

Nicholas Louis Panchy

Personal Information:

Address: Institute for Cyber Enabled Research
Michigan State University
567 Wilson Road, Room 1440
East Lansing, MI 48824-1226
Phone: (828)-423-4718
Email: npanchy@utk.edu

Education:

Graduate: Michigan State University, MI, Ph. D., Genetics, Laboratory of Dr. 2011 to 2017
Shin-Han Shiu
Undergraduate: University of North Carolina at Chapel Hill, NC, B.S. Biology and B.S. 2007 to
2011 Mathematics

Experience:

Research:

2022-present Research Consultant, Institute for Cyber Enabled Research, Michigan State
University, East Lansing, MI
2017-2022 Post-Graduate Researcher, Dr. Tian Hong, Biochemistry & Cellular and
Molecular Biology and National Institute of Mathematical Biological Synthesis,
University of Tennessee Knoxville, TN
2012-2017 Graduate Research Assistant, Dr. Shin-Han Shiu, Genetics Graduate Program
Michigan State University, MI
2010-2011 Undergraduate Research Assistant, Dr. Maria Servedio, Biology Department,
University of North Carolina at Chapel Hill, NC

Teaching:

Summer 2018 - 2020 Coding Workshop Instructor, Summer Research Experience hosted by the
National Institute of Mathematical Biological Synthesis, Organized by Suzanne
Lenhart and Gregory Wiggins, University of Tennessee Knoxville, TN
Summer 2019 Co-Mentor with Dr. Tian Hong, Summer Research Experience hosted by the
National Institute of Mathematical Biological Synthesis, Organized by Suzanne
Lenhart and Gregory Wiggins, University of Tennessee Knoxville, TN
Fall 2018 Guest lectures on Machine Learning for Programming for Biological Data
Analysis (LFSC507), Taught by Dr. Tian Hong, University of Tennessee
Knoxville, TN

- Fall 2016 Graduate Teaching Assistant for Theory and Practice in Bioinformatics (PLB400/810), Taught by Dr. Shin-Han Shiu, Michigan State University, MI
- Summer 2014, 2015 Teaching Assistant for Frontiers and Techniques in Plant Science, Co-taught by Drs. Mark Johnson, Shin-Han Shiu, Marja Timmerman, Cold Spring Harbor Labs NY
- Fall 2012 Graduate Teaching Assistant for Introduction to Genetics (ZOL341), Taught by Dr. Richard Allison, Michigan State University, MI

Outreach:

- 2018, 2019 Instructor “Adventures in STEM” camp at University of Tennessee Knoxville, TN
- 2016, 2017 Instructor for “Code Like a Girl” at Girl’s Math and Science Day, In association with Graduate Women in Science, Michigan State University, MI

Skills

- Actively practicing and teaching scientific programming in Python and R with prior experience in C++, C-sharp, MATLAB, and Mathematica (see <https://github.com/panchyni>)
- Familiar with UNIX operating systems, maintaining UNIX servers on a single laboratory scale, and using institutional/inter-institutional high performance computing clusters
- Experienced with machine learning package in both R and Python
- Experienced with modeling problems using systems of ordinary differential equations using both custom Python scripts and the Tellurium modeling environment
- Experienced with pre-processing, cleaning and investigation of large-scale omics data using both statistical and dimension-reduction based approaches
- Experienced with genome assembling, annotation, and alignment algorithm using both short and long reads

Peer-reviewed Publications:

1. **Panchy N**, Watanabe K, Hong T. Interpretable, Scalable, and Transferrable Functional Projection of Large-Scale Transcriptome Data Using Constrained Matrix Decomposition. *Front Genet.* 2021 Aug 20;12:719099.
2. **Panchy N**, von Arnim AG, Hong T. (2020) Early Detection of Daylengths with a Feedforward Circuit Coregulated by Circadian and Diurnal Cycles. *Biophys J.* 119(9):1878-1895
3. **Panchy N**, Azeredo-Tseng C, Luo M, Randall N, Hong T. (2020) Integrative Transcriptomic Analysis Reveals a Multiphasic Epithelial-Mesenchymal Spectrum in Cancer and Non-tumorigenic Cells. *Front Oncol.* 9:1479
4. **Panchy NL**, Lloyd JP, Shiu SH. (2020) Improved recovery of cell-cycle gene expression in *Saccharomyces cerevisiae* from regulatory interactions in multiple omics data. *BMC Genomics.* 21(1):159
5. Watanabe K, **Panchy N** (co-first author), Noguchi S, Suzuki H, Hong T. (2019) Combinatorial perturbation analysis reveals divergent regulations of mesenchymal genes during epithelial-to-mesenchymal transition. *PJ Syst Biol Appl.* Jun 14;5:21
6. **Panchy NL**, Azodi CB, Winship EF, O'Malley RC, Shiu SH. (2019) Expression and regulatory asymmetry of retained *Arabidopsis thaliana* transcription factor genes derived from whole genome duplication. *BMC Evol Biol* 19(1):77.
7. Wang P, Moore BM, **Panchy NL**, Meng F, Lehti-Shiu MD, Shiu SH. (2018) Factors Influencing Gene Family Size Variation Among Related Species in a Plant Family, Solanaceae. *Genome Biol Evol.* 10(10):2596-2613

