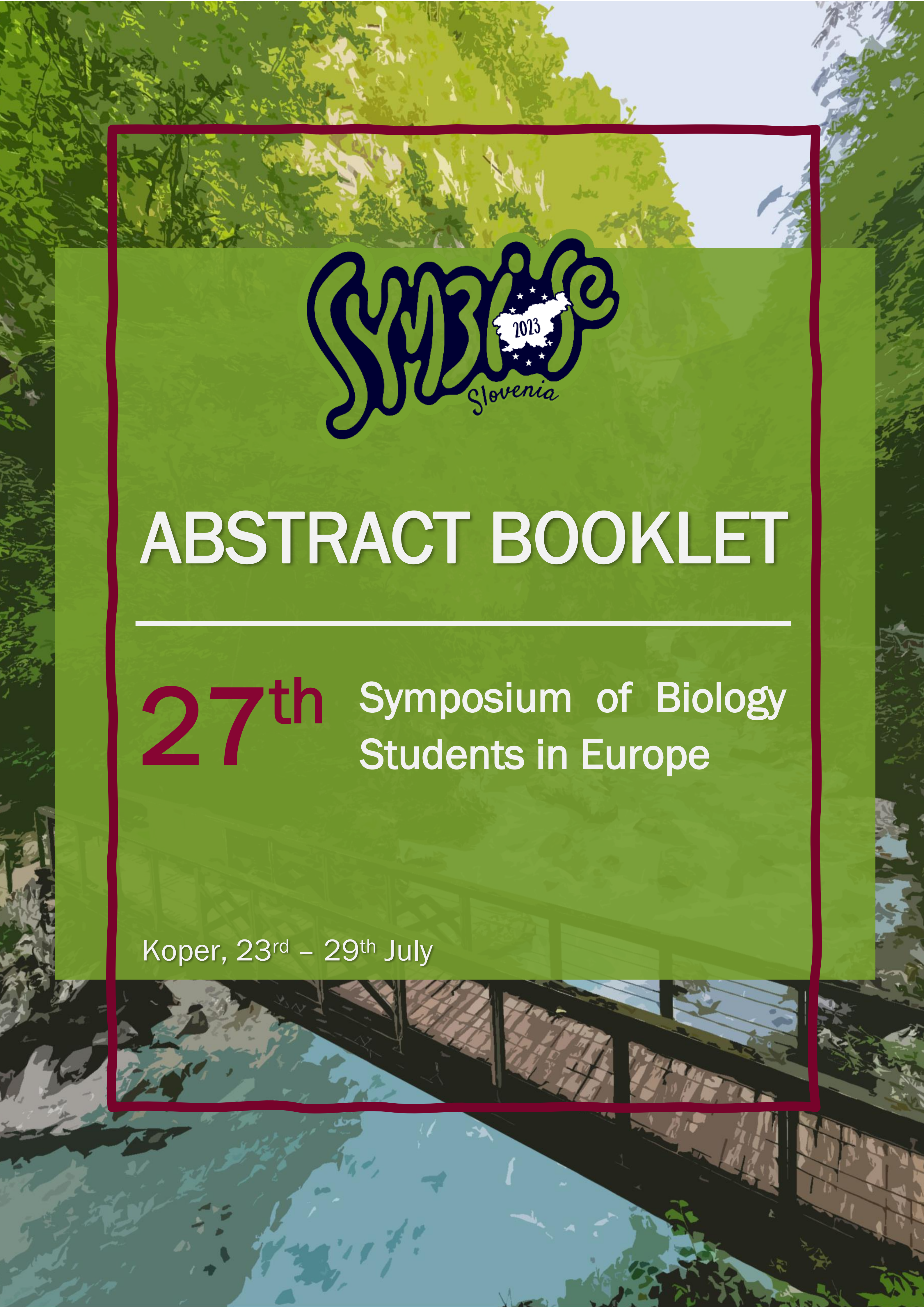

ABSTRACT BOOKLET

27th Symposium of Biology Students in Europe

Koper, 23rd – 29th July

SymBioSE 2023 Slovenia Abstract Booklet
27th Symposium of Biology Students in Europe
Koper, 23rd – 29th July 2023

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Published by · Mladinsko društvo Marezige, Marezige 24, 6273 Marezige

Marezige · 2023

Electronic Edition

Kataložni zapis o publikaciji (CIP) pripravili v Narodni in univerzitetni knjižnici v Ljubljani
COBISS.SI-ID 160891395
ISBN 978-961-96335-0-2 (PDF)

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MODULE 5: STATISTICS, DIDACTICS, SCIENTIFIC ILLUSTRATION

MODULE 6: PROTEIN ENGINEERING, CYTOGENETICS, DNA BARCODING

MODULE 7: HUMAN HEALTH, NEUROLOGY

MODULE 8: CONSERVATION, MONITORING, MIGRATORY BEHAVIOUR

MODULE 9: ENTOMOLOGY, ANIMAL TESTING

MODULE 10: MICROPLASTICS, NANOTECHNOLOGY, PALAEOECOLOGY

SYMBIOSE: CONNECTS BIOLOGISTS

On the cover page of the abstract booklet is pictured one of the bridges located within the Tolmin Gorges, one of the destinations that will be explored during this year's SymBioSE. The Tolmin Gorges are intertwined with bridges and paths leading towards inspiring landscapes that invigorate both a sense of adventure and desire for tranquillity, and provide knowledge, experiences and the opportunity for diverse encounters. Such is the essence of the SymBioSE event itself—a symbolic bridge that connects biologists and all those captivated by it. Each year, this event takes us beyond borders, bridging the gap between nations, fostering the exchange of diverse knowledge, and forging new acquaintances and new experiences. Throughout the journey, you never know who you will meet on the road, where that road will lead you, and who or what will inspire you to delve deeper into research.

Ever since its inception in 1996 by members of a German student association, SymBioSE, the Symposium for Biology Students, has brought together biologists from across Europe. With each passing year, this event has become an annual tradition, hosted by various nations, presenting their own culture and making each symposium a truly distinctive experience. The inaugural gathering in Berlin back in 1997 set the cornerstone for SymBioSE's incredible journey, leaving an indelible mark as a resounding success.

SymBioSE meetings are created to enrich participating students in various ways. Captivating lectures and immersive excursions expose students to a range of knowledge and diverse university systems, broadening their horizons and fostering dynamic discussions and collaborations. Emphasizing the importance of cultural exchange, SymBioSE fosters meaningful connections and cultivates a personal network of collaboration and friendship that spans Europe. Through facilitating student exchanges and international work experiences, SymBioSE contributes to mutual understanding and offers participants a fresh perspective on education. With a steadfast focus solely on science, education and friendship, SymBioSE is an open and inclusive event that transcends politics, welcoming individuals from all backgrounds to come together.

SymBioSE is not just an event; it is a compelling narrative that highlights the beauty and significance of science in our collective human story. The symposium covers a wide spectrum of scientific fields, inviting participants to present their research and ideas through oral contributions, posters, and workshops. From molecular biology, genetics, microbiology, botany, zoology, ecology, and beyond, all areas of biology find a place at SymBioSE.

SCHEDULE OF 2023 SYMBIOSE

	SUN, 23. 7. 2023	MON, 24. 7. 2023		TUE, 25. 7. 2023		WED, 26. 7. 2023		THU, 27. 7. 2023		FRI, 28. 7. 2023		SAT, 29. 7. 2023
06:00						GATHERING (BREAKFAST)						
06:30						BUS TO TOLMIN						
07:00		BREAKFAST		BREAKFAST				BREAKFAST		BREAKFAST		BREAKFAST
07:30										BUS TO IZOLA		
08:00										BEACH + ARCHAEOLOGICAL PARK SIMONOV ZALIV		
08:30				GATHERING (Avla)		TOLMIN GORGES						
09:00		GATHERING (Avla)		**SCIENTIFIC PROGRAMME MODULE 5** (VP1)	**SCIENTIFIC PROGRAMME MODULE 6** (VP3)			GATHERING (Avla)				MOVING OUT
09:30		**SCIENTIFIC PROGRAMME MODULE 1** (VP1)	**SCIENTIFIC PROGRAMME MODULE 2** (VP3)					**SCIENTIFIC PROGRAMME MODULE 7** (VP1)	**SCIENTIFIC PROGRAMME MODULE 8** (VP3)			
10:00	REGISTRATIONS (Avla)											GATHERING
10:30				COFFEE BREAK		SNACK TIME				WALK TO INNORENEW COE		GENERAL ASSEMBLY (+ VOTING) (VP3)
11:00		COFFEE BREAK		INVITED SPEAKER - BIOPSYCHOLOGY (Tramontana)		BUS TO BOVEC		COFFEE BREAK		INVITED SPEAKER - BIOINFORMATICS⍰ (InnoRenew)		
11:30		**SCIENTIFIC PROGRAMME MODULE 3** (VP1)	**SCIENTIFIC PROGRAMME MODULE 4** (VP3)					**SCIENTIFIC PROGRAMME MODULE 9** (VP1)	**SCIENTIFIC PROGRAMME MODULE 10** (VP3)			
12:00				COFFEE BREAK		ADVENTURE PARK SRNICA OR RAFTING OR VIRJE WATERFALL				INNORENEW COE presentation		COFFEE BREAK
12:30				NATIONAL ASSEMBLY (VP2)								CLOSING CEREMONY (Avla)
13:00	Walk to Lunch	Walk to Lunch						Walk to Lunch				
13:30	LUNCH	LUNCH		Walk to Lunch				LUNCH		BUS TO PIRANO	WAIT	
14:00				LUNCH						LUNCH	BUS TO PIRANO	GOODBYE
14:30						BUS TO TRENTA					LUNCH	
15:00	OPENING CEREMONY (VP3)					LUNCH	TRIGLAV NATIONAL PARK MUSEUM			WAIT		
15:30		**WORKSHOP 1** (RLab3)	**WORKSHOP 2** (VP3)	**WORKSHOP 3** (RLab3)	**WORKSHOP 4** (VP3)			**WORKSHOP 5** (VP3)	**WORKSHOP 6** (MP1)	VISIT PIRANO + AQUARIUM PIRAN + MORIGENOS		
16:00	ACCOMMODATION											
16:30						TRIGLAV NATIONAL PARK MUSEUM	LUNCH					
17:00	**POSTER SESSION** + COFFEE + SOCIALISING (Avla)	COFFEE BREAK		COFFEE BREAK				COFFEE BREAK				
17:30		COUNTRY PRESENTATIONS SESSION 1 (Avla)		COUNTRY PRESENTATIONS SESSION 3 (Avla)				COUNTRY PRESENTATIONS SESSION 5 (Avla)				
18:00						BUS TO KOPER						
18:30	DINNER TIME	DINNER TIME		DINNER TIME				DINNER TIME		LOCAL CULINARY DEGUSTATION		
19:00												
19:30	TREASURE HUNT (Koper) + SLOVENIA COUNTRY PRESENTATION (Avla)											
20:00		COUNTRY PRESENTATIONS SESSION 2 (Avla)		COUNTRY PRESENTATIONS SESSION 4 (Avla)				COUNTRY PRESENTATIONS SESSION 6 (Avla)		CONCERT WIND ORCHESTRA PIRANO & BEND-IT! ORCHESTRA		
20:30												
21:00												
21:30		SOCIALISING (Avla)		SOCIALISING (Avla)		SOCIALISING (Avla)		SOCIALISING (Avla)				
22:00	SOCIALISING (Avla)									BUS TO KOPER		
22:30										FAREWELL PARTY (Avla)		
23:00												
23:30												
00:00												

SCIENTIFIC PROGRAMME: POSTER SESSION

ID	Name	Surname	Title	Time	Date
1	Aleksandra	Ružičić	The Effects of Long-Term Palm Oil Intake on Inflammatory and Oxidative Status in the Rat Hypothalamus	17:00 - 18:30	**Sunday, 23.7.**
2	Silja	Töyrylä	Homosexual Behavior of Animals		
4	Laura	Kares	Survival of the Eagel Owl, *Bubo bubo*		
5	Božena	Omasta	Lymphocytic Choriomeningitis Virus Infection Increases Cellular Lipid Droplets Levels		
6	David	Fic	Leaf Micromorphological Changes in Cadmium-Treated Bean Plants (*Phaseolus vulgaris* L.)		
7	Anna S.	Kashnik	Nanoscale Spatial Arrangement of Ibuprofen in the Lipid Bilayer According To Double Electron-Electron Resonance Spectroscopy Data		
8	Jana	Lapinová	Carbonic Anhydrase IX is Upregulated by Adipokine Leptin in Breast and Colorectal Cancer Cells		
9	Laura	Haikonen	The Role of Pine Sawfly Larval Secretions in Ant Self-Medication.		
12	Anđela	Švarc	Analysis of Molecular Diversity of *Cheilosia crassiseta* Loew, 1859 (Diptera, Syrphidae)		
13	Tea	Serdarević	Integrated Strategy for Rehabilitation of Disturbed Land Surfaces and Control of Air Pollution		
14	Klemen	Tršinar	Characteristics of Community Surface Temperature of Intensive and Extensive Meadows Using Thermal Imaging		
15	Melani	Potrč	Aggregation Mechanisms of D(G4C2) Repeats Associated with Neurological Disorders ALS in FTD		
16	Veronika	Vaňová	Generation of SARS-Cov-2 Pseudotypes for Monitoring the Humoral Immune Response Against the Newly Emerged (Sub)Variants		

