Ilias Tagkopoulos

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Education

- **Princeton University**, Princeton, NJ.
  Postdoctoral Research Fellow, Lewis-Sigler Institute, 2009
  Ph.D. in Electrical Engineering, October 2008.
  M.A. in Electrical Engineering, May 2005.
  PEI-STEP Certificate in Environmental and Public Policy, May 2009.
  Advisors: Saeed Tavazoie (MolBio) and Sun-Yuan Kung (ECE)

- **Columbia University**, New York, NY.
  M.Sc. in Electrical Engineering, February 2003.
  Concentration: Microelectronics & Wireless Networks.
  Advisors: Charles Zuckowski (EE) and Dimitrios Anastassiou (EE)

- **University of Patras**, Patras, Greece.
  Diploma in Electrical and Computer Engineering, June 2001.

Work Experience

- **Full Professor**, University of California, Davis `(2019 - now)`
  Department of Computer Science and UC Davis Genome Center.
- **Associate Professor**, University of California, Davis `(2015 - 2019)`
  Department of Computer Science and UC Davis Genome Center.
- **Assistant Professor**, University of California, Davis `(2009 - 2015)`
  Department of Computer Science and UC Davis Genome Center.
- **Advisor and Science Advisory Board member** `(2010 - now)`
  Science advisor to C-level executives and leaders in the CPG, food, petcare, biotechnology and life science industries.
- **Relationship Manager**, DIT - Sales & Research Analytics, Credit Suisse `(2008 - 2009)`
  Liaison between modeling, programming and business teams. Supervised the development of quantitative financial models and solutions within the investment bank. Member of the 2008 Quantitative Associate class and the Fixed Income Derivatives LOCUS team.
- **Research Assistant**, Lewis-Sigler Institute for Integrative Genomics `(2003 - 2008)`
  Developed a multi-scale microbial evolution simulator and machine learning algorithms for biological data integration.
- **Research Assistant**, Columbia Integrated Systems Laboratory (CISL). `(2001 - 2003)`
  Designed and fabricated a biomimetic mixed signal VLSI chip.

Business

- **Founder and owner** `(2015 - now)`
  Founder of various active small businesses (10-35 employees) related to scientific software development (enterprise-level solutions for Machine Learning, bioinformatics, and AI), tourism (sailing vacations), and trade.

Teaching experience

- **ECS 188**: Ethics in the Era of Technology
  UC Davis, 2012-2015
- **ECS 124**: Theory and Practice of Bioinformatics
  UC Davis, 2010-2016
- **ECS 289K**: Computational Systems and Synthetic Biology
  UC Davis, 2009-2013
- **ECS 171**: Machine Learning
  UC Davis, 2014-now
- **ECS 289G**: Deep Learning
  UC Davis, 2017-now

Upcoming publications

- Pereira B, Wang X, **I. Tagkopoulos**, A systems analysis and the genetic basis of E. coli short and long-term response to biocides. (under revision)
- Wai Shun Mak, Steve Bertolani, XiaoKang Wang, Wen Qiao Tang, **I. Tagkopoulos**, David K. Wilson, Justin B. Siegel, Genomic Mining of Aldehyde Deformylating Oxygenases Defines Structural Features that Enable Engineering of Function. (under revision)
- Kim KJ, Rai N, Kim M, **I. Tagkopoulos**. A network-based model for drug repurposing in Rheumatoid Arthritis. (under review)
- Rai N, Pereira B, Kim M, **I. Tagkopoulos**, Understanding the formation and mechanism of anticipatory responses in *Escherichia coli.* (submitted)

Journal Publications

- Pereira, B, **I. Tagkopoulos**. Benzalkonium chlorides: Uses, regulatory status, and microbial resistance. *Applied and Environmental Microbiology*, AEM-00377. doi:10.1128/AEM.00377-19, 2019
- Moon SJ, Jung MB, Kyung-Su P, **I. Tagkopoulos**, and KJ Kim. Compendium of skin molecular signatures identifies key pathological features associated with fibrosis in systemic sclerosis. *Annals of the Rheumatic Diseases*, doi:10.1136/annrheumdis-2018-214778, 2019
- Kim KJ, Kim M, Adamopoulos I, **I. Tagkopoulos**, Compendium of Synovial Signatures Identifies Pathologic Characteristics for Predicting Treatment Response in Rheumatoid Arthritis. *Clinical Immunology*, doi:10.1016/j.clim.2019.03.002, 2019
- Rai N, Huynh L, Kim M, and **I. Tagkopoulos**. Population collapse and adaptive rescue during longterm chemostat fermentation. *Biotechnology and Bioengineering*, 116, 3, 693-703. doi:10.1002/bit.26898, 2019
- Kim K, **I. Tagkopoulos**. Application of machine learning in rheumatic disease research. *The Korean journal of internal medicine*, doi:10.3904/kjim.2018.349, 2018
- Eetemadi A, and **I. Tagkopoulos**. Genetic Neural Networks: an artificial neural network architecture for capturing gene expression relationships. *Bioinformatics*, doi:10.1093/ bioinformatics/bty945, 2018
- Wang X, Zorraquino V, Kim M, **I. Tagkopoulos**, Predicting the evolution of *Escherichia coli* by a data-driven approach. *Nature Communications*, 3562, 2018.
- Kim M., **I. Tagkopoulos** Data integration and predictive modeling methods for multi-omics datasets. Mol. Omics. 2018,14, 8. PubMed PMID:29725673.
- Kim M, Eetemadi A, **I. Tagkopoulos** DeepPep: Deep proteome inference from peptide profiles. *PLoS Computational Biology.* 13(9): e1005661, 2017
- Bjornson, M, Balcke, G, Xiao, Y, de Souza, A, Wang, J, Zhabinskaya, D, **I. Tagkopoulos**, Tissier, A, Dehesh, K. Integrated omics analyses of retrograde signaling mutant delineate interrelated stress response strata. *Plant Journal.* 2017 Jul;91(1):70-84. doi: 10.1111/tpj.13547. Epub 2017 Apr 29.

