ALTENBERG SEMINARS IN THEORETICAL BIOLOGY

Summer 2007:
Biocomplexity

Hörsaal 1, Biozentrum, Althanstrasse 14, at 6.15 p.m.

The Program at a glance:

15 March 2007
John M. BEGGS (Biocomplexity Institute, Department of Physics,
Indiana University, Bloomington, IN, USA):
"The Criticality Hypothesis: How Local Cortical Networks Might Optimize Information Processing"

26 April 2007
Frank BRUGGEMAN (Manchester Centre for Integrative Systems Biology, Manchester Interdisciplinary Biocentre, and Department of Molecular Cell Physiology, Vrije Universiteit Amsterdam):
"Tracing Life Emergence to Its Molecular Mechanisms and Back"

3 May 2007
Paulien HOGEWEG (Theoretical Biology and Bioinformatics group, Utrecht University, The Netherlands)
"Multilevel Evolution and Biocomplexity"

14 June 2007
Astero PROVATA (Statistical Mechanics and Nonlinear Dynamics Laboratory, Institute of Physical Chemistry, National Center for Scientific Research
“Demokritos,” Athens, Greece)
"Complexity and Correlations in the Primary Structure of DNA"

21 June 2007
Rita R. COLWELL (University of Maryland College Park, Johns Hopkins University Bloomberg School of Public Health, and Canon U. S. Life Sciences, Inc.):
"Global Climate and Human Health: The Cholera Paradigm"

The topic

The relationship between the growth rate (annualized biomass production) and body size of plants is scale-invariant over 20 orders of magnitude in body size. This is true of single-celled algae and aquatic ferns as well as of conifers, including the giant sequoia, and turns out to be indifferent to both habitat and phylogenetic affiliation (NIKLAS and ENQUIST 2001). Outbreaks of cholera in Bangladesh closely track Pacific warming, which is largely associated with El Niño-Southern Oscillation weather patterns (PASCUAL et al. 2000; COLWELL seminar). Long-term weather patterns reflecting global warming affect the distribution of species (for instance, certain nonmigratory butterflies in Europe) across space and time (PARMESAN et al. 1999). (Additional examples of biocomplexity research are discussed in HILBORN et al. 2003 and NICHOLSON et al. 2004.)

Classical science typically minimizes the number of independent variables and interference from "external" factors to keep research tasks manageable and fundable. What distinguishes the aforementioned instances of integrative biocomplexity research from reductionistic science is their relevance for organisms ranging from unicellulars to humans and for environments ranging "from polar regions to volcanic vents to tropical forests to agricultural lands to urban centers" (MICHENER et al. 2001: 1019). Biocomplex interactions tend to span multiple hierarchical levels, with their emergent properties, from genes to the biosphere (COLWELL 1998; COVICH 2000; BRUGGEMAN et al. 2002; DEGUET et al. 2006), and are often reflected in nonlinear, chaotic, and unpredictable behaviors (DYKE 1987; BEGGS and NICOLIS seminars).

The analysis of complex data sets representing physical, chemical, biological, behavioral, and social interactions across many scales of resolution can result in novel predictions that are potentially useful to scientists, resource managers, and policy makers in multiple ways. Biocomplexity research draws on advances in geometry, topology, graph theory, control theory for chaotic systems, and in techniques for modeling uncertainty, and on sophisticated simulation methods, among others. It may require interdisciplinary collaborations among disciplines as disparate as oceanography and epidemiology, using, for instance, remote sensing for the indirect detection of cholera bacteria (LOBITZ et al. 2000; COLWELL seminar).

MICHENER et al. (2001: 1018) define biocomplexity as "properties emerging from the interplay of behavioral, biological, chemical, physical, and social interactions that affect, sustain, or are modified by living organisms, including humans." Viewed this way, biocomplexity research is closely related to computational biology, which has been defined as "the development and application of data-analytical and theoretical methods, mathematical modeling and computational simulation techniques to the study of biological, behavioral, and social systems" (http://www.bisti.nih.gov/).

This Altenberg Seminar will document biocomplexity at work at the levels of the cell (BRUGGEMAN), the brain (BEGGS), and evolving populations in their environmental settings, including host-parasite coevolution (COLWELL, HOGEWEG). These "intra-level" approaches will be complemented by cross-level accounts of the emergence of global structural patterns (including morphogenesis) from the nonlinear interactions between constituent elements (COLWELL, HOGEWEG, and NICOLIS in particular).

