

Samuel Anthony Danziger

Sam_Danziger@ieee.org • Seattle, WA • www.SamDanziger.com

RESEARCH FOCUS: My main research interest is using computer models and high-throughput ‘omics experiments to speed up the pace of biological discovery. I use statistical and bioinformatics techniques to model biological systems and develop regulatory networks that identify drivers of patient outcomes. Recently I have focused on deconvolution – determining which immune and stromal cells are present in gene expression data taken from tumor samples.

SELECT PUBLICATIONS:

Danziger, S.A.; McConnell, M.; Gockley, J.; Young, M.H.; Rosenthal, A.; Schmitz, F.; Reiss, D.J.; Farmer, P.; Alapat, D.V.; *et al.*; Ratushny, A.V.; Morgan, G.J.

Bone marrow microenvironments that contribute to patient outcomes in newly diagnosed multiple myeloma: A cohort study of patients in the Total Therapy clinical trials, (2020) *PLoS Medicine* 17 (11), e1003323

Danziger, S.A.; Gibbs, D.L.; Shmulevich, I.; McConnell, M.; Trotter, M.W.B.; Schmitz, F.; Reiss, D.J.; Ratushny, A.V.

ADAPTS: Automated deconvolution augmentation of profiles for tissue specific cells, (2019) *PLoS One* 14 (11), e0224693

Danziger S.A., Zeng J., Wang Y., Brachmann R.K., and Lathrop R.H.

Choosing where to look next in a mutation sequence space: Active Learning of informative p53 cancer rescue mutants, (2007) *Bioinformatics*, 23(13), 104-114

EMPLOYMENT:

January 2020 – Present: *Principal Scientist, Disease Stratification* **Bristol-Myers Squibb**, Seattle WA

- Deconvolved solid tumor samples to stratify patients including lung, prostate and breast cancer
- Developed new techniques for single cell informed deconvolution of heterogenous samples

January 2017 – January 2020: *Senior Scientist, Genome Stratification* **Celgene**, Seattle WA

- Deconvolved bone marrow microenvironment for pre-treatment Multiple Myeloma (MM) patients
- Determined a high-risk deconvolution-based signature for MM along with biological mechanisms
- Developed a GNS-REFS based framework for determining causal models of patient outcomes

September 2015 - Present: *Director of Bioinformatics* **Precyte**, Seattle WA

- Oversaw development of machine learning based indicator cell phenotype classifier

Spring 2010 - January 2017: *Senior Scientist / Bioinformatics (Staff) Scientist*

Center for Infectious Disease Research and Institute for Systems Biology, Seattle WA

- Identified DC6 / DC8 surface protein adhesion types associated with severe malaria
- Integrated genetic and metabolic networks to identify Oaf1 / pyruvate dehydrogenase link
- Co-founded **Precyte** to detect ALS, Alzheimer’s, and Cancer from indicator cells
- Developed Biclustor Sampled Coherence Metric (BSCM) for cMonkey2
- Co-developed PhosphoChain to detect phosphorylation events from gene expression data
- Designed a framework to build regulatory networks from mass spectrometry data
- Built a biomarker discovery pipeline to detect liver-stage resistance to malaria
- Developed machine learning based models that correctly predicted gene expression *in vivo*
- Made an intuitive, accessible yeast oleate response network from microarray, ChIP, and Motif data
- Improved R-based cMonkey gene clustering and Inferelator gene regulation tools
- Deployed resource intensive software on Amazon Elastic Cloud Compute (EC2) resources

EDUCATION:

Biomedical Engineering: Doctor of Philosophy – GPA: 3.91/4.0 (2004-2009)

Biomedical Engineering: Master of Science (2002-2004)

Henry Samueli School of Engineering *University of California Irvine*, Irvine, California
Computer Science: *Master of Science* – GPA: 4.0/4.0 (1997-2002)
Golisano College of Computing and Information Sciences
Electrical Engineering: *Bachelor of Science* – GPA: 3.89/4.0 (1997-2002)
Kate Gleason College of Engineering *Rochester Institute of Technology*, Rochester, New York

COMPUTER LANGUAGES, SOFTWARE AND ENVIRONMENT:

