

VITTORIO ZAMPINETTI

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ACADEMIC EXPERIENCE

Ph.D. student

Applied Math and Computational Biology

November 2021-

Politecnico di Torino, Italy

- Summary: My research involves the definition and analysis of Bayesian inference algorithms such as Variational Inference, as well as maximum likelihood methods (EM), which enable the reconstruction of cancer evolutionary trees from high-dimensional and inherently noisy data. Additionally, I develop efficient methods for sampling trees and generate synthetic data for testing implementations before the application on real data.
- Co-tutelle PhD programme with KTH, Stockholm, under the supervision of Jens Lagergren.
- During summer 2023, I have been a visiting researcher at Memorial Sloan Kettering Cancer Center in New York, in [Sohrab Shah lab](#), working on analysis of whole-genome sequencing data.

MSc

Data Science and Engineering

2019 - 2021

Politecnico di Torino, Italy

- Part of the [ASP](#) programme.
- One-year Erasmus programme at KTH in Stockholm.
- [Master thesis](#) on copy-number aware clonal tree reconstruction using single cell RNA sequence.

BSc

Computer Engineering

2016 - 2019

Università di Firenze, Italy

- [Thesis](#) on the development of an automated tool for cell measurement in 3D images acquired by confocal light sheet microscopy.

ARTICLES

Main author, RECOMB 2024

Accepted article, Oral Presentation

April 2024

Conference at MIT Boston

- Summary: [The paper](#) presents the first Bayesian framework for joint inference of copy number evolution and clonal trees.
- Coordinate Ascent VI (CAVI) and Importance sampling based framework.
- Introduces a novel sampler for labeled directed trees named LARS.

TEACHING

Politecnico di Torino, Italy

Main Teaching Assistant (TA) in [Statistical Models](#).

2021 - 2024

TECHNICAL STRENGTHS

Programming Languages

Python, C/C++, Java, R, Javascript, Matlab

Languages

Italian (fluent), English (fluent), Swedish (basic)

Tools/libraries

L^AT_EX, PyTorch, TensorFlow, JAX, Pyro, NetworkX, Jupyter, MPI, Unix, Vim, Git, HPC clusters