GIOELE LA MANNO

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- Date of Birth: 15 July 1990   ▪ Place of birth: Palermo, Italy   ▪ Nationality: Italian   ▪ Languages: Italian, English

CURRENT APPOINTMENTS

- ♦ Group leader of the Neurodevelopmental Systems Biology Lab, at EPFL (Started 2018-11)
- ♦ EPFL Life Sciences Early Independence Research Scholar (ELSIR) (2018-2023)

EDUCATION AND RESEARCH TRAINING

Karolinska Institutet   PHD STUDIES   January 2014 – October 2018

- ♦ Thesis: "Lineages and molecular heterogeneity in the developing nervous system"
- ♦ Surpervisor: Sten Linnarsson*, Cosupervisors: Ernest Arenas, Jussi Taipale
- ♦ Relevant PhD Courses and Schools: Computational Dynamic Analysis of Biological Processes, Machine Learning, Microfluidic Flows
  * Department of Medical Biochemistry and Biophysics(MBB), Molecular Neurobiology Division, Sten Linnarsson lab.

Karolinska Institutet   RESEARCH ASSISTANT   June – December 2013

- ♦ Project title: "Developing a microfluidic based single cell RNA-seq approach"
  # Department of Medical Biochemistry and Biophysics(MBB), Molecular Neurobiology Division, Sten Linnarsson lab.

Karolinska Institutet   BIOMEDICINE MASTERS PROGRAM (120 ECTS)   August 2011 - June 2013

- ♦ Comprehensive mark: VG (highest grade)
- ♦ Final research project: "Preserving cellular state for single-cell RNA sequencing" PI: Sten Linnarsson, MBB Karolisnka Institutet
- ♦ Other Projects: "Functional analysis of distinct Lgr6+ stem cell populations of murine skin" PI: Maria Kasper, BioNut Karolinska Institutet

University of Palermo   BACHELOR DEGREE IN BIOTECHNOLOGY (180 ECTS)   Autumn 2008 - July 2011

- ♦ Comprehensive mark: 110/110 with distinction and special mention (equiv. 'magna cum laude')
- ♦ Final project: "Over-expression and silencing of p63 in breast cancer stem cells" PI: Giorgio Stassi, Dep. of Surgical and Oncological Sciences UNIPA

GRANTS AND AWARDS

- ▪ 2019-2020 — CZI Seed Network Grant - Oligodendroglia heterogeneity in the human brain - 400,000 $ (synergy of 3 PIs)
- ▪ 2019-2022 — Swedish research council International Fellowship — 330,000 $ over 3 years (refused)
- ▪ 2018-2023 — ELISIR Programme Founding (EPFL) — 1,500,000 $ over 5years
- ▪ 2018 — Selected publication - ScilifeLab Scientific Medley
- ▪ 2018 — EMPIRIS award for research in brain diseases. 10,000 CHF, personal
- ▪ 2014-2017 — KID Doctoral Grant. 270000 SEK per year for a total of 4 years
- ▪ 2012/13 - Swedish Institute Scholarship (within the Bilateral Scholarship Program for research and education). 72000 SEK

SUPERVISION AND TEACHING

- ▪ I am the thesis supervisor of two PhD Students:
  - Alex Lederer (BSc University Pittsburg)   - Irina Khven (MSc Lomonosov University).
- ▪ I currently supervise two Masters students: Halima Schede (EFPL), Anurag Ranjak (EPFL)
- ▪ I was invited to contribute lectures to several bioinformatics courses (inviters include Piero Carninci director of genomics at RIKEN)
- ▪ I assisted the teaching Organic Chemistry labs to Undergraduates (for 4 years)
- ▪ During my PhD I have been training Master students and other PhD students in molecular biology and computational analysis
  - Johanna Stergiadou (KI)   - Leonie Von Berlin (KI)   - Arvin Chireh (KH) -Yizhou Hu (VR)

EVALUATION AND OUTREACH

- ▪ I review papers for several research journals and institutions including Nature Biotechnology, Nature Communications, Bioinformatics, the EMBO Journal, Nucleic Acid Research and the Israel Science Foundation.
- ▪ Our paper on visceral motor neuron diversity had important media outreach, at least a dozen newspapers featured our discoveries
- ▪ In different occasions I gave popular science talks for high school students of UniStem day, an European event for the dissemination and outreach of stem cell science dedicated to high school students.

