

# Joshua Schaaf

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## Education

<b>Temple University</b> , PSM (Professional Science Masters) in Bioinformatics ( <a href="#">Contact</a> ) <ul style="list-style-type: none"><li>GPA: 4.0/4.0 (<a href="#">Diploma</a>)</li><li><b>Relevant Coursework</b> - Machine Learning, Biostatistics, Biological Models in Python, Genomics</li></ul>	Sept 2020 – May 2022 Philadelphia PA, USA
<b>Temple University</b> , BS in Biochemistry, Computer Science Minor <ul style="list-style-type: none"><li>GPA: 3.88/4.0 (<a href="#">Diploma</a>) – <i>Magna Cum Laude</i>, With Distinction</li><li><b>Relevant Coursework</b> - Data Structures, Calculus, Organic Chemistry, Physical Chemistry, Biochemistry</li></ul>	Sept 2017 – May 2021 Philadelphia PA, USA

## Language

**English** – Native, Fluent | **Finnish** – Beginner | **Spanish** – Beginner

## Experience

<b>Bioinformatics Programmer Analyst II</b> , <a href="#">HJF WHIRC</a> – Annandale, VA, USA Support bioinformatic efforts in a cancer proteomics laboratory: Early Career (Stage I) <ul style="list-style-type: none"><li>Develop, deploy, and publish <a href="#">ProteoMixture</a>, a tool to determine relative abundance of tissue types from bulk High-Grade Serous Ovarian Cancer samples</li><li>Design and develop machine learning (ML) methods for classifying/regressing against patient clinical variables using multiomic data</li><li>Lead the development of computer vision-based tissue collection automation efforts</li><li>Develop and maintain statistical data analysis workflows for proteomic, transcriptomic, and clinical data levels for projects spanning multiple cancer types</li><li>Analyze peptide spectral match data from tandem mass tag (TMT) mass spectrometry experiments to generate comprehensive protein abundance reports</li></ul>	January 2023 – Present
<b>Data Analyst</b> , <a href="#">FOXO Technologies</a> – Remote – Davis CA, USA Developed tools to aid identification of epigenetic biomarkers. <ul style="list-style-type: none"><li>Developed, maintained, and tested <a href="#">RAPA</a> (Robust Automated Parsimony Analysis), a Python package leveraging auto-ML platform Data Robot, to perform and plot intra-model recursive feature reduction</li><li>Created interactive dashboards for comparing clustering algorithms of methylation array data</li></ul>	July 2021 – November 2022
<b>Undergraduate Genetic Researcher</b> , <a href="#">Balciunas Lab</a> – Philadelphia PA, USA <ul style="list-style-type: none"><li>Created a genetically modified (floxed) zebrafish line to study the role of a transcription factor in cardiac tissue regeneration</li><li>Analyzed ChIP-seq data to identify binding locations/motifs of transcription factors in the zebrafish genome</li></ul>	December 2018 – May 2021
<b>Undergraduate Biochemistry Researcher</b> , <a href="#">Wang Group</a> – Philadelphia PA, USA <ul style="list-style-type: none"><li>Performed solid-phase peptide synthesis to generate antibody-drug conjugate linkers</li></ul>	May 2018 – September 2018

## Publications

<b>ProteoMixture: A cell type deconvolution tool for bulk tissue proteomic data</b> iScience, Volume 27 (3) Authors: Pang-ning Teng, <b>Joshua Schaaf</b> , ... Nicholas W. Bateman DOI – <a href="https://doi.org/10.1016/j.isci.2024.109198">10.1016/j.isci.2024.109198</a>	March 2024
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Mapping three-dimensional intratumor proteomic heterogeneity in uterine serous carcinoma by multiregion microsampling  
Clinical proteomics, Volume 21 (1)  
Authors: Allison L. Hunt, ... [Joshua Schaaf](#), ... Thomas P. Conrads  
DOI – [10.1186/s12014-024-09451-2](#)

January 2024

## Presentations

(Abstract accepted) [Predicting Immune Cell Admixture in Bulk Proteomics Data Using ProteoMixture](#) ASMS – June 2025

- Abstract ID – 323107
- Poster Session – Informatics: Algorithms and Statistical Advances

[Evaluating the Performance of ProteoMixture, a Proteomics-Based Cell Deconvolution Tool in Pan-Cancer Data for > 1000 Patient Tumors](#) ASMS – June 2024

- Abstract ID – 318970
- Poster Session – Informatics: Algorithms and Statistical Advances

[Conditional Mutagenesis of Zebrafish \*tcf21\*](#) TU URP Symposium – 2019

- Temple University Undergraduate Research Program research symposium

## Awards and Honors

Honors	Awards
<ul style="list-style-type: none"><li>• Temple University <a href="#">Honors Program</a> (2018 – 2021)</li><li>• College of Science and Technology Dean's List (2017 – 2021)</li><li>• Latin Honors <i>Magna Cum Laude</i> (2021)</li><li>• Distinction in Major (2021)</li></ul>	<ul style="list-style-type: none"><li>• <a href="#">Science Scholars Program</a> (2019 – 2021)</li><li>• <a href="#">Natan Luehrmann-Cowen Memorial Award</a> (2021)</li><li>• <a href="#">Temple University Diamond Marching Band Scholarship</a> (2017 – 2018)</li><li>• Temple University Tuition Scholarship (2017 – 2021)</li></ul>

## Skills and Technologies

Python | R | Machine Learning (sklearn, pytorch, tensorflow, keras) | Data Visualization (seaborn, matplotlib, ggplot2) | Computer Vision | Proteomics | git | JavaScript | C | Linux | Mass Spectrometry

## Science Outreach and Communication

[Letters to a Pre-Scientist \(LPS\)](#) September 2024 – Present

I am a pen-pal for a middle-school student from a school in a lower-income community. I help de-mystify science and scientists, and hopefully inspire my student to further consider a career that may have felt out of reach.