

CURRICULUM VITAE

ANN E. LORAINE

Dept. of Bioinformatics and Genomics
University of North Carolina, Charlotte

<http://www.lorainelab.org>
<http://www.bitbucket.org/lorainelab>

1 Education

Ph.D. University of California at Berkeley, Molecular and Cell Biology, 1996

B.A. University of Texas at Austin, Plan II (Honors Liberal Arts), 1989

B.S. University of Texas at Austin, Zoology, 1990

2 Professional Experience

- 2008 – present, *Associate Professor* (with tenure), Dept. of Bioinformatics and Genomics
University of North Carolina Charlotte
- 2004 – 2008, *Assistant Professor*, Departments of Biostatistics and Genetics (joint appointment),
University of Alabama at Birmingham
- 2000 – 2003, *Bioinformatics Scientist*, Affymetrix, Inc
- 1999-2000, *Bioinformatics Software Engineer*, Neomorphic, Berkeley, CA
- 1998-1999, *Programmer/Analyst*, UC Berkeley, Berkeley Drosophila Genome Project
- 1997-1998, *Postdoctoral Trainee*, UC Berkeley, Berkeley Drosophila Genome Project

3 Peer Reviewed Journal Publications

Qin P, **Loraine AE**, McCormick S. Cell-specific cis-natural antisense transcripts (cis-NATs) in the sperm and pollen vegetative cells of *Arabidopsis thaliana*. Accepted (with revisions) to F1000Research

Zubo YO*, Blakley IC*, Yamburenko MV, Worthen JM, Street IH, Franco-Zorrilla JM, Zhang W, Hill K, Raines T, Solano R, Kieber JJ, **Loraine AE****, Schaller GE**. Cytokinin induces genome-wide binding of the type-B response regulator ARR10 to regulate growth and development in *Arabidopsis*. *Proc Natl Acad Sci U S A*. 2017 Jul 18;114(29):E5995-E6004.

*Equal contribution.

**Co-corresponding authors.

<https://www.ncbi.nlm.nih.gov/pubmed/28673986>

<https://bitbucket.org/lorainelab/cytochipseq> (source code repository)

Vanechoutte D, Estrada AR, Lin YC, **Loraine AE**, Vandepoele K. Genome-wide characterization of differential transcript usage in *Arabidopsis thaliana*. *Plant J*. 2017 Oct 14.

<http://www.ncbi.nlm.nih.gov/pubmed/29031026>

Luo Y, Reid R, Freese D, Li C, Watkins J, Shi H, Zhang H, **Loraine A****, Song BH**. Salt tolerance response revealed by RNA-Seq in a diploid halophytic wild relative of sweet potato. *Sci Rep*. 2017

**Co-corresponding authors.

Aug 29;7(1):9624. <http://www.ncbi.nlm.nih.gov/pubmed/28852001>

Raines T*, Blakley IC*, Tsai YC, Worthen JM, Franco-Zorrilla JM, Solano R, Schaller GE, **Loraine AE****, Kieber JJ**. Characterization of the cytokinin-responsive transcriptome in rice. *BMC Plant Biol.* 2016 Dec 8;16(1):260.

*Equal contribution.

**Co-corresponding authors.

<https://www.ncbi.nlm.nih.gov/pubmed/27931185>

<https://bitbucket.org/lorainelab/ricecyto> (source code repository)

Freese NH, Norris DC, **Loraine AE**. Integrated Genome Browser: Visual analytics platform for genomics. *Bioinformatics.* 2016 Jul 15;32(14):2089-95.

<https://www.ncbi.nlm.nih.gov/pubmed/27153568>

<http://www.bioviz.org> (download site)

<https://bitbucket.org/lorainelab/integrated-genome-browser> (source code repository)

Mall T, Eckstein J, Norris D, Vora H, Freese NH, **Loraine AE**. ProtAnnot: an App for Integrated Genome Browser to display how alternative splicing and transcription affect proteins. *Bioinformatics.* 2016 Aug 15;32(16):2499-501.

