

# Cancer Bioinformatics Shared Resource (CBSR)

## Director Alper Uzun, MS PhD



### Overview

Cancer Bioinformatics Shared Resource (CBSR) provide guidance with large consortia data such as from The Cancer Genomic Atlas (TCGA), or assistance for webservers such as cBioPortal, gnomAD, HPA (Human Protein Atlas). Cancer Bioinformatics develop novel tools in cutting edge cancer research at Legorreta Cancer Center (LCC). CBSR consistently updates bioinformatics tools to uphold best practices, from data pre-processing to variant discovery. CBSR also support and provide education in computational biology and bioinformatics from cancer biology perspectives.

### Key Services

- Next-Generation Sequencing (NGS) Sequence Analysis
- Advanced Post-Analysis
- Custom Tool Development for Genomics Data Processing and Interpretation
- Specialized Bioinformatics Consulting Services for Genomics Projects

### Value Added

- Guidance with large consortia data and bioinformatics applications
- Enhance the practical skills of LCC researchers
- Provide a unique edge to LCC researchers with novel tools
- On-demand Consulting

### Major Equipment /Technologies

Ocean State Center for Advanced Resources (Oscar) is Brown University's high performance computing cluster for both research and classes.



### Key Personnel

Cancer Bioinformatics Director, Alper Uzun, MS PhD

### Interaction with Cancer Bioinformatics Shared Resource

Research Group	Role	Description	Program Affiliations
El-Deiry Lab	Coll. & Bio.	RNA-seq Analysis for the tumor treating fields project	Cancer Therapeutics
Lawler Lab	Coll.	Androgen Response Elements Promoters Genes in HLA-E	Cancer Therapeutics
Sobol Lab	Coll.	Glioblastoma, Pediatric Glioblastoma	Cancer Therapeutics
Uzun Lab (Dr. Ece Uzun's Lab)	Coll.	NSF proposal in prep. NIH P01 proposal in prep.	Cancer Biology
Dr. Andre Souza	Coll. & Bio.	APPIC, Glioblastoma, Colorectal Cancer, Bladder Cancer	Cancer Biology
Dr. Ali Amin	Coll.	Bladder Cancer	Cancer Therapeutics
Dr. Benedito A. Carneiro	Coll.	Genetic alterations in urothelial carcinoma.	Cancer Biology
		Senescence and Prostate CA	Cancer Therapeutics

- Collaboration & Bioinformatics support (Coll. & Bio.)
- Collaboration (Coll.)
- Bioinformatics Support (Bio.)

### Key Publications

Hacking S, Chou C, Baykara Y, Wang Y, **Uzun A\***, Gamsiz Uzun ED\*. MMR Deficiency Defines Distinct Molecular Subtype of Breast Cancer with Histone Proteomic Networks. *Int J Mol Sci.* 2023 Mar 10;24(6):5327. \*Equal corresponding authors

De Souza AL, Mega AE, Douglass J, Olszewski AJ, Gamsiz Uzun ED, **Uzun A**, Chou C, Duan F, Wang J, Ali A, Golijanin DJ, Holder SL, Lagos GG, Safran H, El-Deiry WS, Carneiro BA. Clinical features of patients with MTAP-deleted bladder cancer. *Am J Cancer Res.* 2023 Jan 15;13(1):326-339.

Armanious D, Schuster J, Tollefson GA, Agudelo A, DeWan AT, Istrail S, Padbury J, **Uzun A**. Proteinarium: Multi-sample protein-protein interaction analysis and visualization tool. *Genomics.* 2020 Nov;112(6):4288-4296. doi: 10.1016/j.ygeno.2020.07.028. Epub 2020 Jul 20.

