ECE/CS/BioEn 6760
Engineering Genetic Circuits

Chris J. Myers

Lecture 0: Course Overview

Course Information

- Webpage: access using CANVAS
- Meeting time: TTh 2-3:20pm
- Meeting place: MEB 2325
- Office hours: TTh 3:30-4:30pm or by appointment
- Email: myers@ece.utah.edu
- Office: MEB 4112 / 581-6490

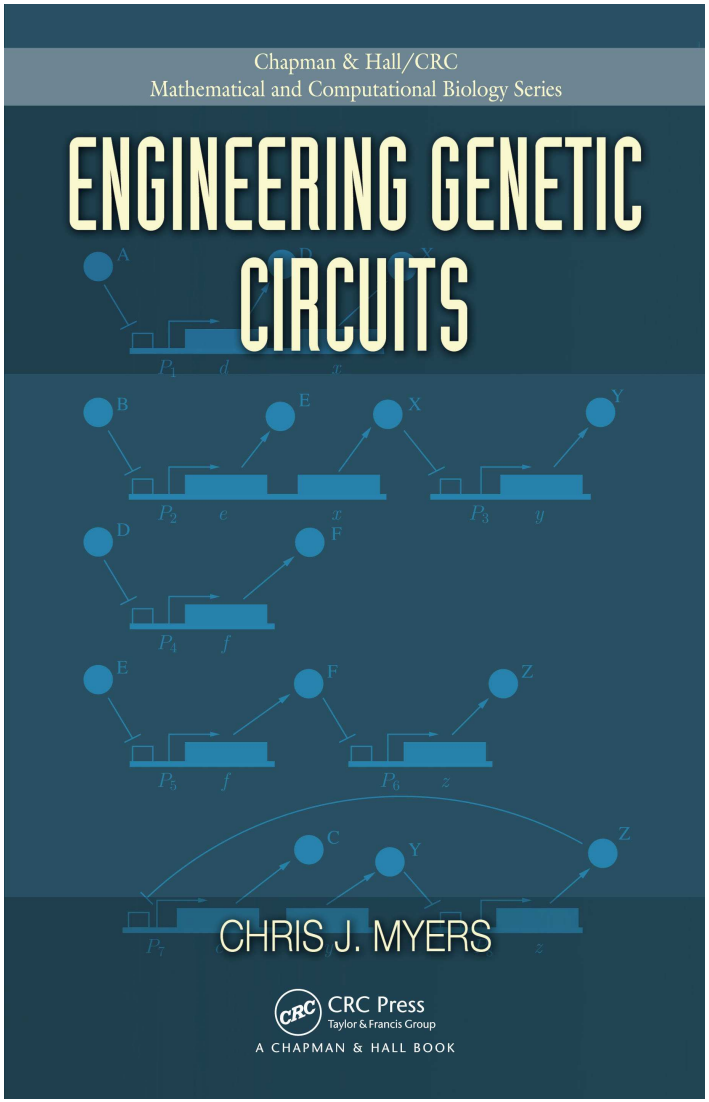
Prerequisites

- Students should have some familiarity with:
  - Genetics, cell biology, molecular biology, or biochemistry, OR
  - Engineering methods for modeling, analysis, and design.

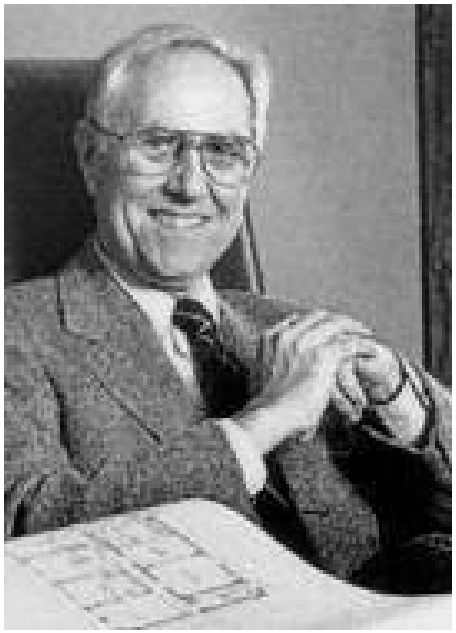
Grading Policy

- Participation - 10 percent
  - Attend class.
  - Participate in class discussions.
- Homework - 40 percent
  - Will learn how to use and create modeling, analysis, and design tools.
  - Use simple system for tutorial.
  - Choose a genetic circuit to use in your assignments.
  - Model, analyze, and design your genetic circuit with these tools.
- Project - 50 percent
  - Design a genetic circuit, or
  - Design and implement a software tool.

Recommended Textbook



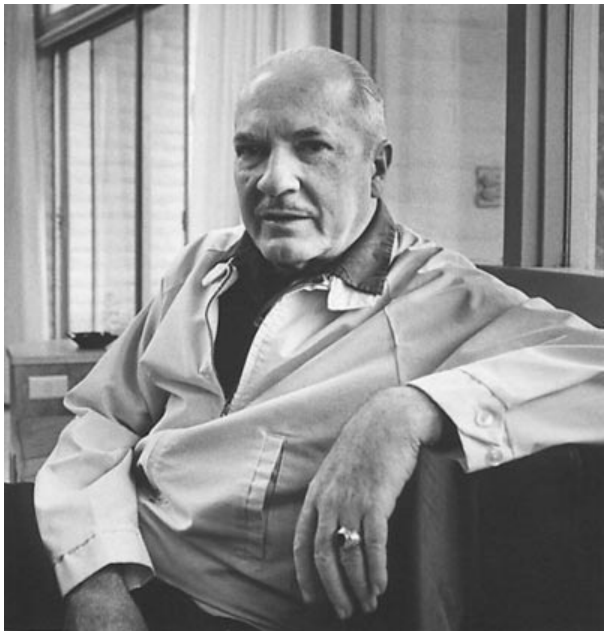
What is Engineering?



Samuel Florman

Engineering is the art or science of making practical.

What is Engineering?



Robert Heinlein

One man's "magic" is another man's engineering.

What are Genetic Circuits?

- A cell includes three main types of biological networks (circuits):
  - *Metabolic networks* are enzymatic processes that transform food into energy, and perform both biosynthesis and biodegradation.
  - *Protein networks* are communication and signaling networks which are composed of basic reactions between two or more proteins.
  - *Genetic regulatory networks*, or *genetic circuits*, regulate gene expression at many molecular levels.

What are Genetic Circuits?

- A cell includes three main types of biological networks (circuits):
  - *Metabolic networks* are enzymatic processes that transform food into energy, and perform both biosynthesis and biodegradation.
  - *Protein networks* are communication and signaling networks which are composed of basic reactions between two or more proteins.
  - *Genetic regulatory networks*, or *genetic circuits*, regulate gene expression at many molecular levels.
- **The focus of this course is the application of engineering methods to the modeling, analysis, and design of genetic circuits.**

What are Genetic Circuits?

- A cell includes three main types of biological networks (circuits):
  - *Metabolic networks* are enzymatic processes that transform food into energy, and perform both biosynthesis and biodegradation.
  - *Protein networks* are communication and signaling networks which are composed of basic reactions between two or more proteins.
  - *Genetic regulatory networks*, or *genetic circuits*, regulate gene expression at many molecular levels.
- **The focus of this course is the application of engineering methods to the modeling, analysis, and design of genetic circuits.**
- **GOAL: faciilitate collaborations between engineers and biologists.**

What is Bioinformatics?

- Biology is now both a lab-based science and an information science.
- Biologists have had to draw assistance from those in mathematics, computer science, and engineering.
- Result was development of *bioinformatics* and *computational biology*.
- Major goal is to extract new biological insights from large and noisy sets of data generated by high throughput technologies.
- Must create and maintain databases with massive amounts of data.
- Must be able to efficiently access, submit, and revise this data.
- Latest software must even analyze and interpret this data.
- Bioinformatics refers to the analysis of *static* data such as sequence analysis of DNA and protein sequences, techniques for finding genes or evolutionary patterns, and *cluster analysis* of microarray data.
- Bioinformatics algorithms are not explicitly covered in this course.

What is Bioinformatics?

- Biology is now both a lab-based science and an information science.
- Biologists have had to draw assistance from those in mathematics, computer science, and engineering.
- Result was development of *bioinformatics* and *computational biology*.
- Major goal is to extract new biological insights from large and noisy sets of data generated by high throughput technologies.
- Must create and maintain databases with massive amounts of data.
- Must be able to efficiently access, submit, and revise this data.
- Latest software must even analyze and interpret this data.
- Bioinformatics refers to the analysis of *static* data such as sequence analysis of DNA and protein sequences, techniques for finding genes or evolutionary patterns, and *cluster analysis* of microarray data.
- Bioinformatics algorithms are not explicitly covered in this course.
- **Results of bioinformatics research are important to this course.**

What is Systems Biology?

- *Systems biology* is the study of the mechanisms underlying complex molecular processes as integrated into systems or pathways made up of many interacting genes and proteins.
- Concerned with the analysis of *dynamic* models.
- Made possible by new experimental methods such as:
  - cDNA microarrays and oligonucleotide chips.
  - Mass spectrometric identification of gel-separated protiens.
  - 2-hybrid systems.
  - Genome-wide location analysis (ChIP-to-chip)
- Systems biology involves:
  - Collection of large experimental data sets,
  - Constructing mathematical models from this data,
  - Designing software to accurately and efficiently analyze these models *in silico* (i.e., on a computer), and
  - Comparing numerical simulations with the experimental data.

What is Systems Biology? (cont)

- Ultimate goal is to develop methods which can give reasonable predictions of experimental results.
- While it will never replace experimental methods, may help experimentalists make better use of their time.
- Also may gain insight into mechanisms used by these biological processes which may not be obtained by experiments.
- Eventually, may be possible that they could have substantial impact on our society such as aiding in drug discovery.
- Systems biology was focus of previous iterations of this course.

What is Systems Biology? (cont)

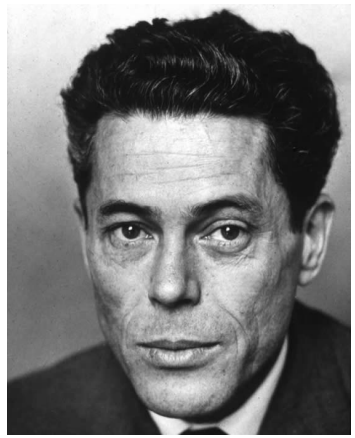
- Ultimate goal is to develop methods which can give reasonable predictions of experimental results.
- While it will never replace experimental methods, may help experimentalists make better use of their time.
- Also may gain insight into mechanisms used by these biological processes which may not be obtained by experiments.
- Eventually, may be possible that they could have substantial impact on our society such as aiding in drug discovery.
- Systems biology was focus of previous iterations of this course.
- **Modeling and analysis methods for systems biology are important for this course, but the applications considered will be different.**

