universität wien
Faculty of Life Sciences

Faculty of Life Sciences at the University of Vienna

Generating knowledge for the future

Nothing in Biology Makes Sense except in the Light of Evolution.

Theodosius Dobzhansky

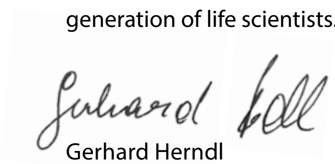
Life Sciences at the University of Vienna

Generating knowledge for the future

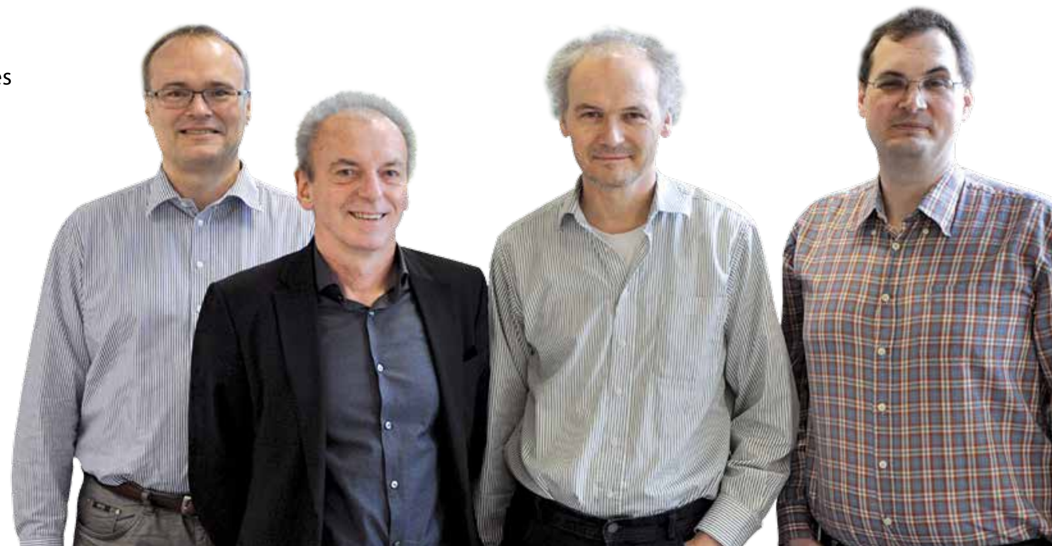
Over the past decade, the Life Sciences have revolutionized our understanding of how life is organized and how organisms and biological systems operate. The Life Sciences encompass a considerable breadth of scientific disciplines and study phenomena of life ranging from the molecular and genetic level within organisms to the interactions with other organisms and the environment. Novel molecular, analytical and imaging techniques developed during the last decades are now widely applied in all fields of Life Sciences and opened new avenues for research. We are now capable of directly assessing the impact of specific environmental stimuli and stressors on the organism and uncover novel aspects of evolution and adaptation. Thus, the principles of life and its organization are currently decoded using more interdisciplinary approaches than ever before in Life Sciences.

At the University of Vienna, the Faculty of Life Sciences reflects the breadth of disciplines dealing with Life on the Earth, covering the disciplines Organismal Systems Biology, Biodiversity and Ecology, Pharmaceutical Sciences and Nutritional Sciences. While multiple interactions between members of the different disciplines represented in the Faculty of Life Sciences are established, there are also exciting collaborations with other Faculties of the University of Vienna and research institutions within and outside Austria.

The Faculty of Life Sciences has significantly contributed to the development of the University of Vienna in the past and will certainly continue to do so in the future. Many high-profile publications, the acquisition of third party funding and prestigious research awards are testimony to the success of the Faculty over the last years. Taken together, the Faculty of Life Sciences at the University of Vienna is well positioned to address the societal challenges of the future and to educate the next generation of life scientists.



Gerhard Herndl
Dean of the Faculty of Life Sciences



Dean and Vice Deans of the Faculty of Life Sciences: Gerhard Ecker, Gerhard Herndl, Ulrich Technau, Karl-Heinz Wagner (f. l. t. r.)

Content

University of Vienna

Faculty of Life Sciences

The Faculty of Life Sciences is one of the largest faculties of the University of Vienna. It covers a broad spectrum of scientific fields: the biological sciences, pharmacy, and nutritional sciences. The Faculty of Life Sciences focuses on a deep understanding of the principles underlying life and on the evolution and diversity of organisms. Its concerns include the multifaceted challenges of the future of humankind such as climate change, nutrition, and the health of an aging human population.

Organismal Systems Biology

Cognition, Brain and Behavior

Evolutionary Anthropology

Evolution of Organismal Complexity

Department of Anthropology
Department of Behavioral Biology
Department of Cognitive Biology
Department of Integrative Zoology
Department of Molecular Evolution and Development
Department of Neurobiology
Department of Theoretical Biology

Ecology

Climate Change Biology

Microbial Ecology and Ecosystems

Symbioses

Department of Ecogenomics and Systems Biology
- *Divison of Archaea Biology and Ecogenomics*
- *Division of Molecular Systems Biology*

Department of Limnology and Bio-Oceanography
- *Division of Bio-Oceanography and Marine Biology*
- *Division of Limnology*

Department of Microbiology and Ecosystem Science
- *Division of Computational Systems Biology*
- *Division of Microbial Ecology*
- *Division of Terrestrial Ecosystem Research*

Botany and Biodiversity Research

Ecology and Biodiversity of Tropical Forests

Patterns and Processes in Plant Evolution and Ecology

Department of Botany and Biodiversity Research
- *Division of Conservation Biology, Vegetation- and Landscape Ecology*
- *Division of Structural and Functional Botany*
- *Division of Systematic and Evolutionary Botany*
- *Division of Tropical Ecology and Animal Biodiversity*

16 Departments

4 Core Facilities

2 Large Instrument Facilities

Pharmaceutical Sciences

Drug Discovery from Nature

Department of Pharmaceutical Chemistry
- *Division of Drug and Natural Product Synthesis*
- *Division of Clinical Pharmacy and Diagnostics*
- *Division of Drug Design and Medicinal Chemistry*

Department of Pharmaceutical Technology and Biopharmaceutics
Department of Pharmacognosy
Department of Pharmacology and Toxicology

Nutritional Sciences

Nutrition-associated Molecular Mechanisms of Ageing

Department of Nutritional Sciences

Computational Life Sciences is developing computational methods and software programs for understanding large-scale biomolecular data.

Facilities

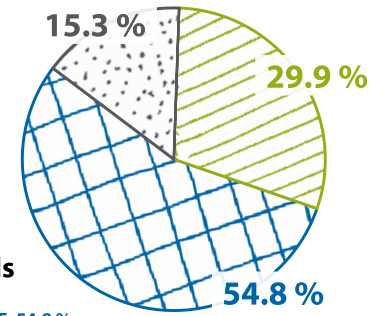
Core Facilities provide state-of-the-art equipment and techniques to all faculty members. They also offer the expertise neccessary to use the instruments and to analyze the research data.

_ Core Facility Botanical Garden
_ Core Facility of Cell Imaging & Ultrastructure Research
_ Core Facility Konrad Lorenz Forschungsstelle (KLF) for Behavior and Cognition
_ Core Facility of Micro-Computed Tomography

Large Instrument Facilities provide access to state-of-the-art equipment to all faculty members. They are operated by dedicated personnel.

_ Large Instrument Facility for Advanced Isotope Research
_ Large Instrument Facility for Mass Spectrometry in Life Sciences

Key figures



Third-party funds

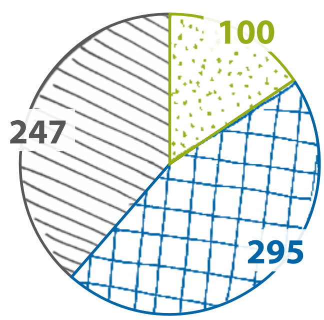
EU: 29.9 %
Austrian Science Fund FWF: 54.8 %
Others (national/international): 15.3 %

In 2013 the volume (in annual expenses) of third-party fundings exceeded 12 Mio. €, more than the half coming from the Austrian Science Fund (see graph).

Personnel (as of Nov. 2014)

Faculty (staff)[1]: 100
Postdocs/Praedocs[2]: 295
Admin/technical staff[2]: 247

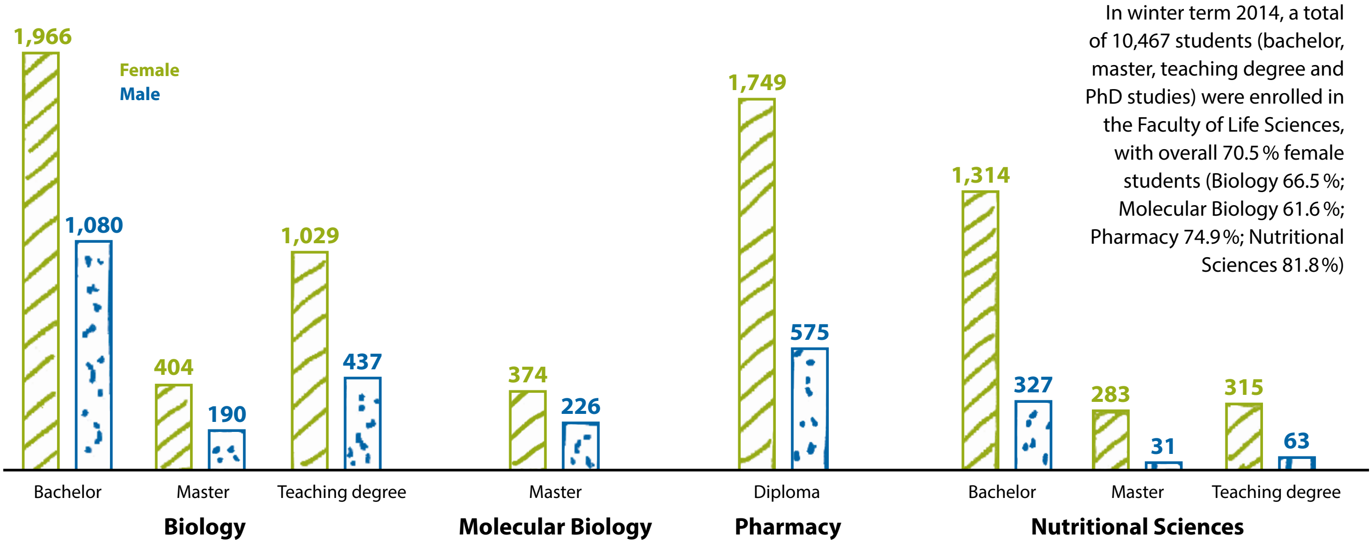
[1] full professors, associate professors/ docents, senior scientists, tenure track positions
[2] financed both by the University or through third-party funds

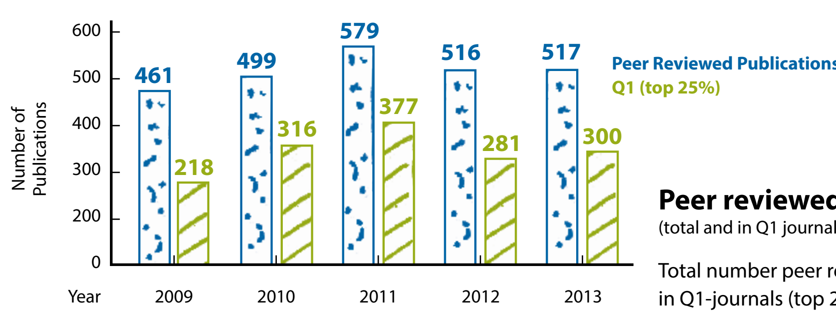


Students

(enrolled in winter term 2014)

In winter term 2014, a total of 10,467 students (bachelor, master, teaching degree and PhD studies) were enrolled in the Faculty of Life Sciences, with overall 70.5 % female students (Biology 66.5 %; Molecular Biology 61.6 %; Pharmacy 74.9 %; Nutritional Sciences 81.8 %)





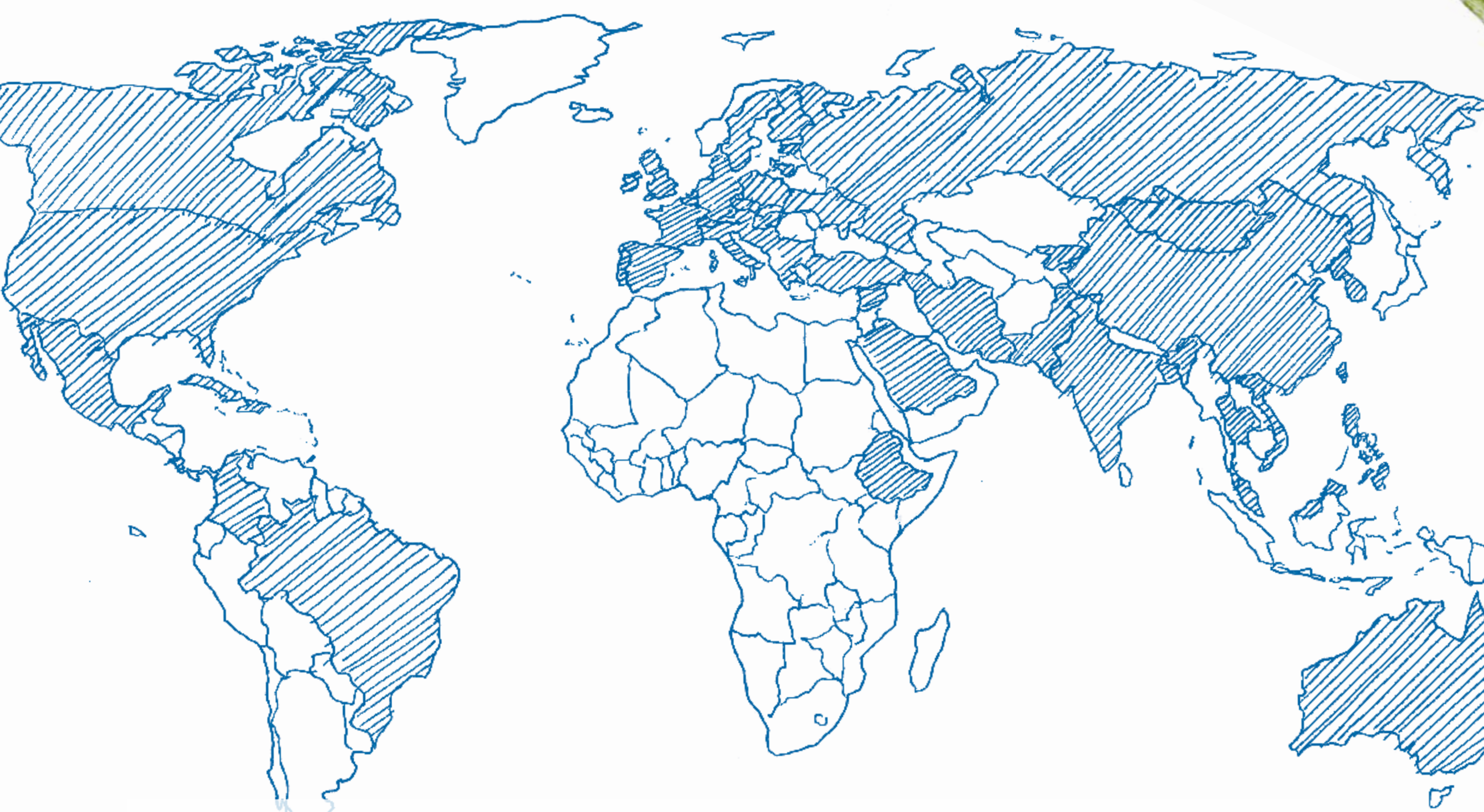
Peer reviewed publications

(total and in Q1 journals)

Total number peer reviewed publications (2009–2013), in Q1-journals (top 25 % of respective subject category)

Internationalisation – origin of PhD students and Postdocs

Currently (Nov. 2014) PhDs and Postdocs from over 50 countries are pursuing their scientific projects at the Faculty of Life Sciences.



Austria	359	United Kingdom	5	Ukraine	3	Malaysia	1	Finland	1
Germany	62	Bosnia & Herzegovina	5	Switzerland	3	Vietnam	1	Mongolia	1
Italy	16	Greece	4	Sweden	3	Bulgaria	1	Thailand	1
India	11	Hungary	4	Macedonia	2	China (Taiwan)	1	Kyrgyzstan	1
Iran, Islamic Republic	11	Netherlands	4	South Korea	2	Canada	1	Philippines	1
USA	11	Spain	4	Ethiopia	2	Palestine Regions	1	Saudi-Arabia	1
Russian Federation	10	Poland	3	Bangladesh	2	Slovenia	1	Australia	1
France	8	Serbia	3	Turkey	1	Lithuania	1	Trinidad & Tobago	1
China	7	Kosovo	3	Brasil	1	Syria, Arab Rep.	1	North Korea	1
Croatia	6	Portugal	3	Mexico	1	Costa Rica	1		
Romania	6	Czech Republic	3	Pakistan	1	Colombia	1	**Total**	**589**

Outstanding Awards and Research Grants

ERC (European Research Council) Advanced Grant
William Tecumseh S. Fitch, Dept. of Cognitive Biology

The Syntax of Mind: A Computational Comparative Approach *(2009–2014)*

This grant funded a highly-interdisciplinary research program designed to determine the computational limits of human and animal cognition and to evaluate the degree to which these limits are shared among different animal species (in cluding primates, birds and reptiles), and among cognitive domains such as music, language and art.

ERC (European Research Council) Advanced Grant
Michael Wagner, Dept. of Microbiology & Ecosystem Science

Nitrification Reloaded – a Single Cell Approach *(2012–2017)*

Nitrification, driven by nitrifying microbes, is a central component of the Earth's biogeochemical nitrogen cycle. Our knowledge on these microbes is dramatically incomplete although their activities are of major ecological and economic importance. This project is designed to use innovative single cell tools to obtain a fundamental understanding of the identity, evolution, metabolism and ecological importance of those bacteria and archaea that catalyze nitrification in nature.

ERC (European Research Council) Advanced Grant
Gerhard J. Herndl, Dept. of Limnology & Bio-Oceanography

Microbial Ecology of the Deep Atlantic Pelagic Realm *(2011–2016)*

The project aims at elucidating the metabolic activity of microbial communities under deep-sea pressure conditions rather than under surface pressure, as commonly done. A recently fabricated high-pressure sampling and incubation system in combination with molecular biology tools is used to assess phylogenetic and functional diversity. This detailed knowledge on the distribution of auto- and heterotrophic deep-sea microbes is essential to refine our view on the oceanic biogeochemical cycles. In 2011 Gerhard J. Herndl also received the *Wittgenstein Award* funded by the Austrian Science Fund (FWF).

ERC (European Research Council) Starting Grant
Matthias Horn, Dept. of Microbiology & Ecosystem Science

The Evolution of the chlamydiae – an Experimental Approach *(2012–2016)*

Chlamydiae are well-known bacterial pathogens of humans and ubiquitous as symbionts of protists. This project aims to better understand their evolutionary history, the development of virulence, and the adaptation to human versus protist hosts using an experimental approach. Simulating and monitoring evolution in "Petri dishes" will provide unique insights into molecular evolution and adaptive processes of chlamydiae, as well as into the mechanisms underlying the evolution of intracellular bacteria. Matthias Horn also received the START award in 2005 for a project on amoeba-associated chlamydiae.

ERC (European Research Council) Starting Grant

Dagmar Woebken, Dept. of Microbiology & Ecosystem Science

Revealing the Function of Dormant Soil Microorganisms and the Cues for their Awakening (DORMANTMICROBES) *(2015–2019)*

Soils harbor the most diverse microbial communities on Earth. However, at a particular point of time the majority of these microorganisms are dormant and only ca. 20% are active. It is hypothesized that this vast diversity of mostly dormant soil microorganism ensures ecosystem functioning under different environmental conditions. The importance of dormant microorganisms in global nutrient cycles and the signals that reactivate them are still largely unknown. With this project we aim to generate essential knowledge on the diversity, the genetics and the function of the dormant majority in terrestrial ecosystems, and thus on the stability of microbial key processes.

FWF START Prize

Ovidiu Paun, Dept. of Botany & Biodiversity Research

Understanding Evolution through Recurrent Allopolyploidization in Dactylorhiza (Orchidaceae) *(2013–2016)*

Hybridization and genome doubling regularly stimulate evolution in flowering plants. Immediately following such events, a genome suffers adjustments in organization and function, thereby shaping the adaptive success and evolutionary fate of the resulting lineages. Using ecologically divergent, sibling orchid species (Dactylorhiza) and the latest genomic approaches, we investigate the molecular drivers of adaptation to distinct environments and the effects of recurrent processes in evolution.

FWF START Prize

Tom J. Battin, Dept. of Limnology & Bio-Oceanography

ARCANET: Architecture of Carbon Fluxes in Fluvial Networks *(2009–2015)*

Streams and rivers were long considered as "pipelines" that transport organic carbon to the oceans. Recent studies have shown that streams emit significant amounts of CO_2 to the atmosphere, which raises the question how can carbon that was stored in soils over extended periods become oxidized in streams despite short residence times therein. We address this question using an interdisciplinary approach across the boundaries of microbiol ecology and geosciences.

FWF START Prize

Thomas Bugnyar, Dept. of Cognitive Biology

Raven Politics: Understanding and Use of Social Relationships *(2008–2014)*

Social life has been suggested as a main driving force for brain evolution in non-human primates, but there are open questions concerning the mechanisms underlying 'intelligent' behavior and the socio-ecological conditions that promote their investment. Corvids offer the possibility to examine these questions because they show similar cognitive skills as primates. We here investigate social complexity in ravens and provide the first comprehensive study on the use of social knowledge in birds.

Organismal Systems Biology

… examines organisms as complex systems by focusing on an integrated analysis of their organisation in time and structure. The dynamics of the physiological, developmental and evolutionary processes of organisms and the neural, social and environmental flows of information are at the core of the research questions.

© Department of Neurobiology

Cognition, Brain and Behavior

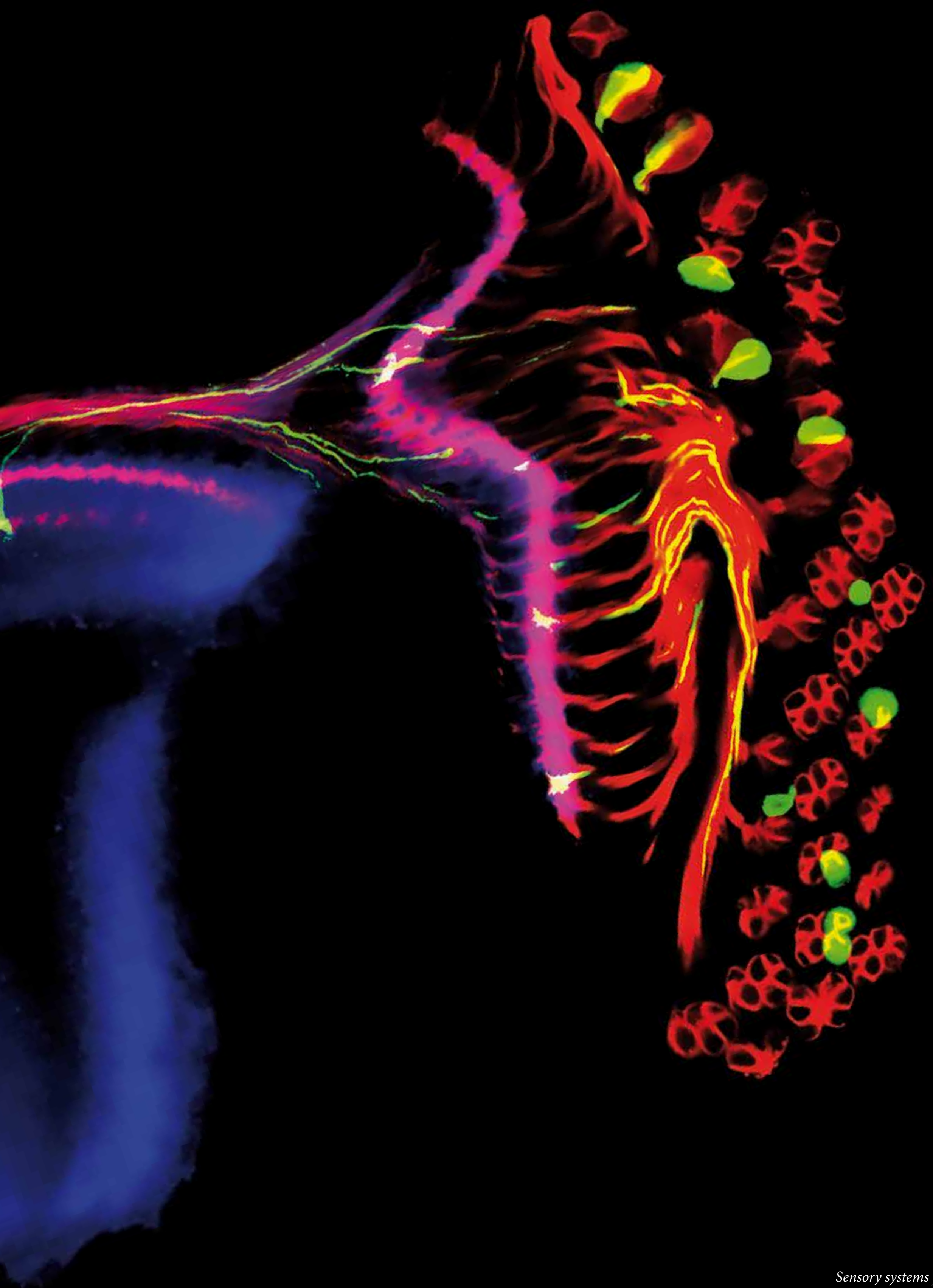
Department of Behavioral Biology · Department of Cognitive Biology · Department of Neurobiology · Core Facility Konrad Lorenz Forschungsstelle

Evolutionary Anthropology

Department of Anthropology · Core Facility Micro-Computed Tomography · Department of Behavioral Biology · Department of Theoretical Biology

Evolution of Organismal Complexity

Department of Integrative Zoology · Department of Molecular Evolution and Development · Department of Neurobiology · Department of Theoretical Biology



Sensory systems provide critical information for context-dependent animal behavior. The image shows the visual system of the fruit fly Drosophila, highlighting the projection of photoreceptors from the retina (green, red) into specific brain regions (blue).