John BEGGS, an applied physicist turned neuroscientist, will review experiments on networks of cortical neurons that appear to be operating at the "edge of chaos" (Stuart KAUFFMAN) and argue that criticality may allow cortical networks to optimize information processing.

The experimental and theoretical biologist Frank BRUGGEMAN will illustrate approaches to network analyses (structural models) and analyses of cellular dynamics (kinetic models) for prokaryotic and eukaryotic networks, and discuss principles of network functioning from the perspective of a working systems biologist.
Throughout her career, theoretical biologist Paulien HOGEWEG has used information-theoretic tools to understand biotic systems at many interconnected levels. In the 1970 she identified the study of information processes in biotic systems as an open and promising research area, for which she coined

the term “bioinformatics.” Today, the term is often used more narrowly to refer only to issues dealing with the management of genome project sequencing data, but HOGEWEG’s original usage largely coincides with what the U.S. National Science Foundation in 1999 called “biocomplexity” (cf. MERVIS 1999). She will survey (inter alia) eco-evolutionary models in which local interactions between replicators lead to pattern formations, and discuss how the dynamics of these patterns influence the evolutionary dynamics of the replicators as well as complex regulatory systems and morphogenesis to tackle the basic questions, “How does biocomplexity evolve?” and “How can we model complex biological systems?”

A long-time collaborator of the Nobel Laureate Ilya PRIGOGINE (1917-2003), Grégoire NICOLIS is the foremost representative of the “Brussels School” in thermodynamics. Their preoccupation with complex systems led them to realize that the linear view of the dominant, molecular biology approach to life must be essentially incomplete long before this view became the mantra.[1] NICOLIS will outline a "bottom-up" approach to biological complexity that emphasizes the emergence of global structural and/or behavioral patterns on various levels of description, arising from the nonlinear interactions between the constituent elements and the nonequilibrium constraints underlying biological activity.

To round off the seminar, the distinguished bacteriologist, geneticist, and oceanographer Rita COLWELL, using the case of cholera as a paradigm for global infectious diseases, will show how many such diseases are intricately related to weather patterns, climate, and seasonality. She will discuss how studies that integrate satellite sensing technology, ground truth measurements, and microbiological analyses provide the basis for predictive modeling of cholera epidemics in Middle Asia and East Africa.

The aims of biocomplexity research are not only theoretical but also eminently practical: “It is not enough to explore and chronicle the enormous diversity of the world’s ecosystems. We must do that — but also reach beyond, to discover the complex chemical, biological, and social interactions in our planet’s systems. From these subtle but very sophisticated interactions and interrelationships, we can tease out the principles of sustainability” (COLWELL 1998: 786).

Note

1. Much work in a similar vein is published in the journal ComPleXus: Modeling in Systems Biology, Social, Cognitive and Information Science, edited by Henri ATLAN since 2003.

References

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COLWELL R (1998) Balancing the biocomplexity of the planet’s living systems: A twenty-first century task for science. BioScience 48: 786-87.

COVICH A (2000) Biocomplexity and the future: The need to unite disciplines. BioScience 50: 1035.

DEGUET J, DEMAZEAU Y, MAGNIN L (2006) Elements about the emergence issue: A survey of emergence definitions. ComPlexUs 3: 24-31.

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HILBORN R, QUINN TP, SCHINDLER DE, ROGERS DE (2003) Biocomplexity and fisheries sustainability. Proceedings of the National Academy of Sciences USA 100: 6564-68.

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MICHENER WK, BAERWALD TJ, FIRTH P, PALMER MA, ROSENBERGER JL, SANDLIN EA, ZIMMERMAN H (2001) Defining and unraveling biocomplexity. BioScience 51: 1018-23.

NICHOLSON JK, HOLMES E, LINDON JC, WILSON ID (2004) The challenges of modeling mammalian biocomplexity. Nature Biotechnology 22: 1268-74.

NIKLAS KJ, ENQUIST BJ (2001) Invariant scaling relationships for interspecific plant biomass production rates and body size. Proceedings of the National Academy of Sciences USA 286: 2922-27.

PARMESAN C, RYRHOLM N, STEFANESCU C, HILL JK, THOMAS CD, DESCIMON H, HUNTLEY B, KAILA L, KULLBERG J, TAMMARU T, TENNENT WJ, THOMAS JA, WARREN M (1999) Poleward shifts in geographic ranges of butterfly species associated with regional warming. Nature 399: 579-83.

