DANIEL R. KICK, PHD

- Experience predicting maize yield across environments using **deep learning, machine learning, statistical modeling** to facilitate crop improvement.
- **Designed funded research project** (USDA NIFA) to create environmentally aware **deep learning models for trait prediction** and **transfer learning** between maize and wheat ($225,000, Grant 2023-67012-39485).
- Initiated and led a multi-institutional research collaboration; collaborated with domain experts.
- **Presented** to scientific and general audiences **36 times** since 2016.
- Invited presentations at University of Michigan, Truman State University, Iowa State University, and University of Georgia's **AI in Plant Breeding Symposium**.
- **Developed data analysis app** used by **>700 students** as of 2021.
- **Data and models** downloaded **700 times** and viewed over **1515 times**.
- **Led 4 teaching assistants** and **mentored 9 research students**.

PROFESSIONAL AND RESEARCH EXPERIENCE

Present | 2021

Research Geneticist

Jacob Washburn Lab, USDA-ARS

- **Secured $225,000** to develop **"Environmentally Aware Deep Learning Based Genomic Selection And Management Optimization For Maize Yield"** from the National Institute of Food and Agriculture (NIFA) (Grant 2023-67012-39485).
- **Initiated and led a multi-institutional research collaboration** and wrote custom libraries for same.
- Employed **deep neural networks, machine learning models, best linear unbiased predictors, and scientific models (i.e. process based)** to improve trait prediction accuracy in diverse environments.
- **Communicated** with stakeholders via **21 presentations** (7 national, 10 regional, 4 outreach).
- **Organized and lead** deep learning community of practice university and government attendees.
- **Mentored** 4 students with projects ranging from high throughput phenotyping experiment, to deep learning model development.
- **Created** and taught a **Python data visualization workshop** titled "Tools and Techniques for a Jupyter Based Scientific Workflow".
- Completed **Software Carpentries instructor certification**, taught **R for Reproducible Scientific Analysis**, and assisted in teaching **Data Management with SQL**.
- Served as a **panel member on "Next-Generation Omics"** at the 2022 University of Missouri Division of Biological Sciences Retreat.
- Designed and completed a professional development curriculum with the guidance of an industry scientists via the **Bayer-University Mentoring Program** and the **Maize Genetics Mentoring Program**.

2021 | 2015

Graduate Researcher

David Schulz Lab, University of Missouri

- **Author on 6 publications**: 4 original research and 2 eLife Insight publications.
- **Assessed the efficacy of machine learning models** to predict cell identity from mRNA and contig abundances. **Applied cluster estimation, hyperparameter tuning, unsupervised machine learning,** and **supervised machine learning**. Identified and learned needed skills primarily through self study. Collaborated with molecular biology project lead. (see *Northcutt[1], Kick[1], et al. 2019*).
- Defined research question and experiments. **Developed novel approaches to quantify changes in cell activity**.
- **Collaborated with electrophysiologists**, assisting with data analysis.
- **Collaborated with computational neuroscientists**, contributing domain expertise.
- **Mentored 5 students** and oversaw their projects.
- Communicated results through **18 presentations** (6 national, 6 regional, 6 outreach).
- Served as a **peer mentor of 3 PhD students** in use of R for reproducible data analysis, created internal documents on same.

CONTACT INFO

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Google Scholar

github.com/DanielKick-USDA

github.com/danielkick

danielkick.com

Education

PhD: Biological Sciences

University of Missouri, Columbia, MO (2021)

Machine Learning Methods for Biomedical Informatics, Quantitative Methods in the Life Sciences, and Grant Writing

Bachelor of Science: Biology

Truman State University, Kirksville, MO (2015)

Next Generation Sequence Data and Analysis, Bioinformatics, **Leadership role** in the biological honors society Tri-Beta

Technical Skills

Python (3 years) experience with `pandas`, `numpy`, `plotly`, `scikit-learn`, `keras`, `pytorch`.