Mind the difference!

Cognition, Brain and Behavior ***The cognitive, neural and hormonal bases of behavior are central to this research focus. The strengths of the focus include its broad comparative perspective, diverse model systems, and research at multiple explanatory levels, from cells to social groups.***

How can we study intelligence in animals?

Our research focuses on the evolution of cognitive processes, the influence of environmental factors on behavioral phenotypes, and the interaction of behavior, genetic and physiological factors. Particularly relevant are social factors including the complexity of social relations, cooperation, communication and stress management. With this approach we have not only generated internationally visible research but also achieved a steady increase of topics, model organisms and research groups. Currently more than 100 researchers at different career stages, from PhD candidates to senior scientists and professors, are working in the realm of Cognition, Brain and Behavior. This positive development is also reflected in teaching. We offer our own master program and participate in the related programs of Anthropology, Evolution and Cognitive Science. Our PhD education follows high international standards and is carried out mainly within the framework of our PhD program "Cognition and Communication".

Approaches to study cognition

Traditionally, animals have been exposed to learning tasks under highly controlled conditions, such as discriminating stimuli by pressing levers in an otherwise sterile box. These methods are useful for studying specific cognitive skills like feature discrimination and concept formation. Yet, they do not tell us much about what the animals can do under naturalistic settings. An alternative way is to start with ecologically relevant questions, inspired by observations in the field. For instance, we may wonder how animals that store food for later consumption manage to find their hidden caches again and protect them from be-

Ravens exhibit sophisticated social behaviors, resembling 'politics'.

How do hormones and behavior interact?

ing stolen. We may thus hypothesize that food-storing animals have evolved an excellent spatial memory. We may also hypothesize that if a species faces high competition for food, then individuals should be sensitive to audience and store food only when they cannot be seen. We can test predictions derived from these hypotheses in lab experiments, where we can control i) the availability of cache locations by allowing animals to store food in a given room, ii) the time to recovery by allowing the animals' access to the room under a give time schedule and iii) whether or not conspecific competitors are visible at caching. Furthermore, we can compare their performance with that of closely related species that do not rely on hidden food. Finally, we can expose our animals to tasks that are not of direct ecological relevance, such as memorizing artificial pictures on a touch screen computer or paying attention to conspecifics foraging outside. This approach may help us determine if the skills shown by our animals during food caching are a special adaptation to this very context or if these skills can, once they have evolved, also be generalized to other domains. In the latter case, we humans use the term 'intelligence'.

The role of endocrinology

Steroid hormones alter behaviors, which in turn can affect the individuals' endocrine physiology. One example for these interactions is the behavioral and physiological stress response. Social factors can modulate stress load in animals in many ways. Social conflicts, for instance, may lead to stress, but the effect can be buffered by socio-positive interactions before and after conflicts. On the physiological level, glucocorticoids (i.e. corticosterone and cortisol) produced by the adrenal cortex are known as reliable indicators of stress. They play a major role in the physiological stress response, mainly by ensuring a sufficient supply of glucose, which is important in emergency situations such as flight or fight. Increased glucocorticoid secretion in response to chronic stress, however, can have detrimental fitness consequences such as inhibited sexual behavior and immune function as well as decreased memory and learning capacity. Glucocorticoids can be measured non-invasively by analyzing their metabolites in saliva or faecal samples. By combining behavioral observations with physiological measurements, we investigate effects of social parameters on stress levels and vice versa in our model species, including common hamsters, guinea pigs and ground squirrels. In addition this method is an important tool to optimize animal keeping and experimental setups by identifying and avoiding stressful situations. In relation to endocrine stress physiology a very important point is to clarify whether specific catechol-O-methyltransferase (COMT) alleles would provide protection or increase sensitivity against environmental »

Effects of reproductive effort and output on hibernation patterns are investigated in common hamsters.

Timber wolves represent an ideal model organism for studying physiology and cognition during (simulated) hunts.

Elephants are vocal learners and show advanced abilities in sound production and comprehension.

> **"We study a wide range of species in captivity and in the field."**

Where is our research conducted?

» or social stressors. This question could yield answers on behavioral adaptations for specific social roles within hierarchal systems in social living animals. Moreover, the analyses of individual molecular biological markers, such as the COMT polymorphism, could deliver information about how individuals can cope with physiological stress reactions.

Reseach sites and model species

Special features of our research focus are the range of study species and the number of unique research sites, most of which are cooperatively run by multiple researchers and departments. While our labs and indoor-keeping facilities are based at the Faculty of Life Sciences in Vienna, large outdoor-facilities are available at Haidlhof Research Station in Bad Vöslau, Konrad Lorenz Research Station in Grünau, Konrad Lorenz Institute in Vienna and Wolf Science Center in Ernstbrunn. Our field sites are distributed across the city of Vienna (e.g. area of Schönbrunn Zoo for crows, Bisamberg for hamsters and ground squirrels), the Austrian Alps and, in collaboration with our international partners in Brazil, French Guiana, Galápagos and Panama.

On the neural level, we use the fruit fly *Drosophila melanogaster* as a model system to i) determine the genetically encoded signals underlying sensory circuit formation and ii) the cellular mechanisms in the modulation of innate behavioral responses. In virtual-reality based behavioral paradigms we are addressing the questions how simple nervous systems integrate complex sensory information in spiders.

Future outlook

An important goal for the future is to strengthen the neurosciences and to integrate research in cognition, brain and behavior more broadly with other groups in Vienna.

Allobates femoralis, a small territorial poison-dart frog exhibits sophisticated spacial cognition.

Goffin cockatoos are very playful and can become amazingly skilled tool-users in captivity.

Common marmosets are used for studying social learning processes and the formation of foraging traditions.

Virtual reality set up for large hunting spiders.

Key References

_ Herbst CT, Stoeger AS, Frey R, Lohscheller J, Titze IR, Gumpenberger M, Fitch WT (2012) How low can you go? Physical production mechanism of elephant infrasonic vocalizations. Science 237:6094.

_ Fitch WT (2014) Toward a computational framework for cognitive biology: unifying approaches from cognitive neuroscience and comparative cognition. Phys Life Rev 11:329.

_ Boeckle M, Bugnyar T (2012) Long-term memory for affiliates in ravens. Curr Biol 22:801-6.

_ Massen JJ, Pašukonis A, Schmidt J, Bugnyar T (2014) Ravens notice dominance reversals among conspecifics within and outside their social group. Nature Comm 5:3679.

_ Scheiber IBR, Weiss BM, Hemetsberger J, Kotrschal K. (Eds). (2013) in: The Social Life of Greylag Geese, Cambridge University Press.

_ Teschke I, Wascher CA, Scriba MF, von Bayern AM, Huml V, Siemers B, Tebbich S (2013) Did tool-use evolve with enhanced physical cognitive abilities? Phil Trans Royal Soc B 268:20120418.

_ Pflüger LS, Valuch C, Gutleb DR, Ansorge U, Wallner B (2014) Colour and contrast of female faces: Attraction of attention and its dependence on male hormone status in Macaca fuscata. Animal Behaviour 94:61–71.

_ Barske J, Schlinger BA, Wikelski M, Fusani L (2011) Female choice for male motor skills. Proc R Soc Lond B Biol Sci 278:3523-3528.

_ Strauss A,Hoffmann IE, Walzl M, Millesi E (2009) Vaginal oestrus during the reproductive and non-reproductive period in European ground squirrels. Anim. Reprod. Sci. 112:362–370.

_ Stowers JR, Fuhrmann A, Hofbauer M, Streinzer M, Schmid A, Dickinson MH, Straw AD (2014) Reverse Engineering Animal Vision with Virtual Reality and Genetics. Computer 47: 38–45. «

Departments

Department of Cognitive Biology
Thomas Bugnyar: cogbio.univie.ac.at

Department of Behavioral Biology
Eva Millesi: www.behaviour.univie.ac.at

Department of Neurobiology
Thomas Hummel: neuro.univie.ac.at

Core Facility Konrad Lorenz Forschungsstelle
Kurt Kotrschal: Fischerau 11, 4645 Grünau, www.klf.ac.at

Who is Homo sapiens *and how did we come to be?*

Evolutionary Anthropology ***spans concerns and insights from genes and other interesting molecules all the way up through behavior, social structure, and human history.***

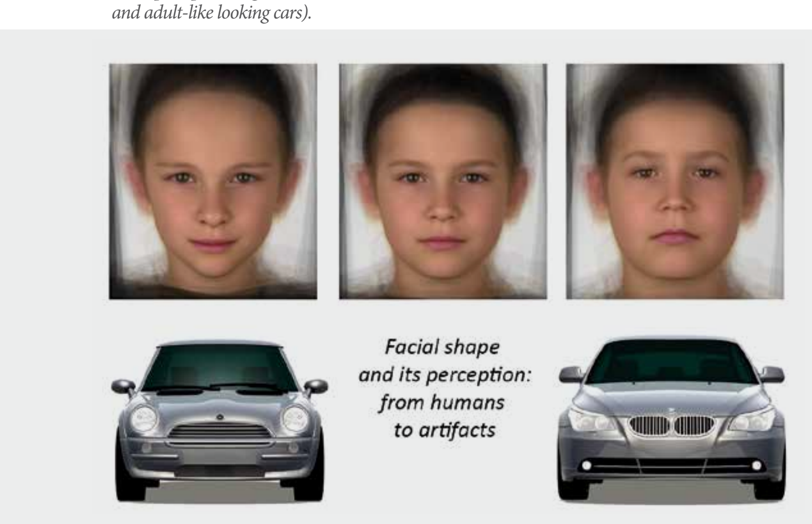
Human Behavior

The Human Behavior research group studies human and non-human primate behavior from an evolutionary perspective. In order to understand the origins and the consequences of behavioral patterns across different social environments or ecological niches, we combine concepts and hypotheses from sociobiology, behavioral genetics, behavioral ecology, evolutionary life history, and evolutionary psychology. To this great range of research questions, we bring a comparably large range of research tools, including multivariate statistics and other "big data" approaches, geometric morphometrics, population genetics, molecular biology, and computer vision. This yields quantitative explanations of human behavior in modern societies based on the principles of the natural sciences. Some of our specific topics are fertility and demographics, cooperative behavior, evolutionary aesthetics, and industrial design. Our findings are published in scientific outlets and also are implemented in applied technologies, such as contemporary systems for surveillance of public spaces like subways (EU-project VANAHEIM) or the design of autonomous robots (CADDY). Other current research foci include the causes and consequences of facial shape variation and its perception, social hierarchies, and evolutionary demographics. A new departure concerns the genetics of complex phenotypes: in collaboration with the University of Veterinary Medicine, Vienna, we are studying DNA polymorphisms and epigenetics as they relate to stress and bonding in humans and other mammals.

Human Ecology

Our Human Ecology group at the Department of Anthropology pays special attention to the interactions between humans and their environment. Among the many possible characterizations of our species and our ancestors, one stands out: our unique ability to accommodate or respond to a wide range of environmental factors, from domes-

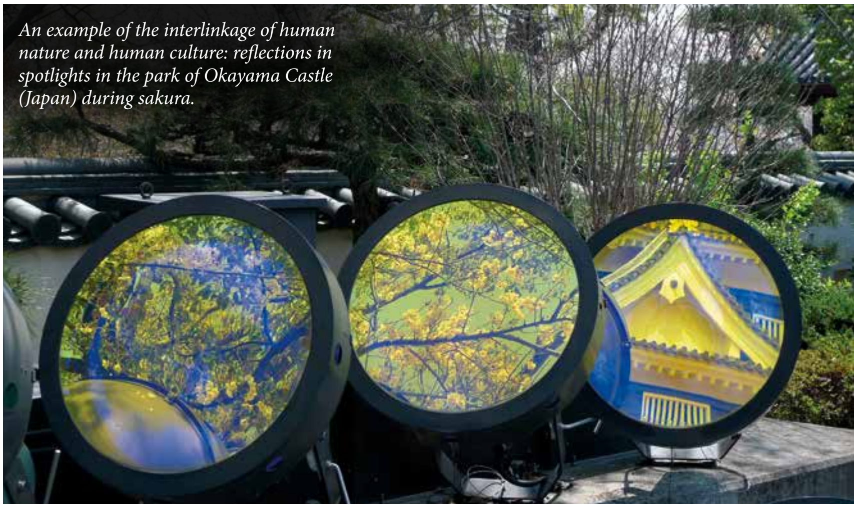
Shape patterns associated with biological causes (e.g. prenatal hormone exposures: upper panel) and social perception (e.g. child- and adult-like looking cars).



The purpose of anthropology is to make the world safe for human differences. Ruth Benedict

Scenery is fine, but human nature is finer.

John Keats



An example of the interlinkage of human nature and human culture: reflections in spotlights in the park of Okayama Castle (Japan) during sakura.

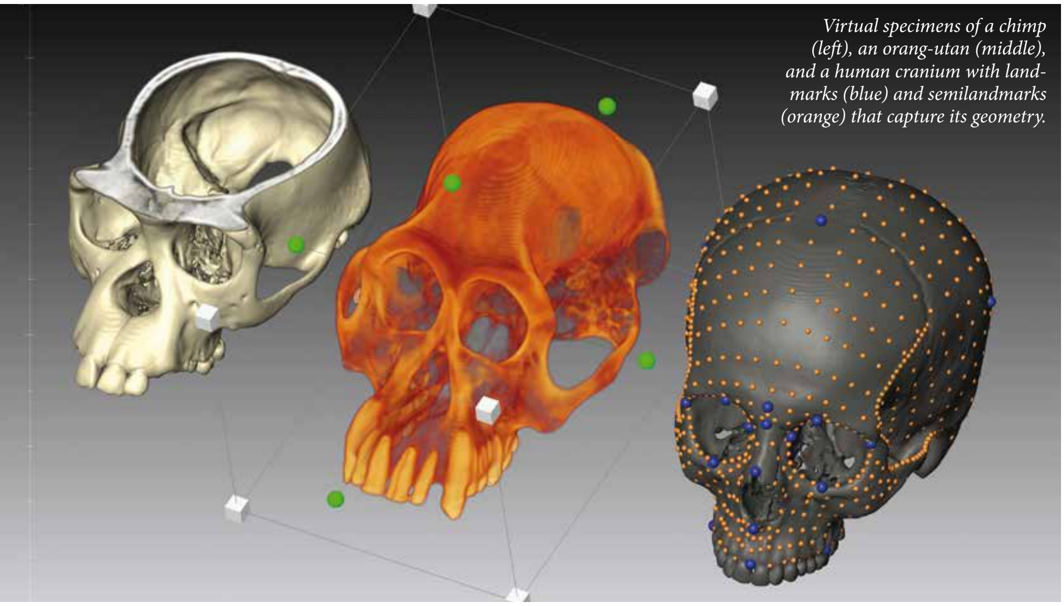
tication of crops to climate change. Over the course of human evolution there have been two stages of environmental influences. Initially, some specific environmental factors affected the details of human phylogenesis (evolution and succession of a variety of *Homo* species). More recently, all these interactions have been refined and amended by steadily more powerful processes of cultural development.
The subject of Human Ecology combines components and viewpoints of both themes: both nature and culture, because they are manifested not only in human properties but also in aspects of their surroundings. Human evolutionary ecology emphasizes in-depth views into human environmental history. Here, processes such as brain evolution, development of human group sizes, and the evolution of speech are of particular interest. Human evolutionary economics deals with the exceptional phylogenetic and organismal situation of *Homo sapiens* along with our unique modes of resource use and resource production. The research questions of this branch range from the beginning of resource production during the Neolithic transition up to present-day problems such as global limitations on resources and sustainable development.
Recent research challenges include global warming, resource allocation and depletion, soil depletion, erosion, and desertification. Connected to each of these phenomena is a broad range of social aspects. Questions of this sort include demographic developments, migration, how decisions are taken and by whom, who is affected, and what the respective distribution aspects are (e. g. access to resources, risks, amendments, impairments).

Human Evolution

The evolutionary origin of our species, *Homo sapiens*, can be understood only by combining fossil evidence with comparisons of extant humans, and other primates, particularly the great apes. Beside genetics used to infer relatedness, variation, or admixture, we need to rely on morphology for two reasons: first, only morphology can tell us about function, growth, and development, and, second, the great majority of fossils do not offer us DNA. Whether we are studying form for its own sake (comparative morphology) or as it relates to organismal function (functional morphology), our preferred way of proceeding is via Virtual Anthropology (VA), a long-term specialty of this department. VA is the computer-based scrutiny of electronic versions of specimens. Virtual visualizations help us to compare great apes to humans. The data here come from computed tomography scans (a kind of 3D X-ray). We capture the whole geometry of these objects, whether external or internal, by rich organized schemes of points (landmarks and semilandmarks) spread out over the surfaces of such a structure (compare figure above). Sophisticated statistics are applied to generate average forms, pictures of variation, or descriptions of trends. Using such tools, we »

Richard J. Borden

The story of our human lineage is continually enlarged, almost daily, by discoveries from physical anthropology, archaeology, and genetics.



Virtual specimens of a chimp (left), an orang-utan (middle), and a human cranium with landmarks (blue) and semilandmarks (orange) that capture its geometry.

Female life history patterns are influenced by evolutionary, ecological, and cultural factors.

» have discovered, for instance, how growth patterns of human and chimp mandibles from fetal stage to adulthood differ; we have discovered the first modern human in Europe living 45,000 years ago; we have demonstrated the role of supporting structures in the faces of South African Australopithecines; and we have identified some possible ancestors of both Neanderthals and modern humans in the Levant. The EU-funded project EVAN trained young scientists all across Europe and created software to facilitate all the analyses mentioned above. We also published the first textbook of methods in this domain.

Human Life History

All organisms pass through particular life stages specific to their species; life history theory seeks to explain these patterns in an evolutionary context. Typically, they have been shaped by natural selection to produce the largest possible number of surviving offspring for the expected physical or ecological environment. Human life history is unique among the animals; it differs even from the patterns characterizing our closest relatives, the great apes. Compared to them, we have higher rates of survival, higher life expectancy, later sexual maturation, shorter birth intervals, and a long period of post-reproductive senescence. For instance, the extended postmenopause, which makes up about one-third of today's average female life expectancy, is exclusive to *Homo sapiens*.

Although human life history clearly has an evolutionary basis, it is nevertheless affected by environmental factors as well. The human body reacts quite sensitively to environmental stress and to changes in dietary habits or physical workload. Our Human Life History research group focuses on the evolutionary basis of these patterns, the interactions between environmental factors and patterns of growth and development involving body composition or obesity, and the evolutionary demography of the corresponding reproductive strategies. This latter topic includes the impact of environmental and social factors on timing of reproduction and number of offspring. It also extends these considerations to aspects of intrauterine and postnatal growth such as age-dependent changes in body fat and its distribution patterns, muscle mass and its dwindling, bone mass, and bone density. We are especially interested in aspects of female life history, because from sexual maturation to menopause, pregnancy outcomes must be interpreted within an evolutionary framework. Investigations such as these are highly interesting to our colleagues in the field of gender studies as well. In 2013, the Emerging Field "Comparative human life history: A multilevel approach" has been established at the Faculty of Life Sciences.

The Dalai Lama

In this century we have made remarkable material progress, but basically we are the same as we were thousands of years ago.

A morphometric representation of 185 women's feet

To grasp the present human condition it is necessary to add the biological evolution of a species and the circumstances that led to its prehistory.

E. O. Wilson

Anthropometrics

Our anthropometrics group focuses on data coming from CT scanners and video cameras. Today's most important bio-anthropological problems deal with how organisms hold together over development, aging, climate change, or evolution. Starting with new tools for analysis of patterns in the information from fossil skulls, we have been developing rigorous new ways to describe that integration for almost any kind of observational data about human forms. Lately these research themes have broadened to include other aspects of human lives, for instance studies of skeletal function (and the associated stresses and strains) and anatomically focused factors affecting these patterns, such as what high heels do to women's feet. There are ties with the subjective assessment of human faces and bodies in social contexts such as dating and even in the world of art. Our group has made Vienna the world's leading center for extending anthropometric methods to concerns like these.

We also work in the rhetoric of the complex systems sciences, critiquing the ways that biologists use words and figures to convince other people – colleagues, journalists, museumgoers, the general public – about the patterns they find in complex new data sets. How do we persuade someone that a new birth defect is real, or a correlation between a gene and behavior? And how can we be confident that our claims are valid? The ways our colleagues report the correlations they uncover in human biology data are often illogical. We develop and teach better rules for this kind of reporting of "how arithmetic turns into understanding" all across human biology. It is this sort of translation that makes our work worth the public's interest, the country's support, and our students' attention in our courses and seminars.

Key References

_ Abend P et al (2015) The sound of female shape: a redundant signal of vocal and facial attractiveness. Evolution and Human Behavior DOI: 10.1016/J.evolhumbehav.2014.10.004.
_ Bookstein FL (2014) Measuring and reasoning. Cambridge University Press, New York.
_ Hershkovitz I et al (2015) Levantine cranium from Manot Cave (Israel) foreshadows the first European modern humans. Nature DOI: 10.1038/nature14134.
_ Kirchengast S & Rühli F (2013) Evolutionary medicine and its implications for endocrinological issues (e.g. menopause). Comparative Endocrinology 186:145–149.
_ Weber GW & Bookstein FL (2011) Virtual Anthropology - A Guide to a New Interdisciplinary Field. Wien, New York: Springer Verlag.
_ Windhager S et al (2014) Variation at genes influencing facial morphology are not associated with developmental imprecision in human faces. PLOS One 9(6), e99009. «

Departments

Department of Anthropology
Harald Wilfing: www.anthropology.at

Department of Behavioral Biology
Eva Millesi: www.behaviour.univie.ac.at

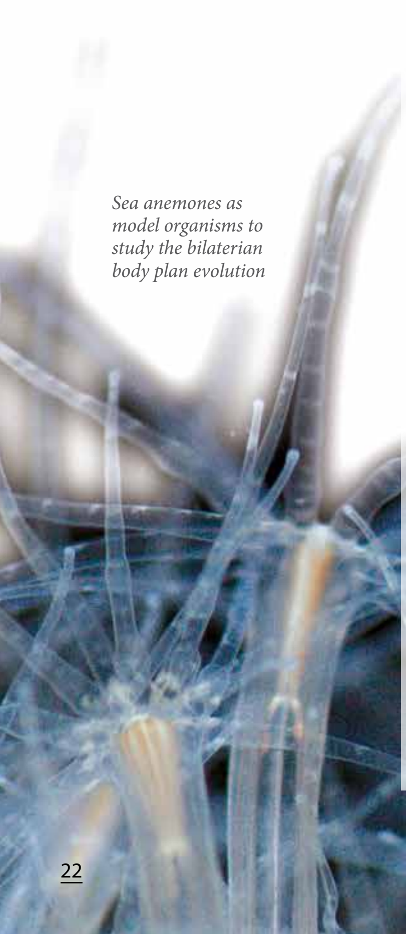
Department of Theoretical Biology
Gerd B. Müller: theoretical.univie.ac.at

Core Facility Micro-Computed Tomography
Gerhard W. Weber: www.micro-ct.at

Living Complexity
From Hydra to Humans

Evolution of Organismal Complexity ***This research focus examines the developmental basis of the evolutionary processes that have led to the great diversity of differentiated cells, organs, and organisms.***

How do organisms develop and evolve?



Sea anemones as model organisms to study the bilaterian body plan evolution

Animals come in a wide variety of shapes and body plans that exhibit fundamentally different constructions. The complexity of these organismal architectures is characterized by the evolution of different cell types, tissues, and organs, as well as their developmental interactions. Since all adult structures are built from much simpler embryonic forms, it is necessary to elucidate the underlying principles of their development in order to understand the evolution of life's complexity. The participating departments address the multiple levels of organization involved in generating biological structures as well as their evolutionary modifications through genetic and environmental influences. Our research applies molecular, morphological, biomathematical, and imaging techniques to the study of various marine invertebrates, arthropods as well as vertebrates, including humans. The combination of experimental and quantitative analyses yields theoretical models that permit comprehensive interpretations of animal complexity and of life's responses to different environmental challenges.

Genes do the trick

Most animal phyla are bilaterally symmetric and thus belong to the Bilateria, which had a common ancestor at least 550 Mio years ago. The evolutionary sister group of the bilaterians are the cnidarians (hydra, jellyfish, corals, sea anemones), representing one of the oldest animal lineages. Cnidarians lack a number of morphological features such as the third germ layer (mesoderm), two well-defined body axes, and a central nervous system. Therefore, cnidarians play a crucial role in our understanding of the evolution of key bilaterian traits. What is the relationship of the main body axis of cnidarians to the two body axes of Bilateria? How does the diffuse nervous system of cnidarians develop and function? Can we trace the origins of the three germ layers that are the founding tissues for all organs in humans and other bilaterians? How did genomic evolution contribute to more complex organisms? In the Department of Molecular Evolution and Development these questions are addressed using molecular tools and resources that have been developed for the sea anemone *Nematostella vectensis*. Interestingly, the human and sea anemone genomes show surprising similarities in gene repertoire and epigenetic organisation. This suggests that complex genomes date back to at least 600 Mio years. By contrast, recent studies revealed that post-transcriptional regulation unexpectedly resembles that of *Arabidopsis*, providing a link of this early metazoan lineage with plants.

It takes nerves

Understanding how the nervous system allows animals to perceive and react to specific environmental stimuli is one of the main challenges in modern neuroscience. Research at the Department of Neurobiology is focusing on the development and function of sensory systems

How is form regulated?

Transgenically labeled neurons (green) and muscles (red) in the sea anemone Nematostella vectensis

by integrating complementary genetic, electrophysiological, and behavioral approaches. The combination of various arthropod model systems (e.g. hunting spiders, bloodsucking bugs, fruit flies) with a broad range of cutting-edge technologies including high-resolution imaging, cell type-specific transgene expression, and virtual reality-based behavior paradigms enables us to decipher the molecular and physiological mechanisms underlying evolutionary adaptations of the nervous system to specific environmental challenges. In addition, the functional characterization of human disease genes in developing invertebrate neurons provides novel insights into brain dysfunction and neurodegeneration. The common focus on sensory circuits with increasing levels of cellular complexity allows the identification of conserved genetic signals and cellular mechanisms in evolving nervous systems.