Recent Projects: R

Older Projects: Bash, C, C++, C#, Java, Matlab, Open GL, Python, Ruby, Sun Grid Engine, Visual Basic

Some Experience: Lisp, ML, Perl, SQL, VHDL, XNA

Recent Software: Docker, Git, Jupyter, MS Office, RStudio, vi

Older Software: Adobe Illustrator, Amber, DESeq2, Eclipse, EdgeR, MaxQuant, Modeller, SAMtools, STAR, Subversion, UCSF Chimera, Visual Studio, Weka

BIOLOGICAL LAB EXPERIENCE:

Polymerase Chain Reaction (PCR), Digestion, Ligation, *Escherichia Coli* and Yeast Transformation, Plasmid Rescue, Single Colony Purification and Basic Laboratory Procedure

HONORS:

UCI Bioinformatics Training Grant (BIT) recipient: (2004-2008)

PROFESSIONAL ORGANIZATIONS:

International Society for Computational Biology (ISCB) (2007)

Order of the Engineer (2004), Institute for Electrical and Electronic Engineers (IEEE) (2001)

ADDITIONAL EMPLOYMENT:

Fall 2009-Winter 2010: *Machine Learning Scientist*

- Developed data mining algorithms to identify strong players stuck at a low rank
- Corrected Riot Games team Elo algorithm using data mining techniques in R
- Designed and implemented Gaussian encounter algorithm for Starflight III project in XNA/C#

Fall 2002-Summer 2009: *Graduate Student Researcher*

University of California, Irvine CA

- Invented bioinformatics and protein engineering software to find desirable mutants
- Created mutant proteins *in silico* using Amber™ molecular dynamics software
- Simulated active learning and analyzed protein structure using Matlab™
- Optimized software to run on a 64 node Sun Grid Engine (SGE) cluster
- Tested mutant p53 protein phenotype *in vivo*
- Collaborated with a mixed team of computer scientists and biologists specializing in e. coli, yeast, oncology, protein structure-function relationships and molecular modeling
- Analyzed *in-vitro* and *in-silico* experimental results for statistical significance
- Administrated multi-user IIS web, ftp, subversion, and SQL server running Windows 2003
- Wrote scientific papers using clear, descriptive language for an international audience

Summer 2001: *Software Scientist*, Winter 2000 – Spring 2000: *Software Co-op*

Annapolis Micro Systems, Annapolis MD

- Led a group writing a Vector Signal and Image Processing Library (VSIPL) using the WILDSTAR™ WILDFFT™ core in ANSI standard C
- Wrote a demonstration for the VSIPL library using Matlab™ scripting language
- Wrote and/or maintained software for internal testing and board repair
- Tested and debugged API for WILDSTAR™ board, including several multi-thread issues
- Expanded API to readback through a JTAG interface for Xilinx Virtex™ series chips.
- Prepared, Tested, and Released software for multiple platforms including Windows NT (both PC and VMIC), Linux, Solaris, and Force

Summer 1999: *Co-op*

Compaq Computer Services (formerly Digital Equipment Corporation), Piscataway NJ

- Supported group developing a Telecommunications Management Information Platform (TeMIP)
- Read / Write testing of True 64 UNIX Alpha box
- Created a database of NE region based Telecom Service Providers

EXTRACURRICULAR LEADERSHIP EXPERIENCE:

VP Financial Affairs - Associated Graduate Students (AGS) (2007-2008)

VP Administrative Affairs - Associated Graduate Students (AGS) (2006-2007)

Chair - Graduate Student Health Insurance Plan (GSHIP) Advisory Board (GAB) (2005-2006)

Engineering Representative - Associated Graduate Students (AGS) (2004-2009)

ALL RESEARCH PAPERS (*First Author):

<https://scholar.google.com/citations?hl=en&user=12smia0AAAAJ>

Danziger, S.A.; McConnell, M.; Gockley, J.; Young, M.H.; Rosenthal, A.; Schmitz, F.; Reiss, D.J.; Farmer, P.; Alapat, D.V.; *et al.*; Ratushny, A.V.; Morgan, G.J.

Bone marrow microenvironments that contribute to patient outcomes in newly diagnosed multiple myeloma: A cohort study of patients in the Total Therapy clinical trials, (2020) *PLoS Medicine* **17** (11), e1003323

Neal, M.L.; Wei, L.; Peterson, E.; Arrieta-Ortiz, M.L.; Danziger, S.A.; Baliga, N.S.; Kaushansky, A.; Aitchison, J.D.

