

Publications in international peer reviewed conference papers and journals

1. Shavit Y., Walker B., Lio' P (2015) Hierarchical block matrices as efficient representations of chromosome topologies and their application for 3C data integration. In press on Bioinformatics.
2. Angione C, Conway M. and Pietro Lio' (2015) Weighted integration of multi-omic layers of conditions in genome-scale models. Accepted in BMC Bioinformatics.
3. Capobianco E. and Liò, P. (2015). Electronic Health Systems: Golden Mine for Precision Medicine? The Journal of Precision Medicine (in press)
4. Claudio Angione and Pietro Lio' (2015) Predictive analytics of environmental adaptability in multi-omic network models. Scientific Reports Oct 20;5:15147. doi: 10.1038/srep15147.
5. S. Haider, Z. Lipinszki, M. R Przewloka, Y. Ladak, P.P. D'Avino, Y. Kimata, P. Lio and D. M. Glover (2015) DAPPER: A data-mining resource for protein-protein interactions. BioData Mining 2015, 8:30.
6. Bartocci E, Lio', P. Computational modeling, formal analysis and tools for systems biology. Plos Computational Biology, (in press).
7. Veličković P. Lio', P. (2015) Molecular multiplex network inference. Journal of Complex Networks (in press)
8. Shavit, Y., Merelli I, Milanese L. & Lio', P. (2015) How computer science can help in understanding the 3D genome architecture. Briefings in Bioinformatics, 2015, Brief Bioinform. Oct 3. pii: bbv085
9. Moni, MA, Haoming Xu, Liò, P (2015). Network regularised Cox regression and multiplex network models to predict disease comorbidities and survival of cancer. Computational Biology and Chemistry (in press).
10. Felicetti, L., Femminella, M., Reali, G., Lio', P. (2015) Applications of molecular communications to medicine: a survey. Nano Communication Networks (in press).
11. Conway, M, Angione, C., Lio' P. (2015) Iterative multi level calibration of metabolic networks. Current Bioinformatics. In press.
12. Angione C, Costanza J. , Carapezza G., Lio' P, Nicosia G. (2015) Multi-target analysis and design of mitochondrial metabolism. PLoS ONE 10(9): e0133825. doi:10.1371/journal.pone.0133825
13. Castellani et al, Lio' P. (2015) Systems medicine of inflammaging. Briefings in Bioinformatics, Aug 24. pii: bbv062.
14. Ascolani G., Occhipinti A., Lio' P. (2015) Modelling circulating tumour cells for personalised survival prediction in metastatic breast cancer. Plos Computational Biology May 15;11(5):e1004199. doi: 10.1371/journal.pcbi.1004199. eCollection 2015.
15. Angione C, Pratanwanich N., Lio' P. (2015) A hybrid of metabolic flux analysis and Bayesian factor modeling for multi-omics temporal pathway activation. ACS Synthetic Biology, 10.1021/sb5003407
16. Bosi, et al. MeDuSa: a multi-draft based scaffolder. (2015) Bioinformatics. 2015 Mar 25. pii: btv171 (pubmed/25810435).

17. Smedley et al. (2015) The BioMart Community Portal: an innovative alternative to large, centralized data repositories. *Nucleic Acids Research*, Apr 20. pii: gkv350.
18. Iuliano A., Occhipinti A, Angelini C., De Feis I. and Lio' P. (2015) Network-based survival analysis methods for pathway detection in cancer. *Lecture Notes in Computer Science LNCS 8623* (in press).
19. Boutorh A, Pratanwanich N, Guessoum A. and Lio' P. (2015) Drug repurposing by optimizing mining of genes target association. *Lecture Notes in Computer Science LNCS 8623* (in press).
20. Capobianco E. and Liò, P. (2015). Comorbidity Networks: beyond disease correlations. *The Journal of Complex Networks* , *jcomplexnetw* (2015) doi: 10.1093/comnet/cnu048
21. Moni MA, Liò P (2015). How to build personalised multi-omics comorbidity profiles. *Frontiers in Cell and Developmental Biology*, section *Systems Biology*. *Front. Cell Dev. Biol.* doi: 10.3389/fcell.2015.00028.
22. Moni, MA, Haoming Xu, Liò, P (2014). CytoCom: a Cytoscape app to visualise, query and analyse disease comorbidity networks. *Bioinformatics* 31:969-71.
23. P Liò (2014) Computing Longevity: Insights from Controls. *Formal Methods in Macro-Biology*. *Lecture Notes in Computer Science Volume 8738*, 2014, pp 40-46
24. M Fondi, P Liò (2015) Genome-Scale Metabolic Network Reconstruction, *Bacterial Pangenomics*, *Methods in Molecular Biology Volume 1231*, 2015, pp 233-256
25. Angione C, Costanza J. , Carapezza G., Lio' P, Nicosia G. (2015) Analysis and Design of Molecular Machines, *Theoretical Computer Science* (in press).
26. M Fondi, P Liò (2015) Genome-Scale Metabolic Network Reconstruction, *Bacterial Pangenomics*, *Methods in Molecular Biology Volume 1231*, 233-256
27. Di Stefano, A., Scata' M. , Lió, P. et al. (2015) Quantifying the Role of Homophily in Human Cooperation Using Multiplex Evolutionary Game Theory. *PLoS One*. 2015 Oct 23;10(10):e0140646. doi: 10.1371/journal.pone.0140646.
28. Alessandro Di Stefano, Aurelio La Corte, Pietro Lió , Marialisa Scatá (2015) Bio-Inspired ICT for Big Data Management in Healthcare. in *Intelligent Agents in Data-intensive Computing*, editors: Kołodziej, J., Correia, L., Manuel Molina, J. Springer.
29. Xiaofeng Lu , Pietro Lio , and Pan Hui A Content Dissemination Model for Mobile Internet to Minimize Load on Cellular Network Electronics, *Communications and Networks IV*, *Proceedings of the 4TH International Conference on Electronics, Communications and Networks*, 12 – 15 December 2014, Beijing, China Edited by Amir Hussain and Mirjana Ivanovic CRC Press 2015, Pages 289–294. Print ISBN: 978-1-138-02830-2
30. Angione C., Bartocci E., Bortolussi L., Lió P., Occhipinti A., Sanguinetti G., (2014) Bayesian Design for Whole Cell Synthetic Biology Models. *Proceedings HSB. Third International Workshop on Hybrid Systems Biology Vienna, Austria, July 23-24, 2014 at CAV 2014.*

31. Vitaly Petrov, Sasitharan Balasubramaniam, Rahmi Lale, Dmitri Moltchanov, Pietro Lio', Yevgeni Koucheryavy (2014) Forward and Reverse Coding for Chromosome Transfer in Bacterial Nanonetworks Nano Communication Networks 5: 1-2. March-April.
32. Angione, C., Pratanwanich, N. and Pietro Lió, P. A hybrid of multi-omics FBA and Bayesian factor modeling to identify pathway crosstalks. Proceedings IWBDA 2014.
33. 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.
34. 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)
35. Korhonen A., Guo Y, Yetisgen-Yildiz M., Stenius U., Narita M. and Lio' P. (2015) Improving Literature-Based Discovery with Text Mining Lecture Notes in Computer Science LNCS 8623
36. Shavit Y., Walker B., Lio' P (2015) Hierarchical block matrices as efficient representations of chromosome topologies and their application for 3C data integration. In press on *Bioinformatics*.
37. Angione C, Conway M. and Pietro Lio' (2015) Weighted integration of multi-omic layers of conditions in genome-scale models. Accepted in *BMC Bioinformatics*.
38. Bardozzo F, Lio P and Tagliaferri R, (2015) Multi omic oscillations in bacterial pathways. *IJCNN2015*, Dublin.
39. Hamey F., Shavit Y., Maciulyte V., Town C., Lio' P. and Tosi S. (2015) Automated Detection of Fluorescent Probes in Molecular Imaging. Lecture Notes in Computer Science LNCS 8623
40. I Merelli, F Tordini, M Drocco, M Aldinucci, P Liò, L Milanese (2015) Integrating Multi-omics features exploiting Chromosome Conformation Capture data. *Frontiers in genetics* Feb 11;6:40. doi: 10.3389/fgene.2015.00040. eCollection 2015.
41. M Fondi, P Liò (2015) Multi -omics and metabolic modelling pipelines: challenges and tools for systems microbiology. *Microbiological Research* Feb;171:52-64. doi: 10.1016/j.micres.2015.01.003. Epub 2015 Jan 7.
42. Shavit, Y., Hamey F. & Lio', P. (2014) FisHical: an R package for iterative FISH-based calibration of Hi-C data. *Bioinformatics* Jul 23. pii: btu491.
43. Shavit, Y., & Lio', P. (2014). Combining wavelet changepoint and Bayes Factor for analysing chromosomal interactions data. *Molecular BioSystems* 10(6):1576-85.
44. Taffi M., Paoletti N., Liò P., Pucciarelli S., Marini M. (2015) 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 04 Jun 2015 doi:10.1016/j.ecolmodel.2014.11.030 (Best Young Researcher Award at ISEM 2016).
45. Taffi, M., Paoletti, N., Angione, C., Pucciarelli, S., Marini, M., Liò, P. (2014) Bioremediation in marine ecosystems: a computational study combining

