Andrea Guarracino

Curriculum Vitae

Department of Genetics, Genomics and Informatics
The University of Tennessee, Memphis, USA
✉ *aguarra1@uthsc.edu*
***Online CV**: andreaguarracino.github.io*
AndreaGuarracino *live:andreaguarracino*

Current position

2022/11/01 - present **Postdoctoral Scholar at the University of Tennessee Health and Science Center**, *Memphis, USA*, Reporting to Prof. Erik Garrison.

- New generation of sequence aligners for aligning whole eukaryotic chromosomes

Collaborations

2022/11/01 - present **E-Visitor at the Human Technopole**, *Milan, Italy*, Reporting to Prof. Nicole Soranzo and Prof. Erik Garrison.

- Development of tools for pangenome graph building, manipulation, and analyses

2019/11/01 - present **Italian Institute for Genomic Medicine and the Candiolo Cancer Institute**, *Candiolo, Italy*, Reporting to Dr. Ilio Vitale.

- Spindle Assembly Checkpoint functionality in colon-rectal cancer stem cells
- Exploiting karyotypic aberrations and chromosomal instability in cancer stem cells for precision immunotherapy

Employment

2021/11/01 - 2022/10/31 **Postdoctoral Associate at the Human Technopole**, *Milan, Italy*, Reporting to Prof. Nicole Soranzo and Prof. Erik Garrison.

- Studying chromosome communities (acrocentric and sex chromosomes) in the human pangenome

2013/03/04 - 2018/10/31 **Computer engineer for multiplatform firmware/software development**, *GISA S.n.c., Italy*, Reporting to Eng. Gaetano Giordano.

- Firmware development in STMicroelectronics microcontrollers for high efficiency embedded systems
- Firmware and library development in open-source hardware and software platforms (Arduino/Genuino)
- Development of multi-management software and desktop applications for embedded systems programming
- Mobile applications development for programming and the control of multi-service machines via Bluetooth
- Implementation of proprietary communication protocols and contact/contactless (RFID) interfaces
- Development and maintenance of websites and e-commerce
- Remote assistance to customers for the usage and programming of multi-service machines, taking feedback to further improve the solutions offered
- Patent application on a universal system for services fruition, with validation, reconstruction, and credit self-reloading management, on read-only and read/write supports (ITUA20165252, A1) (Patent)
- Basic design of simple electrical circuits for controlling actuators and reading analog/digital signals

2012/10/04 - 2013/01/20 **Salesman**, *L'Erborista S.A.S. di Sarno Adele & C, Italy*.

- Selling products, warehouse management and cleaning

2010/11/01 - 2012/03/03 **Web Developer**, *Virtual, Italy*.

- Development of dynamic websites using Java Server Page, JavaScript, ASP.NET, PHP, MySQL

Education

2018/11/01 - 2022/02/08 **Ph.D. in Cellular and Molecular Biology (Bioinformatics)**, *University of Rome Tor Vergata, Italy*, "Investigating chromosomal instability in cancer stem cells", Evaluation: excellent quality.

2016/10/03 - 2018/10/25 **Master's degree in Bioinformatics (LM-6), 110/110 cum laude**, *University of Rome Tor Vergata, Italy*, "Energetic and functional characterization of phosphorylations involved in the co-regulation of protein interactions", GPA: 4.00, A+.

2007/10/01 - 2010/10/29 **Bachelor's degree in Computer Engineering (L-8), 110/110 cum laude**, *University of Salerno, Italy*, "HDR methods for industrial inspection applications", GPA: 4.00, A+.

Research experience

2018/11/01 - present **Bioinformatic analyses of multiomics data**, *University of Rome Tor Vergata, Italy*.

