

Stanford



Markus Covert

Associate Professor of Bioengineering and, by courtesy, of Chemical and Systems Biology

Bio

BIO

Our focus is on building computational models of complex biological processes, and using these models to guide an experimental program. Such an approach leads to a relatively rapid identification and validation of previously unknown components and interactions. Biological systems of interest include metabolic, regulatory and signaling networks as well as cell-cell interactions. Current research involves the dynamic behavior of NF-kappaB, an important family of transcription factors whose aberrant activity has been linked to oncogenesis, tumor progression, and resistance to chemotherapy.

ACADEMIC APPOINTMENTS

- Associate Professor, Bioengineering
- Associate Professor (By courtesy), Chemical and Systems Biology
- Member, Bio-X
- Faculty Fellow, Stanford ChEM-H

HONORS AND AWARDS

- Ezra Taft Benson Presidential Scholar, Brigham Young University (1991-1997)
- Robert Black Postdoctoral Fellow, Damon Runyon Cancer Research Foundation (2004-2006)

PROFESSIONAL EDUCATION

- Ph.D., UCSD , Bioengineering/ Bioinformatics (2003)
- M.S., UCSD , Bioengineering (2002)
- B.S., Brigham Young University , Chemical Engineering (1997)

LINKS

- Lab Website: <https://www.covert.stanford.edu/>

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

Our focus is on building computational models of complex biological processes, and using these models to guide an experimental program. Such an approach leads to a relatively rapid identification and validation of previously unknown components and interactions. Biological systems of interest include metabolic, regulatory and signaling networks as well as cell-cell interactions. Current research involves the dynamic behavior of NF-kappaB, an important family of transcription factors whose aberrant activity has been linked to oncogenesis, tumor progression, and resistance to chemotherapy.

Teaching

COURSES

2019-20

- Bioengineering Departmental Research Colloquium: BIOE 393 (Aut, Win)
- Bon Appétit, Marie Curie! The Science Behind Haute Cuisine: BIOE 32Q (Spr)
- Bon Appétit, Marie Curie! The Science behind French Cooking: OSPPARIS 25 (Win)
- Systems Biology: BIOE 101, BIOE 210 (Aut)

2018-19

- Bon Appétit, Marie Curie! The Science Behind Haute Cuisine: BIOE 32Q (Spr)
- Systems Biology: BIOE 101, BIOE 210 (Aut)

2017-18

- Bon Appétit, Marie Curie! The Science Behind Haute Cuisine: BIOE 32Q (Spr)
- Electricity, Magnetism and Optics with Laboratory: OSPPARIS 53 (Win)
- Engineering Concepts Applied to Physiology: BIOE 300B (Aut)
- Systems Biology: BIOE 101, BIOE 210 (Aut)

2016-17

- Bon Appétit, Marie Curie! The Science Behind Haute Cuisine: BIOE 32Q (Spr)
- Engineering Concepts Applied to Physiology: BIOE 300B (Aut)
- Systems Biology: BIOE 101, BIOE 210 (Aut)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Jay Bhasin, Salil Bhate, Kara Brower, Hannah Kempton, Deze Kong, Linfeng Yang

Postdoctoral Faculty Sponsor

Eran Agmon, Taryn Gillies

Doctoral Dissertation Advisor (AC)

Katie Bodner, Heejo Choi, Mialy DeFelice, Travis Horst, Stevan Jeknic, Takamasa Kudo, Gwanggyu Sun

Master's Program Advisor

Noah Young

Doctoral (Program)

Eliel Akinbami, Jay Bhasin, Katie Bodner, Brianna Chrisman, Tyler Cork, Mialy DeFelice, Nelson Hall, Ali Kight, Mira Moufarrej, Gwanggyu Sun

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Bioengineering (Phd Program)
- Biomedical Informatics (Phd Program)
- Chemical and Systems Biology (Phd Program)

