



Professor Pietro Liò

Position I am Full Professor of Computational Biology in the Artificial Intelligence Division of the Department of Computer Science and Technology of the University of Cambridge

Personal citizenship: Italian; Married, one daughter

Document Curriculum past 4 years achievements: 2019-2023

Affiliations

Department of Computer Science and Technology (Cambridge), J. Thomson Avenue, CB03FD
Cambridge

email

tel

Other Affiliations

Cambridge Center for AI and Medicine (Cambridge)
Fellow and member of the Council of Clare Hall College (Cambridge).

Research Interests

Research Interests AI methodology, AI and Medicine, Bioinformatics and Computational Biology

Which AI methodology I focus on Graph representation learning and higher order graphs; neurosymbolic; explainability; diffusion models

Which targets for AI and medicine I focus on	Develop methodology in Artificial Intelligence and computational Biology that can lead to useful applications and be respectful of societal values particularly cancer and neurodegenerative diseases; developing methods for the integration of multi scale heterogeneous data; model the overall progression of complex diseases which is critical to the timing of therapeutic interventions and design of effective clinical trials; incorporation of models of uncertainties and counterfactuals and go beyond the hypothesis confirmation towards the generation of new hypotheses; develop a fully trustworthy AI, to assist, help doctor and patients
Which targets of Bioinformatics and Computational Biology I focus on	Biological Complexity; Theoretic Information in Biology; Evo-Devo; single cell; dynamical biosystems; Computational Biology as the new AI

Past Positions

Lecturer (part time Lecturer), Chemistry Dept, University Firenze; course held in years: 1988,89,90; fellowship Institute of National Physics of Matter INFM (1995); Research Associate in Statistical Epidemiology, Princess Anne Hospital, University of Southampton. (1996-1997); Research Associate, Dept. of Genetics, Cambridge; (1998-2000); Research Associate Univ. Cambridge Dept. of Zoology, Cambridge, 2001; Research associate at the European Bioinformatics Institute (2002); Lecturer in Bioinformatics algorithms at the Computer Laboratory, University of Cambridge and affiliated Faculty member of the Centre for Computational Biology, Department of Mathematics, University of Cambridge (2004), Director of studies of Computer Science of Fitzwilliam College (2004-2014); Senior Lecturer, The Computer Laboratory, University of Cambridge (2007); Reader in Computational medicine at the Computer Laboratory, University of Cambridge (2013); - Full Professor in Computational Biology (2018).

Visiting Positions (> 1 month)

University of Padova, University of Toronto and Fields Institute (Canada), University of UCSC (USA), University of Texas (College Station, USA).

International Activities

- 2024 Member of Panel for Activities of Pasteur Institutes (France)
- 2022 Member of Panel for Activities of Adapta (Science Foundation Ireland)
- 2021 Member of Panel for Italian ERC Awards (CNR, Italy)

Awards - Honours (recent)

- 2022 Fellow of the Asia-Pacific Artificial Intelligence Association (AAIA)
- 2021 Fellow of the Academia Europaea
- 2019 Member of Ellis, the European Lab for Learning & Intelligent Systems
- 2023 Listed in the "A standardized citation metrics author database annotated for scientific field" (doi.org/10.1371/journal.pbio.3000384)

Listed in the top Italian Scientists: www.topitalianscientists.org/TIS_HTML/Top_Italian_Scientists_Computer_Sciences.htm

Erdos n 3 www.csauthors.net/distance/pietro-lio/paul-erdos

Invited Talks

- 23 April 2024 Invited talk, Department of Computer Science, Bocconi University, Milano
- 15 April 2024 Turing Lecture, Invited talk, Turing-AI, Queen's University, Belfast
- 9 April 2024 Invited talk, Department of Computer Science, University of Padova
- 22 March 2024 Invited talk, AI4H conference, Padova
- 8 September 2023 Invited talk, school of BioPhotonics and AI, Firenze
- August 2023 lecture at the IoT & AI for Sustainable Global Health and Wellbeing 2023 summer school, Cambridge
- 06-07 July Invited, 6th Machine Learning and AI in Bio(Chemical) Engineering Conference
- 21 June Invited, Deep Learning 2023, Trento, Italy
- 7th June Invited talk, 2023 IEEE World AI IoT Congress (AllIoT) (online)
- June 7-10 Teaching First Doctoral Summer School in Data Science, Accounting & Management Summer school, Paestum, Italy
- June 6 Invited talk, WIRN2023, Vietri, Italy
- June 3, 2023 Keynote talk, IEEE AllIoT 2023
- May 2023 Invited talk, IEEE MetroLivEnv
- March 2023 Invited talk - Pujiang Innovation Forum (Online)
- March 2023 Turing Lecture, Invited talk AI- Turing Institute, Teesside
- March 2023 Invited talk - Physics of Life, Harrogate
- 6 March 2023 Invited talk - Statistical learning on LARge scale GRaphs (LARGR), Inria, Universite de Lille
- December 2022 Invited Talk, Istituto Italiano di Cultura Italiano, ENCOUNTERS: across sciences and humanities
- Sept 2022 Invited talk at the Summer School on AI and Medicine, Cambridge (online)
- Sept 2022 Invited talk at the School of Biophotonics, Florence, Italy
- 28 June 2022 Invited talk - ShanghaiTech SIST Distinguished Lecture, at the Jiao Tong University, Shanghai, China
- Jun 2022 Invited talk at CMBE21 (7th International Conference on Computational and Mathematical Biomedical Engineering); Politecnico di Milano
- Dec 2021 Invited talk at Int. Workshop on Future Computing and Networks, Changchun, China
- Jan 2021 Invited talk: Next Generation Internet, NGL.eu, Forward workshop: The Future of search: Search and (hyper) locality, Search in/and Internet of Things, Search and Ethics - European Community

- Jan 2020 Invited talk at the 21st International Conference on Distributed Computing and Networking, ICDCN Conference, Kolkata
- Sept 2019 Invited talk on AI and data social awareness, MyData2019, Helsinki

Research: Active Grants

- 2023 Wisdom, WELL-BEING IMPROVEMENT THROUGH THE INTEGRATION OF HEALTHCARE AND RESEARCH DATA AND MODELS WITHOUT BORDER FOR CHRONIC IMMUNE-MEDIATED DISEASES, Horizon Europe, Trophy (G112412 NRAG/752), Horizon Europe UKRI Underwrite Innovate, Title: Ultrafast Holographic FTIR Microscopy (2022-2026); £ 294k; Charm (G113952 NRAG/750), Horizon Europe UKRI Underwrite Innovate (2022-2026), title: Chemometric Histopathology via Coherent Raman Imaging for Precision Medicine, £ 275k; GO-DS21, European Commission Horizon 2020 (H2020) Societal Challenges, Go-Ds21 : Gene Overdosage And Comorbidities During The Early Lifetime In Down Syndrome (2020-2024), £400k; Few PhD fellowships sponsored by AstraZeneca (2 students; 1 through CCAIM), GSK (2 students; 1 through CCAIM); CMIH: Cambridge Mathematics Of Information In Healthcare (Cmih), EPSRC, 2020-2023

Governance Activities

- 2024 Member of the Student Complaints and Appeal Committee of the University of Cambridge; member of the Postdoc mentorship scheme of the University of Cambridge
- 2021-2023 Member of the Faculty Board of the Dept of Computer Science and Technology; University of Cambridge Steering committee Big Data (The Cambridge Centre for Data-Driven Discovery (C2D3)); University of Cambridge - High performance computing panel; University of Cambridge Computational Biology Steering Committee; Member of the Student Complaints and Appeal Committee of the University of Cambridge; member of the panel for professorships at the Dept of Computer Science and Technology, University of Cambridge; examiner of ACS MPhil, Dept of Computer Science and Technology, University of Cambridge; Member of School of Technology STEC PhD Fellowship Calls Team

Service to the academic community outside the University

- 2023 Member of panel for professorship on Machine Learning and Biology, Copenhagen, Denmark (September 2022); External Examiner at the University of Newcastle for the MSc Bioinformatics, MSc Computational Neuroscience and Neuroinformatics, MSc Computational Systems Biology (2017-2021); Member of the committee of the VPHiUK.Organiser and co-organizer of scientific conferences and workshops: 08/12/2022 Learning on Graph (LoG) Cambridge.

Service to the Underprivileged schools

- 2023 Teaching Sutton College Summer School, Cambridge
- 2022 Teaching Sutton College Cambridge

Collaborations with Industry

2022 member AI panel of GSK

;

Teaching and supervision

- 2023 ACS MPhil course on Graph Representation Networks; Bioinformatics Algorithms
-Undergraduate -Dept Computer science and technology
- 2024 38 PhD students have been awarded the PhD, >40 MPhil students supervised
(MPhil in advanced computing; Part III Systems biology; MPhil in computational
Biology; Part III Physics); >20 PartII students

.

Dissemination to the broader public (only recent)

- 2022-2024 Organisation of CS AI SIG - Special Interest Group, 1/term at Clare Hall College, Cambridge
- Nov 2020 Lecture on AI and medicine, FuturoRemoto exhibition, Napoli
- Oct 2020 Talk on AI and medicine, TEDxCambridge University
- Jul 2019 Bioinformatics for Kids, CambridgeSpark - Cambridge

Publications from Cambridge University Symplectic database

orcid 0000-0001-8956-9815

Erdős number 3

- 2024 >600 publications in journals and international conferences; arxiv and bioarxiv
as preliminary deposit; H-index = 71 (Google Scholar); i10-index=371;
>54000 citations. <https://scholar.google.co.uk/citations?user=3YrWf7EAAAAAJ&hl=en&oi=ao>; <https://orcid.org/0000-0002-0540-5053>;
noteanotherOrcidunderforenamewithdifferentaccent

Publications

- [1] F Ceccarelli, SB Holden, and P Liò. Mugi-mri: Enhancing breast cancer classification through multiplex graph neural networks in dce-mri. Yokohama, Japan.
- [2] M Li, A Micheli, YG Wang, S Pan, P Lió, GS Gnecco, and M Sanguineti. Guest editorial: Deep neural networks for graphs: Theory, models, algorithms, and applications. *IEEE Trans. Neural Networks Learn. Syst.*, 35(4):4367–4372, Apr 2024.
- [3] F Bardozzo, A Terlizzi, C Simoncini, P Lió, and R Tagliaferri. Elegans-ai: How the connectome of a living organism could model artificial neural networks. *Neurocomputing*, 584, Jun 2024.
- [4] T Dong, M Jamnik, and P Liò. Sphere neural-networks for rational reasoning, Mar 2024.
- [5] S Somathilaka, A Ratwatte, S Balasubramaniam, MC Vuran, W Srisa-an, and P Liò. Wet tinym: Chemical neural network using gene regulation and cell plasticity, Mar 2024. Accepted as a full paper by the tinyML Research Symposium 2024.

- [6] K Huang, W Cao, H Ta, X Xiao, and P Liò. Optimizing polynomial graph filters: A novel adaptive krylov subspace approach, Mar 2024.
- [7] A Defilippo, P Veltri, P Lio', and PH Guzzi. Leveraging graph neural networks for supporting automatic triage of patients, Mar 2024.
- [8] E Lawrence, A El-Shazly, S Seal, CK Joshi, P Liò, S Singh, A Bender, P Sormanni, and M Greenig. Understanding biology in the age of artificial intelligence, Mar 2024.
- [9] D Buterez, JP Janet, SJ Kiddle, D Oglic, and P Lió. Transfer learning with graph neural networks for improved molecular property prediction in the multi-fidelity setting. *Nat Commun*, 15(1):1517, Feb 2024.
- [10] D Buterez, JP Janet, SJ Kiddle, D Oglic, and P Lió. Transfer learning with graph neural networks for improved molecular property prediction in the multi-fidelity setting. *Nature Communications*, 15(1).
- [11] F Ceccarelli, L Giusti, S Holden, and P Lio. Integrating structure and sequence: Protein graph embeddings via gnns and llms. Feb 2024.
- [12] X Zhao, Z Li, M Shen, G-B Stan, P Liò, and Y Zhao. Enhancing real-world complex network representations with hyperedge augmentation, Feb 2024. Preprint. Under review. 17 pages, 4 figures, 14 tables. arXiv admin note: text overlap with arXiv:2306.05108.
- [13] D Buterez, JP Janet, D Oglic, and P Lio. Masked attention is all you need for graphs, Feb 2024.
- [14] T Papamarkou, T Birdal, M Bronstein, G Carlsson, J Curry, Y Gao, M Hajij, R Kwitt, P Liò, PD Lorenzo, V Maroulas, N Miolane, F Nasrin, KN Ramamurthy, B Rieck, S Scardapane, MT Schaub, P Veličković, B Wang, Y Wang, G-W Wei, and G Zamzmi. Position paper: Challenges and opportunities in topological deep learning, Feb 2024.
- [15] N Mumenin, MA Yousuf, MA Nashiry, AKM Azad, SA Alyami, P Lio', and MA Moni. Asdnet: A robust involution-based architecture for diagnosis of autism spectrum disorder utilising eye-tracking technology. *IET Computer Vision*, Jan 2024.
- [16] A Bazaga, P Liò, and G Micklem. Hyperbert: Mixing hypergraph-aware layers with language models for node classification on text-attributed hypergraphs, Feb 2024. 11 pages, 2 figures.
- [17] D Georgiev, P Liò, and D Buffelli. The deep equilibrium algorithmic reasoner, Feb 2024.
- [18] K Didi, F Vargas, SV Mathis, V Dutordoir, E Mathieu, UJ Komorowska, and P Lio. A framework for conditional diffusion modelling with applications in motif scaffolding for protein design, Dec 2023. 9 pages.
- [19] A Duval, SV Mathis, CK Joshi, V Schmidt, S Miret, FD Malliaros, T Cohen, P Liò, Y Bengio, and M Bronstein. A hitchhiker's guide to geometric gnns for 3d atomic systems, Dec 2023.
- [20] A Bazaga, P Liò, and G Micklem. Language model knowledge distillation for efficient question answering in spanish, Dec 2023. ICLR 2024 Tiny Paper (6 pages, 2 tables).

- [21] G Bernárdez, L Telyatnikov, E Alarcón, A Cabellos-Aparicio, P Barlet-Ros, and P Liò. Topological network traffic compression. In *GNNet 2023 - Proceedings of the 2nd Graph Neural Networking Workshop 2023*, pages 7–12, Dec 2023.
- [22] AFD Villaforesta, LC Magister, P Barbiero, and P Liò. Digital histopathology with graph neural networks: Concepts and explanations for clinicians, Dec 2023.
- [23] J Yang and P Liò. Unsupervised adaptive implicit neural representation learning for scan-specific mri reconstruction, Dec 2023.
- [24] J Yang and P Liò. Dual-domain multi-contrast mri reconstruction with synthesis-based fusion network, Dec 2023.
- [25] L Liu, Y Cheng, Z Deng, S Wang, D Chen, X Hu, P Liò, C-B Schönlieb, and A Aviles-Rivero. Trafficmot: A challenging dataset for multi-object tracking in complex traffic scenarios, Nov 2023. 17 pages, 7 figures.
- [26] K Huang and P Liò. An effective universal polynomial basis for spectral graph neural networks, Nov 2023.
- [27] D Buterez, JP Janet, SJ Kiddle, D Oglic, and P Liò. Modelling local and general quantum mechanical properties with attention-based pooling. *Commun Chem*, 6(1):262, Nov 2023.
- [28] A Marinoni, P Lio', A Barp, C Jutten, and M Girolami. Improving embedding of graphs with missing data by soft manifolds, Nov 2023.
- [29] I Brant, A Norcliffe, and P Liò. Fourier neural differential equations for learning quantum field theories, Nov 2023. 9 pages, 6 figures.
- [30] X Bi, S Tang, Z Yang, X Deng, B Xiao, and P Lio. Mmctnet: Multi-modal cony-transformer network for predicting good and poor outcomes in cardiac arrest patients. In *Computing in Cardiology*, Jan 2023.
- [31] J Jürß, LC Magister, P Barbiero, P Liò, and N Simidjievski. Everybody needs a little help: Explaining graphs via hierarchical concepts, Nov 2023. 33 pages, 16 figures, accepted at the NeurIPS 2023 GLFrontiers Workshop.
- [32] Z Shen, Y Cheng, RH Chan, P Liò, C-B Schönlieb, and AI Aviles-Rivero. Trident: The nonlinear trilogy for implicit neural representations, Nov 2023.
- [33] M Zhu, S Stanivuk, A Petrovic, M Nikolic, and P Lio. Incorporating llm priors into tabular learners, Nov 2023. Table Representation Learning Workshop at NeurIPS 2023.
- [34] Y Lu, HSDO Borde, and P Liò. Ames: A differentiable embedding space selection framework for latent graph inference, Nov 2023.
- [35] S Kidwai, P Barbiero, I Meijerman, A Tonda, P Perez-Pardo, P Lio, AH van der Maitland-Zee, DL Oberski, AD Kraneveld, and A Lopez-Rincon. A robust mrna signature obtained via recursive ensemble feature selection predicts the responsiveness of omalizumab in moderate-to-severe asthma. *Clin Transl Allergy*, 13(11):e12306, Nov 2023.

- [36] L Liu, Y Cheng, D Chen, J He, P Liò, C-B Schönlieb, and AI Aviles-Rivero. Traffic video object detection using motion prior, Nov 2023. 11 pages, 4 figures.
- [37] M Zhu, K Kobalcyk, A Petrovic, M Nikolic, MVD Schaar, B Delibasic, and P Lio. Tabular few-shot generalization across heterogeneous feature spaces, Nov 2023. Tabular learning, Deep learning, Few shot learning.
- [38] D Crisostomi, I Cannistraci, L Moschella, P Barbiero, M Ciccone, P Liò, and E Rodolà. From charts to atlas: Merging latent spaces into one, Nov 2023. To appear in the NeurReps workshop @ NeurIPS 2023.
- [39] SI Nayan, MH Rahman, MM Hasan, SMRH Raj, MAA Almoyad, P Liò, and MA Moni. Network based approach to identify interactions between type 2 diabetes and cancer comorbidities. *Life Sci*, 335:122244, Dec 2023.
- [40] J Chen, Y Wang, C Bodnar, R Ying, P Lio, and YG Wang. Dirichlet energy enhancement of graph neural networks by framelet augmentation, Nov 2023.
- [41] Y Jiang, Q Ding, YG Wang, P Liò, and X Zhang. Vision graph u-net: Geometric learning enhanced encoder for medical image segmentation and restoration. *Inverse Problems and Imaging*, 2023, Nov 2023.
- [42] A Bazaga, P Liò, and G Micklem. Sqlformer: Deep auto-regressive query graph generation for text-to-sql translation, Oct 2023. 11 pages, 4 figures.
- [43] L Telyatnikov, MS Bucarelli, G Bernardez, O Zaghen, S Scardapane, and P Lio. Hypergraph neural networks through the lens of message passing: A common perspective to homophily and architecture design, Oct 2023.
- [44] JD Boom, M Greenig, P Sormanni, and P Liò. Score-based generative models for designing binding peptide backbones, Oct 2023.
- [45] I Duta, G Cassarà, F Silvestri, and P Liò. Sheaf hypergraph networks, Sep 2023. Accepted at Neural Information Processing Systems (NeurIPS 2023).
- [46] A Bazaga, P Liò, and G Micklem. Unsupervised pretraining for fact verification by language model distillation, Sep 2023. ICLR 2024 Camera Ready.
- [47] X Lu, C Liu, S Zhu, Y Mao, P Lio, and P Hui. Rlpto: A reinforcement learning-based performance-time optimized task and resource scheduling mechanism for distributed machine learning. *IEEE Transactions on Parallel and Distributed Systems*, 34(12):3266–3279, Dec 2023.
- [48] T Shadbahr, M Roberts, J Stanczuk, J Gilbey, P Teare, S Dittmer, M Thorpe, RV Torné, E Sala, P Lió, M Patel, J Preller, AIX-COVNET Collaboration, JHF Rudd, T Mirtti, AS Rannikko, JAD Aston, J Tang, and C-B Schönlieb. The impact of imputation quality on machine learning classifiers for datasets with missing values. *Commun Med (Lond)*, 3(1):139, Oct 2023.
- [49] COVID-19 Host Genetics Initiative. A second update on mapping the human genetic architecture of covid-19. *Nature*, 621(7977):E7–E26, Sep 2023.

- [50] M Mamalakis, HD Vareilles, A Al-Manea, SC Mitchell, I Arartz, LE Morch-Johnsen, J Garrison, J Simons, P Lio, J Suckling, and G Murray. An explainable three dimension framework to uncover learning patterns: A unified look in variable sulci recognition, Sep 2023.
- [51] AA Chowdhury, SM Hasan Mahmud, KK Shahjalal Hoque, K Ahmed, FM Bui, P Lio, MA Moni, and FA Al-Zahrani. Stackfbas: Detection of fetal brain abnormalities using cnn with stacking strategy from mri images. *Journal of King Saud University - Computer and Information Sciences*, 35(8), Sep 2023.
- [52] X Zou, X Zhao, P Liò, and Y Zhao. Will more expressive graph neural networks do better on generative tasks?, Aug 2023. 2nd Learning on Graphs Conference (LoG 2023). 26 pages, 5 figures, 11 tables.
- [53] R Bergna, F Opolka, P Liò, and JM Hernandez-Lobato. Graph neural stochastic differential equations, Aug 2023. 9 main pages, 6 of appendix (15 in total), submitted for the Learning on Graph (LoG) conference.
- [54] N Faruqui, MA Yousuf, M Whaiduzzaman, AKM Azad, SA Alyami, P Liò, MA Kabir, and MA Moni. Safetymed: A novel iomt intrusion detection system using cnn- lstm hybridization. *Electronics (Switzerland)*, 12(17), Sep 2023.
- [55] J Torge, C Harris, SV Mathis, and P Lio. Diffhopp: A graph diffusion model for novel drug design via scaffold hopping, Aug 2023.
- [56] C Harris, K Didi, AR Jamasb, CK Joshi, SV Mathis, P Lio, and T Blundell. Benchmarking generated poses: How rational is structure-based drug design with generative models?, Aug 2023.
- [57] E De Maria, J Despeyroux, A Felty, P Liò, C Olarte, and A Bahrami. Computational logic for biomedicine and neurosciences. In *Symbolic Approaches to Modeling and Analysis of Biological Systems*, pages 187–234. Aug 2023.
- [58] G Ciravegna, F Giannini, P Barbiero, M Gori, P Lio, M Maggini, and S Melacci. Learning logic explanations by neural networks. In *Compendium of Neurosymbolic Artificial Intelligence*, pages 547–558. Aug 2023.
- [59] Z Wang, Q Gao, X Yi, X Zhang, Y Zhang, D Zhang, P Liò, C Bain, R Basset, S Li, Y Guo, S Imoto, J Yao, RJ Daly, and J Song. Surformer: An interpretable pattern-perceptive survival transformer for cancer survival prediction from histopathology whole slide images. *Comput Methods Programs Biomed*, 241:107733, Nov 2023.
- [60] G Ciravegna, F Giannini, P Barbiero, M Gori, P Lio, M Maggini, and S Melacci. Chapter 25. learning logic explanations by neural networks. In *Frontiers in Artificial Intelligence and Applications*. IOS Press, Jul 2023.
- [61] T Azevedo, RAI Bethlehem, DJ Whiteside, N Swaddiwudhipong, JB Rowe, P Lió, T Rittman, and Alzheimer's Disease Neuroimaging Initiative. Identifying healthy individuals with alzheimer's disease neuroimaging phenotypes in the uk biobank. *Commun Med (Lond)*, 3(1):100, Jul 2023.
- [62] R Jain, P Veličković, and P Liò. Neural priority queues for graph neural networks, Jul 2023.

- [63] R Viñas, CK Joshi, D Georgiev, P Lin, B Dumitrascu, ER Gamazon, and P Liò. Hypergraph factorization for multi-tissue gene expression imputation. *Nat Mach Intell*, 5(7):739–753, Jul 2023.
- [64] X Zhang, L Wang, J Helwig, Y Luo, C Fu, Y Xie, M Liu, Y Lin, Z Xu, K Yan, K Adams, M Weiler, X Li, T Fu, Y Wang, H Yu, Y Xie, X Fu, A Strasser, S Xu, Y Liu, Y Du, A Saxton, H Ling, H Lawrence, H Stärk, S Gui, C Edwards, N Gao, A Ladera, T Wu, EF Hofgard, AM Tehrani, R Wang, A Daigavane, M Bohde, J Kurtin, Q Huang, T Phung, M Xu, CK Joshi, SV Mathis, K Azizzadenesheli, A Fang, A Aspuru-Guzik, E Bekkers, M Bronstein, M Zitnik, A Anandkumar, S Ermon, P Liò, R Yu, S Günnemann, J Leskovec, H Ji, J Sun, R Barzilay, T Jaakkola, CW Coley, X Qian, X Qian, T Smidt, and S Ji. Artificial intelligence for science in quantum, atomistic, and continuum systems, Jul 2023.
- [65] G Dominici, P Barbiero, LC Magister, P Liò, and N Simidjievski. Sharcs: Shared concept space for explainable multimodal learning, Jul 2023.
- [66] Y Lishkova, P Scherer, S Ridderbusch, M Jamnik, P Liò, S Ober-Blöbaum, and C Offen. Discrete lagrangian neural networks with automatic symmetry discovery. *IFAC-PapersOnLine*, 56(2):3203–3210, Jul 2023.
- [67] K Yi, B Zhou, Y Shen, P Liò, and YG Wang. Graph denoising diffusion for inverse protein folding, Jun 2023. NeurIPS 2023.
- [68] A Margeloiu, N Simidjievski, P Liò, and M Jamnik. Weight predictor network with feature selection for small sample tabular biomedical data. In *Proceedings of the 37th AAAI Conference on Artificial Intelligence, AAAI 2023*, volume 37, pages 9081–9089, Jun 2023.
- [69] A Margeloiu, N Simidjievski, P Liò, and M Jamnik. Weight predictor network with feature selection for small sample tabular biomedical data. *Proceedings of the AAAI Conference on Artificial Intelligence*, 37(8):9081–9089.
- [70] H Xuanyuan, P Barbiero, D Georgiev, LC Magister, and P Liò. Global concept-based interpretability for graph neural networks via neuron analysis. *Proceedings of the 37th AAAI Conference on Artificial Intelligence, AAAI 2023*, 37:10675–10683, Jun 2023.
- [71] F Bardozzo, A Terlizzi, P Lio, and R Tagliaferri. Elegansai: how a biological neural network would compare with artificial networks?, Jun 2023.
- [72] A Bisercic, M Nikolic, MVD Schaar, B Delibasic, P Lio, and A Petrovic. Interpretable medical diagnostics with structured data extraction by large language models, Jun 2023.
- [73] Z Li, X Zhao, M Shen, G-B Stan, P Liò, and Y Zhao. Hybrid graph: A unified graph representation with datasets and benchmarks for complex graphs, Jun 2023. 16 pages, 5 figures, 11 tables.
- [74] F Ceccarelli, L Giusti, SB Holden, and P Liò. Neural embeddings for protein graphs, Jun 2023. 10 pages, 5 figures.
- [75] FL Opolka, Y-C Zhi, P Liò, and X Dong. Graph classification gaussian processes via spectral features, Jun 2023.

