

CURRICULUM VITAE

ANN E. LORAINE

Dept. of Bioinformatics and Genomics
University of North Carolina, Charlotte
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<http://www.lorainelab.org>

<http://bitbucket.org/lorainelab>

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1 Education

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

Advisor: Wilhelm Gruissem

Ph.D. Thesis Title: Rab proteins from tomato and rab prenyl transferase

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, University of North Carolina at Charlotte
Department of Bioinformatics and Genomics

2004 – 2008

Assistant Professor, University of Alabama at Birmingham

2000 – 2003

Bioinformatics Scientist, Affymetrix

1999-2000

Bioinformatics Software Engineer, Neomorphic

1998-1999

Programmer/Analyst, UC Berkeley, Berkeley Drosophila Genome Project

1997-1998

Postdoctoral Trainee, UC Berkeley, Berkeley Drosophila Genome Project

Advisors: Gerald Rubin and Suzanna Lewis

3 Peer Reviewed Journal Publications

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. <https://www.ncbi.nlm.nih.gov/pubmed/28852001>

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)

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.

<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. doi: 10.1093/bioinformatics/btw068. Epub 2016 Apr 7.

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

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

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/antail6maseq> (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://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://peerj.com/articles/919/>

<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. doi: 10.1186/s13742-015-0046-9. eCollection 2015. PubMed PMID: 25830017; PubMed Central PMCID: PMC4379747.

<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. [Epub ahead of print] PubMed PMID: 25511303; PubMed Central PMCID: PMC4271460.

<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.

<http://bit.ly/berryflav> (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. doi: 10.1104/pp.112.211441. Epub 2013 Apr 16.

<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 now co-publish source code repositories for analyses reported in papers, using BitBucket.org, a free code hosting service. We are beginning to publish 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. doi: 10.1104/pp.113.217026. Epub 2013 Mar 22. PubMed PMID: 23524861; PubMed Central PMCID: PMC3641208.

<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. Epub 2009 Jan 23.

<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. Epub 2008 Jun 23.

<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. Epub 2008 Apr 28.

<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> (Note this version 2.0 of software released with the article.)

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>

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.
<http://psb.stanford.edu/psb-online/proceedings/psb2004/cline.pdf> (PDF)

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.
<http://psb.stanford.edu/psb-online/proceedings/psb2002/cline.pdf> (PDF)

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. doi: 10.1007/978-1-4939-2444-8_24. PubMed PMID: 25757788; PubMed Central PMCID: PMC4387895. <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC4387895/> (PMC author manuscript) <http://bitly.com/rnaseq2014> (Dropbox with workshop data) <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 Manuscripts under Review

D Vaneechoutte, AR Estrada, YC Lin, A Loraine, K Vandepoele. Genome-wide characterization of isoform switching in *Arabidopsis thaliana*. bioRxiv, 136770

3.4 Patents filed

"Engineering larger seeds and higher yields in the oilseed crop *Camelina sativa*" UNCC IR#2016-001. Application number 62/210,557 filed on 08/27/2015. (not pursued)

4 Extramural Funding

4.1 Peer Reviewed National and International Grants

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 (UMd)

Award Amount: \$108, 774 (UNCC sub-contract)

Summary: This project will develop methods for genome editing in plants. My role is to develop an IGB App 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)

Award Amount: \$572,023 (UNCC sub-contract)

Summary: This project will use genomic approaches to investigate how the plant hormone cytokinin controls stem cell (meristem) growth in rice.

Current

Title: Linking Integrated Genome Browser and CyVerse

PI: Loraine

Funder: NIH

Award Amount: \$150,000/year direct costs

Dates: 06/01/2016 – 05/31/2018

Summary: This project will integrate rich client, Java-based software Integrated Genome Browser with CyVerse cloud resources using web services.

Title: Integrated Genome Browser and IGB Apps

PI: Loraine

Prospective funder: NIH

Award Amount: \$250,000/year direct costs

Dates: 07/01/16 - 06/30/21

Summary: This project will transform Integrated Genome Browser (IGB) into a flexible, easy-to-use and highly modular platform for visualization software development.

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

Amount: \$129,994 (UNCC sub-contract)

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.

