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Complex Systems and Changes - Darwin and Evolution: Nature-Culture Interfaces

Hotel Eden Roc, Sant Feliu de Guixols, Spain
15-20 September 2009

Co-Chairs: **Roland Pochet**, Université Libre de Bruxelles, BE, **Alain Peyraube**, CNRS and EHESS, FR
Programme Committee: **Reinhart Ceulemans**, Universiteit Antwerpen, BE, **János László**, Hungarian Academy of Sciences, HU, **Martin Stokhof**, Universiteit van Amsterdam, NL

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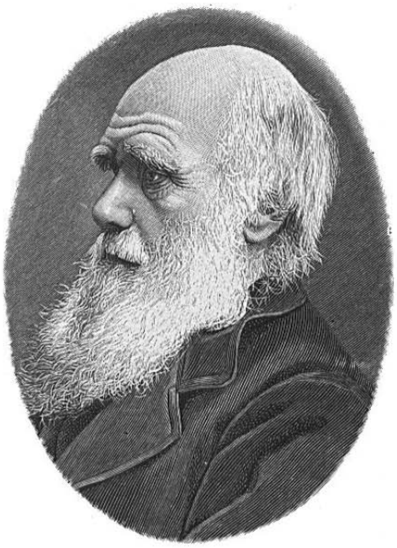

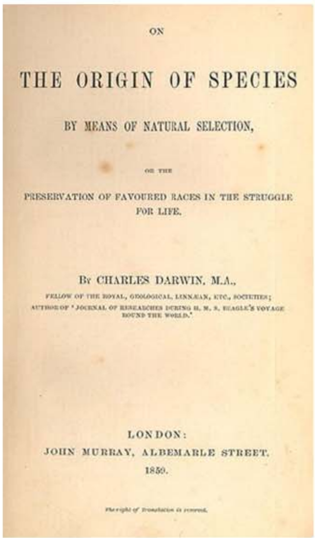

ON

THE ORIGIN OF SPECIES

BY MEANS OF NATURAL SELECTION,

OR THE

PRESERVATION OF FAVOURED RACES IN THE STRUGGLE
FOR LIFE.

BY CHARLES DARWIN, M.A.,

FELLOW OF THE ROYAL, GEOLOGICAL, LINNÆAN, ETC., SOCIETIES;
AUTHOR OF 'JOURNAL OF RESEARCHES DURING H. M. S. BEAGLE'S VOYAGE
ROUND THE WORLD.'

LONDON:
JOHN MURRAY, ALBEMARLE STREET.
1859.

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ABSTRACT BOOK

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Professor Martin Stokhof (Universiteit van Amsterdam, The Netherlands)

Conference Secretary
Ms. Zuzana Vercinska, ESF

PROGRAM

Tuesday 15 September :

Late afternoon/early evening	REGISTRATION
19.30	Welcome drink
20.30	Dinner

Wednesday 16 September :

“The Evolution of Darwin’s Theory”

Chair : Roland Pochet (Université Libre de Bruxelles, BE)

08.30 – 08.45	Conference opening
08.45 – 09.30	Luis Campos (Drew University, US) “The Many Lives of Darwinism”
	Roundtable 1 : “Filling the Cultural Gap” Moderator : Annick Lesne (IHES, FR)
09.30 – 09.35	Arcadi Navarro I Cuartillas (IBE, ES)
09.35 – 09.40	Steven Rose (The Open University, UK)
09.40 – 09.45	Csaba Pléh (Hungarian Academy of Sciences, HU)
09.45 – 10.45	Audience discussion
10.45 – 11.15	Coffee break
11.15 – 12.00	Steven Rose (The Open University, UK) “From Dobzhansky’s Dictum to Developmental Systems Theory”
12.00 – 12.45	Jaume Bertranpetit (Universitat Pompeu Fabra, ES) “Natural Selection in the XXIst Century: What Do We Have That Is Really New? Visions from Molecular Genetics and Complexity”
12.45	Lunch
14.00 – 14.45	Bryan Clarke (University Park, UK) “When it pays to be different”
	Roundtable 2 : Is there a “neo-Darwinism”? Moderator : Annick Lesne (IHES, FR)
14.45 – 14.50	Jaume Bertranpetit (Universitat Pompeu Fabra, ES)
14.50 – 14.55	Antoine Danchin (CNRS, FR)
14.55 – 15.00	Luis Campos (Drew University, US)
15.00 – 16.00	Audience discussion
16.00 – 16.30	Coffee break
	Short Talks
16.30 – 16.45	Susanna Badalyan (Yerevan State University, AM) “Evolution and Phylogenetic Relationships in Fungal Organisms”
16.45 – 17.00	Rachid Bouhadad (USTHB, Algiers, DZ) “Evolutionary History and Biologic Diversity of Desert Fish of Algeria”
17.00 – 17.15	Flavio D’Abramo (University of Rome, La Sapienza, IT) “D'Arcy Thompson, Charles Darwin and Complex Systems”
17.15 – 17.30	Davinder Grover (Punjab Agricultural University, IN) “Heritability for Income, Wealth and Other Economic Phenotypes”
19.00	Dinner

Thursday 17 September :

"Nature-Culture Interfaces 1"

Chair : Alain Peyraube (CNRS, EHESS, FR)

09.00 – 09.45	Vinciane Despret (University of Liège, BE) "Darwin's Choice Of Our Ancestor: Heroic Monkeys, Ugly Primates and Problematic Early Man"
	Roundtable 3 : "What is a phenotype ?" Moderator : Biljana Stojkovic (University of Belgrade, RS)
09.45 – 09.50	Luis Campos (Drew University, US)
09.50 – 09.55	Hans Liljenström (Swedish University of Agricultural Sciences, SE)
09.55 – 10.00	Christine Heller del Riego (Comillas University, ES)
10.00 – 11.00	Audience discussion
11.00 – 11.30	Coffee break
11.30 – 12.15	Eric Green (NHGRI, NIH, US) "*Comparative Genome Sequencing: Using Evolution to Decode the Human Genome*"
	Short Talks
12.15 – 12.30	Ally Harari (Ben Gurion University of the Negev, IL) "Female Sex Pheromones under Sexual Selection"
12.30 – 12.45	Jeffrey Hard (Northwest Fisheries Science Center, US) "Unnatural Selection: Human-induced Evolution in Exploitation of Wild Populations"
12.45	Lunch
14.00 – 14.45	Dan Sperber (EHESS/ ENS/ CNRS, FR) "How Culture Evolves"
	Short Talks
14.45 – 15.00	Mukund Kajale (Deccan College Postgraduate & Research Inst, Deemed University, IN) "Understanding Evolutionary Development of Ancient Indian Biodiversity with Special Reference to the Culture Plants"
15.00 – 15.15	Aliakbar Kiani (University of Tehran, IR) "Using Darwin's Theory to Describe Emerging and Disappearance of Powers in Global Politics"
15.15 – 15.45	Coffee break
15.45 – 17.45	Poster session 1
20.00	Dinner

Friday 18 September :

"Nature-Culture Interfaces 2"

Chair: János László (Hungarian Academy of Sciences, HU)

09.00 – 09.45	Csaba Pléh (Hungarian Academy of Sciences, HU) *"*Evolutionary Psychology: The Nature-Culture Interface*"*
09.45 – 10.30	Heather van der Lely (University College of London, UK) "Genes, Language and Specific Language Impairment: A Window onto an Evolutionary Earlier Stage?"
10.30 – 11.00	Coffee break
11.00 – 12.00	Poster session 2
12.00	Lunch
Afternoon	Half-day excursion
19.00	Dinner

Saturday 19 September :

"Complex Systems"

Chair : Jacques Haiech (University of Strasbourg, FR)