- ecological modelling and flux balance analysis. *Frontiers in Genetics, section Systems Biology*. 5: 319. Published online Sep 12, 2014. doi: 10.3389/fgene.2014.00319 (see also related editorial).
46. 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 *Proc. of Intl. Euromicro PDP 2015: Parallel Distributed and network-based Processing*, 2015.
 47. I. Merelli, P. Liò, L. Milanese (2014). Describing the genes social networks relying on chromosome conformation capture data. *EMBnet.journal*, 19:73-75, oct. 2013. ISSN 2226-6089.
 48. Bartoszek, K & Lio', P. (2014) A Novel algorithm to reconstruct phylogenies using gene frequencies and expression data. *Proceedings of 2014 International Conference on Bioinformatics and Biomedical Technology*. Gdansk 14-16 May, 2014.
 49. Pratanwanich, N. and Liò, P. (2014) Exploring the complexity of pathway-drug relationships using latent Dirichlet allocation. *Computational Biology and Chemistry*. 53:144-52. doi: 10.1016/j.compbiolchem.2014.08.019
 50. 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*.
 51. Moni, M.A. and Lio', P. (2014) Network-based analysis of comorbidities risk during an infection: SARS and HIV case studies. *BMC Bioinformatics* 2014, 15:333
 52. 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.
 53. 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.
 54. Felicetti, L., Femminella, M., Reali, G., Lio', P. Endovascular Mobile Sensor Network for Detecting Circulating Tumoral Cells. 9th International Conference on Body Area Networks. BODYNETS - 9th International Conference on Body Area Networks, September 29–October 1, 2014, London, <http://dx.doi.org/10.4108/icst.bodynets.2014.256917>
 55. L. Felicetti, M. Femminella, G. Reali, P. Lio', A Molecular Communication System in Blood Vessels for Tumor Detection, *ACM NANOCOM 2014*, Atlanta, Georgia, USA, May 13-14, 2014 - DOI: 10.1145/2619955.2619978
 56. L. Felicetti, M. Femminella, G. Reali, P. Lio', 2014 Book chapter Effect of Aging, Disease vs Health Conditions in the design of Nano-Communications in Blood Vessels, published in the Springer book "Modeling, Methodologies and Tools for Molecular and Nano-scale Communications", Springer Nanocom 2014

57. Moni M.A. and Liò, P. (2014). ComoR: a software for disease comorbidity risk assessment. *Journal of Clinical Bioinformatics* 2014, 4:8 doi:10.1186/2043-9113-4-8.
58. Pratanwanich, N. and Liò, P. (2014) Pathway-based Bayesian inference of drug-disease interactions. *Molecular BioSystems* Jun;10(6):1538-48. doi: 10.1039/c4mb00014e.
59. Ascolani, G. and Liò, P. (2014) Modeling TGF-beta in early stages of cancer tissue dynamics. *Plos One* 9(2):e88533
60. 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.
61. 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)
62. Pratanwanich, N. and Liò, P. (2014) Exploring the complexity of pathway-drug relationships using latent Dirichlet allocation. *Computational Biology and Chemistry*. in press.
63. 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*.
64. Moni MA, Liò P (2014). "comoR: a software for disease comorbidity risk assessment". *Journal of Clinical Bioinformatics*, 4(1):8, 2014.
65. 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.
66. Moni, MA, Haoming Xu, Liò, P (2014). "CytoCom: a Cytoscape app to visualise, query and analyse disease comorbidity networks". *Bioinformatics* (in press).
67. Moni MA, Liò P (2014). "How to build personalised multi-omics comorbidity profiles". (accepted with minor revision in *Frontiers of Systems biology*)
68. Moni, MA., Haoming Xu, Liò, P (2014). "Network regulated Cox Regression Model to predict survival and comorbidity of cancer". (Submitted to *Frontiers of Systems biology*)
69. 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 (IWBD A)*. Boston.

70. Angione, C., Bartocci, E., Bortolussi, L., Lio, P., Occhipinti, A., & Sanguinetti, G. (2014, July 23). Bayesian Design for Whole Cell Synthetic Biology Models. In *Proceedings of the Third International Workshop on Hybrid Systems Biology (HSB 2014)*. Vienna.
71. 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
72. 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.
73. 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
74. 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>
75. 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*.
76. Pratanwanich, N., & Lio', P. (2013). Bayesian Inference for Learning Between-Pathway Network: A New Tool for Studying Drug-Disease Interactions. In *HUMAN HEREDITY* Vol. 76 (pp. 99).
77. Pratanwanich, N., & Lio', P. (2014). Pathway-based Bayesian inference of drug-disease interactions. *Mol Biosyst*, 10(6), 1538-1548. doi:10.1039/c4mb00014e
78. 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
79. Ascolani, G., & Lio', P. (2014). Modeling TGF- β in early stages of cancer tissue dynamics.. *PLoS One*, 9(2), e88533. doi:10.1371/journal.pone.0088533
80. Nardi, F., Lio', P., Carapelli, A., & Frati, F. (2014). MtPAN(3): site-class specific amino acid replacement matrices for mitochondrial proteins of Pancrustacea and Collembola. *Mol Phylogenet Evol*, 75, 239-244. doi:10.1016/j.ympev.2014.02.001

81. Bianchi, L., Fernandes, P., & Lio, P. (2013). 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: Libreria universitaria. Retrieved from <http://libreriauniversitaria.it/>
82. Angione, C., Carapezza, G., Costanza, J., Lio, P., & Nicosia, G. (2013). The Role of the Genome in the Evolution of the Complexity of Metabolic Machines. In T. Gilbert, M. Kirkilionis, & G. Nicoli (Eds.), *Proceedings of the European Conference on Complex Systems 2012* (pp. 1063-1070). Bruxelles: Springer.
83. Lio, P., Iacovella, L., Bianchi, L., & Nguyen, V. (2013). Information Filtering and Learning: From Heuristics to Social Eudaimonia. In T. Gilbert, M. Kirkilionis, & G. Nicoli (Eds.), *Proceedings of the European Conference on Complex Systems 2012* (pp. 1051-1057). Bruxelles: Springer.
84. Bansal, A., Azad, S., & Lio, P. (2013). Malaria Incidence Forecasting and Its Implication to Intervention. In T. Gilbert, M. Kirkilionis, & G. Nicoli (Eds.), *Proceedings of the European Conference on Complex Systems 2012* (pp. 919-926). Bruxelles: Springer.
85. Fondi, M., Orlandini, V., Perrin, E., Maida, I., Bosi, E., Papaleo, M. C., . . . Fani, R. (2014). Draft genomes of three Antarctic Psychrobacter strains producing antimicrobial compounds against Burkholderia cepacia complex, opportunistic human pathogens.. *Mar Genomics*, *13*, 37-38. doi:10.1016/j.margen.2013.12.009
86. Iacovella, L., & Lio, P. (2013). Speeding up the transition to collective awareness. *2013 IEEE International Conference on Communications Workshops, ICC 2013*, 220-224.
87. Angione, C., Carapezza, G., Costanza, J., Lio, P., & Nicosia, G. (2013). Rational design of organelle compartments in cells. *EMBnet journal*, *18*(B), 20-22.
88. Angione, C., Carapezza, G., Costanza, J., Lio, P., & Nicosia, G. (2013). Multi objective design for bacterial communication networks. *2013 IEEE International Conference on Communications Workshops, ICC 2013*, 813-817.
89. Lu, X., Lio, P., Hui, P., & Jin, H. (2013). A Location Prediction Algorithm for Mobile Communications Using Directional Antennas. *INTERNATIONAL JOURNAL OF DISTRIBUTED SENSOR NETWORKS*. doi:10.1155/2013/418606
90. Angione, C., Carapezza, G., Costanza, J., Lio, P., & Nicosia, G. (2013). Pareto optimality in organelle energy metabolism analysis.. *IEEE/ACM Trans Comput Biol Bioinform*, *10*(4), 1032-1044. doi:10.1109/TCBB.2013.95

91. Angione, C., Carapezza, G., Costanza, J., Lio', P., & Nicosia, G. (2013). Design and strain selection criteria for bacterial communication networks. *Nano Communication Networks*, 4(4), 155-163.
92. Moni, M. A., Mariani, S., Poli, G., Lio, P., & Vicenzi, E. (2013). Differential impacts of R5 vs. X4 HIV-1 on the transcriptome of primary CD4(+) T cells. *RETROVIROLOGY*, 10, S39.
93. Castiglione, F., Tieri, P., De Graaf, A., Franceschi, C., Lio', P., Van Ommen, B., . . . Ernst, M. (2013). The onset of type 2 diabetes: proposal for a multi-scale model. *JMIR Res Protoc*, 2(2), e44. doi:10.2196/resprot.2854
94. Taffi, M., Paoletti, N., Lio', P., Tesei, L., Merelli, E., & Marini, M. (2013). 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.
95. Di Stefano, A., La Corte, A., Leotta, M., Lio', P., & Scat', M. (2013). It measures like me: An IoTs algorithm in WSNs based on heuristics behavior and clustering methods. *Ad Hoc Networks*, 11(8), 2637-2647.
96. Lio', P. (2013). Methodologies for Systems Medicine: Time to Join the Forces of Bioengineering and Bioinformatics.. In P. Fernandes, J. SolÈ-Casals, A. L. N. Fred, & H. Gamboa (Eds.), *BIOINFORMATICS* (pp. 1S-27). SciTePress.
97. Merelli, I., Lio', P., & Milanese, L. (2013). NuChart: An R Package to Study Gene Spatial Neighbourhoods with Multi-Omics Annotations. *PLoS ONE*, 8(9).
98. Xiaofeng, L., Pan, H., & Lio, P. (2013). Offloading Mobile Data from Cellular Networks Through Peer-to-Peer WiFi Communication: A Subscribe-and-Send Architecture. *CHINA COMMUNICATIONS*, 10(6), 35-46.
99. Angione, C., Costanza, J., Carapezza, G., LiO', P., & Nicosia, G. (2013). A design automation framework for computational bioenergetics in biological networks.. *Mol Biosyst*, 9(10), 2554-2564. doi:10.1039/c3mb25558a
100. Capobianco, E., & Lio', P. (2013). Comorbidity: a multidimensional approach. *Trends in Molecular Medicine*.
101. Angione, C., Costanza, J., Carapezza, G., Lio', P., & Nicosia, G. (2013). Pareto epsilon-dominance and identifiable solutions for BioCAD modeling. *Proceedings - Design Automation Conference*.

