




Marcelo HURTADO

BIOENGINEER


PhD student in COMPUTATIONAL BIOLOGY & BIOINFORMATICS

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EDUCATION

Oct 2023	<div>PhD student </div> <ul style="list-style-type: none">Paul Sabatier University, Toulouse, FranceCancer Research Center of Toulouse (CRCT)Team: NetB(IO)² Supervisor: Vera PancaldiProject: Reinforcement learning approaches to control the tumor microenvironment <div>Current achievements:</div> <ul style="list-style-type: none">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 architectures (Github repository).Apply basic reinforcement learning algorithms into the NLC-CLL model to evaluate cancer cell concentrationDevelop an advanced machine learning framework in R to extract clinically relevant features from bulk RNAseq data (pipeML)
Jan 2017 Dec 2023	<div>B.Sc Bioengineering - Mention in Biotechnology</div> <ul style="list-style-type: none">Universidad de Ingenieria y Tecnologia UTEC Lima, Peru.Courses: Synthetic Biology, Biomedical signals, Medical robotics, bioprocesses, biofluids mechanics.
Aug 2021 Dec 2021	<div>Exchange Program Biotechnology and Biomedical Engineering</div> <ul style="list-style-type: none">Instituto de Estudios Superiores Tecnologicos de Monterrey - Monterrey, Mexico.Courses: Genetic engineering, neuroengineering, biomedical imaging

RESEARCH EXPERIENCE

Apr 2023 Oct 2023	<div>Bioinformatics Engineer Cancer Research Center of Toulouse (CRCT)</div> <ul style="list-style-type: none">Team: NetB(IO)² Principal Investigator: Vera PancaldiTasks: 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 (CellTFusion). <div>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</div>
Jan 2022 March 2022 Aug 2022 Feb 2023	<div>Intern of Bioinformatics Cancer Research Center of Toulouse (CRCT) </div> <ul style="list-style-type: none">Team: NetB(IO)² Principal Investigator: Vera PancaldiTasks: 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	<div>Research Assistant Universidad de Ingenieria y Tecnologia UTEC Lima, Peru.</div> <ul style="list-style-type: none">Department: Bioengineer Department Supervisor: Dr. Alberto DonayreTasks: 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

- ★ 1 Prix de la Fondation Silab Jean Paufigue
- ★ 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

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|--------------------------|--|
| 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

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|--------------------------|---|
| 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. ★8 ★9 ★10

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)
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Dr. Leila **KHAJAVI**
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★ Awards and achievements