

## ABOUT DYNALIFE

In the mid-twentieth century two new scientific disciplines emerged forcefully: molecular biology and information-communication theory. At the beginning cross-fertilisation was so deep that the term genetic code was universally accepted for describing the meaning of triplets of mRNA (codons) as amino acids. However, today, such synergy has not taken advantage of the vertiginous advances in the two disciplines and presents more challenges than answers. These challenges are not only of great theoretical relevance but also represent unavoidable milestones for next generation biology: from personalized genetic therapy and diagnosis, to artificial life, to the production of biologically active proteins. Moreover, the matter is intimately connected to a paradigm shift needed in theoretical biology, pioneered long time ago in Europe, and that requires combined contributions from disciplines well outside the biological realm. The use of information as a conceptual metaphor needs to be turned into quantitative and predictive models that can be tested empirically and integrated in a unified view. The successful achievement of these tasks requires a wide multidisciplinary approach, and Europe is uniquely placed to construct a world leading network to address such an endeavour.

The aim of this Action is to connect involved research groups throughout Europe into a strong network that promotes innovative and high-impact multi and inter-disciplinary research and, at the same time, to develop a strong dissemination activity aimed at breaking the communication barriers between disciplines, at forming young researchers, and at bringing the field closer to a broad general audience.

COST (European Cooperation in Science and Technology) is a funding agency for research and innovation networks. Our Actions help connect research initiatives across Europe and enable scientists to grow their ideas by sharing them with their peers. This boosts their research, career and innovation.

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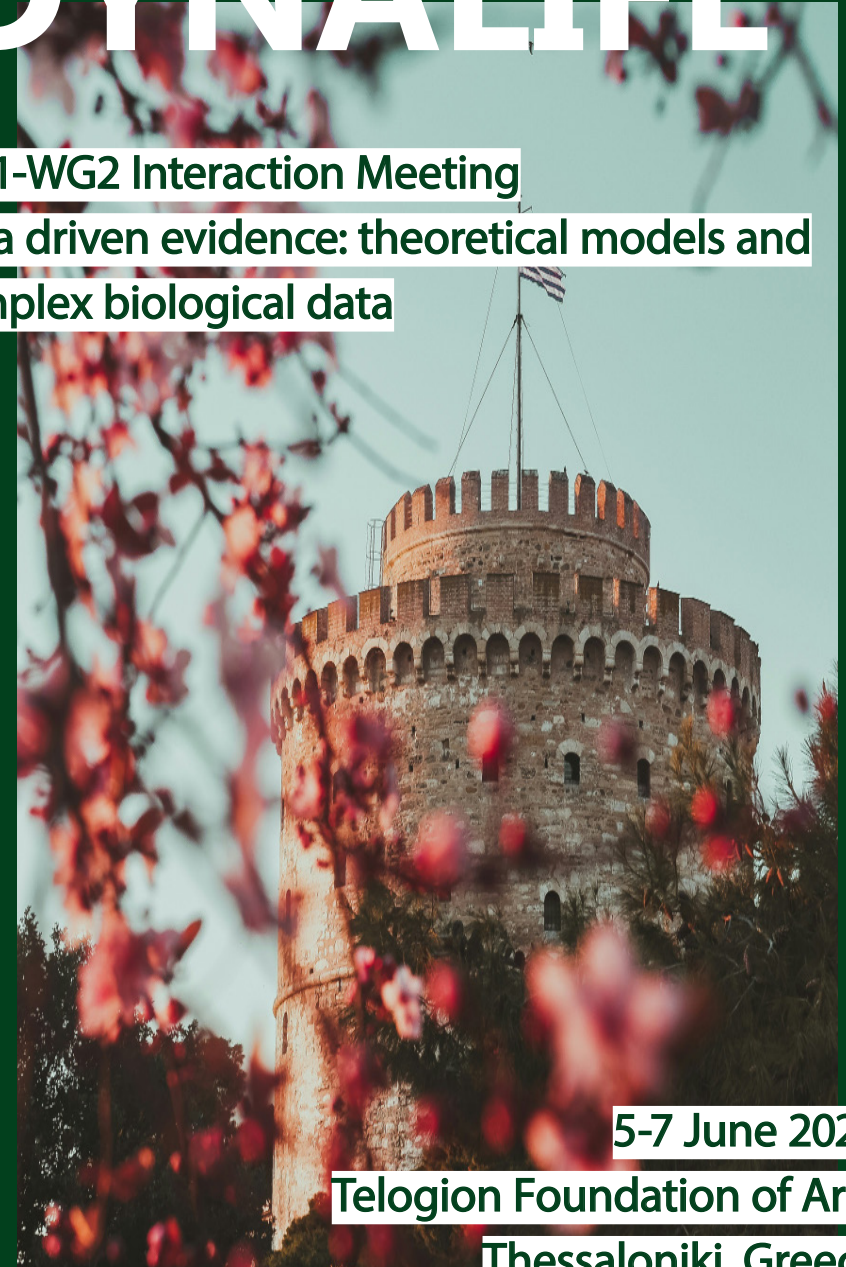


