

Andrea Guarracino

Curriculum Vitae

Department of Genetics, Genomics and Informatics
The University of Tennessee, Memphis, USA
✉ aguarra1@uthsc.edu
📄 **Online CV:** <https://andreaguarracino.github.io>

Computer engineer working on pangenomics.

Current position

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

- Heterologous recombination in the human pangenome ([📄 Guarracino et al., 2023, Nature](#))
- Telomere-to-Telomere Robertsonian translocation characterization
- Nanopore sequencing for studying recombination in yeast
- Development of a new whole-genome aligner ([🔗 wfmash](#))
- Pangenome graph sorting and layout ([📄 Heumos*, Guarracino* et al., 2023, Bioinformatics](#))

Collaborations

2023/11/01 - **Honorary contract holder at the Princess Máxima Center for Pediatric Oncology, Utrecht, present Netherlands**, Reporting to Dr. Ruben van Boxtel and Prof. Pjotr Prins.

- Personalized pangenome references for improved cancer genomics
- 2022/11/01 - **E-Visitor at the Human Technopole, Milan, Italy**, Reporting to Prof. Nicole Soranzo and present Prof. Erik Garrison.
- Building pangenome graphs ([🔗 Garrison*, Guarracino* et al., 2023, bioRxiv](#)) ([🔗 pggg](#), [🔗 smoothxg](#))
- 2019/11/01 - **Italian Institute for Genomic Medicine and the Candiolo Cancer Institute, Candiolo, Italy**, present 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 - **Postdoctoral Associate at the Human Technopole, Milan, Italy**, Reporting to Prof. Nicole Soranzo and Prof. Erik Garrison.

- Unbiased pangenome graphs ([📄 Garrison and Guarracino, 2022, Bioinformatics](#)) ([🔗 seqwish](#))
- Optimized Dynamic Genome/Graph Implementation ([📄 Guarracino et al., 2022, Bioinformatics](#)) ([🔗 ODGI](#))

2013/03/04 - **Computer engineer for multiplatform firmware/software development, GISA S.n.c., Italy**, 2018/10/31 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 an e-commerce
- Remote assistance to customers for the usage and programming of multi-service machines
- Patent application on a universal system for services fruition (ITUA20165252, A1) ([📄 Patent](#))
- Basic design of simple electrical circuits for controlling actuators and reading analog/digital signals

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

2013/01/20 ○ Selling products, warehouse management and cleaning

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

2012/03/03 ○ Development of dynamic websites using Java Server Page, JavaScript, ASP.NET, PHP, MySQL

Education

- 2018/11/01 - **Ph.D. in Cellular and Molecular Biology (Bioinformatics)**, *University of Rome Tor Vergata, Italy*, "Investigating chromosomal instability in cancer stem cells", Evaluation: excellent quality.
2022/02/08
- 2016/10/03 - **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+.
2018/10/25
- 2007/10/01 - **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+.
2010/10/29

Research experience

- 2018/11/01 - **Bioinformatic analyses of multiomics data**, *University of Rome Tor Vergata, Italy*.
2022/02/08
- 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 ([Pietrosanto*, Adinolfi*, Guarracino* et al., 2021, NAR](#))
 - Web server development for RNA sequence and structure motif scan ([Guarracino et al., 2021, NAR](#))
 - 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 - **Previous software development for pangenomics**, *Virtual*.
- 2021/09/21
- Workflow development of a public sequence resource for on-the-fly analyses ([bh20-seq-resource](#))
 - Development of a pangenome graph browser ([Pantograph](#))