- [76] L Giusti, T Reu, F Ceccarelli, C Bodnar, and P Liò. Cin++: Enhancing topological message passing, Jun 2023. 21 pages, 9 figures.
- [77] V Lachi, GM Dimitri, AD Stefano, P Liò, M Bianchini, and C Mocenni. Impact of the covid 19 outbreaks on the italian twitter vaccination debat: a network based analysis, Jun 2023.
- [78] A Breger, I Selby, M Roberts, J Babar, E Gkrania-Klotsas, J Preller, L Escudero Sánchez, AIX-COVNET Collaboration, JHF Rudd, JAD Aston, JR Weir-McCall, E Sala, and C-B Schönlieb. A pipeline to further enhance quality, integrity and reusability of the nccid clinical data. *Sci Data*, 10(1):493, Jul 2023.
- [79] X Mei, Y Yang, M Li, C Huang, K Zhang, and P Lió. A feature reuse framework with texture-adaptive aggregation for reference-based super-resolution, Jun 2023.
- [80] F Caso, G Trappolini, A Bacciu, P Liò, and F Silvestri. Renormalized graph neural networks, Jun 2023.
- [81] K Bujel, Y Gideoni, CK Joshi, and P Liò. Group invariant global pooling, May 2023.
- [82] CK Joshi, AR Jamasb, R Viñas, C Harris, S Mathis, A Morehead, and P Liò. grnade: Geometric deep learning for 3d rna inverse design, May 2023. Previously titled 'Multi-State RNA Design with Geometric Multi-Graph Neural Networks', presented at ICML 2023 Computational Biology Workshop.
- [83] R Viñas, P Scherer, N Simidjievski, M Jamnik, and P Liò. Spatio-relational inductive biases in spatial cell-type deconvolution, 2023.
- [84] D Georgiev, D Numeroso, D Bacciu, and P Liò. Neural algorithmic reasoning for combinatorial optimisation, May 2023.
- [85] F Giannini, S Fioravanti, O Keskin, AM Lupidi, LC Magister, P Lio, and P Barbiero. Interpretable graph networks formulate universal algebra conjectures, May 2023.
- [86] G Wölflein, LC Magister, P Liò, DJ Harrison, and O Arandjelović. Deep multiple instance learning with distance-aware self-attention, May 2023.
- [87] KF Yeh, P Flood, W Redman, and P Liò. Learning linear embeddings for non-linear network dynamics with koopman message passing, May 2023.
- [88] S Dittmer, M Roberts, J Gilbey, A Biguri, I Selby, A Breger, M Thorpe, JR Weir-McCall, E Gkrania-Klotsas, A Korhonen, E Jefferson, G Langs, G Yang, H Prosch, J Stanczuk, J Tang, J Babar, L Escudero Sánchez, P Teare, M Patel, M Wassin, M Holzer, N Walton, P Lió, T Shadbahr, E Sala, J Preller, JHF Rudd, JAD Aston, and CB Schönlieb. Navigating the development challenges in creating complex data systems. *Nature Machine Intelligence*, 5(7):681–686, Jul 2023.
- [89] A Bernstein. Immune infiltrates in breast cancer: Clinical significance from histopathology to prognosis.
- [90] J Yang, X-X Li, F Liu, D Nie, P Lio, H Qi, and D Shen. Fast multi-contrast mri acquisition by optimal sampling of information complementary to pre-acquired mri contrast. *IEEE Trans Med Imaging*, 42(5):1363–1373, May 2023.

- [91] P Scherer. Distributional and relational inductive biases for graph representation learning in biomedicine.
- [92] X Lu, X Zhang, and P Lio. Gat-dns: Dns multivariate time series prediction model based on graph attention network. In *ACM Web Conference 2023 - Companion of the World Wide Web Conference, WWW 2023*, pages 127–131, Apr 2023.
- [93] G Mittone, F Svoboda, M Aldinucci, N Lane, and P Lió. A federated learning benchmark for drug-target interaction. In *ACM Web Conference 2023 - Companion of the World Wide Web Conference, WWW 2023*, pages 1177–1181, Apr 2023.
- [94] P Barbiero, G Ciravegna, F Giannini, ME Zarlenga, LC Magister, A Tonda, P Lio', F Precioso, M Jamnik, and G Marra. Interpretable neural-symbolic concept reasoning, Apr 2023.
- [95] P Barbiero, S Fioravanti, F Giannini, A Tonda, P Lio, and ED Lavore. Categorical foundations of explainable ai: A unifying theory, Apr 2023.
- [96] F Bardozzo, A Terlizzi, P Lió, and R Tagliaferri. *<i>elegansnet</i>*: a brief scientific report and initial experiments, Apr 2023.
- [97] S Del Duca, G Semenzato, A Esposito, P Liò, and R Fani. The operon as a conundrum of gene dynamics and biochemical constraints: What we have learned from histidine biosynthesis. *Genes (Basel)*, 14(4), Apr 2023.
- [98] EL Ambags, G Capitoli, VL Imperio, M Provenzano, MS Nobile, and P Liò. Assisting clinical practice with fuzzy probabilistic decision trees, Apr 2023. 19 pages.
- [99] D Buterez, JP Janet, SJ Kiddle, and P Liò. Mf-pcba: Multifidelity high-throughput screening benchmarks for drug discovery and machine learning. *J Chem Inf Model*, 63(9):2667–2678, May 2023.
- [100] M Hasan, M Abdar, A Khosravi, U Aickelin, P Lio', I Hossain, A Rahman, and S Nahavandi. Survey on leveraging uncertainty estimation towards trustworthy deep neural networks: The case of reject option and post-training processing, Apr 2023.
- [101] A Purificato, G Cassarà, F Siciliano, P Liò, and F Silvestri. Sheaf4rec: Sheaf neural networks for graph-based recommender systems, Apr 2023. 21 pages, 8 figures.
- [102] F Bardozzo, A Terlizzi, P Liò, and R Tagliaferri. Elegansnet: a brief scientific report and initial experiments, Apr 2023. 4 pages, short report before full paper submission.
- [103] P Bongini, F Scarselli, M Bianchini, GM Dimitri, N Pancino, and P Lio. Modular multi-source prediction of drug side-effects with drugnn. *IEEE/ACM Trans Comput Biol Bioinform*, 20(2):1211–1220, 2023.
- [104] M Lu, CN Christensen, JM Weber, T Konno, NF Läubli, KM Scherer, E Avezov, P Lio, AA Lapkin, GS Kaminski Schierle, and CF Kaminski. Ernet: a tool for the semantic segmentation and quantitative analysis of endoplasmic reticulum topology. *Nat Methods*, 20(4):569–579, Apr 2023.

- [105] MS Islam, KF Hasan, S Sultana, S Uddin, P Lio, JMW Quinn, and MA Moni. Hardc : A novel ecg-based heartbeat classification method to detect arrhythmia using hierarchical attention based dual structured rnn with dilated cnn, Mar 2023. 23 pages.
- [106] J Zhu. Deep neural networks for medical image super-resolution.
- [107] T Tilly. Deep learning of regulatory sequence variation in pulmonary arterial hypertension.
- [108] A Petrović, M Nikolić, U Bugarić, B Delibašić, and P Lio. Controlling highway toll stations using deep learning, queuing theory, and differential evolution. *Engineering Applications of Artificial Intelligence*, 119, Mar 2023.
- [109] A Norcliffe, B Cebere, F Imrie, P Lio, and MVD Schaar. Survivalgan: Generating time-to-event data for survival analysis, Feb 2023.
- [110] J Zhu, G Yang, and P Lio. A residual dense vision transformer for medical image super-resolution with segmentation-based perceptual loss fine-tuning, Feb 2023. Preprint submitted to Medical Image Analysis and under review.
- [111] D Kazhdan, B Dimanov, LC Magister, P Barbiero, M Jamnik, and P Lio. Gci: A (g)raph (c)oncept (i)nterpretation framework, Feb 2023.
- [112] FD Giovanni, L Giusti, F Barbero, G Luise, P Lio', and M Bronstein. On over-squashing in message passing neural networks: The impact of width, depth, and topology, Feb 2023. Accepted at ICML 2023; 21 pages.
- [113] A Longa, V Lachi, G Santin, M Bianchini, B Lepri, P Lio, F Scarselli, and A Passerini. Graph neural networks for temporal graphs: State of the art, open challenges, and opportunities, Feb 2023.
- [114] X Zhao, H Stärk, D Beaini, Y Zhao, and P Liò. Task-agnostic graph neural network evaluation via adversarial collaboration, Jan 2023. 11th International Conference on Learning Representations (ICLR 2023) Machine Learning for Drug Discovery (MLDD) Workshop. 17 pages, 6 figures, 4 tables.
- [115] M Waqas, S Aziz, P Liò, Y Khan, A Ali, A Iqbal, F Khan, and FN Almajhdi. Immunoinformatics design of multivalent epitope vaccine against monkeypox virus and its variants using membrane-bound, enveloped, and extracellular proteins as targets. *Front Immunol*, 14:1091941, 2023.
- [116] A Campbell, S Spasov, N Toschi, and P Lio. Dbgdgm: Dynamic brain graph deep generative model, Jan 2023.
- [117] A Sathyanarayanan, TT Mueller, M Ali Moni, K Schueler, ECNP TWG Network members, BT Baune, P Lio, D Mehta, BT Baune, M Dierssen, B Ebert, C Fabbri, P Fusar-Poli, M Gennarelli, C Harmer, OD Howes, JGE Janzing, P Lio, E Maron, D Mehta, A Minelli, L Nonell, C Pisanu, M-C Potier, F Rybakowski, A Serretti, A Squassina, D Stacey, R van Westrhenen, and L Xicota. Multi-omics data integration methods and their applications in psychiatric disorders. *Eur Neuropsychopharmacol*, 69:26–46, Apr 2023.
- [118] CK Joshi, C Bodnar, SV Mathis, T Cohen, and P Liò. On the expressive power of geometric graph neural networks, Jan 2023. ICML 2023.

- [119] Z Yang, G Zhang, J Wu, J Yang, QZ Sheng, S Xue, C Zhou, C Aggarwal, H Peng, W Hu, E Hancock, and P Liò. State of the art and potentialities of graph-level learning, Jan 2023.
- [120] A Purificato, G Cassarà, P Liò, and F Silvestri. Sheaf neural networks for graph-based recommender systems. *CoRR*, abs/2304.09097, 2023.
- [121] L Liu, J Prost, L Zhu, N Papadakis, P Liò, C-B Schönlieb, and AI Avilés-Rivero. Scotch and soda: A transformer video shadow detection framework. In *CVPR*, pages 10449–10458, 2023.
- [122] A Jang, S Patel, S Patel, S Shah, and P Lio. Predicting mortality in systemic sclerosis patients using machine learning approaches. In *JOURNAL OF INVESTIGATIVE DERMATOLOGY*, volume 143, pages S37–S37, 2023.
- [123] F Di Giovanni, L Giusti, F Barbero, G Luise, P Liò, and M Bronstein. On over-squashing in message passing neural networks: The impact of width, depth, and topology. In *Proceedings of Machine Learning Research*, volume 202, pages 7865–7885, Jan 2023.
- [124] CK Joshi, AR Jamasb, R Viñas, C Harris, SV Mathis, and P Liò. Multi-state rna design with geometric multi-graph neural networks. *CoRR*, abs/2305.14749, 2023.
- [125] GM Dimitri, SE Spasov, A Duggento, L Passamonti, P Liò, and N Toschi. Multimodal and multicontrast image fusion via deep generative models. *CoRR*, abs/2303.15963, 2023.
- [126] Z Sun, A Harit, AI Cristea, J Wang, and P Lio. Money: Ensemble learning for stock price movement prediction via a convolutional network with adversarial hypergraph model. *AI Open*, 4:165–174, Jan 2023.
- [127] G Ciravegna, P Barbiero, F Giannini, M Gori, P Liò, M Maggini, and S Melacci. Logic explained networks. *Artif. Intell.*, 314:103822–103822, 2023.
- [128] A Campbell, AG Zippo, L Passamonti, N Toschi, and P Liò. Dbgs! : Dynamic brain graph structure learning. *Proceedings of Machine Learning Research*, 227:1318–1345, Jan 2023.
- [129] LC Magister, P Barbiero, D Kazhdan, F Siciliano, G Ciravegna, F Silvestri, M Jamnik, and P Liò. Concept distillation in graph neural networks. volume 1903 CCIS, pages 233–255. Jan 2023.
- [130] P Barbiero, S Fioravanti, F Giannini, A Tonda, P Liò, and ED Lavore. Categorical foundations of explainable ai: A unifying formalism of structures and semantics. *CoRR*, abs/2304.14094, 2023.
- [131] O Keskin, A Lupidi, F Giannini, S Fioravanti, LC Magister, P Barbiero, and P Liò. Bridging equational properties and patterns on graphs: an ai-based approach. In *Proceedings of Machine Learning Research*, volume 221, pages 156–168, Jan 2023.
- [132] Z Sun, A Harit, AI Cristea, J Wang, and P Lio. A rewiring contrastive patch performermixer framework for graph representation learning. In *Proceedings - 2023 IEEE International Conference on Big Data, BigData 2023*, pages 5930–5939, Jan 2023.
- [133] MM Ahamad, S Aktar, MJ Uddin, M Rashed-AI-Mahfuz, AKM Azad, S Uddin, SA Alyami, IH Sarker, A Khan, P Liò, JMW Quinn, and MA Moni. Adverse effects of covid-19 vaccination:

Machine learning and statistical approach to identify and classify incidences of morbidity and postvaccination reactogenicity. *Healthcare (Basel)*, 11(1), Dec 2022.

- [134] C Bodnar. Topological deep learning: Graphs, complexes, sheaves.
- [135] E Rocheteau. Representation learning for patients in the intensive care unit.
- [136] P Scherer, P Liò, and M Jamnik. Distributed representations of graphs for drug pair scoring. In *Proceedings of Machine Learning Research*, volume 198, Jan 2022.
- [137] M Pándy, W Qiu, G Corso, P Veličković, R Ying, J Leskovec, and P Liò. Learning graph search heuristics, Dec 2022.
- [138] GM Dimitri, S Spasov, A Duggento, L Passamonti, P Lió, and N Toschi. Multimodal and multicontrast image fusion via deep generative models. *Information Fusion*, 88:146–160, Dec 2022.
- [139] T Tilly, K Auckland, R Nibhani, J Martin, N Nihir, NW Morrell, P Lio', and S Graf. Deep learning of regulatory regions discovers enhancer variants implicated in pah. In *EUROPEAN RESPIRATORY JOURNAL*, volume 60, 2022.
- [140] A Jain, C Mishra, and P Liò. A physics-informed search for metric solutions to ricci flow, their embeddings, and visualisation, Nov 2022.
- [141] Y He, P Veličković, P Liò, and A Deac. Continuous neural algorithmic planners, Nov 2022.
- [142] A Margeloiu, N Simidjievski, P Lio, and M Jamnik. Weight predictor network with feature selection for small sample tabular biomedical data, Nov 2022. Accepted to AAAI-2023.
- [143] Y-C Zhi, FL Opolka, YC Ng, P Liò, and X Dong. Transductive kernels for gaussian processes on graphs, Nov 2022.
- [144] P Charoenkwan, C Pipattanaboon, C Nantasenamat, MM Hasan, MA Moni, P Lio', and W Shoombuatong. Psrttca: A new approach for improving the prediction and characterization of tumor t cell antigens using propensity score representation learning. *Comput Biol Med*, 152:106368, Jan 2023.
- [145] HSDO Borde, A Kazi, F Barbero, and P Liò. Latent graph inference using product manifolds, Nov 2022.
- [146] H Mitchell, A Norcliffe, and P Liò. Learning feynman diagrams using graph neural networks, Nov 2022.
- [147] Y Lishkova, P Scherer, S Ridderbusch, M Jamnik, P Liò, S Ober-Blöbaum, and C Offen. Discrete lagrangian neural networks with automatic symmetry discovery, Nov 2022.
- [148] D Buterez, JP Janet, SJ Kiddle, and P Liò. Mf-pcba: Multi-fidelity high-throughput screening benchmarks for drug discovery and machine learning, Nov 2022.
- [149] S Cardozo, GI Montero, D Kazhdan, B Dimanov, M Wijaya, M Jamnik, and P Lio. Explainer divergence scores (eds): Some post-hoc explanations may be effective for detecting unknown

spurious correlations, Nov 2022. Presented at the AIMLAI workshop at the 31st ACM International Conference on Information and Knowledge Management (CIKM 2022).

- [150] L Liu, J Prost, L Zhu, N Papadakis, P Liò, C-B Schönlieb, and AI Aviles-Rivero. Scotch and soda: A transformer video shadow detection framework, Nov 2022. Accepted to CVPR 2023.
- [151] C Purves, P Liò, and C Cangea. Goal-conditioned reinforcement learning in the presence of an adversary, Nov 2022.
- [152] X Lu, A Xue, P Lio, and P Hui. Intelligent decision making based on the combination of deep reinforcement learning and an influence map. *Applied Sciences (Switzerland)*, 12(22), Nov 2022.
- [153] A Margeloiu, N Simidjievski, P Lio, and M Jamnik. Gcondnet: A novel method for improving neural networks on small high-dimensional tabular data, Nov 2022. Accepted at the 2nd Table Representation Learning Workshop at NeurIPS 2023 [selected for oral presentation].
- [154] D Buterez, JP Janet, SJ Kiddle, D Oglic, and P Liò. Graph neural networks with adaptive readouts, Nov 2022. Published at NeurIPS 2022. 10 pages, 5 figures, 1 table.
- [155] JOO Ayorinde, F Citterio, M Landrò, E Peruzzo, T Islam, S Tilley, G Taylor, V Bardsley, P Liò, A Samoshkin, and GJ Pettigrew. Artificial intelligence you can trust: What matters beyond performance when applying artificial intelligence to renal histopathology? *J Am Soc Nephrol*, 33(12):2133–2140, Dec 2022.
- [156] R Borgheresi, A Barucci, S Colantonio, G Aghakhanyan, M Assante, E Bertelli, E Carlini, R Carpi, C Caudai, D Cavallero, D Cioni, R Cirillo, V Colcelli, A Dell'Amico, D Di Gangi, PA Erba, L Faggioni, Z Falaschi, M Gabelloni, R Gini, L Lelii, P Liò, A Lorito, S Lucarini, P Manghi, F Mangiacrapa, C Marzi, MA Mazzei, L Mercatelli, A Mirabile, F Mungai, V Miele, M Olmastroni, P Pagano, F Païar, G Panichi, MA Pascali, F Pasquinelli, JE Shortrede, L Tumminello, L Volterrani, E Neri, and NAVIGATOR Consortium Group. Navigator: an italian regional imaging biobank to promote precision medicine for oncologic patients. *Eur Radiol Exp*, 6(1):53, Nov 2022.
- [157] X Lu, R Pang, and P Lio. Poster: Cfmap: A robust cpu clock fingerprint model for device authentication. In *Proceedings of the ACM Conference on Computer and Communications Security*, pages 3407–3409, Nov 2022.
- [158] R Jain, G Ciravegna, P Barbiero, F Giannini, D Buffelli, and P Lio. Extending logic explained networks to text classification, Nov 2022. Accepted as short paper at the EMNLP 2022 conference.
- [159] P Charoenkwan, N Schaduengrat, P Lio, MA Moni, P Chumnanpuen, and W Shoombuatong. iamp-scm: A novel computational tool for large-scale identification of antimalarial peptides using estimated propensity scores of dipeptides. *ACS Omega*, 7(45):41082–41095, Nov 2022.
- [160] F Imrie, A Norcliffe, P Lio, and MVD Schaar. Composite feature selection using deep ensembles, Nov 2022. Accepted to NeurIPS 2022.
- [161] A Longa, S Azzolin, G Santin, G Cencetti, P Liò, B Lepri, and A Passerini. Explaining the explainers in graph neural networks: a comparative study, Oct 2022.

- [162] P Charoenkwan, P Chumnannpuen, N Schaduengrat, P Lio', MA Moni, and W Shoombuatong. Improved prediction and characterization of blood-brain barrier penetrating peptides using estimated propensity scores of dipeptides. *J Comput Aided Mol Des*, 36(11):781–796, Nov 2022.
- [163] A Schneuing, Y Du, C Harris, A Jambas, I Igashov, W Du, T Blundell, P Lió, C Gomes, M Welling, M Bronstein, and B Correia. Structure-based drug design with equivariant diffusion models, Oct 2022.
- [164] A Lopez-Rincon, S Kidwai, P Barbiero, I Meijerman, A Tonda, PPerez-Pardo, P Lio, A-HM-VD Zee, DL Oberski, and A Kraneveld. A robust mrna signature obtained via recursive ensemble feature selection predicts the responsiveness of omalizumab in moderate-to-severe asthma, Oct 2022.
- [165] SK Dhillon, MD Ganggayah, S Sinnadurai, P Lio, and NA Taib. Theory and practice of integrating machine learning and conventional statistics in medical data analysis. *Diagnostics (Basel)*, 12(10), Oct 2022.
- [166] CN Christensen. Deep learning for image processing in optical super-resolution microscopy.
- [167] S Azzolin, A Longa, P Barbiero, P Liò, and A Passerini. Global explainability of gnns via logic combination of learned concepts, Oct 2022. Camera ready version for ICLR2023 publication.
- [168] N Schaduengrat, N Anuwongcharoen, MA Moni, P Lio', P Charoenkwan, and W Shoombuatong. Stackpr is a new computational approach for large-scale identification of progesterone receptor antagonists using the stacking strategy. *Sci Rep*, 12(1):16435, Sep 2022.
- [169] AA Aslam, RA Baksh, SE Pape, A Strydom, MC Gulliford, LF Chan, and GO-DS21 Consortium. Diabetes and obesity in down syndrome across the lifespan: A retrospective cohort study using u.k. electronic health records. *Diabetes Care*, 45(12):2892–2899, Sep 2022.
- [170] A Campbell, AG Zippo, L Passamonti, N Toschi, and P Lio. Dyndepnet: Learning time-varying dependency structures from fmri data via dynamic graph structure learning, Sep 2022. 19 pages, 5, figures, 9 tables, ICML Workshop.
- [171] X Lu, F Yang, L Zou, P Lio, and P Hui. An lte authentication and key agreement protocol based on the ecc self-certified public key. *IEEE/ACM Transactions on Networking*, 31(3):1101–1116, Jun 2023.
- [172] ME Zarlenga, P Barbiero, G Ciravegna, G Marra, F Giannini, M Diligenti, Z Shams, F Precioso, S Melacci, A Weller, P Lio, and M Jamnik. Concept embedding models: Beyond the accuracy-explainability trade-off, Sep 2022. To appear at NeurIPS 2022.
- [173] H Coggan, H Andres Terre, and P Liò. A novel interpretable machine learning algorithm to identify optimal parameter space for cancer growth. *Front Big Data*, 5:941451, 2022.
- [174] GM Dimitri, G Meoni, L Tenori, C Luchinat, and P Lió. Nmr spectroscopy combined with machine learning approaches for age prediction in healthy and parkinson's disease cohorts through metabolomic fingerprints. *Applied Sciences (Switzerland)*, 12(18), Sep 2022.
- [175] H Xuanyuan, P Barbiero, D Georgiev, LC Magister, and P Lió. Global concept-based interpretability for graph neural networks via neuron analysis, Aug 2022. 9 pages, 5 figures.

- [176] P Charoenkwan, N Schaduangrat, P Lio', MA Moni, W Shoombuatong, and B Manavalan. Computational prediction and interpretation of druggable proteins using a stacked ensemble-learning framework. *iScience*, 25(9):104883, Sep 2022.
- [177] R Viñas, C Joshi, D Georgiev, B Dumitrascu, B Dumitrascu, E Gamazon, and P Liò. Hypergraph factorisation for multi-tissue gene expression imputation, 2022.
- [178] S Patel and P Lio. Efficacy, safety, and applications of skin protectants. *J Drugs Dermatol*, 21(9):977–982, Sep 2022.
- [179] LC Magister, P Barbiero, D Kazhdan, F Siciliano, G Ciravegna, F Silvestri, M Jamnik, and P Lio. Encoding concepts in graph neural networks, Jul 2022.
- [180] X Lu and P Lio. Second international workshop on artificial intelligence to security - aits 2022. In *Proceedings - 52nd Annual IEEE/IFIP International Conference on Dependable Systems and Networks Workshop Volume, DSN-W 2022*, page XVII, Jan 2022.
- [181] D Buterez, JP Janet, S Kiddle, and P Liò. Multi-fidelity machine learning models for improved high-throughput screening predictions, Jul 2022.
- [182] P Qian, J Yang, P Lió, P Hu, and H Qi. Joint group-wise motion estimation and segmentation of cardiac cine mr images using recurrent u-net. In *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, volume 13413 LNCS, pages 65–74, Jan 2022.
- [183] D Buffelli, P Liò, and F Vandin. Sizeshiftreg: a regularization method for improving size-generalization in graph neural networks. Jul 2022. Accepted at NeurIPS 2022.
- [184] L Liu, Z Huang, P Liò, CB Schönlieb, and AI Aviles-Rivero. You only look at patches: A patch-wise framework for 3d unsupervised medical image registration. In *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, volume 13386 LNCS, pages 190–193, Jan 2022.
- [185] E DE MARIA, J DESPEYROUX, A FELTY, P LIÒ, C OLARTE, and A BAHRAMI. Logique calculatoire pour la biomédecine et les neurosciences. In *Approches symboliques de la modélisation et de l'analyse des systèmes biologiques*, pages 201–253. ISTE Group, Jul 2022.
- [186] P Barbiero, G Ciravegna, F Giannini, P Lió, M Gori, and S Melacci. Entropy-based logic explanations of neural networks. In *Proceedings of the 36th AAAI Conference on Artificial Intelligence, AAAI 2022*, volume 36, pages 6046–6054, Jun 2022.
- [187] D Georgiev, P Barbiero, D Kazhdan, P Veličković, and P Liò. Algorithmic concept-based explainable reasoning. In *Proceedings of the 36th AAAI Conference on Artificial Intelligence, AAAI 2022*, volume 36, pages 6685–6693, Jun 2022.
- [188] P Barbiero, G Ciravegna, F Giannini, P Lió, M Gori, and S Melacci. Entropy-based logic explanations of neural networks. In *Proceedings of the AAAI Conference on Artificial Intelligence*, 36:6, Jun 2021.
- [189] D Georgiev, P Barbiero, D Kazhdan, P Veličković, and P Liò. Algorithmic concept-based explainable reasoning. Jul 2021. preprint.

- [190] X Lu, J Zhao, and P Lio. Robust android malware detection based on subgraph network and denoising gcn network. In *MobiSys 2022 - Proceedings of the 2022 20th Annual International Conference on Mobile Systems, Applications and Services*, pages 549–550, Jun 2022.
- [191] Y Wang, YG Wang, C Hu, M Li, Y Fan, N Otter, I Sam, H Gou, Y Hu, T Kwok, J Zalcberg, A Boussioutas, RJ Daly, G Montúfar, P Liò, D Xu, GI Webb, and J Song. Cell graph neural networks enable the precise prediction of patient survival in gastric cancer. *NPJ Precis Oncol*, 6(1):45, Jun 2022.
- [192] F Barbero, C Bodnar, HSDO Borde, M Bronstein, P Veličković, and P Liò. Sheaf neural networks with connection laplacians. Jun 2022. Presented at the ICML 2022 Workshop on Topology, Algebra, and Geometry in Machine Learning.
- [193] K Yi, J Chen, YG Wang, B Zhou, P Liò, Y Fan, and J Hamann. Approximate equivariance $so(3)$ needlet convolution. Jun 2022.
- [194] T Shadbahr, M Roberts, J Stanczuk, J Gilbey, P Teare, S Dittmer, M Thorpe, RV Torne, E Sala, P Lio, M Patel, AIX-COVNET Collaboration, JHF Rudd, T Mirtti, A Rannikko, JAD Aston, J Tang, and C-B Schönlieb. Classification of datasets with imputed missing values: does imputation quality matter?, Jun 2022. 17 pages, 10 figures, 30 supplementary pages.
- [195] P Charoenkwan, N Schaduagratt, MA Moni, P Lio', B Manavalan, and W Shoombuatong. Sapphire: A stacking-based ensemble learning framework for accurate prediction of thermophilic proteins. *Comput Biol Med*, 146:105704, Jul 2022.
- [196] P Charoenkwan, N Schaduagratt, P Lio', MA Moni, B Manavalan, and W Shoombuatong. Neptune: A novel computational approach for accurate and large-scale identification of tumor homing peptides. *Comput Biol Med*, 148:105700, Sep 2022.
- [197] M Lu, C Christensen, J Weber, T Konno, N Läubli, K Scherer, E Avezov, P Lio, A Lapkin, G Kaminski Schierle, and C Kaminski. Ernet: a tool for the semantic segmentation and quantitative analysis of endoplasmic reticulum topology for video-rate super-resolution imaging, 2022.
- [198] P Charoenkwan, S Ahmed, C Nantasenamat, JMW Quinn, MA Moni, P Lio', and W Shoombuatong. Amypred-frl is a novel approach for accurate prediction of amyloid proteins by using feature representation learning. *Sci Rep*, 12(1):7697, May 2022.
- [199] T Azevedo, A Campbell, R Romero-Garcia, L Passamonti, RAI Bethlehem, P Liò, and N Toschi. A deep graph neural network architecture for modelling spatio-temporal dynamics in resting-state functional mri data. *Med Image Anal*, 79:102471, Jul 2022.
- [200] J Yang, T Küstner, P Hu, P Liò, and H Qi. End-to-end deep learning of non-rigid groupwise registration and reconstruction of dynamic mri. *Front Cardiovasc Med*, 9:880186, 2022.
- [201] I Igashov, A Jamasb, A Sadek, F Sverrisson, A Schneuing, P Liò, T Blundell, M Bronstein, and B Correia. Decoding surface fingerprints for protein-ligand interactions, 2022.
- [202] CWJ Goh, C Bodnar, and P Liò. Simplicial attention networks. Apr 2022. Accepted to the ICLR 2022 Workshop on Geometrical and Topological Representation Learning.