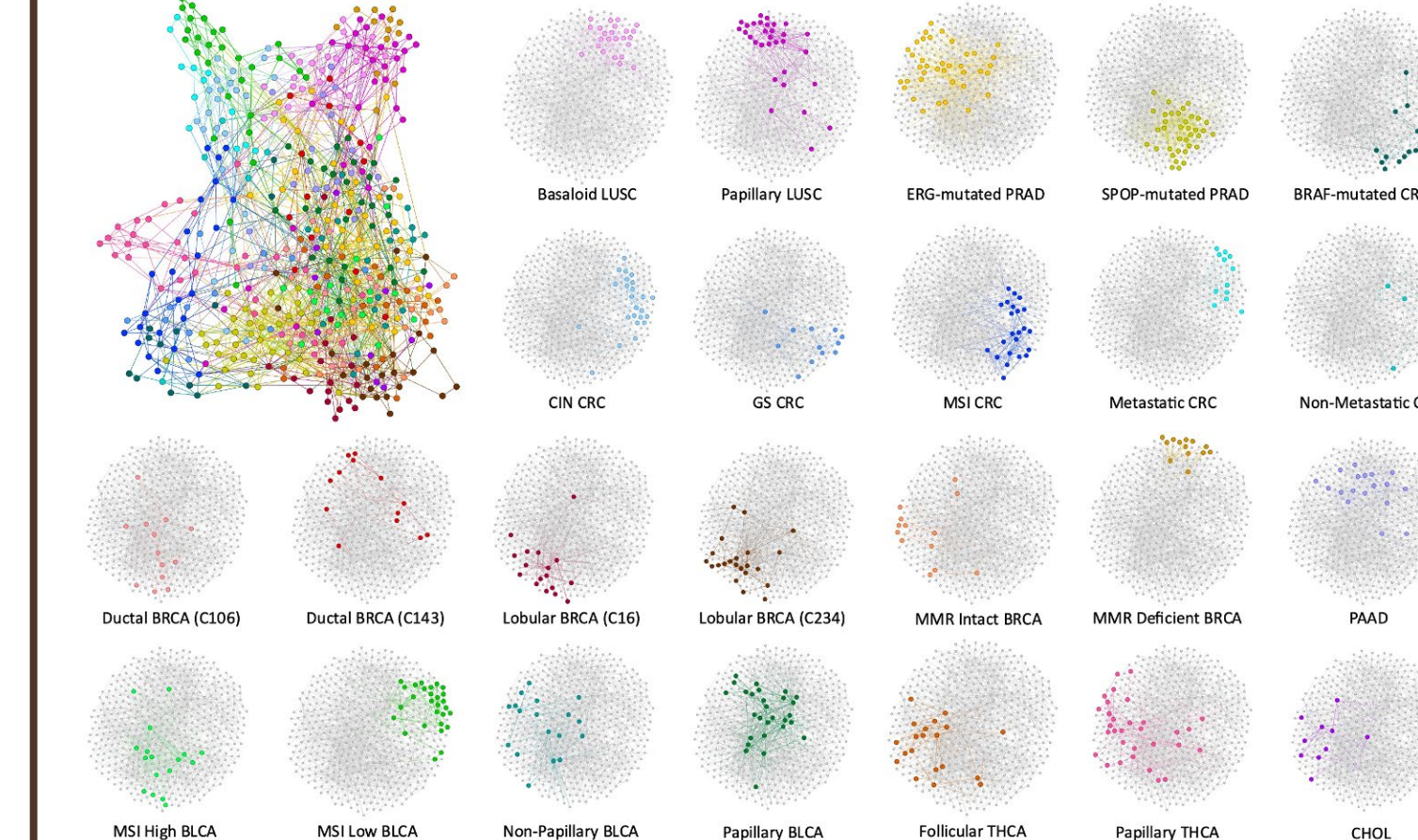
Tollefson GA, Schuster J, Gelin F, Agudelo A, Ragavendran A, Restrepo I, Stey P, Padbury J, **Uzun A**. VIVA (VIsualization of VArants): A VCF File Visualization Tool. *Sci Rep.* 2019 Sep 2;9(1):12648.

Schuster J, Superdock M, Agudelo A, Stey P, Padbury J, Sarkar IN, **Uzun A**. Machine learning approach to literature mining for the genetics of complex diseases. *Database (Oxford).* 2019 Jan 1;2019.