Build bodies and diversify

Research at the Department of Integrative Zoology spans across a wide range of non-model organisms including vertebrates, arthropods, and animals with a ciliated larva in their life cycle, the so-called lophotrochozoans (mollusks and allies). Specimens are analyzed using morphological and molecular methods, including immunolabeling, confocal microscopy, in silico 3D reconstruction, high-speed video analysis, microCT, electron microscopy, and gene expression studies. The data are interpreted in an integrative context and often combine field and laboratory experiments with phylogenetic tools to elucidate the evolution of body plan complexity from a functional, developmental, and ecological perspective. Specific topics currently explored include the morphological and molecular mechanisms that underlie the development and evolution of complex body plan features (e.g. neuromuscular and circulatory systems, feeding structures) as well as the evolution of morphological novelties in arthropods and mollusks. Thereby, ecological features such as the interactions of animals with conspecifics as well as with their environment are also considered. This yields an integrative picture of the driving forces that shape phenotypic diversity.

3D Micro CT of a mouse embryo stained for tubulin expression

Models of life

Progress in our understanding of organismal complexity requires a theoretical analysis and integration of the multiplicity of empirical data. In the Department of Theoretical Biology we concentrate on the quantitative measurement, mathematical formalization, and theoretical modeling of complex biological phenomena, in particular as they exhibit dynamic properties such as in developmental and evolutionary processes. The kind of theoretical biology we are aiming for connects evolutionary developmental biology (EvoDevo) with conceptual advances in other domains of biological research, such as genomics, ecology, and behavior. The aim is a common theoretical foundation for organismal evolution. Applying novel imaging techniques and biometric tools to »

Can development be quantified?

Adopting Micro-CT technology for developmental biology

» phenomena of biological organization at different scales, from embryos to populations, we address questions at the interface of environment, development, and evolution. Our preferred model systems are evolving vertebrate fins and limbs, as well as the vertebrate cranium. It is currently highly debated whether such a pluralistic approach goes beyond the scope of the standard theory of evolution. Are extensions to the classical evolutionary framework required? In the frame of this question, we interpret the results of contemporary organismal systems biology in the context of the ongoing reform of evolutionary theory.

Key References

_ Capek D, Metscher BD and Müller GB (2014). Thumbs Down: a molecular-morphogenetic approach to avian digit homology. J. Exp. Zool. (Mol. Dev. Evol.) 322B:1–12

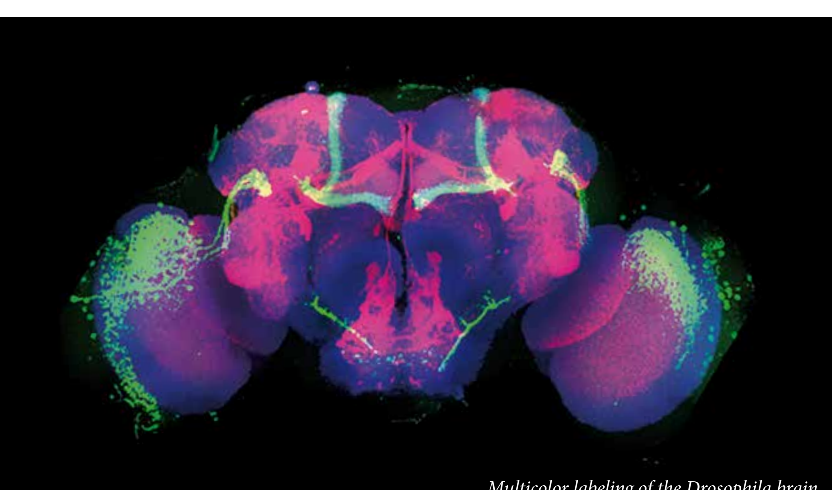
_ Fenk LM, Schmid A (2011). Flicker-induced eye movements and the behavioural temporal cut-off frequency in a nocturnal spider. J Exp Biol. 214:3658–63.

_ Lange A, Nemeschkal HL, Müller GB (2014). Biased polyphenism in polydactylous cats carrying a single point mutation: The Hemingway Model of digit novelty. Evol.Biol. 41:262–275.

_ Mayer C, Brian Metscher BD, Müller GB, Mitteroecker P (2014). Studying developmental variation with geometric morphometric image analysis (GMIA). PloS ONE, in press.

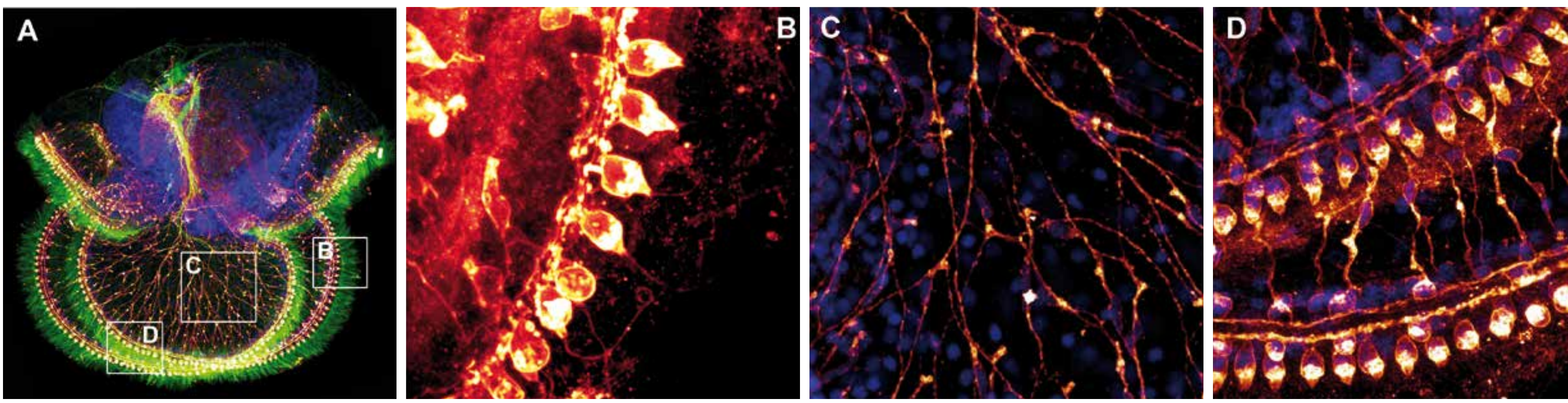
_ Moran Y, Fredman D, Praher D, Li XZ, Wee L, Rent-

How do neural circuits evolve?

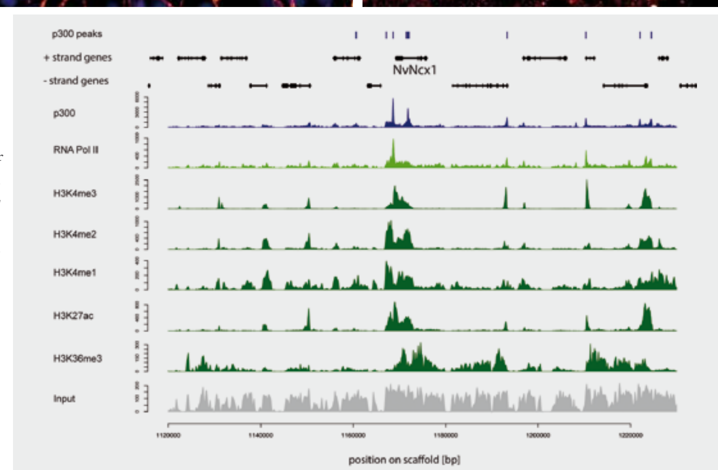


Multicolor labeling of the Drosophila brain

How are complex nervous systems of invertebrate larvae organized?



Multicolor labeling of neural structures in a nemertine larva



The genomic landscape of Nematostella vectensis is characterized by conserved specific histone modifications, marking promoters and enhancers.

zsch, F, Zamore P, Technau U, Seitz H (2014). Cnidarian microRNAs frequently regulate targets by cleavage. Genome Res. 24:639–50.

_ Petrovic M, Hummel T (2008). Temporal identity in axonal target layer recognition. Nature 456:800–3.

_ Scherholz M, Redl E, Wollesen T, Todt C, Wanninger A. (2013). Aplacophoran molluscs evolved from ancestors with polyplacophoran-like features. Curr.Biol. 23: 2130–2134.

_ Schwaiger M, Schönauer A, Rendeiro AF, Pribitzer, C, Schauer A, Gilles AF, Schinko JB, Renfer E, Fredman D, Technau U (2014). Evolutionary conservation of the eumetazoan gene regulatory landscape. Genome Res., 24:639–50.

_ Steinmetz PRH, Kraus JEM, Larroux C, Hammel JU, Amon-Hassenzahl A, Houliston E, Wörheide G, Nickel M, Degnan BM, Technau U.(2012). Independent evolution of striated muscles in cnidarians and bilaterians. Nature 487, 231–234. «

Departments

Department of Integrative Zoology
Andreas Wanninger: zoology.univie.ac.at

Department of Molecular Evolution & Development
Ulrich Technau: molevodevo.univie.ac.at

Department of Neurobiology
Thomas Hummel: www.neuro.univie.ac.at

Department of Theoretical Biology
Gerd B. Müller: theoretical.univie.ac.at

Ecology

… aims at gaining insight into the structures and functions of terrestrial, limnic and marine ecosystems and their microbial, floral and faunal communities. Specific importance is attached to research on microbial communities, their relations to the biotic and abiotic environment, as well as their implications for ecosystem functions in a rapidly changing environment. This thematic area uses approaches of systems biology and state-of-the-art methods of single-cell and stable-isotope analysis, genomics, proteomics, metabolomics and computational methods.

Climate Change Biology

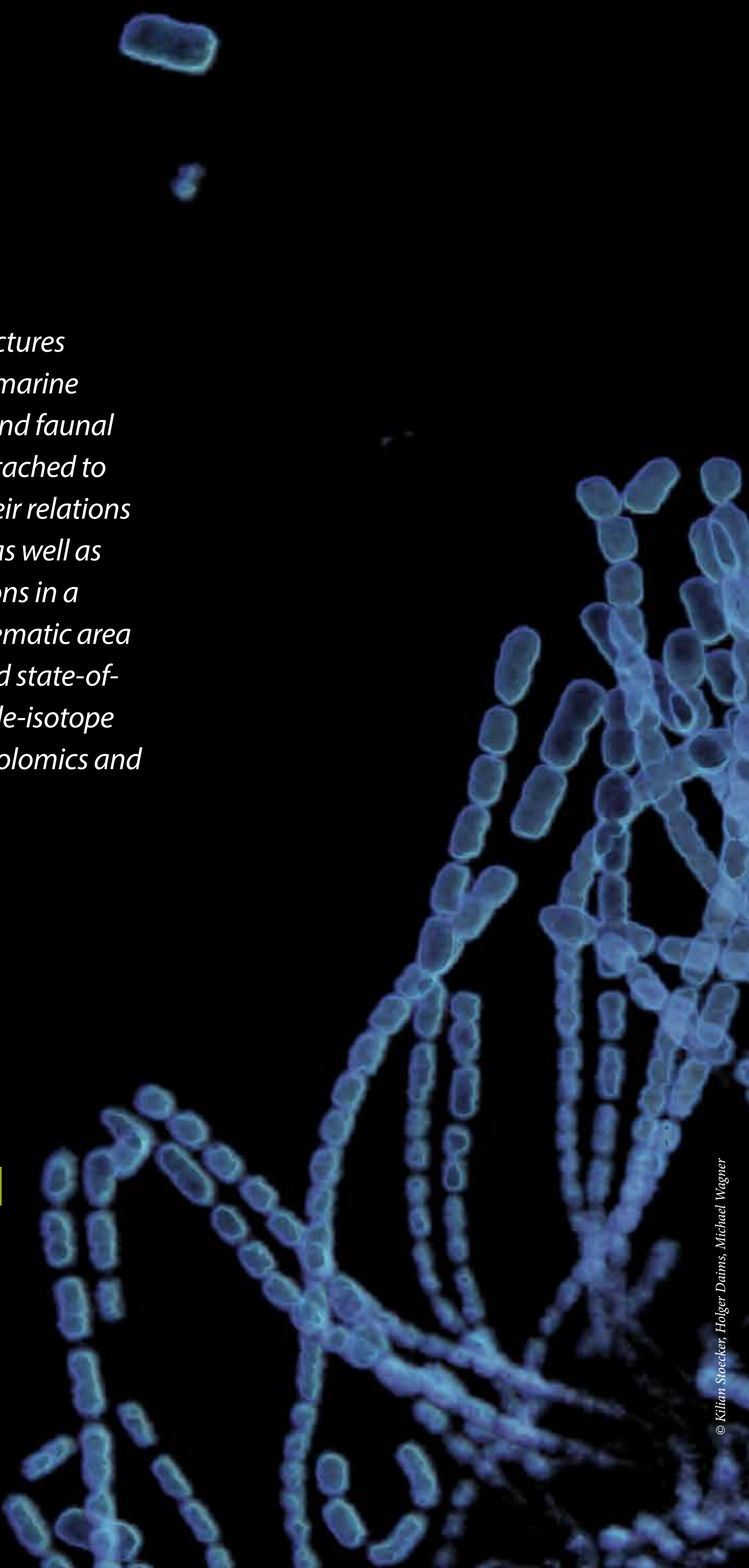
Department of Botany and Biodiversity Research
Department of Limnology and Bio-Oceanography
Department of Microbiology and Ecosystem Science

Microbial Ecology & Ecosystems

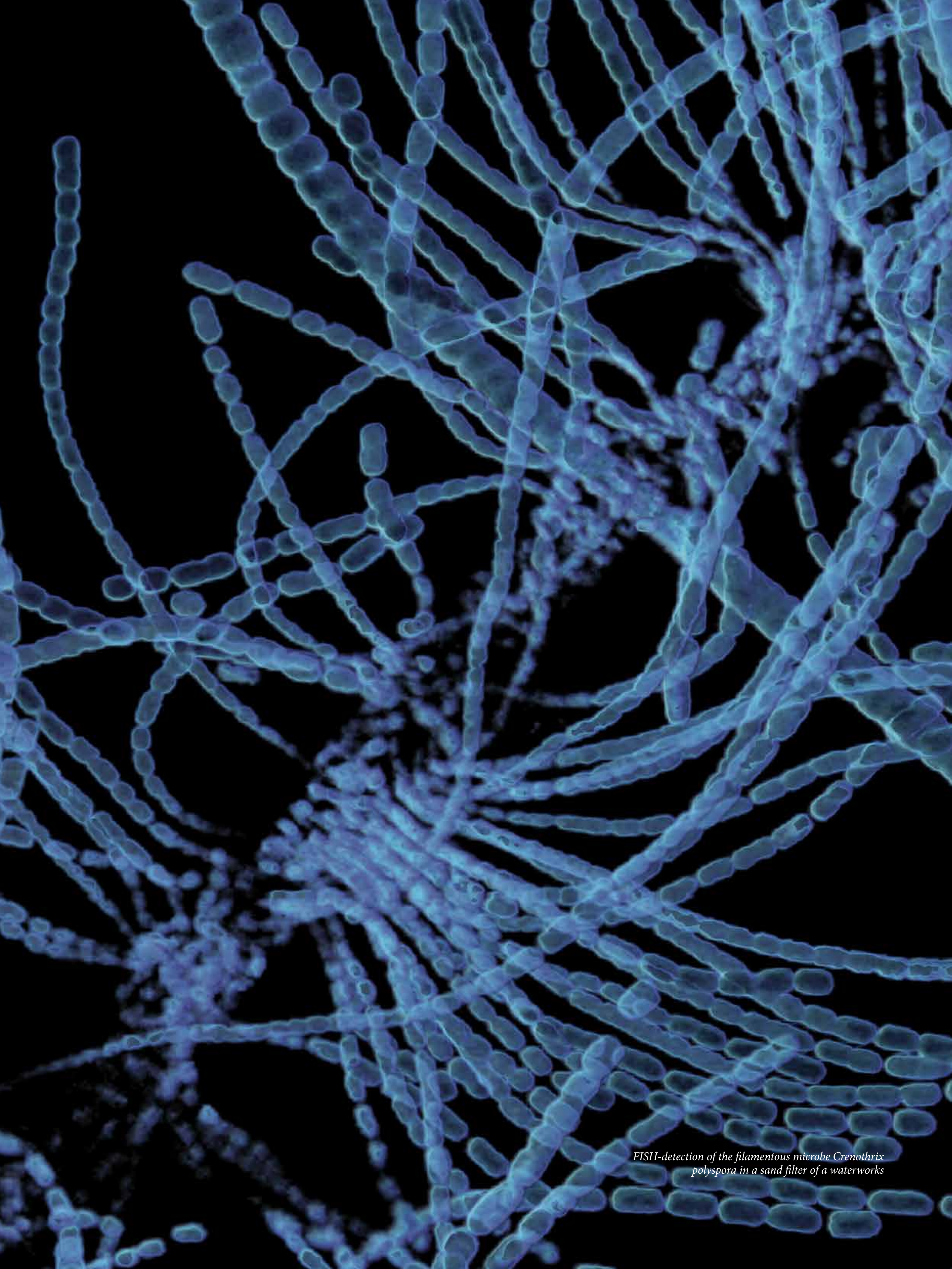
Department of Ecogenomics and Systems Biology
Department of Limnology and Bio-Oceanography
Department of Microbiology and Ecosystem Science

Symbioses

Department of Ecogenomics and Systems Biology
Department of Limnology and Bio-Oceanography
Department of Microbiology and Ecosystem Science



© Kilian Stoecker, Holger Daims, Michael Wagner



FISH-detection of the filamentous microbe Crenothrix polyspora in a sand filter of a waterworks

The heat is on

Climate Change Biology ***This research focus addresses the ecological consequences of climate change for the distribution and diversity of organisms as well as for ecosystem structure and functioning.***

Of all aspects of the physical environment, climate is arguably most influential for the distribution of biota on Earth and strongly affects the structure and functioning of ecosystems. The research focus Climate Change Biology addresses the impact of a changing climate on evolution, physiology and ecology at all levels of biological organization and at all spatial scales from molecules and cells to ecosystems and beyond. It also encompasses feedback loops between the various components of the biological system and the physical environment. The research teams working in this key area have a strong focus on the geographical patterns of plant species diversity as well as on changes in energy and element cycling by the activity of microorganisms and plants and their interaction. We use state-of-the-art analytical and computational tools and methods to both improve our understanding of how climatic change affects biotic controls on biodiversity and ecosystem processes. This approach helps to evaluate the possible consequences of a changing climate at these levels.

Non-climatic range limitations are likely to be the norm, rather than the exception, and pose added risks for species under climate change.[1]

[1] Early, R. and Sax, D.: Climatic niche shifts between species' native and naturalized ranges raise concern for ecological forecasts during invasions and climate change. Global Ecology and Biogeography 23: 1356-65 (2014)

Seed dispersal capacity is a key factor controlling whether plant species will be able to adapt their ranges to changing climatic conditions.

Climate and species distributions

No plant or animal species is present everywhere on Earth. In fact, the majority of terrestrial species occupy ranges that are much smaller than the territory of the European Union, and even within these ranges their distribution is often highly patchy. Ecologists have long been fascinated by these pervasive range limitations and have early hypothesized climatic factors as key to their understanding. Nowadays, this issue has received renewed interest in the context of climate change because sound knowledge on this causality is a prerequisite to assessing the potential consequences of a warmer climate on the distribution and diversity of species. Our work in this research area mainly addresses the relative roles of climate and other factors in determining patterns of bio-

The fate of biological diversity for the next 10 million years will almost certainly be determined during the next 50–100 years by the activities of a single species.[2]

[2] Ehrlich, P.R. & Pringle, R.M.: Where does biodiversity go from here? A grim business-as-usual forecast and a hopeful portfolio of partial solutions. PNAS 105: 11579–11586 (2008)

geography and biodiversity from local to global scales. We thereby use field data collections and experiments as well as advanced methods of analyzing macroecological data. Additionally, we are interested in whether the warming trends of the recent past have already changed biodiversity patterns, or are about to do so. In tackling this question we mainly rely on comparing historical and contemporary species distribution data, with a strong focus on plants of mountain ecosystems, in particular in the European Alps.

Forecasting biodiversity changes under a warming climate

The tight connection between the variation of climatic conditions on Earth and the distribution of species suggests that the effects of climate change on species' geography could be massive. Indeed, evidence from the fossil record demonstrates that range shifts have been a dominant response of species to past climatic perturbations. Forecasting the extent, direction and magnitude of such shifts is not only of theoretical interest but also of eminent applied importance in nature conservation, for example in the context of continental-scale reserve networks. Considerable effort is hence put in developing predictive models of species range shifts and the associated changes of biodiversity. Nonetheless, while the general trend of such range shifts will clearly be directed towards the poles and up in the mountains, actual migration processes might be controlled and modified by a multitude of other factors such as the species' requirements towards other attributes of the physical environment, their intrinsic dispersal capacities, their interactions with other species, or the land-use-driven loss and fragmentation of habitats. We are therefore applying existing and developing new tools for computer-based simulations of species migration under different scenarios of climate and land use change. We primarily apply these tools to plants but are currently expanding our focus especially to invertebrate animals and systems of interdependent plant and animal species such as herbivores and their hosts.

Ecosystem productivity and carbon and nutrient cycling in a future world

Current ecosystems are undergoing rapid and often overlooked changes that are, at least in part, due to climate change. Changes in the cycling of nutrients such as nitrogen and phosphorus and in ecosystem carbon storage are among the most important consequences of climate change: they have a high potential for climate feedbacks as well as a strong impact on a wide range of ecosystem goods and services and thus on the wellbeing of humankind.

Predicting carbon and nutrient cycling in a future climate requires a detailed understanding of the functioning of the underlying microbiological and plant systems and how their community composition and activity is controlled. In this research focus we apply experimental ecosystem manipulations, large-scale transect studies and modeling combined with state-of-the-art analytical approaches to advance the understanding of plant production and microbial processes and their controls in a wide range of ecosystems from the Arctic to the Tropics, in terrestrial and aquatic environments. Currently we are working »

Hyperdiverse tropical forests (here: Costa Rica) respond highly sensitively to climate change

» on the control of microbial decomposition of organic matter in permafrost soils (which hold more than twice the amount of carbon than the current atmosphere), and are addressing large-scale environmental controls on net primary production and carbon sequestration in tropical rain forests. A further focus of this research area is climate change effects on the interaction of plants and microbes and its ecosystem consequences, such as rhizosphere priming (i.e. the enhanced decomposition of soil organic matter by the input of fresh plant material).

Revealing microbial key players and microbial metabolic interactions in climate change

Nutrient cycling in ecosystems is mainly carried out by microorganisms, which compete or synergistically cooperate for nutrients. This effectively controlls organic carbon degradation and gross production of green house gases such as carbon dioxide, methane, and nitrous oxide. Which microorganisms and, more importantly, how microorganisms will respond to global warming in the upcoming decades to centuries is largely unknown but key to understanding climate feedbacks. To address these questions, we apply the entire modern tool kit of genomic and stable isotope labeling methods for studying complex microbial communities in their natural environments. Our research focuses on identifying and revealing the genetic and metabolic features of microbial key players of the carbon, nitrogen, phosphorus and sulfur cycle that have a disproportional negative or positive impact on climate change. We further aim at unravelling the complex metabolic interactions during organic carbon degradation in terrestrial and aquatic environment. This includes the feedbacks of microbial processes on climate change through production and consumption of green house gases.

Global warming accelerates the decomposition of organic matter in permafrost soils (here: northern Siberia), making positive feedbacks to climate change likely

... the biogeochemical carbon cycle in the ocean and on land will continue to respond to climate change and rising atmospheric CO_2 concentrations created during the 21st century.[3]

[3] Ciais et al., 2013: Carbon and Other Biogeochemical Cycles. In: Climate Change 2013: The Physical Science Basis. Contribution of Working Group I to the Fifth Assessment Report of the Intergovernmental Panel on Climate Change [Stocker et al. (eds.)]. Cambridge University Press, Cambridge, UK and New York, NY, USA.

Outlook

Future research in the research focus Climate Change Biology will (a) focus on a more in-depth understanding of the role of biotic interactions (e.g. between microorganisms or microorganisms and plants) on biogeochemical cycles and climate feedbacks, and (b) increasingly integrate the interaction of biota with their biotic and abiotic environment and resulting feedback loops with the human response into predictive modelling. Such models shall stress the the non-equilibrium between vegetation, microbial communities and climate which will likely prevail during the upcoming decades. Such models will promote research on the consequences that such non-equilibrium might have for the functioning of ecosystems and the services they provide to human societies. Such questions also call for a stronger integration between organismal and ecosystem-based approaches to Climate Change Biology issues.

Key References

_ Dullinger S et al. (2012) Extinction debt of high-mountain plants under 21st-century climate warming. Nature Climate Change 2: 619.
_ Hofhansl F, Schnecker J, Singer G, Wanek W (2014) New insights into mechanisms driving carbon allocation in tropical forests. The New Phytologist 205: 137.
_ Mooshammer M et al. (2014) Adjustment of microbial nitrogen use efficiency to carbon:nitrogen imbalances regulates soil nitrogen cycling. Nature Communications 5: 3694.
_ Pauli H et al. (2012) Recent plant diversity changes on Europe's mountain summits. Science 336: 353.
_ Pester M, Knorr K-H, Friedrich MW, Wagner M, Loy A (2012) Sulfate-reducing microorganisms in wetlands – fameless actors in carbon cycling and climate change. Frontiers in Microbiology 3: 72.
_ Singer GA, Fasching C, Wilhelm L, Niggemann J, Steier P, Dittmar T, Battin TJ (2012) Biogeochemically diverse organic matter in Alpine glaciers and its downstream fate. Nature Geoscience 5: 710. «

Microbial processes have a central role in the global fluxes of the key biogenic greenhouse gases (carbon dioxide, methane and nitrous oxide) and are likely to respond rapidly to climate change.[4]

[4] Singh et al., Nature Reviews Microbiology 8, 779–790 (2010)

Recent studies demonstrate that mountain plants are already shifting their distributions in response to a warming climate.