- ◇ Zorraquino V, Kim M, Rai N, **I. Tagkopoulos**, The genetic and transcriptional basis of short and long term adaptation across multiple stresses in Escherichia coli. *Molecular Biology and Evolution.* 2016 Dec 21. pii: msw269. doi: 10.1093/molbev/msw269, PubMed PMID: 28007978.
- ◇ Huynh L, **I. Tagkopoulos**, A Parts Database with Consensus Parameter Estimation for Synthetic Circuit Design. *ACS Synthetic Biology.* 2016 Dec 16;5(12):1412-1420. PubMed PMID: 27454439.
- ◇ Kim M, Rai N, Zorraquino V, **I. Tagkopoulos**, Multi-omics integration accurately predicts cellular state in unexplored conditions for Escherichia coli. *Nature Communications.* 2016 Oct 7;7:13090. doi: 10.1038/ncomms13090. PubMed PMID: 27713404; PubMed Central PMCID: PMC5059772.
- ◇ M. Meisner, J. Rosenheim, **I. Tagkopoulos**, "A data-driven, machine learning framework for optimal pest management in cotton", 7(3), *Ecosphere*, 2016
- ◇ D.A. Carlin, R.W. Caster, X. Wang, S.A. Betzenderfer, C. Chen, V.M. Duong, C.V. Ryklansky, A. Alpekin, N. Beaumont, H. Kapoor, N. Kim, H. Mohabbot, B. Pang, R. Teel, L. Whithaus, **I. Tagkopoulos**, J.B. Siegel, "Kinetic characterization of over 100 glycoside hydrolase mutants enables the discovery of structural features correlated with kinetic constants", *PLoS One*, 11(1), 2016
- ◇ N. Rai, A. Ferreiro, A. Neckelmann, A. Soon, A. Yao, J. Siegel, M.T. Facciotti, **I. Tagkopoulos**, "RiboTALE: a versatile and modular tool for the multi-dimensional control of gene expression", 5, *Scientific Reports*, 2015
- ◇ L. Huynh, **I. Tagkopoulos**. "Fast and Accurate Circuit Design Automation through Bounded Search and Hierarchical Model Switching", Apr 28, 25916918, *ACS Synthetic Biology*, 2015
- ◇ M. Kim, V. Zorraquino-Salvo, **I. Tagkopoulos**, "Prediction of phenotypic characteristics from large-scale gene expression profiles", 11(3): e1004127. doi:10.1371/journal.pcbi.1004127, *PLoS Computational Biology*, 2015
- ◇ Taylor-Teeples M, Lin Lc, Trabucco G, de Lucas M, Turco G, Doherty C, Toal T, Gaudinier A,Young NF, Xiong G, Corwin J, Tsoukalas A, Pauly M, Kliebenstein DJ , **I. Tagkopoulos**, Breton G, Ahnert S, Kay SA, Brady SM, Hazen SP. "Environmental, developmental and genotype-dependent regulation of Xylem cell specification and secondary cell wall biosynthesis in *Arabidopsis thaliana*", 517, 571575, *Nature*, 2015
- ◇ A. Tsoukalas, T. Albertson, **I. Tagkopoulos**, "From data to optimal decision making: A data-driven, probabilistic machine learning approach to decision support for patients with Sepsis", 3(1), *Jour. Med. Int. Res.*, 2015
- ◇ Hnin-Hnin Ma, Nasos Tsoukalas, John Rutledge, **I. Tagkopoulos**. "A systems biology analysis of brain microvascular endothelial cell lipotoxicity", *BMC Systems Biology*, 8:80, 2014
- ◇ J. Carrera, R. Estrela, J. Luo, N. Rai, A. Tsoukalas, **I. Tagkopoulos**. "An integrative, genome-scale model reveals the phenotypic landscape of *Escherichia coli*", 10(7):735, *Molecular Systems Biology*, 2014
- ◇ L. Huynh, **I. Tagkopoulos**. "Optimal part and module selection for synthetic gene circuit design automation", 3(8):556, doi: 10.1021/sb400139h, *ACS Synthetic Biology*, 2014
- ◇ E. Gultepe, J. Green, H. Nguyen, J. Adams, T. Albertson, **I. Tagkopoulos**, "From vital signs to clinical outcomes for patients with sepsis: A machine learning basis for a clinical decision support system", 21:315-325, doi: 10.1136/amiajnl-2013-001815, *Journal of the American Medical Informatics Association (JAMIA)*, 2014
- ◇ A. Pavlogiannis, V. Mozhayskiy, **I. Tagkopoulos**, "A flood-based information flow analysis and network minimization method for bacterial systems", 14:137 DOI:10.1186/1471-2105-14-137, *BMC Bioinformatics*, 2013

