

# Milton Pividori, Ph.D.

Assistant Professor in Biomedical Informatics - University of Colorado Anschutz Medical Campus, USA

## Personal information

Name: Milton Damián Pividori

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Github: <https://github.com/pivlab>

Residence: Philadelphia, Pennsylvania, United States

## Education

- 2016 Ph.D. on Information Systems Engineering  
Research institute for signals, systems and computational intelligence, Santa Fe, Argentina  
Universidad Tecnológica Nacional, Santa Fe, Argentina  
Thesis: Cluster ensembles with applications in bioinformatics  
Advisors: Georgina Stegmayer and Diego Milone
- 2010 B.S. in Information Systems Engineering  
Universidad Tecnológica Nacional, Santa Fe, Argentina

## Employment

- 2023-present Assistant Professor in the Department of Biomedical Informatics,  
University of Colorado Anschutz Medical Campus, CO, USA.
- 2020-2023 Postdoctoral researcher at the Perelman School of Medicine,  
University of Pennsylvania, PA, USA.
- 2017-2020 Postdoctoral scholar at the Section of Genetic Medicine, Department of Medicine,  
University of Chicago, IL, USA.
- 2010-2012 Senior Software Engineer at Folder IT,  
Santa Fe, Argentina.

## Publications

### Articles

**Milton Pividori**, Casey Greene. A publishing infrastructure for AI-assisted academic authoring. *bioRxiv*, doi: 10.1101/2023.01.21.525030, 2023.

Gengjie Jia, Xue Zhong, Hae Kyung Im, Nathan Schoettler, **Milton Pividori**, D. Kyle Hogarth, Anne I. Sperling, Steven R. White, Edward T. Naureckas, Christopher S. Lyttle, Chikashi Terao, Yoichiro Kamatani, Masato Akiyama, Koichi Matsuda, Michiaki Kubo, Nancy J. Cox, Carole Ober, Andrey Rzhetsky, Julian Solway. Discerning asthma endotypes through comorbidity mapping. *Nature Communications*, doi: 10.1038/s41467-022-33628-8, 2022.

**Milton Pividori**, Marylyn Ritchie, Diego Milone, Casey Greene. An efficient not-only-linear correlation coefficient based on machine learning. *bioRxiv*, doi: 10.1101/2022.06.15.496326, 2022.

Van Truong, Jakob Woerner, Tess Cherlin, Yuki Bradford, Daniel Hui, Anastasia Lucas, Manu Shivakumar, Rachit Kumar, **Milton Pividori**, Chelsea Okeh, Chris Jones, Abigail Bossa, Stephen Turner, Marylyn Ritchie, Shefali Verma. Quality control procedures for genome-wide association studies. *Current Protocols*, doi: 10.1002/cpz1.603, 2022.

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\*Alphabetical order.

†Equal contribution.

Yanyu Liang, **Milton Pividori**, Ani Manichaikul, Abraham A. Palmer, Nancy J. Cox, Heather Wheeler, Hae K. Im. Polygenic transcriptome risk scores (PTRS) can improve portability of polygenic risk scores across ancestries. *Genome Biology*, doi: 10.1186/s13059-021-02591-w, 2022.

Binglan Li, Yogasudha Veturi, Anastasia Lucas, Yuki Bradford, Shefali S. Verma, Anurag Verma, Joseph Park, Wei-Qi Wei, Qiping Feng, Bahram Namjou, Krzysztof Kiryluk, Iftikhar Kullo, Yuan Luo, **Milton Pividori**, Hae Kyung Im, Casey S. Greene, Marylyn D. Ritchie. Multi-ancestry gene-trait connection landscape using electronic health record (EHR) linked biobank data. *medRxiv*, doi: 10.1101/2021.10.21.21265225, 2021.

**Milton Pividori**, Sumei Lu, Binglan Li, Chun Su, Matthew E. Johnson, Wei-Qi Wei, Qiping Feng, Bahram Namjou, Krzysztof Kiryluk, Iftikhar Kullo, Yuan Luo, Blair D. Sullivan, Carsten Skarke, Marylyn D. Ritchie, Struan F.A. Grant, Casey S. Greene. Projecting genetic associations through gene expression patterns highlights disease etiology and drug mechanisms. *bioRxiv*, doi: 10.1101/2021.07.05.450786, 2021.

Alvaro Barbeira, Rodrigo Bonazzola, Eric Gamazon, Yanyu Liang, YoSon Park, Sarah Kim-Hellmuth, Gao Wang, Zhuoxun Jiang, Dan Zhou, Farhad Hormozdiari, Boxiang Liu, Abhiram Rao, Andrew Hamel, **Milton Pividori**, [...], Hae Kyung Im. Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. *Genome Biology*, doi: 10.1186/s13059-020-02252-4, 2021.