- I contributed to the organization of "DDPDGenes Parkinson's open day" a scientific dissemination meeting with patients and families.

COMPETENCES AND TECHNICAL SKILLS

- I have extensive experience in data analysis and the development and implementation of algorithms.
- I master python programming language and a wide selection of scientific libraries, I have a good knowledge of Matlab, R and I use C/C++ for high performance computing.
- Beyond my canonical education I extended my theoretical knowledge on many topics studying Linear Algebra, Dynamical Systems, Applied Statistics, Statistical Mechanics, Convex Optimization and Machine learning.
- I worked extensively at the development of single cell RNA sequencing from the early days of the technology, developing new protocols and adapting preexisting one for clinical applications (i.e. myocardial endovascular micro-biopsies).
- Experience in the design of simple custom microfluidics apparatuses and usage of commercial ones (Fluidigm, Dolomite).

PUBLICATIONS

Original research articles: 16   *Citations:* 3071   *h-index:* 13

A cell fitness selection model for neuronal survival during development.
Nature Communications. 2019 Sep 12
Wang Y, Wu H, Fontanet P, Codeluppi S, Akkuratova N, Petitpré C, Xue-Franzén Y, Niederreither K, Sharma A, Da Silva F, Comai G, Agirman G, Palumberi D, Linnarsson S, Adameyko I, Moqrich A, Schedl A, **La Manno G***, Hadjab S*, Lallemend F** [Senior author]

Single-cell transcriptional logic of cell-fate specification and axon guidance in early-born retinal neurons.
Development. 2019 Sep 1
Lo Giudice Q, Leleu M, **La Manno G***, Fabre PJ* [Senior author]

Spatial organization of the somatosensory cortex revealed by cyclic smFISH.
Nature Methods. 2018 Oct 30
Codeluppi S, Borm LE, Zeisel A, **La Manno G***, van Lunteren JA, Svensson CI, Linnarsson S*

Single-cell transcriptomics of traced epidermal and hair follicle stem cells reveals rapid adaptations during wound healing.
Cell Reports. *2018 Oct 16*
Joost S, Jacob T, Sun X, Annusver K, **La Manno G***, Sur I, Kasper M*

Molecular architecture of the mouse nervous system
Cell*. 2018 Aug 08*
Zeisel A, Hochgerner H, Lonnerberg P, Johnsson A, Memic F, van der Zwan J, Haring M, Braun E, Borm L, **La Manno G***, Codeluppi S, Furlan A, Skene N, Harris KD, Hjerling Leffler J, Arenas E, Ernfors P, Marklund U, Linnarsson S*

RNA velocity of single cells.
Nature*. 2018 Aug 08.* **[Part of PhD thesis]**
La Manno G*, Soldatov R, Zeisel A, Braun E, Hochgerner H, Petukhov V, Lidschreiber K, Kastriti M, Lonnerberg P, Furlan A, Fan J, Borm L, Liu Z, van Bruggen D, Guo J, Xialing He, Barker R, Sundstrom E, Castelo-Branco G, Cramer P, Adameyko I, Linnarsson S*, Kharchenko P**

Neuronal atlas of the dorsal horn defines its architecture and links sensory input to transcriptional cell types.
Nature Neuroscience. *23 April 18.*
Häring M, Zeisel A, Hochgerner H, Rinwa P, Jakobsson JET, Lönnerberg P, **La Manno G***, Sharma N, Borgius C, Kiehn O, Lagerström MC, Linnarsson S*, Ernfors P*.*

STRT-seq-2i: dual-index 5' single cell and nucleus RNA-seq on an addressable microwell array.
Scientific reports*. 2017 Nov 27*
Hochgerner H, Lönnerberg P, Hodge R, Mikes J, Heskol A, Hubschle H, Lin P, Picelli S, **La Manno G***, Ratz M, Dunne J, Husain S, Lein E, Srinivasan M, Zeisel A, Linnarsson S.*