### Scientific Impact Scientific Examples for Genomic Tools and Databases

#### Atlas of Protein-Protein Interactions in Cancer (APPIC)

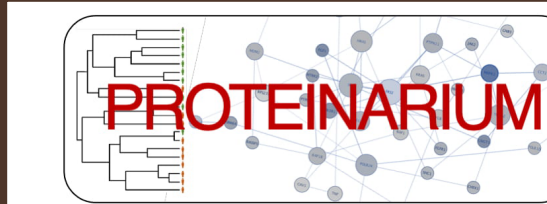
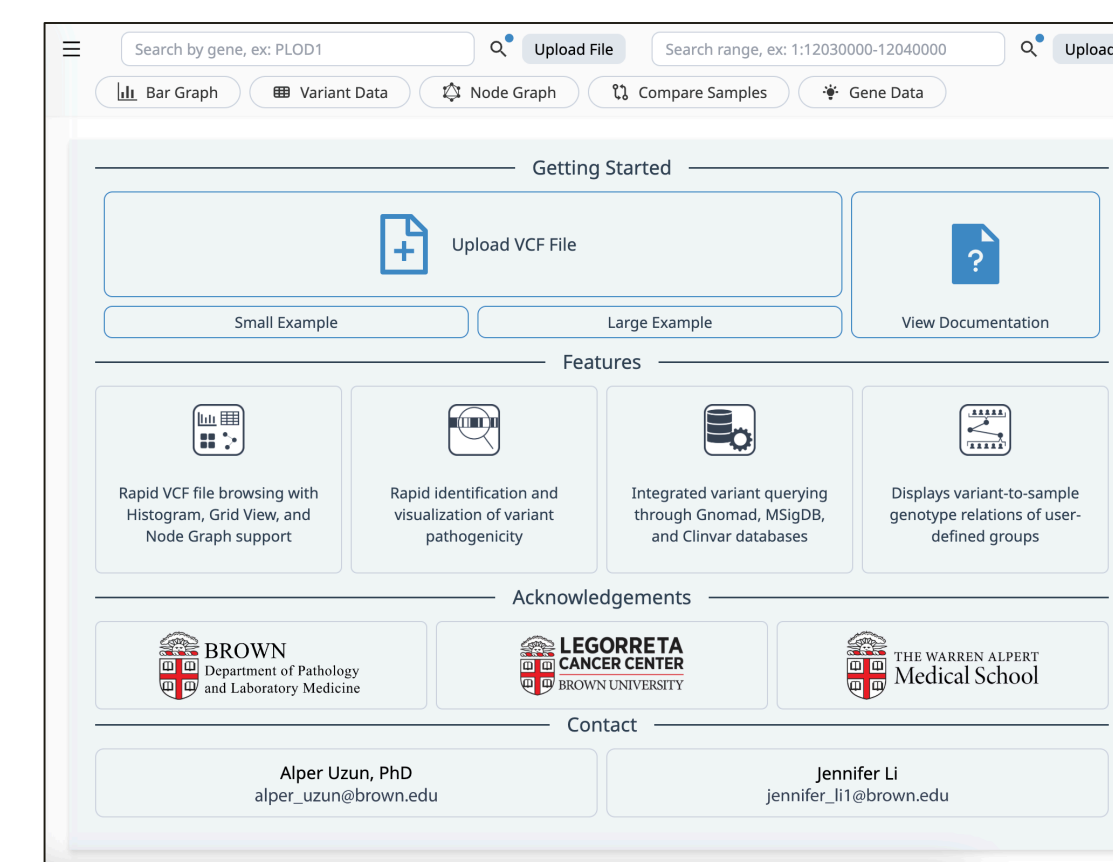
APPIC is a web-based tool that helps users visualize the protein-protein interactions (PPIs) of various cancer types and subtypes. We used publicly available genomic data of cancer patients across 10 tissue types to define the (PPI)s of a total of 26 cancer subtypes. APPIC is available at <https://appic.brown.edu/>



