## NAME AND CONTACT INFORMATION

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| **Dr. Cranos Williams** | North Carolina State University |
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## EDUCATION

**North Carolina State University**                                                                    2008
Ph.D., Electrical Engineering, Dissertation: Engineering Methodologies and Design Concepts
for Systems Biology, Advisor: W.E. Alexander

M.S., Electrical Engineering,                                                                              2002

**North Carolina A&T State University**                                                            2001
B.S., Electrical Engineering,

## EXPERIENCE

**North Carolina State University**
Professor, Dept. of Electrical and Computer Engineering                          2020-Present
Adjunct Professor, Dept. of Plant and Microbial Biology                          2014-Present
Associate Professor, Dept. of Electrical and Computer Engineering          2014-2020
Assistant Professor, Dept. of Electrical and Computer Engineering          2008-2014

## AWARDS AND HONORS

Selected for National Academy of Engineering, Frontiers of Engineering Symposium (2019)
Alcoa Foundation Research Achievement Award (2019)
ECE Department William F. Lane Outstanding Teacher Award (2013)
National Science Foundation Graduate Research Fellowship (2003)
NASA Harriett G. Jenkins Predoctoral Fellowship (2003)
National Consortium for Graduate Degrees for Minorities in Eng. & Science (GEM) Doctoral Fellowship (2003)

## PROFESSIONAL MEMBERSHIP AND SERVICE

Senior Member, Institute of Electrical and Electronic Engineers, 2006 - Present
Member, Editorial Advisory Board, *in-silico* Plants, 2018 – Present
Organization Chair, RiseEnAg (Rapid Innovations in Systems Engineering and Agricultural Sustainability)
Consortium Stakeholder Engagement Workshop, Raleigh, NC, 2019
Organization Committee Chair, Plant Systems Biology and Engineering Workshop, Raleigh, NC, 2014
Journal Reviewer: *in-silico* Plants, PLoS Computational Biology, PLoS Biology, Biotechnology for Biofuels,
EURASIP J. on Bioinformatics and Systems Biology, IEEE J. on Selected Topics in Signal Processing: Special
Issue on Genomic and Proteomic Signal Processing, IEEE Trans. on Signal Processing, 2008 - Present
Grant Panel Reviewer: NSF (2011, 2013, 2014, 2018, 2019); USDA NIFA (2014, 2015), FFAR (2018)
Faculty Search Committees: ECE (2014-2017), Systems and Synthetic Biology Faculty Cluster (2011-2015),
Quantitative and Computational Developmental Biology Faculty Cluster (2015-2017)
Advisees: Ph.D. (7 Current, 4 Graduated), M.S. (0 Current, 3 Graduated) Undergrad (2 Current, 23 Previous)

## SUMMARY - PATENTS, PUBLICATIONS, AND INVITED TALKS

| Activity | Number | Activity | Number |
|---|---|---|---|
| Peer Reviewed Journals (Published | 24 | Conference Proceedings | 15 |
| External / Internal Invited Research Talks | 33 | Patents (Awarded / Submitted) | 1 / 1 |

## OTHER

Grant and Extramural Funding: Total Funding: **$14,228,113** (To CMW Directly: **$1,786,985**)

Interdisciplinary Course Development: Co-instructor – *Systems Biology Modeling of Plant Regulation*. Course
cross listed between Electrical & Computer Engineering & Plant and Microbial Biology

Teaching: Taught 1,307 students in three courses since 2008

Disciplines and Areas of Research Collaborators: Elect & Comp Engineering; Plant & Microbial Biology; Forest
Biotechnology; Ag and Bio Engineering; Chem & Biomolecular Engineering; Environmental Engineering;
Biochemistry; Mech & Aerospace Engineering, NuPulseCV, Inc. (Industry Collaborator)

**Candidate Statement**

My name is Dr. Cranos Williams and I am an associate professor in the electrical and computer engineering (ECE) department at North Carolina State University. Since joining the faculty in 2008, I have focused my research efforts towards building an internationally recognized research program in **Plant Systems Biology and Engineering (PSB/E)** at North Carolina State University. My research efforts have advanced the discovery of novel computational approaches and convergent research strategies for addressing complex societal problems such food security in the 21$^{st}$ century and the identification of effective alternatives to petroleum-based fuels (e.g. biofuels). During my time at NC State, I have 1) aggressively developed and led research initiatives in PSB/E that involve multiple departments/colleges/universities; 2) led/participated in synergistic activities that grew the critical mass of NC State faculty in the area of systems and synthetic biology; 3) provided a unique interdisciplinary research environment for recruiting and mentoring undergraduate/graduate students; and 4) established a national and international presence in Plant Systems Biology and Engineering through participation in national and international workshops and meetings. The accomplishments stated below were achieved from 2008 to 2019.

**RESEARCH SCHOLARSHIP**: I am the founder and sole faculty leader of the EnBiSys (Engineering Computational Methodologies for Multi-hierarchical Biological Systems) Research Laboratory (http://enbisys.ece.ncsu.edu). The EnBiSys Research Laboratory focuses on the development of computational and analytical solutions for modeling and understanding the combinatorial interactions of biomolecular, physiological, and structural processes that impact plant growth, development, and adaptation. I have led, as lead PI or as CoPI, **twelve extramural or internal grants** totaling **$14.2M**, with **$1.7M** going directly to my research program. Results from these grants have led to **24 journal publications**, **10 conference publications**, and **19 external invited talks**. The resulting manuscripts were published in high impact journals such as **IEEE Transactions on Systems, Man, and Cybernetics** (IF: 2.3), **Nature Communications** (IF: 12.353), **the Proceedings of the National Academy** (IF: 9.66), **The Plant Cell** (IF: 8.53), **BMC Systems Biology** (IF: 2.3), **Plant Physiology** (IF: 6.28) and **PLoS Computational Biology** (IF: 4.428). The findings from these projects have provided better insight into the molecular mechanisms associated with stress response in plants, yielded models that describe wood formation in trees, and provided computational algorithms for spatial and temporal tracking of gene expression, molecular experimental design, and multi-scale modeling of biological processes. These findings will ultimately translate to strategies for improving tolerance of crop plants to pathogens and abiotic stresses, increasing the efficiency of biofuel production from plant biomass, and strategies for addressing food security challenges. I was awarded the **Alcoa Foundation Research Achievement Award** in 2019, have one patent that was submitted in 2019 (Patent Application Number: 16401368), and was selected to attend the **National Academy of Engineering 2019 Frontiers of Engineering Symposium**. Specific contributions to science include the following:

      **Automated Tracking of Gene Expression over Space and Time in Microscopy Images.** My collaborators and I have made significant progress towards understanding the morphological response of plants to single and combinatorial stresses through the development of automated computer vision approaches for tracking gene expression over space and time in *Arabidopsis thaliana* roots. In [2], we developed an automated solution for analyzing spatial characteristics of gene expression without the necessity of fluorescent tagged cell walls or cell nuclei. Our solution indicates, segments, and tracks gene expression using a fluorescent imaging channel of a light sheet microscope while determining gene expression location within an organism from a Brightfield (non-fluorescent) imaging channel. We used this approach to extract, analyze, and compare high-dimensional dynamic spatial and temporal cellular data in *A. thaliana* roots in response to single and combinatorial stress conditions at high temporal resolution [1]. Our computational pipeline extracted spatiotemporal metrics from high throughput microscopy images, and allowed us to compare and contrast the timing and behavior of single and combinatorial stress responses in plant roots. Our results showed that the iron deprivation and heat stress responses act in an antagonistic manner at specific time points when *A. thaliana* seedlings are exposed to combinatorial stresses.

**[1]** E. Buckner et al., "High Resolution Spatiotemporal Imaging and Analysis of Dynamic Cell Cycle Progression Patterns Under Iron Deficiency and Heat Stress Conditions," under 2nd review, *Frontiers in Plant Science*, 2019. **[2]** E. Buckner et al., *The 40th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC)*, pp. 818-821, 2018.

**Dynamic Gene Regulatory Network of the Arabidopsis thaliana Iron Deficiency Response (NSF MCB-1247427).** My collaborators and I have made significant progress towards understanding the dynamic transcriptional cascade associated with the iron deficiency response in *A. thaliana*. In [3], we formulated the Clustering and Differential Alignment Algorithm (CDAA), which identified 7 putative regulators previously unlinked to the iron homeostasis response. The CDAA predicted 32 potential regulatory connections of which 53% were experimentally validated. We formulated an integrative modelling approach that was used to generate a dynamic ordinary differential equation model describing the expression these genes and their regulatory interactions under iron deficient conditions [1]. The trained model was able to capture and account for a significant difference in mRNA decay rates under iron sufficient and iron deficient conditions, approximate the expression behavior of currently unknown gene regulators, unveil potential synergistic effects between the modulating transcription factors and predict the effect of double regulator mutants. The presented modelling approach illustrates a framework for experimental design, data analysis and information aggregation in an effort to gain a deeper understanding of various aspects of a biological process of interest.