- M. Dragosits, V. Mozhayskiy, S. Quinones-Soto, **I. Tagkopoulos**, “Evolutionary potential, cross-stress dependencies, and the genetic basis of acquired stress resistance in *E. coli*”, doi:10.1038/msb.2012.76, 9:643, *Molecular Systems Biology*, 2013
- A. Yao, T. Fenton, K. Owsley, P. Seitzer, D. Larsen, H. Lam, J. Lau, A. Nair, J. Tantiongloc, **I. Tagkopoulos**, M. Facciotti, “Promoter activity arising from the fusion of standard BioBrick parts”, 2(2), pp 111120, DOI: 10.1021/sb300114d, *ACS Synthetic Biology*, 2013
- L. Huynh, M. Köppe, **I. Tagkopoulos**, “SBROME: A scalable optimization and module matching framework for automated biosystem design”, DOI: 10.1021/sb300095m2, pp 263-273, *ACS Synthetic Biology*, 2013
- V. Mozhayskiy, **I. Tagkopoulos**, “Microbial evolution in vivo and in silico: methods and applications”, DOI:10.1039/C2IB20095C, 5(2):26277, *Integrative Biology*, 2013
- **I. Tagkopoulos**, “Microbial factories under control: Auto-regulatory control through engineered stress-induced feedback”, 4:1, 1-4, *Bioengineered*, 2013
- Y. Liang, H. Wu, R. Lei, RA. Chong, Y. Wei, X. Lu, **I. Tagkopoulos**, SY. Kung, Q. Yang, G. Hu, Y. Kang, “Transcriptional Network Analysis Identifiies BACH1 as a Master Regulator of Breast Cancer Bone Metastasis”, 287(40):33533-44, *Journal of Biological Chemistry*, 2012
- L. Huynh, J. Kececioglu, M. Köppe, **I. Tagkopoulos**, “Automated Design of Synthetic Gene Circuits through Linear Approximation and Mixed Integer Optimization”, 7(4):e35529, *PLoS ONE*, 2012
- M. Dragosits, D. Nicklas, **I. Tagkopoulos**, “A synthetic biology approach to self-regulatory recombinant protein production in *Escherichia coli*”, 6:2, *Journal of Biological Engineering*, 2012
- V.Mozhayskiy, **I. Tagkopoulos**, “Guided evolution of *in silico* microbial populations in complex environments accelerates evolutionary rates through a step-wise adaptation”, 13:S10, *BMC Bioinformatics*, 2012
- V.Mozhayskiy, **I. Tagkopoulos**, “Horizontal gene transfer dynamics and distribution of fitness effects during microbial *In silico* Evolution”, 13:S13, *BMC Bioinformatics*, 2012
- **I. Tagkopoulos**, Y.Liu, S. Tavazoie, “Predictive Behavior Within Microbial Genetic Networks”, *Science*, 320:1313-7, 2008
- S.Y.Kung, M.W. Mak, and **I. Tagkopoulos**, “Symmetric and Asymmetric Multi-modality Biclustering Analysis for Microarray Data Matrix”, *Journal of Bioinformatics and Computational Biology*, vol 4(2), pp. 275-298, 2006

Selected Peer-Reviewed Conference Publications

- L.Huynh, N. Rai, **I. Tagkopoulos**, ”Parameter inference for gene circuit models”, Proceedings of the 7th International Workshop on Bio-design Automation, IWBDA’15, Seattle, 2015
- L.Huynh, M. Kim, **I. Tagkopoulos**, ”Integration of circuit design automation and genome-scale modeling”, Proceedings of the 6th International Workshop on Bio-design Automation, IWBDA’14, Boston, 2014
- L.Huynh, **I. Tagkopoulos**, ”Optimizing module matching for synthetic gene circuit design automation”, Proceedings of the 5th International Workshop on Bio-design Automation, IWBDA’13, London, 2013
- E. Gultepe, Hien Nguyen, Tim Albertson, **I. Tagkopoulos**, “A Bayesian network for early diagnosis of sepsis patients: a basis for a clinical decision support system”, 2nd IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS), Las Vegas, NV, pp.1-5, 23-25, 2012
- L. Huynh, **I. Tagkopoulos**, “A robust, library-based, optimization-driven method for automatic gene circuit design”, 2nd IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS), Las Vegas, NV, pp.1-6, 24-26, 2012

