

# Pascal Sturmfels

psturm@cs.washington.edu - <https://psturmfels.github.io/>

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EDUCATION	<b>Ph.D. in Computer Science, Institute for Protein Design, University of Washington</b> June 2024 <ul style="list-style-type: none"><li>I was supervised by <a href="#">David Baker</a>. My research focused on developing deep learning models for protein design and structure prediction, and in particular predicting the structure of protein-ligand complexes. I was generally interested in applications in drug discovery, including docking and virtual screening.</li><li>From 2018 to 2020 I worked in the <a href="#">AIMS Lab</a> developing methods for explainable machine learning.</li></ul> <b>B.E in Computer Science, Minor in Mathematics, University of Michigan</b> Fall 2017
EMPLOYMENT	<b>Vilya, Deep Learning Scientist</b> September 2024 - Now <ul style="list-style-type: none"><li>Working on deep learning models for drug discovery, particularly structure prediction and virtual screening</li></ul> <b>Meta AI Research, Research Intern</b> Summer 2022 <ul style="list-style-type: none"><li>Supervised by <a href="#">Alexander Rives</a> and <a href="#">Adam Lerer</a></li><li>Developed large language models for protein sequence diversification tasks</li></ul> <b>Salesforce Research, Research Intern</b> Summer 2020 <ul style="list-style-type: none"><li>Supervised by <a href="#">Nazneen Rajani</a>, <a href="#">Jesse Vig</a> and <a href="#">Ali Madani</a></li><li>Worked on novel, self-supervised pre-training tasks for protein language models</li></ul> <b>MLD3 Lab, Research Assistant</b> September 2017 - May 2018 <ul style="list-style-type: none"><li>Supervised by <a href="#">Jenna Wiens</a></li><li>Designed new CNN architectures for predicting properties from MRI scans</li></ul> <b>Microsoft, Software Engineering Intern</b> Summer 2017 <ul style="list-style-type: none"><li>Worked on the Core Services Engineering and Operations Team (CSEO)</li></ul> <b>CAAR REU, Research Assistant</b> Summer 2016 <ul style="list-style-type: none"><li>Supervised by <a href="#">Samir Khuller</a></li><li>Worked on approximation algorithms for online machine scheduling problems</li></ul> <b>Pachter Lab, Research Assistant</b> May 2015 - July 2016 <ul style="list-style-type: none"><li>Supervised by <a href="#">Lior Pachter</a> and <a href="#">Harold Pimental</a></li><li>Worked on data visualization tools for differential expression analysis.</li></ul>
TEACHING EXPERIENCE	<b>Teaching Assistant, University of Washington</b> <ul style="list-style-type: none"><li>CSE 312: Foundations of Computing Summer 2021</li><li>CSE 427: Computational Biology Spring 2021</li><li>CSE 546: Machine Learning Fall 2018</li></ul> <b>Teaching Assistant, University of Michigan</b> <ul style="list-style-type: none"><li>EECS 445: Machine Learning Fall 2017</li><li>EECS 376: Theory of Computation Winter 2017</li></ul>
PUBLICATIONS	<ul style="list-style-type: none"><li>[1] Krishna, Rohith, Jue Wang, Woody Ahern, <b>Pascal Sturmfels</b>, Preetham Venkatesh, Indrek Kalvet, Gyu Rie Lee et al. "Generalized biomolecular modeling and design with RoseTTAFold All-Atom." Science (2024).</li><li>[2] <b>Sturmfels, Pascal</b>, Roshan Rao, Robert Verkuil, Zeming Lin, Ori Kabeli, Tom Sercu, Adam Lerer, and Alexander Rives. "Seq2MSA: A Language Model for Protein Sequence Diversification." Machine Learning for Structural Biology, NeurIPS Workshop (2022).</li><li>[3] Rutherford, Saige, <b>Pascal Sturmfels</b>, Mike Angstadt, Jasmine Hect, Jenna Wiens, Marion I. van den Heuvel, Dustin Scheinost, Moriah Thomason, and Chandra Sripada. "Observing the origins of human brain development: automated processing of fetal fMRI." Neuroinformatics (2021): 1-13.</li></ul>

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- [6] Erion, Gabriel\*, Joseph D. Janizek\*, **Pascal Sturmfels**\*, Scott Lundberg, and Su-In Lee. "Improving performance of deep learning models with axiomatic attribution priors and expected gradients." *Nature Machine Intelligence* (2021): 1-12.
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- [12] Pimentel, Harold, **Pascal Sturmfels**, Nicolas Bray, Páll Melsted, and Lior Pachter. "The Lair: a resource for exploratory analysis of published RNA-Seq data." *BMC bioinformatics* 17, no. 1 (2016): 490.