

Mirko LEDDA
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RELEVANT SKILLS

Computing	Programming	<ul style="list-style-type: none">• Python, R, Matlab (+ some C and Perl).• Software development and release.• Shell scripting and analysis on high-performance clusters.
	Data science	<ul style="list-style-type: none">• Machine Learning.• Statistics, algebra, calculus and probability theory.• Algorithms and statistical methods development.• Big data management and analysis.
Biology	Bioinformatics	<ul style="list-style-type: none">• High-throughput sequencing (incl. library prep).• Genomics, transcriptomics, metabolomics and GWAS.• Common bioinformatics tools/pipelines.
	Engineering	<ul style="list-style-type: none">• Receptors biochemistry.• Molecular, structural and cell biology.• Bioprocesses and bioreactors.
Business	Management	<ul style="list-style-type: none">• Project management and team building.• Effective oral and written communication.• Teaching, consulting and mentoring.
	Processes	<ul style="list-style-type: none">• Intellectual properties.• Biological lab management.• Safety and quality control (incl. MP, SOP and GLP).

EDUCATION

Ph.D. in Integrative Genetics and Genomics with Emphasis in Biotechnology (DEB)

University of California at Davis, CA, USA

Expected graduation in Early 2019

Thesis title : Hairpin in a haystack: structure-guided search for functional RNA elements
Thesis advisor : Prof. Sharon Aviran, Biomedical Engineering & Genome Center, UC Davis
DEB advisor : Dr. Judith A. Kjelstrom, director, UC Davis Biotechnology Program

B.Sc. in Life Sciences with Emphasis in Biotechnology

2008

University of Applied Sciences (HES-SO), Sion, Switzerland

Topic : Strategies for the study of genes with unknown functions in *Streptomyces*
Advisors : Prof. Sergio Schmid, Institute of Life Technologies, University of Applied Sciences (HES-SO), Sion, Switzerland
Prof. Anna Maria Puglia, Dept. of Biological, Chemical and Pharmaceutical Sciences and Technologies, University of Palermo, Italy

RESEARCH/WORK EXPERIENCE

Ph.D. researcher - UC Davis, CA

2014-Current

Supervisor: Prof. Sharon Aviran

Computational and statistical methods development for nucleic acid structures. My contributions include:

- Characterized the statistical properties of RNA structure profiling data.
- Contributed to, and developed all the statistical bases and strategies for, [RNAprob](#), a tool for data-directed RNA secondary structure prediction using probabilistic modeling.
- Conceived and developed [patteRNA](#), a Machine Learning algorithm for the rapid mining of RNA secondary structure motifs from transcriptome-wide structure profiling data.
- Mentored new lab members and undergraduate summer students.
- Acting as lab manager and lab safety officer.
- Actively consulted in multiple research projects to tackle complex problems.

Research Assistant - Nestlé Research Center, Lausanne, Switzerland

2009-2014

Supervisor: Prof. Johannes le Coutre

Project and Lab manager for research on taste perception physiology. My contributions include:

- Performed genome-wide association studies (GWAS) of human metabolism and taste perception;
 - Discovered and patented new biomarkers of the health-status of the gastrointestinal tract.
 - Developed statistical methods to analyze human taste phenotypic data.
 - Discovered new genetic drivers of bitter taste perception, most notably for caffeine.
- Established the single cell Ca^{2+} -imaging technique in the lab and developed computational tools for automated image data analysis.
- Functionalized and *in vitro* validated of several human, feline and rat GPCRs/TRP channels in mammalian cells (HEK, Hela, CHO, Chem-1 and primary rat DRG neurons).
- Performed receptor-interaction studies using siRNAs and co-expression approaches.
- Developed a method for the expression and purification of water-insoluble proteins in *E. coli*.
- Managed research projects and activities. Produced deliverable on time.
- Mentored students and interns.
- Acted as Lab security officer, supervised supplies and ensured proper functioning of lab equipment.

Soldier specialist in biological weapons - Swiss Army, Labor Spiez, Switzerland 2008-2014

Supervisor: Dr. Christian Beuret

Part-time: 3 weeks per year

- Development and validation of laboratory techniques for rapid identification of pathogenic bacteria, viruses and toxins.
- Team leader for research tasks.