09.00 – 09.45	Antoine Danchin (CNRS, FR) "Natural Selection and Maxwell's Demon"
09.45 – 10.30	Miloš Judaš (University of Zagreb, School of Medicine, Zagreb, HR) "Evolution and development of uniquely human brain: life history framework"
10.30 – 11.00	Coffee break

Co-Chairs : Roland Pochet (Université Libre de Bruxelles, BE) &
Martin Stokhof (Universiteit van Amsterdam, NL)

11.00 – 11.45	Hans Liljenström (Swedish University of Agricultural Sciences, SE) "Evolving Complexity, Cognition, and Consciousness"
11.45 – 12.30	Axel Meyer (University of Konstanz, DE) "Darwin's Mystery of Mysteries: What Have We Learned about the Speciation in the 150 Years since the "Origin"?"
12.30	Lunch
14.30 – 15.15	Allen Orr (University of Rochester, US) "Genetics and the Origin of Species"
15.15 – 16.00	Arcadi Navarro i Cuartiellas (IBE, ES) "Genoeconomics: A New Perspective on Human Evolution"
16.00 – 16.35	Coffee break
16.30 – 17.45	**General Discussion, Conclusions and Forward Look** **Moderator : Jacques Haiech (University of Strasbourg, FR)**
20.00	Get-together & Conference Dinner

Sunday 20 September :

Breakfast & Departure

INVITED SPEAKERS

Wednesday 16th September
08.45 – 09.30

Dr. Luis CAMPOS
Drew University, US

THE MANY LIVES OF DARWINISM

Luis Campos

Over the past 150 years, a rich variety of interpretations and approaches have claimed to be "Darwinian"--deriving inspiration or insight from Darwin and his account of evolution by means of natural selection. In this talk, I will explore some of the more interesting, varied, and competing claims for "Darwinism" that have emerged over the past century and a half, from the late nineteenth-century belief that natural selection could account for all evolutionary phenomena (the Allmacht of natural selection), to the so-called "eclipse of Darwinism" around 1900, up to the more complicated roles "Darwinism" has played in the twentieth century, from the modern synthesis to molecular biology and beyond. The meaning of Darwinism has shifted over time, in both disciplinary and national contexts, and this remains as true a century later as it was when Darwinism first emerged. In this talk, I will suggest that a greater familiarity with this complex history will enable us to better understand the role of new discoveries and disciplines, and how scholarly trends and even anniversary celebrations affect the emergence of new forms of "Darwinism." Understanding the multiple meanings of "Darwinism" will also help us to understand the nature of scientific advance more generally.

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Wednesday 16th September
11.15 – 12.00

Emeritus Professor Steven ROSE
The Open University, UK

FROM DOBZHANSKY'S DICTUM TO DEVELOPMENTAL SYSTEMS THEORY

Steven Rose

Dobzhansky, famously, said 'nothing in biology makes sense except in the light of evolution.' But as Darwin himself said, natural selection is the major but not the only driver of evolutionary change. Furthermore, what evolves becomes a crucial question, asked for all living organisms by developmental systems theory (amongst others). What are the materials of variation? What does the 98.4% similarity between chimpanzee and human genome tell us about the limits of biological evolutionary theory in its attempts to explain 'the human condition.'

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Wednesday 16th September
12.00 – 12.45

Professor Jaume BERTRANPETIT
Institut de Biologia Evolutiva (IBE), Universitat Pompeu Fabra, ES

NATURAL SELECTION IN THE XXI ST CENTURY: WHAT DO WE HAVE THAT IS REALLY NEW? VISIONS FROM MOLECULAR GENETICS AND COMPLEXITY

Jaume Bertranpetit, Hafid Laayouni, Ferran Casals, Ludovica Montanucci, Martin Sikora, Giovanni dall'Olio

In the last years our vision of natural selection has dramatically changed thanks to the wealth of information provided by the description and study of diverse genomes, be them of different species or of different individuals within a species.

Moreover the deep knowledge of the pattern of variation in the human genome (SNPs, haplotypes) has also allowed the unravelling of past selective events. We are able to begin understanding the base of adaptation.

Purifying selection has long been known to be of importance and it is a possible way of interpreting the evolutionary genetics of diseases. Nonetheless the interpretation of diversity data allow a fine measure of function of the different proteins involved in functional networks and can approximate the degree of dispensability and the constraints suffered during the long term functional experiments carried out by natural genetic variants. Differences in the genes involved in serotonin function (including different behaviours for members of gene families) are a nice example.

Balancing selection has been demonstrated only in a few cases, some still not being very clearly accepted. Among the cases, indirect evidences have been suggested for CFTR variants. More recently it has been argued that it has been important in human history in the prion protein gene in conferring resistance to prion diseases, whose spread was suggested to be driven by cannibalism in our ancestors; it has been found to be an artefact. But where it seems to be highly important is in genes related to innate immunity and glycosylation of membrane proteins. The detection of the molecular footprint of positive selection is the goal of many researchers as it may help to recognize the genetic bases for human specific traits ("what makes us humans"). While some cases are clearly recognized, no clear picture is emerging due to the partial view of the genetic bases for complex adaptations. Moreover, it is possible to find the genetic bases for population specific populations, be it in relation to environmental factors (radiation, climate) or to the pressure of infectious diseases.

Now, natural selection is not only recognized and measured, but may be understood it its very basic level in shaping the genome. But the simplistic approach driven by the classical genetics is not going to give interesting answers: only the context of complex functional networks will allow a successful approach.

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Wednesday 16th September
14.00 – 14.45

Professor Bryan CLARKE
University Park, UK

WHEN IT PAYS TO BE DIFFERENT

Bryan Clarke

A simple-minded extrapolation of Darwinian logic suggests that because the fittest individuals survive and reproduce at the expense of the less fit, every population should tend towards genetic homogeneity. The members of a population should all become alike except for the unfortunate ones that carry new disadvantageous mutations, or those that are hybrids between populations.

This extrapolation is misleading. Natural selection often acts to maintain genetic diversity within populations, usually because the success of genetic variants depends on their frequencies, so that a variant is relatively advantageous when it is rare but relatively disadvantageous when it is common. The agents bringing about such selection can be predators, parasites (which include diseases), or competitors. Some striking examples will be discussed.

It is a mistake to ignore the advantages of genetic diversity when considering human populations.

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Thursday 17th September
09.00 – 09.45

Dr. Vinciane DESPRET
University of Liège, BE

DARWIN'S CHOICE OF OUR ANCESTOR: HEROIC MONKEYS, UGLY PRIMATES AND PROBLEMATIC EARLY MAN

Vinciane Despret

Darwin was confronted with a dilemma when he wanted to determine which monkeys could represent our ancestor among the primates. His choice could have been established on the criterion of the morality, what he confessed to have preferred. He however could not, for reasons which we suggest clarifying.

Because the primates were not only at stake: the "savage" indeed, had also to fit into the continuum. Darwin therefore had to opt for another criterion. This choice has determined the whole story of primatology… and even Freud’s theories.

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Thursday 17th September
11.30 – 12.15

Dr. Eric GREEN
National Human Genome Research Institute, NIH, US

COMPARATIVE GENOME SEQUENCING: USING EVOLUTION TO DECODE THE HUMAN GENOME

Eric Green

Comparison is a fundamental tool for analyzing DNA sequence. Comparisons of sequences from species separated over long and short evolutionary distances (i.e., inter-species comparisons) provide clues about the evolutionary forces that have uniquely sculpted each genome into its modern-day form and insights about genome function. Since completion of the human genome sequence by the Human Genome Project, significant attention has turned towards generating sequences from multiple other vertebrate species. Comparative analyses of these sequence data are revealing important insights about the patterns of sequence conservation among species and about the locations of highly conserved sequences that are likely functionally important. Such efforts are a key component of the ENCODE project, a large consortium-based project that aims to establish a complete catalog of functional elements in the human genome. This project is integrating experimental and computational data to provide new insights about the functional roles of evolutionarily conserved sequences. Together, these studies are advancing the utility of comparative sequence analyses and making important contributions towards unraveling the functional and evolutionary complexities of the human genome.

