

Wenbin Mei, PhD

Computational Biology & AI Leader · Predictive Modeling for Target Discovery & Multiplex Gene Editing · Building High-Impact Teams

Cambridge, MA
wenbinmei@gmail.com
wenbinmei.github.io ·
linkedin.com/in/wenbin-mei

SUMMARY

Computational biology and AI leader with 15+ years of experience in genomics, machine learning, and genome editing, including 6+ years as a people leader. I build predictive models that turn biological data into decisions, most recently for target identification and multiplex gene editing at Inari, and the teams that deliver them. I am motivated by applying AI in biology to solve problems with real-world impact, from crops to human health.

- **People leader:** 6+ years as a people leader; built a team of 10+ computational biologists and data analysts across the US and Ghent, Belgium, as Platform Manager; led a cross-functional team of 8–9 computational biologists and ML scientists as Model Capability Lead.
- **Platform impact:** delivered AI models that prioritize gene targets and design edits, now powering Inari's Predictive Design Engine, an agentic AI platform for designing gene edits.
- **Track record:** inventor on 8 patent applications; 19 peer-reviewed papers including *Nature Genetics*, *Science*, *PNAS*, and *Genetics* (2,500+ citations, h-index 18).

EXPERIENCE

Inari Agriculture · Cambridge, MA · 2019 – Present

Predictive Design Engine Tech Lead

Jan 2026 – Present

- Technical lead for the Predictive Design Engine, Inari's agentic AI platform for designing gene edits; co-lead platform strategy and roadmap.
- Advance scientific capabilities through improvements in model architecture, training data, data quality, and benchmarking.
- Lead model capability development across multiple product concepts, aligning model priorities with product goals.

Model Capability Lead

Jan 2024 – Dec 2025

- Led development of strategic predictive modeling solutions for R&D needs.
- Managed a cross-functional team of 8–9 computational biologists and machine learning scientists building AI-enabled models; mentored junior colleagues.

Platform Manager, Computational Biology

Jan 2023 – Jan 2024

- Built a team of 10+ computational biologists and data analysts across the US and Ghent, Belgium; developed strategic initiatives to expand computational biology capabilities for R&D; mentored junior scientists.

Data Analytics & Automation Lead, Science Platform

Oct 2020 – Jan 2023

- Led and managed the Data Analytics & Automation team, developing team members to strengthen bioinformatics support across R&D; partnered cross-functionally to expand data analytics and high-throughput automation capabilities.

Scientist II, Computational Biology

Jan 2019 – Sep 2020

- Major contributor to the Inari maize HapMap, used across science and product teams (**Game Changer Award**, 2020).
- Built population-genetics methods to annotate deleterious SNPs and prioritize variants for CRISPR-Cas editing, leading to a patent application; characterized maize germplasm and annotated plant genomes.

Postdoctoral Researcher · University of California, Davis (Ross-Ibarra Lab)

Jun 2016 – Dec 2018

- Population genomics of structural variation in teosinte; adaptation and functional constraint in plant genomes.
- Collaborated on the NSF-funded Panzea project linking genotype and phenotype in maize.

PhD Research Assistant · University of Florida (Barbazuk Lab)

Sep 2010 – May 2016

- Characterized the genome-wide alternative splicing landscape of maize and other monocots (first-author papers in *Genetics* and *Frontiers in Plant Science*); dissertation provided preliminary data for NSF Plant Genome Research Program award #1547787.
- Integrated epigenomic and transcriptomic data to study splicing regulation; contributed to the NSF-funded *Amborella* and maize W22 reference genome projects.

PATENT APPLICATIONS (8, all assigned to Inari Agriculture)

1. Model for selecting guide RNA molecules. WO2026055608A1 (2026). Inventor 2 of 6.
2. Soybean with improved nodulation. WO2025193889A1 (2025). First inventor.
3. Enhanced nodulation in soybeans. WO2025259666A1 (2025). · Promoter edited soybean plants. WO2025264908A1 (2025).
4. In-frame deletions for modulating protein activity in plants. WO2025128748A1 (2025).
5. Morphogenic regulator combinations for improved plant transformation. WO2025122750A1 (2025). · Morphoregulators for regeneration of maize somatic embryos. WO2023178300A2 (2023).
6. Methods and systems for assessing genetic variants. WO2021035164A1 (2021). Major contributor; deleterious-variant annotation.

SELECTED PUBLICATIONS (19 peer-reviewed; full list at wenbinmei.github.io)

1. Springer NM, Anderson SN, ..., **Mei W**, ..., Brutnell TP. The maize W22 genome provides a foundation for functional genomics and transposon biology. *Nature Genetics* 50:1282–1288 (2018).
2. **Mei W**, Boatwright L, Feng G, Schnable JC, Barbazuk WB. Evolutionarily conserved alternative splicing across monocots. *Genetics* 207:465–480 (2017). Cover article.
3. **Mei W**, Liu S, Schnable JC, Yeh CT, Springer NM, Schnable PS, Barbazuk WB. A comprehensive analysis of alternative splicing in paleopolyploid maize. *Frontiers in Plant Science* 8:694 (2017).
4. Gault CM, Martin F, **Mei W**, et al. Aberrant splicing in maize *rough endosperm3* reveals a conserved role for U12 splicing in eukaryotic multicellular development. *PNAS* 114:E2195–E2204 (2017). MaizeGDB Editor's Choice.
5. Amborella Genome Project (incl. **Mei W**). The *Amborella* genome and the evolution of flowering plants. *Science* 342:1241089 (2013).

EDUCATION

PhD, Botany (Computational Biology) · University of Florida, 2016

MS, Biology · Central Washington University, 2010

BS, Biology · Nanjing Normal University, 2007

SKILLS

Leadership & strategy: computational biology strategy and model roadmaps; building and scaling cross-functional teams across sites; aligning model priorities with R&D and product goals; partnering with executive leadership; mentoring.

AI & modeling: agentic AI for biological design; large language models and biological foundation models; sequence-expression-function-phenotype models; benchmarking and training-data strategy; statistical genomics.

AI-enabled computational biology: target discovery; CRISPR-Cas multiplex edit design; population, functional and comparative genomics; systems biology and multi-omics.

SERVICE

Biology Leadership Council, University of Florida (2023 – present).

Peer review: 36 verified reviews for 18 journals, incl. *The Plant Cell*, *Molecular Plant*, *Genetics*, *G3*, *MBE*.

Inari guilds: Bioinformatics (organizer, 2020); Plant Breeding & Population Genetics (co-organizer, 2019).

CERTIFICATIONS

Generative AI: Working with Large Language Models · Large Language Models: Text Classification for NLP using BERT.

HONORS

Game Changer Award, Inari (2020) · CLAS Dissertation Fellowship, Univ. of Florida (2015) · Graduate School Preeminence Award, Univ. of Florida (2010 – 2014) · Summer Institute in Statistical Genetics Scholarship (2014)

Languages: English (professional), Mandarin & Wu Chinese (native)