Titles and Abstracts

Jonathan Birch
Propositional content in signalling systems

What is propositional content, and when is it reasonable to ascribe propositional content to a signal? These questions are of profound importance to philosophy, biology and the behavioural sciences, yet they are notoriously recalcitrant to naturalistic answers. Recently, Brian Skyrms (2010) has suggested that the propositional content of a signal is determined by its informational content, where the latter is a formal measure of the way in which the signal shifts the probabilities of states of the world. Peter Godfrey-Smith (2013) raises a serious problem for this proposal: if Skyrms is correct, then it is impossible for any signal to carry false propositional content. In this paper, I present and defend an amended version of Skyrms's account that solves this problem. In broad terms, my suggestion is that the propositional content of a signal is determined not by its actual informational content, but rather by the informational content that it would carry at the nearest separating equilibrium of the underlying evolutionary dynamics. Using Maynard Smith's Philip Sidney game as an illustrative case, I show that this amended account allows for ascriptions of false propositional content to signals. I further show that the amended account has an interesting by-product: it allows propositional content to be ascribed to signals much more liberally than Skyrms's original account.

Frédéric Bouchard
How Research on Symbiosis Should Transform Our Understanding of Adaptation

Evolutionary Biology has mostly relied on a 'Modern Synthesis' theoretical foundation that has not changed much since it was proposed by population geneticists and other biologists in the first half of the 20th Century. For most evolutionary biologists, intergenerational change was mediated almost exclusively through genetic change between generations. Various research projects aimed at weakening that assumption by showing how non-genetic inheritance played a non-trivial role in trait formation and transmission: this gave rise to various attempts to enrich, transform or even supplant the 'Modern Synthesis' that played such a key role in our understanding of evolutionary processes. Be it Developmental System Theory, or some epigenetics research programme, niche construction, or even evo-devo to some extent, the centrality of intergenerational genetic change to our understanding of adaptation has been relativized. But all those projects still focus on species or biological systems with relatively homogenous lineages. What has not been fully appreciated is how much symbiosis (especially at the microbiological level) shows the limitations of any attempt to reduce the process of adaptation to within lineage change. Symbionts are in many respects modular traits that can be passed on vertically or horizontally in ways that clearly affect the evolutionary success of the communities they are involved in. Symbiosis has a process of generating new cohesive biological units (new evolutionary individuals) shows the limitation of focusing the study of adaptation exclusively on continuous cohesive genetic units of same species organisms. Inspired by John Dupré an O'Malley's work on the philosophy of microbiology and systems biology, we will see how the common functional history becomes more useful than common genetic history to assess the evolution of many of complex biological systems.

Andrew Buskell
Culture Shock: Information, Representation, and Competition

Philosophers should be puzzled by some of the claims made by contemporary exponents of cultural evolution. For instance, we are told that "[by] information we mean any kind of mental state, conscious or not" (Richerson and Boyd,

2005, p. 5). Richerson and Boyd also say that "[culture] is (mostly) information stored in human brains … transmitted from brain to brain by way of a variety of social learning processes" (Richerson & Boyd p. 61). The 'mostly' in the second quotation seems to go against the implication of the first, namely that informational states must be brain states. Is it possible that they are trying to make room for the notion that some mental states might not be realised in the brain? This issue is further complicated by characterisations of cultural 'competition'. Mesoudi and his co-writers suggest that "an appropriate way to conceptualize what any set of cultural variations are in general competing over is in terms of functional categori es" (Mesoudi et al. 2004 p.4), but then immediately suggest that this can be understood as a Malthusian struggle for neuronal resources (Mesoudi et al. 2004). Do they believe that really think that packets of cultural information 'compete' neuronally? What does this claim amount to? Finally, it's not straightforwardly clear that these claims about brain states can be squared with their own desiderata to account for external warehouses of cultural information. For example, "culturally transmitted information is stored in … extrasomatic codes such as written language, binary computer code, and musical notation." (Mesoudi 2011 p. 3) or perhaps more impressionistically, "the architecture of the church may help store information about the rituals performed within." (Richerson & Boyd p. 61). I will suggest that these three topics, despite offering a range of seemingly contradictory statements, can be made to cooperate. Doing so will ground the cultural evolutionists appropriation of information, show how competition in the cultural transmission pathway might illuminate how to demarcate it from the genetic or epigenetic pathway, and help determine what is the right way to think about external sources of cultural information.