SCIENTIFIC PROGRAMME: ORAL PRESENTATIONS

			Module 1: Medical research, Pharmacology, Antibiotic production			
ID	**Name**	**Surname**	**Title**	**Time**	**Session**	**Date**
5	Aitana	Belloso	Role of Viruses in Cancer Treatment: Cancer Vaccines and Oncolytic Viruses	09:30 - 09:45	**Parallel Session 1**	**Monday, 24.7.**
39	Kalypso Angeliki	Koukouvini	Standardization of Immunoglobulin Study for the Search for New Biomarkers in Chronic Lymphocytic Leukaemia (CLL)	09:45 - 10:00		
17	Livia	Pietrow	Plant Extracts as a Source of Novel Antibiotics	10:00 - 10:15		
42	Sara	Veleska	Screening and Isolation of Soil *Bacillus* spp. for Antibiotic Production	10:15 - 10:30		
			Module 2: Botany research, Ecotoxicology			
ID	**Name**	**Surname**	**Title**	**Time**		
3	Liva	Purmale	Micropropagation of *Mertensia maritima*	09:30 - 09:45		
30	Miriam	Kaltwasser	Phytochrome Mediated Red Light Signalling in Plants and Its Link to Cold Regulated Genes	09:45 - 10:00		
33	Vasiliki	Garefalaki	Pesticide Detection Through an Esterase-Based Fluorescent Biosensor	10:00 - 10:15		
34	Sara	Novaković	Cadmium Effects on Leaf Epidermis of *Phaseolus vulgaris L.*	10:15 - 10:30		
			Module 3: Microbiology, Biotechnology, Biocontrol			
ID	**Name**	**Surname**	**Title**	**Time**	**Session**	
21	Mara-Sophie	Bruhns	The Effect of Bacterial Infection on Survival and Resistance of Different *Drosophila* Host Populations	11:30 - 11:45	**Parallel Session 2**	
27	Sofija	Kostandinovska	Antimicrobial Activity of Actinomycetes Isolated From Compost	11:45 - 12:00		
37	Dzansel	Bukovec	In Vitro Antagonistic Activity of Paenibacillus polimyxa AA15 Against Pathogenic Venturia inaequalis	12:00 - 12:15		
43	Dimitrios-Nikolaos	Kapiris	Using Synthetic Biology and Biotechnology Methods for the Preservation of Marble Monuments	12:15 - 12:30		
			Module 4: Genetics, Genomics, Virology			
ID	**Name**	**Surname**	**Title**	**Time**		
12	Bojan	Brmbota Horvat	Differences of SNPs of the Croatian Population and Their Compatibility Based on SNPs in HLA-A, -B and -C Genes	11:30 - 11:45		
10	Dalibor	Novokmet	The m^6A RNA Methylosome Subunits are Required for Male Fertility in the Moss *Physcomitrium patens*	11:45 - 12:00		
19	Lucas	Prost Boxoen	When Genomes Double Up: The Role of Polyploidy in Plant	12:00 - 12:15		
22	Marta	Falcão	Genome Characterization and Spaciotemporal Dispersal: Analysis of Bagaza Virus Detected in Portugal, 2021	12:15 - 12:30		

SCIENTIFIC PROGRAMME: ORAL PRESENTATIONS

			Module 5: Statistics, Didactics, Scientific illustration			
ID	**Name**	**Surname**	**Title**	**Time**	**Session**	**Date**
16	Joe	de la Mata	Computed Artificial Neural Networks for Predicting Clinical Outcomes	09:00 - 09:15	**Parallel Session 3**	**Tuesday, 25.7.**
26	Sebastian	Neufeld	Conceptualizing and Linking Biological System: A Didactics Approach	09:15 - 09:30		
44	Camilo E.	Pineda	Vertebras as a Starting Exercise for Paleontological Illustration	09:30 - 09:45		
			Module 6: Protein Engineering, Cytogenetics, DNA barcoding			
ID	**Name**	**Surname**	**Title**	**Time**		
25	Sofia	Assis	Engineering of NOV1 Dioxygenase by Directed Evolution to Improve Bio-vanillin Production	09:00 - 09:15		
36	Alona	Yurchenko	Cytogenetic Analysis of Seven Species of Gekkonid and Phyllodactylid Geckos	09:15 - 09:30		
13	Nikola	Pischiutta	First Insights Into the Morphological and Genetic Variability of Stoneflies (Plecoptera) in Medvednica Nature Park	09:30 - 09:45		

			Module 7: Human health, Neurology			
ID	**Name**	**Surname**	**Title**	**Time**	**Session**	**Date**
23	Maria Panagiota	Sarafi	The Invisible Universe of the Human Microbiome	09:30 - 09:45	**Parallel Session 4**	**Thursday, 27.7.**
35	Ramona-Alexandra	Ciaușu	The Incidence of Occupational Diseases Between 2017-2021 in Bacău, Romania	09:45 - 10:00		
24	Ioanna	Koutsotoli	The Impact of Mitochondria in Neurodegenerative Diseases	10:00 - 10:15		
14	Andreea Carmen	Dumitrescu	Why Music, Not Noise? Neural Mechanisms of Music Processing	10:15 - 10:30		
			Module 8: Conservation, Monitoring, Migratory behaviour			
ID	**Name**	**Surname**	**Title**	**Time**		
32	Marc	Villasevil	*Posidonia Oceanica* Seagrass: Conservation Actions in the Balearic Islands	09:30 - 09:45		
9	Jaume Adrià	Badia-Boher	Using Demographic Models to Characterize Population Dynamics and Guide Conservation Action in a Threatened Raptor	09:45 - 10:00		
46	Minja	Krstić	Innovative Methods for Wildlife Monitoring	10:00 - 10:15		
8	Arturo	Esteban-Pineda	A year (and a Half) of Fieldwork Across Europe. The Study of a Migratory Bird: The Black-Tailed Godwit (*Limosa limosa*)	10:15 - 10:30		
			Module 9: Entomology, Animal testing			
ID	**Name**	**Surname**	**Title**	**Time**	**Session**	
6	Alfredo	Escanciano-	Insects in a Changing World	11:30 - 11:45	**Parallel Session 5**	
4	Jennifer	Fischer	Bee Misunderstood – The Fascinating World of The Wild Bees	11:45 - 12:00		
18	Lucas	Gottesleben	Reducing Animal Testing Through Alternatives	12:00 - 12:15		
			Module 10: Microplastics, Nanotechnology, Palaeoecology			
ID	**Name**	**Surname**	**Title**	**Time**		
47	Irma	Hostnik	Presence of Microplastics in Water Column and Tissue of Farmed Mussel (*Mytilus galloprovincialis*) in Slovenian Sea	11:30 - 11:45		
38	Ira	Božić	What Happens With Nanoparticles in the Marine Ecosystem?	11:45 - 12:00		
2	Petra	Hus	What Happens in the Past, Stays in the Past (or not)?	12:00 - 12:15		

SCIENTIFIC PROGRAMME: WORKSHOPS

			Workshop 1			
ID	**Name**	**Surname**	**Title**	**Time**	**Session**	**Date**
1	Adam	Trach	Computational/In Silico Approach of the Potential Role of N-acylethanolamines as Inhibitors of E-protein of Coronavirus SARS-CoV-2	15:30 - 17:00	**Parallel Session 1**	**Monday, 24.7.**
			Workshop 2			
ID	**Name**	**Surname**	**Title**	**Time**		
2	Georgia	Wells	Making Science Interesting Again: Podcasting as a Form of Science Communication	15:30 - 17:00		

			Workshop 3			
ID	**Name**	**Surname**	**Title**	**Time**	**Session**	**Date**
3	Joe	de la Mata	Performing Multivariate Linear Regression Models With R.	15:30 - 17:00	**Parallel Session 2**	**Tuesday, 25.7.**
			Workshop 4			
ID	**Name**	**Surname**	**Title**	**Time**		
4	Marta	Biesiekierska	Scientist – A Man of Many Faces. What Do a Nerd, an Entertainer, and a Salesman Have in Common?	15:30 - 17:00		

SCIENTIFIC PROGRAMME: WORKSHOPS

			Workshop 5			
ID	**Name**	**Surname**	**Title**	**Time**	**Session**	**Date**
5	Mykyta	Osadchyi	Science Writing: How To Get Good at Captivating Others With Your Ideas	15:30 - 17:00	**Parallel Session 3**	**Thursday, 27.7.**
			Workshop 6			
ID	**Name**	**Surname**	**Title**	**Time**		
6	Minja	Krstić	Innovative Methods for Wildlife Monitoring	15:30 - 17:00		

SOCIAL PROGRAMME: COUNTRY PRESENTATIONS

Country	Time	Session	Date
Belgium	17:30 - 17:45	Session 1	Monday, 24.7.
Latvia	17:45 - 18:00		
Ukraine	18:00 - 18:15		
Croatia	20:00 - 20:15	Session 2	
England (UK)	20:15 - 20:30		
Spain	20:30 - 20:45		
Netherlands	20:45 - 21:00		
Bulgaria	17:30 - 17:45	Session 3	Tuesday, 25.7.
Norway	17:45 - 18:00		
Poland	18:00 - 18:15		
Germany	20:00 - 20:15	Session 4	
Italy	20:15 - 20:30		
North Macedonia	20:30 - 20:45		
Finland	20:45 - 21:00		
Austria	17:30 - 17:45	Session 5	Thursday, 27.7.
Romania	17:45 - 18:00		
Russia	18:00 - 18:15		
Greece	20:00 - 20:15	Session 6	
Czech Republic	20:15 - 20:30		
Portugal	20:30 - 20:45		
Serbia	20:45 - 21:00		
Slovakia	21:00 - 21:15		

EXPLORING THE HOST'S BACKGROUND: ACROSS SLOVENIA TO FAMNIT, KOPER

Republic of Slovenia

Slovenia is a picturesque and environmentally diverse country, known for its abundant nature and biodiversity which captivates the interest of biologists and nature enthusiasts. The country's remarkable geographical features encompass stunning coastlines, majestic mountains, and thriving national parks such as Triglav National Park, which provide essential habitats for indigenous, endemic, and protected species. With forest coverage exceeding 58% of the land area, Slovenia harbours a significant proportion of Slovenian endemic species, with two-thirds of them thriving within caves and soil environments. Notably, Slovenia boasts a noteworthy share of European amphibians, mammals, and half of the European bird species that periodically migrate to the country. In addition to its natural allure, Slovenia seamlessly combines its cultural heritage and exhilarating outdoor activities, including the popular pastime of rafting along the Soča River. The Soča River is recognized for sustaining a balanced ecosystem characterized by a diverse array of plant and animal species. Slovenia's captivating appeal is further enhanced by its charming towns, exceptional wines, vibrant festivals, and dedication to sustainable practices.

City of Koper

This year, Koper will be the host city for the upcoming SymBioSE symposium. Koper is a coastal city located in southwestern Slovenia, known as the Primorska region. It is the largest city and the main port of the country. Situated on the Adriatic Sea, it is renowned for its rich history, vibrant atmosphere, and stunning natural surroundings. The city's Old Town, influenced by Venetian architecture, features narrow streets and notable landmarks such as the Praetorian Palace, Cathedral of the Assumption, and Carpaccio Square. The city hosts various festivals, including the Koper Summer Festival, which offers a diverse programme of music, theatre, and other artistic performances. Koper's location makes it a convenient starting point for exploring other parts of Slovenia and neighbouring countries as it is well-connected by road, rail, and sea transportation. Koper and its surrounding region offer diverse natural beauty that is worth experiencing, such as the cliffs and diverse wildlife of the Strunjan Nature Reserve, or the UNESCO World Heritage Site of Škocjan Caves, known for its underground canyons. The Sečovlje Salina Nature Park offers a glimpse into salt production and boasts a wealth of birdlife. Koper's proximity to the Karst region allows visitors to explore limestone landscapes, vineyards, and traditional villages.

University of Primorska

Our host university, the University of Primorska, holds the distinction of being the third largest university in Slovenia, both in terms of age and size. It was established in 2003 by a special law enacted by the National Assembly of the Republic of Slovenia. Situated in the strategic area bordering Croatia and Italy, specifically in Koper, Slovenia, the University of Primorska plays a vital role in the economic and social development of the Primorska region.

Comprising six faculties, the University of Primorska is located in the coastal towns of the Primorska region. Its mission is focused on the pursuit of excellence in the generation and dissemination of knowledge, as well as fostering collaboration to enrich the academic and social spheres, not only in the Mediterranean area but also beyond. These values line up with the core principles of the Symbiosis event, encapsulating everything it stands for.

UP Famnit

The Faculty of Mathematics, Natural Sciences, and Information Technologies (UP FAMNIT) was established in 2006 and offers programmes at all three levels of higher education, along with conducting research in mathematics, computer science, information technology, and natural sciences. A significant collaboration exists between the faculty and the University of Primorska's Andrej Marušić Institute (UP IAM), where a majority of UP FAMNIT's academic staff are actively involved in research activities.

Courses are conducted in both Koper and Izola, reflecting the faculty's commitment to widespread accessibility. In addition to its primary focus on education and research, the faculty also plays a pivotal role in organizing and co-organizing successful international conferences and other scientific events, such as the one we are currently participating in. As this year's organizing committee all studied at UP FAMNIT, we share a close relationship with this esteemed faculty, which has enriched us with invaluable experiences, knowledge, friendships, and adventures.

ŠTUDENTSKI SVET
Univerze na Primorskem

ORGANISING ASSOCIATIONS

Marezige Youth Association

The Marezige Youth Association deals with cultural, sports and educational content. The association's biggest annual project is the MareziJazz international big band festival, which the association has been organising continuously since 2005 and where approximately 10 groups, or 250 musicians, perform every year, and it is visited by several thousand visitors.

The Marezige Youth Association has been very active since its foundation and gathers under its roof young people from the hinterland of the Koper municipality, as the association is not only made up of locals from Marezige, but also from other surrounding villages and Koper itself. The area of activity of the association is the organisation of concerts, seminars, workshops, gatherings and activities that are in any way related to culture, sports and education.

Association Biodiva

The purpose of the Association Biodiva is to promote research, study, and extracurricular activities of students and other members of the association. As a young association, Biodiva wants to create suitable conditions for expanding knowledge, gaining new experiences, and networking between different generations of conservation biologists.

Through various projects, Biodiva wants to contribute to people's awareness of the importance of nature conservation and taking care of our environment. Currently, the biggest projects of the Association are the biological camp Biocamp and the present conference.

ORGANISING COMMITTEE

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Luca Privileggio

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Urška Gerič

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Taja Pajmon Rak

SOCIAL PROGRAMME
Tinkara Kovic
Taja Pajmon Rak

SOCIAL MEDIA
Lucia Nikolić

KEYNOTE SPEAKERS

Genomic Approaches in Wildlife Management and Conservation

Elena Bužan[1 2]

[1] *University of Primorska, Faculty of Mathematics, Natural Sciences and Information Technologies, Glagoljaška 8, 6000 Koper, Slovenia*
[2] *Faculty of Environmental Protection, Trg mladosti 7, 3320 Velenje, Slovenia*

Keywords: conservation, management, metabarcoding, whole genome sequencing

Genetics has been a crucial element in wildlife management and conservation for the past fifty years. Genetic and genomic approaches that are commonly used include single locus analysis, DNA metabarcoding, reduced representation DNA techniques, transcriptome sequencing (RNA-Seq), and whole-genome (re)sequencing. They combine the power of modern genomics techniques with the goals of wildlife management and conservation and give us useful information such as the importance of genetic diversity for species adaptation, genetic requirements for sustainable population management, the effects of habitat change on species extinction, the genetic details of taxonomic differentiation, animal diet preferences, etc.