<https://www.ncbi.nlm.nih.gov/pubmed/27153567>

Krizek BA, Bequette CJ, Xu K, Blakley IC, Fu ZQ, Stratmann JW, **Loraine AE**. RNA-Seq Links the Transcription Factors AINTEGUMENTA and AINTEGUMENTA-LIKE6 to Cell Wall Remodeling and Plant Defense Pathways. *Plant Physiol.* 2016 Jul;171(3):2069-84.

<https://www.ncbi.nlm.nih.gov/pubmed/27208279>

<https://bitbucket.org/lorainelab/antail6rnaseq> (source code repository)

Lambirth KC, Whaley AM, Blakley IC, Schlueter JA, Bost KL, **Loraine AE**, Piller KJ. A Comparison of transgenic and wild type soybean seeds: analysis of transcriptome profiles using RNA-Seq. *BMC Biotechnol.* 2015 Oct 1;15:89.

<https://www.ncbi.nlm.nih.gov/pubmed/26427366>

<https://bitbucket.org/lorainelab/soyseq> (source code repository)

Estrada AD, Freese NH, Blakley I, **Loraine AE**. Analysis of pollen-specific alternative splicing in *Arabidopsis thaliana* via semi-quantitative PCR. *PeerJ.* 2015.

<https://www.ncbi.nlm.nih.gov/pubmed/25945312>

<https://bitbucket.org/lorainelab/pollenas> (source code repository)

Gupta V, Estrada AD, Blakley I, Reid R, Patel K, Meyer MD, Andersen SU, Brown AF, Lila MA, **Loraine AE**. RNA-Seq analysis and annotation of a draft blueberry genome assembly identifies candidate genes involved in fruit ripening, biosynthesis of bioactive compounds, and stage-specific alternative splicing. *Gigascience.* 2015 Feb 13;4:5.

<https://www.ncbi.nlm.nih.gov/pubmed/25830017>

<https://bitbucket.org/lorainelab/blueberrygenome> (source code repository)

Ben-Tov D, Abraham Y, Stav S, Thompson K, **Loraine A**, Elbaum R, de Souza A, Pauly M, Kieber JJ, Harpaz-Saad S. COBRA-LIKE2, a Member of the Glycosylphosphatidylinositol-Anchored COBRA-LIKE Family, Plays a Role in Cellulose Deposition in *Arabidopsis* Seed Coat Mucilage Secretory Cells. *Plant Physiol.* 2015 Mar;167(3):711-24.

<https://www.ncbi.nlm.nih.gov/pubmed/25583925>

Liu R, **Loraine AE**, Dickerson JA. Comparisons of computational methods for differential alternative splicing detection using RNA-seq in plant systems. *BMC Bioinformatics*. 2014 Dec 16;15(1):364.
<https://www.ncbi.nlm.nih.gov/pubmed/25511303>

Yousef GG, Brown AF, Funakoshi Y, Mbeunkui F, Grace MH, Ballington JR, **Loraine A**, Lila MA. Efficient quantification of the health-relevant anthocyanin and phenolic acid profiles in commercial cultivars and breeding selections of blueberries (*Vaccinium* spp.). *J Agric Food Chem*. 2013 May 22;61(20):4806-15.
<https://www.dropbox.com/s/5ve3rfrh93qvfy/Youssef.13.blueberry-anthocyanins.pdf>

Loraine AE, McCormick S, Estrada A, Patel K, Qin P. RNA-seq of *Arabidopsis* pollen uncovers novel transcription and alternative splicing. *Plant Physiol*. 2013 Jun;162(2):1092-109.
<https://www.ncbi.nlm.nih.gov/pubmed/23590974>
<https://bitbucket.org/lorainelab/pollenrnaseq> (source code repository - added after publication*)

* *Starting with the blueberry genome paper (Gupta, et al.), we release source code repositories when publishing a new article. We are beginning to release code for older papers, as well.*

Bhargava A, Clabaugh I, To JP, Maxwell BB, Chiang YH, Schaller GE, **Loraine AE**, Kieber JJ. Identification of cytokinin-responsive genes using microarray meta-analysis and RNA-Seq in *Arabidopsis*. *Plant Physiol*. 2013 May;162(1):272-94.
<https://www.ncbi.nlm.nih.gov/pubmed/23524861>
<https://bitbucket.org/lorainelab/atcytokinin> (source code repository - added after publication*)