**[1]** Koryachko A. et al., *in silico Plants*, Volume 1, Issue 1, 2019, diz005, **https://doi.org/10.1093/insilicoplants/diz005**. **[2]** Koryachko A. et al. Proceedings for the 10th International Conference on Bioinformatics and Computational Biology (BICoB 2018), pp. 142-147, 2018. **[3]** Koryachko A. et al., *PLoS ONE*, 10(8):e0136591-21, 2015. **[4]** A. Koryachko et al., *Current Plant Biology*, 1-10, Jun. 2015.

**Mathematical modelling of Lignin Biosynthesis (NSF DBI-0922391).** My collaborators and I have made unprecedented progress in understanding and modelling lignin biosynthesis through on-going collaborative efforts. This was accomplished through the collection data quantifying lignin biosynthesis in *Populus trichocarpa* in response to 138 transgenic perturbations. These transgenic lines were a result of multi-level knockdowns (or knock-outs when possible) of individual monolignol pathway genes, pair-wise combinations, and whole gene families. Data from all 21 monolignol pathway enzymes, 24 pathway intermediates, and cell wall properties associated with lignin composition and structure were collected and used to computationally model the interactions between several multi-enzymatic reactions in the lignin biosynthesis pathway [3][5][6], establish a predictive kinetic metabolic-flux model for the 21 enzymes and 24 metabolites of the monolignol biosynthetic pathway using *P. trichocarpa* secondary differentiating xylem [4], formulate an integrative systems model by incorporating the dynamic metabolic model with transcript data and phenotypic data to predict how novels combinations of lignin specific knockdowns influenced changes in wood traits (e.g lignin content, lignin composition, saccharification efficiency) [2], and develop a sparse maximum likelihood approach for modeling cross-regulatory influences between monolignol transcripts and proteins [1].

**[1]** M. Matthews et al, *PLoS Computational Biology*, vol. 16, no. 4, 2020. **[2]** Wang J et al., *Nature communications*, 9(1):1579, 2018. **[3]** Chen H., Song J. et al., *The Plant Cell Online,* 26(3):876-893, 2014. **[4]** Wang J. et al., *The Plant Cell Online*, 26(3):894-914, 2014. **[5]** Chen H. et al., *Plant Physiology*, 161:1501-1516, 2013. **[6]** J. Wang et al., *Planta*, vol. 236, no. 3, pp. 795-808, 2012.

**System identification and experimental design in the presence of bounded uncertainty.** We have investigated the development of computational algorithms for estimating unmeasured components and designing the specifications of biological experiments in the presence of uncertain measurements where the uncertainty was characterized as bounded error. We formulated an experimental design framework for models of biological systems when few measurements with known bounded uncertainty were available [1]. We were also able to generate algorithms for estimating bounds on state variables based on measurements containing bounded uncertainty [2][4] and formulated a computational platform that incorporated the use of parallel computing architectures to speed up the calculations [3].

**[1]** Marvel S and **Williams C**, *BMC Systems Biology*, 6(1):21, 2013. **[2]** Marvel S and **Williams C**, *Proceedings of 2012 IEEE International Conference on Systems, Man, and Cybernetics (SMC)*, 72-77,

2012. **[3]** <u>Marvel S</u> et al., *Proceedings of the 2011 International Workshop on Computational Systems Biology*, 140-143, 2011. **[4]** <u>de Luis Balaguer MA</u> and **Williams C**, *2010 IEEE Conference Proceedings of the 44th ASILOMAR Conf. on Signals, Systems, and Computer*, 993-997, 2010.

       **Modularization of biological systems.** Mathematical models that describe biological systems can lack intuitive comprehension due to high levels of complexity. More coarse information that allows a perceptive insight of the system is sometimes needed in combination with the model to understand control hierarchies or lower level functional relationships. In [1], we formulated a method to identify relationships between components of dynamic models of biochemical pathways that reside in different functional groups. We also generated a framework to identify individual components and modules that influence phenotypic traits of interest and predict phenotypical changes under perturbed conditions [2].

**[1]** <u>de Luis Balaguer MA</u> and **Williams C**. *IEEE Transactions on Systems, Man, and Cybernetics, Part B*, 44(8):1473-1484, 2014. **[2]** <u>de Luis Balaguer MA</u> and **Williams C**, *Proceeding of 2014 IEEE International Conference on Systems, Man, and Cybernetics (SMC)*, 1300-1305, 2014.

**TEACHING AND MENTORSHIP**: I have demonstrated myself to be an effective teacher, having taught **1,307 students** over three courses since 2008, with an **average teaching effectiveness** of 4.6 (4.1), 4.6 (4.2), and 4.9 (4.1), respectively ((.) indicates department average). I have graduated **4 doctoral students** and **3 MS Thesis** students. I have **7 current doctoral students** for whom I chair their doctoral committee. My dedication to student diversity is clearly evident, where since 2008 **5 of my 10** past/present doctoral students are women and/or members of an underrepresented group. Similarly, **19 of my 25** past/present undergraduate/high school research students are women and/or members of an underrepresented group. I have also been successful in recruiting undergraduate research students from minority serving institutions, successfully recruiting summer research students from the **University of Puerto Rico, Cayan** and the **University of the Virgin Islands** (UVI). I am a faculty mentor and sit on the executive committee for the **NIH sponsored Molecular Biotechnology Training Program** (MBTP), which allows me to nominate deserving students for the MBTP doctoral traineeships (1 current student awarded) and the Graduate Assistance in Areas of National Need (GAANN) Molecular Biotechnology fellowships (1 current student awarded). I also served as a faculty mentor in the **NC State Initiative for Maximizing Student Diversity Program** (IMSD), which seeks to increase the representation from underrepresented groups in the biomedical and behavioral science workforce through undergraduate and graduate student support (2 past doctoral students awarded). I also co-created and co-teach **a multidisciplinary course** on "Plant Systems Biology," which has served as an effective tool for recruiting interdisciplinary students. In 2013, I was awarded the ECE Department's **William F. Lane Outstanding Teacher Award**.

**ENGAGEMENT WITH INDUSTRY AND THE PLANT SCIENCE COMMUNITY**: I have maintained an active presence in the plant science community by attending meetings that attempt to further shape the science and policies associated with systems and synthetic biology and define the impending challenges associated with increased population and its effect on food security. Since 2008, I have been invited to give talks at and/or participate in meetings such as the **NSF-Engineering and Physical Sciences Research Council Synthetic Biology Sandpit** (Imperial College, London), the **BASF Science Symposium** (Chicago, IL), the **National Academies Keck Futures Initiative Conference** (Irvine, CA), the **Crops In-Silico Symposium and Workshop** (University of Oxford, UK), the **Novo Nordisk Foundation Sponsored Workshop on Crop Resiliency** (Hillerød, Denmark), the **International Symposium on Forest Tree Molecular Biology and Biotechnology** (Harbin, China), and the first **International Plant Systems Biology Workshop** (Roscoff, France). I was invited to serve on the Editorial Advisory Board for the journal in-silico Plants. I also participated in the two of three focus groups as part of the North American Arabidopsis Steering Committee (NAASC) RCN on **Arabidopsis Training in the 21st Century** (Phoenix, AZ) whose goal was to discuss guidelines, skill sets, and core competencies that should be emphasized when training undergraduate/graduate students, postdoctoral researchers and faculty interested in Plant Systems Biology and Engineering. The notes from these meetings resulted in two publications (Friesner et al., 2017 and Argueso et al., 2019), where I am listed as a co-author due to my contributions.

## GRANTS AND EXTRAMURAL FUNDING

Total Funding: **$14,228,113** (To CMW Directly: **$1,786,985**)

"Molecular Mechanisms and Dynamics of Plant-Microbe Interactions at the Root-Soil Interface: InRoot," Novo Nordisk Foundation, 01/01/2020 – 12/31/2025, Jens Stougaard, PI, Stig Uggarhøj Andersonn, Co-PI, Simona Radutoiu, Co-PI, Kasper Røjkjaer Andersen, Co-PI, Dugald Reid, Co-PI, Simon Kelly, Co-PI, Marianne Glasius, Co-PI, Shusei Sato, Co-PI, Thomas Roitsch, Co-PI, Heike Sederoff, Co-PI, Manuel Kleiner, Co-PI, **Cranos Williams, Co-PI**, Ronnie de Jonge, Co-PI, Henrik V. Scheller, Co-PI, Paul Pop, Co-PI, Winnie Edith Svendsen, Co-PI, Jan Madsen, Co-PI. Amount: $11.5M

"Planning Grant: Engineering Research Center for Rapid Innovations in SystEms Engineering and Agricultural Sustainability (RiseEnAg)," National Science Foundation (NSF EEC 1840440), 09/01/2018-8/31/2019, **C. Williams, PI**, R. Sozzani, Co-PI, O. Oralken, Co-PI, M. Kudenov, Co-PI, K. Ogan, Co-PI. Amount: $99,940

"From Lab to Field - Developing agro-textile nanotechnology for accelerating the development of stress tolerant high-yield crops," NC State University College of Agriculture and Life Sciences Research Foundation Grant, 07/01/18 – 06/30/2020, T. Long, PI, **C. Williams, Co-PI**, E. Ford, Co-PI, R. Sozzani, Co-PI, A. Locke, Co-PI, Amount: $49,951

"Natural variation and systems-level properties of gene regulation in Drosophila,"
National Institute of Health (NIH 1R01HD093041-01), 05-2017-05/2022; G. Reeves, PI, **C. Williams, Co-PI**. Amount: $1,799,591

"Collaborative Research: Modeling the regulatory network of InsP6 signaling in plants,"
National Science Foundation (NSF MCB-1615953), 09/2016 – 08/2018; I. Perera, PI, J. Ducoste, Co-PI, **C. Williams, Co-PI**. Amount: $310,155

"Identification of Translational Hormone-Response Gene Networks and Cis-Regulatory Elements,"
National Science Foundation (NSF IOS-1444561), 08/2015 – 07/2020; J. Alonso, PI, A. Stepanova, Co-PI, **C. Williams, Co-PI**, S. Heber, Co-PI. Amount: $3,200,484.

