

Exploring Computational Oncology: A Journey from evolutionary biology to Drug Discovery

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Oncology Research

Guest lecture in Applied Mathematics and Informatics in Drug Discovery

University of Basel

My background and current role

Colombia, Zapatoca



2016

PhD in Life Sciences, UNIL - SIB

Computational biology in plant evolution

Nicolas Salamin

2011

Bachelor and Master in Biology in Colombia

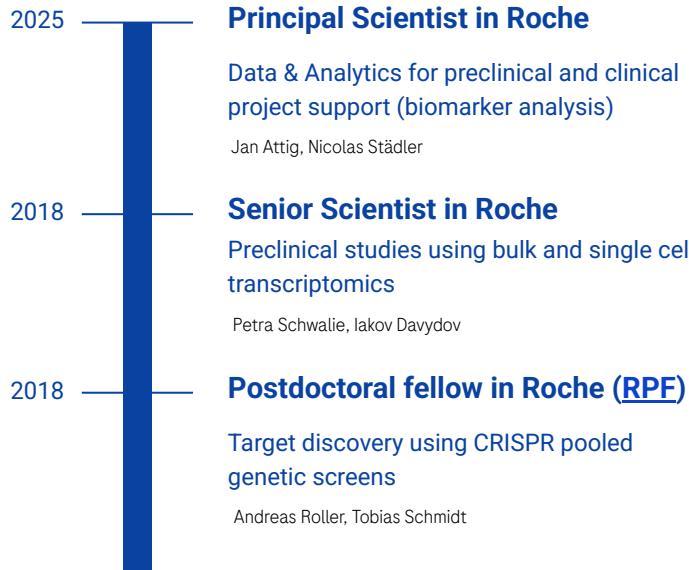
Domestication and genetic diversity of Lima beans in the Americas

Maria Isabel Chacón

Colombia, Zapatoca



Journey from evolutionary biologist to clinical research and development



A key lesson: the principles of modeling, data analysis, and understanding complex, adaptive systems—which I learned in evolutionary biology—are the exact same principles I apply today to human cancer

Pharma research and early development pRED

A global team of scientists dedicated to translating science into medicines

2,900

Employees around the world



Five innovation centres

Basel, Zurich, Munich, New York and Welwyn



Our pipeline consists of approximately **50% LMs¹, 35% SMs² and 15% RMs³, ADCs⁴ and GTs⁵**



pRED has delivered many “**firsts**” for Roche and with that created **new opportunities**

155 publications

in 2024 with at least one of the main authors being from pRED

Since 2014, **> 8,000,000 patients** have been treated with pRED molecules



We are uniquely positioned to apply **artificial intelligence and machine learning**



Multiple disease areas

Cardiovascular and Metabolism, Immunology, Infectious Diseases, Neuroscience, Oncology, Ophthalmology and Rare Diseases