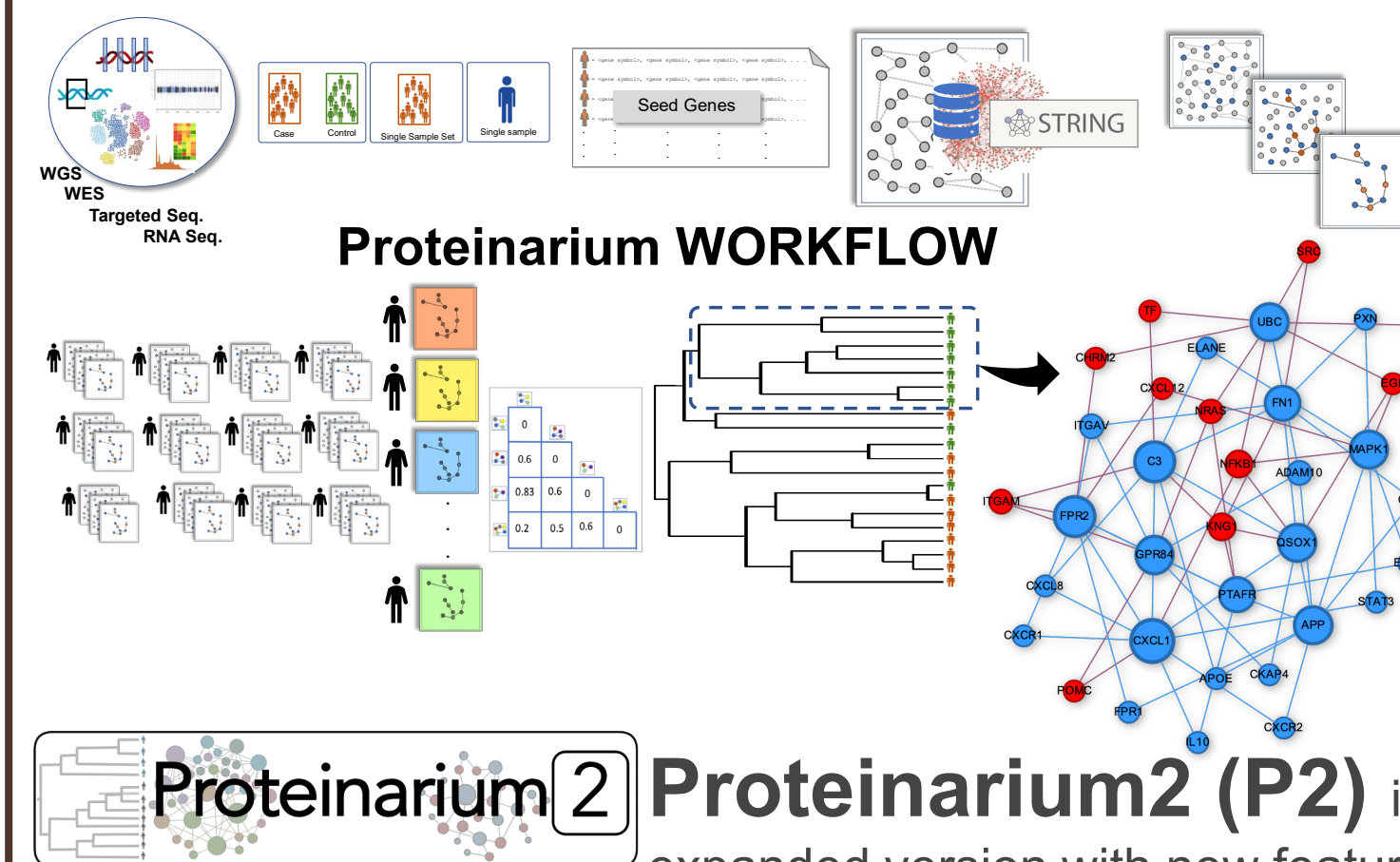
Funding: LCC Pilot Project, Rhode Island Foundation

#### Variant Graph Craft (VGC)

Tool for Analyzing Genetic Variation and Identifying Disease-Causing Variants. VGC is freely downloadable at <https://github.com/alperuzun/VGC>



