

Publications in international peer reviewed conference papers and journals

1. Fondi et al, MeDuSa: A multi-draft based scaffolder. submitted Bioinformatics.
2. P Liò (2014) Computing Longevity: Insights from Controls. Formal Methods in Macro-Biology. Lecture Notes in Computer Science Volume 8738, 2014, pp 40-46
3. M Fondi, P Liò (2015) Genome-Scale Metabolic Network Reconstruction, Bacterial Pangenomics, Methods in Molecular Biology Volume 1231, 2015, pp 233-256
4. Felicetti, L., Femminella, M., Reali, G., Lio', P. (2014) Effect of Aging, Disease vs Health Conditions in the design of Nano-Communications in Blood Vessels Springer book on Modeling, Methodologies and Tools for Molecular and Nano-scale Communications.
5. Azad S, Lio P. (2014) Emerging trends of malaria-dengue geographical coupling in the Southeast Asia region. J Vector Borne Dis. 51(3):165-71.
6. Capobianco E. and Liò, P. (2014). Advances in translational biomedicine from systems approaches. Frontiers in Genetics, 14 August 2014 doi: 10.3389/fgene.2014.00273 (Editorial)
7. Pratanwanich, N. and Liò, P. (2014) Exploring the complexity of pathway-drug relationships using latent Dirichlet allocation. Computational Biology and Chemistry. in press.
8. Pratanwanich, N. and Liò, P. (2014) Who Wrote This? Textual Modeling with Authorship Attribution in Big Data. ICDM 2nd Workshop for High Dimensional Data Mining.
9. Moni MA, Liò P (2014). "comoR: a software for disease comorbidity risk assessment". Journal of Clinical Bioinformatics, 4(1):8, 2014.
10. Moni MA, Liò P (2014). "Network-based analysis of comorbidities risk during an infection: SARS and HIV case studies". BMC bioinformatics 15.1(2014):333.
11. Moni, MA, Haoming Xu, Liò, P (2014). "CytoCom: a Cytoscape app to visualise, query and analyse disease comorbidity networks". Bioinformatics (in press).
12. Moni MA, Liò P (2014). "How to build personalised multi-omics comorbidity profiles". (accepted with minor revision in Frontiers of Systems biology)

13. Moni, MA., Haoming Xu, Liò, P (2014). "Network regulised Cox Regression Model to predict survival and comorbidity of cancer". (Submitted to *Frontiers of Systems biology*)
14. Angione, C., Pratanwanich, N., & Lio, P. (2014, June 11). 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.
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16. Fernandes, P., Lio, P., & Milanesi, L. (2014, July 17-19). CHALLENGES IN BUILDING AN E-HEALTH INFRASTRUCTURE FOR P5 MEDICINE. In Proceedings of The International Conference on e-Health. Lisbon
17. Bartoszek, K., & Lio, P. (2014, May 14). A novel algorithm to reconstruct phylogenies using gene sequences and expression data. In *2014 6th International Conference on Bioinformatics and Biomedical Technology (ICBBT 2014)*. Gdansk.
18. Fondi, M., Maida, I., Perrin, E., Mellera, A., Mocali, S., Parrilli, E., ... Fani, R. (2014). Genome scale metabolic reconstruction and constraints-based modelling of the Antarctic bacterium *Pseudoalteromonas haloplanktis TAC125*. *Environ Microbiol*. doi:10.1111/1462-2920.12513
19. Taffi, M., Paoletti, N., Lio', P., Tesei, L., Pucciarelli, S., & Marini, M. (2014). Estimation and Modelling of PCBs Bioaccumulation in the Adriatic Sea Ecosystem. Retrieved from <http://arxiv.org/abs/1405.6384v1>
20. Petrov, V., Balasubramaniam, S., Lale, R., Moltchanov, D., Lio', P., & Koucheryavy, Y. (2014). Forward and Reverse coding for chromosome transfer in bacterial nanonetworks. *Nano Communication Networks*.
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22. Pratanwanich, N., & Lio', P. (2014). Pathway-based Bayesian inference of drug-disease interactions. *Mol Biosyst*, 10(6), 1538-1548. doi:10.1039/c4mb00014e
23. Shavit, Y., & Lio', P. (2014). Combining a wavelet change point and the Bayes factor for analysing chromosomal interaction data.. *Mol Biosyst*, 10(6), 1576-1585. doi:10.1039/c4mb00142g

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doi:10.1371/journal.pone.0088533
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doi:10.1016/j.ympev.2014.02.001
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