96 patent applications

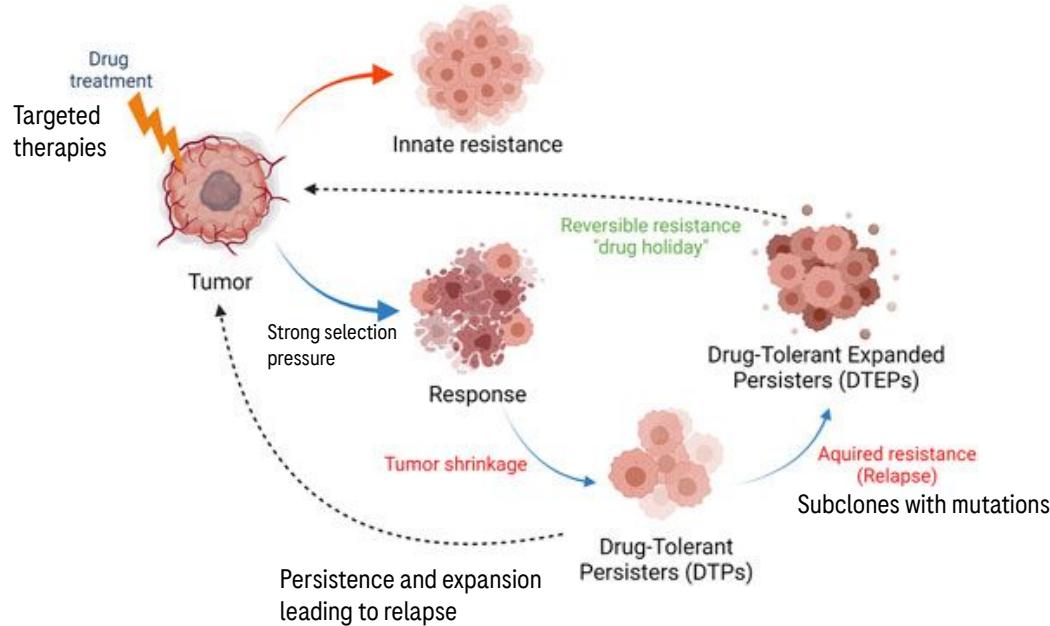
for new inventions in 2024



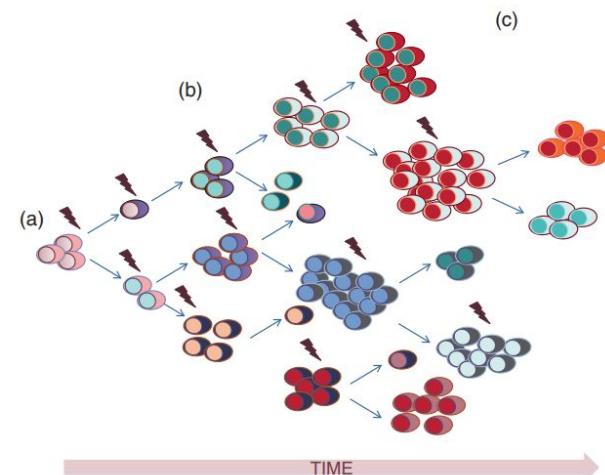
What drives me, what is the challenge?