8. Liu MJ, Sugimoto K, Uygun S, **Panchy NL**, Campbell M, Yandell M, Howe GA, Shiu SH. (2018) Regulatory Divergence In Wound-Responsive Gene Expression In Domesticated And Wild Tomato. *Plant Cell* 30(7):1445-1460
9. Lloyd JP, Tsai ZT, Sowers RP, **Panchy NL**, Shiu SH. (2018) A Model-Based Approach for Identifying Functional Intergenic Transcribed Regions and Noncoding RNAs. *Mol Biol Evol.* 35(6):1422-1436
10. Lehti-Shiu MD, **Panchy N**, Wang P, Uygun S, Shiu SH. (2017) Diversity, expansion, and evolutionary novelty of plant DNA-binding transcription factor families. *Biochim Biophys Acta* 1860(1):3-20.
11. **Panchy N**, Lehti-Shiu MD, Shiu SH. (2016) Evolution of Gene Duplication in Plants. *Plant Physiol.* 171(4):2294-316
12. Poliner E, **Panchy N**, Newton L, Wu G, Lapinsky A, Bullard B, Zienkiewicz A, Benning C, Shiu SH, Farré EM. (2015) Transcriptional coordination of physiological responses in *Nannochloropsis oceanica* CCMP1779 under light/dark cycles. *Plant J* 83(6):1097.
13. Lehti-Shiu MD, Uygun S, Moghe, GD, **Panchy N**, Fang L, Hufnagel D, Jasicki HL, Feig M, Shiu SH (2015) Molecular evidence for functional divergence and decay of a transcription factor derived from whole genome duplication in *Arabidopsis thaliana*. *Plant Physiol.* 168(4):1717-34.
14. Law M, Childs KL, Campbell MS, Stein D, Holt C, **Panchy N**, Lei J, Achawanantakun R, Jiao D, Andorf CM, Lawrence CJ, Ware D, Shiu SH, Sun Y, Jiang N, Yandell M (2015) Automated update, revision and quality control of the *Zea mays* genome annotations using MAKER-P improves the B73 RefGen_v3 gene models and identifies new genes. *Plant Physiol.* 167(1):25-39
15. **Panchy N**, Wu G, Newton L, Tsai CH, Chen J, Benning C, Farre EM, Shiu SH (2014) Prevalence, Evolution, and *cis*-Regulation of Diel Transcription in *Chlamydomonas reinhardtii*. *G3* 4(12):2461-2471
16. Wang Q, Tikhonenko M, Bozack SN, Lydic TA, Yan L, **Panchy NL**, McSorley KM, Faber MS, Yan Y, Boulton ME, Grant MB, Busik JV (2014) Changes in the daily rhythm of lipid metabolism in the diabetic retina. *PLoS One* 9(4):e95028
17. Awad S, **Panchy N**, Ng S-k, Chen J (2012) Inferring the Regulatory Interaction Models of Transcription Factors in Transcriptional Regulatory Networks. *J Bioinform Comput Biol.* 10(5):1250012

Presentations:

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| 2020 | ‘Investigating the progression of EMT in single-cell RNA data using Dimension Reduction’ Biochemistry & Cellular and Molecular Biology Department Colloquium, University of Tennessee Knoxville, Knoxville, TN (October 12) |
| 2018 | ‘Analysis of epithelial and mesenchymal gene expression uncovers the regulatory mechanisms controlling differential expression and reciprocity during epithelial-to- mesenchymal transition’ Department of Mathematics Colloquia, Howard University, Washington DC (October 19) |
| 2018 | ‘Regulation of reciprocal epithelial and mesenchymal gene expression during the epithelial-to-mesenchymal transition’ Biochemistry & Cellular and Molecular Biology Department Colloquium, University of Tennessee Knoxville, Knoxville, TN (October 1) |
| 2017 | ‘Asymmetric evolution of transcription factor expression and regulation in <i>Arabidopsis thaliana</i> .’ ICAR, St. Louis, MO (June 19-23) |