

Charles Blatti

Senior Research Scientist

National Center for Supercomputing Applications

[Affiliate Research Page](#)

Email: blatti@illinois.edu

Created: January 2024

For complex phenotypes, behaviors, and diseases, molecular profiling experiments can capture the characteristics of and interactions between the underlying genes, proteins, and cell types. Modelling and extracting meaningful insights from these large, high-dimensional datasets can accelerate biomarker identification for health interventions.

Top Genes Discovered By:

Cancer Type	STANDARD ONLY	BOTH METHODS	KNOWLEDGE-GUIDED ONLY
AML			NRAS, KRAS
BLCA			RBM5, SMC1A
BRCA	MECOM	TBX3, GATA3	FOXO1
COAD			
GBM			TJP1, EGFR, SPTAN1 ★
HNSCC	★ IRF6	PABPC3, ZNF750, FAT2	CDH1, CTNNB1, EGFR ★★
LUAD			EGFR, FN1
LUSC			CTNNB1, CLOCK
OV			ATF1, ACTG1, HDAC3 ★
READ		AXIN2, ELF3	
UCEC		SRGAP3, SOX17	CTNNB1, WIPF1, GNAI1 ★

Research Interests

- Constructing gene regulatory models from RNA-seq and epigenetic data
- Machine learning on gene-centered heterogeneous knowledge networks
- Interactive tools for visualizing and exploring evolutionary phylogenies
- Variant allele statistics and significance for phenotype-specific populations
- Query interfaces and chatbots for assisting with variant interpretation

Current Projects

- Transcriptomic and protein level changes in response to viral challenge
- GWAS and EWAS analysis of STRONG Kids 2 cohort
- Large language model-based research assistant for leveraging popular variant annotation databases

Keywords

Genome sequencing, transcriptional regulatory networks, knowledge networks, variant interpretation, tumor evolution

Interest Areas for Collaboration/Future Work

Dr. Blatti is interested in working with experimental and clinical researchers who have collected genomic, transcriptomic, or epigenomic data from model organisms or human patients and study participants and who want to relate their molecular profiling results to relevant health and disease phenotypes.