Departments

Department of Microbiology & Ecosystem Science
Division of Terrestrial Ecosystem Research
Andreas Richter: www.ecosystem-research.net
Division of Microbial Ecology
Michael Wagner: www.microbial-ecology.net

Department of Limnology and Bio-Oceanography
Division of Limnology
Jakob Schelker: limbo.univie.ac.at/lab_schelker.php
Division of Bio-Oceanography
Gerhard J. Herndl: www.microbial-oceanography.eu/staff/herndl.html

Department of Botany & Biodiversity Research
Division of Conservation Biology, Vegetation- and Landscape Ecology
Stefan Dullinger: cvl.univie.ac.at

Microorganisms

Stewards of Planet Earth

Microbial Ecology and Ecosystems ***The research focus 'Microbial Ecology and Ecosystems' examines the diversity and function of microorganisms. It characterizes the biogeochemical transformations in natural and anthropogenic ecosystems driven by microbial activities. As all life relies on microbial processes, this knowledge is essential to understand the biology of our planet and the consequences of perturbations induced by human activities.***

How are microbes adapted to live in the dark, cold and nutrient-poor deep ocean?

Collecting water samples from 4000 m depth on board RV Pelagia using a rosette sampling system.

Life on Earth would not be possible without a continuous recycling of the chemical elements. These essential biogeochemical cycles are mainly catalyzed by microorganisms, which are ubiquitous in all ecosystems and reach an enormous diversity and abundance. Despite the ecological importance of these microbial communities and of the biogeochemical transformations they perform, there are major gaps in our basic understanding of their ecology.

In most ecosystems, the microbial key players still remain to be characterized with regard to their community structure, functional diversity, and interactions with other organisms. Resolving these questions is a main goal of this research theme. Several research groups are studying various aspects of this theme with a special emphasis on carbon, nitrogen, and sulfur cycling by bacteria and archaea in aquatic and terrestrial environments and on interactions within the microbial community in specific habitats. A major challenge is that most microorganisms cannot be cultured and studied in the laboratory by traditional methods. Cutting-edge molecular and isotope techniques overcome this obstacle and are used to study microorganisms directly in their habitats, even at the resolution of single microbial cells.

Microbial life at high pressure and low temperature

The Microbial Oceanography group focuses on the role of bacteria, archaea and viruses in me-

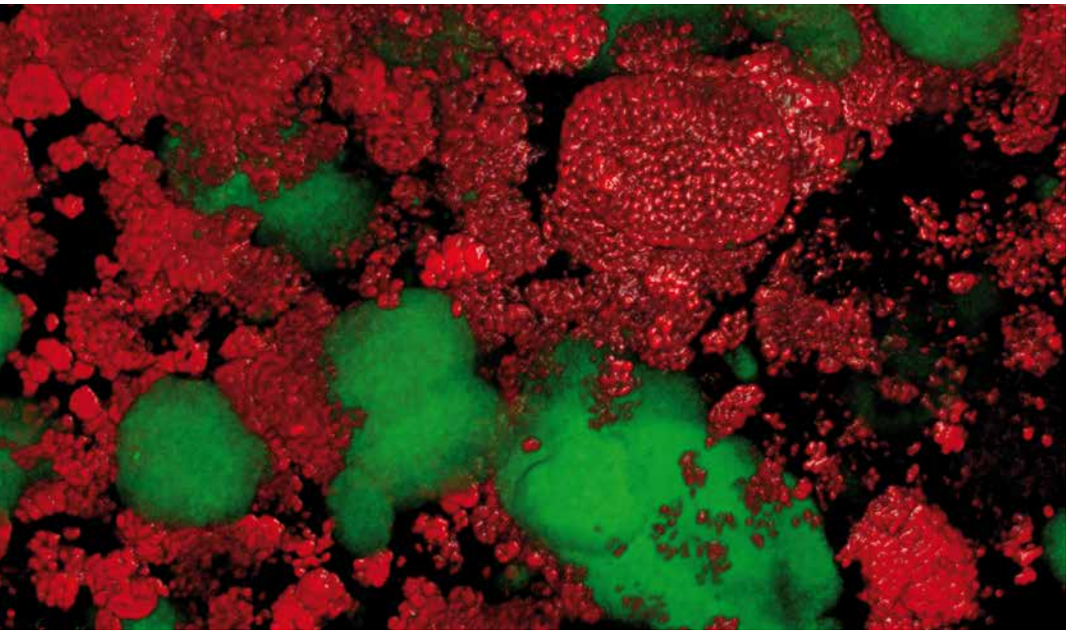
Did the first microbial life forms evolve in hot environments?

Searching for Archaea in hot springs of Iceland

diating the biogeochemical fluxes in the ocean, with an emphasis on the deep oceanic water column. Deep-sea systems are characterized by high pressure and a water temperature varying from 0–2 °C. While it has been known for a long time that some specific microbes are adapted to these high-pressure conditions, the contribution of these 'pressure-loving' microbes to the total deep-sea microbial community remains enigmatic. Therefore, the main research questions addressed are the effects of high-pressure conditions on deep-sea microbial communities and their metabolic pathways and activity. Viruses infect specific microbial species and are ten times more abundant than microbes in surface waters. In the deep ocean, however, viruses are up to 100 times more abundant than microbes. How this high viral abundance is maintained in the deep sea is unknown. It is likely that the deep-sea microbial community is not randomly distributed in the water column but centered on 'marine snow' particles, which provide a rain of organic matter from the sunlit surface waters into the deep sea. This particle rain represents the food source for the heterotrophic deep-sea food webs. Also, it has been found that there is a large community of autotrophic microbes in the deep ocean fixing carbon dioxide and using a plethora of energy sources. It is estimated that the dark ocean's carbon dioxide fixation is of the same order of magnitude as heterotrophic microbial biomass production. The fate of this newly synthesized organic carbon and its role in fueling the deep-sea food webs is the focus of future research.

Archaea: from the extremes to normality

Beside bacteria, a second fundamentally different group of microorganisms, the archaea, started to thrive on this planet probably even 1 billion years before plants and animals developed. Archaea have unique cell membranes and metabolisms and, despite their typical prokaryotic cell structures and often extreme life styles, they share many features of information-processing systems with higher organisms (eukaryotes). Therefore, archaea play a crucial role for understanding the evolution of microbial life and metabolisms as well as the evolution of key eukaryotic traits. Most archaea are found in extreme environments, in particular in hot springs. Recent studies, however, have shown that some archaea are also important players in global carbon and nitrogen cycles; in particular, ammonia-oxidizing archaea are found in virtually any terrestrial and aquatic environment on Earth. Did archaea originate in hot springs, where they are found in huge diversity? Can we find archaea that are direct ancestors of eukaryotes? What is the basis of the ecological success of archaea in moderate environments? Do these archaea directly compete with bacteria? These and further questions are addressed by the Archaea Biology and Ecogenomics Division of the »



FISH image of nitrifying microbes in the environment

» Department of Ecogenomics and Systems Biology using environmental genomics, systems biology and classical microbiological approaches.

Cycling of carbon, nitrogen and sulfur affect the health of our planet

A key process of the nitrogen cycle is nitrification driven almost exclusively by two groups of microorganisms, which aerobically oxidize ammonia via nitrite to nitrate. The activities of these nitrifiers are of major ecological and economic importance because they produce the potent greenhouse gas N_2O as a by-product, and largely contribute to the inefficiency of ammonium fertilization in agriculture, causing massive eutrophication events and dead zones in water bodies. At the same time it is the activity of nitrifiers in wastewater treatment that prevents eutrophication of aquatic ecosystems. Another key process of the nitrogen cycle is nitrogen fixation, where microorganisms known as diazotrophs incorporate dinitrogen gas from the atmosphere into organic compounds. This makes the nitrogen available to other microorganisms, plants, and animals, which all lack this capability. Analogous to nitrogen cycling, microorganisms play an equally important role for sulfur cycling. Dissimilatory sulfate reduction is a key step in this cycle and is exclusively catalyzed by specialized anaerobic microorganisms. Despite the importance of these biogeochemical cycles for the health and ecological functioning of our planet, we have just begun to understand their microbiology. Most of our current knowledge on key microbial processes such as nitrification, nitrogen fixation, and sulfate reduction stems from work with a few cultured model organisms that hardly represent the microbes driving these processes in most environments. The Department of Microbiology and Ecosystem Science uses modern (meta)genomic, transcriptomic and proteomic approaches as well as fluorescence and chemical imaging methods such as Raman microspectroscopy and NanoSIMS combined with cultivation

Single-cell techniques offer new insights into the ecology of microbes.

What are the most important carbon-, nitrogen- and sulfur-cycling microbes, and what are their characteristics?

methods and highly sensitive analytics to reveal and characterize environmentally relevant bacteria and archaea. Research efforts have led to the discovery of many important carbon-, nitrogen- and sulfur-cycling microorganisms and of unexpected physiological properties of these fascinating microbes.

Key References

_ Alves RJE, Wanek W, Zappe A, Richter A, Svenning MM, Schleper C, Urich T (2013) Nitrification rates in Arctic soils are associated with functionally distinct populations of ammonia-oxidizing archaea. ISME Journal 7(8): 1620–1631.
_ Hatzenpichler R, Lebedeva EV, Spieck E, Stoecker K, Richter A, Daims H, Wagner M (2008) A moderately thermophilic ammonia-oxidizing crenarchaeote from a hot spring. P Natl Acad Sci USA 105: 2134–2139.
_ Herndl GJ, Reinthaler T (2013) Microbial control of the dark end of the biological pump. Nature Geoscience, 6: 718–724
_ Hubert C et al.(2009) A constant flux of diverse thermophilic bacteria into the cold Arctic seabed. Science 325: 1541–1544.
_ Jiao N, Herndl GJ, Hansell DA, Benner R, Kattner G, Wilhelm SW, Kirchman DL, Weinbauer MG, Luo T, Chen F, Azam F (2010) Microbial production of recalcitrant dissolved organic matter: long-term carbon storage in the global ocean. Nature Rev. Microbiol., 8: 593–599
_ Koch H et al.(2014). Growth of nitrite-oxidizing bacteria by aerobic hydrogen oxidation. Science 345: 1052–1054.
_ Milucka J, Ferdelman TG, Polerecky L, Franzke D, Wegener G, Schmid M, Lieberwirth I, Wagner M, Widdel F, Kuypers MMM (2012). Zero-valent sulphur is a key intermediate in marine methane oxidation. Nature 491: 541–546.
_ Offre P, Spang A, Schleper C (2013). Archaea in biogeochemical cycles. Annu Rev Microbiol.: 67:437–57.
_ Swan BK et al. (2011) Potential for chemolithoautotrophy among ubiquitous bacteria lineages in the dark ocean. Science, 333: 1296–1300
_ Zebec Z, Manica A, Zhang J, White MF, Schleper C (2014). CRISPR-mediated targeted mRNA degradation in the archaeon Sulfolobus solfataricus. Nucleic Acids Res. 42(8):5280-8. «

Departments
Department of Ecogenomics and Systems Biology
Christa Schleper: genetics-ecology.univie.ac.at/schleper.html

Department of Limnology and Bio-Oceanography
Gerhard J. Herndl: www.microbial-oceanography.eu/staff/herndl.html

Department of Microbiology and Ecosystem Science
Andreas Richter: http://131.130.57.230/cms/index.php?id=289
Michael Wagner: www.microbial-ecology.net/wagner

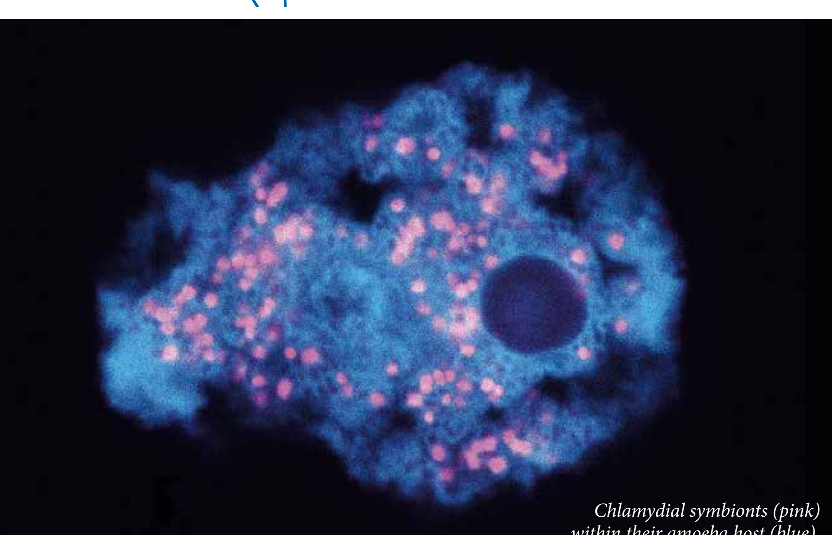
No one lives alone

***Symbiosis** is a fundamental principle of nature. Nearly all living beings on our planet rely on associations with other species, and oftentimes these partners are microbial symbionts. In this research focus processes and molecular mechanisms involved in microbial symbioses, their ecology and evolution are studied using diverse model systems ranging from protists to animals and plants.*

What makes a symbiont?

Ancient invaders

Amoebae are ubiquitous and important predators of microbes. They also serve as hosts for a variety of bacterial symbionts, several of which are most closely related to pathogens of humans, such as *Chlamydia*. We study these symbionts and environmental counterparts of human pathogens to understand the evolutionary history of bacteria living within eukaryotic host cells. Using state-of-the-art molecular methods, we could show that both extant chlamydial pathogens and symbionts use similar mechanisms to invade and manipulate their host cells. These mechanisms have evolved hundreds of millions of years ago, likely during interplay with primordial protists, and only later served to successfully infect humans. Currently we investigate molecular differences and similarities of symbionts and pathogens, and uses evolution experiments to investigate factors driving host adaptation and development of virulence in these microbes. The analysis of these bacteria is vital to our understanding of intracellular symbioses, the evolution of intracellular pathogens and bacterial mechanisms used to infect and exploit eukaryotic host cells.

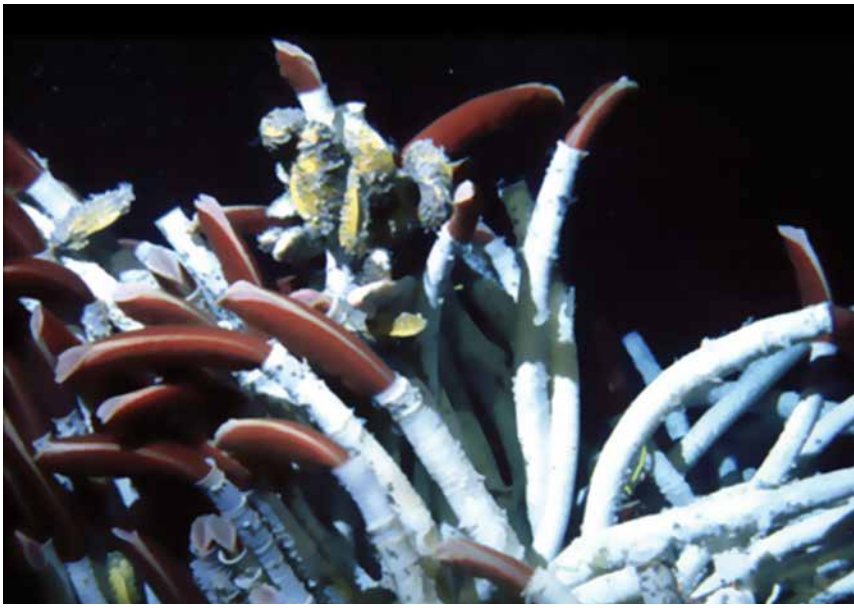


Chlamydial symbionts (pink) within their amoeba host (blue).

To live without a gut

The giant tubeworm *Riftia pachyptila* is one of the fastest-growing invertebrate we know of. Instead of a gut, it houses the endosymbiont *Candidatus Endoriftia persephone*. Endoriftia uses hydrogen sulphide percolating from deep-sea vents and oxygen from surrounding water for carbon fixation, thereby also nourishing the host. The tubeworm larvae, however, must acquire Endoriftia in each generation anew. We used artificial settlement devices deployed with a submersible to recover larvae. With molecular and electron microscopy techniques we reconstructed the infection process of the symbiont through the host skin. Likewise, the symbiont must be released back into the environment for replenishment of the free-living population. In experiments we simulated the cessation of a vent using high-pressure flow-through aquaria. We found that Endoriftia escapes the tubeworm upon host death. Currently we inves-

How to infect and escape a host?



Giant tubeworms at a hydrothermal vent at 2.500 m depth in the Pacific Ocean

tigated how the symbiont colonizes aquaria surfaces where it starts to proliferate. Such studies underline the significance of transmission and escape processes in the persistence of cooperation in ecological and evolutionary time scales.

Dressed to cooperate

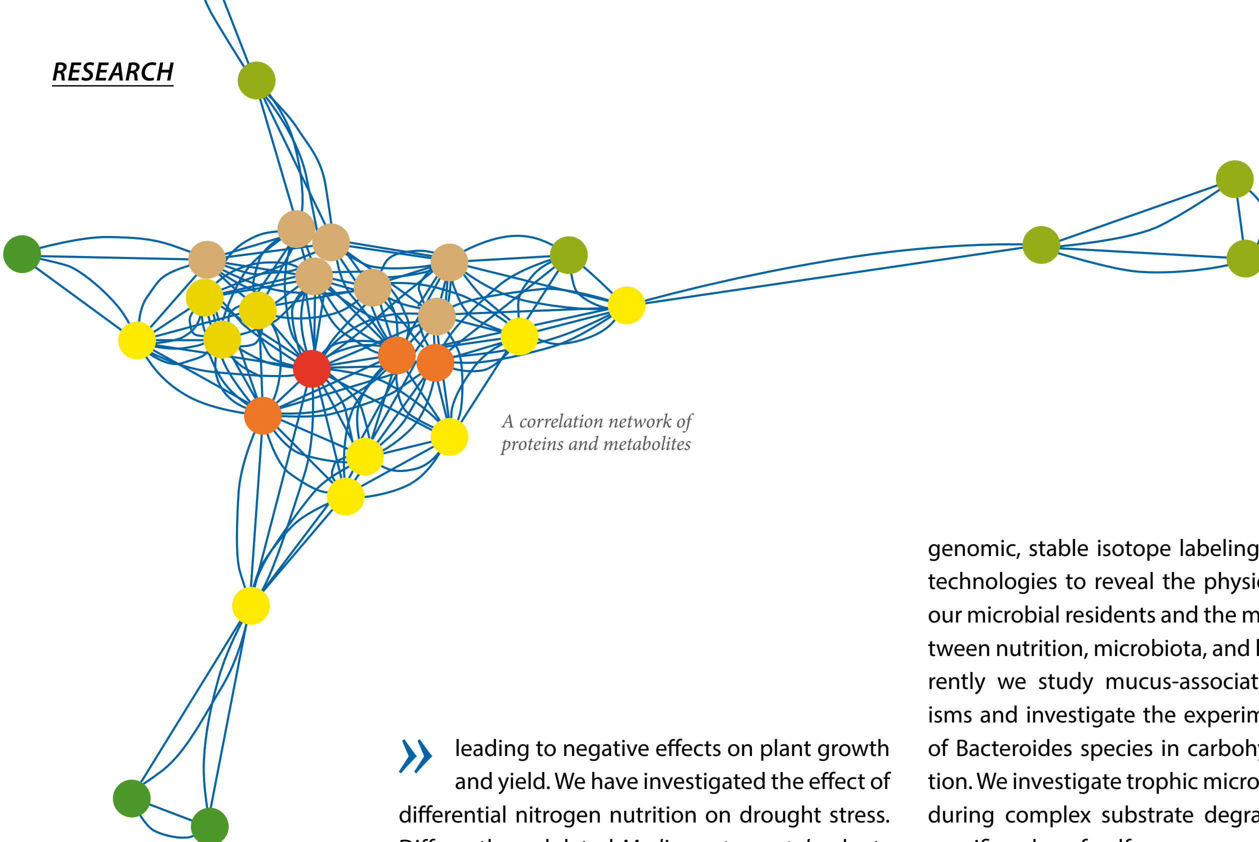
Stilbonematid roundworms are coated by sulphur-oxidizing *Gammaproteobacteria*. What makes these marine ectosymbioses unique is the high specificity maintained from birth to adulthood in spite of four molting events. This is in stark contrast with the vast and complex microbial populations engaging – for example – the human skin. Applying molecular, biochemical and omics techniques, We study worm-secreted molecules, which mediate specific host-symbiont attachment. Among these are the sugar-binding Mermaid proteins. Their function resembles that of human immunoreceptors, making them biomedically relevant. Another exotic feature is that symbiont reproduction is often drastically different from that of conventional bacteria. By applying state-of-the-art microscopy and image analysis we have shown that some symbionts divide lengthwise when rod-shaped while others manage to divide regularly after growing so long to be perceivable by the naked eye. We currently study the molecular mechanisms underlying symbiosis specificity. At the same time, we also seek to understand whether the animal host can time bacterial proliferation and, if so, how.

Scanning electron microscopy image of the up to 1 cm long Eubostrichus dianeae roundworm and its "fur" made of filamentous bacterial cells.

Stay green during drought

Legumes can grow on nitrogen-poor soil when interacting with nitrogen (N) -fixing rhizobia in root nodules, facilitating metabolic exchanges between partners. Drought is a major stress »

What controls a symbiont?



A correlation network of proteins and metabolites

» leading to negative effects on plant growth and yield. We have investigated the effect of differential nitrogen nutrition on drought stress. Differently nodulated *Medicago truncatula* plants with *S. meliloti* or *S. medicae* were compared with N-fertilized plants. Physiological and molecular responses were assessed using metabolomic and proteomic techniques. On the molecular level, we found a priming effect apparently responsible for a so-called "Stay-Green effect". While N-fertilized plants showed accelerated leaf senescence during drought, leaves of nodulated plants remained green. Nodulated plants invested more into reprogramming of the leaf metabolism, yielding protective compounds. Currently we investigate the underlying mechanism of how symbiotic interaction facilitates legume shoot biomass maintenance and protective compound synthesis under drought. In addition we test putative biomarkers. The results will help understand the underlying Stay-Green effect for improved drought tolerance.

Our own social network of microbial friends

Trillions of symbiotic microorganisms live in and on the human and animal body. This microbiota, largely residing in the intestinal tract, has important beneficial functions; its disturbance leads to disease. Genomic and postgenomic studies have revealed exciting insights into the composition and metabolic potential of the host-associated microbiota and intriguing correlative associations with human and animal nutrition, behavior, and disease. Nonetheless, the true functions of individual microbiota members and their contributions to host physiology and health remain largely undetermined. We combine modern (post) genomic, stable isotope labeling, and single cell technologies to reveal the physiological roles of our microbial residents and the manifold links between nutrition, microbiota, and host health. Currently we study mucus-associated microorganisms and investigate the experimental evolution of Bacteroides species in carbohydrate degradation. We investigate trophic microbial interactions during complex substrate degradation and the specific roles of sulfur-compounds-metabolizing microorganisms in host nutrition, health, and disease. This research has a high potential to provide both significant advances in scientific understanding of microbiota function and the basis for novel therapeutic applications.

Let's talk about symbiosis

Members of this research focus conceive their goals as joint endeavors. Manifold collaborations in science and a consolidated educational program are key in this transdisciplinary research field, creating an open environment of exchange of knowledge, ideas and techniques. The goal is to foster this cooperative approach and reach out to other disciplines at the University of Vienna such as chemistry, physics and mathematics.

Key References

_ Berry D et al. (2012) Phylotype-level 16S rRNA analysis reveals new bacterial indicators of health state in acute murine colitis. ISME J. 6: 2091.

_ Berry D et al. (2013) Host-compound foraging by intestinal microbiota revealed by single-cell stable isotope probing. Proc. Natl. Acad. Sci. USA 110: 4720.

_ Bright M, Espada-Hinojosa S, Lakouvardos I, Volland J-M (2014) The giant ciliate Zoothamnium niveum and its thiotrophic epibiont Canditatus Thiobios zoothamnicoli: a model system to study interspecies cooperation. Front. Microbiol. 5: 1–13.

More microbial than human. Our body is an ecosystem for ten times more microbial cells than human cells.

Why are microorganisms so important for animals and humans?