Madison Cooley, Casey Greene, Davis Issac, **Milton Pividori**<sup>\*</sup>, Blair Sullivan. Parameterized algorithms for identifying gene co-expression modules via weighted clique decomposition. *SIAM Conference on Applied and Computational Discrete Algorithms 2021 (ACDA21)*, doi: 10.1137/1.9781611976830.11, 2021.

Gengjie Jia, Yu Li, Xue Zhong, Kanix Wang, **Milton Pividori**, Rabab Al-omairy, Aniello Esposito, Hatem Ltaief, Chikashi Terao, Masato Akiyama, Koichi Matsuda, David E. Keyes, Hae Kyung Im, Takashi Gojobori, Yoichiro Kamatani, Michiaki Kubo, Nancy J. Cox, Xin Gao, Andrey Rzhetsky. The continuous space of human diseases mapped to genetic loci predicts disease trajectories and risk. *In revision*, 2021.

**Milton Pividori**<sup>†</sup>, Padma S. Rajagopal<sup>†</sup>, Alvaro Barbeira, Yanyu Liang, Owen Melia, Lisa Bastarache, YoSon Park, Xiaoquan Wen, GTEx Consortium, Hae K. Im. PhenomeXcan: Mapping the genome to the phenome through the transcriptome. *Science Advances*, 6(37):eaba2083, doi: 10.1126/sciadv.aba2083, 2020.

Abhay Hukku, **Milton Pividori**, Francesca Luca, Roger Pique-Regi, Hae Kyung Im, Xiaoquan Wen. Probabilistic colocalization of genetic variants from complex and molecular traits: promise and limitations. *American Journal of Human Genetics*, doi: 10.1016/j.ajhg.2020.11.012, 2020.

Leandro Bugnon, Cristian Yones, Jonathan Raad, Matías Gerard, Mariano Rubiolo, Gabriela Merino, **Milton Pividori**, Leandro Di Persia, Diego Milone, Georgina Stegmayer. DL4papers: a deep learning approach for the automatic interpretation of scientific articles. *Bioinformatics*, 36(11):3499-3506, doi: 10.1093/bioinformatics/btaa111, 2020.

**Milton Pividori**<sup>†</sup>, Nathan Schoettler<sup>†</sup>, Dan Nicolae, Carole Ober, Hae Kyung Im. Shared and distinct genetic risk factors for childhood-onset and adult-onset asthma: genome-wide and transcriptome-wide studies. *The Lancet Respiratory Medicine*, 7(6):509-522, doi: 10.1016/S2213-2600(19)30055-4, 2019.

Alvaro Barbeira, **Milton Pividori**, Jiamao Zheng, Heather Wheeler, Dan Nicolae, Hae Kyung Im. Integrating predicted transcriptome from multiple tissues improves association detection. *PLOS Genetics*, 15(1):e1007889, doi: 10.1371/journal.pgen.1007889, 2019.

Georgina Stegmayer, Leandro Di Persia, Mariano Rubiolo, Matias Gerard, **Milton Pividori**, Cristian Yones, Leandro Bugnon, Tadeo Rodriguez, Jonathan Raad, Diego Milone. Predicting novel microRNA: a comprehensive comparison of machine learning approaches. *Briefings in Bioinformatics*, 20(5):1607-1620, doi: 10.1093/bib/bby037, 2019.

**Milton Pividori**, Andres Cernadas, Luis de Haro, Fernando Carrari, Georgina Stegmayer, Diego Milone. Clustermatch: discovering hidden relations in highly-diverse kinds of qualitative and quantitative data without standardization. *Bioinformatics*, 35(11):1931-1939, doi: 10.1093/bioinformatics/bty899, 2019.

**Milton Pividori**, Hae Kyung Im. ukbREST: efficient and streamlined data access for reproducible research in large biobanks. *Bioinformatics*, 35(11):1971-1973, doi: 10.1093/bioinformatics/bty925, 2019.

**Milton Pividori**, Georgina Stegmayer, Diego Milone. Diversity control for improving the analysis of consensus clustering. *Information Sciences*, 361:120-134, doi: 10.1016/j.ins.2016.04.027, 2016.

Georgina Stegmayer, **Milton Pividori**, Diego H. Milone. A very simple and fast way to access and validate algorithms in reproducible research. *Briefings in Bioinformatics*, 17(1):180-183, doi: 10.1093/bib/bbv054, 2016.

**Milton Pividori**, Georgina Stegmayer, Diego H. Milone. A method to improve the analysis of cluster ensembles. *Ibero-American Journal of Artificial Intelligence*, 17(53):46-56, doi: 10.4114/intartif.vol17iss53, 2014.

