

FRANCESCO G. BRUNDU

Research Scientist

francesco.brundu_at_gmail.com
github: fbrundu
Full publications list: [Francesco G. Brundu](#)

Francesco G. Brundu currently works as a Postdoctoral Research Scientist at Columbia University. He specializes in computational methodologies applied to biological data. Since 2019 he has been collaborating on projects related to Schizophrenia through several models (human organoids, mouse), being able to complement his interests in mind/behavior with computational methodologies. He is very passionate about his work in these projects and he aspires to deepen his expertise on computational models for intelligence, which already have a disrupting impact when leveraged for the analysis of the growing amounts of data.

EXPERIENCE

Post-Doctoral Research Scientist

Columbia University - Program for Mathematical Genomics

SEP 2017 - PRESENT, NEW YORK CITY

Research Focus: Single-Cell Transcriptome Analysis

Research Projects Key Achievements:

- Identification of Cancer-Associated Fibroblasts (CAF) sub-population in Intrahepatic Cholangiocarcinoma (Affò et al., under review)
- Cell subtype identification in mouse models of T-Cell development (Belver et al., *Cancer Discovery*, 2019)

Key Responsibilities:

- Literature review (Bioinformatics, Machine Learning, Cancer genomics, Neuroscience, Cell Biology)
- Analysis strategy (objective definition, data selection, algorithms evaluation)
- Design and development of data analysis pipelines and novel methodologies
- Oral presentation of results to collaborators and lab members
- Manuscript preparation and submission
- Student mentoring

PI: Raúl Rabadán

EDUCATION

PhD - Computer and Control Engineering

Politecnico di Torino

JAN 2014 - JUL 2017, TORINO

Thesis: Distributed service infrastructure for monitoring, management and simulation in Smart Cities ([Poster presentation](#)).

Key achievements:

- District Web Service infrastructure for data integration and simulation to the purpose of energy reduction (Brundu et al., *IEEE Transactions on Industrial Informatics*, 2017).

Additional achievements:

- Preprocessing and analysis of Colorectal Cancer gene expression through bulk RNA-Seq and microarray data (Isella et al., *Nature Communications*, 2017).

Advisor: Enrico Macii

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Skills

Programming

Python, C (prior), C++ (prior), SQL, R

Scientific Computing

pandas, numpy, scipy, scikit-learn

Shell

Bash scripting, AWK, GNU parallel

Computational Biology

Single-cell RNA-Seq

- Data preprocessing
- Sample integration
- Cell type identification
- Differential Expression
- Gene Regulatory Networks

Other

Docker, GIT, REST, AWS (EC2, S3, Batch), pymc3

Languages

English, Italian

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MSc - Computer Engineering

Politecnico di Torino

OCT 2010 - MAR 2013, TORINO

BSc - Computer Engineering

Politecnico di Torino

OCT 2006 - SEP 2010, TORINO