

James V. Talwar

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EDUCATION

University of California San Diego, Jacobs School of Engineering Sept. 2018 – Present
PhD candidate in Bioinformatics and Systems Biology; GPA: 3.98/4.00; Advisor: Hannah Carter, PhD La Jolla, CA

University of California San Diego, Jacobs School of Engineering Sept. 2021 – March 2023
MS in Computer Science: Artificial Intelligence; GPA: 3.98/4.00 La Jolla, CA

- **Selected Coursework:** Neural Networks, Recommender Systems, Probabilistic Reasoning, Algorithm Design and Analysis, Graduate Networked Systems

University of Pennsylvania, School of Engineering and Applied Science Sept. 2010 – May 2014
Bachelor of Science in Engineering, Bioengineering and Mathematics (Major/Minor) Philadelphia, PA

- **Honors:** Dean's List; Graduation Honor *Cum Laude*

SKILLS

Programming Languages: Python, Java, Go, R, MATLAB, Arduino, LabVIEW

Open Source Libraries: PyTorch, Keras, DGL, LangChain, Tensorflow

SELECTED PROJECTS

Inferring Interactive Effects and Improving Genetic Risk Scores through Deep Learning Apr. 2020 – Present

- **Vision Adapted Disease Elucidating Transformer (VADeR):** Formulated and developed a novel vision transformer inspired architecture for capturing global, disease-specific epistatic interactions from SNP-level data in breast and prostate cancer.
- **Sequence Informing Transformer Archetype (SITh):** Conceptualized and implemented a self-supervised transformer modeling approach for inferring genomic regulatory grammar by capturing local genomic sequence interdependencies.

Generalized Realignment of Innocuous and Essential Variants Otherwise Utilized as Skewed Jul. 2023 – Present

- Devised and developed **grievous**, a command-line tool for guaranteeing cross-cohort variant consistency.
- Code and documentation available at: <https://github.com/jvtalwar/GRIEVOUS>

Domain Retrieval-Augmented Generation On Novel Bioinformatics Resources Ensuring Accurate Truthful Help Nov. 2023 – Present

- Created and designed **DRAGONBREATH**, a personalized assistant for bioinformatics software, backed by state-of-the-art large language models and enhanced with retrieval-augmented generation.
- Demo available upon request.

Identifying Immune Surveillance Contributions to Elusive Melanoma Risk Jun. 2019 – Jun. 2023

- Identified previously uncharacterized MHC-mechanisms of melanoma predisposition through autoimmune disease associations and driver mutation antigen presentation.
- Code available at: <https://github.com/cartercompbio/MelMHC>

TEACHING

Medical Scientist Training Program: Bioinformatics Bootcamp (RNA-seq) Summer 2021, 2022

- **Teaching Assistant:** Constructed course websites; Developed course materials and lectures; Ran interactive bioinformatics tutorials.
- Course materials can be found at: <https://github.com/jvtalwar/2022-MSTP-Bioinformatics-Bootcamp>

INDUSTRY EXPERIENCE

Intheon

Jun. 2014 – Aug. 2014

Engineering Intern at startup company specializing in neurotechnology

San Diego, CA

- Investigated mapping real-time EEG signals to spatial brain activities using signal strength and direction.
- Developed interactive three-dimensional brain visualization models and updated GUI libraries.

ResMed

Jun. 2013 – Aug. 2013

Engineering Intern at global medical device company

Dublin, Ireland

- Constructed hardware and wrote software resulting in the development of an automated light sensor test system for non-contact sleep monitor evaluation.

SELECTED PUBLICATIONS AND POSTERS

1. **J.V. Talwar**, D. Laub, M.S. Pagadala, A. Castro, M. Lewis, G.E. Luebeck, B.R. Gorman, C. Pan, F.N. Dong, K. Markianos, C.C. Teerlink, J. Lynch, R. Hauger, S. Pyarajan, P.S. Tsao, G.P. Morris, R.M. Salem, W.K. Thompson, K. Curtius, M. Zanetti, H. Carter. Autoimmune alleles at the major histocompatibility locus modify melanoma susceptibility. *Am. J. Hum. Genet.* (2023).
2. A. Klie, D. Laub, **J.V. Talwar**, H. Stites, T. Jores, J.J. Solvason, E.K. Farley, H. Carter. Predictive analyses of regulatory sequences with EUGENE. *Nat. Comput. Sci.* (2023).
3. M. Pagadala, T.J. Sears, V.H. Wu, E. Pérez-Guijarro, H. Kim, A. Castro, **J.V. Talwar**, C. Gonzalez-Colin, S. Cao, B.J. Schmiedel, S. Goudarzi, D. Kirani, J. Au, T. Zhang, T. Landi, R.M. Salem, G.P. Morris, O. Harismendy, S.P. Patel, L.B. Alexandrov, J.P. Mesirov, M. Zanetti, C. Day, C.C. Fan, W.K. Thompson, G. Merlino, J.S. Gutkind, P. Vijayanand, H. Carter. Germline modifiers of the tumor immune microenvironment implicate drivers of cancer risk and immunotherapy response. *Nat. Commun.* (2023).
4. M.S. Pagadala, J.A. Linscott, **J.V. Talwar**, T.M. Seibert, B. Rose, J. Lynch, M. Panizzon, R. Hauger, M.H. Hansen, J.D. Sammon, M.H. Hayn, K. Kader, H. Carter & S.T. Ryan. PRState: Incorporating genetic ancestry in prostate cancer risk scores for men of African ancestry. *BMC Cancer.* (2022).
5. **J. Talwar** and H. Carter. Assessing cancer drug response prediction from gene expression. Poster presented at: AACR Annual Meeting 2020; April 27-28, 2020 and June 22-24, 2020; Philadelphia, PA