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Thursday 17th September
14.00 – 14.45

Dr. Dan SPERBER
EHESS/ ENS/ CNRS, FR

HOW CULTURE EVOLVES

Dan Sperber

Explaining the evolution culture in a naturalistic perspective faces two challenges. The best understood challenge is that of identifying the natural factors that make the existence of culture possible and that play a causal role in its perpetuation and evolution. A less well understood and deeper challenge is that of developing a naturalistic understanding of what culture is made of. I suggest a way to meet both challenges at once. Culture, I argue, can be viewed as the distribution in a human population of mental representations, artifacts and practices that are linked through causal chains where mental and environmental events alternate. These causal chains crisscross and mesh in a way that determines both our individual thoughts and actions and our common institutions. The relative stability and evolution of culture is made possible not by a mechanisms of replication of 'memes' but by a combination of 'preservative' and 'constructive' mental and social processes. Recognising the role of constructive processes in cultural transmission helps us to appreciate that apparent imperfections in cultural production are not, properly speaking, "copy errors" or "mutations". Moreover, constructive biases, when shared in populations, help allow representations, practices and artefacts to reach a cultural level of distribution and stability. The resulting story about cultural evolution is not a memetic one, but it is Darwinian.

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Friday 18th September
09.00 – 09.45

Professor Csaba PLEH
Hungarian Academy of Sciences (HAS), HU

DARWIN AND THE NATURE-CULTURE CONTINUITY ISSUE REGARDING CULTURE

Csaba Pléh

The talk shall use a historical essay format. Controversies and proposed solutions regarding the tensions arising from a postulated human nature and the inherent variability of cultural phenomena will be surveyed with some possible suggestion for a way out. Three issues shall be specifically analyzed.

Continuity of mechanisms. Several models were proposed for the nature-culture interface postulating some kind of common or analogue mechanisms of variation-selection-stabilization cycles from Mach through Karl Bühler and Karl Popper to Daniel Dennett's tower of selection. The critical issues in this approach are whether these parallels are only structural homologies due to optimalisation or is there agenetic-historical continuity between them. Furthermore, the issue is always raised if there is an interaction and downward feedback between the postulated mechanism?

Cultural selection models as particular applications of the idea of homologue mechanism have become much discussed lately. The memetic ideas of Richard Dawkins emphasize conservative cultural transmission and the analogy of identical replication, while the epidemiological approach of Dan Sperbercontroversy. The talk will compare the two approaches both regarding the postulated psychological mechanism, and regarding the possible diversities of cultural diffusion. The diffusion models have to take into account the tensions between variability and postulated universals and the relativity issue in cultural studies the light of Darwinism.

Evolutionary algorithms are too slow, was an issue already raised in late 19th century. James Baldwin proposed a hierarchy of speeding effects starting from trial and error learning through imitation to environmental feedback, the infamous Badwin effect. This latter factor has a long story with advocators and critiques from Piaget through Chomsky to Dennett. The new models of cultural learning and the recent analysis of imitation like phenomena proposed by Michael Tomasello and György Gergely and Gergely Csibra in their model of natural pedagogy attempt a new synthesis in this regard. These approaches are examples for the promises of a new interpretation of the Darwinian message. One promise is the combination of the proximal interpretation of Darwinism in neuroscience with the proposal of particular evolutionary adaptations for culture, and the second is the promise of the Evo-Devo attitude, i.e. a combination of developmental studies with evolutionary considerations

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Friday 18th September
09.45 – 10.30

Professor Heather VAN DER LELY
University College London, UK

GENES, LANGUAGE AND SPECIFIC LANGUAGE IMPAIRMENT: A WINDOW ONTO AN EVOLUTIONARY EARLIER STAGE?

Heather van der Lely

In this paper I present evidence supporting the theory that grammar is an adaptation shaped by natural selection motivated originally by its design features. Complex grammar conforms to a universal design in humans and is learnt quickly in a manner that resembles fear and human sexual desire rather than cultural learning. Further, the evolutionary advantages of a human-specific complex grammar are illustrated when we consider the cultural costs of not having a typical grammar system. I will bring data from children with "Specific Language Impairment (SLI)" to support this hypothesis. SLI is a developmental impairment in the acquisition of language that persists into adulthood.

First, SLI has a multi genetic basis and illustrates how multiple genes are required for normal grammar. Recently, variants of two genes FOXP2, and a gene down-stream from FOXP2, CNTNAP2, have been identified as associated with SLI. In humans FOXP2 shows an evolutionary specific form, little variation within humans compared to other species, indicating that it has been selected for. Further whereas most children acquire language without effort at an early age, children with SLI encounter severe difficulty in acquiring their first language. These genetic factors from SLI are characteristic of an evolutionary adaptive trait.

Second, I will present evidence from investigations of children and teenagers from a sub-group of SLI, "Grammatical"(G)-SLI. G-SLI individuals' core deficit is in just those aspects of language that are specific to humans, i.e., grammar. I will argue that G-SLI provides evidence for the dissociation of grammar from other cognitive traits. Behavioural and neural-imaging data reveal that the cognitive mechanisms underlying grammar appear to be domain specific, and uniquely impaired in G-SLI. Whereas a neural correlate associated with grammatical violations, that is the Early Left Anterior Negativity (ELAN), is missing in teenagers with G-SLI, a normal neural correlate (N400) associated with semantic processing is found. Moreover, G-SLI teenagers appear to compensate for their syntactic deficit by using their relatively good semantic processing. These data indicate that grammar is a design feature of language that is specialised and independent, and is not a manifestation of more general cognitive abilities.

Third, the social and communicative advantages that language brings are illustrated by a recent UK Government report (The Bercow Report 2009). Two children in every classroom across Europe have problems learning language due to Specific Language Impairment (SLI). Extrapolation from UK data indicates this is costing Europe more than 250 billion Euros over a life-span. That’s 1% of GDP, enough to bail out a medium-sized bank. Language is one of the key skills children need to succeed in education and later in life. Without this skill, the potential of our children is lost. The complexity of grammar provides its expressive power, fast acquisition and efficient use by adults. Natural selection is the most plausible explanation for its evolution. Further research is required to establish whether good grammatical skills (as opposed to language) are likely to be selected for in a mate as a sign of potential economic and social success.

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Saturday 19th September
09.00 – 09.45

Professor Antoine DANCHIN
CNRS, FR

NATURAL SELECTION AND MAXWELL'S DEMON

Antoine Danchin

Information is central to Biology, essentially via the genetic program and information transfers between the program embodied by nucleic acids and its expression. Physics witnesses a revolutionary shift of emphasis from the standard categories of Reality, matter, energy, space and time, to information as an authentic fifth category. In this context, I use comparative genomics to investigate the role of a concept that has often been considered as quite fuzzy, and which is at the centre of many heated controversies, Natural Selection. The role of this process is explored at the level of the separation between the process of reproduction, from the process of replication. Analysis of gene persistence in bacterial genomes permits identification of a core genome, the paleome, reminiscent of a scenario of the origin of life. The paleome, which is made of approximately 500 genes, comprises genes deemed essential, which code for the constructor and the replicator of the cell, supporting life. It also comprises a set of genes, often non essential, which code for energy-dependent degradation functions, permitting reproduction of life. I conjecture that Natural Selection is the degradative process that makes room for accumulation of information, using energy to prevent degradation of information-rich entities, as would Maxwell's demons behave. Making the parallel with the process of accumulation of information in the physical world, and which asks for erasing the memory to make room for novel information using energy to prevent destruction of functional entities, I remark that the commonplace observation that babies are born very young, suggests that the genes coding for degradative processes are used by ageing cells to make a young progeny, thereby trapping information in any available form. I further show that comparative genomics suggests that polyphosphate (a mineral) could play the role of the essential energy reservoir that is used in the process. A brief discussion about adaptive mutations shows that they could be the explicit manifestation of the process of accumulation of information, further suggesting that the process of cancer could be initiated in stem cells which acquire adaptive mutations leading to immortalisation.