Publications

PUBLICATIONS

- **Live-cell measurements of kinase activity in single cells using translocation reporters** *NATURE PROTOCOLS*
Kudo, T., Jeknic, S., Macklin, D. N., Akhter, S., Hughey, J. J., Regot, S., Covert, M. W.
2018; 13 (1): 155–69
- **Deep Learning Automates the Quantitative Analysis of Individual Cells in Live-Cell Imaging Experiments.** *PLoS computational biology*
Van Valen, D. A., Kudo, T., Lane, K. M., Macklin, D. N., Quach, N. T., DeFelice, M. M., Maayan, I., Tanouchi, Y., Ashley, E. A., Covert, M. W.
2016; 12 (11)
- **High-sensitivity measurements of multiple kinase activities in live single cells.** *Cell*
Regot, S., Hughey, J. J., Bajar, B. T., Carrasco, S., Covert, M. W.
2014; 157 (7): 1724-1734
- **Accelerated discovery via a whole-cell model.** *Nature methods*
Sanghvi, J. C., Regot, S., Carrasco, S., Karr, J. R., Gutschow, M. V., Bolival, B., Covert, M. W.
2013; 10 (12): 1192-1195
- **A Whole-Cell Computational Model Predicts Phenotype from Genotype** *CELL*
Karr, J. R., Sanghvi, J. C., Macklin, D. N., Gutschow, M. V., Jacobs, J. M., Bolival, B., Assad-Garcia, N., Glass, J. I., Covert, M. W.
2012; 150 (2): 389-401
- **Single-cell NF-kappa B dynamics reveal digital activation and analogue information processing** *NATURE*
Tay, S., Hughey, J. J., Lee, T. K., Lipniacki, T., Quake, S. R., Covert, M. W.
2010; 466 (7303): 267-U149
- **A Noisy Paracrine Signal Determines the Cellular NF-kappa B Response to Lipopolysaccharide** *SCIENCE SIGNALING*
Lee, T. K., Denny, E. M., Sanghvi, J. C., Gaston, J. E., Maynard, N. D., Hughey, J. J., Covert, M. W.
2009; 2 (93)
- **Combinatorial processing of bacterial and host-derived innate immune stimuli at the single-cell level.** *Molecular biology of the cell*
Gutschow, M. V., Mason, J. C., Lane, K. M., Maayan, I., Hughey, J. J., Bajar, B. T., Amatya, D. N., Valle, S. D., Covert, M. W.
2018: mbcE18070423
- **Combining Comprehensive Analysis of Off-Site Lambda Phage Integration with a CRISPR-Based Means of Characterizing Downstream Physiology** *MBIO*
Tanouchi, Y., Covert, M. W.
2017; 8 (5)
- **Measuring Signaling and RNA-Seq in the Same Cell Links Gene Expression to Dynamic Patterns of NF- κ B Activation.** *Cell systems*
Lane, K., Van Valen, D., DeFelice, M. M., Macklin, D. N., Kudo, T., Jaimovich, A., Carr, A., Meyer, T., Pe'er, D., Boutet, S. C., Covert, M. W.
2017; 4 (4): 458-469 e5
- **High-resolution imaging and computational analysis of haematopoietic cell dynamics in vivo.** *Nature communications*
Koechlein, C. S., Harris, J. R., Lee, T. K., Weeks, J., Fox, R. G., Zimdahl, B., Ito, T., Blevins, A., Jung, S., Chute, J. P., Chourasia, A., Covert, M. W., Reya, et al
2016; 7: 12169-?
- **NetworkPainter: dynamic intracellular pathway animation in Cytobank** *BMC BIOINFORMATICS*
Karr, J. R., Guturu, H., Chen, E. Y., Blair, S. L., Irish, J. M., Kotecha, N., Covert, M. W.
2015; 16
- **Summary of the DREAM8 Parameter Estimation Challenge: Toward Parameter Identification for Whole-Cell Models.** *PLoS computational biology*
Karr, J. R., Williams, A. H., Zucker, J. D., Raue, A., Steiert, B., Timmer, J., Kreutz, C., Wilkinson, S., Allgood, B. A., Bot, B. M., Hoff, B. R., Kellen, M. R., Covert, et al
2015; 11 (5)
- **Summary of the DREAM8 Parameter Estimation Challenge: Toward Parameter Identification for Whole-Cell Models.** *PLoS computational biology*