Teaching

- 2020/10/26 - **Teacher in 'Data Structures for Bioinformatics' (2 CFU/ECTS)**, creating new material for present the course. Master's degree in Bioinformatics, *University of Rome Tor Vergata, Italy* ([Material](#))
- 2024/06/19 - **Instructor/organizer in 'Computational Pangenomics'**, creating new material for the course.
2024/06/21 *University of Rome La Sapienza, Rome, Italy* ([Website](#), [Certificate](#))
- 2024/05/18 - **Instructor/organizer/chair in 'MemPanG24 Pangenomics'**, creating new material for the course. *University of Tennessee Health and Science Center, Memphis, USA* ([Website](#), [Material](#), [Certificate](#))
2024/05/22
- 2024/04/17 **Teacher in the 'PhD Program in Genetics, Molecular and Cellular Biology'**, introducing pangenomics and PGGB. *University of Pavia, Italy (Virtual)* ([Flier](#), [Invitation](#))
- 2024/04/09 **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, Netherlands (Virtual)* ([Website](#))
- 2023/11/13 - **Instructor in 'Pangenome & RefGraph Workshop'**, creating new material and analyzing new human genome assemblies. *H3ABioNet, Cape Town, South Africa* ([Material](#), [Invitation](#))
2023/11/17
- 2023/10/08 - **Instructor/organizer in 'Complex Trait Community & Rat Genome'**, creating new material for the workshop. *University of Tennessee Health and Science Center, Memphis, USA* ([Website](#), [Certificate](#))
2023/10/12
- 2023/05/30 - **Instructor/organizer in 'MemPanG23 Pangenomics'**, creating new material for the course.
2023/06/02 *University of Tennessee Health and Science Center, Memphis, USA* ([Website](#), [Material](#), [Certificate](#))

- 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, Netherlands (Virtual)* ([Website](#))
- 2022/05/23 - **Instructor in 'CPANG22 Computational PANGenomics'**, creating new material for the course. 2022/05/27 *Instituto Gulbenkian de Ciência, Oeiras, Portugal* ([Website](#), [Material](#), [Certificate](#))
- 2018 - 2021 **Tutor in 'Bioinformatics' (6 CFU/ECTS)**, reviewing the practicals and assisting the students. Bachelor's degree in Biological Science, *University of Rome Tor Vergata, Italy* ([Certificate](#))
- 2019/12/16 - **Exam assistance for 'Computational Proteogenomics' (2 CFU/ECTS)**, Master's degree in Bioinformatics, *University of Rome Tor Vergata, Italy*
- 2019/06/07 - **Exam assistance for 'Molecular Biology' (8 CFU/ECTS)**, Bachelor's degree in Biological Science, *University of Rome Tor Vergata, Italy*
- 2019/06/07 - **Exam assistance for 'Bioinformatics' (6 CFU/ECTS)**, Bachelor's degree in Biological Science, 2021/07/21 *University of Rome Tor Vergata, Italy*

Symposia

- 2024/06/30 - **Organizer of the "Human genetic variability in the Pangenomic era" symposia**, *Society for Molecular Biology & Evolution 2024 (SMBE24), Mexico*, ([Call for abstracts](#), [Certificate](#))

Mentoring

- 2023/10/01 - **Dissecting the intracellular response to replication and mitotic stress in colorectal cancer for the design of novel effective (immuno)therapies**, PhD program in Systems Medicine, Computational Biology curricula, *SEMM European School of Molecular Medicine, Italy*
present
- 2021/09/02 - **Machine learning to detect *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 - **Effect analysis 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 - **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 - **Machine Learning methods applied to kinase-substrate interaction prediction**, Master's degree in Bioinformatics, *University of Rome Tor Vergata, Italy*
- 2020/03/02 - **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 - **Study of normalization techniques' effects in gene expression correlation analyses**, Bachelor's degree in Biological Science, *University of Rome Tor Vergata, Italy*

Invitations

- 2024/02/26 **Seminar on "Heterologous recombination in the human pangenome"**, University of Rome La Sapienza, *Italy* ([Invitation](#), [Brochure](#))
- 2023/09/14 - **Invited speaker on "Heterologous recombination in the human pangenome"**, Joint Meeting AGI-SIMAG, *Cortona, Italy* ([Invitation](#), [Brochure](#))
- 2023/09/13 **Seminar on "Heterologous recombination in the human pangenome"**, University of Rome Tor Vergata, *Italy* ([Invitation](#))

Publications

See them on [Google Scholar](#).

Journal Articles (*first authorship)

