liangwei.yin@cea.fr | yinliangwei1@gmail.com | +33 07 52 72 42 60

YIN, LIANGWEI (he/him)

A computational biologist aims to uncover novel molecular mechanisms and treatment targets for complex diseases, with diverse bioinformatics skills: multi-omics analysis, network biology, survival analysis, methods development, machine learning.

Education

Ph. D.	University Grenoble Alpes, France	2025.12
-Visiting PhD Student	University of Helsinki	2025.05-2025.06
M.Sc. Bioinformatics	Miami University, USA	2021.12
B.Sc. Biotechnology	Hubei University of Chinese Medicine, China	2018.06

Research Experience

02/2023-12/2025 PhD Candidate

Bioinformatics and machine learning/ Advisor: Dr. Christophe Battail

Summary of this role: designed, and performed computational experiments in modeling treatment response of advanced kidney cancers.

Project I: Network Modeling of Immunotherapy Response in Kidney Cancer

a. Designed and led a study applying sample-specific gene co-expression networks (ssGCNs) to identify molecular patterns of immunotherapy response in advanced kidney cancer.
b. Inferred and validated individual gene networks using the SWEET method.
c. Refined network distance by referencing cohort-level gene networks to associate with survival outcomes and treatment efficacy.
d. Generated gene connectivity and gene association matrices; performed unsupervised clustering of patients and correlated network features with somatic mutations and clinical variables.
e. Developed novel entropy and centrality metrics to quantify pathway perturbations using sample-specific pathway networks.
f. Integrated network-derived features with gene expression in machine learning models, improving immunotherapy response prediction across tumor sites using leave-one-out cross-validation and cross-study testing.

Project II: Transcriptional Assessment of **Immune-Infiltrated Tumor Organoids** in Clear Cell Renal Cell Carcinoma (ccRCC)

a. Conducted differential expression analysis across tumor tissue, dissociated tumors, PDTOs, and immune-infiltrated PDTOs to identify key transcription factors and pathways.
b. Applied gene ontology (GO) and GSEA to characterize molecular transitions during organoid formation and immune infiltration.
c. Evaluated immune signatures using ESTIMATE and ssGSEA for 28 immune cell types, quantifying tumor purity, and immune landscape.
d. Predicted immunotherapy responsiveness using TIDE scores and expression profiling of immune checkpoints, T cell exhaustion markers, and tumor-intrinsic features.

Project III: Cell-Type-Specific Gene Regulatory Networks in Tumor Progression (In collaboration with Dr. Marieke L. Kuijjer)

a. Curated and preprocessed public single-cell RNA-seq data of 437,747 cells in ccRCC; performed clustering and annotated cell types via canonical markers.
b. Reconstructed cell-type-specific gene regulatory networks using Scorpion, identifying key TF–target interactions associated with tumor grade (ISUP).
c. Quantified TF and gene influence via outdegree/indegree metrics; visualized GRNs and mapped interactions into sample-specific networks (via LIONESS) for TCGA-KIRC bulk RNA-seq.
d. Conducted clustering and survival analysis using intersected gene regulatory features to identify

prognostic signatures.

Skills: gene co-expression network construction, gene regulatory network construction, graph theory, survival models, unsupervised clustering, supervised learning, single sample pathway scores, immunotherapy predictive signatures, cell deconvolution.

08/2019-12.2021 Master Graduate Assistant
Cellular, Molecular, Structural Biology/Advisor: Dr. Meixia Zhao

Focus: Comparative genomics, chromatin dynamics, and mutation effects on recombination in maize.

Project I: Comparative Genomics of Maize Subgenomes

a. Analyzed genomic, epigenomic, and transcriptomic features of duplicated genes across maize subgenomes, focusing on pericentromeric and chromosomal arm regions.
b. Identified subgenome blocks and quantified gene duplications, transposable elements (TEs), and recombination rates; computed Ka, Ks, and ω to evaluate evolutionary divergence.
c. Conducted transcriptomic and proteomic profiling to determine dominant homeolog expression.
d. Assessed epigenetic landscapes by analyzing TE proximity, TE content, and methylation patterns using whole-genome bisulfite sequencing (WGBS) and small RNA-seq.
e. Performed ChIP-seq analysis to examine enrichment of histone marks (H2A.Z, H3K4me1, H3K4me3, H3Kac) over duplicated gene regions.
f. Investigated chromatin accessibility by comparing accessible chromatin region (ACR) distributions and intensities near homeologs; used Hi-C data to evaluate chromatin loop associations and their evolutionary conservation across subgenomes.
g. Studied evolutionary consequences of conserved ACRs' retention or deletion on expression of homologous genes.

Project II: Effects of ***mop1*** **Mutation** on Recombination in Maize

a. Conducted DNA extraction and sample preparation for resequencing to evaluate recombination patterns in mop1 mutants versus wildtype lines.
b. Performed indel marker-based genotyping to quantify recombination frequency across genomic intervals.
c. Carried out SNP calling and variant analysis to investigate genome-wide recombination differences influenced by RNA-directed DNA methylation deficiency (mop1 mutation).

