IUBS

IUBS 2015
Frontiers in Unified Biology

Abstracts and Program

of the

32nd International Union of Biological Sciences
General Assembly and Conference

14–16 December 2015
Berlin, Germany

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Preface

It is with great pleasure that we welcome you to Berlin in December 2015 on the occasion of the 32nd General Assembly of the International Union of Biological Sciences, IUBS. We anticipate inspiring exchanges between colleagues from all over the world and from all biological sub-disciplines – and beyond – in order to promote biological research across these disciplines. We also hope to communicate insights derived from biological research to a broad audience, especially in relation to the many challenges facing humankind today. To do so, a unified approach to the biological sciences is needed.

We will be meeting to discuss key topics within the Unified Biology perspective, and how this must play a key role when addressing the large challenges facing humanity today. Through plenary talks and discussions we aim to unite the perspectives of the "Common Future" debate of the last century with the "Future Earth" approach of this century.

We will have symposia and posters on topics such as societal interfaces with biology, biological consequences of climate change and its lessons from the past, urban biology, biological nomenclature, informatics, and bio-education.

During the General Assembly, IUBS delegates will also discuss future collaborations and scientific programs that will be implemented during the next triennium.

We hope and encourage you to get involved in this exchange and fundamental debate. We look forward to welcoming you in Berlin.

Nils Chr. Stenseth
IUBS President

Regine Jahn
Conference Chairwoman
IUBS Executive Committee Member

Program of the 32nd International Union of Biological Sciences

Monday, 14 December	**Room “Cambridge”**	09:00 – 12:00 **IUBS General Assembly | for delegates only**
		14:00 – 18:00 **Keynote Speakers & Panel: Our Common Future**
	BGBM Tropical House	19:00 – 21:00 **Reception**

Tuesday, 15 December		**Symposia (3 parallel sessions)**	
		09:00 – 13:00	**14:00 – 18:00**
	Room “Cambridge”	**Symposium 1** Biological Consequences of Global Change: current challenges	**Symposium 4** Integrative Climate Change Biology – Biodiversity, functional traits, and lessons from the past
	Room “Oxford”	**Symposium 2** Building an Informatics Agenda that will deliver a Unified Biology	**Symposium 5** BioNomenclature: Making nomenclatural codes, concepts and tools fit for modern research
	Room “Sorbonne”	**Symposium 3** Unified Biology Education for sustainable and equitable world	**Symposium 6** The Science-Policy Interface

Wednesday, 16 December		**General Assembly and Symposium**
		09:00 – 13:00
	Room “Cambridge”	**IUBS General Assembly | for delegates only**
	Room “Oxford”	**Symposium 7** From Urban Biology to sustainable BiodiverCities

Monday 2015•12•14

09:00 – 12:00: IUBS General Assembly | for delegates only

14:00 – 14:15: Opening

14:15 – 18:00: Keynote Speakers & Panel: Our Common Future

- **14:15 – 14:45: Nils Christian Stenseth,** President, IUBS: *The 21st Century is the Century of Biology: from Darwin to the DNA helix and beyond*
- **14:45 – 15:15: Thomas Brooks,** Head, Science & Knowledge Unit, IUCN: *Does Conservation Work?*

15:15 – 15:45: Coffee Break

- **15:45 – 16:15: Anne Larigauderie,** Executive Secretary, IPBES: *IPBES: Biodiversity Science for Decision Making*
- **16:15 – 16:45: Paul Shrivastava,** Executive Director, Future Earth: *Enlivening Biological Sciences for Sustainable Development*

16:45 – 18:00: Panel, all keynote speakers: Our Common Future

19:00 – 21:00: Reception at the Botanic Garden and Botanical Museum, Freie Universität Berlin, Königin-Luise-Str. 6-8.

Tuesday 2015•12•15

09:00 – 13:00: Symposia (3 parallel sessions)

1. Biological Consequences of Global Change: current challenges

2. Building an Informatics Agenda that will deliver a Unified Biology

3. Unified Biology Education for sustainable and equitable world

13:00 – 14:00 Lunch Break

14:00 – 18:00: Symposia (3 parallel sessions)

4. Integrative Climate Change Biology – Biodiversity, functional traits, and lessons from the past

5. BioNomenclature: Making nomenclatural codes, concepts and tools fit for modern research

6. Biology and the Societal Interfaces

18:30 – 19:30 Poster Session

20:00 – 22:00 Public Open Event: Zoological Nomenclature – Quo vadis?

Wednesday 2015•12•16

09:00 – 13:00: Symposium 7

7. From Urban Biology to sustainable BiodiverCities

09:00 – 13:00: IUBS General Assembly | for delegates only

Symposium 1

Biological Consequences of Global Change: Current Challenges

Organizers: Zhibin Zhang[1], Yury Dgebuadze[2], Chunxu Han[3]
[1] China National Committee for the International Union of Biological Sciences (CCIUBS)
[2] Russia National Committee for the International Union of Biological Sciences (RCIUBS)
[3] International Society of Zoological Sciences (ISZS)

Outline
Global Change is an international phenomenon and needs international cooperation and collaboration. To understand the biological consequences of global change it also needs a unified biology, i.e. the interaction and employment of multi-disciplines of biology and beyond. The Biological Consequences of Global Change (BCGC) Program was initiated as an international research program by the International Society of Zoological Sciences (ISZS) in 2008, supported by the Chinese Academy of Sciences (CAS) as a key international cooperation program and adopted in 2009 by the International Union of Biological Sciences (IUBS) as a new international research program. In 2012, it was reviewed as the core of the programs at the IUBS. Currently, there are over 20 scientists involved from Australia, Chile, China, France, India, Norway, Russia, Israel, Germany, South Africa, Mexico and the United States. For details of the BCGC program, please visit the website at:
www.blogbalzoology.org

Chair: Zhibin Zhang, Institute of Zoology, Chinese Academy of Sciences, China.

9:00 - 9:10 | Chunxu Han (Secretary General, International Society of Zoological Sciences (ISZS)): **The IUBS/ISZS's program, Biological Consequences of Global Change (BCGC).**

9:10 - 9:30 | Yury Dgebuadze (Russian Academy of Sciences (RAS); Deputy Director, A. N. Severtsov Institute of Problems of Ecology and Evolution Russia): **Global Change and Fish Diversity in Central Asia.**

9:30 - 9:50 | Jürgen Heinze (Universität Regensburg, Germany): **Ants in a Globalized World.**

9:50 - 10:10 | Fuwen Wei (Institute of Zoology, Chinese Academy of Sciences, China): **Global climate shifts drive the population fluctuation of giant pandas.**

10:10 - 10:30 | Christelle Robinet (INRA- Zoologie Forestiere, France): **A model insect for global change, the pine processionary moth.**

10:30-10:50 | Xianfeng Yi (College of Life Science, Jiangxi Normal University, Nanchang, Jiangxi, China): **Temperature-directed seed masting and its influences on population fluctuations of small rodents.**

10:50-11:00 Coffee Break

Chair: Yury Dgebuadze Russian Academy of Sciences (RAS), A.N. Severtsov Institute of Problems of Ecology and Evolution, Russia.

11:00 - 11:20 | **Zhibin Zhang** (Institute of Zoology, Chinese Academy of Sciences, China): **Population dynamics on Brandt's vole under global change: large-scale manipulative experiments reveal accumulative effects of livestock grazing on Brant's vole populations in steppe grassland.**

11:20 - 11:40 | **Hongxuan He** (Institute of Zoology, Chinese Academy of Sciences, China): **Wildlife Borne Diseases Surveillance and Prevention in China.**

11:40 - 12:00 | **Abraham Haim** (Faculty of Science and Science Education, University of Haifa, Israel): **Biological Consequence of Global Change – The Disappearance of Dark Nights.**

12:00 - 12:20|
Xinhai Li (Institute of Zoology, Chinese Academy of Sciences): **Historical declines of 11 mammals in China and associated driving forces.**

12:20 - 12:35|
Hiroyuki Takeda (Department of Biological Sciences, Graduate School of Science, University of Tokyo, Japan): **Epigenetic and environment in fish.**

12:35 - 12:45 |
Wenhua Xiong (Executive Editor, Integrative Zoology (INZ)): **Introduction on INZ's efforts for BCGC.**

12:45 - 12:55 |
Nils Chr. Stenseth (Centre for Ecology and Evolution, Department of Biosciences, University of Oslo, Norway): **Concluding comments.**

12:55 - 13:00 |
Zhibin Zhang: Wrap-up

Symposium 2

Building an Informatics Agenda that will deliver a Unified Biology

Organizer & David Patterson
IUBS Executive Committee. University of Sydney, Australia

Outline

IUBS has set itself the agenda of promoting a unified Biology. This complements the trend of a century for a detailed, particular, and exact approach to Biology. One way to unify biology is to take advantage of the new sciences of informatics. Our goal is to assemble a team who will promote a new and transformative agenda for an infrastructure that is capable of linking events involving particles as small as photos to particles as big as the complete biosphere; or events that last for less than a billionth of second to those that have endured for over 3 billion years. We will use this opportunity to bring together world leaders and visionaries who are expert informaticians.

Chair: Rich Pyle (Bishop Museum, Hawaii; ICB; ZooBank & ICZN)

09:00 – 9:30 | **David Patterson** (University Sydney, Australia): **Building an informatics agenda that will deliver a unified biology: Introduction**

09:30 – 10:00 | **David Shorthouse** (Canadensys, Montreal Canada): **Names based cyberinfrastructure for biology.**

10:00 – 10:30 | **Robert Hanner** (BOLD, University Guelph, Canada): **Integrating molecular perspectives into taxonomy, ecology, and biosurveillance.**

10:30 – 10.50 | **Gabriele Dröge** (BGBM, Freie Universität Berlin, Germany): **The Global Genome Biodiversity Network (GGBN).**

10:50 – 11:30 Coffee Break

11:30 - 12:00 | **Dora A. L. Canhos** (CRIA, Brasil): **Challenges in building an infrastructure for all of biology.**

12:00 – 12:20 | **Anton Güntsch** (BGBM, Freie Universität Berlin, Germany): **GFBio – A sustainable federated national infrastructure for biological data management.**

12:20 – 12:40 | **Donat Agosti** (Plazi, Switzerland): **Nothing in Science makes sense except as open access.**

12.40 – 13.00 | **General Discussion**

Symposium 3

Unified Biology Education for sustainable and equitable world

Organizer & Chair: LS Shashidhara[1]
[1] Indian Institute of Science Education and Research (IISER), Maharashtra, India & IUBS Executive Committee

Outline

Talks and discussions would focus on (i) integrated biology education for sustainable and equitable world; (ii) ways of connecting field biology to lab biology and make the education and research multidisciplinary; (iii) developing inexpensive modules/tools for education and research in field biology that can be effectively used in countries with less resources in their Schools/Colleges and Universities.

Schedule

09:00 – 09:15 | Nils Christian Stenseth (Centre for Ecological and Evolutionary Synthesis, Norway): **Opening Remarks: BioEd: What can IUBS - and the ICSU Bio-cluster – do today for Future Earth?**

09:15 – 10:00 | KN Ganeshaiah (School of Ecology and Conservation, University of Agricultural Sciences, GKVK Bengaluru, India): **Broadening Biology Education: need to augment arts and science for a better biology.**

10:00 – 10:45 | Eric Warrant (Department of Biology, University of Lund, Sweden):
Teaching basic concepts of animal vision and navigation to school children using dung beetles as model organisms.

10:45 – 11:15 Coffee Break

11:15 – 11:45 | John Buckeridge (Earth & Oceanic Systems Group, RMIT University, Melbourne, Australia): **Biology and Palaeobiology Education: are we failing to provide the appropriate foundations?**

11:45 – 12:30 | LS Shashidhara (Indian Institute of Science Education and Research (IISER) Pune, Maharashtra): **Integrated Biology Education for Sustainable and Equitable world**

12:30 – 13:00 | Panel discussion

Symposium 4

Integrative Climate Change Biology - Biodiversity, functional traits, and lessons from the past

Organizers & Chairs: Jussi T. Eronen[1], A. Michelle Lawing[2] & Jason Head[3]
[1] University of Helsinki, Finland
[2] Texas A&M University, USA
[3] University of Cambridge, UK

Outline

New biological problems require new, unified approaches. One of the great problems for biology in the 21st Century is to understand how organisms, species, and ecosystems respond to climatic changes. One of the great complexities of biotic responses to climate change is scale: spatial scales range from the individual to hemispheres, the processes, temporal scales range from years to millennia, and the scales of response are varied, including ill health, increased productivity, extirpation, range expansion, selective adaptation, ecosystem reorganization, and extinction. Each scale is associated with a different biological subdiscipline: smaller, shorter scales are the domain of conservation biology; medium scales are the domain of ecology; and long, large scales are the domain of paleontology. This symposium brings together scientists who are studying climate change biology at all these scales with the aim of fostering communication, sharing data, and exchanging methods. The speakers include paleontologists working in deep time and on the Anthropocene, ecosystem scientists working on largescale responses of species ranges to changing climate, phylogeneticists working on evolutionary turnover due to extinction and cladogenesis, and ecologists working on decadal scale changes in species abundance and distribution. The unifying concept used by all of them is an ataxic approach that focuses on the role of functional traits in responding to global change, and use of those traits as metrics for measuring the rates and magnitudes of responses in a way that can be used to amalgamate data across temporal and spatial scales in the hope of better forecasting changes to come in the Late Anthropocene.

Schedule

14:00 – 14:30 | Mikael Fortelius (University of Helsinki): **Mass Extinctions, Past and Present.**

14:30 – 15:00 | Susanne Fritz (Senckenberg BiK-F): **Diversity in space and time – wanted dead and alive.**

15:00 – 15:45 | Jason J. Head (University of Cambridge, UK), **Jussi Eronen** (Senckenberg BiK-F & University of Helsinki, Finland, & Senckenberg Biodiversity and Climate Research Centre, Frankfurt, Germany), **P. David Polly** (Indiana University, Bloomington, IN, USA): **Ecometrics and global change: using modern fossil functional traits to estimate biotic response to environmental transitions.**

15:45 – 16:15 Coffee Break

16:15 – 16:40 | Raymond Katebaka (African Union of Conservationists (AUC), Makerere University, Kampala, Uganda): **Assessment of the Potential Impact of Biodiversity Change on Waterfowl of Lake Victoria.**

16:40 – 17:05 | Johannes Müller (NHM Berlin): **Cenozoic cooling and reptile evolution.**

17:05 – 17:30 | Jan Schnitzler (Senckenberg BiK-F): **Diversification dynamics from extant and fossil lineages.**

17:30 – 18:00 | Nils Christian Stenseth (Centre for Ecological and Evolutionary Synthesis, Norway): **Climate Change and mammals/birds.**

Symposium 5

BioNomenclature: Making the Nomenclatural Codes, concepts and tools fit for modern research

Organizers & Chairs: Ellinor Michel[1], Regine Jahn[2] & Nicholas Turland[2]
[1]NHM London
[2]Botanischer Garten und Botanisches Museum, Freie Universität Berlin

Outline

Streamlining the process of doing robust, well-referenced, repeatable taxonomy is recognised as among the highest priorities for improving our scientific grasp on the biodiversity crisis. A key component in this is ensuring that naming processes, systems and infrastructures are fit for purpose and adaptable for the future. Nomenclature is the anchor for biological information; it needs to be consistent, understandable and not a burden to use. This symposium will cover nomenclatural issues across the range of codes - zoology; plants, algae and fungi; bacteria; and viruses. Common problems include recognition of taxa using molecular data, online taxonomic information management systems (cybertaxonomy infrastructures), open nomenclature, links with taxonomic systems and harmonisation of practice. Approaches to these problems vary. By bringing together key players, we aim to discover commonalities and derive ways to accelerate the recognition and description of new species in the future.