- Germline and somatic variants analyses on Whole-Exome sequencing (WES) data: quality control, sample matching, rRNA contamination, read trimming and mapping, variant calling, and functional prediction
- Microsatellite instability (MSI) status on paired tumor-normal and tumor-only WES data
- Variant calling and differential expression analyses on RNA-seq data
- Neoantigen prediction and prioritization by integrating WES data and RNA-seq data
- Analysis of Assay for Transposase-Accessible Chromatin using sequencing (ATAC-seq) data
- Normalization and correlation analysis of transcriptomic microarray data (Affymetrix)
- Proteomic and phosphoproteomic analyses of Reverse Phase Protein microarray (RPPA) data
- RNA structural characterization and conservation research (Pietrosanto, Adinolfi, Guarracino *et al.*, 2021)
- Web server development for RNA sequence and structure motif scan (Guarracino *et al.*, 2021)
- Energetic and functional analyses of phosphorylations applied *in silico* on 3D structures of protein complexes
- Cox modeling and survival analysis on patient cohorts (from TCGA and cBioPortal platforms)
- Basic procedures on High Performance Computing (HPC) machines

2020/04/05 - present **Software development for pangenomics**, *Virtual*.

- Developing of tools to construct pangenome graphs of any complexity and scale (pggb, smoothxg)
- Optimized Dynamic Genome/Graph Implementation (ODGI) development to analyze and manipulate pangenome graphs, scaling up to large collections of eukaryotic genomes (Guarracino *et al.*, 2022)
- Development of a new algorithm for sorting pangenome graphs to simplify downstream analyses on them (Path-guided Sorting, Path-guided Layout)
- Development of a new gap-affine pairwise aligner to align whole eukaryotic chromosomes (wfmash)
- Software and workflows development for PubSeq, a free and open online public sequence resource with on-the-fly analysis (bh20-seq-resource)
- Pangenome graph browser development (Pantograph)

Teaching

2020/10/26 - present **Teacher in 'Data Structures for Bioinformatics' (2 CFU/ECTS)**, creating new material for the course. Master's degree in Bioinformatics, *University of Rome Tor Vergata, Italy* (Material)

2023/02/28 - 2023/02/28 **Teacher in 'Advanced Bioinformatics: Data Mining and Data Integration for Life Science (1.5 CFU/ECTS)'**, introducing pangenomics and PGGB (PanGenome Graph Builder). *Utrecht Bioinformatics Center, Utrecht* (Website)

2022/05/23 - 2022/05/27 **Instructor in 'CPANG22 Computational PANGenomics'**, creating new material for the course. *Instituto Gulbenkian de Ciência, Oeiras, Portugal* (Website, Material, Poster, Certificate)

2019/10/07 - 2020/12/07 **Tutor in 'Bioinformatics' (6 CFU/ECTS)**, reviewing the practical lessons and assisting the students. Bachelor's degree in Biological Science, *University of Rome Tor Vergata, Italy*

2019/12/16 - 2021/03/29 **Exam assistance for 'Computational Proteogenomics' (2 CFU/ECTS)**, Master's degree in Bioinformatics, *University of Rome Tor Vergata, Italy*

2019/06/07 - 2021/07/21 **Exam assistance for 'Molecular Biology' (8 CFU/ECTS) and 'Bioinformatics' (6 CFU/ECTS)**, Bachelor's degree in Biological Science, *University of Rome Tor Vergata, Italy*

Mentoring

2021/09/02 - 2022/04/20 **Machine learning to automatically detect the *C. elegans* bodies from microscope images and measure their growth over time**, Master's degree in Bioinformatics, *University of Rome Tor Vergata, Italy*

2021/04/20 - 2021/11/02 **Analysis of the effect of SARS-CoV-2 mutations on the pairing between the viral genome and human miRNAs**, Bachelor's degree in Biological Science, *University of Rome Tor Vergata, Italy*