International *Arabidopsis* Informatics Consortium. Taking the next step: building an *Arabidopsis* information portal. *Plant Cell*. 2012 Jun;24(6):2248-56.
<https://www.ncbi.nlm.nih.gov/pubmed/22751211>

Humphry M, Bednarek P, Kemmerling B, Koh S, Stein M, Göbel U, Stüber K, Pislewska-Bednarek M, **Loraine A**, Schulze-Lefert P, Somerville S, Panstruga R. A regulon conserved in monocot and dicot plants defines a functional module in antifungal plant immunity. *Proc Natl Acad Sci U S A*. 2010 Dec 14;107(50):21896-901.
<https://www.ncbi.nlm.nih.gov/pubmed/21098265>

English AC, Patel KS, **Loraine AE**. Prevalence of alternative splicing choices in *Arabidopsis thaliana*. *BMC Plant Biol*. 2010 Jun 4;10(1):102.
<https://www.ncbi.nlm.nih.gov/pubmed/20525311>
<http://bitbucket.org/lorainelab/altspliceanalysis>

Mutwil M, Usadel B, Schütte M, **Loraine A**, Ebenhöf O, Persson S. Assembly of an interactive correlation network for the *Arabidopsis* genome using a novel heuristic clustering algorithm. *Plant Physiol*. 2010 Jan;152(1):29-43.
<https://www.ncbi.nlm.nih.gov/pubmed/19889879>

- Helt GA, Nicol JW, Erwin E, Blossom E, Blanchard SG Jr, Chervitz SA, Harmon C, **Loraine AE**. Genoviz Software Development Kit: Java tool kit for building genomics visualization applications. BMC Bioinformatics. 2009 Aug 25;10:266.
<https://www.ncbi.nlm.nih.gov/pubmed/19706180>
<https://bitbucket.org/lorainelab/genoviz-sdk> (source code repository)
- Nicol JW, Helt GA, Blanchard SG Jr, Raja A, **Loraine AE**. The Integrated Genome Browser: free software for distribution and exploration of genome-scale datasets. Bioinformatics. 2009 Oct 15;25(20):2730-1.
<https://www.ncbi.nlm.nih.gov/pubmed/19654113>
<https://bitbucket.org/lorainelab/integrated-genome-browser> (source code repository)
- Cui X, **Loraine AE**. Consistency analysis of redundant probe sets on Affymetrix three-prime expression arrays and applications to differential mRNA processing. PLoS ONE. 2009;4(1):e4229.
<https://www.ncbi.nlm.nih.gov/pubmed/19165320>
- Dybvig K, Zuhua C, Lao P, Jordan DS, French CT, Tu AH, **Loraine AE**. Genome of *Mycoplasma arthritidis*. Infect Immun. 2008 Sep;76(9):4000-8.
<https://www.ncbi.nlm.nih.gov/pubmed/18573899>
- French CT, Lao P, **Loraine AE**, Matthews BT, Yu H, Dybvig K. Large-scale transposon mutagenesis of *Mycoplasma pulmonis*. Mol Microbiol. 2008 Jul;69(1):67-76.
<https://www.ncbi.nlm.nih.gov/pubmed/18452587>
- Srinivasasainagendra V, Page GP, Mehta T, Coulibaly I, **Loraine AE**. CressExpress: a tool for large-scale mining of expression data from Arabidopsis. Plant Physiol. 2008 Jul;147(3):1004-16.
<https://www.ncbi.nlm.nih.gov/pubmed/18467456>
<http://www.cressexpress.org> (Version 2.0, revised from Version 1.0 released in 2008.)
- Yao J, Chang C, Salmi ML, Hung YS, **Loraine A**, Roux SJ. Genome-scale cluster analysis of replicated microarrays using shrinkage correlation coefficient. BMC Bioinformatics. 2008 Jun 18;9:288.
<https://www.ncbi.nlm.nih.gov/pubmed/18564431>
- Shriner D, Baye TM, Padilla MA, Zhang S, Vaughan LK, **Loraine AE**. Commonality of functional annotation: a method for prioritization of candidate genes from genome-wide linkage studies. Nucleic Acids Res. 2008 Mar;36(4):e26.
<https://www.ncbi.nlm.nih.gov/pubmed/18263617>
- Wei H, Persson S, Mehta T, Srinivasasainagendra V, Chen L, Page GP, Somerville C, **Loraine A**. Transcriptional coordination of the metabolic network in Arabidopsis. Plant Physiol. 2006 Oct;142(2):762-74.
<https://www.ncbi.nlm.nih.gov/pubmed/16920875>
- Shapero MH, Zhang J, **Loraine A**, Liu W, Di X, Liu G, Jones KW. MARA: a novel approach for highly

