

TIANYUAN LIU

Computational Genomics · MSCA Doctoral Fellow, I2SysBio (CSIC–Universitat de València)
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Computational genomics researcher developing quality-control and benchmarking methods for long-read transcriptomics and epigenomics; first author of TUSCO (*Nature Communications*, 2026), PaintOmics 4 (*Nucleic Acids Research*, 2022) and a *Nature Genetics* review of long-read epigenome profiling (2025); contributor to the LRGASP long-read benchmark (*Nature Methods*, 2024). Combines method development with hands-on single-molecule epigenomics: established Hia5/Fiber-seq chromatin-accessibility profiling at the bench. PhD defence expected late 2026.

EDUCATION

2023–2026 PhD in Bioinformatics

Institute for Integrative Systems Biology (I2SysBio), CSIC–Universitat de València, Valencia, Spain
Thesis: long-read multiomics methods for isoform regulatory biology. Supervisor: Prof. Ana Conesa.

2021–2023 MPhil

School of Engineering, Cardiff University, Cardiff, United Kingdom
Supervisor: Dr Peter Theobald. Built a multi-tissue transcriptomic atlas of porcine postnatal development from 1,924 PigGTEx RNA-seq profiles, and modelled its cross-species transferability.

2016–2020 BEng in Bioengineering

Huazhong Agricultural University, Wuhan, China

RESEARCH EXPERIENCE

2023–2026 Marie Skłodowska-Curie Doctoral Fellow

Genomics of Gene Expression Lab (Prof. A. Conesa), I2SysBio, CSIC–Universitat de València
Quality-control and benchmarking methods for long-read transcriptomics (TUSCO, SQANTI3, SQANTI-SIM) and epigenomics (SQANTI-EPI); LLM-based interpretation of multi-omics networks (TELLME).

DEC 2024 Research Secondment

Nicassio Lab, Center for Genomic Science, IIT@SEMM (IFOM–IEO Campus), Milan, Italy
LongTREC MSCA secondment, Dec 2024–Feb 2025: wet-lab single-molecule epigenomics. Established Hia5 directed-methylation (Fiber-seq) chromatin-accessibility profiling on H1 hESC and HEK293 cell lines; delivered a draft SOP to the host lab.

2019–2020 Research Intern

Genetics Institute, University of Florida, Gainesville, FL, USA
MirCure: quality control and curation of animal and plant microRNAs (sup. A. Conesa, G. Ylla).

PUBLICATIONS

T Liu = candidate; entries led by T Liu are first-author. 8 research articles (4 first-author) · 2 reviews (1 first-author).

Peer-reviewed original research (8)

- 2026 T Liu, A Paniagua, F Jetzinger, L Ferrández-Peral, A Frankish, A Conesa. “TUSCO: benchmarking transcriptome reconstruction with endogenous single-isoform controls” *Nature Communications*.
- 2026 T Liu, R Lei, IM Khan, P Theobald. “Tissue identity is the dominant determinant of cross-species transferability of a porcine developmental programme” *BMC Genomics*.
- 2024 FJ Pardo-Palacios, D Wang, F Reese, ..., T Liu, ..., A Conesa. “Systematic assessment of long-read RNA-seq methods for transcript identification and quantification” *Nature Methods* 21(7), 1349–1363.
- 2024 FJ Pardo-Palacios, A Arzalluz-Luque, ..., T Liu, et al. “SQANTI3: curation of long-read transcriptomes for accurate identification of known and novel isoforms” *Nature Methods* 21(5), 793–797.
- 2023 J Mestre-Tomás, T Liu, F Pardo-Palacios, A Conesa. “SQANTI-SIM: a simulator of controlled transcript novelty for long-read RNA-seq benchmarking” *Genome Biology* 24(1), 286.

- 2022 **T Liu**, P Salguero, ..., A Conesa. "PaintOmics 4: new tools for the integrative analysis of multi-omics datasets supported by multiple pathway databases" *Nucleic Acids Research* 50(W1), W551–W559.
- 2020 **T Liu**, L Balzano-Nogueira, A Lleo, A Conesa. "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.
- 2020 G Ylla, **T Liu**, A Conesa. "MirCure: a tool for quality control, filter and curation of microRNAs of animals and plants" *Bioinformatics* 36(Suppl. 2), i618–i624.

Reviews and perspectives (2)

- 2025 **T Liu**, A Conesa. "Profiling the epigenome using long-read sequencing" *Nature Genetics* 57(1), 27–41.
- 2025 C Monzó, **T Liu**, A Conesa. "Transcriptomics in the era of long-read sequencing" *Nature Reviews Genetics* 26(10), 681–701.

