Tianyuan Liu | Computational Genomics Researcher

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About

Computational genomics researcher specializing in long-read sequencing technologies and transcriptome analysis. Part of the LongTREC (Long-read Transcriptomics Research and Education Consortium) Marie Skłodowska-Curie Actions program. Research focuses on developing computational methods for analyzing long-read RNA sequencing data, with particular expertise in isoform regulatory biology and multiomics integration.

Education

Institute for Integrative Systems Biology   **Spanish National Research Council (CSIC-UV)**
PhD Student & Early Stage Researcher, Valencia, Spain   *2023–Present*
Advisor: Dr. Ana Conesa
LongTREC Marie Skłodowska-Curie Actions program
Focus: Long-read multiomics methods for isoform regulatory biology

Huazhong Agricultural University (HZAU)   **China**
Bachelor of Engineering in Bioengineering   *2016–2020*
Comprehensive education in bioengineering with focus on computational biology and bioinformatics applications

Research Focus

Main Topic: Long-read multiomics methods to understand isoform regulatory biology

Areas: Quality control methods, isoform detection, epigenome profiling, transcriptome assembly, differential analysis

Research Experience

Institute for Integrative Systems Biology, CSIC-UV   **Valencia, Spain**
PhD Student & Early Stage Researcher   *2023–Present*
Developing computational methods for isoform regulatory biology
Contributing to major software projects like SQANTI3
Collaborating with international research networks

University of Florida, Genetics Institute   **USA**
Research Experience   *2019–2020*
Supervised by Dr. Ana Conesa and Dr. Guillem Ylla
Working on MirCure project for microRNA quality control and curation methods

Publications

Peer-Reviewed Articles..

1. **Liu, T.**, & Conesa, A. (2025). Profiling the epigenome using long-read sequencing. *Nature Genetics*, 57(1), 27–41.
2. Monzó, C., **Liu, T.**, & Conesa, A. (2025). Transcriptomics in the era of long-read sequencing. *Nature Reviews Genetics*, 1–21.
3. Pardo-Palacios, F.J., Arzalluz-Luque, A., Kondratova, L., Salguero, P., Mestre-Tomás, J., Amorín, R., Estevan-Morió, E., **Liu, T.**, et al. (2024). SQANTI3: curation of long-read transcriptomes for accurate identification

of known and novel isoforms. *Nature Methods*, 21(5), 793–797.

4. Pardo-Palacios, F.J., Wang, D., Reese, F., Diekhans, M., Carbonell-Sala, S., ..., **Liu, T.**, ..., Conesa, A. (2024). Systematic assessment of long-read RNA-seq methods for transcript identification and quantification. *Nature Methods*, 21(7), 1349–1363.
5. Mestre-Tomás, J., **Liu, T.**, Pardo-Palacios, F., & Conesa, A. (2023). SQANTI-SIM: a simulator of controlled transcript novelty for lrRNA-seq benchmark. *Genome Biology*, 24(1), 286.
6. **Liu, T.**, Salguero, P., Petek, M., Martínez-Mira, C., Balzano-Nogueira, L., Conesa, A., et al. (2022). PaintOmics 4: New tools for the integrative analysis of multi-omics datasets supported by multiple pathway databases. *Nucleic Acids Research*, 50(W1), W551–W559.
7. **Liu, T.**, Balzano-Nogueira, L., Lleó, A., & Conesa, A. (2020). Transcriptional differences for COVID-19 disease map genes between males and females indicate a different basal immunophenotype relevant to the disease. *Genes*, 11(12), 1447.
8. Ylla, G., **Liu, T.**, & Conesa, A. (2020). MirCure: a tool for quality control, filter and curation of microRNAs of animals and plants. *Bioinformatics*, 36(Supplement_2), i618–i624.

Preprints & Under Review...

9. **Liu, T.**, Paniagua, A., Jetzinger, F., Ferrández-Peral, L., Frankish, A., & Conesa, A. (2025). Transcriptome Universal Single-isoform COntrol (TUSCO): A Framework for Evaluating Transcriptome Reconstruction Quality. *bioRxiv*, 2025.08.23.671926. (Under review at *Nature Communications*)

Conference Presentations

2025: Transcriptome Universal Single-isoform Control (TUSCO): A Framework for Evaluating Transcriptome Quality. *Oral presentation*, ISMB/ECCB 2025, Liverpool, United Kingdom. Track: iRNA: Integrative RNA Biology.

Major Projects

SQANTI3
Comprehensive quality control and curation pipeline for long-read transcriptomes. Contribution: Report generation and documentation.
SQANTI-SIM
Simulator of controlled transcript novelty for long-read RNA-seq benchmarking. Contribution: Added PBSIM integration to the simulation framework.
PaintOmics 4
Advanced web-based platform for integrative analysis of multi-omics datasets with support for multiple pathway databases. Technologies: JavaScript, web-based interface, multi-omics integration.
MirCure
Specialized tool for microRNA quality control, filtering, and curation in both animals and plants. Language: R, bioinformatics pipeline.
DeCovid
Tool for conducting wide-spread transcriptional analysis for COVID-19 Disease Map genes. Features: Differential expression analysis, GO enrichment, interactive web interface.

Technical Skills

Programming Languages...
Python, R, JavaScript, HTML/CSS, Bash/Shell

Technologies & Tools..
PacBio, Oxford Nanopore, Bioconductor, Docker, Git/GitHub, Nextflow, Conda/Mamba

Data Analysis & Methods...
Statistical analysis, machine learning, data visualization, pipeline development, reproducible research

High-Performance Computing...
SLURM, cluster workflows, cloud integration

Last updated: October 3, 2025