- Submitted DongAhn Yoo, Arang Rhie, Prajna Hebbar, Francesca Antonacci, Glennis A. Logsdon, Steven J. Solar, Dmitry Antipov, Brandon D. Pickett, Yana Safonova, Francesco Montinaro, Yanting Luo, Joanna Malukiewicz, Jessica M. Storer, Jiadong Lin, Abigail N. Sequeira, Riley J. Mangan, Glenn Hickey, Graciela Monfort Anez, Parithi Balachandran, Anton Bankevich, Christine R. Beck, Arjun Biddanda, Matthew Borchers, Gerard G. Bouffard, Emry Brannan, Shelise Y. Brooks, Lucia Carbone, Laura Carrel, Agnes P. Chan, Juyun Crawford, Mark Diekhans, Eric Engelbrecht, Cedric Feschotte, Giulio Formenti, Gage H. Garcia, Luciana de Gennaro, David Gilbert, Richard E. Green, **Andrea Guarracino**, Ishaan Gupta, Diana Haddad, Junmin Han, Robert S. Harris, Gabrielle A. Hartley, William T. Harvey, Michael Hiller, Kendra Hoekzema, Marlys L. Houck, Hyeonsoo Jeong, Kaivan Kamali, Manolis Kellis, Bryce Kille, Chul Lee, Youngho Lee, William Lees, Alexandra P. Lewis, Qihui Li, Mark Loftus, Yong Hwee Eddie Loh, Hailey Loucks, Jian Ma, Yafei Mao, Juan F. I. Martinez, Patrick Masterson, Rajiv C. McCoy, Barbara McGrath, Sean McKinney, Britta S. Meyer, Karen H. Miga, Saswat K. Mohanty, Katherine M. Munson, Karol Pal, Matt Pennell, Pavel A. Pevzner, David Porubsky, Tamara Potapova, Francisca R. Ringeling, Joana L. Rocha, Oliver A. Ryder, Samuel Sacco, Swati Saha, Takayo Sasaki, Michael C. Schatz, Nicholas J. Schork, Cole Shanks, Linnea Smeds, Dongmin R. Son, Cynthia Steiner, Alexander P. Sweeten, Michael G. Tassia, Francoise Thibaud-Nissen, Edmundo Torres-Gonzalez, Mihir Trivedi, Wenjie Wei, Julie Wertz, Muyu Yang, Panpan Zhang, Shilong Zhang, Yang Zhang, Zhenmiao Zhang, Sarah A. Zhao, Yixin Zhu, Erich D. Jarvis, Jennifer L. Gerton, Iker Rivas-Gonzalez, Benedict Paten, Zachary A. Szpiech, Christian D. Huber, Tobias L. Lenz, Miriam K. Konkel, Soojin V. Yi, Stefan Canzar, Corey T. Watson, Peter H. Sudmant, Erin Molloy, Erik Garrison, Craig B. Lowe, Mario Ventura, Rachel J. O'Neill, Sergey Koren, Kateryna D. Makova, Adam M. Phillippy, and Evan E. Eichler. Complete sequencing of ape genomes. *bioRxiv*. Cold Spring Harbor Laboratory, Submitted. **Contribution: Pangenome alignment/Divergence.**
- Submitted Emilia Volpe, Luca Corda, Elena Di Tommaso, Franca Pelliccia, Riccardo Ottalevi, Danilo Licastro, Giulio Formenti, Mattia Capulli, **Andrea Guarracino**, Evelyne Tassone, and Simona Giunta. The complete human diploid reference genome of rpe-1 identifies the phased epigenetic landscapes from multi-omics data. *bioRxiv*. Cold Spring Harbor Laboratory, Submitted. **Contribution: Support for the analyses and figures, Figure 2, paper writing.**
- Submitted Flavia Villani, **Andrea Guarracino**, Rachel R Ward, Tomomi Green, Madeleine Emms, Michal Pravenec, Pjotr Prins, Erik Garrison, Robert W. Williams, Hao Chen, and Vincenza Colonna. Pangenome reconstruction in rats enhances genotype-phenotype mapping and novel variant discovery. *bioRxiv*. Cold Spring Harbor Laboratory, Submitted. **Contribution: Pangenome graph building and analyses, structural variant calling, paper writing.**
- Submitted Ling Li, Zhiping Wu, **Andrea Guarracino**, Flavia Villani, Deihui Kong, Ariana Mancieri, Aijun Zhang, Laura Saba, Hao Chen, Hana Brozka, Karel Vales, Anna N. Senko, Gerd Kempermann, Ales Stuchlik, Michal Pravenec, Pjotr Prins, Junmin Peng, Robert W. Williams, and Xusheng Wang. Genetic modulation of protein expression in rat brain. *bioRxiv*. Cold Spring Harbor Laboratory, Submitted. **Contribution: Pangenome graph analysis, paper editing.**
- In review Sergey Koren, Zhigui Bao, **Andrea Guarracino**, Shujun Ou, Sara Goodwin, Katharine M Jenike, Julian Lucas, Brandy McNulty, Jimin Park, Mikko Rautianinen, Arang Rhie, Dick Roelofs, Harrie Schneiders, Ilse Vrijenhoek, Koen Nijbroek, Doreen Ware, Michael C. Schatz, Erik Garrison, Sanwen Huang, William Richard McCombie, Karen H Miga, Alexander H.J. Wittenberg, and Adam M Phillippy. Gapless assembly of complete human and plant chromosomes using only nanopore sequencing. *bioRxiv*. Cold Spring Harbor Laboratory, In review. **Contribution: Human centromere analysis.**
- In review Simon Heumos, Michael L Heuer, Friederike Hanssen, Lukas Heumos, Andrea Guarracino, Peter Heringer, Philipp Ehmele, Pjotr Prins, Erik Garrison, and Sven Nahnsen. Cluster efficient pangenome graph construction with nf-core/pangenome. *bioRxiv*. Cold Spring Harbor Laboratory, In review. **Contribution: software development, paper editing.**