Systems Biology Example: Phage λ


Esther Lederberg

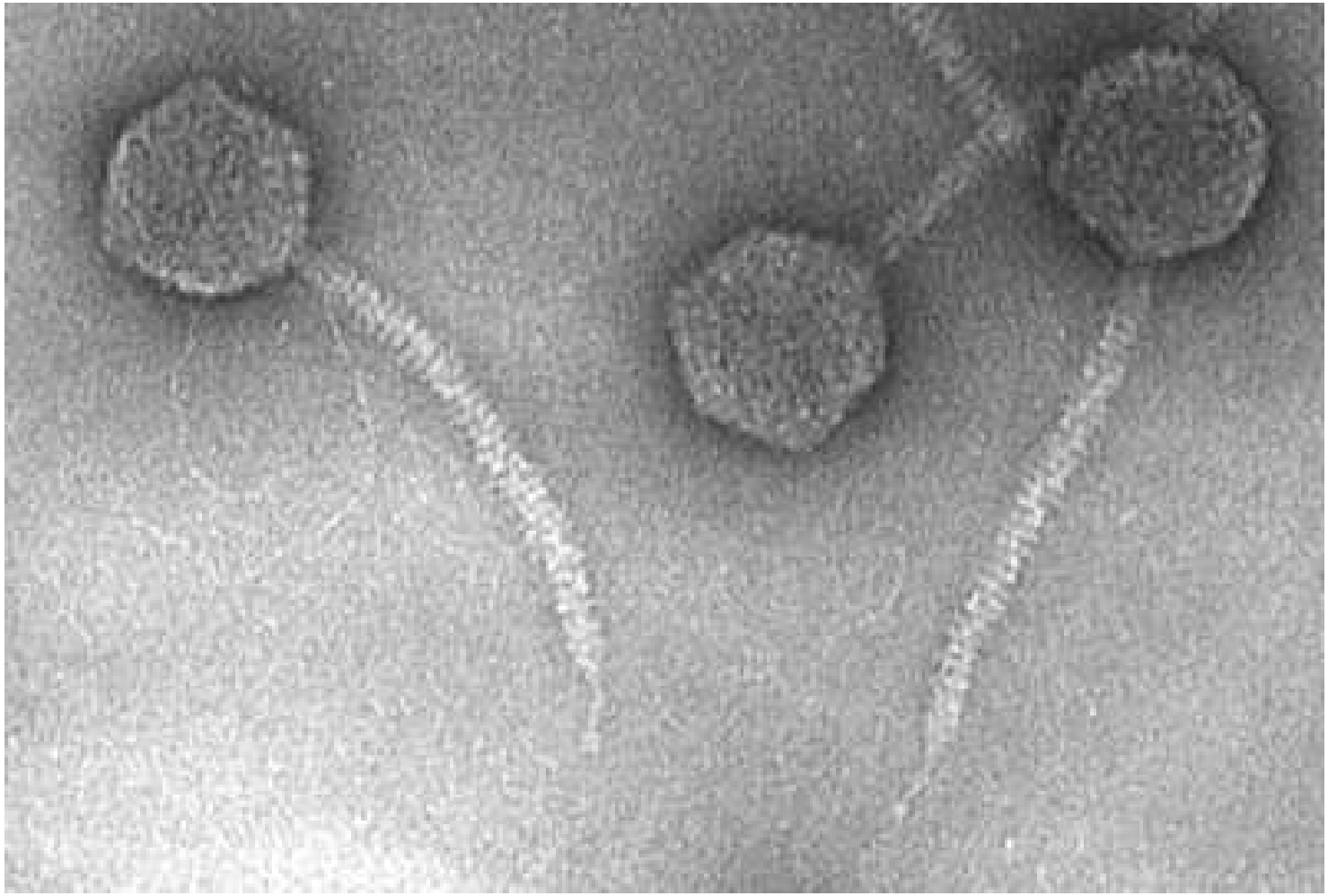

Andre Lwoff


Francois Jacob


Jacques Monod

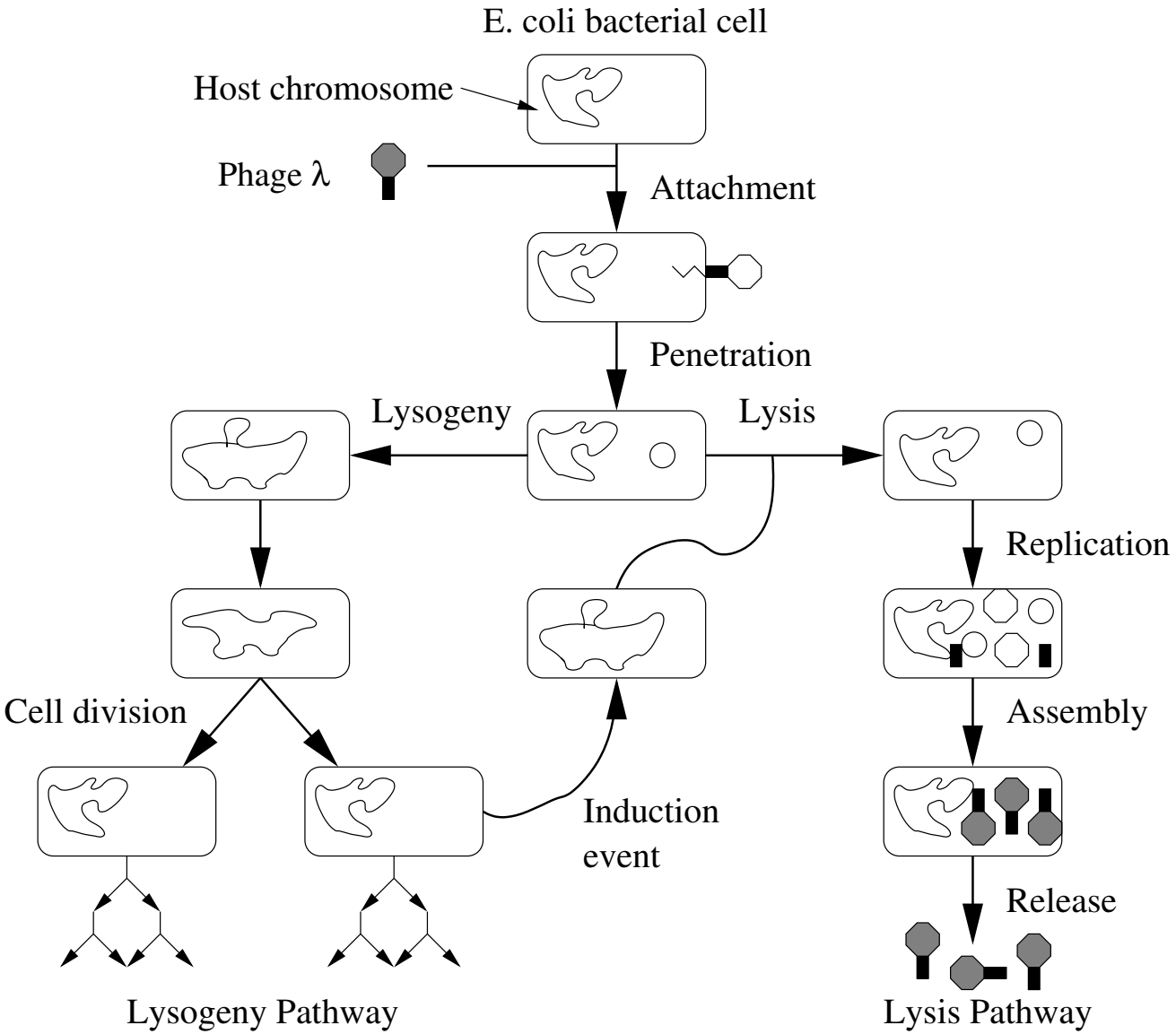
- In 1953, Lwoff et al. discovered that a strain of *E. Coli* when exposed to UV light *lyse* spewing forth λ viruses.
- Some of the newly infected *E. Coli* would soon lyse while others grow and divide normally until exposed to UV light.
- In other words, some cells follow a *lysis* pathway while other followed a *lysogeny* pathway.
- The decision between the lysis and the lysogeny developmental pathway is made by a fairly simple genetic circuit.

Systems Biology Example: Phage λ

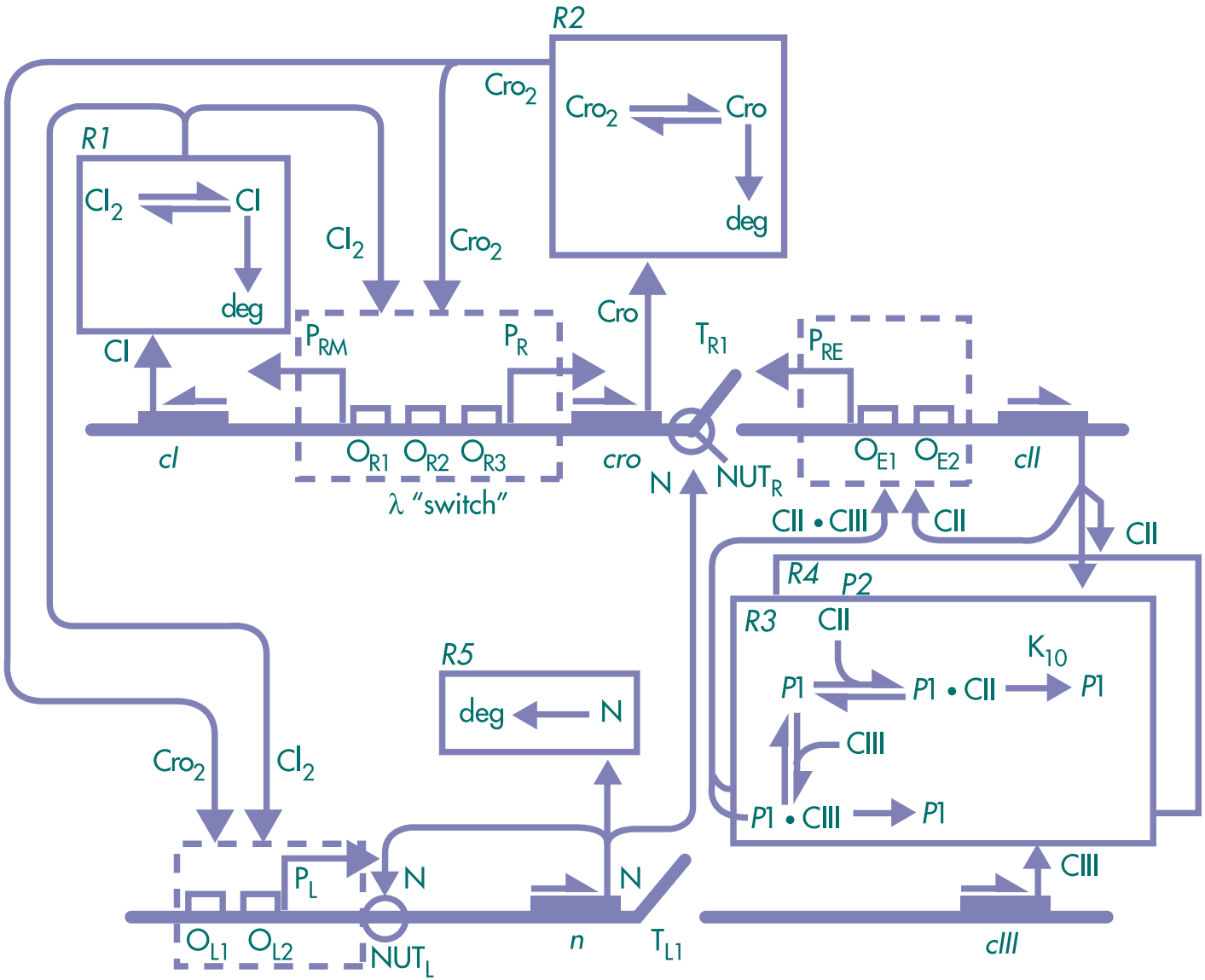


(Courtesy of Maria Schnos and Ross Inman, Institute for Molecular Virology, University of Wisconsin, Madison)