R (8 years) experience with `tidyverse`, `lme4`, `caret`, `ggplot2`, `shiny`, & package creation.

Miscellaneous Experience with high performance computing (`bash`, `slurm`), virtual environments (`conda`, `singularity`), version control (`git`, `GitHub`), literate programming (`Quarto`, `Rmarkdown`, `Jupyter`, `nbdev`), Scientific modeling (crop growth modeling `APSIM Next Generation`), basic `SQL` (`SQLite`).

For a pdf with links scan here.

2021 | 2020

Lead Teaching Assistant, Animal Physiology Lab

Biological Sciences, University of Missouri

- **Developed statistics web application used by more than 700 students** as of 2021 with **shiny** (source, deployed) for data visualization, testing assumptions, and fitting **frequentist**, **non-parametric**, and **Bayesian** models.
- Led 4 Teaching Assistants and coordinated adaptation of lab curriculum to be fully online due to COVID-19 pandemic.
- **Mentored** next Lead Teaching Assistant, created documentation on best practices.

2020 | 2018

Teaching Assistant, Animal Physiology Lab

Biological Sciences, University of Missouri

- Iteratively refined curriculum, modeled student grade distributions to identify and adjust for differences in grading.

2018

Curriculum Consultant, Animal Physiology Lab

Biological Sciences, University of Missouri

- Redesigned and updated course material to incorporate data analysis and primary literature.

2016 | 2015

Teaching Assistant, Animal Physiology Lab

Biological Sciences, University of Missouri

- Delivered weekly lectures, ensured experiments were conducted safely, provided timely feedback on assignments.

2015 | 2013

Undergradute Researcher

University of Missouri, University of Connecticut, and Truman State University

- Designed a hydroponic system for maize root phenotyping –(2014-2015), Quantified retinal minor splicisome expression using immunohistochemistry – (2014), Measured effectiveness of oligonucleotide treatment for spinal muscular atrophy in mice – (2013).

HONORS AND AWARDS (SHOWING 4/5)

2025 | 2023

NIFA Fellowship (AFRI EWD)

$225,000 awarded (Grant # 2023-67012-39485) over two years to create and environmentally aware deep learning genomic selection models and prepare the recipient to transition into industry.

2019

J. Perry Gustafson Award for Outstanding Graduate Research in the Life Sciences

This $2,000 award is granted for the quality of their research and academic achievements.

2018 | 2016

NIH T32 Training Grant Recipient

This provides a $27,000 yearly stipend and $750 yearly to facilitate presenting research at scientific conferences.

2015

Cum Laude & President's Recognition, Truman State University

SELECTED PUBLICATIONS (SHOWING 3/9 PUBLISHED)

2023

Ensemble of Best Linear Unbiased Predictor, Machine Learning, and Deep Learning Models Predict Maize Yield Better Than Each Model Alone

Daniel R. Kick, Jacob D. Washburn *in Silico* Plants

2023

Yield Prediction Through Integration of Genetic, Environment, and Management Data Through Deep Learning

Daniel R. Kick, Jason G. Wallace, James C. Schnable, Judith M. Kolkman, Baris Alaca, Timothy M. Beissinger, David Ertl, Sherry Flint-Garcia, Joseph L. Gage, Candice N. Hirsch, Joseph E. Knoll, Natalia de Leon, Dayane C. Lima, Danilo Moreta, Maninder P. Singh, Teclemariam Weldekidan, Jacob D. Washburn G3: Genes, Genomes, Genetics

2019

Molecular profiling of single neurons of known identity in two ganglia from the crab Cancer borealis

Adam J. Northcutt[1], ***Daniel R. Kick***[1], Adriane G. Otopalik, Benjamin M. Goetz, Rayna M. Harris, Joseph M. Santin, Hans A. Hofmann, Eve Marder, and David J. Schulz (***[1] denotes co-first authorship***) Proceedings of the National Academy of Sciences