"Implementation and Analysis of Novel Real-Time QRS Detection Algorithms,"
NuPulse, Inc., 02/2015 – 12/2017; **C. Williams, PI**, T. Nagle, Co-PI. Amount: $187,604.

"High-Resolution in Vivo Imaging of Stem Cell Divisions with Light Sheet Microscopy," NC State Research and Innovation Seed Funding Program, 07/01/15 – 06/30/16, R. Sozzani, PI, **C. Williams, Co-PI**, T. Horn, Co-PI, Amount: $24,723

"INSPIRE: Dynamic Regulatory Modeling of the Iron Deficiency Response in Arabidopsis thaliana,"
National Science Foundation (NSF MCB-1247427), 08/2012 – 08/2017; **C. Williams, PI**, T. Long, Co-PI, J. Ducoste, Co-PI, J. Tuck, Co-PI. Amount: $999,758.

"Exploring Frontiers in Plant Systems Biology,"
National Science Foundation (NSF EFRI-1249698), 10/2012 – 09/2013; **C. Williams, PI**, T. Long, Co-PI, H. Sederoff, Co-PI. Amount: $48,516.

"Modeling of Cellulose, Hemicellulose and Lignin-Carbohydrate Complex Formation and Regulation to Understand Plant Cell Wall Structure,"
Department of Energy (DOE Project ID: 0017541), 09/2011 – 08/2017; V. Chiang, PI, R. Sederoff, Co-PI, H. Chang, Co-PI, D. Muddiman, Co-PI, **C. Williams, Co-PI**. Amount: $2,249,825.

"Regulation and Modeling of Lignin Biosynthesis,"
National Science Foundation (NSF DBI-0922391), 09/2009 – 08/2016; V. Chiang, PI, R. Sederoff, Co-PI, J. Ralph, Co-PI, J. Ducoste (Co-PI), F. Isik, Co-PI, **C. Williams, (Senior Personnel)**. Amount: $3,738,870.

"Improving Predictive Models of Biochemical Pathways in the Presence of Uncertainty," NC State Faculty Research and Professional Development Fund, 07/01/09 – 06/30/10, **C. Williams, PI**, Amount: $4,947

## PEER REVIEWED PUBLICATIONS

Journal Publications (Advisees of CMW indicated by underline)

1. L. Van den Broeck, <u>M. Gordon</u>, D. Inzé, **C. Williams**, R. Sozzani, "Gene regulatory network inference: connecting plant biology and mathematical modeling," *Frontier in Genetics, Bioinformatics and Computational Biology*, vol. 11, 2020, p. 457.
2. <u>M. Matthews</u>, J. Wang, R. Sederoff, V. Chiang, and **C. M. Williams**, "Modeling cross-regulatory influences on monolignol transcripts and proteins in *Populus trichocarpa* under single and combinatorial gene knockdowns," *PLoS Computational Biology,* vol 16, no 4, 2020.
3. <u>E. Buckner</u>, I. Madison, H. Chou, C. E. Melvin, R. Sozzani, **C. Williams**, Terri A. Long, "High Resolution Spatiotemporal Imaging and Analysis of Dynamic Cell Cycle Progression Patterns Under Iron Deficiency and Heat Stress Conditions," *Frontiers in Plant Science*, vol. 10, pp. 1487, 2019. (CW and TL co-corresponding authors)
4. N. Clark, <u>E. Buckner</u>, A. P. Fisher, E. C. Nelson, T. T. Nguyen, A. R. Simmons, M. A. de Luis Balaguer, T. Butler-Smith, P. J. Sheldon, D. C. Bergmann, **C. M. Williams**, R. Sozzani, "Stem-cell-ubiquitous genes spatiotemporally coordinate division through regulation of 2 stem-cell-specific gene networks," *Nature Communications*, vol. 10, no. 1, pp. 1-11, 2019.
5. A. Koryachko, A. Matthiadis, <u>S. Haque</u>, D. Muhammad, J. Ducoste, J. Tuck, T. Long, **C. Williams**, "Dynamic modeling of the iron deficiency modulated transcriptome response in Arabidopsis thaliana roots," *in silico Plants*, Volume 1, Issue 1, 2019, diz005, **https://doi.org/10.1093/insilicoplants/diz005**. (CW and TL co-corresponding authors)
6. C. T. Argueso, S. M. Assmann, K. D. Birnbaum, S. Chen, J. R. Dinneny, C. J. Doherty, A. L. Eveland, J. Friesner, V. R. Greenlee, J. A. Law, A. Marshall-Colón, G. A. Mason, R. O'Lexy, S. C. Peck, R. J. Schmitz, L. Song, D. Stern, M. J. Varagona, J. W. Walley, and **C. M. Williams**, "Directions for research and training in plant omics: Big Questions and Big Data," *Plant Direct*, vol. 3, no. 4, pp. e00133–16, Apr. 2019. (SMA corresponding author)
7. J. P. Wang, <u>M. L. Matthews</u>, P. P. Naik, **C. M. Williams**, J. J. Ducoste, R. R. Sederoff, and V. L. Chiang, "Flux modeling for monolignol biosynthesis.," *Current opinion in Biotechnology*, vol. 56, pp. 187–192, Dec. 2018.
8. <u>S. Haque</u>, J. S. Ahmad, N. M. Clark, **C. M. Williams**, and R. Sozzani, "Computational prediction of gene regulatory networks in plant growth and development.," *Current Opinion in Plant Biology*, vol. 47, pp. 96–105, Nov. 2018. (CW and RS co-corresponding authors).
9. J. Wang, <u>M. Matthews</u>, **C. Williams**, R. Shi, C. Yang, S. Tunlaya-Anukit, H. Chen, Q. Li, Jie L., C. Lin, P. Naik, Y. Sun, P. Loziuk, T. Yeh, H. Kim, E. Gjersing, T. Shollenberger, C. Shuford, J. Song, Z. Miller, Y. Huang, C. Edmunds, B. Liu, Y. Sun, Y. Lin, W. Li, H. Chen, I. Peszlen, J. Ducoste, J. Ralph, H. Chang, D. Muddiman, M. Davis, C. Smith, F. Isik, R. Sederoff, and V. Chiang, "Improving wood properties for wood utilization through multi-omics integration in lignin biosynthesis," *Nature communications*, 9(1), 1579, 2018.
10. P. Naik, J. Wang, J. Liu, H. Chen, R. Shi, C. M. Shuford, Q. Li, C.Y. Lin, D. C. Muddiman, R. Sederoff, V. Chiang, **C. Williams**, and J. Ducoste, "Assessing the Impact of the *4cl* Complex on the Robustness of Monolignol Biosynthesis Using Metabolic Pathway Analysis," accepted for publication to PLoS ONE, 2018.
11. Joanna Friesner, Sarah Assmann, Ruth Bastow, Julia Bailey-Serres, James Beynon, Volker Brendel, Robin Buell, Alexander Buksch, Jose Dinneny, Colleen Doherty, Andrea Eveland, Malia Gehan, Michael Gonzales, Erich Grotewold, Ute Kramer, Cody Markelz, Molly Megraw, Blake C. Meyers, Jim Murray, Nicholas J. Provart, Sue Rhee, Roger Smith, Edgar Spalding, Crispin Taylor, Tracy Teal, Keiko Torii, Chris Town, Matthew Vaughn, Richard Vierstra, Doreen Ware, Olivia Wilkins, **Cranos Williams**, Siobhan M. Brady, "The Next Generation of Training for Arabidopsis Researchers: Optimizing Training in Bioinformatics and Quantitative Biology for the Future," *Plant physiology* 175, no. 4 (2017): 1499-1509.
12. M. A. de Luis Balaguer, A. P. Fisher, N. M. Clark, M. G. Fernandez-Espinosa, B. K. Möller, D. Weijers, J. U. Lohmann, **C. Williams**, O. Lorenzo, and R. Sozzani, "Predicting gene regulatory networks by combining spatial and temporal gene expression data in Arabidopsis root stem cells," *Proc Natl Acad Sci USA*, vol. 114, no. 36, pp. E7632–E7640, Sep. 2017.
13. D. Muhammad, <u>S. Schmittling</u>, **C. Williams**, T. A. Long, "More than Meets the Eye: Emergent Properties of Transcription Factors Networks in Arabidopsis," BBA - Gene Regulatory Mechanisms, Special Issue: Plant Gene Regulatory Mechanisms, vol. 1860, pp. 64-74, 2016. (DM and SS co-first authors)
14. Jack P Wang, Sermsawat Tunlaya-Anukit, Rui Shi, Ting-Feng Yeh, Ling Chuang, Fikret Isik, Chenmin Yang, Jie Liu, Quanzi Li, Philip L Loziuk, Punith P Naik, David C Muddiman, Joel J Ducoste, **Cranos M Williams**, Ronald R Sederoff, Vincent L Chiang, "A Proteomic-Based Quantitative Analysis of the Relationship Between Monolignol Biosynthetic Protein Abundance and Lignin Content Using Transgenic Populus trichocarpa," Recent Advances in Polyphenol Research, vol. 5, pp. 89, 2016.
15. <u>A. Koryachko</u>, A. Matthiadis, D. Muhammad, J. Foret, S. M. Brady, J. J. Ducoste, J. Tuck, T. A. Long, and **C. Williams**, "Clustering and Differential Alignment Algorithm: Identification of Early Stage Regulators in the

