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Personal information

Researcher, Developer and Data Steward at the AIMMS Institute & Faculty of Science, Vrije Universiteit Amsterdam

Qualifications

Biochemistry, PhD, University of Stellenbosch
1 Jan 2000 → 31 Dec 2004

Employment

Research Associate

Systems Bioinformatics
Vrije Universiteit Amsterdam
1 Jan 2014 → present

Research outputs

- MEMOTE for standardized genome-scale metabolic model testing**
Lieven, C., Beber, M. E., Olivier, B. G., Bergmann, F. T., Ataman, M., Babaei, P., Bartell, J. A., Blank, L. M., Chauhan, S., Correia, K., Diener, C., Dräger, A., Ebert, B. E., Edirisinghe, J. N., Faria, J. P., Feist, A. M., Fengos, G., Fleming, R. M. T., García-Jiménez, B., Hatzimanikatis, V. & 49 others, van Helvoirt, W., Henry, C. S., Hermjakob, H., Herrgård, M. J., Kaafarani, A., Kim, H. U., King, Z., Klamt, S., Klipp, E., Koehorst, J. J., König, M., Lakshmanan, M., Lee, D. Y., Lee, S. Y., Lee, S., Lewis, N. E., Liu, F., Ma, H., Machado, D., Mahadevan, R., Maia, P., Mardinoglu, A., Medlock, G. L., Monk, J. M., Nielsen, J., Nielsen, L. K., Nogales, J., Nookaew, I., Palsson, B. O., Papin, J. A., Patil, K. R., Poolman, M., Price, N. D., Resendis-Antonio, O., Richelle, A., Rocha, I., Sánchez, B. J., Schaap, P. J., Malik Sheriff, R. S., Shoaie, S., Sonnenschein, N., Teusink, B., Vilaça, P., Vik, J. O., Wodke, J. A. H., Xavier, J. C., Yuan, Q., Zakhartsev, M. & Zhang, C., 1 Mar 2020, In : Nature Biotechnology. 38, 3, p. 272-276 5 p.
- A systematic assessment of current genome-scale metabolic reconstruction tools**
Mendoza, S. N., Olivier, B. G., Molenaar, D. & Teusink, B., 7 Aug 2019, In : Genome Biology. 20, 1, 158.
- The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 2 Core Release 2**
Hucka, M., Bergmann, F. T., Chaouiya, C., Dräger, A., Hoops, S., Keating, S. M., König, M., Novère, N. L., Myers, C. J., Olivier, B. G., Sahle, S., Schaff, J. C., Sheriff, R., Smith, L. P., Waltemath, D., Wilkinson, D. J. & Zhang, F., 20 Jun 2019, In : Journal of Integrative Bioinformatics. 16, 2, p. 1-183 183 p.
- Harmonizing semantic annotations for computational models in biology**
Neal, M. L., König, M., Nickerson, D., Misirli, G., Kalbasi, R., Dräger, A., Atalag, K., Chelliah, V., Cooling, M. T., Cook, D. L., Crook, S., De Alba, M., Friedman, S. H., Garny, A., Gennari, J. H., Gleeson, P., Golebiewski, M., Hucka, M., Juty, N., Myers, C. & 8 others, Olivier, B. G., Sauro, H. M., Scharm, M., Snoep, J. L., Touré, V., Wipat, A., Wolkenhauer, O. & Waltemath, D., 22 Mar 2019, In : Briefings in bioinformatics. 20, 2, p. 540-550 11 p.
- Correction to: Meeting report from the fourth meeting of the Computational Modeling in Biology Network (COMBINE)**
Waltemath, D., Bergmann, F. T., Chaouiya, C., Czauderna, T., Gleeson, P., Goble, C., Golebiewski, M., Hucka, M., Juty, N., Krebs, O., Le Novère, N., Mi, H., Moraru, I. I., Myers, C. J., Nickerson, D., Olivier, B. G., Rodriguez, N., Schreiber, F., Smith, L., Zhang, F. & 1 others, Bonnet, E., 9 Aug 2018, In : Standards in Genomic Sciences. 13, 1, p. 1-1 1 p., 17.
- The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 1 Core**
Hucka, M., Bergmann, F. T., Dräger, A., Hoops, S., Keating, S. M., Le Novère, N., Myers, C. J., Olivier, B. G., Sahle, S., Schaff, J. C., Smith, L. P., Waltemath, D. & Wilkinson, D. J., 19 Jun 2018, In : Journal of Integrative Bioinformatics. 15, 1
- Simulation Experiment Description Markup Language (SED-ML) Level 1 Version 3 (L1V3)**
Bergmann, F. T., Cooper, J., König, M., Moraru, I., Nickerson, D., Le Novère, N., Olivier, B. G., Sahle, S., Smith, L. & Waltemath, D., 19 Mar 2018, In : Journal of Integrative Bioinformatics. 15, 1, p. 1-98 98 p.