- L.Huynh, J.Kececioglu, **I. Tagkopoulos**, "Scaling responsibly, Towards a reusable, modular, automated gene circuit design", Proceedings of the 4rth International Workshop on Bio-design Automation, IWBDA'12, San Francisco, 2012
- R. Miller, V.Mozhayskiy, **I. Tagkopoulos**, KL. Ma, "EVEVis: A Multi-Scale Visualization System for Dense Evolutionary Data", 1st IEEE Symposium on Biological Data Visualization, pp. 143-150, Providence, Rhode Island, 2011
- V.Mozhayskiy, R. Miller, KL. Ma, **I. Tagkopoulos**, "A Scalable Multi-scale Framework for Parallel Simulation and Visualization of Microbial Evolution", TeraGrid'11; Salt Lake City, Utah, 2011, DOI:10.1145/2016741.2016749 **(Best Paper Award)**
- V.Mozhayskiy, **I. Tagkopoulos**, "*In silico* Evolution of Multi-scale Microbial Systems in the Presence of Mobile Genetic Elements and Horizontal Gene Transfer", ISBRA'11, Lecture Notes in Bioinformatics, LNBI 6674, pp.262-273, Springer, 2011
- L.Huynh, J.Kececioglu, **I. Tagkopoulos**, "Automated Design of Synthetic Gene Circuits through Linear Approximation and Mixed Integer Optimization", Proceedings of the 3rd International Workshop on Bio-design Automation, IWBDA'11, San Diego, 2011.
- **I. Tagkopoulos**, D. Serpanos, "Gene Classification and Regulatory Prediction Based on Transcriptional Modeling." Proceedings of the IEEE Symposium on Signal Processing and Information Technology, ISSPIT'05, pp. 29-34, Proceedings of the Firth IEEE International Symposium on Signal Processing and Information Technology, Athens, Greece, 2005.
- **I. Tagkopoulos**, "A Transcriptional Approach to Gene Clustering", CIBCB'05, Proceedings of the IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology, pp.1-7, San Diego, California, 2005. **(student paper award)**
- **I. Tagkopoulos**, N. Slavov, S.Y. Kung, "Multi-class Biclustering and Classification Based on Modeling of Gene Regulatory Networks", BIBE'05, Proceedings of the 5th IEEE Symposium on Bioengineering and Bioinformatics, pp. 89-96, Minneapolis, Minnesota, 2005.
- S.Y.Kung, M.W. Mak, and **I. Tagkopoulos**, "Multi-Metric and Multi-Substructure Biclustering Analysis for Gene Expression Data", CSB'05, Proceedings of the IEEE Computational Systems Bioinformatics Conference, pp.123-134, Stanford, California, 2005.
- **I. Tagkopoulos**, C.Zukowski, G.Cavelier, D.Anastassiou, "A Custom FPGA for the Simulation of Gene Regulatory Networks", GLSVLSI'03, Proceedings of the 13th ACM Great Lakes Symposium on VLSI, pp. 135-141, Washington D.C., 2003.
- N.D.Zervas, **I. Tagkopoulos**, V. Spiliotopoulos, D.Soudris, C.E.Goutis, "Comparison of DWT Scheduling Algorithms Alternatives on Programmable Platforms", ISCAS'01, Proceedings of the International Symposium on Circuits and Systems, , pp. 761-764, vol. 2, Sidney, Australia, 2001.

Selected Abstracts and Posters

- M. Kim, **I. Tagkopoulos**, "A Deep Learning proteome reconstruction method for short peptide signatures", invited oral presentation, Blue Waters Symposium, Oregon, US, 2016
- **I. Tagkopoulos**, "Multi-omics modeling, integration and simulation", invited oral presentation, DOE requirements workshop, Bethesda, US, 2016
- M. Kim, N. Rai, **I. Tagkopoulos**, "Deep learning integration for bacterial models", invited oral presentation, 4^{rth} Conference on Quantitative Biology, q-bio'16, Oahu, Hawaii, 2016
- M. Kim, N. Rai, V. Zorraquinno, L. Huynh, **I. Tagkopoulos**, "Deep learning and predictive models of a multi-omics dataset for *Escherichia coli*", Oral presentation, 3rd Conference on Quantitative Biology, q-bio'15, Maui, Hawaii, 2015
- M. Kim, **I. Tagkopoulos**, "A graph-based integrative learning framework for whole-cell modeling", NetSci'14, Berkeley, US, 2014
- J. Carrera, L. Huynh, **I. Tagkopoulos**, "A automated synthetic gene circuit design tool based on mathematical optimization", Poster, 1st Conference on Quantitative Biology, q-bio'13, Honolulu, Hawaii, 2013