102. Lio, P. (2013). Pathways to P4 medicine. *BIOINFORMATICS 2013 - Proceedings of the International Conference on Bioinformatics Models, Methods and Algorithms*, IS15-IS20.
103. Moni, M. A., Lio', P., & Milanesi, L. (2013). 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*, 196-201.
104. Balasubramaniam, S., Ben-Yehuda, S., Pautot, S., Jesorka, A., Lio', P., & Koucheryavy, Y. (2013). A review of experimental opportunities for molecular communication. *Nano Communication Networks*, 4(2), 43-52.
105. Carapezza, G., Umeton, R., Costanza, J., Angione, C., Stracquadanio, G., Papini, A., . . . Nicosia, G. (2013). Efficient behavior of photosynthetic organelles via Pareto optimality, identifiability, and sensitivity analysis.. *ACS Synth Biol*, 2(5), 274-288. doi:10.1021/sb300102k
106. Brillì, M., Lio, P., Lacroix, V., & Sagot, M. F. (2013). Short and long-term genome stability analysis of prokaryotic genomes.. *BMC Genomics*, 14, 309. doi:10.1186/1471-2164-14-309
107. Castiglione, F., Diaz, V., Gaggioli, A., Lio, P., Mazza, C., Merelli, E., . . . von Ammon, R. (2013). Physio-Environmental Sensing and Live Modeling. *JOURNAL OF MEDICAL INTERNET RESEARCH*, 15(1). doi:10.2196/ijmr.2092
108. Aldinucci, M., Bracciali, A., Lio', P., Sorathiya, A., & Torquati, M. (2010). StochKit-FF: Efficient Systems Biology on Multicore Architectures.. In M. R. Guarracino, F. Vivien, J. L. Trff, M. Cannataro, M. Danelutto, A. Hast, . . . M. Alexander (Eds.), *Euro-Par Workshops* Vol. 6586 (pp. 167-175). Springer. doi:10.1007/978-3-642-21878-1_21
109. Coello, C. A. C., Greensmith, J., Krasnogor, N., Lio', P., Nicosia, G., & Pavone, M. (Eds.) (2012). Artificial Immune Systems - 11th International Conference, ICARIS 2012, Taormina, Italy, August 28-31, 2012. Proceedings. In *ICARIS* Vol. 7597. Springer. doi:10.1007/978-3-642-33757-4
110. Bartocci, E., Lio', P., Merelli, E., & Paoletti, N. (2012). Multiple Verification in Complex Biological Systems: The Bone Remodelling Case Study.. *T. Comp. Sys. Biology*, 14, 53-76. doi:10.1007/978-3-642-35524-0_3
111. Angione, C., Lio', P., & Nicosia, G. (2012). How to Compute with Metabolism in Bacteria?. *ERCIM News*, 2012.

112. Lio', P., Nicosia, G., & Stibor, T. (Eds.) (2011). Artificial Immune Systems - 10th International Conference, ICARIS 2011, Cambridge, UK, July 18-21, 2011. Proceedings. In *ICARIS Vol. 6825*. Springer.
doi:10.1007/978-3-642-22371-6
113. Lio', P., Merelli, E., & Paoletti, N. (2012). Disease processes as hybrid dynamical systems. *EPTCS 92, 2012*, pp. 152-166.
doi:10.4204/EPTCS.92.11
114. Leung, I. X. Y., Chan, S. Y., Hui, P., & Lio', P. (2011). Intra-City Urban Network and Traffic Flow Analysis from GPS Mobility Trace.
<http://arxiv.org/abs/1105.5839v1>
115. Lio', P., Bianchi, L., Nguyen, V., & Kitchovich, S. (2013). Risk Perception, Heuristics and Epidemic Spread. In P. Manfredi, & A. D'Onofrio (Eds.), *Modeling the Interplay Between Human Behavior and the Spread of Infectious Diseases* (pp. 139-152).
116. Shavit, Y., & Lio', P. (2013). CytoHiC: a cytoscape plugin for visual comparison of Hi-C networks.. *Bioinformatics*, 29(9), 1206-1207.
doi:10.1093/bioinformatics/btt120
117. Balasubramaniam, S., & Lio', P. (2013). Multi-hop conjugation based bacteria nanonetworks.. *IEEE Trans Nanobioscience*, 12(1), 47-59.
doi:10.1109/TNB.2013.2239657
118. Vicenzi, E., Lio', P., & Poli, G. (2013). The puzzling role of CXCR4 in human immunodeficiency virus infection.. *Theranostics*, 3(1), 18-25.
doi:10.7150/thno.5392
119. Costanza, J., Carapezza, G., Angione, C., Lio', P., & Nicosia, G. (2012). 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.
120. Lio', P., Paoletti, N., Moni, M. A., Atwell, K., Merelli, E., & Viceconti, M. (2012). Modelling osteomyelitis.. *BMC Bioinformatics*, 13 Suppl 14, S12.
doi:10.1186/1471-2105-13-S14-S12
121. Costanza, J., Carapezza, G., Angione, C., Lio', P., & Nicosia, G. (2012). Robust design of microbial strains.. *Bioinformatics*, 28(23), 3097-3104.
doi:10.1093/bioinformatics/bts590
122. Haider, S., Cordeddu, L., Robinson, E., Movassagh, M., Siggins, L., Vujic, A., . . . Foo, R. (2012). The landscape of DNA repeat elements in human heart failure.. *Genome Biol*, 13(10), R90. doi:10.1186/gb-2012-13-10-r90

123. Peng, C., Jin, X., Wong, K. C., Shi, M., & LiO', P. (2012). Correction: Collective Human Mobility Pattern from Taxi Trips in Urban Area.. *PLoS One*, 7(8). doi:10.1371/annotation/f0d48839-ed4b-4cb2-822a-d449a6b4fa5d
124. Lio', P., Angelini, C., De Feis, I., & Nguyen, V. A. (2012). Statistical approaches to use a model organism for regulatory sequences annotation of newly sequenced species.. *PLoS One*, 7(9), e42489. doi:10.1371/journal.pone.0042489
125. Paoletti, N., Lio', P., Merelli, E., & Viceconti, M. (2012). Multilevel computational modeling and quantitative analysis of bone remodeling.. *IEEE/ACM Trans Comput Biol Bioinform*, 9(5), 1366-1378. doi:10.1109/TCBB.2012.51
126. Xiaofeng, L., Hu, P., & Lio, P. (2012). High Delivery Performance Opportunistic Routing Scheme for Delay Tolerant Networks. *CHINA COMMUNICATIONS*, 9(6), 145-153. Retrieved from
127. Lu, X. F., Towsley, D., Lio, P., & Xiong, Z. (2012). An adaptive directional MAC protocol for ad hoc networks using directional antennas. *Science China Information Sciences*, 55(6), 1360-1371.
128. Massaro, E., Bagnoli, F., Guazzini, A., & LiO', P. (2012). Information dynamics algorithm for detecting communities in networks. *Communications in Nonlinear Science and Numerical Simulation*, 17(11), 4294-4303.
129. Laise, P., Fanelli, D., Lio, P., & Arcangeli, A. (2012). Modeling TGF-beta signaling pathway in epithelial-mesenchymal transition. *AIP ADV*, 2(1), . doi:10.1063/1.3697962
130. Peng, C., Jin, X., Wong, K. C., Shi, M., & LiO', P. (2012). Collective human mobility pattern from taxi trips in urban area.. *PLoS One*, 7(4), e34487. doi:10.1371/journal.pone.0034487
131. Lu, X., Xin, Y., & Lio, P. (2011). 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*, 488-492.
132. Lio', P., & Balasubramaniam, S. (2012). Opportunistic routing through conjugation in bacteria communication nanonetwork. *Nano Communication Networks*, 3(1), 36-45.
133. Lu, X., Hui, P., & Lio', P. (2011). Evolving model of opportunistic routing in delay tolerant networks. *Proceedings - 2011 7th International Conference on Mobile Ad-hoc and Sensor Networks, MSN 2011*, 276-281.

134. Merelli, E., Paoletti, N., & Lio, P. (2011). Methodological Bridges for Multi-Level Systems. In E. Giacobino, & R. Pfeifer (Eds.), *Procedia Computer Science* Vol. 7 (pp. 180-182). Budapest: Elsevier.
135. Khoo, W. M., & Lio', P. (2011). Unity in diversity: Phylogenetic-inspired techniques for reverse engineering and detection of malware families. *Proceedings - 1st SysSec Workshop, SysSec 2011*, 3-10.
136. Nazri, A., & Lio', P. (2012). Investigating meta-approaches for reconstructing gene networks in a mammalian cellular context.. *PLoS One*, 7(1), e28713. doi:10.1371/journal.pone.0028713
137. Umeton, R., Stracquadanio, G., Papini, A., Costanza, J., Lio', P., & Nicosia, G. (2012). Identification of sensitive enzymes in the photosynthetic carbon metabolism.. *Adv Exp Med Biol*, 736, 441-459. doi:10.1007/978-1-4419-7210-1_26
138. Movassagh, M., Choy, M. K., Knowles, D. A., Cordeddu, L., Haider, S., Down, T., Lio', P., Foo, R. S. (2011). Distinct epigenomic features in end-stage failing human hearts.. *Circulation*, 124(22), 2411-2422. doi:10.1161/CIRCULATIONAHA.111.040071
139. Lio', P., & Sasitharan Balasubramaniam, S. B. (2011). Opportunistic routing through conjugation in bacteria communication nanonetwork. *Nano Communication Networks*, 2(October 2011). doi:10.1016/j.nancom.2011.10.003
140. Bagnoli, F., & Lio', P. (2011). HOW THE MUTATIONAL-SELECTION INTERPLAY ORGANIZES THE FITNESS LANDSCAPE. *J NONLINEAR MATH PHY*, 18, 265-286. doi:10.1142/S1402925111001532
141. Lio', P., & Verma, D. (2011). *Biologically Inspired Networking and Sensing*. Medical Info Science Reference.
142. Balasubramaniam, S., Leibnitz, K., Lio', P., Botvich, D., & Murata, M. (2011). Biological Principles for Future Internet Architecture Design. *IEEE COMMUN MAG*, 49(7), 44-52.
143. Yoneki, E., Crowcroft, J., Lio', P., Walton, N., Vojnovic, M., & Whitaker, R. (2011). Message from the Workshop on the Future of Social Networking. *COMPUT COMMUN REV*, 41(3), 14-18. doi:10.1145/2002250.2002254
144. Giampieri, E., Remondini, D., de Oliveira, L., Castellani, G., & Lio', P. (2011). Stochastic analysis of a miRNA-protein toggle switch.. *Mol Biosyst*, 7(10), 2796-2803. doi:10.1039/c1mb05086a
145. Lio', P., Merelli, E., Paoletti, N., & Viceconti, M. (2011). A combined process algebraic and stochastic approach to bone remodeling. *Electronic Notes in Theoretical Computer Science*, 277(1), 41-52.

