

# Xiang Ge (Xiangge) Luo

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## Education

### ETH Zurich

#### PHD CANDIDATE IN COMPUTATIONAL BIOLOGY

- Thesis: Modeling tumor mutation trees for evolution-guided precision oncology
- Advisor: Prof. Dr. Niko Beerenwinkel | Second advisor: Dr. Jack Kuipers
- Doctoral committee: Prof. Dr. Benjamin Raphael, Prof. Dr. Jasmine Foo

Basel, Switzerland

2020.11 - 2025.12

### ETH Zurich

#### MASTER OF SCIENCE IN STATISTICS

- GPA: 5.88/6 – Graduated with distinction
- Thesis: Learning Bayesian networks from ordinal data
- Advisor: Dr. Jack Kuipers

Zurich, Switzerland

2018.09 - 2020.09

### University of Waterloo

#### BACHELOR OF MATHEMATICS

- GPA: 92% – Graduated with distinction, Dean's Honours List

Waterloo, Canada

2013.09 - 2018.04

## Research Experience

### Computational Biology Group, ETH Zurich

#### SCIENTIFIC ASSISTANT

- Advisor: Prof. Dr. Niko Beerenwinkel
- Developed mathematical and statistical models to infer cancer evolution from cross-sectional single-cell phylogenies, aiming to predict drug resistance and facilitate evolution-guided precision oncology.

Basel, Switzerland

2020.11 - present

### Institute of Molecular Systems Biology, ETH Zurich

#### SEMESTER STUDENT

- Advisor: Prof. Dr. Mattia Zampieri
- Analyzed E. coli drug response metabolomics data to investigate regulatory and functional relationships between metabolites.

Zurich, Switzerland

2019.03 - 2019.07

### Seminar for Statistics, ETH Zurich

#### STATISTICS LAB STUDENT

- Advisor: Dr. Markus Kalisch
- Analyzed mouse experimental data using mixed models to assess bone loss and identify early osteoporosis markers.

Zurich, Switzerland

2019.03 - 2019.06

### Department of Statistics and Actuarial Science, University of Waterloo

#### UNDERGRADUATE RESEARCHER

- Advisor: Prof. Dr. Alexander Schied
- Derived the Nash equilibrium for risk-averse investors in a market impact game with transient price impact and quadratic transaction costs over finite and infinite horizons.

Waterloo, Canada

2017.09 - 2017.12

## Awards & Scholarships

2025	ISMB/ECCB 2025 Ian Lawson Van Toch Memorial Award for Best Student Paper, ISCB	United Kingdom
2025	ISMB/ECCB 2025 Conference Fellowship & Dependent Care Grant, ISCB (USD 950)	United Kingdom
2024	SIB Remarkable Outputs 2023 Award, Swiss Institute of Bioinformatics	Switzerland
2018	Undergraduate Student Research Award, NSERC (CAD 4,500)	Canada
2018	President's Research Award, University of Waterloo (CAD 1,500)	Canada
2016	President's International Experience Award, University of Waterloo (CAD 1,500)	Canada
2014	Isabel Farrar Undergraduate Entrance Scholarship, University of Waterloo (CAD 4,000)	Canada
2014	President's Scholarship of Distinction, University of Waterloo (CAD 2,000)	Canada

## Publications

**Xiang Ge Luo**, Jack Kuipers, Kevin Rupp, Koichi Takahashi and Niko Beerenwinkel. Bayesian inference of fitness landscapes via tree-structured branching processes. *Bioinformatics*, 41:i160-i169, 2025. **(ISMB/ECCB 2025, acceptance rate 17%)**

**Xiang Ge Luo**, Jack Kuipers and Niko Beerenwinkel. Joint inference of exclusivity patterns and recurrent trajectories from tumor mutation trees. *Nature Communications*, 14:3676, 2023. (**RECOMB 2022**, acceptance rate 21.3%)

**Xiang Ge Luo**, Giusi Moffa and Jack Kuipers. Learning Bayesian networks from ordinal data. *Journal of Machine Learning Research*, 22:1-44, 2021.

**Xiangge Luo** and Alexander Schied. Nash equilibrium for risk-averse investors in a market impact game with transient price impact. *Market Microstructure and Liquidity*, 5:2050001, 2020.

## Conferences, Seminars & Workshops

2025.07	<b>Contributed talk</b> , ISMB/ECCB 2025 Conference	Liverpool, UK
	• Bayesian inference of fitness landscapes via tree-structured branching processes	
2025.04	<b>Poster</b> , 6th Zurich Precision Oncology Symposium	Zurich, Switzerland
	• FiTree: fitness inference from single-cell phylogenies applied to acute myeloid leukemia data	
2025.03	<b>Invited talk</b> , D-BSSE Departmental Seminar Series, ETH Zurich	Basel, Switzerland
	• Fitness inference from single-cell phylogenies using tree-structured branching processes	
2025.02	<b>Contributed talk</b> , PhyloBasel Seminar Series, ETH Zurich	Basel, Switzerland
	• Bayesian inference of fitness landscapes via tree-structured branching processes	
2024.06	<b>Award talk</b> , SIB Days – The Swiss Bioinformatics Summit	Virtual
	• Mining tumor mutation trees with TreeMHN for evolution-guided precision oncology	
2023.06	<b>Contributed talk</b> , SKINTEGRITY.CH Annual Retreat	Spiez, Switzerland
	• Joint inference of exclusivity patterns and recurrent trajectories from tumor mutation trees	
2022.06	<b>Contributed talk</b> , Mutual Hazard Networks Workshop	Virtual
	• Joint inference of exclusivity patterns and recurrent trajectories from tumor mutation trees	
2022.05	<b>Contributed talk</b> , RECOMB 2022 Conference	San Diego, USA
	• Joint inference of exclusivity patterns and recurrent trajectories from tumor mutation trees	
2022.04	<b>Contributed talk</b> , OLISSIPO Exchange Week	Lisbon, Portugal
	• Joint inference of exclusivity patterns and recurrent trajectories from tumor mutation trees	
2022.03	<b>Poster</b> , Ascona Workshop 2022	Ascona, Switzerland
	• Joint inference of exclusivity patterns and recurrent trajectories from tumor mutation trees	

## Teaching

Spring 2023	<b>Teaching Assistant</b> , Statistical Models in Computational Biology	ETH Zurich
Spring 2022	<b>Head Teaching Assistant</b> , Statistical Models in Computational Biology	ETH Zurich
Spring 2022	<b>Teaching Assistant</b> , LSZGS Advanced Block Course Computational Biology	ETH Zurich
Spring 2021	<b>Teaching Assistant</b> , Statistical Models in Computational Biology	ETH Zurich

## Supervision

2025	<b>Marie Dogo</b> , Master Student, Mines Paris - PSL
2023	<b>Laura Quintas</b> , Master Student, INESC-ID (Co-supervised with Monica Baciu-Dragan)
2023	<b>Laurenz Keller</b> , Master Student, ETH Zurich (Co-supervised with Pawel Piotr Czyn)
2022	<b>Jiayi Wang</b> , Master Student, ETH Zurich (Co-supervised with Pawel Piotr Czyn)

## Academic Services

**Journal Reviewer** for Genome Research, Bioinformatics      **Conference Reviewer** for RECOMB, ISMB

## Languages and Skills

<b>Coding</b>	Python, R, C++, MATLAB, Git, Snakemake, bash, $\text{\LaTeX}$
<b>Languages</b>	English (working proficiency), Mandarin (native), Cantonese (native)