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Saturday 19th September
09.45 – 10.30

Professor Judas MILOS
University of Zagreb, School of Medicine, Zagreb, HR

EVOLUTION AND DEVELOPMENT OF UNIQUELY HUMAN BRAIN: LIFE HISTORY FRAMEWORK

Judas Milos

The human brain is much larger than expected for primate of our body size and much more complex. It also has other unique (species-specific) features – e.g., it takes at least two decades to develop and attain mature level of functioning. While fully developed human brain obviously serves well the needs of human survival, the puzzle remains: How humans manage to survive and thrive by letting their brains grow and mature so slowly? I suggest that we should seek the answer in the realm of life-history theory, which can bridge the gap between developmental neuroscience and evolutionary developmental biology (evodevo).

I will briefly explain what is the life-history theory, compare major lifehistory parameters of apes and humans (including rhesus monkeys as an outgroup) and highlight unique features of human life-history strategy. The correlates of slow maturation and long life in mammals are: (1) enlarged brains; (2) large body size; (3) enhanced learning and sociality; and (4) increased parental investment. Relative brain size is quite similar in newborns of apes and humans (7-12% of adult body mass); however, the postnatal decrease in relative brain size in humans is significantly lower than in apes. With respect to postnatal growth curves, primates delay body growth and reproductive development but do not delay brain growth. While brain growth in apes is rapid before birth and relatively slower after birth, brain growth in humans is rapid both before and (for about a year) after the birth. The time course of human growth is unexceptional both before birth and after initiation of the subadult growth spurt (in fact, growth spurt periods are shorter than expected). However, human growth is much longer than expected (on the basis of body size) mainly because of an extremely long EARLY postnatal growth period – the attributes of early growth periods appear to be highly evolvable or responsive to selective pressures. Human gestation is characterized by „energy expensive“ strategy and reflects heavy maternal investment in gestation. Human development from birth to the subadult spurt is characterized by „time expensive“ stragegy – low growth rates distributed over a long period, thus spreading metabolic burdens of infants and children over time. The childhood (defined as period from 3 to 7 years, i.e. from weaning to the onset of juvenile period) is uniquely human life-history stage. Finally, large brains are costly: humans use over 2.5 times more of the resting metabolic rate (RMR) to maintain their brains than do other anthropoids – human brain is an expensive tissue. In conclusion, evolutionary causes of prolonged human ontogeny are most readily interpreted as requirements of the developing brain. Prolonged ontogeny: (1) May be partly an adaptation to limit the already high total brain energy requirements during childhood – shifting juvenile metabolic risk costs to the perinatal period and distributing metabolic costs to the mother, another caretaker, or group of older individuals; (2) May ensure the retention of a functionally juvenile (i.e., highly plastic) brain for a long period of time; (3) Promotes prolongation of experience-expectant and experience-dependent periods while enabling variability in the timing of brain ontogeny among regions; and (4) May promote comparatively high plasticity into the adult period.

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Saturday 19th September
11.00 – 11.45

Professor Hans LILJENSTROM
Swedish University of Agricultural Sciences, SE

EVOLVING COMPLEXITY, COGNITION AND CONSCIOUSNESS

Hans Liljenström

All through the history of the universe there is an apparent tendency for increasing complexity, with the organization of matter in evermore elaborate and interactive systems. The living world in general, and the human brain in particular, provides the highest complexity known. It seems obvious that all of this complexity must be the result of physical, chemical and biological evolution, but it was only with Darwin that we began to get a scientific understanding of biological evolution. Darwinian principles are guiding in our understanding of such complex systems as the nervous system, but also for the evolution of human society and technology. Living organisms have to survive in a complex and changing environment. This implies response and adaption to environmental events and changes at several time scales. The interaction with the environment depends on the present state of the organism, as well as on previous experiences stored in its molecular and cellular structures. At a longer time scale, organisms can adapt to slow environmental changes, by storing information in the genetic material carried over from generation to generation.

This phylogenetic learning is complemented by ontogenetic learning, which is adaptation at a shorter time scale, occuring in non-genetic structures. The evolution of a nervous system is a major transition in biological evolution and allows for an increasing capacity for information storage and processing, increasing chances of survival. Such neural knowledge processing, cognition, shows the same principal features as non-neural adaptive processes. Similarly, consciousness might appear, to different degrees, at different stages in evolution.

Both cognition and consciousness depends critically on the organization and complexity of the organism. In this presentation, I will briefly discuss general principles for evolution of complexity, focussing on the evolution of the nervous system, which provides organisms with ever increasing capacity for complex behaviour, cognition and consciousness. I will also discuss some computational approaches, as tools for understanding relations between structure, dynamics and function of the nervous system.

References:

Baltscheffsky, H., Blomberg C., Liljenström H., Lindahl B.I.B., and Århem P., Eds. (1997) On the Origin and Evolution of Life, J. theor. Biol. 187(4).

Århem, P., Liljenström, H. and Svedin, U., Eds. (1997) Matter Matters?- On the Material Basis of the Cognitive Activity of Mind, Heidelberg: Springer.

Liljenström, H. and Svedin, U., Eds. (2005) Micro-Meso-Macro: Addressing Complex Systems Couplings, London: World Scientific.

Liljenström, H. and Århem, P., Eds. (2007) Consciousness Transitions – Phylogenetic, Ontogenetic and Physiological Aspects. Amsterdam: Elsevier.

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Saturday 19th September
11.45 – 12.30

Professor Axel MEYER
University of Konstanz, DE

DARWIN'S MYSTERY OF MYSTERIES: WHAT HAVE WE LEARNED ABOUT THE SPECIATION IN THE 150 YEARS SINCE THE "ORIGIN"?

Axel Meyer

Some science historians and evolutionary biologist claim that Darwin in his opus magnum did not explain sufficiently how speciation works and was wrong on the nature of species as well. In this talk I will revisit some of these historical arguments and use research on the famous species flocks of cichlid fishes from the largest East African Lakes, Victoria, Malawi and Tanganyika to illustrate the points. These extraordinarily diverse fish assemblages are well-known examples for phenomena such as adaptive radiations and explosive rates of speciation. They are composed of several hundred of extremely young species each and are the most species-rich, and diverse species flocks known, in terms of morphology, and ecology as well as behavior. The understanding of the phylogenetic relationships among East African cichlid fish species flocks has increased dramatically during the last 20 years since the application of molecular data for molecular phylogenetic, phylogeographic and population genetic research on cichlids. Phylogenetic analyses of recent molecular data in the context of the geological history of the East African lakes helped to elucidate some aspects of the evolutionary history and the evolutionary processes that can explain the origin of these extraordinary fish faunas. In the last decade advances and insights were made for the understanding of both phylogenetic patterns as well as evolutionary processes. New comparative developmental and genomic approaches began to yielded insights into the genetic and genomic underpinnings of the phenotypic diversity of cichlid fish diversity.

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Saturday 19th September
14.00 – 14.45

Dr. Allen ORR
University of Rochester, US

GENETICS AND THE ORIGIN OF SPECIES

Allen Orr

The study of speciation has been characterized by a number of major developments since the publication of Darwin's *Origin of Species*. In the most recent two developments, the study of speciation has been brought together with genetics and, later, with the study of molecular evolution. I will review these developments. In particular, I will discuss classical genetic studies of reproductive isolation, especially hybrid sterility and inviability. I will also discuss recent efforts to identify "speciation genes" at the DNA sequence level, reviewing recent work from several laboratories, including my own. As we will see, the attempt to connect the studies of speciation and molecular evolution has revealed an important role for natural selection in speciation.