multiplexed locus-specific SNP genotyping using high-density DNA oligonucleotide arrays. *Nucleic Acids Res.* 2004 Dec 15;32(22):e181.

<https://www.ncbi.nlm.nih.gov/pubmed/15601992>

Loraine AE, Helt GA, Cline MS, Siani-Rose MA. Exploring alternative transcript structure in the human genome using BLOCKs and InterPro. *J Bioinform Comput Biol.* 2003 Jul;1(2):289-306.

<https://www.ncbi.nlm.nih.gov/pubmed/15290774>

<https://www.dropbox.com/s/g1mu0nylqzu6rk2/Loraine.03.JBCB.AltSpliceProteinEffects.pdf>

Liu G, **Loraine AE**, Shigeta R, Cline M, Cheng J, Valmeekam V, Sun S, Kulp D, Sani-Rose MA. NetAffx: Affymetrix probesets and annotations. *Nucleic Acids Res.* 2003 Jan 1;31(1):82-6.

<https://www.ncbi.nlm.nih.gov/pubmed/12519953>

Loraine AE, Helt GA. Visualizing the genome: techniques for presenting human genome data and annotations. *BMC Bioinformatics.* 2002 Jul 30;3:19.

<https://www.ncbi.nlm.nih.gov/pubmed/12149135>

FlyBase Consortium. The FlyBase database of the *Drosophila* Genome Projects and community literature. *Nucleic Acids Research*, 1999 Jan 1;27(1):85-88.

<https://www.ncbi.nlm.nih.gov/pubmed/9847148>

Helt GA, Lewis S, **Loraine AE**, Rubin GM. BioViews: Java-based tools for genomic data visualization. *Genome Res.* 1998 Mar;8(3):291-305.

<https://www.ncbi.nlm.nih.gov/pubmed/9521932>

Yalovsky S, **Loraine AE**, Gruissem W. Specific Prenylation of Tomato Rab Proteins by Geranylgeranyl Type-II Transferase Requires a Conserved Cysteine-Cysteine Motif. *Plant Physiol.* 1996 Apr;110(4):1349-1359.

<https://www.ncbi.nlm.nih.gov/pubmed/12226265>

Loraine AE, Yalovsky S, Fabry S, Gruissem W. Tomato Rab1A homologs as molecular tools for studying Rab geranylgeranyl transferase in plant cells. *Plant Physiol.* 1996 Apr;110(4):1337-47.

<https://www.ncbi.nlm.nih.gov/pubmed/8934628>

3.1 Peer Reviewed Conference Publications

Kim K, Zakharkin S, **Loraine AE**, Allison DB. Picking the most likely candidates for further development: Novel intersection-union tests for addressing multi-component hypotheses in comparative genomics. Proceedings of the American Statistical Association Joint Statistical Meeting, ENAR Section [CD-ROM], Toronto, Ontario, Canada, Aug 8 - 12, 2004.

<http://www.uab.edu/cngi/pdf/2004/JSM%202004%20-IUTs%20Kim%20et%20al.pdf> (PDF)

Cline MS, Shigeta R, Wheeler RL, Siani-Rose MA, Kulp D, **Loraine AE**. The effects of alternative splicing on transmembrane proteins in the mouse genome. *Pac Symp Biocomput.* 2004;:17-28.

<https://www.ncbi.nlm.nih.gov/pubmed/14992489>

Loraine AE, Helt GA. Visualization techniques for genomic data. Proc IEEE Comput Soc Bioinform Conf. 2002;1:321-6. Review.

Loraine AE, Helt GA, Cline MS, Siani-Rose MA. Protein-based analysis of alternative splicing in the human genome. Proc IEEE Comput Soc Bioinform Conf. 2002;1:118-24.