Phage λ Developmental Pathways

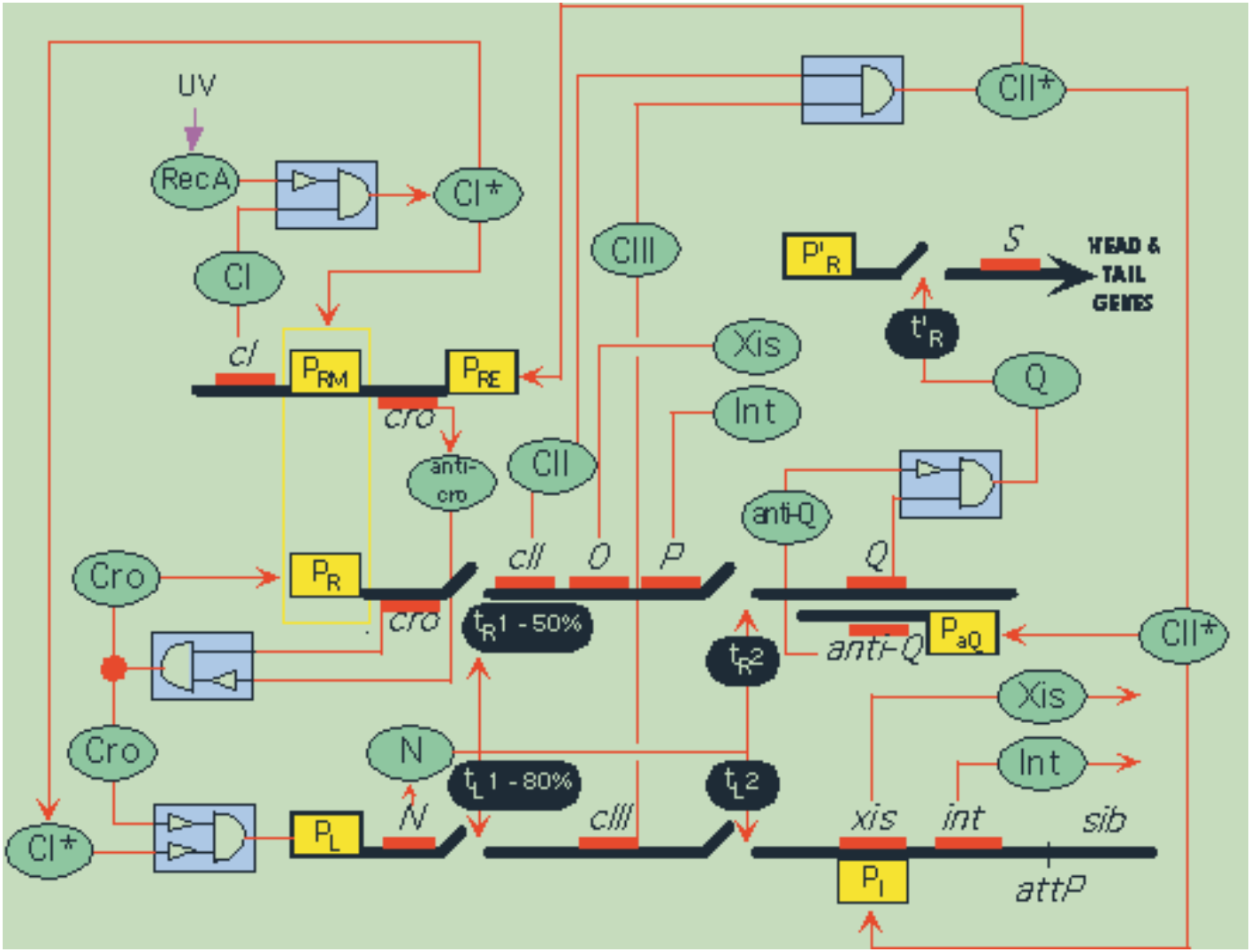


Phage λ Decision Circuit



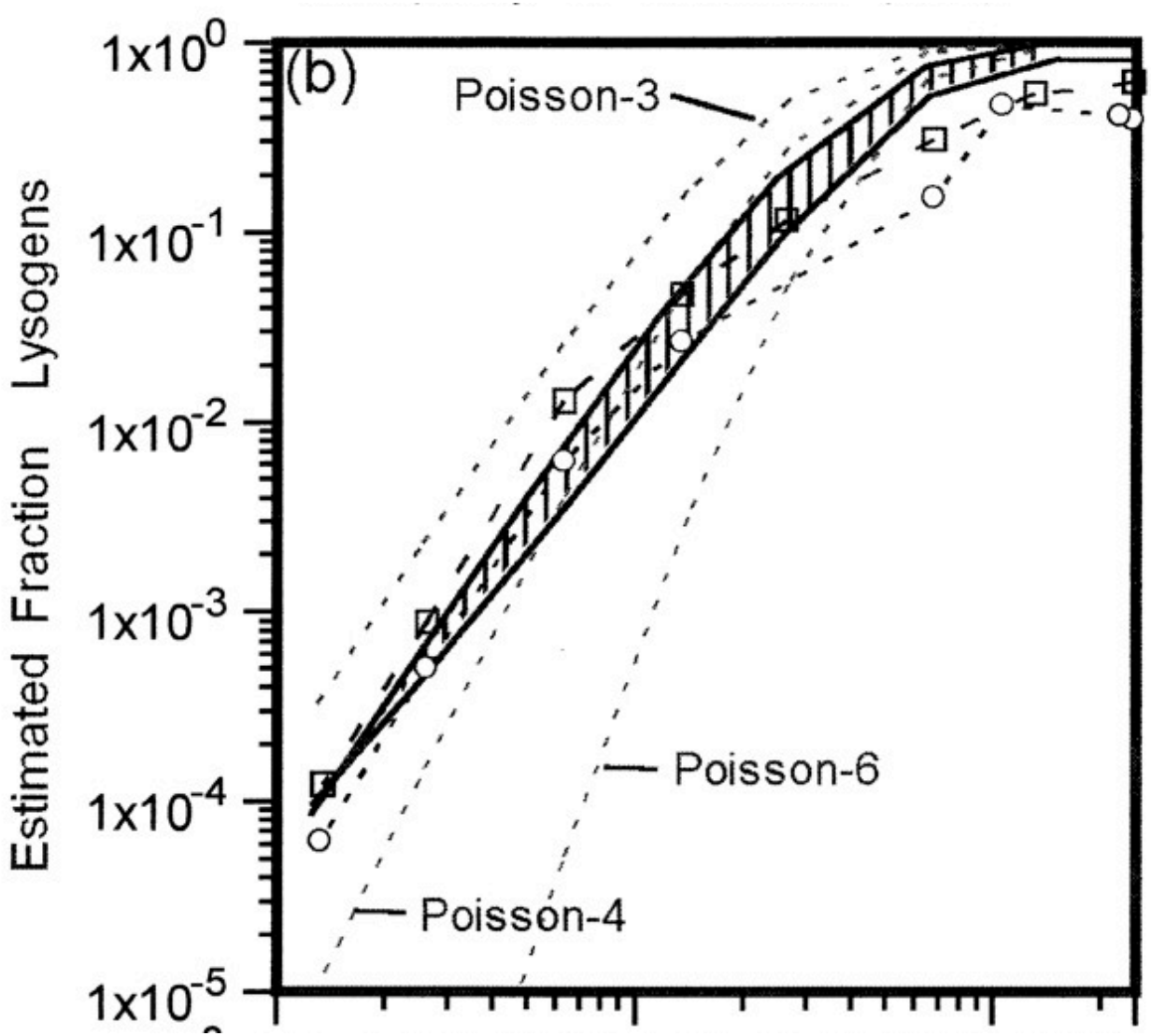
YGG 01-0052

Another Representation of the Phage λ Decision Circuit



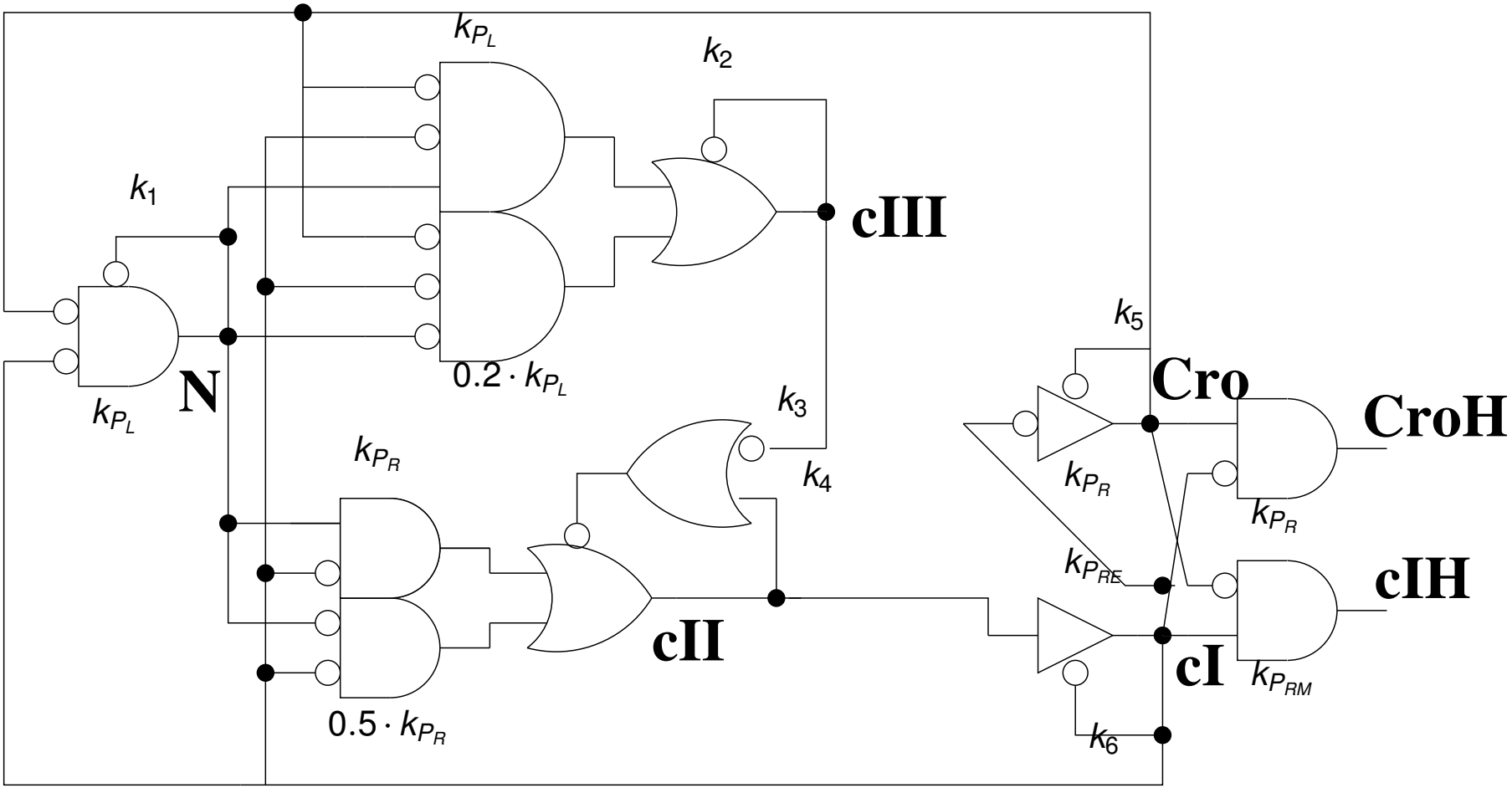
McAdams/Shapiro, Science (1995)

Stochastic Simulation Results for the Phage λ Circuit

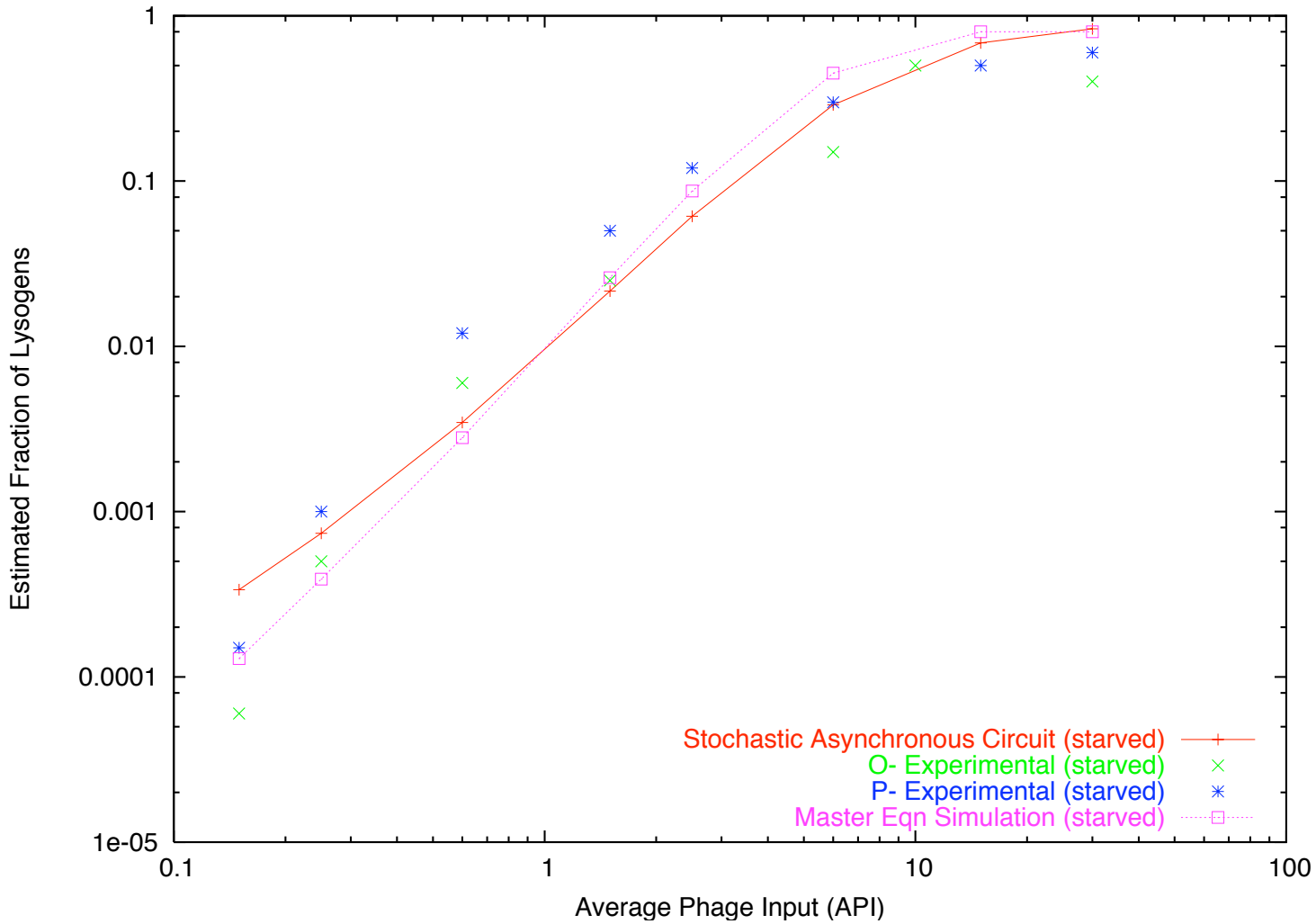


Arkin/Ross/McAdams, Genetics (1998)

