Enio Gjerga

Nationality: German **Date of birth:** 23/04/1991 **Gender:** Male

Phone number: (+49) 17685132057 **Email address:** enio.gjerga@gmail.com

Website: https://enio23.github.io/

Work: Innere Medizin III INF 669, 69120 Heidelberg (Germany)

ABOUT ME

A postdoctoral scientist specializing in computational and systems biology, focusing on developing tools for integrating multi-omics data and alternative splicing effects to elucidate molecular mechanisms underlying pathologies.

WORK EXPERIENCE

Postdoctoral Scientist

Klaus Tschira Institute for Integrative Computational Cardiology & Innere Medizin III [01/03/2021 – Current]

City: Heidelberg | **Country:** Germany

Postdoc with Prof. Christoph Dieterich at the DieterichLab.

- Integration of multi-omics data to shed light into the molecular mechanisms leading to the development of cardiomyopathies.
- Development of computational tools used for the understanding of Alternative Splicing effects to protein signalling networks.
- Identification of essential parameter settings for direct RNA sequencing with Nanopore Sequencing.
- Development of computational tools for the joint modelling of extra- and intra-cellular interaction systems.
- Computational tools and analyses scripts developed in R.

Postdoctoral Scientist

Charité – Universitätsmedizin Berlin [01/05/2020 – 01/12/2020]

City: Berlin | **Country:** Germany

Development of Bioinformatics workflows for the analysis of RNA-seq and Proteomics data.

SyMBioSys ITN Early Stage Researcher - PhD candiadte

Institute for Computational Biomedicine, BioQuant Zentrum, Universitätsklinikum Heidelberg [01/09/2018 – 24/04/2020]

Address: Im Neuenheimer Feld 267, 69120 Heidelberg (Germany) | **Website:** https://www.bioquant.uni-heidelberg.de

Under the supervision of Prof. Dr. Julio Saez-Rodriguez (julio.saez@bioquant.uni-heidelberg.de).

Thesis title: Identification of both structure and parameters of large signalling models.
From September 2018 continued my PhD project as a visiting researcher in BioQuant Zentrum at Heidelberg University.

SyMBioSys ITN Early Stage Researcher - PhD candidate

RWTH Aachen - Faculty of Mechanical Engineering [25/08/2016 – 24/04/2020]

Address: Kackertstraße 9, 52072 Aachen (Germany) | **Website:** http://www.h2020symbiosys.eu/

Under the supervision of Prof. Dr. Julio Saez-Rodriguez at the saezlab.

Thesis Title: Identification of both structure and parameters of large signalling models.

- Development of computational tools used for the modelling large-scale cell signalling networks
- Integration of optimization techniques with simulation analysis in order to provide information about the behaviour of cell signalling systems.
- Statistical and data exploration analysis of molecular data (mainly of proteomics and transcriptomic).
- Computational tools developed in R.

Master Thesis Project

Helmholtz Institut - RWTH Aachen [15/02/2016 – 15/08/2016]

Address: Pauwelsstraße 20, D-52074 Aachen (Germany) | **Website:** http://www.hia.rwth-aachen.de

Under the supervision of Univ.-Prof. Dr.-Ing. Klaus Radermacher and Dipl.-Ing. Christoph Haenisch.

Thesis title: Registration of 3D ultrasound volume images and segmentation of bone surfaces using statistical shape models.

Under the supervision of Univ.-Prof. Dr.-Ing. Klaus Radermacher and Dipl.-Ing. Christoph Haenisch.

Thesis title: Registration of 3D ultrasound volume images and segmentation of bone surfaces using statistical shape models.

- 3D reconstruction and segmentation of the knee joint based on ultrasound imagery.
- The Image Registration process consisted of applying optimization algorithms for identifying the 3D rigid transformation matrix parameters and statistical shape models for efficient segmentation.
- Codes were written in MATLAB and C++.