- In review Jonas A Gustafson, Sophia B Gibson, Nikhita Damaraju, Miranda PG Zalusky, Kendra Hoekzema, David Twesigomwe, Lei Yang, Anthony A Snead, Phillip A Richmond, Wouter De Coster, Nathan D Olson, **Andrea Guarracino**, Qiuhui Li, Angela L Miller, Joy Goffena, Zachery Anderson, Sophie HR Storz, Sydney A Ward, Maisha Sinha, Claudia Gonzaga-Jauregui, Wayne E Clarke, Anna O Basile, Andre Corvelo, Catherine E Reeves, Adrienne Helland, Rajeeva Lochan Musunuri, Mahler Revsine, Karynne E Patterson, Cate Paschal, Christina Zakarian, Sara Goodwin, Tanner D Jensen, Esther Robb, 1000 Genomes ONT Sequencing Consortium, University of Washington Center for Rare Disease Research (UW-CRDR), Genomics Research to Elucidate the Genetics of Rare Diseases (GREGoR) Consortium, W. Richard McCombie, Fritz J Sedlazeck, Justin M Zook, Stephen B Montgomery, Erik Garrison, Mikhail Kolmogorov, Michael C Schatz, Jr. Richard N McLaughlin, Harriet Dashnow, Michael C Zody, Matthew Loose, Miten Jain, Evan E Eichler, and Danny E Miller. Nanopore sequencing of 1000 genomes project samples to build a comprehensive catalog of human genetic variation. *medRxiv*. Cold Spring Harbor Laboratory Press, In review. **Contribution: Pangenome graph building and analyses, paper method section writing.**
- Accepted* 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. *Nature Methods*. Cold Spring Harbor Laboratory, Accepted*. **Contribution: Software development, experiments, paper writing, documentation, testing.**
- Accepted Davide Bolognini, Alma Halgren, Runyang Nicolas Lou, Alessandro Raveane, Joana L. Rocha, **Andrea Guarracino**, Nicole Soranzo, Jason Chin, Erik Garrison, and Peter H Sudmant. Global diversity, recurrent evolution, and recent selection on amylase structural haplotypes in humans. *Nature*. Cold Spring Harbor Laboratory, Accepted. **Contribution: Pangenome graph analysis, genome assembly, paper writing and editing.**
- 2024 Simon* Heumos, **Andrea Guarracino***, Jan-Niklas M Schmelzle, Jiajie Li, Zhiru Zhang, Jörg Hagmann, Sven Nahnsen, Pjotr Prins, and Erik Garrison. Pangenome graph layout by Path-Guided Stochastic Gradient Descent. *Bioinformatics*, page btae363, 07 2024. **Contribution: Algorithm implementation and evaluation, paper writing.**
- 2023 Zuyu Yang, **Andrea Guarracino**, Patrick J. Biggs, Michael A. Black, Nuzla Ismail, Jana Renee Wold, Tony R. Merriman, Pjotr Prins, Erik Garrison, and Joep de Ligt. Pangenome graphs in infectious disease: a comprehensive genetic variation analysis of neisseria meningitidis leveraging oxford nanopore long reads. *Frontiers in Genetics*, volume 14. Frontiers Media SA, August 2023. **Contribution: Pangenomic analyses and support, paper editing.**
- 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 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 L. Gerton, Patrick G. S. 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 E. G. Sauria, Fritz J. Sedlazeck, Kishwar Shafin, Valery A. Shepelev, Alaina Shumate, Jessica M. Storer, Likhitha Surapaneni, Angela M. Taravella Oill, Françoise Thibaud-Nissen, Winston Timp, Marta Tomaszkiwicz, 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 J. O'Neill, Michael C. Schatz, Karen H. Miga, Kateryna D. Makova, and Adam M. Phillippy. The complete sequence of a human y chromosome. *Nature*, volume 621, pages 344–354. Springer Science and Business Media LLC, August 2023. **Contribution: Variants and Liftover.**
- 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.**
- 2023 Noé Cochetel, Andrea Minio, **Andrea Guarracino**, Jadran F. Garcia, Rosa Figueroa-Balderas, Mélanie Massonnet, Takao Kasuga, Jason P. Londo, Erik Garrison, Brandon S. Gaut, and Dario Cantu. A super-pangenome of the north american wild grape species. *Genome Biology*, volume 24. Springer Science and Business Media LLC, December 2023. **Contribution: Support for pangenome graph building and graph read mapping.**