2020/04/28 - 2020/11/05	**Analysis of repeated sequences in lincRNA candidates for exon shuffling**, Bachelor's degree in Biological Science, *University of Rome Tor Vergata, Italy*
2020/03/09 - 2021/03/12	**Machine Learning methods applied to kinase-substrate interaction prediction**, Master's degree in Bioinformatics, *University of Rome Tor Vergata, Italy*
2020/03/02 - 2020/12/17	**Natural Language Processing techniques for protein encoding applied to phosphorylation prediction**, Master's degree in Bioinformatics, *University of Rome Tor Vergata, Italy*
2019/12/13 - 2020/06/11	**Study of normalization techniques' effects in gene expression correlation analyses**, Bachelor's degree in Biological Science, *University of Rome Tor Vergata, Italy*

Peer-review for international journals

2021/02/26 - present	**Human Genomics** (Journal), 🔗 Review identifiers
2021/02/23 - present	**PLOS ONE** (Journal), 🔗 Review identifiers

Publications

See the Google Scholar Profile.

Journal Articles (*first authorship)

In revision	Arang Rhie, Sergey Nurk, Monika Cechova, Savannah J Hoyt, Dylan J Taylor, Nicolas Altemose, Paul W Hook, Sergey Koren, Mikko Rautiainen, Ivan A Alexandrov, Jamie Allen, Mobin Asri, Andrey V Bzikadze, Nae-Chyun Chen, Chen-Shan Chin, Mark Diekhans, Paul Flicek, Giulio Formenti, Arkarachai Fungtammasan, Carlos Garcia Giron, Erik Garrison, Ariel Gershman, Jennifer Gerton, Patrick GS Grady, **Andrea Guarracino**, Leanne Haggerty, Reza Halabian, Nancy F Hansen, Robert Harris, Gabrielle A Hartley, William T Harvey, Marina Haukness, Jakob Heinz, Thibaut Hourlier, Robert M Hubley, Sarah E Hunt, Stephen Hwang, Miten Jain, Rupesh K Kesharwani, Alexandra P Lewis, Heng Li, Glennis A Logsdon, Julian K Lucas, Wojciech Makalowski, Christopher Markovic, Fergal J Martin, Ann M Mc Cartney, Rajiv C McCoy, Jennifer McDaniel, Brandy M McNulty, Paul Medvedev, Alla Mikheenko, Katherine M Munson, Terence D Murphy, Hugh E Olsen, Nathan D Olson, Luis F Paulin, David Porubsky, Tamara Potapova, Fedor Ryabov, Steven L Salzberg, Michael EG Sauria, Fritz J Sedlazeck, Kishwar Shafin, Valery A Shepelev, Alaina Shumate, Jessica M Storer, Likhitha Surapaneni, Angela M Taravella Oill, Francoise Thibaud-Nissen, Winston Timp, Marta Tomaszkiewicz, Mitchell R Vollger, Brian P Walenz, Allison C Watwood, Matthias H Weissensteiner, Aaron M Wenger, Melissa A Wilson, Samantha Zarate, Yiming Zhu, Justin M Zook, Evan E Eichler, Rachel O'Neill, Michael C Schatz, Karen H Miga, Kateryna D Makova, and Adam M Phillippy. The complete sequence of a human y chromosome. ***Nature***, In revision. ***Contribution: Variants and Liftover.***
In preparation	Erik Garrison*, **Andrea Guarracino***, Simon Heumos, Flavia Villani, Zhigui Bao, Lorenzo Tattini, Jörg Hagmann, Sebastian Vorbrugg, Santiago Marco-Sola, Christian Kubica, David G. Ashbrook, Kaisa Thorell, Rachel L. Rusholme-Pilcher, Gianni Liti, Emilio Rudbeck, Sven Nahnsen, Zuyu Yang, Mwaniki N. Moses, Franklin L. Nobrega, Yi Wu, Hao Chen, Joep de Ligt, Peter H. Sudmant, Nicole Soranzo, Vincenza Colonna, Robert W. Williams, and Pjotr Prins. Building pangenome graphs. *bioRxiv*. Cold Spring Harbor Laboratory, In preparation. ***Contribution: Software development, experiments, paper writing, documentation, testing.***
2023	**Andrea Guarracino***, Silvia Buonaiuto, Leonardo Gomes de Lima, Tamara Potapova, Arang Rhie, Sergey Koren, Boris Rubinstein, Christian Fischer, Human Pangenome Reference Consortium, Jennifer L. Gerton, Adam M. Phillippy, Vincenza Colonna, and Erik Garrison. Recombination between heterologous human acrocentric chromosomes. *Nature*, volume 617, pages 335–343, May 2023. ***Contribution: pangenomic analyses, figures from 1 to 5, paper writing.***

