RNA is an important factor in influenza adaptation and host range. Evolutionary constraints imposed by RNA folding were traced in host-specific covariations of paired nucleotides in conserved structures predicted for two segments of the influenza genome. Two transitions, determined by the covariations, are suggested to occur in the subtype H2N2/H3N2 lineage of human influenza strains after 1957 pandemic. The specific basepairs are inherited and remarkably stable in currently circulating human H3N2 strains, distinguishing this lineage from both all avian influenza A viruses and human H1N1 strains.

Structure-function relationships in the enod40 RNA, a noncoding plant RNA involved in cell development and symbiotic interactions with bacteria or fungi, have been further investigated. A study of evolution of enod40 RNA structural motifs has become possible after multiple enod40 homologues have been detected in various plant families (Gultyaev & Roussis, 2007). Furthermore, comparative analysis of RNA-binding proteins interacting with enod40 RNA reveals protein domains and amino acid residues involved in protein-RNA recognition. A striking similarity of plant enod40-binding proteins to some metazoan RNA-binding proteins, revealed in this study, will be further investigated.

2. Innovations and Constraints in Evolution (dr. F. Galis, Prof. dr. J.A.J. Metz)

This project focuses on innovations and mechanisms that facilitate evolutionary changes at the organismal level, in particular the constraining effects of internal selection, i.e., selection caused by characteristics of the developmental system. The main focus is on the conservation of the early organogenesis stage and on the conservation of adult traits that are determined during that stage (i.e., the number of cervical vertebrae in mammals and the number of digits in tetrapods), with the goal of understanding the interplay between genetic architecture, developmental mechanisms and stabilising selection.

A first subproject on Evo-Devo largely concentrates on the role of internal selection as a conserving evolutionary force. A collaborative experimental program is going on with the Pathology department of the VUMC (Free University Medical Center). A central question in understanding biological diversity is how developmental pathways constrain evolution: the fundamental constancy of gene networks and developmental mechanisms underlying body plans is poorly understood. Such understanding is essential i.a. to determine how data obtained from model organisms generalize. Because many adult traits are determined during early organogenesis, early developmental events have a persisting influence. In this project we focus on how such projected effects constrain the power of natural selection in shaping adaptive evolution. Our working hypothesis is that strong integration between the patterning of the embryonic axes is the root cause of the conservation of body plans. Due to this integration, positive mutational changes of some character cause that many negative pleiotropic effects (abnormalities) elsewhere that they are nearly excluded (so-called internal selection).

In 2007 we have continued our collaboration with the Pathology department of the VUmc (Free University Medical Center), in particular with Dr. Liliane Wijnaendts. We have continued our study on the incidence of an abnormal number of cervical vertebrae in fetuses and infants that died in hospital. Variations of the number of cervical vertebrae indicate a disturbance of the early organogenesis stage. Our study shows that such disturbances lead to multiple, mainly negative, effects and that cervical ribs are reliable indicators of medical risks. Our study further shows that the multiple effects are the result of the extremely strong interactivity of morphogenetic and patterning processes during the early patterning of the embryonic axes. As a result, mutations with an effect on this stage almost always have many negative side-effects (pleiotropic effects). These side-effects constrain evolutionary change (pleiotropic constraints to evolutionary change). In 2007 we have investigated the importance of relaxed selection for the breaking of such pleiotropic constraints in evoluiton. We have shown how such breaking of constraints can occur under relaxed selection regimes and how this can lead to evolutionary novelties. We have published an article on this in Integrative and Comparative Biology.

We have started a collaboration with Prof. Stefan van Dongen from Antwerp University. In this study we are investigating whether fluctuating asymmetry (random differences between left and right, as opposed to the deliberate natural asymmetry in animals) is a good indicator of developmental instability. Research in the area of fluctuating asymmetry has been disappointing and it has been hypothesized that this is due to the fact that individuals with the largest asymmetry die early and are not part of investigations on fluctuating asymmetry. To test this hypothesis we are investigating the relationship between fluctuating asymmetry and the presence or absence of congenital abnormalities in human individuals that died early (the fetuses and infants that died in the VUmc hospital mentioned above).

In 2007 we have also continued research in collaboration with Dr. E. Teske, veterinary oncologist at the University of Utrecht. In this collaboration we study variations in the number of digits and cervical vertebrae in dogs. Such variations, in particular variations in the number of digits, are much more common in dogs than in humans. Dogs, therefore provide us with a better study system to find out more about associations between these variations and associated medical risks, in particular cancer. Our results suggest that variations of traits that are highly conserved (e.g. the number of digits and cervical vertebrae in mammals) provide more of a medical risk than traits that are less highly conserved (the number of teeth and mammae). We will continue this line of research.

3. Ecological Dynamics and ESS Theory (dr. P. Haccou, Prof. dr. J.A.J.Metz)

This project considers the population dynamics of single species as well as processes involving the interaction between several species on ecological time scales. In one direction novel mathematical tools are developed for the translation from complex individual level causes to population dynamical consequences. In the opposite direction the ESS route allows the prediction, based on their population dynamical consequences, of properties of individuals. In addition statistical methods are developed for analysing ecological data as well as data on individuals, in a manner useful for evolutionary theorising.