A system-level gene regulatory network model for Plasmodium falciparum, (2020) *Nucleic Acids Research*, In Press

Aguilar, B.; Gibbs, D.L.; Reiss, D.J.; McConnell, M.; Danziger, S.A.; Dervan, A.; Trotter, M.W.B.; Bassett, D.; Hershberg, R.; Ratushny, A.V.;

A generalizable data-driven multicellular model of pancreatic ductal adenocarcinoma, (2020) *GigaScience* **9** (7), g1aa075

Wall, M.A.; Turkarslan, S.; Wu, W.J.; Danziger, S.A.; Reiss, D.J.; Mason, M.; Dervan, A.P.; Trotter, M.W.; Bassett, D.; Hershberg, R.M., De Lomana, A.L.G

Genetic program activity delineates risk, relapse, and therapy responsiveness in Multiple Myeloma, (2020) *BioRxiv*

Mason, M.J.; Schinke, C.; Eng, C.L.P.; Towfic, F.; Gruber, F.; Dervan, A.; White, B.S.; Pratapa, A.; Guan, Y.; Chen; Danziger, S.A.; *et al.*

Multiple Myeloma DREAM Challenge reveals epigenetic regulator PHF19 as marker of aggressive disease, (2019) *Leukemia*, 1-9

Danziger, S.A.; Gibbs, D.L.; Shmulevich, I.; McConnell, M.; Trotter, M.W.B.; Schmitz, F.; Reiss, D.J.; Ratushny, A.V.

ADAPTS: Automated deconvolution augmentation of profiles for tissue specific cells, (2019) *PLoS One* **14** (11), e0224693

Danziger, S.A.; McConnell, M.; Gockley, J.; Young, M.; Rosenthal, A.; Schmitz, F.; Reiss, D.; Farmer, P.; Ashby, C.; Bauer, M.A.

Baseline and on-treatment bone marrow microenvironments predict myeloma patient outcomes and inform potential intervention strategies, (2018) *Blood* **132** (Supplement 1), 1882

Dervan, Andrew P; Mason, Michael; Towfic, Fadi; Amatangelo, Michael; Auclair, Daniel; Bassett, Douglas; Dai, Hongyue; Dalton, W.S.; Danziger, S.A.; Flynt, E.

Crowdsourcing a High-Risk Classifier for Multiple Myeloma Patients, (2017) *Blood* **130** (Supplement 1), 265

Danziger, S.A.; Dervan, A.P.; Schmitz, F.; Walker, B.A.; Copeland, W.; Fitch, A.; Newhall, K.; Ashby, C.; Bauer, M.; Barlogie, B.

Deconvolution of the immune microenvironment can predict the outcome of myeloma patients and inform potential intervention strategies, (2017) *Blood* **130** (Supplement 1), 1751

Zuck, M; Austin, L.S.; Danziger, S.A.; Aitchison, J.D.; and Kaushansky, A.

The promise of systems biology approaches for revealing host pathogen interactions in malaria, (2017) *Frontiers in Microbiology* **8**, 2183

Kessler A., Dankwa S., Bernabeu M., Harawa V., Danziger S.A., Duffy F., Kampondeni S.D., Potchen M.J., Dambrauskas N., Vigdorovich V., Oliver B.G., Hochman S.E., Mowrey W.B., MacCormick I.J.C., Mandala W.L., Rogerson S.J., Sather D.N., Aitchison J.D., Taylor T.E., Seydel K.B., Smith J.D., and Kim K.

Linking EPCR-Binding PfEMP1 to Brain Swelling in Pediatric Cerebral Malaria, (2017) *Cell Host & Microbe* **22** (5), 601-614.e5

Wang Z., Danziger S.A., Heavner B.D., Ma S., Smith J.J., Li S., Herricks T., Simeonidis E., Baliga N.S., Aitchison J.D., and Price N.D.