Arabidopsis thaliana Iron Deficiency Response.," PLoS ONE, vol. 10, no. 8, pp. e0136591–21, 2015. (TL and CW: co-corresponding authors, AK and AM co-first authors)

16. A. Koryachko, A. Matthiadis, J. Ducoste, J. Tuck, T. Long, and **C. Williams**, "Computational approaches to identify regulators of plant stress response," Current Plant Biology, pp. 1–10, Jun. 2015, doi:10.1016/j.cpb.2015.04.001. (invited review, TL and CW: co-corresponding authors)

17. C. Lin, J. Wang, Q. Li, H. Chen, J. Liu, P. Loziuk, J. Song, **C. Williams**, D. Muddiman, R. Sederoff, and V. Chiang, "4-Coumaroyl and Caffeoyl Shikimic Acids Inhibit 4-Coumaric Acid: Coenzyme A Ligases and Modulate Metabolic Flux for 3-Hydroxylation in Monolignol Biosynthesis of *Populus trichocarpa*," *Molecular Plant*, vol. 8, no. 1, pp. 176-187, 2015.

18. H. Chen, J. Song, J. Wang, Y. Lin, J. Ducoste, C. Shuford, J. Liu, Q. Li, R. Shi, A. Nepomuceno, F. Isik, D. Muddiman, **C. Williams**, R. Sederoff, and V. Chiang, "Systems Biology of Lignin Biosynthesis in *Populus trichocarpa*: Heteromeric 4-Coumaric Acid:Coenzyme A Ligase Protein Complex Formation, Regulation, and Numerical Modeling," *The Plant Cell Online,* vol. 26, no. 3, pp. 876-893, 2014. (HC and JS, co-first authors, equal credit; CW, RS, and VC, co-corresponding authors)

19. J. Wang, P. Naik, H. Chen, R. Shi, C. Lin, J. Jiu, C. Shuford, J. Ducoste, Q. Li, **C. Williams**, D. Muddiman, R. Sederoff, and V. Chiang, "Complete Proteomic-Based Enzyme Reaction and Inhibition Kinetics Reveal How Monolignol Biosynthetic Enzyme Families Affect Metabolic Flux and Lignin in *Populus trichocarpa*, " *The Plant Cell Online*, vol. 26, no. 3, pp. 894-914, 2014.

20. M. A. de Luis Balaguer and **C. Williams**, "Hierarchical modularization of biochemical pathways using Fuzzy-C Means clustering," IEEE Transactions on Systems, Man, and Cybernetics, Part B, vol. 44 (8), pp. 1473-1484, 2014.

21. H. Chen, J. Song, **C. Williams**, C. Shuford, J. Liu, J. Wang, Q. Li, R. Shi, E. Gokce, J. Ducoste, D. Muddiman, R. Sederoff, and V. Chiang, "Monolignol pathway 4-coumaric acid: CoA ligases in *Populus trichocarpa*: Novel Specificity, Metabolic Regulation, and Simulation of CoA Ligation Fluxes," Plant Physiology, vol. 161, pp. 1501-1516, 2013.

22. S. Marvel and **C. Williams**, "Set membership experimental design for biological systems," BMC Systems Biology, vol. 6, no. 1, pp. 21, 2013.

23. B. Nabavi and **C. Williams**, "A novel cost function to estimate parameters of oscillatory biochemical systems," EURASIP Journal on Bioinformatics and Systems Biology, vol. 2012, no. 1, pp. 1-17, 2012.

24. J. Wang, C. Shuford, Q. Li, J. Song, Y. Lin, Y. Sun, H. Chen, **C. Williams**, D. Muddiman, R. Sederoff, and V. Chiang. "Functional redundancy of the two 5-hydroxylases in monolignol biosynthesis of Populus trichocarpa: LC–MS/MS based protein quantification and metabolic flux analysis". Planta, vol. 236, no. 3, pp. 795-808, 2012. .

*Books and Book Chapters*
1. W. E. Alexander and C. Williams, Digital Signal Processing: Principles, Algorithms and System Design, Academic Press, 2016.

*Conference Proceeding, Refereed*
1. M. Gordon and **C. Williams**, "PVC Detection Using a Convolutional Autoencoder and Random Forest Classifier," in Proceedings for Pacific Symposium on Biocomputing (PSB) 2019, pp. 42-53, https://doi.org/10.1142/9789813279827_0005.

2. E. Buckner, C. Melvin, C. Ottley, A. Balaguer, R. Sozzani, and **C. Williams**, "Tracking Gene Expression via Light Sheet Microscopy and Computer Vision in Living Organisms," The 40th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC), pp. 818-821, 2018.

3. A. Koryachko, S. Haque, and **C. Williams**, "Scalable approach to data driven transcriptome dynamics modeling," in Proceedings for the10th International Conference on Bioinformatics and Computational Biology (BICoB 2018), pp. 142-137, 2018.

4. Z. Qazi and **C. Williams**, "Controller structure for optimized region of attraction of Polynomial Systems," in Proceeding of the 49th ASILOMAR Conf. on Signals, Systems, and Computer, pp. 952 – 959, 2015.

5. M. de Luis Balaguer and **C. Williams**, "An HMM approach to identify components that influence phenotypes," in Proceeding of 2014 IEEE International Conference on Systems, Man, and Cybernetics (SMC), pp. 1300-1305, 2014.

6. M. Matthews and **C. Williams**, "Region of attraction estimation of biological continuous Boolean models," in Proceeding of 2012 IEEE International Conference on Systems, Man, and Cybernetics (SMC), pp. 1700 - 1705, 2012.

7.  S. Marvel and **C. Williams**, "Set membership state and parameter estimation for nonlinear differential equations with sparse discrete measurements," in Proceedings of 2012 IEEE International Conference on Systems, Man, and Cybernetics (SMC), pp. 72-77, 2012.
8.  S. Nabavi and **C. Williams**, "A novel cost function for parameters estimation in oscillatory biochemical systems," in 2012 Proceeding of IEEE SoutheastCon, pp. 1-8, 2012.
9.  S. Marvel, M. de Luis Balaguer, and **C. Williams**, "Parameter estimation in biological systems using interval methods with parallel processing," in Proceedings of the 2011 International Workshop on Computational Systems Biology, pp. 140-143, 2011.
10. M. de Luis Balaguer and **C. Williams**, "Estimation of component concentrations in biological systems via Interval Analysis," in 2010 IEEE Conference Proceedings of the 44th ASILOMAR Conf. on Signals, Systems, and Computer, pp. 993 – 997, 2010.
11. W. Edmonson, S. Ocloo, **C. Williams**, and W. Alexander, "The use of interval methods in signal processing and control for systems biology," in Proceedings of the 1st IEEE Symposium on Foundations of Computational Intelligence, pp. 136–142, 2007.
12. **C. Williams**, W. Alexander, W. Edmonson, "Estimating the unmeasured dynamics of biological systems using a constrained real-coded genetic algorithm," in 2006 IEEE Conference Proceedings of the 40th ASILOMAR Conf. on Signals, Systems, and Computer, pp. 1855-1859, 2006.
13. N. Cahill, **C. Williams**, S. Chen, L. Ray, and M. Goodgame, "Incorporating spatial information into entropy estimates to improve multimodal image registration," IEEE International Symposium on Biomedical Imaging, pp. 832-835, 2006.
14. **C. Williams**, W. Alexander, and T. Pompey, "Independent and principal component analyses of the global stress response of *Bacillus subtilis*," IEEE International Workshop on Genomic Signal Processing and Statistics, May 2005.
15. T. Pompey, **C. Williams**, J. Kim, and W. Alexander, "Analyzing the reliability of ICA estimates of *Bacillus subtilis*," IEEE International Workshop on Genomic Signal Processing and Statistics, May 2005.