_ Bulgheresi S, Gruber-Vodicka HR, Heindl NR, Dirks U, Kostadinova M, Breiteneder H, Ott JA (2011) Sequence variability of the pattern recognition receptor Mermaid mediates specificity of marine nematode symbioses. ISME J. 5: 986.
_ Domman D, Horn M, Embley TM, Williams TA. (2015) Plastid establishment did not require a chlamydial partner. Nature Comm. 6: 6421.
_ Nussbaumer AD., Fisher C.R., Bright M. 2006. Horizontal endosymbiont transmission in hydrothermal vent tubeworms. Nature 441: 345–8.
_ Pende N, Leisch N, Gruber-Vodicka HR, Heindl NR, Ott JA, den Blaauwen T, Bulgheresi S. (2014) Size-independent symmetric division in extraordinarily long cells. Nature Comm. 5: 4803.
_ Sixt BS, Siegl A, Müller C, Watzka M, Wultsch A, Tziotis D, Montanaro J, Richter A, Schmitt-Kopplin P, Horn M. (2013) Metabolic features of Protochlamydia amoebophila elementary bodies - a link between activity and infectivity in Chlamydiae. PLoS Pathogens 9: e1003553.
_ Staudinger C, Mehmeti V, Turetschek R, Lyon D, Egelhofer V, Wienkoop S (2012) Possible role of nutritional priming for early salt and drought stress responses in Medicago truncatula. Front. Plant Proteomics. 3: 285. «

Departments
Department of Ecogenomics and Systems Biology
Silvia Bulgheresi: genetics-ecology.univie.ac.at/bulgheresi.html
Stefanie Wienkoop: homepage.univie.ac.at/stefanie.wienkoop/index.html

Department of Limnology and Bio-Oceanography
Monika Bright: www.hydrothermalvent.com

Department of Microbiology and Ecosystem Science
Matthias Horn: www.microbial-ecology.net/horn
David Berry: www.microbial-ecology.net/berry
Alexander Loy: www.microbial-ecology.net/loy

Botany and Biodiversity

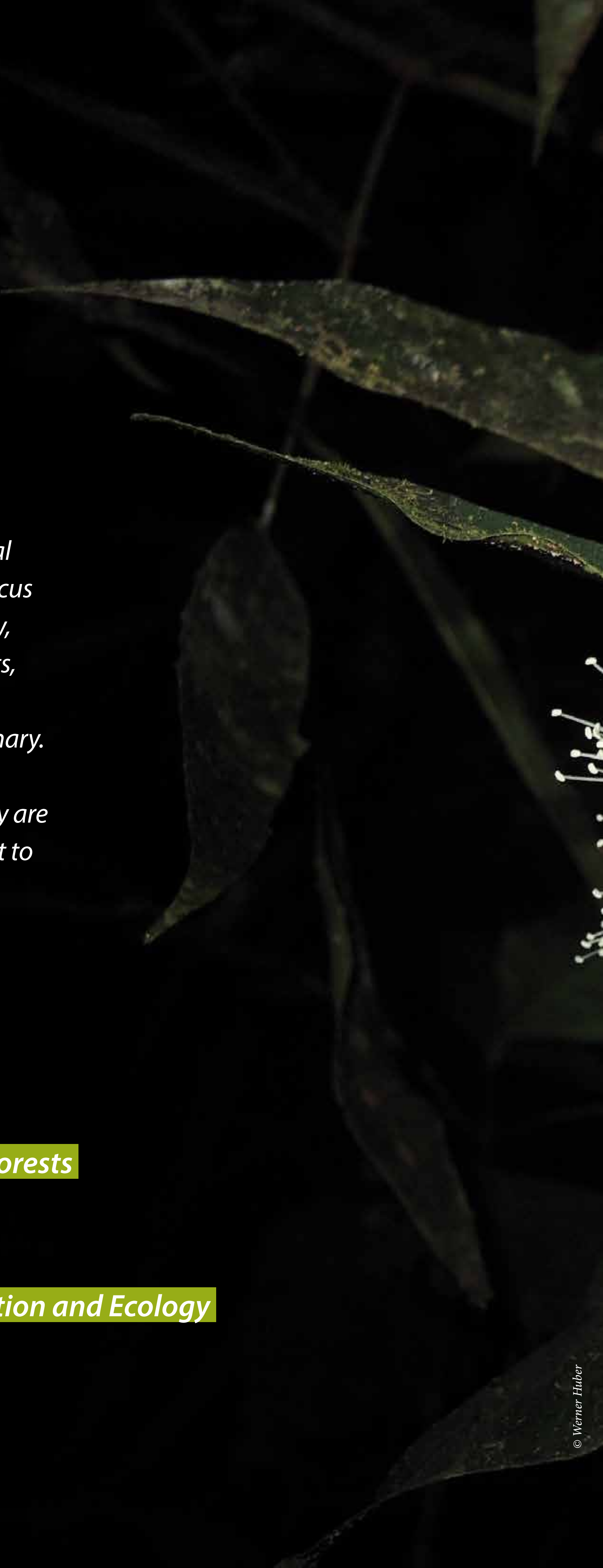
… studies biodiversity in all relevant ecological and evolutionary dimensions. The research focus combines expertise from ecology, morphology, and evolutionary biology. It investigates plants, fungi, and animals. As a consequence both its research and teaching are highly interdisciplinary. In addition, science-based rationales for management and conservation of biodiversity are developed in response to the worldwide threat to biodiversity by human activities.

Ecology and Biodiversity of Tropical Forests

Department of Botany and Biodiversity Research
Department of Microbiology and Ecosystem Science
Tropical Research Station La Gamba (Costa Rica)

Patterns and Processes in Plant Evolution and Ecology

Department of Botany and Biodiversity Research
Department of Ecogenomics and Systems Biology
Core Facility Botanical Garden



Rose apple (Syzygium jambos, Myrtaceae) – *its showy flowers attract a broad range of pollinators*

Biodiversity matters

Ecology and Biodiversity of Tropical Forests ***This research focus studies tropical forests as global centers of biodiversity and their resilience to land use and climate change. The research focus is on cascading effects of global changes on tropical biodiversity, tropical ecosystems and on measures to decelerate biodiversity loss.***

In this research focus we analyze the effects of global change on tropical biodiversity and ecosystem processes. We aim to understand underlying mechanisms and functions, i.e. ecosystem functions, in order to improve future measures of land management and conservation.

Tropical forests are key drivers of global energy and matter cycles.

Tropical Research Station La Gamba in Costa Rica – main building and office.

Tropical forests in a changing environment

Although tropical forests cover only one sixth of the Earth's land surface, they play a key role in global carbon, water, and energy cycles: They contain about 40 % of the global terrestrial organic carbon pool, account for more than one third of terrestrial productivity, and comprise more than half of the world's plant and animal species. Moreover, at a regional scale, tropical rainforests provide important ecosystem services such as water recharge and erosion control, as well as timber and food production. Loss of tropical rainforests therefore has major impacts on global productivity, biodiversity and climate, and on regional ecosystem services. Increasing human pressures through land-use change (deforestation, fragmentation) and climate change can have detrimental effects on biodiversity and the functioning of tropical forests. Despite the importance of tropical rainforests, the knowledge of their potential responses to global change and increased human pressures is highly fragmentary. We also still do not understand how biodiversity loss will affect ecosystem functioning. To fill this gap, it is important to study the resistance and resilience of biodiversity and the functioning of tropical forests to global changes.

Biodiversity affects ecosystem functions

Biodiversity has been demonstrated to impact ecosystem functions. In grasslands, recent biodiversity-ecosystem function (BDEF) research demonstrated that not species diversity (species

How are biodiversity and ecosystem functions related in tropical forests?

Species-rich primary tropical rainforests cover the rugged terrain near La Gamba, Costa Rica.

numbers) but rather species composition and particularly the functional diversity positively drive ecosystem functions such as resource use (light, water and nutrients) and plant productivity. Higher levels of functional diversity imply larger numbers of plant or animal functional types and a greater breadth of functional traits. While this biodiversity-ecosystem function relationship has been well established in grasslands, much less is known from forests, and even less from tropical forests.

Scientific key questions

Fundamental questions of this research focus therefore concern the importance of high biodiversity levels for the functioning of tropical forest ecosystems, the impact of global change on biodiversity and ecosystem functions of tropical forests, and measures to decelerate biodiversity loss in the tropics.

Methods and approaches

Answering these questions calls for integrating different scientific disciplines, for instance through collaborations of working groups of the University of Vienna as well as of other national universities (University of Natural Resources and Life Sciences, BOKU) and international universities (Universidad de Costa Rica). The scientific efforts are centered around the Tropical Research Station La Gamba in Costa Rica, which is affiliated with the University of Vienna and provides ideal conditions to perform research on tropical lowland forests and a multitude of land-use systems (e.g. oil palm and tree plantations, pastures). Central to this research focus, a unique biodiversity experiment in La Gamba and an extensive monitoring network of forest plots in the Golfo Dulce region in SW Costa Rica was recently established. The "Finca Amable" BDEF experiment was started in 2012 and sets out to understand the effect of plant functional diversity on resource use, plant productivity and animal interactions. Three functional groups of trees i. e. light-demanding (pioneer) trees, shade-tolerant (late successional) trees and legumes were planted at 80 plots, in combinations of one to three, with the level of species diversity held constant. Moreover, 20 one-hectare plots were established in replicated types of forest across a topographic and regional tectonic gradient in southwest Costa Rica. They are now the basis for studies of vegetation and animal community composition, ecosystem functions and major regional drivers »

Tropical biodiversity is strongly endangered through global change.

Large tropical trees contain the bulk of biomass in forests but are inherently difficult to measure and identify.

Observational and manipulative ecosystem studies help elucidate biodiversity-ecosystem function relations.

» and linkages of biodiversity, functional trait variation and ecosystem processes. Both approaches yield new insights into the coupling of biodiversity and ecosystem functioning in tropical forests and help to increase the international visibility of Austrian tropical research.

Outlook

The BDEF initiative has been financed by the Association of "Regenwald der Österreicher" (Finca Amable experiment) and the Federal Ministry of Science and Research Austria (plot network). Current research activities and collaborations shall lead to future projects to be financed by national science funds (FWF Austria, Costa Rica) and enable long-term ecological research (LTER). Data from the plot network will be integrated into the national Costa Rican LTER network, enabling to integrate and synthesize drivers of vegetation structure, tree biomass, and plant diversity at the national scale.

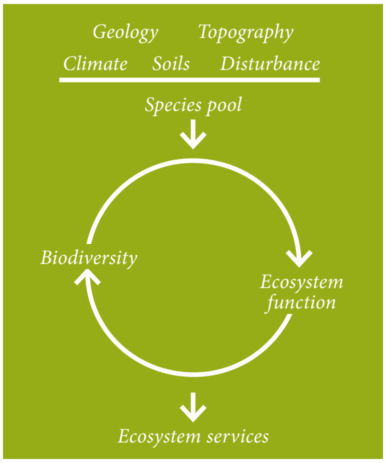
Key References

_ Brehm G, Strutzenberger P, Fiedler K (2013) Phylogenetic diversity of geometrid moths decreases with elevation in the tropical Andes. Ecography 36: 1247–1253.

_ Hietz P, Turner BL, Wanek W, Richter A, Nock CA, Wright SJ (2011) Long-term change in the nitrogen cycle in tropical forests. Science 334: 664–666.

_ Höbinger T, Schindler S, Seaman BS, Wrbka T, Weissenhofer A (2011) Impact of oil palm plantations on the structure of the agroforestry mosaic of La Gamba, Southern Costa Rica: potential implications for biodiversity. Agrof. Sys. 85: 367–381.

_ Hofhansl F, Wanek W, Drage S, Huber W, Weissenhofer A, Richter A (2012) Controls of hydrochemical fluxes via stemflow in tropical lowland rainforests: effects of meteorology and vegetation characteristics. J. Hydrol. 452: 247–258.



State factors select for the species pool and drive biodiversity and ecosystem functions at the landscape scale

Students at work in the laboratory of the Tropical Research Station La Gamba – soil extractions and data evaluation.

Does species richness or functional diversity drive ecosystem responses?

_ Hofhansl F, Schnecker J, SingerG, Wanek W (2015) New insights into mechanisms driving carbon allocation in tropical rainforests. New Phytol. 205, 137–146.
_ Kessler M et.al. (2012) Can joint carbon and biodiversity management in tropical agroforestry landscapes be optimized? PLoS ONE 7(10): e47192.
_ Laurance WF et al. (2012) Averting biodiversity collapse in tropical forest protected areas. Nature 489: 290–294. «

Departments and Divisions

Department of Botany & Biodiversity Research
Jürg Schönenberger: www.botanik.univie.ac.at
- Division of Conservation Biology, Vegetation- and Landscape Ecology (CVL)
- Division of Structural and Functional Botany (SFB)
- Division of Systematic and Evolutionary Botany
- Division of Tropical Ecology and Animal Biodiversity

Department of Microbiology & Ecosystem Science
- Division of Terrestrial Ecosystem Research
- Wolfgang Wanek: http://131.130.57.230/cms/index.php?id=432

Tropical Research Station La Gamba, Costa Rica: www.lagamba.at

The secret life of plants

Evolution and Ecology of Plant Diversity ***This research focus addresses the evolutionary and ecological processes that have given rise to present patterns of plant diversity. It also examines how to maintain plant diversity in the future.***

Plants are the backbone of life on Earth and like all other groups of organisms, plants have had an evolutionary history during which they have changed and diversified. This research focus is concerned with the processes leading to present-day patterns of plant diversity. In connection with the question on how plant diversity may be maintained in the long-term, we also study anthropogenic influences on plants and their environments. Two recent examples include the structural, ecological, and metabolomic circumscription of a novel pollination system discovered in South Ameria and the integration of high-resolution tomography data with metobolomic profiling of floral development. Another important aim is to closely connect our research with our teaching efforts. In order to intensify these efforts, we have recently established the two new master programs "Botany" and "Ecology & Ecosystems".

Organisms are crucial in all of comparative biology.

A stingless bee collecting resin on the flowers of the genus Clusia *(Costa Rica).*

Organismal Biology

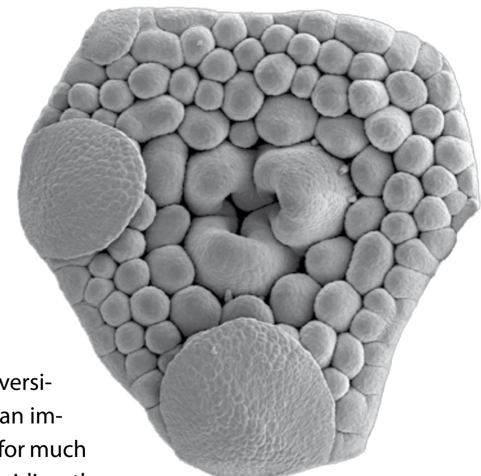
Organisms are crucial in comparative biology as they connect morphology, physiology and ecology to the fields of comparative genomics, evolutionary development, and molecular phylogenetics. This research focus is deeply rooted in organismal biology, i. e. the study of structure, function, ecology, and evolution at the level of the organism. Our research is solidly grounded in a detailed familiarity with the organisms we study and we are convinced that such an organismal approach is most efficient and produces the most reliable results when studying evolutionary and ecological processes and patterns.

Evolution and Systematics

Processes of evolution and mechanisms of speciation are the ultimate driving forces shaping the diversity of life. Ordering this diversity is the mission of systematics, which is a highly synthetic approach integrating multiple lines of evidence in order to develop hypotheses of phylogenetic relationships between organisms and how they should be arranged in a hierarchical system, i.e. in taxonomic classifications. We specialize in microevolution at the populational

Nothing in biology makes sense except in the light of evolution.

Dobzhansky 1973



Young developmental stage of a flower of Camellia sinensis *(tea) as seen in a scanning electron microscope.*

level as well as macroevolution and taxonomy of various plant groups. In connection with these efforts, we regularly conduct fieldwork in alpine regions, in the tropics, and on oceanic islands around the world. In addition we curate an internationally important herbarium, we cultivate thousands of plants in our botanical garden, we specialize in methods of phylogenetic and biogeographic analysis, and we study mechanisms of plant speciation.

Structural Plant Biology

Function and form are inseparable, and in order to understand biological function, an organism's structure as well as its phylogenetic relationship needs to be taken into account. Modern techniques for structural research such as high-resolution computer tomography and morphometric analyses are opening new possibilities for further integrating comparative structural studies with results from sample-based approaches such as genomics, proteomics, and metabolomics. In this research focus, researchers are interested in the functionality of structural plant features in order to understand the development and the evolution of flowers, pollination mechanisms, plant-ant interactions, and phylogenetic relationships of various plant lineages.

Ecology and Conservation

Speciation and extinction are driven by interactions of individuals and populations with their physical and biotic environments. Organismal ecology focuses on these interactions and how they shape the distribution of species in space and time, their assembly to biological communities, and the resulting patterns of biodiversity from local to global scales. The human impact has become of major importance for much of the world's biodiversity. Hence, providing the scientific foundation for biodiversity conservation has become an important part of ecology. In this research focus, collection and experiments in the field as well as advanced techniques of data analysis and computer simulations are used to identify the determinants of current plant species distribution. This approach also helps to predict how future changes in environmental conditions, in particular those related to various facets of global change such as climate warming, land use alteration, or alien species introductions, will affect species ranges and biodiversity patterns. Based on the horticultural skills of the Botanical Garden and extensive field work, we combine experience from *ex situ* cultivation with *in situ* conservation to optimize actions in safeguarding threatened species and their ecosystems. We actively contribute to the development of national and international strategies for plant protection and environmental conservation.

Function and form are inseparable.

Green Systems Biology

Plants have shaped human life from the outset. With increasing problems in the areas of global climate change and limited fossil energy resources, plant biology and biotechnology are becoming dramatically important. One key issue is to improve plant productivity and stress resistance in agriculture as a response to restricted land area and increasing envi- »

Participants of the first eFLOWER Summer School (University of Vienna, July 2013), which was supported by this Research Focus.

Flowers of Impatiens parasitica, *an epiphytic species native to India.*

» ronmental pressures. Another aspect is the development of CO_2-neutral plant resources for fiber/biomass and biofuels. At the same time we have to conserve and protect natural diversity and species richness as a foundation of life on Earth. Consequently, plant biology and ecology will become more important for all socio-economic aspects of our life than ever before. The latest developments in biological and bio-analytical research will lead to a paradigm shift towards trying to understand organisms at a systems level and in their eco-systemic context. Systems biology combines molecular data, genetic evolution, environmental cues, and species interactions with the understanding, modeling, and prediction of active biochemical networks up to whole species populations. This approach relies on developing new technologies to analyse molecular data, especially genomics, metabolomics, and proteomics data. The ambitious aim of these 'omic' technologies is to extend our understanding beyond the analysis of separate parts of the system and will lead to a novel understanding of plant metabolism and its interaction with the environment.

Outlook

Particular promising avenues for future research are expected to emerge at the interfaces of different research fields such as (1) „omics" data and morphometric analyses based on high-resolution 3D-data, (2) broad-scale structural data sets and the reconstruction of character evolution, (3) large ecological data sets and phylogenetic analyses, and (4) plant-animal interactions and community ecology/macroecology.

Key References

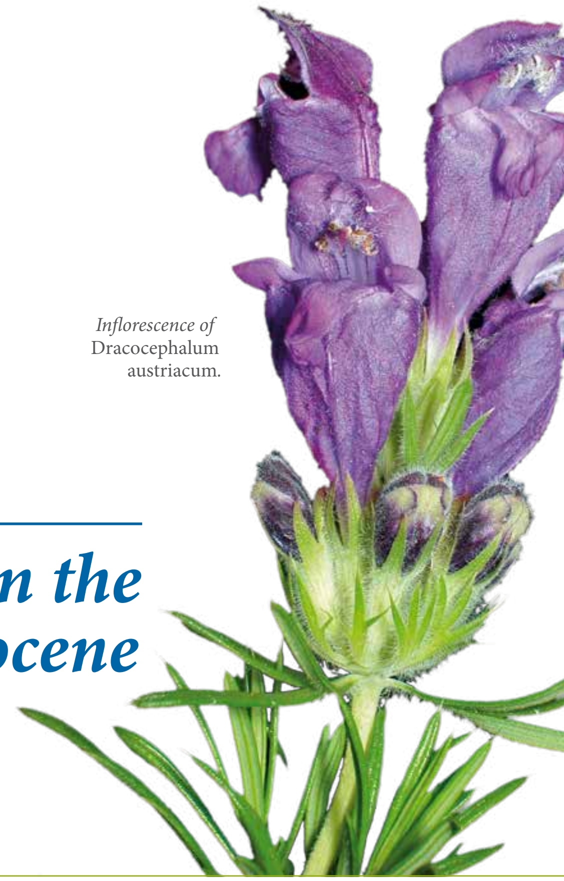
_ Dellinger AS, Penneys DS, Staedler YM, Fragner L, Weckwerth W, Schönenberger J (2014) A specialized bird pollination system involving a bellows mechanism for pollen transfer and staminal food body rewards. Curr. Biol. 24: 1–5

_ Bellaire A, Ischebeck T, Staedler YM, Weinhaeuser I, Mair A, Parameswaran S, Ito T, Schönenberger J, Weckwerth W (2014) Metabolism and Development – integration of micro-CT data and metabolite profiling reveals metabolic reprogramming from floral initiation to silique development. New Phytol. 202: 322–335.

_ Dullinger S et al. (2012) Extinction debt of high-mountain plants under 21st-century climate warming Nat. Clim. Change 2: 619–622.

From single genomes, proteomes and metabolomes to ecosystems research.

_ Essl F et al. (2011) Socioeconomic legacy yields an invasion debt. Proc. Nat. Acad. Sci. 108: 203–207.
_ Kiehn M (2011) Globale Strategie zur Erhaltung der Pflanzen (GSPC) Umsetzung in Österreich "Roadmap 2011–2020": www.plants2020.net/national-casestudies
_ Schumacher F, Grünweis FM, Knickmann B, Maier R, Prehsler D, Tod F, Kiehn M (2013) Projekte und Initiativen des Botanischen Gartens der Universität Wien (HBV) zur Erhaltung von Steppenpflanzen am Beispiel von Artemisia pancicii und Dracocephalum austriacum. Pp. 385–394 in Baumbach, H. & Pfützenreuter, S. (Eds.): "Steppenlebensräume Europas – Gefährdung, Erhaltungsmaßnahmen und Schutz". – Erfurt, Ministerium für Landwirtschaft, Forsten, Umwelt und Naturschutz (TMLFUN) des Landes Thüringen
_ Takayama K et al. (2014) Relationships and genetic consequences of contrasting modes of speciation among endemic species of Robinsonia (Asteraceae, Senecioneae) of the Juan Fernandez Archipelago, Chile, based on AFLPs and SSRs. New Phytol. doi: 10.1111/nph.13000
_ Weckwerth W (2011) Green systems biology – From single genomes, proteomes and metabolomes to ecosystems research and biotechnology. J. Proteom. 75: 284–305. «



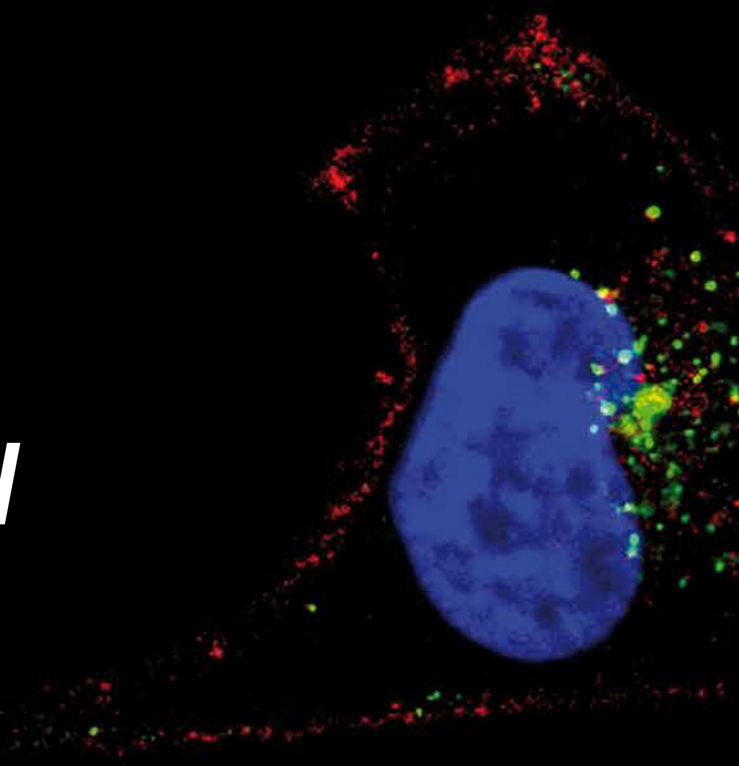
Inflorescence of Dracocephalum austriacum.

Ecology in the Anthropocene

Departments and Divisions
Department of Botany and Biodiversity Research
Jürg Schönenberger: www.botanik.univie.ac.at/botanik
Division of Conservation Biology, Vegetation- and Landscape Ecology: cvl.univie.ac.at
Division of Structural and Functional Botany: www.botanik.univie.ac.at/sfb
Division of Systematic and Evolutionary Botany: systematics.univie.ac.at

Department of Ecogenomics and Systems Biology
Division of Molecular Systems Biology
Wolfram Weckwerth: www.univie.ac.at/mosys

Core Facility Botanical Garden
www.botanik.univie.ac.at/hbv

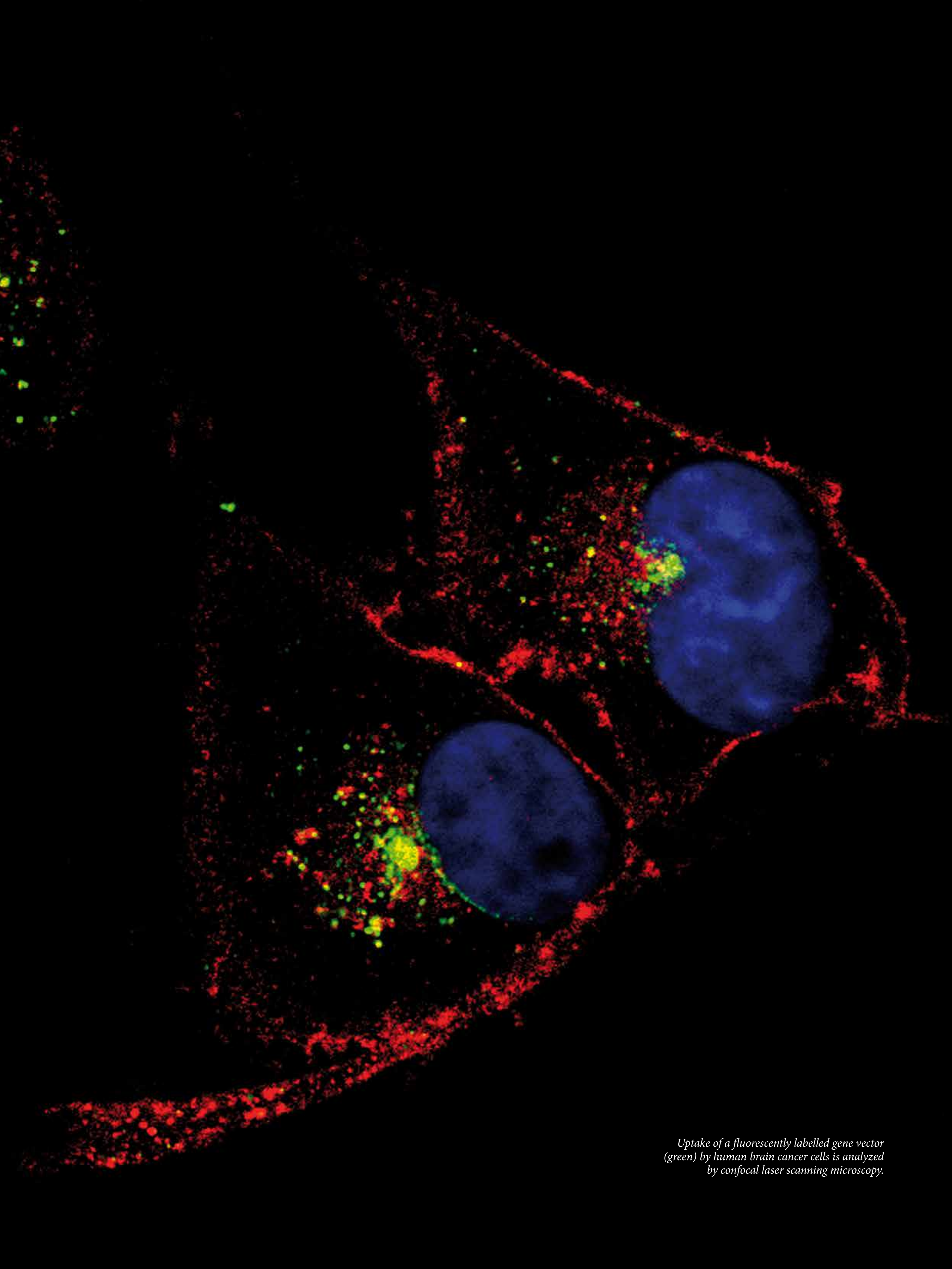


Pharmaceutical Sciences

… aim at the discovery, development, and appropriate use of medications for the welfare and the safety of the public. They are focusing on identifying and characterizing of both new biologically active natural products and synthetic drugs. They strive to understand their interactions with human targets on a molecular level using in silico, in vitro, and in vivo models.
Based on this knowledge, new lead compounds and disease-relevant targets are investigated and delivery systems for pharmaceutically active ingredients are developed.