2023 Santiago Marco-Sola, Jordan M Eizenga, **Andrea Guarracino**, Benedict Paten, Erik Garrison, and Miquel Moreto. Optimal gap-affine alignment in O(s) space. ***Bioinformatics***, 02 2023. ***Contribution: testing, evaluation, Figure 2.***

2023 Wen-Wei Liao, Mobin Asri, Jana Ebler, Daniel Doerr, Marina Haukness, Glenn Hickey, Shuangjia Lu, Julian K. Lucas, Jean Monlong, Haley J. Abel, Silvia Buonaiuto, Xian H. Chang, Haoyu Cheng, Justin Chu, Vincenza Colonna, Jordan M. Eizenga, Xiaowen Feng, Christian Fischer, Robert S. Fulton, Shilpa Garg, Cristian Groza, **Andrea Guarracino**, William T. Harvey, Simon Heumos, Kerstin Howe, Miten Jain, Tsung-Yu Lu, Charles Markello, Fergal J. Martin, Matthew W. Mitchell, Katherine M. Munson, Moses Njagi Mwaniki, Adam M. Novak, Hugh E. Olsen, Trevor Pesout, David Porubsky, Pjotr Prins, Jonas A. Sibbesen, Jouni Sirén, Chad Tomlinson, Flavia Villani, Mitchell R. Vollger, Lucinda L. Antonacci-Fulton, Gunjan Baid, Carl A. Baker, Anastasiya Belyaeva, Konstantinos Billis, Andrew Carroll, Pi-Chuan Chang, Sarah Cody, Daniel E. Cook, Robert M. Cook-Deegan, Omar E. Cornejo, Mark Diekhans, Peter Ebert, Susan Fairley, Olivier Fedrigo, Adam L. Felsenfeld, Giulio Formenti, Adam Frankish, Yan Gao, Nanibaa' A. Garrison, Carlos Garcia Giron, Richard E. Green, Leanne Haggerty, Kendra Hoekzema, Thibaut Hourlier, Hanlee P. Ji, Eimear E. Kenny, Barbara A. Koenig, Alexey Kolesnikov, Jan O. Korbel, Jennifer Kordosky, Sergey Koren, HoJoon Lee, Alexandra P. Lewis, Hugo Magalhães, Santiago Marco-Sola, Pierre Marijon, Ann McCartney, Jennifer McDaniel, Jacquelyn Mountcastle, Maria Nattestad, Sergey Nurk, Nathan D. Olson, Alice B. Popejoy, Daniela Puiu, Mikko Rautiainen, Allison A. Regier, Arang Rhie, Samuel Sacco, Ashley D. Sanders, Valerie A. Schneider, Baergen I. Schultz, Kishwar Shafin, Michael W. Smith, Heidi J. Sofia, Ahmad N. Abou Tayoun, Françoise Thibaud-Nissen, Francesca Floriana Tricomi, Justin Wagner, Brian Walenz, Jonathan M. D. Wood, Aleksey V. Zimin, Guillaume Bourque, Mark J. P. Chaisson, Paul Flicek, Adam M. Phillippy, Justin M. Zook, Evan E. Eichler, David Haussler, Ting Wang, Erich D. Jarvis, Karen H. Miga, Erik Garrison, Tobias Marschall, Ira M. Hall, Heng Li, and Benedict Paten. A draft human pangenome reference. *Nature*, volume 617, pages 312–324, May 2023. ***Contribution: paper editing, pangenome graph creation, pangenome visualization, population genetic analysis.***