In my talk, I will explore the latest advances in the field of genomics and discuss how they can support wildlife conservation and management. I will also discuss the challenges that this field faces, such as data accessibility, ethical considerations, and the integration of genomics with other conservation disciplines. As case examples, my presentation will focus on genomics of the Northern chamois (*Rupicapra rupicapra*) and wild cat (*Felix silvestris*) as well as on diet analysis of the wild boar (*Sus scrofa*), grey wolf (*Canis lupus*) and Eurasian lynx (*Lynx lynx*). Moreover, considering differences in their population densities, spatial behaviour, dietary characteristics, and life-history strategies, we tried to assess the effects of habitat fragmentation and hybridisation on populations genetic structure and dietary profile determined by metabarcoding. We used genomics information to gain better insight into the influence of external and intrinsic factors on population dynamics and structure of these species, which would allow us to conduct sustainable, science-based population management.

Genomic data is a strong tool for resolving numerous management problems, and it can be less expensive than intense field work. Given the rapid advancements in computing and sequencing technology, we may see a not-too-distant future in which simpler methods, analysis, and interpretation will make genomic tools available to managers.

The Human Gut-Brain Connection: Roles of Microbiome in Mood and Behaviour

Tina Tinkara Peternelj[1]

[1]University of Primorska, Faculty of Mathematics, Natural Sciences and Information Technologies, Glagoljaška 8, 6000 Koper, Slovenia

Keywords: brain, gut, microbiome, behaviour, wellbeing

The microbiota-gut-brain axis (MGBA) is a complex system integrating neural, hormonal and immunological signalling pathways between the gut and the brain, where microbiota and its metabolites play crucial roles. It is a dynamic bidirectional network where the brain controls gastrointestinal functions and the gut influences central nervous system homeostasis.

Trillions of microbial cells (primarily bacteria, but also fungi, macrophages, viruses, archaea), its genes and metabolites form the human microbiome, representing the invisible world around and within us. The microbiome is concentrated in the gut but demonstrates systemic effects, taking part in host food digestion and metabolism, gut mucosal barrier, immune system education and regulation, stress response, integrity of blood-brain barrier and brain neuroplasticity. We now know that the gut microbiome can affect our cognition, mood, personality, sleep and eating patterns. Dysbiotic microbiota has been associated with many chronic diseases, including neurodegenerative diseases and psychiatric disorders. Importantly, neuroinflammation has been shown as a pathological hallmark of many diseases and crosstalk between immune function, our emotional lives and behavioural tendencies has been suggested.

A number of approaches have been used to probe the MGBA, such as dietary interventions, probiotic agents, microbiome transplants, psychotherapeutic strategies and, indeed, long-term lifestyle changes. Empirical data is coming mainly from animal studies; however, several interventions have demonstrated promising results. Therefore, further and well-designed human studies are warranted to identify research gaps and provide deeper insights into our relationship with the microbes, at individual, community and global levels. Finally, the gut-brain connection's potential to help human health has emerged as a hot topic in clinical studies, yet scientists are only scratching the surface. Nevertheless, each individual can access several strategies to support healthy microbiome and optimize gut-brain connection leading to overall wellness.

ORAL PRESENTATIONS

Role of Viruses in Cancer Treatment: Cancer Vaccines and Oncolytic Viruses

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Keywords: oncolytic virus, immunotherapy, cancer, viral vectors, review

Cancer is a major cause of death worldwide. This situation nowadays places its treatment and potential cure as one of the greatest challenges in human medicine. Among all the therapies developed to date, the use of viruses has grown exponentially in recent years. This biological therapy includes cancer vaccines and oncolytic viruses [1].

Oncolytic virotherapy is a therapeutic approach that uses replication-competent viruses to kill tumours. The ability of oncolytic viruses to selectively replicate in cancer cells leads to direct cell lysis and induction of anti-tumour immune response [2].

Cancer vaccine are designed to direct the immune response against tumour-associated antigens, creating a long-lasting immunological memory that controls tumour growth and prevents tumour recurrence [3]. Many classical cancer vaccines have used non-replicative viruses as vectors to express tumour antigens and/or immunomodulatory molecules [2].

The state of the art of the use of viruses as anti-tumour therapy will be reviewed, summarising the current knowledge about the molecular mechanisms existing in the host tumoral environment-virus interaction, current examples, potential therapy combinations, limitations and future perspectives [4,5].

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Standardization of Immunoglobulin Study for the Search for New Biomarkers in Chronic Lymphocytic Leukaemia (CLL)

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Keywords: chronic lymphocytic leukaemia, immunogenetics; immunoglobulin; blood cancer

Chronic lymphocytic leukaemia (CLL) is the most common adult leukaemia in the West, characterized by the clonal expansion and accumulation of mature B cells in the blood, bone marrow, and secondary lymphoid organs.[1] Some patients remain stable for years, while the progression of the disease may be faster and more aggressive in others.[2] In this context, the assessment of molecular biomarkers such as gene mutations, gene expression profiling, peptides and proteins can assist in disease prognostication and accurate patient staging. Ample evidence supports the notion that the clonotypic B-cell receptor (BcR) plays a critical role in the pathogenesis of CLL. These findings complemented immunogenetic studies reporting a remarkably skewed BcR immunoglobulin (IG) gene repertoire, which culminated in the identification of highly similar, stereotyped BcR IG in 40% of cases. The aim of this study is the in-depth study of immunoglobulins from patients with CLL at the primary sequence level, through the application of a multiplex PCR amplification strategy of the clonotypic IGHV-IGHD-IGHJ gene rearrangements, sequencing based on the Sanger and metadata analysis with the purpose-built IMGT/V-QUEST tool. This analysis will be expanded to the three-dimensional level via the application of molecular modelling methodologies.

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Plant Extracts as a Source of Novel Antibiotics

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Keywords: antibiotics, plant extracts, natural products

As antibiotic resistance is emerging, the need for novel ways of fighting bacterial infections is increasing. With rising resistance levels, and lowered antibiotic discovery rates, the demand for new antibiotics presents a serious issue **[1]**. Plant extracts have historically been an important source of medicinal compounds. Within the field of antibiotic discovery, however, plant-derived compounds remain underrepresented. Despite the estimated number of 370,000 distinct plant species, only about a thousand plants have been reported to exhibit antibacterial activities**[2]**. The Dutch extract library is a unique collection comprising 2240 extracts of plants commonly cultivated in the Netherlands, including many extracts derived from agricultural waste streams. We here present the results of a bioactivity screen conducted with extracts from this library. In the entirety of the library, we found a set of extracts that display potent antimicrobial effects against a broad panel of bacteria. Notably, some extracts were found to kill MRSA and VRSA, important resistant strains that affect >150,000 people each year in the European Union alone **[3]**. In order to further explore the antibiotic potential of the extracts, their haemolytic activity was also assessed. The most promising extracts thus identified remain to be fractionated and further analysed using mass spectrometry approaches to characterize the compound(s) responsible for the antibacterial activity.

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Screening and Isolation of Soil *Bacillus* spp. for Antibiotic Production

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Keywords: *Bacillus*, soil, inhibition, agar-well diffusion method, antimicrobial activity

One of the most important secondary metabolites produced by bacteria for commerce is the antibiotic, which is used in many different contexts. Today's antibiotics are primarily made by bacteria. Because of their ability to create necessary antibiotics like bacitracin and other antibiotics that always impede the growth of other organisms, *Bacillus* species are the most common soil bacteria. Many *Bacillus* species from distinct ecological settings have been described. *Bacillus* spp. perform a wide range of ecological tasks in the soil ecosystem, from cycling nutrients to imparting stress tolerance to plants, thanks to their abundance of genetic diversity and metabolic variety. This study's primary goal was to identify and isolate *Bacillus* species from soil samples that have antibacterial activity against six test microorganisms. In various climatic circumstances, soil samples from Vodno, North Macedonia, were gathered. The initial soil sample was taken in the winter, and the subsequent one in the spring. After being serially diluted, these samples were plated on nutrient agar. After the initial tests, nineteen bacteria were determined to be the most active. Using the agar-well diffusion method, the antibacterial activity was assessed against Gram-positive and Gram-negative microorganisms. Ten of the isolates exhibited inhibitory activity against *Bacillus subtilis* ATCC 6633, *Escherichia coli* ATCC 8739, and *Salmonella enterica* ATCC 10708. The growth of *Listeria monocytogenes* ATCC 13393 and *Staphylococcus aureus* ATCC 6538 were both suppressed by seven of the isolated strains. These isolates demonstrated antibacterial activity and could be exploited to create novel antibiotics for use in medicine or agriculture.

Micropropagation of *Mertensia maritima*

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Keywords: oyster plant, oyster leaf, *in vitro*, multiplication medium

Mertensia maritima is endangered plant species with edible leaves and flowers. Plant tissue culture of two *M. maritima* genotypes – *Mertensia maritima* and *Mertensia maritima* var. *asiatica* – was initiated from seeds. Seeds were surface sterilized using commercial bleach "Domestos" (15% for 15 min). Seeds were placed on hormone-free Murashige and Skoog (MS) mineral medium containing 30 g L^{-1} sucrose and 6 g L^{-1} agar, pH 5.8. After two months, plantlets were transferred to fresh MS medium supplemented with 0.5 mg L^{-1} 6-benzylaminopurine (BAP), followed by subcultivation every 5 weeks. Different multiplication media were tested: (i) 0.5 mg L^{-1} BAP; (ii) 1 mg L^{-1} thidiazuron (TDZ) and 0.2 mg L^{-1} 1-naphthaleneacetic acid (NAA); (iii) 2 mg L^{-1} kinetin and 0.2 mg L^{-1} NAA. Differences between the genotypes and media were observed (Figure 1).

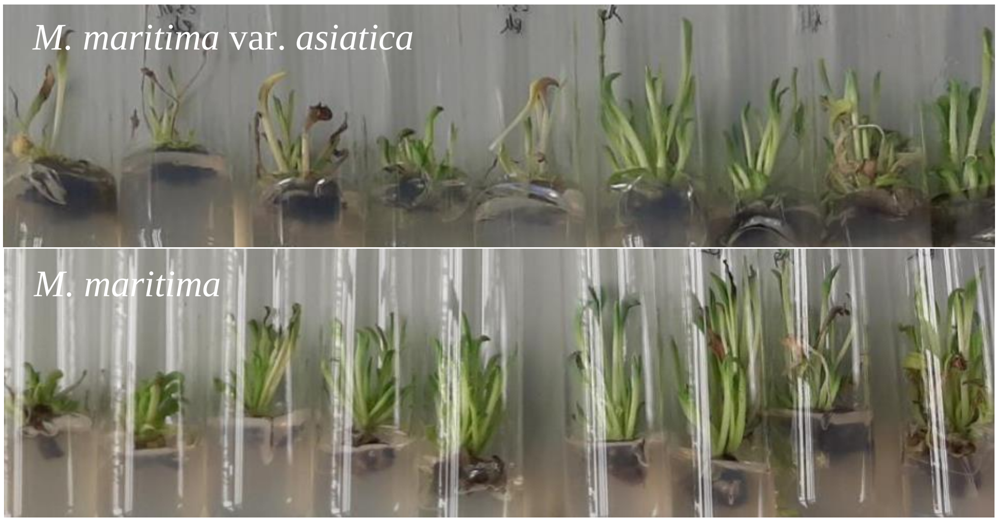

Figure 1. Development of *Mertensia maritima* and *Mertensia maritima* var. *asiatica* on MS medium supplemented with 1 mg L^{-1} TDZ and 0.2 mg L^{-1} NAA.

Further research is required, but preliminary results showed higher multiplication rate for *M. maritima* than *M. maritima* var. *asiatica* on all media tested. The medium with 2 mg L^{-1} kinetin and 0.2 mg L^{-1} NAA was not suitable for *M. maritima* var. *asiatica* multiplication.

Phytochrome Mediated Red Light Signalling in Plants and Its Link to Cold Regulated Genes

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Keywords: plant physiology, phytochromes, red light signalling, cold regulation, *Arabidopsis thaliana*

Plants are exposed to many different external stimuli. Sensing those and reacting accordingly is of utmost importance since their sessile lifestyle requires adjustment to outer conditions. Light is one of the most important of those outer stimuli since different light conditions, wavelengths, intensities, and durations contain a lot of information about the time, season, and place that a plant is growing in. For this reason, plants evolved several light receptors with absorption spectra of different wavelengths. One class of those photoreceptors, called phytochromes, is responsible for red- and far-red-light dependent signalling. Phytochromes are responsible for many processes in the plant, including seedling development, growth phase transition, shade avoidance, and flowering [1]. Phytochromes are activated when the inactive pr-form of the protein is converted into the active pfr-form by absorption of red light. Pfr-phytochrome can be converted back into the inactive pr-form by far-red light absorption. Phytochrome can therefore be described as a molecular red/far-red light switch. Environmental cues derived from red light (pr/pfr-ratios) are integrated into physiological responses via different proteins interacting with active pfr-phytochrome in the nucleus. For example, two cold regulated genes in *Arabidopsis thaliana*, COR27 and COR28, physically interact with phytochrome [2]. COR27/28 act as regulators, finetuning photomorphogenesis, and presenting a trade-off mechanism between flowering and freezing tolerance. COR27/28 integrate red-light signals via different other downstream interactors. In this study the interaction and Co-Localisation of Phytochrome and COR27/28 in phytochrome nuclear bodies [3] is investigated. Potential other interactors of COR27/28 are also tested in interaction assays, alongside the analysation of chromatin status of light regulated genes in dependence of COR27/28.