- V. Mozhayskiy, M. Dragosits, **I. Tagkopoulos**, “Guided step-wise adaptation of microbial populations insilico and in vivo”. 7th Annual Systems-to-Synthesis Symposium, San Diego, CA, 2012
- **I. Tagkopoulos**, ”Self-regulatory circuits for recombinant protein production”, Poster, 11th Conference on Microbial Genetics and Ecology, BAGECO’11, Corfu, Greece, 2011
- **I. Tagkopoulos**, ”Microbial Evolution in Stressful Environments: Theory and Experiments”, Poster, 11th Conference on Microbial Genetics and Ecology, BAGECO’11, Corfu, Greece, 2011
- V.Mozhayskiy, **I. Tagkopoulos**, “Facilitated Variation of *In Silico* Microbial Populations Affects Evolutionary Rates”, Poster and Talk, 7^{th} International Symposium on Bioinformatics Research and Applications, Changsha, China, May 2011
- V.Mozhayskiy, **I. Tagkopoulos**, ”Large-scale Evolutionary Simulations of Complex Microbial Behaviors in Dynamic Environments”, Poster, 9th Annual International Conference on Computational Systems Bioinformatics, CSB’10, Stanford, 2010
- **I. Tagkopoulos**, ”Advancing Broader Impacts of CISE Projects: Scientific Discovery and Public Dissemination”, Abstract, Invited Participant in NSF Broader Impacts for Research and Discovery Summit, Washington, D.C., 2010
- V.Mozhayskiy, **I. Tagkopoulos**, ”Emergence of Robust Biological Networks in Petascale Simulations of Bacterial Evolution”, Abstract, Extreme Scale I/O and Data Analysis Workshop, NSF/NCSA/TACC, Austin, TX, 2010
- V.Mozhayskiy, **I. Tagkopoulos**, ”Simulations of Microbial Evolution in Fluctuating Environments”, Poster, 18th Annual International Conference on Intelligent Systems for Molecular Biology, ISMB’10, Boston, 2010

SELECTED INVITED TALKS

- **Automating innovation discovery through ML and AI**, Mars Inc., McLean, VA, October 2019
- **Accelerating biological discoveries through optimal experimental design**, Dartmouth University, Hanover, NH, March 2019
- **Machine Learning meets biology**, AutoDesk/ATUM Synthetic Biology symposium, CA, March 2018
- **A science and discovery analytics integration platform**, Waltham Center for Pet Nutrition, UK, March 2018
- **From data to products: using AI to make recipies**, Industry/Academia meeting in Flavor, Nice, FR, March 2018
- **A disease prediction platform for companion animals**, UCSD, CA, September 2017
- **AI-based clinical decision support for Vets**, Banfield Pet Hospitals, Vancouver, WA, February 2017
- **Multi-omics predictive modeling for agriculture**, Bayer, Inc., CA, January 2017
- **Large data integration and predictive analytics for health and nutrition**, Mars Inc., McLean, VA, October 2016
- **An AI-based platform for microbiome analysis**, Second Genome, Inc., CA, Oct 2016
- **Use of EMR patient records and machine learning to predict onset of sepsis**, Engineering in Sepsis workshop, UIUC, May 2016
- **A recommendation system for patients with sepsis**, LLNL, April 2016
- **Multi-omics integration and predictive analytics in HPC environments**,DOE BER-ACSR requirements workshop, North Bethesda, MD, March 2016
- **Predictive analytics and AI in medical informatics**, LLNL/LBNL conference, Monterrey, CA, September 2015