Schedule

14:00 - 14:20 | David Hawksworth, John McNeill, Werner Greuter (NHM London, & Univ. Complutense de Madrid, Spain; RBG Edinburgh, UK; BGBM, Freie Universität Berlin; all ICB): **The BioCode: from vision to reality.**

14:20 - 14:40 | Mike Adams (Int'l Committee on the Taxonomy of Viruses (ICTV) & ICB): **Challenges and developments in virus taxonomy.**

14:40 – 15:00 | Brian Tindall (Leibniz-Institut DSMZ, Germany & ICB): **The Bacteriological Code: A model to follow or one to avoid?**

15:00 - 15:20 | Nicholas Turland (BGBM, Freie Universität Berlin, Germany & ICB): **Fit for purpose, or out of shape? The present and future Code for algae, fungi, and plants.**

15:20 – 15:40 | Paul Kirk (RBG Kew, UK & Institute of Microbiology (CAS) & Index Fungorum & ICB): **Mycologists lead the way... but it's not all plain sailing.**

15:40 – 16:00 | Wolf-Henning Kusber & Regine Jahn (BGBM, Freie Universität Berlin, Germany & ICB): **Algae: Diverse codes for diverse taxa?**

16:00 – 16:20 Coffee Break

16:20 – 16:40 | Rafael Govaerts (RBG Kew, UK; IPNI): **Follow the names: Biodiversity Informatics in a botanical context.**

16:40 – 17:00 | Gary Rosenberg (ANSP / Drexel University, USA): **Infiltration of the International Code of Zoological Nomenclature by the Biological Species Concept.**

17:00 – 17:20 | Rich Pyle (Bishop Museum, Hawaii; ICB; ZooBank & ICZN): **ZooBank, registration & the digital future for nomenclature.**

17:20 – 17:40 | Nico Cellinese & Hilmar Lapp (Univ. of Florida, Gainesville, USA & PhyloCode & ICB; Duke Univ., USA): **Integrating data at the Tree of Life scale using computable clade definitions.**

17:40 – 18:00 | Christine Flann (Naturalis Biodiversity Center, NL & Species 2000 & Catalogue of Life): **Catalogue of Life – View on nomenclature & big picture aims.**

Symposium 6

Biology and the Societal Interfaces

Organizers & Chairs: Cornelia Löhne[1] & Kathrin Vohland[2] & Lily Rodriguez[3]
[1] Forschungsmuseum Alexander König, Bonn
[2] Museum für Naturkunde Berlin
[3] Universität Bonn

Outline

The biodiversity crisis shows how vulnerable (human) life on Earth is. Biological Sciences are a key to ensure a sustainable development of our planet: Many solutions stem from biological sciences, such as genetic and physiological adaptations to climate change and other unfavourable environments, or the increasingly acknowledged implementation of biomimicry into technologies, products and processes. Biological sciences provide a valid basis for global political negotiations on biodiversity and climate change, but are at the same time affected by political decisions and regulations. Furthermore, the links between science and citizens become more diverse and intensive: Private people engage with biology, for example as citizen scientists supporting biodiversity monitoring programmes, or people in garages as do-it-yourself biologists. In this symposium we would like to reflect the important interactions between biological research, policy and society, and discuss how we may intensify and improve these links even more.

Schedule

A) The Science-Policy Interface:

14:00 – 14:20 | Cornelia Löhne (ZFMK, Germany) & **Kathrin Vohland** (MfN Berlin, Germany): **Biology and the Societal Interface – Setting the scene.**

14:20 – 14:50 | Carsten Neßhöver (Helmholtz Centre for Environmental Research – UFZ, Leipzig, Germany): **Engaging in science-policy interfacing – a growing need for the biological sciences.**

14:50 – 15:10 | Chris H.C. Lyal (Natural History Museum London, UK): **The Nagoya Protocol on Access and Benefit Sharing – Challenges and opportunities for biological scientists from international policy.**

15:10 – 15:30 | Lily Rodriguez (University of Bonn, Germany): **ABS – Delivering benefits and identifying non-commercial research in biological sciences.**

15:30 – 15:45 | Plenary discussion

15:45 – 16:15 Coffee Break

B) Science, sustainable development, and Citizens

16:15 - 16:45 | **Heidi Ballard** (UC Davis, USA): **Synergies between citizen science and learning about nature.**

16:45 – 17:05 | **Rüdiger Trojok** (ITAS/KIT, Germany): **What is DIYBio – theory, practice and perspectives.**

17:05 – 17:25 | **Katrin Reuter** (MfN Berlin, Germany): **Transdisciplinary Biodiversity Research.**

17:25 – 17:45 | **Matthias Geiger** (ZFMK, Germany): **Engaging citizens in the inventory and DNA barcoding of fauna and flora – Experiences from the German Barcode of Life Project.**

17:45 – 18:00 | **Plenary discussion**

Symposium 7

From Urban Biology to sustainable BiodiverCities

Organizers & Chairs: Ingo Kowarik[1] & Kerstin Elbing[2]
[1] Technische Universität Berlin
[2] VBIO

Outline

The number of megacities inhabited by more than ten million people is increasing continuously. It is estimated that in 2030 already 60% of the world's population will live in cities. Thus, the sustainable development of cities as a living environment is one of the major challenges for politics and society. Some stakeholders even claim that there will be no sustainable world without sustainable cities. The United Nations Sustainable Development Goals (SDG), upon which will be decided in autumn 2015, has as one of its goals (no. 11) that cities and human settlements shall be designed to be "inclusive, secure, resilient and sustainable”. There are a couple of approaches, how to achieve the goal of sustainable cities, that are discussed by different stakeholders and on different levels. They all have in common that environmental and economic as well as socio-cultural factors are taken into account. Cities are no longer perceived as cultural entities distinct from nature. In fact, cities form a global network that is woven into the global ecosystem at every point. This Symposium is dedicated to the natural resources of the city and its biological aspects of a sustainable urban development. The Symposium takes up the tradition of "Urban Ecology", a research field whose basic principles were developed originally in the City of Berlin (West). The focus of the lectures will be laid on the urban biodiversity. The talks will present status and function of biological diversity in the city, the urban-rural gradient of biodiversity and the importance of biodiversity and ecosystem services for the city and its socio-economic implications. The "Berlin Biodiversity Strategy" will show starting points how “nature” can be promoted in a modern, liveable metropolis.

Schedule

09:00–09:40 | **Ingo Kowarik** (Technische Universität Berlin, Germany): **Integration of biodiversity into urban development. The case of Berlin.**

09:40–10:15 | **Eva Knop** (University of Bern, Switzerland): **Biodiversity and ecosystem functioning in and of cities.**

10:15–10:50 | **Sonja Knapp** (Helmholtz Centre for Environmental Research – UFZ, Halle, Germany): **Effects of urbanization on plant biodiversity - insights into functions and phylogenetics.**

10:50–11:10 Coffee Break

11:10–11:45 | Assaf Shwartz (Haifa, Israel): **Aligning the agendas of public health and conservation: Which elements of biodiversity provide well-being benefits to city dwellers?**

11:45–12:20 | Divya Gopal (Bangalore, India): **Urban biodiversity and people in Bangalore, an Indian megacity.**

12:20–12:55 | Ulrike Sturm (MfN, Berlin, Germany): **Discover your city – Urban nature as an experience in everyday life.**

Poster Session Tuesday, 18:30-19:30

Gisela Baumann (Botanischer Garten & Botanisches Museum Berlin, Freie Universität Berlin, Germany): **Out of the cellar – into the web. Opening up natural history collections to the public via Europeana**

Lars Binder (University of Leipzig, Germany): **New insights into the cell cycle control mechanisms of histone genes**

Anoop Karumampoyil Das (Centre for Conservation Ecology MES Mampad College, University of Calicut, India): **Functional diversity of aquatic insects in water-filled tree holes in the tropical forests of the Western Ghats, India**

Song Ge (Institute of Botany, Chinese Academy of Sciences, Beijing, China**): Insights into the role of differential gene expression on speciation of two Oryza species**

Marian-Traian Gomoiu (Romanian Academy / National Institute for Research and Development of Marine Geology and Geoecology, Constanta, Romania): **The Current Situation and Prospects of Romanian Biological Oceanography**

Bakhtiyor Karimov (Scientific-consulting Center "ECOSERVICE", Tashkent, Uzbekistan): **Climate change and increasing water salinization vulnerability mitigation strategies for fisheries sector development in desert and arid lands of Aral Sea Basin**

Alexey Kotov (A.N. Severtsov Institute of Ecology and Evolution, Moscow, Russia): **Discrimination of the 'traditional' taxonomy and the 'descriptive' science - evidence of a deep crysis in all Natural Sciences, not in taxonomy only?**

David Lazarus (Museum für Naturkunde, Berlin, Germany): **Biodiversity-Climate Interactions in Modern Oceans and deep Time: Integrating Plankton and Oceanographic Data with the Marine Microfossil Record**

Santiago Merino (National Natural History Museum, Spain): **Strangers Spreading Diseases: The Role of Introduced Species as Vectors of Blood Parasites for Endemic Threatened Forest Bird Species in Chile**

Dorota Myszkowska (Jagiellonian University Medical College; delegate of the International Association for Aerobiology (IAA), Krakow, Poland): **Practical applications of aerobiological studies**

Katrin Reuter (Museum für Naturkunde Berlin (MfN), Berlin, Germany): **Network-Forum: a science-policy interface for biodiversity research in Germany**

Livia Schäffler (Museum für Naturkunde Berlin (MfN), Berlin, Germany): **The Leibniz Network on Biodiversity (LVB) – Objectives and Priorities**

Lutz Suhrbier (BGBM, Freie Universität Berlin, Germany): **AnnoSys – A Generic Online Annotation Management System and Repository for Sustainable Collection Data**

Makamas Sutthacheep (Ramkhamhaeng University, Marine Biodiversity Research Group, Faculty of Science, Bangkok Thailand): **Impacts of Climate Change Induced Coral Bleaching on Ecosystem Services in the Gulf of Thailand**

Bulent Teke (Department of Animal Breeding and Husbandry, Ondokuz Mayis University, Veterinary Faculty, Samsun, Turkey): **Effects of the lairage time on beef cattle**

Jacob Wickham (International Society of Zoological Sciences, Beijing, China): **Biological Consequences of Global Change**

Thamasak Yeemin (Ramkhamhaeng University, Marine Biodiversity Research Group, Faculty of Science Huamark, Bangkok, Thailand): **Science-Based Policies for Tourism Management at a Marine National Park**

Abstracts of talks & posters

CHALLENGES AND DEVELOPMENTS IN VIRUS TAXONOMY

Adams, Mike

International Committee on Taxonomy of Viruses (ICTV) and ICB, 24 Woodland Way,
Stevenage, Herts SG2 8BT, UK.

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What is now the International Committee on Taxonomy of Viruses (ICTV) was set up in 1966 to develop an international and universal classification for viruses, irrespective of the host (vertebrate, plant, prokaryote etc). The practice of virus taxonomy differs from other types of biological classification because ICTV not only regulates a Code of Nomenclature but also considers and approves the creation of all virus taxa (currently orders, families, subfamilies, genera and species). Priority of publication is not the determining factor. Species names are frequently derived from the common (vernacular) name of the virus (usually in English) used to establish the species. Changes to approved taxonomy are currently made annually and the latest release is published on a web site that provides links to the proposal documents that justify the changes (http://www.ictvonline.org/virusTaxonomy.asp).

There are often difficulties in creating higher levels of taxonomy because of the huge diversity of viruses and the mosaicism evident amongst the genomes of many related viruses. The other most obvious challenge is the vast amount of sequence data that is being generated from metagenomic surveys, sometimes of environmental samples (faeces, soil, water etc). These data are revealing the presence of many viruses that are largely uncharacterized and for which host organisms are often unknown. The lack of biological data make such viruses difficult to classify using current criteria, so processes need to be found to integrate the phylogenetic information they provide into future taxonomic schemes.

With funding from the Wellcome Trust, the ICTV is making major changes to its operation and conducting a wide-ranging review of its procedures and policies. Web-based resources are being developed to assist taxonomic assignment of sequence data and to provide automated systems for submission and evaluation of taxonomic proposals. Specialist meetings are being organised to discuss and develop policies for naming 'sequence-only' data and for classifying bacteriophages, where mosaicism is a particularly acute problem. ICTV Reports have recently been large and expensive encyclopaedias. This information will be migrated to an open-access web site that can be updated on a rolling basis and with links to other biological databases.

NOTHING IN SCIENCE MAKES SENSE EXCEPT AS OPEN ACCESS

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Science covers all aspects of life and its findings are reported in millions of articles and books that have been collected, though never completely, in libraries small and large. These publications form an impressive physical corpus of knowledge that depends on human eyes to extract structured information and facts from a narrative designed primarily for human consumption. With the advent of the digital age, and access provided through the Internet, all the data and information in those articles could be converted into one seamless Open Knowledge Management System (OKMS) accessible from anywhere in the world. It could be mined for structured information and be the basis for new discoveries, a foundation for a knowledge-driven economy, and not least, closing a gap of access - at least in science - between the developed and developing economies.

With linked open data in mind, such a system is on the verge of becoming a reality. The prerequisite is, of course, open access to digital, machine-readable, semantically-enhanced, linked scientific research results. With the help of ontologies and reference systems, research data can be analysed not just from one domain but across several domains, and thus potentially provide new insights. One of the most successful examples of this is the use of geographic location to bring together seemingly disparate facts such as on a given point in Google Maps information on traffic jams, restaurants and best prices for a steak. Through this shared property of geolocation, it is possible to mine, analyse and visualize data that otherwise appear disconnected. In Biology, scientific names of taxa lend themselves as such a reference system, if implemented, allowing accessing all the facts known about a specific taxon.

Based on the experience of successfully implementing a semantic publishing workflow in taxonomic biology, the steps needed to arrive at one of the world's most advanced publication system will be explained and discussed. This system is based on the widely used Journal and Archival Tag Suite (JATS) standard which has been enhanced through the TaxPub extension to cover the semantics of taxonomy. This way an article becomes the source for various databases such as the Global Biodiversity Information Facility (GBIF) and National Center for Biodiversity Informatics (NCBI), and at the same time its content can be visualized and mined by third parties.

Though efforts are underway to digitize the backlog of already published literature, a case is made for a decisive effort to prevent losing any structured data in the publishing workflow. We have to ensure that the necessary infrastructure is built to provide machine access to the rapidly growing corpus of scientific research results to build an Open Knowledge Management System. The Berlin, Bouchout and The Hague Declarations show the scientific community’s commitment towards such an OKMS, complemented with respective actions by governments and funding bodies.

SYNERGIES BETWEEN CITIZEN SCIENCE, NATURAL HISTORY MUSEUMS, AND LEARNING ABOUT NATURE

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Through their unique combination of specimen collections, scientific and public education expertise, and wide audience reach and trust, natural history museums (NHMs) are obvious settings for bridging conservation science and education through citizen science. Building on over 100 years of amateur naturalist contributions to biodiversity science, a wide range of NHM-based citizen science programs have emerged recently. Yet no comparative studies of the conservation outcomes of this work exist. Here we ask, what is the evidence that NHM citizen science contributes to conservation, what kinds of programs and strategies do so, and how could this approach be better realized for conservation goals? We analyze 43 citizen science programs across three museums (one UK, two US) to assess whether and how they contribute to conservation-relevant outcomes. We find evidence that they support conservation, both directly through site and species management, and indirectly through research, education and policy impacts. This study has implications for better understanding the role NHMs can play in maximizing the socio-ecological impacts of citizen science, including bringing citizen science to new audiences, mobilizing volunteers to collect and analyze data required to study species invasions and impacts of global changes, and conducting community-relevant research in urban systems. We conclude that NHM citizen science provides multiple entry-points and levels of engagement for participants in science and access to new means of studying biodiversity, all under one “roof” – both physical and virtual.

OUT OF STORAGE - ONTO THE WEB OPENING UP NATURAL HISTORY COLLECTIONS TO THE PUBLIC VIA EUROPEANA

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Natural history institutions increasingly recognize the value of digitized specimens not only for biodiversity research but also for education, creative developments, or as an information resource for the general public. The technical developments of the Global Biodiversity Information Facility (GBIF) were instrumental for implementing centralized portals mediating access to a wide range of distributed natural history collection information systems. Today, a growing number of natural history collections are being digitized, not only providing textual metadata on the collection objects, but also increasingly multimedia representations. However, searching and browsing multimedia content can be like finding a needle in the haystack for users when confronted with hundreds of web interfaces and millions of records of cultural heritage institutions. Moreover, intellectual property right information associated with multimedia objects is inhomogeneous and often concealed or not accessible at all. Finally, many collections cannot afford to build up and sustain IT-services and tools, so existing objects often remain hidden from researchers and the public. www.Europeana.eu is the cross-domain central portal to Europe's digitized cultural and scientific heritage. Its newest version links to over 46 million digital objects such as images, texts, sounds, and videos. Some of these are world famous, others are hidden treasures from Europe's museums, galleries, archives, libraries and audio-visual collections. Europeana's vision is to make cultural heritage as easily accessible and as freely reusable as possible. Every digital object is provided with licenses giving explicit information about conditions for re-use. Since 2011, OpenUp! is a growing network of European institutions providing natural history objects to Europeana. This includes digitized specimens, natural history artwork, animal sounds, and videos. The OpenUp! natural history aggregator for Europeana is coordinated by the Freie Universität Berlin, Botanic Garden und Botanical Museum Berlin (BGBM). Collections provide standardised metadata via the BioCASe Provider Software (Biological Collection Access Service), feeding into the aggregation process that includes the harvest, transformation and transfer of metadata to Europeana. Harvests are repeated at regular intervals to ensure availability of up-to-date information on the Europeana data portal. In addition, scientific metadata items are enriched by common names of plants and animals to increase the accessibility of objects by non-scientific users. So far, 23 partners from 12 European countries take part in the OpenUp! network and contribute more than 2.2 million records. Data providers benefit from reaching new audiences, increasing web traffic to institutional websites, and gaining better visibility towards research funding organizations and within society. Europeana is an inspiring approach on how to make cultural heritage in its entirety accessible to the public, and how to open it up for re-use. By presenting natural history objects in the cultural context via Europeana, natural history collections can broaden their audience and achieve a better representation of their field in the public space.