Drug Discovery from Nature

Department of Pharmaceutical Chemistry
Department of Pharmacognosy
Department of Pharmacology and Toxicology
Department of Pharmaceutical Technology and Biopharmaceutics



Uptake of a fluorescently labelled gene vector (green) by human brain cancer cells is analyzed by confocal laser scanning microscopy.

From nature to medicines

Drug Discovery from Nature ***The objective of this key research area is to identify new active agents from nature (plants, microorganisms, etc.) and to understand their mechanisms of action using a broad spectrum of models and methods ranging from*** *in silico* ***experiments to*** *in vivo* ***imaging approaches. Smart delivery strategies are necessary to develop active agents towards medicines.***

How to find the needle in the haystack most effectively?

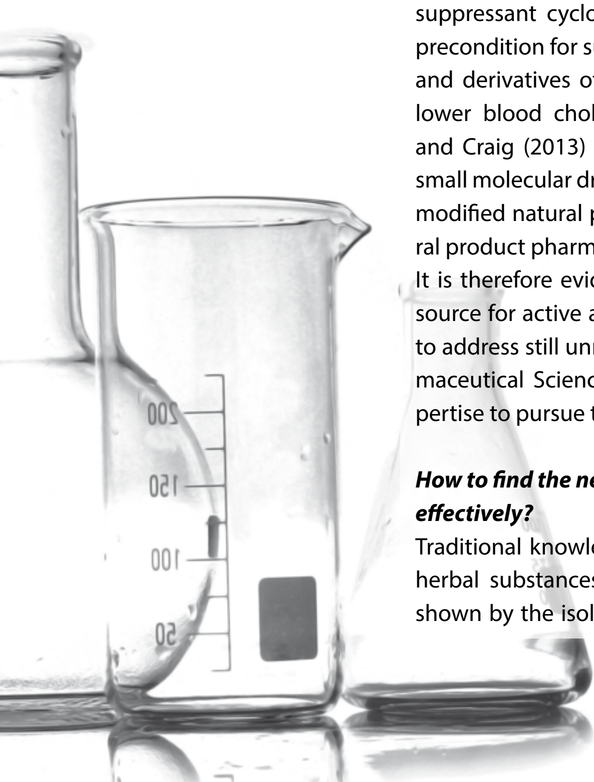
The history of modern drug discovery and development started with morphine. Friedrich Sertürner, a young assistant at a pharmacy in Paderborn, isolated this natural compound from opium in 1804 and named the drug *morphium* after Morpheus, the Greek god of dreams.

Subsequently many more seminal discoveries were made using nature as a source for new chemical entities. Aspirin was obtained by acetylating salicylic acid, a compound from willow bark. Compounds from microbes changed our lives by being discovered as effective antibiotics, with penicillin as the first representative. The immunosuppressant cyclosporine was an indispensable precondition for successful organ transplantation and derivatives of lovastatin are widely used to lower blood cholesterol. Analyses by Newman and Craig (2013) showed that about 50 % of all small molecular drugs are either natural products, modified natural products, or inspired by a natural product pharmacophore.

It is therefore evident that revisiting nature as a source for active agents is a rewarding approach to address still unmet medicinal needs. The Pharmaceutical Sciences in Vienna hold unique expertise to pursue this goal.

How to find the needle in the haystack most effectively?

Traditional knowledge about the medical use of herbal substances provides a starting point, as shown by the isolation of morphine from opium 200 years ago. Today this is achieved by collaborations between phytochemists extracting and isolating compounds from the natural sources and pharmacological/biological groups providing models monitoring biological activity. To increase effectivity, computational methods are included: virtual libraries of natural products are screened *in silico* using various pharmacophore models. These pharmacophore models can be designed by analyzing available ligands of certain receptors or the structure of the receptor itself, if respective data are available. Thus, virtual hits (a match between compound and receptor in the computer) can be generated and will then be evaluated and validated in suitable biological models. This objective was pursued e. g. for the discovery of magnolol derivatives as PPARγ agonists by the Department of Pharmacognosy in collaboration with groups from Innsbruck. In general, this interdisciplinary approach requires collaborative expertise of Pharmacognosy, Pharmaceutical Chemistry and Pharmacology.



What are the best models predicting activity in humans?

What are the best models predicting activity in humans?

In silico models are very helpful to get a first indication for activity. Nevertheless, suitable biological/pharmacological models are mandatory to identify active compounds. As a compromise between easy and fast handling, and a certain degree of complexity (and thus also validity), in most cases initially cell lines are used. The Departments of Pharmacology and Toxicology, of Pharmacognosy as well as the Division of Clinical Pharmacy and Diagnostics (Department of Pharmaceutical Chemistry) currently cover several models ranging from cancer cells to cellular models for osteoporosis, cardiovascular and metabolic disease, models for certain channels and transporters or nuclear receptors as well as the possibility to identify antimicrobial and fungicidal terpenoids. Thus, cellular models are designed to detect either certain phenotypic changes in cells or the (de)activation of specific targets (e. g. receptors). To further validate active compounds, systems with increasing complexity are used (ranging from combinations of different cell types to animal models). Modern imaging systems are available to evaluate efficacy and safety in relevant disease models as provided by the Division of Clinical Pharmacy and Diagnostics.

How to ensure compound supply?

Natural products may pose the challenge of sustainable supply. Effective compounds are sometimes produced by nature only in small amounts, complicating the isolation of larger amounts and eventually even leading to ecological problems. Chemical synthesis of natural products is not only helpful to solve this problem, but also to generate libraries of related compounds by systematic variation of their core skeleton and/or the side chains. Driven by feedback from biological assays, these natural-product-inspired, fully synthetic new compounds are optimized with regard to activity as well as bioavailability. Currently, this iterative approach is used in the Division of Drug Synthesis (Department of Pharmaceutical Chemistry), for the discovery of new, highly active anti-cancer agents. In particular, ellipticine and olivacine targeting topoisomerase II as well as the topoisomerase I poisons luotonin A and calothrixin B are subject of extensive structural modification. In collaboration with colleagues from the Vienna University of Technology, the Department of Pharmacology & Toxicology generated libraries of valerenic acid and piperine and characterized them *in vitro* and *in vivo*. This work resulted amongst others in the discovery of valerenic acid prodrugs as potential anticonvulsant compounds and piperine analogues with pronounced anxiolytic activity.

If synthesis is not efficient due to a high structural complexity of the compound, biotechnological methods may be used for a sustainable supply of the biological material containing the active ingredient, as is being currently done by a group at the Department of Pharmacognosy.

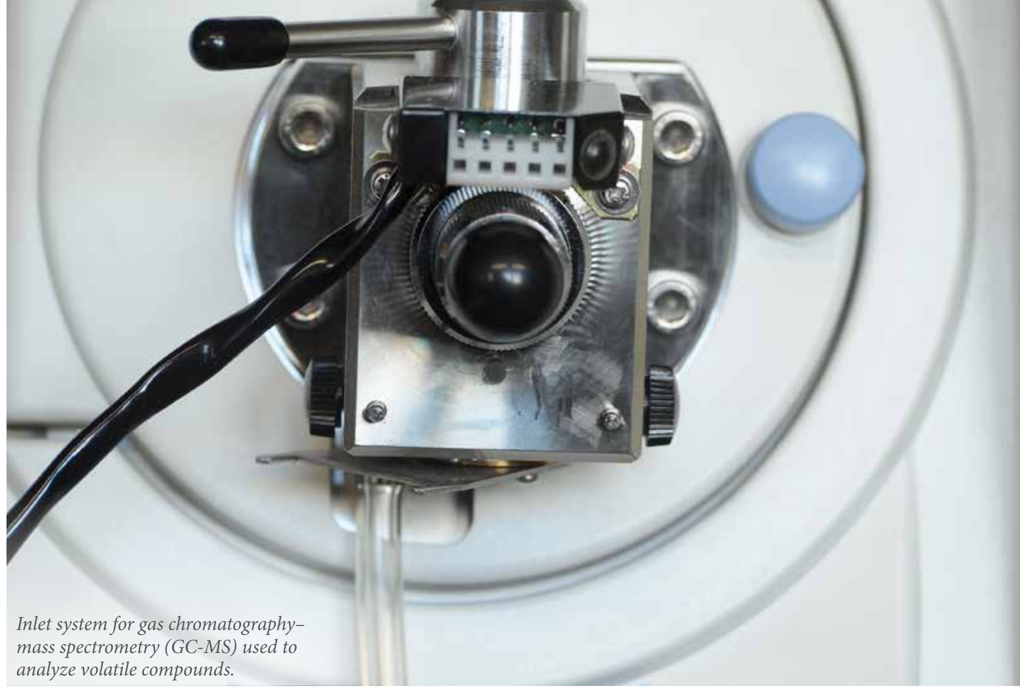
Adventitious shoots of Charybdis maritima *(L.) Speta in vitro*

How to ensure compound supply?

How to identify toxicity early?

One very important issue is the early identification of potential toxicity. First information is obtained via innovative *in silico* strategies and novel software tools to better predict the toxicological profiles of small molecules in the computer (Division of Drug Design and Medicinal Chemistry, Department of Pharmaceutical Chemistry). In addition, screens are implemented to identify so-called "anti-targets", such as the hERG »

“Biotechnological methods may be used for a sustainable supply of the biological material containing the active ingredient.”



Inlet system for gas chromatography–mass spectrometry (GC-MS) used to analyze volatile compounds.

» channel. Blocking this ion channel may result in cardiotoxicity. Thus, these screens help to identify potential cardiotoxic risks early (Department of Pharmacology & Toxicology).

How to identify the target?

Having a promising active agent in hand poses the crucial question: how does the compound act? Target identification is an extremely challenging task and is best accomplished by combining several expertises: *in silico* profiling may give hints whether known targets are addressed. More unbiased approaches are cells signaling studies and *target fishing*. The latter approaches may lead even to new targets, which is advantageous for developing new concepts for treating diseases. In part these areas are already flourishing, as seen in the many mechanistic studies performed e.g. on anticancer cyclodepsipeptides or on resveratrol. In the future, especially the area of *target fishing* will be developed with collaborative efforts of the Departments of Pharmaceutical Chemistry, of Pharmacognosy and of Pharmacology and Toxicology.

How to identify toxicity early?

What has to be done once an active and non-toxic new drug is found?

Drugs need to be delivered at the right time to the desired area. To succeed, smart delivery and targeting concepts need to be developed. To deliver drugs towards specific tissues, dosage forms are created that contain sugar-binding proteins, such as wheat germ agglutinin from *Triticum vulgare*, a dietary lectin that binds to the cell membrane of eukaryotic cells followed by uptake into the cell. These cytoadhesive and cytoinvasive characteristics are exploited to utilize this lectin as a shoehorn to shuttle conjugated drugs or drug-loaded nanoparticles into cells. Delivering drugs through the skin may have advantages in terms of reduced side effects and reduced agent inactivation. Thus, one important aim is to develop effective delivery systems through the skin, which can be monitored by state-of the art high-tech analysis such as specific infrared spectroscopic techniques. These and many more concepts of drug delivery and targeting are implemented at the Department of Pharmaceutical Technology and Biopharmaceutics.

In summary, the key research area *Drug Discovery from Nature* is highly collaborative and includes all Departments of Pharmaceutical Sciences.

Key References

_ Cragg GM, Newman DJ (2013) Natural products: a continuing source of novel drug leads. Biochim Biophys Acta. 1830:3670–95

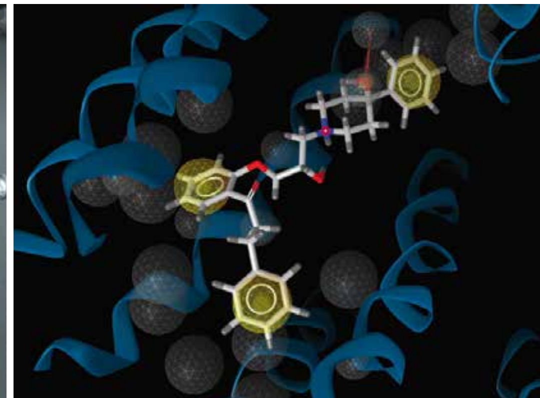
_ Fakhrudin N et al. (2010) Computer-aided discovery, validation, and mechanistic characterization of novel neolignan activators of peroxisome proliferator-activated receptor gamma. Mol Pharmacol. 77:559–66

_ Riha J et al. (2014) Resveratrol and its major sulfated conjugates are substrates of organic anion transporting polypeptides (OATPs): Impact on growth of ZR-75-1 breast cancer cells. Mol Nutr Food Res 58: 1830–42

_ Dornetshuber R, Heffeter P, Mohr T, Hazemi P, Seger C, Berger W, Lemmens-Gruber R (2013) Destruxins: fungal-derived cyclohexadepsipeptides

How to identify the target?

Microplate reader: the readout of cellular assays by quantification of luminescence or fluorescence



In silico profiling may give hints whether known targets are addressed.

with multifaceted anticancer and antiangiogenic activities. Biochem Pharmacol 86:361–77
_ Haider N, Nuß S (2012) Weinreb amidation as the cornerstone of an improved synthetic route to A-ring-modified derivatives of luotonin A. Molecules. 17:11363-78
_ Schöffmann A et al. (2014) Efficient modulation of γ-aminobutyric acid type A receptors by piperine derivatives. J Med Chem. 57:5602-19, 2014.
_ Wawrosch C, Schwaiger S, Stuppner H, Kopp B (2014) Lignan formation in hairy root cultures of Edelweiss (Leontopodium nivale ssp. alpinum (Cass.) Greuter). Fitoterapia 97:219–23
_ Kratz JM, Schuster D, Edtbauer M, Saxena P, Mair CE, Kirchebner J, Matuszczak B, Baburin I, Hering S, Rollinger JM (2014) Experimentally validated HERG pharmacophore models as cardiotoxicity prediction tools. J Chem Inf Model 54:2887–901
_ Bollmann F et al. (2014) Resveratrol post-transcriptionally regulates pro-inflammatory gene expression via regulation of KSRP RNA binding activity. Nucleic Acids Res. 42:12555–69
_ Neutsch L, Gabor F, Wirth M (2014) Glycan-targeted drug delivery for intravesical therapy: in the footsteps of uropathogenic bacteria. Ther Deliv. 5:537–53
_ Hoppel M, Reznicek G, Kählig H, Kotisch H, Resch GP, Valenta C (2015) Topical delivery of acetyl hexapeptide-8 from different emulsions: Influence of emulsion composition and internal structure. Eur J Pharm Sci. 68:27–35. «

Digitalis grandiflora

Departments of the Center of Pharmaceutical Sciences
Department of Pharmaceutical Chemistry
Thierry Langer: merian.pch.univie.ac.at/pch

Department of Pharmacognosy
Verena Dirsch: pharmakognosie.univie.ac.at

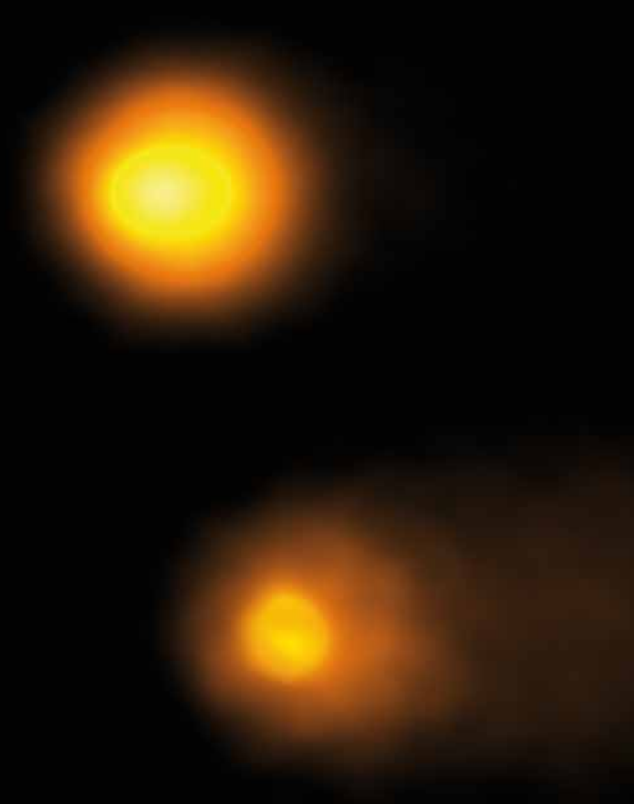
Department Pharmacology and Toxicology
Steffen Hering: www.univie.ac.at/ptox

Department of Pharmaceutical Technology and Biopharmaceutics
Helmut Viernstein: www.univie.ac.at/pharm-technologie

What has to be done once an active and non-toxic new drug is found?

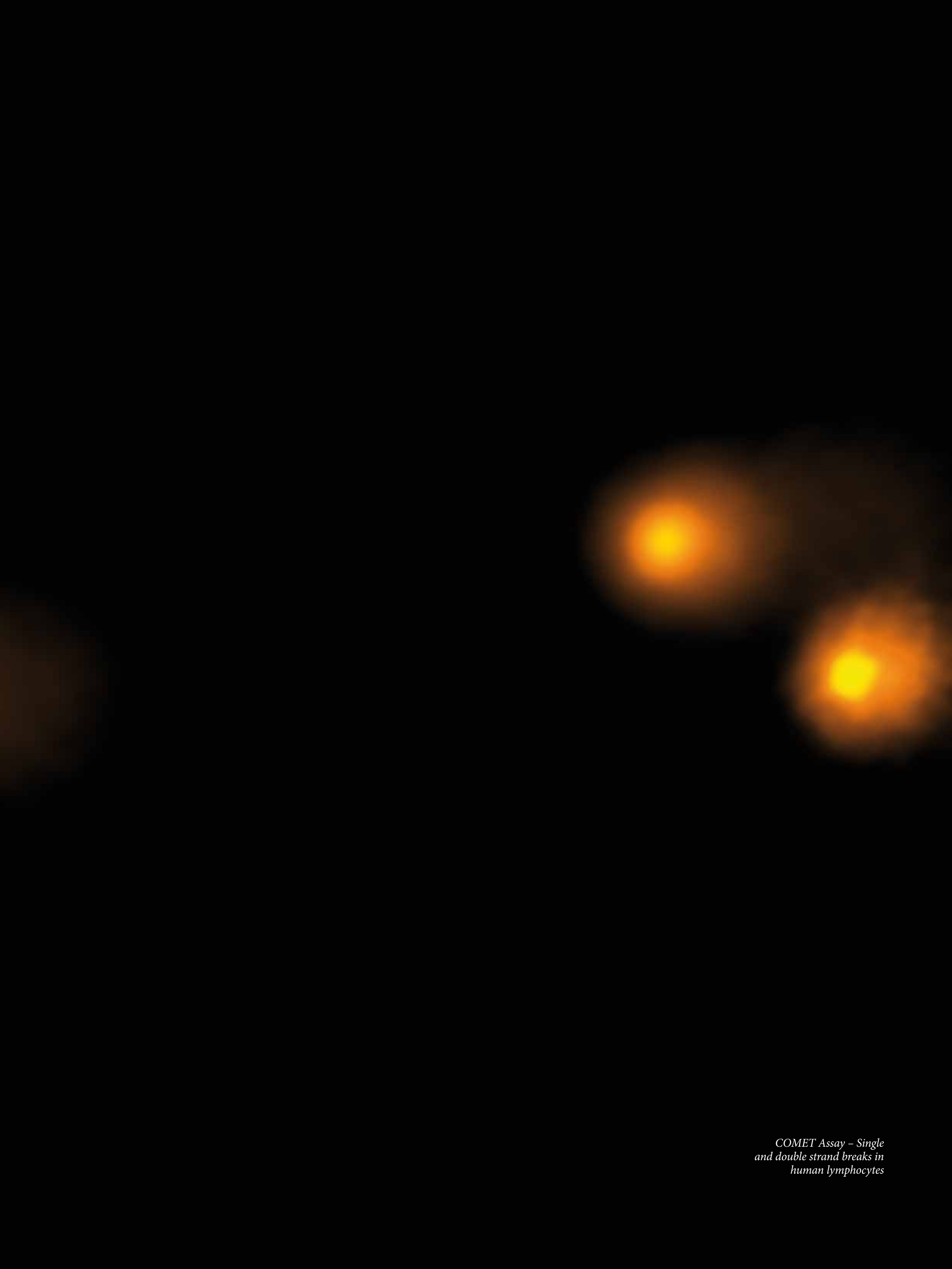
Nutritional Sciences

… study the interaction between the organism and its nutrition. The focus is on molecular and cellular research with an orientation towards systems biology. We apply genomic, transcriptional, proteomic and metabolic strategies, thereby also contributing to the development of biomarkers for predicting long-term diseases and identifying gene variants involved in the development of nutrition-related phenotypic expressions. A key research area of the Nutritional Sciences are molecular mechanisms of ageing.



Nutrition-associated molecular mechanisms of ageing

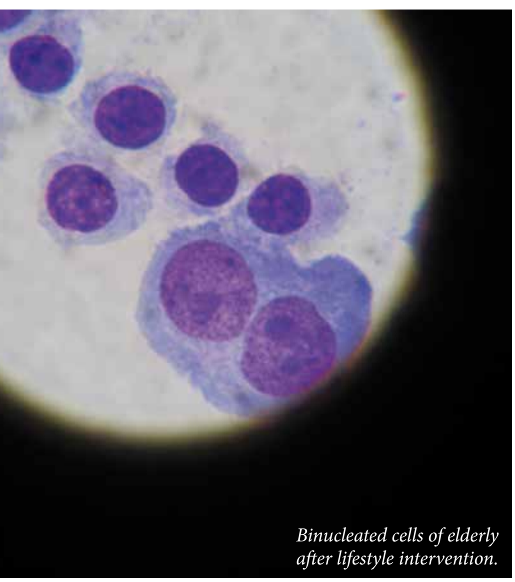
Department of Nutritional Sciences



COMET Assay – Single and double strand breaks in human lymphocytes

Nutrition and Ageing

Nutrition-associated Molecular Mechanisms of Ageing ***Although nutrition as part of a healthy lifestyle is recognised as one of the driving factors for healthy ageing, the exact mechanisms on the biochemical and molecular level are not fully understood. This research focus studies the effects of the human diet and other lifestyle factors on ageing processes, supported by animal and in vitro experiments.***



Binucleated cells of elderly after lifestyle intervention.

Ageing goes hand in hand with altered DNA repair and defence mechanisms against DNA-damage. As life expectancy is steadily increasing, the number of people changing from home-living to an institutionalized situation is also rising. This is often accompanied by malnutrition, depression and inactivity. The aim of a recent cohort study was to examine the effect of age, nutritional status and aerobic fitness on DNA-damage in adults and more than 100 institutionalized women and men (65–98 years of age) living in Vienna. Chromosomal damage (frequency of micronuclei, MN) increased with age in adults and showed, surprisingly, a levelling-off at about 60 years of age. Furthermore, a significant negative linear correlation between chromosomal damage and physical activity parameters was observed. This "plateau-like effect" of the MN frequency above the age of 60–70 years indicates a higher resistance against chromosomal damage of the "survivors" of the regular life span. The data show for the first time that aerobic fitness and an appropriate diet could protect against chromosomal damage also at high age. Interestingly, DNA damage was not a matter of ageing, as single and double strand breaks were not increased in elderly when compared to younger adults.

Summary: Appropriate lifestyle protects against chromosomal damage at high age.

Lifestyle activities and Ageing – Lessons learned from a long-lasting lifestyle intervention study

A long-term intervention study over a period of 18 months dealt with the impact of a dietary supplementation in combination with progressive resistance exercise on the molecular mechanisms involved in the development of sarcopenia and its prevention. More than 100 institutionalized elderly in their 7th to 10th decade of life were examined. The average age was 83 years, which made the study internationally unique. Blood, Urine, DNA, RNA as well as muscle biopsies of muscular tissue of study participants have been collected. First data show improvements in functional parameters (e.g. chair rise and 6-min walking test) concomitant with effects on the Transforming growth factor-ß (TGF-β)superfamily (reduced expression of TGF- receptor (βRI) levels in leukocytes). The TGF-β superfamily has been shown to play an important role in a

Is ageing linked to increased DNA damage?

Impact of active lifestyle on ageing

wide range of physiological as well as pathological processes including ageing, immune modulation, atherosclerosis and cancer development. Furthermore, small non-coding RNAs such as microRNAs (miRNAs) are of interest because they can affect gene expression and are involved in regulating the ageing process on the level of organism lifespan, tissue ageing or cellular senescence. DNA damage was decreased in cells exposed to H_2O_2 after the intervention, and chromosomal damage was reduced by more than 20%. At the same time antioxidant enzyme activities increased significantly. Nutritional status was improved and particularly the increase in vitamin B12 status was negatively correlated with decreased chromosomal damage after intervention.

Summary: Lifestyle intervention was effective on the molecular level in highly aged institutionalized elderly.

Hyperbilirubinaemia & Ageing – A new link

Very recent data demonstrate that mildly elevated serum bilirubin levels (hyperbilirubinaemia) are strongly associated with a lower prevalence of all-cause mortality as well as chronic diseases, particularly Cardiovascular diseases (CVDs), cancer and type 2 diabetes.

