FORMATO EUROPEO PER IL CURRICULUM VITAE

INFORMAZIONI PERSONALI

Nome	**Pagliarini Roberto**
Indirizzo	**Dipartimento di matematica, Informatica and Fisica – Università Degli studi di Udine - Polo Scientifico Rizzi, Via delle Scienze 206, 33100, Udine, Italia**
Telefono	**0432 553489**
E-mail	**roberto.pagliarini@uniud.it**
Nazionalità	Italiana
Data di nascita	23/07/1981

ESPERIENZA LAVORATIVA

• Date (da – a)	Da Febbraio 2023
• Università degli studi di Udine	Dipartimento di Matematica, Informatica e Fisica
• Qualifica	Ricercatore a tempo determinato
• Date (da – a)	Luglio 2016 – Febbraio 2023
• IRCCS Ospedale San Raffaele	Divisione di Genetica e Biologia Molecolare
• Qualifica	Senior Postdoctoral Fellow
• Date (da – a)	Giugno 2011 – Giugno 2016
• Istituto Telethon di Genetica e Medicina	Systems and Synthetic Biology Lab
• Qualifica	Postdoctoral Fellow
• Date (da – a)	Gennaio 2011 – Giugno 2011
• Università degli studi di Verona	Facoltà di Scienze Matematiche, Fisiche e Informatiche
• Qualifica	Postdoctoral Fellow
• Date (da – a)	Luglio 2009 – Marzo 2010
• University of Cranfield	School of Health
• Qualifica	Visiting Scientist

ISTRUZIONE E FORMAZIONE

• Date (da – a)	Gennaio 2008 – Dicembre 2010
• Università degli studi di Verona	Facolta' di Scienze Matematiche, Fisiche e Informatiche – Scuola di Scienze, Ingegneria e Medicina
• Titolo Conseguito	Dottorato di ricerca (PhD) in Informatica – Doctoris Europaei
• Date (da – a)	Anno Accademico 2006/2007
• Università degli studi di Verona	Facolta' di Scienze Matematiche, Fisiche e Informatiche
•Titolo conseguito	Laurea Magistrale in Informatica

ATTIVITÀ DIDATTICHE

• Date	Anno Accademico 2022/2023
• Università degli Studi di Udine	Laurea in Informatica
• Occupazione	Collaboratore alla didattica per il corso di "Algoritmi e Strutture Dati e Laboratorio"
• Date	Anni Accademici 2016/2017, 2018/2019, 2019/2020, 2020/2021, 2021/2022
• Università Vita-Salute San Raffaele	Laurea Magistrale in Medicina e Chirurgia
• Occupazione	Tutor alla didattica per le attività del corso di "Biologia Molecolare"
• Date	Anno Accademico 2010/2011
• Università degli Studi di Verona	Laurea in Biotecnologie
• Occupazione	Tutor alla didattica per le attività del corso di "Informatica"
• Date	Anno Accademico 2010/2011
• Università degli Studi di Verona	Laurea in Matematica Applicata
• Occupazione	Tutor alla didattica per le attività del corso di "Calcolo Numerico"
• Date	Anno Accademico 2008/2009
• Università degli Studi di Verona	Laurea in Matematica Applicata
• Occupazione	Tutor alla didattica per le attività del corso di "Calcolo delle Probabilità e Statistica"

MADRELINGUA	**ITALIANA**
ALTRE LINGUA	
	INGLESE
• Capacità di lettura	ECCELLENTE
• Capacità di scrittura	ECCELLENTE
• Capacità di espressione orale	BUONO

RICONOSCIMENTI

- "Post-Doctoral Fellowship-year 2018": Fondazione Umberto Veronesi.
- "Bando Ricerca Finalizzata Anno 2016 – Giovani Ricercatori (PI)" : Ministero Italiano Della Salute

PUBBLICAZIONI SCIENTIFICHE

Peer-reviewed Journal Papers

[1] M. Steidl, E. Nigro, A. Kallehauge Nielsen, R. Pagliarini, L. Cassina, M. Lampis, C. Podrini, M. Chiaravalli, V. Mannella, G. Distefano, M. Yang, M. Asnalayan, G. Musco, R. Roepman, C.Frezza, A. Boletta. Primary Cilia Sense Nutrient Availability and Respond to Glutamine via Asparagine Synthetase. Nature Metabolism, 5(3), pp. 385–397, 2023.

[2] R. Pagliarini, C. Podrini. Metabolic Reprogramming and Reconstruction: Integration of Experimental and Computational Studies to Set the Path Forward in ADPKD. Frontiers in Medicine, 8:740087, 2021.