Cline M, Liu G, **Loraine AE**, Shigeta R, Cheng J, Mei G, Kulp D, Siani-Rose MA. Structure-based comparison of four eukaryotic genomes. Pac Symp Biocomput. 2002;:127-38.
<https://www.ncbi.nlm.nih.gov/pubmed/11928469>

3.2 Book Chapters

Loraine AE, Blakley IC, Jagadeesan S, Harper J, Miller G, Firon N. Analysis and Visualization of RNA-Seq Expression Data Using RStudio, Bioconductor, and Integrated Genome Browser. Methods Mol Biol. 2015;1284:481-501.

<https://www.ncbi.nlm.nih.gov/pubmed/25757788>

<http://bitly.com/rnaseq2014> (Dropbox with workshop materials)

<http://bitbucket.org/lorainelab/tomatopollen> (workshop source code)

Gulledge AA, Vora H, Patel K, **Loraine AE**. A protocol for visual analysis of alternative splicing in RNA-Seq data using integrated genome browser. Methods Mol Biol. 2014;1158:123-37. doi: 10.1007/978-1-4939-0700-7_8. PubMed PMID: 24792048; PubMed Central PMCID: PMC4070736.
<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC4070736/> (PMC author manuscript)

Loraine A. Co-expression analysis of metabolic pathways in plants. Methods Mol Biol. 2009;553:247-64. <http://bit.ly/coexpr> (PDF)

Ye J, Cui X, **Loraine A**, Bynum K, Kim NC, White G, De Luca M, Garfinkel MD, Lu X, Ruden DM. Methods for nutrigenomics and longevity studies in *Drosophila*: effects of diets high in sucrose, palmitic acid, soy, or beef. Methods Mol Biol. 2007;371:111-41.

3.3 Peer Reviewed Extended Abstracts/Short Papers

Budagyan B, **Loraine AE**. Gene length and alternative transcription in the fruit fly. IEEE Computational Systems Bioinformatics, Stanford, August, 2004. <http://ieeexplore.ieee.org/document/1332480>

Loraine AE, Salmi ML, Stout SC, Roux SJ. Gene Ontology-based analysis of gene expression changes in early development in *Ceratopteris*. IEEE Computational Systems Bioinformatics Conference, Stanford, CA, August, 2005. <http://ieeexplore.ieee.org/document/1540555>

Cui X, **Loraine AE**. Global correlation analysis between redundant probe sets using a large collection of Arabidopsis ATH1 expression profiling data. Proc LSS Comp Sys Bioinform Conf. 2006;223-227.
<http://www.lifesciencessociety.org/CSB2006/toc/223.2006.html>

4 Extramural Funding

4.1 Peer Reviewed National and International Grants

Current

Title: Integrated Genome Browser and IGB Apps

Project Number: 5R01GM103463

PI: Loraine

Funder: NIH NIGMS, NHGRI

Dates: 07/01/16 - 06/30/20

Summary: This project maintains and develops Integrated Genome Browser (IGB).

Title: Linking Integrated Genome Browser and CyVerse

Project Number: 1R01GM121927

PI: Loraine

Funder: NIH NIGMS

Dates: 06/01/2017 – 05/31/2020

Summary: This project links Integrated Genome Browser with NSF-funded CyVerse cloud computing resources.

Title: Regulation of floral growth and patterning in *Arabidopsis*.

PI: Beth Krizek (University of South Carolina)

Co-PI: Ann Loraine

Funder: NSF

Dates: 05/01/14 - 04/30/19

Summary: This project investigates the role of conserved, DNA-binding proteins ANT and AIL6 in determining the position and growth pattern of floral organs in plants, using *Arabidopsis* as a model.

Pending

Title: ECA-PGR: Developing multiplexed transcriptional regulation systems for plant genome reprogramming

PI: Yiping Qi (University of Maryland)

Co-PIs: Ann Loraine, Steven Mount (University of Maryland)

Prospective Funder: National Science Foundation (U.S.)

Summary: This project will develop methods for genome editing in plants. My role is to develop tools to visualize genome editing target sites.