TEACHING EXPERIENCE

Guest Lecturer - Quantitative Genetics and Selection Theory (PLS298), UC Davis

2018

IOR: Prof. Steve Knapp

Level: Graduate

Duties: Gave a 1h30 lecture on fundamental concepts in Machine Learning.

Evaluation: Very positive oral feedback from the students.

Lecturer - Machine Learning Workshop for the Plant Sciences Dept., UC Davis

2017

IOR: Mirko Ledda

Level: Undergraduate, Graduate and Professor

Duties: Organized a 4h workshop on Machine Learning for the Ross-Ibarra, Knapp and Runcie Labs.

Evaluation: Very positive oral feedback. Prof. Ross-Ibarra tweeted about it [here](#).

Guest Lecturer - Topics in BME: Computational Genomics (BIM189C), UC Davis

2017

IOR: Prof. Sharon Aviran

Level: Upper level undergraduate

Duties: Gave two 2h lectures on fundamental concepts in Machine Learning.

Evaluation: 4.7/5 - 67% excellent and 33% very good ratings.

TEACHING EXPERIENCE (CONTINUED)

- Teaching assistant** - Quantitative Genetics and Selection Theory (PLS298), UC Davis 2016
IOR: Prof. Steve Knapp
Level: Graduate
Duties: Taught R programming and the mathematical bases of selection theory in lab sessions.
Evaluation: Very positive oral feedback from the students.
- Course development** - Quantitative Genetics and Selection Theory (PLS298), UC Davis 2015
IOR: Prof. Steve Knapp
Level: Graduate
Duties: Prepared the teaching material for this newly proposed class.

AWARDS

- UC Davis Graduate Student Travel Award** - UC Davis 2017
Competitive award to cover the cost to attend, as a speaker, the *2017 [BC]2 Basel Computational Biology Conference* in Basel, Switzerland.
- Registration Bursary** - Wellcome Genome Campus Scientific Conferences 2016
Competitive award to cover the cost to attend, as a speaker, the *2016 Computational RNA Biology Conference* in Cambridge, UK.
- Summer Graduate Student Researcher Award** - UC Davis 2016
3-month support for graduate research in engineering, computer science, and disciplines with engineering-related applications and methods.

MEMBERSHIP

- Student member** - The RNA Society 2018
- Nominated for membership** - Phi Kappa Phi ($\Phi K \Phi$) Honor Society 2018
- Nominated for membership** - Golden Key International Honour Society 2015-2018

COMMUNITY SERVICE

- Graduate Student Association (GSA) representative** - UC Davis 2015-Current
Representative for the IGG graduate program.
- IGG Annual Colloquium organizer** - UC Davis 2017
Member of the organizing committee.
- DEB volunteer for the Teen Biotech Challenge 2017** - DEB, UC Davis 2017
Judge for System and Computational Biology websites.
- Mentor for Topics in BME: Computational Genomics (BIM189C)** - UC Davis 2017
Mentored three students for their final projects.
- DEB volunteer for the Teen Biotech Challenge 2016** - DEB, UC Davis 2016
Judge for System and Computational Biology websites.
- Volunteer for "Science in the Siskiyous"** - Dunsmuir High School, Dunsmuir, CA, USA 2015
Presented biology research and taught basic genetic concepts to three 9th to 12th grade high-school classes.
- Volunteer for "Science vs Fiction"** - Senior Center, Davis, CA, USA 2015
Presented common scientific misconceptions followed by an open discussion with seniors.
- Mentor for the IGG program** - UC Davis 2015
Mentor for all incoming international IGG students and mentor for a 1st year IGG student.

