

Andrea Fossati

PHD STUDENT · SYSTEM BIOLOGY

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Summary

I am a PhD student in System Biology at ETH Zurich developing next generation interactomics technologies. I provided the first tools for complex-centric prediction of novel protein complexes. I've been programming since high school and spend my extra time working on a selection of projects to improve my current skill-set. 3+ years of experience in mass spectrometry based proteomics. Proficient in machine learning, network analysis and statistical modeling.

Software skills

Languages	Python, R, Perl, C++, Bash
ML/Deep learning	Scikit-learn, Tensorflow, Keras, pyTorch
MS data analysis	MaxQuant, Mascot, Trans Proteomic Pipeline, OpenSwath, Spectronaut, Skyline
Database	SQL, mySQL

Education

Institute of Molecular System Biology, ETH Zurich

DR. SC. ETH ZURICH

Zurich, Switzerland

Feb. 2017 - Expected May 2020

- 'Identification of protein communities in high dimensional data', Supervisors Prof. Ruedi Aebersold and Dr. Matthias Gstaiger

University of Parma

M.SC IN PHARMACEUTICAL BIOTECHNOLOGY

Parma, Italy

Dec. 2014 - Oct. 2016

- Graduated 110/110 summa cum laude

Research Experience

Institute of Molecular system Biology, ETH Zurich, Aebersold Lab

PHD STUDENT

Zurich, Switzerland

Feb. 2017- May 2020

- Developed ML frameworks for inference of putative protein complexes and differential analysis of co-fractionation data
- Developed targeted assays (SRM/PRM/DIA) for analysis of histone modifications
- Designed, purified and characterized antibodies for endogenous immunoprecipitation
- Implemented deep learning framework for analysis of spatial proteomics data
- Integrated RNA-seq and proteomics data for modeling gene silencing kinetic

Institute of Molecular Biochemistry and Biophysics, Karolinska Institutet, Zubarev Lab

RESEARCH ASSISTANT

Stockholm, Sweden

Oct. 2016 - Jan. 2017

- Preparation of clinical samples (lung biopsies) and targeted MS (DIA/PRM) acquisition
- Developed a fragment ion scoring algorithm for classification of isobaric and near-isobaric peptides based differential average charge state

Institute of Molecular Biochemistry and Biophysics, Karolinska Institutet, Zubarev Lab

MASTER STUDENT

Stockholm, Sweden

Feb. 2016 - Oct. 2016

- Performed thermal proteome profiling in various cell lines and bacteria following drug perturbation
- Developed an isotope-clustering algorithm for accurate monoisotopic peak assignment based on isotopic enrichment
- Performed cell culture and shotgun proteomics analysis in bacteria

Department of Analytical Chemistry, University of Parma, Careri Lab

BACHELOR STUDENT

Parma, Italy

Mar. 2014 - Dec. 2014

- Developed MRM method for analysis of neurotoxins
- Investigated different HPLC column chemistries and MS fragmentation schemes for neurotoxins identification via targeted MS

Teaching

Computational methods in system biology for omics analysis, Graduate

PhD program in Molecular Life
Science, ETH Zurich

LECTURER & ORGANIZER

Feb. 2020

- Introduced concepts of system biology such as constraints-based modeling, information flux and multi-omics integration
- Integrated of omics datasets using non linear dimensionality reduction (tSNE, uMAP...)
- Visualized high dimensional datasets using network analysis softwares (Cytoscape) and showed add-on libraries for network analysis and partitioning
- Introduced the students to R programming, tidy universe and the language of graphic (ggplot)

Functional Proteomics course, Undergraduate

M. Sc in Biology, ETH Zurich

LECTURER & ORGANIZER

Apr.2019 - May 2019

- Introduced the students to search engine algorithms and challenges in peptide spectrum matching in data dependent and data independent acquisition with a focus on the statistical issues of both acquisition schemes
- Analyzed phospho-interactomics data with the attendees using different quantitation (MS1 based or spectral counting) and discussed the problem of data filtering in interactomics data. I then discussed the solution available in the field (empirical versus probabilistic models)
- Introduced the student to the basics of network analysis and application for the investigation of interactome rewiring following drug perturbation