NEW INSIGHTS INTO THE CELL CYCLE-DEPENDENT CONTROL MECHANISMS OF HISTONE GENES

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Histones are among the most evolutionary conserved proteins in eukaryotes. They are essential for DNA packaging and the regulation of genes. The regulation of histone mRNA expression has been studied extensively, but detailed molecular mechanisms remain unresolved. mRNA levels of core histones peak in S phase which is achieved by cell cycle-dependent transcriptional regulation as well as by modulation of mRNA stability. For many histones multiple copies of genes exist coding for the same protein but differing in their promoter regions. In general, mechanisms of gene expression have been studied for groups of histones rather than for individual genes because of the high similarity of related histone genes. Here, we compare for the first time the regulation of individual histone genes of the H3.1 histone group to gain a more detailed understanding of potentially differing control mechanisms.

We have found for a specific group of histones that there are remarkable differences in the mechanisms of gene expression between the individual members. We have identified a subgroup of those genes showing a strong activation of promoter activity when cells progress from G0/G1 to S-phase.

We observe that such genes are controlled by cell cycle-dependent elements (CDE) and cell cycle genes homology regions (CHR) in their promoters. Binding of the multiprotein complex DREAM to these elements coincides with repression of the genes in G0 and G1 phases suggesting that DREAM is a central transcriptional repressor of these histone genes. Another subgroup does not harbour CDE/CHR promotor elements and does not bind DREAM in G0 and G1. These genes are mainly regulated by a cycle-dependent modulation of mRNA stability rather than promoter activity.

These different mechanisms of regulating genes coding for the same protein could resemble a backup mechanism that reduces the danger of severe cellular defects as a result of perturbation of one particular mechanism of histone expression.

DOES CONSERVATION WORK?

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In 2010, most of the world's governments agreed to the 2011–2020 Strategic Plan for Biodiversity and its 20 Aichi Targets, the most powerful set of commitments to environmental sustainability that the world has ever had, and much of this has now been incorporated into the establishment of the new UN Sustainable Development Goals. However, indicators for the Aichi Targets reveal that biodiversity continues to decline across multiple dimensions. Is environmental sustainability an unattainable goal? I argue that these indicators only reveal half of the story, and must be complemented by documentation of the impacts of actions. In other words, what would have happened in the absence of conservation intervention? I examine this question regarding the impacts of conservation overall in reducing species extinction risk, as well as for the specific case of the impacts of protected areas in reducing habitat conversion and extinction risk. In each case, the data reveal that biodiversity loss would be proceeding much faster in the absence of conservation action. Such monitoring relative to counterfactual scenarios represents an exciting frontier for unified biology. The overall message is while the world is still far from achieving absolute targets for environmental sustainability, the state of nature would be far worse were it not for conservation efforts to date. Conservation works – we just need much more of it.

BIOLOGY AND PALAEOBIOLOGY EDUCATION: ARE WE FAILING TO PROVIDE THE APPROPRIATE FOUNDATIONS?

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Abstract: This presentation looks at trends in bioscience education, and notes with concern the continuing move away from courses (or course content) that provides sufficient grounding for systematic taxonomy. Questions to be addressed include: Do graduates need to be able to effectively navigate codes of nomenclature? Are there employment opportunities in systematic taxonomy? Can we undertake effective environmental impact assessment simply through recognition of phyla (and their abundance) in a system? Finally, is systematic taxonomy a 19th Century anachronism now that we have rapid and relatively cheap DNA sequencing available?

INTEGRATING DATA AT THE TREE OF LIFE SCALE USING COMPUTABLE CLADE DEFINITIONS

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Improving our understanding of Life, whether the biology of individual species such as our own, or the mechanisms and processes governing biodiversity at large, critically depends on integrating, querying, and aggregating biological data from many different organisms. To this day, the most fundamental and common way to accomplish this goal relies on organism names, making these one of the pillars of querying and managing our biological knowledge and data. However, traditionally defined names, based in Linnaean nomenclature, suffer from two major limitations to their usefulness when it comes to integrating and communicating data. First, because they are simple text-strings, the meaning intended by those who coin a name and those who apply it is inaccessible to machines. As a result, exactly which organism a name is or is not meant to include is often ambiguous, and names are therefore often applied inconsistently. Second, there are many groups of organisms that do not yet and may never have a Linnaean name, but for which molecular or macroscopic characteristics have been discovered that constitute valuable biological knowledge. We propose to address these challenges by generating a mechanism, called phyloreferencing, that allows referring to any group of organisms of shared evolutionary descent by a machine-interpretable definition of the unique pattern of descent that distinguishes the group from all others. Phyloreferences build on a large body of theoretical and applied work on phylogenetic taxonomy. With the recent synthesis and continuous update of a universal phylogenetic Tree of Life, phyloreferences will have immediate and broad practical applications for communicating, integrating, and querying biological data across the Tree. In contrast to authoritative nomenclatural naming, the goal for phyloreferences is that users can construct them instantly for any group of shared evolutionary descent for which they wish to communicate discoveries. To accomplish our goals, we are using standards and tools developed for the Web, specifically the Web Ontology Language (OWL), ontologies, and machine reasoning. Ontology and reasoning technologies have already shown their power for biological knowledge integration and discovery and are increasingly being adopted for evolutionary research as well. Phyloreferences will be designed with the goal that any element, whether node, branch, apomorphy, or clade on the Tree of Life can be referenced in a way that is unambiguous and has fully computable semantics defined by patterns of evolutionary relatedness.

FUNCTIONAL DIVERSITY OF AQUATIC INSECTS IN WATER-FILLED TREE HOLES IN THE TROPICAL FORESTS OF THE WESTERN GHATS, INDIA

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Water filled tree holes forming as a permanent or ephimeral freshwater aquatic habitats occupied by an array of invertebrates largely shared by aquatic insects. In a sub-tropical forest of the Western Ghats, in Silent Valley National Park (SVNP) and New Amaramblam Reserved Forest (NARF) we investigated the functional variation in the aquatic insects in water-filled tree holes. The sampling effort comprised of search at 150 water filled tree holes in the study area. This investigation showed that occurrence of 28 different species with an average of 3-5 species in a tree hole. Most of the recorded organisms (96.8%) belong to order Odonata, Heteroptera, Diptera, Coleoptera, Trichoptera. Altogether, 7505 macrofauna individuals were recorded from 150 tree hole aquatic habitats of SVNP and NARF. Aquatic insects belonging to the orders Coleoptera, Diptera, Trichoptera, Heteroptera, and Odonata together comprised of 96.8% of entire collection. The remaining 3.2% were the representatives of the taxa from Dermaptera, Annelida, Collembola, Gastropoda, Diplopoda, Geckonidae and Anura. Out of 16 aquatic insect taxa recorded, nine were Dipterans, four Coleopterans and one each from order Trichoptera, Heteroptera, and Odonata respectively. About 13 aquatic insect taxa in the tree hole aquatic habitat found in their larval stage and three aquatic insect groups such as Hydrophilidae, Dytiscidae of Coleoptera and Heteroptera were found in adult stage. Structural characteristics and community structure, number of taxa, its abundance, number of predators and saprophages in study area were summarized. The predator aquatic insect taxa recorded were belonging to three taxa namely Toxyrinchites of Culcidae, Agabus of Dytiscidae, and an Anisopteran nymph of Odonata. Of these Anisoptera act as the top predator in tree hole aquatic habitat. Remaining taxa were saprophages grouped into macrosparophages, microsparphages and filter feeders based on feeding relation on coarse particulate organic matter, fine particulate organic matter and dissolved organic matter respectively. Community composition was more similar within the tree hole aquatic habitats of SVNP and highly variable between SVNP and NARF. The feeding relationship of community is mainly organized based on detritus food web in which saprophage group were most represented in terms of abundance and taxa richness. The saprophages includes Scirtidae and Tipulidae. Scirtidae which is commonly called as marsh beetles is the most abundant and highly characteristics group of tree hole aquatic habitat in the study area. They use its specialized mouth parts to shred the leaf litters and in turn largely facilitates the conversion of coarse particulate organic matter (CPOM) into fine particulate organic matter (FPOM). The indirect ordination shows that variability on abundance in tree hole during pre-monsoon and post monsoon sample. Pre monsoon samples was most of them in negative PC1 and post monsoon samples was in positive PC1. Taxa abundance and characteristics ordination the PC1 reflects the earlier pattern. And no apparent variability among the tree hole characteristics as they are point towards the positive PC1. The PC 2 axis instigates the positive PC2 taxa is more abundant in high water volume tree holes. Negative PC2 taxas was

more abundant in higher litter quantity containing tree holes. There it observes divergence in trophic relations as micro and macro saprophages. It showed the importance of habitat characteristics as water volume and energy sources as litter quantity on community composition in aquatic habitats. It was found that water filled tree holes which are persistent are having high species diversity and longer food web and tree holes were a perfect analogy to much more complex and larger ecosystems.

GLOBAL CHANGE AND FISH DIVERSITY IN CENTRAL ASIA

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All continents of our planet recently are facing a great challenge of global change (GCH) including global warming and human activity consequences such as environmental degradation, habitat transformation, pollution, global transportation, etc. One of the consequences of GCH is the loss of the natural continental and local biodiversity. A good example of the impact of GCH on biodiversity is the situation with fish variety in the waters of Central Asia. As a result of GCH influence a bias in ratio of ecological guilds, declining of local diversity, changes in distribution, and life history of many species of fish are observed. In the course of long-term research on periodically drying water bodies of the Central Asian Lake Valley a unique phenomenon of cyclic diversification of Altai osmans (genus *Oreoleuciscus*, Cyprinidae) at a later stage of ontogeny was found. Actually, it was demonstrated how a dwarf riverine form of Altai osmans turned into a lacustrine one as a result of periodical fluctuations of range size of this species. One of the main factors, influencing on fish populations, is mining in the rivers. In particular, in upper reaches of rivers of Arctic Ocean basin, where mining is going on, substantial silting of the grounds has led to violation of spawning condition of valuable fishes. An increase of water turbidity, the lowering of flow velocity and heterogeneity of environment at separate sections, chemical pollution led to a drastic fall in number of such species as taimen, lenok, graylings, minnows, burbot and to a growth of populations of the species which adapted to a new environments (golden carp, dace). Anthropogenic load on the water bodies of the Central-Asian waters is connected, also with construction of hydraulic structures (dams first of all), and intensification of fishery. Globalization of many processes has greatly increase risk of biological invasion of alien species and destruction of native ecosystem functions. Biological invasion process supposes that introduced species on the one hand have to adapt to new climate of the region of introduction and on the other hand discomfort aboriginal species. This allows presuming corresponding alterations in the regulation of the vulnerability of ecosystems to invasions. When warming aboriginal ecosystems are more vulnerable due to the growth of primary production, where the role of native species in the regulation process is reduced, since many of them are poorly adapted to the new conditions. It is obvious that alien species from the warmer climatic zones receive a competitive advantage. Data obtained during the last two decades in Central-Asian waters confirm the correctness of these assumptions. The analysis of the alien species composition showed that several species of fish are spreading to the North and East in basins of Ob, Yenisei and Amur rivers and occupying mainly reservoirs. Evaluation of modern condition of water ecosystems and distribution and population parameters of fish of Central-Asian waters should be remain the main purpose of research for the years immediately ahead.

THE GLOBAL GENOME BIODIVERSITY NETWORK (GGBN)

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The Global Genome Biodiversity Network (GGBN) was formed with the principal aim of making high-quality well-documented collections that store DNA or tissue samples of biodiversity, discoverable for research. This is achieved through the GGBN Data Portal (http://data.ggbn.org), which links globally distributed databases and bridges the gap between biodiversity repositories, sequence databases and research results. Many genome sequencing projects with the potential to revolutionize biodiversity research consider access to adequate samples to be a major bottleneck in their workflow. This is linked not only to accelerating biodiversity loss and demands to improve conservation efforts but also to a lack of standardized methods for providing access to genomic samples. Biodiversity biobank-holding institutions urgently need to set a standard of collaboration towards excellence in collections stewardship, information access and sharing and ethical use of such collections. GGBN meets these needs by enabling and supporting accessibility and the efficient coordinated expansion of biodiversity biobanks worldwide.

CATALOGUE OF LIFE - VIEW ON NOMENCLATURE & BIG PICTURE UNIFICATION

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The Catalogue of Life (CoL) has recently been making big picture plans with other global biodiversity data aggregators. There was a summit early in 2015 that cemented the commitment of CoL, the Global Biodiversity Information Facility (GBIF), Encyclopedia of Life (EOL), Biodiversity Heritage Library (BHL) and the Barcode of Life Database (BOLD) to pool resources and work to finally complete a single shared taxonomic index. As well as this CoL are active in seeking funding to work with the Global Names Architecture (GNA), Nomenclators, BHL and next generation publishers to maximise the data now digitally available. Global names resolution is becoming more and more important to be able to link all names used for a given organism and direct them to the correct accepted name according to a taxonomic expert. The CoL has a strong role in the last step, but cannot always ensure full synonymy and does not include name usages in the way that GNA does. It is more and more obvious that we all need to work together.

The CoL is primarily concerned with taxonomy and take names as given by Global Species Databases (GSDs). We are very keen to work with nomenclators on ensuring the nomenclatural accuracy of names in the CoL. It would be ideal to set up a way of checking nomenclature via the large nomenclators (International Plant Name Index, ZooBank, Index of Organism Names, Index Fungorum etc). Alongside this, investigating the possibilities of using registration in animal and fungi names and in the future, plant names, to contribute newly described names and funnel them to the appropriate GSD providers would be beneficial to all users of species data. In line with the focus of the IUBS meeting, what is important is unification of all our work to enable users to progress with science, conservation and policy.

DIVERSITY IN SPACE AND TIME: WANTED DEAD AND ALIVE

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Even though extinct and extant biodiversity have likely been generated by similar fundamental processes, research in ecology and evolution is largely split between paleontological and neontological studies. We provide a conceptual framework that capitalizes on data and methods from both disciplines to investigate fundamental processes, and highlight the opportunities arising from a combined approach. We demonstrate our framework by testing the diversity-productivity relationship through geological history in large terrestrial mammals, combining >14,000 occurrences for 690 fossil genera with regional terrestrial net primary productivity estimated from fossil plant communities. Our results show a consistent mammalian diversity-productivity relationship over the last 20 million years across North America and Europe. However, mammalian diversity today is much lower than expected from the fossil relationship, suggesting a combination of human impacts and Pleistocene climate variability has strongly reduced primary productivity and driven many mammalian species in to decline or to extinction. This example presents new insights on the long-term persistence of a general ecological pattern in the fossil record and discovers human impacts on these patterns, highlighting the need for integrative analyses across time and space.

BROADENING BIOLOGY EDUCATION:
NEED TO AUGMENT ARTS AND SCIENCE FOR A BETTER BIOLOGY

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Teaching the concepts of biology relies mostly on laboratory experiments and observational exercises. This is because education and research in biology is getting more and more specialized, compartmentalized and, suffers from a reductionist approach. In fact biology education is being shaped more by the patterns of education in physical sciences and as a result biology has become gradually isolated from arts and natural philosophy. In this presentation, I show that biology education could gain a lot by taking recourse to historical lessons especially for teaching the current issues of ecological sustainability and conservation of bio-resources.

