# Fabio Zanini

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## Research

**Group Leader, Data Driven Biomedicine lab, University of New South Wales**, since Fall 2019.

Single cell analyses of infection, immunology, and lung development; machine learning on cell atlases.

**Postdoctoral Scholar in Bioengineering, Stanford University**, 2016-2019.

*Research topic*: Single-cell transcriptomics of *flavivirus* infection *in vitro* and *in vivo*.
*P.I.*: Prof. Stephen R. Quake

**PhD in Bioinformatics, Max Planck Institute for Developmental Biology and Universität Tübingen**, 2015.

*Thesis*: Population Genomics of Intrapatient HIV Evolution.
*Supervisors*: Dr. Richard Neher and Prof. Daniel Huson

**M.Sc. and Diplom in Physics, Università degli Studi di Trento and Universität Tübingen**, 2011.

**B.Sc. in Physics, Università degli Studi di Trento**, 2008.

## Selected Publications

Google Scholar: `https://scholar.google.com/citations?user=XMDw5-4AAAAJ` (469 citations, h-index 13).

Github: `https://github.com/iosonofabio/` (70+ repositories).

F. Zanini *et al.*, S. R. Quake, C. M. Alvira, D. N. Cornfield. Progressive Increases in Mesenchymal Cell Diversity Modulate Lung Development and are Attenuated by Hyperoxia. bioRxiv (2021)

F. Zanini *et al.*, D. N. Cornfield, S. R. Quake, C. M. Alvira. Phenotypic diversity and sensitivity to injury of the pulmonary endothelium during a period of rapid postnatal growth. bioRxiv (2021)

Z. Yao*, F. Zanini* *et al.*, S. R. Quake, S. Einav. The transcriptional landscape of Venezuelan equine encephalitis virus (TC-83) infection. PLOS NTD (2021)

The Tabula Muris Consortium (F. Zanini: Logistical coordination, Organ collection and processing, Computational data analysis, Writing group). A single-cell transcriptomic atlas characterizes ageing tissues in the mouse. Nature (2020)

F. Zanini*, B. Berghuis*, R. C Jones, B. Nicolis di Robilant, R. Y Nong, J. Norton, M. F Clarke, S. R. Quake. northstar: leveraging cell atlases to identify healthy and neoplastic cells in transcriptomes from human tumors. Scientific Reports (2020)

R. Domingo-Gonzales*, F. Zanini*, X. Che, M. Liu, R. C. Jones, M. A. Swift, S. R. Quake, D. N. Cornfield, C. M. Alvira. Diverse homeostatic and immunomodulatory roles of immune cells in the developing mouse lung at single cell resolution. eLife (2020)

F. Zanini*, M. Robinson*, D. Croote, M. Kumar Sahoo, A. M Sanz, E.Ortiz-Lasso, L. Luis Albornoz, F. R Suarez, J. G Montoya, L. Goo, B. A Pinsky, S. R. Quake, S. Einav. Virus-inclusive single cell RNA sequencing reveals the molecular signature predictive of progression to severe dengue. PNAS (2018)

The Tabula Muris Consortium (F. Zanini: as above). Single-cell transcriptomics of 20 mouse organs creates a Tabula Muris. Nature (2018)

F. Zanini, S. Y. Pu, E. Bekerman, S. Einav, S. R. Quake. Single-cell transcriptional dynamics of flavivirus infection. eLife (2018)

F. Zanini, J. Brodin, J. Albert, R. A Neher. Error rates, PCR recombination, and sampling depth in HIV-1 whole genome deep sequencing. Virus research (2017)

F. Zanini, V. Puller, J. Brodin, J. Albert, R. A. Neher. In vivo mutation rates and the landscape of fitness costs of HIV-1. Virus Evolution (2017)

F. Zanini J. Brodin, L. Thebo, C. Lanz, G. Bratt, J. Albert, R. A Neher. Population genomics of intrapatient HIV-1 evolution. eLife 4 (2015)

F. Zanini and R. A. Neher. Quantifying selection against synonymous mutations in HIV-1 env evolution. Journal of virology (2013)

F. Zanini and R. A. Neher. FFPopSim: an efficient forward simulation package for the evolution of large populations. Bioinformatics (2012)

# Patents

F. Zanini *et al.* Antibodies against dengue virus and related methods, US Provisional Application No. 62/715,628 (2018)

# Grants and Awards

US National Institutes of Health R01 (with C. Alvira, n. 2), 2021-2024 (accepted).

US National Institutes of Health R01 (with C. Alvira), 2021-2024.

Chan Zuckerberg Initiative Grant for Essential Open Source Software, 2020-2021.

UNSW Cellular Genomics Future Institute Seed Grant, 2021-2022.

Symbiont Award at the Pacific Symposium on Biocomputing, 2018.

EMBO long-term postdoctoral fellowship, 2016-2018.

Excellent Master Student Award, Università degli Studi di Trento, 2011.

Double Degree Scholarship (Italy-Germany), 2008-2010.

# Teaching and Outreach

I routinely teach Scientific Programming for biomedicine students and researchers.

Guest lecturer on single cell biology for University of Sydney and CZ Biohub.

Supervising 5 students and 2 postdocs since starting my own lab (2019-2020).

Former member of the selection committee for the Symbiont Research Award (2018-2020).

Former mentor at the Stanford Inclusive Postdoc:Grad Program “Someone like me”, 2018.

Open source and open science advocate.

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