Evan Charney
Behavior Genetics and Postgenomics

The science of genetics is undergoing a paradigm shift. Recent discoveries, including the activity of retrotransposons, the extent of copy number variations, somatic and chromosomal mosaicism, the nature of the epigenome as a regulator of DNA expressivity, and the prevalence of alternative splicing, are challenging a series of dogmas concerning the nature of the genome and the relationship between genotype and phenotype. According to four widely held dogmas, DNA is the unchanging template of heredity, is identical in all the cells and tissues of the body, is the sole agent of inheritance, and every protein in the human body is coded for by a particular gene. Rather than being an unchanging template, DNA appears subject to a good deal of environmentally induced change. Instead of identical DNA in all the cells of the body, somatic mosaicism appears to be the normal human condition. DNA can no longer be considered the sole agent of inheritance. We now know that the epigenome, which regulates gene expressivity, can be inherited via the germline. And given that the human body contains anywhere from 100,000 – 1 million proteins but only 25,000-30,000 genes, and that alternative splicing occurs in 90% of all genes, every protein is not coded for by a particular gene.

These developments are particularly significant for behavior genetics for at least three reasons: First, epigenetic regulation, DNA variability, and somatic mosaicism appear to be particularly prevalent in the human brain and probably are involved in much of human behavior; second, they have important implications for the validity of heritability and gene association studies, the methodologies that largely define the discipline of behavior genetics; and third, they appear to play a critical role in development during the perinatal period and, in particular, in enabling phenotypic plasticity in offspring. I examine one of the central claims to emerge from the use of heritability studies in the behavioral sciences, the principle of minimal shared maternal effects, in light of the growing awareness that the maternal perinatal environment is a critical venue for the exercise of adaptive phenotypic plasticity. This consideration has important implications for both developmental and evolutionary biology.

David R. Crawford
Information Transmission and Entropy in Fisher's Genetical Theory

Fisher's treatment of genetics and organism-environment adaptation provides a platform for examining how a population can be said to gain information about its environment over generational time. Adaptation consists in successive rounds of survival and reproduction: viability and fecundity selection result in population-level 'learning' about the environment; reproductive dynamics constitute the transmission of this information from parent to offspring generation. We can quantify Fisher's notion of adaptation as "conformity in many particulars between two complex entities" (between population gene frequencies and environmental factors) in terms of Shannon entropy such that the informational capacity of a gene pool in a given environment is constrained by locus number and polymorphism, and a normalized form of Fisher's genetic variance in fitness measure. In a similar vein, the accuracy of learning is constrained by the Boltzmann entropy of organism-environment interactions and the accuracy of transmission is constrained by the Boltzmann entropy of reproductive dynamics. This analysis yields three conclusions: first, a population gains environmental information only in the retrospective sense that organisms have adapted to a particular environment -- information does not accumulate past changes in the selective environment; second, population learning is highly sensitive to the dynamics of several stochastic processes; third, this informational analogy for adaptation provides a quantitative framework for experimental use of organisms to gain environmental information (e.g., use of clonal plants to measure soil features).

Antoine C. Dussault
Ecosystem Health: A Normative but Non-Etiological Account of Ecosystem Function

Many ecological scientists and philosophers have expressed skepticism with regard to the scientific appropriateness of the concept of ecosystem health. Their main reason can be stated in the form of a dilemma. According to the critics, as the concept of ecosystem health is normative, either it will be grounded in ethical considerations and therefore fail to be a value-free as science would require; or either it will have to make use of the etiological account of functions, which is known for its ability to generate a naturalized form of normativity, but which would require the implausible postulate that ecosystems are levels of selection.

The goal of my presentation is to combine insights from McLaughlin's (2001) self-reproduction account and Krohs's (2011; 2009) design account of functions in order to open way out of this dilemma. Using resources from these two accounts of functions, I will explain how norms of proper ecosystem functioning can legitimately be grounded in ecologists' empirical investigation on ecosystem dynamics. I will tie this conceptual analysis to Robert Costanza's (1992) index of ecosystem health, defined as the mathematical product of ecosystem vigor, organization and resilience.

