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Erwin received his Ph.D. in biomedical engineering from the University of Virginia in May 2009. His research focused on developing computational systems biology-based tools for reconstructing and analyzing intracellular biochemical reaction networks *in silico*, with the goal of better understanding fundamental diseases and identifying therapeutic targets. Erwin has co-authored 13 peer-reviewed publications in leading technical journals in the field as well as one book chapter, attended several international conferences to present his work, and been involved with two patent disclosures and multiple Federal grants. Erwin received his M.S. in biomedical engineering (2007) and B.S. in computer science (2005) from the University of Virginia.

Before joining CRA, Erwin was a 2009-10 AAAS Science & Technology Policy Fellow, and he worked on various computing research initiatives – including health information technology – at the National Science Foundation. Previously, he was Director of Innovation Networking at the University of Virginia, reporting to the university’s Vice President for Research. In that role, he headed up BMEplanet, a global network for bioengineering established by the university.

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Recent peer-reviewed publications:

Gianchandani, E.P., A.K. Chavali, and J.A. Papin. 2009. The application of flux balance analysis to systems biology. *Wiley Interdisciplinary Reviews: Systems Biology and Medicine* 2 (3): 372-82 (doi 10.1002/wsbm.60).

Gianchandani, E.P., and T.C. Skalak. 2009. BMEplanet: A global collaboration network for bioengineering. *IEEE Engineering in Medicine & Biology* 28(5): 56-7.

Gianchandani, E.P., A.R. Joyce, B.Ø. Palsson, and J.A. Papin. 2009. Functional states of the genome-scale *Escherichia coli* transcriptional regulatory system. *PLoS Computational Biology* 5 (6): e1000403.

Wieghaus, K.A.*, E.P. Gianchandani*, R.A. Neal, M.A. Paige, M.L Brown, J.A. Papin**, and E.A. Botchwey**. 2009. Phthalimide neovascular factor 1 (PNF1) stimulates pro-angiogenic gene transcription and promotes microvascular network expansion *in vivo*. *Biotechnology & Bioengineering* 103(4): 796-807.

Mandell, J.W., G.F. Glass, E.P. Gianchandani, C.N. Locke, S. Amos, T.D. Bourne, D. Schiff, and J.A. Papin. 2009. Dephosphorylation of beta-arrestin 1 in glioblastomas. *Journal of Neuropathology and Experimental Neurology* 68(5): 535-41.

†Chavali, A.K.*, E.P. Gianchandani*, S.M. Peirce-Cottler, M.B. Lawrence, and J.A. Papin. 2008. Characterizing emergent properties of immunological systems with multi-cellular rule-based computational modeling. *Trends in Immunology* 29(20): 589-99.

Wieghaus, K.A.*, E.P. Gianchandani*, M.A. Paige, M.L. Brown, E.A. Botchwey, and J.A. Papin. 2008. Novel pathway compendium analysis elucidates mechanism of a pro-angiogenic synthetic small molecule. *Bioinformatics* 24(20): 2384-90.

Lee, J.M.*, E.P. Gianchandani*, J.A. Eddy, and J.A. Papin. 2008. Dynamic analysis of integrated signaling, metabolic, and regulatory networks. *PLoS Computational Biology* 4(5): e1000086.

Gianchandani, E.P.*, M.A. Oberhardt*, A.P. Burgard, C.D. Maranas, and J.A. Papin. 2008. Predicting biological system objectives de novo from internal state measurements. *BMC Bioinformatics* 9(1): 43.

++Wieghaus, K.A., E.P. Gianchandani, M.L. Brown, J.A. Papin, and E.A. Botchwey. 2007. Mechanistic interrogation of phthalimide neovascular factor 1 (PNF1) using network analysis tools. *Tissue Engineering* 13(10): 2561-75.

†Gianchandani, E.P.*, J.A. Papin*, N.D. Price, A.R. Joyce, and B.Ø. Palsson. 2006. Matrix formalism to describe functional states of transcriptional regulatory systems. *PLoS Computational Biology* 2(8): e101.

Lee, J.M., E.P. Gianchandani, and J.A. Papin. 2006. Flux balance analysis in the era of metabolomics. *Briefings in Bioinformatics* 7(2): 140-50.

Gianchandani, E.P., D.L. Brautigam, and J.A. Papin. 2006. Systems analyses characterize integrated functions of biochemical networks. *Trends in Biochemical Sciences* 31(5): 284-91.

Papin, J.A., E.P. Gianchandani, and S. Subramaniam. 2005. Mapping the genotype-phenotype relationship in cellular signaling networks: building bridges over the unknown, in: *Systems Biology, Volume II: Networks, Models, and Applications*, eds. Isidore Rigoutsos and Gregory Stephanopoulos.

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++Selected by Tissue Engineering as an "Editor's top pick—hot paper" for October 2007.

†Featured on journal cover.