Email : orr@pas.rochester.edu

Saturday 19th September
16.00 – 16.45

Professor Arcadi NAVARRO i CUARTIELLAS
Institut de Biologia Evolutiva (IBE), ES

GENOECONOMICS: A NEW PERSPECTIVE ON HUMAN EVOLUTION

Arcadi Navarro i Cuartiellas

Since the publication, almost 150 years ago, of the Origin of Species the scientific study of the evolution of human-specific traits has been the focus of many efforts coming from very different areas of science. Indeed, Darwin himself published an extremely influential treatise "The Descent of Man" in 1871.

Nowadays, after a century an a half of research, impressive results have accumulated, particularly about those traits that, presumably, would “make us human”, setting us apart from the rest of primates, and about how these trait would have evolved. Over the last few years, a new area of research, genoeconomics, has started to make important contributions towards the study of hominization. I will review the foundations and promises of this new branch of science and discuss a few of the pitfalls that may hinder its advance.

E-mail : arcadi.navarro@upf.edu

SHORT TALKS

Wednesday 16th September
16.30 – 16.45

Professor Susanna BADALYAN
Department of Botany, Yerevan State University, AM

EVOLUTION AND PHYLOGENETIC RELATIONSHIPS IN FUNGAL ORGANISMS

S.M. Badalyan[1], K.W. Hughes[2], U. Kües[3]
[1]Laboratory of Fungal Biology and Biotechnology, Yerevan State University, AM
[2]Department of Ecology and Evolutionary, University of Tennessee, US
[3]Molecular Wood Biotechnology and Technical Mycology, Büsgen-Institute, Georg-August-University Göttingen, DE

The kingdom of Fungi (Mycota) is recognized as evolutionary one of the oldest and phylogenetically complex clades of life originated 1.5 billion years ago. Fungi are found in different ecosystem as mutualists, pathogens, parasites or saprobes. The described fungal biodiversity (around 76.000 species) is only represents 5-10% of the total number of species currently presents on Earth. However including a large number of microscopic, undescribed and unculturable fungi it could be even higher than 1.5 million species. Fungi are including mayor phyla Ascomycota, Basidiomycota, Zygomycota, Chytridiomycota and Oomycota which were traditionally classified in the Plant kingdom. Based on "morphological" and "molecular" characteristics the Fungi are monophyletic group diverged from common ancestor with the animals. Presently they are part of large clade Opisthokonts in which evolutionary and phylogenetic relationships are still unclear. The problem in estimating of fungal species is the absence of reliable definition of a fungal species. With the development of molecular and evolutionary phylogenetics, fungal species concepts are evolving from morphological and biological concepts to phylogenetically and DNA-based species concepts using combined sequence data from nuclear and mitochondrial ribosomal DNAs and protein-coding genes. Our results to study of phylogenetically significant characteristics of Coprinoid mushrooms, Flammulina velutipes and Pleurotus ostreatus species complexes collections are also discussing.

Wednesday 16th September
16.45 – 17.00

Professor Rachid BOUHADAD
FSB, University of Sciences and Technology - Houari Boumediene, Algiers, DZ

EVOLUTIONARY HISTORY AND BIOLOGIC DIVERSITY OF DESERT FISH OF ALGERIA

Rachid Bouhadad

The algerian sahara possesses a hydrographical fossil basin which testifies the presence of the ancient sahara 10,000 years ago. This important cathment gathers several wetlands (isolated points of water, streams, lakes) where live an ichtyological fish fauna poorly studied. The Subgenus Barbus is represented by two important species with B. amguidensis (tetraploid) largely distributed in the Hoggar and Tassili region eventhough B. deserti (diploid) is enclosed to the hoggar region (threatned species). The genus Clarias caught in Iherir Valley (Tassili region) is represented only by C. gariepinus (endemic), the area distribution of this species look to be restricted. Two species Tilapia zilli and Gambusia affinis had been introduced years ago and acclimated in large areas in the Tassili region. Evolution and diversity are the purposes of this survey.

Wednesday 16th September
17.00 – 17.15

Flavio D’ABRAMO
Department of Philosophical and Epistemological Studies, University of Rome, IT

D'ARCY THOMPSON, CHARLES DARWIN AND COMPLEX SYSTEMS

Flavio D’Abramo

I will show descriptions of complex systems within Charles Darwin's and D'Arcy Thompson's works. Then I will highlight some paths we are running thanks to their heritage.

Wednesday 16th September
17.15 – 17.30

Professor Davinder GROVER
Department of Economics and Sociology, Punjab Agricultural University, IN

HERITABILITY FOR INCOME, WEALTH AND OTHER ECONOMIC PHENOTYPES

Davinder Grover

It is normally believed that personality encompassing various actions and reactions to material as well as non material provocations in life is vastly determined by the genes, a person acquires from his/her parents. Genoeconomics spot many ways in which individual behaviour and social institutions/ environment moderate or amplify genetic differences over the generations. More generally, economic and or social institutions may either reduce or amplify the inequalities produced by genetic variation. Genetic mechanisms and its interaction with environmental factors jointly influence economic behaviour. Generally, cognitive factors influence income, and or decision making about savings, wealth and other economic phenotypes including risk bearing/ avoiding attitudes, etc. To what extent, such economic phenotypes travel generation to generation through simply acquiring and transmitting genes. This quarry was probed from household/families in Ludhiana - a commercial city of India basically with a view to find out the similarities or dissimilarities of actions and reactions to various economic provocations by family members over 2-3 generations. The probable actions/reactions to particular decision making situation by them were gathered using research instrument that contained a set of questions/situations. Based on quick observations, the similar (not exactly same) economic phenotypes over generations were found in around two-thirds families. In rest of the cases, the probable economic actions were quite contradictory, generation to generation, may be because of rapid changes that have taken place in economic environment through all these years. Analysis suggests that genetic characters do determine the personal behaviour towards various economic activities to some extent, but just not superimpose. The rapid transformation taken place in an economic and social environment also influence the economic behaviour of human being, generation to generation.

Thursday 17th September
12.15 – 12.30

Dr. Ally HARARI
Department of Life Sciences, Ben Gurion University of the Negev, IL

FEMALE SEX PHEROMONES UNDER SEXUAL SELECTION

Ally Harari

In natural selection, species-specific sex pheromones of moths play a significant role through species recognition. The role of sex pheromone, and especially pheromone produced by females, in sexual selection, is currently under debate. Pheromones are thought to be responsible for reproductive isolation between closely related species and thus, variation in pheromone characteristics within a population is expected to be low due to stabilizing selection. Accordingly, females with a pheromone that deviates from the population mean are expected to be less attractive to males. Nevertheless, recently accumulated evidence demonstrates males' sensitivity to a wide variety of conspecific pheromone characteristics.

Female sex pheromones are produced in minute amounts (ng), but the costs of their pheromone production has been little investigated. I tested the cost of female producing sex pheromone and studied the role of female moth pheromones as secondary sexual ornaments that honestly advertise the individual female quality, using two moth species: Agrotis segetum and Lobesia botrana. The results indicate that female pheromone may be used as an honest signal for female size and physical conditions.