We received a grant from the Dutch government to study introgression of modified genes through hybridization between cultivars and their wild relatives in collaboration with the section plant ecology and the Centre of environmental sciences, Leiden University. The theoretical part of the study focuses on deriving introgression hazard rates based on generalized branching process models, under different eological and agricultural scenarios.

We were invited by Evolutionary Ecology Research to submit a manuscript (cited about 20 times on the basis of a pre-print on the IIASA web-site) about necessary and sufficient conditions for evolution to optimise, this manuscript has been retyped and updated. On the suggestion of the referees the paper will be split into two to bring out its separate messages a little more sharply.

In collaboration with dr. I. Oliveiri (Montpellier, France) we developed a model for haplodiploid sex allocation when there is uncertainty about egg and sperm supplies. We are now studying the ESS strategy in relation to reliability of cues about the realized supply. Furthermore, we study the ESS sex allocation in haplodiploids with partial sibmating, when a proportion of the females is unmated.

In collaboration with dr. I. Oliveiri (Montpellier, France) and X. Martini (Toulouse, France) we developed a model to study the evolution of larval feromones in relation to cannibalism in ladybugs.

In collaboration with dr. Y. Iwasa (Fukuoka, Japan) we examinethe evolution of epigenetic inheritance in relation to environmental stress in fluctuating environments, in relation to cue reliability.

In collaboration with U. Hogsbro Thygessen and J. Beyer (Kopenhagen, Denmark) we developed a foraging model to study optimal habitat switching in uncertain environments, by predatory fish.

4. Adaptive Dynamics (Prof. dr. J.A.J. Metz, dr. P. Haccou)

This project considers evolutionary time-scales and the species level as well as between-species interaction. The aim here is the construction of an overarching theory of phenotypic evolution, as a direct dynamical extension of the evolutionary statics of ESS theory. This theory also deals with co-evolution and with the treelike structure of character evolution through adaptive speciation.

In the canonical equation of adaptive dynamics, which tells how traits change over evolutionary time as a consequence of the relatively scarce production of new favourable mutations which then undergo selection in the environment produced by the current community, appears a scalar term, consisting of a product of ratios of various life history statistics times the size of the population that produces the mutants, that might be called the effective population size for adaptive evolution. It was proved that for all possible ecological scenarios this effective size is equal to another, time honoured, effective size that crops up in the theory of random genetic drift. In other words, if one wishes to study random drift for some model ecology or chooses to study the adaptive evolution of some mechanistic parameters for it, one ends up calculating the same effective size as a speed parameter. Technically this coincidence is useful as it allows exchanging formulas (and techniques for deriving such formulas) between two rather disparate areas of research. There is also a more practical consequence. Random drift forms the background model for many statistical inference methods for molecular evolution despite some obvious shortcomings, one of which is that the observed variances tend to be way above the theoretically predicted ones. A consensus is appearing that the main cause of the latter shortcoming is that neutral genetic variation hitchhikes with adaptively substituting genes, a process dubbed genetic draft. The result about the equality of the effective sizes tells that under reasonable provisos genetic drift and draft have proportional speeds. Hence, even though the standard background model may be basically wrong, a fair fraction of the results based on assuming that model may still be relatively trustworthy.

The process of evolutionary branching from a k-morphism to a (k+1)-morphism has been studied, for the case of an adaptive dynamics with an underlying Lotka-Volterra community dynamics. Necessary conditions for the occurrence of branching have been derived, as well as a geometric representation of these conditions.

PERSONNEL

Prof. Dr. J.A.J. (Hans) Metz	Professor UL (0-appointment)
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Dr. A.P. (Sacha) Gultyaev	Assistant Professor UL
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GRANTS

- NWO: Simulation and Analysis of Complex Histories of Evolution (SACHE). Exchange program with the Limnological Institute, Siberian Branch of the Russian Academy of Sciences, Irkutsk, funded by the Russian Foundation for Basic Research, on speciation in Lake Baikal. 1/4/2004-1/4/2007. Total amount: € 115,000.
- NWO + minsteries VROM, EZ, LNV & OCW: Quantifying introgression risks of transgenes with hazard rates, using carrot as a model species. 1/11/2007 - 1/5/2012. In collaboration with CML and section plant ecology IBL. Total amount: € 778,795
- EU FP7 collabotorive project: Effect of natural viral RNA sequence variation on influenza virus RNA function. 1/1/2008-1/1/2010. € 235,000

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Wajnberg, E. & Haccou, P. 2007 Statistical tools for a sound behavioural ecology of insect parasitoids. In: E. Wajnberg, C. Bernstein, J.J.M. van Alphen (eds) Behavioural Ecology of Insect Parasitoids: From Theoretical Approaches to Field Applications. Blackwell Publishing Ltd.

Yokomizo, H., Haccou, P., Iwasa, Y. 2007 Optimal conservation strategy in fluctuating environments with species interactions: resource-enhancement of the native species versus extermination of the alien species. Journal of Theoretical Biology 244:46-58