- ◇ **High-performance simulations of multi-omics bacterial models**, Blue Waters Symposium, OR, June 2015
- ◇ **Integration of Multi-omics data for predictive analytics**, Department of Bioengineering, University of California, San Diego, CA, June 2015
- ◇ **Big Data on Small Organisms: Integrative Predictive Modeling with Deep Learning**, Simons Foundation, NY, May 2015
- ◇ **An integrative, data-driven whole-cell model for systems and synthetic biology**, Mosanto Fellows, St. Louis, April 2015
- ◇ **Deep learning and predictive models of a multi-omics dataset for *Escherichia coli***, 3rd Conference on Quantitative Biology, q-bio'15, Maui, Hawaii, 2015
- ◇ **Multi-scale, genome-wide, omics modeling and simulation**, PepTalk15, San Diego, January 2015
- ◇ **Integrative modeling for targeted experimentation in Systems and Synthetic Biology**, Life Sciences, University of Warwick, July 2014
- ◇ **A genome-scale, integrative model for *E. coli* for targeted experimentation**, Biodesign Institute, UIUC, May 2014
- ◇ **Petascale simulations in microbial evolution: Challenges and Applications**, NCSA, May 2014
- ◇ **An integrative E. coli genome-scale model for automated design in synthetic biology**, 2nd Conference on Quantitative Biology, q-bio'14, Big Island, Hawaii, February 2014
- ◇ **An integrative genome-scale model for *E. coli***, DOE Joint Genome Institute (JGI), November 2013
- ◇ **The emergence and genetic basis of cross-stress behavior in *E. coli***, Department of Microbiology, UC Davis, April 2013
- ◇ **The Evolution of Cross-stress Protection in *E. coli***, Department of Microbiology and Environmental Toxicology, UCSC, February 2013
- ◇ **Self-regulatory Recombinant Protein Production through an Integrative Synthetic Biology Approach**, Engineering Genes, Vectors, Constructs and Clones, PepTalk, Palm Springs, January 2013
- ◇ **Multiscale Predictive Models for Synthetic Circuits: Potential and Pitfalls**, Biology and Mathematics in the Bay Area (BaMBA VII), UCSF, November 2011
- ◇ **The Future of Science**, Institute for the Future, Gordon and Betty Moore Foundation, Palo Alto, September 2011
- ◇ **A model-based, synthetic biology approach to recombinant protein production**, 11th Conference on Microbial Genetics and Ecology, BAGECO'11, Corfu, Greece, 2011
- ◇ **An Integrated Approach to Synthetic Biology and Evolution**, Progress in Biotechnology Seminar, UC Davis Biotechnology Seminar Series, Davis, May 2011
- ◇ **Large-scale Evolutionary Simulations of Complex Microbial Behaviors in Dynamic Environments**, 9th Annual International Conference on Computational Systems Bioinformatics, Stanford, 2010
- ◇ **Microbial Evolution in Stressful Environments: Theory and Experiments**, Math Biology Seminar, Department of Mathematics, UC Davis, Davis, April 2011
- ◇ **Emergence of Robust Biological Networks in Petascale Simulations of Bacterial Evolution**, Extreme Scale I/O and Data Analysis Workshop, NSF/NCSA/TACC, Austin, TX, 2010

◇ **Extrapolating in Petascale: Dynamic optimization of simulation environments through process migration**, National Center for Supercomputing Applications Workshop, NCSA, Urbana-Champaign, 2010

◇ **Multiscale models of microbial evolution**, Center for Population Biology, UC Davis, Davis, April 2010

◇ **Emergence of Predictive Capacity within Microbial Networks**, School of Computing, Georgia Institute of Technology, Atlanta, Georgia, May 2009

◇ **LOCUS: An integrative tool for Fixed Income, FX, and other investment instruments**, Credit Suisse, New York, April 2009

Honors & Awards

- **Frontiers of Engineering**, National Academy of Engineering (83 nationwide) `(2016)`
- **IGEM Grand Prize**, First Place, World Championship, Boston, MA `(2014 - 2015)`
- **NSF CAREER award** ($600,000), National Science Foundation, DC. `(2013 - 2018)`
- **Science, Technology& Env. Policy Award** ($60,000), Princeton, NJ. `(2006 - 2008)`
- **Burroghs Wellcome Fellowship** ($130,000), Princeton, NJ. `(2004 - 2006)`
- **Princeton Graduate Fellowship** ($54,000), Princeton, NJ. `(2003 - 2004)`
- **Stanley J. Seeger Fellowship** ($5,000), Princeton, NJ. `(2003 - 2008)`
- **Paul Nichoplas Excellence Award** ($5,000), Columbia University, NY. `(2002 - 2003)`
- **Geroundelis Foundation Scholarship** ($4,000), Boston, MA. `(2001 - 2002)`
- **Teaching Assistant Award** ($500), Columbia University, NY. `(March 2002)`
- **Honorary Distinction Award** ($1,000), Technical Chamber of Greece. `(July 2001)`
- **Erasmus Scholarship** ($5,000), University of Aachen (RWTH), Germany. `(Fall 1998)`

Research Funding

◇ **Petascale Simulations of Complex Biological Behavior in Fluctuating Environments**
National Science Foundation, NSF-OCI 0941360, PI: Tagkopoulos
Dates: 10/2009 - 09/2014, Funds: $115,000 and allocation on the Blue Waters Supercomputer

◇ **A Model-Based System for the Automated Design of Synthetic Genetic Circuits by Mathematical Optimization**
National Science Foundation, NSF-CCF 1146926, PI: Tagkopoulos, co-PI: Matthias Koeppe (UC Davis, Math), John Kececioglu (University of Arizona, CS)
Dates: 10/2011 - 09/2014, Funds: $300,000

◇ **Modeling and Simulation of Microbial Evolution**
NSF Teragrid, TG-ASC110007, PI: Tagkopoulos, co-PI: Vadim Mozhayskiy
Dates: 03/2011 - 12/2012, 1,500,000 SU in supercomputing systems

◇ **An integrative framework for MD-based protein-DNA binding prediction**
NSF XSEDE, DEB130003, PI: Tagkopoulos, co-PI: Vadim Mozhayskiy
Dates: 01/2013 - 12/2013, 600,000 SU in supercomputing systems