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the European Union

# DYNALIFE

WG1-WG2 Interaction Meeting

Data driven evidence: theoretical models and complex biological data



5-7 June 2024

Telogion Foundation of Arts

Thessaloniki, Greece

**WEDNESDAY, 5 JUNE 2024**

09:00 – 10:00	<b>REGISTRATION</b>	13:05 – 13:25	Michel Planat (CNRS, Université de Franche-Comté, France) <b>Topology and dynamics of transcriptome (dys)regulation</b>
10:00 – 10:15	<b>WELCOME</b>	13:30 – 14:40	<b>LUNCH BREAK</b>
10:15 – 11:15	<b>KEYNOTE LECTURE 1</b> Marcos de la Pena (CSIC-UPV, Spain) <b>A new RNA world of infectious agents with minimal circular genomes</b>	14:40 – 15:00	Slobodan Zdravkovic (University of Belgrade, Serbia) <b>Helicoidal-Peyrard-Bishop model for DNA dynamics and micro-manipulation experiments</b>
11:15 – 11:45	<b>BREAK</b>	15:00 – 15:20	Dalibor Chevizovich (Vinca Institute of Nuclear Sciences, University of Belgrade, Serbia) <b>Migration of single excitation and loss of information contained in DNA</b>
11:45 – 12:05	Diego Gonzalez (IMM-CNR, Italy) <b>Biological void is highly structured: nullomers and genomic rare sequences</b>	15:20 – 15:40	Julyan Cartwright (CSIC-Universidad de Granada, Spain) <b>Directed self-assembly, genomic assembly complexity and the formation of biological structure, or, what are the genes for nacre?</b>
12:05 – 12:25	Ivan Marqués Campillo (University of Balearic Islands, Spain) <b>Genomic Sequences, Fractals and the ambiguity of Nullomers.</b>	15:40 – 16:00	Elena Pohl (University of Veterinary Medicine, Austria) <b>Mechanism of the proton transport mediated by ATP/ADP carrier</b>
12:25 – 12:45	Ozgur YILDIRIM (Yildiz Technical University, Turkey) <b>On the stable difference schemes solution of nonlinear system of sine-Gordon equations corresponding to DNA dynamics</b>	16:00 – 16:20	Marco Patriarca (National Institute of Chemical Physics and Biophysics-Tallinn, Estonia) <b>Diffusion processes on periodic and disordered substrates</b>
12:45 – 13:05	Stefano Piotto (University of Salerno, Italy) <b>Synonymous codon utilization in proteins: preserving function over sequence and investigating cross-species nullomer and antimicrobial peptide (AMP) correlations</b>		

**PARTICIPANTS**

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**09**  
Panagiotis Sarantidis  
(Aristotle University of Thessaloniki, Greece)  
**Exploring Biological Networks with Deep Learning Methods and Omics data of Cancer Patients**