- [203] R Vignani, M Scali, and P Liò. Molecular markers and genomics for food and beverages characterization. In *Handbook of DNA Profiling*, pages 889–909. Apr 2022.
- [204] J Huang, Y Fang, Y Nan, H Wu, Y Wu, Z Gao, Y Li, Z Wang, P Lio, D Rueckert, YC Eldar, and G Yang. Data and physics driven learning models for fast mri – fundamentals and methodologies from cnn, gan to attention and transformers. Apr 2022. 14 pages, 3 figures, submitted to IEEE SPM.
- [205] L Liu, Z Huang, P Liò, C-B Schönlieb, and AI Aviles-Rivero. Pc-swinmorph: Patch representation for unsupervised medical image registration and segmentation. Mar 2022. 10 pages, 7 figures, 2 tables.
- [206] C Tong, E Rocheteau, P Veličković, N Lane, and P Liò. Predicting patient outcomes with graph representation learning. *Studies in Computational Intelligence*, 1013:281–293, Jan 2022.
- [207] S Ahmad, P Charoenkwan, JMW Quinn, MA Moni, MM Hasan, P Lio', and W Shoombuatong. Scorpion is a stacking-based ensemble learning framework for accurate prediction of phage virion proteins. *Sci Rep*, 12(1):4106, Mar 2022.
- [208] P Charoenkwan, N Schaduengrat, MM Hasan, MA Moni, P Lió, and W Shoombuatong. Empirical comparison and analysis of machine learning-based predictors for predicting and analyzing of thermophilic proteins. *EXCLI J*, 21:554–570, 2022.
- [209] CN Christensen, M Lu, EN Ward, P Lio, and CF Kaminski. Spatio-temporal vision transformer for super-resolution microscopy. Feb 2022. 8 pages, 9 figures. Source code: <https://github.com/charlesnchr/vsr-sim>.
- [210] P Bongini, F Scarselli, M Bianchini, GM Dimitri, N Pancino, and P Liò. Modular multi-source prediction of drug side-effects with drugnn, Feb 2022.
- [211] T Azevedo. Data-driven representations in brain science: Modelling approaches in gene expression and neuroimaging domains.
- [212] C Bodnar, FD Giovanni, BP Chamberlain, P Liò, and MM Bronstein. Neural sheaf diffusion: A topological perspective on heterophily and oversmoothing in gnns. Feb 2022. Accepted to NeurIPS 2022. Contains 29 pages, 10 figures.
- [213] G Meoni, L Tenori, S Schade, C Licari, C Pirazzini, MG Bacalini, P Garagnani, P Turano, PROPAG-AGEING Consortium, C Trenkwalder, C Franceschi, B Mollenhauer, and C Luchinat. Metabolite and lipoprotein profiles reveal sex-related oxidative stress imbalance in de novo drug-naive parkinson's disease patients. *NPJ Parkinsons Dis*, 8(1):14, Feb 2022.
- [214] S Zafeiriou, M Bronstein, T Cohen, O Vinyals, L Song, J Leskovec, P Lio, J Bruna, and M Gori. Guest editorial: Non-euclidean machine learning. *IEEE Transactions on Pattern Analysis and Machine Intelligence*, 44(2):723–726, Feb 2022.
- [215] Y Chen, CB Schonlieb, P Lio, T Leiner, PL Dragotti, G Wang, D Rueckert, D Firmin, and G Yang. Ai-based reconstruction for fast mri-a systematic review and meta-analysis. *Proceedings of the IEEE*, 110(2):224–245, Feb 2022.

- [216] E Zago, A Dal Molin, GM Dimitri, L Xumerle, C Pirazzini, MG Bacalini, MG Maturo, T Azevedo, S Spasov, P Gómez-Garre, MT Perrián, S Jesús, L Baldelli, L Sambati, G Calandra-Buonaura, P Garagnani, F Provini, P Cortelli, P Mir, C Trenkwalder, B Mollenhauer, C Franceschi, P Liò, C Nardini, and PROPAG-AGEING Consortium. Early downregulation of hsa-mir-144-3p in serum from drug-naïve parkinson's disease patients. *Sci Rep*, 12(1):1330, Jan 2022.
- [217] A Chaturvedi, A Tiwari, S Chaturvedi, and P Lio. System neural network: Evolution and change based structure learning. *IEEE Transactions on Artificial Intelligence*, 3(3):426–435, Jun 2022.
- [218] M Barsacchi, H Andres-Terré, and P Lió. Metabolically driven latent space learning for gene expression data. In *Deep Learning In Biology and Medicine*, pages 131–155. Jan 2022.
- [219] T Azevedo, RAI Bethlehem, D Whiteside, N Swaddiwudhipong, J Rowe, P Lió, and T Rittman. Identifying healthy individuals with alzheimer neuroimaging phenotypes in the uk biobank, 2022.
- [220] C Pisanu, G Severino, I De Toma, M Dierssen, P Fusar-Poli, M Gennarelli, P Lio, E Maffioletti, E Maron, D Mehta, A Minelli, M-C Potier, A Serretti, D Stacey, R van Westrhenen, L Xicota, European College of Neuropsychopharmacology (ECNP) Pharmacogenomics & Transcriptomics Network, BT Baune, and A Squassina. Transcriptional biomarkers of response to pharmacological treatments in severe mental disorders: A systematic review. *Eur Neuropsychopharmacol*, 55:112–157, Feb 2022.
- [221] P Charoenkwan, W Chiangjong, C Nantasenamat, MA Moni, P Lio', B Manavalan, and W Shoombuatong. Scmthp: A new approach for identifying and characterizing of tumor-homing peptides using estimated propensity scores of amino acids. *Pharmaceutics*, 14(1), Jan 2022.
- [222] B Zhou, X Liu, Y Liu, Y Huang, P Liò, and YG Wang. Well-conditioned spectral transforms for dynamic graph representation. In *Proceedings of Machine Learning Research*, volume 198, Jan 2022.
- [223] P Scherer, M Trebacz, N Simidjievski, R Viñas, Z Shams, H Andrés-Terré, M Jamnik, and P Liò. Unsupervised construction of computational graphs for gene expression data with explicit structural inductive biases. *Bioinform.*, 38(5):1320–1327, 2022.
- [224] F Barbero, C Bodnar, HS de Ocariz Borde, M Bronstein, P Veličković, and P Liò. Sh ea f neu ra l netwo rk s w ith co nn ectio n laplacians. In *Proceedings of Machine Learning Research*, volume 196, pages 28–36, Jan 2022.
- [225] A Campbell, L Qendro, P Liò, and C Mascolo. Robust and efficient uncertainty aware biosignal classification via early exit ensembles. In *ICASSP, IEEE International Conference on Acoustics, Speech and Signal Processing - Proceedings*, volume 2022-May, pages 3998–4002, Jan 2022.
- [226] G Aghakhanyan, A Barucci, S Colantonio, V Colcelli, F Pasquinelli, R Gini, P Lio, M Mazzei, P Erba, V Miele, and E Neri. Navigator: An imaging biobank to precisely prevent and predict cancer, and facilitate the participation of oncologic patients to diagnosis and treatment. In

- [227] AR Jamasb, R Viñas, EJ Ma, C Harris, K Huang, D Hall, P Lió, and TL Blundell. Graphin - a python library for geometric deep learning and network analysis on biomolecular structures and interaction networks. In *Advances in Neural Information Processing Systems*, volume 35, Jan 2022.
- [228] A Margeloiu, N Simidjievski, P Lio', and M Jamnik. Graph-conditioned mlp for high-dimensional tabular biomedical data. *CoRR*, abs/2211.06302, 2022.
- [229] SA Tailor, FL Opolka, P Liò, and ND Lane. Do we need anisotropic graph neural networks? In *ICLR 2022 - 10th International Conference on Learning Representations*, Jan 2022.
- [230] J Fan, J Pei, X Bi, B Xiao, and P Lio. Context correlation aware network for cardiac segmentation. In *Proceedings - IEEE International Conference on Multimedia and Expo*, volume 2022-July, Jan 2022.
- [231] ME Zarlenga, P Barbiero, G Ciravegna, G Marra, F Giannini, M Diligenti, Z Shams, F Precioso, S Melacci, A Weller, P Liò, and M Jamnik. Concept embedding models. *CoRR*, abs/2209.09056, 2022.
- [232] FL Opolka and P Liò. Bayesian link prediction with deep graph convolutional gaussian processes. In *Proceedings of Machine Learning Research*, volume 151, pages 4835–4852, Jan 2022.
- [233] B Day, R Viñas, N Simidjievski, and P Liò. Attentional meta-learners for few-shot polythetic classification. In *Proceedings of Machine Learning Research*, volume 162, pages 4867–4889, Jan 2022.
- [234] R Viñas, H Andrés-Terré, P Liò, and K Bryson. Adversarial generation of gene expression data. *Bioinform.*, 38(3):730–737, 2022.
- [235] FL Opolka, Y-C Zhi, P Liò, and X Dong. Adaptive gaussian processes on graphs via spectral graph wavelets. In G Camps-Valls, FJR Ruiz, and I Valera, editors, *AISTATS*, volume 151 of *Proceedings of Machine Learning Research*, pages 4818–4834. PMLR, 2022.
- [236] A Manouchehrinia, A Ebrahimi, UK Wiil, NA Kiani, P Lio, T Olsson, and I Kockum. A susceptibility network analysis of disease pathways leading to multiple sclerosis. In *MULTIPLE SCLEROSIS JOURNAL*, volume 28, pages 172–173, 2022.
- [237] H Stärk, D Beaini, G Corso, P Tossou, C Dallago, S Günnemann, and P Liò. 3d infomax improves gnns for molecular property prediction. In *Proceedings of Machine Learning Research*, volume 162, pages 20479–20502, Jan 2022.
- [238] Z Ma, J Xuan, YG Wang, M Li, and P Li². Path integral based convolution and pooling for graph neural networksthis article is an updated version of: Ma z, xuan j, wang y g, li m and li² p 2020 path integral based convolution and pooling for graph neural networks advances in neural information processing systems vol 33 ed h larochelle, m ranzato, r hadsell, m f balcan and h lin (new york: Curran associates) pp 16421–33. *Journal of Statistical Mechanics: Theory and Experiment*, 2021(12), Dec 2021.

- [239] Y Chen, C-B Schönlieb, P Liò, T Leiner, PL Dragotti, G Wang, D Rueckert, D Firmin, and G Yang. Ai-based reconstruction for fast mri – a systematic review and meta-analysis, Dec 2021.
- [240] X Lu, F Wang, C Jiang, and P Lio. A universal malicious documents static detection framework based on feature generalization. *Applied Sciences (Switzerland)*, 11(24), Dec 2021.
- [241] J Deasy, N Simidjievski, and P Liò. Heavy-tailed denoising score matching. Dec 2021.
- [242] A Iuliano, A Occhipinti, C Angelini, I De Feis, and P Liò. Cosmonet: An r package for survival analysis using screening-network methods. *Mathematics*, 9(24), Dec 2021.
- [243] S Banerjee, P Lio, P Jones, and R Cardinal. A class-contrastive human-interpretable machine learning approach to predict mortality in severe mental illness. *npj Schizophrenia*.
- [244] P Charoenkwan, C Nantasenamat, MM Hasan, MA Moni, P Lio', B Manavalan, and W Shoom-buatong. Stackdppiv: A novel computational approach for accurate prediction of dipeptidyl peptidase iv (dpp-iv) inhibitory peptides. *Methods*, 204:189–198, Aug 2022.
- [245] D Buterez, I Bica, I Tariq, H Andrés-Terré, and P Liò. Cellvgae: an unsupervised scrna-seq analysis workflow with graph attention networks. *Bioinformatics*, 38(5):1277–1286, Feb 2022.
- [246] J Deasy. Relaxing assumptions in deep probabilistic modelling.
- [247] B Zhou, X Liu, Y Liu, Y Huang, P Liò, and Y Wang. Spectral transform forms scalable transformer. Nov 2021.
- [248] J Yang, X-X Li, F Liu, D Nie, P Lio, H Qi, and D Shen. Fast t2w/flair mri acquisition by optimal sampling of information complementary to pre-acquired t1w mri. Nov 2021.
- [249] P Drotár, AR Jamasb, B Day, C Cangea, and P Liò. Structure-aware generation of drug-like molecules, Nov 2021.
- [250] P Spivakovsky-Gonzalez. Computational tools for metabolic modeling and gene duplication analysis.
- [251] FL Opolka, Y-C Zhi, P Liò, and X Dong. Adaptive gaussian processes on graphs via spectral graph wavelets. Oct 2021.
- [252] GM Dimitri, E Beqiri, MM Placek, M Czosnyka, N Stocchetti, A Ercole, P Smielewski, P Lió, and CENTER-TBI Collaborators. Modeling brain-heart crosstalk information in patients with traumatic brain injury. *Neurocrit Care*, 36(3):738–750, Jun 2022.
- [253] H Stärk, D Beaini, G Corso, P Tossou, C Dallago, S Günnemann, and P Liò. 3d infomax improves gnns for molecular property prediction. *39th International Conference on Machine Learning (ICML 2022)*, Oct 2021. 39th International Conference on Machine Learning (ICML 2022). Also accepted at NeurIPS 2021 ML4PH, AI4S, and SSL workshops and as oral at ELLIS ML4Molecules. 24 pages, 7 figures, 18 tables.
- [254] J Zhu, C Tan, J Yang, G Yang, and P Lio'. Arbitrary scale super-resolution for medical images. In *International Journal of Neural Systems*, volume 31, Oct 2021.

- [255] J King, RV Torné, A Campbell, and P Liò. An investigation of pre-upsampling generative modelling and generative adversarial networks in audio super resolution, Sep 2021.
- [256] JD Moss, FL Opolka, B Dumitrascu, and P Lió. Approximate latent force model inference. Sep 2021. Accepted with oral presentation at the Science-Guided AI Symposium at AAAI 2021.
- [257] G Corso, R Ying, M Pándy, P Veličković, J Leskovec, and P Liò. Neural distance embeddings for biological sequences, Sep 2021.
- [258] P Barbiero, R Viñas Torné, and P Lió. Graph representation forecasting of patient's medical conditions: Toward a digital twin. *Front Genet*, 12:652907, 2021.
- [259] M Zhu, P Lio, and J Moss. Modular neural ordinary differential equations. Sep 2021. 4 pages.
- [260] Y Wang, YG Wang, C Hu, M Li, Y Fan, N Otter, I Sam, H Gou, Y Hu, T Kwok, J Zalcborg, A Boussioutas, R Daly, G Montúfar, P Liò, D Xu, G Webb, and J Song. Cell graph neural networks enable the digital staging of tumor microenvironment and precise prediction of patient survival in gastric cancer, 2021.
- [261] X Lu, Y Liao, C Liu, P Lio, and P Hui. Heterogeneous model fusion federated learning mechanism based on model mapping. *IEEE Internet of Things Journal*, 9(8):6058–6068, Apr 2022.
- [262] L Baldelli, S Schade, S Jesús, SR Schreglmann, L Sambati, P Gómez-Garre, C Halsband, G Calandra-Buonaura, AD Adarmes-Gómez, F Sixel-Döring, C Zenesini, C Pirazzini, P Garagnani, MG Bacalini, KP Bhatia, P Cortelli, B Mollenhauer, C Franceschi, PROPAG-AGEING consortium, P Mir, C Trenkwalder, and F Provini. Heterogeneity of prodromal parkinson symptoms in siblings of parkinson disease patients. *NPJ Parkinsons Dis*, 7(1):78, Sep 2021.
- [263] F Castiglione, D Deb, AP Srivastava, P Liò, and A Liso. From infection to immunity: Understanding the response to sars-cov2 through in-silico modeling. *Front Immunol*, 12:646972, 2021.
- [264] P Charoenkwan, C Nantasenamat, MM Hasan, MA Moni, P Lio', and W Shoombuatong. ibitter-fuse: A novel sequence-based bitter peptide predictor by fusing multi-view features. *International Journal of Molecular Sciences*, 22(16).
- [265] G Ciravegna, P Barbiero, F Giannini, M Gori, P Lió, M Maggini, and S Melacci. Logic explained networks. *Artificial Intelligence*, 103822, 2022, Aug 2021.
- [266] X Lu and P Lio. International workshop on application of intelligent technology in security - aits 2021. In *Proceedings - 51st Annual IEEE/IFIP International Conference on Dependable Systems and Networks Workshops, DSN-W 2021*, pages XIV–XV, Jun 2021.
- [267] E Bellini, F Bagnoli, M Caporuscio, E Damiani, F Flammini, I Linkov, P Lio, and S Marrone. Resilience learning through self adaptation in digital twins of human-cyber-physical systems. In *Proceedings of the 2021 IEEE International Conference on Cyber Security and Resilience, CSR 2021*, pages 168–173, Jul 2021.

- [268] A Amor, P Lio', V Singh, RV Torné, and HA Terre. Graph representation learning on tissue-specific multi-omics. Jul 2021. This paper was accepted at the 2021 ICML Workshop on Computational Biology.
- [269] LC Magister, D Kazhdan, V Singh, and P Liò. Gcexplainer: Human-in-the-loop concept-based explanations for graph neural networks. Jul 2021. Accepted as 3rd ICML Workshop on Human in the Loop Learning, 2021.
- [270] L Qendro, A Campbell, P Liò, and C Mascolo. High frequency eeg artifact detection with uncertainty via early exit paradigm. Jul 2021. ICML 2021 Workshop on Human In the Loop Learning.
- [271] AR Jamasb, B Day, C Cangea, P Liò, and TL Blundell. Deep learning for protein-protein interaction site prediction. *Methods Mol Biol*, 2361:263–288, 2021.
- [272] COVID-19 Host Genetics Initiative. Mapping the human genetic architecture of covid-19. *Nature*, 600(7889):472–477, Dec 2021.
- [273] V Fanfani, R Vinas Torne, P Lio', and G Stracquadanio. Discovering cancer driver genes and pathways using stochastic block model graph neural networks. 2021.
- [274] C Bodnar, F Frasca, N Otter, YG Wang, P Liò, G Montúfar, and M Bronstein. Weisfeiler and lehman go cellular: Cw networks, Jun 2021.
- [275] MR Islam, MA Moni, MM Islam, M Rashed-Al-Mahfuz, MS Islam, MK Hasan, MS Hossain, M Ahmad, S Uddin, A Azad, SA Alyami, MAR Ahad, and P Lio. Emotion recognition from eeg signal focusing on deep learning and shallow learning techniques. *IEEE Access*, 9:94601–94624, Jan 2021.
- [276] N Zubić and P Liò. An effective loss function for generating 3d models from single 2d image without rendering. *IFIP Advances in Information and Communication Technology*, 627:309–322, Jan 2021.
- [277] C Bodnar, C Cangea, and P Liò. Deep graph mapper: Seeing graphs through the neural lens., 2021.
- [278] B Day, R Viñas, N Simidjievski, and P Liò. Attentional meta-learners for few-shot polythetic classification. Jun 2021. Accepted at ICML 2022.
- [279] A Tangherloni, F Ricciuti, D Besozzi, P Liò, and A Cvejic. Analysis of single-cell rna sequencing data based on autoencoders. *BMC Bioinformatics*, 22(1):309, Jun 2021.
- [280] AD Vecchio, A Deac, P Liò, and P Veličković. Neural message passing for joint paratope-epitope prediction. May 2021. ICML Workshop on Computational Biology 2021 , 5 pages, 2 figures.
- [281] A Del Vecchio, A Deac, P Liò, and P Veličković. Neural message passing for joint paratope-epitope prediction, May 2021.
- [282] T Azevedo, GM Dimitri, P Lió, and ER Gamazon. Multilayer modelling of the human transcriptome and biological mechanisms of complex diseases and traits. *NPJ Syst Biol Appl*, 7(1):24, May 2021.

- [283] J Zhu, C Tan, J Yang, G Yang, and P Lio'. Miassr: An approach for medical image arbitrary scale super-resolution. May 2021.
- [284] S Spasov. Encoding parameter and structural efficiency in deep learning.
- [285] V Shankar, R Tibshirani, and RN Zare. Massexplorer: a computational tool for analyzing desorption electrospray ionization mass spectrometry data. *Bioinformatics*, May 2021.
- [286] K Chen, H Xu, Y Lei, P Lio, Y Li, H Guo, and M Ali Moni. Integration and interplay of machine learning and bioinformatics approach to identify genetic interaction related to ovarian cancer chemoresistance. *Brief Bioinform*, 22(6), Nov 2021.
- [287] B Day, A Norcliffe, J Moss, and P Liò. Meta-learning using privileged information for dynamics. Apr 2021. Published as a workshop paper at the Learning to Learn and SimDL workshops at ICLR 2021. 4 pages, 3 pages of appendices.
- [288] D D'Agostino, P Liò, M Aldinucci, and I Merelli. Advantages of using graph databases to explore chromatin conformation capture experiments. *BMC Bioinformatics*, 22(Suppl 2):43, Apr 2021.
- [289] MM Ahamad, S Aktar, MJ Uddin, M Rashed-Al-Mahfuz, AKM Azad, S Uddin, S Alyami, I Sarker, P Liò, JMW Quinn, and MA Moni. Adverse effects of covid-19 vaccination: machine learning and statistical approach to identify and classify incidences of morbidity and post-vaccination reactogenicity, 2021.
- [290] SA Tailor, FL Opolka, P Liò, and ND Lane. Adaptive filters and aggregator fusion for efficient graph convolutions. *arxiv*. Short versions to appear at the GNNsSys Workshop at MLSys 2021 and the Hardware-Aware Efficient Training Workshop at ICLR 2021.
- [291] A Lipov and P Liò. A multiscale graph convolutional network using hierarchical clustering. *Advances in Intelligent Systems and Computing*, 1364 AISC:489–506, Jan 2021.
- [292] CN Christensen, E Ward, P Lio, and C Kaminski. MI-sim: Universal reconstruction of structured illumination microscopy images using transfer learning. *Biomedical Optics Express*.
- [293] D Kazhdan, B Dimanov, HA Terre, M Jamnik, P Liò, and A Weller. Is disentanglement all you need? comparing concept-based & disentanglement approaches. Apr 2021. Presented at the RAI, WeaSul, and RobustML workshops at The Ninth International Conference on Learning Representations (ICLR) 2021.
- [294] R Viñas, T Azevedo, ER Gamazon, and P Liò. Deep learning enables fast and accurate imputation of gene expression. *Front Genet*, 12:624128, 2021.
- [295] GM Dimitri, E Beqiri, M Czosnyka, A Ercole, P Smielewski, P Lio, CENTER-TBI High Resolution Substudy Participants, and Investigators. Analysis of cardio-cerebral crosstalk events in an adult cohort from the center-tbi study. *Acta Neurochir Suppl*, 131:39–42, 2021.
- [296] S Banerjee, P Liò, P Jones, and R Cardinal. A human-interpretable machine learning approach to predict mortality in severe mental illness, 2021.

- [297] E Rocheteau, P Liò, and S Hyland. Temporal pointwise convolutional networks for length of stay prediction in the intensive care unit. *ACM CHIL 2021 - Proceedings of the 2021 ACM Conference on Health, Inference, and Learning*, pages 58–68, Apr 2021.
- [298] SA Tailor, FL Opolka, P Liò, and ND Lane. Do we need anisotropic graph neural networks?, Apr 2021.
- [299] A Norcliffe, C Bodnar, B Day, J Moss, and P Liò. Neural ode processes. Mar 2021. ICLR 2021. 9 pages, 6 figures, 7 pages of appendices.
- [300] GM Dimitri, S Spasov, A Duggento, L Passamonti, P Lio', and N Toschi. Multimodal image fusion via deep generative models, 2021.
- [301] JM Weber, CP Lindenmeyer, P Liò, and AA Lapkin. Teaching sustainability as complex systems approach: a sustainable development goals workshop. *International Journal of Sustainability in Higher Education*, 22(8):25–41, Mar 2021.
- [302] D Buterez, I Bica, I Tariq, H Andrés-Terré, and P Liò. Cellvgae: An unsupervised scrna-seq analysis workflow with graph attention networks. 2020.
- [303] M Rashed-Al-Mahfuz, MA Moni, P Lio', SMS Islam, S Berkovsky, M Khushi, and JMW Quinn. Deep convolutional neural networks based ecg beats classification to diagnose cardiovascular conditions. *Biomed Eng Lett*, 11(2):147–162, May 2021.
- [304] X Zheng, B Zhou, J Gao, YG Wang, P Lio, M Li, and G Montufar. How framelets enhance graph neural networks. *INTERNATIONAL CONFERENCE ON MACHINE LEARNING, VOL 139*, 139, 2021.
- [305] M Roberts, D Driggs, M Thorpe, J Gilbey, M Yeung, S Ursprung, AI Aviles-Rivero, C Etman, C McCague, L Beer, JR Weir-McCall, Z Teng, E Gkrania-Klotsas, A Ruggiero, A Korhonen, E Jefferson, E Ako, G Langs, G Gozaliasl, G Yang, H Prosch, J Preller, J Stanczuk, J Tang, J Hofmanninger, J Babar, LE Sánchez, M Thillai, PM Gonzalez, P Teare, X Zhu, M Patel, C Cafolla, H Azadbakht, J Jacob, J Lowe, K Zhang, K Bradley, M Wasson, M Holzer, K Ji, MD Ortet, T Ai, N Walton, P Lio, S Stranks, T Shadbahr, W Lin, Y Zha, Z Niu, JHF Rudd, E Sala, and CB Schönlieb. Common pitfalls and recommendations for using machine learning to detect and prognosticate for covid-19 using chest radiographs and ct scans. *Nature Machine Intelligence*, 3(3):199–217, Mar 2021.
- [306] Z Shams, B Dimanov, S Kola, N Simidjievski, HA Terre, P Scherer, U Matjašec, J Abraham, M Jamnik, and P Liò. Rem: An integrative rule extraction methodology for explainable data analysis in healthcare, 2021.
- [307] R Viñas, H Andrés-Terré, P Liò, and K Bryson. Adversarial generation of gene expression data. *Bioinformatics*.
- [308] E Rocheteau, C Tong, P Veličković, N Lane, and P Liò. Predicting patient outcomes with graph representation learning, Jan 2021.
- [309] F Bardozzo, P Lió, and R Tagliaferri. Signal metrics analysis of oscillatory patterns in bacterial multi-omic networks. *Bioinform.*, 37(10):1411–1419, 2021.

- [310] Z Nain, HK Rana, P Liò, SMS Islam, MA Summers, and MA Moni. Pathogenetic profiling of covid-19 and sars-like viruses. *Briefings Bioinform.*, 22(2):1175–1196, 2021.
- [311] I Sebenius, A Campbell, SE Morgan, ET Bullmore, and P Lio. Multimodal graph coarsening for interpretable, mri-based brain graph neural network. In *IEEE International Workshop on Machine Learning for Signal Processing, MLSP*, volume 2021-January, Jan 2021.
- [312] R Vignani, M Scali, and P Liò. Molecular markers and genomics for food and beverages characterization. In *Handbook of DNA Profiling*, pages 1–21. Springer Singapore, 2021.
- [313] F Bagnoli, D Lorini, and P Lió. Modeling social groups, policies and cognitive behavior in covid-19 epidemic phases. basic scenarios. *Substantia*, 4(1), Jan 2021.
- [314] F Bagnoli and P Lio. How the mutational-selection interplay organizes the fitness landscape. *J NONLINEAR MATH PHY*, 18:265–286, Aug 2011.
- [315] L Qendro, A Campbell, P Liò, and C Mascolo. Early exit ensembles for uncertainty quantification. In *Proceedings of Machine Learning Research*, volume 158, pages 181–195, Jan 2021.
- [316] D Beaini, S Passaro, V Létourneau, WL Hamilton, G Corso, and P Liò. Directional graph networks. In *Proceedings of Machine Learning Research*, volume 139, pages 748–758, Jan 2021.
- [317] X Wei, C Pu, Z He, and P Lio. Deep reinforcement learning-based vaccine distribution strategies. In *Proceedings - 2021 2nd International Conference on Electronics, Communications and Information Technology, CECIT 2021*, pages 427–436, Jan 2021.
- [318] N Zubic and P Liò. An effective loss function for generating 3d models from single 2d image without rendering. In I Maglogiannis, J MacIntyre, and L Iliadis, editors, *AIAI*, volume 627 of *IFIP Advances in Information and Communication Technology*, pages 309–322. Springer, 2021.
- [319] X Lu, S Fu, C Jiang, and P Lió. A fine-grained iot data access control scheme combining attribute-based encryption and blockchain. *Secur. Commun. Networks*, 2021:5308206:1–5308206:1, 2021.
- [320] B Dimanov. Interpretable deep learning: Beyond feature-importance with concept-based explanations.
- [321] C Pirazzini, T Azevedo, L Baldelli, A Bartoletti-Stella, G Calandra-Buonaura, A Dal Molin, GM Dimitri, I Doykov, P Gómez-Garre, S Hägg, J Hällqvist, C Halsband, W Heywood, S Jesús, J Jylhävä, KM Kwiatkowska, MA Labrador-Espinosa, C Licari, MG Maturo, G Mengozzi, G Meoni, M Milazzo, MT Perrián-Tocino, F Ravaioli, C Sala, L Sambati, S Schade, S Schreglmann, S Spasov, L Tenori, D Williams, L Xumerle, E Zago, KP Bhatia, S Capellari, P Cortelli, P Garagnani, H Houlden, P Liò, C Luchinat, M Delledonne, K Mills, P Mir, B Mollenhauer, C Nardini, NL Pedersen, F Provini, S Strom, C Trenkwalder, P Turano, MG Bacalini, C Franceschi, and PROPAG-AGEING Consortium. A geroscience approach for parkinson’s disease: Conceptual framework and design of propag-ageing project. *Mech Ageing Dev*, 194:111426, Mar 2021.