8. **SBML Level 3 Package: Flux Balance Constraints version 2**
Olivier, B. G. & Bergmann, F. T., 9 Mar 2018, In : Journal of Integrative Bioinformatics. 15, 1, p. 1-39 39 p.
9. **The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 2 Core**
Hucka, M., Bergmann, F. T., Dräger, A., Hoops, S., Keating, S. M., Le Novère, N., Myers, C. J., Olivier, B. G., Sahle, S., Schaff, J. C., Smith, L. P., Waltemath, D. & Wilkinson, D. J., 9 Mar 2018, In : Journal of Integrative Bioinformatics. 15, 1, p. 1-182 182 p.
10. **Alignment of microbial fitness with engineered product formation: Obligatory coupling between acetate production and photoautotrophic growth**
Du, W., Jongbloets, J. A., van Boxtel, C., Hernández, H. P., Lips, D., Olivier, B. G., Hellingwerf, K. J. & dos Santos, F. B., 13 Feb 2018, In : Biotechnology for Biofuels. 11, 38, p. 1-13 13 p., 38.
11. **Probing the genome-scale metabolic landscape of *Bordetella pertussis*, the causative agent of whooping cough**
dos Santos, F. B., Olivier, B. G., Boele, J., Krumpochova, P., Klau, G. W., Giera, M. & Teusink, B., 1 Nov 2017, In : Applied and Environmental Microbiology. 83, 21
12. **Model-based quantification of metabolic interactions from dynamic microbial-community data**
Hanemaaijer, M., Olivier, B. G., Röling, W. F. M., Bruggeman, F. J. & Teusink, B., 1 Mar 2017, In : PLoS ONE. 12, 3, e0173183.
13. **Constraint-based stoichiometric modelling from single organisms to microbial communities.**
Gottstein, W. G., Olivier, B. G., Bruggeman, F. J. & Teusink, B., 2016, In : Journal of the Royal Society Interface. 13, 124, 20160627.
14. **Genome-scale reconstruction of the *Streptococcus pyogenes* M49 metabolic network reveals growth requirements and indicates potential drug targets.**
Levering, J., Fiedler, T., Sieg, A., van Grinsven, K. W., Hering, S., Veith, N., Olivier, B. G., Klett, L., Hugenholtz, J., Teusink, B., Kreikemeyer, B. & Kummer, U., 2016, In : Journal of Biotechnology. 232, p. 25-37
15. **Integrating highly quantitative proteomics and genome-scale metabolic modeling to study pH adaptation in the human pathogen *Enterococcus faecalis***
Grosseholz, R., Ching-Chiek, K., Veith, N., Fiedler, T., Strauss, M., Olivier, B. G., Collins, B. C., Schubert, O. T., Bergmann, F., Kreikemeyer, B., Aebersold, R. & Kummer, U., 2016, In : NPJ systems biology and applications. 16017.
16. **Modeling and simulation tools: from systems biology to systems medicine**
Olivier, B. G., Swat, M. J. & Mone, M. J., 2016, In : Methods in Molecular Biology. 1386, p. 441-463
17. **Modelling? Using standards can help you.**
Olivier, B. G. & Teusink, B., 2016, In : ERCIM NEWS. 104, p. 34-38
18. **Top 10 metrics for life science software good practices.**
Artaza, H., Chue Hong, N., Corpas, M., Corpuz, A., Hooft, R., Jimenez, R. C., Leskosek, B., Olivier, B. G., Stourac, J., Svobodova Varekova, R., van Parys, T. & Vaughan, D., 2016, In : F1000Research. 5, ELIXIR-2000.
19. **Using a genome-scale metabolic model of *Enterococcus faecalis* V583 to assess amino acid uptake and its impact on central metabolism**
Veith, N., Solheim, M., van Grinsven, K. W. A., Olivier, B. G., Levering, J., Grosseholz, R., Hugenholtz, J., Holo, H., Nes, I., Teusink, B. & Kummer, U., Mar 2015, In : Applied and Environmental Microbiology. 81, 5, p. 1622-1633 12 p.
20. **Fast flux module detection using matroid theory.**
Reimers, A. C., Bruggeman, F. J., Olivier, B. G. & Stougie, L., 2015, In : Journal of Computational Biology. 22, p. 414-424 5.
21. **Interplay between constraints, objectives, and optimality for genome-scale stoichiometric models.**
Maarleveld, T. R., Wortel, M. T., Olivier, B. G., Teusink, B. & Bruggeman, F. J., 2015, In : PLoS Computational Biology. 7, 11, 4.
22. **Systems Biology Markup Language (SBML) Level 2 Version 5: Structures and Facilities for Model Definitions.**
Hucka, M., Bergmann, F. T., Dräger, A., Hoops, S., Keating, S. M., Le Novère, N., Myers, C. J., Olivier, B. G., Sahle, S., Schaff, J. C., Smith, L. P., Waltemath, D. & Wilkinson, D. J., 2015, In : Journal of Integrative Bioinformatics. 12, p. 271 2.
23. **Systems modeling approaches for microbial community studies: from metagenomics to inference of the community structure**
Hanemaaijer, M. J., Röling, W. F. M., Olivier, B. G., Khandelwal, R. A., Teusink, B. & Bruggeman, F. J., 2015, In : Frontiers in Microbiology. 6, 213.
24. **The Systems Biology Markup Language (SBML) Level 3 Package: Flux Balance Constraints.**
Olivier, B. G. & Bergmann, F. T., 2015, In : Journal of Integrative Bioinformatics. 12, p. 269 2.
25. **COMBINE archive and OMEX format: One file to share all information to reproduce a modeling project**
Bergmann, F. T., Adams, R., Moodie, S., Cooper, J., Glont, M., Golebiewski, M., Hucka, M., Laibe, C., Miller, A. K., Nickerson, D. P., Olivier, B. G., Rodriguez, N., Sauro, H. M., Scharm, M., Soiland-Reyes, S., Waltemath, D., Yvon, F. & Le Novère, N., 14 Dec 2014, In : BMC Bioinformatics. 15, p. 1-9 9 p., 326.