Stochastic Asynchronous Circuit Model for Phage λ



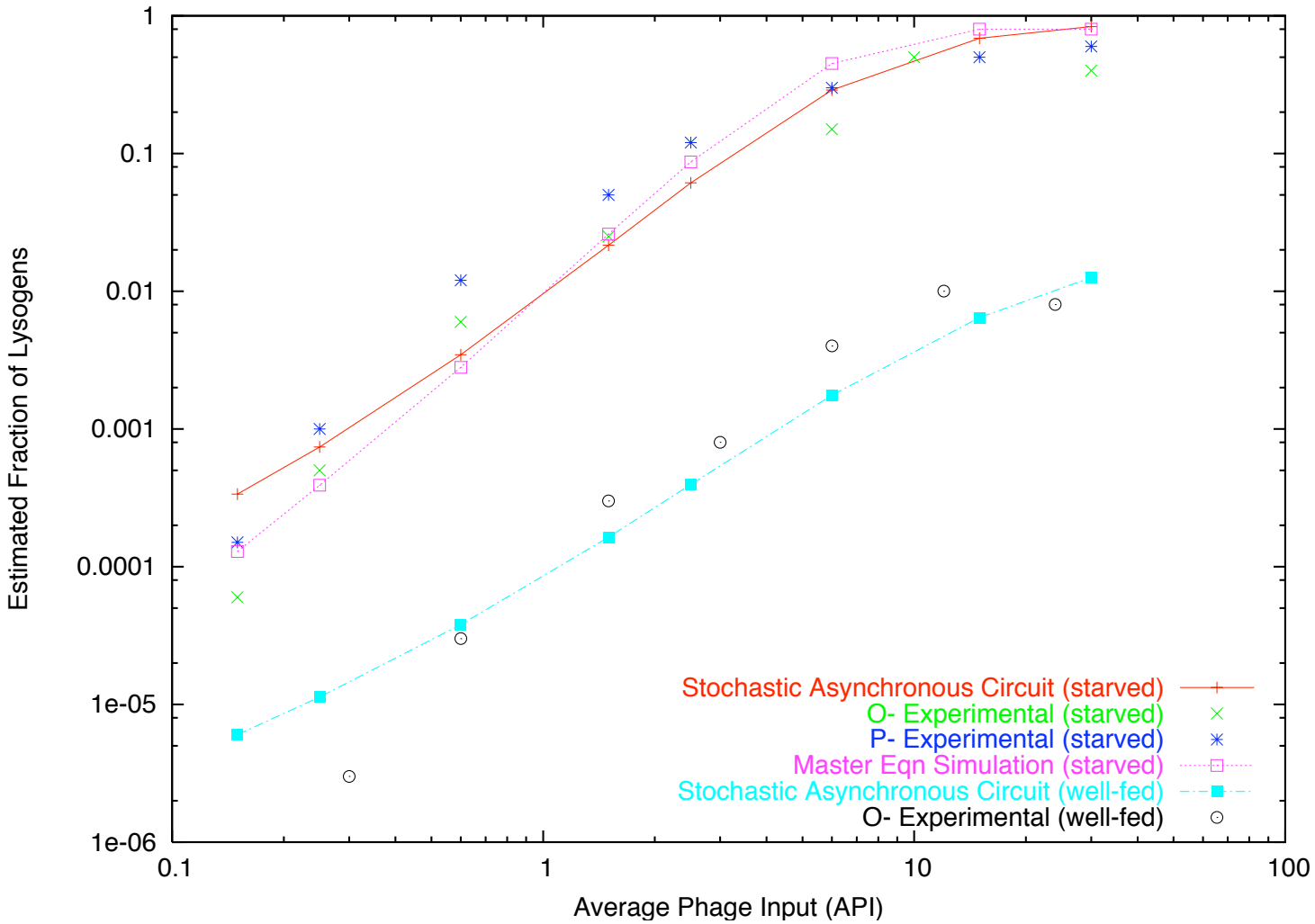
Stochastic Asynchronous Circuit Results



SAC results generated in only 7 minutes.

Kuwahara et al., Trans. on Comp. Sys. Bio. (2006)

Stochastic Asynchronous Circuit Results



SAC results generated in only 7 minutes.

Kuwahara et al., Trans. on Comp. Sys. Bio. (2006)

Systems Biology Versus Synthetic Biology

Drew Endy

What is Synthetic Biology?

Biology has at least 50 more interesting years
– James Watson (1984).

What is Synthetic Biology?

Biology has at least 50 more interesting years
– James Watson (1984).

- *Synthetic biology* has likely extended this much further.
- Synthetic biology involves:
  - Designing new biological systems to achieve a desired function.
  - Creating systems that actually agree with our models.
- Potential applications:
  - Produce drugs and bio-fuels.
  - Consume toxic waste.
  - Destroy tumors.
- **Synthetic biology is the focus of this course.**

Genetic Engineering vs. Synthetic Biology

- *Genetic engineering* (last 40 years) consists of experimental techniques to produce artificial DNA sequences.
- Synthetic biology adds:
  - *Standards* - create repositories of parts that can be easily composed.
  - *Abstraction* - high-level models to facilitate design.
  - *Decoupling* - separate design from construction.

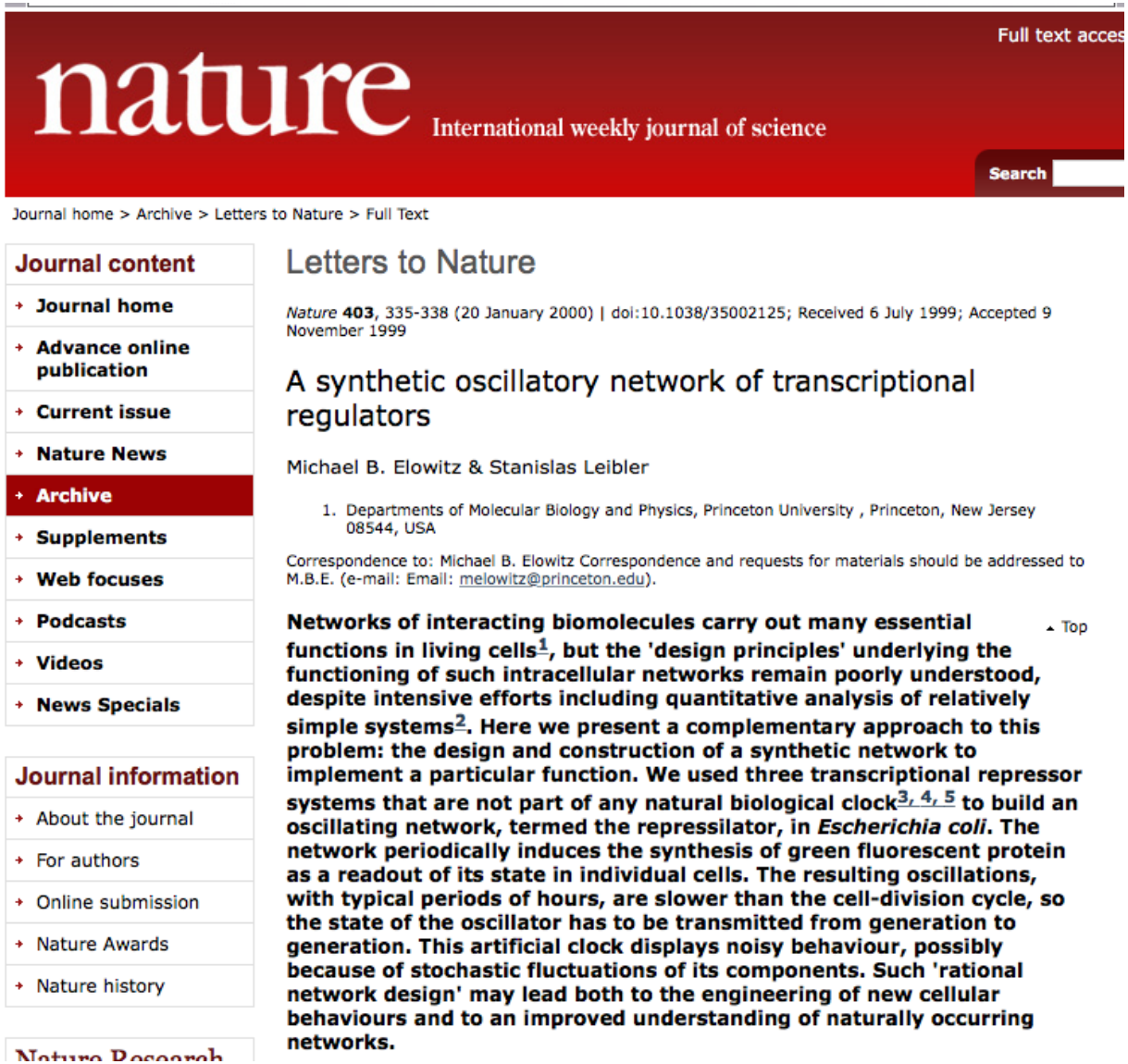
(source: Drew Endy)

Genetic Engineering vs. Synthetic Biology

- *Genetic engineering* (last 40 years) consists of experimental techniques to produce artificial DNA sequences.
- Synthetic biology adds:
  - *Standards* - create repositories of parts that can be easily composed.
  - *Abstraction* - high-level models to facilitate design.
  - *Decoupling* - separate design from construction.
- **In other words, synthetic biology makes genetic engineering a "real" engineering discipline.**

(source: Drew Endy)

A Brief History of Synthetic Biology



nature International weekly journal of science

Full text acces

Search

Journal home > Archive > Letters to Nature > Full Text

Journal content

- Journal home
- Advance online publication
- Current issue
- Nature News
- Archive
- Supplements
- Web focuses
- Podcasts
- Videos
- News Specials

Journal information

- About the journal
- For authors
- Online submission
- Nature Awards
- Nature history

Nature Research

Letters to Nature

Nature **403**, 335-338 (20 January 2000) | doi:10.1038/35002125; Received 6 July 1999; Accepted 9 November 1999

A synthetic oscillatory network of transcriptional regulators

Michael B. Elowitz & Stanislas Leibler

1. Departments of Molecular Biology and Physics, Princeton University , Princeton, New Jersey 08544, USA

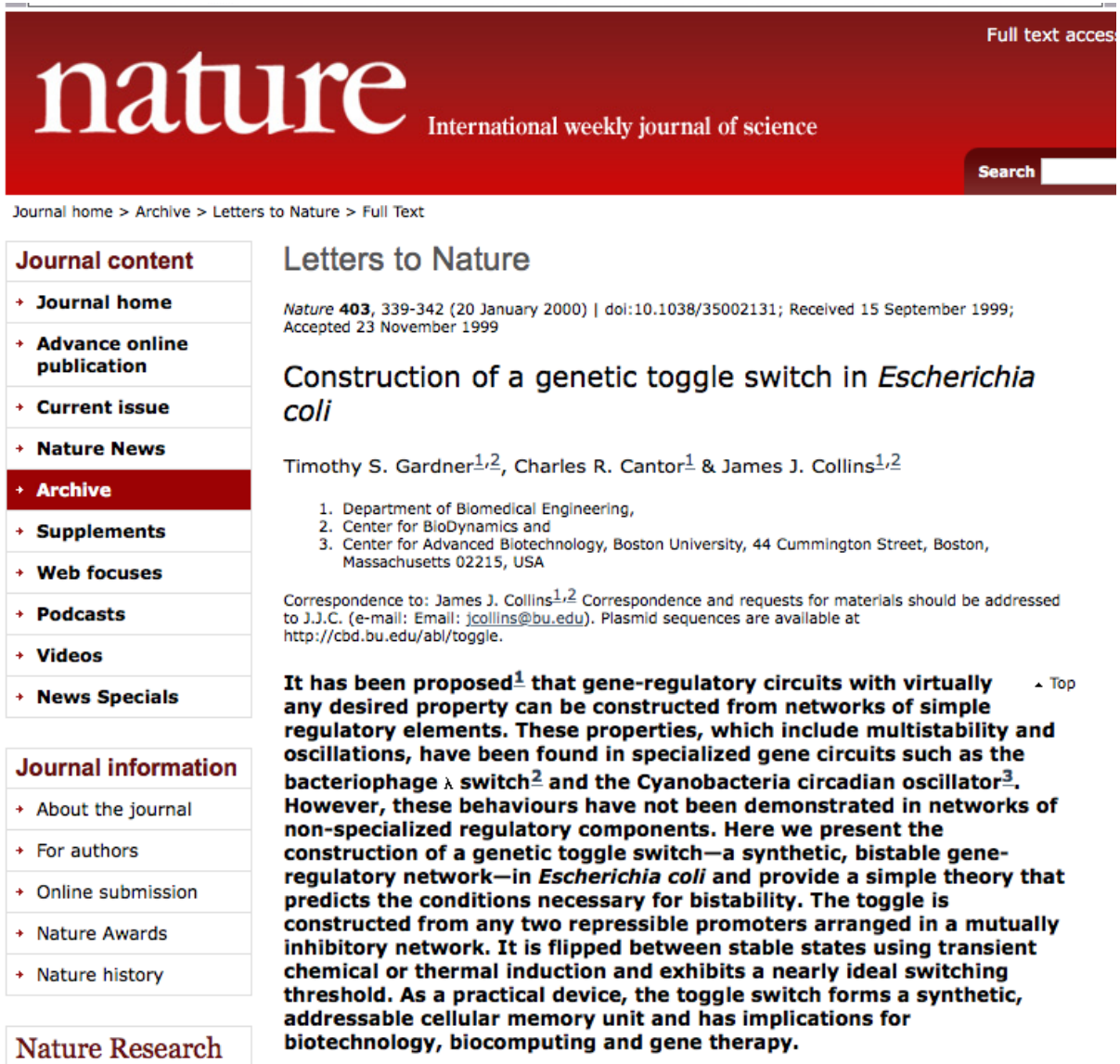
Correspondence to: Michael B. Elowitz Correspondence and requests for materials should be addressed to M.B.E. (e-mail: Email: melowitz@princeton.edu).