Internship

AZ Maria Middelares [01/02/2015 – 15/07/2015]

Address: Buitenring Sint-Denijs 30, 9000 Ghent (Belgium) | **Website:** http://www.mariamiddelares.be

Under the supervision of Prof. Pascal Verdonck.

- 3D delineation and volume estimation of the Striatum of the Brain and Liver Cancer tissues.
- Development of tools used to quantify the severity of Parkinson Disease and Liver Cancer for making proper treatment planning.
- Software tools developed in MATLAB.

EDUCATION AND TRAINING

Bachelor in Electronic Engineering

Polytechnic University of Tirana [01/09/2009 – 01/08/2012]

Address: Bul. "Dëshmorët e Kombit, Sheshi Nënë Tereza Nr. 4, 4001 Tirana (Albania) | **Website:** http://www.upt.al/

As a Bsc. graduated in Electronic Engineering I obtained the skills of designing, conceive applications of data processing systems and maintaining electronic systems and sensor networks, database management, etc.. This background allows me to lead information processing laboratories of enterprises and companies in the area of industrial production, in medicine or in the environment.

Thesis title: Data Network Simulation and DDoS Attack against it.

Master of Science in Electronic Engineering/Clinical Engineering Profile

Polytechnic University of Tirana [01/09/2012 – 01/08/2014]

Address: Bul. "Dëshmorët e Kombit, Sheshi Nënë Tereza Nr. 4, 4001 Tirana (Albania) | **Website:** http://www.upt.al/

As an Msc. graduated in Electronic Engineering/Clinical Profile I obtained the skills necessary to be employed in the area of data processing in sanitary and biomedical systems and electronic systems. As the Master program was still mainly based on the subjects related to electronics, as a graduate I could have still been employed in industries that handle automation and robotic; companies that work in informative systems and sensor networks as well as in services sector companies and in the public administration.
Thesis title: Retinal Tears Detection based on Image Processing with MATLAB.

CEMACUBE Erasmus Mundus Master of Science in Biomedical Engineering (Ghent University & VU Brussles - 1st year)

Ghent University & Free University of Brussels (VUB) [01/09/2014 – 01/09/2015]

Address: St. Pietersnieuwstraat 33, 9000 Ghent (Belgium) | **Website:** http://www.ugent.be

I finished the first year of the Master in Biomedical Engineering at Ghent University & Free University of Brussels (VUB) where I obtained a vast set of general knowledge regarding this field. The main subjects of the first year were Modelling of Physiological Systems, BiomedicalImaging, Medical Physics, Biomaterials, Biomechanics.

CEMACUBE Erasmus Mundus Master of Science in Biomedical Engineering (RWTH Aachen University 2nd year)

RWTH Aachen University [01/10/2015 – 24/08/2016]

City: Aachen | **Country:** Germany

On the second year of the program, I specialised in Medical Imaging where I to deepened my knowledge of Medical Imaging Instrumentations and Image Processing Techniques. The main subjects include Image Processing and Management and Image-Guided Therapy/Molecular Imaging. The second semester I mainly worked on my thesis I had the first introduction to various optimisation techniques, applied statistics and image/data processing methods.
Thesis title: Registration of 3D ultrasound volume images and segmentation of bone surfaces using statistical shape models.

After the completion of the CEMACUBE Erasmus Mundus program, I obtained a joint Msc. degree in Biomedical Engineering from Ghent University, VU Brussels and RWTH Aachen University.