Computational methods for Genome and Sequence analysis, undergraduate

B. Sc in Biology, ETH Zurich

LECTURER

Oct. 2017 - Nov. 2017

- Introduced algorithms for reads alignment (Smith-Waterman, Burrows Wheeler Transform, NGS), corresponding algorithm complexity and big O notation
- Explained the basics of Python programming and used data wrangling libraries such as Numpy and Pandas
- Coded a data preprocessing pipeline from raw reads data
- Developed and supervised the exams

Software projects

PCprophet

PRINCIPAL DEVELOPER

- Developed a software tool for analyzing co-fractionation datasets generated from biochemical fractionation experiments
- Implemented a machine learning framework for prediction of novel complexes across conditions
- Added Bayesian framework for statistical assessment of altered protein-protein interaction or complexes across conditions
- Utilized: Python3, Sklearn, Pandas, Numpy, NetworkX, Git

APprophet

PRINCIPAL DEVELOPER

- Developed a software tool for affinity purified natively fractionated samples
- Implemented a deep neural network for prediction and scoring of novel PPI from affinity-purified size fractionated samples
- Designed a novel statistical scoring to separate false and true interaction partners
- Utilized: Python3, Tensorflow, Keras, Numpy, Cython, Git, Docker

pyLOC

PRINCIPAL DEVELOPER

- Developed a software tool for analysis and integration of 2D fractionation experiments
- Implemented a convolutional neural network for data-driven assignment of protein complexes to localization
- Introduced a novel score for representing a complex in 2D coordinates
- Utilized: Python3, Tensorflow, Keras, Numpy, Pandas, Git

CCprofiler

CONTRIBUTOR

- Utilized: R, Git

Others

Aebersold lab

Institute for Molecular System
Biology, ETH Zurich, Zurich,
Switzerland

MASS SPECTROMETER OPERATOR

Feb. 2017 - Feb. 2020

- Gained expertise in maintenance and clean up of Orbitrap and Triple TOF mass spectrometer
- Performed quadrupole clean up on Triple TOF systems
- Performed routine maintenance and troubleshooting
- Optimized EVOSEP-ONE DIA methods and performed routine maintenance on the EVOSEP ONE system
- Organized sample queues

HPLC OPERATOR

Feb. 2018 - Feb. 2020

- Gained expertise in maintenance and clean up of Agilent HPLC used for size fractionation
- Performed routine clean-up and evaluation of standard
- Organized sample queues

Presentation & Posters

Human Proteome Organization 2019 conference

Adelaide, Australia

POSTER

Sep. 2019

- Time resolved assessment of nuclear protein complex dynamics via SEC-MS

European Proteomic Association 2019 conference

Potsdam, Germany

POSTER

Mar. 2019

- High throughput analysis of protein complexes during X-chromosome inactivation

Life Science2 Swiss Proteomics Meeting

Montreux, Switzerland

PRESENTATION

May. 2019

- Systematic assessment of epigenetic remodeling during mammalian dosage compensation

Life Science annual meeting Meeting

Zurich, Switzerland

PRESENTATION

Feb. 2019

- Nuclear proteome dynamics upon epigenetic silencing: a lecture from chromatin biology

Department of Biology symposium

Davos, Switzerland

POSTER

Jun. 2018

- Investigation of Polycomb complexes interplay in X-chromosome inactivation

Honors & Awards

2019 **HUPO travel grant**, Human Proteome Association 2019

Adelaide, Australia

2019 **EUPA travel grant**, European Proteomic Association 2019

Potsdam, Germany

2016 **Erasmus + Traineeship**, Support grant for master thesis

Stockholm, Sweden

2011-2015 **Study grant**, Study grant for high performing students

Parma, Italy