PRESENTATIONS AND POSTERS

[BCJ2 Basel Computational Biology Conference - Congress Center, Basel, Switzerland 2017
Ledda M. and Aviran S., patteRNA: Transcriptome-wide search for functional RNA elements via structural data signatures. *Speaker - 20min talk*

Genome Research Day - 23andMe, Mountain View, CA 2017
Ledda M. and Aviran S., Transcriptome-wide search for functional RNA elements via structural data signatures. *Poster*

Computational RNA Biology Conference - Wellcome Trust, Cambridge, UK 2016
Ledda M., Deng F., Vaziri S., and Aviran S., Data-directed RNA secondary structure prediction using probabilistic modeling. *Speaker - 15min talk*

PUBLICATIONS (* INDICATES CO-AUTHORSHIP)

Ledda M. and Aviran S. (2018)
patteRNA: transcriptome-wide search for functional RNA elements via structural data signatures, *Genome Biology* 19(28) [\[doi\]](#)

Choudhary K., Shih N.P., Deng F., **Ledda M.**, Li B. and Aviran S. (2016)
Metrics for rapid quality control in RNA structure probing experiments, *Bioinformatics* 32(23): 2575-3583 [\[doi\]](#)

Deng F.*, **Ledda M.***, Vaziri S. and Aviran S. (2016)
Data-directed RNA secondary structure prediction using probabilistic modeling, *RNA* 22(8): 1109-19 [\[doi\]](#)

Michlig González S., Meylan Merlini J., Beaumont M., **Ledda M.**, Tavenard A., Mukherjee R., Camacho S and le Coutre J. (2016)
Acute Effects of single ingestion of TRPV1, TRPA1 and TRPM8 agonists on the energetic metabolism and the autonomic activity in healthy subjects, *Scientific Reports* 6: 20795 [\[doi\]](#)

Rueedi R.*, **Ledda M.***, Nicholls A.W., Salek R.M., Marques-Vidal P., Morya E., Sameshima K., Montoliu I., Da Silva L., Collino S., Martin F-P., Rezzi S., Steinbeck C., Waterworth D.M., Waeber G., Vollenweider P., Beckmann J.S., le Coutre J., Mooser V., Bergmann S., Genick U.K., Kutalik Z. (2014)
Genome-wide association study of metabolic traits reveals novel gene-metabolite-disease links, *PLoS Genetics* 10(2) [\[doi\]](#)

Ledda M.*, Kutalik Z.*, Destito M.C.S., Souza M.M., Cirillo C. a., Zamboni A., Martin N., Morya E., Sameshima K., Beckmann J.S., le Coutre J., Bergmann S., Genick U.K. (2013)
GWAS of human bitter taste perception identifies new loci and reveals additional complexity of bitter taste genetics, *Human Molecular Genetics* 23: 259-267 [\[doi\]](#)

Godinot N., Yasumatsu K., Barcos M.E., Pineau N., **Ledda M.**, Viton F., Ninomiya Y., le Coutre J. and Damak S. (2013)
Activation of tongue-expressed GPR40 and GPR120 by non caloric agonists is not sufficient to drive preference in mice, *Neuroscience* 250: 20-30 [\[doi\]](#)

Montoliu I.*, Genick U.*, **Ledda M.**, Collino S., Martin F.P., Le Coutre J. and Rezzi S. (2013)
Current status on genome-metabolome-wide associations: An opportunity in nutrition research, *Genes and Nutrition* 8: 19-27 [\[doi\]](#)

Genick U.K., Kutalik Z., **Ledda M.**, Souza Destito M.C., Souza M.M., Cirillo C. a., Godinot N., Martin N., Morya E., Sameshima K., Bergmann S., le Coutre J. (2011)
Sensitivity of genome-wide-association signals to phenotyping strategy: The PROP-TAS2R38 taste association as a benchmark, *PLoS One* 6(11) [\[doi\]](#)

Manuscripts submitted / in-preparation

Radecki P.*, **Ledda M.***, Aviran S. (2018)

Automated recognition of RNA structure motifs by their SHAPE data signatures, *Genes* submitted

PATENTS

Genick U.K., **Ledda M.**, Montoliu I., Le Coutre J., Rezzi S., Collino S., Martin F.P., Da Silva L.

Genetic and urine-derived markers of human metabolic and gut microbial states

European Patent Office *EP2687845 A1* (issued in 2014)

US Patent Office *US Patent 20,150,160,191* (Issued in 2015)

HOBBIES/INTERESTS

- Soccer - Alpine Ski - GoKart
- Hiking, traveling and taking (too) many pictures
- Building servers at home

References upon request