◇ **An EMR-based, probabilistic clinical support system for the diagnosis and treatment of sepsis patients**
CITRIS seed funding, PI: Tagkopoulos, co-PI: Tim Albertson (UCDMC), Hien Nguyen (UCDMC), Shawn Newsam (UC Merced) Dates: 06/2012 - 06/2014, Funds: $50,000

◇ **Guiding clinical decisions for sepsis patients: A data-driven, probabilistic approach to EHR data mining**
CTSC seed funding, PI: Tagkopoulos, co-PI: Tim Albertson (UCDMC) Dates: 06/2013 - 06/2014, Funds: $20,000

◇ **Evolution and dynamics of associative memory in bacterial populations**
Department of Defense, PI: Tagkopoulos
Dates: 07/2012 - 06/2015, Funds: $495,000

- **Instrumentation for Adaptive Evolution in Bacteria**
  Department of Defense, PI: Tagkopoulos
  Dates: 06/2013 - 05/2014, Funds: $250,000
- **CAREER: Integrative Synthetic Biology: A Scalable Framework for Modular Multilevel Design**
  National Science Foundation, PI: Tagkopoulos
  Dates: 02/2013 - 02/2018, Funds: $600,000
- **Elucidating the Genetic Basis and Evolutionary Potential of Cross-stress Behavior in Escherichia coli**
  National Science Foundation, PI: Tagkopoulos
  Dates: 07/2013 - 06/2015, Funds: $212,000
- **An integrated systems biology approach to elucidate viral resistance signaling networks in tomato**
  National Science Foundation, PI: Dinesh-Kumar Savithramma, Co-PIs: Gilbertson, Ullman, Tagkopoulos
  Dates: 07/2014 - 06/2019, Funds: $1,624,000
- **EVOPROG: General-purpose programmable evolution machine on-a-chip**
  CORDIS FP7-ICT 610730, PI: Alfonso Jaramillo (UoWarwick), Co-PIs: Isalan, Rodriguez, de Lorenzo, Cronin, Tagkopoulos
  Dates: 10/2013 - 09/2016, Funds: $3,821,000
- **FIGARO:Flexible and Precise Irrigation Platform to Improve Farm Scale Water Productivity**
  CORDIS FP7-ICT 610730, PI: Netafim LTD, Israel, 17 Universities
  Dates: 10/2012 - 09/2017, Role: Participant as an external expert in Decision Support Systems (DSS)
- **Big Data on Small Organisms: Petascale Simulations of Data-driven Whole-cell Microbial Models**
  National Science Foundation, NSF-ACI, PI: Tagkopoulos
  Dates: 06/2015 - 06/2018, Funds: $40,000 and allocation on the Blue Waters Supercomputer
- **Developing advanced chemical and computational methods for assessing organoleptic properties of olive oil**
  Bi-national Agricultural Research & Development Fund, BARD US-4962-16, PI: Wang
  Dates: 06/2016 - 06/2019, Funds: $305,000
- **ABI Innovation: EAGER: Towards an optimal experimental design framework with Omics Data**
  National Science Foundation, NSF-DBI, PI: Tagkopoulos
  Dates: 09/2017 - 09/2019, Funds: $300,000
- **Predictive multi-omics profiling**
  MARS Inc. PI: Tagkopoulos
  Proprietary algorithms and models for multi-omics profiling. Undisclosed data and amounts (Multi-year R01-level funding). Dates: 09/2016 - now

Trainees

- **Current:**
  - Dr. Navneet Rai, Postdoctoral Research Associate
  Ph.D. in Synthetic Biology, Indian Institute of Technology, Bombay, India
  - Dr. Bo Mi Lee, Postdoctoral Research Associate
  Ph.D. in Structural Engineering, UCSD, CA, USA

  - Ameen Eetemadi, 6^{th} year Ph.D. Candidate in Computer Science, UC Davis
  - Beatriz Pereira, 5^{rth} year Ph.D. Candidate in Microbiology, UC Davis
  - Xiaokang Wang, 6^{th} year Ph.D. Candidate in Biomedical Engineering, UC Davis

- Cheng-En Tan, 4^{nd} year Ph.D. Candidate in Computer Science, UC Davis
- Trevor Chan, 2^{nd} year Ph.D. Candidate in Computer Science, UC Davis
- Kit Sang Chu, 2^{nd} year Ph.D. Candidate in Biophysics, UC Davis
- Zhi Zang, 1^{st} year Ph.D. Candidate in Computer Science, UC Davis

