Roberto Semeraro

Education

2013-2017	PhD program in "Information Engineering" Department of Information Engineering - University of Florence. Thesis: "*A new morphological approach for synthetic genomic samples generation*" **Supervisor**: Stefano Ruffo, Alberto Magi
2011-2013	Master Degree in molecular biotechnology (110/110 cum laude) University of Florence, Department of Biology Thesis: "*Comparative analysis of Sinorhizobium meliloti metabolism*" **Supervisor**: Prof. A. Mengoni, Dott. M. Galardini
2007-2011	Bachelor Degree in Biotechnology (103/110) University of Florence**,** Department of Evolutionary Biology Thesis "*Comparative analysis of transport systems in Burkholderia genus*" **Supervisor**: Prof. R. Fani, Dott. M. Fondi

Research Experience

2014-current	PhD Fellowship in collaboration with Dott. Alberto Magi at Laboratory of Bioinformatics for Omic Sciences - Department of Experimental and Clinical Medicine, University of Florence, Italy
February/March 2014	Visitor Fellow in collaboration with Prof. Marco Rinaldo Oggioni at the University of Leicester (UK). Project title "Characterization of a glycosyl hydrolase of *Streptococcus pneumoniae* and impact assessment of adhesion and biofilm"

Scientific activity and achievements

My research interests focus on genomic informatics and transcriptomics, with the aim of understanding the molecular mechanisms that underlie the regulation of gene expression, particularly in the context of diseases.
From 2015 to 2018, I mainly worked in the field of cancer research, been awarded with three research grants. In this context, I released several computational methods for the analysis of tumor sequencing data, by studying the impact of single nucleotide variations (SNV), InDels and structural variants on disease progress and onset. In 2018, I released a tumor sample simulator called Xome-Blender. In the meantime, I also had the chance to be one of the first researchers to work on data generated by third generation sequencing platforms based on nanopore sensing. As a result, I developed a method, called PyPore, for visualization and processing of long read datasets, along with other variant detection tools.

In the last three years, I focused my attention on single-cell techniques, posing particular attention on their impact on medical and clinical applications, and producing several works to confirm this.

Teaching Activities

January/February 2023	Computational Systems Biology - Centro didattico Morgagni, Firenze
24th September 2018	Introduction to Bionformatics Resources for Vector Genomics Studies - Polo d'innovazione di genomica, genetica e biologia, Siena

Conference, Workshop and Seminars

28th October 2016	Fifth edition of the Tuscan meeting of Bioinformatic and Systems Biology - Florence.
1st October 2015	Algorithms in Bioinformatics and in Omics applications - Siena.

Conferences and Courses Organization

4th October 2019	Co-chair of the Eighth edition of the Tuscan meeting of Bioinformatic and Systems Biology - Florence.

Editorial Activities

Review Editor for Computational Genomics Frontiers in Genetics.

Publications

Citation statistics

Papers in international peer-reviewed journals: 24

Total Citations (Scopus): 283

Total Citations (Scholar): 435

H-index (Scopus): 9

H-index (Scholar): 9

Journal Article

- Galardini, M., Mengoni, A., Biondi, E. G., **Semeraro, R.**, Florio, A., Bazzicalupo, M.,... & Mocali, S. (2014). DuctApe: a suite for the analysis and correlation of genomic and OmniLog™ phenotype microarray data. Genomics, 103(1), 1-10.
- Magi, A., D'Aurizio, R., Palombo, F., Cifola, I., Tattini, L., **Semeraro, R.**, ... & Gensini, G. F. (2015). Characterization and identification of hidden rare variants in the human genome. BMC Genomics, 16(1), 340.
- Magi A, **Semeraro R.**, Mingrino A, Giusti B and D'Aurizio R. (2017) Nanopore sequencing data analysis: state of the art, applications and challenges. Briefings In Bioinformatics.