LANGUAGE SKILLS

Mother tongue(s): Albanian

Other language(s):

English

LISTENING C2 **READING** C2 **WRITING** C2

SPOKEN PRODUCTION C2 **SPOKEN INTERACTION** C2

Italian

LISTENING C2 **READING** C1 **WRITING** B2

SPOKEN PRODUCTION B2 **SPOKEN INTERACTION** B2

German

LISTENING B2 **READING** B2 **WRITING** B1

SPOKEN PRODUCTION B1 **SPOKEN INTERACTION** B1

Levels: A1 and A2: Basic user; B1 and B2: Independent user; C1 and C2: Proficient user

PUBLICATIONS

Publications

- First/Co-first authorships
  - **Enio Gjerga, Matthias Dewenter, Thiago Britto-Borges, Johannes Grosso, Frank Stein, Jessica Eschenbach, Mandy Rettel, Johannes Backs, Christoph Dieterich.** "Transverse aortic constriction multi-omics analysis uncovers pathophysiological cardiac molecular mechanisms". *Database*, Volume 2024, 2024, baae060, https://doi.org/10.1093/database/baae060.
  - **Isabel S. Naarmann-de Vries, Enio Gjerga, Catharina L.A. Gandor and Christoph Dieterich.** 2023. "Adaptive sampling for nanopore direct RNA-sequencing". RNA 2023. 29: 1939-1949 rna.079727.123.
  - **Enio Gjerga, Isabel S Naarmann-de Vries, Christoph Dieterich.** 2023. "Characterizing alternative splicing effects on protein interaction networks with LINDA". *Bioinformatics*, Volume 39, Issue Supplement_1, June 2023, Pages i458–i464, https://doi.org/10.1093/bioinformatics/btad224
  - **Anika Liu, Panuwat Trairatphisan, Enio Gjerga, Athanasios Didangelos, Jonathan Barratt, Julio Saez-Rodriguez.** 2019. "From expression footprints to causal pathways: contextualizing large signaling networks with CARNIVAL". *npj Syst Biol Appl* **5,** 40 (2019) doi:10.1038/s41540-019-0118-z.
  - **Enio Gjerga, Panuwat Trairatphisan, Attila Gabor, Hermann Koch, Celine Chevalier, Francesco Ceccarelli, Aurelien Dugourdd, Alexander Mitsos, Julio Saez-Rodriguez.** 2019/2020. "Converting networks to predictive logic models from perturbation signalling data with CellNOpt". https://doi.org/10.1093/bioinformatics/btaa561.
  - **Enio Gjerga, Aurelien Dugourd, Luis Tobalina, Abel Sousa, Julio Saez-Rodriguez.** 2021. "PHONEMeS: efficient modeling of signaling networks derived from large-scale mass spectrometry data". Journal of Proteome Research 20 (4), 2138-2144. https://doi.org/10.1021/acs.jproteome.0c00958.
  - **Enio Gjerga, Panuwat Trairatphisan, Attila Gabor, Julio Saez-Rodriguez.** 2019**.** "Literature and data-driven based inference of signalling interactions using timecourse data". 2019. *IFAC-PapersOnLine*. https://doi.org/10.1016/j.ifacol.2019.12.235.

- Secondary authorships, Collaborations
  - **Alexander Schäfer, Enio Gjerga, Richard WD Welford, Imke Renz, Francois Lehembre, Peter MA Groenen, Julio Saez-Rodriguez, Ruedi Aebersold and Matthias Gstaiger.** 2019. "Elucidating Essential Kinases of Endothelin Signalling by Logic Modelling of Phosphoproteomics Data." *Molecular Systems Biology 15 (8): e8828.* https://doi.org/10.15252/msb.20198828.
  - **Aurelien Dugourd, Christoph Kuppe, Marco Sciacovelli, Enio Gjerga, Attila Gabor, Kristina B Emdal, Vitor Vieira, Dorte B Bekker-Jensen, Jennifer Kranz, Eric MJ Bindels, Ana SH Costa, Abel Sousa, Pedro Beltrao, Miguel Rocha, Jesper V Olsen, Christian Frezza, Rafael Kramann, Julio Saez-Rodriguez.** 2021. "Causal integration of multi-omics data with prior knowledge to generate mechanistic hypotheses". *Molecular Systems Biology* 17 (1), e9730. https://doi.org/10.15252/msb.20209730.
  - **Thiago Britto-Borges, Annekathrin Ludt, Etienne Boileau, Enio Gjerga, Federico Marini & Christoph Dieterich.** 2022. "Magnetique: an interactive web application to explore transcriptome signatures of heart failure". J Transl Med 20, 513 (2022). https://doi.org/10.1186/s12967-022-03694-z.

