

Erik P. Storrs

5449 Odell Street | Saint Louis, MO 63139
314-809-0604 | epstorrs@gmail.com | storrs.io | github.com/estorrs

Education

Washington University, Saint Louis, MO
PhD in Computational and Systems Biology
Li Ding Lab

August 2019 - May 2025

Saint Louis University, Saint Louis, MO
Bachelor of Science, double major in Computer Science and Geology
Minor in Environmental Science
Awards:

August 2012 - May 2017

Magna cum laude (GPA: 3.78 / 4.0)

Dean's List: 7 semesters

Selected to represent the Department of Math and Computer Science at the SLU Senior Legacy Symposium

Work Experience

Washington University School of Medicine

May 2025 - Present

Bioinformatician (*Li Ding Lab*)

- Managed imaging data, including H&E, IHC, and multiplex IHC images
- Developed tools and methods for analysis of 3-dimensional -omics datasets
- Developed deep learning models for application in spatial datasets

Washington University School of Medicine / McDonnell Genome Institute

November 2018 - August 2019

Research Assistant (*Li Ding Lab*)

- Helped to implement high-throughput pipelines for genomics data
- Applied concepts in machine learning and deep learning to cancer proteogenomics

Inventr

October 2017 - September 2018

Co-founder and CTO

- Designed, deployed, and maintained information retrieval services in support of a patent search application
- Developed and deployed backend services within a cloud-based architecture
- Implemented user-facing frontend services
- Gathered user feedback to inform product development decisions

CareOtter

June 2017 - March 2018

Data Scientist

- Implemented a suggestion engine in support of an Allscripts electronic health record system
- Responsible for interfacing with DevOps team to coordinate deployment within a Kubernetes cluster

Washington University School of Medicine

May 2014 - August 2014

Lab Assistant

- Helped to develop nanotechnology used for biomedical imaging and target-specific drug delivery
-

Research Projects

3D reconstruction and neighborhood annotation in multi-modal imaging datasets

Overview: Developed Mushroom, a tool for the generation of 3D cellular neighborhoods in multi-modal serial section datasets

Description: Used a specialized vision transformer (ViT) to annotate 3D neighborhood volumes and a graph clustering approach for integration of data type-specific volumes. The method was then applied in a pan-cancer analysis of the tumor-TME boundary in 15 cases. Additionally, 3D DEG analysis was applied to identify transition DEGs in Prostate and Breast cancer.

Languages used: Python

Github: <https://github.com/ding-lab/mushroom>

Single cell analysis of genomic subtypes in pancreatic adenocarcinoma (PDAC)

Overview: Used scRNA-seq data to identify a community of stromal and immune cell states with implications for patient overall survival and distinct developmental characteristics.

Description: Based on scRNA-seq, we partitioned malignant cells into Classical and Basal subtypes, CAFs into myofibroblast (myCAF) and inflammatory (iCAF) fibroblast, and TAMs into C1QC+, FCN1+, SPP1+ Macrophages. We found an association with Basal malignant cells, myCAFs, and SPP1+ TAMs and overall patient survival. Additionally, we found the developmental status of CAFs and Malignant cells were linked to this community of cell states and overall survival.

Languages used: Python, R

Classification of cell types in single cell datasets

Overview: Developed a variational autoencoder (VAE)-based model to identify cell types in single-cell datasets across a variety of cancer types.

Description: Developed Pollock, a variational autoencoder for classification of cell types, that was designed to be compatible with popular single-cell methods and analysis platforms, such as Scanpy and Seurat. Additionally, a set of pretrained cancer reference models were provided, along with the ability to extract interpretability scores from the model to identify genes driving cell type classifications.

Languages used: Python, R

Github: <https://github.com/ding-lab/pollock>

Genomic pipeline development

Overview: Containerized a variety of tools for genomic analysis of tumor sequencing data and incorporate into a pipeline using common workflow language (CWL)

Description: Used docker to containerize tools, such as expression quantification, mutation calling, and fusion detection, for analysis RNA and DNA sequencing datasets. Pipeline was orchestrated in CWL and designed to run on the Washington University high performance computing cluster.

Languages used: CWL, Bash, Python

Github: <https://github.com/ding-lab/pecgs-pipeline>

Classification of ancestry with genomic data

Overview: Developed a machine learning model to classify patients' ancestry based on WGS sequencing data

Description: Using data from the thousand genomes project as a reference, a model was built to call overlapping mutations and classify sample ancestry. We used a hybrid approach, where mutations were reduced to low dimensional space via PCA, and the resulting components were input to a random forest model that annotated ancestry.

Languages used: Python

Github: <https://github.com/ding-lab/ancestry>

Personal Projects

Remote viewer for spatial transcriptomics experiments

Overview: Developed Cosilico Viewer, a web application for viewing spatial transcriptomics experiments in the browser.

Description: Built a browser-based viewer using Svelte and OpenLayers for remote visualization of spatial datasets stored in Zarr format on S3-compatible storage. Developed a complementary Python library for programmatic upload, download, and management of spatial experiments. Used Supabase as the backend for authentication, database, and storage services.