### Book chapters

Ma. de los Milagros Gutiérrez, Jorge Roa, **Milton Pividori**, Georgina Stegmayer, Jorge Vega. FAIA: a framework for intelligent agents development. *La Tecnología Educativa al Servicio de la Educación Tecnológica: Experiencias e investigaciones en la UTN*, Ed. UTN, ISBN 978-987-25855-9-4, 2010.

Jorge Roa, **Milton Pividori**, Ma. De los Milagros Gutiérrez, Georgina Stegmayer. How to develop intelligent agents in an easy way with FAIA. *Quality and Communicability for Interactive Hypermedia Systems: Concepts and Practices for Design*, Ed. IGI-Global, ISBN 978-1-61520-763-3, pp. 120-140, 2009.

### Grants and awards

2022 (*awarded*): NIH Pathway to Independence Award (K99/R00). Title: "Computational approaches to characterize heterogeneity and improve risk stratification in complex disease phenotypes." Impact score: 21.

2019: BSD Career Advancement for Postdocs (CAP) Travel Award. Funded by: Postdoctoral Association, Division of Biological Sciences, University of Chicago, USA.

2019: Title: "Characterizing the function of understudied genes using large biobanks genotype and phenotype data." Funded by: Small Grants Program, BSD Office of Diversity and Inclusion, University of Chicago, USA.

2018-2020: Title: "Computational tool for genetic data fusion for obtaining high-biomass crops under environmental stress conditions." Funded by: Ministry of Science, Technology and Productive Innovation, (Santa Fe), Argentina. Director: Georgina Stegmayer.

2014: Member in PICT 2014-2627. Title: "Data mining in bioinformatics: integration and analysis based on artificial intelligence." Funded by: National Agency of Scientific and Technological Promotion, Argentina. Director: Diego Milone.

2013-2015: Member in PIP 2013-2015 #117. Title: "Data mining in bioinformatics: integrated approach based on artificial intelligence." Funded by: National Agency of Scientific and Technological Promotion, Argentina. Director: Georgina Stegmayer.

2013-2015: Member in CAI+D 2011 #054. Title: "Models and algorithms for data mining in bioinformatics." Funded by: School of Engineering and Water Sciences, Universidad Nacional del Litoral, Argentina. Director: Georgina Stegmayer.

2013-2015: Member in UTN-FRSF 25/O153. Title: "Data mining in bioinformatics." Funded by: Universidad Tecnológica Nacional, Argentina. Director: Georgina Stegmayer.

2008-2010 Member in UTN-FRSF 25/O103. Title: "FAIA: framework for intelligent agents development for artificial intelligence problems." Funded by: Universidad Tecnológica Nacional, Argentina. Director: Georgina Stegmayer.

### Teaching

2014-2015: Teaching assistant in the graduate course "Data mining in bioinformatics." School of Engineering and Water Sciences, Universidad Nacional del Litoral.

2014-2015: Co-director in undergraduate thesis in Informatics Engineering, School of Engineering and Water Sciences, Universidad Nacional del Litoral. *Thesis title*: "Development of a computational tool for ensemble clustering applied to heterogeneous biological data sets." *Student*: Marcos Yedro.

2013-2014: Co-director in undergraduate thesis in Information System Engineering, Universidad Tecnológica Nacional (Regional School of Santa Fe). *Thesis title*: "Design and development of a web application for the bioinformatics tool \*omeSOM." *Students*: Juan Pablo De Marco and Matías Gabriel Tardivo.

2009-2010: Teaching assistant in the undergraduate course “Artificial Intelligence.” Universidad Tecnológica Nacional (Regional School of Santa Fe).

## Presentations

### *Invited talks*

2023: “A publishing infrastructure for AI-assisted academic authoring.” Statistical Genetics Journal Club, Department of Medicine, University of Chicago.

2022: “An interpretable gene module-based approach for genetic studies.” Rising Stars in Genetics and Genomics Symposium, Department of Human Genetics, University of Utah.

2021: “Interpretable computational approaches to precision medicine.” Research Seminar Series, Division of Biomedical Informatics & Personalized Medicine, University of Colorado Anschutz Medical Campus.

2019: “Shared and distinct genetic risk factors for childhood-onset and adult-onset asthma: genome-wide and transcriptome-wide studies.” Webinar journal club organized by the Assembly on Allergy, Immunology, and Inflammation, American Thoracic Society.

### *Conference works (selected)*

**Milton Pividori**, Marylyn Ritchie, Diego Milone, Casey Greene. An efficient not-only-linear correlation coefficient based on machine learning. *International Society for Computational Biology (ISCB) Rocky Mountain Bioinformatics Conference*, 2022. Accepted for an **oral presentation**.

**Milton Pividori**, Padma S. Rajagopal, Alvaro Barbeira and Hae Kyung Im. Biclustering of a large gene to phenome catalog of associations unveils hidden connections between complex traits and genes. *American Society of Human Genetics*, 2019. Accepted for a **platform talk**.