Induction of functional dopamine neurons from human astrocytes in vitro and mouse astrocytes in a Parkinson's model.
Nature Biotechnology. *2017 Oct 10*
Rivetti di Val Cervo P, Romanov RA, Spigolon G, Masini D, Martín-Montañez E, Toledo EM, **La Manno G**, *Feyder M, Pifl C, Ng YH, Sánchez SP, Linnarsson S, Wernig M, Harkany T, Fisone G, Arenas E.*

Molecular analysis of the midbrain dopaminergic niche during neurogenesis
bioRxiv. *2017 Jun 26*
Toledo EM, **La Manno G**, *Rivetti Val Cervo P, Gyllborg D, Islam S, Villaescusa S, Linnarsson S, Arenas E*

Visceral motor neuron diversity delineates a cellular basis for nipple- and pilo-erection muscle control.
Nature Neuroscience *2016 Oct 19* **[Part of PhD thesis]**
Furlan A, **La Manno G**, *Lübke M, Häring M, Abdo H, Hochgerner H, Kupari J, Usoskin D, Airaksinen MS, Oliver G, Linnarsson S, Ernfors P.*

Molecular Diversity of Midbrain Development in Mouse, Human, and Stem Cells.
Cell. *2016 Oct 6.* **[Part of PhD thesis]**
La Manno G, *Gyllborg D, Codeluppi S, Nishimura K, Salto C, Zeisel A, Borm LE, Stott SR, Toledo EM, Villaescusa JC, Lönnerberg P, Ryge J, Barker RA, Arenas E, Linnarsson S.*

Single-Cell Transcriptomics Reveals that Differentiation and Spatial Signatures Shape Epidermal and Hair Follicle Heterogeneity.
Cell Systems. *2016 Sep 28*
Joost S, Zeisel A, Jacob T, Sun X, **La Manno G**, *Lönnerberg P, Linnarsson S, Kasper M*

Oligodendrocyte heterogeneity in the mouse juvenile and adult central nervous system.
Science. *2016 June 10*
Marques S, Zeisel A, Codeluppi S, van Bruggen D, Mendanha Falcão A, Xiao L, Li H, Häring M, Hochgerner H, Romanov RA, Gyllborg D, Muñoz- Manchado AB, **La Manno G**, *Lönnerberg P, Floriddia EM, Rezayee F, Ernfors P, Arenas E, Hjerling-Leffler J, Harkany T, Richardson WD, Linnarsson S, Castelo-Branco G.*

Cell types in the mouse cortex and hippocampus revealed by single-cell RNA-seq.
Science *2015 March 6*
Zeisel A, Muñoz-Manchado AB, Codeluppi S, Lönnerberg P, **La Manno G**, *Juréus A, Marques S, Munguba H, He L, Betsholtz C, Rolny C, Castelo- Branco G, Hjerling-Leffler J, Linnarsson S.*

Quantitative single-cell RNA-seq with unique molecular identifiers.
Nature Methods *2014 February*
Islam S, Zeisel A, Joost S, **La Manno G**, *Zajac P, Kasper M, Lönnerberg P, Linnarsson S.*

PATENTS

I contributed to the two related patents (Licensed to Wafergen Bio-Systems Inc.):
- "*Method that allows pooling down from chip to the 96 well device*" [WAFER-34667/US-1 62/256,968]
- "*Method for dual end barcoding chemistry*" [WAFER-34667/US-2]

I co-invented and patented (Legal rights sold to Fluidigm Corp. in 2015):
- "*Method for capturing and encoding nucleic acid from a plurality of single cells*" [PCT/EP2014/070824].

INVITED TALKS AND LECTURES

Invited seminar talk at ETH Zurich D-BSSE – October 2019, Basel, Switzerland

Contributed talk at Single Cell Genomics Conference – September 2019, Stockholm, Sweden

Lecture at EPFL Python bootcamp - July 2019, Lausanne, Switzerland

Invited symposium talk at IZKF Erlangen – June 2019, Kloster Banz, Germany

Invited seminar talk, Life Science PhD seminar series - University of Milan – June 2019, Milan, Italy

Invited conference talk at Heidelberg Forum for Young Scientists – June 2019, Heidelberg, Germany

Invited talk, Life Science PhD seminar series - University of Milan – May 2019, Milan, Italy

Invited seminar at Max Planck Institute for Molecular Genetics – May 2019, Berlin, Germany

"RNA velocity: differentiation predicts differentiation" Invited Talk at World Congress of Hair Research - April 2019, Sitges. Barcelona.