- Karr, J. R., Williams, A. H., Zucker, J. D., Raue, A., Steiert, B., Timmer, J., Kreutz, C., Wilkinson, S., Allgood, B. A., Bot, B. M., Hoff, B. R., Kellen, M. R., Covert, et al
2015; 11 (5): e1004096
- **Single-cell variation leads to population invariance in NF- κ B signaling dynamics.** *Molecular biology of the cell*
Hughey, J. J., Gutschow, M. V., Bajar, B. T., Covert, M. W.
2015; 26 (3): 583-590
 - **NetworkPainter: dynamic intracellular pathway animation in Cytobank.** *BMC bioinformatics*
Karr, J. R., Guturu, H., Chen, E. Y., Blair, S. L., Irish, J. M., Kotecha, N., Covert, M. W.
2015; 16: 172-?
 - **WholeCellSimDB: a hybrid relational/HDF database for whole-cell model predictions** *DATABASE-THE JOURNAL OF BIOLOGICAL DATABASES AND CURATION*
Karr, J. R., Phillips, N. C., Covert, M. W.
2014
 - **Nonlytic viral spread enhanced by autophagy components** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Bird, S. W., Maynard, N. D., Covert, M. W., Kirkegaard, K.
2014; 111 (36): 13081-13086
 - **Nonlytic viral spread enhanced by autophagy components.** *Proceedings of the National Academy of Sciences of the United States of America*
Bird, S. W., Maynard, N. D., Covert, M. W., Kirkegaard, K.
2014; 111 (36): 13081-13086
 - **The future of whole-cell modeling** *CURRENT OPINION IN BIOTECHNOLOGY*
Macklin, D. N., Ruggero, N. A., Covert, M. W.
2014; 28: 111-115
 - **Incorporation of flexible objectives and time-linked simulation with flux balance analysis.** *Journal of theoretical biology*
Birch, E. W., Udell, M., Covert, M. W.
2014; 345: 12-21
 - **WholeCellSimDB: a hybrid relational/HDF database for whole-cell model predictions.** *Database : the journal of biological databases and curation*
Karr, J. R., Phillips, N. C., Covert, M. W.
2014; 2014
 - **Accelerated discovery via a whole-cell model** *NATURE METHODS*
Sanghvi, J. C., Regot, S., Carrasco, S., Karr, J. R., Gutschow, M. V., Bolival, B., Covert, M. W.
2013; 10 (12): 1192-?
 - **Towards a whole-cell modeling approach for synthetic biology** *CHAOS*
Purcell, O., Jain, B., Karr, J. R., Covert, M. W., Lu, T. K.
2013; 23 (2)
 - **Single-Cell and Population NF- κ B Dynamic Responses Depend on Lipopolysaccharide Preparation** *PLOS ONE*
Gutschow, M. V., Hughey, J. J., Ruggero, N. A., Bajar, B. T., Valle, S. D., Covert, M. W.
2013; 8 (1)
 - **WholeCellKB: model organism databases for comprehensive whole-cell models.** *Nucleic acids research*
Karr, J. R., Sanghvi, J. C., Macklin, D. N., Arora, A., Covert, M. W.
2013; 41 (Database issue): D787-92
 - **Accelerated discovery via a whole-cell model** *Nature Methods*.
Sanghvi, J. C., Regot, S., Carrasco, G. S., Karr, J. R., Gutschow, M. V., Bolival, B., Covert, M.
2013
 - **WholeCellViz: data visualization for whole-cell models.** *BMC bioinformatics*
Lee, R., Karr, J. R., Covert, M. W.
2013; 14 (1): 253-?

- **WholeCellKB: model organism databases for comprehensive whole-cell models** *NUCLEIC ACIDS RESEARCH*
Karr, J. R., Sanghvi, J. C., Macklin, D. N., Arora, A., Covert, M. W.
2013; 41 (D1): D787-D792
- **Single-cell and population NF- κ B dynamic responses depend on lipopolysaccharide preparation.** *PloS one*
Gutschow, M. V., Hughey, J. J., Ruggero, N. A., Bajar, B. T., Valle, S. D., Covert, M. W.
2013; 8 (1)
- **Determining Host Metabolic Limitations on Viral Replication via Integrated Modeling and Experimental Perturbation** *PLOS COMPUTATIONAL BIOLOGY*
Birch, E. W., Ruggero, N. A., Covert, M. W.
2012; 8 (10)
- **Neuron-to-neuron transmission of alpha-synuclein fibrils through axonal transport** *ANNALS OF NEUROLOGY*
Freundt, E. C., Maynard, N., Clancy, E. K., Roy, S., Bousset, L., Sourigues, Y., Covert, M., Melki, R., Kirkegaard, K., Brahic, M.
2012; 72 (4): 517-524
- **Competing pathways control host resistance to virus via tRNA modification and programmed ribosomal frameshifting** *MOLECULAR SYSTEMS BIOLOGY*
Maynard, N. D., Macklin, D. N., Kirkegaard, K., Covert, M. W.
2012; 8
- **High-throughput, single-cell NF-kappa B dynamics** *CURRENT OPINION IN GENETICS & DEVELOPMENT*
Lee, T. K., Covert, M. W.
2010; 20 (6): 677-683
- **The virus as metabolic engineer** *BIOTECHNOLOGY JOURNAL*
Maynard, N. D., Gutschow, M. V., Birch, E. W., Covert, M. W.
2010; 5 (7): 686-694
- **A Forward-Genetic Screen and Dynamic Analysis of Lambda Phage Host-Dependencies Reveals an Extensive Interaction Network and a New Anti-Viral Strategy** *PLOS GENETICS*
Maynard, N. D., Birch, E. W., Sanghvi, J. C., Chen, L., Gutschow, M. V., Covert, M. W.
2010; 6 (7)
- **Computational modeling of mammalian signaling networks** *WILEY INTERDISCIPLINARY REVIEWS-SYSTEMS BIOLOGY AND MEDICINE*
Hughey, J. J., Lee, T. K., Covert, M. W.
2010; 2 (2): 194-209
- **Genome-scale metabolic networks** *WILEY INTERDISCIPLINARY REVIEWS-SYSTEMS BIOLOGY AND MEDICINE*
Terzer, M., Maynard, N. D., Covert, M. W., Stelling, J.
2009; 1 (3): 285-297
- **A dynamic network of transcription in LPS-treated human subjects** *BMC SYSTEMS BIOLOGY*
Seok, J., Xiao, W., Moldawer, L. L., Davis, R. W., Covert, M. W.
2009; 3
- **Integrating metabolic, transcriptional regulatory and signal transduction models in Escherichia coli** *BIOINFORMATICS*
Covert, M. W., Xiao, N., Chen, T. J., Karr, J. R.
2008; 24 (18): 2044-2050
- **Integrated Flux Balance Analysis Model of Escherichia coli** *Bioinformatics.*
Covert, M. W., Xiao, N., Chen, T. J., Karr, J. R.
2008; 18 (24): 2044-2050
- **Achieving stability of lipopolysaccharide-induced NF-kappa B activation** *SCIENCE*
Covert, M. W., Leung, T. H., Gaston, J. E., Baltimore, D.
2005; 309 (5742): 1854-1857
- **Integrated regulatory and metabolic models** *Computational Systems Biology, Academic Press, New York*
Covert, M.W.