History is a potential database of successful and failed experiments of mankind's attempts to manage natural resources for improving his living status and comfort. It contains in it, several long-term experiments –both intended and accidental, that are difficult, costly and unnecessary to repeat. The results thereof from these historical experiments are often visible vividly or would be represented in art forms. Thus a carefully mining of history and arts could provide us very interesting lessons on use and abuse of our ecosystem and natural resources. In this paper I show that concepts such as ecological balance, sustainable use of resources and dispersal of crops can be effectively taught using specific examples from history, art and archaeology. Based on these examples I urge for broadening the biology education through augmenting the arts and history in to it.

ENGAGING CITIZENS IN THE INVENTORY AND DNA BARCODING OF FAUNA AND FLORA

- EXPERIENCES FROM THE GERMAN BARCODE OF LIFE PROJECT

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GBOL (https://www.bolgermany.de/) is currently the largest DNA barcoding campaign in Europe, financed by the German Federal Ministry for Education and Research. The consortium of Natural History collections and Universities works on the construction of a DNA barcode reference library for the country's fauna and flora. GBOL has five regional and thematic nodes and is flanked by complementing projects (Barcoding Fauna Bavarica (BFB), FREDIE for European freshwater fishes and some invertebrate taxa, barcoding of the North Sea Fauna) and supported by more than 225 specialized citizen scientists. The latter play a crucial role, because the taxonomic workforce and expertise in natural history museums and universities is insufficient. We describe the efforts required to motivate voluntary helpers and the importance of a national web portal for communication in the native language, and the necessity for a close cooperation with the international platform BOLD. To maximize synergies a strong commitment to common data standards and repositories is needed, as well as better trans-boundary cooperation between nations, which both would accelerate database completion and increase cost-efficiency.

THE CURRENT SITUATION AND PROSPECTS OF ROMANIAN BIOLOGICAL OCEANOGRAPHY

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The Black Sea represents a "unicum hydrobiologicum" characterized by several features:
- It is a meromictic sea; It is an euxinic azoic domain below depths of 150 - 200 m; It has an intense exchange of waters with the Mediterranean Sea; It receives a large amount of fresh water, especially in its northwest sector through the Danube, Dnieper and Dniester Rivers; It holds a circum-marine belt filter-up represented by bivalves (*Mytilus galloprovincialis* with its cocoenotic forms and *Modiolula phaseolina*); In its north-western part it hosts a large area covered with red algae of the genus *Phyllophora*; It has been subject to intense environmental pressures; It recorded numerous manifestations of eutrophication and scrolling chain reactions in the last decades of the 20th century; Decrease or limits in native biodiversity and decrease in the bio-productive potential; Specific biodiversity has been enriched by the appearance and development of alien species populations.

The current situation of Romanian oceanography: Following the political and socio-economic changes triggered by the events of December 1989 and especially after Romania's accession to EU, Romanian Oceanography made evident progress: Institutional diversification; Building young elite of researchers trained in the country and abroad through doctorates and courses; Sustained cooperation, national and international partnerships and joint research projects; Harmonizing the Romanian researches with those in the EU Member States; The endowment of infrastructure with modern facilities and equipment.

Recent ecological events in the Black Sea ecosystems: Decrease in environmental pressures; Decreasing pollutant / fertilizing discharges into the Danube; Reduction of the quantities of domestic sewage from coastal settlements; Improvement in the quality of wastewater discharged into the sea through sewage plants; Adopting and implementing a national / international set of guidelines concerning marine environment.

The Black Sea ecosystem restoration - Certainties & Uncertainties

Rehabilitation signals are fragile and few: Recurrence of absent species in samples collected from 1970 until1990/95. Recurrence of extinct species in the last 20 - 30 years can be considered a good sign, but there are questions: a. How often do these species reappear? b. Why are the communities "thriving" in 1960-1970 still in a poor state? We refer here to the red algae *Phyllophora*, to other macrophyte algae belt (*Cystoseria barbata*) in the southern Romanian coast, once so prosperous, to the bottoms covered with sea grass *Zostera*, to crustaceans or shellfish populations.

What should to be done for the improvement of Romanian Marine Research?

Reorganization of research, development and innovation in the maritime field (MRDI): New ways of financing MRDI activities from public sources; Stimulating private investments in MRDI; Reducing MRDI system fragmentation; Transparency in R & D public funding; The analysis of the major paradigms of deep-sea diversity (McClain R. C. and Schlacher A T., 2015).

URBAN BIODIVERSITY AND PEOPLE IN BANGALORE, AN INDIAN MEGACITY

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The importance of urban biodiversity has been widely acknowledged in recent times. Conventional uses of diversity in cities across the world mainly deal with environmental services and aesthetics. However, biodiversity, especially that of plants, rises to prominence in the context of marginalized communities and cultural practices prevalent in developing countries.

The unconventional interaction of civilians with plant diversity in a densely populated Indian city like Bangalore is inspiring as it leads the path towards conservation of urban greens and urban wildlife. Tailored to local conditions that include urban poverty and predominance of cultural practices, these informal systems of governance seem to be self-sustaining on the long run.

Bangalore’s slums accommodate roughly 1.4 million people, accounting to about 15% of the total population. Slum residents often have limited/no access to basic necessities such as clean water, sanitation and sturdy housing units. In these extreme conditions, floral diversity in slums seem to cater to various uses including; urban agriculture; health through traditional plant based medicines; structural uses as support for houses, clothes line, etc. Despite space constraints, slum residents were found to be growing a rich diversity of potted plants for different needs.

Another informal system of green governance prevails in the form of sacred nature. Nature worship is a common cultural practice in Bangalore, like other Indian cities. People protect and nurture sacred trees and sacred sites; and cutting such trees is considered a taboo. With this cultural norm, sacred trees act as keystone species wherein other non-sacred flora and fauna within a sacred site, also enjoy the benefits of cultural conservation practices. These sites are often home to native and spontaneous species. Where as other land use types of Bangalore such as parks, domestic gardens, streets and institutions are dominated by exotics with limited non-aesthetic uses.

In a city with high population density and high proportion of urban poverty, urban greenery, green spaces and plant diversity play a crucial role in the everyday functioning of civilian populations. There are many lessons to learn from these unconventional interactions of people with plant diversity that aids the path towards sustainable cities.

FOLLOW THE NAME – PERSPECTIVES FOR PLANTS

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Since the 1890's, names of plants have been compiled and managed at the Royal Botanic Gardens, Kew. Until 1970 this was done on paper which was limiting in that corrections could not easily be made. Since 1971 the names were digitised and in 2003 they were combined with the Gray card index (covering American plant names from 1900) and the APNI (covering all Australian plant names) to make IPNI (the International Plant Names Index). To keep the data relevant in the 21st century, new names need not only be added but existing names need to be curated and user feedback checked and incorporated. Data are also used to write scientific papers with a global perspective and data are provided to other data aggregators and in particular to the World Checklist of Selected Plants families (WCSP), which is Kew's global taxonomic species concept index. Both IPNI and WCSP are now being used to create the Plants of the World Online Portal (POWOP), Kew's answer to the 2020 target 1 of the GSPC: "An online flora of all known plants".

Curation of the data is essential to ensure a quality product that can be used for other purposes. This does not just involve adding new names and maintaining the IT systems but more importantly, curating the existing one million names to contemporary rules and requirements. The ICN, the code that governs plant names, changes every 6 years, which may have consequences for existing names. The way publications, dates and linked names were recorded has changed a lot over the years, this is continuously being standardised to international agreed standards. The data also need to incorporate the latest trends like linking protologues to the actual online publications and adding DOI's.

In the most recent ICN, electronic publication was accepted as an effective place of publication of new names. This has resulted in a growing number of homemade electronic-only publications. Finding such new names has made the job of the curators even more challenging. Not in the least because some of them vanish as quickly as they appeared. Kew has therefore now become involved in a trial for plant name registration, in line with what the ICN mandates for fungal name registration. It is hoped that registration will make the adding of new names more efficient, though there are undoubtedly also additional tasks involved.

Unfortunately, core data sources like IPNI and WCSP, although used by most botanists, are rarely directly cited. Continued funding for the massive effort it entails to maintain these core database is therefore not assured.

INSIGHTS INTO THE ROLE OF DIFFERENTIAL GENE EXPRESSION ON SPECIATION OF TWO ORYZA SPECIES

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Ecological speciation is a common mechanism by which new species arise. Despite great efforts, the role of gene expression in ecological divergence and speciation is poorly understood. Here, we conducted a genome-wide gene expression investigation of two Oryza species that are evolutionarily young and distinct in ecology and morphology. Using digital gene expression technology and the paired-end RNA sequencing method, we obtained 21,415 expressed genes across three reproduction-related tissues. Of them, approximately 8% (1,717) differed significantly in expression levels between the two species and these differentially expressed genes are randomly distributed across the genome. Moreover, 62% (1,064) of the differentially expressed genes exhibited a signature of directional selection in at least one species. Importantly, the genes with differential expression between species evolved more rapidly at the 50 flanking sequences than the genes without differential expression relative to coding sequences, suggesting that cis-regulatory changes are likely adaptive and play an important role in the ecological divergence of the two species. Finally, we showed evidence of significant differentiation between species in phenotype traits and observed that genes with differential expression were overrepresented with functional terms involving phenotypic and ecological differentiation between the two species, including reproduction- and stress-related characteristics. Our findings demonstrate that ecological speciation is associated with widespread and adaptive alterations in genome-wide gene expression and provide new insights into the importance of regulatory evolution in ecological speciation in plants.

Key words: ecological speciation, expression evolution, adaptation, wild rice.

GFBIO – A SUSTAINABLE FEDERATED NATIONAL INFRASTRUCTURE FOR BIOLOGICAL DATA MANAGEMENT

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The DFG-funded 'German Federation for Biological Data' (GFBio) is a consortium of national institutions providing environmentally related biological data and services. GFBio aims to provide a sustainable, service oriented, national data infrastructure facilitating data sharing and stimulating data intensive science in the fields of biological and environmental research. GFBio addresses data management requirements of a large range of stakeholders including individual scientists, natural history collections as well as larger research networks. Special consideration is given to genome data, ecological and environmental data as well as collection related data.

GFBio services include i) a portal mediating access to data submission, helpdesk, and data retrieval functions ii) data visualisation and analysis modules, iii) terminology services supporting data retrieval, data integration, and semantic enrichment, and iv) a set of (domain-specific) data archives.

In its second project phase, which started in October 2015, an important aspect of the project will be the development of a sustainable business model for GFBio. This involves the identification of core services, their description, and assessment of costs. On this basis a model for sustainable financing of the infrastructure is developed.

IUBS/ISZS’S INTRODUCTION OF IUBS/ISZS'S PROGRAM, BIOLOGICAL CONSEQUENCES OF GLOBAL CHANGE (BCGC)

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Global change is now one of the most discussed topics in the world. Understanding the impact of global change is extremely important for the sustainable development of human society.

Therefore, in 2008, the International Society of Zoological Sciences (ISZS) initiated an international research program, Biological Consequences of Global Change (BCGC). It was first supported by the Chinese Academy of Sciences (CAS). In 2009, BCGC was adopted by the International Union of Biological Sciences (IUBS) as a new international research program. In 2012, the program was evaluated highly at IUBS and was considered as the core of IUBS scientific programs. Currently, there are over 20 scientists from Australia, Chile, China, France, India, Norway, Russia, Israel, Germany, South Africa and the United States involved.

The focus of the BCGC program is to organize a diverse group of international experts, with expertise in many scientific disciplines, and develop an understanding of the consequences of global change and human activity on evolutionary mechanisms, biological structures, endangered species and biological disasters.

The BCGC program provides a platform for scientists around the world to collaborate on topics, such as the impact of global change on biodiversity, ecological infectious diseases, agricultural pests, invasive species and many other topics of interest. The program is expanding its research networks to include more scientists and scientific disciplines from various places around the globe.

INTEGRATING MOLECULAR PERSPECTIVES INTO TAXONOMY, ECOLOGY, AND BIOSURVEILLANCE

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The concomitant rise of genomics and informatics has ushered in a new paradigm of collaborative, open access research that serves as a model for achieving the power and vision of a “unified” biological science. The International Nucleotide Sequence Database Collaboration (INSDC) has built an elegant infrastructure to archive and reuse primary research data that indexes it with the downstream knowledge products created from said data. As DNA sequencing and the digital revolution permeate other areas of biology, for the first time we have the potential to address one of the grand questions in biology concerning "how many species" inhabit our planet. Doing so requires the integration, maintenance and support of diverse information systems via the semantic web that currently exist as data silos with varied funding mechanisms and governance models, which collectively constitute the “eBiosphere”. Closing the gaps between silos has led to important advances in ecology, taxonomy and biosurveillance. This talk will focus on experiences gained via the International Barcode of Life (iBOL.org) project and highlight socio-economically relevant outcomes, closing with remarks on the need for an overarching plan to support the infrastructure required for the digital unification of the biological sciences.

THE BIOCODE: FROM VISION TO REALITY

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The realization that a unified Code of nomenclature applicable to all organisms was ideal emerged during a meeting of the IUBS/IUMS International Committee on Bionomenclature (ICB) held in Egham (UK) in March 1994. Later that year, the IUBS General Assembly in Paris passed a resolution urging the ICB to "expedite work towards a unified system of bionomenclature". Representatives of all five Codes then met at Egham in May 1995 and produced recommendations on unified terms and a first draft of a possible BioCode. The draft was widely circulated and developed over several international meetings, particularly the International Congress of Systematic and Evolutionary Biology (ICSEB) meeting in Budapest in 1996, with the last major revision being published in 2011 and considered by the ICSEB meeting in Berlin that same year. At that occasion it was resolved to make additional revisions, mainly to allow for the advent of electronic publication and registration, for eventual adoption by IUBS and IUBS. The BioCode aimed to utilize elements of the existing Codes that best served stability. It was, however, recognized from the first that a prerequisite was a list of validly published names to be retained, as any retroactive imposition would be too disruptive. Implementation was, therefore, seen as necessarily proceeding on a group-by-group basis as robust listings were achieved. It was envisaged as running along with the main Codes, with a gradual switching over as lists were developed and approved. This was the vision, and the BioCode, with some updating needed prior to endorsement, has not gone away. The reality is that the BioCode remains unadoptable in the absence of the required basal lists of protected names, and that progress on generating such lists has been negligible to slow. It could, however, become the Code of choice in some groups urgently in need of a basal list, such as the cyanobacteria, and it was also promoted by some mycologists as the way forward prior to the changes that were made at the International Botanical Congress in Melbourne in 2011. The BioCode slumbers, waiting to be woken up, spruced up, and spring into action as and when required.

WILDLIFE BORNE DISEASES SURVEILLANCE AND PREVENTION IN CHINA

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Wildlife borne diseases is an important issue for human health, wildlife population and agriculture development. Since SARS in 2003, wildlife borne diseases has taken a big part of major emerging infectious disease events, such as human infection with H7N9 influenza virus happened earlier this year. The complex role wildlife play in these events cannot be neglected and need to be further investigated.

In China, a surveillance system of wildlife borne diseases has been established since 2005. National Research Center for Wildlife borne Diseases is the main Technical Support Unit under the system. Measures has been widely used to serve for wildlife borne diseases surveillance and management, including remote conduct and monitoring system, zero report system, and data submission and direct inform system. Collaboration with other departments, institutes and university has also been carried out for addressing wildlife diseases issues. International cooperation is developed as well. Asia-Pacific Wildlife Diseases Network, a communication network for exchange of ideas and information among persons working on wildlife disease issues, was initiated by Chinese Academy of Sciences and United States Department of Agriculture in 2010. The members of the network are from more than 10 countries in Asia-Pacific region and several international organizations. Activities, including workshops focused on wildlife borne diseases held each year by the Network improve communications and collaborations to a great extent.

Since 2013, more than 600 avian influenza A(H7N9) infections confirmed have been confirmed and reported in humans, of which more than 30% were fatal. The novel virus was originated from multiple reassortment events among wild birds, ducks and chicken. In Zhejiang Province, the severely affected area of H7N9 avian influenza cases, we found almost all positive samples came from chickens and ducks in live poultry markets. These results strongly suggest that the live poultry market is the place where the novel H7N9 viruses emerged recently and acquired the capability of infecting humans directly through reassortment among different influenza viruses from birds and domestic chickens/ducks as well as accumulation of new mutations in important positions of different viral genes.