"RNA velocity in single cells: concept, estimations and applications" *selected for a contributed talk at Single Cell Genomics Conference - October 2018, Broad Institute of MIT and Harvard, Cambridge MA*

"An introduction to RNA velocity" *lecture* Single cell RNA sequencing course Scilife Lab - May 2018, Stockholm, Sweden "RNA velocity of single cells unveils the dynamics of commitment ad fate choice" *invited talk for the Sfn virtual conference* Advances in Single Cell Genomics to Study Brain Cell Types - May 2018

"Introduction to data analysis and machine learning" *lecture at* Bioinformatics analysis of gene regulation in omics data and its application in medical problems RIKEN/KI 8th International PhD Course - March 2018, Stockholm, Sweden

"Differentiation and branching of neural cell types unveiled by RNA velocity" *selected for a contributed talk at* Single Cell Analysis Meeting at Cold Spring Harbor Laboratory - November 2017, New York, USA

"Machine learning for single cell transcriptomics" invited *lecture at* Single Cell Data Analysis Course, University of Helsinki - September 2017, Helsinki, Finland

"A single cell atlas of brain development" *invited talk at* Single cell symposium, University of Helsinki - September 2017, Helsinki, Finland

"Introduction to Machine learning" *lecture at* EMBnet COST.CHARME training school *"Big Data for Life Sciences"* - September 2017, Uppsala, Sweden

"Single cell RNA-seq unveils the molecular diversity of midbrain development in human, mouse and stem cells". *Invited talk at* ESHG (European Society of Human Genetics Conference) - May 2017, Copenhagen, Denmark

"Single-cell RNA-seq: a high throughput technology to explore cell type diversity" *invited seminar for the* international seminar series of the Masters Programme in Medical Biotechnology and Molecular Medicine of University of Palermo - March 2017, Palermo, Italy

"Machine learning: introduction and applications" *lecture at* Bioinformatics analysis of gene regulation in omics data and its application in medical problems RIKEN/KI 7th International PhD Course - February 2017, Yokohama, Japan

"Molecular diversity of midbrain development: from cell type homologies to replacement therapies". *Invited talk at* Annual Meeting of the Computational and Molecular Methodologies for Life Sciences Research Programme - December 2016, Turku, Finland

"Single-cell transcriptomics of the nervous system" *invited talk at* SciLifeLab Medical and Population Genetics and Genomics Workshop - October 2015, Uppsala, Sweden

"Conserved principles of brain development revealed by comparative single-cell RNA-seq in mouse and human ventral midbrain" *selected for a contributed talk at* Single Cell Genomics Conference - September 2015, Utrecht, Netherlands

OTHER PRESENTATIONS

"Constructing gene expression atlases by RNA tomography" *poster at* Quantitative Principles of Biology EMBO Conference - November 2017, Heidelberg. Germany

"RNA velocity in single cells reveals differentiation directionality and dynamics" *poster at* Single Cell Genomics Conference - October 2017, Weizmann Institute, Rehovot. Israel

"Cell Type Learning: From The Conservation Of The Ventral Midbrain To Replacement Therapies" *poster at* Single Cell genomics Conference - September 2016, Hinxton, Cabridge, UK

"Comparative single-cell RNA-seq in mouse and human ventral midbrain reveals conserved principles of brain development" *lightning talk and poster presentation at* the 3rd Human Brain Project Education Workshop December 2015, Manchester, UK

OPEN SOURCE SCIENTIFIC SOFTWARE

I contributed to the implementations and maintenance of the following software
(available at https://github.com/linnarsson-lab):

velocyto: a package for the analysis of expression dynamics in single cell RNA seq data

cytograph: A tool for building analysis pipeline for big single cell RNA sequencing projects

loompy: core implementation of loom file format, the standard format for single-cell RNA-seq data

py-fitsne: a python frontend for the fast tsne algorithm described by Linderman et al. 2017.

ceftools: an older file format designed to store smaller single-cell RNA-seq datasets

BackSPIN: official implementation of the clustering algorithm described in Zeisel et al. 2015

cmdstan-py: an alternative, lightweight, python interface to the Bayesian Modeling language Stan

nbregression: negative binomial generalized linear model for single cell expression data.