Thursday 17th September
12.30 – 12.45

Dr. Jeffrey HARD
Conservation Biology Division, Northwest Fisheries Science Center, US

UNNATURAL SELECTION: HUMAN-INDUCED EVOLUTION IN EXPLOITATION OF WILD POPULATIONS

Jeffrey Hard, Fred W. Allendorf

Human harvest of wild populations imposes selection that can reduce the frequencies of those phenotypes among breeders. Hunting, fishing, and other forms of human exploitation contrast with agriculture and aquaculture, where the most desirable individuals are selected for breeding to increase the frequency of particular phenotypes. There has been surprisingly little consideration of human-induced selection in the wild until recently. Although Darwin himself recognized the potential for exploitation to cause evolution, he did not apply his evaluation of methodological, unconscious, and natural selection to wild animals and plants. We consider the potential effects of human exploitation on the genetics and sustainability of wild populations. We consider how harvesting can affect the mating system and thereby modify sexual selection in a way that might affect viability. Determining whether phenotypic changes in harvested populations are due to evolution, rather than phenotypic plasticity or environmental variation, has been challenging. However, it is likely that some undesirable changes observed in exploited populations over time are due to selection against particular phenotypes that arise from natural or sexual selection—a process we call "unnatural" selection. Evolution induced by human harvest can increase the risk of population collapse, and might greatly increase the time it will take over-harvested populations to recover once harvest is curtailed because harvesting often creates strong selection differentials, whereas curtailing harvest will generally result in less intense selection in the opposing direction.

Thursday 17th September
14.45 – 15.00

Professor Mukund KAJALE
Dept. of Archaeology, Deccan College Postgraduate & Research Inst., Deemed University, IN

UNDERSTANDING EVOLUTIONARY DEVELOPMENT OF ANCIENT INDIAN BIODIVERSITY WITH SPECIAL REFERENCE TO THE CULTURE PLANTS

Mukund Kajale

The development of human civilization has largely been possible becuase of the domestication of plants and animals and the manipulation of natural environment at the hands of Man. The domestication itself has been a Man aided co-evolutionary process and the factual evidences forwhich are recovered from archaeological sites belonging various chrono-cultural deposits right from Palaeolithic, Mesolithic, Neolithic, Chalcolithic, Megalithic and subsequent Historical sites.

The author being a student of Archaeology (Environmental Archaeology, Palaeo-environment), Botany (Archaeobotany) and Quaternary Geology (Palaeoecology), proposes to put forth datasets from his studies on archaeological plant remains in the Indian sub-continent to understand evolutionary devlopment of subsistence, cultivation and domestication of plants and agricultural systems in Indian sub-continent.

India has been a land of contradictions (like many other parts of globe), deterioration of environment, erosion of agrobiodiversity and conservation of natural biodiversity through cultural and religious practices have been going on simultaneously.

I propose to illustrate various facets of evolution of ancient Indian plant biodiversity through ages in light of Darwinian evolutionary concepts along with certain limitations and ateempt conceptualisation of sustainable human devlopment for this part of the globe.

Thursday 17th September
15.00 – 15.15

Aliakbar Kiani
Dept. of International Relations, Faculty of Law and Political science, University of Tehran, IR

USING DARWIN'S THEORY TO DESCRIBE EMERGING AND DISAPPEARANCE OF POWERS IN GLOBAL POLITICS

Aliakbar Kiani

We are living in the era of sharp changes in the global atmosphere. It is because of expanded capabilities of communication and influence that serves actors in their willing directions. What is current world actor's main goal? What is clear is pursuing national interest toward securing safety and progress of nation and authorities. But obviously the definition of these elements has changed during these decades. Previously security meant being sure of not have foreign attack or to some extend safety in life and economic programs that all where dependent to national hard power. But now the importance of weapons has reduced and it is the strength of social structure of a community that protect a nation stability and advance. New global framework does not allow the actors to take up challenging agendas in hard power competition. Globalization proved for international parties that they have to develop their capability in trade, life welfare and applying human capitals. Naturally those who have potentials for such programs or trying to provide them are more likely to survive rather than the rest. Being able to work with the others is a vital factor not fighting. Therefore it's not competition which guaranties surviving but is ability in cooperation. And each nation has to develop this variable in its existence.

Consequently there will not be more challenge outside the states but inside them for institutionalization this paradigm and enforcing it. Those who fail to promote this character will disappear. Nations have to win their inner struggle to survive.

POSTERS

DIFFICULTIES IN COMPARATIVE BEHAUVORAL SCIENCE

Mohamud Abdiselam
Tom Patrick Institute, University Aurangabad, IN

The comperative investigation of human and non human animal behaviour had many independent origins which have hampered research to the present day. Comparative psychologists attempted to discover general behaviour organising mechanisms across especies and comparative ethologies were interested in the ecological function and the evolitionary history of specific examination of animal behavour has been conducted by psychologists and bilogists seperatly resulting in serious theoretical terminology and methaodological defference. Recent developments however have recognised the importance of establishing a unified field to integrate the study of behavioural mechanisms into a functional and evolutionary framework. A meaningful comparative social cognition research agenda requires a clear understanding of both the evolutionary history and the developmental constraints of the behaviour being studied.

INTRODUCTION OF THE MOLECULAR ANALYSIS IN THE CUBAN GAUCHER DISEASE POPULATION: A NEW DIAGNOSTIC TEST

Arlet María Acanda de la Rocha
Faculty of National Center of Medical Genetic, Havana City, CU

Gaucher disease is the most common lysosomal storage disorder. It is inherited as an autosomal recesive trait, caused by a deficiency of the enzyme beta-glucocerebrosidase, which leads to the progressive accumulation of glucocerebrosidase in the lysosomes of macrophages in various tissues. Gaucher disease is classified into three types according to the presence and severity of the neurologic symptoms and has a striking phenotypic variability. The gene for glucocerebrosidase was localized to 1q21, distributed in 11 exons and 10 introns. Over 200 mutations have been identified worldwide, although only a few are the most common in the general non-jewish population. The diagnostic of this disease in Cuba was the established histologically examine and by measuring the acid-beta-glucosidase activity of leukocytes, but both of them are not always reliable. The aim of this study was the introduction at first time in Cuba, of the molecular study of the most frequent mutations N370S, L444P, G377S and 55del for distinguished the pseudogene carriers. Genomic DNA was extracted from peripheral blood leukocytes using standard methods (Miller et al., 1988). A total of 2 patients and their 1rst grade relatives were studied; the diagnosis of the Gaucher disease type 1 was confirmed by clinical evaluation of these families. These 4 mutations was determined by PCR technique and enzymatic digestion and subjected to electrophoresis on 3% agarose gel. For the first time in Cuba we standardize the mutations N370S, L444P, G377S and 55del using direct study of the gene. It allows the introduction of the molecular diagnostic in the Cuban Health National System, which may be helpful to predict the severity and the rate of progression of clinical manifestations and has an important impact on the Cuban molecular medicine.

EVOLUTION IN ENVIRONMENTAL AND TECHNICAL SYSTEMS

Nikolai Bobylev
Environmental Assessment and Policy Research Group, Technische Universität Berlin, DE

The presentation will explore similarities and distinct features of evolution process in different systems and interface between those systems. Thanks to Darwin the concept of evolution revolutionized biology, and now the term evolution is used in a variety of disciplines reflecting Darwinian view of the world. The presentation will focus on ecological and environmental systems, expanding them to include artificial or manmade components. One can argue that technological parts of ecosystems can represent evolution of pure natural ecosystems to nature-technical systems, or combination of natural and manmade environment.

Interestingly, analysis of pure technical systems, e.g. infrastructures, can reveal some similarities with natural systems in their development. Analysis of these similarities is important as it can reveal development trends, which would not been clearly visible and theoretically grounded by drawing on just outlook of progress in technology. One example can be evolution of urban physical infrastructure systems under factor of economical effectiveness. Need for infrastructures adaptation to climate change can be analyzed drawing on evolution theory as well. The presentation will give example of interdependence and convergence characteristics changes under factors of environmental change.

VARIATION IN WING SHAPE OF ARTIFICIALLY SELECTED LINEAGES OF DROSOPHILA MELANOGASTER AND EFFECTS OF SELECTION OVER CORRELATED TRAITS AND PHENOTYPIC PLASTICITY

Daniel Corrêa, Blanche Christine Bitner-Mathe
Departamento de Genética, Instituto de Biologia, Universidade Federal do Rio de Janeiro, BR

Evolution of biological structures can be constrained by the interconnections of traits, altering the response to natural selection. The wing of D. melanogaster has been largely used in studies of morphological evolution. Artificial selection programs are useful tools for testing several assumptions under this topic.