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Pesticide Detection Through an Esterase-Based Fluorescent Biosensor

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Keywords: fluorescent biosensors, pesticides, organophosphates, carboxylesterase

The use of pesticides in agricultural activity is inevitable, but it comes with serious hazards to the ecosystem, including humans. European regulation of pesticides is strict, yet there is continuous need for monitoring the presence of pesticides and their biotransformation derivatives in food products. One of the most toxic groups of chemicals used as pesticides are organophosphate (OP) compounds, and recent investigation trends have moved towards development of efficient methodologies for the detection of OPs. These include fluorescent biosensors based on carboxylesterases. Here, a double mutant of the thermostable esterase EST2 from the bacterium *Alicyclobacillus acidocaldarius* was studied as a potential OP biosensor. The enzyme was modified with the fluorescent probe IAEDANS and used to screen a collection of sixteen pesticides. Indeed, the fluorescent double mutant was able to detect the OP paraoxon, resulting in fluorescence quenching of 18±1%. These results were also confirmed by enzymatic activity assays, where the activity was completely inhibited in the presence of equimolar amounts of paraoxon (in the nanomolar range). Additionally, methyl-paraoxon resulted in fluorescence quenching of 14±2%. The detection method has a linearity range between 0.1-0.4μM for paraoxon and blind samples within that range were successfully quantified. This study is a starting point towards the development of fluorescence-based biosensors for the screening of enzyme mutants with different pesticide selectivity profiles. Applications of such enzyme-based biosensors can include environmental monitoring and food traceability by controlling the presence of toxic organophosphate pesticides.

Cadmium Effects on Leaf Epidermis of *Phaseolus vulgaris L.*

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Keywords: cadmium, contamination, stomata, leaf, bean

Cadmium (Cd) is one of the major environmental contaminants because of great anthropological impact. Also, cadmium has a negative effect on plants, inhibiting carbon fixation, reducing chlorophyll synthesis and photosynthetic activity. We studied the effects of cadmium on epidermal characters of prophylls and first trifoliate leaves of three *Phaseolus vulgaris* L. genotypes. Two genotypes are cadmium resistant and one is cadmium sensitive. Using light and scanning electron microscopy (SEM), comparative analyses of adaxial and abaxial epidermal micromorphological features have been carried out. SEM analyses revealed the presence of nonglandular (with straight and hooked apical part) and glandular trichomes on both leaf types of all analysed genotypes. Statistical analysis (Duncan test, Student's t-test) showed that cadmium had more significant effect on foliage leaves than on prophylls. On prophylls in cadmium-sensitive genotype, cadmium caused a decrease in stomata number and increase in length, width and surface area of stomata. On foliage leaves, of all genotypes, cadmium caused an increase in stomata number and increase in overall size of stomata. The number of trichomes on foliage leaves was increased because of the cadmium effect, while their number has not changed on prophylls. However, analyses showed that cadmium has no effect on stomata index, neither in prophylls, nor in foliage leaves. In conclusion, our research showed that cadmium has the greatest effect in stomata number and size.

The Effect of Bacterial Infection on Survival and Resistance of Different *Drosophila* Host Populations

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Keywords: *Drosophila*, survival, bacterial load, resistance

When infected by a pathogen, the host system reacts on multiple levels. The host immune system has evolved towards maintaining the host's fitness and ultimately getting rid of the pathogen. In this project the overarching aim was to characterise host population responses to different infections. Two different host *Drosophila melanogaster* lab populations, e.g. OregonR and BerlinK, were tested for the effects of bacterial infection on both resistance (bacterial load) and survival rates. Female adult flies were injected with two different pathogenic bacteria species in three different doses. Their survival was followed for 4 weeks and bacterial load was measured at several time points. The aim here was to characterise the survival curves and examine the time after injection at which most of the mortality occurs for each of the host genotypes. Another question targeted with these experiments was whether the flies clear the infection or sustain a persistent bacterial load[1]. The results will give insight to the decomposition of virulence. Is the bacterial infection dose dependent? Which bacterial strain is more virulent? Does the virulence depend on host or pathogen factors? Can we decompose the virulence into resistance, tolerance, exploitation, per parasite pathogenicity?

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Antimicrobial Activity of Actinomycetes Isolated From Compost

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Keywords: actinomycetes, compost, screening, antimicrobial activity

It is absolutely necessary to develop new broad range antimicrobial medicines to tackle infections that often emerge and are multi-drug resistant. Actinomycetes are a large and varied class of aerobic, gram-positive, mycelial bacteria that are crucial to soil cycles on an ecological level. The economic significance of many as manufacturers of biologically active compounds, including antibiotics, vitamins, and enzymes, is widely known. Therefore, the objective of this work was to isolate various bioactive actinomycetes strains from compost that were able to produce antimicrobial secondary metabolites. A total of 4 compost samples were processed during different seasons. Twenty-five strains of Actinomycetes were isolated from compost samples. By examining microscopic and colony characteristics, several isolates were classified. Preliminary screening was done using the cross-streak method against three gram-positive and gram-negative bacteria, and three fungi. The secondary screening of the antibacterial activities of the isolates was performed using the Kirby-Bauer disc diffusion method. Fourteen of the isolates were active against at least one of the test organisms. Only one of the isolates showed antibacterial activity against one gram-negative test bacteria, while the other isolates showed antibacterial activity against gram-positive test bacteria. According to the findings of the current study, Actinomycetes from compost represent a powerful source of new antibiotics. Actinomycetes can be isolated, characterized, and studied to find new species of Actinomycetes.

In Vitro Antagonistic Activity of *Paenibacillus polimyxa* AA15 Against Pathogenic *Venturia inaequalis*

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Keywords: apple scab, in vitro, antagonism, *Paenibacillus*, biocontrol

This work aimed to determine the antifungal activity of *Bacillus spp.* and *Paenibacillus spp.* under in vitro conditions against the fungus *Venturia inaequalis*, which is the cause of apple scab. One of the most critical diseases at the world level is scab disease, which causes significant economic losses of up to 100% of apple production by affecting commercial quality. Consequently, the control of this disease depends on using fungicides which are dangerous for the environment and human health. The preceding shows the great need for research into new strategies for controlling apple scab, like using biocontrol agents as an alternative for disease management. The V. inaequalis strain was isolated from fruits with disease symptoms. In the laboratory tests, three bacterial isolates of *Paenibacillus polymxa*, strain AA/9, AA/11, AA/15 and five of *Bacillus velezensis*, strain AA/1, AA/2-1, AA/2-2, AA/19-2 and AA/20 were used. In vitro, tests on apples were carried out to confirm the results. The best growth of *V. inequalis* was observed on the *Sabouraud dextrose* agar plate, with a colony size of 43 cm. The antagonism by *Paenibacillus polymxa* AA/15 and *Bacillus veleznsis* AA/11 isolates against *V. inaequalis* was classified according to the radial growth inhibition zone in Miller Hinton broth + Sabouraud dextrose broth media. We obtained tremendously good results from all isolates, where *Paenibacillus polymxa* AA/15 was separated by a narrow margin with a pure inhibitory zone of 25mm. Microdilution method for assessment of their antifungal activity was conducted. We proved that isolates of *Paenibacillus polymxa* stain AA/11 and AA/15 exhibit antifungal activity against the pathogenic fungus up to 10^{-5} dilution. The obtained results are promising, with which chemical fungicides could be replaced.

Using Synthetic Biology and Biotechnology Methods for the Preservation of Marble Monuments

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Keywords: bacteria, fungi, biodeterioration, antimicrobial peptide, cultural heritage

Biodegradation is the degradation of materials into environmentally acceptable products such as water, carbon dioxide, and biomass by the action of naturally available microorganisms which either nest and grow, or feed on it, under normal environmental conditions. Biodeterioration is any kind of undesirable change caused by organisms. The definition involves organic and inorganic materials (from artefacts) and activities of organisms (biodeteriogens). Basic consequences of biodeterioration are mechanical, aesthetical, and chemical. These phenomena are threatening marble monuments all over the world, so their limitation is a matter of great importance for the preservation of cultural heritage. Antimicrobial peptides are an important component of the innate immune system of many organisms, with inhibitory or killing action, against pathogens. Tachyplecin is an antimicrobial peptide, with action against Gram+ and Gram– Bacteria, Firmicutes, Fungi and Viruses. Compared to traditional antibiotics, antimicrobial peptides such as tachyplecin have the advantage of not producing drug resistance and have a unique antibacterial mechanism. The experimental procedures involve the transformation of Escherichia coli strains with recombinant plasmids containing the desired nucleotide sequence that produces tachyplecin, using synthetic biology and biotechnology methods. Following the characterization of the expression and purity of the peptide under study, the efficacy of tachyplecin as a biocidal product is evaluated in microorganisms found in marble. The use of the antimicrobial peptide prevents the development of resistance of microorganisms, thus eliminating the need to create even more modern biocides, constituting a useful tool for combating biodegradation and preserving cultural heritage.

Differences of SNPs of the Croatian Population and Their Compatibility Based on SNPs in HLA-A, -B and -C Genes

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Keywords: HLA, SNPs, DNA

The human leukocyte antigen (HLA) system is an essential part of the immune system and is controlled by genes located on chromosome 6. Multiple scientific research demonstrates that people with differing DNA markers (HLA genes) find each other's scent to be pleasant in the first place and are more likely to have a long-lasting romantic relationship. With the help of my mentor, dr. Olga Zaytseva, I have been studying the correlation between HLA genes and their influence on human partnership and the immune system. This study has been carried out amongst fifty individuals. After we received their genotyped results, we then compared the data we received from my algorithm with a questionnaire that all participants filled out.

While I was waiting for the genotyped results of the DNA samples - during SymBioSE 2022 - I invented an algorithm that would automatically calculate the percentage of compatibility between two individuals based on SNP markers in their HLA genes. The algorithm looks for differences in the SNP markers of HLA genes; the more different the HLA genes are, the better the match. Other scientific research has also proven that more different nucleotides in parents result in a more robust immune system in offspring. The use of artificial intelligence and machine learning, has enabled our system to be able to predict the formation of HLA genes in future humans with unparalleled accuracy.

The goal of this service (which we are still working on) is to offer future parents an insight into the genetic health data of their child (before conception). The system currently behaves reliably, accurately and delivers its genetic prediction results with unparalleled accuracy.

The m^{6}A RNA Methylosome Subunits are Required for Male Fertility in the Moss *Physcomitrium patens*

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Keywords: development, m^{6}A, male sterility, mRNA methylation, *P. patens*

Methylation of mRNA is a conserved mechanism of gene expression control across all eukaryotic lineages. Methylation of adenine (m^{6}A) in mRNA transcripts affects gene expression by modulating many aspects of mRNA metabolism such as maturation, and stability. *Arabidopsis thaliana* mutants lacking core components of the m^{6}A methylosome, the MTA and FIP37, are embryo lethal, and complemented rescued plants with decreased m^{6}A methylation show massive over-proliferation of shoot apical meristem. Epimethylome analysis of these mutants showed that m^{6}A methylation affects transcripts of key meristem regulators such as *STM* and *WUS*. Core components of the m^{6}A methylosome have been detected in the moss *Physcomitrium patens*, a representative of early land plants. Unlike in *A. thaliana* with complex meristems, *P. patens* shoots contain a single apical stem cell. To understand the function of m^{6}A RNA modification in *P. patens*, we generated knock-out mutants of the *MTA* and *FIP37* homologs. The mutants are not affected in gametophyte development but are unable to produce sporophytes. Analytical crossing with fluorescent transgenic strains revealed male sterility in both *Δmta* and *Δfip37* mutants. We are currently working on epimethylome and ultrastructural analyses of these mutants which could uncover conserved molecular components regulated by m^{6}A RNA methylation with essential functions for plant development and reproduction.

When Genomes Double Up: The Role of Polyploidy in Plant Evolution

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Keywords: Polyploidy, gene expression, transcriptomic plasticity, Chlamydomonas

Polyploidy, defined as the duplication of entire genomes, is a widespread phenomenon observed across prokaryotic and eukaryotic organisms, but mostly prevalent in plants. Despite the complexity and variability in the repercussions of polyploidization across diverse systems and species, it has frequently been perceived as an evolutionary dead end. There is mounting evidence correlating polyploidization with responses to environmental change or stress, leading to an increased acknowledgment of its adaptive potential in the short term. Intriguing patterns of gene retention following whole-genome duplication once polyploidy has been established, which might serve as key insights into significant long-term evolutionary transitions and an overall increase in biological complexity. Challenging the prevalent view of polyploidy as an evolutionary dead-end, polyploidy is now seen as a potent catalyst that might drive biodiversity and complexity, particularly in the context of angiosperm evolution. It thereby offers a fresh perspective on understanding the adaptive and evolutionary potentials of polyploid organisms.

Genome Characterization and Spaciotemporal Dispersal Analysis of Bagaza Virus Detected in Portugal, 2021

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Keywords: Flavivirus, BAGV; genome, Alectoris rufa, phylogenetic analysis

In September 2021, Bagaza virus (BAGV), a member of the Ntaya group from the Flavivirus genus, was detected for the first time in Portugal, in the heart and the brain of a red-legged partridge found dead in a hunting ground in Serpa (Alentejo region; southern Portugal). BAGV was first isolated from a pool of Culex mosquitoes in 1966, in the Bagaza district of the Central African Republic. Subsequently, it has been detected in mosquitoes (*Cx. Perexiguus, Cx. Univittatus*) collected in other African countries, India, and the United Arab Emirates. In vertebrates, BAGV-associated infections were first reported in red-legged partridges, ring-necked pheasants, and common pigeons in Spain in 2010, and a few years later, in 2016, in Himalayan monal pheasants from South Africa. Here we report the genomic characterization of the full-length sequence of the Bagaza virus detected (BAGV/PT/2021), including phylogenetic reconstructions and spaciotemporal analyses. Phylogenies inferred from nucleotide sequence alignments, complemented with the analysis of amino acid alignments, indicated that the Bagaza strain from Portugal is closely related to Bagaza strains previously detected in Spain, suggesting a common ancestor that seems to have arrived in the Iberia Peninsula in the late 1990s to early 2000s. In addition, our findings support previous observations that Bagaza virus and Israel turkey meningoencephalitis virus (ITV) belong to the same viral species. Furthermore, in order to speed up the diagnosis of Bagaza virus and other flaviviruses common in Europe, such as West Nile virus and USUTU virus, a PCR capable of detecting the three infections was developed and standardized. This PCR is now being used in several field samples in order to try to detect flavivirus circulating in Portugal.