CONFERENCES AND SEMINARS

Conferences

- Oral presentations
  - Fourth CoLoMoTo meeting (Paris, July 17-19 2017). **Presentation title:** Efficient modelling of signalling networks derived from mass spectrometry phosphoproteomics data using Integer Linear Programming.
  - ECCB 2018 (Athens, 8-12 September 2018). **Presentation title:** Advances in computational methods for the modelling of signalling networks.
  - BIOMS Symposium 2018 (Heidelberg, October 1-2 2018). **Presentation title:** Modelling of signalling networks by using multiple boolean logic formalisms.

    - GCB 2019 (Heidelberg, September 17-19 2019). **Presentation title:** Topological analysis of causal signalling models contextualised by gene expression data.
    - FOSBE 2019 (Valencia, October 15-18 2019). **Presentation title:** Literature and data-driven based inference of signalling interactions using time-course data.
    - ISMB/ECCB 2023 (Lyon, July 23-27 2023). **Presentation title:** Characterizing alternative splicing effects on protein interaction networks with LINDA.

- Poster presentations
    - HUPO 2017 (Dublin, September 17-21 2017). **Poster title:** Modelling signalling networks from mass spectrometry phosphoproteomics using Integer Linear Programming.
    - ECCB 2018 (Athens, 8-12 September 2018). **Poster title:** Handling time-course data for the modelling of signalling networks using large-scale phosphoproteomics data.
    - ECCB 2022 (Sitges, 12-20 September 2022). **Poster title:** Characterizing alternative splicing effects on protein interaction networks with LINDA.
    - ECCB 2024 (Turku, 16-20 September 2024). **Poster title:** LINDA+: Characterizing of alternative splicing effects on intra-cellular and cell-cell interaction networks.

- Chairing
    - SyMBioSys Final Symposium (Athens, September 9 2018). Multi-omic data in biological systems modelling.

COMMUNICATION AND INTERPERSONAL SKILLS

Communication and interpersonal skills

Excellent presentation and interpersonal communication skills, acquired through the practising of the public speaking (mainly in various conferences and workshops) and living in an international environment.

JOB-RELATED SKILLS

Job-related skills

- Computational Biology.
- Systems Biology.
- Modelling of protein and molecular interaction networks.
- Optimization techniques.
- Graph theory.
- Analysis and processing of biological and molecular data.
- Omics data: proteomics, bulk RNA-seq, single-cell and single nuclei RNA-seq, secretomics, metabolomics, gene sequencing.
- Functional analysis and integration of omics data.
- Nanopore sequencing.
- Machine learning application in Biology.
- Application of system optimization and engineering principles in Biology.
- Protein folding with AlphaFold.
- Modelling or protein interactions with AlphaFold Multimer.
- Structural biology.
- Programming and statistical analysis with R.
- Containerization with Docker and Singularity.
- Unix & shell scripting.
- Git.

TEACHING

Concepts of Modelling in Biological Systems

Graduate course, *Heidelberg University*, 2022-2024.

Course for the Medical Informatics (Profile Bioinformatics). 2022, 2023. In this course I describe the fundamental principles for doing mathematical modelling of Biological System.

Introduction to Programming with R

Undergraduate course, *Heidelberg University*, 2023

Course for the undergraduate medical students of Heidelberg University, teaching basic concepts of programming with R. The course was organized around a simple clinical inflammation data-set provided here.

Proteomics and Integrative Proteomics & Transcriptomics Analysis Techniques

Graduate course, *Heidelberg University*, 2022

Teaching for the Heidelberg Biosciences International Graduate School (HBIGS). The course focused on the presenting step-by-step analysis of Proteomics data as well as the integrative analysis of Proteomics and Transcriptomics.