*Conference Extended Abstracts / Posters, Refereed*
1.  A. Koryachko, A. Matthiadis, D. Muhammad, J. Ducoste, J. Tuck, T. Long, and **C. Williams**, "Revealing gene regulatory interactions of the iron deficiency response in Arabidopsis Thaliana," presented at the 15th International Conference on Systems Biology, October 2014 (Poster)
2.  **C. Williams** and S. Ocloo, "Design of experiments using bounded approaches," in Proceedings of the 11th International Conference on Systems Biology, October 2010, (Extended Abstract).
3.  M. de Luis Balaguer and **C. Williams**, "An interval method for state estimation in biological systems", in Proceedings of the 11th International Conference on Systems Biology, October 2010, (Extended Abstract).
4.  **C. Williams**, W. Alexander, and W. Edmonson, "Optimal control formulation of constrained Least-Squares estimation for biochemical pathway estimation," in Proceedings of the 8th International Conference on Systems Biology, October 2007, (Extended Abstract).

Patents
1.  R. Smith, N. Chinta, R. McCormick, D. Ivers, **C. Williams**, D. Badheka, H. T. Nagle, S. Dasari, S. Samadi, "Predictive QRS Detection and R-to-R Timing Systems and Methods," U.S. Patent Application 16401368, Filed May 02, 2019.
2.  S. Chen, L. Ray, N. Cahill, M. Goodgame, and **C. Williams**, "Method of image registration using mutual information," U.S. Patent 7,263,243, Aug. 28, 2007.

## INVITED ORAL/POSTER PRESENTATIONS
*Research-related (Conference w/ Proceeding)*: (Oral, Refereed)
1.  "An HMM approach to identify components that influence phenotypes," M. de Luis Balaguer and **C. Williams**, 2014 IEEE International Conference on Systems, Man, and Cybernetics (SMC), 2014.
2.  "Set membership state and parameter estimation for nonlinear differential equations with sparse discrete measurements," **C. Williams** and S. Marvel, *Referred Conference*, IEEE International Conference on Systems, Man, and Cybernetics (SMC), Seoul, Korea, 2012.

*Research-related (Conference w/o Proceedings)*: (Oral, Refereed)
1.  "Set-based Parameter and State Estimation in Nonlinear Differential Equations Using Sparse Measurements," **C. Williams** and S. Marvel, *Refereed Conference*, SIAM Conference on Uncertainty Quantification, Raleigh, NC, 2012.

2. "Predictive models of regulatory and metabolic pathways for monolignol biosynthesis," **C. Williams**, H. Chen, J. Song, J. Ducoste, C. M. Shuford, Q. Li, J. Liu, R. Shi, D. Muddiman, R. Sederoff, and V. Chiang, *Refereed Conference*, Plant and Animal Genome Conference XX, San Diego, CA, 2012.

*Research-related, invited (external)*: (15 Oral Presentations, 3 Poster Presentations)
1. "Multiscale Modeling of Lignin Biosynthesis in *Populus trichocarpa*," **C. Williams**, Plant and Animal Genome International Conference, San Diego, CA., January 2020.
2. "Dynamic modeling of the iron deficiency modulated transcriptome response in *Arabidopsis thaliana* roots," **C. Williams**, University of Tennessee, Chattanooga, March 2018.
3. "Dynamic modeling of the iron deficiency modulated transcriptome response in *Arabidopsis thaliana* roots," **C. Williams**, *Poster Presentation*, International Plant Systems Biology Conference, Roscoff, France, 2018.
4. "Systematically uncovering modes of regulation and control in monolignol biosynthesis," **C. Williams**, Forest Tree Molecular Biology and Biotechnology Symposium, Harbin, China, 2018
5. "Dynamic modeling of the iron deficiency modulated transcriptome response in Arabidopsis thaliana roots," **C. Williams**, University of North Carolina - Chapel Hill, April 2018.
6. "Integrative Dynamic Modeling using Diverse Biological Datasets," **C. Williams**, Crops In Silico Symposium and Workshop, University of Oxford, UK, July, 2017.
7. "Integrative Dynamic Modeling using Diverse Biological Datasets," **C. Williams**, Systems Biology Group, BASF, Raleigh, NC, July 2017.
8. "Plant Systems Biology and Engineering: Promoting Scientific Discovery through the Integration of Engineering and Biology," **C. Williams**, University of the Virgin Islands, Jan. 2017.
9. "EnBiSys Research Lab: Engineering Analytical and Computational Methodologies for Understanding Multi-Hierarchical Biology Systems," **C. Williams**, Systems Biology Group, BASF, Raleigh, NC, Oct. 2016.
10. "Clustering and Differential Alignment Algorithm: Identification of Early Stage Regulators in the Arabidopsis Thaliana Iron Deficiency Response," **C. Williams** et al., Pittcon: Symposia - Big Data in Analytical Sciences - Challenges and Solutions, Atlanta, GA, 2016.
11. "Set Membership Experimental Design for Biological Systems," **C. Williams**, *Technical Presentation*, Institute of Bioinformatics Seminar Series, University of Georgia, Athens, GA, 2013.
12. "Engineering Programmable Plant Systems" **C. Williams** and E. May, *Technical Presentation*, NSF EFRI FY 2014 Topic Solicitation, Office of Emerging Frontiers in Research and Innovation, Directorate of Engineering, National Science Foundation, 2013.
13. "Plant Systems Biology and Engineering – Overview," **C. Williams**, Plant Systems Biology and Engineering Workshop, North Carolina State University, Raleigh, NC, 2012.
14. "NSF-EPSRC Synthetic Biology Horizon Scanning Session – Bioprocess Engineering," **C. Williams**, *Technical Presentation*, NSF-EPSRC Synthetic Biology Sandpit, Imperial College London, 2011.
15. "Plant Systems Engineering: Predictive Modeling of Plant Metabolism, Development, and Adaptation," **C. Williams**, *Technical Presentation*, NSF EFRI FY 2012 Topic Solicitation, Office of Emerging Frontiers in Research and Innovation, Directorate of Engineering, National Science Foundation, 2011.
16. "Design of Experiments using Bounded Approaches," **C. Williams**, *Poster Presentation*, National Academies Keck Futures Initiative Conference on Ecosystem Services, Irvine, CA, 2011.
17. "Bounded System Identification for Biological Systems," **C. Williams**, *Invited Seminar*, Sandia National Laboratories, 2010.
18. "State Estimation of Biological Processes in the Presence of Bounded Uncertainty," **C. Williams**, *Poster Presentation*, Minority Faculty Development Forum, Massachusetts Institute of Technology, 2010.
19. "Dynamic Transitions of Pluripotent Cells," **C. Williams**, *Technical Presentation*, Computational Cell Biology Course, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 2009.

*Research-related, invited (internal)*: (16 Oral Presentations)
1. "From Lab to Field: Developing agro-textile nanotechnology for accelerating the development of stress tolerant high-yield crops" **C. Williams**, CALS Innovation Grant Update Meeting, April 2018.
2. "From Lab to Field: Developing agro-textile nanotechnology for accelerating the development of stress tolerant high-yield crops," **C. Williams**, INTRYSyC Seminar Series, Feb. 2018.
3. "Molecular and computational approaches to elucidating plant stress response," joint presentation by T.A. Long and **C. Williams**, VIB-NC State Minisymposium, Oct. 2017.
4. "Plant Systems Biology and Engineering: Sensing and Predictive Modeling of Plant Metabolism, Development, and Adaptation," **C. Williams**, College of Engineering Committee Meeting, North Carolina State University, 2016.