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Computed Artificial Neural Networks for Predicting Clinical Outcomes

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Keywords: machine learning, neural networks, biostatistics, biomedicine, bioinformatics

Regression models are statistical models to analyse the relationship between different independent variables and a dependent variable known as response outcome. Numerous clinical data measures or variables (e.g. blood pressure, age, clinical biomarkers, etc.) present a strong relationship with clinical outcomes of interest (e.g. risk to develop a disease, death outcome, etc.) and this relationship can be studied through regression models. If a model finds a strong correlation between some clinical variables and the response clinical outcome, this regression can be used to predict the clinical outcome for patients based on the values of these variables. For instance, we can predict how likely it is that a patient will survive a disease given the administration of different treatments and that the patient presents some co-morbidities.

Machine-learning methods have been designed to maximise the optimization of regression models and improve the precision at predicting outcomes. Inspired by the mechanics of animal neural networks, a state-of-the-art machine-learning model was designed in the early 1940s for computing regression models with a similar functioning to sensory processing in animal brains. Artificial Neural Networks (ANNs) generate regression models for classifying subjects in different categories given a large set of independent variables. This methodology, albeit it requires a complex computation, uses a feedback algorithm to improve the learning mechanism of the computer in finding the strongest regression of the independent variables with the response outcome.

During this presentation I will introduce the concept of statistical regression models and will explain the mechanics and functioning of ANNs with non-biomedical and medical applications.

Conceptualizing and Linking Biological Systems: A Didactics Approach

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Keywords: didactics, concepts, principles, biological systems

Biology consists of complex systems, a plethora of interactions and scales from ions to ecosystems. Still, biological study programmes are often very discipline driven (e.g. genetics, botany, microbiology) instead of emphasizing reoccurring concepts. However, linking the mechanisms of different organisms and levels of organization can help in understanding the “big picture” of life. Based on the lectures and courses of the B.Sc. Biology programme in Freiburg, we try to find, explain and connect these concepts with corresponding principles in a self-paced E-Learning environment that spans the first four semesters (basic modules). By using ILIAS, the already established digital learning platform of the University of Freiburg, we have easy access to other contents as well as an integration into existing course-structures of present students. We already defined the main concepts (structure and function, matter- and energy-conversion, information and communication, control and regulation, individual and evolutionary development), principles they comprise (e.g. form-follows function, surface area expansion) and therefore related competencies. Currently, we are working on fleshing out 3-4 suitable phenomena (e.g. convolution of mitochondrial membrane) on different organizational levels (e.g. molecules, cells, organs, ecosystems) for each principle. The talk will cover the main concepts, current state of the project and some examples (phenomena in different organizational levels).

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Vertebras as a Starting Exercise for Palaeontological Illustration

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Keywords: fossil, illustration, palaeontology, vertebras

While paleontological illustration skills and live reconstitutions of extinct species have become an iconographic exercise among young palaeontologists, scientific illustration is not widely practiced. Making scientifically accurate skeletal drawings is an important tool in science communication, because it improves the interpretation of anatomical descriptions and simplifies the information. This exercise encourages dialogue between palaeontologists (experienced in fossils) and illustrators (experienced in drawing techniques), reconciling the needs of palaeontology with intrinsic competences of illustration, while both can learn about the fossil itself. To explore this idea, the drawing of four different vertebrae (dolphin, human thoracic, fossil Bovidae and mammoth spinous process) was proposed as the beginning exercise for a palaeontological illustration lesson. The choice of vertebras as drawing models allows an upgrowing complexity approach, given by anatomy, symmetry, size, or completeness. In this case, the illustrator (less trained in fossil/bone drawings) acquires, during each task, knowledge about procedures and conventions of illustration applied to palaeontology, as well as the correct use of several tools and techniques, such as: correct positioning of each vertebra, choice of different views, transfer to graph paper (in real or reduced scale), analogical techniques (graphite, black ink) for highlighting bone edges and fading cracks/fractures, and preparing drawings for scanning and digital post-production. All this to obtain the best and most reliable possible result for a publishable version. This exercise is easily applicable to other bones and fossils, as long an increasing degree of morphological complexity is accomplished. With this exercise, the illustrator acquires important knowledge about the application of osteological illustration in palaeontology, as well as the skills to draw much more complex fossils. The constant feedback between the palaeontologist and the illustrator is the finest way to learn before proceeding with an illustration work in a much more confident, autonomous and competent way, once the exercise is over.

Engineering of NOV1 Dioxygenase by Directed Evolution to Improve Bio-vanillin Production

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Keywords: lignin valorisation, isoeugenol, vanillin, directed evolution

The sustainable enzymatic conversion of lignin-derived phenolics into valuable products can valorise lignin bio-wastes. NOV1 from *Novosphingobium aromatocivorans* is a dioxygenase that converts lignin-derived isoeugenol into vanillin, a common and valuable flavour and fragrance. This reaction holds the potential to replace the mostly used petroleum-based vanillin and valorise lignin biowaste.

Directed evolution is a protein engineering method that allows improvement of a given enzyme by mimicking evolution. This process consists of iterative rounds of random mutagenesis and variant selection that will be used as parents for the next round. In previous work, two rounds of directed evolution were applied, resulting in the hit 1D6 variant, which showed a k_{cat} 4-fold higher in comparison to the wild type and about 35-fold longer half-life at 25 °C.

In this project, a third round of directed evolution was done, using 1D6 as parent. A library of variants was constructed by random mutagenesis and, after the screening of 1500 variants, 16G3 variant emerged, displaying 1.5-fold activity and 2.1-fold stability as compared to 1D6 parent. The characterization of 16G3, which harbours 4 non-synonymous mutations, shows no improvement in k_{cat} but almost halved the K_m (from 1.7 to 1.0 mM), resulting in a 2-fold increased k_{cat}/K_m. Kinetic stability was also enhanced as 16G3 displayed a half-life time of 53 h at 25 °C, 40-fold longer than the wild type.

Overall, these results show the potential of applying directed evolution to engineer NOV1 enzyme for improved catalytic and stability properties. Future work will continue NOV1 engineering and focus on the structure-function relationship underlying the effect of the mutations introduced by the engineering process.

Cytogenetic Analysis of Seven Species of Gekkonid and Phyllodactylid Geckos

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Keywords: fish, Gekkota, heterochromatin, karyotype, sex chromosomes

Geckos are one of the richest reptiles' clades with over 2200 recognized species in this group, which has a well-demonstrated variability in diploid chromosome number (2n = 16–48) and sex determination systems. Geckos possess all of the major vertebrate sex determining mechanisms, including genetic sex determination (with both male and female heterogamety - ZW and XY, respectively), and temperature-dependent sex determination. However, only a small part of the gecko species has been studied by cytogenetic methods. In this project, we used conventional methods (karyotype reconstruction, C-banding), as well as molecular (fluorescence in situ hybridization with probes for rDNA loci and telomeric repeats) cytogenetic analyses in seven species of geckos, namely *Blaesodactylus boivini*, *Chondrodactyluslaevigatus*, *Gekko badenii*, *Gekko cf. lionotum*, *Hemidactylus sahgali*, *Homopholis wahlbergii* (Gekkonidae), and *Ptyodactylus togoensis* (Phyllodactylidae) to better understand karyotype evolution in geckos. Four of the studied species demonstrated the presence of interstitial telomeric repeats, but we could not conclude whether they are remnants of previous chromosomal rearrangements or formed by the accumulation of telomere-like satellite motifs. The presence of sex chromosomes was not found in any of the studied species, although they were previously identified by cytogenetic and/or genomic methods in a number of species from the genera Hemidactylus and Gekko. Our studied species have either poorly differentiated sex chromosomes, or perhaps environmental sex determination. Future research should examine the effects of temperature and conduct genome-wide analysis to determine how sex is determined in these species.

First Insights Into the Morphological and Genetic Variability of Stoneflies (Plecoptera) in Medvednica Nature Park

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Keywords: EPT group, biodiversity, protected area, DNA barcoding, phylogeographic structure

Mount Medvednica is located in the near vicinity of Zagreb, the capital city of Croatia, hence urbanization and frequent changes in watercourses have a strong impact on fauna. However, the biota in this area is understudied. This is especially true for aquatic insects of order Plecoptera (stoneflies) that belong to the EPT (Ephemeroptera, Plecoptera, Trichoptera) group, and which is considered one of the groups of organisms most sensitive to environmental pollution [1,2]. A total of 101 stonefly specimens were collected at 12 localities in Medvednica Nature Park. Adult individuals were determined to the species level using morphological identification and, additionally, with DNA barcoding. The DNA barcoding method is based on the sequencing of a standardized mitochondrial gene fragment of cytochrome *c* oxidase subunit I (*COI*) in the length of 658 bp, and represents an important tool for providing the first insight into genetic diversity and phylogenetic relationships, for confirming presence of cryptic and undescribed species, as well as for associating immature and adult life stages [3]. The study confirmed the presence of 14 species of stoneflies. Detailed analyses of genetic diversity and examination of the phylogeographic structure were performed on four species with wider distribution range and with more sequences available in databases (*Isoperla grammatica, Brachyptera seticornis, Leuctra prima, Leuctra braueri*, and undescribed species *Leuctra* sp. ZB). Given the lack of similar studies in this area, the conducted research created the basis for future detailed morphological, genetic, and ecological studies of stoneflies and for tracking the effect of pollution through biomonitoring of this group. The study is part of the project *DNA barcoding of Croatian faunal biodiversity*, funded by the Croatian Science Foundation, which has the main goals: to provide first insight into genetic diversity of selected groups of Croatian fauna and to revise distributional ranges of particular species.

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The Invisible Universe of the Human Microbiome

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Keywords: microbiome, biofilm, symbiosis, dysbiosis

Microbiome is the full collection of genes of all microbes in a community. The genes in human microbiome outnumber the genes in their genome by about 100 to 1. We have recently started to understand the role of microbes in our bodies and, as it turns out, they are far more important than we could ever imagined. The term “microbes” is used to describe many different types of life forms with different sizes and characteristics, such as: bacteria, archaea, fungi. Every human being acquires their biofilm of microbes from the environment at birth. As we grow up, our microbial profiles change along with us. Indeed, it is shaped by family, friends, and social contacts in general.[1] A few microbes can cause diseases[2] like asthma, obesity, and diabetes, but most of them are essential for good health. In fact, we can optimize our gut and brain bacteria to improve our health. In addition to the effects of symbiosis, several metagenomic studies suggest that dysbiosis in the commensal microbiota is also associated with inflammatory disorders and various types of cancer throughout the body.[3] Dysbiosis is a major imbalance of the communities, and generated by diseases, genetics, or even bad lifestyle. Furthermore, research has shown that microbes can alter behaviour and help us figure out how they affect the brain. So, if we learn more about the microbes, we are coming to understand how restoring the balance may lead to more focused and effective treatments.

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The Incidence of Occupational Diseases Between 2017-2021 in Bacău, Romania

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Keywords: occupational diseases, work environment, silicosis

The International Labour Organisation [1] and the World Health Organisation estimates that 5–7% of global fatalities are attributable to work-related illnesses and occupational injuries [2]. Globally, 2.3 million deaths take place due to occupational injuries and work-related diseases annually [3]. In Bacău County during 2017-2021, according to data from the Public Health Department, 93 cases of occupational diseases were registered. In 2017, 17 cases were registered, 47 in 2018, 15 in 2019, 6 in 2020 and 8 in 2021. The aim of the study is to highlight the variation in the incidence of cases of occupational diseases and their interrelation with exposure to professional risk factors in the work environment. The types of occupational diseases that were registered are occupational diseases due to overuse of the locomotor apparatus: 51 cases (55%), silicosis: 34 cases (37%), diseases due to exposure to noise and vibration: 6 cases (6%), occupational asthma: one case (1%) and occupational tuberculosis: one case (1%). The main fields of activity where occupational diseases have been registered are metallurgy and forestry. Occupational diseases impose considerable costs on workers, their families, the health system, and society because they reduce productivity and work capacity.

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The Impact of Mitochondria in Neurodegenerative Diseases

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Keywords: Alzheimer’s disease, Huntington’s disease, mitochondrial dysfunction, neuronal cell death, Parkinson’s disease

Mitochondria are usually known as the powerhouse of the cells, because of their significant role in energy production, which is necessary for the survival of the organism. Some organs (like the brain) have higher energy needs than others and the biochemical processes of mitochondria in these cells have a critical role. In addition, cells in the central nervous system heavily rely on mitochondrial integrity. Mitochondrial dysfunction is one important pathological process in the etiology of neurological disorders. Extensive evidence from animal and clinical studies support this view. For instance, Huntington's disease, Parkinson's disease, Amyotrophic lateral sclerosis and Alzheimer's disease involves mitochondrial dysfunction and the most central pathological feature of the neurodegenerative diseases is apoptosis that is regulated by mitochondria.[1] Further evidence suggest that structural changes in mitochondria, including increased mitochondrial fragmentation and decreased mitochondrial fusion, are critical factors associated with mitochondrial dysfunction and cell death in aging and age-related diseases. Some mitochondrial abnormalities include abnormal mitochondrial enzyme activities, mitochondrial DNA defects, abnormal gene expression, deficiencies in proteostasis of mitochondrial proteins, abnormal mitophagy, oxidative stress and mitochondrial-driven inflammation. [2]These mechanisms will be briefly analyzed, so the impact they have in the development of neurodegenerative diseases, can be clearly understandable. In our days, the outbreak of diseases, such as Alzheimer’s and Parkinson’s, lead to an extended need for new therapeutic methods that may arise as a result of understanding the etiology of neurological disorders.

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Why Music, not Noise? Neural Mechanisms of Music Processing

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Keywords: neural processing, music, emotions, auditory cortex, EEG

Music is an important part of every culture and, for many, a part of daily life. It can be pleasing or displeasing to listen to, it can be cheerful, it can be sad or it can be scary. Without doubt, music evokes emotions – but how exactly do we perceive it at a neural level and why are our emotional states so easily influenced by it? Moreover, why are there so many individual differences in how exactly we enjoy and interpret music? How can we effectively use it in therapy? Is it truly intrinsic to human culture or is it more deep-rooted in evolution than we would be inclined to think? In this presentation, I will start by summarizing findings from literature explaining what we know and do not know about music perception in humans - from the ear, to the auditory cortex, to integration in the brain and subjective experiences of music – as well as non-humans: takeaways from other species that have the capacity to enjoy or even create music. In this context, I will also present some of my own research on this topic done with the help of the Cognitive Brain Research Unit at the University of Helsinki and my coordinator at the University of Bucharest.