Completed

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

PI: Loraine

Funder: NIH

Award Amount: \$1,449,035 (\$200,000/year direct costs)

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. The grant was renewed in 2016 as title: "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

Amount: \$683,982 (UNCC sub-contract)

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

Dates: May 1, 2010 – April 30, 2016 (in one-year no cost extension)

Amount: \$47,000

Summary: The project helped build a community of researchers interested in using pollen as a model system in plant 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: NSF

Award Amount: \$507,341 (UNCC sub-contract)

Dates: 09/01/10 - 08/31/15

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

Dates: July 1, 2008 – June 30, 2011

Amount: \$600,000

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, office of Steve Leath

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

Award Amount: \$310,888

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 (26 since 2008)

Bioinformatics

1. Adam English “Prevalence of alternative splicing in *Arabidopsis*,” Fall, 2008 – Spring 2010. Current position: Senior Bioinformatics Software Engineer at Baylor University.
2. Archana Raja “Testing Integrated Genome Browser,” Spring, 2009 – Spring 2010. Current position: Bioinformatics Analyst, Evan Eichler Lab, University of Washington.
3. Nathaniel Watson “Assembling a blueberry transcriptome,” Spring 2010. Current position: Bioinformatics Analyst, Stanford University Medical School.
4. Peter Pham “RNA-Seq analysis of pollen-specific gene expression,” Summer 2010.
5. Afshan Jalali, “PollenNetwork.org – Web site for Pollen Researchers,” Summer 2011.
6. Adam Baxter “Assembly and annotation of a blueberry transcriptome,” Spring 2011-Fall 2011. Current Position: Consultant, Red Hat.
7. Katy Kubiak, “Testing Integrated Genome Browser,” Spring 2012. Current position: Greenwood Genetics Institute.
8. Natascha Moestl, “Alternative splicing under drought and heat stress,” Spring 2013.
9. Anuja Jain, “Alternative splicing in floral development,” Spring 2013.

10. Chris Ball, “Charting expression of cytokinin signaling genes during seed development in the oilseed crop *Camelina sativa*, a relative of *Arabidopsis thaliana*” Spring 2015. Current position: Bioinformatics Analyst, NC State University
11. Daniella Freese, “Integrated Genome Browser,” Summer 2016. Current position: Software consultant, Stackleader.com, Concord, NC.

Computer Science & IT graduate programs

1. Hiral Vora “Integrated Genome Browser,” Fall 2008 – Spring 2010. Current position: Senior Software Engineer, Deutsche Bank.
2. Vikram Bishnoi “Integrated Genome Browser,” Summer 2010 – Spring 2011. Current position: Assistant Vice-President, Bank of America.
3. David Norris, “Integrated Genome Browser,” Spring 2011 – Spring 2012. Current Position: Owner and Co-Founder, Stackleader.com, Concord, NC.
4. Zhong Ren, “Integrated Genome Browser,” Summer 2011 – Spring 2012. Current Position: Bioinformatics Analyst, Columbia University.
5. Anuj Puram, “Integrated Genome Browser,” Spring 2012 - Spring 2013.
6. Vineeth Sai Santosh Mylapur, “PollenNetwork.org – Web site for Pollen Researchers.” Summer, 2012. Current Position: IBM.
7. Praveen Babu Patchalla, “PollenNetwork.org – Web site for Pollen Researchers,” Fall 2012. Current Position: Software Developer, Client Network Services, Inc.
8. Fuquan Wang, “Integrated Genome Browser,” Summer 2012 – Spring 2013. Current position: Software Engineer, Amazon.
9. Nikhil Dahake, “CressExpress 2.0”, Summer 2014 – Fall 2014. Current position: Software Engineer, Amazon.
10. Tarun Santosh Kanaparathi, “Integrated Genome Browser,” Fall 2013 – Fall 2014. Current position: Software Engineer, Empirix, Inc.
11. Tarun Mall, “Integrated Genome Browser,” Fall 2015 – present. Current position: Software Engineer, Amazon.
12. Devdatta Kulkarni, “Integrated Genome Browser,” May 2016 – May 2017. Current Position: Software Engineer
13. Deepti Joshi, “Integrated Genome Browser,” May 2017 – present.
14. Ashwini Kadam, “Integrated Genome Browser,” May 2017 – present.
15. Sanket Patil, “Integrated Genome Browser,” May 2017 – present.