- 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, Françoise 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 Korf, 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. Grzymiski, 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.

Awards

- 2023/09/13 **Student Travel Grant, 600 CHF (632.36 EUR)**, International Genome Graph Symposium 2022, Cortona, Switzerland ([Certificate](#))

Talks & Poster

- July 2024 *IGGSy 2024*, The complete sequence of Robertsonian chromosomes, ([Presentation](#))
- May 2024 *The Biology of Genomes*, Aligning pangenomes with hierarchical wavefront algorithm, ([Poster](#))
- July 2023 *SMBE23*, Recombination between heterologous human acrocentric chromosomes, ([Poster](#))
- July 2023 *SMBE23*, Building a Pangenome Graph for the HXB/BXH Recombinant Inbred Rat Strain Family: Enhanced Discovery of Complex Variants and Validation with Sanger Sequencing, ([Poster](#))
- 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*, Chr. 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*, Analysis of human SARS-CoV-2 infection and host-virus interaction, ([Abstract](#), [Poster](#))

Training Activity

- 2023/07/17 - **A multidisciplinary approach to epistasis detection**, *Lorentz Center, Leiden, Netherlands* ([Poster](#))
- 2021/03/22 - **nf-core hackaton**, *nf-core/pangenome pipeline development* ([Link](#), [nf-core/pangenome](#))
- 2020/11/09 - **BioHackathon Europe**, *Federated Interoperable Annotated Variation Graphs* ([Link](#))
- 2020/07/08 **Overcoming Challenges in Academic Writing**: Articles and Grant Applications ([Certificate](#))
- 2021/04/21 **English language certification**, ESB Level 1 (B2 CEFR), Pass with distinction ([Certificate](#))
- 2020/04/05 - COVID-19-BH20 Biohackathon, *Groups: Pangenome, Pangenome Browser, Machine Learning, Gene Expression, Public Sequence Resource* ([Link](#))
- 2017/09/27 - ELIXIR-IIB / Best practices for RNA-Seq data analysis, *Software Carpentry Workshop and Elixir-ITA / University of Salerno, Italy* ([Certificate](#))

Misc

- 2020/10/20 Associate Member of the **Human Pangenome Reference Consortium** ([Collection](#))
- 2021/07/09 Chair at **Deciphering the complexity in neurodegeneration and cancer** workshop ([Poster](#))
- 2020/06/07 - 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](#))

Achievements

- 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*

Computer skills

Programming C/C++, Rust, Java, Python, R, HTML/CSS, Javascript, Bash, LaTeX, Assembly
O.S. Linux, Windows

Referees

Prof. Manuela Helmer-Citterich

Full Professor

Molecular Biology

University of Rome Tor Vergata, Italy

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Ilio Vitale, Ph.D.

Group Leader

Italian Institute for Genomic Medicine, Italy

Candiolo Cancer Institute

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Prof. Erik Garrison

Assistant Professor

Genomics, Genetics, and Informatics

University of Tennessee Health Science Center, USA

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Prof. Pjotr Prins

Associate Professor

Genomics, Genetics, and Informatics

University of Tennessee Health Science Center, USA

✉ jprins@uthsc.edu

Online version of this CV for certificates and other information: <https://andreaguarracino.github.io/>