◇ **Past:**
- Dr. Ki-Jo Kim, MD, Ph.D., Visiting Scholar (2016-2018)
currently: Associate Professor, Catholic University of Korea
- Dr. Nasos Tsoukalas, Postdoctoral Research Associate
Ph.D. in Electrical Engineering, University of Patras, Greece
currently: Research Scientist at New York University - Abu Dhabi
- Dr. Violeta Zorraquino Salvo, Postdoctoral Research Associate
Ph.D. in Microbiology, University of Pablona
currently: Research Scientist, Zymergen Inc.
- Dr. Javier Carrera, Ph.D. in Synthetic Biology, Universite de Evry, France
currently: Postdoctoral Research Associate at Stanford University
- Dr. Semarhy Quinones-Soto, Ph.D. in Microbiology, University of California-Davis
currently: Faculty Instructor at Sacramento State University, Sacramento, CA
- Dr. Jiyeon Park, Ph.D. in Microbiology, University of Illinois, Urbana-Champaign
currently: Research staff at the Pacific Northwest National Laboratory, Richland, WA
- Dr. Martin Dragosits, Ph.D. in Biotechnology, BOKU, Austria
- Dr. Vadim Mozhayskiy, Ph.D. in Physical Chemistry, USC
currently: Thermo-Fisher
- Dr. Linh Huynh, Computer Science, UC Davis
currently: Postdoctoral Associate in UC Davis
- Dr. Minseung Kim, Computer Science, UC Davis
currently: Team Lead in Machine Learning, PIPA LLC
- Dr. Matthew Meisner, Population & Ecology (with S. Schreiber, J. Rosenheim)
currently: Head of Data Analytics at Farmer's Business Network, Inc.
- Nicholas Joodi, currently data scientist in Scribd.
- Eren Gultepe, currently Ph.D. Candidate in Neuroscience, Queen's University
- Daniel Nicklas, currently Ph.D. Candidate in Biomedical Engineering, UC Davis
- Roy Runyu Shi, currently Ph.D. Candidate in Computer Science, CMU-SV **- Mohammad Gharehyazie**, currently Ph.D. Candidate in Computer Science, UC Davis
- Andreas Pavlogiannis, currently Ph.D. Candidate in Computer Science, IST, Austria
- Adam Sumner, currently at Dynamic Bio, Inc.

PHD COMMITTEES

- Krishna Kumar Singh, Ph.D. Candidate in Computer Science (Advisor: YJ. Lee)
- David Haley, Ph.D. Candidate in Computer Science (Advisor: D. Doty)
- Alex Carlin, Ph.D. Candidate in Chemistry (Advisor: J. Siegel)
- Steven Bertolani, Ph.D. Candidate in Chemistry (Advisor: J. Siegel)
- Yuitian Cui, Ph.D Candidate in Chemistry (Advisor: J. Siegel)
- William Wright, Ph.D Candidate in Mathematics (Advisor: M. Friedlander)
- Aubrey Gress, Ph.D. Candidate in Computer Science (Advisor: I. Davidson)
- Victor Missirian, Ph.D. Candidate in Computer Science (Advisor: V. Filkov)
- Spencer Mathews, Ph.D. Candidate in Biophysics (Advisor: J. Crutchfield)
- Christopher Schwarz, Ph.D. Candidate in Computer Science (Advisor: O. Carmichael)
- Jishang Wei, Ph.D. Candidate in Computer Science (Advisor: KL. Ma)
- Yu-Hsuan Chan, Ph.D. Candidate in Computer Science (Advisor: KL. Ma)
- Xiang Wang, Ph.D. Candidate in Computer Science (Advisor: I. Davidson)
- Kristin Lui, Ph.D. Candidate in Mathematics (Advisor: I. Davidson)
- Rushell Neches, Ph.D. Candidate in Microbiology (Advisor: J. Eisen)
- Leonid Shamis, M.Sc. Candidate in Computer Science (Advisor: I. Davidson)

Panel Service

- **National Science Foundation**, Panelist, Broader Impact Panel (CISE Division) `(2010)`
- **National Science Foundation**, Panelist, Proposal Review Panel (BIO Division) `(2011)`
- **National Science Foundation**, Panelist, Proposal Review Panel (BIO Division) `(2012)`
- **National Science Foundation**, Consortium for Mathematics, Panelist and author `(2012)`
- **National Science Foundation**, Panelist, Proposal Review Panel (CISE Division) `(2013a)`
- **National Science Foundation**, Panelist, Proposal Review Panel (CISE Division) `(2013b)`
- **National Science Foundation**, Panelist, Proposal Review Panel (CISE Division) `(2014)`
- **National Institutes of Health**, Panelist, Scientific Review Group (NHLBI) `(2015a)`
- **National Institutes of Health**, Panelist, Scientific Review Group (NHLBI) `(2015b)`
- **Department of Energy**, Panelist, BER-ASCR requirements review workshop `(2016)`
- **National Science Foundation**, Panelist, Proposal Review Panel (BIO Division) `(2016)`
- **National Science Foundation**, Panelist, Proposal Review Panel (BIO Division) `(2018)`
- **US Department of Agriculture**, Panelist, Proposal Review Panel `(2019)`

Activities & Broader Impacts

Reviewer for various journals (NPG, AAAS, BMC, Bioinformatics, AMIA, EMBO, ACM, IEEE Transactions, NAR, ACS, among others). REU advisor (6-8 students), UC Davis Biotechnology (2-3 students) and IGEM synthetic biology team advising (6-10 students per year, providing space, mentorship, funding).