Languages/Frameworks used: Javascript (Svelte), Python, Supabase (Postgres, Deno, S3 storage)

Github: <https://github.com/estorrs/cosilico-viewer>

Demo link: https://lighthearted-kulfi-ce56ba.netlify.app/portal/demo_429ed69f-28e9-4663-8e71-222a7fbc7533

Blog

Overview: Blog posts on deep learning methods, particularly as they apply to biomedical imaging and genomics

Website: storrs.io

Technologies and Software

Imaging and spatial analysis

Languages: Python

Libraries: NumPy, Scipy, scikit-image, tifffile, Pillow, Scanpy, Squidpy

Software: Fiji/ImageJ, QuPath, HALO, QiTissue, Omero

Deep Learning

Languages: Python

Libraries: PyTorch, TensorFlow (to a lesser extent than PyTorch), scikit-learn

Models: Transformers, Autoencoders, CNNs, (topical blog posts at storrs.io)

Single-cell genomics

Languages: Python, R

Libraries: Scanpy, Seurat

Pipeline orchestration and development

Languages: CWL, Bash, Python

Platforms: Linux, Docker, AWS

Application development

Frontend languages/frameworks: Javascript (Svelte, React)

Backend: Supabase (Postgres, Deno, S3 storage)

Publications

Storrs, E.P., Chati, P.*, Usmani, A.*,..., Chaudhuri, A. (2023) 'High-dimensional deconstruction of pancreatic cancer identifies tumor microenvironmental and developmental stemness features that predict survival', NPJ precision oncology, 7(1), p. 105.

Storrs, E.P.*, ..., Ding, L. (2022) 'Pollock: fishing for cell states', Bioinformatics advances, 2(1), p. Vbac028.

- Mo, C.K.*, Liu, J.*, Chen, S.#, **Storrs, E.P.#**, Targino da Costa, A.L.N.#,, Ding, L. (2024) 'Tumour evolution and microenvironment interactions in 2D and 3D space', *Nature*, 634 (8036), 1178-1186
- Liu, J., ..., **Storrs, E.P.**, ..., Ozbek, U. (2024) 'Multi-scale signaling and tumor evolution in high-grade gliomas', *Cancer cell*, 42 (7), 1217-1238.
- Kołodziejczak-Guglas, I., ..., **Storrs, E.P.**, ..., Wiznerowicz, M. (2025) 'Proteomic-based stemness score measures oncogenic dedifferentiation and enables the identification of druggable targets', *Cell Genomics* 5 (6).
- Rodrigues, F.M., ..., **Storrs, E.P.**, ..., Ding, L. (2025) 'Precision proteogenomics reveals pan-cancer impact of germline variants', *Cell* 188 (9), 2312-2335. E26
- Iglesia, M.D., ..., **Storrs, E.P.**, ..., Ding, L. (2024) 'Differential chromatin accessibility and transcriptional dynamics define breast cancer subtypes and their lineages', *Nature Cancer* 5 (11), 1713-1736.
- Rodrigues, F.M., ..., **Storrs, E.P.**, ..., Ding, L. (2024) 'Germline predisposition in multiple myeloma', *Iscience* 28 (1).
- Liang, W.-W.,, **Storrs, E.P.**,, Ding, L. (2023) 'Integrative multi-omic cancer profiling reveals DNA methylation patterns associated with therapeutic vulnerability and cell-of-origin', *Cancer cell*, 41(9), pp. 1567–1585.e7.
- Li, Y., **Storrs, E.P.**, ... Ding, L. (2023) 'Pan-cancer proteogenomics connects oncogenic drivers to functional states', *Cell*, 186(18), pp. 3921–3944.e25.
- Yao, L., ..., **Storrs, E.P.**, ... Ding, L. (2023) 'Single-Cell Discovery and Multiomic Characterization of Therapeutic Targets in Multiple Myeloma', *Cancer research*, 83(8), pp. 1214–1233.
- Cui Zhou, D., ..., **Storrs, E.P.**, ..., Ding, L. (2022) 'Spatially restricted drivers and transitional cell populations cooperate with the microenvironment in untreated and chemo-resistant pancreatic cancer', *Nature genetics*, 54(9), pp. 1390–1405.
- Liu, R., ...**Storrs, E.P.**, Ding, L. (2021) 'Co-evolution of tumor and immune cells during progression of multiple myeloma', *Nature communications*, 12(1), p. 2559.

Abstracts and presentations

- Storrs, E.P.**, ..., Ding, L., (2024) 'Mushroom: a tool for identification of 3D cellular neighborhoods in multi-modal spatial datasets', AACR Minisymposium (Oral presentation)
- Storrs, E.P.***, Chati, P.*, Usmani, A.*, ..., Chaudhuri, A. (2023) 'High-dimensional deconstruction of pancreatic cancer identifies co-occurring TME features associated with survival', AACR Minisymposium (Oral presentation, talk presented by P. Chati)
- Storrs, E.P.** (2023) 'Deconstruction of pancreatic ductal adenocarcinoma identifies survival-associated tumor microenvironmental communities', Cancer Genomics Consortium (Oral presentation, Poster)
- Storrs, E.P.** (2019) 'Pollock: fishing for cell states', Human Tumor Atlas Network Annual Meeting (Oral presentation, Poster)