146. Gilks, W. R., Nye, T. M. W., & Lio', P. (2011). A Variance-Components Model for Distance-Matrix Phylogenetic Reconstruction. *STAT APPL GENET MOL*, 10(1), . doi:10.2202/1544-6115.1574
147. Schwarz, E., Whitfield, P., Nahnsen, S., Wang, L., Major, H., Leweke, F. M., Lio' P. . . Bahn, S. (2011). Alterations of primary fatty acid amides in serum of patients with severe mental illness.. *Front Biosci (Elite Ed)*, 3, 308-314. Retrieved from <http://www.ncbi.nlm.nih.gov/pubmed/21196311>
148. Balocco, C., & Lio', P. (2011). Assessing ventilation system performance in isolation rooms. *ENERG BUILDINGS*, 43(1), 246-252. doi:10.1016/j.enbuild.2010.09.020
149. Kitchovitch, S., & Lio', P. (2011). Community structure in social networks: applications for epidemiological modelling.. *PLoS One*, 6(7), e22220. doi:10.1371/journal.pone.0022220
150. Umeton, R., Stracquadanio, G., Sorathiya, A., Papini, A., Lio', P., & Nicosia, G. (2011). Design of robust metabolic pathways. *Proceedings - Design Automation Conference*, 747-752.
151. Song, Y., & Lio', P. (2011). Epileptic EEG detection via a novel pattern recognition framework. *5th International Conference on Bioinformatics and Biomedical Engineering, iCBBE 2011*.
152. Lio', P., Merelli, E., & Paoletti, N. (2011). Multiple verification in computational modeling of bone pathologies. In *EPTCS Vol. 67* (pp. 82-96). Aachen, Germany <http://combio.abo.fi/compmod11/>.
153. Paoletti, N., Lio', P., Merelli, E., & Viceconti, M. (2011). Osteoporosis: A multiscale modeling viewpoint. *Proceedings of the 9th International Conference on Computational Methods in Systems Biology, CMSB'11*, 183-193.
154. Van Der Wath, R. C., Van Der Wath, E. C., & Lio', P. (2011). 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*, 311-317.
155. Lio', P., & Verma, D. (2011). Biologically inspired networking and sensing: Algorithms and architectures. *IEEE Network*, 24, 4. doi:10.1109/MNET.2010.5464220.
156. Aldinucci, M., Bracciali, A., Lio', P., Sorathiya, A., & Torquati, M. (2011). 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.

157. Hebenstreit, D., Gu, M., Haider, S., Turner, D. J., Lio', P., & Teichmann, S. A. (2011). EpiChIP: gene-by-gene quantification of epigenetic modification levels.. *Nucleic Acids Res*, 39(5), e27. doi:10.1093/nar/gkq1226
158. Sorathiya, A., Bracciali, A., & Lio', P. (2010). An integrated modelling approach for R5-X4 mutation and HAART therapy assessment. *SWARM INTELL-US*, 4(4), 319-340. doi:10.1007/s11721-010-0046-4
159. Lio', P., Guazzini, A., Passarella, A., & Conti, M. (2010). Modeling perisaccadic time perception. *Journal of Biomedical Science and Engineering*, 3(12), 1133-1142. doi:10.4236/jbise.2010.312147
160. Brilli, M., Fani, R., & Lio', P. (2010). Bioinformatics of gene families. In U. Bastolla, M. Porto, E. Roman, & M. Vendruscolo (Eds.), *Structural Approaches to Sequence Evolution* (pp. 368 pages).
161. Botta, M., Haider, S., Leung, I. X., Lio', P., & Mozziconacci, J. (2010). Intra- and inter-chromosomal interactions correlate with CTCF binding genome wide.. *Mol Syst Biol*, 6, 426. doi:10.1038/msb.2010.79
162. Papini, A., Mosti, S., Lio, P., & Haider, S. (2010). BIOLIP, a biotechnology-oriented database of oil content in plants, algae, fungi and cyanobacteria. In *JOURNAL OF BIOTECHNOLOGY* Vol. 150 (pp. S204-S205). doi:10.1016/j.jbiotec.2010.09.012
163. Papini, A., Nicosia, G., Stracquadanio, G., Lio', P., & Umeton, R. (2010). Key Enzymes for the Optimization of CO₂ Uptake and Nitrogen Consumption in the C-3 Photosynthetic Carbon Metabolism. In *JOURNAL OF BIOTECHNOLOGY* Vol. 150 (pp. S525-S526). doi:10.1016/j.jbiotec.2010.09.846
164. Lu, X. F., Wicker, F. D., Towsley, D., Xiong, Z., & Lio', P. (2010). Detection Probability Estimation of Directional Antennas and Omni-Directional Antennas. *WIRELESS PERS COMMUN*, 55(1), 51-63. doi:10.1007/s11277-009-9785-1
165. Emiliani, G., Fondi, M., Lio', P., & Fani, R. (2010). Evolution of Metabolic Pathways and Evolution of Genomes. In A. Loy (Ed.), *Geomicrobiology* (pp. 485 pages). Springer Verlag.
166. Balocco, C., & Lio', P. (2010). Modelling infection spreading control in a Hospital isolation room. *Journal of Biomedical Science and Engineering*, 3(7), 653-663. doi:10.4236/jbise.2010.37089

167. Lio', P., & Brillì, M. (2010). Transcription factors and gene regulatory networks. In M. Buchanan, G. Caldarelli, & P. D. L. Rios (Eds.), *Networks in Cell Biology* (pp. 271 pages). Cambridge Univ Pr.
168. Lio', P., & Song, Y. (2010). 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. doi:10.4236/jbise.2010.36078
169. Lio', P., & Verma, D. (2010). Biologically Inspired Networking. *IEEE NETWORK*, 24(3), 4.
170. Brillì, M., & Lio', P. (2010). The structural and dynamical properties of biological systems. In S. Boccaletti, V. Latora, & Y. Moreno (Eds.), *Handbook on Biological Networks* (pp. 441 pages). World Scientific Pub Co Inc.
171. Cheng, T. M., Lu, Y. E., Guest, P. C., Rahmoune, H., Harris, L. W., Wang, L., Lio', P. . . Bahn, S. (2010). Identification of targeted analyte clusters for studies of schizophrenia.. *Mol Cell Proteomics*, 9(3), 510-522. doi:10.1074/mcp.M900372-MCP200
172. Song, Y., Azad, S., & Lio', P. (2010). 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*, 436-441.
173. Sorathiya, A., Bracciali, A., & Lio', P. (2010). An integrated modelling approach for R5-X4 mutation and HAART therapy assessment. *Swarm Intelligence*, 1-22.
174. Stracquadanio, G., Umeton, R., Papini, A., Lio, P., & Nicosia, G. (2010). Analysis and optimization of C3 photosynthetic carbon metabolism. *10th IEEE International Conference on Bioinformatics and Bioengineering 2010, BIBE 2010*, 44-51.
175. Guazzini, A., Lio', P., Bagnoli, F., Passarella, A., & Conti, M. (2010). Cognitive network dynamics in chatlines. In *ICCS 2010 - INTERNATIONAL CONFERENCE ON COMPUTATIONAL SCIENCE, PROCEEDINGS* Vol. 1 (pp. 2349-2356). doi:10.1016/j.procs.2010.04.265
176. Guazzini, A., Lio', P., Bagnoli, F., Passarella, A., & Conti, M. (2010). Cognitive network dynamics in chatlines. *Procedia Computer Science*, 1(1), 2355-2362.
177. Angelini, C., De Feis, I., Nguyen, V. A., Van Der Wath, R., & Lio', P. (2010). 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.

178. Nguyen, V. A., & Lio', P. (2010). Filling in the gaps of biological network. In S. Do'eroski, S. Rogers, & G. Sanguinetti (Eds.), *Machine Learning in Systems Biology, Proceedings of the Fourth International Workshop Edinburgh, Scotland October 15-16, 2010* (pp. 147-149). Edinburgh.
179. Xie, S., Lawniczak, A. T., Song, Y., & Lio', P. (2010). 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*, 337-342.
180. Xie, S., Lawniczak, A. T., & Lio', P. (2010). Features extraction via wavelet kernel PCA for data classification. *Proceedings of the 2010 IEEE International Workshop on Machine Learning for Signal Processing, MLSP 2010*, 438-443.
181. Sorathiya, A., Bracciali, A., & Lio', P. (2010). Formal reasoning on qualitative models of coinfection of HIV and Tuberculosis and HAART therapy.. *BMC Bioinformatics*, 11 Suppl 1, S67. doi:10.1186/1471-2105-11-S1-S67
182. Aldinucci, M., Bracciali, A., & Lio', P. (2010). Formal Synthetic Immunology. *Ercim News*, 82, 40-41.
183. Chan, T. M., Leung, K. S., Lee, K. H., & Lio', P. (2010). Generic Spaced DNA Motif Discovery Using Genetic Algorithm. In *2010 IEEE CONGRESS ON EVOLUTIONARY COMPUTATION (CEC)* (pp.).
184. Lio', P., & Verma, D. (2010). Guest Editorial: Biologically inspired networking. *IEEE Network*, 24(3), 4.
185. Bartoszek, K., Lio', P., & Sorathiya, A. (2010). INFLUENZA DIFFERENTIATION AND EVOLUTION. In A. T. Lawniczak, D. Makowiec, & B. N. Di Stefano (Eds.), *SUMMER SOLSTICE 2009 INTERNATIONAL CONFERENCE ON DISCRETE MODELS OF COMPLEX SYSTEMS* Vol. 3 (pp. 417-452).
186. Pappas, V., Verma, D. C., & Lio', P. (2010). Morphogenesis in computer networks. *33rd IEEE Sarnoff Symposium 2010, Conference Proceedings*.
187. Kitchovitch, S., & Lio, P. (2010). Risk perception and disease spread on social networks. In *ICCS 2010 - INTERNATIONAL CONFERENCE ON COMPUTATIONAL SCIENCE, PROCEEDINGS* Vol. 1 (pp. 2339-2348). doi:10.1016/j.procs.2010.04.264 *Procedia Computer Science*, 1(1), 2345-2354.