2022 **Andrea Guarracino***, Simon Heumos*, Sven Nahnsen, Prins Pjotr, and Erik Garrison. ODGI: understanding pangenome graphs. ***Bioinformatics***, 2022. ***Contribution: paper writing, documentation, made the figures and the table, and implemented several tools.***

2022 Gerardo Pepe, **Andrea Guarracino**, Francesco Ballesio, Luca Parca, Gabriele Ausiello, and Manuela Helmer-Citterich. Evaluation of potential miRNA sponge effects of SARS genomes in human. ***Non-coding RNA Research***, volume 7, pages 48–53. Elsevier BV, March 2022. ***Contribution: genomes collection, filtering, deduplication, alignment, and variant calling.***

2022 Martina Musella, **Andrea Guarracino**, Nicoletta Manduca, Claudia Galassi, Eliana Ruggiero, Alessia Potenza, Ester Maccafeo, Gwenola Manic, Luca Mattiello, Sara Soliman Abdel Rehim, Michele Signore, Marco Pietrosanto, Manuela Helmer-Citterich, Matteo Pallocca, Maurizio Fanciulli, Tiziana Bruno, Francesca De Nicola, Giacomo Corleone, Anna Di Benedetto, Cristiana Ercolani, Edoardo Pescarmona, Laura Pizzuti, Francesco Guidi, Francesca Sperati, Sara Vitale, Daniele Macchia, Massimo Spada, Giovanna Schiavoni, Fabrizio Mattei, Adele De Ninno, Luca Businaro, Valeria Lucarini, Laura Bracci, Eleonora Aricò, Giovanna Ziccheddu, Francesco Facchiano, Stefania Rossi, Massimo Sanchez, Alessandra Boe, Mauro Biffoni, Ruggero De Maria, Ilio Vitale, and Antonella Sistigu. Type I IFNs promote cancer cell stemness by triggering the epigenetic regulator KDM1B. ***Nature Immunology***. Springer Science and Business Media LLC, 8 2022. ***Contribution: made Figure 6.a, 7.a, and 7.b, contributed for Figure 6.c, 6.e, performed RNA-seq, ATAC-seq, and microarray data analysis, correlation analyses, TF-binding motif enrichment, and survival analyses.***

2022 Erich D. Jarvis, Giulio Formenti, Arang Rhie, **Andrea Guarracino**, Chentao Yang, Jonathan Wood, Alan Tracey, Francoise Thibaud-Nissen, Mitchell R. Vollger, David Porubsky, Haoyu Cheng, Mobin Asri, Glennis A. Logsdon, Paolo Carnevali, Mark J.P. Chaisson, Chen-Shan Chin, Sarah Cody, Joanna Collins, Peter Ebert, Merly Escalona, Olivier Fedrigo, Robert S. Fulton, Lucinda L. Fulton, Shilpa Garg, Jay Ghurye, Ana Granat, Edward Green, Ira Hall, William Harvey, Patrick Hasenfeld, Alex Hastie, Marina Haukness, Erich B. Jaeger, Miten Jain, Melanie Kirsche, Mikhail Kolmogorov, Jan O. Korbel, Sergey Koren, Jonas Korlach, Joyce Lee, Daofeng Li, Tina Lindsay, Julian Lucas, Feng Luo, Tobias Marschall, Jennifer McDaniel, Fan Nie, Hugh E. Olsen, Nathan D. Olson, Trevor Pesout, Daniela Puiu, Allison Regier, Jue Ruan, Steven L. Salzberg, Ashley D. Sanders, Michael C. Schatz, Anthony Schmitt, Valerie A. Schneider, Siddarth Selvaraj, Kishwar Shafin, Alaina Shumate, Catherine Stober, James Torrance, Justin Wagner, Jianxin Wang, Aaron Wenger, Chuanle Xiao, Aleksey V. Zimin, Guojie Zhang, Ting Wang, Heng Li, Erik Garrison, David Haussler, Justin M. Zook, Evan E. Eichler, Adam M. Phillippy, Benedict Paten, Kerstin Howe, Karen H. Miga, and Human Pangenome Reference Consortium. Automated assembly of high-quality diploid human reference genomes. ***Nature***, 10 2022. ***Contribution: pangenome alignments, Jaccard, PCA and MHC analyses, figure 2.***