My motivation and the grand challenge

The evolutionary arms race of cancer

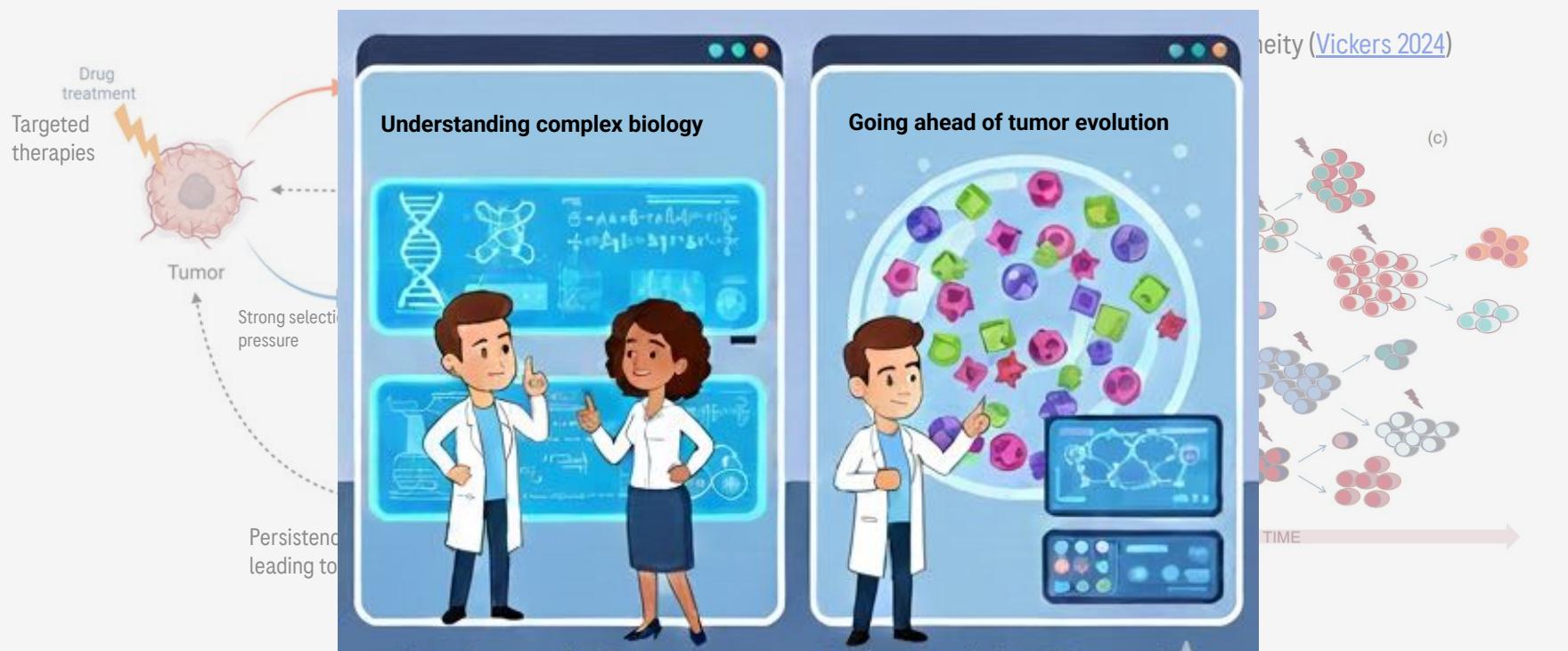


Tumor heterogeneity ([Vickers 2024](#))



My motivation and the grand challenge

The evolutionary arms race of cancer

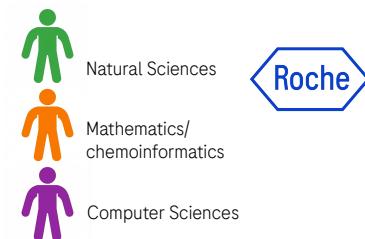




How [computational] oncology drug discovery works?

What do we do at Roche?

How drug discovery works and what is my contribution... and how our skills are essential

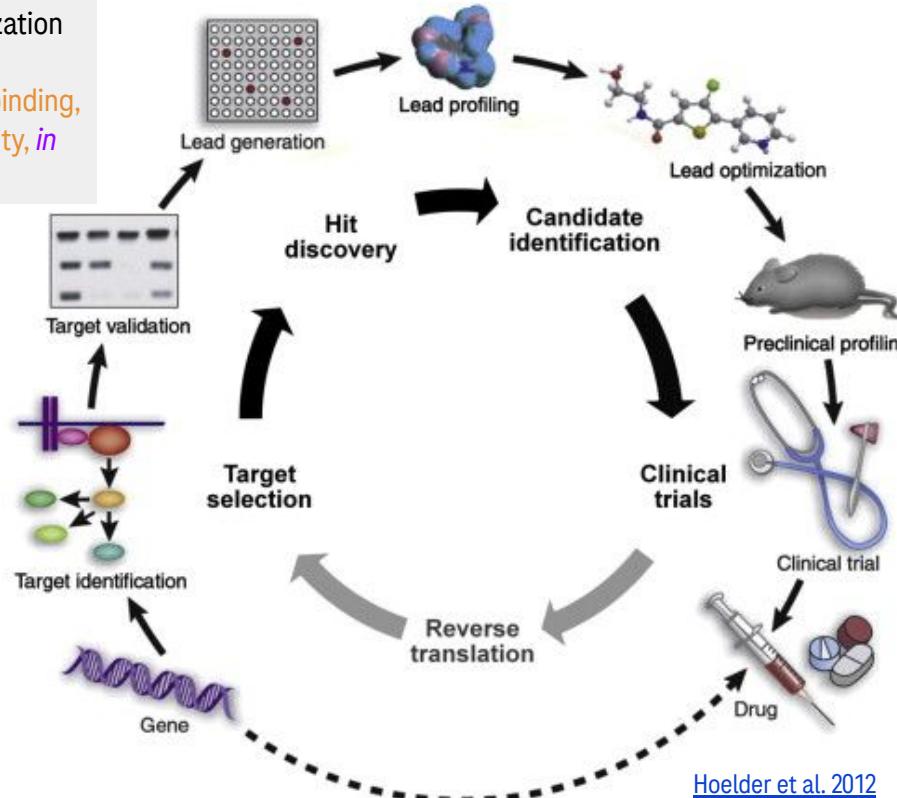


Molecule production, characterization and performance:

