YIN LIANGWEI

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

EDUCATION

PhD student	University Grenoble Alpes. France	2025.12
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 student

Bioinformatics and machine learning/ Advisor: Dr. Christophe Battail

Project I: Sample-specific gene co-expression network (ssGCN) analysis identifies gene co-expression patterns of immunotherapy response in advanced kidney cancer

a. Adjusted network distance in Pearson Correlation-Based ssGCNs

- Inference and validation of sample-specific networks using an existing method (SWEET).
- Adjusted network distance using different cohort-level gene networks.
- Correlated adjusted network distance with survival probability and treatment response.

b. Gene connectivity and gene-gene associations

- Gene connectivity and gene association matrix were generated from ssGCNs.
- Unsupervised clustering of patients using selected network features.
- Evaluation of network features in terms of somatic mutation and clinical features.

c. Sample-specific pathway level entropy and centrality scores

- Refine the entropy by the distribution of edges inside sample-specific pathway networks.
- Weigh the influence of gene connectivity and gene associations inside pathway networks.
- Identify significant perturbed pathway based on pathway entropy and topology scores.

d. Network features improved gene-expression-based ML for predicting treatment response

- Leave One Out Cross Validation to assess the predictive power of network features.
- Across-study prediction using network features from primary sites of tumor to predict treatment response of tumor metastasis.

Project II: Transcriptomic evaluation of immune-infiltrated patient-derived tumor organoids as preclinical models in clear cell renal cell carcinoma (ccRCC)

a. Differential gene expression analysis for the formation of patient-derived tumor organoids (PDTOs)

- Identify differential genes, TFs, and pathways in the comparisons between tumor tissue, dissociated tumors, PDTO, and infiltrated-PDTOs.
- Gene ontology and gene set enrichment analysis for identified DEGs.

b. Tumor and immune signatures of infiltrated-PDTOs

- Simplified pathway signatures of ccRCC subtypes in tumor tissue and infiltrated-PDTO.
- Employed the ESTIMATE algorithm to infer immune infiltration level and tumor purity.
- Performed single sample gene set enrichment analysis (ssGSEA) of 28 immune cells to quantify immune infiltrating level.

c. Prediction of immunotherapy response

- Performed TIDE score to identify responder and non-responder.

- Examined the expression of predictive genes, including immune checkpoints, T cell exhaustion genes, tumor-intrinsic mutators, and etc.

Project III: Cell-type gene regulatory networks along tumor progression in ccRCC

a. Curation of publicly available single cell data of ccRCC.

- Integration, quality control, and batch effect adjustment of single cell data, composing 437,747 cells.
- Clustering and cell type annotation using canonical cell markers.

b. Construction of Cell-type gene regulatory networks using Scorpion.

- Identify significant interactions between TFs and target genes along tumor grade (ISUP grade).
- Identify TFs and genes by outdegree and indegree, associated with tumor progression.
- Visualization of gene regulatory network.

c. Mapping cell-type gene interaction into sample-specific network

- Construction of sample-specific gene regulatory networks using Lioness for bulk-seq data from TCGA-KIRC.
- Identification of cell-type gene interaction using the intersection between cell-specific interactions, cell-specific genes, and sample specific interactions.
- Clustering and survival analysis based on intersected cell-type interactions for bulk-seq samples

Skills: gene co-expression network construction, gene regulatory network construction, network 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

Project I: Analysis of maize subgenomes reveals no pronounced bias in pericentromeric regions

a. Evolutionary features of whole genome duplicated genes in different genomic locations

- Identify subgenome blocks and compare number of duplicates, transposons (TEs), and recombination rates of duplicates.
- Calculate and compare evolutionary rates (nucleotide substitution rates: Ka, Ks, w).
- Transcriptome and protein abundance profiling of dominant expressed homeologs.

b. Epigenetic features of duplicated genes in different genomic locations

- Examine genome-wide TE variation: the distance of duplicates to its nearest TEs and the proportion of TE contents over the flanking regions of duplicates.
- Dissect RNA-directed DNA methylation pathway: whole genome bisulfite sequencing (WGBS) analysis and small RNA analysis.
- Perform ChIP-seq analysis to explore the enrichment of covalent histone marks (H2A.Z, H3K4me1, H3Kme3, H3Kac) over duplicates.

c. Distribution and evolution of chromatin accessible regions (ACRs) of two subgenomes

- Compare the distribution of ACRs flanking duplicates and peak values of ACRs.
- Compare chromatin loops of distal ACRs to duplicates from HIC-seq data.
- Identify syntenic ACRs in maize subgenomes and compare their evolutionary rates (K).
- Examine effects of the retention and deletion of conserved ACRs on its targeted homologous genes.

Project II: *Mop1* mutation affects recombination rates in maize

a. Sample preparation for DNA resequencing experiments.

b. Examine recombination rates of *mop1* mutant and wildtype by genotyping with indel markers.
c. SNPs (single nucleotide polymorphism) calling analysis.

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.

PROFESSIONAL EXPERIENCE

Data analyst Shanghai Transmedia (Clinical data) 2019, 2022

- Tracked, collected, filtered, and analyzed clinical data
- Worked directly with the marketing from big pharmacy companies such as Johnson

Clinical coordinator Mingma Shanghai (Genetic Consulting) 2018

- Sorting out clinical information of rare-disease patients
- Manage product tracking forms and ensure product quality
- Serve as the coordinator between researchers and the managers
- Learn the workflow of genetic counseling in ACMG

TEACHING EXPERIENCE

2024/2023 Co-Instructor (20 hours)
AI4omics, University Grenoble Alpes
Biotechnology of DNA system (Intro. Bioinformatics), University Grenoble Alpes

2021/2020/2019 Teaching Assistant
BIO115, 116, 256 (Intro. Bioinformatics, intro Biology Lab), Miami University

PUBLICATION

Liangwei Yin, Léonard Lugand, Jules Russick, Joel Lemaoult, Christophe Battail. (2025). Transcriptomic evaluation of immune-infiltrated patient-derived tumor organoids as preclinical models in renal cell carcinoma. (In preparation)

Yin, L., Traversa, P., Elati, M., Moreno, Y., Marek-Trzonkowska, N., & Battail, C. (2024). Sample-specific network analysis identifies gene co-expression patterns of immunotherapy response in clear cell renal cell carcinoma. (biorxiv ► *iScience*)

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, Liangwei, Gen Xu, Jinliang Yang, and Meixia Zhao. "The heterogeneity in the landscape of gene dominance in maize is accompanied by unique chromatin environments." *Molecular Biology and Evolution* 39, no. 10 (2022): msac198.

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.

JOURNAL REVIEWER

HELIYON (36), 2024-2025