- **Semeraro, R.**, Orlandini V. and Magi A. (2018) Xome-Blender: A novel cancer genome simulator. PLoS ONE 13(4):e0194472.
- D'Aurizio R., **Semeraro R.**, and Magi A. (2018) Using XCAVATOR and EXCAVATOR2 to identify CNVs from WGS, WES, and TS Data. Current Protocols in Human Genetics, e65.
- Calvani M, Cavallini L, Tondo A, Spinelli V, Ricci L, Pasha A, Bruno G, Buonvicino D, Bigagli E, Vignoli M, Bianchini F, Sartiani L, Lodovici M, **Semeraro R.**, Fontani F, De Logu F, Dal Monte M, Chiarugi P, Favre C, Filippi L. (2018) β3-Adrenoreceptors Control Mitochondrial Dormancy in Melanoma and Embryonic Stem Cells. Oxidative Medicine and Cellular Longevity 2018:6816508.
- Magi A, Bolognini D, Bartalucci N, Mingrino A, **Semeraro R.**, Giovannini L, Bonifacio S, Parrini D, Pelo E, Mannelli F, Guglielmelli P, Vannucchi AM. (2019) Nano-GLADIATOR: real-time detection of copy number alterations from nanopore sequencing data. Bioinformatics, btz241.
- **Semeraro R.**, Magi A. (2019) PyPore: a python toolbox for nanopore sequencing data handling. Bioinformatics, btz269
- Peired, A. J., Antonelli, G., Angelotti, M. L., Allinovi, M., Guzzi, F., Sisti, A., **Semeraro, R.** ... & Melica, M. E. (2020). Acute kidney injury promotes development of papillary renal cell adenoma and carcinoma from renal progenitor cells. Science Translational Medicine, 12(536).
- Magi, A., Giangregorio, T., **Semeraro, R.**, Carangelo, G., Palombo, F., Romeo, G., ... & Pippucci, T. (2020). AUDACITY: A comprehensive approach for the detection and classification of Runs of Homozygosity in medical and population genomics. Computational and structural biotechnology journal, 18, 1956-1967.
- Mazzoni, A., Maggi, L., Capone, M., Vanni, A., Spinicci, M., Salvati, L., **Semeraro, R.**, ... & Annunziato, F. (2021). Heterogeneous magnitude of immunological memory to SARS-CoV-2 in recovered individuals. Clinical & translational immunology, 10(5), e1281.
- Martignano, F., Munagala, U., Crucitta, S., Mingrino, A., **Semeraro, R.**, Del Re, M., ... & Conticello, S. G. (2021). Nanopore sequencing from liquid biopsy: analysis of copy number variations from cell-free DNA of lung cancer patients. Molecular cancer, 20(1), 1-6.
- Magini, P., Mingrino, A., Gega, B., Mattei, G., **Semeraro, R.**, Bolognini, D., ... & Magi, A. (2022). Third Generation Cytogenetic Analysis (TGCA): diagnostic application of long-read sequencing. The Journal of Molecular Diagnostics.
- Melica, M. E., Antonelli, G., **Semeraro, R.**, Angelotti, M. L., Lugli, G., Landini, S., ... & Romagnani, P. (2022). Differentiation of crescent-forming kidney progenitor cells into podocytes attenuates severe glomerulonephritis in mice. Science Translational Medicine, 14(657), eabg3277.
- Carangelo, G., Magi, A., & **Semeraro, R.** (2022). From multitude to singularity: An up-to-date overview of scRNA-seq data generation and analysis. Frontiers in Genetics, 13, 994069.
- De Chiara, L., Conte, C., **Semeraro, R.**, Diaz-Bulnes, P., Angelotti, M. L., Mazzinghi, B., ... & Romagnani, P. (2022). Tubular cell polyploidy protects from lethal acute kidney injury but promotes consequent chronic kidney disease. Nature Communications, 13(1), 1-19.
- Vanni, A., Mazzoni, A., **Semeraro, R.**, Capone, M., Maschmeyer, P., Lamacchia, G., ... & Annunziato, F. (2023). Clonally expanded PD-1-expressing T cells are enriched in synovial fluid of juvenile idiopathic arthritis patients. European Journal of Immunology, 2250162.

- Magi, A., Mattei, G., Mingrino, A., Caprioli, C., Ronchini, C., Frigè, G., **Semeraro, R.**, ... & Pelicci, P. G. (2023). High-resolution Nanopore methylome-maps reveal random hyper-methylation at CpG-poor regions as driver of chemoresistance in leukemias. Communications Biology, 6(1), 382.