Gilbert syndrome (GS) is a benign condition characterized by moderately elevated unconjugated bilirubin levels. Bilirubin conjugation and excretion into the bile is decreased, thereby increasing the circulating unconjugated bilirubin concentration. This syndrome affects up to 10 % of the general population.

In a cross sectional human study as well as a hyperbilirubinaemic animal model (Gunn rat), we investigated whether the condition is linked to biomarkers of lipid metabolism and adiposity or to novel lipid associated cardiovascular disease (CVD) risk markers: all of them increased within the ageing process.

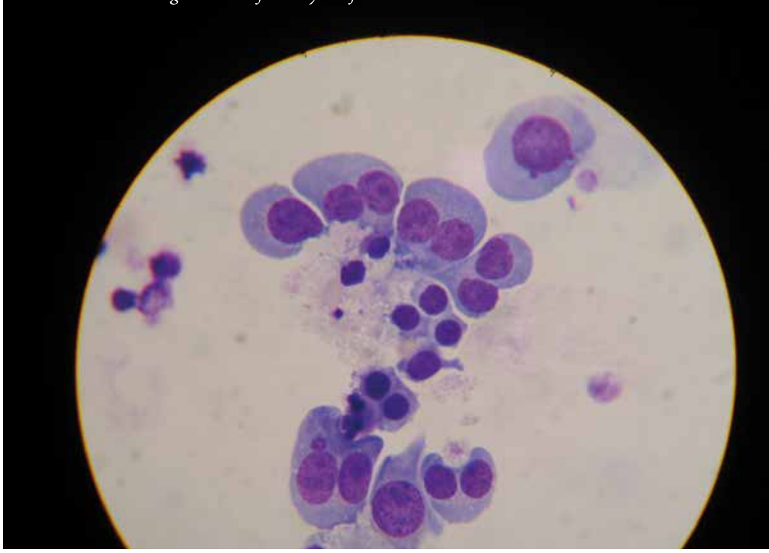
Interestingly, we found that GS subjects had a significantly improved lipid profile with lower LDL cholesterol, triglycerides and a lower inflammatory state. When control and GS groups were subdivided into younger and older cohorts, older GS subjects demonstrated reduced lipid variables compared to matched controls. These data were strongly supported by lipid analyses in the rodent model. These novel and surprising findings indicate that elevated circulating bilirubin, particularly the benign condition of Gilbert's Syndrome, is associated with reduced concentrations of lipid and inflammation biomarkers and a trend to decreased body mass index (BMI). Furthermore we demonstrated that older subjects, who are generally at greater disease risk, are likely to benefit more from a mild congenital hyperbilirubinemia.

Summary: Mildly elevated bilirubin plasma levels protects against age-related diseases.

Type 2 Diabetes and Ageing

Type 2 Diabetes, one of the most common chronic diseases and a growing health care problem worldwide, is mainly related to ageing. »

Various parameters to investigate chromosomal damage in cells of elderly subjects.



Resistance exercise session with tera bands

» It is well recognized that diabetes is linked to increased risk of micro- and macro-vascular complications in the ageing population. Our aim was to study the effects of a healthy, vegetable-based diet in a parallel, randomized, intervention-study in elderly individuals between 60 and 80 years of age, focusing on the cellular and molecular level. Cytogenetic damage in a novel cellular test with buccal cells at baseline was significantly higher in participants with diabetes mellitus compared to healthy individuals. Further analysis of baseline data revealed significantly higher chromosomal damage in participants with higher waist circumference, fasting plasma glucose, glycated hemoglobin and cardiovascular disease risk. Diabetic individuals of the intervention group (vegetable-based intervention) showed significantly reduced HbA1c and DNA strand breaks. This study clearly shows the strong effect of a healthy diet on physiological and molecular markers of aged type 2 diabetics.

Summary: A healthy diet improves type 2 diabetes conditions and reduces DNA damage

Carbohydrate metabolism and ageing

The incidence of obesity and metabolic disorders such as type 2 diabetes in the ageing society has dramatically increased. Little is known about the mechanism of dietary fructose in the insulin signaling pathway (IIS) and its effect on gene expression patterns in glucose and lipid metabolism. We found that fructose feeding transcriptionally activated *sir-2.1* overexpression in *C. elegans*, which activates target genes normally regulated/inhibited by insulin signaling through the insulin receptor. Fructose up-regulated stress-responsive genes such as superoxide dismutase and induced gluconeogenesis by overexpression of *pyc-1* (the coding gene for pyruvate carboxylase) and pyruvate carboxykinase – *pck-1* (the main control point for the regulation of gluconeogenesis). Activation of gluconeogenic genes by binding of DAF16/FOXO to their promoters was found to be a fructose-induced and *sir-2.1*-mediated process. Fructose feeding was accompanied with alterations in IIS by high abundances of insulin receptor mRNA attributed to a DAF-16/FOXO feedback regulated process. Free fructose in mixtures with glucose activated acetyl-CoA carboxylase – *pod-2* gene expression, the first step in fatty acid biosynthesis. In addition, *lpd-2*, which is part of a conserved pathway regulating lipogenesis, was transcriptionally induced by fructose. Our findings show that fructose feeding alters post-receptor insulin signaling of DAF-16/FOXO via a *sir-2.1*-mediated process and interferes with glucose homeostasis and lipid metabolism.

Outlook

We are living in an ageing society, which makes a closer look at biochemical and molecular aspects

Is there a link between hyperbilirubinaemia and ageing?

Concerted training with elderly is much more effective than sole workouts

> *"Working with elderly people in clinical studies is sometimes challenging, but outcomes and the translation from scientific results to society is fascinating."*
>
> ***Marlies Wallner, former PhD student***

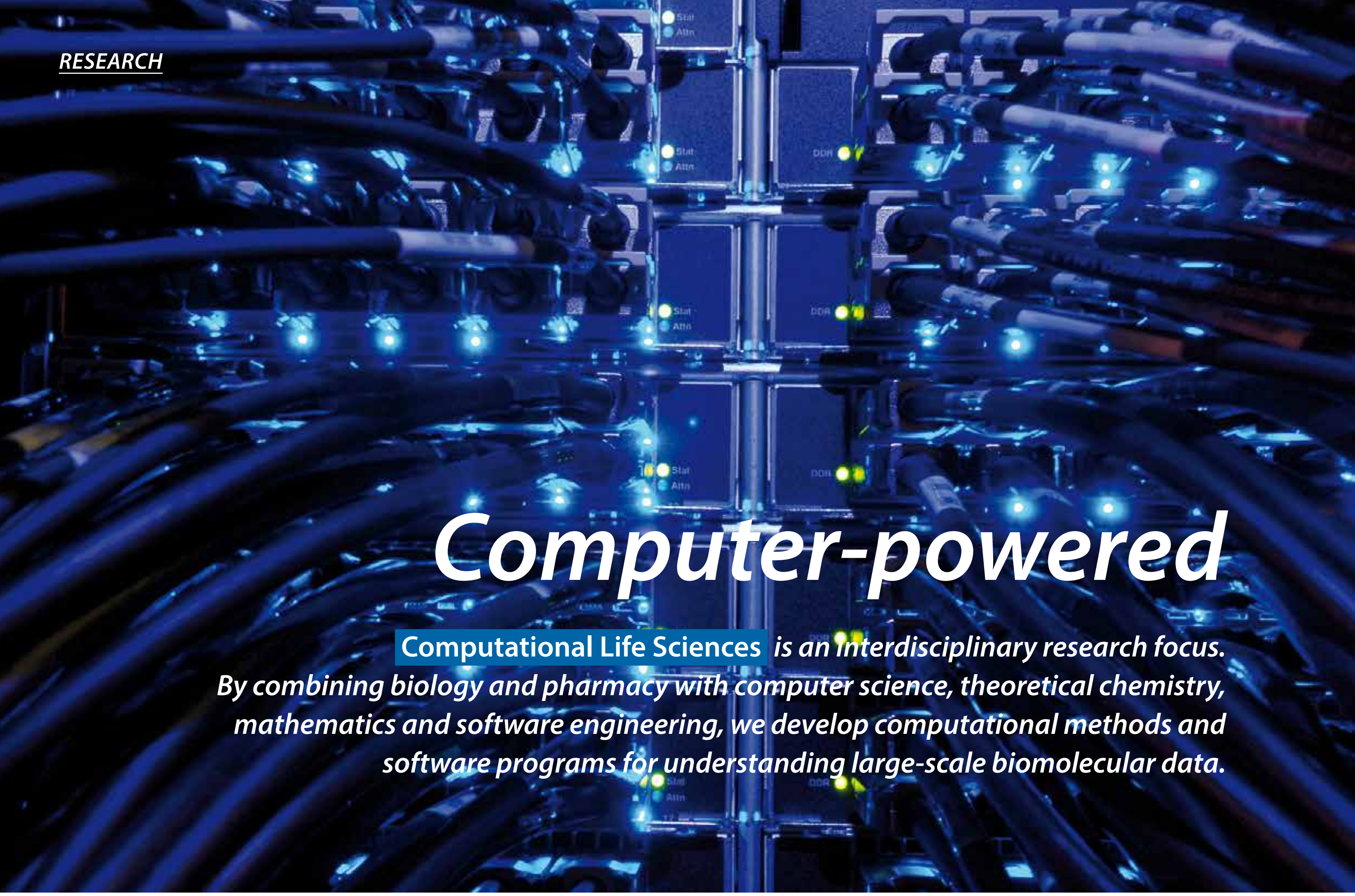
of age-related diseases so important. The aim is to better understand the ageing process itself and its triggers and ultimately to develop disease-prevention strategies. These links will further be explored by using human, animal as well as *in vitro* models.

Key References

_ Franzke B, et al. (2014): The influence of age and aerobic fitness on chromosomal damage in Austrian institutionalised elderly. Mutagenesis 29:441–445.
_ Franzke B, Halper B, Hofmann M, Oesen S, Jandrasitz W, Baierl A, Tosevska A, Strasser EM, Wessner B, Wagner KH (2015); Vienna Active Ageing Study Group. The impact of six months strength training, nutritional supplementation or cognitive training on DNA damage in institutionalised elderly. Mutagenesis 3o:147–153
_ Halper B, Hofmann M, Oesen S, Franzke B, Vidotto C, Wagner KH, Wessner B (2015) Influence of age and physical fitness on miRNA-21, TGF-β and its receptors in leukocytes of healthy women. Ex. Immunolog. Rev. 21:133–142
_ Müllner E, Brath H, Nersesyan A, Nitz M, Petschnig A, Wallner M, Knasmüller S, Wagner KH. (2013): Nuclear anomalies in exfoliated buccal cells in healthy and diabetic individuals and the impact of a dietary intervention. Mutagenesis 29:1–6.
_ Müllner E, et al. (2013): Vegetables and PUFA-rich plant oil reduce DNA strand breaks in individuals with type 2 diabetes. Mol Nutr Food Res. 57(2):328–38.
_ Ortbauer M, Lassi M, Aichert M, Mairhofer E, Zöchmeister C, König J (2014): Fructose induces sir-2.1 overexpression in C. elegans and alters downstream insulin signaling and glucose homeostasis. Genes & Nutrition (submitted).
_ Wallner M, Antl N, Rittmannsberger B, Schreidl S, Najafi K, Bulmer AC, Wagner KH (2013): Anti-genotoxic potential of bilirubin in vivo: Damage to DNA in hyperbilirubinemic human and animal models. Cancer Prev. Res. 6(10):1056–63.
_ Wallner M, Marculescu R, Doberer D, Wolzt M, Wagner O, Vitek L, Bulmer AC, Wagner KH. (2013): Protection from age-related increase in lipid biomarkers and inflammation contributes to cardiovascular protection in Gilbert's syndrome. Clin Sci (Lond.) 125(5):257–64. «

Can type 2 diabetes be improved by dietary intervention?

Department of Nutritional Sciences
Jürgen König, Karl-Heinz Wagner: nutrition.univie.ac.at



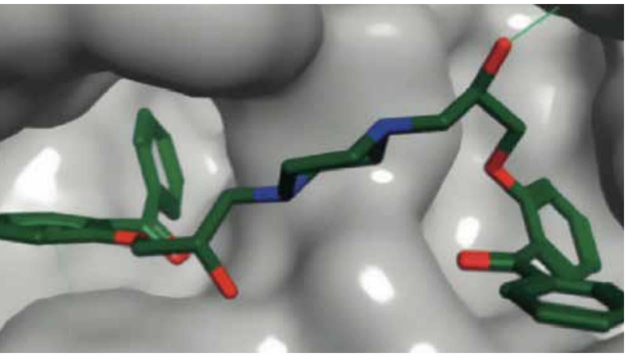
Computer-powered

***Computational Life Sciences** is an interdisciplinary research focus. By combining biology and pharmacy with computer science, theoretical chemistry, mathematics and software engineering, we develop computational methods and software programs for understanding large-scale biomolecular data.*

Rational design of new drug candidates?

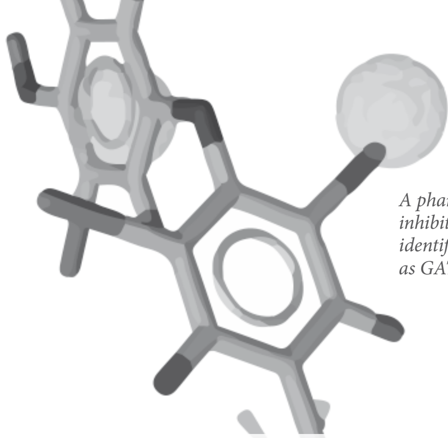
The increased efficiency of experimental methods has led to an unseen "information gain" in life sciences. Modern high-throughput molecular and imaging techniques generate up to Terabytes of raw data in each experiment. We address the challenge to interconnect and interpret these data by developing novel and sophisticated computational and mathematical solutions.

Fit of a benzophenone type inhibitor into the binding site of the drug efflux pump P-glycoprotein



Bits, bytes and the molecules of life
Molecular methods are still revolutionizing life sciences and enable us to study the molecular principles of life. This would be impossible without the massive support of information technology. We develop and cross-link the new discipline of computational life sciences.

Small molecules and proteins: pharmacoinformatics
The discovery and development of a new drug is a complex and time- and resource-intensive process, which heavily relies on computational techniques. These range from the discovery and validation of new targets, the identification and optimization of their ligands, up to the prediction of bioavailability and toxicity in living organisms. The increasing number of available protein structures, together with sophisticated techniques, allows us to analyze and predict the molecular basis of drug-protein interactions.



A pharmacophore model for tiagabine-type inhibitors of the GABA-transporter GAT1 identifies the tyroid hormone liotyronine as GAT1 inhibitor.

How to integrate data from heteroge-neous sources?

This is key for a rational design of new drug candidates and the understanding of their selectivity and toxicity on a whole organism level.
The researchers at the Division of Drug Design and Medicinal Chemistry develop tools and methods for predicting ligand-protein interactions, for *in silico* screening of large compound libraries, predicting of toxicity, as well as for decision support in drug discovery programs.

Data integration is key for understanding

The large number of publicly available databases exemplifies the huge information gain in life sciences. Such data, however, are provided in different formats using different standards and ontologies. This renders queries across multiple data sources time consuming and requires a lot of manual intervention. Semantic, schema-free integration of multiple data sources is one of the approaches pursued by the pharmacoinformatics Research Group to approach this problem. A first realization is exemplified in the Open PHACTS Discovery Platform, an open access platform integrating data from different domains (compound – target – pathway – disease). This has been developed by a large consortium coordinated by the pharmacoinformatics research group.

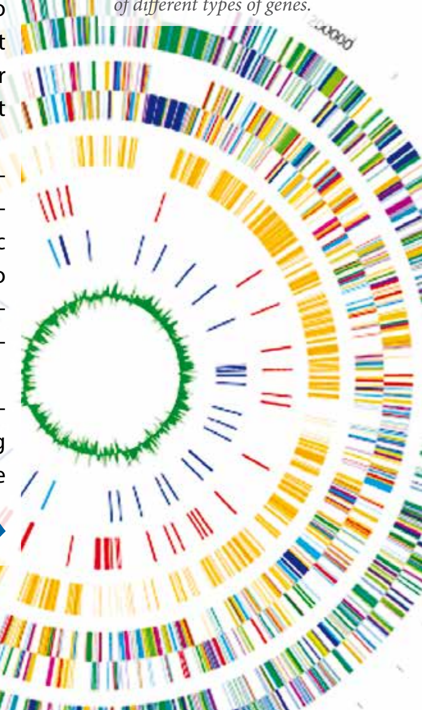
In silico genomics

Life on Earth has evolved for several billion years. Living organisms inhabit virtually every environment, surviving and thriving in extremes of heat, cold, radiation, pressure, salt, acidity, and darkness. Often in these environments, only “simple” microorganisms are found and the only nutrients come from inorganic matter. The diversity and range of environmental adaptations indicate that even tiny microbes long ago “solved” many problems for which scientists and engineers are still actively seeking solutions.
These secrets are enclosed in the genomes, which encode the construction plans of cells and organisms. The first complete bacterial genome was deciphered in 1995. Since then the number of complete genomes sequenced is growing exponentially. Only powerful computers and sophisticated bioinformatics software enable us to investigate these massive data.
CUBE, the Division of Computational Systems Biology, is involved in many genome-sequencing projects. We also create new software for the annotation and analysis of genome sequences and comparative genomics.

What are the secrets of mul-tifaceted life?

Microbial molecular interactions

Annoying for most of us, but dangerous or even life threatening for particular persons: infections by pathogenic bacteria are never welcome. However, pathogenic lifestyles in nature are no bad habit – they have developed in evolution. It is simply the balance of the complex molecular interplay between microorganisms and us that determines the role of a species we encounter.
The CUBE team investigates molecular mechanisms of host-microbial interactions. This research is motivated by the tremendous public health impact of microbial infections, but also by the growing knowledge about beneficial microbes around us and in our personal microbiomes.
The main goal of our work is to develop computational approaches to predict interacting molecules directly in genome sequences. These include adhesins (making cellular contacts), inter-cell secretion machineries and »



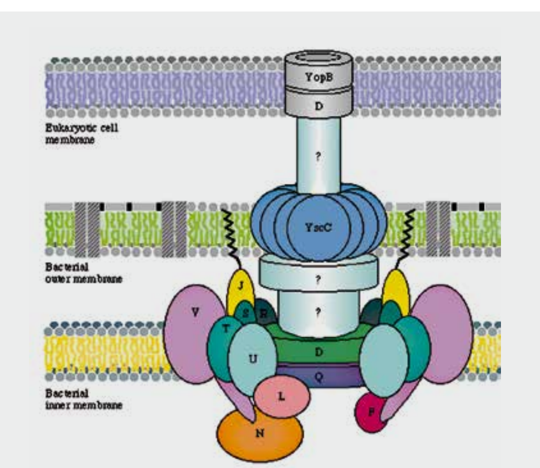
Microbial genome: Even the smallest microbial genomes consist of many thousands of base pairs. This circular representation of a chlamydial chromosome indicates the locations of different types of genes.

What makes a pathogen pathogenic?

» secreted molecules. Comparative genomics studies help us to discover novel genes and to predict molecular principles involved in microbial molecular interactions.

Modeling in Systems Biology

All of us start early in modeling – listening to fairytales told by parents and grandparents. A model, just as a fairytale, is a simplified abstraction of reality. It focuses on the principal elements involved and how these work together, piling up to what we call world. To become a proper model in Systems Biology, a story needs to be formalized into mathematical or computational terms. This enables transcending qualitative statements to quantitative ones and facilitates the validation between model and evidence. Choosing a particularly suitable modeling approach crucially involves a lot of crosstalk between scientists from the wet- and dry-labs, the typical cycle between hypothesis, model and experiment. This is the same strategy the modelers A. Hodgkin and A. Huxley applied back in the 1960s, when they deciphered the fundamental mechanism of nerval communication: the initiation and propagation of the action potential.



Type III secretion system: The Type III secretion system is one of the typical molecular pathogenicity factors. It facilitates the secretion of effector proteins from the bacterial cell directly into host cells.

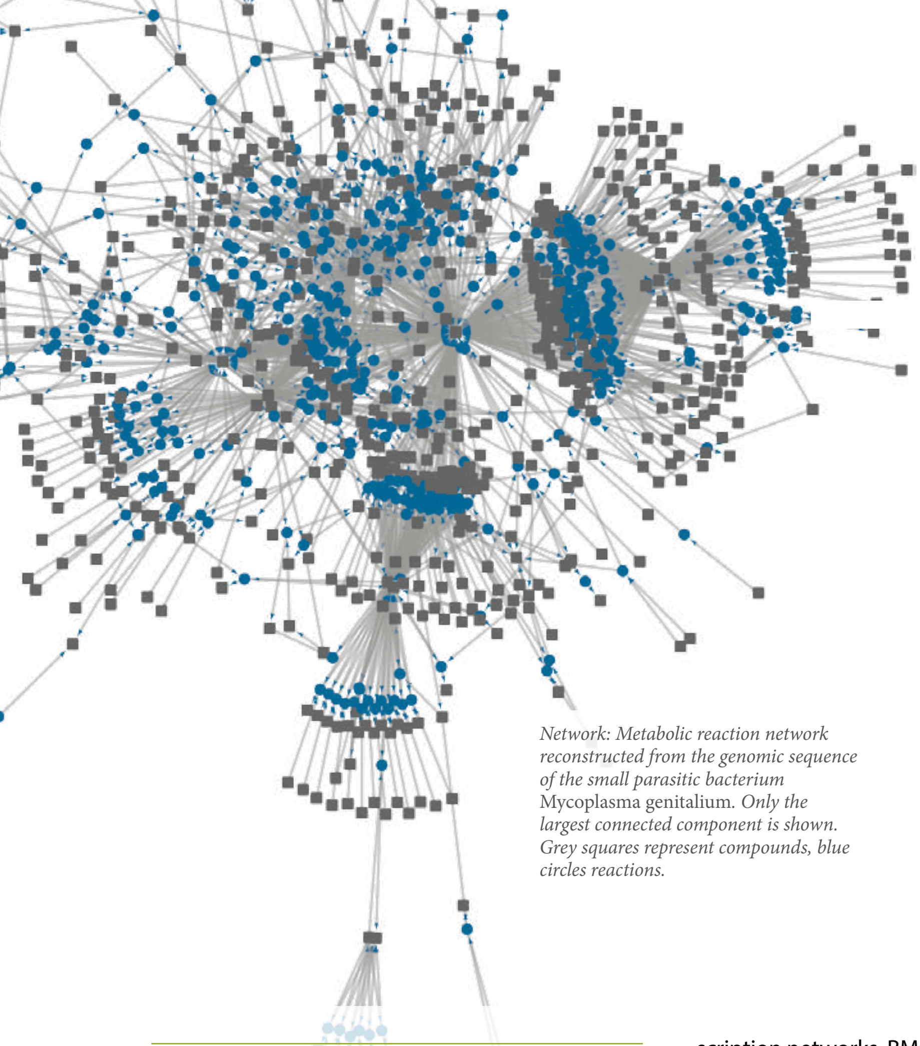
The research question and available data determine if one designs an ordinary differential equation model to cover molecular processes or rather applies network analysis to pinpoint organizational properties of ecological communities. Modeling is scale-free. Also, modeling is a fundamental cornerstone for Systems Biology because it links experiment and interpretation in today's high-throughput biological and biomedical research.

Networking Biology

With the advent of economic high-throughput methods for the system-wide study of molecules, genes and communities, science is confronted not only with enormously big data, but also with a previously unknown degree of complexity in the data. The goal is to integrate the molecular parts list with their interactions in order to catch up with reality. Clearly, interactions between biological entities play a key role in regulation, adaptation and productivity at the micro- and macro-scale. Organizing these interactions system-wide results in a complicated network of dependencies between the players.
Interestingly, recurrent topological features of such biological networks have been identified and explained by evolutionary processes. One example is the pronounced robustness and resilience of biological communities, from transcription factors to microbes, caused by the particular organization of their interactions.
The challenge of interpreting high-throughput data requires computational methods and power. Network analysis facilitates the understanding by prescinding from details and focusing on the community level. At CUBE we study interaction organization and design principles of biological networks across scales, particularly cellular patterns and microbial communities.

The significance of computational life sciences will further increase as the field moves towards system-wide combination of distinct data types for better understanding biological and biomedical processes.

Getting from genes to ecosystems?



Network: Metabolic reaction network reconstructed from the genomic sequence of the small parasitic bacterium Mycoplasma genitalium. Only the largest connected component is shown. Grey squares represent compounds, blue circles reactions.

How can we interpret the massive amount of high-throughput data?

Key References

_ Azzaoui K et al. (2013). Scientific competency questions as basis for the development of a semantically enriched Open Pharmacological Space. Drug Discov Today 18:843–52

_ Berry D, Widder S (2014). Deciphering microbial interactions and detecting keystone species with co-occurrence networks. Front Microbiol.

_ Chapman JA et al. (2010). The dynamic genome of Hydra. Nature 464, 592–596.

_ Heinz E et al. (2012). The Genome of the Obligate Intracellular Parasite Trachipleistophora hominis: New Insights into Microsporidian Genome Dynamics and Reductive Evolution.

_ PLOS Pathog. e1002979.

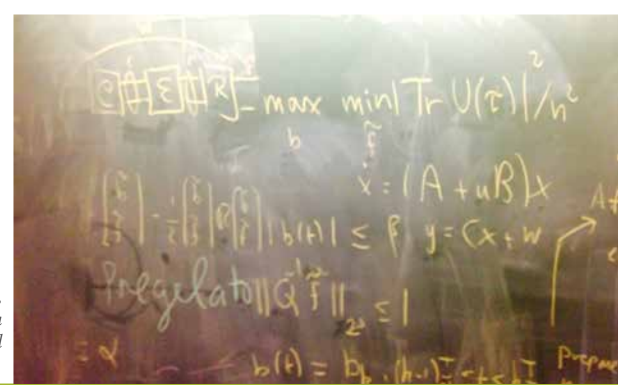
_ Klepsch F et al. (2014). Ligand and Structure-Based Classification Models for Prediction of P-Glycoprotein Inhibitors. J Chem Inf Model 54:218–229

_ Maixner F et al. (2014). Metagenomic Analysis Reveals Presence of Treponema denticola in a Tissue Biopsy of the Iceman. PLOS ONE e99994.