Compound screening for protein binding, compound stability and selectivity, *in* *silico* binding prediction.

Target Identification and validation
requires disease understanding,
hypothesis generation and validation

Does target contribute to cancer growth?
Will inhibition lead to tumor regression or increased survival?

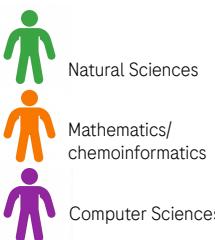


Preclinical models Confidence on growth inhibition, target modulation, safety

Clinical trial execution, patient monitoring, reverse translation
Hypothesis-driven trials
Understanding of resistance and finding predictive biomarkers

What can we do next?

The power of scale (data), modeling, and hypothesis generation

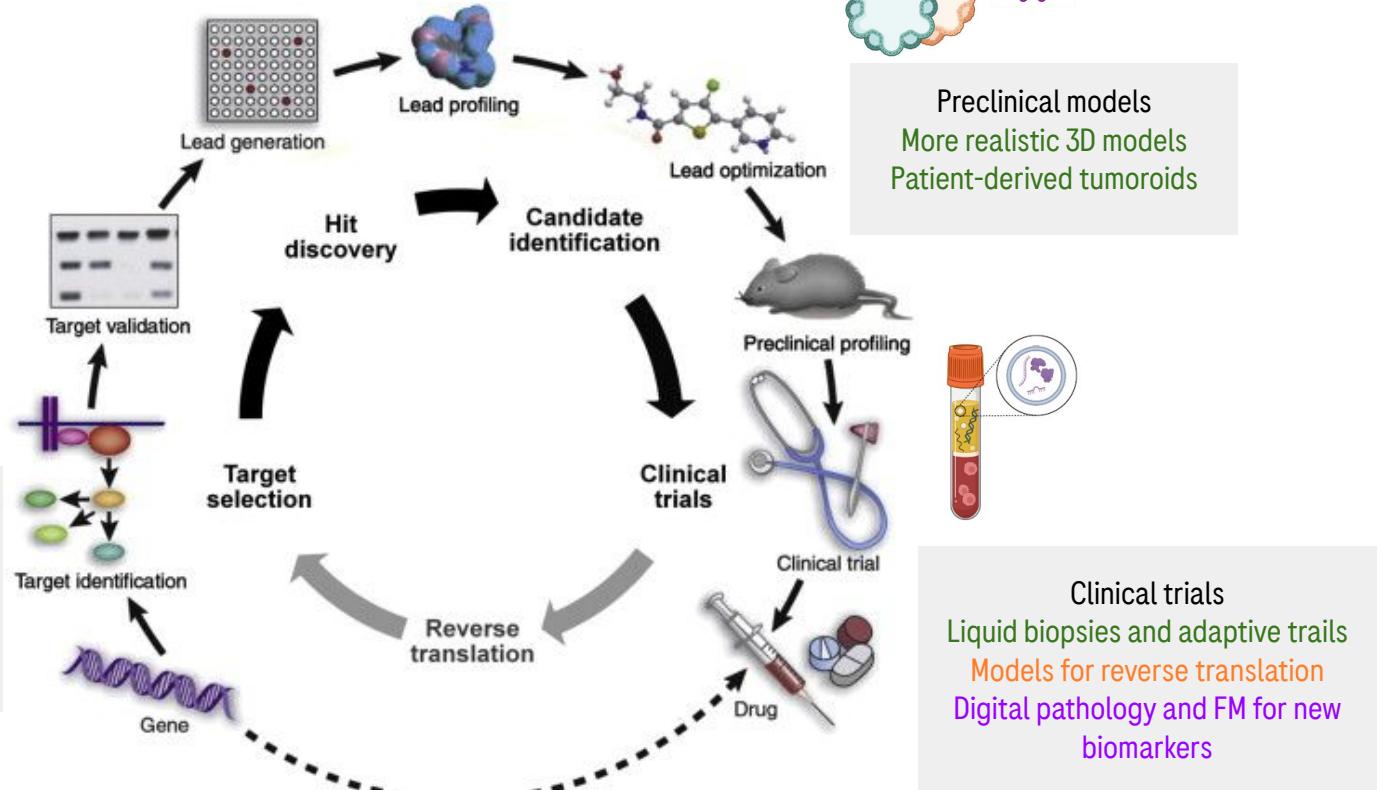


Target Identification and validation

Drug repurposing

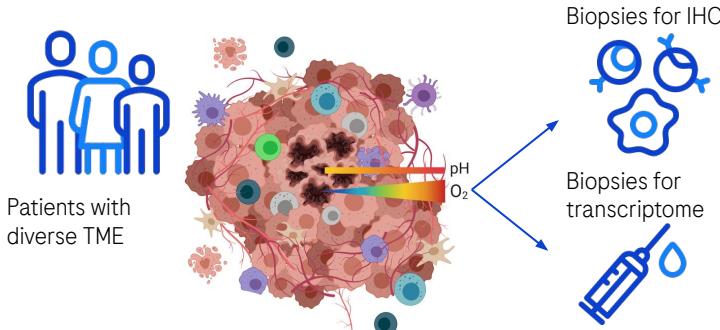