- [322] F Caccuri, P D'Ursi, M Uggeri, A Bugatti, P Mazzuca, A Zani, F Filippini, M Salmona, D Ribatti, M Slevin, A Orro, W Lu, P Liò, RC Gallo, and A Caruso. Evolution toward beta common chain receptor usage links the matrix proteins of hiv-1 and its ancestors to human erythropoietin. *Proc Natl Acad Sci U S A*, 118(2), Jan 2021.
- [323] F Castiglione, D Deb, A Srivastava, P Liò, and A Liso. From infection to immunity: understanding the response to sars-cov2 through in-silico modeling, 2020.
- [324] J Deasy, P Liò, and A Ercole. Dynamic survival prediction in intensive care units from heterogeneous time series without the need for variable selection or curation. *Scientific Reports*, 10(1).
- [325] D Kazhdan, B Dimanov, M Jamnik, and P Liò. Meme: Generating rnn model explanations via model extraction. Dec 2020. Presented at the HAMLETS workshop at the 34th Conference on Neural Information Processing Systems (NeurIPS 2020).
- [326] D D'Agostino, P Liò, M Aldinucci, and I Merelli. Neohic: A web application for the analysis of hi-c data. In *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, volume 12313 LNBI, pages 98–107, Jan 2020.
- [327] M van Der Schaar, AM Alaa, A Floto, A Gimson, S Scholtes, A Wood, E McKinney, D Jarrett, P Lio, and A Ercole. How artificial intelligence and machine learning can help healthcare systems respond to covid-19. *Machine Learning*, 110:1–14, Jan 2021. amended Scholtes author spelling & updated status, vol, pagination. amended subtype from "review" (=book review) to "article".
- [328] M Trębacz, Z Shams, M Jamnik, P Scherer, N Simidjievski, HA Terre, and P Liò. Using ontology embeddings for structural inductive bias in gene expression data analysis. *arxiv*. 4 pages + 2 page references, 15th Machine Learning in Computational Biology (MLCB) meeting, 2020.
- [329] X Lu, Y Liao, P Lio, and H Pan. An asynchronous federated learning mechanism for edge network computing. *Jisuanji Yanjiu yu Fazhan/Computer Research and Development*, 57(12):2571–2582, Dec 2020.
- [330] MM Ahamad, S Aktar, M Rashed-Al-Mahfuz, S Uddin, P Liò, H Xu, MA Summers, JMW Quinn, and MA Moni. A machine learning model to identify early stage symptoms of sars-cov-2 infected patients. *Expert Systems with Applications*, 160:113661–113661, Dec 2020.
- [331] M Trębacz, Z Shams, M Jamnik, P Scherer, N Simidjievski, HA Terre, and P Liò. Using ontology embeddings for structural inductive bias in gene expression data analysis, Nov 2020.
- [332] T Azevedo, A Campbell, R Romero-Garcia, L Passamonti, RAI Bethlehem, P Liò, and N Toschi. A deep graph neural network architecture for modelling spatio-temporal dynamics in resting-state functional mri data. 2020.
- [333] CPE Rollins, JR Garrison, M Arribas, A Seyedsalehi, Z Li, RCK Chan, J Yang, D Wang, P Liò, C Yan, Z-H Yi, A Cachia, R Uptegrove, B Deakin, JS Simons, GK Murray, and J Suckling. Evidence in cortical folding patterns for prenatal predispositions to hallucinations in schizophrenia. *Transl Psychiatry*, 10(1):387, Nov 2020.

- [334] X Lu, X Wang, P Lio, and P Hui. Dadim: A distance adjustment dynamic influence map model. *Future Generation Computer Systems*, 112:1122–1130, Nov 2020.
- [335] D Kazhdan, B Dimanov, M Jamnik, P Liò, and A Weller. Now you see me (cme): Concept-based model extraction, Oct 2020.
- [336] J Moss and P Lió. Gene regulatory network inference with latent force models. Oct 2020.
- [337] D Beaini, S Passaro, V Létourneau, WL Hamilton, G Corso, and P Liò. Directional graph networks, Oct 2020.
- [338] V Wichitwechkarn, B Day, C Bodnar, M Wales, and P Liò. The role of isomorphism classes in multi-relational datasets. Sep 2020. 7 pages main text, 1 page of references and an ethics statement, 3 pages of appendices.
- [339] B Day, C Cangea, AR Jamasb, and P Liò. Message passing neural processes. Sep 2020. 18 pages, 6 figures. The first two authors contributed equally.
- [340] P Scherer, M Trbacz, N Simidjievski, Z Shams, HA Terre, P Liò, and M Jamnik. Incorporating network based protein complex discovery into automated model construction. Sep 2020. 7 Pages, 2 Figures.
- [341] M Scata, A Di Stefano, A La Corte, and P Lio. A multiplex social contagion dynamics model to shape and discriminate d2d content dissemination. *IEEE Transactions on Cognitive Communications and Networking*, 7(2):581–593, Jan 2021.
- [342] K Dmitry, Z Shams, and L Pietro. Marleme: A multi-agent reinforcement learning model extraction library. In *2020 International Joint Conference on Neural Networks (IJCNN)*. Glasgow, UK, IEEE.
- [343] P Barbiero, R Viñas Torné, and P Lió. Graph representation forecasting of patient’s medical conditions: towards a digital twin. 2020.
- [344] Y Zhao, D Wang, D Bates, R Mullins, M Jamnik, and P Lio. Learned low precision graph neural networks. Sep 2020.
- [345] G Yeghikyan, FL Opolka, M Nanni, B Lepri, and P Lio. Learning mobility flows from urban features with spatial interaction models and neural networks**to appear in the proceedings of 2020 ieee international conference on smart computing (smartcomp 2020). In *Proceedings - 2020 IEEE International Conference on Smart Computing, SMARTCOMP 2020*, pages 57–64, Sep 2020.
- [346] X Lu, S Zhang, P Hui, and P Lio. Continuous authentication by free-text keystroke based on cnn and rnn. *Computers and Security*, 96, Sep 2020.
- [347] Z Nain, HK Rana, P Liò, SMS Islam, MA Summers, and MA Moni. Pathogenetic profiling of covid-19 and sars-like viruses. *Briefings in Bioinformatics*, Aug 2020.
- [348] A Di Stefano, M Scatá, B Attanasio, A La Corte, P Lió, and SK Das. A novel methodology for designing policies in mobile crowdsensing systems. *Pervasive and Mobile Computing*, 67, Sep 2020.

- [349] F Bardozzo, P Liò, and R Tagliaferri. Signal metrics analysis of oscillatory patterns in bacterial multi-omic networks, Aug 2020.
- [350] D Wang. Neural diagrammatic reasoning.
- [351] E Rocheteau, P Liò, and S Hyland. Temporal pointwise convolutional networks for length of stay prediction in the intensive care unit, Jul 2020.
- [352] S Spasov, AD Stefano, P Lio, and J Tang. Grade: Graph dynamic embedding. Jul 2020.
- [353] A Jamasb, R Viñas, E Ma, C Harris, K Huang, D Hall, P Lió, and T Blundell. Graphein - a python library for geometric deep learning and network analysis on protein structures and interaction networks. 2020.
- [354] ED Maria, J Despeyroux, A Felty, P Liò, C Olarte, and A Bahrami. Computational logic for biomedicine and neurosciences. Jul 2020.
- [355] E de Maria, J Despeyroux, A Felty, P Liò, C Olarte, and A Bahrami. Computational logic for biomedicine and neurosciences, Jul 2020.
- [356] S Glass, S Spasov, and P Liò. Riccinets: Curvature-guided pruning of high-performance neural networks using ricci flow. Jul 2020. To appear at ICML 2020, AutoML Workshop. Contains 11 pages, 5 figures.
- [357] GM Dimitri, S Spasov, A Duggento, L Passamonti, P Lio, and N Toschi. Unsupervised stratification in neuroimaging through deep latent embeddings. In *Annu Int Conf IEEE Eng Med Biol Soc*, volume 2020, pages 1568–1571. United States, Jul 2020.
- [358] D Kazhdan, Z Shams, and P Lio. Marleme: A multi-agent reinforcement learning model extraction library. *Proceedings of the International Joint Conference on Neural Networks*, Jul 2020.
- [359] GM Dimitri, E Beqiri, MM Placek, M Czosnyka, A Ercole, P Smielewski, and P Lio. Introducing brain-heart crosstalks information in clinical decision support systems for tbi patients, through icm+. In *2020 11th Conference of the European Study Group on Cardiovascular Oscillations: Computation and Modelling in Physiology: New Challenges and Opportunities, ESGCO 2020*, Jul 2020.
- [360] A-C Filip, T Azevedo, L Passamonti, N Toschi, and P Lio. A novel graph attention network architecture for modeling multimodal brain connectivity. In *Annu Int Conf IEEE Eng Med Biol Soc*, volume 2020, pages 1071–1074. United States, Jul 2020.
- [361] T Azevedo, L Passamonti, P Lio, and N Toschi. A deep spatiotemporal graph learning architecture for brain connectivity analysis. In *Annu Int Conf IEEE Eng Med Biol Soc*, volume 2020, pages 1120–1123. United States, Jul 2020.
- [362] E Rocheteau, P Liò, and S Hyland. Predicting length of stay in the intensive care unit with temporal pointwise convolutional networks. Jun 2020. Machine Learning for Health (ML4H) at NeurIPS 2020 - Extended Abstract. Also accepted for spotlight presentation at Healthcare Systems, Population Health, and the Role of Health-Tech (HSYS) at ICML 2020. The full length version of this paper can be found at arXiv:2007.09483.

- [363] K Stankevičiūtė, T Azevedo, A Campbell, R Bethlehem, and P Liò. Population graph gnns for brain age prediction. 2020.
- [364] Z Ma, J Xuan, YG Wang, M Li, and P Lio. Path integral based convolution and pooling for graph neural networks, Jun 2020.
- [365] V Karavias, B Day, and P Liò. Uncertainty in neural relational inference trajectory reconstruction. Jun 2020. 4 main pages, 1 page of supplementary materials. Accepted for presentation at the Graph Representation Learning and Beyond workshop at ICML 2020.
- [366] MS John, JA Nagoth, KP Ramasamy, P Ballarini, M Mozzicafreddo, A Mancini, A Telatin, P Liò, G Giuli, A Natalello, C Miceli, and S Pucciarelli. Horizontal gene transfer and silver nanoparticles production in a new *marinomonas* strain isolated from the antarctic psychrophilic ciliate *euplotes focardii*. *Scientific Reports*, 10(1):10218–10218, Jun 2020.
- [367] A Lipov and P Liò. A multiscale graph convolutional network using hierarchical clustering, Jun 2020.
- [368] D Wang, M Jamnik, and P Lio. Abstract diagrammatic reasoning with multiplex graph networks, Jun 2020.
- [369] J Deasy, N Simidjievski, and P Liò. Constraining variational inference with geometric jensen-shannon divergence, Jun 2020.
- [370] I Bica, H Andrés-Terré, A Cvejic, and P Liò. Unsupervised generative and graph representation learning for modelling cell differentiation. *Sci Rep*, 10(1):9790, Jun 2020.
- [371] D Wang, M Jamnik, and P Lio. Extrapolatable relational reasoning with comparators in low-dimensional manifolds, Jun 2020.
- [372] P Barbiero and P Lió. The computational patient has diabetes and a covid. 2020.
- [373] A Norcliffe, C Bodnar, B Day, N Simidjievski, and P Liò. On second order behaviour in augmented neural odes, Jun 2020.
- [374] R Viñas, T Azevedo, E Gamazon, and P Liò. Gene expression imputation with generative adversarial imputation nets. 2020.
- [375] A Campbell and P Liò. tvgp-vae: Tensor-variate gaussian process prior variational autoencoder. Jun 2020. 8 pages, 2 Figures.
- [376] PDL Flood, R Viñas, and P Liò. Investigating estimated kolmogorov complexity as a means of regularization for link prediction. Jun 2020. Published as a Workshop Paper at the Causal Discovery & Causality-Inspired Machine Learning Workshop at Neural Information Processing Systems, 2020.
- [377] CPE Rollins, J Garrison, M Arribas, A Seyedsalehi, Z Li, RCK Chan, J Yang, D Wang, P Lio, C Yan, Z-H Yi, A Cachia, R Upthegrove, B Deakin, J Simons, G Murray, and J Suckling. The neurodevelopment of anomalous perception: Evidence in cortical folding patterns for prenatal predispositions to hallucinations in schizophrenia. 2020.

- [378] C Tan, J Zhu, and P Lio'. Arbitrary scale super-resolution for brain mri images. *IFIP Advances in Information and Communication Technology*, 583 IFIP:165–176, Jan 2020.
- [379] T Azevedo, GM Dimitri, P Lio, and E Gamazon. Multilayer modelling and analysis of the human transcriptome. 2020.
- [380] D Georgiev and P Liò. Neural bipartite matching. May 2020.
- [381] P Spivakovsky, P Lio, and MS Clark. Physim: A new phylogenetic tool for modeling trait evolution and speciation, 2020.
- [382] X Lu, X Zhou, W Wang, P Lio, and P Hui. Domain-oriented topic discovery based on features extraction and topic clustering. *IEEE Access*, 8:93648–93662, Jan 2020.
- [383] G Yeghikyan, FL Opolka, M Nanni, B Lepri, and P Lio'. Learning mobility flows from urban features with spatial interaction models and neural networks. Apr 2020. 9 pages, 5 figures, to be published in the Proceedings of 2020 IEEE International Conference on Smart Computing (SMARTCOMP 2020).
- [384] TT Müller and P Lio. Peclides neuro: A personalisable clinical decision support system for neurological diseases. *Front Artif Intell*, 3:23, 2020.
- [385] G Corso, L Cavalleri, D Beaini, P Liò, and P Veličković. Principal neighbourhood aggregation for graph nets, Apr 2020.
- [386] C Bodnar, B Day, and P Lió. Proximal distilled evolutionary reinforcement learning. *AAAI 2020 - 34th AAAI Conference on Artificial Intelligence*, pages 3283–3290, Jan 2020.
- [387] CN Christensen, EN Ward, P Lio, and CF Kaminski. MI-sim: A deep neural network for reconstruction of structured illumination microscopy images. Mar 2020.
- [388] Y Zhao, D Wang, X Gao, R Mullins, P Lio, and M Jamnik. Probabilistic dual network architecture search on graphs, Mar 2020.
- [389] P Scherer and P Lio. Learning distributed representations of graphs with geo2dr. Mar 2020. 9 Pages, Revised version accepted at ICML 2020 GRL+ Workshop.
- [390] J Deasy, A Ercole, and P Liò. Adaptive prediction timing for electronic health records. Mar 2020.
- [391] X Lu, Y Liao, P Lio, and P Hui. Privacy-preserving asynchronous federated learning mechanism for edge network computing. *IEEE Access*, 8:48970–48981, Jan 2020.
- [392] J Deasy, E Rocheteau, K Kohler, D Stubbs, P Barbiero, P Liò, and A Ercole. Forecasting ultra-early intensive care strain from covid-19 in england, v1.1.4, 2020.
- [393] T Azevedo, L Passamonti, P Liò, and N Toschi. Towards a predictive spatio-temporal representation of brain data. Feb 2020. To appear in the Workshop on AI for Affordable Healthcare (AI4AH) at ICLR 2020. 8 pages, 2 figures.
- [394] M Barsacchi, HA Terre, and P Lió. Geese: Metabolically driven latent space learning for gene expression data. 2018.

- [395] AG Rakowski, P Veličković, E Dall'Ara, and P Liò. Chronomid-cross-modal neural networks for 3-d temporal medical imaging data. *PLoS One*, 15(2):e0228962, 2020.
- [396] HK Rana, MR Akhtar, MB Islam, MB Ahmed, P Lió, F Huq, JMW Quinn, and MA Moni. Machine learning and bioinformatics models to identify pathways that mediate influences of welding fumes on cancer progression. *Sci Rep*, 10(1):2795, Feb 2020.
- [397] I Merelli, P Liò, I Kotenko, and D D'Agostino. Latest advances in parallel, distributed, and network-based processing. *Concurrency and Computation: Practice and Experience*, 32(10), May 2020.
- [398] FL Opolka and P Liò. Graph convolutional gaussian processes for link prediction, Feb 2020.
- [399] C Bodnar, C Cangea, and P Liò. Deep graph mapper: Seeing graphs through the neural lens, Feb 2020.
- [400] R Kusztos, GM Dimitri, and P Lió. Neural models for brain networks connectivity analysis. In *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, volume 11925 LNBI, pages 212–226, Jan 2020.
- [401] F Bardozzo, P Lio', and R Tagliaferri. A machine learning approach to investigate regulatory control circuits in bacterial metabolic pathways. volume 2016, pages 13–13. 5 pages, 3 figures.
- [402] F Bardozzo, P Lio', and R Tagliaferri. A machine learning approach to investigate regulatory control circuits in bacterial metabolic pathways, Jan 2020.
- [403] A Di Stefano, DDF Maesa, SK Das, and P Liò. Resolution of blockchain conflicts through heuristics-based game theory and multilayer network modeling. In *ACM International Conference Proceeding Series*, volume Part F165625, Jan 2020.
- [404] C Cangea, P Velickovic, and P Liò. Xflow: Cross-modal deep neural networks for audiovisual classification. *IEEE Trans. Neural Networks Learn. Syst.*, 31(9):3711–3720, 2020.
- [405] SE Spasov and P Liò. Dynamic neural network channel execution for efficient training. *30th British Machine Vision Conference 2019, BMVC 2019*, Jan 2020.
- [406] AD Stefano, M Scatà, B Attanasio, AL Corte, P Lió, and SK Das. A novel methodology for designing policies in mobile crowdsensing systems. *Pervasive Mob. Comput.*, 67:101230–101230, 2020.
- [407] N Simidjievski, C Bodnar, I Tariq, P Scherer, H Andres Terre, Z Shams, M Jamnik, and P Liò. Variational autoencoders for cancer data integration: Design principles and computational practice. *Front Genet*, 10:1205, 2019.
- [408] H Andres Terre. Interpreting deep learning for cell differentiation. supervised and unsupervised models viewed through the lens of information and perturbation theory.
- [409] MS Satu, K Chandra Howlader, TM Niamat Ullah Akhund, JMW Quinn, P Lio, and MA Moni. Comorbidity effects of mitochondrial dysfunction to the progression of neurological disorders: Insights from a systems biomedicine perspective. In *2019 22nd International Conference on Computer and Information Technology, ICCIT 2019*, Dec 2019.

- [410] J Yang, D Wang, C Rollins, M Leming, P Liò, J Suckling, G Murray, J Garrison, and A Cachia. Volumetric segmentation and characterisation of the paracingulate sulcus on mri scans. Nov 2019.
- [411] T George and P Lio. Unsupervised machine learning for data encoding applied to ovarian cancer transcriptomes, 2019.
- [412] R Viñas, H Andrés-Terré, P Liò, and K Bryson. Adversarial generation of gene expression data, 2019.
- [413] T Akter, M Shahriare Satu, MI Khan, MH Ali, S Uddin, P Lio, JMW Quinn, and MA Moni. Machine learning-based models for early stage detection of autism spectrum disorders. *IEEE Access*, 7:166509–166527, Jan 2019.
- [414] C Cangea, P Velickovic, and P Lio. Xflow: Cross-modal deep neural networks for audiovisual classification. *IEEE Trans Neural Netw Learn Syst*, Nov 2019. Early Access.
- [415] P Scherer, H Andres-Terre, P Lio, and M Jamnik. Decoupling feature propagation from the design of graph auto-encoders. Oct 2019. 4 pages (considering single anonymous naming during original submission, now a few lines over 4). Originally submitted to NeurIPS 2019 Graph Representation Learning Workshop.
- [416] I Bica, H Andrés-Terré, A Cvejic, and P Liò. Unsupervised generative and graph representation learning for modelling cell differentiation, 2019.
- [417] J Deasy, A Ercole, and P Liò. Impact of novel aggregation methods for flexible, time-sensitive ehr prediction without variable selection or cleaning. Sep 2019. 5 pages, 3 tables, 1 figure, preprint under review at the Machine Learning for Health workshop at NeurIPS 2019.
- [418] J Deasy, P Liò, and A Ercole. Dynamic survival prediction in intensive care units from heterogeneous time series without the need for variable selection or curation. *Sci Rep*, 10(1):22129, Dec 2020.
- [419] J Deasy, P Liò, and A Ercole. Dynamic survival prediction in intensive care units from heterogeneous time series without the need for variable selection or pre-processing, Sep 2019.
- [420] D Taylor, S Spasov, and P Liò. Co-attentive cross-modal deep learning for medical evidence synthesis and decision making. Sep 2019. 7 pages, 2 figures, Machine Learning for Health (ML4H) at NeurIPS 2019 - Extended Abstract, clarified graph and math notation, typos corrected.
- [421] C Maj, T Azevedo, V Giansanti, O Borisov, GM Dimitri, S Spasov, Alzheimer’s Disease Neuroimaging Initiative, P Lió, and I Merelli. Integration of machine learning methods to dissect genetically imputed transcriptomic profiles in alzheimer’s disease. *Frontiers in Genetics*, 10(726).
- [422] C Cangea, E Belilovsky, P Liò, and A Courville. Videonavqa: Bridging the gap between visual and embodied question answering. Aug 2019. To appear at BMVC 2019. 15 pages, 5 figures.
- [423] A Tangherloni, F Ricciuti, D Besozzi, P Liò, and A Cvejic. Analysis of single-cell rna sequencing data based on autoencoders, 2019.

- [424] G Ascolani and P Liò. Modeling breast cancer progression to bone: how driver mutation order and metabolism matter. *BMC Medical Genomics*, 12(Suppl 6).
- [425] T Müller and P Lio'. Peclides neuro a personalisable clinical decision support system for neurological diseases, 2019.
- [426] V Prokhorov, MT Pilehvar, D Kartsaklis, P Lio, and N Collier. Unseen word representation by aligning heterogeneous lexical semantic spaces. *Proceedings of the AAAI Conference on Artificial Intelligence*, 33(01):6900–6907.
- [427] V Singh and P Lio'. Towards probabilistic generative models harnessing graph neural networks for disease-gene prediction. Jul 2019. Workshop on Computational Biology (WCB) at ICML 2019.
- [428] H Andrés-Terré and P Lió. Perturbation theory approach to study the latent space degeneracy of variational autoencoders. Jul 2019.
- [429] L Xiaofeng, J Fangshuo, Z Xiao, Y Shengwei, S Jing, and P Lio. Assca: Api sequence and statistics features combined architecture for malware detection. *Computer Networks*, 157:99–111, Jul 2019.
- [430] J Weber, P Lio', and A Lapkin. Identification of strategic molecules for future circular supply chains using large reaction networks. 2019.
- [431] C Bodnar, B Day, and P Lió. Proximal distilled evolutionary reinforcement learning, Jun 2019.
- [432] E Webb, B Day, H Andres-Terre, and P Lió. Factorised neural relational inference for multi-interaction systems. May 2019. 4 page workshop paper accepted for presentation at the ICML 2019 Workshop on Learning and Reasoning with Graph-Structured Representations with 6 pages of supplementary materials and figures.
- [433] E Rossi, F Monti, M Bronstein, and P Liò. ncna classification with graph convolutional networks. May 2019.
- [434] SE Spasov and P Lio. Dynamic neural network channel execution for efficient training, May 2019.
- [435] E Luzhnica, B Day, and P Liò. On graph classification networks, datasets and baselines, May 2019. Submitted to the ICML 2019 Workshop on Learning and Reasoning with Graph-Structured Data.
- [436] T Azevedo, L Passamonti, P Lió, and N Toschi. A machine learning tool for interpreting differences in cognition using brain features. In *IFIP Advances in Information and Communication Technology*, volume 559, pages 475–486, Jan 2019.
- [437] A Deac, Y-H Huang, P Veličković, P Liò, and J Tang. Drug-drug adverse effect prediction with graph co-attention. May 2019. 8 pages, 5 figures.
- [438] J Despeyroux, A Felty, P Liò, and C Olarte. A logical framework for modelling breast cancer progression. In *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, volume 11415 LNCS, pages 121–141, Jan 2019.