5. "EnBiSys Research Lab: Develop Engineering Tools for Plant Systems Biology," **C. Williams**, Technical Presentation, BASF / NCSU Site Visit, North Carolina State University, 2015.
6. "Developing Engineering Tools for Plant Systems Biology," **C. Williams**, Technical Presentation, Biochemistry Seminar Series, Biochemistry Department, NC State University, 2014.
7. "EnBiSys Research Laboratory: Engineering Analytical and Computational Solutions for Multi-Hierarchical Biological Systems," **C. Williams**, Technical Presentation, Plant Biology Seminar Series, Plant Biology Department, NC State University, 2013.
8. "Systems Biology of Lignin Biosynthesis in *Populus trichocarpa*: Heteromeric 4-Coumaric acid: CoA Ligase (4CL) Protein Complex Formation, Regulation and Numerical Modeling," **C. Williams**, *Technical Presentation*, NSF Project: Regulation and Modeling of Lignin Biosynthesis Scientific Advisory Board Meeting, NC State University, 2013
9. "Set Membership Experimental Design for Biological Systems," **C. Williams**, *Technical Presentation*, Biomath Seminar Series, Department of Mathematics, NC State University, 2013.
10. "Plant Systems Biology and Engineering," *Presentation*, ECE Scientific Advisory Board Meeting, NC State University, 2012
11. "Mathematical Modeling of Ptr4CL3 and Ptr4CL5 Enzyme Complex," **C. Williams**, *Technical Presentation*, NSF Project: Regulation and Modeling of Lignin Biosynthesis Scientific Advisory Board Meeting, NC State University, 2012.
12. "Functional Model of Lignin Biosynthesis – Systems Model Overview," **C. Williams**, *Technical Presentation*, NSF Project: Regulation and Modeling of Lignin Biosynthesis Scientific Advisory Board Meeting, NC State University, 2011.
13. "Plant Systems Engineering: Predictive Modeling of Plant Metabolism, Development, and Adaptation," **C. Williams**, *Technical Presentation*, Blue Sky Research Meeting, Department of Electrical and Computer Engineering, North Carolina State University, 2011.
14. "Regulation and Modeling of Lignin Biosynthesis – Systems Model Overview," **C. Williams**, *Technical Presentation*, NSF Project: Regulation and Modeling of Lignin Biosynthesis Scientific Advisory Board Meeting, North Carolina State University, 2010.
15. "Plant Systems Biology: Understanding the Complex Dynamics of Biochemical Networks", **C. Williams**, *Invited Seminar*, Seminar Series on Plant Biology, Department of Plant Biology, North Carolina State University, 2008.
16. "Computational Tools for Estimating the Unknown or Unmeasured Characteristics of Biochemical Pathways," **C. Williams**, *Invited Seminar*, Botany 824N: Molecular Approaches to Plant Development, North Carolina State University, 2008.

## MULTIDISCIPLINARY/INTERDISCIPLINARY ACTIVITIES

Engineering / Plant Science Consortium for Rapid Innovations in SystEms Engineering and Agricultural Sustainability (RiseEnAg)
**Cranos Williams (Lead)**; Partnering Institutions: Ali Karimoddini (Elect. & Comp. Eng., NC A&T Univ); Gerrit Hoogenboom (Ag. & Bio. Eng., Univ. of Florida); Cristina Davis (Mech. & Aero. Eng., Univ. of California - Davis); Chandra Krintz (Computer Science, Univ. of California – Santa Barbara)

**Consortium Vision**: Enable long-term global food security and safety through integrated engineered systems for improving the health of the plant (pre-harvest resilience), the health of the produce (post-harvest fruit quality), and consumer food safety.

**Consortium Mission:** RiseEnAg will drive the fundamental research needed to enable the tools of innovation and discovery necessary to address these challenges in four key areas: 1) Sensors for monitoring a crop's physical, biochemical, and molecular parameters and use of synthetic biology for signal amplification; 2) Platforms that allow sensors to network over an internet-of-things backbone for data collection (e.g. rural or poorly connected areas); 3) Multiscale crop modeling, data mining, and machine learning approaches, tailored to heterogeneous agricultural datasets, on-field noise, and experimental limitations; and 4) Cyberinfrastructure for integrating private and public datasets to enable information exchange between center stakeholders.

**Activities**:

- Awarded NSF Planning Grant to build interdisciplinary and convergent research team, engage stakeholders, and grow industry partnerships to identify solutions in this space (NSF EEC 1840440, **C. Williams, PI**).
- Held **2-day Stakeholder Engagement Workshop** (May 2nd-May 3rd, 2019) for Ag growers/producers and Ag-Biotech representatives to 1) to identify the needs and concerns of producers, plant breeders, researchers, and Extension agents and 2) establish a tailored business model for **RiseEnAg** to partner with Ag-Business and Ag-Biotech stakeholders, where research conducted within the consortium will be able to provide increased value to our stakeholders within a pre-competitive research space (**C. Williams**, Organization Chair)

North Carolina Plant Science Initiative (NC PSI)
Interdisciplinary initiative for addressing the grand scientific and technical challenges associated with agriculture in North Carolina. Goals are to:
- Integrate the work of agricultural scientists with engineers, mathematicians, social scientists, computer scientists, and economist to deliver sound, science-based solutions
- Facilitate innovative partnerships between universities, industry, and government
- Make North Carolina the premier destination for plant sciences

**CMW Activities and Contributions**:
- Member of the Research Taskforce of the NC PSI, which was formed to help guide the scientific research and technology planning of the NC PSI
- *Co-Lead* of the Plant Data Sciences Technical Platform
- Led three planning meetings comprised of academic, industry, and production leaders; goal was to define the main tenants of the Plant Data Sciences Platform
- Summarized and compiled findings; finding presented to the executive committee in the form of a white paper

Chancellor's Faculty Excellence Program
**Funded Area**: "Modeling the Living Embryo: Quantitative and Computational Developmental Biology"
*Lead Faculty*: Troy Ghashghaei (Molecular Biomedical Sciences, CVM) and Nanette Nascone-Yoder (Molecular Biomedical Sciences, CVM)
*Proposing Faculty*:
Ke Cheng, Jorge Piedrahita, Phillip Sannes, Jeffrey Yoder, Heather Shive, Scott Bailey, Sharon Lubkin, Mansoor Haider, Alun Lloyd, Robert Anholt, Patricia Estes, James Mahaffey, Trudy Mackay, Heather Patisaul, Antonio Planchart, Emilie Rissman, Reade Roberts, David Muddiman, Seth Kullman, Michael Cowley, Keith Weninger, Balaji Rao, Greg Reeves, **Cranos Williams**, Nancy Allbritton, Matthew Fisher, Zhen Gu, Elizabeth Loboa, Anne Taylor, Linyou Cao, Albena Ivanisevic, Yaroslava Yingling, Shadow Huang, Jose Alonso, Robert Franks, Candace Haigler, Tzung-Fu Hsieh, Imara Perera, Marcela Rojas-Pierce, Anna Stepanova, Qiuyun Xiang, Ross Sozzani, Max Scott, Colleen Doherty, Charles Stuber
Participating Colleges: College of Vet. Medicine, College of Agriculture and Life Sciences, **College of Engineering**, College of Sciences
Status: Awarded (**4 Faculty Positions**)

**CMW Contributions**:
- Member, *Modeling the Living Embryo: Quantitative and Computational Developmental Biology*, Chancellor's Faculty Excellence Cluster Hire Program, 2015, 2016, 2017

Chancellor's Faculty Excellence Program
**Funded Area**: "Integrated Synthetic and Systems Biology (ISSB) at NCSU"
*Lead Faculty*: Heike Sederoff (CALS, Plant Biology) and Alex Deiters (PAMS, Chemistry)
*Proposing Faculty*:
**College of Ag. & Life Sciences**: Trudy McKay (Genetics), Bill Thompson (Plant Biology), Terri Long (Plant Biology), Margaret Daub (Plant Biology), Linda-Hanley-Bowdoin (Molecular and Structure Biochemistry)
**College of Engineering**: Joel Ducoste (Civil, Constr. & Environ. Eng.), **Cranos Williams (Elect. & Comp. Eng.)**, Bob Kelly (Chem. & Bio. Eng.), Jason Haugh (Chem. & Bio. Eng.), Bala Rao (Chem. & Bio. Eng.), Greg Reeves (Chem. & Bio. Eng.), Bala Rao (Chem. & Bio. Eng.), and Chase Beisel (Chem. & Bio. Eng.)

*College of Physical & Mathematical Sciences*: Keith Weninger (Physics), Robert Riehn (Physics), and Gavin Williams (Chemistry)
*College of Natural Resources*: Vincent Chiang (Forestry & Environ. Resources) and Ronald Sederoff (Forestry & Environ. Resources)
*College of Vet. Medicine*: Jeff Yoder (Molecular Biomedical Sciences)
North Carolina State University
Status: Awarded **(3 Faculty Positions)**

**CMW Contributions**:
- Lead contributor to Systems Biology Chancellor's Faculty Excellence proposal
- Member, *Synthetic and Systems Biology Cluster Search Committee*, Chancellor's Faculty Excellence Cluster Hire Program, 2015, 2014, 2013, 2012, 2011

MULTIDISCIPLINARY WORKSHOPS
- Under-represented Minority Awards Co-Leader, International Conference on Arabidopsis Research, St. Louis, MI, June 2017
- Organization Committee, *Plant Systems and Synthetic Biology: Solutions to Global Food Security Workshop*, North Carolina State University, October 17-18, 2014.
- Organization Committee Chair, *Plant Systems Biology and Engineering Workshop*, North Carolina State University, November 1-3, 2012. (http://research.ece.ncsu.edu/plantsysbioeng/)