Top

Networks of interacting biomolecules carry out many essential functions in living cells[1], but the 'design principles' underlying the functioning of such intracellular networks remain poorly understood, despite intensive efforts including quantitative analysis of relatively simple systems[2]. Here we present a complementary approach to this problem: the design and construction of a synthetic network to implement a particular function. We used three transcriptional repressor systems that are not part of any natural biological clock[3, 4, 5] to build an oscillating network, termed the repressilator, in *Escherichia coli*. The network periodically induces the synthesis of green fluorescent protein as a readout of its state in individual cells. The resulting oscillations, with typical periods of hours, are slower than the cell-division cycle, so the state of the oscillator has to be transmitted from generation to generation. This artificial clock displays noisy behaviour, possibly because of stochastic fluctuations of its components. Such 'rational network design' may lead both to the engineering of new cellular behaviours and to an improved understanding of naturally occurring networks.

The Beginning: January 2000

A Brief History of Synthetic Biology



nature
International weekly journal of science
Full text acces
Search
Journal home > Archive > Letters to Nature > Full Text

Journal content
- Journal home
- Advance online publication
- Current issue
- Nature News
- Archive
- Supplements
- Web focuses
- Podcasts
- Videos
- News Specials

Journal information
- About the journal
- For authors
- Online submission
- Nature Awards
- Nature history

Nature Research

Letters to Nature

Nature **403**, 339-342 (20 January 2000) | doi:10.1038/35002131; Received 15 September 1999; Accepted 23 November 1999

Construction of a genetic toggle switch in *Escherichia coli*

Timothy S. Gardner[1,2], Charles R. Cantor[1] & James J. Collins[1,2]

1. Department of Biomedical Engineering,
2. Center for BioDynamics and
3. Center for Advanced Biotechnology, Boston University, 44 Cummington Street, Boston, Massachusetts 02215, USA

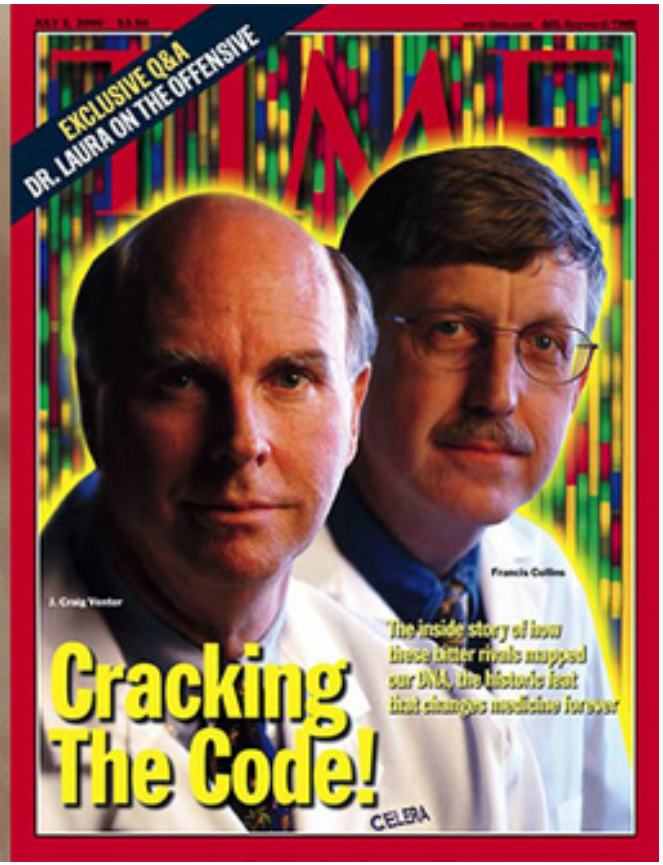
Correspondence to: James J. Collins[1,2] Correspondence and requests for materials should be addressed to J.J.C. (e-mail: Email: jcollins@bu.edu). Plasmid sequences are available at http://cbd.bu.edu/abl/toggle.

Top

It has been proposed[1] that gene-regulatory circuits with virtually any desired property can be constructed from networks of simple regulatory elements. These properties, which include multistability and oscillations, have been found in specialized gene circuits such as the bacteriophage λ switch[2] and the Cyanobacteria circadian oscillator[3]. However, these behaviours have not been demonstrated in networks of non-specialized regulatory components. Here we present the construction of a genetic toggle switch—a synthetic, bistable gene-regulatory network—in *Escherichia coli* and provide a simple theory that predicts the conditions necessary for bistability. The toggle is constructed from any two repressible promoters arranged in a mutually inhibitory network. It is flipped between stable states using transient chemical or thermal induction and exhibits a nearly ideal switching threshold. As a practical device, the toggle switch forms a synthetic, addressable cellular memory unit and has implications for biotechnology, biocomputing and gene therapy.

The Beginning: January 2000

A Brief History of Synthetic Biology



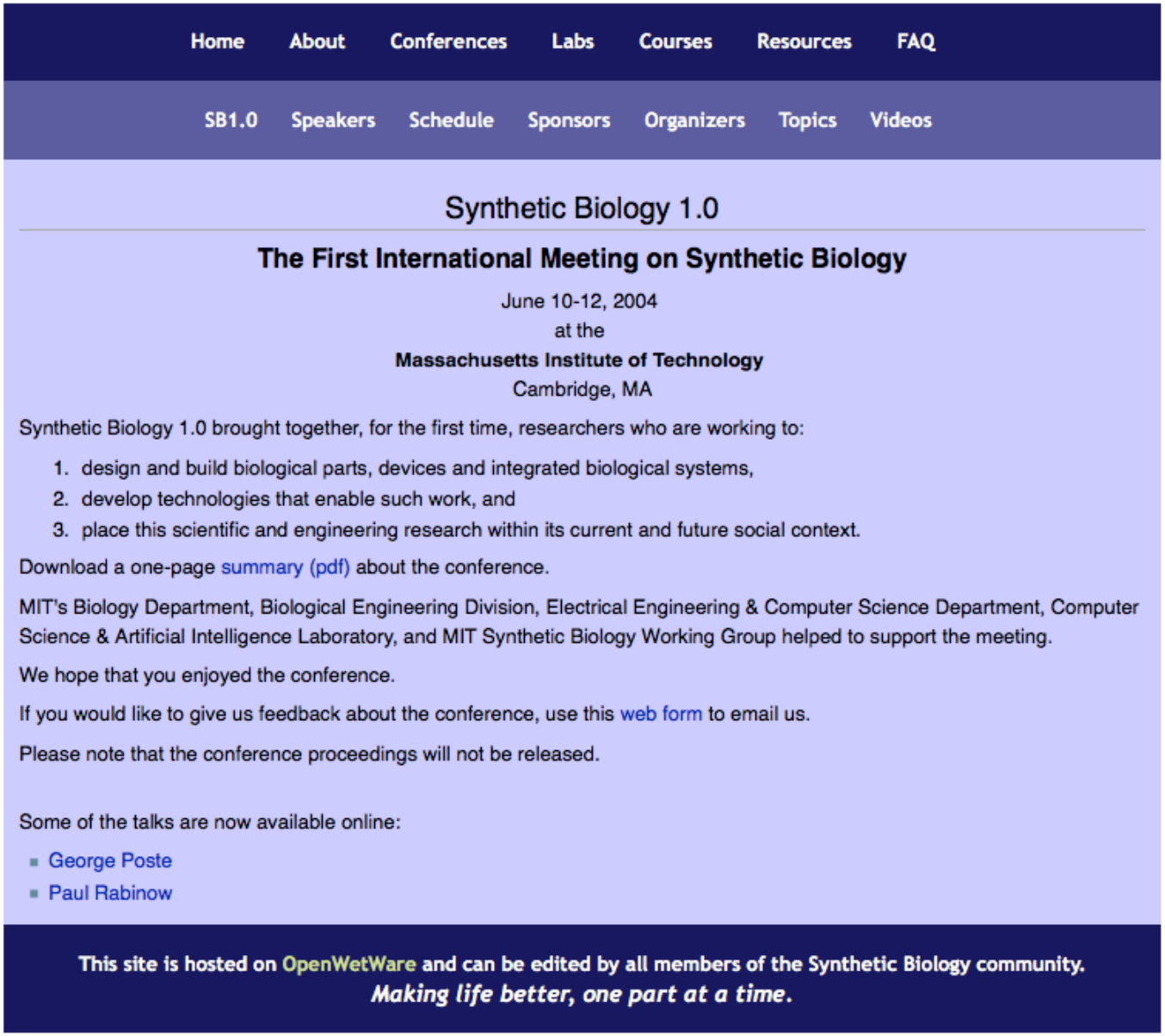
Human Genome Project

Published February 2001

Cost of $3 billion

1990 $\rightarrow$ 2003

A Brief History of Synthetic Biology



Home About Conferences Labs Courses Resources FAQ

SB1.0 Speakers Schedule Sponsors Organizers Topics Videos

Synthetic Biology 1.0

The First International Meeting on Synthetic Biology

June 10-12, 2004
at the
Massachusetts Institute of Technology
Cambridge, MA

Synthetic Biology 1.0 brought together, for the first time, researchers who are working to:

1. design and build biological parts, devices and integrated biological systems,
2. develop technologies that enable such work, and
3. place this scientific and engineering research within its current and future social context.

Download a one-page summary (pdf) about the conference.

MIT's Biology Department, Biological Engineering Division, Electrical Engineering & Computer Science Department, Computer Science & Artificial Intelligence Laboratory, and MIT Synthetic Biology Working Group helped to support the meeting.

We hope that you enjoyed the conference.

If you would like to give us feedback about the conference, use this web form to email us.

Please note that the conference proceedings will not be released.

Some of the talks are now available online:

- George Poste
- Paul Rabinow

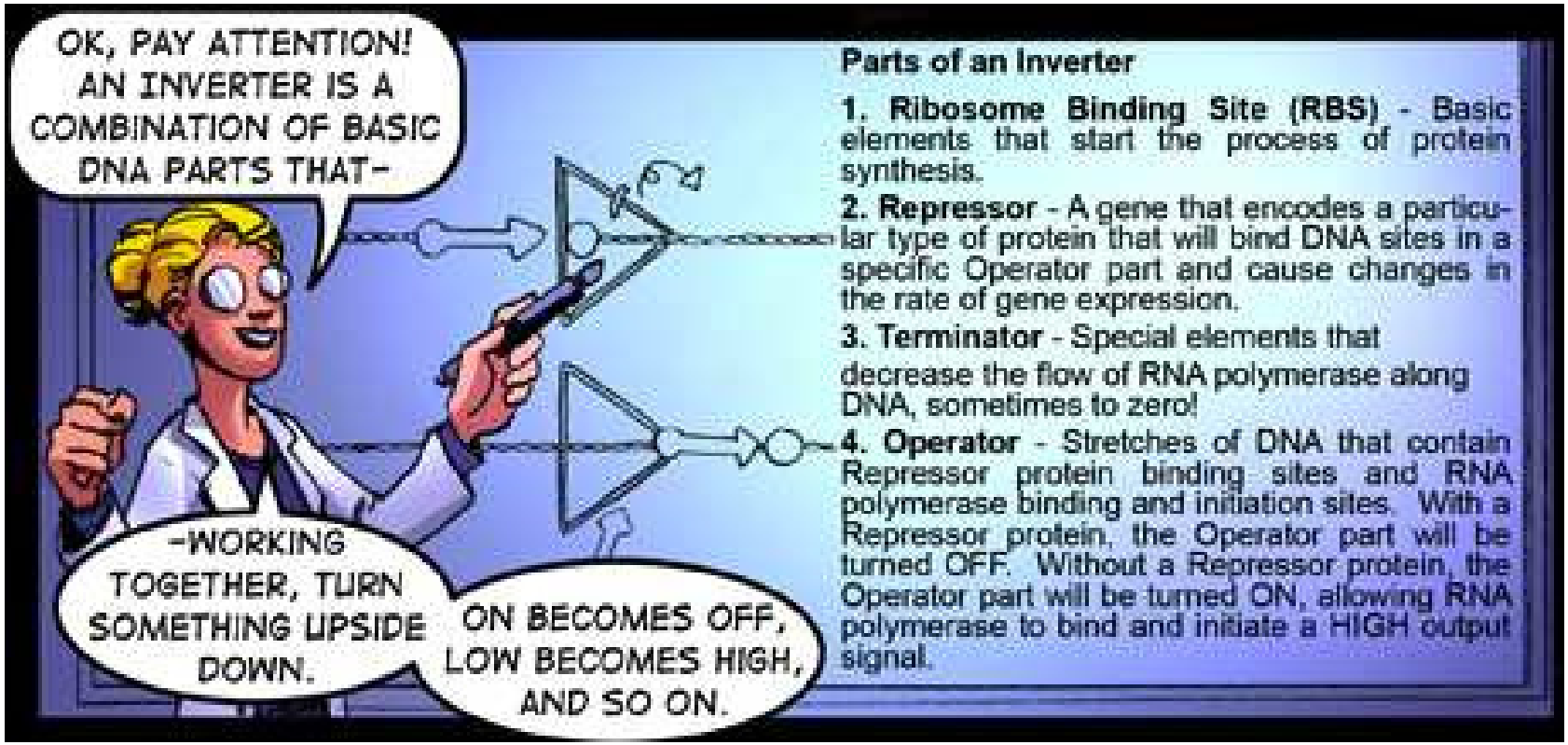
This site is hosted on OpenWetWare and can be edited by all members of the Synthetic Biology community.
Making life better, one part at a time.