PASCUAL M, RODÓ X, ELLNER SP, COLWELL R, BOUMA MJ (2000) Cholera dynamics and El Niño-Southern Oscillation. Science 289: 1766-69.

Abstracts and biographical notes

John M. BEGGS
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The Criticality Hypothesis:
How Local Cortical Networks Might Optimize Information Processing

15 March 2007

Abstract

Early theoretical and simulation work independently undertaken by Packard, Langton, and Kauffman suggested that adaptability and computational power would be optimized in systems at the "edge of chaos," at a critical point in a phase transition between total randomness and boring order. This provocative hypothesis has received much attention, but biological experiments supporting it have been relatively few. Here we review recent experiments on networks of cortical neurons, showing that they appear to be operating near the critical point. Simulation studies capture the main features of these data and suggest that criticality may allow cortical networks to optimize information processing. These simulations lead to predictions that could be tested in the near future, possibly providing further experimental evidence for the criticality hypothesis.

Biographical note

John Beggs has been Assistant Professor at Indiana University's Biocomplexity Institute, Department of Physics, since 2003. He studied applied physics at Cornell University (BS, 1985), engineering at Cornell University (M Eng, 1989), and obtained his PhD in behavioral neuroscience from Yale University in 1998. From 1986 to 1988, while in the U.S. Peace Corps, he taught calculus and physics at Samoa College. In 1998-99 he was a postdoctoral fellow in computational neuroscience at Yale.

Selected publications

(submitted) The criticality hypothesis: How local cortical networks might optimize information processing. Philosophical Transactions of the Royal Society A

(submitted) Self-sustaining neural system models: Minimal requirements for a functionally useful system (with D Hsu, A. Tang, and M. Hsu). Neurocomputing.

(submitted) Beggs, J.M., Network connectivity and neuronal dynamics (with W Chen and J Klukas). In: The Handbook of Brain Connectivity (McIntosh R, Jirsa VK, eds). Springer.

(2006) Neuronal avalanches and criticality: A dynamical model for homeostasis (with D Hsu). Neurocomputing 69: 1134-1136.

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Tracing Life Emergence to its Molecular Mechanisms and Back

26 April 2007

Abstract

Organisms resemble very complicated systems. The minimal genome necessary and sufficient for supporting cellular life for one strictly defined growth condition has been estimated to be around 250 genes. To quantitatively describe how such a "minimal" organism functions is already a challenge. Organisms growing in more complicated environments have much larger genomes (E. coli 4377 genes, yeast 5770 genes, man ~25000 genes). At any one given time only a fraction of the total number of genes is expressed and functional. Organisms have developed sophisticated control and regulatory mechanisms to adapt adequately to new changes in environmental conditions. By developing quantitative methods and theoretical concepts and by integrating approaches developed in engineering, analytical chemistry and physics, systems biology is facing this complexity. I will illustrate approaches to network analyses (structural models) and analyses of cellular dynamics (kinetic models) for prokaryotic and eukaryotic networks. I will discuss some of the principles of network functioning that have been discovered. I will also briefly discuss the philosophical foundations of systems biology and how it differs from classical biological disciplines.

Biographical note

Frank J. BRUGGEMAN is a Lecturer in the Systems Biology Group within the Manchester Interdisciplinary Biocentre (School for Chemical Engineering and Analytical Science, Faculty for Physical Sciences, University of Manchester, United Kingdom) and Post-Doc in the Department of Molecular Cell Physiology at the Vrije Universiteit of Amsterdam, The Netherlands. He obtained his doctoral (M. Sc.) in Biology in 1999 at the University of Leiden and his Ph. D. in 2005 at the Vrije Universiteit of Amsterdam. He is interested in the philosophy of biology (complex systems, emergence, reductionism, (mechanistic) explanation, modularity), regulation and adaptation of cellular physiology, and application of (dynamical-systems and control) theory to the (experimental) analysis of cellular phenomena. Dr. BRUGGEMAN has published over 30 scientific papers. He has worked on philosophy (mechanistic explanation and emergence) and systems biology (modular response analysis, modelling of ammonium assimilation in Escherichia coli, MAPK signalling, pH homeostasis in muscle, robustness, phytohormone transport).

Selected publications

(2006) Effects of sequestration on signal transduction cascades (with N BLÜTHGEN, S LEGEWIE, H HERZEL, HV WESTERHOFF, and BN KHOLODENKO). FEBS [Federation of European Biochemical Society] Journal 273: 895-906.