Posidonia Oceanica Seagrass: Conservation Actions in the Balearic Islands

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Keywords: Posidonia, seagrass, conservation.

The marine phanerogam *Posidonia oceanica*, is a seagrass endemic to the Mediterranean Sea, largely extended at depths down to 40 m. Despite its large distribution, the rapid warming of the Mediterranean threatens its future persistence as the marine biodiversity linked to the meadows, particularly key ecosystems already stressed by other anthropic factors. With the support of scientific reports and the will to preserve, actions established and promoted through regulations by local governments are key to maintaining a strong and resilient roadmap to success. Public institutions and other companies that benefit from the Posidonia meadows contribute to promoting its conservation as enforced by the nature protection laws developed in the last decades. In the Balearic Islands, the administration, non-governmental organizations and stakeholders have joined forces through these new regulations. Intensive and uncontrolled anchoring[1] or the increase of marine traffic[2] are leading the species into severe damage. Also, the unsupervised removal of leaves washed ashore are exposing the coastline to regression over increasing extreme climate events.[3] Local authorities of the Balearic Islands aim to minimize these anthropic stressors over the seagrass lifecycle but also the uncontrolled removal of washed ashore leaves. In this presentation we will present the current conservation policies and actions to preserve the *P. oceanica* seagrass meadows, and show the effects and results implied by the Balearic local authorities regulations.

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Using Demographic Models to Characterize Population Dynamics and Guide Conservation Action in a Threatened Raptor

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Keywords: raptor, demography, threatened species, population dynamics, ecology

Expanding our understanding on the dynamics and demography of threatened species provides valuable knowledge on the main factors that drive these populations to increase, decrease or become extinct [1]. This can easily help conservation efforts to be efficiently focused on the key aspects of threatened populations and provide improved results globally [2]. Raptors are long-lived animals that are particularly sensitive to human-related mortality, to the extent that they are among the most threatened animal groups in the world [3]. However, our knowledge on their demography is limited due to their complex life cycles and population dynamics, which makes it difficult to manage imperilled raptor populations effectively. Throughout the course of my thesis, we took advantage of an intensive 13-year monitoring dataset on the regionally imperilled Bonelli's eagle (*Aquila fasciata*) in Catalonia to characterize its long-term dynamics with the ultimate aim of providing valuable insights for raptor conservation. In particular, we used novel quantitative methodologies such as spatial mark-recapture models, integrated population models, and fine-scale viability analyses to understand the demographic patterns of the population for the last 40 years, assess the reliability of our population estimates, and pinpoint parameters to be targeted by conservation action [4]. We expect the results of my thesis to provide valuable knowledge in the fields of ecology and demography that will help guide the conservation of threatened long-lived animals.

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Innovative Methods for Wildlife Monitoring

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Keywords: monitoring, wildlife, app, camera trapping

Monitoring (checking the distribution, numbers, etc.) of wildlife populations is fundamental for successful conservation or management plans of wildlife populations, whether we are talking about hunting or strictly protected species. Regular and systematic monitoring of several species is also required by Slovenian and European legislation. Not only researchers but also nature lovers today can make an exceptional contribution to better monitoring and understanding wildlife populations and their needs.

To conduct easier, better, and more systematic monitoring of selected species of wild animals, we developed an application called SRNA in cooperation with the Hunting Association of Slovenia and three research institutions (the University of Primorska, University of Ljubljana and Faculty of Environmental Protection of Velenje). The app allows those interested to record the observations of different animal species in nature.

Participants will learn about modern methods of monitoring wildlife in Slovenia using innovative SRNA app and camera traps. In the introductory part, participants will learn how to identify different wildlife species through an interactive quiz and how to use the SRNA app. They will learn how to enter and monitor data in the app. They will see videos taken by cameras in the field and will be given a brief introduction to the process of catching and monitoring of early mortality of European roe deer fawns in Slovenia.

A year (and a Half) of Fieldwork Across Europe. The Study of a Migratory Bird: The Black-Tailed Godwit (*Limosa limosa*)

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Keywords: black-tailed godwit, fieldwork, bird migration

Black-tailed godwits (*Limosa limosa*) are a classic example of long-distance migrators. In Europe we can find two subspecies: the one that winters below the Sahara desert in Africa and reproduces in central Europe (*L. l. limosa*) and the one that migrates less and winters in SW Europe while reproducing in Iceland (*L. l. islandica*) [1]. To try to study the possible consequences that this difference in effort between the migration of both subspecies can have in their physiology, reproductive success or survival rate, we organized the fieldwork in two parts. First, we captured over a hundred birds on their stopover grounds in SW Spain (Badajoz) and Western Portugal (Lisboa) in several ringing attempts carried out during the first weeks of 2022. We colour-ringed and measured them, took blood and feather samples and deployed several GPS transmitters to a few individuals. In that way, we could follow the same individuals to their breeding locations in the Netherlands and Germany and study their reproduction and take new samples. Additionally, and even though none of our birds went to Iceland, we also travelled there to capture families from the Icelandic subspecies and be able to compare their blood and feather samples in the lab after the summer. We are planning to do the same fieldwork in 2023. This talk will cover all the adventures experienced working with this magnificent species as well as give some preliminary results on the experiments done.

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Insects in a Changing World

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Keywords: climate change, insects, behavioural ecology, physiology

It is a fact that climate change is leading to a change in biodiversity patterns in many parts of the world. These changes result in shifts in the behaviour and distribution of many species (Kannan & James, 2009). In the case of insects, there is a growing interest in research due to the services they can provide and their use in various industries such as agriculture and food, acting as pollinators or in pest control (Harvey et al. 2023). However, in order to understand the mechanisms by which insect populations vary, it is relevant to first understand the physiological and behavioural effects that insects may suffer from increased temperature, aspects that have not been taken into account as joint variables in insect studies (Zachariassen, 1996) until very recently. It is important to note that much of the scientific literature addressing these issues mentions that there is often no link between studies in physiology and in ethology and therefore some of the most significant results collected may not be fully complete (Terblanche & Hoffmann, 2020).

Considering this background, this presentation will serve as an introduction to the project I will be working on during my PhD, where I will try to address the possible combination of the effects that temperature change may have on two predator-prey systems with similar function species at four different sites in Europe to see if these changes have to do with latitude and the possible adaptations of the different species to these changes at both metabolic and behavioural levels.

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Bee Misunderstood – The Fascinating World of The Wild Bees

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Keywords: pollinator, wild bee, ecology, Apidae

Within the wider public and press the term “bee” often gets associated with the domesticated honeybee. Wild bees are often not recognized as bees at all and knowledge about them is lacking. But there are around 20,000 bee species classified worldwide and about 720 species in Austria (as of 2016) [2]. Wild bees are not only of ecological importance for the pollination of a high number of wild plant species, they can also contribute to the pollination of agricultural crops [1, 2]. Due to various drivers there is a reported decline of wild and domesticated pollinators [1]. While the threat for honey bees is already widely acknowledged, the disappearance of wild bees is often not even noticed. Hence their conservation is of importance, but unfortunately the lack of knowledge within the wider public and on a political level can lead to problems when it comes to suitable management methods [3]. In this oral presentation I want to introduce you to the fascinating diversity of wild bees and hence the complexity of their requirements in habitats, nesting materials and often very specialized food resources. I want to talk further about their importance, current threats and why the focus on honey bees regarding biodiversity might be a problem.

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Reducing Animal Testing Through Alternatives

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Keywords: reduction, replacement, refinement; animal testing, alternatives

Animal testing remains one of the most controversial issues in biomedical research. In 2021, around 2 million animals were used for animal experiments in Germany [1]. Unfortunately, it is currently not possible to completely avoid animal testing. However, Directive 2010/63/EU strongly reinforces the adoption of the 3Rs (Refinement, Reduction and Replacement) for the use of animals for scientific and educational purposes. Against this background, two platforms, LAS interactive and 3R-SMART, aim to support people involved in animal testing and the 3Rs.

LAS interactive is a platform that includes an information platform on laboratory animal science topics (vtk online) and fee-based online training courses for people working with laboratory animals (las campus).

In addition, LAS interactive allows online course participants to acquire basic knowledge about the use of animals in experiments (Reduction) and how better animal welfare can have a positive impact on animal experiments (Refinement).

3R-SMART is an open platform that allows different 3R stakeholders to present their 3R efforts on the platform and provides educational content on alternative methods in the form of texts, explanatory videos, or lecture recordings, as well as news and updates, a calendar of upcoming events and a forum to exchange ideas in the field of 3R.

Together, these platforms can provide sustainable support for a wider knowledge of laboratory animal science and the implementation of the 3Rs.

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Presence of Microplastics in Water Column and Tissue of Farmed Mussel (*Mytilus galloprovincialis*) in the Slovenian Sea

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Keywords: microplastics, water pump, mussel, water column, sea, concentration of microwaste, concentration of microplastics, FTIR

Microplastic in the sea is a global problem, since the sea is an environment where plastics are coming from different surroundings. The Slovenian Sea is small part of the Adriatic, but still an important area of aquaculture. Some researchers found connections between water and mussels; that is why we analysed micro-waste and microplastics in sea water and mussel (*Mytilus galloprovincialis)* from three locations in Trieste bay – Seča, Strunjan and Debeli rtič. These are important farming areas providing most of the seafood grown in Slovenia.

Seawater samples were taken using a water pump and filtered using a 100 µm pore size inox sieve (in-situ sampling). For each sampling side tree parallels of 1 m^3 seawater were taken. Seawater was sampled at two depths to compare the level of micro-plastics and micro-waste in between depth. 18 m^3 seawater filtrates were analysed. In addition to seawater, mussels were collected from the same depth as water. For each sampling point we analysed 50 mussels. A total of 300 mussels were analysed, 100 for each aquaculture side.

Analyses were made with usage of Fourier-transform infrared spectroscopy (FTIR) and micro-FTIR.

Presence of micro-waste and micro-plastics was confirmed in all water samples. The upper sample layer of side called Debeli rtič was the most contaminated; we proved the highest concentrations of micro-waste and micro-plastics. Micro-waste was found in 75.7% of the mussels. The highest number for micro-waste per mussel was found in mussels from the Strunjan shellfish farm.

What Happens With Nanoparticles in the Marine Ecosystem?

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Keywords: nanoparticles, nanotechnology, marine, ecotoxicology

Nanotechnology is the manipulation of organic or inorganic material on a nanoscopic level while changing its properties. As a novel technology, it has promising use in many spheres of human life, such as biomedical research and pharmacology, construction and electronics, waste management and soil and water remediation, as a way of dealing with anthropogenic pollution; as coatings, conductors, insulators, indicators, adsorbents etc. The problem arises because of the inherent nature of nanoparticles themselves which is their tendency to aggregate, their high reactivity to other molecular structures (especially organics) and their cytotoxic and genotoxic properties. Commercial use of engineered nanomaterials has grown rapidly in the last two decades. Similarly, the world, especially the aquatic environment, faces a problem with these nanoparticles entering the food web possibly through bioaccumulation and biomagnification either as a suspension in the water or as a part of the sediment, often acting as immunomodulators and gene expression alterants. A lot has been discovered through recent scientific research regarding nanoparticles and their impact on the aquatic wildlife, even using some species of invertebrates as bioindicators for nanoparticle pollution. Since the implementation of nanomaterials in manufactured goods and scientific research will only rise in the future, safety and controlled disposal measures should be implemented for environmental protection and human health.

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What Happens in the Past, Stays in the Past (or not)?

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Keywords: foraminifera, paleoecology, reconstruction, micropaleontology

Foraminifera (lat. Foraminifera) are unicellular organisms that live mainly in marine environments as a part of plankton or benthos, belonging to the Rhizopoda cluster. Because of their short generation time, large abundance, and fast response to stressful conditions, foraminifera are excellent bioindicators. Furthermore, estuaries are complex coastal environments rich with some rare biota, and benthic foraminifera are the most common biological proxies used in paleoenvironmental reconstructions. This study will focus on the Holocene paleoenvironmental record of the Krka River salt-wedge estuary, specifically the Prokljan lake. The sediment core PROK-3 was analysed and interpreted through laboratory and statistical methods. Laboratory methods were micropaleontological analysis, radiocarbon dating, organic C/N analysis, and grain size. The results showed that sediments deposited during the last ~9 600 years were under the significant influence of sea level variability and different conditions. The core was divided into 3 zones. Zone 1 was in the basal part of the core. It was dominated by Ammonia tepida and implies by all analyses on the terrestrial environment. Zone 2 is the transition zone; A. tepida is still present but Haynesina sp. starts to dominate. It implies that the sea level rose during Holocene. Finally, Zone 3 is the typical marine environment with marine species like Haynesina sp., Elphidium translucens, Aubygna perlucida, Bulimina aculeata, and Miliolinella subrotunda. The results are important for the reconstruction of the Quaternary paleoenvironments along the eastern Adriatic coast, which is still insufficiently explored.

The presented data are part of the Croatian Science Foundation project "Sediments between source and sink during a Late Quaternary eustatic cycle: The Krka and the Mid Adriatic Deep System-QMAD".

POSTER PRESENTATION

The Effects of Long-Term Palm Oil Intake on Inflammatory and Oxidative Status in the Rat Hypothalamus

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Keywords: palm oil, hypothalamus, inflammation, oxidative stress

Palm oil has become the most consumed oil worldwide, yet its impact on health remains controversial. While some studies suggest potential benefits of consuming palm oil, others advise against it due to its high content of saturated fatty acids. Despite data on the effects of long-term palm oil intake on peripheral tissues, little is known about its impact on the brain, particularly the hypothalamus, which has a key role in regulating energy homeostasis. The present study aimed to investigate the effects of long-term intake of palm oil on markers of inflammation and oxidative stress in the hypothalamus.

Male *Wistar* rats were fed a palm oil-enriched diet (POD) prepared by soaking standard briquette chow in commercially available palm oil, for 21 weeks. The control group received standard chow. Body weight gain was measured weekly. After overnight fasting, blood samples were collected for serum measurement of IL-6. The rats were then perfused and hypothalami were isolated. Retroperitoneal and gonadal depots of white adipose tissue were extracted and weighed to measure visceral adiposity. Total hypothalamic RNA was transcribed to analyse the expression of NF-κβ, TLR 4, IL-6, IL-1β and Nrf 2 by RT-qPCR. Variations in the total redox status of the hypothalamus were measured by electron paramagnetic resonance spectroscopy.