**10**  
Hamid Khoshfekar Rudhari  
(Oslo University Hospital, Norway)  
**Polygenic Risk Score Analysis for Juvenile Idiopathic Arthritis**

**11**  
He Li  
(Radboud University, Netherlands)  
**Statistical Integration of Multi-Omics for Outcome Variables**

**12**  
Aleksej Gaj  
(Institute of Information Theory and Automation, Czech Academy of Sciences, Czech Republic)  
**Agent-based cooperation in shared environment**

**13**  
Anna Krakovská  
(Slovak Academy of Sciences, Slovakia)  
**Selection of methods derived from dynamical systems theory**

**14**  
Nicolina Pop  
(Politehnica University Timisoara, Romania)

**Study of dynamical systems by Modified Optimal Homotopy Asymptotic method**

**15**  
Persefoni Talimtzí  
(Aristotle University of Thessaloniki, Greece)  
**Evaluation of systematic reviews of prognostic models for COVID-19: an overview of systematic reviews**

**16**  
Mahmut Sinan Taspınar  
(Ataturk University, Turkey)  
**A comparison nonlinear models to describe the growth of laying hens**

**17**  
Ariane Gabriel Talleé Kakeu  
(Hochschule Mannheim (Germany) and University of Dschang (Cameroon), Germany)  
**Isomorphisms of Maximal Self-Complementary  $C^3$ -Codes**

**18**  
Chanelle Olivade Kamga  
(Hochschule Mannheim, Germany)  
**Personal Interest in Mathematical Biology**

**19**  
Vuk Jovovic  
(Non Government Organization PRONA and University of Montenegro, Montenegro)  
**Bridging Theory and Practice: My Academic and Professional Path in Mathematics**

16:20 – 16:40 **BREAK**  
16:40 – 17:00 Peter Wills  
(University of Tübingen, Germany)  
**Emergent computational control of molecular processes via genetic coding**

17:00 – 17:20 Nataša Mišić  
(R&D Institute Lola Belgrade, Serbia)  
**Predicting structural disorder of proteins using the wavelet transforms**

17:20 – 18:20 **MC MEETING**

18:30 – 19:30 **“FAKE FOR REAL” GUIDED TOUR**

19:30 **WELCOME DRINKS**

### **THURSDAY, 6 JUNE 2024**

09:15 – 09:45 **REGISTRATION**

09:45 – 10:45 **KEYNOTE LECTURE 2**  
Haeran Cho  
(University of Bristol, UK)  
**Data segmentation: Univariate mean change and beyond**

10:45 – 11:10 Guillem Rigail  
(INRAE, France)  
**DiffSegR: an RNA-seq data driven method for differential expression analysis using changepoint detection**

11:10 – 11:35 Israel Martinez Hernandez  
(Lancaster University, UK)  
**Changepoint method for a time-dependent sequence of 0-1 values**

11:35 – 12:00 **BREAK**

12:00 – 12:45 **ORAL POSTER PRESENTATIONS**

12:45 – 13:30 **POSTER SESSION**

13:30 – 15:00 **LUNCH BREAK**

15:00 – 16:00 **KEYNOTE LECTURE 3**  
Mark Robinson  
(University of Zurich, Switzerland)  
**Analysis of spatial omics data using functional data analysis**

16:00 – 16:20 Said el Bouhaddani  
(UMC Utrecht, Netherlands)  
**Augmenting multi-omics integration with prior-informed imputation and drug information**

16:20 – 16:40 Rosember Guerra Urzola  
(Tilburg University, Netherlands)  
**Optimal penalized sparse PCA**

16:40 – 17:00 Dragana Dudic  
(Faculty of Computer Science and Informatics, University Union Nikola Tesla, Serbia)  
**Integration of single cell transcriptome sequencing data of head and neck cancer cells**