(2005a) From complexity to what really matters: control of MAPK signaling (with JJ HORNBERG , B BINDER, B SCHOEBERL, R HEINRICH, and HV WESTERHOFF). Oncogene 24: 5533-42.

(2005b) The multifarious short-term regulation of ammonia assimilation of Escherichia coli: Dissection using an in silico replica (with BOOGERD FC and WESTERHOFF HV). FEBS Journal 272: 1965-85.

(2005c) Principles behind the multifarious control of signal transduction: ERK phosphorylation and kinase/phosphatase control (with JJ HORNBERG, B BINDER, C GEEST, M BIJ DE VAATE, J LANKELMA, R HEINRICH, and HV WESTERHOFF. FEBS Journal 272: 244-58.

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(2002b) Modular response analysis of cellular regulatory networks (with HV WESTERHOFF, JB HOEK, and BN KHOLODENKO). Journal of Theoretical Biology 218: 507-20.

(2002c) BioComplexity: A pluralist research strategy is necessary for a mechanistic explanation of the "live" state (with HV WESTERHOFF HV and FC BOOGERD). Philosophical Psychology 15: 411-40.

Paulien Hogeweg
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Multilevel Evolution and Biocomplexity

3 May 2007

Abstract

How does biocomplexity evolve? And how can we model complex biological systems? I will discuss modeling approaches that attempt to shed light on both these questions. Central in our approach is to consider local information processing and the multi-scale consequences thereof. I will discuss eco-evolutionary models in which local interactions between replicators lead to pattern formations, and discuss how the dynamics of these patterns influences the evolutionary dynamics of the replicators. Second, I will discuss genome evolution models and (the evolution of) complex genotype-phenotype mapping, in particular complex regulatory systems and morphogenesis. I will address the question when "individual based complexity" or "population (eco-system) based complexity" evolves. Throughout I will focus on “side-effects” and their evolutionary consequences.

Biographical note

Paulien HOGEWEG is the Director of the Theoretical Biology and Bioinformatics Group at Utrecht University. The aim of her research is to understand biotic systems as dynamic information-processing systems at many interconnected levels. In the 1970 she identified the study of information processes in biotic systems as an open and promising research area, for which she coined the term “bioinformatics.” She has explored this area ever since and developed the required new methodology and methods for both bioinformatic pattern analysis and bioinformatic modeling. The research of her group has covered many areas from sequence analysis and RNA evolution to morphogenesis, eco-evolutionary processes (including host-parasite coevolution), and behavior. Her research newly focuses on “adaptive genomics” in which she combines static (pattern analysis of genomic data) and dynamic (multi-level modeling) bioinformatics approaches to study the interface between gene regulation and evolution in uni- and multicellular organisms. Her experience with both static and dynamic bioinformatics is rather unique and gives exciting opportunities to convert the flood of genomic data into theory.

Selected publications

(2006) Feed-forward loop circuits as a side effect of genome evolution (with OX CORDERO). Molecular Biology and Evolution 23: 1931-36.

(2005) Interlocking of selforganization and evolution. In: Selforganization and Evolution of Social Systems (HEMELRIJK CK, ed), 166-89. Cambridge UP.

(2003a) Computing an organism: On the interface between informatic and dynamic processes. Biosystems 64: 97-109.

(2003b) Multilevel selection in models of prebiotic evolution: Compartments and spatial self-organization (with N. TAKEUCHI). Origins of Life and Evolution of the Biosphere 33: 375-403.

(2001) How amoeboids self-organize into a fruiting body: Multicellular coordination in Dictyostelium discoideum (with AFM MAREE). Proceedings of the National Academy of Sciences USA 98: 3879-83.

(2000) Evolving mechanisms of morphogenesis: On the interplay between differential adhesion and cell differentiation. Journal of Theoretical Biology 203: 317-33.

Astero PROVATA
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Complexity and Correlations in the Primary Structure of DNA

Thursday 14 June

Abstract

The complexity in the structure of DNA, even at the primary level, has been the subject of numerous investigations during the past decade. With the recent advances of the various genomic projects we are now able not only to know the exact DNA sequences of whole chromosomes but also the precise location of many functional units (exons, introns, promoters, regulatory elements, etc.). We are far behind, however, in understanding the full genome organization and the laws that govern genomic complexity, functionality, and evolution.
In the present discussion I will demonstrate the existence of nontrivial (long-range) correlations in the genome of higher eukaryotes, and in particular in the hierarchical organization of coding and noncoding sequences in the arrangement of oligonucleotides and in the dispersion of promoters. I will also discuss evolutionary models describing genomic, dynamical modifications due to mutations, replications, sequence deletions, and other genomic modulating mechanisms. These models, which are designed to be in the category of open, non-conservative dynamical systems, can predict the nontrivial statistical features characterizing the current genome structure.