MULTIDISCIPLINARY SEMINAR INVITATIONS
- Invited Participant, Crop Resiliency Workshop, Novo-Nordisk, Denmark, 2018.
- Invited Participant: "Workshop on Training and Education in Plant Biology," North American Arabidopsis Steering Committee Focus Group, Santa Fe, NM, Feb. 2017
- Invited Participant: "Workshop on Next Generation of Training for Arabidopsis Research," North American Arabidopsis Steering Committee Focus Group, Phoenix, AZ, June 2016.
- Invited Participant, Plant Sciences Initiative Task Force 2: Research & Technology, North Carolina State University, 2016
- Invited Participant, BASF Science Symposium, Chicago, Illinois, 2015
- Invited Participant: *Interdisciplinary and Innovation: Strategies for Effective Team Research*, NSF EFRI Workshop, National Science Foundation, Arlington, VA, 2014.
- Invited Panelist, *Session 4: Role of Systems and Synthetic Biology in Addressing Food Security Issues for the Future*, Plant Systems and Synthetic Biology: Solutions to Global Food Security Workshop, North Carolina State University, 2014
- Invited Presenter, *National Academies Keck Futures Initiative Conference on Ecosystem Services*, Irvine CA, 2011
- Participant, *AFOSR Spring Review*, Air Force Office of Scientific Research, Arlington, VA, 2011
- Invited, *NCSU-COE Early Career Visit to NSF*, National Science Foundation, Arlington, VA, 2011
- Invited Presenter, *Minority Faculty Development Forum*, Massachusetts Institute of Technology, Cambridge, MA, 2010
- Invited Presenter, *Computational Cell Biology Course*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 2009. *Description: The three-week interdisciplinary course on the mathematics of dynamical systems, computational simulation techniques, cell biology and molecular biology. ASEE Engineering Research Council Annual Conference*, Arlington, VA, 2009
- Invited, *Minority Faculty Development Forum*, Georgia Institute of Technology, Atlanta, GA, 2009.


**STUDENT SYMPOSIUM/CONFERENCE PRESENTATIONS**
(Advisee of CMW indicated)
1. Samiul Haque, Sarah Bell, Edgar Lobaton, Natalie Nelson, Michael Kudenov, Mike Boyette, and **Cranos Williams**, *"Sweetpotato Shape Classification using Computer Vision and Supervised Machine Learning"*, National Sweetpotato Collaborators Annual Meeting, January 2020, Nashville, TN, USA.
2. Haque, S., Muhammad, D., Chou H., Ducoste, J.J., Tuck, J.M., Long, T.A. and **Williams, C.M.**, "Epidermal Gene Regulatory Network of Arabidopsis Thaliana under Iron Deficiency," 2019 Society for Experimental Biology Annual Meeting, Seville, Spain, 2-5 July 2019.

3. <u>Megan Matthews</u> and **Cranos Williams**, "Computational Model for Predicting Monolignol Transcript and Protein Abundances in *Populus trichocarpa* under Single and Combinatorial Monolignol Gene Knockdowns", Plant and Animal Genome Conference, 2019, California.

4. <u>Max Gordon</u> and **Cranos Williams**, "PVC Detection Using a Convolutional Autoencoder and Random Forest Classifier," Pacific Symposium on Biocomputing (PSB) January 2019, Hawaii, Hawaii.

5. <u>Eli Buckner</u> and **Cranos Williams**, "Tracking Gene Expression via Light Sheet Microscopy and Computer Vision in Living Organisms," Oral Presentation, Annual Molecular Biotechnology Training Program (MBTP) Symposium, North Carolina State University, Nov. 2018.

6. <u>Eli Buckner</u> and **Cranos Williams**, "Tracking Gene Expression via Light Sheet Microscopy and Computer Vision in Living Organisms," *40th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC)*, July 2018, Hawaii.

7. <u>Alex Koryachko</u> and **Cranos Williams**, "Identification of key gene regulatory mechanisms underlying iron deficiency response in *Arabidopsis thaliana*," Poster Presentation, Annual Molecular Biotechnology Training Program (MBTP) Symposium, North Carolina State University, Nov. 2016.

8. <u>Megan Matthews</u> and **Cranos Williams**, "Developing a Metabolic Objective Approach to Infer Regulatory Relationships Between Metabolic Pathway Enzymes," Poster Presentation, Annual Molecular Biotechnology Training Program (MBTP) Symposium, North Carolina State University, Nov. 2016.

9. <u>Zohaib Qazi</u> and **Cranos Williams**, "Causal inference using RNASeq data," Poster Presentation, Annual Molecular Biotechnology Training Program (MBTP) Symposium, North Carolina State University, Nov. 2016.

10. Anna Matthiadis, <u>Alexandr Koryachko</u>, Durreshahwar Muhammad, Joel Ducoste, James Tuck, **Cranos Williams**, and Terri Long. "Computational approaches to predict regulatory relationships: New players in the Arabidopsis thaliana iron deficiency response," American Society of Plant Biology (ASPB) Meeting, Austin, Texas, July 2016.

11. Anna Matthiadis, <u>Alexandr Koryachko</u>, Durreshahwar Muhammad, Joel Ducoste, James Tuck, **Cranos Williams**, and Terri Long. "Algorithm application to identify novel regulators in the *Arabidopsis thaliana* iron deficiency response," Systems Biology and New Approaches Session, 26th International Conference on Arabidopsis Research (ICAR), Paris, France, July 2015.

12. Anna Matthiadis, <u>Alexandr Koryachko</u>, Durreshahwar Muhammad, Joel Ducoste, James Tuck, **Cranos Williams**, and Terri Long. "Algorithm application to identify novel regulators in the *Arabidopsis thaliana* iron deficiency response," Ionomics Workshop, 26th International Conference on Arabidopsis Research (ICAR), Paris, France, July 2015.

13. Durre Muhammad, Daniel Schmitt, <u>Alexandr Koryachko</u>, Anna Matthiadis, Devarshi Selote, Rosangela Sozzani, **Cranos Williams**, Terri Long. "The roles of iron-responsive transcription factors in gene regulatory networks involved in key processes of iron homeostasis." 25th International Conference on Arabidopsis Research (ICAR), Poster Presentation, Vancouver, Canada, July 2014.

14. Anna Matthiadis, <u>Alexandr Koryachko</u>, Durreshahwar Muhammad, Joel Ducoste, James Tuck, **Cranos Williams**, and Terri Long. "Using a systems biology approach to identify key transcriptional regulators in the Arabidopsis thaliana iron deficiency response." 9th International BioMetals Symposium, Poster Presentation, Duke University, July 2014.

15. Anna Matthiadis, <u>Alexandr Koryachko</u>, Terri Long, and **Cranos Williams**. "Creating a dynamic gene regulatory model of the iron deficiency response in Arabidopsis thaliana." 9th Annual Graduate Student Research Symposium, Poster Presentation, North Carolina State University, March 2014.

16. <u>L. Blakey</u> (UG) and **C. Williams**, "A Mathematical Representation of the Lignin Biosynthesis Pathway," <u>Annual Biomedical Research Conference for Minority Students (ABRCMS)</u>, November 2014, November 2013.

17. <u>M. Rahhal</u> (UG) and **C. Williams**, "Logic Gate Representation of Gene Regulatory Networks: T-Helper Cell Differentiation," Undergraduate Summer Research Symposium, NC State University, August 2013.

18. <u>L. Blakey</u> (UG) and **C. Williams**, "A Mathematical Representation for the Mechanistic Model of the Lignin Biosynthesis Pathway," Undergraduate Summer Research Symposium, NC State University, August 2013.

19. <u>M. Rahhal</u> (UG) and **C. Williams**, "Modeling Biological Systems: Evaluation of Systems Biology Toolbox and Wolfram Systems Modeler," State of NC Undergraduate Research and Creativity Symposium (SNCURCS**)**, November 2012.

20. <u>R. Damptey</u> (UG) and **C. Williams**, "Assessing the Dynamics of Biochemical Pathways Using Continuous Boolean Approximations," 2012 <u>Annual Biomedical Research Conference for Minority Students (ABRCMS)</u>, November 2012. (**Received Research Award in the area of Molecular and Computational Biology)**

21. <u>M. Rahhal</u> (UG) and **C. Williams**, "Modeling Biological Systems: Evaluation of Systems Biology Toolbox and Wolfram System Modeler", Undergraduate Summer Research Symposium, NC State University, August 2012.

22. L. Weldegebriel (UG) and **C. Williams**, "Regulated Flux Balance Analysis of Lignin Biosynthesis", Undergraduate Summer Research Symposium, NC State University, August 2012.
23. R. Damptey (UG) and **C. Williams**, "Assessing the Dynamics of Biochemical Pathways Using Continuous Boolean Approximations", Undergraduate Summer Research Symposium, NC State University, August 2012.
24. J. Song, H. Chen, C. M. Shuford, Q. Li, J. Liu, R. Shi, D. Muddiman, **C. Williams**, J. Ducoste, R. Sederoff, and V. Chiang, "Multi-Enzyme System Modeling for Regulated Metabolic Pathways," Presented at $1^{st}$ Korean Student Technical and Leadership Conference, Chicago, IL, 2012.
25. M. Matthews and **C. Williams**, "Estimating Regions of Attractions for Quadratic Nonlinear Biochemical Systems," Presented at $10^{th}$ Annual OPT-ED Alliance Day Conference, NC State University, October 2011.
26. R. Damptey *(UG)* and **C. Williams**, "Parameter Estimation of Continuous Boolean Approximations of Enzyme Kinetics," Presented at the 2011 Annual Biomedical Research Conference for Minority Students, St. Louis, Missouri, November 2011.
27. J. Smith *(UG)*, **C. Williams**, and J. Ducoste, "Steady State Analysis of Biological Systems Using Mathematical Modeling," Presented at the 2011 Annual Biomedical Research Conference for Minority Students, St. Louis, Missouri, November 2011.
28. R. Damptey *(UG)* and **C. Williams**, "Parameter Estimation of Continuous Boolean Approximations of Enzyme Kinetics," Presented at the $10^{th}$ Annual OPT-ED Alliance Day Conference, NC State University, October 2011.
29. R. Damptey *(UG)* and **C. Williams**, "Assessing the Dynamics of Biochemical Pathways Using Continuous Boolean Approximations," Presented at the Undergraduate Summer Research Symposium, NC State University, August 2011.