5.3 Bachelors Students Supervised

1. Francesca Weaks, North Carolina A&T, Summer, 2008
2. Roshonda Barner, North Carolina A&T, Summer 2008, 2009, and 2010
3. Kristen Sagliani, UNC Charlotte, Summer 2009
4. Jesseca Nguyen, NSCU, Summer 2011
5. Darius Bost, North Carolina A&T, Summer 2012
6. Shelvasha Burkes, UNC Charlotte, Summer 2013
7. Brittney David, UNC Charlotte, 2013-2015
8. Mason Meyer, Lenoir Rhyne University, Summer 2014
9. Tiffany Kennedy, North Carolina A&T, Summer 2014

10. Jennifer Daly, UNC Charlotte, Spring 2017 - present

5.4 Non-Degree Students Supervised (e.g., certificate students)

1. Brock Overcash, Salisbury High School, Summer 2012 (now attending George Tech)
2. Tanner Deal, A.L. Brown High School (Kannapolis), Summer 2015 (now attending UNC Charlotte)
3. Jessi Davis, A.L. Brown High School (Kannapolis), Summer 2016

5.5 Postdoctoral Trainees Supervised

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: Scientist, 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). Dr. Freese led outreach and training efforts for the Integrated Genome Browser project while learning bioinformatics data analysis and project management. After joining the team, Dr. Freese applied for and won a National Science Foundation Postdoctoral Fellowship to investigate epigenetic control of alternative splicing in rice. The fellowship began Sept. 1, 2015.

6 Teaching

6.1 Courses Taught

6.1.1 Graduate Courses

UNCC:

BINF6111/8111 Bioinformatics Programming I, Fall 2008, 2009, 2010
BINF6112/8112 Bioinformatics Programming II, Spring 2009, 2010, 2011
BINF6153 Career Development in Bioinformatics, Spring 2014
BINF 6151 Professional Communications, Fall 2014, 2015
BINF 6152 Program and Professional Orientation, Fall 2013, 2015
BINF 6150 Biotechnology and Genomics Laboratory, Fall 2015
BINF 6153 Career Development in Bioinformatics, Spring 2015, 2016
WiNGS Teaching Assistant Training, Spring 2013, 2014

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

6.1.2 Undergraduate Courses

UNCC:

BINF2111 Introduction to Bioinformatics Programming, Fall 2012

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

7 Service and Outreach

7.1 Outreach

Organized and taught the 2013 and 2014 UNC Charlotte Workshop in Next-Generation Sequencing Workshop meetings, which included a research symposium followed by day-long series of workshops introducing bioinformatics data analysis methods and software.

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

7.2 External Service

Advisory Board Member, Biochemical Spatial NeTwork Resource (BioSNTR), <http://sdepacor.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 (for project highlights, see: <http://bit.ly/salmonSAB>)

NSF:

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, 2008, 2009, 2011, 2012

NIH:

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

7.2.1 Presentations (selected from more than 40 since 2002)

- “Genome browsing.” 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.” University of Maryland Plant Biology Dept. Seminar, Sept. 2014
- “Explore, analyze, and share genomic data using Integrated Genome Browser.” Bioinformatics Open Source Conference, Boston, July 2014. (Video available from: http://www.open-bio.org/wiki/BOSC_2014_Schedule)
- “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.
- “Visualizing the genome with Integrated Genome Browser, the next generation of genomic analysis tools,” 24th Annual Plant Molecular Biology Retreat, Oct 1-2, 2010, Asheville, NC.
- “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.

“Co-expression analysis of metabolic pathways in Arabidopsis,” Twelfth International Conference of The Forum for Interdisciplinary Mathematics on Statistics, Combinatorics, Mathematics, and Applications, Auburn University, Auburn, AL, Dec. 2-4, 2005.

“Integrated Genome Browser: Visualizing alternative mRNA processing,” NSF Microarray Research Coordination Network, Mohonk Mountain House, New Paltz, NY, September, 2005

“Transcript variation: introducing a new layer of complexity in expression analysis,” NSF Microarray Research Coordination Network, Mohonk Mountain House, New Paltz, NY, September, 2004

“Visualizing the genome: Techniques for Presenting Human Genome Data and Annotations” Cambridge Healthtech Institute’s Data Visualization and Interpretation Conference, Baltimore, MD, September, 2003.

“Developing Visualization Software for Genomics: A Necessary Collaboration” Bay Area Bioinformatics Discussion Group, Stanford, CA, September, 2002

7.2.2 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

7.2.3 Program Committees

IEEE Computer Society Bioinformatics Conference, 2003

Life Sciences Society Computational Systems Bioinformatics Conference, 2004-2010

Bioinformatics Open Source Conference, 2009

7.2.4 Editorial Boards/Panels

Academic Editor, PeerJ