Biographical note

Astero Provata is currently Research Director at the National Center for Scientific Research "Demokritos," Institute of Physical Chemistry (Athens), where she leads the Statistical Mechanics and Nonlinear Dynamics Laboratory.
Her research interests include the theory and applications of statistical mechanics and nonlinear dynamics, critical phenomena, reactive dynamics, pattern formation, fractals, population dynamics, bioinformatics, genome organization, and genomic statistics. Her most recent interests are focused on the detection, analysis, and interpretation (evolutionary-wise) of long- and short-range correlations in coding and noncoding DNA, promoter sequences, and ologonucleotides, and the use of entropic indices to quantify the complexity between different classes of organisms.

Selected publications

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(2001) An evolutionary model about the origin of non-randomness, long-range correlations and fractality in the genome (with Y. Almirantis). Bioessays 23: 647-656.

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Global Climate and Human Health: The Cholera Paradigm

21 June2007

Abstract

Vector borne diseases have long been recognized to be climate driven, but it is now clear that many infectious diseases are intricately related to weather patterns, climate, and seasonality. Epidemics of cholera, a devastating disease occurring predominantly in third world countries, has been shown to be directly correlated with environmental parameters including sea surface temperature, sea surface height, and salinity, among others. Recent studies incorporating satellite sensing technology, ground truth measurements, and microbiological analyses have provided the basis for predictive modeling of cholera epidemics in Bangladesh, India, and East Africa. These findings will be discussed as a paradigm for global infectious diseases in this century.

Biographical note

Dr. Rita COLWELL is Distinguished University Professor both at the University of Maryland at College Park and at Johns Hopkins University Bloomberg School of Public Health, and Chairman of Canon US Life Sciences, Inc. Her interests are focused on global infectious diseases, water, and health, and she is currently developing an international network to address emerging infectious diseases and water issues, including safe drinking water for both the developed and developing world.
Dr. COLWELL served as the 11th Director of the National Science Foundation, 1998-2004. In her capacity as NSF Director, she served as Co-chair of the Committee on Science of the National Science and Technology Council. Her major interests include K-12 (primary and secondary education) science and mathematics education, graduate science and engineering education, and the increased participation of women and minorities in science and engineering.
Dr. COLWELL has held many advisory positions in the U.S. Government, non-profit science policy organizations, and private foundations, as well as in the international scientific research community. She is a nationally respected scientist and educator, and has authored or co-authored 16 books and more than 700 scientific publications. She produced the award-winning film, Invisible Seas, and has served on editorial boards of numerous scientific journals.
Before going to NSF, Dr. COLWELL was President of the University of Maryland Biotechnology Institute and Professor of Microbiology and Biotechnology at the University Maryland. She was also a member of the National Science Board from 1984 to 1990.
Dr. COLWELL has previously served as Chairman of the Board of Governors of the American Academy of Microbiology and also as President of the American Association for the Advancement of Science, the Washington Academy of Sciences, the American Society for Microbiology, the Sigma Xi National Science Honorary Society, and the International Union of Microbiological Societies. Dr. COLWELL is a member of the National Academy of Sciences, the Royal Swedish Academy of Sciences, the Royal Society of Canada, the American Academy of Arts and Sciences, and the American Philosophical Society. She is President-Elect of the American Institute of Biological Sciences (AIBS).
Dr. COLWELL has also been awarded 47 honorary degrees from institutions of higher education, and is the recipient of the Order of the Rising Sun, Gold and Silver Star, bestowed by the Emperor of Japan. Dr. COLWELL is an honorary member of the microbiological societies of the UK, Australia, France, Israel, Bangladesh, and the U.S., and has held several honorary professorships, including one at the University of Queensland, Australia. A geological site in Antarctica, Colwell Massif, has been named in recognition of her work in the polar regions.
Born in Beverly, MA, Dr. COLWELL holds a BS in Bacteriology and an MS in Genetics from Purdue University, and a PhD in Oceanography from the University of Washington.

Selected publications

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(2000a) Nonculturable Microorganisms in the Environment (with DJ GRIMES). ASM Press.

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