

Marcelo HURTADO

BIOENGINEER

PhD student in COMPUTATIONAL BIOLOGY & BIOINFORMATICS

EDUCATION

Oct 2023

PhD student

- Paul Sabatier University, Toulouse, France
- Cancer Research Center of Toulouse (CRCT)
- **Team:** NetB(IO)² | **Supervisor:** Vera Pancaldi
- **Project:** Reinforcement learning approaches to control the tumor microenvironment

Current achievements:

- Develop a multiscale ABM of NLC-CLL differentiation using the **Physicell** software ([Github repository](#)).
- Develop a **Python** and **Bash** pipeline for Physicell model exploration (including parameter exploration, sensitivity analysis and genetic algorithms) for running in **HPC arquitectures** ([Github repository](#)).
- Apply basic reinforcement learning algorithms into the NLC-CLL model to evaluate cancer cell concentration
- Develop an advanced machine learning framework in **R** to extract clinically relevant features from bulk RNAseq data ([pipeML](#))

Jan 2017

Dec 2023

B.Sc Bioengineering - Mention in Biotechnology

- Universidad de Ingenieria y Tecnologia UTEC Lima, Peru.
- **Courses:** Synthetic Biology, Biomedical signals, Medical robotics, bioprocesses, biofluids mechanics.

Aug 2021

Dec 2021

Exchange Program | Biotechnology and Biomedical Engineering

- Instituto de Estudios Superiores Tecnologicos de Monterrey - Monterrey, Mexico.
- **Courses:** Genetic engineering, neuroengineering, biomedical imaging

RESEARCH EXPERIENCE

Apr 2023
Oct 2023

Bioinformatics Engineer | Cancer Research Center of Toulouse (CRCT)

- **Team:** NetB(IO)² | **Principal Investigator:** Vera Pancaldi
- **Tasks:** Analysis of transcriptomics data to evaluate patient profiles of early and late stage NSCLC patients.
- **Achievements:** Develop a novel framework for characterizing TME patient profiles by constructing transcriptional regulatory networks (TRNs) based on inferred transcription factor (TF) activity and cell type deconvolution from bulk RNA-seq data ([CellITFusion](#)).

Hurtado M et al. (2024). Transcriptomics profiling of the non-small cell lung cancer microenvironment across disease stages reveals dual immune cell-type behaviors. *Front. Immunol.* 15:1394965. doi: 10.3389/fimmu.2024.1394965

Jan 2022
March 2022

Intern of Bioinformatics | Cancer Research Center of Toulouse (CRCT)

- **Team:** NetB(IO)² | **Principal Investigator:** Vera Pancaldi
- **Tasks:** Analysis of tumor cell composition on NSCLC patients using computational tools based on transcriptomics data.
- **Achievements:** Develop of an algorithm that integrates a combination of multiple first or second-generation deconvolution methods and several cell type signatures to ensure robust and accurate profiling of cell composition starting from bulk RNAseq data ([multideconv](#)).

Jan 2021
Aug 2021

Research Assistant | Universidad de Ingenieria y Tecnologia UTEC Lima, Peru.

- **Department:** Bioengineer Department | **Supervisor:** Dr. Alberto Donayre
- **Tasks:** Design of a bioactive polymer based on self-assembling and antimicrobial peptides for wound applications.
- **Achievements:** Propose a genetic cassette for the production of self-assembling peptides with antimicrobial properties via the implementation of genetic engineering techniques and cloning methods ([Gibson assembly, restriction enzymes, golden gate](#)).



Awards and achievements

AWARDS AND ACHIEVEMENTS

- 1 Prix de la Fondation Silab Jean Paufique
- 2 Best poster presentation award
- 3 Campus France - France Excellence Eiffel PhD scholarship
- 4 Toulouse Foundation Cancer Sante - PhD scholarship
- 5 CARe Graduate School Univ. Paul Sabatier - Doctoral School Fellowship
- 6 CARe Graduate School Univ. Paul Sabatier - M2 internship fellowship
- 7 Research for Peruvian Undergraduates (REPU) program - International stage fellowship
- 8 iGEM Design League - Gold medal, Best Human Practices, Best aligned with SGD
- 9 ERASMUS+ Fellowship