- [439] A Tangherloni, S Spolaor, L Rundo, MS Nobile, P Cazzaniga, G Mauri, P Liò, I Merelli, and D Besozzi. Genhap: a novel computational method based on genetic algorithms for haplotype assembly. *BMC Bioinformatics*, 20(Suppl 4).
- [440] A Di Stefano, M Scatà, A La Corte, SK Das, and P Liò. Improving qoe in multi-layer social sensing: A cognitive architecture and game theoretic model. In *SocialSense'19 Proceedings of the Fourth International Workshop on Social Sensing*, pages 18–23. Montreal, Canada, Association for Computing Machinery, Apr 2019.
- [441] FL Opolka, A Solomon, C Cangea, P Veličković, P Liò, and RD Hjelm. Spatio-temporal deep graph infomax. 6 pages, 2 figures, Representation Learning on Graphs and Manifolds Workshop of the International Conference on Learning Representations (ICLR).
- [442] FL Opolka, A Solomon, C Cangea, P Veličković, P Liò, and RD Hjelm. Spatio-temporal deep graph infomax, Apr 2019.
- [443] HK Rana, MR Akhtar, MB Islam, MB Ahmed, P Liò, JMW Quinn, F Huq, and MA Moni. Genetic effects of welding fumes on the development of respiratory system diseases. *Comput Biol Med*, 108:142–149, May 2019.
- [444] S Bakas, M Reyes, A Jakab, S Bauer, M Rempfler, A Crimi, RT Shinohara, C Berger, SM Ha, M Rozycki, M Prastawa, E Alberts, J Lipkova, J Freymann, J Kirby, M Bilello, H Fathallah-Shaykh, R Wiest, J Kirschke, B Wiestler, R Colen, A Kotrotsou, P Lamontagne, D Marcus, M Milchenko, A Nazeri, M-A Weber, A Mahajan, U Baid, E Gerstner, D Kwon, G Acharya, M Agarwal, M Alam, A Albiol, A Albiol, FJ Albiol, V Alex, N Allinson, PHA Amorim, A Amrutkar, G Anand, S Andermatt, T Arbel, P Arbelaez, A Avery, M Azmat, B Pranjali, W Bai, S Banerjee, B Barth, T Batchelder, K Batmanghelich, E Battistella, A Beers, M Belyaev, M Bendszus, E Benson, J Bernal, HN Bharath, G Biros, S Bisdas, J Brown, M Cabezas, S Cao, JM Cardoso, EN Carver, A Casamitjana, LS Castillo, M Catà, P Cattin, A Cerigues, VS Chagas, S Chandra, Y-J Chang, S Chang, K Chang, J Chazalon, S Chen, W Chen, JW Chen, Z Chen, K Cheng, AR Choudhury, R Chylla, A Clérigues, S Coleman, RGR Colmeiro, M Combalia, A Costa, X Cui, Z Dai, L Dai, LA Daza, E Deutsch, C Ding, C Dong, S Dong, W Dudzik, Z Eaton-Rosen, G Egan, G Escudero, T Estienne, R Everson, J Fabrizio, Y Fan, L Fang, X Feng, E Ferrante, L Fidon, M Fischer, AP French, N Fridman, H Fu, D Fuentes, Y Gao, E Gates, D Gering, A Gholami, W Gierke, B Glocker, M Gong, S González-Villá, T Grosgees, Y Guan, S Guo, S Gupta, W-S Han, IS Han, K Harmuth, H He, A Hernández-Sabaté, E Herrmann, N Himthani, W Hsu, C Hsu, X Hu, X Hu, Y Hu, Y Hu, R Hua, T-Y Huang, W Huang, SV Huffel, Q Huo, HV Vivek, KM Iftakharuddin, F Isensee, M Islam, AS Jackson, SR Jambawalikar, A Jesson, W Jian, P Jin, VJM Jose, A Jungo, B Kainz, K Kamnitsas, P-Y Kao, A Karnawat, T Kellermeier, A Kermi, K Keutzer, MT Khadir, M Khened, P Kickingereider, G Kim, N King, H Knapp, U Knecht, L Kohli, D Kong, X Kong, S Koppers, A Kori, G Krishnamurthi, E Krivov, P Kumar, K Kushibar, D Lachinov, T Lambrou, J Lee, C Lee, Y Lee, M Lee, S Lefkovits, L Lefkovits, J Levitt, T Li, H Li, W Li, H Li, X Li, Y Li, H Li, Z Li, X Li, Z Li, X Li, W Li, Z-S Lin, F Lin, P Lio, C Liu, B Liu, X Liu, M Liu, J Liu, L Liu, X Llado, MM Lopez, PR Lorenzo, Z Lu, L Luo, Z Luo, J Ma, K Ma, T Mackie, A Madabushi, I Mahmoudi, KH Maier-Hein, P Maji, CP Mammen, A Mang, BS Manjunath, M Marcinkiewicz, S McDonagh, S McKenna, R McKinley, M Mehl, S Mehta, R Mehta, R Meier, C Meinel, D Merhof, C Meyer, R Miller, S Mitra, A Moiyadi, D Molina-Garcia, MAB

Monteiro, G Mrukwa, A Myronenko, J Nalepa, T Ngo, D Nie, H Ning, C Niu, NK Nuechterlein, E Oermann, A Oliveira, DDC Oliveira, A Oliver, AFI Osman, Y-N Ou, S Ourselin, N Paragios, MS Park, B Paschke, JG Pauloski, K Pawar, N Pawlowski, L Pei, S Peng, SM Pereira, J Perez-Beteta, VM Perez-Garcia, S Pezold, B Pham, A Phophalia, G Piella, GN Pillai, M Piraud, M Pisov, A Popli, MP Pound, R Pourreza, P Prasanna, V Prkovska, TP Pridmore, S Puch, É Puybureau, B Qian, X Qiao, M Rajchl, S Rane, M Rebsamen, H Ren, X Ren, K Revanuru, M Rezaei, O Rippel, LC Rivera, C Robert, B Rosen, D Rueckert, M Safwan, M Salem, J Salvi, I Sanchez, I Sánchez, HM Santos, E Sartor, D Schellingerhout, K Scheufele, MR Scott, AA Scussel, S Sedlar, JP Serrano-Rubio, NJ Shah, N Shah, M Shaikh, BU Shankar, Z Shboul, H Shen, D Shen, L Shen, H Shen, V Shenoy, F Shi, HE Shin, H Shu, D Sima, M Sinclair, O Smedby, JM Snyder, M Soltaninejad, G Song, M Soni, J Stawiaski, S Subramanian, L Sun, R Sun, J Sun, K Sun, Y Sun, G Sun, S Sun, YR Suter, L Szilagyi, S Talbar, D Tao, D Tao, Z Teng, S Thakur, MH Thakur, S Tharakan, P Tiwari, G Tochon, T Tran, YM Tsai, K-L Tseng, TA Tuan, V Turlapov, N Tustison, M Vakalopoulou, S Valverde, R Vanguri, E Vasiliev, J Ventura, L Vera, T Vercauteren, CA Verrastro, L Vidyaratne, V Vilaplana, A Vivekanandan, G Wang, Q Wang, CJ Wang, W Wang, D Wang, R Wang, Y Wang, C Wang, G Wang, N Wen, X Wen, L Weninger, W Wick, S Wu, Q Wu, Y Wu, Y Xia, Y Xu, X Xu, P Xu, T-L Yang, X Yang, H-Y Yang, J Yang, H Yang, G Yang, H Yao, X Ye, C Yin, B Young-Moxon, J Yu, X Yue, S Zhang, A Zhang, K Zhang, X Zhang, L Zhang, X Zhang, Y Zhang, L Zhang, J Zhang, X Zhang, T Zhang, S Zhao, Y Zhao, X Zhao, L Zhao, Y Zheng, L Zhong, C Zhou, X Zhou, F Zhou, H Zhu, J Zhu, Y Zhuge, W Zong, J Kalpathy-Cramer, K Farahani, C Davatzikos, KV Leemput, and B Menze. Identifying the best machine learning algorithms for brain tumor segmentation, progression assessment, and overall survival prediction in the brats challenge. Nov 2018. The International Multimodal Brain Tumor Segmentation (BraTS) Challenge.

- [445] J Zhu, G Yang, and P Lio. How can we make gan perform better in single medical image super-resolution? a lesion focused multi-scale approach. In *Proceedings - International Symposium on Biomedical Imaging*, volume 2019-April, pages 1669–1673, Apr 2019.
- [446] S Spasov, L Passamonti, A Duggento, P Liò, N Toschi, and Alzheimer's Disease Neuroimaging Initiative. A parameter-efficient deep learning approach to predict conversion from mild cognitive impairment to alzheimer's disease. *Neuroimage*, 189:276–287, Apr 2019.
- [447] E Luzhnica, B Day, and P Lio'. Clique pooling for graph classification. Mar 2019. Under review as a workshop paper at RLGM 2019 @ ICML.
- [448] MD Ganggayah, NA Taib, YC Har, P Lio, and SK Dhillon. Predicting factors for survival of breast cancer patients using machine learning techniques. *BMC Medical Informatics and Decision Making*, 19(48).
- [449] D Wang, M Jamnik, and P Lio. Unsupervised and interpretable scene discovery with discrete-attend-infer-repeat. Mar 2019.
- [450] HL Smith, A Stevens, B Minogue, S Sneddon, L Shaw, L Wood, T Adeniyi, H Xiao, P Lio, SJ Kimber, and DR Brison. Systems based analysis of human embryos and gene networks involved in cell lineage allocation. *BMC Genomics*, 20(1):171, Mar 2019.
- [451] A Serra, MD Guida, P Lió, and R Tagliaferri. Hierarchical block matrix approach for multi-view clustering. In *Lecture Notes in Computer Science (including subseries Lecture Notes*

in *Artificial Intelligence and Lecture Notes in Bioinformatics*), volume 10834 LNBI, pages 200–212, Jan 2019.

- [452] R Vignani, P Liò, and M Scali. How to integrate wet lab and bioinformatics procedures for wine dna admixture analysis and compositional profiling: Case studies and perspectives. *PLoS One*, 14(2):e0211962, 2019.
- [453] A Di Stefano, M Scatà, S Vijayakumar, C Angione, A La Corte, and P Liò. Social dynamics modeling of chrono-nutrition. *PLoS Comput Biol*, 15(1):e1006714, Jan 2019.
- [454] T Müller and P Lió. Personalisable clinical decision support system. *ERCIM News*, 116:19–20.
- [455] AG Rakowski, P Veličković, E Dall’Ara, and P Liò. Chronomid - cross-modal neural networks for 3-d temporal medical imaging data, Jan 2019.
- [456] V Prokhorov, MT Pilehvar, D Kartsaklis, P Liò, and N Collier. Unseen word representation by aligning heterogeneous lexical semantic spaces. In *AAAI*, pages 6900–6907. AAAI Press, 2019.
- [457] LM Aiello, C Cherifi, H Cherifi, R Lambiotte, P Lió, and LM Rocha. *Preface*, volume 812. Jan 2019.
- [458] V Parmar and P Lió. Multi-omic network regression: Methodology, tool and case study. *Studies in Computational Intelligence*, 813:611–624, Jan 2019.
- [459] K Bartoszek and P Liò. Modelling trait-dependent speciation with approximate bayesian computation. *Acta Physica Polonica B, Proceedings Supplement*, 12(1):25–47, Jan 2019.
- [460] J Zhu, G Yang, and P Lió. Lesion focused super-resolution. In ED Angelini and BA Landman, editors, *Medical Imaging: Image Processing*, volume 10949 of *SPIE Proceedings*, pages 109491L–109491L. SPIE, 2019.
- [461] S Pernice, L Follia, G Balbo, L Milanese, G Sartini, N Totis, P Lió, I Merelli, F Cordero, and M Beccuti. Integrating petri nets and flux balance methods in computational biology models: A methodological and computational practice. *Fundamenta Informaticae*, 171(1-4):367–392, Jan 2019.
- [462] A Tangherloni, S Spolaor, L Rundo, MS Nobile, P Cazzaniga, G Mauri, P Liò, I Merelli, and D Besozzi. Genhap: a novel computational method based on genetic algorithms for haplotype assembly. *BMC Bioinform.*, 20-S(4):172:1–172:1, 2019.
- [463] P Veličković, W Fedus, WL Hamilton, P Liò, Y Bengio, and RD Hjelm. Deep graph infomax. To appear at ICLR 2019. 17 pages, 8 figures.
- [464] P Veličković, W Fedus, WL Hamilton, Y Bengio, P Liò, and R Devon Hjelm. Deep graph infomax. In *7th International Conference on Learning Representations, ICLR 2019*, Jan 2019.
- [465] P Lio and P Zuliani. *Automated Reasoning for Systems Biology and Medicine Preface*, volume 30. 2019.
- [466] A Tangherloni, L Rundo, S Spolaor, MS Nobile, I Merelli, D Besozzi, G Mauri, P Cazzaniga, and P Liò. High performance computing for haplotyping: Models and platforms. In *Lecture*

- [467] A Tangherloni, S Spolaor, L Rundo, MS Nobile, P Cazzaniga, G Mauri, P Liò, I Merelli, and D Besozzi. Genhap: A novel computational method based on genetic algorithms for haplotype assembly, Dec 2018.
- [468] K Bartoszek and P Liò. Modelling trait dependent speciation with approximate bayesian computation, Dec 2018.
- [469] E Del Prete, A Facchiano, and P Liò. Reusing microarray clinical data from a complex disease with bioinformatics tool, Nov 2018.
- [470] H Xiao, K Bartoszek, and P Lio'. Multi-omic analysis of signalling factors in inflammatory comorbidities. *BMC Bioinformatics*, 19(Suppl 15):439, Nov 2018.
- [471] HK Rana, MR Akhtar, MB Ahmed, P Lio', J Quinn, F Huq, and MA Moni. Genetic effects of welding fumes on the progression of neurodegenerative diseases, 2018.
- [472] A Mancini, F Eyassu, M Conway, A Occhipinti, P Liò, C Angione, and S Pucciarelli. Ciliategem: an open-project and a tool for predictions of ciliate metabolic variations and experimental condition design. *BMC Bioinformatics*, 19(Suppl 15):442, Nov 2018.
- [473] MH Rahman, S Peng, C Chen, P Lio', and MA Moni. Genetic effect of type 2 diabetes to the progression of neurological diseases, 2018.
- [474] MA Moni, HK Rana, MB Islam, MB Ahmed, P Liò, F Huq, and JMW Quinn. Early detection of neurological dysfunction using blood cell transcript profiles, Nov 2018.
- [475] S Vijayakumar, M Conway, P Lió, and C Angione. Seeing the wood for the trees: a forest of methods for optimization and omic-network integration in metabolic modelling. *Briefings in Bioinformatics*, 19(6):1218–1235, Nov 2018.
- [476] C Cangea, A Grauslys, P Liò, and F Falciani. Structure-based networks for drug validation. Nov 2018. Machine Learning for Health (ML4H) Workshop at NeurIPS 2018 arXiv:1811.07216.
- [477] E Del Prete, A Facchiano, and P Liò. Bioinformatics methodologies for coeliac disease and its comorbidities. *Brief Bioinform*, 21(1):355–367, Jan 2020.
- [478] V Prokhorov, MT Pilehvar, D Kartsaklis, P Lio, and N Collier. Unseen word representation by aligning heterogeneous lexical semantic spaces, Nov 2018.
- [479] S Haider, CQ Yao, VS Sabine, M Grzadkowski, V Stimper, MHW Starmans, J Wang, F Nguyen, NC Moon, X Lin, C Drake, CA Crozier, CL Brookes, CJH van de Velde, A Hasenburg, DG Kieback, CJ Markopoulos, LY Dirix, C Seynaeve, DW Rea, A Kasprzyk, P Lambin, P Lio', JMS Bartlett, and PC Boutros. Pathway-based subnetworks enable cross-disease biomarker discovery. *Nat Commun*, 9(1):4746, Nov 2018.
- [480] C Cangea, P Veličković, N Jovanović, T Kipf, and P Liò. Towards sparse hierarchical graph classifiers. Nov 2018. To appear in the Workshop on Relational Representation Learning (R2L) at NIPS 2018. 6 pages, 3 figures.

- [481] SE Spasov, L Passamonti, A Duggento, P Lio, and N Toschi. A multi-modal convolutional neural network framework for the prediction of alzheimer's disease. In *Annu Int Conf IEEE Eng Med Biol Soc*, volume 2018, pages 1271–1274. United States, Jul 2018.
- [482] C Sheehan, B Day, and P Liò. Introducing curvature to the label space. Oct 2018. Under review as a workshop paper at MetaLearn, NIPS 2018, 4 pages, 2 figures.
- [483] J Zhu, G Yang, and P Lio. Lesion focused super-resolution, Oct 2018.
- [484] V Parmar and P Lio. Multi-omic network regression: Methodology, tool and case study, Oct 2018.
- [485] X Lu, C Liang, S Zhang, P Lio, and S Jing. Terminal sensitive data protection by adjusting access time bidirectionally and automatically. In *Proceedings - International Conference on Computer Communications and Networks, ICCCN*, volume 2018-July, Oct 2018.
- [486] P Veličković, W Fedus, WL Hamilton, P Liò, Y Bengio, and RD Hjelm. Deep graph infomax, Sep 2018.
- [487] L Felicetti, M Femminella, G Reali, and P Liò. Applications of molecular communications to medicine: a survey, Aug 2018.
- [488] Z Benmounah, S Meshoul, M Batouche, and P Lio. Parallel swarm intelligence strategies for large-scale clustering based on mapreduce with application to epigenetics of aging. *Applied Soft Computing*, 69:771–783.
- [489] I Saggese, E Bona, M Conway, F Favero, M Ladetto, P Liò, G Manzini, and F Mignone. Stable: a novel approach to de novo assembly of rna-seq data and its application in a metabolic model network based metatranscriptomic workflow. *BMC Bioinformatics*, 19(Suppl 7):184, Jul 2018.
- [490] F Bardozzo, P Lió, and R Tagliaferri. A study on multi-omic oscillations in escherichia coli metabolic networks. *BMC Bioinformatics*, 19(Suppl 7):194, Jul 2018.
- [491] E Bartocci, P Lio, and N Paoletti. Guest editors' introduction to the special section on the 14th international conference on computational methods in systems biology (cmsb 2016). *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(4):1122–1123, Jul 2018.
- [492] A Iuliano, A Occhipinti, C Angelini, I De Feis, and P Liò. Combining pathway identification and breast cancer survival prediction via screening-network methods. *Front Genet*, 9:206, 2018.
- [493] I Merelli, P Lio, and I Kotenko. Message from organizing chairs. In *Proceedings - 26th Euromicro International Conference on Parallel, Distributed, and Network-Based Processing, PDP 2018*, page xxi, Jun 2018.
- [494] G Ascolani and P Lió. Modelling the order of driver mutations and metabolic mutations as structures in cancer dynamics. May 2017.
- [495] P Veličković, L Karazija, ND Lane, S Bhattacharya, E Liberis, P Liò, A Chieh, O Bellahsen, and M Vegreville. Cross-modal recurrent models for weight objective prediction from multimodal

time-series data. *PervasiveHealth: Pervasive Computing Technologies for Healthcare*, Jan 2018.

- [496] DP Martins, M Barros, M Pierobon, M Kandhavelu, P Lio, and S Balasubramaniam. Computational models for trapping ebola virus using engineered bacteria. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(6).
- [497] L Karazija, P Veličković, and P Liò. Automatic inference of cross-modal connection topologies for x-cnns, May 2018.
- [498] E Liberis, P Velickovic, P Sormanni, M Vendruscolo, and P Liò. Parapred: antibody paratope prediction using convolutional and recurrent neural networks. *Bioinformatics*, 34(17):2944–2950, Sep 2018.
- [499] A Mathur, T Zhang, S Bhattacharya, P Velickovic, L Joffe, ND Lane, F Kawsar, and P Liò. Using deep data augmentation training to address software and hardware heterogeneities in wearable and smartphone sensing devices. In L Mottola, J Gao, and P Zhang, editors, *IPSN '18 Proceedings of the 17th ACM/IEEE International Conference on Information Processing in Sensor Networks*, pages 200–211. Porto, Portugal, IEEE, Apr 2018.
- [500] S Haider, C Yao, V Sabine, M Grzadkowski, V Stimper, MHW Starmans, J Wang, F Nguyen, N Moon, X Lin, C Drake, C Crozier, C Brookes, CJH van de Velde, A Hasenburg, D Kieback, C Markopoulos, L Dirix, C Seynaeve, D Rea, A Kasprzyk, P Lambin, P Lio, JMS Bartlett, and P Boutros. Network-based biomarkers enable cross-disease biomarker discovery, 2018.
- [501] M Scatà, A Di Stefano, A La Corte, and P Liò. Quantifying the propagation of distress and mental disorders in social networks. *Sci Rep*, 8(1):5005, Mar 2018.
- [502] D Wang, R Zhang, J Zhu, Z Teng, Y Huang, F Spiga, M Hong-Fei Du, JH Gillard, Q Lu, and P Liò. Neural network fusion: a novel ct-mr aortic aneurysm image segmentation method. In *Proc SPIE Int Soc Opt Eng*, volume 10574. United States, Mar 2018.
- [503] P He, T Nakano, Y Mao, P Lio, Q Liu, and K Yang. Stochastic channel switching of frequency-encoded signals in molecular communication networks. *IEEE Communications Letters*, 22(2):332–335, Feb 2018.
- [504] GM Dimitri, S Agrawal, A Young, J Donnelly, X Liu, P Smielewski, P Hutchinson, M Czosnyka, P Lio, and C Haubrich. Simultaneous transients of intracranial pressure and heart rate in traumatic brain injury: Methods of analysis. *Acta Neurochirurgica: Supplementum*, 126:147–151, 2018.
- [505] F Tordini, M Aldinucci, P Viviani, I Merelli, and P Liò. Scientific workflows on clouds with heterogeneous and preemptible instances. *Advances in Parallel Computing*, 32:605–614, Jan 2018.
- [506] S Vijayakumar, M Conway, P Lió, and C Angione. Optimization of multi-omic genome-scale models: Methodologies, hands-on tutorial, and perspectives. volume 1716, pages 389–408. 2018.
- [507] I Bica, P Veličković, H Xiao, and P Liò. Multi-omics data integration using cross-modal neural networks. In *ESANN 2018 - Proceedings, European Symposium on Artificial Neural Networks, Computational Intelligence and Machine Learning*, pages 385–390, Jan 2018.

- [508] D Wang, M Jamnik, and P Lio. Investigating diagrammatic reasoning with deep neural networks. pages 390–398. Edinburgh, Springer International Publishing AG.
- [509] P Veličković, A Casanova, P Liò, G Cucurull, A Romero, and Y Bengio. Graph attention networks. *6th International Conference on Learning Representations, ICLR 2018 - Conference Track Proceedings*, Jan 2018.
- [510] P Velickovic, L Karazija, ND Lane, S Bhattacharya, E Liberis, P Liò, A Chieh, O Bellahsen, and M Vegreville. Cross-modal recurrent models for weight objective prediction from multimodal time-series data. In N Minsky and V Osmani, editors, *PervasiveHealth*, pages 178–186. ACM, 2018.
- [511] 26th euromicro international conference on parallel, distributed and network-based processing, pdp 2018, cambridge, united kingdom, march 21-23, 2018. In I Merelli, P Liò, and IV Kotenko, editors, *PDP*. IEEE Computer Society, 2018.
- [512] T Brouwer, J Frellsen, and P Liò. Comparative study of inference methods for bayesian nonnegative matrix factorisation. In M Ceci, J Holmén, L Todorovski, C Vens, and S Dzeroski, editors, *ECML/PKDD (1)*, volume 10534, pages 513–529. Skopje, Springer, Dec 2017.
- [513] T Brouwer and P Lio'. Prior and likelihood choices for bayesian matrix factorisation on small datasets. Dec 2017.
- [514] El Athanasiadis, JG Botthof, H Andres, L Ferreira, P Lio, and A Cvejic. Single-cell rna-sequencing uncovers transcriptional states and fate decisions in haematopoiesis. *Nat Commun*, 8(1):2045, Dec 2017.
- [515] M Peychev, P Veličković, and P Liò. Quantifying the effects of enforcing disentanglement on variational autoencoders. Nov 2017. Accepted to the Workshop on Learning Disentangled Representations at the 31st Annual Conference on Neural Information Processing Systems (NIPS 2017), 5 pages, 2 figures.
- [516] L Bianchi and P Liò. Opportunities for community awareness platforms in personal genomics and bioinformatics education. *Briefings in Bioinformatics*, 18(6):1082–1090, Nov 2017.
- [517] P Veličković, G Cucurull, A Casanova, A Romero, P Liò, and Y Bengio. Graph attention networks, Oct 2017.
- [518] K Heffernan, P Liò, and S Teufel. Multilayer data and document stratification for comorbidity analysis. In *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, volume 10477 LNBI, pages 209–219, Jan 2017.
- [519] E Del Prete, A Facchiano, and P Liò. A gene set enrichment analysis of multiomic celiac disease data, Oct 2017.
- [520] L Felicetti, M Femminella, T Ivanov, P Lio, and G Realì. A big-data layered architecture for analyzing molecular communications systems in blood vessels. In *Proceedings of the 4th ACM International Conference on Nanoscale Computing and Communication, NanoCom 2017*, Sep 2017.

- [521] P Veličković, L Karazija, ND Lane, S Bhattacharya, E Liberis, P Liò, A Chieh, O Bellahsen, and M Vegreville. Cross-modal recurrent models for weight objective prediction from multimodal time-series data, Sep 2017.
- [522] A Tangherloni, S Spolaor, L Rundo, MS Nobile, I Merelli, P Cazzaniga, D Besozzi, G Mauri, and P Liò. Genhap: A novel computational method based on genetic algorithms for haplotype assembly, Sep 2017.
- [523] E Liberis, P Veličković, P Sormanni, M Vendruscolo, and P Liò. Paratope prediction using convolutional and recurrent neural networks. 2017.
- [524] C Cangea, P Veličković, and P Liò. Xflow: Cross-modal deep neural networks for audiovisual classification, Sep 2017.
- [525] GM Dimitri, S Agrawal, A Young, J Donnelly, X Liu, P Smielewski, P Hutchinson, M Czosnyka, P Lió, and C Haubrich. A multiplex network approach for the analysis of intracranial pressure and heart rate data in traumatic brain injured patients. *Appl Netw Sci*, 2(1):29, 2017.
- [526] MA Moni and P Lio'. Genetic profiling and comorbidities of zika infection. *J Infect Dis*, 216(6):703–712, Sep 2017.
- [527] V Prokhorov, MT Pilehvar, D Kartsaklis, P Lió, and N Collier. Learning rare word representations using semantic bridging. Jul 2017.
- [528] M Barandalla, H Shi, H Xiao, S Colleoni, C Galli, P Lio, M Trotter, and G Lazzari. Global gene expression profiling and senescence biomarker analysis of hesc exposed to h2o2 induced non-cytotoxic oxidative stress. *Stem Cell Res Ther*, 8(1):160, Jul 2017.
- [529] O Oshota, M Conway, M Fookes, F Schreiber, R Chaudhuri, L Yu, F Morgan, S Clare, J Choudhary, N Thomson, P Lio, D Maskell, P Mastroeni, and AJ Grant. Transcriptome and proteome analysis of salmonella enterica serovar typhimurium systemic infection of wild type and immune-deficient mice. *PLoS ONE*, 12(8), Jul 2017.
- [530] T Brouwer and P Lio. Bayesian hybrid matrix factorisation for data integration. In *Proceedings of Machine Learning Research*, volume 54, pages 557–566. Fort Lauderdale, FL, USA, Journal of Machine Learning Research, Apr 2017. <http://www.aistats.org/aistats2017/> <http://proceedings.mlr.press/v54/>.
- [531] GM Dimitri and P Lió. Drugclust: A machine learning approach for drugs side effects prediction. *Comput Biol Chem*, 68:204–210, Jun 2017.
- [532] L Felicetti, M Femminella, P Liò, and G Reali. Effect of aging, disease versus health conditions in the design of nano-communications in blood vessels. In *Modeling and Optimization in Science and Technologies*, volume 9, pages 447–471. Jan 2017.
- [533] SS Kashaf, C Angione, and P Lió. Making life difficult for clostridium difficile: augmenting the pathogen’s metabolic model with transcriptomic and codon usage data for better therapeutic target characterization. *BMC Syst Biol*, 11(1):25–25, Feb 2017.
- [534] P Narula, V Piratla, A Bansal, S Azad, and P Lio. Parameter estimation of tuberculosis transmission model using ensemble kalman filter across indian states and union territories. *Infection, Disease and Health*, 21(4):184–191, Dec 2016.

- [535] M Moni and P Lio. Infectome, diseasome and comorbidities of zika infection. In *INTERNATIONAL JOURNAL OF INFECTIOUS DISEASES*, volume 53, pages 14–14, 2016.
- [536] M Scatà, A Di Stefano, P Liò, and A La Corte. The impact of heterogeneity and awareness in modeling epidemic spreading on multiplex networks. *Scientific Reports*, 6(37105):1–13, Nov 2016.
- [537] F Tordini, M Aldinucci, L Milanesi, P Liò, and I Merelli. The genome conformation as an integrator of multi-omic data: The example of damage spreading in cancer. *Front Genet*, 7:194, 2016.
- [538] T Brouwer, J Frellsen, and P Lio'. Fast bayesian non-negative matrix factorisation and tri-factorisation, Oct 2016.
- [539] F Tordini, M Drocco, C Misale, L Milanesi, P Liò, I Merelli, M Torquati, and M Aldinucci. Nuchart-ii: The road to a fast and scalable tool for hi-c data analysis. *International Journal of High Performance Computing Applications*, 31(3):196–211, May 2017.
- [540] P Veličković, D Wang, ND Lane, and P Liò. X-cnn: Cross-modal convolutional neural networks for sparse datasets, Oct 2016.
- [541] M Scatà, A Di Stefano, A La Corte, P Liò, E Catania, E Guardo, and S Pagano. Combining evolutionary game theory and network theory to analyze human cooperation patterns. *Chaos, Solitons and Fractals*, 91:17–24, Oct 2016.
- [542] E Alarcon, RG Cid-Fuentes, A Davy, L Felicetti, M Femminella, P Lio, G Reali, and J Solé-Pareta. Molcomm1: The molecular communication markup language. In *Proceedings of the 3rd ACM International Conference on Nanoscale Computing and Communication, ACM NANOCOM 2016*, Sep 2016.
- [543] A Iuliano, A Occhipinti, C Angelini, I De Feis, and P Lió. Cancer markers selection using network-based cox regression: A methodological and computational practice. *Front Physiol*, 7:208, 2016.
- [544] N Pratanwanich, P Lió, and O Stegle. Warped matrix factorisation for multi-view data integration. In *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, volume 9852 LNAI, pages 789–804, Jan 2016.
- [545] F Tordini, I Merelli, P Liò, L Milanesi, and M Aldinucci. Nuchart: Embedding high-level parallel computing in r for augmented hi-c data analysis. In *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, volume 9874 LNCS, pages 259–272, Jan 2016.
- [546] C Angione, P Liò, S Pucciarelli, B Can, M Conway, M Lotti, H Bokhari, A Mancini, U Sezerman, and A Telatin. Bioinformatics challenges and potentialities in studying extreme environments. In *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, volume 9874 LNCS, pages 205–219, Jan 2016.
- [547] G Reali and P Lio. Simulation tools for molecular communications. *IEEE TCSIM Newsletter*.

