

Speakers, Lecture topics and References

Research talks:

Nagasuma Chandra: From genome sequence to systems models of *Mycobacterium tuberculosis*: Insights for drug discovery

Kunihiko Kaneko: Multi-level evolutionary dynamics

Andreas Wagner: On the origins of evolutionary innovations (two talks including survey)

Lecture courses:

Matthias Heinemann

Topic: Principles of metabolism

1. Introduction into metabolism (basics, stoichiometric models, flux balance analysis, ^{13}C flux analysis, metabolomics)
2. Flux-sensing in metabolism (principle how cells regulate their metabolism, kinetic model of metabolism, consequences of flux sensing)
3. Options for the last lecture (to be decided based on participant interest, etc.)
 - (a) metabolism on the single cell-level (incl. measurement techniques, bistability in metabolism)
 - (b) multidimensional optimality of microbial metabolism
 - (c) new predictive flux balance analysis

Suckjoon Jun

Topic to be announced

Pankaj Mehta

Topic: Energy, information and computation in cells

The tremendous advances in our ability to understand and manipulate cellular information processing networks raises several fundamental physics questions: How do the molecular components of cellular circuits exploit energy consumption to improve information processing? Can one utilize ideas from thermodynamics to improve the design of synthetic cellular circuits? The lectures demonstrate these ideas using several simple examples and discuss the implications of these theoretical ideas for the emerging field of synthetic biology.

References:

1. Hopfield, John J. "Kinetic proofreading: a new mechanism for reducing errors in biosynthetic processes requiring high specificity." *Proceedings of the National Academy of Sciences* 71.10 (1974): 4135-4139.
2. Berg, Howard C., and Edward M. Purcell. "Physics of chemoreception." *Biophysical journal* 20.2 (1977).
3. Mehta, Pankaj, Alex H. Lang, and David J. Schwab. "Landauer in the age of synthetic biology: energy consumption and information processing in biochemical networks." *arXiv preprint arXiv:1505.02474* (2015).

Yitzhak Pilpel

Topic: Evolution of gene expression

The lectures will discuss various methods to study how gene expression evolves; these will include comparative genomics, synthetic gene approaches, and experimental evolution. A special emphasis will be given to evolution of networks that control transcription and translation. Results from simple model systems will be discussed, including bacteria and yeast, and in addition cancerous cells.

Some relevant references will include (PDFs can be downloaded from the Pilpel lab's website <http://longitude.weizmann.ac.il>):

1. Mitchell et al nature 2009
2. Tuller et all Cell 2010
3. Yona et al pnas 2012
4. Yona et al eLife 2013
5. Gingold et al. Cell 2014
6. Yona et al Cell 2015

Nathan Price

Topic: Modeling of metabolism and its regulation

1. Introduction to metabolic modeling and gene regulatory networks
 2. Concepts and approaches for integrated modeling of gene regulatory and metabolic networks
 3. Research talk on integrated modeling of regulatory-metabolic networks
- Lectures would cover, among other things, stoichiometric models and flux balance analysis, including single cell FBA simulations in *E. coli* and yeast.

Matthew Scott

Topic: Quantitative methods in bacterial physiology

1. Historical case studies - Monod (1949), Schaechter et al (1958), Neidhardt & Magasanik (1960)
2. Mathematical methods - cell doubling and exponential growth, bacterial 'growth laws'
3. Interfacing mechanistic models with host physiology - Case study on growth-dependent susceptibility to ribosome targeting antibiotics

References:

1. Monod (1949)
<http://www.annualreviews.org/doi/pdf/10.1146/annurev.mi.03.100149.002103>
2. Schaechter et al (1958)
<http://mic.microbiologyresearch.org/content/journal/micro/10.1099/00221287-19-3-592>
3. Neidhardt & Magasanik (1960)
<http://www.sciencedirect.com/science/article/pii/0006300260907575>
4. Scott et al (2010)
<http://www.sciencemag.org/content/330/6007/1099.short>
5. Grulich et al (2015)
<http://msb.embopress.org/content/11/3/796.abstract>

Gary Stormo

Topic: Regulation of gene expression in bacteria

1. Overview of transcriptional regulation: lac and lambda examples
positive, negative, effector on/off cases
Savageau's demand theory
brief introduction to Alon's work on network motifs, characteristics and advantages of different strategies
2. TF motifs
basic PWM model, its limitations and extensions
obtaining model parameters from various datatypes: motif discovery, phylogenetic conservation, experimental data including new high-throughput technique
recognition models and protein design for specificity
3. post-transcriptional models
several examples including RNA-protein interactions, riboswitches, frame-shifting, etc
opportunities for autoregulation, molecular mimicry ideas and examples

References: Shen-

Orr et al (2002)

<http://www.nature.com/ng/journal/v31/n1/full/ng881.html>

Breaker 2011

<http://www.cell.com/molecular-cell/abstract/S1097-2765%2811%2900645-9>

Gary D. Stormo, Modeling the specificity of protein-DNA interactions, *Quantitative Biology* (2013), 1(2): 115-130

Tom Kuhlmann

Topic: Quantitative characterization of the molecular basis of evolution

1. Molecular mechanisms of mutation and evolution – point mutation, horizontal gene transfer, and transposition
2. Statistics and models of mutations and their effects – temporal and spatial randomness and Target Theory
3. Modern experimental methods and real time measurement of mutations in individual live cells

References:

1. Luria and Delbruck (1943): <http://www.genetics.org/content/28/6/491.short>
2. Knudson (1971): <http://www.pnas.org/content/68/4/820.full.pdf>
3. Babic et al (2008): <http://www.ncbi.nlm.nih.gov/pubmed/18339941>
4. Elez et al (2010): <http://www.ncbi.nlm.nih.gov/pubmed/20674359>