

# Jai Mehta

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## Education

### University of Tennessee

BS in Honors Computer Science, Chemistry

Minors in Pre-Health Professions, Molecular Biophysics

Aug. 2023 – May 2027

GPA: 4.00/4.00

### Wilson Central High School

Salutatorian, High School Diploma

May 2023

GPA: 4.55/4.00

## Coursework

**Computer Science Courses:** Data Structures, Algorithms, Computer Organization, Discrete Structures, Probability and Statistics, Linear Algebra, Calculus I & II

**Medical Courses:** Cellular and Molecular Biology, General Chemistry (with Lab), Organic Chemistry I & II (with Lab), Biochemistry, Physics I & II

## Experience

### Researcher and Software Developer

Systems Immunology Lab, Osaka University

Osaka, Japan

Dec. 2024 – Present

- Building a Clonotype to Paratope converter using IMGT and MiXCR inputs that takes a V gene name, J gene name, and CDR3b sequence, and provides the complete amino acid sequence.
- Working on changing the amino acid sequence numbering to improve a multiple sequence alignment algorithm.

### Teaching Assistant

Introductory Computer Science in C++, COSC 102

Knoxville, TN

Aug. 2024 – Present

- Hosted weekly office hours to assist students with labs
- Assisted in topics related to learning Linux, basic data structures, dynamic memory, recursion, file I/O, searching algorithms, and binary logic.

### Research Member

Emrich Lab

Knoxville, TN

Aug. 2024 – Present

- Utilizing scRNA-seq data to further understand cell state plasticity.

### Research Intern

Oak Ridge National Lab, Center for Molecular Biophysics

Oak Ridge, TN

Nov. 2023 – Present

- Tested an in-house Machine Learning model against other models to evaluate Area Under the Receiver Operating Characteristic Curve (AUC-ROC) scores regarding prediction of T Cell Receptor to epitope binding specificity.
- Currently using AlphaFold-2 to predict MHC to peptide binding affinity.

### Research Intern

Yu Lab, St. Jude Children's Research Hospital

Memphis, TN

July 2024 – Aug. 2024

- Evaluated a multi-informational clustering algorithm using scATAC-seq data with scRNA-seq labels to observe misclassification levels between cell phenotypes. Utilized Euclidean and Cosine distance estimation methods.
- Tested "Memory-like" and "Effector-like" cell states defined by a Gaussian Mixture Model using Joint Embedding, Differential Expression, and Gene Set Enrichment Analysis on clinical CAR T data.
- Combined clinical CAR T data, ran through Gaussian Mixture Model, and tested to observe similarities between individual clinical datasets and combined data.

## **Presentations and Talks**

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### **Defining Effector and Memory-like Cell State In in-vivo CAR T Cells from Multi-center Clinical Trials**

- UTK Undergraduate Research and Fellowships Discovery Day, Knoxville, TN, Sep. 2024.
- SASE National Conference, Computational Sciences Division, Boston, MA, Oct. 2024.

**Panelist** for *Student Panel for Undergraduate Research, Knoxville, TN, Nov. 2024.*

## **Selected Awards**

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<b>Tau Beta Pi Honors</b>	2024
<b>Cook Grand Challenge Engineering Honors</b>	2023
<b>Chancellor's University Honors</b>	2023
<b>National Merit Scholar</b>	2023
<b>Distinguished Tennessean Scholar</b>	2023
<b>Ned McWherter's Scholar</b>	2023
<b>John Tummins Memorial Scholarship</b>	2023
<b>National Youth Science Camp Attendee</b>	2023
<b>Eagle Scout</b>	2022

## **Technologies**

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**Programming Languages:** C++, Assembly, R, Java, R, Python, Bash

**Skills:** SciKit-Learn, ScanPy, Seurat, MacOS, Windows, Linux, Raspberry Pi, Arduino, Vim, Jupyter Notebook, GitHub, LaTeX, Single Cell Analysis, Machine Learning, High Performance Computing