Understanding disease states (scRNA)

In-silico perturbations



Transcriptome-based classifier for TME and patients outcome

Roller et al. 2024

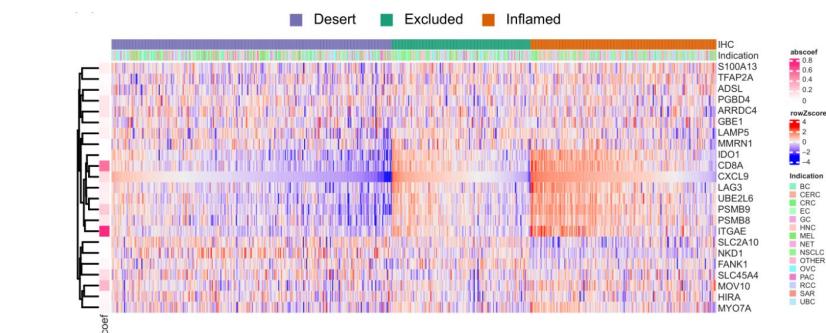
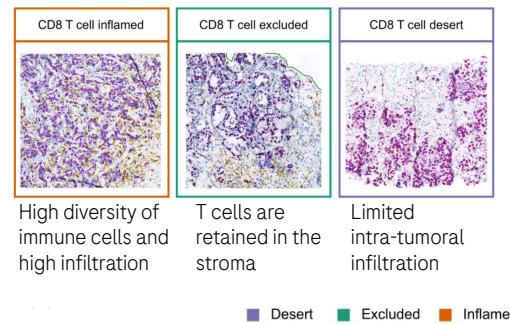


We developed a transcriptome-based classifier that could accurately **predict different spatial CD8+T cell infiltration** patterns in the TME



TME: Tumor micro environment

IHC: Immunohistochemistry staining



Inflamed phenotypes → immune cells, fibroblasts, endothelial and mast cells.
Desert phenotypes → stromal genes and immunosuppressive environment
 Classifier has lower performance for **excluded** in which spatial relationships are more difficult to capture by bulk transcriptomics.



Lessons learned and tips

My key lessons learned

What are good skills?