Title: Research-PGR: Genomic analysis of cytokinin function in rice apical meristems

PI: Joe Kieber (UNC Chapel Hill)

Co-PIs: Ann Loraine, Eric Schaller (Dartmouth), Rosangela Sozzani (NC State University)

Prospective Funder: National Science Foundation (U.S.)

Summary: This project will use integrative genomic and bioinformatics approaches to illuminate how the plant hormone cytokinin governs rice plant productivity, focusing on cytokinin signaling in meristems.

Completed

Title: Continued maintenance and development of software: Integrated Genome Browser and the Genoviz SDK, visualization software for next-generation genomics.

PI: Loraine

Project Number: 8R01GM103463

Funder: NIH NIGMS (U.S.)

Dates: 07/01/11 - 06/30/16

Summary: This project developed the Integrated Genome Browser (IGB) and its foundation library of genomics visualization software components, the Genoviz SDK. This grant was renewed in 2016 as: “Integrated Genome Browser and IGB Apps.”

Title: Genomic approaches to understanding cytokinin signaling and function in rice.

PI: Joe J. Kieber (UNC Chapel Hill)

Co-PIs: Ann Loraine, Eric Schaller (Dartmouth University)

Funder: NSF Plant Genome Research Program (U.S.)

Dates: 10/01/12 - 09/30/16

Summary: This project used integrative genomic and bioinformatics approaches to illuminate how the plant hormone cytokinin regulates rice plant productivity.

Title: Collaborative Proposal: Research Coordination Network on Integrative Pollen Biology

UNCC PI: Ann Loraine

Lead PI: Alice Cheung (U Mass Amherst)

Co-PIs: Heven Sze (University of Maryland); Bruce McClure (University of Missouri) and Sheila McCormick (USDA/UC Berkeley).

Funder: National Science Foundation (U.S.)

Dates: May 1, 2010 – April 30, 2016

Summary: The project helped build a community of researchers using pollen as a model system in plant cell biology.

Title: Arabidopsis 2010: Analysis of the cytokinin-regulated transcriptional network

PI: Joe Kieber

Co-PIs: Ann Loraine, Eric Schaller (Dartmouth University), Dennis Mathews (University of New Hampshire)

Funder: National Science Foundation (U.S.)

Dates: Sept. 1, 2010 – Aug. 31, 2015

Summary: This project used integrative genomic approaches to dissect the transcriptional regulatory network underlying how the plant hormone regulates many aspects of development in plants.

Title: Arabidopsis 2010: Visualization software and data server for *Arabidopsis*

PI: Ann Loraine

Funder: National Science Foundation Arabidopsis 2010 Program (U.S.)

Dates: July 1, 2008 – June 30, 2011

Summary: This project developed the Integrated Genome Browser and companion data servers for the *Arabidopsis* research community.

4.2 Other Grants

Title: Bioinformatics-intensive probe of the blueberry genome

Lead PI: Ann Loraine

Co-PIs: Mary Ann Lila, Allan Brown of NC State University

Funder: University of North Carolina General Administration

Award dates: January 1, 2009 – June 30, 2011

Goal: This project annotated a draft blueberry genome assembly using data from an RNA-Seq experiment investigating gene expression changes during blueberry fruit development, maturation, and ripening.

5 Student Supervision

5.1 Doctoral Students

1. Vikas Gupta, University of Aarhus (visiting student from University of Aarhus, Denmark, March-July, 2013). Gupta co-authored our 2015 paper on blueberry genomics. Current Position: Bioinformatics Scientist, CLC Genomics.
2. Ruolin Liu, Iowa State University (with thesis advisor Julie Dickerson). Liu was lead author on our paper investigating alternative splicing data analysis methods.
3. Kevin Lambirth, Biology Dept., UNC Charlotte (with thesis advisor Ken Bost). Kevin was a USDA Kannapolis fellow in my lab co-mentored with Ken Bost. His project investigated how soy transgenes affect native gene expression in soybean.