26. **Meeting report from the fourth meeting of computational modeling in biology network (COMBINE).**
Waltemath, D., Bergmann, F. T., Chaouiya, C., Czauderna, T., Gleeson, P., Goble, C. A., Golebiewski, M., Hucka, M., Juty, N., Krebs, O., Le Novere, N., Mi, H., Moraru, I. I., Myers, C. J., Nickerson, D., Olivier, B. G., Rodriguez, N., Schreiber, F., Smith, L., Zhang, F. & 1 others, Bonnet, E., 2014, In : Standards in Genomic Sciences. 2014, 9, p. 1285-1301 5279417.
27. **Basic concepts and principles of stoichiometric modeling of metabolic networks.**
Maarleveld, T. R., Khandelwal, R. A., Olivier, B. G., Teusink, B. & Bruggeman, F. J., 2013, In : Biotechnology Journal. 8, 9, p. 997-1008
28. **Community flux balance analysis for microbial consortia at balanced growth**
Khandelwal, R. A., Olivier, B. G., Roling, W. F. M., Teusink, B. & Bruggeman, F. J., 2013, In : PLoS ONE. 8, 5
29. **StochPy: a comprehensive, userfriendly tool for simulating stochastic biological processes**
Maarleveld, T. M., Olivier, B. G. & Bruggeman, F. J., 2013, In : PLoS ONE. 8, 11
30. **FAME, the flux analysis and modelling environment**
Boele, J., Olivier, B. G. & Teusink, B., 2012, In : BMC Systems Biology. 6, 8.
31. **Optimal flux spaces of genome-scale stoichiometric models are determined by a few subnetworks**
Kelk, S. M., Olivier, B. G., Stougie, L. & Bruggeman, F. J., 2012, In : Scientific Reports. 2, 580, 580.
32. **What it takes to understand and cure a living system: computational systems biology and a systems biology-driven pharmacokinetics-pharmacodynamics platform.**
Swat, M., Kielbasa, S. M., Polak, S., Olivier, B. G., Bruggeman, F. J., Quinton Tulloch, M., Snoep, J. L., Verhoeven, A. J. & Westerhoff, H. V., 2011, In : Interfaces. 1, p. 16-23
33. **Enzymes or redox couples? The kinetics of thioredoxin and glutaredoxin reactions in a systems biology context**
Pillay, C. S., Hofmeyr, J. H. S., Olivier, B. G., Snoep, J. L. & Rohwer, J. M., 1 Jan 2009, In : Biochemical Journal. 417, 1, p. 269-275 7 p.
34. **Comparing the regulatory behaviour of two cooperative, reversible enzyme mechanisms**
Olivier, B. G., Rohwer, J. M., Snoep, J. L. & Hofmeyr, J. H. S., Sep 2006, In : Systems Biology. 153, 5, p. 335-337 3 p.
35. **Towards building the silicon cell: A modular approach**
Snoep, J. L., Bruggeman, F., Olivier, B. G. & Westerhoff, H. V., Feb 2006, In : BioSystems. 83, 2-3 SPEC. ISS., p. 207-216 10 p.
36. **Modelling cellular systems with PySCeS**
Olivier, B. G., Rohwer, J. M. & Hofmeyr, J. H. S., 15 Feb 2005, In : Bioinformatics. 21, 4, p. 560-561 2 p.
37. **Web-based kinetic modelling using JWS Online**
Olivier, B. G. & Snoep, J. L., 1 Sep 2004, In : Bioinformatics. 20, 13, p. 2143-2144 2 p.
38. **JWS online cellular systems modelling and microbiology**
Snoep, J. L. & Olivier, B. G., Nov 2003, In : Microbiology. 149, 11, p. 3045-3047 3 p.
39. **The regulatory design of an allosteric feedback loop: the effect of saturation by pathway substrate.**
Hofmeyr, J. H. S. & Olivier, B. G., Apr 2002, In : Biochemical Society Transactions. 30, 2, p. 19-25 7 p.
40. **Modelling cellular processes with Python and Scipy**
Olivier, B. G., Rohwer, J. M. & Hofmeyr, J. H. S., 2002, In : Molecular Biology Reports. 29, 1-2, p. 249-254 6 p.