

PETR TAUS

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EXPERIENCE

Computational Biologist II | Immunai

March 2022 - present

Joined Immunai as a member of the single-cell curation team, focusing on the analysis of single-cell data, development of the curation single-cell pipeline, and construction of single-cell atlases, including the cancer cell atlas. Successfully transitioned to an external-facing scientific team within 10 months, where I have been leveraging single-cell multi-omics and data science to bridge the gap between causal immunology and translational biology. In this role, I have taken on the position of computational biology lead for projects focusing on selection of cancer indications for a clinical trial and on target nomination in inflammatory diseases.

Research Assistant | Medical Genomics group, CEITEC Masaryk University, Brno

February 2018 - February 2022

Worked with next-generation sequencing data, including whole-exome sequencing, bulk RNA-seq, and single-cell RNA-seq datasets. Leveraged mutation data, pathway analysis, and machine learning to identify mutation subtypes of chronic lymphocytic leukemia (CLL). Subsequently, established capabilities for single-cell data analysis at the institute, leading to involvement in multiple projects spanning different groups and research topics. In the project that I led, I utilized single-cell data and machine learning to explore cellular origin of CLL.

Research visits

Lab of Prof. Julio Saez-Rodriguez, Heidelberg University, Germany

August - October 2021 (3 months)

Acquired a deep understanding of the methods for extracting mechanistic insights from single-cell RNA-seq data developed in the lab. Played a role in the development of the decoupleR, an R package for benchmarking and applying methods for mechanistic signatures inference from omics data.

Genomics Core Facility, EMBL, Heidelberg, Germany

November 2018 (1 month)

Worked on the analysis of whole-exome sequencing data under the supervision of Tobias Rausch.

Bioinformatics Research Centre, Aarhus University, Denmark

March - July 2017 (5 months)

Analyzed tumor-infiltrating leukocytes from bulk RNA-seq expression data in primary bladder cancer tumors and built a classification model to predict the progression of the disease.

EDUCATION

September 2018 - February 2023

PhD in Computational Biology

CEITEC PhD School, Masaryk University, Brno, Czechia

2015 - 2017

MSc in Immunology (Summa cum laude)

Charles University, Prague, Czechia

September 2015 - January 2016

Study visit at University of Gothenburg, Sweden

Molecular Biology and Bioinformatics (Pass with distinction)

2012 - 2015

BSc in Molecular Biology and Biochemistry of Organisms

Charles University, Prague, Czechia

Relevant courses

2023 - Deep Learning specialization on Coursera

11/09/2023 - Introduction to Spatial Transcriptomics Data Analysis workshop, Basel, Switzerland

2022 - Machine Learning specialization on Coursera

11-12/12/2019 - R: Mastering the Tidyverse, Brno, Czechia

25/2-1/3/2019 - Big Data and Machine Learning, Uppsala, Sweden

Spring 2019 - Machine Learning and Data Mining, Faculty of Informatics, Masaryk University

Spring 2019 - Complex Networks, Faculty of Informatics, Masaryk University

23-26/10/2018 - Analysis of High Throughput Sequencing Data, EMBL-EBI, Hinxton, UK

09/09/2018 - Interactive visualizations to guide health diagnostics and personalized medicine workshop, Athens, Greece

06/2018 - R for Machine Learning course during a one-week stay at EMBL, Heidelberg, Germany

21-24/05/2018 - Systems Dynamics of Biological Networks through Computational Modelling, Brno, Czechia

11/2017 - Advanced R Programming on Coursera

COMPETENCES AND TECHNICAL SKILLS

- Extensive experience in analyzing and interpreting biological signal from diverse omics datasets, including single-cell/bulk RNA-seq, CITE-seq, VDJ-seq, and whole-exome sequencing.
- Proficient in the R programming language; good knowledge of Python, UNIX/Linux, and Git/GitHub.
- Working knowledge of machine learning and deep learning techniques.
- Strong knowledge of immunology, particularly in the context of malignant and inflammatory diseases.
- Wet-lab experience in molecular biology and biochemistry.