- [548] P He, Y Mao, Q Liu, P Liò, and K Yang. Channel modelling of molecular communications across blood vessels and nerves. In *2016 IEEE International Conference on Communications, ICC 2016*, Jul 2016.
- [549] X Lu, P Lio, and P Hui. Distance-based opportunistic mobile data offloading. *Sensors (Basel)*, 16(6), Jun 2016.
- [550] C Angione and P Lió. Erratum: Predictive analytics of environmental adaptability in multi-omic network models. *Sci Rep*, 6:26266, May 2016.
- [551] P Veličković and P Liò. Muxstep: an open-source c++ multiplex hmm library for making inferences on multiple data types. *Bioinformatics*, 32(16):2562–2564, Aug 2016.
- [552] E Schwarz, R Izmailov, P Liò, and A Meyer-Lindenberg. Protein interaction networks link schizophrenia risk loci to synaptic function. *Schizophr Bull*, 42(6):1334–1342, Nov 2016.
- [553] E Capobianco and P Lio. Electronic health systems: Golden mine for precision medicine. *The journal of precision medicine*, Mar 2016.
- [554] X Lu and P Lio. Privacy information security classification and comparison between the westerner and chinese. In *Proceedings - 2015 International Conference on Identification, Information, and Knowledge in the Internet of Things, IIKI 2015*, pages 13–18, Mar 2016.
- [555] C Angione, M Conway, and P Lió. Multiplex methods provide effective integration of multi-omic data in genome-scale models. *BMC Bioinformatics*, 17 Suppl 4(Suppl 4):83, Mar 2016.
- [556] F Nardi, F Frati, and P Liò. Animal inference on human mitochondrial diseases. *Comput Biol Chem*, 62:17–28, Jun 2016.
- [557] C Sansom, F Castiglione, and P Lio. Metabolic disorders: how can systems modelling help? *Lancet Diabetes Endocrinol*, 4(4):306, Apr 2016.
- [558] M Conway, C Angione, and P Liò. Iterative multi level calibration of metabolic networks. *Current Bioinformatics*, 11(1):93–105, Feb 2016.
- [559] E Bartocci and P Lió. Computational modeling, formal analysis, and tools for systems biology. *PLoS Comput Biol*, 12(1):e1004591, Jan 2016.
- [560] P Velickovic, D Wang, ND Lane, and P Liò. X-cnn: Cross-modal convolutional neural networks for sparse datasets. In *SSCI*, pages 1–8. IEEE, 2016.
- [561] P Veličković, D Wang, ND Lane, and P Liò. X-cnn: Cross-modal convolutional neural networks for sparse datasets. *SSCI 2016: 1-8*. To appear in the 7th IEEE Symposium Series on Computational Intelligence (IEEE SSCI 2016), 8 pages, 6 figures. Minor revisions, in response to reviewers' comments.
- [562] E Bartocci, P Lio, and N Paoletti. *Preface*, volume 9859 LNCS. Jan 2016.
- [563] Computational methods in systems biology - 14th international conference, cmsb 2016, cambridge, uk, september 21-23, 2016, proceedings. In E Bartocci, P Liò, and N Paoletti, editors, *CMSB*, volume 9859 of *Lecture Notes in Computer Science*. Springer, 2016.

- [564] A Di Stefano, A La Corte, P Lió, and M Scatá. Bio-inspired ict for big data management in healthcare. In *Studies in Big Data*, volume 14, pages 1–26. Jan 2016.
- [565] L Felicetti, M Femminella, G Reali, and P Liò. Applications of molecular communications to medicine: A survey. *Nano Communication Networks*, 7:27–45, Jan 2016.
- [566] P Veličković and P Lió. Molecular multiplex network inference using gaussian mixture hidden markov models. *Journal of Complex Networks*, 4(4):561–574, Dec 2016.
- [567] Y Shavit, BJ Walker, and P Lio'. Hierarchical block matrices as efficient representations of chromosome topologies and their application for 3c data integration. *Bioinformatics*, 32(8):1121–1129, Apr 2016.
- [568] F Tordini, M Drocco, I Merelli, L Milanese, P Liò, and M Aldinucci. Nuchart-ii: A graph-based approach for analysis and interpretation of hi-c data. In *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, volume 8623, pages 298–311, Jan 2015.
- [569] A Korhonen, Y Guo, S Baker, M Yetisgen-Yildiz, U Stenius, M Narita, and P Liò. Improving literature-based discovery with advanced text mining. In *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, volume 8623, pages 89–98, Jan 2015.
- [570] A Boutorh, N Pratanwanich, A Guessoum, and P Liò. Drug repurposing by optimizing mining of genes target association. In *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, volume 8623, pages 209–218, Jan 2015.
- [571] FK Hamey, Y Shavit, V Maciulyte, C Town, P Liò, and S Tosi. Automated detection of fluorescent probes in molecular imaging. In *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, volume 8623, pages 68–75, Jan 2015.
- [572] A Iuliano, A Occhipinti, C Angelini, I De Feis, and P Lió. Applications of network-based survival analysis methods for pathways detection in cancer. In *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, volume 8623, pages 76–88, Jan 2015.
- [573] P Liò, O Miglino, G Nicosia, S Nolfi, and M Pavone. Advances in artificial life: Synthesis and simulation of living systems: Editorial. *Artif Life*, 21(4):395–397, 2015.
- [574] A Di Stefano, M Scatà, A La Corte, P Liò, E Catania, E Guardo, and S Pagano. Quantifying the role of homophily in human cooperation using multiplex evolutionary game theory. *PLoS One*, 10(10):e0140646, 2015.
- [575] C Angione and P Lió. Predictive analytics of environmental adaptability in multi-omic network models. *Sci Rep*, 5:15147, Oct 2015.
- [576] H Xu, MA Moni, and P Liò. Network regularised cox regression and multiplex network models to predict disease comorbidities and survival of cancer. *Comput Biol Chem*, 59 Pt B:15–31, Dec 2015.

- [577] Y Shavit, I Merelli, L Milanesi, and P Lio'. How computer science can help in understanding the 3d genome architecture. *Brief Bioinform*, 17(5):733–744, Sep 2016.
- [578] F Bardozzo, P Lió, and R Tagliaferri. Multi omic oscillations in bacterial pathways. In *Proceedings of the International Joint Conference on Neural Networks*, volume 2015-September, Sep 2015.
- [579] C Angione, J Costanza, G Carapezza, P Lió, and G Nicosia. Analysis and design of molecular machines. *Theoretical Computer Science*, 599:102–117, Sep 2015.
- [580] S Haider, Z Lipinski, MR Przewloka, Y Ladak, PP D'Avino, Y Kimata, P Lio', and DM Glover. Dapper: a data-mining resource for protein-protein interactions. *BioData Min*, 8:30, 2015.
- [581] GC Castellani, G Menichetti, P Garagnani, M Giulia Bacalini, C Pirazzini, C Franceschi, S Collino, C Sala, D Remondini, E Giampieri, E Mosca, M Bersanelli, S Vitali, IFD Valle, P Liò, and L Milanesi. Systems medicine of inflammaging. *Brief Bioinform*, 17(3):527–540, May 2016.
- [582] P Narula, S Azad, and P Lio. Bayesian melding approach to estimate the reproduction number for tuberculosis transmission in indian states and union territories. *Asia Pac J Public Health*, 27(7):723–732, Oct 2015.
- [583] D Smedley, S Haider, S Durinck, L Pandini, P Provero, J Allen, O Arnaiz, MH Awedh, R Baldock, G Barbiera, P Bardou, T Beck, A Blake, M Bonierbale, AJ Brookes, G Bucci, I Buetti, S Burge, C Cabau, JW Carlson, C Chelala, C Chrysostomou, D Cittaro, O Collin, R Cordova, RJ Cutts, E Dassi, A Di Genova, A Djari, A Esposito, H Estrella, E Eyra, J Fernandez-Banet, S Forbes, RC Free, T Fujisawa, E Gadaleta, JM Garcia-Manteiga, D Goodstein, K Gray, JA Guerra-Assunção, B Haggarty, D-J Han, BW Han, T Harris, J Harshbarger, RK Hastings, RD Hayes, C Hoede, S Hu, Z-L Hu, L Hutchins, Z Kan, H Kawaji, A Keliet, A Kerhornou, S Kim, R Kinsella, C Klopp, L Kong, D Lawson, D Lazarevic, J-H Lee, T Letellier, C-Y Li, P Lio, C-J Liu, J Luo, A Maass, J Mariette, T Maurel, S Merella, AM Mohamed, F Moreews, I Nabihoudine, N Ndegwa, C Noiro, C Perez-Llamas, M Primig, A Quattrone, H Quesneville, D Rambaldi, J Reecy, M Riba, S Rosanoff, AA Saddiq, E Salas, O Sallou, R Shepherd, R Simon, L Sperling, W Spooner, DM Staines, D Steinbach, K Stone, E Stupka, JW Teague, AZ Dayem Ullah, J Wang, D Ware, M Wong-Erasmus, K Youens-Clark, A Zadissa, S-J Zhang, and A Kasprzyk. The biomart community portal: an innovative alternative to large, centralized data repositories. *Nucleic Acids Res*, 43(W1):W589–W598, Jul 2015.
- [584] X Lu, P Lio, and P Hui. A content dissemination model for mobile internet to minimize load on cellular network. In *Electronics, Communications and Networks IV - Proceedings of the 4th International Conference on Electronics, Communications and Networks, CECNet2014*, pages 289–294, Jan 2015.
- [585] MA Moni and P Liò. How to build personalized multi-omics comorbidity profiles. *Front Cell Dev Biol*, 3:28, 2015.
- [586] Z Liu, L Tang, and J Yan. A random early detection based active queue management algorithm in power optical communication network. In *Electronics, Communications and Networks IV*, pages 277–281. CRC Press, Jun 2015.

- [587] M Taffi, M Taffi, N Paoletti, P Liò, S Pucciarelli, and M Marini. Bioaccumulation modelling and sensitivity analysis for discovering key players in contaminated food webs: The case study of pcbs in the adriatic sea. *Ecological Modelling*, 306:205–215, Jun 2015.
- [588] G Ascolani, A Occhipinti, and P Liò. Modelling circulating tumour cells for personalised survival prediction in metastatic breast cancer. *PLoS Comput Biol*, 11(5):e1004199, May 2015.
- [589] C Angione, N Pratanwanich, and P Lió. A hybrid of metabolic flux analysis and bayesian factor modeling for multiomic temporal pathway activation. *ACS Synth Biol*, 4(8):880–889, Aug 2015.
- [590] E Bosi, B Donati, M Galardini, S Brunetti, M-F Sagot, P Lió, P Crescenzi, R Fani, and M Fondi. Medusa: a multi-draft based scaffolder. *Bioinformatics*, 31(15):2443–2451, Aug 2015.
- [591] P Narula, P Sihota, S Azad, and P Lio. Analyzing seasonality of tuberculosis across indian states and union territories. *J Epidemiol Glob Health*, 5(4):337–346, Dec 2015.
- [592] I Merelli, F Tordini, M Drocco, M Aldinucci, P Liò, and L Milanese. Integrating multi-omic features exploiting chromosome conformation capture data. *Front Genet*, 6:40, 2015.
- [593] N Pratanwanich and P Lio. Who wrote this? textual modeling with authorship attribution in big data. In *IEEE International Conference on Data Mining Workshops, ICDMW*, volume 2015-January, pages 645–652, Jan 2015.
- [594] M Fondi and P Liò. Multi -omics and metabolic modelling pipelines: challenges and tools for systems microbiology. *Microbiol Res*, 171:52–64, Feb 2015.
- [595] E Capobianco and P Liò. Comorbidity networks: Beyond disease correlations. *Journal of Complex Networks*, 3(3):319–332, Sep 2015.
- [596] C Angione, G Carapezza, J Costanza, P Lio, and G Nicosia. Design and strain selection criteria for bacterial communication networks, Jan 2015.
- [597] C Di Serio, P Liò, A Nonis, and R Tagliaferri. *Preface*, volume 8623. Jan 2015.
- [598] F Tordini, M Drocco, C Misale, L Milanese, P Lió, I Merelli, and M Aldinucci. Parallel exploration of the nuclear chromosome conformation with nuchart-ii. In *Proceedings - 23rd Euromicro International Conference on Parallel, Distributed, and Network-Based Processing, PDP 2015*, pages 725–732, Jan 2015.
- [599] F Tordini, M Drocco, C Misale, L Milanese, P Lio, I Merelli, and M Aldinucci. Parallel exploration of the nuclear chromosome conformation with *nuchart-ii*. In *23RD EUROMICRO INTERNATIONAL CONFERENCE ON PARALLEL, DISTRIBUTED, AND NETWORK-BASED PROCESSING (PDP 2015)*, pages 725–732, 2015.
- [600] C Angione, J Costanza, G Carapezza, P Lió, and G Nicosia. Multi-target analysis and design of mitochondrial metabolism. *PLoS One*, 10(9):e0133825–e0133825, 2015.
- [601] M Fondi and P Liò. Genome-scale metabolic network reconstruction. *Methods Mol Biol*, 1231:233–256, 2015.

- [602] C Di Serio, P Liò, A Nonis, and R Tagliaferri. Computational intelligence methods for bioinformatics and biostatistics: 11th international meeting, cibb 2014 cambridge, uk, june 26–28, 2014 revised selected papers. In *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, volume 8623, Jan 2015.
- [603] X Lu, Z Qu, P Lio, P Hui, Q Li, P Lu, and R Bie. Directional communication with movement prediction in mobile wireless sensor networks. *Personal and Ubiquitous Computing*, 18(8):1941–1953, Dec 2014.
- [604] L Felicetti, M Femminella, G Reali, and P Liò. Endovascular mobile sensor network for detecting circulating tumoral cells. In *BODYNETS 2014 - 9th International Conference on Body Area Networks*, pages 111–117, Nov 2014.
- [605] MA Moni, H Xu, and P Liò. Cytocom: a cytoscape app to visualize, query and analyse disease comorbidity networks. *Bioinformatics*, 31(6):969–971, Mar 2015.
- [606] MA Moni and P Liò. Network-based analysis of comorbidities risk during an infection: Sars and hiv case studies. *BMC Bioinformatics*, 15(1):333, Oct 2014.
- [607] M Taffi, N Paoletti, C Angione, S Pucciarelli, M Marini, and P Liò. Bioremediation in marine ecosystems: a computational study combining ecological modeling and flux balance analysis. *Front Genet*, 5:319, 2014.
- [608] S Azad and P Lio. Emerging trends of malaria-dengue geographical coupling in the southeast asia region. *J Vector Borne Dis*, 51(3):165–171, Sep 2014.
- [609] N Pratanwanich and P Lio. Exploring the complexity of pathway-drug relationships using latent dirichlet allocation. *Comput Biol Chem*, 53 Pt A:144–152, Dec 2014.
- [610] E Capobianco and P Lió. Advances in translational biomedicine from systems approaches. *Front Genet*, 5:273, 2014.
- [611] Y Shavit, FK Hamey, and P Lio. Fishical: an r package for iterative fish-based calibration of hi-c data. *Bioinformatics*, 30(21):3120–3122, Nov 2014.
- [612] C Angione, E Bartocci, L Bortolussi, P Lio, A Occhipinti, and G Sanguinetti. Bayesian design for whole cell synthetic biology models. In *Proceedings of the Third International Workshop on Hybrid Systems Biology (HSB 2014)*. Vienna.
- [613] M Fondi, I Maida, E Perrin, A Meller, S Mocali, E Parrilli, ML Tutino, P Liò, and R Fani. Genome-scale metabolic reconstruction and constraint-based modelling of the antarctic bacterium *pseudoalteromonas haloplanktistac125*. *Environ Microbiol*, 17(3):751–766, Mar 2015.
- [614] C Angione, N Pratanwanich, and P Lio. A hybrid of multi-omics fba and bayesian factor modeling to identify pathway crosstalks. In *Proceedings of the 6th International Workshop on Bio-Design Automation (IWBDa)*. Boston.
- [615] M Taffi, N Paoletti, P Liò, L Tesei, S Pucciarelli, and M Marini. Estimation and modelling of pcbs bioaccumulation in the adriatic sea ecosystem. May 2014. 24 pages, 4 figures, 7 tables.

- [616] M Taffi, N Paoletti, P Liò, S Pucciarelli, and M Marini. Bioaccumulation modelling and sensitivity analysis for discovering key players in contaminated food webs: The case study of pcbs in the adriatic sea. *Ecological Modelling*, 306:205–215, Jun 2014.
- [617] HB Raju, Z Englander, E Capobianco, NF Tsinoremas, and JK Lerch. Identification of potential therapeutic targets in a model of neuropathic pain. *Front Genet*, 5:131, 2014.
- [618] MA Moni and P Liò. comor: a software for disease comorbidity risk assessment. *J Clin Bioinforma*, 4:8, 2014.
- [619] K Bartoszek and P Lio. A novel algorithm to reconstruct phylogenies using gene sequences and expression data. Gdansk, May 2014.
- [620] L Felicetti, M Femminella, G Reali, and P Liò. A molecular communication system in blood vessels for tumor detection. *Proceedings of the 1st ACM International Conference on Nanoscale Computing and Communication, NANOCOM 2014*, Jan 2014.
- [621] Y Shavit and P Lio'. Combining a wavelet change point and the bayes factor for analysing chromosomal interaction data. *Mol Biosyst*, 10(6):1576–1585, Jun 2014.
- [622] N Pratanwanich and P Lió. Pathway-based bayesian inference of drug-disease interactions. *Mol Biosyst*, 10(6):1538–1548, Jun 2014.
- [623] X Lu, P Lio, P Hui, and Z Qu. Nodes density adaptive opportunistic forwarding protocol for intermittently connected networks. In *Proceedings - 2014 International Conference on Identification, Information and Knowledge in the Internet of Things, IIKI 2014*, pages 297–300, Mar 2014.
- [624] V Petrov, S Balasubramaniam, R Lale, D Moltchanov, P Lio', and Y Koucheryavy. Forward and reverse coding for chromosome transfer in bacterial nanonetworks. *Nano Communication Networks*, 2014.
- [625] G Ascolani and P Liò. Modeling tgf- in early stages of cancer tissue dynamics. *PLoS One*, 9(2):e88533, 2014.
- [626] F Nardi, P Liò, A Carapelli, and F Frati. Mtpan(3): site-class specific amino acid replacement matrices for mitochondrial proteins of pancrustacea and collembola. *Mol Phylogenet Evol*, 75:239–244, Jun 2014.
- [627] M Fondi, V Orlandini, E Perrin, I Maida, E Bosi, MC Papaleo, L Michaud, A Lo Giudice, D de Pascale, ML Tutino, P Liò, and R Fani. Draft genomes of three antarctic psychrobacter strains producing antimicrobial compounds against burkholderia cepacia complex, opportunistic human pathogens. *Mar Genomics*, 13:37–38, Feb 2014.
- [628] M Scatà, A Di Stefano, E Giacchi, A La Corte, and P Liò. The bio-inspired and social evolution of node and data in a multilayer network. In *DCNET 2014 - Proceedings of the 5th International Conference on Data Communication Networking, Part of ICETE 2014 - 11th International Joint Conference on e-Business and Telecommunications*, pages 41–46, Jan 2014.

- [629] F Nardi, P Liò, A Carapelli, and F Frati. Mtpan³: Site-class specific amino acid replacement matrices for mitochondrial proteins of pancrustacea and collembola. *Molecular Phylogenetics and Evolution*, 75(1):239–244, Jan 2014.
- [630] P Liò. Computing longevity: Insights from controls. *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, 8738 LNBI:40–46, Jan 2014.
- [631] PL Fernandes, P Liò, and L Milanesi. Challenges in building an e-health infrastructure for p5 medicine. In *Proceedings of the International Conferences on ICT, Society and Human Beings 2014, Web Based Communities and Social Media 2014, e-Commerce 2014, Information Systems Post-Implementation and Change Management 2014 and e-Health 2014 - Part of the Multi Conference on Computer Science and Information Systems, MCCSIS 2014*, pages 389–393, Jan 2014.
- [632] L Jacovella and P Lio. Speeding up the transition to collective awareness. *2013 IEEE International Conference on Communications Workshops, ICC 2013*, pages 220–224, Dec 2013.
- [633] C Angione, G Carapezza, J Costanza, P Lio, and G Nicosia. Multi objective design for bacterial communication networks. *2013 IEEE International Conference on Communications Workshops, ICC 2013*, pages 813–817, Dec 2013.
- [634] C Angione, G Carapezza, J Costanza, P Lio, and G Nicosia. Pareto optimality in organelle energy metabolism analysis. *IEEE/ACM Trans Comput Biol Bioinform*, Aug 2013.
- [635] C Angione, G Carapezza, J Costanza, P Lió, and G Nicosia. Design and strain selection criteria for bacterial communication networks. *Nano Communication Networks*, 2013.
- [636] X Lu, P Lio, P Hui, and H Jin. A location prediction algorithm for mobile communications using directional antennas. *INTERNATIONAL JOURNAL OF DISTRIBUTED SENSOR NETWORKS*, (ARTN 418606), 2013.
- [637] A Di Stefano, A La Corte, M Leotta, P Lió, and M Scatá. It measures like me: An iots algorithm in wsns based on heuristics behavior and clustering methods. *Ad Hoc Networks*, 2013.
- [638] F Castiglione, P Tieri, A De Graaf, C Franceschi, P Liò, B Van Ommen, C Mazzà, A Tuchel, M Bernaschi, C Samson, T Colombo, GC Castellani, M Capri, P Garagnani, S Salvioli, VA Nguyen, I Bobeldijk-Pastorova, S Krishnan, A Cappozzo, M Sacchetti, M Morettini, and M Ernst. The onset of type 2 diabetes: proposal for a multi-scale model. *JMIR Res Protoc*, 2(2):e44, Oct 2013.
- [639] M Taffi, N Paoletti, P Liò, L Tesei, E Merelli, and M Marini. A systems biology and ecology framework for pops bioaccumulation in marine ecosystems. *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, 8130 LNBI:238–239, Oct 2013.
- [640] I Merelli, P Liò, and L Milanesi. Describing the genes social networks relying on chromosome conformation capture data. *EMBnet.journal*, 19(B):73–73.

- [641] MA Moni, S Mariani, G Poli, P Lio, and E Vicenzi. Differential impacts of r5 vs. x4 hiv-1 on the transcriptome of primary cd4₊ t cells. *RETROVIROLOGY*, 10(ARTN P114):S39–S39, 2013.
- [642] P Lio, L Bianchi, V Nguyen, and S Kitchovich. Risk perception, heuristics and epidemic spread. In P Manfredi and A D’Onofrio, editors, *Modeling the Interplay Between Human Behavior and the Spread of Infectious Diseases*, pages 139–152. Jan 2013.
- [643] C Angione, J Costanza, G Carapezza, P Lió, and G Nicosia. A design automation framework for computational bioenergetics in biological networks. *Mol Biosyst*, 9(10):2554–2564, Oct 2013.
- [644] I Merelli, P Liò, and L Milanesi. Nuchart: An r package to study gene spatial neighbourhoods with multi-omics annotations. *PLoS ONE*, 8(9), Sep 2013.
- [645] E Capobianco and P Lio’. Comorbidity: a multidimensional approach. *Trends in Molecular Medicine*, 2013.
- [646] X Lu, P Hui, and P Lio. Offloading mobile data from cellular networks through peer-to-peer wifi communication: A subscribe-and-send architecture. *CHINA COMMUNICATIONS*, 10(6):35–46, 2013.
- [647] S Balasubramaniam, S Ben-Yehuda, S Pautot, A Jesorka, P Lio’, and Y Koucheryavy. A review of experimental opportunities for molecular communication. *Nano Communication Networks*, 4(2):43–52, Jun 2013.
- [648] C Angione, J Costanza, G Carapezza, P Lió, and G Nicosia. Pareto epsilon-dominance and identifiable solutions for biocad modeling. *Proceedings - Design Automation Conference*, Jul 2013.
- [649] P Liò. Pathways to p4 medicine. *BIOINFORMATICS 2013 - Proceedings of the International Conference on Bioinformatics Models, Methods and Algorithms*, May 2013.
- [650] MA Moni, P Liò, and L Milanesi. Comparing viral (hiv) and bacterial (staphylococcus aureus) infection of the bone tissue. *BIOINFORMATICS 2013 - Proceedings of the International Conference on Bioinformatics Models, Methods and Algorithms*, pages 196–201, May 2013.
- [651] M Brilli, P Liò, V Lacroix, and M-F Sagot. Short and long-term genome stability analysis of prokaryotic genomes. *BMC Genomics*, 14:309, May 2013.
- [652] Y Shavit and P Lio’. Cytohic: a cytoscape plugin for visual comparison of hi-c networks. *Bioinformatics*, 29(9):1206–1207, May 2013.
- [653] S Balasubramaniam and P Lio’. Multi-hop conjugation based bacteria nanonetworks. *IEEE Trans Nanobioscience*, 12(1):47–59, Mar 2013.
- [654] F Castiglione, V Diaz, A Gaggioli, P Lio, C Mazza, E Merelli, CGM Meskers, F Pappalardo, and R von Ammon. Physio-environmental sensing and live modeling. *JOURNAL OF MEDICAL INTERNET RESEARCH*, 15(1), Jan 2013.

- [655] G Carapezza, R Umeton, J Costanza, C Angione, G Stracquadanio, A Papini, P Lió, and G Nicosia. Efficient behavior of photosynthetic organelles via pareto optimality, identifiability, and sensitivity analysis. *ACS Synth Biol*, 2(5):274–288, May 2013.
- [656] E Vicenzi, P Liò, and G Poli. The puzzling role of cxcr4 in human immunodeficiency virus infection. *Theranostics*, 3(1):18–25, 2013.
- [657] C Angione, G Carapezza, J Costanza, P Lió, and G Nicosia. The role of the genome in the evolution of the complexity of metabolic machines. pages 1063–1069, Jan 2013.
- [658] Proceedings of the twelfth european conference on the synthesis and simulation of living systems: Advances in artificial life, ecal 2013, sicily, italy, september 2-6, 2013. In P Liò, O Miglino, G Nicosia, S Nolfi, and M Pavone, editors, *ECAL*. MIT Press, 2013.
- [659] P Liò. Methodologies for systems medicine: Time to join the forces of bioengineering and bioinformatics. In P Fernandes, J Solé-Casals, ALN Fred, and H Gamboa, editors, *BIOINFORMATICS*, pages IS–27. SciTePress, 2013.
- [660] A Bansal, S Azad, and P Lio. Malaria incidence forecasting and its implication to intervention strategies in south east asia region. In *Springer Proceedings in Complexity*, pages 919–926. Jan 2013.
- [661] A Bansal, S Azad, and P Lio. Malaria incidence forecasting and its implication to intervention. In T Gilbert, M Kirkilionis, and G Nicoli, editors, *Proceedings of the European Conference on Complex Systems 2012*, number Springer Proceedings in Complexity in Springer Proceedings in Complexity, pages 919–926, Bruxelles, 2013. Bruxelles, Springer. Springer Proceedings in Complexity Proceedings of the European Conference on Complex Systems 2012.
- [662] P Liò, L Jacovella, and V Nguyen. Information filtering and learning: From heuristics to social eudaimonia. pages 1051–1056, Jan 2013.
- [663] L Bianchi, P Fernandes, and P Lio. Improving collective awareness and education about the privacy and ethical issues connected with the genome technologies. In *The Future of Education, Conference Proceedings 2013*, Florence, 2013. Florence, Libreria universitaria.
- [664] S Xie, AT Lawnizak, P Lio, and S Krishnan. Feature extraction by multi-scale principal component analysis and classification in spectral domain. *Engineering*, 05(10):268–271, 2013.
- [665] N Pratanwanich and P Lio. Bayesian inference for learning between-pathway network: A new tool for studying drug-disease interactions. In *HUMAN HEREDITY*, volume 76, pages 99–99, 2013.
- [666] E Bartocci, P Liò, E Merelli, and N Paoletti. Multiple verification in complex biological systems: The bone remodelling case study. *Trans. Comp. Sys. Biology*, 14:53–76, 2012.
- [667] C Angione, G Carapezza, J Costanza, P Lio, and G Nicosia. Rational design of organelle compartments in cells. *EMBnet. journal*, 18(B):20–22, Apr 2013.
- [668] E Massaro, F Bagnoli, A Guazzini, and P Lió. Information dynamics algorithm for detecting communities in networks. *Communications in Nonlinear Science and Numerical Simulation*, 17(11):4294–4303, Nov 2012.