In our lab, divergent lineages have been produced by artificial selection on the shape (SH) of the D. melanogaster wing at 22°C, generating both elongated and rounded shaped wings. Here we test the effects of the artificial selection, temperature and lineage on shape, size, wing vein patterns and phenotypic plasticity. We also characterized the wing of eight out of the twelve strains of Drosophila species with whole genome sequenced to analyze the extent of shape variation within the selected lineages in a phylogenetic context. Replicas from the 64th generation were grown in two developmental temperatures (16°C and 25°C). Two methods of shape descriptions were used, being the adjustment of the fittest ellipse to wing contour and GLS procrustes methods. Principal components analyses were conducted to resume vein position data for both methods. Analysis of variance indicates the selection program as the main effect causing differences in wing shape but no significant differences in size. The developmental temperature is the principal effect causing variation in size. Principal components (CP) from both methods were significantly different across selection directions and temperatures. Phenotypic plasticity response seems not to have changed for any trait as seen by the interaction between selection and final temperature. It shows that selection can dramatically change the mean of a trait without disturbing phenotypic plasticity mechanisms. The genetic architecture controlling wing shape seems to be at least partially detached from those responsible for wing size, allowing a deep change in the first without compromising the other.

According to CP1 procrustes, patterns of wing venation seem to have changed in response to the selection program. The species experiment showed that the selection program not only produced wings with shape outranging that exhibited by D. melanogaster, but also invaded variation found in phylogenetic distant species.

There seem to be a hidden variation, not exhibited in natural populations, that can be presented when the environment puts the population under harsh selection. Selection seems to have disturbed some mechanisms that preserve that variation undercover.

MODELING OF SELF-ORGANIZATION II BRAIN AS AN ADAPTIVE COMPLEX SYSTEM

Maryam Esmaeili
MACS – Lab (Modelling and Application of Complex Systems Laboratory), University of Lugano, CH

Large-scale neural networks are thought to be an essential substrate for the implementation of cognitive function by the brain. If so, then a thorough understanding of cognition is not possible without knowledge of how these large-scale neural networks of cognition (neurocognitive networks) operate individually and socially. In this paper, we aim at providing a theoretical framework for modeling of behavior of brain as a cooperative multi-agent system. In this work entities are neurocognitive networks as some expert agents that they only do what they think in their on best expertness. We formulate the dynamic interaction among those expert agents as competitive and cooperative problems. We obtain the equilibrium behavior in the long run, and characterize the collective behavior of these expert agents as responsible of intricacies of cognition. We show how complex collective behavior of neurocognitive networks can emerge from the locally optimal behavior of each agent. We also describe why and how these neural networks organize themselves into a multilevel hierarchical organization with nesting structures.

MULTICELLULAR AND MULTIINDIVIDUAL - COULD IT BE THE SAME EVOLUTIONARY PARADIGM

Srecko Gajovic
Croatian Institute for Brain Research, School of Medicine, University of Zagreb, HR

The time line of evolution has one impressive feature. The time required for the appearance of life on the earth is several times shorter than the transition from unicellular toward multicellular organisms. The major problem that was necessary to be solved to achieve multicellular organisms was to devise the complicated system of cell to cell communication and coordination. Nevertheless, upon achieving this step, the individual cells lost their individuality when integrated in the multicellular organism, and could be replaced, differentiated or shed according to the need of the multicellular organism.

The technological advance the humanity has mastered recently includes some enormous achievements in particular in genetics and biomedicine. These are expected to be reflected in the improvement of quality of life and specifically in combating the diseases which affect humans. Another aspect is the awareness that the life span is genetically determined, therefore the insight in genes regulated the longevity of humans is expected soon.

Having this in mind some speculations about human future include as well the improvement of the humans as a species. The most speculations include the merging of technological gadgets and humans (e.g. creating cyborgs), claiming that this is already the case in people with e.g. heart pacemakers. Others advocate the application of genetic technology to humans in which the newly designed human species would appear with enhanced features.

Here I propose the different speculation, which takes basis in evolutionary change from unicellular to multicellular organisms. In order to achieve the higher level of complexity human individuals are already connected in a complex network of civilisation. The advances in technology like brain to brain interfaces could increase the communication abilities and quality of data transfer. As a result a novel being consisting of more human individuals could appear. Simple versions of these multiindividual associations are already present, i.e. the people participating on this conference. Still this occasional cooperation of humans, although it gave evolutionary advantage to the other primates, and currently produces the conference proceedings output available to the next generation, cannot be considered unique and self perpetuating.

BIOGENESIS OF LYSOSOME: AN EVOLUTIONARY ANALYSIS OF LYSOSOMAL ASSOCIATED MEMBRANE PROTEIN -1 (LAMP-1)

Manish Dwivedi, Vijay Tripathi, Dwijendra Gupta
Institute of Interdisciplinary Studies, Department of Biochemistry and Center
of Bioinformatics, Allahabad, IN

Over 20 distinct transport processes facilitating mainly the export of degradation products across the lysosomal membrane have been characterized functionally. However, biogenesis of lysosomes and the machinery regulating their interaction with other compartments are still incompletely understood. The lysosomal associated membrane proteins LAMP-1 and LAMP-2 are major constituents of the lysosomal membrane. Using different bioinformatics tools, we have established the phylogenetic relationship among LAMP-1 proteins from different organisms. The phylogenetic analysis reveals the structural as well as qualitative similarities and dissimilarities of LAMPs. Here our work based on ClustalW (multiple sequence alignment of LAMP-1 proteins), MEGA4 and BioEdit software revealed the phylogeny, amino acid composition, entropy and hydrophobicity profile of LAMP-1 that can help predict the nature, structure and localization of amino acid of the membrane proteins in the lysosomal membrane. This information can provide a proper platform to disclose the molecular basis of different metabolic disorders associated with the lysosomal membrane proteins like Lysosomal Storage diseases, I-cell disease etc. and to solve the question related to biogenesis of lysosomes.

PERSONALITY TRAITS IN THE MATE CHOICE: HOMOGAMY AND/OR SEXUAL IMPRINTING

Petra Gyuris
Department of Psychology, University of Pécs, HU

We have made an attempt at demonstrating the effect of sexual imprinting mechanism on human mate choice. In our former studies, we had focused on facial similarities between couples, now we wondered if homogamy is represented in personality characters, as well. Two hundred ninety six participants (49 couples and their parents) filled in the Caprara' s BIG FIVE Questionnaire. The couples were also asked to complete the s-EMBU retrospective attachment test (including Emotional warmth, Rejection, Overprotection scales). Significant resemblances were found between the males' wife and mother in Social Desirability and Conscientiousness traits of the BFQ. Our results on the effects of maternal rearing behavior style on their son's mating revealed controversial patterns. Scores on Rejection scale of s-EMBU were associated with Emotional Lability, and Emotional Warmth with Agreeableness trait, which supports our expectation. However, another analysis of maternal rearing has shown that those men who developed an unfavorable attachment with their mother during childhood would be attracted to women who are similar to her in Emotional Lability and Social Desirability traits, which seems to contradict our hypothesis. As for women's mate choice, only one tendency has been revealed for supporting the sexual imprinting hypothesis: those women who had experienced high Emotional Warmth from their father during childhood chose men who resembled their father in Conscientiousness factor of the BFQ.

DOES RECOMBINATION RATE EVOLVE WITH GENETIC DIFFERENTIATION IN HUMANS?