A Brief History of Synthetic Biology

iGEM 2004: 5 teams, 31 participants, $\sim$50 parts

A Brief History of Synthetic Biology

A Brief History of Synthetic Biology



(From “Adventures in Synthetic Biology” - Endy et al.)

A Brief History of Synthetic Biology

iGEM 2005: 13 teams, 125 participants, $\sim$125 parts

A Brief History of Synthetic Biology

A Brief History of Synthetic Biology

iGEM 2006: 32 teams, 723 participants, ∼724 parts

A Brief History of Synthetic Biology

A Brief History of Synthetic Biology

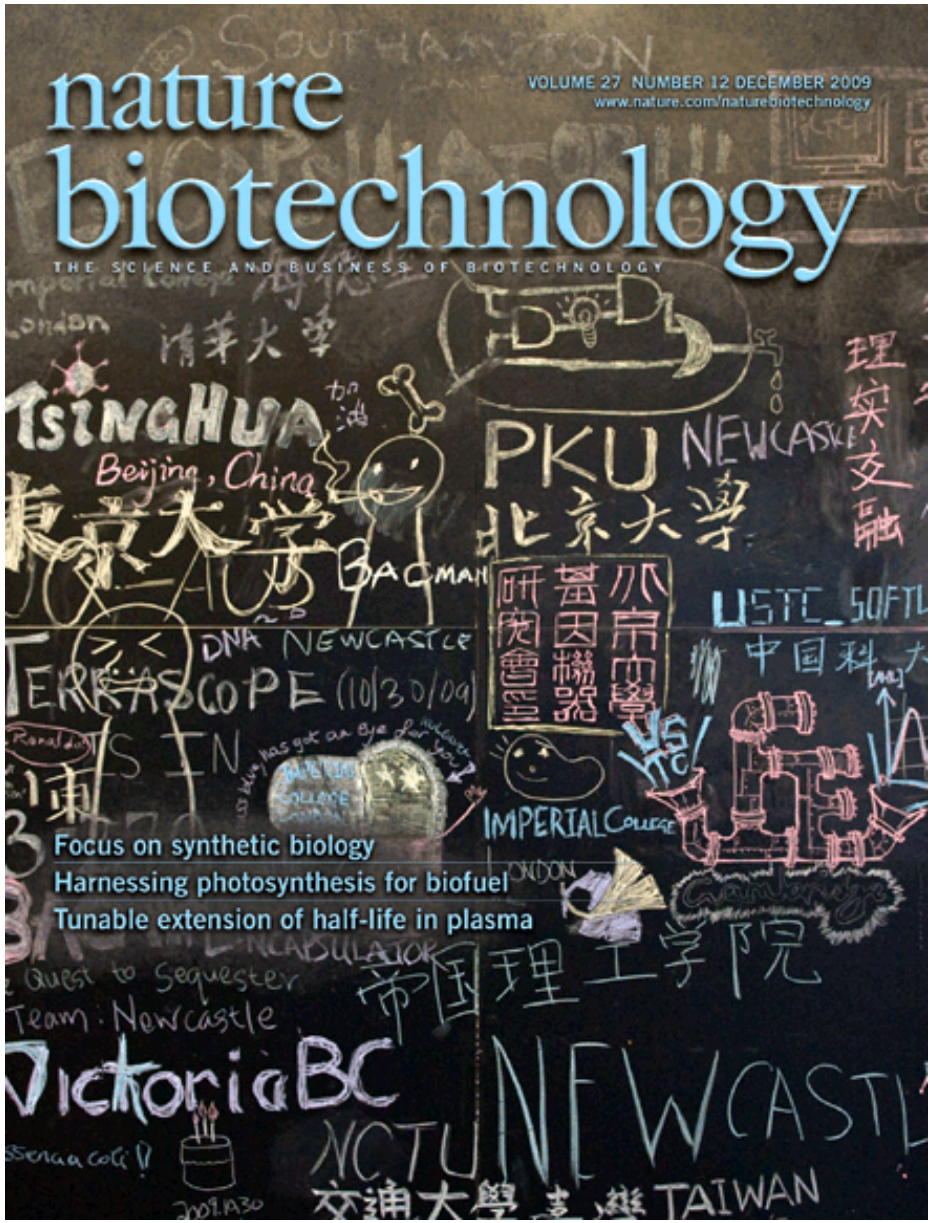
iGEM 2007: 54 teams, 777 participants, ∼800 parts