- [669] J Costanza, G Carapezza, C Angione, P Liò, and G Nicosia. Multi-objective optimisation, sensitivity and robustness analysis in fba modelling. *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, 7605 LNBI:127–147, Oct 2012.
- [670] J Costanza, G Carapezza, C Angione, P Liò, and G Nicosia. Robust design of microbial strains. *Bioinformatics*, 28(23):3097–3104, Dec 2012.
- [671] S Haider, L Cordeddu, E Robinson, M Movassagh, L Siggins, A Vujic, M-K Choy, M Goddard, P Lio, and R Foo. The landscape of dna repeat elements in human heart failure. *Genome Biol*, 13(10):R90, Oct 2012.
- [672] P Liò, C Angelini, I De Feis, and V-A Nguyen. Statistical approaches to use a model organism for regulatory sequences annotation of newly sequenced species. *PLoS One*, 7(9):e42489, 2012.
- [673] P Liò, N Paoletti, MA Moni, K Atwell, E Merelli, and M Viceconti. Modelling osteomyelitis. *BMC Bioinformatics*, 13 Suppl 14(Suppl 14):S12, 2012.
- [674] P Liò, E Merelli, and N Paoletti. Disease processes as hybrid dynamical systems, Aug 2012.
- [675] C Peng, X Jin, KC Wong, M Shi, and P Liò. Correction: Collective human mobility pattern from taxi trips in urban area. *PLoS One*, 7(8), 2012. PMID: PMC3435422.
- [676] N Paoletti, P Liò, E Merelli, and M Viceconti. Multilevel computational modeling and quantitative analysis of bone remodeling. *IEEE/ACM Trans Comput Biol Bioinform*, 9(5):1366–1378, 2012.
- [677] S Xie, AT Lawniczak, S Krishnan, and P Lio. Wavelet kernel principal component analysis in noisy multiscale data classification. *ISRN Computational Mathematics*, 2012:1–13, Jul 2012.
- [678] C Angione, G Carapezza, J Costanza, P Lio, and G Nicosia. Computing with metabolic machines. In *EPiC Series in Computing*. EasyChair.
- [679] X Lu, H Pan, and P Lio. High delivery performance opportunistic routing scheme for delay tolerant networks. *CHINA COMMUNICATIONS*, 9(6):145–153, 2012.
- [680] C Peng, X Jin, K-C Wong, M Shi, and P Liò. Collective human mobility pattern from taxi trips in urban area. *PLoS One*, 7(4):e34487, 2012.
- [681] P Laise, D Fanelli, P Lio, and A Arcangeli. Modeling tgfbeta signaling pathway in epithelial-mesenchymal transition. *AIP ADV*, 2(1), Mar 2012.
- [682] XF Lu, D Towsley, P Lio, and Z Xiong. An adaptive directional mac protocol for ad hoc networks using directional antennas. *Science China Information Sciences*, 55(6):1360–1371, Jun 2012.
- [683] P Laise, D Fanelli, P Lio, and A Arcangeli. Modeling tgfbeta signaling pathway in epithelial-mesenchymal transition. *AIP Advances*, Special Topic: Physics of Cancer.
- [684] P Lio and S Balasubramaniam. Opportunistic routing through conjugation in bacteria communication nanonetwork. *Nano Communication Networks*, 3(1):36–45, Mar 2012.

- [685] A Nazri and P Lio. Investigating meta-approaches for reconstructing gene networks in a mammalian cellular context. *PLoS One*, 7(1):e28713, 2012.
- [686] H Kim, WM Khoo, and P Lio. Polymorphic attacks against sequence-based software birthmarks. Beijing, China, 2012.
- [687] C Angione, P Liò, and G Nicosia. How to compute with metabolism in bacteria? *ERCIM News*, 2012(91), 2012.
- [688] P Lio and D Verma. Biologically inspired networking and sensing: Algorithms and architectures preface. In *BIOLOGICALLY INSPIRED NETWORKING AND SENSING: ALGORITHMS AND ARCHITECTURES*, pages VIII–XI. 2012.
- [689] Artificial immune systems - 11th international conference, icaris 2012, taormina, italy, august 28-31, 2012. proceedings. In CAC Coello, J Greensmith, N Krasnogor, P Liò, G Nicosia, and M Pavone, editors, *ICARIS*, volume 7597 of *Lecture Notes in Computer Science*. Springer, 2012.
- [690] WM Khoo and P Lió. Unity in diversity: Phylogenetic-inspired techniques for reverse engineering and detection of malware families. *Proceedings - 1st SysSec Workshop, SysSec 2011*, pages 3–10, Dec 2011.
- [691] E Massaro, A Guazzini, F Bagnoli, and P Liò. Information dynamics algorithm for detecting communities in networks, Dec 2011.
- [692] P Lio and D Verma. Preface. *Biologically Inspired Networking and Sensing: Algorithms and Architectures*, Dec 2011.
- [693] X Lu, P Hui, and P Lio. Evolving model of opportunistic routing in delay tolerant networks. *Proceedings - 2011 7th International Conference on Mobile Ad-hoc and Sensor Networks, MSN 2011*, pages 276–281, Dec 2011.
- [694] P Lio and D Verma. Biologically inspired networking and sensing: Algorithms and architectures. *Biologically Inspired Networking and Sensing: Algorithms and Architectures*, pages 1–297, Dec 2011.
- [695] X Lu, Y Xin, and P Lio. Admac: An adaptive directional mac protocol for mobile ad hoc networks. *Proceedings - 2011 4th IEEE International Conference on Broadband Network and Multimedia Technology, IC-BNMT 2011*, pages 488–492, Dec 2011.
- [696] M Movassagh, MK Choy, DA Knowles, L Cordeddu, S Haider, T Down, L Siggins, A Vujic, I Simeoni, C Penkett, M Goddard, P Lio, MR Bennett, and RSY Foo. Distinct epigenomic features in end-stage failing human hearts. *Circulation*, 124(22):2411–2422, Nov 2011.
- [697] R Umeton, G Stracquadanio, A Papini, J Costanza, P Liò, and G Nicosia. Identification of sensitive enzymes in the photosynthetic carbon metabolism. *Adv Exp Med Biol*, 736:441–459, 2012.
- [698] P Liò, E Merelli, N Paoletti, and M Viceconti. A combined process algebraic and stochastic approach to bone remodeling. *Electronic Notes in Theoretical Computer Science*, 277(1):41–52, Oct 2011.

- [699] P Lio and SB Sasitharan Balasubramaniam. Opportunistic routing through conjugation in bacteria communication nanonetwork. *Nano Communication Networks*, 2(October 2011), Oct 2011.
- [700] P Lio, Emanuela Merelli, NP Nicola Paoletti, and MV Marco Viceconti. A combined process algebraic and stochastic approach to bone remodeling. *Electronic Notes in Theoretical Computer Science*, 277(27):41–52, Oct 2011.
- [701] N Paoletti, P Liò, E Merelli, and M Viceconti. Osteoporosis: A multiscale modeling viewpoint. *Proceedings of the 9th International Conference on Computational Methods in Systems Biology, CMSB'11*, pages 183–193, Oct 2011.
- [702] P Liò, E Merelli, and N Paoletti. Multiple verification in computational modeling of bone pathologies, Sep 2011.
- [703] M Aldinucci, A Bracciali, P Liò, A Sorathiya, and M Torquati. Stochkit-ff: Efficient systems biology on multicore architectures. *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, 6586 LNCS:167–175, Aug 2011.
- [704] P Lio and D Verma. *Biologically Inspired Networking and Sensing*. Medical Info Science Reference, Jul 2011.
- [705] S Kitchovitch and P Liò. Community structure in social networks: applications for epidemiological modelling. *PLoS One*, 6(7):e22220, 2011.
- [706] Y Song and P Liò. Epileptic eeg detection via a novel pattern recognition framework. *5th International Conference on Bioinformatics and Biomedical Engineering, iCBBE 2011*, Jul 2011.
- [707] E Yoneki, J Crowcroft, P Lio', N Walton, M Vojnovic, and R Whitaker. Message from the workshop on the future of social networking. *COMPUT COMMUN REV*, 41(3):14–18, Jul 2011.
- [708] S Balasubramaniam, K Leibnitz, P Lio', D Botvich, and M Murata. Biological principles for future internet architecture design. *IEEE COMMUN MAG*, 49(7):44–52, Jul 2011.
- [709] E Giampieri, D Remondini, L de Oliveira, G Castellani, and P Lió. Stochastic analysis of a mirna-protein toggle switch. *Mol Biosyst*, 7(10):2796–2803, Oct 2011.
- [710] R Umeton, G Stracquadanio, A Sorathiya, A Papini, P Liò, and G Nicosia. Design of robust metabolic pathways. *Proceedings - Design Automation Conference*, pages 747–752, Jan 2011.
- [711] IXY Leung, S-Y Chan, P Hui, and P Lio'. Intra-city urban network and traffic flow analysis from gps mobility trace. May 2011. 23 pages, 6 figures, 2 tables, 1 algorithm.
- [712] WR Gilks, TMW Nye, and P Lio. A variance-components model for distance-matrix phylogenetic reconstruction. *STAT APPL GENET MOL*, 10(1), 2011.
- [713] RC Van Der Wath, EC Van Der Wath, and P Lió. Parallel hematopoietic stem cell division rate estimation using an agent-based model on the grid. *Proceedings - 19th International*

Euromicro Conference on Parallel, Distributed, and Network-Based Processing, PDP 2011, pages 311–317, Apr 2011.

- [714] P Lio, Emanuela Merelli, and NP Nicola Paoletti. Multiple verification in computational modeling of bone pathologies. In *EPTCS*, volume 67, pages 82–96. Aachen, Germany <http://combio.abo.fi/compmod11/>, 2011.
- [715] E Merelli, N Paoletti, and P Lio. Methodological bridges for multi-level systems. In E Giacobino and R Pfeifer, editors, *Procedia Computer Science*, volume 7, pages 180–182, Budapest, 2011. Budapest, Elsevier.
- [716] C Balocco and P Lio. Assessing ventilation system performance in isolation rooms. *ENERG BUILDINGS*, 43(1):246–252, Jan 2011.
- [717] Artificial immune systems - 10th international conference, icaris 2011, cambridge, uk, july 18-21, 2011. proceedings. In P Liò, G Nicosia, and T Stibor, editors, *ICARIS*, volume 6825 of *Lecture Notes in Computer Science*. Springer, 2011.
- [718] E Schwarz, P Whitfield, S Nahnsen, L Wang, H Major, FM Leweke, D Koethe, P Lio, and S Bahn. Alterations of primary fatty acid amides in serum of patients with severe mental illness. *Front Biosci (Elite Ed)*, 3(1):308–314, Jan 2011.
- [719] D Hebenstreit, M Gu, S Haider, DJ Turner, P Liò, and SA Teichmann. Epichip: gene-by-gene quantification of epigenetic modification levels. *Nucleic Acids Res*, 39(5):e27, Mar 2011.
- [720] P Lio, A Guazzini, A Passarella, and M Conti. Modeling perisaccadic time perception. *Journal of Biomedical Science and Engineering*, 3(12):1133–1142, Dec 2010.
- [721] TM Chan, KS Leung, KH Lee, and P Lio. Generic spaced dna motif discovery using genetic algorithm. In *2010 IEEE CONGRESS ON EVOLUTIONARY COMPUTATION (CEC)*, 2010.
- [722] G Emiliani, M Fondi, P Lio, and R Fani. Evolution of metabolic pathways and evolution of genomes. In A Loy, editor, *Geomicrobiology*. Springer Verlag, Jul 2010.
- [723] M Botta, S Haider, IXY Leung, P Lio, and J Mozziconacci. Intra- and inter-chromosomal interactions correlate with ctcf binding genome wide. *Mol Syst Biol*, 6:426, Nov 2010.
- [724] M Brilli, R Fani, and P Lio. Bioinformatics of gene families. In U Bastolla, M Porto, E Roman, and M Vendruscolo, editors, *Structural Approaches to Sequence Evolution*. Nov 2010.
- [725] A Papini, G Nicosia, G Stracquadanio, P Lio, and R Umeton. Key enzymes for the optimization of co2 uptake and nitrogen consumption in the c-3 photosynthetic carbon metabolism. In *JOURNAL OF BIOTECHNOLOGY*, volume 150, pages S525–S526, Nov 2010.
- [726] A Papini, S Mosti, P Lio, and S Haider. Biolip, a biotechnology-oriented database of oil content in plants, algae, fungi and cyanobacteria. In *JOURNAL OF BIOTECHNOLOGY*, volume 150, pages S204–S205, Nov 2010.
- [727] VA Nguyen and P Lio. Filling in the gaps of biological network. pages 147–149. Edinburgh.
- [728] A Sorathiya, A Bracciali, and P Lio. An integrated modelling approach for r5-x4 mutation and haart therapy assessment. *SWARM INTELL-US*, 4(4):319–340, Dec 2010.

- [729] Y Song, S Azad, and P Lio. A new approach for epileptic seizure detection using extreme learning machine. *BIOSIGNALS 2010 - Proceedings of the 3rd International Conference on Bio-inspired Systems and Signal Processing, Proceedings*, pages 436–441, Sep 2010.
- [730] G Stracquadanio, R Umeton, A Papini, P Lio, and G Nicosia. Analysis and optimization of c_3 photosynthetic carbon metabolism. *10th IEEE International Conference on Bioinformatics and Bioengineering 2010, BIBE 2010*, pages 44–51, Sep 2010.
- [731] C Angelini, I De Feis, VA Nguyen, R Van Der Wath, and P Liò. Combining replicates and nearby species data: A bayesian approach. *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, 6160 LNBI:191–205, Aug 2010.
- [732] K Bartoszek, P Lio, and A Sorathiya. Influenza differentiation and evolution. In AT Lawniczak, D Makowiec, and BN Di Stefano, editors, *SUMMER SOLSTICE 2009 INTERNATIONAL CONFERENCE ON DISCRETE MODELS OF COMPLEX SYSTEMS*, volume 3, pages 417–452, 2010.
- [733] M Aldinucci, A Bracciali, P Liò, A Sorathiya, and M Torquati. Stochkit-ff: Efficient systems biology on multicore architectures, Jul 2010.
- [734] C Balocco and P Lio. Modelling infection spreading control in a hospital isolation room. *Journal of Biomedical Science and Engineering*, 3(7):653–663, Jul 2010.
- [735] V Pappas, DC Verma, and P Lio. Morphogenesis in computer networks. *33rd IEEE Sarnoff Symposium 2010, Conference Proceedings*, Jun 2010.
- [736] P Lio and Y Song. A new approach for epileptic seizure detection: sample entropy based feature extraction and extreme learning machine. *Journal of Biomedical Science and Engineering*, 3(6):556–567, Jun 2010.
- [737] S Kitchovitch and P Lio. Risk perception and disease spread on social networks. In *ICCS 2010 - INTERNATIONAL CONFERENCE ON COMPUTATIONAL SCIENCE, PROCEEDINGS*, volume 1, pages 2339–2348, 2010.
- [738] P Lio and D Verma. Guest editorial: Biologically inspired networking. *IEEE Network*, 24(3):4, May 2010.
- [739] A Guazzini, P Lio, F Bagnoli, A Passarella, and M Conti. Cognitive network dynamics in chatlines. In *ICCS 2010 - INTERNATIONAL CONFERENCE ON COMPUTATIONAL SCIENCE, PROCEEDINGS*, volume 1, pages 2349–2356, 2010.
- [740] P Liò and DC Verma. Biologically inspired networking [guest editorial]. *IEEE Netw.*, 24(3):4–4, 2010.
- [741] P Lio and D Verma. Biologically inspired networking. *IEEE NETWORK*, 24(3):4–4, May 2010.
- [742] A Sorathiya, A Bracciali, and P Liò. Formal reasoning on qualitative models of coinfection of hiv and tuberculosis and haart therapy. *BMC Bioinformatics*, 11 Suppl 1(Suppl 1):S67, Jan 2010.

- [743] V-A Nguyen, Z Koukolikova-Nicola, F Bagnoli, and P Lio. Noise and nonlinearities in high-throughput data, Jan 2010.
- [744] P Lio and M Brilli. Transcription factors and gene regulatory networks. In M Buchanan, G Caldarelli, and PDL Rios, editors, *Networks in Cell Biology*. Cambridge Univ Pr, Jun 2010.
- [745] M Ostilli, E Yoneki, IXY Leung, JFF Mendes, P Lio, and J Crowcroft. Statistical mechanics of rumour spreading in network communities. In *ICCS 2010 - INTERNATIONAL CONFERENCE ON COMPUTATIONAL SCIENCE, PROCEEDINGS*, volume 1, pages 2325–2333, 2010.
- [746] M Aldinucci, A Bracciali, and P Lio. Formal synthetic immunology. *Ercim News*, 82:40–41, 2010.
- [747] S Xie, AT Lawniczak, and P Liò. Features extraction via wavelet kernel pca for data classification. *Proceedings of the 2010 IEEE International Workshop on Machine Learning for Signal Processing, MLSP 2010*, pages 438–443, Jan 2010.
- [748] S Xie, AT Lawniczak, Y Song, and P Liò. Feature extraction via dynamic pca for epilepsy diagnosis and epileptic seizure detection. *Proceedings of the 2010 IEEE International Workshop on Machine Learning for Signal Processing, MLSP 2010*, pages 337–342, Jan 2010.
- [749] S Kitchovitch, YD Song, R van der Wath, and P Lio. Substitution matrices and mutual information approaches to modeling evolution. In T Stutzle, editor, *LEARNING AND INTELLIGENT OPTIMIZATION*, volume 5851, pages 259–272, 2009.
- [750] TMK Cheng, Y-E Lu, PC Guest, H Rahmoune, LW Harris, L Wang, D Ma, V Stelzhammer, Y Umrana, MT Wayland, P Lió, and S Bahn. Identification of targeted analyte clusters for studies of schizophrenia. *Mol Cell Proteomics*, 9(3):510–522, Mar 2010.
- [751] Y-E Lu, SGB Roberts, P Liò, R Dunbar, and J Crowcroft. Size matters: Variation in personal network size, personality and effect on information transmission. In *CSE (4)*, pages 188–193. IEEE Computer Society, 2009.
- [752] VA Nguyen and P Lio. Measuring similarity between gene expression profiles: a bayesian approach. In *BMC GENOMICS*, volume 10, Sep 2009.
- [753] SK Xie, P Lio, and AT Lawniczak. A comparative study of noise effect on wavelet based de-noising methods. In *IEEE TIC-STH 09: 2009 IEEE TORONTO INTERNATIONAL CONFERENCE: SCIENCE AND TECHNOLOGY FOR HUMANITY*, pages 919–926, 2009.
- [754] SK Xie, P Lio, and AT Lawniczak. A case study of ica with multi-scale pca of simulated traffic data. In C Alippi, M Polycarpou, C Panayiotou, and G Ellinas, editors, *ARTIFICIAL NEURAL NETWORKS - ICANN 2009, PT II*, volume 5769, pages 358–367, 2009.
- [755] S Kitchovitch, I Leung, YD Song, and P Lio. Using mutual information and models of evolution for improved pattern detection. In J Zhang, GZ Li, and JY Yang, editors, *2009 INTERNATIONAL JOINT CONFERENCE ON BIOINFORMATICS, SYSTEMS BIOLOGY AND INTELLIGENT COMPUTING, PROCEEDINGS*, pages 215–221, 2009.
- [756] K Xu, P Hui, VOK Li, J Crowcroft, V Latora, and P Lio. Impact of altruism on opportunistic communications. In *2009 FIRST INTERNATIONAL CONFERENCE ON UBIQUITOUS AND FUTURE NETWORKS*, pages 153–158, 2009.

- [757] Y-E Lu, SGB Roberts, TMK Cheng, R Dunbar, P Liò, and J Crowcroft. On optimising personal network size to manage information flow. In J Wang, S Zhou, and D Zhang, editors, *CIKM-CNIKM*, pages 19–26. ACM, 2009.
- [758] A Guazzini, P Lio, A Passarella, and M Conti. Information processing and timing mechanisms in vision. In C Alippi, M Polycarpou, C Panayiotou, and G Ellinas, editors, *ARTIFICIAL NEURAL NETWORKS - ICANN 2009, PT I*, volume 5768, pages 325–334, 2009.
- [759] SY Chan, IXY Leung, and P Liò. Fast centrality approximation in modular networks. *International Conference on Information and Knowledge Management, Proceedings*, pages 31–38, Dec 2009.
- [760] M Fondi, G Emiliani, P Liò, S Gribaldo, and R Fani. The evolution of histidine biosynthesis in archaea: insights into the his genes structure and organization in luca. *J Mol Evol*, 69(5):512–526, Nov 2009.
- [761] A Sorathiyar, P Lio, and L Sguanci. Mathematical model of hiv superinfection and comparative drug therapy. In PS Andrews, J Timmis, NDL Owens, U Aickelin, E Hart, A Hone, and AM Tyrrell, editors, *ARTIFICIAL IMMUNE SYSTEMS, PROCEEDINGS*, volume 5666, pages 41–53, 2009.
- [762] L Milanese, P Romano, G Castellani, D Remondini, and P Liò. Trends in modeling biomedical complex systems. *BMC Bioinformatics*, 10 Suppl 12(Suppl 12):I1, Oct 2009.
- [763] E Schwarz, FM Leweke, S Bahn, and P Liò. Clinical bioinformatics for complex disorders: a schizophrenia case study. *BMC Bioinformatics*, 10 Suppl 12(Suppl 12):S6, Oct 2009.
- [764] P Hui, K Xu, VOK Li, J Crowcroft, V Latora, and P Lio. Selfishness, altruism and message spreading in mobile social networks. In *IEEE INFOCOM 2009 - IEEE CONFERENCE ON COMPUTER COMMUNICATIONS WORKSHOPS*, pages 284–289, 2009.
- [765] A Sorathiya, T Jucikas, S Pieciewicz, S Sengupta, and P Lio. Searching for glycomics role in stem cell development. In F Masulli, R Tagliaferri, and GM Verkhivker, editors, *COMPUTATIONAL INTELLIGENCE METHODS FOR BIOINFORMATICS AND BIOSTATISTICS*, volume 5488, pages 198–209, 2009.
- [766] G Bella and P Lio. Formal analysis of the genetic toggle. In P Degano and R Gorrieri, editors, *COMPUTATIONAL METHODS IN SYSTEMS BIOLOGY, PROCEEDINGS*, volume 5688, pages 96–110, 2009.
- [767] RC van der Wath, A Wilson, E Laurenti, A Trumpp, and P Liò. Estimating dormant and active hematopoietic stem cell kinetics through extensive modeling of bromodeoxyuridine label-retaining cell dynamics. *PLoS One*, 4(9):e6972, Sep 2009.
- [768] L Bianchi and P Lio. La legge e il dna. *Le Scienze, Italian Edition Scientific American*, (September 2009), Sep 2009.
- [769] XF Lu, FD Wicker, D Towsley, Z Xiong, and P Lio. Detection probability estimation of directional antennas and omni-directional antennas. *WIRELESS PERS COMMUN*, 55(1):51–63, Sep 2010.

- [770] M Brilli, M Fondi, P Lio, and R Fani. The origin and evolution of nitrogen fixation genes. *ORIGINS LIFE EVOL B*, 39(3-4):310–311, Aug 2009.
- [771] A Wilson, E Laurenti, G Oser, RC van der Wath, W Blanco-Bose, M Jaworski, S Offner, C Dunant, L Eshkind, E Bockamp, P Lio, HR MacDonald, and A Trumpp. Hematopoietic stem cells reversibly switch from dormancy to self-renewal during homeostasis and repair (vol 135, pg 1118, 2008). *CELL*, 138(1):209–209, Jul 2009.
- [772] A Wilson, E Laurenti, G Oser, RC van der Wath, W Blanco-Bose, M Jaworski, S Offner, C Dunant, L Eshkind, E Bockamp, P Lio, HR MacDonald, and A Trumpp. Hematopoietic stem cells reversibly switch from dormancy to self-renewal during homeostasis and repair (doi:10.1016/j.cell.2008.10.048). *Cell*, 138(1):209, Jul 2009.
- [773] TMK Cheng, YE Lu, and P Lió. Identification of structurally important amino acids in proteins by graph-theoretic measures. *Proceedings of the KDD-09 Workshop on Statistical and Relational Learning in Bioinformatics, StReBio '09*, pages 7–11, Nov 2009.
- [774] IXY Leung, P Hui, P Lio, and J Crowcroft. Towards real-time community detection in large networks. *PHYS REV E*, 79(6), Jun 2009.
- [775] XF Lu, D Towsley, P Lio, F Wicker, and Z Xiong. Minimizing detection probability routing in ad hoc networks using directional antennas. *EURASIP J WIREL COMM*, (256714), 2009.
- [776] U Lee, E Magistretti, M Gerla, P Bellavista, P Lio, and KW Lee. Bio-inspired multi-agent data harvesting in a proactive urban monitoring environment. *AD HOC NETW*, 7(4):725–741, Jun 2009.
- [777] CB Carla Balocco, P Lio, and Luca Sani. Simulazione di un sistema di ventilazione per il controllo degli agenti eziologici nei reparti infettivi. un caso reale. *CDA CONDIZIONAMENTO DELL'ARIA RISCALDAMENTO REFRIGERAZIONE*, May 2009(May 2009):1–9, May 2009.
- [778] VA Nguyen, Z Koukolikova-Nicola, F Bagnoli, and P Lio. Noise and non-linearities in high-throughput data. *J STAT MECH-THEORY E*, (P01014), Jan 2009.
- [779] M Brilli and P Lio. The structural and dynamical properties of biological systems. In S Boccaletti, V Latora, and Y Moreno, editors, *Handbook on Biological Networks*. World Scientific Pub Co Inc, Mar 2010.
- [780] P Lio. Modeling space and clocks constraints in visual information processing. *Frontiers in Neuroinformatics*, 3.
- [781] GB Giampaolo Bella and P Lio. Analysing the microrna-17-92/myc/e2f/rb compound toggle switch by theorem proving. In *Proc. of the 9th Workshop on Network Tools and Applications in Biology (Nettab'09)*, volume Liberodiscrivere (2009), pages 59–62, Catania, 2009. Catania, Italy <http://www.nettab.org/2009/>, Liberodiscrivere (2009).
- [782] M Brilli, A Mengoni, M Fondi, M Bazzicalupo, P Liò, and R Fani. Analysis of plasmid genes by phylogenetic profiling and visualization of homology relationships using blast2network. *BMC Bioinformatics*, 9:551, Dec 2008.
- [783] P Liò. Topological and dynamical properties of genetic and social networks. *PAMM*, 7(1):2070007–2070008, Dec 2007.

- [784] A Wilson, E Laurenti, G Oser, RC van der Wath, W Blanco-Bose, M Jaworski, S Offner, CF Dunant, L Eshkind, E Bockamp, P Lió, HR Macdonald, and A Trumpp. Hematopoietic stem cells reversibly switch from dormancy to self-renewal during homeostasis and repair. *Cell*, 135(6):1118–1129, Dec 2008.
- [785] RC van der Wath and P Lio. A stochastic single cell based model of brdu measured hematopoietic stem cell kinetics. In M Heiner and AM Uhrmacher, editors, *COMPUTATIONAL METHODS IN SYSTEMS BIOLOGY, PROCEEDINGS*, volume 5307, pages 387–401, 2008.
- [786] P Lió, AT Lawniczak, S Xie, and J Xu. Wavelet-domain statistics of packet switching networks near traffic congestion. *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, 5151 LNCS:268–279, Dec 2008.
- [787] SM Allen, M Conti, J Crowcroft, R Dunbar, P Lio, JF Mendes, R Molva, A Passarella, I Stavrakakis, and RM Whitaker. Social networking for pervasive adaptation. In GD Serugendo, editor, *SASOW 2008: SECOND IEEE INTERNATIONAL CONFERENCE ON SELF-ADAPTIVE AND SELF-ORGANIZING SYSTEMS WORKSHOPS, PROCEEDINGS*, pages 49–54, 2008.
- [788] XF Lu, F Wicker, P Lio', and D Towsley. Security estimation model with directional antennas. In *2008 IEEE MILITARY COMMUNICATIONS CONFERENCE: MILCOM 2008, VOLS 1-7*, pages 3808–3813, 2008.
- [789] XF Lu, P Hui, P Lio, and Z Xiong. Identity privacy protection by delayed transmission in pocket switched networks. In M Guo, ZJ Wang, F Tang, and CZ Xu, editors, *EUC 2008: PROCEEDINGS OF THE 5TH INTERNATIONAL CONFERENCE ON EMBEDDED AND UBIQUITOUS COMPUTING, VOL 2, WORKSHOPS*, pages 272–277, 2008.
- [790] F Bagnoli, A Guazzini, and P Lio. Human heuristics for autonomous agents. In P Lio, E Yoneki, and DC Verma, editors, *BIO-INSPIRED COMPUTING AND COMMUNICATION*, volume 5151, pages 340–351, 2008.
- [791] U Lee, E Magistretti, M Gerla, P Bellavista, P Lio, and KW Lee. Bio-inspired multi-agent collaboration for urban monitoring applications. In P Lio, E Yoneki, and DC Verma, editors, *BIO-INSPIRED COMPUTING AND COMMUNICATION*, volume 5151, pages 204–216, 2008.
- [792] YE Lu, P Lio, and S Hand. Beta random projection. In P Lio, E Yoneki, and DC Verma, editors, *BIO-INSPIRED COMPUTING AND COMMUNICATION*, volume 5151, pages 319–331, 2008.
- [793] VA Nguyen, Z Koukolikova-Nicola, F Bagnoli, and P Lio. Bayesian inference on hidden knowledge in high-throughput molecular biology data. In TB Ho and ZH Zhou, editors, *PRICAI 2008: TRENDS IN ARTIFICIAL INTELLIGENCE*, volume 5351, pages 829–838, 2008.
- [794] XF Lu, YC Chen, I Leung, Z Xiong, and P Lio. A novel mobility model from a heterogeneous military manet trace. In D Coudert, D SimplotRyl, and I Stojmenovic, editors, *AD-HOC, MOBILE AND WIRELESS NETWORKS, PROCEEDINGS*, volume 5198, pages 463–474, 2008.