To investigate the origin of the novel virus, active surveillance of avian influenza was performed on migratory birds. The results showed that the wild bird H9N2 viruses, serving as a gene pool, contribute to the internal genes of H7N9 subtypes viruses. In order to assess the biological properties of H7N9 viruses that may recruit internal genes from genetically distinct H9N2 viruses circulating among wild birds, we generated 63 H7N9 reassortants derived from an avian H7N9 and a wild-bird-origin H9N2 virus. Compared with the wild-type parent, 25/63 reassortants had increased pathogenicity in mice. A reassortant containing PB1 of the H9N2 virus was highly lethal to mice and chickens but was not transmissible to guinea pigs by airborne routes; however, three substitutions associated with adaptation to mammals conferred airborne transmission to the virus. The emergence of the H7N9-pandemic reassortant virus highlights that continuous monitoring of H7N9 viruses is needed, especially at the domestic poultry/wild bird interface.

ECOMETRICS AND GLOBAL CHANGE: USING MODERN AND FOSSIL FUNCTIONAL TRAITS TO ESTIMATE BIOTIC RESPONSE TO ENVIRONMENTAL TRANSITIONS

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Ecometrics, the quantitative analysis of functional trait-environment relationships, in an important innovation for reconstructing short- and long-term histories of environmental transitions and in forecasting biotic responses to anthropogenic climate change. Measured at community or assemblage scales, ecometrics are anatomical, physiological, or behavioural traits that are functionally dependant upon specific environmental properties, which are themselves, determined by local to global climatic conditions. Spatial and temporal changes in environmental factors drive the performance and distribution of traits, resulting in biotic histories ranging from local extirpation to adaptive radiations. Because functional traits are not specific to a particular taxon, they can be examined across a wide range of temporal and geographic intervals. This taxon-free approach allows for comparisons between fossil and modern trait records, including forward models that predict trait success in response to future climate change and inverse models that reconstruct past environmental variables from trait distributions in the fossil record. Examples of well-defined ecometrics include the relationships of tooth morphology in ungulate mammals to precipitation, body size in poikilothermic animals to ambient temperature, and limb morphology in carnivore mammals to vegetation cover.

ANTS IN A GLOBALIZED WORLD

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Ants (Formicidae) play important roles in almost all terrestrial ecosystems as predators, seed dispersers, direct or indirect herbivores, and soil engineers. Through human commerce, dozens of ant species have been transferred between continents and many of these "tramps" have become established as invasive species throughout the world. Species, such as the Red imported fire ant, the Argentine ant, or the Yellow crazy ant, are listed among the 100 worst invaders in the global invasive species database, because they have reached enormous population densities and fundamentally change the native fauna and flora. Others, such as *Cardiocondyla* spp., are less conspicuous but nevertheless make up a significant part of the ant communities in plantations, parks or tropical beaches in the tropics.

Aim of the presentation is to highlight traits that allow ant species to become successful invaders and examine the present and future impact of invasive ant species in the times of global change.

CLIMATE CHANGE AND INCREASING WATER SALINIZATION VULNERABILITY MITIGATION STRATEGIES FOR FISHERIES SECTOR DEVELOPMENT IN DESERT AND ARID LANDS OF ARAL SEA BASIN

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The Aral Sea Basin (ASB) coincides with most of Central Asia and has an area of 1.58 million km2. Prior to 1960, the only fish available on the internal market was caught mainly from the Aral Sea. The sea was rich in valuable freshwater fish species. Fishery activities in the Aral Sea yielded about 45 000 t of fish annually. During the last decades of the last century water inflow into the Aral Sea significantly dropped as a result of development and poorly managed large scale irrigation systems to fulfill the water needs for cotton production. The salinity of water increased from about 10g/L in 1960s to more than 130 g/L in 2000s due to high evaporation, which has led to gradual elimination of all 20 fish species. The increase of water salinization deltaic water bodies was caused above all by anthropogenic factor - diversion of large volumes of mineralized unconventional return waters from agricultural fields to rivers, existing lakes and natural depressions. Desiccation of the Aral Sea and its deltas significantly diminished also the area of lakes and wetlands – important areas for the aquatic biodiversity conservation. The last recorded catch in 1983 was just 50 t. Fisheries sector in ASB faces for climate change problems more than in most areas in the world. In most of desert and arid territories of ASB air temperature has gone up by 2.8oC during the 20s century. According to predictions possible increase in annual mean air temperature by 2030 against basic norms in 1961-1990 may vary between 1.5-2.5oC and precipitation will decrease by 3%. This results in glacier reduction, increased evaporation and acute water scarcity, especially in Aral Sea disaster zone. Therefore, climate change related impacts have become emerging threats affecting resilience and sustainability of fisheries and aquaculture in the region. The impact of climate change on biodiversity is not well-known. Countries of the region are not informed by knowledge related to the impact on aquaculture and fisheries and have not developed required strategies and good management practices to mitigate the impacts. Fisheries and aquaculture are especially vulnerable for changing climate because in aquatic ecosystem growth of fish and development of their natural food base depend on the surrounding environment. Our field investigations during 2013-2015 have revealed that the economic threats on fish farming extreme in the region and the vulnerability mitigation strategies of fisheries sector to climate change and increasing water salinization impacts should include above all considerable improvement o: water management measures taking into account needs of fisheries sector and introduction of climate smart aquaculture and fisheries practices: fisheries enhancement (culture based fisheries), integrated agriculture-aquaculture multi-trophic farming (IMTF) systems, tank and cage culture to increase the overall resilience of fisheries and aquaculture sector.

ASSESSMENT OF THE POTENTIAL IMPACT OF BIODIVERSITY CHANGE ON WATERFOWL OF LAKE VICTORIA

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To correctly assess the impact of biodiversity changes on waterfowl, it is necessary to utilize appropriate phenological, biodiversity and socio-economic data. Where such data is scarce, it is possible to make initial assessments using less complex methods that require only the waterfowl as indicators of biodiversity loss. For such methods, the annual waterfowl census is assumed to consist of an economic growth term and biodiversity loss terms. The relative biodiversity loss in the lake is then expressed as function of the first moments to contribute the potential impact changes. The analysis will indicate whether biodiversity loss on the island has a positive or negative effect on economies in future. The method was tested using Musambwa waterfowl census over the period 1999-2005. In general, the results indicate that small future annual biodiversity changes will have a negative effect on potential environmental changes. If economic activities and biodiversity indicator loss continues to follow the changes observed in 2004/2005, then effective conservation measures are recommended.

MYCOLOGISTS LEAD THE WAY... BUT IT'S NOT ALL PLAIN SAILING

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Registration of names for organisms interpreted as ‘fungi’ in the ICN (Fungi, fungus-like organisms in the Chromista/Stramenipila, organisms in the Mycetozoa, Labyrinthulea, Phytomyxea and their ‘allies’, but excluding the Microsporidia) became mandatory from 1st January 2013. Prior to that date the Nomenclature Committee for Fungi voted, following extensive discussion, to approve three repositories – Fungal Names, Index Fungorum, MycoBank – with a mechanism agreed in August 2012 to synchronize content. In reality, the best plans of mice and mycologists floundered on the rocks of … lack of resources. However, a functioning system is in place which more-or-less works as planned. Areas which require attention will be highlighted and options for the future will be suggested.

EFFECTS OF URBANIZATION ON PLANT BIODIVERSITY - INSIGHTS INTO FUNCTIONS AND PHYLOGENETICS

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Urban areas are projected to triple until 2030 with the highest rates of urbanization being likely to occur in the world's biodiversity hotspots. Past urbanization, too concentrated in areas with an originally high biodiversity. Urbanization drives extinctions of native species and immigrations of non-native species, threatening life's diversity, which developed over millions of years. At the same time, it changes environmental conditions in a way that causes shifts in the functional composition of species assemblages; i.e., certain functional traits of plant species (e.g. morphological of physiological characteristics) are more frequent in urban than rural areas. In this talk, I will present an overview on the effects of urbanization on the functional composition of plant species assemblages, including results from urban areas across the world. Further, I will show that urbanization reduces the phylogenetic distinctness of plant assemblages (a measure for species relatedness, i.e., the intrinsic evolutionary history of species assemblages). Although todays urban areas are rich in plant species, they are depauperate concerning phylogenetic diversity – a pattern that is related to the high number of non-native plants in urban areas and to functional traits. I will discuss the consequences of functional and phylogenetic changes and suggest ways how to decrease the future loss of biodiversity within urban areas.

BIODIVERSITY AND ECOSYSTEM FUNCTIONING IN AND OF CITIES

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Cities are growing rapidly, yet it is unclear how urbanization alters biodiversity and ecosystem functioning at various spatial scales. To investigate the impact of urbanization on biodiversity and ecosystem functioning on the ecosystem scale, we assessed 4 arthropod groups (bugs, beetles, leafhoppers, spiders) in 6 Swiss cities and 6 intensively managed agricultural areas nearby. Compared to intensively managed agricultural land, urban ecosystems supported a similar or even higher number of species and density of most indicator groups. Species evenness was partially reduced in cities suggesting the presence of urban exploiters. Species turnover between cities was reduced for most indicator groups compared to species turnover between rural areas, suggesting that urbanization leads to a large scale biotic homogenization. Further, based on species traits we analyzed functional redundancy and response diversity (as a measure for ecosystem resilience) of urban and rural arthropod communities. The results suggest that in the urban ecosystem the arthropod communities are less resilient to disturbances compared to rural communities, whereas the functional redundancy of the communities was similar in both ecosystems.

To investigate how urbanization alters ecosystem functioning in cities, we used a tri-trophic plant-aphid-parasitoid model. In a field experiment including five cities and nearby farmed areas, we used potted Vicia faba plants and manipulated the presence of Megoura viciae aphids and that of naturally occurring aphid predators. We show that predators reduce aphid abundances less in the urban than in the agricultural ecosystem, suggesting that urbanization limits top-down control of aphids by predators. Surprisingly, differences between ecosystems regarding the indirect predator effect on plant biomass were not explained by the differentially strong herbivore suppression. Instead, the urban environment limited plant biomass per se, thereby mitigating the scope of a predator effect. Our results show that urbanization can influence direct and indirect trophic interactions through effects on biotic top-down forces and on plant growth.

Within cities, a high amount of vegetated area increased species richness and abundance of most arthropod groups, whereas evenness showed no clear pattern. In contrast, patch connectivity seems to be less important for arboreal arthropods in an urban context. On a patch scale, we investigated how urban plant community composition affects plant-pollinator networks and the composition of pollens transported. More specifically, we were interested whether invasive plant species reduce nestedness of plant-pollinator networks, and whether pollens of garden plants are frequently transported. We found that invasive species reduce nestedness of plant-pollinator interaction networks. Further, while the pollen of invasive plant species is frequently transported by pollinators, garden plants are hardly integrated into the pollen-transport network. Overall, species can reach high diversity and density in cities, but specific measures are necessary to enhance species which are typical for the biogeographic region and vary in their response to disturbances. Further, managements which reduce the presence of invasive plant species and favour wild plant species would be beneficial for urban pollinators.

DISCRIMINATION OF "TRADITIONAL" TAXONOMY AND "DESCRIPTIVE" SCIENCE – EVIDENCE OF A DEEP CRISIS IN ALL NATURAL SCIENCES, NOT IN TAXONOMY ONLY?

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I define ‘traditional taxonomy’ as the approach based on deep, long-term investigations of a taxonomic group, performed by specialists. The alternative is a ‘machinism’ based on the idea that a new method applied at once, or a sequence of some technical operations, is more important for resolving taxonomic problems than are long-term routine (‘descriptive’) efforts. It is apriori accepted by many ‘modern style’ molecular biologists, that traditional taxonomy is an archaic science and even not science at all. Traditional taxonomy is apriori discriminated by high-, and even many medium-rank journals. Unfortunately, many ‘traditional’ taxonomists for a complex of reasons, i.e. aforementioned apriori discrimination, avoid submitting their papers to even medium-rank journals, preferring local or national proceedings. As a result, a large portion of taxonomic work is hidden from a wider scientific audience. I believe that taxonomy is potentially strong enough to be worthily represented among other directions of science, and that traditional taxonomists themselves are partly responsible for the situation, when our direction of studies is regarded as a low-grade science. We need to form a ‘taxonomic environment’ and a ‘taxonomic culture’ in ‘good’ scientific journals and increase the number of taxonomic papers in them.

The phrase ‘Descriptive science’ is used as a bad word by many journal editors. In reality, it means that the creation of some hypotheses and models based on sophisticated, sometimes unrealistic, assumptions is regarded to be more valuable as compared with direct describing some natural objects, processes and situations. But the latter is the ‘positive’ knowledge, and just such knowledge is discriminated. In contrast to many optimistic reports on a rapid recent progress in Natural Sciences, I have to conclude that the latter are now in a deep crisis.

ALGAE: DIVERSE CODES FOR DIVERSE TAXA?

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Biology requires a precise, coherent and simple system for the naming of organisms used internationally, dealing both with the nomenclatural terms and with the scientific names that are applied to the individual taxonomic groups of organisms (Draft BioCode, Preamble 1). When the first BioCode was drafted in 1988, the scientific sub communities had already decades of expertise in developing successful nomenclatural rules for their special organism groups. The BioCode, initially planned to supersede the specific codes, eventually became a framework to harmonize the single codes.

Because “the nomenclature of algae, fungi, and plants is independent of zoological and bacteriological nomenclature” (Principle 1 International Code of Nomenclature for algae, fungi, and plants or Melbourne Code, ICN), ambiregnal taxa (taxa ruled by two codes) are a problem for nomenclature and vice versa.

Based on ambiregnal taxa we demonstrate what happens when two codes with conflicting sets of rules apply to one single taxon at a specific rank. Cyanophyta respective Cyanobacteria, Dinophyta respective Dinozoa, Euglenophyta respective Euglenozoa are key groups to test which rules of which code are suitable for solving problems in order to achieve unambiguousness and name stability. Each single code has its strengths and weaknesses. Aspects to be discussed are names registration, recommended standards, epitypification, citations, classifications, and infraspecific taxa.

In the scientific community, the resulting problems are often dismissed but they become evident when we take, for example, cross-domain data analysis into account. We provide an insight into the practice of phycological taxonomists to evaluate how much of their work is influenced by different codes.

The call for Unified Biology also calls for a unified code. The BioCode could serve as a forward-looking framework within which nomenclatural problems faced by scientists from independent sub communities can be discussed in order to harmonize the different special codes, to transfer best practices among the codes, and to address the problems presented by ambiregnal taxa (see Jahn 2014).

Finally, we present a new approach which aims at registering algal names with special focus on the name’s metadata and open access provision to overcome information loss and ambiguities because of uncoordinated rules and community standards.

Jahn, R. in: Nationale Akademie der Wissenschaften Leopolina, 2014: Herausforderungen und Chancen der integrativen Taxonomiefür Forschung und Gesellschaft - Taxonomische Forschung im Zeitalter der OMICS-Forschung. Online- Supplement zur Stellungnahme. Deutsche Akademie der Naturforscher Leopoldina e.V. Nationale Akademie der Wissenschaften, Halle/Saale.

IPBES: BIODIVERSITY SCIENCE FOR DECISION MAKING

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IPBES, the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services, was established in 2012, as a mechanism to provide policy relevant knowledge on biodiversity and ecosystem services in response to requests from policy makers. Its membership currently includes 124 governments. Its entire work programme has been approved by governments in response to their request for scientific information. There are currently close to one thousand experts from all regions of the world involved in these assessments and in the other work performed by IPBES, such as on capacity building, or indigenous and local knowledge systems.

IPBES will be launching at its next Plenary in February 2016, its two first assessments, on pollinators, pollinations and food production; and on scenarios and models of biodiversity and ecosystem services. IPBES will also decide at that same Plenary on the possible initiation of a global assessment of biodiversity and ecosystem services, almost 15 years after the Millennium Ecosystem Assessment, which would be released in 2019. This assessment would form a contribution to the report of the Convention on Biological Diversity on the implementation of the Strategic Plan 2011-2020 and its 20 Aichi Targets, and to the next Strategic Plan 2021-2030.

IPBES initiated in 2015 a set of four regional assessments of biodiversity and ecosystem services in Africa, the Americas, Asia Pacific, and Europe and Central Asia, as well as an assessment of land degradation and restoration.

The talk will provide an update on progress in the implementation of the second year of work of IPBES, including on the on-going assessments of biodiversity and ecosystem services. It will also highlight different ways for scientists to get involved.

BIODIVERSITY-CLIMATE INTERACTIONS IN MODERN OCEANS AND IN DEEP TIME: INTEGRATING PLANKTON AND OCEANOGRAPHIC DATA WITH THE MARINE MICROFOSSIL RECORD

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The pelagic realm is the largest biome on Earth. This mostly single-celled plankton ecosystem contributes ca 50% of planetary oxygen production and provides the only major long-term removal mechanism for the earth's atmospheric CO2. Several plankton groups have an extraordinarily good fossil record, preserved in deep-sea sediments and recovered for study by the deep sea drilling programs (DSDP, ODP and currently IODP). Studies of this geologic record suggest close links between the plankton ecosystem and climate at several time-scales, including major perturbations of the global carbon cycle and mass extinctions. We still know remarkably little about the components that make up this system, how it is structured and functions in the modern ocean, and how it is linked to climate dynamics in the past. In particular, responses to climate change are poorly understood, from small-scale ecosystem regime shifts to major extinctions.