A Brief History of Synthetic Biology

A Brief History of Synthetic Biology

iGEM 2008: 88 teams, 1248 participants, 1387 parts

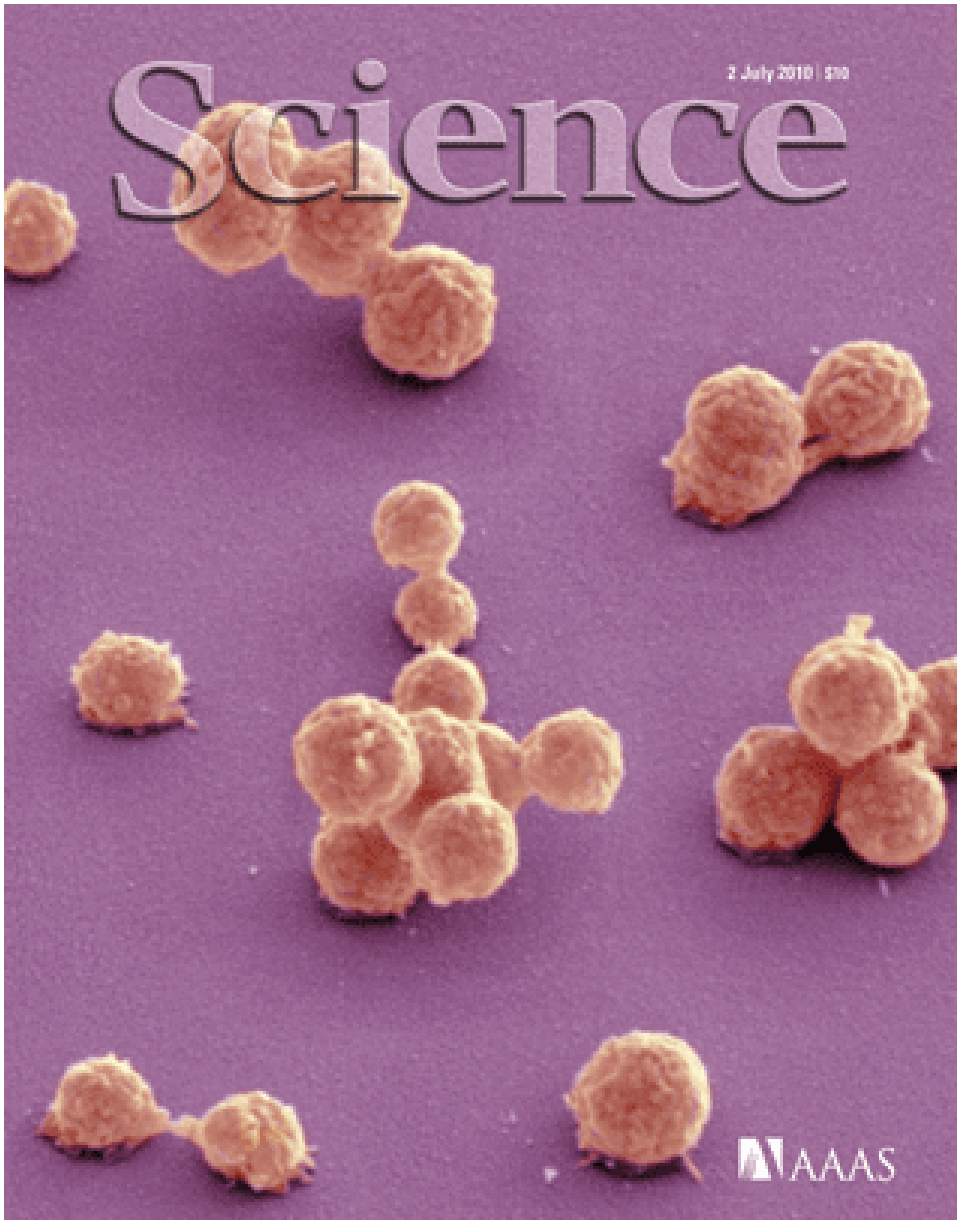
A Brief History of Synthetic Biology



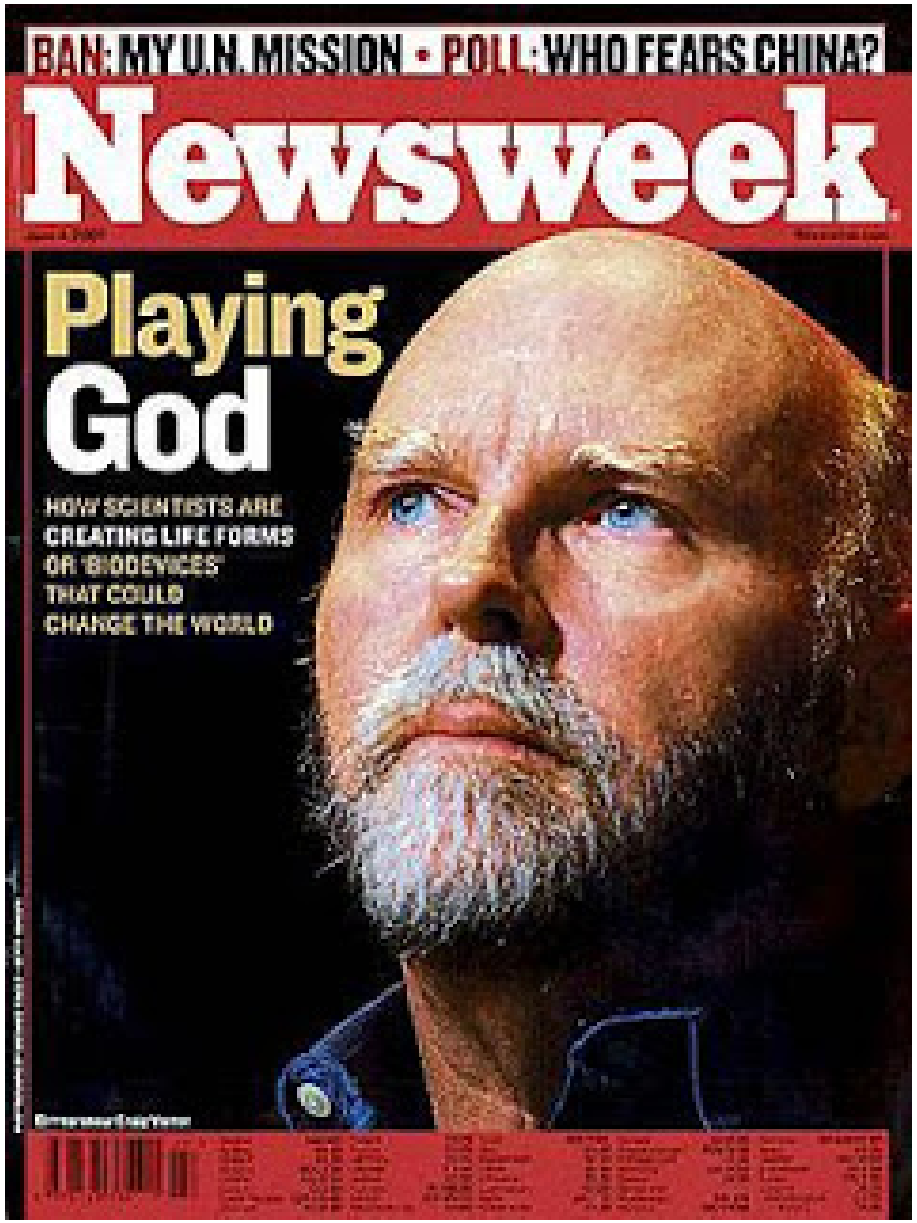
A Brief History of Synthetic Biology

iGEM 2009: 113 teams, 1840 participants, 1348 parts

A Brief History of Synthetic Biology



A Brief History of Synthetic Biology



A Brief History of Synthetic Biology

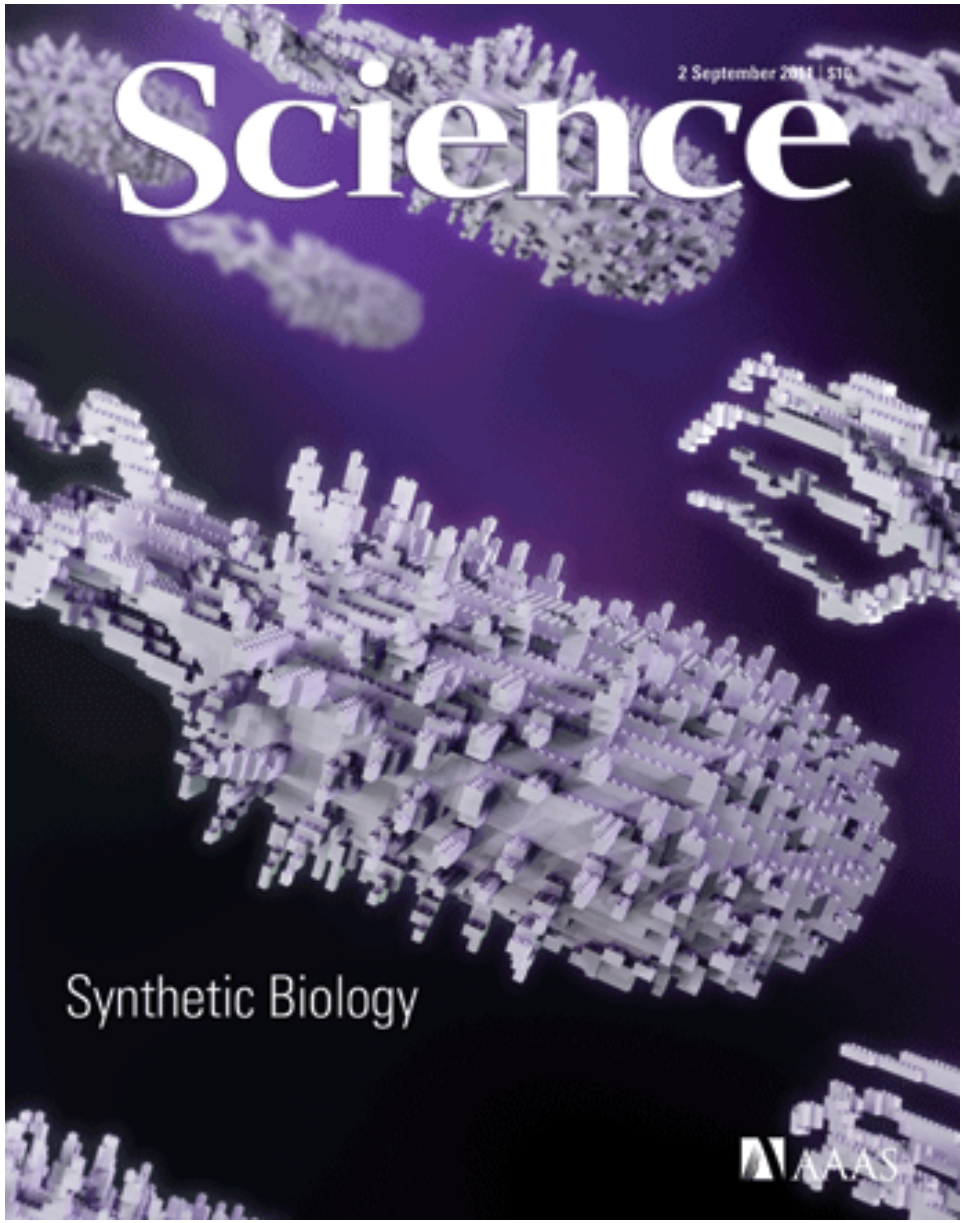
iGEM 2010: 128 teams, 2327 participants, 1863 parts

A Brief History of Synthetic Biology

A Brief History of Synthetic Biology

SB 5.0, Stanford University, June 2011

A Brief History of Synthetic Biology



Essential information for synthetic DNA sequences

To the Editor:

Following a discussion by the workgroup for Data Standards in Synthetic Biology, which met in June 2010 during the Second Workshop on Biodesign Automation in Anaheim, California, we wish to highlight a problem relating to the reproducibility of the synthetic biology literature. In particular, we have noted the very small number of articles reporting synthetic gene networks that disclose the complete sequence of all the constructs they describe.

To our knowledge, there are only a few examples where full sequences have been released. In 2005, a patent application[1] disclosed the sequences of the toggle switches published four years earlier in a paper by Gardner *et al.*[2]. The same year, Basu *et al.*[3] deposited their construct sequences for programmed pattern formation into GenBank[3]. Examples of synthetic DNA sequences derived from standardized parts that have been made available in GenBank include the refactored genome of the bacteriophage

gaps between key components are almost never reported, presumably because they are not considered crucial to the report. Yet, synthetic biology relies on the premise that synthetic DNA can be engineered with base-level precision.

Missing sequence information in papers hurts reproducibility, limits reuse of past work and incorrectly assumes that we know fully which sequence segments are important. For example, many synthetic biologists are currently realizing that translation initiation rates are dependent on more than the Shine-Dalgarno sequence[8]. Sequences upstream of the start codon are crucial for translation rates, yet are underreported. Similarly, it has been demonstrated that intron length can affect the dynamics of genetic oscillators[9]. Many more such examples are likely to emerge.

Because full sequence disclosure is critical, we wonder why the common requirement by many journals to provide GenBank entries for genomes and natural sequences has

and welcome contributions from the greater community.

COMPETING FINANCIAL INTERESTS

The authors declare no competing financial interests.

Jean Peccoud[1], J Christopher Anderson[2], Deepak Chandran[3], Douglas Densmore[4], Michal Galdzicki[5], Matthew W Lux[1], Cesar A Rodriguez[6], Guy-Bart Stan[7] & Herbert M Sauro[3]

[1]Virginia Bioinformatics Institute, Virginia Tech, Blacksburg, Virginia, USA. [2]Department of Bioengineering, QB3: California Institute for Quantitative Biological Research, University of California, Berkeley, California, USA. [3]Department of Bioengineering, University of Washington, Seattle, Washington, USA. [4]Department of Electrical and Computer Engineering, Boston University, Boston, Massachusetts, USA. [5]Biomedical and Health Informatics, University of Washington, Seattle, Washington, USA. [6]BIOFAB, Emeryville, California, USA. [7]Department of Bioengineering and Centre for Synthetic Biology and Innovation, Imperial College London, London, UK.
e-mail: peccoud@vt.edu

1. Gardner, T.S. & Collins, J.J. US patent 6,841,376 (2005).
2. Gardner, T.S., Cantor, C.R. & Collins, J.J. *Nature* **403**, 339–342 (2000).
3. Basu, S., Gerchman, Y., Collins, C.H., Arnold, F.H. & Weiss, R. *Nature* **434**, 1130–1134 (2005).

A Brief History of Synthetic Biology

nature biotechnology

Home | Current issue | News & comment | Research | Archive | Authors & referees | About the journal

home ▸ archive ▸ issue ▸ computational biology ▸ perspective ▸ full text

NATURE BIOTECHNOLOGY | COMPUTATIONAL BIOLOGY | PERSPECTIVE

日本語要約

The Synthetic Biology Open Language (SBOL) provides a community standard for communicating designs in synthetic biology

Michal Galdzicki, Kevin P Clancy, Ernst Oberortner, Matthew Pocock, Jacqueline Y Quinn, Cesar A Rodriguez, Nicholas Roehner, Mandy L Wilson, Laura Adam, J Christopher Anderson, Bryan A Bartley, Jacob Beal, Deepak Chandran, Joanna Chen, Douglas Densmore, Drew Endy, Raik Grünberg, Jennifer Hallinan, Nathan J Hillson, Jeffrey D Johnson, Allan Kuchinsky, Matthew Lux, Goksel Misirli, Jean Peccoud, Hector A Plahar, Evren Sirin, Guy-Bart Stan, Alan Villalobos, Anil Wipat, John H Gennari, Chris J Myers & Herbert M Sauro

– Show fewer authors

Affiliations | Contributions | Corresponding author

Nature Biotechnology **32**, 545–550 (2014) | doi:10.1038/nbt.2891

Received 09 November 2013 | Accepted 20 December 2013 | Published online 06 June 2014

A Brief History of Synthetic Biology

iGEM 2011: 165 teams, 2586 participants, 1355 parts

A Brief History of Synthetic Biology

A Brief History of Synthetic Biology

Theory

Cell

A Whole-Cell Computational Model Predicts Phenotype from Genotype

Jonathan R. Karr,[1,4] Jayodita C. Sanghvi,[2,4] Derek N. Macklin,[2] Miriam V. Gutschow,[2] Jared M. Jacobs,[2] Benjamin Bolival, Jr.,[2] Nacyra Assad-Garcia,[3] John I. Glass,[3] and Markus W. Covert[2,*]
[1]Graduate Program in Biophysics
[2]Department of Bioengineering
Stanford University, Stanford, CA 94305, USA
[3]J. Craig Venter Institute, Rockville, MD 20850, USA
[4]These authors contributed equally to this work
*Correspondence: mcovert@stanford.edu
http://dx.doi.org/10.1016/j.cell.2012.05.044

SUMMARY

Understanding how complex phenotypes arise from individual molecules and their interactions is a primary challenge in biology that computational approaches are poised to tackle. We report a whole-cell computational model of the life cycle of the human pathogen *Mycoplasma genitalium* that

First, until recently, not enough has been known about the individual molecules and their interactions to completely model any one organism. The advent of genomics and other high-throughput measurement techniques has accelerated the characterization of some organisms to the extent that comprehensive modeling is now possible. For example, the mycoplasmas, a genus of bacteria with relatively small genomes that includes several pathogens, have recently been the subject of an exhaustive experimental effort by a European consortium to determine

A Brief History of Synthetic Biology

iGEM 2012: 190 teams, 3696 participants, 1708 parts

A Brief History of Synthetic Biology

A Brief History of Synthetic Biology

A Brief History of Synthetic Biology

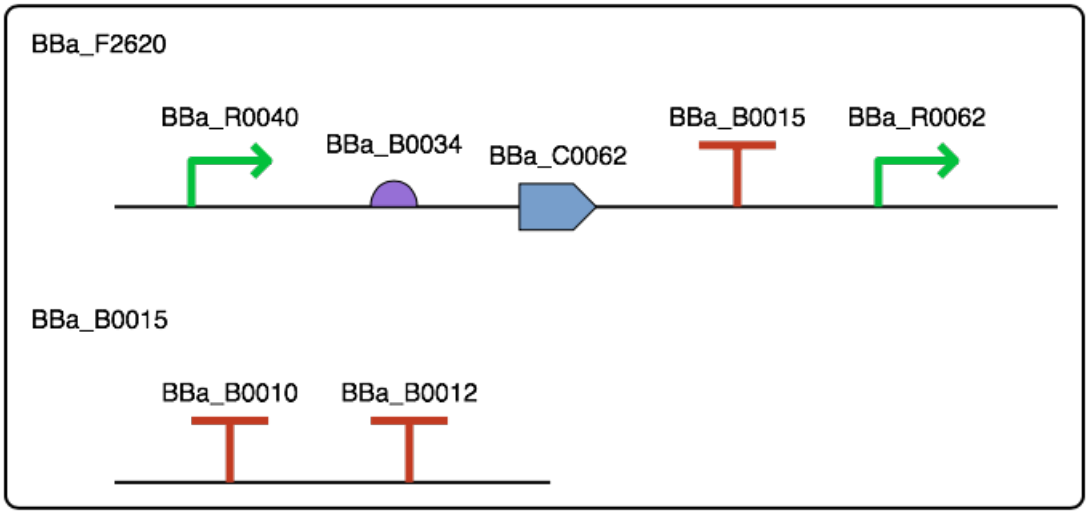
A Brief History of Synthetic Biology

PLOS | BIOLOGY

COMMUNITY PAGE

SBOL Visual: A Graphical Language for Genetic Designs

Jacqueline Y. Quinn[1☯], Robert Sidney Cox III[2☯], Aaron Adler[3], Jacob Beal[3], Swapnil Bhatia[4], Yizhi Cai[5], Joanna Chen[6,7], Kevin Clancy[8], Michal Galdzicki[9], Nathan J. Hillson[6,7], Nicolas Le Novère[10], Akshay J. Maheshwari[11], James Alastair McLaughlin[12], Chris J. Myers[13], Umesh P[14], Matthew Pocock[12,15], Cesar Rodriguez[16], Larisa Soldatova[17], Guy-Bart V. Stan[18], Neil Swainston[19], Anil Wipat[12], Herbert M. Sauro[20]*