Skills: Maize fieldwork; Genotyping; Python (numpy, pandas, matplotlib), MySQL; cloud computing (ohio supercomputer center), Linux; DNA-seq, RNA-seq, Chip-seq, whole genome Bisulfite-seq and small RNA-seq analysis; BWA, GATK, Bcftools, Hisat2, Cufflinks, HTSeq, MACS2, ChromHMM, Bismark, Bowtie/Bowtie2, Bedtools.

Teaching

Co-Instructor, *University Grenoble Alpes (UGA), France*

- **AI4omics (2024):** Co-taught 4-hour publication review on the integration of AI and multi-omics in biomedical research.
- **Biotechnology of DNA System – Introduction to Bioinformatics (2023–2024):** Delivered 20 hours of instruction across two years, covering biotechnology principles and practical data analysis for life science master students.

Teaching Assistant, *Miami University, Ohio, USA*

- **BIO256 – Introduction to Bioinformatics (2021):** Supported hands-on instruction in sequence analysis and functional annotation.
- **BIO115 & BIO116 – Introductory Biology Lab (2020–2021):** Led undergraduate lab sessions on basic experimental techniques and biological concepts.

Conference & Workshop

liangwei.yin@cea.fr | yinliangwei1@gmail.com | +33 07 52 72 42 60

ISMB/ECCB 2025 – Liverpool, UK
Poster: Transcriptomic evaluation of immune-infiltrated patient-derived tumor organoids as preclinical models in ccRCC

3D Cell Cultures & Bioinformatics Methods Workshop 2024 – Grenoble, France
Talk: Gene expression and co-expression network analysis in tumor models

COBICA 2024 – Grenoble, France
Poster: Sample-specific gene co-expression network (ssGCN) analysis reveals immunotherapy response patterns in kidney cancer

ISMB/ECCB 2023 – Lyon, France
Attendee

63rd Annual Maize Genetics Meeting 2021 – Virtual
Poster: Comparative genomic analysis of maize subgenome reveals minimal pericentromeric bias

Industry

Data Analyst – *Shanghai Transmedia* (Clinical Data) | *2019, 2022*
- Collected, filtered, and analyzed clinical datasets for pharmaceutical clients.
- Collaborated with marketing teams of large pharmaceutical companies, including Johnson & Johnson.

Clinical Coordinator – *Mingma Shanghai (Genetic Consulting) | 2018*
- Managed clinical data for rare disease cases and coordinated between researchers and management.
- Oversaw product tracking forms and ensured adherence to product quality standards.
- Gained exposure to ACMG guidelines and workflows in clinical genetic counseling.

Award & Service

IDEX Mobility Scholarship, *University Grenoble Alpes — 2024*
Awarded for research internships in computational biology.

Doctoral Student Funding, *EDISCE Doctoral School — 2024*
Travel/research grant (350 USD equivalent) to support PhD-related activities.

Peer Reviewer, *HELIYON, BIOINFORMATICS ADVANCE — 2024–Present*
Conducted peer reviews, contributing to the evaluation of manuscripts in computational biology.

Publication

Yin, L., Lugand, L., Russick, J., Lemaoult, J., & Battail, C. (2025). Transcriptomic evaluation of immune-infiltrated patient-derived tumor organoids as preclinical models in renal cell carcinoma (Manuscript in preparation).

Yin, L., Traversa, P., Elati, M., Moreno, Y., Marek-Trzonkowska, N., & Battail, C. (2025). Sample-specific network analysis identifies gene co-expression patterns of immunotherapy response in clear cell renal cell carcinoma. *iScience*.

Hasan, M.M., **Yin, L**., Wang, M. *et al. mop1* affects maize recombination landscapes by modulating methylation of MITEs near genes in open chromatin. *Nat Commun* 16, 10476 (2025).

Li, T., **Yin, L.,** Stoll, C. E., Lisch, D., & Zhao, M. (2023). Conserved noncoding sequences and de novo Mutator insertion alleles are imprinted in maize. *Plant Physiology*, *191*(1), 299-316.

Yin, L., Xu, G., Yang, J., & Zhao, M. (2022). The heterogeneity in the landscape of gene dominance in maize is accompanied by unique chromatin environments. *Molecular Biology and Evolution*, 39(10), msac198.

liangwei.yin@cea.fr | yinliangwei1@gmail.com | +33 07 52 72 42 60

Zhao, M., Ku, J. C., Liu, B., Yang, D., **Yin, L**., Ferrell, T. J., ... & Lisch, D. (2021). The mop1 mutation affects the recombination landscape in maize. *Proceedings of the National Academy of Sciences*, *118*(7), e2009475118.

Reference

Christophe Battail, Advisor,
Research Director, IRIG - CEA Grenoble,
christophe.battail@cea.fr

Eric Bonnet, CSI member,
Research Director, François Jacob Institute of biology,
bonnet@cnrgh.fr

Natalia Marek-Trzonkowska, Co-Advisor,
Professor, University of Gdańsk,
natalia.marek-trzonkowska@ug.edu.pl