In addition to limited primary knowledge, our lack of understanding is compounded by poor data integration between different disciplines. Taxonomic descriptions are still only partially digital or online, and primarily in numerous specialist databases. Occurrences for many taxa in modern oceans are still mostly in literature archives, particularly for species-level data, although substantial syntheses have appeared in the last few years for a few groups, e.g. in COPEPOD (NOAA), the World Ocean Database Plankton (NCEI) and most recently the static tabular (Excel file) compilations of the MAREDAT project (http://www.earth-syst-sci-data.net/special_issue7.html). Living culture collections are very incomplete and their databases isolated. Environmental/climate data on oceans are in very different, earth science repositories such as the NCEI system. Data on past plankton occurrences are partially synthesised in the NSB database (www.nsb-mfn-berlin.de) but much data is still in literature archives. Past environmental (paleoceanographic) data is mostly either in the WDC Pangea system or literature archives.

Lack of data integration between taxonomic catalogs and occurrences causes biodiversity and other metrics to be clouded by synonyms, misspellings etc; occurence data cannot easily be compared to physical environment and climate conditions; and modern and past plankton ecosystem studies remain ships that pass in the night.

Several recent and new, proposed projects are addressing data integration problems. Online taxonomic catalogs have been built for a few groups (mostly those with a substantial fossil record) and software tools that can extract and integrate certain types of data across domains have been developed. New proposals (Germany, UK) hope to extend these efforts in the next years, better linking taxonomic, living and fossil occurrence, and (paleo)environmental data together.

POPULATION DYNAMICS OF BRANDT'S VOLE UNDER GLOBAL CHANGE: LARGE-SCALE MANIPULATIVE EXPERIMENTS REVEAL ACCUMULATIVE EFFECTS OF LIVESTOCK GRAZING ON BRANDT'S VOLE POPULATIONS IN STEPPE GRASSLAND

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Livestock grazing as one of the major human disturbances has been causing problems with respect to both pest impacts and biodiversity losses in the steppe grassland ecosystems of Inner Mongolia. In this study, by using large replicated enclosures which prevented immigration and emigration of rodents and excluded all rodent predators, we investigated the accumulative effects of sheep grazing on the population dynamics of Brandt's voles in the steppe grassland of Inner Mongolia, China, between 2010-14. We found the response of vole populations to livestock grazing was not obvious (but with a non-significant positive trend) in the initial years and negative in the following years. The negative effect of grazing was predominantly caused by grazing-induced changes in both food quantity and food quality. Our results provide new insights into impacts of grazing on small rodents in the context of a sheep-plant-rodent system and we call for more flexible management of livestock grazing to optimize livestock production while maintaining species diversity and ecosystem health.

Keywords: Livestock grazing, Food quantity and quality, Secondary compounds, Crude protein, Small rodents, Population dynamics, Grassland

HISTORICAL DECLINES OF 11 MAMMALS IN CHINA AND ASSOCIATED DRIVING FORCES

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Many species have dramatically declined during past hundreds years due to accelerated impacts of human activities and climate change. We derived historical species occurrences of 11 mammals based on historical literatures and current publications from 1500 to 2000. We used eight indices to represent the distribution of species, i.e. the mean, maximum and minimum values of latitude and longitude, and habitat areas on the basis of minimum convex polygon (MCP) and kennel density. Our results showed that Asian elephant (Elephas maximus) and Asian rhinoceros (Rhinoceros unicornis, Dicerorhinus sumatrensis, Rhinoceros sondaicus) had clear southward contraction; the giant panda (Ailuropoda melanoleuca), the Bactrian camel (Camelus Bactrianus), and the Asian wild horse (Equus przewalskii Poliakov) had significant westward retreat; tiger (Panthera tigris), water deer (Hydropotes inermis) and musk deer (Moschus sifanicus, Moschus berezovskii) also declined dramatically yet without a directional pattern. The speeds of declination vary in species. In order to detect the driving forces of range contraction, we used multiple regressions to quantify the linear association between species range indices and climate variables (five temperature series and three precipitation series), as well as human population size. We also used a machine learning technique, random forest, to quantify the nonlinear and interactive effects of the climate variables and human population. We found that temperature was associated with the retreat of the Asian elephant and Asian rhinoceros, whereas the retreat of most other mammals was closely associated with human impact (represented large population size). Our results implied that human activities imposed a great impact in causing range contraction of mammals in China, especially in past 100 years.

CAN NITROGEN DEPOSITION SHAPE THE INTERACTION BETWEEN SEEDS AND FOOD HOARDING ANIMALS?

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The environmental impacts of anthropogenic nitrogen deposition have been well studied; however, response of the interaction between seeds and food hoarding animals to N deposition has been less investigated. This study was designed to explore the impacts of acute N deposition on seed chemical traits and food hoarding behaviors of small rodents in the northeastern deciduous forests in China. In May 2015, nitrogen was added to Korean pine trees as NH4NO3 of 50 g N m−2 yr−1. Seeds were collected in September to measure seed chemical traits and test food hoarding behaviors of rodents. Results showed that acute N addition significantly enhanced the proportion of seed kernel and changed the contents of protein, fat, and total N. Moreover, seed odor emission was significantly influenced by N addition. Acute N addition increased seed scatterhoarding by *Tamias sibiricus* and *Apodemus peninsulae*. N addition decreased cache recovery by *A. peninsulae* but increased cache recovery by *T. sibiricus*. Our results suggest that nitrogen deposition can shape the interaction between seeds and food hoarding animals.

Keywords: Nitrogen deposition; Seed chemical trait; Seed odor; Food hoarding

THE NAGOYA PROTOCOL ON ACCESS AND BENEFIT SHARING – CHALLENGES AND OPPORTUNITIES FOR BIOLOGICAL SCIENTISTS FROM INTERNATIONAL POLICY

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The Nagoya Protocol is a legally-binding international agreement which governs access to genetic resources (GR) in providing countries, and compliance with contractual agreements by users of those resources. Since it came into force in October 2014 it has been ratified by more than 60 countries and the EU; other countries are expected to follow. Countries which have ratified may choose to regulate access to their GR through legislation, generally implemented through a permit system involving a contract to share benefits arising from utilization of the GR. They also are required to monitor GR utilization within their jurisdiction, and take measures to address situations of non-compliance. In the EU compliance is managed under a Regulation (which came into force October 2014), an Implementing Act (from October 2015), and national legislation. The Nagoya Protocol is already having an impact on biological researchers and collections as they work to understand the new legal and procedural environment and develop means of compliance. Tools are becoming available to help manage the new requirements, and challenges now are to implement and improve these tools, raise awareness in relevant sectors, and share benefits with provider countries effectively. It is to be hoped that non-monetary benefits arising from biodiversity research can increasingly be targeted to support conservation and sustainable use of biodiversity.

STRANGERS SPREADING DISEASES: THE ROLE OF NONINDIGENOUS SPECIES AS VECTORS OF BLOOD PARASITES FOR ENDEMIC THREATENED FOREST BIRD SPECIES IN CHILE

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We assessed the presence of blood parasites in two avian communities with endemic threatened birds in Chile. Our aim was to check whether non-endemic, probably introduced bird species, are acting as vectors of blood parasites to threatened endemic birds in those communities. First, we studied the parasites infecting Austral Thrush (*Turdus falcklandii*) and Green Backed Firecrown (*Sephanoides sephaniodes*) in the Juan Fernandez archipelago, as a potential source of blood parasites for the endemic Juan Fernandez Firecrown (*Sephanoides fernandensis*) and Juan Fernández Tit-Tyrant (*Anairetes fernandezianus*). Second, we studied the potential effect of house sparrows (*Passer domesticus*) as vectors of blood parasites for the endemic avifauna of Pampa del Tamarugal, habitat of the Tamarugo conebill (*Conirostrum tamarugense*). Our data indicated that the Austral Thrush could be responsible of the introduction of some parasites also isolated from the Juan Fernández Tit-Tyrant and it represents a potential threat to the endemic firecrown due to its role as reservoir of blood parasites. On the other hand, the occurrence of house sparrows infected with a generalist Plasmodium haplotype implied in the extinction of Hawaiian avifauna, along with the occurrence of the suitable vector (*Culex pipiens quinquefasciatus*) in the same region of the Pampa del Tamarugal, might facilitate a host-switching event with unknown consequences for Tamarugo Conebill populations. However, we only found conebills infected by parasites of the genus *Leucocytozoon*, a parasite absent in house sparrows. The spread of non-endemic species could increase the probability of switching events of blood parasites between bird species.

INTEGRATING PHYSIOLOGY WITH DEEP TIME AND CLIMATE: EXAMPLES FROM ECTOTHERMIC VERTEBRATES

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There is a growing recognition that integrative efforts combining deep-time information from the fossil record with modern macroecological approaches can yield novel insights into our understanding of the effects of climatic and environmental change on biological species and communities. Here we illustrate how physiological traits derived from field-based studies in evolutionary ecology can be successfully incorporated in such a framework. Using ectothermic vertebrates, and primarily turtles as examples we show that physiological and behavioural traits such as modes of thermoregulation and preferred body temperature in conjunction with phylogenetic hypotheses and data from the fossil record can generate empirically testable predictions on extinction risk and past distributions. Our studies also indicate that climate cooling since the mid Cenozoic might have had a significant influence on the evolutionary success of many groups of reptiles. Whereas we advocate for further studies along similar directions, a proper integration of neontological and paleontological data is hampered by our still poor knowledge of modern phenotypes below the family level, which currenly prevents many groups of organisms from being successfully integrated into such transdisciplinary approaches.

PRACTICAL APPLICATIONS OF AEROBIOLOGICAL STUDIES

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Aerobiology is defined as the study of airborne particles of biological origin, including their sources, liberation, dispersal, deposition and impact on other living organisms or the environment. It is then essentially a multidisciplinary field gathering scientists and professionals from many disciplines, with many practical applications. Pollen grains and fungal spores monitoring in the air is important for diagnostics, therapy and prophylaxis of allergy. Information is widely available in the media and the Internet. The European pollen information and Patient's Hay-fever Diary are available on the website of the European Aeroallergen Network (polleninfo.org). Measurement of specific allergens (Bet v1, Ole e1, Phl p5) in the frame of the EU-HIALINE project showed variable allergenic potency of pollen grains. Aerobiological methods allow to capture and identify spores of pathogens before plant infection and to undertake appropriate preventive measures, e. g. to optimize the time and dose of fungicide treatments. They provide information about crop production, gene transfer (e.g, GMOs), and distribution of cultivated, wild and invasive wind-pollinated species using also immunological and molecular biology methods. A number of well tested atmospheric dispersion and transport models are available for aerobiological studies (indoors and outdoors) and the choice of model depends on the species, the availability of source maps and the spatial scale studied. Aerobiological data is a significant indicator of climate change. Since aerobiological processes are responsive to temperature and precipitation, recent changes in climate are manifested in the aerobiological data. Earlier start dates of the pollen season, longer vegetation period and changes in the intensity were observed. Next to climate influences, mainly increasing CO_2 concentrations can lead to a higher pollen production.

Aerobiology is considered for studies on flowering phenology of anemophilous plants. Airborne pollen provides a mean value on the timing and intensity of flowering population, adding important information to traditional field observations for individual plants.

Indoors, many applications were developed to assess air quality and exposure to allergens or pathogens in public and private spaces, and in occupational environment, e.g. in operating theaters, composting facilities or even to prevent bioterrorism. Many studies are similarly dedicated to the preservation of cultural heritage, to identify hazardous situations and to test the efficacy of preventive measures. Aerobiological knowledge is also used for climate reconstruction from fossil pollen data and has important applications in forensics.

ENGAGING IN SCIENCE-POLICY INTERFACING - A GROWING NEED FOR THE BIOLOGICAL SCIENCES

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The last two decades have seen some major developments in the science and policy landscapes on biodiversity. With GBIF, GEOBON and other initiatives, major data and observation related networks are forming and start to be relevant for global policies processes like the Convention on Biological Diversity (CBD) and the newly established Intergovernmental Platform on Biodiversity and Ecosystem Services (IPBES). On the regional level, for example in Europe, similar developments are on the way.

While already the integration within the field of biodiversity is a challenge, as the mentioned initiatives show, the ambition becomes even larger by the current tendency to have biodiversity embedded in the wider societal context as can be seen in the Sustainable Development Goals, or, on the science side, the Future Earth programme.

This diverse landscape pushes the biological sciences into a growing need to get engaged into according interfacing processes – with other scientists, but also with society in interfaces like IPBES. The talk will outline the according challenges from a European as well as international perspective, identifying some major challenges that the biological sciences need to address in order to be perceived as credible and relevant in such interface processes. These challenges include:

- Taking the step from data and information collection and provision to knowledge relevant in interfaces like IPBES
- Getting engaged with other forms of knowledge (in science and beyond) when addressing questions posed by policy
- Developing further the suite of methods of knowledge integration, from systematic review to expert consultation and to adaptive management approaches to name just a few
- Increasing institutional capacities and knowledge about interfaces in order to be able to get involved in them

The talk will then finally reflect on the concrete relevance of these aspects, internationally in the context of IPBES and on the European scale with respect to EU policies.

UNIFYING BIOLOGY THROUGH INFORMATICS: INTRODUCTION

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In line with its agenda to promote a Unified Biology, the International Union of Biological Sciences is exploring how we can call on informatics to unify biology. The products of research are now almost wholly digital. From this emerge opportunities to share and re-use data on all processes involving all elements of biology. The spectrum of processes ranges from sub-femtosecond reactions of photosynthetic molecules to the impact of photons through to the 3.5 billion year processes that have created and maintain the biosphere. The development of a framework capable of linking information from all subdisciplines presents sociological, technical and political challenges. The sociological challenges include a readiness by individuals, teams, and programmes to prepare and offer all new data openly and freely for re-use, to more readily re-use information from others, and to ensure that credit is given to creators of data and to those who ensure they are readily available. The technical challenges involve the assembly of nodes that will discover content in each discipline area, acquire content, provide custody for it, curate it such that the content is available in standard formats, and make it openly available to end users, both human and machines. Additional technical issues include the universal application of dereferenceable identifiers to all data atoms, an ontological framework to describe content, and an annotation system to enable quality control and quality enhancement. The political challenge is to realize an additional funding model that is suited to a cyberinfrastructure. The current research paradigm is well suited to the process of discovery. It supports many groups who tackle the same problems, but this redundancy increases the likelihood of breakthroughs. This also introduces an element of competition. The short term funding for research ensures that the cutting edge is always moving forward. But, the research funding paradigm is not well suited to the development of a stable, reliable and persistent infrastructure that will place a high premium on service. IUBS is well placed to make the case for an additional funding paradigm.

ZOOBANK, REGISTRATION, AND THE DIGITAL FUTURE OF NOMENCLATURE

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ZooBank was first proposed as the official online register for zoological nomenclature in 2005, and was first launched as a voluntary registration system on January 1st, 2008. A revised version was released on September 4, 2012 to coincide with the publication of an amendment to the International Code of Zoological Nomenclature, which established rules for publishing new names and nomenclatural acts electronically (including mandatory registration for such published works in ZooBank). During this time, ZooBank has grown to include nearly 150,000 registered names within nearly 62,000 registered publications, authored by almost 37,000 taxonomists, contributed by approximately 3,000 users. Despite the growing user base and registered content, ZooBank contains less than ten percent of the total names and works within zoology since the time of Linneaus, and many new names not published electronically are not registered. For ZooBank to serve as an effective tool for the future of digital taxonomy, its content must be dramatically expanded, and the services it offers must be expanded and improved. We are currently in an awkward time in history, where information exchange amongst scientists is rapidly shifting towards electronic documents, but the major Codes of nomenclature are only beginning to develop robust registration systems. As the International Commission for Zoological Nomenclature (ICZN) begins drafting the next (fifth) edition of the ICZN Code, a major paradigm shift is needed to embrace the digital future of taxonomy and nomenclature. I will present an outline for a proposal to restructure the next ICZN Code as two parts; one part representing an improved version of the 4th Edition of the Code, and the other part representing a much simplified process to establish new names in Zoology through the registration process itself. I also advocate that the International Committee on Bionomenclature (ICB) play a leadership role in defining how the next generation of taxonomists can best leverage digital information technologies to harmonize the process of nomenclature across all domains of life.