2005

- **Computational Systems Biology.** *Integrated regulatory and metabolic models*
Covert, M. W.
Academic Press.2005
- **Integrating high-throughput and computational data elucidates bacterial networks** *NATURE*
Covert, M. W., Knight, E. M., Reed, J. L., Herrgard, M. J., Palsson, B. O.
2004; 429 (6987): 92-96
- **Reconstruction of microbial transcriptional regulatory networks** *CURRENT OPINION IN BIOTECHNOLOGY*
Herrgard, M. J., Covert, M. W., Palsson, B. O.
2004; 15 (1): 70-77
- **Identifying constraints that govern cell behavior: A key to converting conceptual to computational models in biology?** *BIOTECHNOLOGY AND BIOENGINEERING*
Covert, M. W., Famili, I., Palsson, B. O.
2003; 84 (7): 763-772
- **Reconciling gene expression data with known genome-scale regulatory network structures** *3rd International Conference on Systems Biology 2002*
Herrgard, M. J., Covert, M. W., Palsson, B. O.
COLD SPRING HARBOR LAB PRESS, PUBLICATIONS DEPT.2003: 2423-34
- **Constraints-based models: Regulation of gene expression reduces the steady-state solution space** *JOURNAL OF THEORETICAL BIOLOGY*
Covert, M. W., Palsson, B. O.
2003; 221 (3): 309-325
- **Transcriptional regulation in constraints-based metabolic models of Escherichia coli** *JOURNAL OF BIOLOGICAL CHEMISTRY*
Covert, M. W., Palsson, B. O.
2002; 277 (31): 28058-28064
- **Genome-scale metabolic model of Helicobacter pylori 26695** *9th International Conference on Microbial Genomes*
Schilling, C. H., Covert, M. W., Famili, I., Church, G. M., Edwards, J. S., Palsson, B. O.
AMER SOC MICROBIOLOGY.2002: 4582-93
- **Metabolic modelling of microbes: the flux-balance approach** *Environ Microbiol.*
Edwards, J. S., Covert, M. W., Palsson, B. O.
2002; 3 (4): 133-40
- **Regulation of gene expression in flux balance models of metabolism** *JOURNAL OF THEORETICAL BIOLOGY*
Covert, M. W., Schilling, C. H., Palsson, B.
2001; 213 (1): 73-88
- **Metabolic modeling of microbial strains in silico** *TRENDS IN BIOCHEMICAL SCIENCES*
Covert, M. W., Schilling, C. H., Famili, I., Edwards, J. S., Goryanin, I. I., Selkov, E., Palsson, B. O.
2001; 26 (3): 179-186
- **Encyclopedia of Microbiology.** *Genomic Engineering of Bacterial Metabolism*
Edwards, J. S., Schilling, C. H., Covert, M. W., Smith, S. J., Palsson, B. O.
Academic Press.2000