SOFTWARE

Lead developer

- IN DEV. **SQANTI-EPI** — quality control for long-read epigenomic data (Fiber-seq, m6A).
- 2026 **TUSCO** — transcriptome benchmark using endogenous single-isoform controls.
- 2022 **PaintOmics 4** — web platform for pathway-based integrative multi-omics analysis.
- 2020 **MirCure** — quality control, filtering and curation of animal and plant microRNAs.

Contributor

- 2024 **SQANTI3** — reference QC and curation framework for long-read transcriptomes; report module, docs.
- 2023 **SQANTI-SIM** — simulator of controlled transcript novelty; PBSIM integration.

AI systems

- IN DEV. **TELLME** — multi-agent LLM service (ELIXIR, co-developer) turning multi-omics networks and enrichment results into citation-grounded narratives.
- IN DEV. **AutoRefactor** — autonomous AI refactoring agent (founder) combining static analysis, automated test generation and mutation testing, with Git-native atomic rollback.

GRANTS AND FELLOWSHIPS

- 2023–2026 **Marie Skłodowska-Curie Doctoral Fellowship**
Horizon Europe MSCA Doctoral Networks — LongTREC (grant agreement No. 101072892)
 Named doctoral fellow, competitively awarded within the LongTREC Doctoral Network. Network meetings: Nice (2024), Barcelona mid-term (2025), Norwich (2025).

TALKS AND PRESENTATIONS

Invited

- Nov 2026 **SEBiBC 2026, Toledo, Spain**
 Invited workshop talk: "AI-assisted improvements in code efficiency and sustainability" (forthcoming).

Contributed (talk)

- 2026 **ISMB 2026, Washington, DC, USA**
 "SQANTI-epi: functional and quality annotation of single-molecule epigenomic data." HiTSeq track.

- 2026 **VALT 2026, Valencia, Spain**
 “SQANTI-Epi: single-molecule chromatin accessibility for transcriptomics.”
- 2025 **ISMB/ECCB 2025, Liverpool, United Kingdom**
 “TUSCO: a framework for evaluating transcriptome reconstruction quality.” iRNA track.
- OCT 2024 **LRUA24, Uppsala, Sweden**
 “Transcript identification and quantification.” LongTREC workshop at Long-Read Sequencing Uppsala.

Posters

- OCT 2025 **JB1 2025, Madrid, Spain**
 “TUSCO: a framework for evaluating transcriptome reconstruction quality.”
- OCT 2024 **SEBiBC 2024**
1st Congress of the Spanish Society of Bioinformatics and Computational Biology, Feria Valencia, Spain
 “BUGSI: benchmarking universal genes with single isoforms — a framework for evaluating transcriptome quality.” Poster with flash talk (C-0344).
- SEP 2024 **ECCB 2024, Turku, Finland**
 “SQANTI-SIM: a simulator of controlled transcript novelty for long-read RNA-seq benchmarking.” Poster 729.

TEACHING AND SERVICE

Instruction

- JUN 2026 **Instructor, VALT 2026 Summer Course**
I2SysBio, Valencia, Spain
 Long-read epigenomics and quality-control evaluation.
- OCT 2025 **Workshop instructor**
I2SysBio, Valencia, Spain
 Institute workshop: “How to Make Your Science Easier with AI Support”.
- 2025 **Instructor, LongTREC Summer School**
Earlham Institute, Norwich, United Kingdom
 Data quality and QC metrics; hands-on long-read mapping and QC with SQANTI-reads.

Service

- 2024–2025 **Coordinator, LongTREC seminar series**
 Organized the consortium’s monthly internal webinar across its 12 partner institutions.
- OCT 2024 **Coordinator, LRUA24 LongTREC workshop**
 Coordinated LongTREC fellow contributions to the workshop programme at LRUA24, Uppsala.

Supervision

- 2026 **Supervisor, MSc thesis (TFM)**
Máster en Bioinformática y Ciencias de Datos, ENS-ISCIII, Madrid, Spain
 AlphaFold modelling of novel long-read transcripts (G. Potel Sebastián, Jun–Dec 2026, I2SysBio).
- 2025 **Co-mentor, MSc student**
Genomics of Gene Expression Lab, I2SysBio, Valencia, Spain
 Co-mentored a Master’s student (W. Maessen).

TECHNICAL SKILLS

Programming — Python, R, Rust, JavaScript, Bash/Shell.

Bioinformatics — Nextflow, Snakemake, Bioconductor, Conda/Mamba, Docker, Git; PacBio SMRT and Oxford Nanopore.

AI & machine learning — LLM application design; RAG and GraphRAG; knowledge graphs (LangChain, Neo4j); transformers; gradient-boosted trees (LightGBM, XGBoost).

Wet-lab — mammalian cell culture (H1 hESC, HEK293), nuclei isolation, Hia5/Fiber-seq library prep, high-molecular-weight (HMW) DNA extraction; BSL-2 certified.