Combining inferred regulatory and reconstructed metabolic networks enhances phenotype prediction in yeast, (2017) *PLoS computational biology* **13** (5), e1005489

Danziger S.A., Miller L.R., Signh K., Peskind E.R., Li G., Lipshutz R., Aitchison J.D., and Smith J.J.
An indicator cell assay for blood-based diagnostics, (2017) *PloS one* **12** (6), e0178608

Zuck M., Austin L.S., Danziger S.A., Aitchison J.D., and Kaushansky A.

The promise of Systems Biology approaches for revealing host pathogen interactions in malaria, (2017) *Frontiers in microbiology* **8**

Bernabeu M., Danziger S.A., Avrila M., Vazb M., Babar P., Braziera A.J., Herricks T.E., Maki J.N., Pereira L., Mascarenhas A., Gomes E., Chery L., Aitchison J.D., Rathod P.K., and Smith J.D.

Severe adult malaria is associated with specific PfEMP1 adhesion types and high parasite biomass, (2016) *Proceedings of the National Academy of Sciences* **113** (23), E3270-E3279

Jung S., Danziger S.A., Panchaud A., von Haller P., Aitchison J.D., and Goodlett D.R.

Systematic Analysis of Yeast Proteome Reveals Peptide Detectability Factors for Mass Spectrometry, (2015) *Journal of Proteomics & Bioinformatics*, **8**(10), 231-239

Danziger, S.A., Reiss, D.J., Ratushny, A.V., Smith, J.J., Plaisier, C.L., Aitchison, J.D., and Baliga, N.S.

Bicluster Sampled Coherence Metric (BSCM) provides an accurate environmental context for phenotype predictions, (2015) *BMC Systems Biology* **9**, S1

Finney O.C.*, Danziger S.A.*, Molina D.M., Vignali M., Takagi A., Ji Mi., Staniscic D.I., Siba P.M., Liang X., Aitchison J.D., Mueller I., Gardner M.J., and Wang R.

Predicting anti-disease immunity using proteome arrays and sera from children naturally exposed to malaria, (2014) *Molecular & Cellular Proteomics*, **13**(10), 2646–2660

Danziger S.A., Ratushny A.V., Smith J.J., Saleem R.A., Wan Y., Arens C.E., Armstrong A.M., Sitko K., Chen W.-M., Chiang J.-H., Reiss D.J., Baliga N.S., and Aitchison J.D.

Molecular mechanisms of system responses to novel stimuli are predictable from public data, (2014) *Nucleic Acids Research*, **42**(3), 1442–1460

Cooney L.A., Gupta M., Thomas S., Mikolajczak S., Choi K.Y., Gibson C., Jang I.K., Danziger S.A., Aitchison J., Gardner M.J., Kappe S.H.I., and Wang R.

Short-Lived Effector CD8 T Cells Induced by Genetically Attenuated Malaria Parasite Vaccination Express CD11c, (2013) *Infection and Immunity*, **81**(11), 4171–4181

Wan Y., Zuo X., Zhuo Y., Zhu M., Danziger S.A., and Zhou Z.

The functional role of SUMO E3 ligase Mms21p in the maintenance of subtelomeric silencing in budding yeast, (2013) *Biochemical and Biophysical Research Communication*, **438**(4), 746–752

Chen W.-M.*, Danziger S.A.*, Chiang J.-H., and Aitchison J.D.

PhosphoChain: a novel algorithm to predict kinase and phosphatase networks from high-throughput expression data, (2013) *Bioinformatics* **29**(19), 2435–2444

Baronio R., Danziger S.A., Hall L.V., Salmon K., Hatfield G.W., Lathrop R.H., and Kaiser P.

All-codon scanning identifies p53 cancer rescue mutations, (2010) *Nucleic Acids Research*, **38**(20), 7079-7088

Danziger S.A., Baronio R., Ho L., Hall L., Salmon K., Hatfield G.W., Kaiser P., and Lathrop R.H.

Predicting Positive p53 Cancer Rescue Regions Using Most Informative Positive (MIP) Active Learning, (2009) *PLoS Computational Biology*, **5**(9), e1000498

Danziger S.A., Zeng J., Wang Y., Brachmann R.K., and Lathrop R.H.

