

# STEVEN FOLTZ, PhD

Staff Scientist II, Children's Hospital of Philadelphia  
Laboratory of Kai Tan, PhD

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<https://github.com/envest>

*cancer bioinformatics expert with 10+ years experience — trained educator — positive team leader*

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## RESEARCH FLUENCY AND SKILLS

- Bioinformatics pipeline and tool development for cancer multiomics and clinical data analysis
  - Data science, open software development, and visualization best practices in R and python
  - Unix scripting and project management in high-performance / cloud computing environments
  - Next-gen sequencing data processing using bulk DNA and RNA-seq and single-cell multiomics
  - Machine learning algorithm development for biomarker discovery and label prediction
  - Biostatistics analyses and regression, including statistical genetics and survival analysis
  - Cross-disciplinary and multi-institutional collaboration with clinical and wet lab scientists
  - Classroom and boardroom communication of technical material for wide-ranging audiences
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## EDUCATION AND WORK EXPERIENCE

**Staff Scientist II, Children's Hospital of Philadelphia** Since May 2023  
Laboratory of Kai Tan, PhD  
*Focus:* Single-cell multiomics analysis of pediatric tumor evolution and minimal residual disease

**Postdoctoral Fellow, University of Pennsylvania** July 2020 – May 2023  
Laboratory of Casey Greene, PhD, and the Childhood Cancer Data Lab at ALSF  
*Focus:* Cross-platform bioinformatics data integration for machine learning in pediatric oncology

**PhD, Washington University in St. Louis** June 2014 – March 2020  
Division of Biology and Biomedical Sciences, Human and Statistical Genetics Program  
Laboratory of Li Ding, PhD

- Led pan-cancer computational projects utilizing tumor and normal tissue sequencing data to understand patterns of germline and somatic variation
- Developed integrative data analysis tools and pipelines, including variant calling and quality control using bulk DNA and RNA, single-cell RNA, and linked-read DNA sequencing
- Discovered gene fusions from The Cancer Genome Atlas (9,624 patients, 33 cancer types) and a large multiple myeloma cohort (742 patients), highlighting clinically-relevant events

**Biostatistician, Virginia Commonwealth University** August 2013 – May 2014  
**MS Biostatistics, University of Washington** September 2011 – August 2013  
**BS Mathematics, Presbyterian College** August 2006 – May 2010