GRANTS AND AWARDS

2020 - Interdisciplinary school in 3D genomics fellowship (canceled due to Covid-19)

2019 - European human genetics conference fellowship

2019 - Brno PhD talent award (~12000 EUR; awarded annually to top 25 students from the South Moravian region)

2018 - 2021 - Scholarship for excellent students, CEITEC PhD School, Brno

2017 - Charles University student research grant, Prague

2017 - Erasmus+ scholarship for a traineeship

2014 and 2016 - Scholarship for excellent study results, Charles University, Prague

2015 - NEURON Prima ZOOM Award 2015 for the best science video (nationwide contest)

2015 - Erasmus+ scholarship for a study visit

SUPERVISION AND TEACHING

2021 - 2023 - Initiated, prepared, and taught a new course titled “Data analysis in R for experimental and molecular biologists” at the Faculty of Science, Masaryk University. The course is now continued by my former colleagues.

2019 - 2021 - Received a grant from the South Moravian region to supervise gifted high school students in computational biology research projects. The thesis of my student was awarded 1st place regionally and 9th nationally in a highly competitive student competition.

2018 - 2022 - Provided training and supervision in the analysis of single-cell RNA-seq data for PhD students with a background in bioinformatics/molecular biology.

PUBLICATIONS

Cerebral organoids derived from patients with Alzheimer’s disease with PSEN1/2 mutations have defective tissue patterning and altered development

Vanova T, Sedmik J, Raska J, Amruz Cerna K, **Taus P**, Pospisilova V, Nezvedova M, Fedorova V, Kadakova S, Klimova H, Capandova M, Orviska P, Fojtik P, Bartova S, Plevova K, Spacil Z, Hribkova H, Bohaciakova D

Cell Reports, 2023

Distinct p53 phosphorylation patterns in chronic lymphocytic leukemia patients are reflected in circumjacent pathways’ activation upon DNA damage

Mancikova V, Pesova M, Pavlova S, Helma R, Zavacka K, Hejret V, **Taus P**, Hynst J, Plevova K, Malcikova J, Pospisilova S

Molecular Oncology, 2022

Single-cell RNA sequencing analysis of T helper cell differentiation and heterogeneity

Jarousek R, Mikulova A, Dadova P, **Taus P**, Kurucova T, Plevova K, Tichy B, Kubala L

BBA Molecular Cell Research, 2022

decoupleR: Ensemble of computational methods to infer biological activities from omics data

Badia-i-Mompel P, Vélez J, Braunger J, Geiss C, Dimitrov D, Müller-Dott S, **Taus P**, Dugourd A, Holland C, Ramirez Flores R, Saez-Rodriguez J,

Bioinformatics Advances, 2022

Identification of clinically relevant subgroups of chronic lymphocytic leukemia through discovery of abnormal molecular pathways

Taus P, Pospisilova S, Plevova K

Frontiers in Genetics, 2021

CONFERENCES

09/2023 - Computational Biology conference, Basel, Switzerland

Poster presentation: Curation and integration of cancer single-cell RNA-seq data for meta-analysis

06/2022 - Tooth Morphogenesis and Differentiation conference, Prague, Czechia

Invited workshop: Single-cell RNA-seq analysis

11/2021 - International Conference Analytical Cytometry, Ostrava, Czechia

Oral presentation: Data mining of publicly available scRNA-seq datasets: application of machine learning to interrogate normal cellular counterparts of chronic lymphocytic leukemia

11/2019 - Cancer Genomics, EMBL, Heidelberg, Germany

Poster presentation: Identification of novel chronic lymphocytic leukemia subtypes using germline pathway mutation scores and ensemble clustering

06/2019 - European human genetics conference, Gothenburg, Sweden

Poster presentation: Identification of novel chronic lymphocytic leukemia subtypes using pathway mutation scores and consensus clustering

06/2019 - Joint PhD retreat of CEITEC, IMG and IST Austria

Oral presentation: Identification of novel chronic lymphocytic leukemia subtypes using pathway mutation scores and machine learning

02/2017 - LS2 Annual Meeting in Zurich, Switzerland

Poster presentation: Experimental verification of in silico predicted protein binder to FOXO4 transcription factor