[3] Podrini C.*, Rowe I.*, Pagliarini R.*, Costa A. S. H., Chiaravalli M., Di Meo I., Kim H., Distefano G., Tiranti V., Qian F., di Bernardo D., Frezza C., Boletta A. Dissection of Metabolic Reprogramming in Polycystic Kidney Disease Reveals a Complex and Coordinated Rewiring of Bioenergetic Pathways. Communications Biology, 1:194, 2018.

[4] L. Drusian., E.A. Nigro, V. Mannella., R. Pagliarini, M. Pema, A.S.H. Costa, F. Benigni.,A. Larcher, M. Chiaravalli, E. Gaude , F. Montorsi, U. Capitanio, G. Musco, C. Frezza, A. Boletta. mTORC1 Upregulation Leads to Accumulation of the Oncometabolite Fumarate in a Mouse Model of Renal Cell Carcinoma Cell Reports, 24 (5), pp. 1093-1104, 2018.

[5] R. Pagliarini, R. Castello, F. Napolitano, R. Borzone, P. Annunziata, G. Mandrile, M. De Marchi, N. Brunetti -Pierri, D. di Bernardo. In silico modelling of liver metabolism in a human disease reveals a key enzyme for histidiene and histamine homeostasis . Cell Reports, 15, 2292-2300, 2016.

[6] R. Pagliarini, R. Castello, R. Borzone, P. Annunziata, G. Mandrile, M. De Marchi, N. Brunetti -Pierri, D. di Bernardo. In-silico modelling of Primary Hyperoxaluria Type 1, a human inborn error of liver metabolism, unravels a key enzyme for histamine homeostasis. Inflammation Research, Volume 64, Supplement 1, 2015.

[7] R. Pagliarini, M. Sangiovanni, A. Peron, D. di Bernardo. Combining Flux Balance Analysis and Model Checking for Metabolic Network Validation and Analysis. Natural Computing, Natural Computing. Vol. 14, Issue 3, pp. 341 -354, 2015.

[8] V. Manca, A. Castellini, G. Franco, L. Marchetti, R. Pagliarini. Metabolic P Systems: A Discrete Model for Biological Dynamics. Chinese Journal of Electronics, Vol.22, No.4, 2013.

[9] R. Pagliarini, D. di Bernardo. A genome-scale modeling approach to study inborn errors of liver metabolism: toward an in silico patient . Journal of Computational Biology, 20(5), 2013.

[10] R. Pagliarini, O. Agrigoroaiei, G. Ciobanu, V. Manca. An Analysis of Correlative and Static Causality in P Systems. Lecture Notes in Computer Science, Volume 7762, pp 323-341, 2013.

[11] V. Manca, L. Marchetti, R. Pagliarini. MP Modelling of Glucose-Insulin Interactions in the Intravenous Glucose Tolerance Test. International Journal of Natural Computing Research, vol. 3, Issue2 , 2011 , pp. 13 -24

[12] G. Franco, V. Manca, R. Pagliarini. Regulation and Covering Problems in MP Systems. Lecture Notes in Computer Science, Volume 5957, pp. 242-251, 2010.

[13] A. Castellini, G. Franco and R. Pagliarini. Data analysis pipeline from laboratory to MP models. Natural Computing. Vol. 10, Issue 1, pp. 55-76, 2011.

[14] R. Pagliarini, G. Franco, V. Manca. An algorithm for initial fluxes of MP systems. International Journal of Computers, Communications & Control. Vol. IV, No. 3, pp. 263-272, 2009.

[15] V. Manca, R. Pagliarini, S. Zorzan. A photosynthetic process modelled by a metabolic P system. Natural Computing, Vol. 8, pp. 847-864, 2009.

[16] V. Manca, R. Pagliarini, S. Zorzan. Toward an MP model of Non Photochemical Quenching. Lecture Notes in Computer Science, volume 5391, pp. 299-310, 2009.

Refereed Conferences with Proceedings

[1] R. Pagliarini, A. Boletta. In SILICO Simulations Predict a Causative Link between Increased Glycolysis and Metabolic Reprogramming in Autosomal Dominant Polycystic Kidney Disease. In 16th IEEE Conference on Computational Intelligence in Bioinformatics and Computational Biology, CIBCB 2019.

[2] R. Pagliarini, L. Bianco, V. Manca, C. Bessant. Linking bistable dynamics to Metabolic P Systems. In Proceedings of the Eighth Brainstorming Week on Membrane Computing. Seville, Spain, February 2010.

[3] L. Bianco, R. Pagliarini, C. Bessant. Towards a GPU-aided simulation of nuclear receptors modulation. International Workshop on High Performance Computational Systems Biology, October 2009.

[4] R. Pagliarini, V. Manca. The discovery of initial fluxes of Metabolic P Systems. In Proceedings of the Seventh Brainstorming Week on Membrane Computing. Seville, Spain, February 2009.