ORAL PRESENTATIONS

01/12/2025 04/12/2025	<i>CellTFusion: A novel approach to unravel cell states via cell type deconvolution and TF activity estimated from bulk RNAseq data identifies clinically relevant cell niches</i> Bioinformatics and Computational Biology Conference - Napoli, Italy.
26/11/2025 28/11/2025	<i>Estimating tumour microenvironment cellular states from bulk RNAseq produces biomarkers of clinical outcome across stages</i> 21èmes Journées annuelles du Cancéropôle GSO - Agen, France.
20/07/2025 24/07/2025	<i>CellTFusion: A novel approach to unravel cell states via cell type deconvolution and TF activity estimated from bulk RNAseq data identifies clinically relevant cell niches</i> European Conference on Computational Biology - ISMB/ECCB 2025 - Liverpool, UK.
07/11/2024	<i>"CellTFusion: Transcriptional regulatory networks unravel cell states from immune cell type deconvolution and uncovers cell niches predictive of cancer progression"</i> Journee Bioinfo/Biostat GenoToul - Toulouse, France.
26/11/2023 01/12/2023	<i>"Transcriptional regulatory networks unravel cell states from immune cell type deconvolution and uncovers cell niches predictive of cancer progression"</i> EMBO Workshop Computational models of life: From molecular biology to digital twins Sant Feliu de Guíxols, Spain.
22/11/2023 24/11/2023	<i>"Transcriptional regulatory networks unravel cell states from immune cell type deconvolution and uncovers cell niches predictive of cancer progression"</i> 19th Annual Meeting of the Canceropole GSO - Arcachon, France. ★
25/09/2023 29/09/2023	<i>"Transcriptional regulatory networks unravel cell states from immune cell type deconvolution and uncovers cell niches predictive of cancer progression"</i> Institut Curie Computational Systems Biology of Cancer 6th edition - Paris, France. ★

COURSES AND WORKSHOPS

02/12/2024 06/12/2024	Health Data Challenge 2024: Multimodal data integration to quantify tumor heterogeneity in cancer research. Aussois, France.
29/06/2024 05/07/2024	14th Summer school on medicines. University of Sao Paulo, Ribeirao Preto Medical School.
21/04/2024 26/04/2024	Computational Systems Biology for Complex Human Disease: from static to dynamic representations of disease mechanisms. Wellcome Genome Campus, Hinxton, United Kingdom.
26/11/2023 01/12/2023	EMBO Workshop. Computational models of life: From molecular biology to digital twins. Sant Feliu de Guíxols, Spain.
25/09/2023 29/08/2023	6th course on Computational Systems Biology of Cancer: models of data, data for models. Institut Curie, Paris, France.



PUBLICATIONS

Marku, M.*, Chenel, H.*,..., **Hurtado M.**, et al. Data driven network inference and longitudinal transcriptomics unveil dynamic regulation in Chronic Lymphocytic Leukaemia models. *npj Syst Biol Appl* (2026). <https://doi.org/10.1038/s41540-025-00645-4>

Bertin A*, Bucher E*, ..., **Hurtado M.**, et al. (2025). PhysiGym: bridging the gap between the Gymnasium reinforcement learning application interface and the PhysiCell agent-based model software. *bioRxiv* 2025.09.18.677030; doi: <https://doi.org/10.1101/2025.09.18.677030>

Hurtado M., et al. (2025). multideconv - Integrative pipeline for cell type deconvolution from bulk RNAseq using first and second generation methods. *bioRxiv*. <https://doi.org/10.1101/2025.04.29.651220>

Hurtado M.*, Khajavi L*., et al. (2024). Transcriptomics profiling of the non-small cell lung cancer microenvironment across disease stages reveals dual immune cell-type behaviors. *Front. Immunol.* 15:1394965. doi: 10.3389/fimmu.2024.1394965

SOFTWARE DEVELOPMENT

- **multideconv**: R pipeline for cell type deconvolution from bulk RNAseq using first and second generation methods.
- **pipeML**: A robust R machine learning pipeline for classification tasks and survival analysis.
- **CellTFusion**: R package for the integration of immune-cell type deconvolution features and prior-knowledge networks of TFs-gene interactions to characterize potential cell states of the tumor microenvironment using bulk RNAseq data.

LEADERSHIP & OUTREACH



Team leader - iGEM Desing League 2021 Synthetic Biology competition.

Project LECCHAIN: Improving vaccine thermal tolerance and stability of SARS-CoV-2 antigen using plant lectins.

Press release:

- [Centro Bio](#)
- [Peru21](#)
- [Press coverage](#)
- [ElComercio](#)

Team leader - Synthetic biology group 2020 | Universidad de Ingenieria y Tecnologia UTEC Lima, Peru.

MENTORING

Assistant Professor - Computation and Informatics Tools in Bioinformatics.
CINVESTAV - IPN (Online).

REFERENCES

Dr. Vera **PANCALDI**

Principal Investigator (NetBIO)
Cancer Research Center of Toulouse
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Dr. Leila **KHAJAVI**

Bioinformatics Department, Evotec.
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Dr. Alfredo **CARDENAS-RIVERA**

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Northeastern University, Boston-USA
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Awards and achievements