**Milton Pividori**, Nathan Schoettler, Dan Nicolae, Carole Ober and Hae Kyung Im. Shared and distinct genetic risk factors for childhood-onset and adult-onset asthma: genome-wide and transcriptome-wide studies. *UK Biobank 2019 Scientific Conference*, 2019. Selected in the **top 10 posters in the UK Biobank Early-Career Researcher of the Year Competition** (link to announcement webpage).

**Milton Pividori**, Georgina Stegmayer and Diego Milone. Cluster ensembles for big data mining problems. *AGRANDA 2015 (Argentine Symposium on Big Data)*, 44 *JAIIO (Argentine Conference on Informatics)*, ISSN 2451-7569, pp. 52-54, 2015.

**Milton Pividori**, Georgina Stegmayer, Fernando Carrari and Diego Milone. Consensus clustering from heterogeneous measures of *S. Lycopersicum*. *4CAB2C (IV Argentine Conference on Computational Biology and Bioinformatics)*, 2013. Selected to receive an **honor mention**.

**Milton Pividori**, Georgina Stegmayer and Diego Milone. A novel method to control the diversity in cluster ensembles. *ASAI 2013 (Argentine Symposium on Artificial Intelligence)*, 42 *JAIIO (Argentine Conference on Informatics)*, ISBN 1850-2784, pp. 121-132, 2013.

### *Other conferences works*

**Milton Pividori**, Marylyn D. Ritchie, Diego H. Milone, Casey S. Greene. An efficient not-only-linear correlation coefficient based on machine learning. *Intelligent Systems for Molecular Biology (ISMB)*, 2022.

**Milton Pividori**, Olivia Cheng, Casey Greene. PhenoPLIER: integrating transcriptome-wide association studies with gene co-expression patterns. *Cold Spring Harbor Labs - Biological Data Science*, 2020.

Nathan Schoettler, **Milton Pividori**, Dan Nicolae, Hae Kyung Im, Carole Ober. Genetic Risk Factors for Asthma Age of Onset Implicate Epithelial Barrier Dysfunction and Innate Immune Genes in Earlier Onset Asthma. *Advances in asthma pathogenesis*, 2019.

**Milton Pividori** and Hae Kyung Im. ukbrest: REST API for easy and efficient access to UK Biobank data. *2017 Annual Meeting of the International Genetic Epidemiology Society (IGES)*.

**Milton Pividori** and Hae Kyung Im. Assessing the phenome-wide consequences of gene expression variation using UK Biobank. *GTEEx Project Community Scientific Meeting 2017. Selected for a talk.*

**Milton Pividori**, Georgina Stegmayer, Andrés Cernadas, Mariana Conte, Fernando Carrari and Diego Milone. A novel approach for highly-diverse multi-omics data fusion applied to tomato germplasm selection. *ISCB-LA 2016 (International Society for Computational Biology - Latin America 2016), 2016. Selected for a talk.*

Andrés Cernadas, Mariana Conte, **Milton Pividori**, Ester Marina Insani, Marisa Gisela López, Ramón Asís, Matilde D'Angelo, María Inés Zanor, Silvana Boggio, Estela Valle, Pablo Asprelli, Iris Peralta, Diego Milone, Georgina Stegmayer and Fernando Carrari. Computational clustering integration of metabolomics, transcriptomics and agronomical data for germplasm selection in a highly diverse tomato landrace collection. *LAMPS 2016 (2nd. Latin American Metabolic Profiling Symposium), 2016.*

### Seminar talks

2015: MapReduce for Big Data processing. School of Engineering and Water Sciences, Universidad Nacional del Litoral, Argentina.

2015: Amazon EC2: cloud computing. School of Engineering and Water Sciences, Universidad Nacional del Litoral, Argentina.

2009: Introduction to Version Control Systems. Regional School of Santa Fe, Universidad Tecnológica Nacional, Argentina.

2009: Business Intelligence using Free Software. Regional School of Santa Fe, Universidad Tecnológica Nacional, Argentina.

### Service

2016-2020: Reviewer in Bioinformatics, Briefings in Bioinformatics, Information Sciences, G3 (Genes, Genomes, Genetics), npj Systems Biology and Applications, GigaScience (see more in my Publons profile).

2017-2020 Committee member, Argentine Symposium on Artificial Intelligence (ASAI).

2008-2012: Founder and member of the "Free Software Group." Regional School of Santa Fe, Universidad Tecnológica Nacional, Argentina.

2008-2010: Student Representative at the Information Systems Department Council. Regional School of Santa Fe, Universidad Tecnológica Nacional, Argentina.

### Professional associations

2018-present: American Society of Human Genetics (ASHG).

2008-2014: Argentinian Society of Informatics (SADIO).

### Languages

Spanish (native), English