Choosing where to look next in a mutation sequence space: Active Learning of informative p53 cancer rescue mutants. (2007) *Bioinformatics*, **23(13)**, 104-114

Danziger S.A.*, Swamidass S.J.*, Zeng J., Dearth L.R., Lu Q., Chen J.H., Cheng J., Hoang V.P., Saigo H., Luo R., Baldi P., Brachmann R.K., and Lathrop R.H.

Functional census of mutation sequence spaces: the example of p53 cancer rescue mutants. (2006) *IEEE/ACM transactions on computational biology and bioinformatics*, **3**, 114-125

Danziger S.A. and Anderson P.G.

Next generation optical character recognition using the polynomial method. (2002) Rochester Institute of Technology. (Patentable invention disclosure, released in 2003)

PRESENTATIONS AND POSTERS:

Poster – Baseline and on-Treatment Bone Marrow Microenvironments Predict Myeloma Patient Outcomes and Inform Potential Intervention Strategies

Danziger, S.A.; McConnell, M.; Gockley, J.; Young, M.; Rosenthal, A.; Schmitz, F.; Reiss, D.; Farmer, P.; Ashby, C.; Bauer, M.A.; Rhee, F.V.; Davies F.E.; Zangari M.; Petty, N.; Copeland, W.B.; Fox, B.A.; Hoering A.; Fitch, A.; Newhall, K; Barlogie, B.; Walker, B.A.; Trotter, M.; Hershberg, R.; Dervan, A.; Ratushny, A.; and Morgan, G. *American Society of Hematology (ASH) 2018 Annual Meeting*. Atlanta, GA

Poster – Crowdsourcing a High-Risk Classifier for Multiple Myeloma Patients

Dervan, A.P.; Mason, M.; Towfic, F.; Amatangelo, M.; Auclair, D.; Bassett, D.; Dai, H.; Dalton, W.S.; Danziger, S.; Flynt, E.; et al. *American Society of Hematology (ASH) 2017 Annual Meeting*. Atlanta, GA

Poster - Deconvolution of the Immune Microenvironment Can Predict the Outcome of Myeloma Patients and Inform Potential Intervention Strategies. (Presented by F. Schmitz)

Danziger S.A., Dervan A.P., Schmitz F., Walker B.A., Copeland W., Fitch A., Newhall K., McConnell M., Gockley J., Ashby T.C., Bauer M., Barlogie B., Foy T., Trotter M., Hershberg R., Ratushny A., and Morgan G.J. (2017) *American Society of Hematology (ASH) 2017 Annual Meeting*. Atlanta, GA

Poster - The Fat-Response Network.

Danziger S.A., Ratushny A., Plaisier C., Reiss D., Smith J., Wan Y., Baliga N., and Aitchison J. (2010) *3rd joint conference on Systems Biology, Regulatory Genomics, and DREAM – Reverse Engineering Challenges*. New York, NY

Presentation - Machine Learning discovers p53 cancer rescue regions.

Danziger S.A., Baronio R., Hall L.V. Ho L., Salmon K.A., Hatfield G.W, Kaiser P., and Lathrop R.H. (2009) *Center for Machine Learning & Intelligent Systems*. Irvine, CA

Presentation - Choosing where to look next in a mutation sequence space: Active Learning of informative p53 cancer rescue mutants. Danziger S.A., Zeng J., Brachmann R.K., and Lathrop R.H. (2007) *International Society for Computational Biology (ISMB) 2007*. Vienna, Austria

Presentation - Helping to Cure Cancer: Computer Science and Biology.

Danziger S.A. (2007) *Ask-A-Scientist Night: Hillview Elementary*. Whittier, CA

Presentation - In Silico Protein Behavior: Predicting the Activity of p53 Tumor Suppressor Protein Mutants Using Features Derived From Homology Modeling. Danziger S.A., Zeng J., Brachmann R.K., and Lathrop R.H. (2006) *9th Annual UCI Chao Family Cancer Center Retreat*. Rancho Mirage, CA

Poster - Predicting Mutant Protein Function Using Computer Models.

Danziger S.A, Brachmann R.K., and Lathrop R.H. (2005) *2005 National Library of Medicine (NLM) Informatics Training Programs Conference*. Bethesda, MD

Poster - Predicting Mutant Protein Function Using Computer models.

Danziger S.A, Brachmann R.K., and Lathrop R.H. (2005) *Samueli Scholars Luncheon*. Irvine, CA