- [795] F Stajano, L Bianchi, P Liò, and D Korff. Forensic genomics: Kin privacy, driftnets and other open questions. *Proceedings of the ACM Conference on Computer and Communications Security*, pages 15–22, Dec 2008.
- [796] YE Lu, P Lió, and S Hand. On low dimensional random projections and similarity search. *International Conference on Information and Knowledge Management, Proceedings*, pages 749–758, Dec 2008.
- [797] IXY Leung, G Gibbs, F Bagnoli, A Sorathiya, and P Lio. Contact network modeling of flu epidemics. In H Umeo, S Morishita, K Nishinari, T Komatsuzaki, and S Bandini, editors, *CELLULAR AUTOMATA, PROCEEDINGS*, volume 5191, pages 354–361, 2008.
- [798] RC van der Wath and P Lio. A stochastic multi-agent model of stem cell proliferation. In H Umeo, S Morishita, K Nishinari, T Komatsuzaki, and S Bandini, editors, *CELLULAR AUTOMATA, PROCEEDINGS*, volume 5191, pages 500–505, 2008.
- [799] X Lu, F Wicker, I Leung, P Liò, and Z Xiong. A location prediction algorithm for directional communication. *IWCMC 2008 - International Wireless Communications and Mobile Computing Conference*, pages 159–164, Oct 2008.
- [800] S Xie, AT Lawniczak, and P Lió. Parametric & non-parametric analysis of mean treatment effects of number of packets in transit in data network model. *Canadian Conference on Electrical and Computer Engineering*, pages 2021–2026, Sep 2008.
- [801] C Angelini, L Cutillo, I De Feis, P Lio, and R van der Wath. Combining experimental evidences from replicates and nearby species data for annotating novel genomes. In LM Ricciardi, A Buonocore, and E Pirozzi, editors, *COLLECTIVE DYNAMICS: TOPICS ON COMPETITION AND COOPERATION IN THE BIOSCIENCES*, volume 1028, pages 277–291, 2008.
- [802] IXY Leung, P Hui, P Lio', and J Crowcroft. Towards real-time community detection in large networks, Aug 2008.
- [803] TMK Cheng, Y-E Lu, M Vendruscolo, P Lio', and TL Blundell. Prediction by graph theoretic measures of structural effects in proteins arising from non-synonymous single nucleotide polymorphisms. *PLoS Comput Biol*, 4(7):e1000135, Jul 2008.
- [804] Z Koukolikova-Nicola, P Lio, and F Bagnoli. Inference on missing values in genetic networks using high-throughput data. In E Marchiori and JH Moore, editors, *EVOLUTIONARY COMPUTATION, MACHINE LEARNING AND DATA MINING IN BIOINFORMATICS, PROCEEDINGS*, volume 4973, pages 106–116, 2008.
- [805] P Liò and M Bishop. Modeling sequence evolution. *Methods Mol Biol*, 452:255–285, 2008.
- [806] A Kershenbaum, V Pappas, KW Lee, P Lio, B Sadler, and D Verma. A biologically-inspired manet architecture. *Proceedings of SPIE - The International Society for Optical Engineering*, 6981, Jun 2008.
- [807] A Kershenbaum, V Pappas, KW Lee, P Lio, B Sadler, and D Verma. A biologically-inspired manet architecture - art. no. 698106. In R Suresh, editor, *DEFENSE TRANSFORMATION AND NET-CENTRIC SYSTEMS 2008*, volume 6981, pages 98106–98106, 2008.

- [808] A Wilson, G Osee, R van der Wath, W Blanco-Bose, E Laurenti, C Dunant, P Lio, HR MacDonald, and A Trumpp. Haematopoietic stem cells reversibly switch from dormancy to self-renewal during homeostasis and repair. *SWISS MED WKLY*, 138:46S–46S, Apr 2008.
- [809] P Lio, M Brilli, and R Fani. Topological metrics in blast data mining: Plasmid and nitrogen-fixing proteins case studies. In M Elloumi, J Kung, M Linial, RF Murphy, K Schneider, and C Toma, editors, *BIOINFORMATICS RESEARCH AND DEVELOPMENT, PROCEEDINGS*, volume 13, pages 207–220, 2008.
- [810] P Lio, C Angelini, I DeFeis, V Nguyen, L Cutillo, and R va der Wath. Statistical issues for combining replicates and nearby species data and different omics. In *Proceedings The Art and Science of Statistical Bioinformatics The 27th Leeds Annual Statistical Research Workshop 15th - 17th July 2008*, pages 50–54, Leeds, 2008. Leeds, S. Barber, P.D. Baxter, A. Gusnanto & K.V. Mardia (eds) Leeds University Press.
- [811] P Lio and M Bishop. Modeling sequence evolution. *Methods Mol Biol.*, 452:255–285, 2008.
- [812] E Schwarz, FM Leweke, S Bahn, and P Lio. Combining molecular and physiological data of complex disorders. In M Elloumi, J Kung, M Linial, RF Murphy, K Schneider, and C Toma, editors, *BIOINFORMATICS RESEARCH AND DEVELOPMENT, PROCEEDINGS*, volume 13, pages 362–376, 2008.
- [813] Bio-inspired computing and communication, first workshop on bio-inspired design of networks, biowire 2007, cambridge, uk, april 2-5, 2007, revised selected papers. In P Liò, E Yoneki, J Crowcroft, and DC Verma, editors, *BIOWIRE*, volume 5151 of *Lecture Notes in Computer Science*. Springer, 2008.
- [814] RC van der Wath, E van der Wath, A Carapelli, F Nardi, F Frati, L Milanesi, and P Lio. Bayesian phylogeny on grid. In M Elloumi, J Kung, M Linial, RF Murphy, K Schneider, and C Toma, editors, *BIOINFORMATICS RESEARCH AND DEVELOPMENT, PROCEEDINGS*, volume 13, pages 404–416, 2008.
- [815] F Bagnoli, P Liò, and L Sguanci. Risk perception in epidemic modeling. *Phys Rev E Stat Nonlin Soft Matter Phys*, 76(6 Pt 1):061904, Dec 2007.
- [816] AT Lawniczak, P Lio, S Xie, and JY Xu. Wavelet spectral analysis of packet traffic near phase transition point from free flow to congestion in data network model. In *2007 CANADIAN CONFERENCE ON ELECTRICAL AND COMPUTER ENGINEERING, VOLS 1-3*, pages 364–367, 2007.
- [817] AT Lawniczak, S Xie, PP Liò, and J Xu. Study of packet traffic fluctuations near phase transition point from free flow to congestion in data network model. *Canadian Conference on Electrical and Computer Engineering*, pages 360–363, Dec 2007.
- [818] YE Lu, P Lio, and S Hand. Beta random projection. In *ISM WORKSHOPS 2007: NINTH IEEE INTERNATIONAL SYMPOSIUM ON MULTIMEDIA - WORKSHOPS, PROCEEDINGS*, pages 323–328, 2007.
- [819] M Brilli, R Fani, and P Liò. Current trends in the bioinformatic sequence analysis of metabolic pathways in prokaryotes. *Brief Bioinform*, 9(1):34–45, Jan 2008.

- [820] C Papetti, P Lio, L Ruber, T Patarnello, and R Zardoya. Antarctic fish mitochondrial genomes lack nd6 gene. *J MOL EVOL*, 65(5):519–528, Nov 2007.
- [821] R Fani, M Brilli, M Fondi, and P Lio. The role of gene fusions in the evolution of metabolic pathways: the histidine biosynthesis case. In *BMC EVOLUTIONARY BIOLOGY*, volume 7, 2007.
- [822] A Carapelli, P Lio, F Nardi, E van der Wath, and F Frati. Phylogenetic analysis of mitochondrial protein coding genes confirms the reciprocal paraphyly of hexapoda and crustacea. In *BMC EVOLUTIONARY BIOLOGY*, volume 7, 2007.
- [823] L Sguanci, F Bagnoli, and P Lio. Modeling hiv quasispecies evolutionary dynamics. In *BMC EVOLUTIONARY BIOLOGY*, volume 7, 2007.
- [824] EM Weston, AE Friday, and P Liò. Biometric evidence that sexual selection has shaped the hominin face. *PLoS One*, 2(8):e710, Aug 2007.
- [825] E van der Wath, L Moutsianas, R van der Wath, A Visagie, L Milanese, and P Lio. Grid methodology for identifying co-regulated genes and transcription factor binding sites. *IEEE T NANOBIOSCI*, 6(2):162–167, Jun 2007.
- [826] C Caretta-Cartozo, P De Los Rios, F Piazza, and P Lio. Bottleneck genes and community structure in the cell cycle network of s-pombe. *PLOS COMPUT BIOL*, 3(6):968–976, Jun 2007.
- [827] L Bianchi and P Lio. Forensic dna and bioinformatics. *BRIEF BIOINFORM*, 8(2):117–128, Mar 2007.
- [828] F Chen, V Archambault, A Kar, P Lio, PP D'Avino, R Sinka, K Lilley, ED Laue, P Deak, L Capalbo, and DM Glover. Multiple protein phosphatases are required for mitosis in drosophila. *CURR BIOL*, 17(4):293–303, Feb 2007.
- [829] P Liò, M Brilli, and R Fani. Phylogenetics and computational biology of multigene families. In *Structural Approaches to Sequence Evolution*, pages 191–205. Springer Berlin Heidelberg, 2007.
- [830] YE Lu, S Hand, and P Lio. Keyword searching in structured overlays via content distance addressing. In G Moro, S Bergamaschi, S Joseph, JH Morin, and AM Ouksel, editors, *Databases, Information Systems, and Peer-to-Peer Computing*, volume 4125, pages 259–272, 2007.
- [831] C Angelini, L Cutillo, I De Feis, R Van der Wath, and P Lio. Identifying regulatory sites using neighborhood species. In E Marchiori, JH Moore, and JC Rajapakse, editors, *Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, Proceedings*, volume 4447, pages 1–10, 2007.
- [832] C Caretta-Cartozo, P De Los Rios, F Piazza, and P Liò. Bottleneck genes and community structure in the cell cycle network of s. pombe. *PLoS Computational Biology*, 3(6):0968–0976, Jan 2007.
- [833] L Milanese, P Lio, and V Breton. Bioinformatics challenges in life science. In *IST-Africa 2007 Conference Proceedings, Paul Cunningham and Miriam Cunningham (Eds), IIMC International*

Information Management Corporation, 2007, ISBN: 1-905824-04-1. Maputo, Mozambique, 2007.

- [834] R Fani, D Caramelli, and P Liò. From prebiotic chemistry to the evolution of man: The first conference of the s.i.b.e. (italian society of evolutionary biology) in florence. *Rivista di Biologia - Biology Forum*, 99(3):357–360, Dec 2006.
- [835] M Brilli, R Fani, and P Lio. Motifscorer: using a compendium of microarrays to identify regulatory motifs. *BIOINFORMATICS*, 23(4):493–495, Feb 2007.
- [836] A Ambesi-Impiombato, M Bansal, P Liò, and D di Bernardo. Computational framework for the prediction of transcription factor binding sites by multiple data integration. *BMC Neurosci*, 7 Suppl 1(Suppl 1):S8, Oct 2006.
- [837] P Li and MJ Bishop. Nucleic acid and protein sequence analysis and bioinformatics. Wiley-VCH Verlag GmbH & Co. KGaA.
- [838] R Fani, M Brilli, and P Liò. Inference from proteobacterial operons shows piecewise organization: a reply to price et al. *J Mol Evol*, 63(4):577–580, Oct 2006.
- [839] R Fani, D Caramelli, and P Liò. [it happened... from prebiotic chemistry to human evolution. in florence, the first congress of s.i.b.e. september, 4-6, 2006]. *Riv Biol*, 99(3):357–360, 2006.
- [840] L Sguanci, P Lio', and F Bagnoli. The influence of risk perception in epidemics: a cellular agent model, Jul 2006.
- [841] F Bagnoli, P Lio, and L Sguanci. Modeling viral coevolution: Hiv multi-clonal persistence and competition dynamics. *PHYSICA A*, 366(1):333–346, Jul 2006.
- [842] L Sguanci, F Bagnoli, and P Lio. Mathematical model of hiv superinfection dynamics and r5 to x4 switch. Mar 2006. 21 pages, 14 figures.
- [843] L Sguanci, P Lio, and F Bagnoli. Modeling evolutionary dynamics of hiv infection. In C Priami, editor, *COMPUTATIONAL METHODS IN SYSTEMS BIOLOGY, PROCEEDINGS*, volume 4210, pages 196–211, 2006.
- [844] R Fani, D Caramelli, and P Lio. It happened... from prebiotic chemistry to human evolution. In *Rivista di biologia*, number 99, pages 357–360. Firenze, 2006.
- [845] YE Lu, S Hand, and P Lio. Keyword searching in hypercubic manifolds. In G Caronni, N Weiler, M Waldvogel, and N Shahmehri, editors, *Fifth IEEE International Conference on Peer-to-Peer Computing, Proceedings*, pages 150–151, 2005.
- [846] TMW Nye, P Lio, and WR Gilks. A novel algorithm and web-based tool for comparing two alternative phylogenetic trees. *BIOINFORMATICS*, 22(1):117–119, Jan 2006.
- [847] F Bagnoli, P Lio', and L Sguanci. Modeling viral coevolution: Hiv multi-clonal persistence and competition dynamics, Sep 2005.
- [848] A Carapelli, F Nardi, R Dallai, J Boore, P LiÒ, and F Frati. Relationships between hexapods and crustaceans based on four mitochondrial genes. In *Crustacean Issues*, pages 295–306. CRC Press, Apr 2005.

- [849] R Fani, M Brilli, and P Lio. The origin and evolution of operons: The piecewise building of the proteobacterial histidine operon. *J MOL EVOL*, 60(3):378–390, Mar 2005.
- [850] F Piazza and P Lio. Statistical analysis of simple repeats in the human genome. *PHYSICA A*, 347:472–488, Mar 2005.
- [851] P Lio. Phylogenetic and structural analysis of mitochondrial complex i proteins. In *GENE*, volume 345, pages 55–64, Jan 2005.
- [852] G Rustici, J Mata, K Kivinen, P Lio, CJ Penkett, G Burns, J Hayles, A Brazma, P Nurse, and J Bahler. Periodic gene expression program of the fission yeast cell cycle. *Nat Genet*, 36(8):809–17–809–17, 2004. 15195092 1061-4036 (Print) Comparative Study Journal Article Research Support, Non-U.S. Gov't.
- [853] MG Tadesse, M Vannucci, and P Lio. Identification of dna regulatory motifs using bayesian variable selection. *BIOINFORMATICS*, 20(16):2553–2561, Nov 2004.
- [854] P Lio and N Goldman. Phylogenomics and bioinformatics of sars-cov. *TRENDS MICROBIOL*, 12(3):106–111, Mar 2004.
- [855] P Lio and M Vannucci. Investigating the evolution and structure of chemokine receptors. In *GENE*, volume 317, pages 29–37, Oct 2003.
- [856] P Lio. Il genoma della sars. *Le Scienze Italian Edition of Scientific American*, June 2003(June 2003), Jun 2003.
- [857] P Liò. Dimensionality and dependence problems in statistical genomics. *Brief Bioinform*, 4(2):168–177, Jun 2003.
- [858] P Lio. Statistical bioinformatic methods in microbial genome analysis. *BIOESSAYS*, 25(3):266–273, Mar 2003.
- [859] P Lio. Wavelets in bioinformatics and computational biology: state of art and perspectives. *BIOINFORMATICS*, 19(1):2–9, Jan 2003.
- [860] N Skaer, D Pistillo, JM Gibert, P Lio, C Wulbeck, and P Simpson. Gene duplication at the achaete-scute complex and morphological complexity of the peripheral nervous system in diptera. *TRENDS GENET*, 18(8):399–405, Aug 2002.
- [861] P Lio. Investigating the relationship between genome structure, composition, and ecology in prokaryotes. *MOL BIOL EVOL*, 19(6):789–800, Jun 2002.
- [862] P Lio and N Goldman. Modeling mitochondrial protein evolution using structural information. *J MOL EVOL*, 54(4):519–529, Apr 2002.
- [863] P Liò and N Goldman. Modeling mitochondrial protein evolution using structural information. *J Mol Evol*, 54(4):519–529, Apr 2002.
- [864] P Lio. Una vita per le proteine. *Le Scienze Italian Edition of Scientific American*, February 2002(February 2002), Feb 2002.

- [865] P Lio. Structure and evolution of the histidine biosynthetic pathway. In M Brilli, P Lio, A Lazcano, and R Fani, editors, *Origins of Life and Evolution of the Biosphere*, volume 22, pages 488–488. Oaxaca, Mexico, Springer, 2002.
- [866] RF Renato Fani, SC Silvia Casadei, and P Lio. Origin and evolution of nif genes. In *NITROGEN FIXATION: FROM MOLECULES TO CROP PRODUCTIVITY*, volume 38, of *Current Plant Science and Biotechnology in Agriculture, 2002, Volume 38, Section III*, 177-178, DOI: 10.1007/0-306-47615-0_85, pages 177 – 178. 2002.
- [867] M Brilli, P Lio, A Lazcano, and R Fani. Evolution of tim barrel: Multiple gene elongation events in hisA. In *Origins of Life and Evolution of the Biosphere*, volume 22, pages 487–487. Oaxaca, Mexico, Springer, 2002.
- [868] T Massingham, LJ Davies, and P Lio. Analysing gene function after duplication. *BIOESSAYS*, 23(10):873–876, Oct 2001.
- [869] P Lio. Dal genoma al fisioma. Jul 2001.
- [870] S Whelan, P Lio, and N Goldman. Molecular phylogenetics: state-of-the-art methods for looking into the past. *TRENDS GENET*, 17(5):262–272, May 2001.
- [871] P Lio. Le nuove sfide della filogenesi molecolare. *Le Scienze Italian Edition of Scientific American*, February 2001(Febbraio 2001), Feb 2001.
- [872] M Vannucci and P Lio. Non-decimated wavelet analysis of biological sequences: applications to protein structure and genomics. *Sankhyā: The Indian Journal of Statistics, Series B*, 63b2:218–233, 2001.
- [873] P Bogani, A Simoni, P Lio, A Germinario, and M Buiatti. Molecular variation in plant cell populations evolving in vitro in different physiological contexts. *Genome*, 44(4):549–558, Aug 2001.
- [874] P Lio and M Vannucci. Finding pathogenicity islands and gene transfer events in genome data. *BIOINFORMATICS*, 16(10):932–940, Oct 2000.
- [875] E Hagelberg, N Goldman, P Lio, S Whelan, W Schiefenhover, JB Clegg, and DK Bowden. Evidence for mitochondrial dna recombination in a human population of island melanesia: correction. *P ROY SOC LOND B BIO*, 267(1452):1595–1596, Aug 2000.
- [876] P Lio. Siamo uomini non dna robot,. May 2000.
- [877] P Lio and M Vannucci. Wavelet change-point prediction of transmembrane proteins. *Bioinformatics*, 16(4):376–382, Apr 2000.
- [878] NS Thomas, J Wilkinson, P Lio, I Doull, NE Morton, and ST Holgate. Investigation of the genetic factors underlying asthma and atopy in outbred uk populations. *REV MAL RESPIR*, 17(1BIS):177–182, Feb 2000.
- [879] NS Thomas, J Wilkinson, P Lio, I Doull, NE Morton, and ST Holgate. [genetic factors involved in asthma and atopy. studies in british families]. *Rev Mal Respir*, 17(1 Pt 2):177–182, Feb 2000.

- [880] R Fani, R Gallo, and P Liò. Molecular evolution of nitrogen fixation: the evolutionary history of the *nifd*, *nifk*, *nife*, and *nifn* genes. *J Mol Evol*, 51(1):1–11, Jul 2000.
- [881] E Hagelberg, N Goldman, P Lió, S Whelan, W Schiefenhövel, JB Clegg, and DK Bowden. Evidence for mitochondrial dna recombination in a human population of island melanesia. *Proc Biol Sci*, 266(1418):485–492, Mar 1999.
- [882] E Hagelberg, M Kayser, M Nagy, L Roewer, H Zimdahl, M Krawczak, P Lió, and W Schiefenhövel. Molecular genetic evidence for the human settlement of the pacific: analysis of mitochondrial dna, y chromosome and hla markers. In *Philos Trans R Soc Lond B Biol Sci*, volume 354, pages 141–152. England, Jan 1999.
- [883] P Liò and N Goldman. Using protein structural information in evolutionary inference: trans-membrane proteins. *Mol Biol Evol*, 16(12):1696–1710, Dec 1999.
- [884] E Mori, P Liò, S Daly, G Damiani, B Perito, and R Fani. Molecular nature of rapd markers from *haemophilus influenzae* rd genome. *Res Microbiol*, 150(2):83–93, Mar 1999.
- [885] P Liò and N Goldman. Review: Models of molecular evolution and phylogeny. *Genome Research*, 8(12):1233–1244, Dec 1998.
- [886] P Liò and N Goldman. Models of molecular evolution and phylogeny. *Genome Res*, 8(12):1233–1244, Dec 1998.
- [887] F Bagnoli and P Lio'. Selection, mutations and codon usage in bacterial model, Aug 1998.
- [888] P Lio and S Ruffo. Searching for genomic constraints. *NUOVO CIMENTO D*, 20(1):113–127, Jan 1998.
- [889] P Liò, N Goldman, JL Thorne, and DT Jones3. Passml: combining evolutionary inference and protein secondary structure prediction. *Bioinformatics*, 14(8):726–733, 1998.
- [890] P Lio. Correlation methods for genomic constraints analysis. *Annals of Human Genetics*, 61(6):542, Dec 1997.
- [891] P Lio. Comparison of multipoint analyses for complex inheritance: lddm and asthma. *Annals of Human Genetics*, 61(6):541–542, Dec 1997.
- [892] R Fani, E Tamburini, E Mori, A Lazcano, P Liò, C Barberio, E Casalone, D Cavalieri, B Perito, and M Polsinelli. Paralogous histidine biosynthetic genes: evolutionary analysis of the *saccharomyces cerevisiae* *his6* and *his7* genes. *Gene*, 197(1-2):9–17, Sep 1997.
- [893] J Dewar, A Wheatley, J Wilkinson, ST Holgate, NS Thomas, P Lio, NE Morton, and IP Hall. Association of the *gln 27 beta(2)*-adrenoceptor polymorphism and ige variability in asthmatic families. In *CHEST*, volume 111, pages S78–S79, Jun 1997.
- [894] P Liò and NE Morton. Comparison of parametric and nonparametric methods to map oligogenes by linkage. *Proc Natl Acad Sci U S A*, 94(10):5344–5348, May 1997.
- [895] JC Dewar, J Wilkinson, A Wheatley, NS Thomas, I Doull, N Morton, P Lio, JF Harvey, SB Liggett, ST Holgate, and IP Hall. The glutamine 27 *beta2*-adrenoceptor polymorphism is

associated with elevated ige levels in asthmatic families. *J Allergy Clin Immunol*, 100(2):261–265, Aug 1997.

- [896] NE Morton and P Lio. Oligogenic linkage and map integration. In IH Pawlowitzki, JH Edwards, and EA Thompson, editors, *GENETIC MAPPING OF DISEASE GENES*, pages 17–21, 1997.
- [897] NS Thomas, J Wilkinson, P Lio, I Doull, NE Morton, and ST Holgate. Investigation of the genetic factors underlying asthma and atopy in outbred uk populations. In CS Hong, JT Choung, JH Chung, J Jang, TY Jang, KS Jung, YK Kim, BJ Lee, HR Lee, and CS Park, editors, *5TH WEST-PACIFIC ALLERGY SYMPOSIUM / 7TH KOREA-JAPAN JOINT ALLERGY SYMPOSIUM*, pages 81–86, 1997.
- [898] P Bogani, P Liò, MC Intrieri, and M Buiatti. A physiological and molecular analysis of the genus nicotiana. *Mol Phylogenet Evol*, 7(1):62–70, Feb 1997.
- [899] P Liò, A Politi, S Ruffo, and M Buiatti. Analysis of genomic patchiness of haemophilus influenzae and saccharomyces cerevisiae chromosomes. *J Theor Biol*, 183(4):455–469, Dec 1996.
- [900] P Liò, A Politi, M Buiatti, and S Ruffo. High statistics block entropy measures of dna sequences. *J Theor Biol*, 180(2):151–160, May 1996.
- [901] P Alifano, R Fani, P Liò, A Lazcano, M Bazzicalupo, MS Carlomagno, and CB Bruni. Histidine biosynthetic pathway and genes: structure, regulation, and evolution. *Microbiol Rev*, 60(1):44–69, Mar 1996.
- [902] P Lio. Long range properties of dna sequences. In Bellacicco, Vulpiani, and Koch, editors, *Collana Franco Angeli Editore*. Roma.
- [903] P Bogani, A Simoni, P Lio', A Scialpi, and M Buiatti. Genome flux in tomato cell clones cultured in vitro in different physiological equilibria. ii. a rapd analysis of variability. *Genome*, 39(5):846–853, Oct 1996.
- [904] F VICARIO, GG VENDRAMIN, P ROSSI, P LIO, and R GIANNINI. Allozyme, chloroplast dna and rapd markers for determining genetic-relationships between abies-alba and the relic population of abies nebrodensis. *THEOR APPL GENET*, 90(7-8):1012–1018, Jun 1995.
- [905] F Bagnoli and P Liò. Selection, mutations and codon usage in a bacterial model. *J Theor Biol*, 173(3):271–281, Apr 1995.
- [906] F Bagnoli, G Guasti, and P Lio. Translation optimization in bacteria: Statistical models. In M Peyrard, editor, *NONLINEAR EXCITATIONS IN BIOMOLECULES*, pages 405–411, 1995.
- [907] R Fani, C Bandi, M Bazzicalupo, G Damiani, F Di Cello, S Fancelli, L Gerace, A Grifoni, P Lio, and E Mori. Phylogenetic studies of the genus azospirillum. In *Related Microorganisms:: Genetics - Physiology - Ecology (NATO ASI Series / Ecological Sciences)*. Hungary, Springer Verlag, 1994.
- [908] R Fani, P Liò, and A Lazcano. Molecular evolution of the histidine biosynthetic pathway. *J Mol Evol*, 41(6):760–774, Dec 1995.

- [909] P Liò, M Bazzicalupo, A Grifoni, E Mori, and R Fani. Cloning and analysis of an azospirillum brasilense iteron and hsluv operon containing region. In *Azospirillum VI and Related Microorganisms*, pages 143–148. Springer Berlin Heidelberg, 1995.
- [910] P Liò, S Ruffo, and M Buiatti. Third codon g + c periodicity as a possible signal for an "internal" selective constraint. *J Theor Biol*, 171(2):215–223, Nov 1994.
- [911] R Fani, P Liò, I Chiarelli, and M Bazzicalupo. The evolution of the histidine biosynthetic genes in prokaryotes: a common ancestor for the hisa and hisf genes. *J Mol Evol*, 38(5):489–495, May 1994.
- [912] R Fani, A Grifoni, G Damiani, P Lio, and E Mori. Nucleotide sequence of azospirillum rapid markers. In *Azospirillum VI and Related Microorganisms:: Genetics - Physiology - Ecology (NATO ASI Series / Ecological Sciences)*. Springer Verlag, 1994.
- [913] P Lio. Physio-environmental sensing and live modeling. *interactive Journal of Medical Research (i-JMR)*, 2(1).