188. Ostilli, M., Yoneki, E., Leung, I. X. Y., Mendes, J. F. F., Lio', P., & Crowcroft, J. (2010). Statistical mechanics of rumour spreading in network communities. In *ICCS 2010 - INTERNATIONAL CONFERENCE ON COMPUTATIONAL SCIENCE, PROCEEDINGS* Vol. 1 (pp. 2325-2333). doi:10.1016/j.procs.2010.04.262
189. Milanesi, L., Romano, P., Castellani, G., Remondini, D., & Lio', P. (2009). Trends in modeling Biomedical Complex Systems. *BMC BIOINFORMATICS*, 10, . doi:10.1186/1471-2105-10-S12-11
190. Fondi, M., Emiliani, G., Lio', P., Gribaldo, S., & Fani, R. (2009). The evolution of histidine biosynthesis in archaea: insights into the his genes structure and organization in LUCA. *J Mol Evol*, 69(5), 512-526. doi:10.1007/s00239-009-9286-6
191. Bianchi, L., & Lio', P. (2009). La legge e il DNA. *Le Scienze, Italian Edition Scientific American*, (September 2009). Retrieved from <http://www.lescienze.it/>
192. Nguyen, V. A., & Lio', P. (2009). Measuring similarity between gene expression profiles: a Bayesian approach. In *BMC GENOMICS* Vol. 10 (pp.). doi:10.1186/1471-2164-10-S3-S14
193. Brilli, M., Fondi, M., Lio', P., & Fani, R. (2009). The Origin and Evolution of Nitrogen Fixation Genes. *ORIGINS LIFE EVOL B*, 39(3-4), 310-311.
194. Wilson, A., Laurenti, E., Oser, G., van der Wath, R. C., Blanco-Bose, W., Jaworski, M., Lio', P. . . Trumpp, A. (2009). Hematopoietic Stem Cells Reversibly Switch from Dormancy to Self-Renewal during Homeostasis and Repair (vol 135, pg 1118, 2008). *CELL*, 138(1), 209. doi:10.1016/j.cell.2009.06.020
195. Lee, U., Magistretti, E., Gerla, M., Bellavista, P., Lio', P., & Lee, K. W. (2009). Bio-inspired multi-agent data harvesting in a proactive urban monitoring environment. *AD HOC NETW*, 7(4), 725-741. doi:10.1016/j.adhoc.2008.03.009
196. Leung, I. X. Y., Hui, P., Lio', P., & Crowcroft, J. (2009). Towards real-time community detection in large networks. *PHYS REV E*, 79(6), . doi:10.1103/PhysRevE.79.066107
197. Carla Balocco, C. B., Lio', P., & Luca Sani. (2009). 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.

198. Xie, S. K., Lio', P., & Lawniczak, A. T. (2009). A Case Study of ICA with Multi-scale PCA of Simulated Traffic Data. In C. Alippi, M. Polycarpou, C. Panayiotou, & G. Ellinas (Eds.), *ARTIFICIAL NEURAL NETWORKS - ICANN 2009, PT II* Vol. 5769 (pp. 358-367).
199. Xie, S. K., Lio', P., & Lawniczak, A. T. (2009). 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* (pp. 919-926).
200. Bella, G., & Lio', P. (2009). 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 (Nettabí09)* Vol. Liberodiscrivere (2009) (pp. 59-62). Catania: Liberodiscrivere (2009).
201. Schwarz, E., Leweke, F. M., Bahn, S., & Lio', P. (2009). Clinical bioinformatics for complex disorders: a schizophrenia case study.. *BMC Bioinformatics*, 10 Suppl 12, S6. doi:10.1186/1471-2105-10-S12-S6
202. van der Wath, R. C., Wilson, A., Laurenti, E., Trumpp, A., & Lio', P. (2009). Estimating dormant and active hematopoietic stem cell kinetics through extensive modeling of bromodeoxyuridine label-retaining cell dynamics.. *PLoS One*, 4(9), e6972. doi:10.1371/journal.pone.0006972
203. Chan, S. Y., Leung, I. X. Y., & Lio', P. (2009). Fast centrality approximation in modular networks. *International Conference on Information and Knowledge Management, Proceedings*, 31-38.
204. Bella, G., & Lio', P. (2009). Formal Analysis of the Genetic Toggle. In P. Degano, & R. Gorrieri (Eds.), *COMPUTATIONAL METHODS IN SYSTEMS BIOLOGY, PROCEEDINGS* Vol. 5688 (pp. 96-110).
205. Wilson, A., Laurenti, E., Oser, G., van der Wath, R. C., Blanco-Bose, W., Jaworski, M., . . . Trumpp, A. (2009). 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.
206. Cheng, T. M. K., Lu, Y. -E., & Lio', P. (2009). 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*, 7-11.
207. Xu, K., Hui, P., Li, V. O. K., Crowcroft, J., Latora, V., & Lio', P. (2009). Impact of Altruism on Opportunistic Communications. In *2009 FIRST INTERNATIONAL CONFERENCE ON UBIQUITOUS AND FUTURE NETWORKS* (pp. 153-158).

208. Guazzini, A., Lio', P., Passarella, A., & Conti, M. (2009). Information Processing and Timing Mechanisms in Vision. In C. Alippi, M. Polycarpou, C. Panayiotou, & G. Ellinas (Eds.), *ARTIFICIAL NEURAL NETWORKS - ICANN 2009, PT I* Vol. 5768 (pp. 325-334).
209. Sorathiya, A., Lio', P., & Sguanci, L. (2009). Mathematical Model of HIV Superinfection and Comparative Drug Therapy. In P. S. Andrews, J. Timmis, N. D.
210. L. Owens, U. Aickelin, E. Hart, A. Hone, . . . A. M. Tyrrell (Eds.), *ARTIFICIAL IMMUNE SYSTEMS, PROCEEDINGS* Vol. 5666 (pp. 41-53).
211. Lu, X. F., Towsley, D., Lio', P., Wicker, F., & Xiong, Z. (2009). Minimizing Detection Probability Routing in Ad Hoc Networks Using Directional Antennas. *EURASIP J WIREL COMM*, . doi:10.1155/2009/256714
212. Nguyen, V. A., Koukolikova-Nicola, Z., Bagnoli, F., & Lio', P. (2009). Noise and non-linearities in high-throughput data. *J STAT MECH-THEORY E*, . doi:10.1088/1742-5468/2009/01/P01014
213. Lu, Y. -E., Roberts, S. G. B., Cheng, T. M. K., Dunbar, R., Lio', P., & Crowcroft, J. (2009). On optimising personal network size to manage information flow.. In J. Wang, S. Zhou, & D. Zhang (Eds.), *CIKM-CNIKM* (pp. 19-26). ACM. doi:10.1145/1651274.1651279
214. Sorathiya, A., Jucikas, T., Pieciewicz, S., Sengupta, S., & Lio', P. (2009). Searching for Glycomics Role in Stem Cell Development. In F. Masulli, R. Tagliaferri, & G. M. Verkhivker (Eds.), *COMPUTATIONAL INTELLIGENCE METHODS FOR BIOINFORMATICS AND BIOSTATISTICS* Vol. 5488 (pp. 198-209).
215. Hui, P., Xu, K., Li, V. O. K., Crowcroft, J., Latora, V., & Lio', P. (2009). Selfishness, Altruism and Message Spreading in Mobile Social Networks. In *IEEE INFOCOM 2009 - IEEE CONFERENCE ON COMPUTER COMMUNICATIONS WORKSHOPS* (pp. 284-289).
216. Lu, Y. -E., Roberts, S. G. B., Lio', P., Dunbar, R., & Crowcroft, J. (2009). Size Matters: Variation in Personal Network Size, Personality and Effect on Information Transmission.. In *CSE (4)* (pp. 188-193). IEEE Computer Society. doi:10.1109/CSE.2009.179
217. Kitchovitch, S., Song, Y. D., van der Wath, R., & Lio', P. (2009). Substitution Matrices and Mutual Information Approaches to Modeling Evolution. In T. Stutzle (Ed.), *LEARNING AND INTELLIGENT OPTIMIZATION* Vol. 5851 (pp. 259-272).
218. Milanesi, L., Romano, P., Castellani, G., Remondini, D., & Lio', P. (2009). Trends in modeling Biomedical Complex Systems.. *BMC Bioinformatics*, 10 Suppl 12, I1. doi:10.1186/1471-2105-10-S12-I1

219. Kitchovitch, S., Leung, I., Song, Y. D., & Lio, P. (2009). Using Mutual Information and Models of Evolution for improved pattern detection. In J. Zhang, G. Z. Li, & J. Y. Yang (Eds.), *2009 INTERNATIONAL JOINT CONFERENCE ON BIOINFORMATICS, SYSTEMS BIOLOGY AND INTELLIGENT COMPUTING, PROCEEDINGS* (pp. 215-221). doi:10.1109/IJCBS.2009.77
220. Wilson, A., Laurenti, E., Oser, G., van der Wath, R. C., Blanco-Bose, W., Jaworski, M., Lio', P., Trumpp, A. (2008). Hematopoietic stem cells reversibly switch from dormancy to self-renewal during homeostasis and repair.. *Cell*, 135(6), 1118-1129. doi:10.1016/j.cell.2008.10.048
221. Wilson, A., Osee, G., van der Wath, R., Blanco-Bose, W., Laurenti, E., Dunant, C., Lio' P., Trumpp, A. (2008). Haematopoietic stem cells reversibly switch from dormancy to self-renewal during homeostasis and repair. *SWISS MED WKLY*, 138, 46S.
222. Bagnoli, F., Guazzini, A., & Lio', P. (2008). Human Heuristics for Autonomous Agents. CoRR, abs/0801.3048.
223. Kershenbaum, A., Pappas, V., Lee, K. W., Lio', P., Sadler, B., & Verma, D. (2008). A Biologically-Inspired MANET Architecture. In *Proceedings of SPIE, the International Society for Optical Engineering* (pp. 698106.1-698106.9).
224. Kershenbaum, A., Pappas, V., Lee, K. W., Lio', P., Sadler, B., & Verma, D. (2008). A biologically-inspired MANET architecture - art. no. 698106. In R. Suresh (Ed.), *DEFENSE TRANSFORMATION AND NET-CENTRIC SYSTEMS 2008* Vol. 6981 (pp. 98106).
225. Lu, X., Wicker, F., Leung, I., Lio', P., & Xiong, Z. (2008). A location prediction algorithm for directional communication. *IWCMC 2008 - International Wireless Communications and Mobile Computing Conference*, 159-164.
226. Lu, X. F., Chen, Y. C., Leung, I., Xiong, Z., & Lio', P. (2008). A novel mobility model from a heterogeneous military MANET trace. In D. Coudert, D. SimplotRyl, & I. Stojmenovic (Eds.), *AD-HOC, MOBILE AND WIRELESS NETWORKS, PROCEEDINGS* Vol. 5198 (pp. 463-474).
227. van der Wath, R. C., & Lio', P. (2008). A Stochastic Multi-agent Model of Stem Cell Proliferation. In H. Umeo, S. Morishita, K. Nishinari, T. Komatsuzaki, & S. Bandini (Eds.), *CELLULAR AUTOMATA, PROCEEDINGS* Vol. 5191 (pp. 500-505).
228. van der Wath, R. C., & Lio', P. (2008). A Stochastic Single Cell Based Model of BrdU Measured Hematopoietic Stem Cell Kinetics. In M. Heiner,

& A. M. Uhrmacher (Eds.), *COMPUTATIONAL METHODS IN SYSTEMS BIOLOGY, PROCEEDINGS* Vol. 5307 (pp. 387-401).