Sebastien Dutreuil
A review of the Gaia hypothesis and a discussion of the three kinds of computational models it uses

The Gaïa hypothesis (GH), proposed by Lovelock and Margulis (1973), is typically construed (by philosophy of biology) as a misleading comparison of the Earth with an organism followed by the hype of new-agers; the comparison being misleading since Earth does not reproduce it can not therefore undergo natural selection (Dawkins 1982). If this account is about the current state of GH, it is wrong; if it is about GH as it was 30 years ago it is at best incomplete and conceptually imprecise.

In the first section I will give a general overview of the (scientific) development of the GH that has been undertaken by Earth scientists (and ecologists). This will allow me to clarify the explanan-

dum of the GH (that has nothing to do with the metaphor mentionned above) and to present the empirical discoveries as well as the theoretical propositions of the past 40 years; parallells will be drawn with the development of biology (niche construction, organisms as ecosystem engineers) and philosophy of biology (nature of selection, levels of selection, biological individuality).

In the second section I will narrow down the scope on the models used by GH. I will argue that GH uses three kinds of computational model that differ regarding their target system: (i) "precise models" aim to represent the world as it actually is, (ii) "abstract models" focus on a higher level of description by abstracting away from contingent details about life to explore what may be construed as essential properties of life (similar models are found in the Artificial life tradition), (iii) "what-if" models represent worlds that contradict in relevant respects the actual one. This will allow me first to argue, contra Kirchner, that (ii) and (iii) are legitimate scientific models and, second, to precise the seemingly ambiguous epistemological status of one of the most famous model developed by GH: Daisyworld.

Section 1 and 2 are linked: it is the nature of the questions raised by GH that requires the use of these three kinds ofcomputational models.

Leonore Z. Fleming
The Origin of New Levels of Hierarchy and Why Selection is Not the Answer

The evolutionary transitions literature is pervaded by two main questions: 1) how a new level of hierarchy arises, and 2) how a new level of hierarchy is maintained. Because of the selective framework under which both questions are posed, explanations for the first question usually fall into the realm of the second. In this paper I provide a theory for the first question that is outside of the typical selective framework. I am not concerned with giving adaptive explanations; instead, I focus on the background conditions that allow groups and new levels to form spontaneously such that selective and maintenance ac-

counts can then be applied. I appeal to the Zero Force Evolutionary Law, network theory, and some empirical examples in biology to justify my account.

Michel Morange
Information and Transmission in Epigenetics

My purpose is to question the important, but ambiguous position occupied by epigenetics in extant biological research. For that, I will use the results of the debates about the meaning of " information" in "genetic information." Asking the question "What is epigenetic information?" is a way to distinguish genetics and epigenetics.

Kriti Sharma
Signal Transduction With and Without "Information"

Signal transduction—often defined as the conversion of signals (information) outside of a cell into biochemical changes inside of a cell—may be one of the most straightforward and least controversial uses of "information and transmission" in the biological sciences. Even in this seemingly least problematic of uses, however, I argue that information language may be misplaced, in that it obscures rather than clarifies some of the most intriguing aspects of the phenomenon of interest (namely, organismal sensing and responsiveness). I offer a brief intellectual history of the standard signal transduction concept, highlighting the role of early cybernetic theory in the very inception of an analogy between energy transducers and signal transduction in the cell. I then examine how the standard account both relies on and reinforces at least two dubious assumptions, namely (a) that both energy and information can be described as kinds of intrinsically existent substances that make things happen in the world, and (b) that certain biological processes are "informative" (i.e. whereby the environment remains radically separate from and external to the organism and yet can produce some change in the organism) and others are "assimilative"

(i.e. whereby the environment becomes or constitutes the organism, as in photosynthesis or ingestion). Finally, I offer a view of signal transduction that does not rely on these assumptions of the standard view, and thus provides an account of sensing and responsiveness without relying on a notion of information and transmission or transduction.