POD induced a statistically significant increase in body weight and visceral adiposity, consistent with the reported downsides of palm oil consumption. However, no significant changes were observed in the circulating level of IL-6 or in the hypothalamic expression of NF-κβ, TLR 4, IL-6 and IL-1β. Similarly, total redox status and Nrf 2 expression remained unchanged. These results suggest that long-term intake of palm oil does not induce inflammation and oxidative stress in the hypothalamus. Our study contributes to the ongoing debate and highlights the importance of further research on the prolonged consumption of palm oil.

Homosexual Behaviour Of Animals

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Keywords: animal behaviour, sexual selection, homosexuality, adaptation

Homosexual behaviour of animals has usually been explained by disruptive behaviour. Recently, researchers have been unravelling some possible evolutionary origins for these behaviours and reasons for their manifestations in present species **[1]**. Here in my Bachelor´s thesis I have explored studies that tested both adaptive and non-adaptive reasons for the preservation of the same-sex sexual behaviour. I also compare the same-sex sexual behaviour between monogamous and polygamous bird species. Studies have found only a few non-adaptive reasons for same-sex sexual behaviour in animals. While studying the sexual behaviour of insects, researchers found that the most common maladaptive same-sex sexual behaviour was found to be wrong sex identification. However, numerous adaptive reasons were found, for example, social glue and intrasexual conflict **[2]**. The same-sex sexual behaviour differs a lot between monogamous and polygamous bird species. Studies have shown that female-female couples appeared in bird species who are monogamous and biparental. Same-sex mating was beneficial in populations where there were not enough males to mate with **[3]**. Male-male sexual behaviour occurred mostly in polygynous nests with at least one nesting female. Monogamous male-male couples were born only momentarily **[4]**.The studies that I explored found a lot of evidence that same-sex sexual behaviour in animals has an evolutionary benefit. Most of the articles I studied state that same-sex behaviour has adaptive value. On the other hand, some research results contradict each other. This topic has been discussed relatively little and many of the discoveries have been a by-product of some unrelated research. Same-sex sexual behaviour in animals has proven to be evolutionarily important so it would be very purposeful to study the phenomenon more in the future.

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Survival of the Eagle Owl, *Bubo bubo*

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Keywords: survival

My master thesis is about survival of the Eurasian eagle owl, B*ubo bubo*. **The work is still in progress**, but the results will be ready during the spring of 2023.

According to *BirdLife* (2021), about 250 bird species breed in Finland. The last time Finland's threatened birds were assessed was in 2019, which resulted in a red list. The red list includes all species that have been found to be extinct, endangered, poorly known or near-threatened species. Currently, even every other bird species breeding in Finland belongs to the red list in some way (pp. 4–7). The Eurasian eagle owl is one of these species (Hyvärinen et al., 2019).

Survival is the probability that an individual will survive for a given period. Through my research questions, I aim to investigate whether there has been a change in the survival of the Eurasian eagle owl between 1972 and 2021. I use the ringing data of the Eurasian eagle owl obtained from the Ringing Centre of the Helsinki Natural History Museum. The data has been collected from all over Finland between 1972 and 2021. During the study period, 17,314 individuals were collected, and 3,844 controls were collected. I perform preservation analyses on the data using dead recovery models in Mark software. The model is used to estimate the probability of discovery and the probability of survival. The aim is to fit different models to the data to explain the variation in survival being tested, for example, year and age variation. Model selection is done using the AIC and finally the model or models that best explain the variation in survival are selected. The research will be carried out at the University of Oulu.

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Lymphocytic Choriomeningitis Virus Infection Increases Cellular Lipid Droplets Levels

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Keywords: LCMV, virus-host interactions, lipid metabolism, lipid droplets

During their life cycle, viruses require macromolecules to produce new infectious virions. As viruses are entirely dependent on the metabolic machinery of host cells, they need to rewire and adjust cellular metabolic pathways according to their needs. In our research, we focus on metabolic alterations induced by infection with lymphocytic choriomeningitis virus (LCMV), a prototypic virus of the *Arenaviridae* family. Our previous results showed that LCMV infection increases fatty acid biosynthesis by enhancing the activity of lipogenic enzymes; thus, we addressed the question whether LCMV infection affects cellular lipid composition.

First, we extracted total cellular lipids from both mock- and LCMV-infected MRC5 cells at different time intervals post-infection (hpi) and performed a thin-layer chromatography. At 48 hpi, LCMV infection caused a 1.7-fold increase in triglycerides (TAGs) and a 1.6-fold increase in steryl esters (SEs), both of which are the main components of lipid droplets. In addition, we observed a 1.3-fold increase in SEs at 72 hpi. Following that, we stained LDs in mock- and LCMV-infected cells using Oil Red O dye, which revealed an increase in LD levels in LCMV-infected cells at 48 and 72 hpi when compared to mock-infected cells. These results suggest that the previously observed increase in fatty acid synthesis leads to the increase in TAGs and later LDs, which are required during the later stages of LCMV infections. However, the exact mechanism underlying this process, as well as the role of LDs in the LCMV life cycle, remains to be elucidated.

Leaf Micromorphological Changes in Cadmium-Treated Bean Plants (*Phaseolus vulgaris* L.)

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Keywords: cadmium, contamination, bean, leaf, stomata, trichomes

Cadmium (Cd) is one of the major environmental pollutants due to its wide industrial use. The negative impact that cadmium has on plants is reflected in changes of the anatomical characteristics of the plant tissues as well as in reduction of chlorophyll synthesis and photosynthetic activity. We studied the effects of cadmium on epidermal features of three *Phaseolus vulgaris* L. genotypes, two cadmium resistant (CP-PV-59, CP-PV-76) and one cadmium sensitive (CP-PV-283). Cadmium impact was studied on adaxial and abaxial epidermises of prophylls and foliage leaves. The characters such as stomata and trichome number, length, width, index and area of stomata were subject of this study. Analyses and measurements of epidermal prints were carried out using a light microscope, while their micromorphological characteristics were the subject of scanning electron microscopy (SEM). SEM analyses revealed presence of nonglandular (with straight and hooked apical part) and glandular trichomes on both leaf types of all analysed genotypes. Statistical analysis (Duncan test, Student's t-test) showed that cadmium had more significant effect on foliage leaves than on prophylls. Our study reveals that cadmium has the greatest influence on the dimension of stomata and their number on both types of the leaves, while it had small effect on trichome number and on stomata index.

Nanoscale Spatial Arrangement of Ibuprofen in the Lipid Bilayer According to Double Electron-Electron Resonance Spectroscopy Data

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Keywords: non-steroidal anti-inflammatory drug, NSAID, model biological membranes, lipid bilayer, PELDOR, sl-ibuprofen

In this work, we study the nanoscale spatial arrangement of the non-steroidal anti-inflammatory drug (NSAID) ibuprofen in model biological membranes. Currently, NSAIDs are being improved to increase their bioavailability, the possibility of use in combination with other drugs, and to reduce the negative impact on the gastrointestinal tract. The study of the molecular mechanisms of the interaction of drugs with lipid membranes is important for the development of drugs, improving their delivery and uptake by cells, which reduces possible side effects.

EPR data showed that spin-labelled ibuprofen is bounding to the model lipid membranes. The immersion depth into the membrane was found with pulsed EPR (^{2}H ESEEM spectroscopy) in D_2O hydrated bilayers, the results indicate that spin label is buried in the hydrophobic bilayer interior [1].

Double electron-electron resonance spectroscopy (PELDOR) provides information on the nanoscale spatial arrangement of spin-labelled molecules. Here, PELDOR was applied to study (mono-) spin-labelled ibuprofen (ibuprofen-SL) in a bilayer of palmitoyl-oleoyl-sn-glycerophosphocholine (POPC). The results obtained by PELDOR show that the ibuprofen-SL molecules are located within a plane in each bilayer leaflet. At their low molar concentration in the bilayer χ, the found surface concentration of ibuprofen-SL is two times higher than χ, which can be explained by alternative assembling in the two leaflets of the bilayer. When $\chi > 2$ mol%, these assemblies merge. The findings shed new light on the nanoscale spatial arrangement of ibuprofen in biological membranes. These data may be useful in the development of theoretical models of the interaction of ibuprofen with the membrane in the future [2]. This work was supported by RSF, Grant № 21-13-00025.

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Carbonic Anhydrase IX is Upregulated by Adipokine Leptin in Breast and Colorectal Cancer Cells

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Keywords: obesity, hypoxia, carbonic anhydrase IX, colorectal cancer, breast cancer

The alterations in the adipose tissue (AT) caused by obesity are contributing factors to numerous human diseases, including breast (BC) and colorectal (CRC) cancer. Dysfunctional AT secretes several adipokines, *e.g.* leptin, which are involved in carcinogenesis and affect tumour growth, invasion, and metastatic spread. Circulating levels or leptin are proportional to the total AT mass; increased in obese and decreased in lean subjects. Moreover, excess body fat also results in the development of hypoxia, a state characterized by low oxygen concentration. Carbonic anhydrase IX (CA IX) is one of the most potent hypoxia-induced proteins, creating extracellular acidosis which further promotes cancer cell migration and invasion. Its expression correlates with the poor prognosis of cancer patients and resistance to therapy.

The aim of the presented work was to investigate the effect of leptin on the biological characteristics of two types of cancer cells. HCT116 and ZR-75-1 cell lines representing CRC and BC, respectively, were treated with increasing leptin concentrations and cultivated under normoxic and hypoxic conditions. Subsequently, the effect of leptin treatment on cell proliferation (MTT assay) as well as on CA IX expression (real-time PCR, Western blot) was analysed. We confirmed that leptin does not significantly affect cell viability. Our data also shows that leptin upregulated CA IX expression at the gene and protein levels in both CRC and BC cells. While the highest leptin concentration mostly induced CA IX expression in HCT116 cells, ZR-75-1 cells were found to be more sensitive to leptin treatment.

Overall, the obtained results demonstrate that leptin treatment induces CA IX protein and *CA9* gene expression. Future investigations, including functional analysis, will allow us to unravel the significance of leptin-induced CA IX expression in cancer cells and thereby better understand the molecular mechanisms linking obesity and cancer.

Acknowledgement: *VEGA 2/0076/20, APP0434, IMTS: 313011V344*

The Role of Pine Sawfly Larval Secretions in Ant Self-Medication.

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Keywords: self-medication, Formica fusca, Diprionidae

Ants are eusocial insects and have many complex mechanisms in place to protect the colony from harm. As one example some species such as *Formic fusca* have been proven to practice self-medication as a means to defend against pathogens threatening the colony. Pine sawfly larvae defend themselves against predation by secreting unpalatable fluids. These defensive secretions, however, have antifungal properties derived from resin acids in the larval diet **[1]**. This makes them a potential source of medicine for ants suffering from a fungal infection. In theory, ants could collect the larval secretions by preying on larvae or by collecting empty cocoons that still contain some of the fluid after the insect has matured.

We want to find out if ants of the species *Formica fusca* can utilize the secretions produced by pine sawfly larvae to fend off fungal infection. This will be studied by gathering 30 wild *F. fusca* colonies and dividing these colonies each into four treatments. Treatment 1: Ants get infected with the fungus *Beauveria bassiana* and get a choice between normal ant food and ant food laced with sawfly (*Diprion pini)* larval secretions. Treatment 2: Ants get sham treated and get a choice between normal ant food and ant food laced with larval secretions. Treatment 3: Ants get sham treated and receive only normal ant food. Treatment 4: Ants get sham treated and receive only ant food laced with larval secretions. In addition, we want to test how ants react to both living *D. pini* larvae and the empty cocoons. The experiment will be conducted later this spring in May, and the collected data will be analysed in June. In July, I should have results to present.

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Analysis of Molecular Diversity of *Cheilosia crassiseta* Loew, 1859 (Diptera, Syrphidae)

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Keywords: COI, 28S, ITS2, molecular taxonomy

The genus *Cheilosia* is one of the most diverse and speciose genera of hoverflies (Diptera, Syrphidae) and is recognized as an insect pollinator of exceptional importance in both natural and agricultural ecosystems. Considering the pollinator decline in many ecosystems worldwide, it is necessary to properly identify and delineate existing species. The aim of this study is to use molecular data to confirm delineation of three morphologically similar hoverfly species currently known under one species name, *Cheilosia crassiseta*. We analysed 35 specimens from Slovenia, Montenegro and Switzerland. The genomic DNA was extracted from the insect legs and used for PCR amplification and sequencing of one mitochondrial, (5' end of the COI gene) and two nuclear (28S rRNA gene and ITS2 region), markers. Sequences were used for Maximum parsimony and Maximum likelihood trees construction. The highest sequence variability was found for the COI gene, followed by ITS2 region and 28S rRNA. However, applied molecular markers failed to confirm species delineation within *Cheilosia crassiseta*. The exception was one specimen collected on Triglav in Slovenia that forms a separate branch on both COI trees outside of the *Cheilosia crassiseta* clade and do not match to any of the known *Cheilosia* species based on a BLAST search of NCBI database and a search of DNA barcodes in BOLD systems, which makes it a possible new species whose status is yet to be confirmed.

Acknowledgement: This research received support from the SYNTHESYS+ project http://www.synthesys.info/ which is financed by European Community Research Infrastructure Action under the H2020 Integrating Activities Programme, (grant agreement number 823827), and by the Ministry of Science, Technological Development, and Innovations of the Republic of Serbia (grant agreement number 451-03-47/2023-01/200358).