## TEACHING EXPERIENCE

**ECE492-030/ECE592-038 (PB495-011/PB595-011) – Systems Biology Modeling of Plant Regulation**
- The objective of this course is to provide an introduction to the field of systems biology with a focus on mathematical modeling, gene regulatory network and metabolic pathway construction in plants.

| ECE492-030/ECE592-038 (PB495-011/PB595-011) – Course Enrollment | | | |
|---|---|---|---|
| Year | Total Enrollment | ECE492 (592) | PB495 (595) |
| 2017F | **11** | 0 (3) | 2 (6) |
| 2016F | **7** | 0 (5) | 0 (2) |
| 2015F | **11** | 2 (2) | 4 (3) |
| 2014F | **16** | 3 (5) | 0 (8) |

**ECE 220 – Analytical Foundations of Electrical and Computer Engineering**
- The objective of this course is to provide the mathematical foundation for students in electrical and computer engineering. Topics includes signals and systems signal and systems, linear algebra, complex numbers, systems of linear equations, time-based and Laplace-based approaches for solving ordinary differential equations, and Fourier series analysis of signal and systems.

| ECE 220 – Course Enrollment | | | |
|---|---|---|---|
| Year | Total Enrollment | On-Campus | Distance Ed. |
| 2018S | **150** | 102 | 48 |
| 2016S | **185** | 145 | 40 |
| 2015S | **102** | 59 | 43 |
| 2014S | **91** | 91 | 0 |
| 2013S | **91** | 91 | 0 |

**ECE 513 – Digital Signal Processing**
- Digital processing of analog signal. Offline and real-time processing for spectrum estimation, filter design, and multirate signal processing. Analysis of FIR and IIR filter structures for efficient implementation. Advanced topics include design of quadrature mirror filter banks and discrete wavelet transforms.

| ECE 513 – Course Enrollment | | | |
|---|---|---|---|
| Year | Total Enrollment | On-Campus | Distance Ed. |
| 2017F | **55** | 52 | 3 |
| 2015F | **71** | 61 | 10 |
| 2014F | **72** | 61 | 11 |

| | | | |
|---|---|---|---|
| 2013F | **53** | 47 | 6 |
| 2012F | **104** | 95 | 9 |
| 2011F | **90** | 80 | 10 |
| 2010F | **85** | 78 | 7 |
| 2009F | **86** | 81 | 5 |

**ECE 492/592 – Analysis of Nonlinear Complex Systems**
- Multidisciplinary course that introduces theoretical and computational systems analysis tools that are applied to nonlinear models of biological systems. This course covers analysis tools that include but are not limited to matrix algebra, phase plane analysis, qualitative assessment of systems behavior around equilibrium points, stability analysis, limit cycle analysis, bifurcation, parameter estimation, and sensitivity analysis.

| ECE 492-011 / 592-006 – Course Enrollment | | | |
|---|---|---|---|
| **Year** | **Total Enrollment** | **592-006 (ECE / Other[1])** | **492-011 (ECE / Other[1])** |
| 2012Spr | **2** | 2 (1 / 1) | 0 (0 / 0) |
| 2011Spr | **11** | 5 (4 / 1) | 6 (6 / 0) |
| 2010Spr | **10** | 8 (4 / 4) | 2 (2 / 0) |
| 2009Spr | **6** | 4 (3 / 1) | 2 (0 / 2) |

[1] 'Other' includes Departments of Biomedical Eng., Civil Eng., Natural Resources, Plant Biology, and Forestry

## STUDENT MENTORSHIP AND ADVISING
- Currently directing the theses of __7__ Ph.D. students.
- Graduated __4__ Ph.D. student and __3__ Master's with Thesis students
- Mentored __25__ undergraduate/high school students on research projects

*Doctoral Dissertations Completed as Chair*
1. M. A. de Luis Balaguer, "Computational learning strategies for assessing modular influences on biological phenotypes," Ph.D. EE dissertation, Dept. Elect. & Comp. Eng., NC State Univ., Raleigh, NC, 2013.
2. J. Song, "Mechanistic Model Development for Multi-Enzymatic Reactions in Lignin Biosynthesis," Ph.D. EE dissertation, Dept. Elect. & Comp Eng. NC State Univ., Raleigh, NC 2014
3. A. Koryachko, "Computational Methodologies for Unraveling Gene Regulation Mechanisms Underlying Iron Deficiency Response in Arabidopsis thaliana Root," Ph.D, EE dissertation, Dept. Elect. & Comp. Eng. NC State Univ., Raleigh, NC 2018
4. M. Matthews, "Multi-Scale Modeling of Lignin Biosynthesis and Other Wood Properties in Populus trichocarpa," Ph.D. EE dissertation, Dept. of Elect. & Comp. Eng., NC State Univ., Raleigh, NC 2019

*Master's Thesis Completed as Chair*
1. M. Matthews, "Region of attraction estimation of biological continuous Boolean models," M.S. EE thesis, Dept. Elect. & Comp. Eng., NC State Univ., Raleigh, NC, 2012
2. S. Nabavi, "Kinetic parameter estimation in oscillatory biochemical systems," M.S. EE thesis, Dept. Elect. & Comp. Eng., NC State Univ., Raleigh, NC, 2011
3. S. Marvel, "Set membership experimental design for biological systems," M.S. EE thesis, Dept. Elect. & Comp. Eng., NC State Univ., Raleigh, NC, 2011

## PROFESIONAL SERVICE AND ACTIVITIES
- NSF Ad-hoc Reviewer, Systems and Synthetic Biology Cluster, Division of Molecular and Cellular Biosciences, Directorate for Biology Sciences, National Science Foundation, 2019.
- Member, Executive Committee, NIH/NC State Molecular Biotechnology Training Program, 2018-Present
- Member, Editorial Advisory Board, *in-silico* Plants, 2018 - Present
- Grant Reviewer, Foundation for Food and Agriculture Research, 2018
- NSF Grant Panelist, *System and Synthetic Biology Cluster*, Division of Molecular and Cellular Biosciences, Directorate for Biological Sciences, National Science Foundation, 2018.
- Invited Participant, NSF ERC Planning Grant Workshop, American Society for Engineering Education, Arlington, VA, 2018

- Invited Participant, BASF Visit to NCSU: Bioinformatics and Metabolic Engineering Session, 2016
- Mentor, Duke Preparing Future Faculty Mentor Program, *Mentee: Patrick Wang*, 2014/2015
- Grant Panelist, *Animal Health Panel*, National Institute of Food and Agriculture, USDA, 2014, 2015
- NSF Grant Panelist, Emerging Frontiers in Research and Innovation - REM, Office of Emerging Frontiers in Research and Innovation, Directorate for Engineering, 2014
- NSF Grant Panelist, *Biochemical Engineering & Biotechnology*, Division of Chemical, Bioengineering, Environmental, and Transport Systems, Directorate for Engineering, 2013
- Workshop Chair, *Plant Systems Biology and Engineering Workshop*, Sponsored by National Science Foundation, North Carolina State University, November 2012
- Session Chair, IEEE Conference on Systems, Man, and Cybernetics, Seoul, South Korea, 2012
- Session Chair, SIAM Conference on Uncertainty Quantification, Raleigh, NC, 2012
- NSF Grant Panelist, *Systems / Synthetic Biology and Evolutionary Networks Panel*, Networks and Regulation Cluster, MCB, Directorate for Biological Sciences, NSF, Arlington, VA, 2011
- Participant, Air Force Office of Scientific Review (AFOSR) Spring Review, 2011
- Journal Reviewer, *IEEE Journal on Selected Topics in Signal Processing*: Special Issue on Genomic and Proteomic Signal Processing, 2007
- Journal Reviewer, *in Silico* Plants, PLoS Computational Biology, Biotechnology for Biofuels, EURASIP Journal on Bioinformatics and Systems Biology, IEEE Journal on Selected Topics in Signal Processing: Special Issue on Genomic and Proteomic Signal Processing, IEEE Transactions on Signal Processing, IEEE International Workshop on Genomic Signal Processing and Stat.