2022 Erik Garrison and **Andrea Guarracino**. Unbiased pangenome graphs. ***Bioinformatics***, 11 2022. ***Contribution: Bottleneck parallelization, bug fixings, experiments in multiple species.***

2021 **Andrea Guarracino***, Gerardo Pepe*, Francesco Ballesio, Marta Adinolfi, Marco Pietrosanto, Elisa Sangiovanni, Ilio Vitale, Gabriele Ausiello, and Manuela Helmer-Citterich. BRIO: a web server for RNA sequence and structure motif scan. ***Nucleic Acids Research***, 05 2021. ***Contribution: wrote the paper, made the figures and the table, refactored and completed the web server, and refined the datasets.***

2021 Pietrosanto Marco*, Marta Adinolfi*, **Andrea Guarracino***, Fabrizio Ferrè, Gabriele Ausiello, Ilio Vitale, and Manuela Helmer-Citterich. Relative Information Gain: Shannon entropy-based measure of the relative structural conservation in RNA alignments. ***NAR Genomics and Bioinformatics***, volume 3, 02 2021. ***Contribution: wrote the paper, contributed to Figure 2, made Figure 3, 4, and 5, and fixed, refactored and completed the framework.***

2021 Giuseppe Novelli, Jing Liu, Michela Biancolella, Tonino Alonzi, Antonio Novelli, J. J. Patten, Dario Cocciadiferro, Emanuele Agolini, Vito Luigi Colona, Barbara Rizzacasa, Rosalinda Giannini, Benedetta Bigio, Delia Goletti, Maria Rosaria Capobianchi, Sandro Grelli, Justin Mann, Trevor D. McKee, Ke Cheng, Fatima Amanat, Florian Krammer, **Andrea Guarracino**, Gerardo Pepe, Carlo Tomino, Yacine Tandjaoui-Lambiotte, Yurdagul Uzunhan, Sarah Tubiana, Jade Ghosn, Luigi D. Notarangelo, Helen C. Su, Laurent Abel, Aurélie Cobat, Gai Elhanan, Joseph J. Grzymski, Andrea Latini, Sachdev S. Sidhu, Suresh Jain, Robert A. Davey, Jean-Laurent Casanova, Wenyi Wei, and Pier Paolo Pandolfi. Inhibition of HECT E3 ligases as potential therapy for COVID-19. ***Cell Death & Disease***, volume 12, pages 1–18, March 2021. ***Contribution: made Figure 4, and provided in silico 3D structures analysis.***

2021 Luca Mattiello, Sara Soliman Abdel Rehim, Martina Musella, Antonella Sistigu, **Andrea Guarracino**, Sara Vitale, Francesca Corradi, Claudia Galassi, Francesca Sperati, Gwenola Manic, Ruggero De Maria, and Ilio Vitale. The Targeting of MRE11 or RAD51 Sensitizes Colorectal Cancer Stem Cells to CHK1 Inhibition. ***Cancers***, volume 13, page 1957, January 2021. ***Contribution: made Figure 1.A, and helped in analyzing survival data.***