**Proteinarium** is multi-sample protein-protein interaction analysis and Visualization Tool. Proteinarium identifies clusters of samples with shared networks. The software is freely downloadable at <https://github.com/alperuzun/Proteinarium>

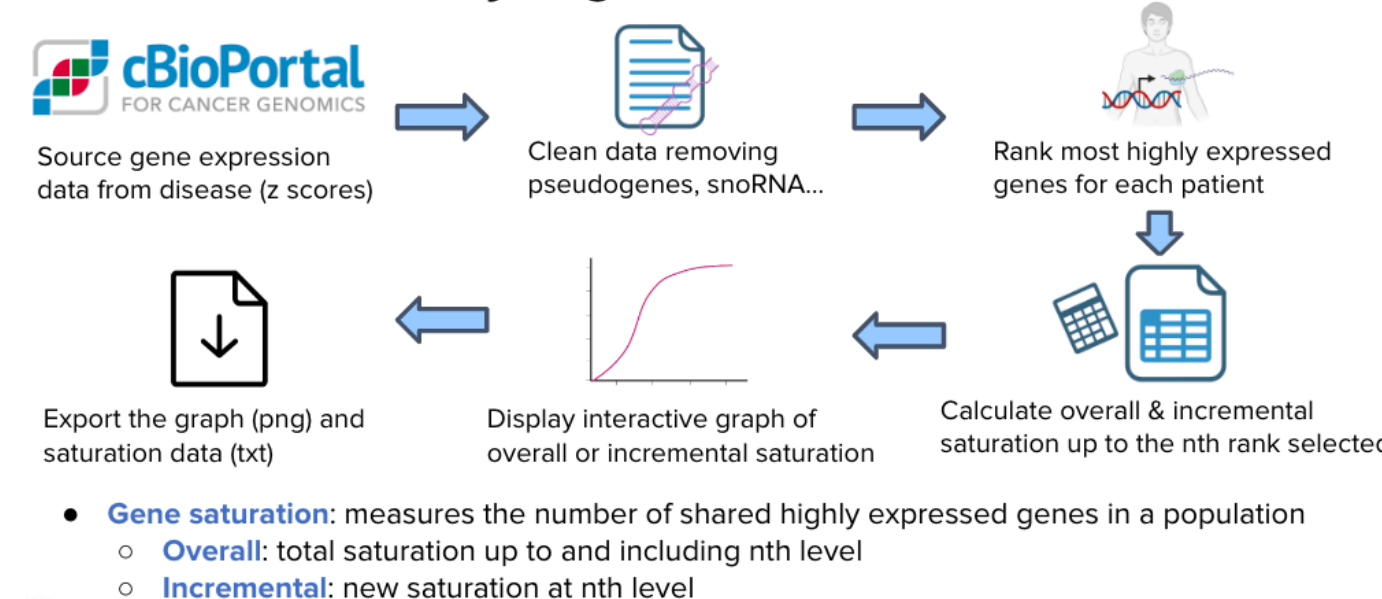


**Proteinarium2 (P2)** is expanded version with new features and databases. P2 is a web application available at <https://proteinarium.brown.edu/>

Funding: NIH, Burroughs Wellcome Fund

**THRESHOLD** analyzes transcriptomic data across large samples of patients (ex: TCGA data) to understand the cohesion of the most upregulated/downregulated genes in a given disease. THRESHOLD identifies consistently regulated genes in diseases, offering unique features such as user-determined saturation types and restriction parameters. THRESHOLD is freely downloadable <https://github.com/alperuzun/THRESHOLD>

#### Analyzing Gene Saturation



### Future Plans

**Fee Management & Sustainability:** Collaborate with administration to develop a cost-effective model and ensure a self-reliant bioinformatics platform.

**Bioinformatics Workshops:** Interactive sessions with cancer genomics data & tools.

**Seminar Series:** Regular talks by experts in cancer genomics & bioinformatics.

**Data Clinics:** Personalized help for bioinformatics challenges; bring questions, get solutions.

**Case Studies & Tutorials:** In-depth guides using real data, like TCGA, for effective learning.

**Online Repository:** Always-accessible resources & FAQs for self-paced learning.