Book Chapters

[1] G. Gambardella*, R. Pagliarini*, F. Gregoretti, G. Oliva, D. di Bernardo. Differential Equation Based Reverse-Engineering Algorithms: Pros and Cons. Gene Network Inference, Springer-Verlag Berlin Heidelberg, 2014.

[2] L. Marchetti, V. Manca, R. Pagliarini, A. Bolling-Fischer. MP Modelling for Systems Biology: two case studies. Applications of membrane

computing in systems and synthetic biology. Applications of Membrane Computing in Systems and Synthetic Biology, volume 7 of Emergence, Complexity and Computation, pages 223 –245. Springer International Publishing, 2014.

Poster Papers, Abstracts and Posters

[1] C. Podrini, I. Rowe, R. Pagliarini, S. Raineri, I. Di Meo, M. Chiaravalli, V. Tiranti, D. di Bernardo , A. Boletta. Global Profiling in Polycystic Kidney Disease Reveals a Metabolic Rewiring Reminiscent of Cancer. ASN Kidney Week 2016.

[2] R. Pagliarini, R. Castello, F. Napolitano, R. Borzone, P. Annunziata, G. Mandrile, M. De Marchi, N. Brunetti -Pierri, D. di Bernardo. A Computational Systems-Level Approach to Decipher Inborn Errors of Metabolism.13th Annual Meeting of the Bioinformatics Italian Society. University of Salerno, Italy, 15-17 June 2016.

[3 R. Pagliarini, R. Castello, N. Brunetti, D.di Bernardo. A Large-scale Computational Model of Inborn Error of Liver Metabolism Unravels Previously Unrecognized Metabolic Derangements and Novel Therapeutic Options. Sixth Annual RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges. Toronto, Canada, 2013.

[4] M. Sangiovanni, R. Pagliarini, D. di Bernardo, A. Peron. A Spin-based model checking approach for genome-scale metabolic networks validation and analysis. 4th International Workshop on Interactions between Computer Science and Biology. Florence, Italy, 2013.

[5] R. Pagliarini, D. di Bernardo. A genome-scale modelling approach to study inborn errors of liver metabolism: towards an in -silico patient. Fifth Annual RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges. San Francisco, USA, 2012.

[6] V. Manca, L. Marchetti, R. Pagliarini. Application of the MP theory for discovering biological models. 12th International Conference on Systems Biology. Mannheim Germany, 2011.

[7] R. Pagliarini, V. Manca. Inference of Biological Pathways by Integrating Different Kinds of Correlation Indexes . In Proceedings of XII International Congress on Molecular Systems Biology , Lleida, Spain , 8 -12 May 2011, pp. 102-102.

ATTIVITÀ DI RICERCA

- Natural Computing
- Reverse Engineering of Biological Networks
- Computational Biology
- Systems Biology
- Mathematical modelling of biological phenomena
- Inborn Errors of Human Metabolism
- Mathematical modelling of cancer metabolism

TALKS

- ”Reverse engineering and modelling of metabolic networks: the case of Mendelian disorders”- 13th May 2014, BioPreDyn: The systems biology modeling cycle - building mechanistic dynamical models, EMBL-EBI, Hinxton, Cambridge, U. K., 12-15th May 2014.
- “Computational Modelling of Inborn Errors of Liver Metabolism” - 19th June 2013, National Research Council (CNR), Naples, Italy.
- “Systems biology of genetic diseases/integration of gene networks and metabolic networks” – 14th June 2013, BioPreDyn Workshop, Centre de Regulacio Genomica (CRG), Barcelona, Spain, 11-15th June 2013.
- “Developing a mathematical modeling framework for linking signaling, regulation, and metabolism: metabolic processes under th e influence of hormones and genetic disorders as case studies” – 5th March 2013, 1st BioPreDyn Annual Metting, Naples, Italy, 4-6th March 2013.
- In silico simulations predict a causative link between increased glycolysis and metabolic reprogramming in autosomal dominant polycystic kidney disease. 16th IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology. Certosa di Pontignano, Italy, July 9-11, 2019.
- A Computational Systems-Level Approach to Decipher Inborn Errors of Metabolism.13th Annual Meeting of the Bioinformatics Italian Society. University of Salerno, Italy, 15-17 June 2016.
- “Differential Flux-balance Analysis: a new computational approach to identify alterations in human metab olic disorders” – 25th February 2015, BioPreDyn Annual

Meeting 2015, Barcelona, Spain, 24 -25th February 2015.

▪ “An analysis of correlative and quantitative causality in P systems” – 29th August 2013, CMC13 - The 13th International Conference on Membrane Computing, Budapest, Hungary, 28-31th August 2012.