229. Brilli, M., Mengoni, A., Fondi, M., Bazzicalupo, M., Lio', P., & Fani, R. (2008). Analysis of plasmid genes by phylogenetic profiling and visualization of homology relationships using Blast2Network.. *BMC Bioinformatics*, 9, 551. doi:10.1186/1471-2105-9-551
230. Nguyen, V. A., Koukolikova-Nicola, Z., Bagnoli, F., & Lio', P. (2008). Bayesian Inference on Hidden Knowledge in High-Throughput Molecular Biology Data. In T. B. Ho, & Z. H. Zhou (Eds.), *PRICAI 2008: TRENDS IN ARTIFICIAL INTELLIGENCE* Vol. 5351 (pp. 829-838).
231. van der Wath, R. C., van der Wath, E., Carapelli, A., Nardi, F., Frati, F., Milanesi, L., . Lio', P. (2008). Bayesian phylogeny on grid. In M. Elloumi, J. Kung, M. Linial, R. F. Murphy, K. Schneider, & C. Toma (Eds.), *BIOINFORMATICS RESEARCH AND DEVELOPMENT, PROCEEDINGS* Vol. 13 (pp. 404-416).
232. Lu, Y. E., Lio', P., & Hand, S. (2008). Beta Random Projection. In P. Lio, E. Yoneki, & D. C. Verma (Eds.), *BIO-INSPIRED COMPUTING AND COMMUNICATION* Vol. 5151 (pp. 319-331).
233. Lee, U., Magistretti, E., Gerla, M., Bellavista, P., Lio', P., & Lee, K. W. (2008). Bio-Inspired Multi-agent Collaboration for Urban Monitoring Applications. In P. Lio, E. Yoneki, & D. C. Verma (Eds.), *BIO-INSPIRED COMPUTING AND COMMUNICATION* Vol. 5151 (pp. 204-216).
234. Lio', P., Yoneki, E., Crowcroft, J., & Verma, D. C. (Eds.) (2008). 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 BIOWIRE Vol. 5151. Springer.
235. Angelini, C., Cutillo, L., De Feis, I., Lio', P., & van der Wath, R. (2008). Combining experimental evidences from replicates and nearby species data for annotating novel genomes. In L. M. Ricciardi, A. Buonocore, & E. Pirozzi (Eds.), *COLLECTIVE DYNAMICS: TOPICS ON COMPETITION AND COOPERATION IN THE BIOSCIENCES* Vol. 1028 (pp. 277-291).
236. Schwarz, E., Leweke, F. M., Bahn, S., & Lio', P. (2008). Combining molecular and physiological data of complex disorders. In M. Elloumi, J. Kung, M. Linial, R. F. Murphy, K. Schneider, & C. Toma (Eds.), *BIOINFORMATICS RESEARCH AND DEVELOPMENT, PROCEEDINGS* Vol. 13 (pp. 362-376).
237. Leung, I. X. Y., Gibbs, G., Bagnoli, F., Sorathiya, A., & Lio', P. (2008). Contact Network Modeling of Flu Epidemics. In H. Umeo, S. Morishita, K. Nishinari, T. Komatsuzaki, & S. Bandini (Eds.), *CELLULAR AUTOMATA, PROCEEDINGS* Vol. 5191 (pp. 354-361).

238. Brilli, M., Fani, R., & Lio', P. (2008). Current trends in the bioinformatic sequence analysis of metabolic pathways in prokaryotes.. *Brief Bioinform*, 9(1), 34-45. doi:10.1093/bib/bbm051
239. Stajano, F., Bianchi, L., Lio', P., & Korff, D. (2008). Forensic genomics: Kin privacy, driftnets and other open questions. *Proceedings of the ACM Conference on Computer and Communications Security*, 15-22.
240. Bagnoli, F., Guazzini, A., & Lio', P. (2008). Human Heuristics for Autonomous Agents. In P. Lio, E. Yoneki, & D. C. Verma (Eds.), *BIO-INSPIRED COMPUTING AND COMMUNICATION* Vol. 5151 (pp. 340-351).
241. Lu, X. F., Hui, P., Lio', P., & Xiong, Z. (2008). Identity Privacy Protection by Delayed Transmission in Pocket Switched Networks. In M. Guo, Z. J. Wang, F. Tang, & C. Z. Xu (Eds.), *EUC 2008: PROCEEDINGS OF THE 5TH INTERNATIONAL CONFERENCE ON EMBEDDED AND UBIQUITOUS COMPUTING, VOL 2, WORKSHOPS* (pp. 272-277).
242. Koukolikova-Nicola, Z., Lio', P., & Bagnoli, F. (2008). Inference on missing values in genetic networks using high-throughput data. In E. Marchiori, & J. H. Moore (Eds.), *EVOLUTIONARY COMPUTATION, MACHINE LEARNING AND DATA MINING IN BIOINFORMATICS, PROCEEDINGS* Vol. 4973 (pp. 106-116).
243. Lio', P., & Bishop, M. (2008). Modeling sequence evolution. *Methods Mol Biol*, 452, 255-285.
244. Lio', P., & Bishop, M. (2008). Modeling sequence evolution.. *Methods Mol Biol*, 452, 255-285. doi:10.1007/978-1-60327-159-2_13
245. Lu, Y. E., Lio', P., & Hand, S. (2008). On low dimensional random projections and similarity search. *International Conference on Information and Knowledge Management, Proceedings*, 749-758.
246. Xie, S. K., Lawniczak, A. T., & Lio', P. (2008). Parametric & non-parametric analysis of mean treatment effects of number of packets in transit in data network model. In *2008 CANADIAN CONFERENCE ON ELECTRICAL AND COMPUTER ENGINEERING, VOLS 1-4* (pp. 1931-1936).
247. Cheng, T. M., Lu, Y. E., Vendruscolo, M., Lio', P., & Blundell, T. L. (2008). Prediction by graph theoretic measures of structural effects in proteins arising from non-synonymous single nucleotide polymorphisms.. *PLoS Comput Biol*, 4(7), e1000135. doi:10.1371/journal.pcbi.1000135
248. Lu, X. F., Wicker, F., Lio', P., & Towsley, D. (2008). Security Estimation Model with Directional Antennas. In *2008 IEEE MILITARY COMMUNICATIONS CONFERENCE: MILCOM 2008, VOLS 1-7* (pp. 3808-3813).

249. Allen, S. M., Conti, M., Crowcroft, J., Dunbar, R., Lio', P., Mendes, J. F., ... Whitaker, R. M. (2008). Social Networking for Pervasive Adaptation. In G. D. Serugendo (Ed.), *SASOW 2008: SECOND IEEE INTERNATIONAL CONFERENCE ON SELF-ADAPTIVE AND SELF-ORGANIZING SYSTEMS WORKSHOPS, PROCEEDINGS* (pp. 49-54).
250. Lio', P., Angelini, C., DeFeis, I., Nguyen, V., Cutillo, L., & va der Wath, R. (2008). 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* (pp. 50-54). Leeds: S. Barber, P.D. Baxter, A. Gusnanto & K.V. Mardia (eds) Leeds University Press.
251. Lio', P., Brilli, M., & Fani, R. (2008). Topological metrics in Blast data mining: Plasmid and nitrogen-fixing proteins case studies. In M. Elloumi, J. Kung, M. Linial, R. F. Murphy, K. Schneider, & C. Toma (Eds.), *BIOINFORMATICS RESEARCH AND DEVELOPMENT, PROCEEDINGS* Vol. 13 (pp. 207-220).
252. Lio', P., Lawniczak, A. T., Xie, S., & Xu, J. (2008). 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.
253. Bagnoli, F., Lio', P., & Sguanci, L. (2007). Risk perception in epidemic modeling.. *Phys Rev E Stat Nonlin Soft Matter Phys*, 76(6 Pt 1), 061904. Retrieved from <http://www.ncbi.nlm.nih.gov/pubmed/18233866>
254. Papetti, C., Lio', P., Ruber, L., Patarnello, T., & Zardoya, R. (2007). Antarctic fish mitochondrial genomes lack ND6 gene. *J MOL EVOL*, 65(5), 519-528. doi:10.1007/s00239-007-9030-z
255. Caretta-Cartozo, C., De Los Rios, P., Piazza, F., & Lio', P. (2007). Bottleneck genes and community structure in the cell cycle network of *S. pombe*. *PLOS COMPUT BIOL*, 3(6), 968-976. doi:10.1371/journal.pcbi.0030103
256. van der Wath, E., Moutsianas, L., van der Wath, R., Visagie, A., Milanesi, L., & Lio', P. (2007). Grid methodology for identifying co-regulated genes and transcription factor binding sites. *IEEE T NANOBIOSCI*, 6(2), 162-167. doi:10.1109/TNB.2007.897470
257. Bianchi, L., & Lio', P. (2007). Forensic DNA and bioinformatics. *BRIEF BIOINFORM*, 8(2), 117-128. doi:10.1093/bib/bbm006