TRANSDISCIPLINARY BIODIVERSITY RESEARCH

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Despite political efforts to halt the loss of biodiversity and despite a growing body of research, biodiversity decline measured as genetic, species, functional or ecosystem diversity continues. In light of this development transdisciplinary methods are needed which produce knowledge that can be applied to real-world problems related to biodiversity and at the same time further scientific progress.

Since the invention of the term "biodiversity" in the 1980ies, the conservation and sustainable use of biological diversity has become integral part of political agendas. One result of the United Nations Conference on Environment and Development (UNCED) in 1992 was the Convention on Biological Diversity (CBD). Furthermore, to strengthen the dialogue between the scientific community, governments, and other knowledge holders the Intergovernmental Platform on Biodiversity and Ecosystem Services (IPBES) was set up in 2012. Parallel to the political processes regarding biodiversity, biodiversity research has established as an own scientific field. With (a) its origins in conservation biology, (b) due to the different scales that biodiversity research operates on, and (c) as biodiversity research provides evidence for management and policy decisions, biodiversity research is inherently connected with value questions. It makes a difference, whether research focusses on ecosystem functions or on the conservation of biodiversity, for example. These, often unconscious, value judgements are not reflected in the scientific discourse that mainly relates biodiversity research to natural sciences methods and disciplines. Nevertheless, they are crucial for addressing the societal causes of biodiversity decline and implementing the diverse political frameworks.

In transdisciplinary research, real-world problems are the starting point. Real-world problems usually involve different knowledge holders and different stakeholders, different problem perceptions, and different answers to questions regarding who has a problem, who caused the problem and who is able and responsible for solving it. Transdisciplinary research projects create boundary objects that transform different perspectives into a common starting point for research questions. One important criterion of transdisciplinary research is the involvement of non-academic knowledge holders and stakeholders during the whole research process. It is the aim of transdisciplinary research to provide solutions for real-world problems as well as new scientific insights.

Examples for transdisciplinary research projects can mainly be found in sustainability science. The talk suggests the use, adaption and development of transdisciplinary methods within biodiversity research by outlining the "added value" of transdisciplinary biodiversity research as well as its challenges.

NETWORK-FORUM: A SCIENCE-POLICY INTERFACE FOR BIODIVERSITY

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The German Network-Forum for Biodiversity Research (NeFo) is the national focal point for scientist, policy-makers and other stakeholders working in the field of biodiversity research and policies. NeFo was set up to improve the information and knowledge exchange both between and within these different stakeholder groups (e.g. between different research disciplines). Our aim is to increase the awareness of the value of biodiversity among policy makers and the society, and the important role scientists play to analyse the drivers of biodiversity change in order to identify solutions for its conservation.

Currently, NeFo has a particular focus on the newly established Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES), which had its first plenary in January 2013 (IPBES-1) and the fourth meeting will be held in February 2016 (IPBES-4). NeFo aims at facilitating the involvement of the German biodiversity community in this IPBES process. Our capacity building comprises national and pan-European workshops, provision of information about IPBES and the possibilities for participation. Beyond, we support the German ministries engaged in IPBES by e.g. identifying (scientific) topics relevant for IPBES, feeding in of comments on IPBES documents and representatively attending important IPBES meetings.

A MODEL INSECT FOR GLOBAL CHANGE, THE PINE PROCESSIONARY MOTH

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The pine processionary moth, *Thaumetopoea pityocampa*, is an insect species occurring in Europe, North Africa and Minor Asia, causing sanitary and phytosanitary problems. Since the early 1990s, it has been extending its distribution northwards and towards higher elevations. This range expansion is acknowledged by IPCC experts to be one of the few responses to climate change among forest insects for which a direct causal relationship has been proven. Higher temperatures in winter facilitate larval foraging, colony survival and ultimately the species spread. In France, the northern edge of the species distribution is considered as a bio-indicator of climate warming since 2007. Mapping of the species edge at 5-year intervals revealed an average northwards progression at a speed of ca. 5 km per year. Although the attenuation of the cold constraint largely explains the large-scale range expansion, human-mediated dispersal has likely accelerated the species spread. Pioneer colonies were discovered far beyond the main range since the 2000s, probably resulting from the transplantation of large potted trees with soil infested by pupae. The establishment of these pioneer colonies is nevertheless enhanced by more suitable climate conditions. A large part of Western Europe has already become favorable to pine processionary moth establishment, and the favorable areas are assumed to extend to the North and the West in the future under IPCC climate change scenarios. Another factor that has not been fully studied until now is the effects of climate change on the species phenology. Stage-specific thermal thresholds of subsequent life stages and inter-populational heterogeneity in phenology need to be considered to better understand how phenology shift could eventually alter the species distribution, and whether climate change may remain so beneficial for the species in the future.

ABS –DELIVERING BENEFITS AND IDENTIFYING NON-COMMERCIAL RESEARCH IN BIOLOGICAL SCIENCES

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Access and benefit sharing (ABS) refers to how genetic resources, derivatives and associated traditional knowledge are accessed and how the benefits that result from their use are shared between the countries using the resources and the providers of these materials. Therefore, even basic research is nowadays worldwide subject to regulations related to the Convention of Biological Diversity (CBD) and the Nagoya Protocol. However, special considerations should be given to research with no commercial intention, contributing to the conservation and sustainable use of biodiversity, the other two aims of the Convention. To assess the contributions of basic and applied non-commercial research on biological sciences, to the objectives of the CBD, we conducted two surveys, one in Germany (n= 118), with researchers in academia. The global survey (n= 929) included members of IUBS and the Species Survival Commission of IUCN. Benefits included capacity building, collaborations, technology transfer, socio-economic benefits. At least half of the projects, in the German dataset, and more than two thirds of the projects, in the global dataset contribute to the conservation and sustainable use of biodiversity, ranging from raising awareness in environmental issues, to the development of new science-related policies in the provider country. When trying to characterize non-commercial research according to the field of research, methods used to conduct research or domain of research, none of these variables was significant (on Chi-square tests for independence). Nevertheless, the study shows some trends that can help provider countries to define their access policies, regarding facilitated access.

INFILTRATION OF THE INTERNATIONAL CODE OF ZOOLOGICAL NOMENCLATURE BY THE BIOLOGICAL SPECIES CONCEPT

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A fundamental principle of zoological nomenclature is that the rules of nomenclature should not restrict taxonomic freedom. Yet in disallowing the naming of varieties and forms after 1960, the International Code of Zoological Nomenclature does restrict taxonomic freedom and expression. Under the Biological Species Concept, it has been widely accepted that subspecies must not overlap in geographic distribution. When two subspecies are found to be sympatric, they are usually either synonymized or elevated to the level of full species. However, the Code does not and should not enforce a geographic definition of subspecies. A taxonomist could choose to recognize sympatric subspecies as an initial stage in sympatric speciation. However, if one preferred to keep a geographic definition of subspecies, which is a matter of taxonomy, incipient sympatric speciation could instead be recognized as, for example, host races, but such cannot be named under the current Code.

The banning of infrasubspecific names has also reduced the level of precision possible in referring to organisms by names. Once the subspecies became the only allowed infraspecific rank, variation that did not have appropriate geographic patterning often went unnamed. The polytypic species concept erased precision. Synonyms were forgotten rather than used as varietal names, even if the taxonomist could distinguish them. Years later, molecular genetics has shown that many subtle morphological differences correspond to what is now recognized as species-level variation, so that now one often cannot tell what species an author who used a polytypic concept meant, unless vouchers exist. Varietal names allow a neutral level of precision that has been lost with the infiltration of the Code by the Biological Species Concept.

In addition to restoring taxonomic freedom, are there other advantages of reinstating the variety group in zoology? Yes, it could provide a mechanism to set aside the taxonomic burden of dealing with variety-group names in the species group. The mechanism would be to recognize priority within each group, with limited precedence of variety-group names in the species group. For variety-groups names treated as valid at subspecies or species rank, or as senior homonyms, before 201X, precedence in the species-group would be from the same date as priority in the varietal group. For variety-group names treated as subspecies or species after that date, precedence in the species group would date from their elevation in rank. Thus an author discovering a species-group taxon that had no valid species-group name, but had an available variety-group name, could choose whether to name a new species-group taxon or elevate the varietal name into the species group. This choice might depend, for example, on whether good type material existed for the variety-group name. Other advantages of use of a variety group might be found in molecular systematics or in dealing with chronological variation in paleontology, allowing naming agnostic to some of the taxonomic considerations of the species-group.

THE LEIBNIZ NETWORK ON BIODIVERSITY (LVB) – OBJECTIVES AND PRIORITIES

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The dramatic loss of biodiversity represents one of the greatest challenges of our time. Biological diversity has a high intrinsic value and is fundamental to human wellbeing in securing food and clean water supply, protecting health, and enhancing resilience to climate change. The Leibniz Network on Biodiversity (Leibniz-Verbund Biodiversität – LVB) pools competencies and resources of 20 member institutes in order to develop solutions for the conservation and sustainable use of biodiversity through interdisciplinary research. Providing policy makers with scientific knowledge, we contribute to the implementation of agreements on biodiversity and aim at reconciling biodiversity-related targets with those of competing policy fields. Finally, the LVB supports citizen science initiatives that promote public engagement in biodiversity research and raise awareness for the value of biological diversity – from the genetic to the ecosystem level – as well as for our responsibility to preserve it.

DIVERSIFICATION DYNAMICS FROM EXTANT AND FOSSIL LINEAGES

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Present-day patterns of biological diversity are driven by processes that have acted over long periods of time and that govern the appearance of new species, their evolution, and ultimately their extinction. Most studies to date have relied on a single source of data to understand the tempo and mode of biotic evolution: either molecular phylogenies or fossil occurrences. This situation is caused in part by limited interaction between molecular systematists and paleobiologists, but also by different data, methods and assumptions, which render comparisons statistically difficult. First, I present a Bayesian framework to estimate speciation and extinction rates based on fossil occurrences. The approach jointly estimates species-specific times of speciation and extinction and the rates of the underlying birth–death process based on the fossil record. Rates of speciation and extinction are allowed to vary through time independently of each other, and the probability of preservation and sampling is explicitly incorporated in the model to estimate the lifespan of each lineage. The estimated parameters of the birth–death process implemented here are directly comparable with those obtained from dated molecular phylogenies, representing an important step towards the integration of molecular and fossil information to infer diversification dynamics. Second, I demonstrate how information from fossils can be integrated into molecular phylogenies of extant taxa when studying the evolution of functional traits. Extinct species may be integrated into a molecular phylogeny based on taxonomic knowledge, while sampling from the estimated times of speciation and extinction of each fossil lineage.

The fit of different macroevolutionary models (Brownian Motion, Ornstein-Uhlenbeck, Accelerating/Decelerating evolution) were compared using AIC regression with and without the integration of fossils. Results show that the integration of fossil data into the analyses of trait evolution significantly affects model selection, estimated evolutionary rates, as well as reconstructed trait values at the root of the phylogenetic tree. These analyses highlight the importance of integrating extant and extinct species when studying macroevolutionary processes.

INTEGRATED BIOLOGY EDUCATION FOR SUSTAINABLE AND EQUITABLE WORLD

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In 21st century, we hope to address some of the fundamental questions on origins of life, systems level understanding of ecosystems, plant/animal-microbe interactions, human diseases, human brain, etc. Much more than this, the needs of providing nutrition-rich food to billions of people, preventing devastating diseases and protecting our habitat for future generations, integrated approaches to biology education and research is the focus in all countries, be developed or developing. Efforts are being made all over the world to train large number of biologists for the future. In this context, a paradigm shift is needed in the way we teach Biology in Schools, Colleges and Universities. Life, while is a continuum of physic-chemical worlds, is several order more complex than any non-living system we know. Furthermore, it is continuously changing/evolving due to stochastic forces and upon its interactions with the changing environment. Thus, inquiry-driven and research-based education is must to obtain even minimal understanding of biology.

In this session at IUBS GA 2015, we would like to discuss ways of developing inexpensive teaching modules on basic concepts of biology (such as Evolution, Ecology, Genetics etc) based on observational field biology that can be effectively used in countries with less resources in their schools/colleges and universities. At pedagogical level, we should use more of ICT tools, such as mobile phones. Developing teaching modules based on mobile phones would reach out to deepest corners of the world.

ENLIVENING BIOLOGICAL SCIENCES FOR SUSTAINABLE DEVELOPMENT

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We are living in the context of great social and ecological acceleration, pushing planetary boundaries, in an era some are calling "the anthropocene". Human impacts on planetary systems are driving the change. Science in this era needs to deal with the challenges of climate change and sustainable development on a planetary scale. This talk introduces Future Earth approach to stakeholder engaged transdisciplinary approaches to science. I offer some thoughts on how enlivening biological sciences to meet our quest for sustainability.

ALIGNING THE AGENDAS OF PUBLIC HEALTH AND CONSERVATION: WHICH ELEMENTS OF BIODIVERSITY PROVIDE WELL-BEING BENEFITS TO CITY DWELLERS?

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Urbanization is a global process that both contributes to the lasting biodiversity crisis and separates people from the experience of nature. This is profoundly concerning, first because interaction with nature leads to a variety of health and well-being benefits, but also since this estrangement can undermine people's action and public support for biodiversity conservation. Planning green cities that host a rich biodiversity could deliver the needed win-win solutions that succeed in aligning the agendas of public health and conservation. However, fledgling work on how to grow cities to reduce their biodiversity impact suggests that compact development forms can reduce ecological impacts on the regional scale better than sprawling green developments, although this response may tradeoff with people's access to nature and the associated outcomes. Unpicking this tradeoff requires a more profound understanding of the social and ecological benefits of conserving urban biodiversity.

A systematic multidisciplinary literature review reveals that empirical research does not convincingly show the importance of urban areas for general conservation. Only few studies demonstrated that cities can directly contribute to conservation efforts, by hosting viable populations of rare or endangered species, or by providing green corridors for the passage of natural populations. From a social perspective, most studies that have explored the restorative role of nature have looked at nature/green as a black box. They show that green infrastructure or nature can provide services for people (notably cultural services), but only few studies explored the role of species diversity per se in providing those services.

We further explored the relationship between species diversity and well-being in France and in Israel and unveil a "people-biodiversity paradox", consisting of a fundamental mismatch between: (i) the preferences people say they have for biodiversity and how this relates to their subjective well-being; and (ii) people's limited ability to perceive biodiversity, which prevents them from benefiting fully from the direct interaction with nature. In Israel, we also found that most relationships between measures of well-being, observed and perceived species richness (notably trees and flowers) were mediated by the respondents' connectedness to nature. Thus, people who perceived themselves as more connected to nature benefited more from species-rich gardens, while such benefits were absent or even negative for people who were less connected to nature. Altogether our results indicate that the relationship between biodiversity and well-being is not as straightforward as commonly argued. We therefore call for a fundamental shift in approach recognizing that much of the biodiversity present in cities is not necessarily perceived by nor provides benefits to people. We argue that the challenge of urban ecology today is to identify the specific elements of nature that benefit people, across different socio-economic levels and urban locations, and explore how they relate to biodiversity indicators of conservation value to promote sustainable planning of cities.

THE 21ST CENTURY IS THE CENTURY OF BIOLOGY: FROM DARWIN TO THE DNA HELIX AND BEYOND

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This presentation will briefly summarize the history of biology since Darwin's contribution through The Origin, emphasizing the interlinkage of ecology and evolution, the former being the driving force behind evolution and the lather determining the nature of the ecological interaction. The presentation will also discuss the need to counter the fragmentation within biology: we need to bridge the gaps between the various sub-disciplines of biology, emphasizing the unified approach to biology.

DISCOVER YOUR CITY – URBAN NATURE AS AN EXPERIENCE IN EVERYDAY LIFE

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Conservation has an educational mandate that becomes even more relevant in the urban context. Urban areas offer the opportunity to give a large number of people an understanding of environmental processes and nature conservation. This is especially important for those who seldom visit conservation areas, where wildlife education has been situated traditionally. Urban citizens may value more the availability of green areas than their ecological value and contribution to biodiversity. The effort to foster a positive emotional relationship with nature where citizens live and work is still too little.

Mobile devices have become almost ubiquitous. Using mobile devices in informal learning can offer the opportunity to make learning a part of everyday life. The learner has the freedom to choose what, where and when to learn. Information can be used in the individual context, is available at the point where it is needed and can be shared with others.