Integrated Strategy For Rehabilitation Of Disturbed Land Surfaces And Control Of Air Pollution (RECAP)

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Keywords: abiotic, biocrust, cyanobacteria, microbiota, substrates

Land degradation affects more than 40% of terrestrial ecosystems worldwide, impairing their functionality. Biocrust carpet engineering, utilizing cyanobacteria as primary colonizers, has been proposed as a potential solution. However, rehabilitation efforts are often hindered by the lengthy recovery period caused by limited moisture availability during the initial phase. The RECAP project aims to address this challenge by introducing a novel approach to land rehabilitation. It involves the utilization of tailored geo-prebiotic polysaccharide supports to establish a sustainable relationship between microbiota and abiotic constituents in degraded land surfaces. The project encompasses ecophysiological characterization of cyanobacterial strains, preparation and selection of polysaccharide supports, cultivation experiments, performance and safety assessments, and result dissemination. The project's commercially promising outcomes are intended to be patented. The RECAP concept, comprising customized polysaccharides and cyanobacterial strains, offers a viable solution for rehabilitating various degraded lands, substrates, and addressing air pollution concerns. It provides ecologically friendly and economically feasible methods for the sustainable restoration and development of damaged land surfaces impacted by industrial activities and desertification, both domestically in Serbia and internationally. Additionally, RECAP has the potential to mitigate future famine risks by reclaiming and enhancing arable lands and pastures. Policymakers and land remediation authorities will benefit from the findings and insights generated by the RECAP project.

Characteristics of Community Surface Temperature of Intensive and Extensive Meadows Using Thermal Imaging

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Keywords: plant species richness, vegetation, canopy surface temperature, urban and suburban areas

Extensive meadows are among the most diverse and species-rich habitats in Europe. Intensification of management in recent decades has converted many species-rich meadows into species-poor plant communities, and there is strong evidence that declining plant species richness is affecting many important ecosystem functions. In our study, we focused on the role of grassland plant species richness in regulating canopy surface temperature, which may be important for processes such as herbivory or flower visitation and may also influence microbial processes in the soil. We investigated several aspects of biodiversity and land use that influence the surface temperature of different types of grasslands in urban and suburban areas. The study is based on 27 vegetation plots and thermal imaging of the same plots. The vegetation plots were divided into urban (intensive meadows) and suburban (extensive meadows) plots. Vegetation data were collected in July 2022, and we used thermal images from an infrared camera (IR) to calculate the mean and variation in surface temperature of the grassland communities. We found that species richness and the presence of different functional plant types increased spatial variation in canopy surface temperatures, creating a heterogeneous pattern of 'heat-scape' pattern within the meadow. Diverse plant communities tend to have taller and more densely packed canopies than less diverse communities. As a result, they absorb more radiation, have greater transpiring leaf surface area, and are better coupled to the atmosphere, resulting in cooler canopy surfaces.

Aggregation Mechanisms of D(G_4C_2) Repeats Associated With Neurological Disorders ALS in FTD

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Keywords: DNA, oligonucleotides, quadruplex, dynamic light scattering, diffusion coefficient

DNA is a molecule classified as nucleic acid and consists of four organic nitrogen DNA bases named adenine, thymine, guanine, and cytosine. The best-known form of DNA is the so-called double helix, but DNA molecules can also form other structures of high order. Guanine-rich DNA sequences self-assemble into highly stable fourfold structures known as DNA quadruplexes. We have studied the G-rich DNA sequences d(G_4C_2)$_n$ with n = 1, 2, 4, that are found in the *C0orf72* gene. A large number of these G_4C_2 repeats are associated with some fatal neurological disorders, especially amyotrophic lateral sclerosis (ALS) and frontotemporal dementia (FTD). The formation of quadruplexes from G_4C_2 repeats thus limits the normal functioning of the cellular process and the functioning of the gene. Measurements were made by using dynamic light scattering. We determined translational diffusion coefficients and consequently resolve the length of the larger aggregates formed in the solution. The diffusion coefficient of the sequence G_4C_2 is $0.20 \cdot 10^{-10}$ m^2/s, which means that the G_4C_2 forms extremely long aggregates with lengths beyond 80 nm. The sequence (G_4C_2)$_2$ is characterized by a relatively short stacked dimeric quadruplex since the diffusion coefficient value was calculated to be $1.40 \cdot 10^{-10}$ m^2/s. The sequence (G_4C_2)$_4$ forms aggregates of multimers corresponding to seven stacked intramolecular quadruplexes. The diffusion coefficient of this sequence is $0.80 \cdot 10^{-10}$ m^2/s [1]. We found that all three sequences assemble into a longer structure than previously reported. We confirmed that sequences indeed form G-quadruplexes and could thus be associated with the formation of neurodegenerative disorders.

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Generation of SARS-Cov-2 Pseudotypes for Monitoring the Humoral Immune Response Against the Newly Emerged (Sub)Variants

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Keywords: SARS-CoV-2, pseudotypes, neutralisation assays, humoral immune response

The occurrence of new (sub)variant-driven infection waves across the globe indicates that the coronavirus disease 2019 (COVID-19) pandemic is not over. Continuous emergence of new severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variants can be anticipated.

Because of the occurrence of new mutations in the virus genome, there is a need for monitoring the ability of the human immune system to neutralize the newly occurring (sub)variants, in case of potential immune escape. However, the accessibility of the specific virus (sub)variant is initially very limited and often delayed to the time point when the variant is already prevalent globally. Therefore, other options have been sought to perform neutralisation assays even before the clinical samples with the new variant are available in a given region. An approach called "pseudotyping" has already been shown in numerous studies. It is considered a solid and reliable substitute for the live virus for testing neutralisation activity because of its safety (BSL2 conditions) and versatility.

In this study, we generated SARS-CoV-2 pseudotypes based on a vesicular stomatitis virus (VSV) system which lacks envelope G glycoprotein (VSVΔG) and bears S protein from different SARS-CoV-2 variants. For the pseudotype visualization and quantification, the green fluorescence protein (GFP) is used, which is incorporated into the VSVΔG genome. To create a complete VSVΔG-GFP-S pseudotype, the cell transfection with plasmids with targeted S protein and the infection of the cells was done. Several other methods for verification of pseudotype product were used, such as immunofluorescence for specific verification of the spike protein presence, or titration for pseudovirus quantification. Moreover, pseudotype-based neutralization assays are compared with live virus-based neutralization assays using the same sera samples. Altogether, we generated and characterized SARS-CoV-2 pseudotypes that are going to be used in the broader study of the humoral immune system.

WORKSHOPS

Computational/*In Silico* Approach of the Potential Role of N-acylethanolamines as Inhibitors of E-protein of Coronavirus SARS-CoV-2

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Keywords: coronavirus, SARS-CoV-2, E-protein, N-acylethanolamines, molecular docking

Today, the worldwide coronavirus SARS-CoV-2 pandemic puts a special emphasis on the search for non-toxic biologically active compounds that can have anti-coronavirus effects and can be used to develop a cure.

N-acylethanolamines is a class of minor lipids that demonstrate high biological properties. These molecules are part of the endocannabinoid retrograde neurotransmitter system in humans and mammals. Early work by the Department of Lipid Biochemistry at the O.V. Palladin Institute of Biochemistry showed that saturated N-stearoylethanolamine has powerful antiviral activity against H1N1 influenza, herpes simplex, and hepatitis C viruses.

It was also identified that the E-protein plays an important role in the coronavirus genome implementation and can be used as a target for antiviral substances.

In this project, molecular docking was used to model the potential of N-acylethanolamines to bind with the active sites of the E-protein. Molecular docking and spatial structure preparation of N-acylethanolamines were carried out using the program AutoDockTools 1.5.6. After conducting the molecular docking, we obtained affinity for the active site of each N-acylethanolamine, then calculated the inhibition constant, and determined the binding sites with suitable receptors. The results indicate that all N-acylethanolamines can bind with the active site of the E-protein of coronavirus SARS-CoV-2; however N-stearoylethanolamine has the highest affinity to the active site and inhibition constant. Our results support the hypothesis of using N-stearoylethanolamine as a potential anti-coronavirus SARS-CoV-2 active compound in the human organism.

The workshop aims to introduce the use of bioinformatics tools for *in silico* experiments, with a focus on hands-on learning using the AutoDockTools environment. Attendees will gain a solid understanding of the computational approach, from preparation to final analysis, through explanations and practical tasks. The goal is to allow participants to independently analyse molecular docking results for a further *in vitro* stage of research.

Making Science Interesting Again: Podcasting as a Form of Science Communication

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Keywords: podcast, presenting, science communication, deep-sea, marine biology

Science is often put into a box of 'too boring/too difficult/too clever for me' by the general public, and even within the scientific community, certain subjects are seen as 'not as important' as others.[1] Working as a deep-sea science communicator, I have repeatedly heard the deep-sea labelled as 'out of sight, out of mind' by colleagues, a viewpoint often reflected in the media. Becoming frustrated with how the deep-sea was being relayed, we started 'The Deep-Sea Podcast' as a chance to speak with people directly about our field. Our subsequent (and admittedly unexpected) success has opened the door to a hoard of opportunities and experiences, proving an effective method of communicating science to a wider audience.

Making use of more captivating forms of science communication is vital in making science interesting again to the general public. Furthermore, culturing an appreciation for your own field of science is fundamental in order to disseminate research, secure funding and work more closely across disciplines.

The goal of this workshop is to leave you feeling more prepared about how to present your science in an engaging and interesting way. These skills can then be used in a variety of applications, like podcasting, presenting or public speaking.

We will brainstorm ideas of how to define your own personal style/format, how to think about your audience and their expectations, and how to feel confident whilst presenting. I have utilised these skills in my own career, whilst giving talks, creating content and producing the podcast. We have now reached the Top 2.5% of all global podcasts and regularly chart under Life Science podcasts in the UK, USA, Germany and Australia, proving that even with niche topics, an engaging medium can be impactful.

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Performing Multivariate Linear Regression Models With R

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Keywords: multivariate regression, predictive models, biostatistics, biomedicine, bioinformatics

Regression models are statistical models to analyse the relationship between different independent variables and a dependent variable known as response outcome. Numerous clinical data measures or variables (e.g. Blood Pressure, age, clinical biomarkers, etc.) present a strong relationship with clinical outcomes of interest (e.g. risk to develop a disease, death outcome, etc.) and this relationship can be studied through regression models. If a model finds a strong correlation between some clinical variables and the response clinical outcome, this regression can be used to predict the clinical outcome for patients based on the values of these variables. For instance, we can predict how likely it is that a patient will survive a disease given the administration of different treatments and that the patient presents some co-morbidities.

During this workshop I will introduce you to specific terminology and concepts of statistical regression models, and I will show you how to perform linear regression models adjusting for multiple variables (covariates) following a script with R programming language that includes some exercises for understanding the functioning of the code. Please be aware that you will need a computer with the latest version of RStudio (https://posit.co/download/rstudio-desktop/) installed for this workshop.

Scientist – A Man of Many Faces. What Do a Nerd, an Entertainer, and a Salesman Have in Common?

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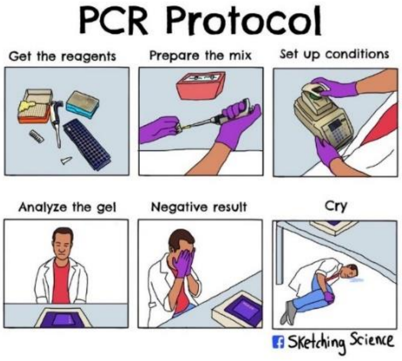
Keywords: grant proposals, academic writing, presentations

Living in fast-changing surroundings is full of challenges. Especially when you are a scientist and you are living in the 21st century. Trends change like in a kaleidoscope, and you want to keep up with it, while not losing your identity. In a constant stream of information, it's difficult to not get lost in the noise. To calm your senses and clear your vision. And everything starts with a vision.

A popular illustration [1] presenting the steps of a PCR protocol is as follows:



Writing a good grant proposal or publication looks more or less the same. If you're skilled (and/or lucky enough…) you may avoid the last two steps. Still, your piece of work will be analysed. Or using a more proper and probably one of the most hated words in the scientific universe: reviewed. Someone will see it. And you want your vision to be clearly seen.

This workshop will be focused on creating your scientific vision (project idea) and working on putting it into real existence (grant proposal, publication, presentation). You will be guided through the scientific chaos to the land of splendour and the Nobel prize (almost). In the end, you will find out what a nerd, an entertainer, and a salesman have in common.

This is supported by the Doctoral Research Grant funded by the University of Lodz.

References:

[1]: Sketching Science, https://sketchingscience.org/

Science Writing: How To Get Good at Captivating Others With Your Ideas

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Keywords: science writing, blog article writing

We live in a world full of brilliant novel ideas. Maybe you're even an owner of one. But to let those ideas shine, we have to know how to effectively communicate them to others. Some may say that's even more important than creating them. Yet throughout our education, we are rarely taught how to do it with excellence. In this workshop, I want to change that. I will help you transform your writing skills so that your ideas come across clearly and so that you can grip others with what you have to say.

I am an undergraduate student of medical biology, who is currently working as a science writer for a biohacking magazine.

In this workshop, I will bring you on a journey to carefully observe how a poorly written text undergoes a magical transformation into something brilliant. You will learn how non-academic blog post writing is different from academic writing, how to identify what makes it good, and how to excel at this writing style. I will share my personal tips about how to spice up a blog post, and what common mistakes people make. In the end, you will write something of your own, and get as much feedback as you want (or as the schedule allows us). By the end of the workshop, your writing skills will improve by at least 1% (hopefully).

Innovative Methods for Wildlife Monitoring

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Keywords: monitoring, wildlife, app, camera trapping

Monitoring (checking the distribution, numbers, etc.) of wildlife populations is fundamental for successful conservation or management plans of wildlife populations, whether we are talking about hunting or strictly protected species. Regular and systematic monitoring of several species is also required by Slovenian and European legislation. Not only researchers but also nature lovers today can make an exceptional contribution to better monitoring and understanding wildlife populations and their needs.

To conduct easier, better, and more systematic monitoring of selected species of wild animals, we developed an application called SRNA in cooperation with the Hunting Association of Slovenia and three research institutions (the University of Primorska, University of Ljubljana and Faculty of Environmental Protection of Velenje). The app allows those interested to record the observations of different animal species in nature.

At the workshop, participants will learn about modern methods of monitoring wildlife in Slovenia using the innovative SRNA app and camera traps. In the introductory part, participants will learn how to identify different wildlife species through an interactive quiz and how to use the SRNA app. They will learn how to enter and monitor data in the app. They will see videos taken by cameras in the field and will be given a brief introduction to the process of catching and monitoring of early mortality of European roe deer fawns in Slovenia. The second part of the workshop will take place outdoors, close to the facility where the workshops will be organised, weather permitting. Participants will have an interactive challenge to find hidden animals (mock-ups) and record the data in a wildlife research app for Slovenia.

SUPPORTERS

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