258. Brilli, M., Fani, R., & Lio', P. (2007). MotifScorer: using a compendium of microarrays to identify regulatory motifs. *BIOINFORMATICS*, 23(4), 493-495. doi:10.1093/bioinformatics/btl607
259. Sguanci, L., Bagnoli, F., & Lio', P. (2007). Modeling HIV quasispecies evolutionary dynamics. In *BMC EVOLUTIONARY BIOLOGY* Vol. 7 (pp.). doi:10.1186/1471-2148-7-S2-S5
260. Carapelli, A., Lio', P., Nardi, F., van der Wath, E., & Frati, F. (2007). Phylogenetic analysis of mitochondrial protein coding genes confirms the reciprocal paraphyly of Hexapoda and Crustacea. In *BMC EVOLUTIONARY BIOLOGY* Vol. 7 (pp.). doi:10.1186/1471-2148-7-S2-S8
261. Fani, R., Brilli, M., Fondi, M., & Lio', P. (2007). The role of gene fusions in the evolution of metabolic pathways: the histidine biosynthesis case. In *BMC EVOLUTIONARY BIOLOGY* Vol. 7 (pp.). doi:10.1186/1471-2148-7-S2-S4
262. Lu, Y. E., Lio', P., & Hand, S. (2007). Beta random projection. In *ISM WORKSHOPS 2007: NINTH IEEE INTERNATIONAL SYMPOSIUM ON MULTIMEDIA - WORKSHOPS, PROCEEDINGS* (pp. 323-328). doi:10.1109/ISM.Workshops.2007.61
263. Weston, E. M., Friday, A. E., & Lio', P. (2007). Biometric evidence that sexual selection has shaped the hominin face.. *PLoS One*, 2(8), e710. doi:10.1371/journal.pone.0000710
264. Caretta-Cartozo, C., De Los Rios, P., Piazza, F., & Lio', P. (2007). Bottleneck genes and community structure in the cell cycle network of *S. pombe*. *PLoS Computational Biology*, 3(6), 0968-0976.
265. Angelini, C., Cutillo, L., De Feis, I., Van der Wath, R., & Lio', P. (2007). Identifying regulatory sites using neighborhood species. In E. Marchiori, J. H. Moore, & J. C. Rajapakse (Eds.), *Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, Proceedings* Vol. 4447 (pp. 1-10).
266. Lu, Y. E., Hand, S., & Lio', P. (2007). Keyword searching in structured overlays via content distance addressing. In G. Moro, S. Bergamaschi, S. Joseph, J. H. Morin, & A. M. Ouksel (Eds.), *Databases, Information Systems, and Peer-to-Peer Computing* Vol. 4125 (pp. 259-272).
267. Chen, F., Archambault, V., Kar, A., Lio', P., D'Avino, P. P., Sinka, R., . . . Glover, D. M. (2007). Multiple protein phosphatases are required for mitosis in *Drosophila*. *CURR BIOL*, 17(4), 293-303. doi:10.1016/j.cub.2007.01.068
268. Lawniczak, A. T., Xie, S., Lio', P. P., & Xu, J. (2007). 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*, 360-363.

269. Lawniczak, A. T., Lio', P., Xie, S., & Xu, J. Y. (2007). 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* (pp. 364-367).
270. Fani, R., Brillì, M., & Lio', P. (2006). Inference from proteobacterial operons shows piecewise organization: a reply to Price et al.. *J Mol Evol*, 63(4), 577-580. doi:10.1007/s00239-006-0074-2
271. Fani, R., Caramelli, D., & Lio', P. (2006). [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. Retrieved from <http://www.ncbi.nlm.nih.gov/pubmed/17342847>
272. Bagnoli, F., Lio', P., & Sguanci, L. (2006). Modeling viral coevolution: HIV multi-clonal persistence and competition dynamics. *PHYSICA A*, 366(1), 333-346. doi:10.1016/j.physa.2005.10.055
273. Nye, T. M. W., Lio', P., & Gilks, W. R. (2006). A novel algorithm and web-based tool for comparing two alternative phylogenetic trees. *BIOINFORMATICS*, 22(1), 117-119. doi:10.1093/bioinformatics/bti720
274. Ambesi-Impiombato, A., Bansal, M., Lio', P., & di Bernardo, D. (2006). Computational framework for the prediction of transcription factor binding sites by multiple data integration.. *BMC Neurosci*, 7 Suppl 1, S8. doi:10.1186/1471-2202-7-S1-S8
275. Fani, R., Caramelli, D., & Lio', P. (2006). From prebiotic chemistry to the evolution of man: The First Conference of the S.I.B.E. (Italian Society of Evolutionary Biology) in Florence | Dalla chimica prebiotica all'evoluzione dell'uomo a Firenze il Primo Congresso della S.I.B.E.. *Rivista di Biologia - Biology Forum*, 99(3), 357-360.
276. Sguanci, L., Lio, P., & Bagnoli, F. (2006). Modeling evolutionary dynamics of HIV infection. In C. Priami (Ed.), *COMPUTATIONAL METHODS IN SYSTEMS BIOLOGY, PROCEEDINGS* Vol. 4210 (pp. 196-211).
277. Sguanci, L., Lio', P., & Bagnoli, F. (2006). The influence of risk perception in epidemics: A cellular agent model. In S. E. Yacoubi, B. Chopard, & S. Bandini (Eds.), *CELLULAR AUTOMATA, PROCEEDINGS* Vol. 4173 (pp. 321-329).
278. Piazza, F., & Lio', P. (2005). Statistical analysis of simple repeats in the human genome. *PHYSICA A*, 347, 472-488. doi:10.1016/j.physa.2004.08.038

279. Fani, R., Brilli, M., & Lio', P. (2005). The origin and evolution of operons: The piecewise building of the proteobacterial histidine operon. *J MOL EVOL*, 60(3), 378-390. doi:10.1007/s00239-004-0198-1
280. Lio', P. (2005). Phylogenetic and structural analysis of mitochondrial complex I proteins. In *GENE* Vol. 345 (pp. 55-64). doi:10.1016/j.gene.2004.11.033
281. Lu, Y. E., Hand, S., & Lio', P. (2005). Keyword searching in hypercubic manifolds. In G. Caronni, N. Weiler, M. Waldvogel, & N. Shahmehri (Eds.), *Fifth IEEE International Conference on Peer-to-Peer Computing, Proceedings* (pp. 150-151).
282. Carapelli, A., Nardi, F., Dallai, R., Boore, J. L., Lio', P., & Frati, F. (2005). Relationships between hexapods and crustaceans based on 4 mitochondrial genes. In S. Koenemann, & R. A. Jenner (Eds.), *Crustacea and arthropod relationships* (pp. 423 pages). CRC.
283. Tadesse, M. G., Vannucci, M., & Lio', P. (2004). Identification of DNA regulatory motifs using Bayesian variable selection. *BIOINFORMATICS*, 20(16), 2553-2561. doi:10.1093/bioinformatics/bth282
284. Rustici, G., Mata, J., Kivinen, K., Lio', P., Penkett, C. J., Burns, G., . . . Bahler, J. (2004). Periodic gene expression program of the fission yeast cell cycle.. *Nat Genet*, 36(8), 809-817. doi:10.1038/ng1377
285. Lio', P., & Goldman, N. (2004). Phylogenomics and bioinformatics of SARS-CoV. *TRENDS MICROBIOL*, 12(3), 106-111.
286. Lio', P., & Vannucci, M. (2003). Investigating the evolution and structure of chemokine receptors. In *GENE* Vol. 317 (pp. 29-37). doi:10.1016/S0378-1119(03)00666-8
287. Lio', P. (2003). Dimensionality and dependence problems in statistical genomics.. *Brief Bioinform*, 4(2), 168-177. <http://www.ncbi.nlm.nih.gov/pubmed/12846397>
288. Lio', P. (2003). Il genoma della Sars. *Le Scienze Italian Edition of Scientific American*, June 2003(June 2003). Retrieved from <http://www.lescienze.it/>
289. Lio', P. (2003). Statistical bioinformatic methods in microbial genome analysis. *BIOESSAYS*, 25(3), 266-273. doi:10.1002/bies.10231
290. Lio', P. (2003). Wavelets in bioinformatics and computational biology: state of art and perspectives. *BIOINFORMATICS*, 19(1), 2-9.
291. Skaer, N., Pistillo, D., Gibert, J. M., Lio', P., Wulbeck, C., & Simpson, P. (2002). Gene duplication at the achaete-scute complex and morphological

- complexity of the peripheral nervous system in Diptera. *TRENDS GENET*, 18(8), 399-405.
292. Lio', P. (2002). Investigating the relationship between genome structure, composition, and ecology in prokaryotes. *MOL BIOL EVOL*, 19(6), 789-800.
293. Lio', P., & Goldman, N. (2002). Modeling mitochondrial protein evolution using structural information. *J MOL EVOL*, 54(4), 519-529. doi:10.1007/s00239001-0052-7
294. Lio, P. (2002). Structure and evolution of the histidine biosynthetic pathway. In M. Brilli, P. Lio, A. Lazcano, & R. Fani (Eds.), *Origins of Life and Evolution of the Biosphere Vol. 22* (pp. 488). Oaxaca, Mexico: Springer
295. Lio', P., & Goldman, N. (2002). Modeling mitochondrial protein evolution using structural information.. *J Mol Evol*, 54(4), 519-529. doi:10.1007/s00239-001-0052-7
296. Lio', P. (2002). Una vita per le proteine. *Le Scienze Italian Edition of Scientific American, February 2002*(February 2002).
297. Brilli, M., Lio', P., Lazcano, A., & Fani, R. (2002). Evolution of TIM barrel: Multiple gene elongation events in HisA.. In *Origins of Life and Evolution of the Biosphere Vol. 22* (pp. 487). Oaxaca, Mexico: Springer.
298. Renato Fani, R. F., Silvia Casadei, S. C., & Lio', P. (2002). Origin and Evolution of nif Genes. In *NITROGEN FIXATION: FROM MOLECULES TO CROP PRODUCTIVITY* (Vol. 38,, pp. 177-178). doi:10.1007/0-306-47615-0_85
299. Massingham, T., Davies, L. J., & Lio', P. (2001). Analysing gene function after duplication. *BIOESSAYS*, 23(10), 873-876.
300. Bogani, P., Simoni, A., Lio', P., Germinario, A., & Buiatti, M. (2001). Molecular variation in plant cell populations evolving in vitro in different physiological contexts.. *Genome*, 44(4), 549-558. Retrieved from <http://www.ncbi.nlm.nih.gov/pubmed/11550888>
301. Lio', P. (2001). Dal Genoma al Fisioma. Retrieved from <http://www.lescienze.it/>
302. Whelan, S., Lio, P., & Goldman, N. (2001). Molecular phylogenetics: state-of-the-art methods for looking into the past. *TRENDS GENET*, 17(5), 262-272.
303. Lio, P. (2001). Le nuove sfide della filogenesi molecolare. *Le Scienze Italian Edition of Scientific American, February 2001*(February 2001).