Hafid Laayouni, Ferran Casals, Ludovica Montanucci, Jan Graffelman, David Comas, Elena Bosch, Marta Melé, Arcadi Navarro, Francesc Calafell, Jaume Bertranpetit
CEXS, Pompeu Fabra University, ES

Recombination varies greatly among species and the recombination landscape between humans and chimpanzees is poorly conserved; shorter evolutionary time frames are needed to understand its evolution. Here, we analyze the recent evolution of recombination in humans through the analysis of a 500000 SNPs in 28 worldwide human populations. We found a high, negative and highly significant correlation between similarity in the recombination rates among all neighboring SNPs and genetic differentiation between populations. This correlation is broadly maintained when considering presence/absence of recombination hot spots and after correcting for effective population size. This result indicates a rapid pace of evolution of recombination, within the time span of differentiation of modern humans. These results are discussed in the context of association studies and different recombination rates in Human populations.

NEW APPROACH FOR DETECTING RECOMBINATION EVENTS IN A SET OF DNA SEQUENCES: TOWARDS THE ANCESTRAL RECOMBINATION GRAPH AND ITS PHYLOGEOGRAPHIC USE

Marta Mele
CEXS, Pompeu Fabra University, ES

Traditionally, the nonrecombinant genome, i.e., mtDNA or Y chromosome, has been used for phylogeography, notably for ease of analysis. The topology of the phylogeny structure in this case is a tree which is easy to comprehend and it is somewhat easy to infer. The main point for it is that it is only based on mutation, and most of the evolutionary reconstructions are based on it. However, recombination is an undeniable genetic fact for most part of the genome. Driven by the need for a more complete analysis in phylogenetics and phylogeography, we address the problem of estimating the ancestral recombination graph (ARG) from a collection of extant sequences and obtain a new set of genetic information based on recombinations: instead of haplotypes we obtain "recotypes". We exploit the coherence that is observed in the human haplotypes as patterns and present a network model of patterns to reconstruct the ARG. We test our model on simulations that closely mimic the observed haplotypes and observe promising results. This method intends to retrieve historical recombinations that have shaped the variation in a set of sequences with the possibility of using such events as markers for the spread of a species in a geographic region, giving rise to a phylogeography based on recombination. The present results show that this is a powerful tool (even more than SNP variation) to discriminate among human populations and trace back population history and evolution.

BECOMING IN THE CONTACT ZONE

Jovan Mircetic
Department of Genetics and Evolution, University of Belgrade, RS

This lecture seeks ways of thinking productively about metaphors in biology and the way these metaphors organize and influence experimental practice in biology. Although the biological framework has been shifted away from the ideas of essence and inner truth since the Darwin’s theory of evolution, we still encounter highly problematic conceptions of body and organism which are often interpreted in an essentialist manner. Using the figure of multispecies entity, firmly grounded in modern molecular biology discourse (as the result of sequencing the human genome and growing knowledge about different “species” inhabiting “the human” body) there will be an attempt to destabilize notions of unitarity of organism by offering mode of becoming rather than being as the one that is constituting for biology today. As an illustration of the general concept I will use various kinds of critical tools, hermeneutical deconstruction being one of them, in analyzing modern immunology discourse (for its main interest in subjects of distinguishing between self and the other). Also, I will discuss different reciprocal influences between science and cultural matrix which science is embedded in as an attempt to figure the ways in which knowledge is produced.

EVOLUTIONARY ANALYSIS OF THE N-GLYCAN METABOLIC PATHWAY ACROSS 5 PRIMATES: A NETWORK APPROACH

Ludovica Montanucci, Hafid Laayouni, Jaume Bertranpetit
CEXS, Pompeu Fabra University, ES

Biological function is the result of a large number of interacting molecules organized in a complex network. The impact of network architecture on the sequence evolution still poorly understood. Here, we analyse the N-Glycan metabolic pathway across 5 species of primates. Glycans have an important biological role in multicellular organs and organisms, since they are mediating the interaction between cells and the surrounding matrix.

Glycans at the cell surface may act as pathogen receptors, making them good candidates to show signatures of adaptation. The work consists in the detection of the selection pressures that acted on orthologous genes to be further analyzed in the context of the pathway they are involved in. This approach rely on the observation that the functional network which each gene takes part to, represent a major constraint in its evolutionary process and only by taking it into account we can achieve a deeper understanding of the evolution of the function which often arise as a combined effect of many different genes. Results are analysed focusing on the strength of purifying selection along the pathway in relation to the position of the gene (upstream vs. downstream genes) and looking at levels of selective constraints in relation at the number of interacting proteins to investigate if the architecture of the pathway constrains gene sequence evolution.

INTERCONNECTIONS BETWEEN ADULT THEORY OF MIND AND MACHIAVELLISM AND THEIR EFFECT ON THE PUBLIC GOODS GAME

Tünde Paál, Tamás Bereczkei
Department of General and Evolutionary Psychology, University of Pécs, HU

Theory of mind - the ability to attribute independent mental states and processes to others - plays an important role in our social lives. It enables us to engage in manipulation, and supposedly has a strong connection with Machiavellism, the tendency to use others in order to reach our own goals. In the present, ongoing study, we intend to explore this connection with the use of the computerized version of the Public Goods game with punishment condition. Our hypothesis is that different levels of theory of mind and Machiavellism lead to the use of different strategies of decision-making and thus different levels of financial success in this game. Theory of mind is examined by asking adult participants to analyze stories; Machiavellism is measured by using the MACH IV Questionnaire developed by Christie and Geis. Our results so far indicate that there is a positive correlation between the level of Machiavellism and the level of financial success; we plan the further, detailed analysis of the connections between theory of mind, Machiavellism and the various decision-making and punishment strategies used in the Public Goods game.

HISTORY: SOCIAL-DARWINIST REALISM OR HUMANITARIAN IDEALISM IN XXI CENTURY?

Oleg Semenov
Department of International relations and Regional studies, Nizhni Novgorod Lobachevsky State University, RU

Nowadays it is more and more obvious that strategic analysis of history and international relations is moving towards technical modernism, depreciating humanitarian values and factors. The question is, whether such deformation relates only to theories and concepts or history itself is becoming just a sum of economic and technical potentials. Social-Darwinism at the beginning of XXI century seems to be quite popular as it gives the well-reasoned strategic picture of modern processes: collapse of USSR was predictable as the Soviet system militated mechanisms of natural selection, the whole system of international relations in future will imply the "democracy of minority" and freedom of those who are powerful. Even more, due to modern social-Darwinists the global aim of new century is to finally establish the survivance of the fittest, whish is the natural logic of history without any spiritual mysticism. Instead of powerful and aggressive USSR we have weak, offended and dishonoured ordinary country, which perfectly fits into positivist scheme of history. So the main problem is which paradigm will be dominant in new world order: value-oriented idealism with global system of checks and balances or hegemony of social-Darwinist dictate of powerful superpowers.

IDENTIFICATION OF NON-CODING REGIONS CONSERVED SPECIFICALLY IN PRIMATES

Mahoko Takahashi, Naruya Saitou
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Evolutionary process toward human within primate lineage is one of the active study fields. Despite widespread interest in primate evolution, little information exists about its genetic mechanism. Regulatory elements contained in non-protein-coding sequences are considered as candidates for important causes to drive evolution.

To identify the regulatory region which might affect primate evolution, we performed a comprehensive MegaBLAST search and identify primate specific HCNS (human, chimpanzee, orangutan and rhesus) and compared with rodent specific (mouse and rat) and mammalian specific HCNSs (4 primates, mouse, horse, dog, and cow). A total of 191 primate specific, 834 rodent specific and 1048 mammalian specific HCNS are identified. We examined the statistically over-represented GO terms assigned to the most flanking genes located within 1Mb of the HCNSs by chi-square-analysis. These three HCNSs are highly associated with genes involved in development, transcriptional regulation and regulation of metabolic process. However, primate specific HCNS show more association with negative metabolic process (transcriptional repressor activity) while rodent specific HCNS show more association with positive metabolic process. The newly extracted primate specific HCNS might contain primate specific regulatory elements, and might affect to develop primate specific characteristics.

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