Learn to speak multiple languages

Biology, code, maths,
communication between
collaborators in a project is key



High-performing algorithms
don't matter if they are
biologically implausible,
or based on biased-data



Power of collaboration

Team sport, only the synergy
of disciplines: computational
prediction and experimental
findings bring us success

Tips for our path

My favorite to go Ten simple rules for doing a postdoc in pharma (Zhang 2021)

| | |
|---|---|
| Embrace the mess | Real world & experimental data is dirty, master data wrangling |
| 80/20 rule | 80% of our impact comes from 20% of our data, models and code. Focus on interpretability and robustness |
| Take a biology class | Focus on systems/molecular biology, genomics, built your biological intuition |
| Learn R and Python, code is our new pipette | Learn version control (Git), command-line environment, workflow engines |
| Get comfortable with probabilities | Computational biology needs understanding p-values, confidence intervals and null hypotheses |



We need the rigor (math), the efficiency (CS), and the domain knowledge (Nat Sci) to solve the world's most critical health problems, only in that way we can build the future of medicine.

“She stood in the storm, and when the wind did not blow her way, she adjusted her sails.”

- Elizabeth Edwards

Doing now what patients need next

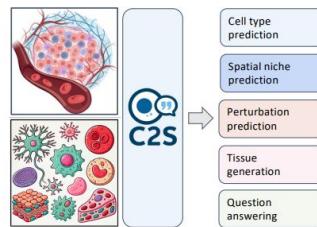
For what do we use LLM?



• Scaling Large Language Models For Next-Generation Single-Cell Analysis Van Dijk lab @ Yale

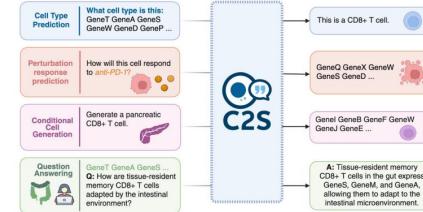
Vision: Teaching LLMs to Simulate the Virtual Cell

- Model **predicts** cellular responses under context
- **Integrates** multimodal data (genomics, text, spatial, drugs)
- Conditions on **microenvironment** (cytokines, neighbors, tissue)
- **Natural-languagee** interface for reasoning & design



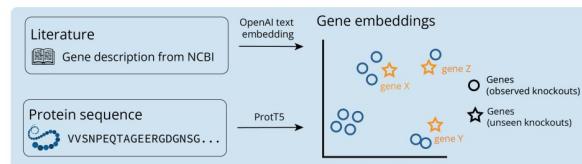
Cell2Sentence: LLMs that Learn Single-Cell Biology

- **Analogy:** Genes ≈ Words | Cells ≈ Sentences | Tissues ≈ Paragraphs.
- Cell2Sentence (*ICML, 2024*): Training LLMs directly on massive single-cell datasets (>50M cells).
- **Capabilities:** Deep semantic understanding of cell types, states, gene programs. Enables “reading” and “writing” biology.



• LLM for unseen perturbation prediction Kaspar Märtens

LLM embedding approach



Our last year's work [1] showed that **LLM-derived gene embeddings**

- **Literature** embeddings, using NCBI gene descriptions [2]
- **Protein sequence** embeddings

are informative for unseen perturbation outcome prediction, and outperformed existing methods

[1] Märtens et al (2024), Enhancing generative perturbation models with LLM-informed gene embeddings

[2] Chen, & Zou (2024). GenePT: a simple but effective foundation model for genes and cells built from ChatGPT

Slides taken from a workshop, please do not distribute, see at the material published.

How to prepare for this career path?

Pointers to Pharma postdoc programs

- Take every opportunity to learn
- Always balance decisions on what makes the most impact (for your career and others) but mostly what makes you happy!
- Ten simple rules for doing a postdoc in pharma

“Change is constant”:
reorganization or
reprioritization

“Collaboration,
collaboration” ...
common goal

“Final reward or incentive” in
industry requires extensive
disciplines collaboration.

Expansion of your
personal network
(interdisciplinary)