5.2 Masters Students (25 since 2008)

Bioinformatics

Adam English, Archana Raja, Nathaniel Watson, Peter Pham, Afshan Jalali, Adam Baxter, Katy Kubiak, Natascha Moestl, Anuja Jain, Chris Ball, Daniella Freese

Computer Science

Hiral Vora, Vikram Bishnoi, Zhong Ren, Anuj Puram, Vineeth Sai Santosh Mylapur, Praveen Babu Patchalla, Fuquan Wang, Nikhil Dahake, Tarun Santosh Kanaparthi, Tarun Mall, Devdatta Kulkarni, Deepti Joshi, Ashwini Kadam, Sanket Patil

5.3 Postdoctoral Trainees

1. Hairong Wei, 2004-2005 (UAB), Current Position: Associate Professor, Michigan Technology University
2. Mahyar Sabripour, 2005-2006 (UAB), Current Position: Senior Scientist, Isis Pharmaceuticals.
3. Ketan Patel, 2008-2010 (UNCC), Current Position: Research Fellow, Centers for Disease Control, Atlanta, GA
4. Jeremy Villalobos, 2011 (UNCC), Current Position: Practical Android Apps, Charlotte, NC
5. Kevin Thompson, 2011-2012 (UNCC), Current Position: Scientist, Mayo Clinic
6. Nowlan Freese, 2014-present (UNCC)

5.4 Courses Taught

5.4.1 Graduate Courses

UNCC:

BINF6111/8111 Bioinformatics Programming I, Fall 2008, 2009, 2010
BINF6112/8112 Bioinformatics Programming II, Spring 2009, 2010, 2011
WiNGS Teaching Assistant Training, Spring 2013, 2014
BINF 6153 Career Development in Bioinformatics, Spring 2014, 2015, 2016
BINF 6151 Professional Communications, Fall 2014, 2015
BINF 6152 Program and Professional Orientation, Fall 2013, 2015
BINF 6150 Biotechnology and Genomics Laboratory, Fall 2015

UAB:

BST 676, Statistical Bioinformatics, Summer 2006

California State University, East Bay:

Stat 6031: Introduction to Statistics for Bioinformatics, Bioinformatics Certificate Program, Winter Quarter, 2004

5.4.2 Undergraduate Courses

UNCC:

BINF2111 Introduction to Bioinformatics Programming, Fall 2012

BINF 3121 Statistics for Bioinformatics, Fall 2016, Spring 2017, Fall 2017, Spring 2018

6 Service and Outreach

6.1 Outreach

I organized and taught the 2013 and 2014 UNC Charlotte Workshop in Next-Generation Sequencing Workshop, a symposium followed by a day of hands-on workshops introducing bioinformatics data analysis methods and software.

I organized and taught a workshop titled “Introducing RNA-Seq data analysis using R and Integrated Genome Browser” at Plant Biology 2017, the annual meeting of the American Society of Plant Biologists, in Honolulu, HI, June 24, 2017

6.2 External Service

Advisory Board Member, Biochemical Spatial NeTwork Resource (BioSNTR),

<http://sdepscor.org/2016/biosntr-partners-4-6-million-nsf-grant-five-year-saint-louis-university-grapevine-root-system-research/>, 2016-present

Arabidopsis Biological Resource Center (Ohio State University) Advisory Committee,

<https://abrc.osu.edu/advisory-committee>, 2016-2018

External Reviewer, UT-ORNL Graduate School of Genome Science and Technology, University of Tennessee, Knoxville, Oct. 2011.

External Advisor for Genome British Columbia-funded project titled “Genomics Tools for Fisheries Management (FishManOmics)” 2009-10

Ad hoc reviewer for Genome British Columbia, Sector Innovation Program (2017)

National Science Foundation (U.S.):

Chair, iPlant Site Visit Panel, NSF Division of Biological Infrastructure, Tucson, AZ, Jan. 25-28, 2012.

Co-Chair, Modules and Use-Case Working Group, International Arabidopsis Informatics Consortium (NSF Research Coordination Network); Attended Design Workshop Dec 11-14, 2011, Atlanta, GA.