2021 Gwenola Manic, Martina Musella, Francesca Corradi, Antonella Sistigu, Sara Vitale, Sara Soliman Abdel Rehim, Luca Mattiello, Eva Malacaria, Claudia Galassi, Michele Signore, Matteo Pallocca, Stefano Scalera, Frauke Goeman, Francesca De Nicola, **Andrea Guarracino**, Rosa Pennisi, Fabrizio Antonangeli, Francesca Sperati, Marta Baiocchi, Mauro Biffoni, Maurizio Fanciulli, Marcello Maugeri-Saccà, Annapaola Franchitto, Pietro Pichierri, Ruggero De Maria, and Ilio Vitale. Control of replication stress and mitosis in colorectal cancer stem cells through the interplay of PARP1, MRE11 and RAD51. ***Cell Death & Differentiation***, pages 1–23, February 2021. ***Contribution: bioinformatics support.***

2021 Mariana G. Ferrarini, Avantika Lal, Rita Rebollo, Andreas J. Gruber, **Andrea Guarracino**, Itziar Martinez Gonzalez, Taylor Floyd, Daniel Siqueira de Oliveira, Justin Shanklin, Ethan Beausoleil, Taneli Pusa, Brett E. Pickett, and Vanessa Aguiar-Pulido. Genome-wide bioinformatic analyses predict key host and viral factors in SARS-CoV-2 pathogenesis. ***Communications Biology***, volume 4, page 590, December 2021. ***Contribution: differential expression analyses, including batch effects exploration, and GO/pathway enrichment analyses.***

In Conference Proceedings

2020 Flavia Villani, Francesco Porto, **Andrea Guarracino**, Robert W. Williams, Pjotr Prins, Gianluca Della Vedova, Erik Garrison, and Vincenza Colonna. Population genomics analyses on pangenome graphs. *Bioinformatics and Computational Biology Conference*, page Abstract, November 2020.

2020 Francesco Porto, Flavia Villani, **Andrea Guarracino**, Christian Fischer, Hao Chen, Robert W Williams, Vincenza Colonna, Gianluca Della Vedova, Erik Garrison, and Pjotr Prins. Scalable variant detection in pangenome models. *T2T-HPRC*, page Abstract, September 2020.

Talks & Poster presentations

Sept. 2022 *CTC-RG 2022*, Initial effort in generating a rat pangenome, (Abstract)

July 2022 *IGGSy 2022*, Chromosome communities in the human pangenome, (Presentation)

Oct. 2021 *Biodiversity Genomics 2021*, Chromosome communities in the human pangenome, (Abstract, Presentation)

Sept. 2021 *AGI2021*, A pangenome for the expanded BXD family of mice, (Abstract, Poster)

Sept. 2021 *GCB 2021*, ODGI: scalable tools for pangenome graphs, (Abstract, Presentation)

June 2021 *EACR*, Control of replication stress and mitosis in cancer stem cells, (Poster)

May 2021 *EMBL in Italy*, Identification of RNA sequence and structure motifs for protein interaction,(Poster)

May 2021 *The Biology of Genomes*, The PanGenome Graph Builder, (Abstract, Poster)

Nov. 2020 *BBCC*, Population genomics analyses on pangenome graphs, (Abstract, Poster)

Sept. 2020 *EG VCBM*, Graph Layout by Path-Guided Stochastic Gradient, (Abstract, Poster)

Sept. 2020 *T2T-HPRC*, Graph Layout by Path-Guided Stochastic Gradient, (Abstract, Poster)

Sept. 2020 *T2T-HPRC*, Scalable Variant Detection In Pangenome Models, (Abstract, Poster)

July 2020 *BCC*, COVID-19 PubSeq: Public SARS-CoV-2 Sequence Resource, (Abstract, Poster, Talk)

July 2020 *ISMB*, Pantograph: Scalable Interactive Graph Genome Visualization, (Abstract, Poster)

July 2020 *ISMB*, Semantic Variation Graphs - A Pangenome Ontology, (Abstract, Poster, BestPosterPrize)

July 2020 *ISMB*, Comprehensive analysis of human SARS-CoV-2 infection and host-virus interaction, (Abstract, Poster)

Proficiency in English

I am a native Italian speaker, and I am fluent in English being involved in multiple contexts for my research:

- **English language certification**: 21 Apr 2018 - ESB Level 1 Certificate in ESOL International All Modes (B2 CEFR); Final Grade: Pass with Distinction; Candidate Number: IT-0042274 (Certificate)
- I am an Associate Member in the **Human Pangenome Consortium** (HPRC) where I attend regular international meetings and present my work on pangenome graphs building and analysis
- I am in the **Variation Graph Team** (VG team), regularly attending their international meetings
- I worked on a **SARS-CoV-2 publication** with researchers from 11 countries (Ferrarini, Lal *et al.*, 2021)
- I was a helper during the **Google Summer of Code** (GSOC) for the "Parallel Graph Traversal for Variation Graphs" project (Blog)

Training Activity

2021/03/22 - 2021/03/24	nf-core hackaton - March 2021, *nf-core/pangenome pipeline development* (Link, nf-core/pangenome)
2020/11/09 - 2020/11/13	BioHackathon Europe, *Federated Interoperable Annotated Variation Graphs* (Link)
2020/07/08	Overcoming Challenges in Academic Writing: Tips for Writing Articles and Grant Applications (Certificate)
2020/04/05 - 2020/04/11	COVID-19-BH20 Biohackathon, *Groups: Pangenome, Pangenome Browser, Machine Learning, Gene Expression, Public Sequence Resource* (Link)
2017/09/27 - 2017/09/29	ELIXIR-IIB / Best practices for RNA-Seq data analysis, *Software Carpentry Workshop and Elixir-ITA / University of Salerno, Italy* (Certificate)

Computer skills

Programming languages	Python, R, C/C++, Rust, Java, HTML/CSS, Javascript, Bash, LaTeX, Assembly
Operating systems	Linux, Windows

Achievements

2021/07/09	Chair at the **Deciphering the complexity in neurodegeneration and cancer** workshop (Poster)
2020/10/12 - present	Associate Member of the **Human Pangenome Reference Consortium** (Link)
2020/06/07 - 2020/08/30	Helper for **Parallel Graph Traversal for Variation Graphs**, *Google Summer of Code* (Blog)
2020/05/06	Quote in the newspaper **Le Monde**: SARS-CoV-2 et Covid-19: jouons sur les mots (Article)

Awards

2020	Best Poster Prize on "Semantic Variation Graphs: Ontologies for Pangenome Graphs", *ISMB*
2016 - 2018	Scholarships during the Master's degree in Bioinformatic, *University of Rome Tor Vergata, Italy*
2007 - 2010	Scholarships during the Bachelor's degree in Computer Engineering, *University of Salerno, Italy*
2007	100/100 cum laude grade in the high school diploma, *IIS Basilio Focaccia, Italy*, (Info)
2007	Highest votes average (9.44/10) in all fifth-grade classes, *IIS Basilio Focaccia, Italy*, (Info)
2006	Highest votes average (9.33/10) in all fourth-grade classes, *IIS Basilio Focaccia, Italy*
2005	Highest votes average (9.22/10) in all third-grade classes, *IIS Basilio Focaccia, Italy*

Referees

Prof. Manuela Helmer-Citterich
Full Professor
Molecular Biology
University of Rome Tor Vergata, Italy
✉ citterich@uniroma2.it

Ilio Vitale, Ph.D.
Group Leader
Italian Institute for Genomic Medicine, Italy
Candiolo Cancer Institute
✉ iliovit@gmail.com

Prof. Erik Garrison
Assistant Professor
Genomics, Genetics, and Informatics
University of Tennessee Health Science Center, USA
✉ egarris5@uthsc.edu

Prof. Pjotr Prins
Assistant Professor
Genomics, Genetics, and Informatics
University of Tennessee Health Science Center, USA
✉ jprins@uthsc.edu

See https://github.com/AndreaGuarracino/andreaguarracino.github.io for certificates, abstracts, posters, and other information.
Online version of this CV: https://andreaguarracino.github.io/.