_ Richter L et al. (2012). Diazepam-bound GABAA receptor models identify new benzodiazepine binding-site ligands. Nature Chem Biol 8, 455–464.

_ Widder S et al. (2012), Evolvability of feed-forward loop architecture biases its abundance in transcription networks. BMC Syst Biol, 6:7.

_ Widder S et al. (2014). Fluvial network organization imprints on microbial co-occurrence networks. Proc Natl Acad Sci U S A.; 111(35):12799-804. «



Brainstorming, visualized on a blackboard

Departments and Divisions

Department of Pharmaceutical Chemistry

Division of Drug Design & Medicinal Chemistry

Gerhard Ecker: pharminfo.univie.ac.at

Thierry Langer: merian.pch.univie.ac.at

Department of Microbiology & Ecosystem Science

Division of Computational Systems Biology

Thomas Rattei, Stefanie Widder: cube.univie.ac.at

Botanical Garden

Rondeletia odorata, *discovered and described by Nikolaus Joseph von Jacquin, flowers in the Coffee-family research collection.*

At the time of its foundation in 1754 the site of the Botanical Garden (Hortus Botanicus Vindobonensis) at the Rennweg was situated at the outskirts of Vienna. Today it is surrounded by the densely populated third district of Vienna. The initial garden covered an area of 1 ha, was outlined in baroque style, mainly contained plants of pharmaceutical relevance, and mainly served as a tool for educating future physicians and botanists at the university level. Today the Botanical Garden harbors ca. 11,500 plant species on an area of nearly 8 ha. Mostly laid out in a 19th century landscape garden, plants are displayed in systematic or plant-geographical contexts. Smaller zones in the garden are devoted to specific topics (e. g. useful plants, vegetation types and flora of Austria, plant morphology, genetics and evolution). Through its design and management, the garden also provides small patches of (semi-)natural environments for native plants and animals.

Fields of activities at the Botanical Garden today are academic research and teaching, conservation ex-situ and in-situ, legal frameworks and practice of plant-exchange, networking and sharing of expertise nationally and internationally (teaching, education, horticulture, conservation), education of gardeners for scientific collections, transfer of horticultural knowledge, public outreach and science education (exhibitions, information, guided tours, education programs …), and management of the open area as a recreation area for the public. The Botanical Garden has strong links with research and teaching at the Department of Botany and Biodiversity Research at the location Rennweg, but also with other organization units at the University of Vienna, especially in the Faculty of Life Sciences. Annually, up to 10,000 parts of 400 different species are provided for lectures and courses in biology.

An important vision and mission of the Botanical Garden is to strengthen its scientific and teaching dimensions in- and outside of the academic context and to link these activities with a further improvement of its public outreach. Building activities, structural and thematic changes of collections and displays, and scientific programs are planned for the future to realize elements of this vision. This will secure and extend its role as a center of botanical research, documentation, and information and as a place of direct experience concerning plants, nature and biodiversity. «

Research goes public: traits of pollination and dispersal ecology are shown in displays close to the main alley of the garden – with the alpine garden in the background.

Plant-animal interactions are often seen at the Botanical Garden – a starting point for scientific studies, conservation actions and creation of public awareness on environmental issues.

Core Facility Botanical Garden
Michael Kiehn: www.botanik.univie.ac.at/hbv
Mechelgasse / Praetoriusgasse, 1030 Vienna

Cell Imaging and Ultrastructure Research

Microscopy and imaging are indispensable for progress in Life Sciences. Though cells have been known for 350 years we still keep detecting new features, and our understanding of how cells function is far from complete. Keeping pace with our aim to understand biological structures at all levels of resolution requires advanced techniques of light and electron microscopy. To concentrate both sophisticated microscopes and expertise, our Core Facility Cell Imaging and Ultrastructure Research (CIUS) was founded.

We support research groups of the faculty, the university and other institutions in their investigations, and we train students in becoming familiar with state-of-the-art microscope techniques. Research conducted by our own group ensures close ties to the scientific community and inspiration for methodological progress.

For Live Cell Imaging, we apply ultraviolet, video-enhanced contrast- and confocal fluorescence microscopy. This enables us to observe structures in living cells that are below the resolution of conventional light microscopes and that have so far been visible only in fixed cells in the electron microscope.

Further analysis of ultrastructure and chemical composition is possible by Electron Microscopy (EM). We apply both scanning EM for surface visualization and transmission EM for visualizing structures within cells in ultrathin sections. Besides studying fine structures, we investigate the chemical composition of the samples by X-ray elemental analysis (EDX) and energy loss spectroscopy. Best possible sample preparation is a prerequisite for any of these applications.

Correlative Microscopy of biological structures by both live cell imaging and EM have proven to be a source of vital information about cellular dynamics. We develop protocols and applications, which comprise the immediate freezing of the living state and subsequent steps for cryo-processing of the samples for EM.

Documentation of biological objects at all levels of magnification is a prerequisite for teaching and for disseminating our scientific results to the general public. Our educational films about our techniques and research topics take advantage of experience and equipment of low magnification microscopy and macrography.

Our Research is focused on the organization of biological samples at various levels of complexity comprising tissues, cells, their organelles and their extracellular products. We analyze their dynamic properties, and we study their reactions to various physiological and ecological conditions.

Our Teaching Activities include lectures, seminars, internships and excursions related to our research topics and our techniques, and we supervise Bachelor, Master and PhD theses. We advise students and guests using hands-on training and international training courses on best possible application of our techniques for their research.

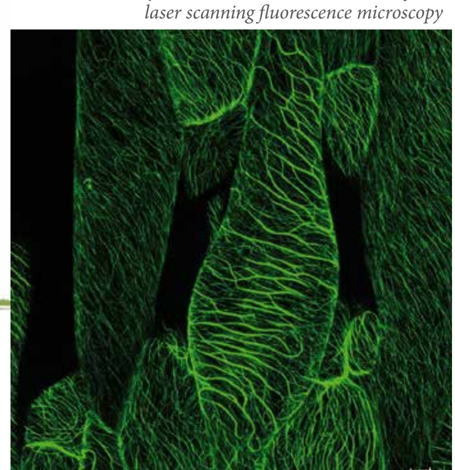
A detailed list of our instrumentation can be found on our website: cius.univie.ac.at «

Cells of protonemata of the moss Physcomitrella patens, *light microscope: bright field*

Head of a sciarid fly (Scanning EM)

Fly sitting on a leaf of Drosera rotundifolia *(Sundew), an insectivorous plant*

Microtubules in cells of Arabidopsis thaliana *labelled by Green Fluorescent Protein, Confocal laser scanning fluorescence microscopy*



Core Facility Cell Imaging & Ultrastructure Research
Irene Lichtscheidl: cius.univie.ac.at
Althanstraße 14, 1090 Vienna

EDX-Spectrum of Thlaspi caerulescens, *a hyperaccumulator plant for zinc*

Konrad-Lorenz-Research station for Behavior and Cognition

Today the Konrad Lorenz Forschungsstelle (KLF for Behavior and Cognition) is a small but internationally well renowned field station, mainly for research into the social complexity and cognition of free-living and aviary birds.

History of the KLF

When Konrad Lorenz (Nobel Laureate in 1973) retired from his directorship at the German Max Planck Institute at Seewiesen, he returned to Austria and found a great place in the Grünau area where he could continue research with his semi-tame flock of Greylag geese, notably his longitudinal (i.e. over generations) study on social dynamics. Mediated by Otto König, Lorenz was invited to come by HM Ernst August, Duke of Cumberland. Buildings were adapted, ponds created and soon Lorenz and co-workers started to move the geese from Seewiesen to Grünau. The first years were still funded by the German Max Planck Society. The Austrian Academy of Sciences took over in 1980.

After Konrad Lorenz died in February 1989, the Konrad Lorenz Research Station (KLF) continued to operate from July 1990 under the scientific directorship of John Dittami (1949–2014), the local directorship of Kurt Kotrschal, assisted by Josef Hemetsberger. Since 2012 the KLF is "Core Facility for Behavior and Cognition" of the University of Vienna. Co-directors are now Thomas Bugnyar, Eva Millesi and Josef Hemetsberger. Basic funding is mainly provided from the University of Vienna and from the state of Upper Austria, as well as from other federal and private sources, including competitive grant money for research, notably from the Austrian Science Fund (FWF).

Research at the KLF

Our main research models are greylag geese (*Anser anser*), ravens (*Corvus corax*), crows (*Corvus corone*), jackdaws (*Corvus monedula*) and bald ibises (*Geronticus eremita*). Our research questions are fundamentally directed at social mechanisms and how social complexity is linked with the evolution of intelligence. For example, we ask how individuals live together in social groups, what costs and benefits are involved, how personality, individual stress management, steroid hormones (determined from faeces) and social careers are related. Out of this, research on dogs and wolves developed in Vienna and Ernstbrunn (www.wolfscience.at, mensch-tier-beziehung.univie.ac.at)

KLF researchers maintain collaborations with a number of other research institutions in Austria and abroad. These include the Department of Cognitive Biology and its research station Haidlhof (University of Vienna), Institutes of the University of Veterinary Medicine Vienna, Schönbrunn Zoo, (Vienna). «

The brains of Common ravens (Corvus corax) *match the relative brain sizes of chimpanzees. Scientists test how clever they are.*

Northern Bald Ibis is a critically endangered bird. Since 1997 the KLF is maintaining a free-flying, self-sustaining colony for basic research

The free-roaming flock of Greylag geese, a direct legacy of Konrad Lorenz, is still an important model for research into the social complexity of birds.

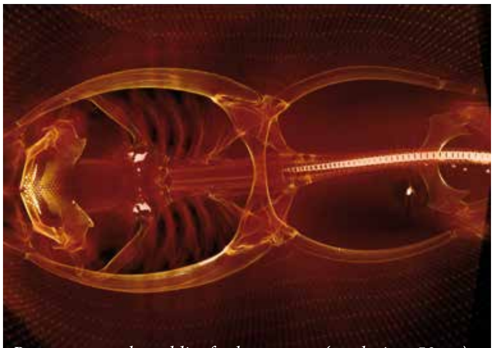
Core Facility Konrad Lorenz Forschungsstelle
Kurt Kotrschal: klf.univie.ac.at
Fischerau 11, A–4645 Grünau

Vienna Micro-CT Lab

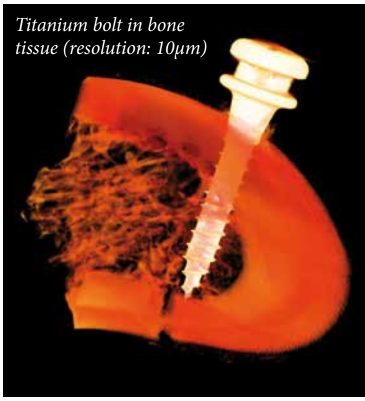
Micro-Computed Tomography

The Vienna Micro-CT Lab (www.micro-ct.at) is operative since 2009. It is specialised in the high-resolution digitalisation (in the micro-meter range) of biological, medical, and technical objects. Because many studies today rely on the acquisition of 3D data from objects for morphological analyses throughout their volume (see for instance, Virtual Anthropology), computed tomographic (CT) methods are of great importance to provide such data. In contrast to medical CTs (operating in the range of ~500–200 µm), our µCT starts at 80 µm as lowest resolution but can go down as far as 3 µm, depending on the size of the object. Our Viscom X8060 II was constructed according to our specific needs. In contrast to conventional micro-computed tomographs, it can receive quite large objects such as human skulls or even complete thighbones in its recording chamber. We can also perform "spiral scans", which means that long objects such as bones or violins can be scanned without interruption, thus avoiding artefacts. The machine features a state-of-the-art digital flat panel detector (3197 x 2239 pixel) and a transmission microfocus X-ray tube delivering up to 190 kV voltage and 80 W power. This enables penetrating even very dense objects such as fossils, titanium implants, or geological drilling cores.

We usually scan skeletal and dental parts of recent humans and primates as well as hominin fossils from all over the world. As a Core Facility of the Faculty of Life Science, we also collaborate with other units, scanning animals and their skeletal parts, plants, or paleontological material. Our partners from the Dental Clinic and the Pathophysiological Centre at Vienna Medical University use the machine for their purposes. Because it is one of a few devices in Central Europe that can handle large and dense objects, we also receive many inquiries from Austrian (e. g. Natural History Museum Vienna, the Geology Department, University Clinic Innsbruck) and international research institutions (e. g. Croatian Natural History Museum, Max Planck Institute Leipzig, Penn State University, University of Kansas). The lab also offers a student training course to teach the handling of the machine. The latest development is a project funded by the Austrian National Bank to investigate the current status and geometry of precious violins such as those from Stradivari or Stainer. Clearly, 3D high-resolution data will gain even more importance in the future in many other areas. «



Potamotrygon leopoldi – freshwater ray (resolution: 50µm)



Titanium bolt in bone tissue (resolution: 10µm)

Fossil skull from Israel (Qafzeh 11), ~ 100,000 years old (resolution: 70µm)

Core Facility Micro-Computed Tomography
Gerhard W. Weber: www.micro-ct.at
Althanstraße 12–14, 1090 Vienna

SILVER – Stable Isotope Laboratory Vienna for Environmental Research

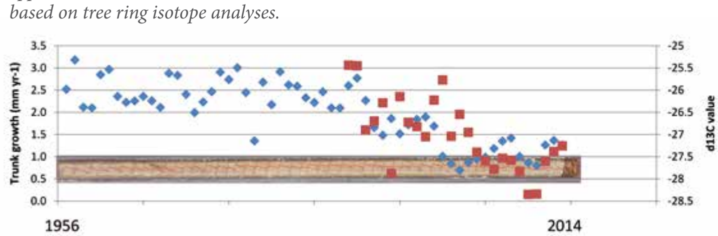
Isotopes of an element differ in their number of neutrons and therefore in mass, but exhibit the same chemical behavior. Almost all of the light chemical elements (hydrogen, carbon, nitrogen, oxygen, sulfur) that constitute living organisms are found in more than one isotopic form, with most of these isotopes being stable, i.e. being not radioactive. The ratio between the light and heavy stable isotopes of an element (e.g. the ratio of 12C over 13C) varies in nature, bearing information of physicochemical and biological processes, as well as of sources and sinks of the matter and/or compounds. Moreover, compounds highly enriched in heavy stable isotopes can be used to trace the fate and transformations of compounds in complex environmental systems, which is not possible by any other approach.

SILVER is the largest facility for determining stable isotope ratios of light elements in environmental samples in Austria and one of the leading laboratories for ecological research with stable isotopes in Europe. In addition to determining the bulk isotopic composition of solid samples by elemental analysis – isotope ratio mass spectrometry (IRMS), SILVER has specialized on compound-specific isotope analysis in ecology and biology. This is important to address fundamental research questions ranging from Global Climate Change and biogeochemical processes to the human microbiome. SILVER was founded in 2006 and is part of the Large Instrument Facility for Advanced Isotope Research at the Faculty of Life Sciences of the University of Vienna.

SILVER currently encompasses five state-of-the art continuous-flow isotope ratio mass spectrometers with a range of front ends such as elemental analyzers, a high-temperature pyrolysis system, headspace gas samplers, trace gas pre-concentrators, and an HPLC- and a GC-Interface. The different configurations allow for bulk and compound-specific analysis of hydrogen, carbon, nitrogen and oxygen isotopes in almost any type of environmental sample. «

Coupling of liquid and gas chromatography to isotope ratio mass spectrometers enables compound-specific enables of biomolecules.

Stable isotope analyses have broad applications, such as climate reconstructions based on tree ring isotope analyses.



Overview of the SILVER laboratory, with isotope ratio mass spectrometers for bulk, trace gas, and compound-specific isotope analyses.

SILVER Laboratories
Large Instrument Facility for Advanced Isotope Research

Andreas Richter, Wolfgang Wanek: nanosims.univie.ac.at/isotope-ratio-mass-spectrometry-silver
Althanstraße 14, 1090 Wien

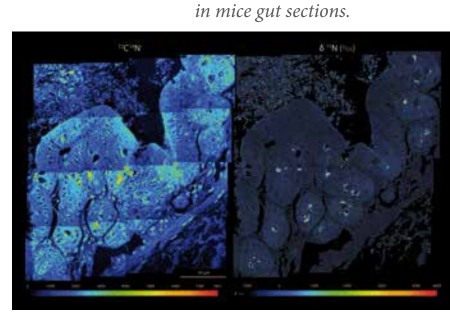
Nano-Secondary Ion Mass Spectrometry

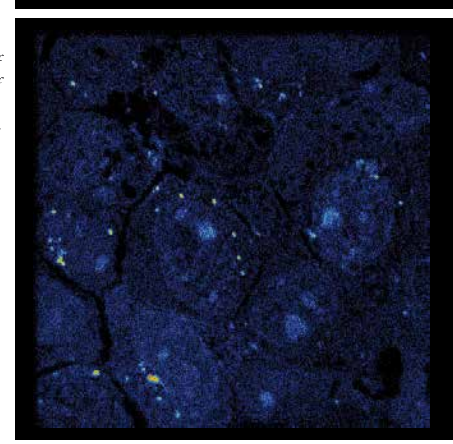
High-resolution chemical imaging helps visualize and quantify the chemical composition of cells and thus offers unique research opportunities in the Life Sciences. Analytical nanometer-scale secondary ion mass spectrometry (NanoSIMS) imaging is perfectly suited to measure and visualize the distribution of virtually any elements and their stable isotopes of interest in biological material. The CAMECA NanoSIMS 50L, which is available since 2010 at the Large Instrument Facility for Advanced Isotope Research, offers a spatial resolution for element/ isotope mapping down to 50 nm and thus even allows highly sensitive analyses at the sub-cellular level. Our NanoSIMS instrument is the only one in Austria and we support research groups in the faculty, university and many other national and international institutions in their chemical imaging efforts. Current applications of our NanoSIMS focus on microbial ecology and cancer research. In microbial ecology we combine NanoSIMS with stable isotope probing and cell identification techniques such as fluorescence in situ hybridization to obtain previously inaccessible information about the functional role of microorganisms in their environment. Using this approach, previously unrecognized physiological properties of bacteria and archaea thriving in soils, microbial mats, deep groundwater samples and within corals as well as mice guts could be deciphered.

In cancer research, we perform, in collaboration with colleagues from the Faculty of Chemistry, NanoSIMS measurements of isotopically labeled metal-based anticancer drugs within individual malignant cells and tumor tissue.

Applications for NanoSIMS projects within the fields of biology, chemistry, medicine and earth sciences can be submitted to the Large Instrument Facility for Advanced Isotope Research at any time. «

NanoSIMS-based detection of mucin-eating microbes in mice gut sections.





NanoSIMS image of the distribution of cisplatin in human colon cancer cells

Panoramic view of the NanoSIMS Laboratory

Large Instrument Facility for Advanced Isotope Research
Michael Wagner, Arno Schintlmeister:
nanosims.univie.ac.at
Althanstraße 14, 1090 Wien

Degree Programs
at the Faculty of Life Sciences

The range of degree programs offered at the Faculty is the largest among the natural science degree programs at the University of Vienna. The Directorates of Studies (SPL) 30 (Biology), 31 (Molecular Biology), 32 (Pharmacy), 33 (Nutritional Sciences) and 47 (Doctoral Studies, DSPL) are in charge of more than 10,000 students, which is more than 10 % of the students enrolled at the University of Vienna. The Life Sciences StudiesServiceCentre administers all the programs of our Faculty. It serves as a student information centre at faculty level for all questions concerning degree programs and graduation.

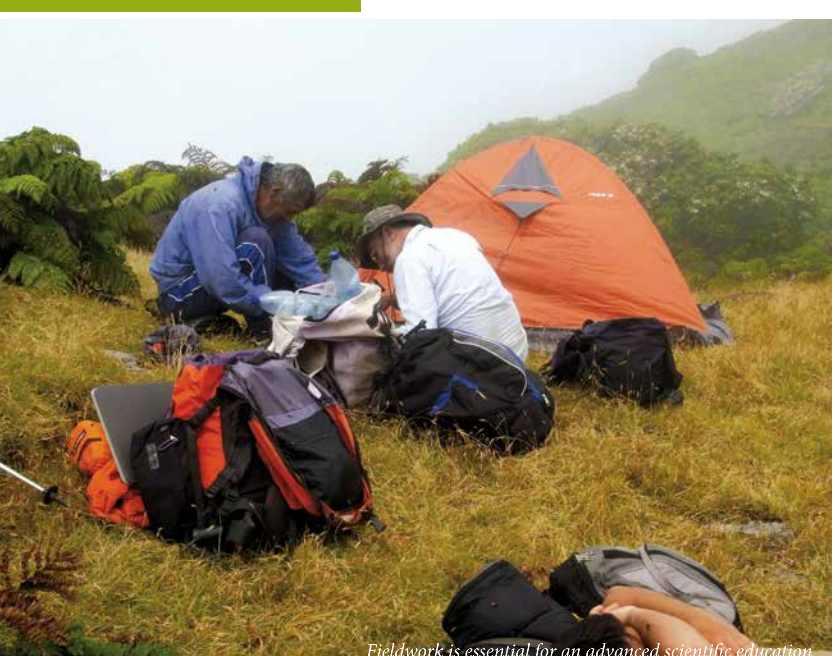
"Students can choose from a broad variety of study programs. Applied courses in the lab or field work are triggers for the success of the programs."

Degree Programs in Biology

The degree programs aim at providing various levels of basic and advanced scientific education in all core fields of Biology. The following study programs are offered: some of the master programs and the PhD program are given in English:

(1) Bachelor's program in Biology (duration: 6 semesters); teacher education in Biology & Environmental Studies (duration: 8 semesters)
(2) Master's programs (duration: 4 semesters): Anthropology; Behavior, Neurobiology & Cognition; Botany; Conservation Biology & Biodiversity Management; Ecology & Ecosystems; Evolutionary Biology; Zoology as well as parts of the interdisciplinary master program Environmental Sciences
(3) Parts of the Master's programs in Molecular Biology (duration: 4 semesters): Genetics & Developmental Biology; Molecular Biology; Molecular Microbiology, Microbial Ecology & Immunobiology
(4) PhD program in Life Sciences (duration: 6 semesters)

A total of 533 students graduated in the year 2013.



Fieldwork is essential for an advanced scientific education

© Patricio Lopez, University of Vienna

Degree Programs in Pharmacy

The degree program in Pharmacy is running as a 9-semester diploma program. The program aims at communicating the knowledge and skills necessary for handling the relevant pharmaceutical tasks competently and efficiently, and independently. This includes knowledge concerning the development, production, quality assurance, composition, preparation and storage, biological effects and interactions of pharmaceutical substances/pharmaceutical drugs, as well as their safe use.

A total of 127 students graduated in the year 2013. In 2015 it is planned to implement the Bachelor and Master programs.

Degree Programs in Nutritional Sciences

The University of Vienna is offering the only Nutritional Sciences high-level education program in Austria covering bachelor, master and PhD education. The following study programs are offered:

(1) Bachelor's program in Nutritional Sciences (duration: 6 semesters)
(2) Master's program in Nutritional Sciences (duration: 4 semesters)

Students choose from a large variety of lectures, seminars and courses

Practical courses in the lab are highly demanded by students

Seminars give the opportunity for small-group-discussions

(3) Diploma program: teacher education in Home Economics and Nutrition (duration: 9 semesters)
(4) Bachelor's program in Home Economics and Nutrition (2013) teacher education (duration: 8 semesters)
(4) PhD program in Life Sciences (duration: 6 semesters)
(5) Doctoral program in Natural Sciences (duration: 4 semesters) curriculum is running until 2017.

A total of 228 students graduated in the year 2013.

Altogether 82 PhD or Dr. rer. nat. students of all three degree programs of the Faculty graduated in 2013.

Insights and Alumni

The structure of the entire Faculty's bachelor study programs is focused on transmitting basic principles of the respective fields in the first semesters, but students will also gain experience in academic work and research under supervision, at least at the end of the bachelor's program. The master's programs are all research-led, and the current modifications of the curricula have been aimed at reflecting the Faculty's research areas in the individual master's programs. The master thesis is very often the first step into a research career, which can be followed by a PhD thesis. Doctoral candidates – almost all are integrated into the working groups of the Faculty-perform research work supported by master's and diploma students, usually supervised by excellent researchers of the Faculty. Every year many of our alumni are able to fill attractive positions in industry or academia, which reflects the state of the art and conscientious education.

The degree programs of the Faculty have been shown to be very attractive for female students, which is reflected in the fact that they account for more than 60 % of the Faculty students.

Approximately 10 % of the students come from abroad; a much higher rate is seen in the PhD programs, which are highly international and cooperative. The bachelor programs are routinely given in German, most of the masters have courses and lectures in English, some master's programs are being restructured so that enrollment will be possible for English-speaking students as well. «

StudiesServiceCenter Life Sciences
ssc-lebenswissenschaften.univie.ac.at
UZA II, Room 2C 323, Althanstraße 14, 1090 Vienna
ssc.lebenswissenschaften@univie.ac.at

Rennweg 14

University of Vienna

Faculty of Life Sciences

Dean's Office

University of Vienna
UZA II (Geozentrum)
Althanstraße 14
1090 Vienna

University Center Althanstraße

(UZA I and UZA II)
Althanstraße 14,
1090 Vienna

UZA I

_ Organismal Systems Biology

_ Ecology

UZA I

UZA II

Acknowledgements
The Dean's team expresses sincere thanks to Friedrich Barth and Friedrich Schiemer for taking the initiative in planning the events of the Faculty of Life Sciences on the occasion of the 650-year-anniversary of the University of Vienna.

Imprint

Faculty of Life Sciences
University of Vienna
Althanstraße 14
1090 Vienna, Austria
Phone: +43-1-4277-50001
dekanat.lewi@univie.ac.at
lifesciences.univie.ac.at

Editors
Friedrich Barth
Thomas Hummel
Ulrich Technau

Project Management
Ursula Gerber

Texts
Contributions from researchers of the Faculty of Life Sciences

Cover
Gregor Eder

Graphic Design
Starmühler Agentur & Verlag
Schellinggasse 1, 1010 Wien
www.starmuehler.at
Christine Starmühler
Sofie Mayer

Print
Ueberreuter
Paper: Magna satin 300/135 g/m²

UZA II

_ *Nutritional Sciences*

_ *Pharmaceutical Sciences*

Rennweg 14, 1030 Vienna

_ *Botany and Biodiversity Research*