Ulrich Stegmann
Information concepts in the life sciences: inferring theoretical roles from actual usage

The nature and legitimacy of information concepts in the life sciences have been under philosophical and historical scrutiny since the 1990s. Many philosophers and historians of biology doubt that they play any substantial theoretical roles. Some philosophers and biologists, on the other hand, have defended the legitimacy of information concepts. I suggest that a common approach to this debate, assessing to what extent standard philosophical theories of information and representation apply, should be supplemented with another approach: paying attention to how information concepts are actually used in the many domains of the life sciences. I argue that considering actual usage in detail can reveal specific theoretical and heuristic roles. In this talk I will present some first results of this approach, focusing on historical and present-day examples of actual usage of information concepts in molecular genetics and animal behavior studies.

Orlin Vakarelov
Information Models for Biology

In recent debates about the role of the concept of information in biology – especially related to the heritability and control function of DNA – the question of whether information has only "metaphorical" use has been important. Some (e.g. Griffiths) have argued that, except for some technical uses of Shannon information theory, such informational descriptions are only metaphors.

At best, they have no explanatory significance; at worst, they propagate dogmas, such as genetic determinism. Others (e.g. Levy) have embraced the "metaphorical" use of information – along fictionalist lines – as having genuine explanatory significance: Metaphor is an important and widespread cognitive devise in the practice of science. Many central and explanatorily important concepts (e.g. energy) are metaphorical.

I will argue that the debate over the metaphorical nature of information – whether informational ascriptions are real or metaphorical and whether it is bad if they are metaphorical – is somewhat misguided. Following a semantic approach to theories, I will argue that the role of information should be analyzed into two questions: (1) What is the informational model used in the description/explanation? (2) How does the model connect to the biological system? Elements of such an approach can be seen in, e.g., Godfrey-Smith. Such an analysis is essential because the "concept" of information, which as an abstract theoretical (but not always technical) concept, enters only through the models. I will focus the discussion primarily on question (1), setting aside the more empirical question (2).

Information, as has been recognized universally, is a heteronomous concept. The reason for this is that it is associated with different models, which are sufficiently related to justify a qualified use of a similar term. I will identify and distinguish a collection of information models that have been (or could be) used in biology (if question (2) is answered favorably – a big if). I will identify a collection of models that are not appropriate for the questions of heritability, morphogenesis and metabolic control, as they enter the realm of the cognitive. Some models are familiar, such as the Shannon communication channel model, the coding-optimization model or the programing-code model. Others have been used implicitly, such as the information medium model and some semantic information models. Other models have seen less use, such as the information medium network model, and structure generation models connected to algorithmic information.

Schedule

Smith Warehouse Garage
Duke University

Friday June 7, 2013

14:00	**Robert Brandon** Welcome and Introduction
14:00-15:30	**Ulrich Stegmann** *"Information Concepts in the Life Sciences: Inferring Theoretical Roles from Actual Usage"*
15:30-15:45	Break
15:45-16:45	**Evan Charney** *"Behavior Genetics and Postgenomics"* Robert Brandon commenter
16:45-17:00	Break
17:00-17:30	**Orlin Vakarelov** *"Information Models for Biology"*
17:30-18:00	**Antoine C. Dussault** *"Ecosystem Health: A Normative but Non-Etiological Account of Ecosystem Function"* (Idea)
18:00-19:00	Reception
19:30	Dinner at Revolution

Saturday 8 June 2013

9:30-10:00	Breakfast
10:00-10:30	**David Crawford** *"Information Transmission and Entropy in Fisher's Genetical Theory"* (Idea)
10:30-11:00	**Kriti Sharma** *"Signal Transduction With and Without 'Information'"* (Idea)
11:00-11:15	Break
11:15-12:15	**Sebastien Dutreuil** *"A review of the Gaia hypothesis and a discussion of the three kinds of comptutational models it uses."* Tyler Curtain commenter
12:15-13:30	Lunch
13:30-14:30	**Leonore Fleming** *"The Origin of New Levels of Hierarchy and Why Selection is Not the Answer"*
14:30-14:45	Break
14:45-15:45	**Jonathan Birch** *"Propositional content in signalling systems"* Francoise Longy commenter
15:45-16:00	Break
16:00-17:00	**Michel Morange** *"Information and Transmission in Epigenetics"*
17:00-17:15	Break
17:15-18:15	**Frédéric Bouchard** *"How Research on Symbiosis Should Transform Our Understanding of Adaptation"*
18:30	Party at Robert Brandon's House

Please contact the organizers with any questions by emailing cm136@duke.edu or using philbio.org/contact