Grant review panelist, 2007-2009, 2011-2012, 2017

National Institutes of Health (U.S.):

Standing member, Biodata Management and Analysis Section [BDMA] Study Section, Term: June 2017 – July 2022

RFA Panel: BD2K Open Educational Resources and Courses for Skills Development (R25) ZRG1 BST-N (55) Jun. 26, 2015

RFA Panel: BD2K Software and Analysis Methods for BioMedical Big Data in Targeted Areas of High Need (U01) ZRG1 BST-N (50), Oct. 2014

Ad hoc member, Biodata Management and Analysis Study Section, February 2011, June 2013, October 2015

RFA Panel: Bioinformatics and Software Development Special Emphasis Panel, ZRG1 BST-F 10 October, 2008

RFA Panel: National Cancer Institute Special Emphasis Panel, Advanced Genomic Data Analysis and Visualization Methods for The Cancer Genome Atlas, ZCA1 SRRB-U (M1), April 2008

6.2.1 Presentations (selected from more than 40 since 2002)

“Using RNA-Seq and genetics to investigate condition and tissue-specific alternative splicing in plant species,” Nov. 24, 2017, Cell and Systems Biology Dept. seminar, University of Toronto, Toronto, ON.

“Genome browsing on some-one else’s computer” Genome Informatics, Nov. 1-4, 2017, Cold Spring Harbor Laboratory, NY

“Genome browsing past and present” 3rd EMBO Conference on Visualizing Biological Data (VIZBI 2016), March 2016, EMBL Heidelberg.

“Role of *SR45a* in alternative splicing and stress response,” Gene Regulation Session, Plant Biology 2015 (presented by April Estrada, with Loraine as Session Chair)

“RNA-Seq analysis of blueberry fruit development and ripening.” Center for Bioinformatics and genomics/Computational Biology Seminar, University of Maryland, College Park, Sept. 16, 2014

“Explore, analyze, and share genomic data using Integrated Genome Browser.” Bioinformatics Open Source Conference, Boston, July 2014.

“Splicing under stress: RNA-Seq analysis of alternative splicing in *Arabidopsis*.” Penn State University, March 2014.

“RNA-Seq analysis of blueberry fruit identifies candidate genes involved in ripening and secondary metabolism.” Plant Animal Genome Conference, Jan. 2014

“Alternative splicing under stress: Noise or adaptation.” 30th Annual Mid-Atlantic Plant Molecular Biology Society Conference, Aug. 2013

“Regulation of alternative splicing under abiotic stress in *Arabidopsis*.” 75th Annual meeting of the Northeast Section of the American Society of Plant Biologists, Durham, NH, May 6-7, 2011

“Alternative splicing and stress adaptation in plant cells.” 19th Annual Plant Animal Genome Conference,” San Diego, CA, Jan 15-19, 2011.

“EST revival: Transcriptome sequencing and annotation via high-throughput cDNA sequencing,” Seminar at NC State University, April 20, 2010

“Effects of water deprivation stress on RNA splicing patterns in *Arabidopsis*.” 11th Annual Plant Biology Minisymposium, University of Maryland, College, Park. March 27, 2010.

“Integrated Genome Browser and DAS2: Free tools for sharing and exploring genome-scale data sets.” Mid Atlantic Section ASPB Annual Spring Meeting, Bowie State University, Bowie, MD March 26, 2010.

“Nodes, neighbors, and networks: Mining the co-expression network in *Arabidopsis*,” seminar for the Plant Biology Department, Carnegie Institution, Stanford, CA, May, 2007.

“Transcriptional coordination of the metabolic network in *Arabidopsis thaliana*.” 17th International Conference on Arabidopsis Research, June 28-July 2, 2006, Madison, WI.

“Mining microarray expression data,” Center for Computational Biology and Bioinformatics Seminar Series, Indiana University Purdue University, Indianapolis, IN, April, 2006.

“Co-expression analysis of metabolic pathways in Arabidopsis,” Plant and Animal Genome Conference XIV, San Diego, CA, January 14-18, 2006.

6.2.2 Journal/Conference Reviewer

Referee for:

Plant Physiology, Nucleic Acids Research, PLoS Genetics, Genes and Immunity, PLoSOne, Bioinformatics, BMC Bioinformatics, BMC Plant Biology, BMC Systems Biology, Journal of Computational Biology and Bioinformatics, ACM Symposium on Applied Computing, American Journal of Botany, GigaScience

6.2.3 Program Committees

IEEE Computer Society Bioinformatics Conference, 2003

Life Sciences Society Computational Systems Bioinformatics Conference, 2004-2010

Bioinformatics Open Source Conference, 2009

6.2.4 Editorial Boards/Panels

Academic Editor, PeerJ