The project Stadtnatur entdecken shows how to foster nature experience in everyday life in an urban context. A transdisciplinary team develops an application for mobile devices which is going to provide contextualized information about urban nature in Berlin.

I will present the application more in detail and show exemplary how we want to motivate citizens to discover their city from a new perspective and to experience urban nature in everyday life.

ANNOSYS – A GENERIC ONLINE ANNOTATION MANAGEMENT SYSTEM AND REPOSITORY FOR SUSTAINABLE COLLECTION DATA

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With 2-3 billion preserved specimens world-wide, natural history collections preserve a record of the world’s biodiversity, providing the baseline data for research in many biological subdisciplines. Traditionally, annotations are paper notes (identifications, comments, type designations) made by specialists and attached to the physical specimens. These annotations document the scientific work with the specimens, improve and actualise the specimen related data, thus increasing their value for future research.

AnnoSys (https://annosys.bgbm.org/) is an online annotation system for networked specimen and species occurrence data. It is a sustainable data quality tool, allowing specialists to correct and enrich the data in publicly available data portals that provide access to such data. AnnoSys supports the creation of and search for annotations using community-specific criteria, such as the identification with a scientific name, the place where the specimen was gathered or the observation was made, nomenclatural type information, etc.

Within its first project phase, AnnoSys developed workflows and methods supporting online Annotations of collection metadata that have been published in the networks of the Global Biodiversity Information Facility (GBIF) and the Biological Collection Access Service (BioCASe). The current online version can be accessed from nine biodiversity data portals providing collection and observation data in the botanical, bacterial and zoological domains.

The data portal integration includes on the one hand the display of available annotations for a given collection or observation data object, on the other hand it allows users to access AnnoSys' web interface where they can edit, manage and publish further annotations. In addition, the web interface enables collection curators (on request) to communicate and vindicate decisions with regard to acceptance or rejection of annotations referring to data objects from their collections. All registered AnnoSys users can subscribe to a message system in order to receive information about annotations in their area of interest (e.g. those referring to specific taxonomic groups, localities or their own collections).

AnnoSys can be adapted to a variety of application domains and data standards, because it uses a generic annotation context model based on international interdisciplinary standard developments (W3C Open Annotation Data Model). The AnnoSys repository archives annotations and the related original collection data. Both are publicly retrievable and integrable with other systems through several types of web services.

In the current project phase, AnnoSys is being extended with respect to data types (to include annotations of species checklists) and with respect to the technical protocols supported.

AnnoSys is funded by the German Research Foundation (DFG). The project title is “Internationalisation and realisation of the comprehensive online annotation system AnnoSys – application potential in terms of disciplines and standards” (BE 2283/4-2).

IMPACTS OF CLIMATE CHANGE INDUCED CORAL BLEACHING ON ECOSYSTEM SERVICES IN THE GULF OF THAILAND

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Coral reef ecosystems provide a lot of economic benefits, especially reef tourism, recreational fisheries, fisheries production, coastal protection and natural products. However, coral reef ecosystem services are threatened by various anthropogenic and natural stresses. A case study in the Gulf of Thailand revealed that the low *Acropora* coverage at the study sites before the 2010 coral bleaching event was still a result of the previous severe coral bleaching event in 1998. Densities of juvenile *Acropora* colonies before the 2010 coral bleaching were also very low at the study sites, with no recruitment for several years. Several *Acropora* species that were previously observed in these coral reefs are presently at risk for local extinction or may have already disappeared. Quantifying coral reef ecosystem services in the Gulf of Thailand has been documented with emphasis on linking coral reef conditions with various types of ecosystem services. Given coral reef management and restoration plans in Thailand as an example, the coral reefs are categorized into four different groups depending on their threats and type of uses. The coral reef that is in a degraded status and is used for tourism is the priority area for coral reef restoration. The coral reef restoration plan concentrates on using passive restoration in four strategies and fifteen measures, by reducing threats from tourism, water pollution, sedimentation and fisheries. The active coral restoration by numerous asexual and sexual reproduction methods and techniques will be carefully considered prior to applying at appropriate reef sites. The major concerns are simple and cheap restoration methods, community involvement, high tolerant species to bleaching and multi-species transplantation. The coral reef management and restoration project in tourist hot spots in the Gulf of Thailand is a good case study for adapting to impacts of coral reef bleaching in Asia-Pacific. The project was initiated and funded by the network of provinces in the eastern Thailand. It aims to survey and establish an ecological and socio-economic database for managing the coral reefs and enhance their resilience to climate change. In addition, artificial substrates for coral recruitment and ecotourism are provided at tourist hotspots with the participation of local communities in managing natural resources and environment, wherein public awareness and education are enhanced. The project shows effective collaboration between scientists, local communities and local government officials as decision-makers to integrate scientific data into policy and adaptation measures. The coral reef restoration sites can be used to support ecotourism and learning opportunities for students. Continuing efforts in capacity building, public awareness and education can enhance resilience in coastal communities. Strengthening the long-term monitoring, evaluation and reporting of the project can provide lessons for conservation of coral reefs in tourist hotspots influenced by climate change.

EPIGENETICS AND THE ENVIRONMENT – FISH AS A POTENTIAL MODEL (PERSPECTIVE)

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In eukaryotic cells, the epigenetic code, a combination of epigenetic modifications, greatly influences the expression of genes. The epigenetic modification includes cytosine methylation of CpG dinucleotides of the genomic DNA as well as chemical modifications (methylation and acetylation) to histone proteins of the chromatin that pack the DNA strand. The possible impact of the environment on epigenetic modifications in the chromatin has become an attracting topic in modern biology. Previous studies have shown that environmentally induced changes in gene expression are often associated with altered DNA methylation patterns or with altered histone modifications. These changes in the epigenetic code are even suggested to be transmitted across generations and thereby, to facilitate rapid adaptation of organisms to ever-changing environment.

My laboratory has been working on epigenetic regulation of developmental key genes using the genome of medaka (Japanese killifish) as a model. We recently established a platform with which we can decode the epigenetic code genome-wide at a single-base resolution in fish genomes. We are now comparing conservation and change in the epigenetic code between two closely related medaka species, one from northern Japanese population and the other from southern one with several million-year separation. This kind of analysis can be applied to wild-type species living under various kind of environmental stresses such as climate change and chemical pollution. I will discuss the potential use of fish epigenome in environmental science.

EFFECTS OF THE LAIRAGE TIME ON BEEF CATTLE

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There are several factors that affect beef quality. The muscle glycogen concentration during slaughter is the most significant. pH values increase above 5.8, unless there are enough stored glycogen. This increase can cause serious quality problems, such as dark cutting in extreme cases. Even optimum conditions are provided, stress is inevitable during transport. When the transport duration increases, the welfare of animals is affected badly and because of physiological stress meat quality decreases. In other words slaughter weight reduces, final pH increases, muscle luminosity decreases and there results dark, firm, dry (DFD) meat due to stress. This transport stress is recovered by application of lairage to animals before slaughter. The main benefits of lairage are; less negative effects of transport, easy evisceration resulting less contamination of the carcass by its gut contents. Basic requirements for lairage are sufficient space to lie down, recovery duration, available water and feed. As a rule the cattle are hold in lairage and handled to remove fatigue arising from transportation. Even so; a definite period of lairage at the abattoir to recover from physical and psychological stress caused by transport and to optimise meat quality. The application of lairage durations ranging from several hours to more than 24 hours can be realized, when arrival time, holding capacity and number of animals to be slaughtered are considered. The objective of the review was to examine the effects of the lairage time on beef cattle.

THE BACTERIOLOGICAL CODE: A MODEL TO FOLLOW OR ONE TO AVOID?

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The Bacteriological Code has served as the inspiration for topics such as the implementation of a system of registering/indexing names as an integral part of the rules and introducing a set of protected names that serves to maintain continuity with those names of the past that were considered to be valuable, while removing those names of the past that were not considered to be useful, as well as building on new names. Implemented in the 1975 revision of the Code and carried forward in subsequent revisions there has been an assumption that "all is well". However, a closer analysis of the Code and putting it into the context of a simple set of logical statements highlights a number of serious problems. The current system has continued to work because those implementing the Code were either not aware of the problems, interpreted the Code inaccurately or simply ignored certain issues.

WHAT IS DIYBIO - THEORY, PRACTICE AND PERSPECTIVES

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What is Biohacking, also known as Do It Yourself Biology or more generally 'citizen science'? Since the early 2000 citizens have begun to connect globally to exchange knowledge on biological arts and science and the concepts of open source sharing of information became popular. Soon, the Hackteria network emerged and started to organize hackathons and workshops to build cheap and generic lab equipment for biotechnology for stationary as well as mobile laboratories. Simple and lean innovation such as turning a Webcam into a Microscope, using CD-ROM for Spectrophotometry and the assembly plans for a DIY thermocycler were developed. Also highly sophisticated projects using scrap electronics could be undertaken. An optical tweezer from DVD burner could be used for single cell manipulation – at about 1/1000 of the cost of commercially available equipment. With such tools citizen scientist managed to make fluorescent plants, genetically programming yeast cells and make beer and bread out of it and conduct other projects in the domain of synthetic biology.

Recently, the maturing DIYbiotechnology is being used to tackle the antibiotic crisis in the project Biostrike. Since years antibiotic resistance is on the rise all across the globe and industry has done little to counter the development. A solution could be the phage therapy, which was developed in the 1950ies in the sowjet union but then forgotten by western scientists. Combining frugal innovation, cheap DIY biotechnology and old publically available knowledge on phages now allows citizen scientists to work on a solution to the antibiotic crisis. Recent advances in DIY electrowetting on dielectric will help to increase efficiency of the citizen research. Digitally reprogramming of Phage DNA sequences in combination with low cost and automated laboratory methods could in future lead to a personalized phage therapy. By establishing open standards and sharing information and technology, academics, artists and interested citizencs in industrialized as well as developing countries can contribute to the solution of the crisis.

FIT FOR PURPOSE, OR OUT OF SHAPE? THE PRESENT AND FUTURE CODE FOR ALGAE, FUNGI, AND PLANTS

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How fit for purpose is the International Code of Nomenclature for algae, fungi, and plants? Major changes were introduced in 2011 at the Melbourne International Botanical Congress (IBC): electronic publication, the end of the Latin requirement for a validating description/diagnosis, the end of dual nomenclature for pleomorphic fungi, the end of morphotaxa for fossils, mandatory registration of fungal names, lists of protected and suppressed fungal names, the Appendices of the Code in a searchable online database, and not least a new name for the Code itself. But what are the drawbacks of the current Code? What could be improved at the 2017 Shenzhen and subsequent Congresses? Greater transparency on how the Code is governed by its users? Greater autonomy for governance of fungal nomenclature? Mandatory registration of plant and algal names? Lists of protected names of plants and algae? With each IBC, the Code becomes arguably more precise, but certainly more complex. Is this trend sustainable? Will the Code eventually become so complex that it is navigable by only a few nomenclature specialists?

TEACHING BASIC CONCEPTS OF ANIMAL VISION AND NAVIGATION TO SCHOOL CHILDREN USING DUNG BEETLES AS MODEL ORGANISMS

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Ball-rolling dung beetles have remarkably stereotyped and highly robust navigational behaviours that rely on their well-developed sense of vision. In order to escape the ferocious competition of the dung pile, these beetles roll balls of dung away from the pile in the most efficient manner possible – in a straight line in any direction. Such straight-line navigation relies on the use of an external compass, and in dung beetles this compass depends on celestial visual cues. Depending on the species, dung beetles use the disk of the sun, or the pattern of polarised light produced around the sun (which is invisible to humans), as a compass cue for visual navigation in a straight line. By using cheap Polaroid filters, mirrors or small cardboard hats that cover the view of the sky, it is possible to manipulate the orientation abilities of these beetles during ball rolling in predictable ways. These simple experiments can be performed by children in developing countries where these types of dung beetles are common (e.g. Africa). They can be used to teach children that insects have good eyesight, and that vision – and familiar visual cues like the sun – are used to help animals navigate. Such experiments would not only help children improve their basic knowledge of animal senses and how animals navigate, but also enhance their appreciation and love for the natural world that is literally on their door step. In my talk I will showcase the different experiments that might be incorporated into a teaching module, and the simple and inexpensive equipment that would be needed.

GLOBAL CLIMATE SHIFTS DRIVE THE POPULATION FLUCTUATION OF GIANT PANDAS

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The evolutionary history of the panda lineage dates back 7~8 million years ago, and ultimately leads to only one extant species, the giant panda (*Ailuropoda melanoleuca*). The pandas have thrived for millions of years, but now face a high risk of extinction. Although the importance of global climate change and anthropogenic disturbances in shaping the demography of animal populations is well recognized, their contributions to the giant panda population dynamics remain largely unknown. Using the previously deep-sequenced genome and population resequencing of 34 wild giant pandas, we reconstructed a continuous demographic history of the giant panda from its origin to the present, revealing two population expansions, two bottlenecks, and two population divergences. Evidence indicates that for millions of years, global climate shifts were drivers of population fluctuations but recent human activities have likely caused population divergence and the serious recent decline. For the current six geographic populations, we identified three genetic populations and signals of local adaptation. To improve survivability of this species, panda populations with distinct genetic composition need carefully selected conservation measures. However, one conservation measure that would equally serve all three populations is the removal of the anthropogenic activities that have negatively affected pandas for the last 3,000 years.

BIOLOGICAL CONSEQUENCES OF GLOBAL CHANGE (BCGC)

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Global change is now one of the most discussed topics in the world. Understanding the impact of global change is extremely important for the sustainable development of our human society. In 2008, the International Society of Zoological Sciences (ISZS) initiated an international research program, Biological Consequences of Global Change (BCGC). The focus of the BCGC program is to organize a diverse group of international experts, with expertise in many scientific disciplines, and develop an understanding of the consequences of global change and human activity on evolutionary mechanisms, biological structures, endangered species and biological disasters. The goals of the program are to promote understanding of BCGC as to improve management of the earth, international collaboration, influence and leadership of IUBS and ISZS. The major questions to be addressed in the program are the impact of global change on biological disasters, like disease and pest outbreaks, its relation to alien species invasion, abundance and range shifts of endangered species, community structure and biodiversity of ecosystems.

SCIENCE-BASED POLICIES FOR TOURISM MANAGEMENT AT A MARINE NATIONAL PARK IN THE ANDAMAN SEA

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Managing marine protected areas for conservation and tourism is a difficult task. Relationship between tourism, livelihood and conservation is recognized as dynamic and complex system. Perceptions of the multiple stakeholders on environmental and ecological aspects are very important in driving the process of tourism in marine protected areas. Researchers, policy makers and managers have recognized that stakeholders' attitudes and behavior towards the environment and conservation can lead to the success or failure of the sustainable tourism. The aim of this study was to examine the environmental impacts of tourism at Ko Tachai, Mu Ko Similan National Park, in the Andaman Sea and to determine the factors that might influence stakeholders' intentions to engage in environmentally responsible behavior, based on field surveys and focus group interviews. Ko Tachai is among the most intensive tourism activities in the Andaman Sea for recreation and the tourist numbers are over carrying capacity of the island. The coral reef degradation at Ko Tachai before the intensive tourism period caused by a few coral bleaching events, the 2004 Indian Ocean tsunamis, outbreaks of crown-of-thorns starfish and exposure during low tides of the shallow reefs. The intensive tourism activities have resulted in coral damages from boat anchors, boat groundings, tourist walking from coral reefs to the beach and sediment resuspension. The indirect impacts were sewages from accommodations on the island and tourist boats and large volumes of solid waste. Most coral fragments were the blue coral *Heliopora coerulea* and a branching coral *Porites cylindrica* at the shallow reef site. The marine national park, relevant government institutions, local government authorities, local communities, tourists and tourism enterprises have to work in collaboration to minimize the environmental impacts on the island. The perception of stakeholder groups on economic benefits, awareness, information access and sharing, governance structure, and resource use rights is urgently needed to be transformed for better environmental management. Improvement of ecological understanding, education, knowledge sharing, legislation and regulations, and collaborative planning and management is essential to enhance stakeholders' perceptions and assist in developing policies for sustainable tourism in the marine protected area. The marine national park policy needs to include interventions that inform the stakeholders concerning tourism and resource use activities and their environmental impacts on the island, especially coral reef, sandy beach and terrestrial ecosystems. Policy interventions are also required to encourage the stakeholders for participating in the marine national park planning and decision process, particularly the entrance fees for conservation, sustainable tourism and environmental management. Lessons learned from managing Ko Tachai can be applied to other marine protected areas in the region.

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