17:00 – 17:15 **BREAK**

17:15 – 18:00 **WG2 MEETING**  
Jeanine

18:00 – 18:30 **DISCUSSION NULLOMERS**  
Diego and Michel

18:30 – 19:00 **DISCUSSION TRANSPORT**  
Slobodan and Dalibor

20:00 **DINNER**

### **FRIDAY, 7 JUNE 2024**

09:00 – 09:30 **REGISTRATION**

09:30 – 10:30 **KEYNOTE LECTURE 4**  
Nevena Ilieva  
(Institute of Information and Communication Technologies at the Bulgarian Academy of Sciences, Bulgaria)  
**Understanding biological data through in silico studies: the h1FNy glycosylation puzzle**

10:30 – 11:00 **BREAK**

11:00 – 11:20 Pablo Rojas  
(University of Kassel, Germany)  
**Learning from dynamical systems through observed dynamics**

11:20 – 11:40 Stella Logotheti  
(National Technical University of Athens, Greece)  
**Cancer radiotherapy-related cardiovascular diseases: providing multidisciplinary and omics-based solutions to a complex clinical condition**

11:40 – 12:00 Athanasios Rafail Rousomanis  
(Democritus University of Thrace, Greece)

**Integrating Graph Neural Networks and Pathway-level Biomarker Discovery in classifying High-Grade Serous Ovarian Carcinomas**

12:00 – 13:00 **DISCUSSIONS**

13:00 – 14:00 **LUNCH BREAK**

14:00 – 14:20 Siavash Fakhimi Derakhshan  
(Adaptive System Department, Institute of Information Theory and Automation, Czech Academy of Sciences, Czechia)  
**Policy Learning via Fully Probabilistic Design**

14:20 – 14:40 Rafayel Petrosyan  
(American University of Armenia / L.A. Orbeli Institute of Physiology NAS RA, Armenia)  
**Characterization of short single-stranded DNAs**

14:40 – 15:00 Luis Mandel  
(NTT DATA, Germany)  
**Exploring Molecular Symmetry, Language Modelling, and Data Integrity in Biological and Computational Sciences**

15:00 – 15:20 Tomislav Stankovski  
(Ss. Cyril and Methodius University in Skopje, Faculty of Medicine, North Macedonia)  
**Coupling functions for inference of interaction mechanisms: application to brain and cardiovascular oscillatory interactions**

15:20 – 15:40 Yanis Saidani  
(Aix Marseille Université, France)  
**The use of nanobodies to modulate the interaction between membrane receptors for cancer treatment**

15:40 – 16:00 Atle Bones  
(NTNU, Norway)  
**Genome editing and gene conversion**

16:00 – 16:20 **BREAK**

16:20 – 17:20 **CORE GROUP MEETING**

### **POSTER SESSION**

**01**  
Clara Gracio  
(University of Évora, Portugal)  
**Application of the results of Symbolic Dynamics in the study of nullomers**

**02**  
María José López-Galiano  
(University of Valencia, Spain)  
**Reservoirs of ancestral Delta-viruses replicate in water molds**

**03**  
Claudia Arbeitman  
(University of Kassel, Germany)  
**Molecular dynamics and machine learning in the study of signal propagation in protein-kinase A**

**04**  
Dimitrios Trygoniaris  
(Aristotle University of Thessaloniki, Greece)  
**Mitigating Class Imbalance in CAD Risk Prediction: A Model-Agnostic Ensemble approach**

**05**  
Adam Jedlicka  
(Department of Adaptive Systems, Institute of Information Theory and Automation, Czech Republic)  
**Exploration in Reinforcement Learning**

**06**  
Andrej Novak  
(University of Zagreb, Croatia)  
**Enhancing Clinical Predictions through Interpretable Machine Learning: An Analysis with XGBoost, LightGBM, and CATBoost**

**07**  
Maria Katsioulas  
(Aristotle University of Thessaloniki, Greece)  
**Exploring Federated Learning Approaches and Platforms in Medical AI models**

**08**  
Christina Papangelou  
(Aristotle University of Thessaloniki, Greece)  
**Addressing the uncertainty of machine learning models in genomic medicine using conformal predictions**