▪”A genome-scale modelling approach to study inborn errors of liver metabolism: towards an in -silico patient” – 15th November 2012, Fifth Annual RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges. San Francisco, USA, 12-15th November 2012.

▪“Metabolic P Systems practical” – 9th February 2010, Cranfield University, Cranfield, U. K.

▪ “Metabolic P Systems: an overview” -9th February 2010, Cranfield University, Cranfield, U. K.

▪ “MP analysis of the stochastic Schlogel’s reaction” – 4th February 2010, Eight Brainstorming Week on Membrane Computing, Sevilla, Spain 1-5th February 2010.

▪ “MetaPlab, a virtual laboratory for Metabolic P systems: use examples and main structures” – 24th August 2009. Tenth Workshop on Membrane Computing, Curtea de Arges, Romania, 24-27th August 2009.

▪ “Modelling and inferring biological phenomena by using Metabolic P Systems” – 24th April 2009. University of Verona, Department of Computer Science, Verona, Italy.

▪ “Multi-agent systems simulating the physiological role of plasmic membrane” – 22nd April 2009. University of Verona, Department of Computer Science, Verona, Italy.

▪ “Log-Gain theory for Metabolic P systems: work in progress” – 19th March 2009. University of Verona, Department of Computer Science, Verona, Italy.

▪ “Inferring the initial fluxes of a metabolic process” – 3rd February 2009, Seventh Brainstorming Week on membrane Computing, Sevilla, Spain 2-6th February 2009.

▪ “Towards an MP model of non-photochemical quencing” – 20th July 2008. Ninth Workshop on Membrane Computing, Edinburgh, U.K., 29 - 31th July 2008.

▪ “Quantum P Systems: Background, Definition and Computational Power” – 17th September 2008. University of Verona, Department of Computer Science, Verona, Italy.

▪ “The R language: what is it?” – 12th September 2008. University of Verona, Department of Computer Science , Verona, Italy.

▪ “Reverse-engineering of gene networks” – 11th September 2008. University of Verona, Department of Computer Science, Verona, Italy.

PARTECIPAZIONE A CONFERENZE

Il simbolo * denota un talk alla conferenza.

- DCGB Institutional Retreat, Brescia, Italy, 22-26th September, 2023 *.
- 16th IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology *. Certosa di Pontignano, Italy, 9-11 July, 2019.
- 13th Annual Meeting of the Bioinformatics Italian Society *. University of Salerno, Italy, 15-17 June 2016.
- Sixth Annual RECOMB/ISCB Conference on Regulatory and Systems Genomics *, with DREAM Challenges. Toronto, Canada, 8-
- BioPreDyn Workshop *, Centre de Regulacio Genomica (CRG), Barcelona, Spain, 11-15th June 2013.
- 4th International Workshop on Interactions between Computer Science and Biology *. Florence, Italy, 6th June 2013.
- 1st BioPreDyn Annual Metting *, Naples, Italy, 4-6th March 2013.
- Fifth Annual RECOMB/ISCB Conference on Regulatory and Systems Genomics *, with DREAM Challen ges. San Francisco, USA, 12-15th November, 2012.
- The 13th International Conference on Membrane Computing *, Budapest, Hungary, 28-31th August 2012.
- Tigem Institutional Retreat, Sorrento, Italy, 22-23th October, 2012.
- 12th International Conference on Systems Biology *, Mannheim, Germany, 28th August – 1st September 2011.
- XII International Congress on Molecular Systems Biology *, Lleida, Spain, 8-12th May 2011,
- Eight Brainstorming Week on Membrane Computing *, Sevilla, Spain, 1-5th February 2010.
- Tenth Workshop on Membrane Computing *, Curtea de Arges, Romania, 24-27th August 2009.
- Seventh Brainstorming Week on Membrane Computing *, Sevilla, Spain, 2-6th February 2009.
- The Architecture of Biological Complexity – Biocomplex 2008, Trento, Italy, 4-6th November 2008.
- Ninth Workshop on Membrane Computing *, Edinburgh, U.K., 29-31th July 2008.

ATTIVITÀ DI REFEREE

- STAR Protocols, by Cell Press
- Review Editor of Optimization
- International Journal of Computers, Communications & Control
- IEEE International Conference on Bioinformatics & Biomedicine (BIBM)
- Gecco
- PPNS
- ECCB 2012
- ECCB 2016

PRIVACY

Autorizzo il trattamento dei miei dati personali ai sensi dell’art. 13 D. Lgs. 30 giugno 2003 n°196 – “Codice in materia di protezione dei dati personali” e dell’art. 13 GDPR 679/16 – “Regolamento europeo sulla protezione dei dati personali"

Data, 01/05/2023