304. Lio', P., & Vannucci, M. (2000). Finding pathogenicity islands and gene transfer events in genome data. *BIOINFORMATICS*, *16*(10), 932-940.
305. Hagelberg, E., Goldman, N., Lio', P., Whelan, S., Schiefenhovel, W., Clegg, J. B., . . . Bowden, D. K. (2000). Evidence for mitochondrial DNA recombination in a human population of island Melanesia: correction. *P ROY SOC LOND B BIO*, *267*(1452), 1595-1596.
306. Fani, R., Gallo, R., & Lio', P. (2000). Molecular evolution of nitrogen fixation: the evolutionary history of the nifD, nifK, nifE, and nifN genes.. *J Mol Evol*, *51*(1), 1-11. Retrieved from <http://www.ncbi.nlm.nih.gov/pubmed/10903367>
307. Lio', P. (2000). Siamo uomini non DNA robot, Newton (June 2000, in Italian).
308. Lio', P., & Vannucci, M. (2000). Wavelet change-point prediction of transmembrane proteins.. *Bioinformatics*, *16*(4), 376-382. Retrieved from <http://www.ncbi.nlm.nih.gov/pubmed/10869036>
309. Thomas, N. S., Wilkinson, J., Lio', P., Doull, I., Morton, N. E., & Holgate, S. T. (2000). Investigation of the genetic factors underlying asthma and atopy in outbred UK populations. *REV MAL RESPIR*, *17*(1BIS), 177-182.
310. Thomas, N. -S., Wilkinson, J., Lio', P., Doull, I., Morton, N. -E., & Holgate, S. -T. (2000). Investigation of the genetic factors underlying asthma and atopy in outbred UK populations | Facteurs genetiques impliquees dans l'asthme et l'atopie. Etudes dans les familles britanniques. *Revue des Maladies Respiratoires*, *17*(1 BIS), 177-182.
311. Lio', P., & Goldman, N. (1999). Using protein structural information in evolutionary inference: transmembrane proteins.. *Mol Biol Evol*, *16*(12), 1696-1710. Retrieved from <http://www.ncbi.nlm.nih.gov/pubmed/10605112>
312. Hagelberg, E., Goldman, N., Lio', P., Whelan, S., Schiefenhovel, W., Clegg, J. B., . . . Bowden, D. K. (1999). Evidence for mitochondrial DNA recombination in a human population of island Melanesia.. *Proc Biol Sci*, *266*(1418), 485-492. doi:10.1098/rspb.1999.0663
313. Mori, E., Lio' P., Daly, S., Damiani, G., Perito, B., & Fani, R. (1999). Molecular nature of RAPD markers from Haemophilus influenzae Rd genome.. *Res Microbiol*, *150*(2), 83-93. Retrieved from <http://www.ncbi.nlm.nih.gov/pubmed/10209764>
314. Hagelberg, E., Kayser, M., Nagy, M., Roewer, L., Zimdahl, H., Krawczak, M., . . . Schiefenhovel, W. (1999). 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* Vol. 354 (pp. 141-152). ENGLAND. doi:10.1098/rstb.1999.0367

315. Lio', P., & Goldman, N. (1998). Models of molecular evolution and phylogeny.. *Genome Res*, 8(12), 1233-1244. Retrieved from <http://www.ncbi.nlm.nih.gov/pubmed/9872979>
316. Lio', P., Goldman, N., Thorne, J. L., & Jones, D. T. (1998). PASSML: Combining evolutionary inference and protein secondary structure prediction. *Bioinformatics*, 14(8), 726-733.
317. Lio', P., & Ruffo, S. (1998). Searching for genomic constraints. *NUOVO CIMENTO D*, 20(1), 113-127.
318. Fani, R., Tamburini, E., Mori, E., Lazcano, A., Lio', P., Barberio, C., . . . Polsinelli, M. (1997). Paralogous histidine biosynthetic genes: evolutionary analysis of the *Saccharomyces cerevisiae* HIS6 and HIS7 genes.. *Gene*, 197(1-2), 9-17. Retrieved from <http://www.ncbi.nlm.nih.gov/pubmed/9332345>
319. Dewar, J. C., Wilkinson, J., Wheatley, A., Thomas, N. S., Doull, I., Morton, N., Lio', P. . . Hall, I. P. (1997). The glutamine 27 beta2-adrenoceptor polymorphism is associated with elevated IgE levels in asthmatic families.. *J Allergy Clin Immunol*, 100(2), 261-265. Retrieved from <http://www.ncbi.nlm.nih.gov/pubmed/9275150>
320. Dewar, J., Wheatley, A., Wilkinson, J., Holgate, S. T., Thomas, N. S., Lio', P., . . . Hall, I. P. (1997). Association of the Gln 27 beta(2)-adrenoceptor polymorphism and IgE variability in asthmatic families. In *CHEST* Vol. 111 (pp. S78-S79).
321. Lio', P., & Morton, N. E. (1997). Comparison of parametric and nonparametric methods to map oligogenes by linkage.. *Proc Natl Acad Sci USA*, 94(10), 5344-5348. Retrieved from <http://www.ncbi.nlm.nih.gov/pubmed/9144239>
322. Bogani, P., Lio', P., Intrieri, M. C., & Buiatti, M. (1997). A physiological and molecular analysis of the genus *Nicotiana*.. *Mol Phylogenet Evol*, 7(1), 62-70. doi:10.1006/mpev.1996.0356
323. Lio', P. (1997). Comparison of multipoint analyses for complex inheritance: IDDM and asthma. *Annals of Human Genetics*, 61(6), 541-542.
324. Lio', P. (1997). Correlation methods for genomic constraints analysis. *Annals of Human Genetics*, 61(6), 542.
325. Thomas, N. S., Wilkinson, J., Lio', P., Doull, I., Morton, N. E., & Holgate, S. T. (1997). Investigation of the genetic factors underlying asthma and atopy in outbred UK populations. In C. S. Hong, J. T. Choung, J.

H. Chung, J. Jang, T. Y. Jang, K. S. Jung, . . . C. S. Park (Eds.), *5TH WEST-PACIFIC ALLERGY SYMPOSIUM / 7TH KOREA-JAPAN JOINT ALLERGY SYMPOSIUM* (pp. 81-86).

326. Morton, N. E., & Lio', P. (1997). Oligogenic linkage and map integration. In I. H. Pawlowitzki, J. H. Edwards, & E. A. Thompson (Eds.), *GENETIC MAPPING OF DISEASE GENES* (pp. 17-21).
327. Lio', P., Politi, A., Ruffo, S., & Buiatti, M. (1996). Analysis of genomic patchiness of *Haemophilus influenzae* and *Saccharomyces cerevisiae* chromosomes.. *J Theor Biol*, *183*(4), 455-469. doi:10.1006/jtbi.1996.0235
328. Bogani, P., Simoni, A., Lio', P., Scialpi, A., & Buiatti, M. (1996). Genome flux in tomato cell clones cultured in vitro in different physiological equilibria. II. A RAPD analysis of variability.. *Genome*, *39*(5), 846-853. Retrieved from <http://www.ncbi.nlm.nih.gov/pubmed/18469940>
329. Lio', P., Politi, A., Buiatti, M., & Ruffo, S. (1996). High statistics block entropy measures of DNA sequences.. *J Theor Biol*, *180*(2), 151-160. doi:10.1006/jtbi.1996.0091
330. Alifano, P., Fani, R., Lio', P., Lazcano, A., Bazzicalupo, M., Carlomagno, M. S., . . . Bruni, C. B. (1996). Histidine biosynthetic pathway and genes: Structure, regulation, and evolution. *MICROBIOL REV*, *60*(1), 44-&.
331. Fani, R., Lio', P., & Lazcano, A. (1995). Molecular evolution of the histidine biosynthetic pathway.. *J Mol Evol*, *41*(6), 760-774. Retrieved from <http://www.ncbi.nlm.nih.gov/pubmed/8587121>
332. VICARIO, F., VENDRAMIN, G. G., ROSSI, P., Lio', P., & GIANNINI, R. (1995). 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.
333. Bagnoli, F., & Lio', P. (1995). Selection, mutations and codon usage in a bacterial model.. *J Theor Biol*, *173*(3), 271-281. doi:10.1006/jtbi.1995.0062
334. Bagnoli, F., Guasti, G., & Lio', P. (1995). Translation optimization in bacteria: Statistical models. In M. Peyrard (Ed.), *NONLINEAR EXCITATIONS IN BIOMOLECULES* (pp. 405-411).
335. Lio', P., Ruffo, S., & Buiatti, M. (1994). Third codon G + C periodicity as a possible signal for an "internal" selective constraint.. *J Theor Biol*, *171*(2), 215-223. doi:10.1006/jtbi.1994.1225

336. Fani, R., Lio', P., Chiarelli, I., & Bazzicalupo, M. (1994). 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. Retrieved from <http://www.ncbi.nlm.nih.gov/pubmed/8028028>
337. Fani, R., Grifoni, A., Damiani, G., Lio, P., & Mori, E. (1994). Nucleotide Sequence of Azospirillum RAPD markers. In *Azospirillum VI and Related Microorganisms:: Genetics - Physiology - Ecology (NATO ASI Series / Ecological Sciences)*. Springer Verlag.
338. Fani, R., Bandi, C., Bazzicalupo, M., Damiani, G., Di Cello, F., Fancelli, S., Lio, P. . . Mori, E. (1994). Phylogenetic Studies of the Genus *Azospirillum*. In *Related Microorganisms:: Genetics - Physiology - Ecology (NATO ASI Series / Ecological Sciences)*. Hungary: Springer Verlag.
339. Lio, P. (1994) Long Range Properties of DNA Sequences. In Bellacicco, Vulpiani, & Koch (Eds.), *Collana Franco Angeli Editore*. Roma.