A Brief History of Synthetic Biology

iGEM 2013: 215 teams, 4027 participants, 1708 parts

A Brief History of Synthetic Biology

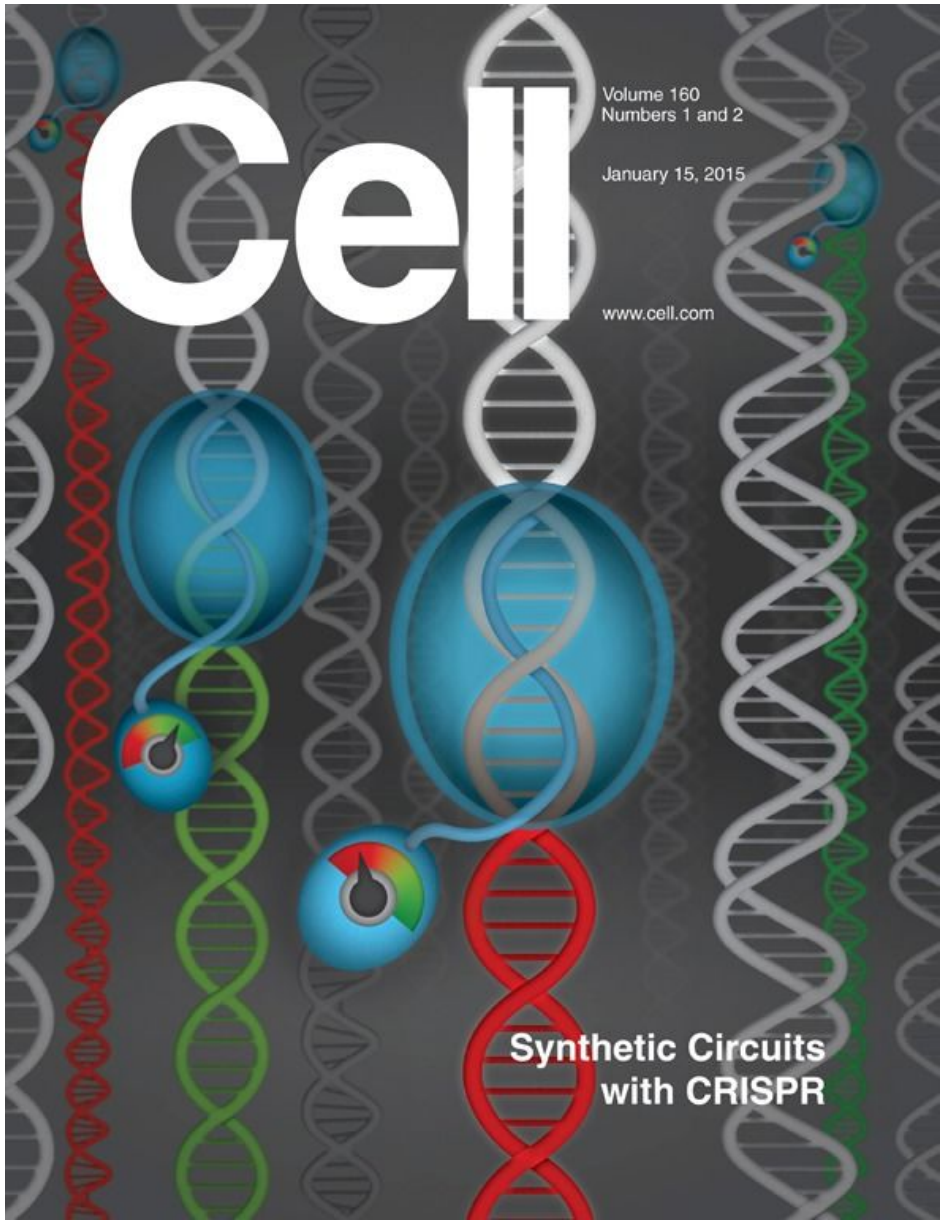
A Brief History of Synthetic Biology

A Brief History of Synthetic Biology

A Brief History of Synthetic Biology

iGEM 2014: 245 teams, 4515 participants

A Brief History of Synthetic Biology

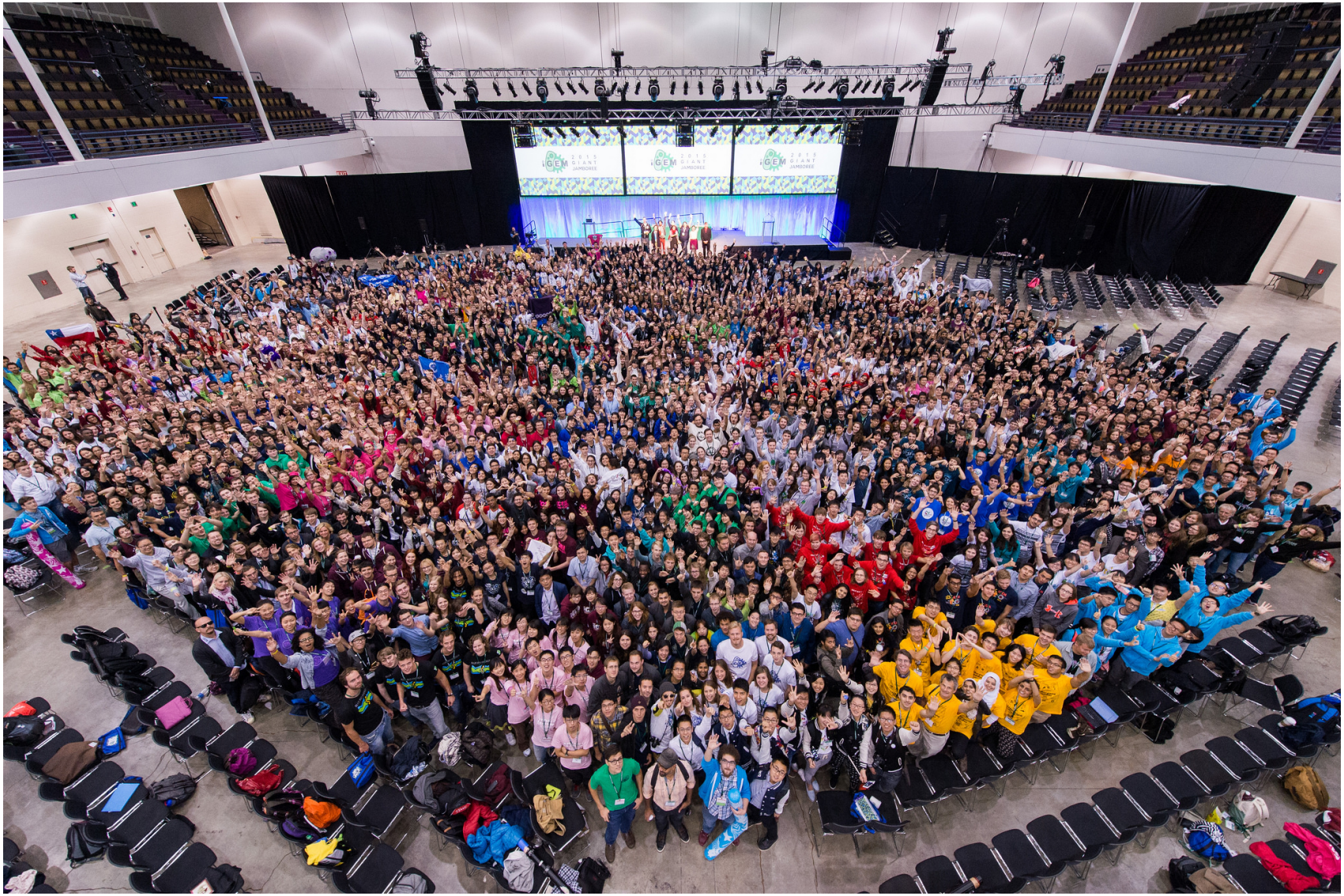


A Brief History of Synthetic Biology

Sharing Structure and Function in Biological Design with SBOL 2.0

Nicholas Roehner,[*,†] Jacob Beal,[‡] Kevin Clancy,[§] Bryan Bartley,[⊥] Goksel Misirli,[∥] Raik Grünberg,[¶] Ernst Oberortner,[#] Matthew Pocock,[▽] Michael Bissell,[⊗] Curtis Madsen,[∥] Tramy Nguyen,[■] Michael Zhang,[■] Zhen Zhang,[■] Zach Zundel,[▲] Douglas Densmore,[†] John H. Gennari,[●] Anil Wipat,[∥] Herbert M. Sauro,[⊥] and Chris J. Myers[■]

A Brief History of Synthetic Biology

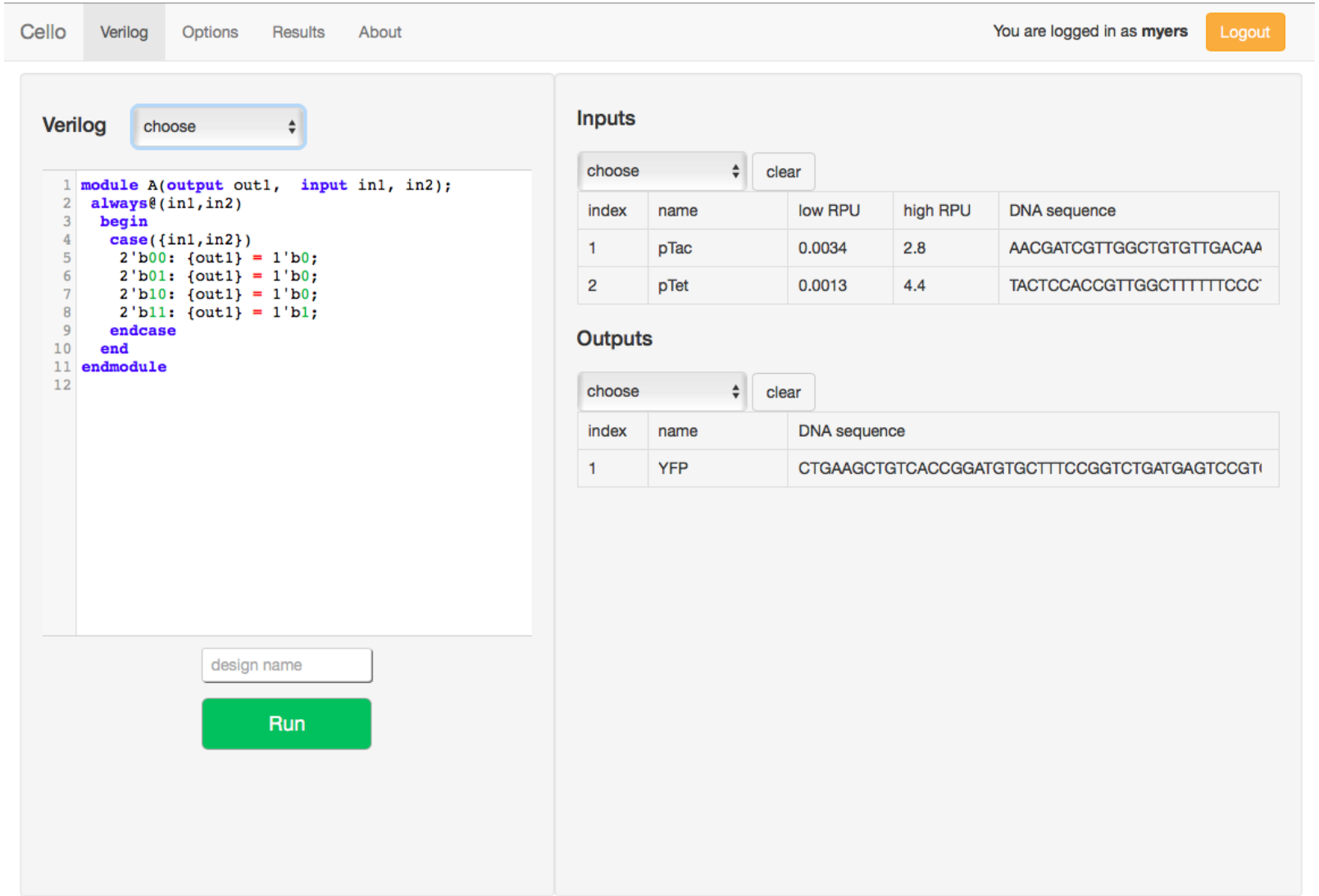


iGEM 2015: 280 teams, 5018 participants

A Brief History of Synthetic Biology

SYNTHETIC
BIOLOGY

A Brief History of Synthetic Biology



Nielsen et al., Science (2016)

A Brief History of Synthetic Biology

ACS SyntheticBiology

Viewpoint

pubs.acs.org/synthbio

Improving Synthetic Biology Communication: Recommended Practices for Visual Depiction and Digital Submission of Genetic Designs

Nathan J. Hillson,[*,†,‡,§,∥] Hector A. Plahar,[†,‡,∥] Jacob Beal,[*,⊥] and Ranjini Prithviraj[#]

[†]Fuels Synthesis and Technology Divisions, DOE Joint BioEnergy Institute (JBEI), Emeryville, California 94608, United States

[‡]Biological Systems and Engineering Division, Lawrence Berkeley National Lab, Berkeley, California 94720, United States

[§]DOE Joint Genome Institute, Walnut Creek, California 94598, United States

[∥]Synthetic Biology Engineering Research Center, Emeryville, California 94608, United States

[⊥]Raytheon BBN Technologies, Cambridge, Massachusetts 02138, United States

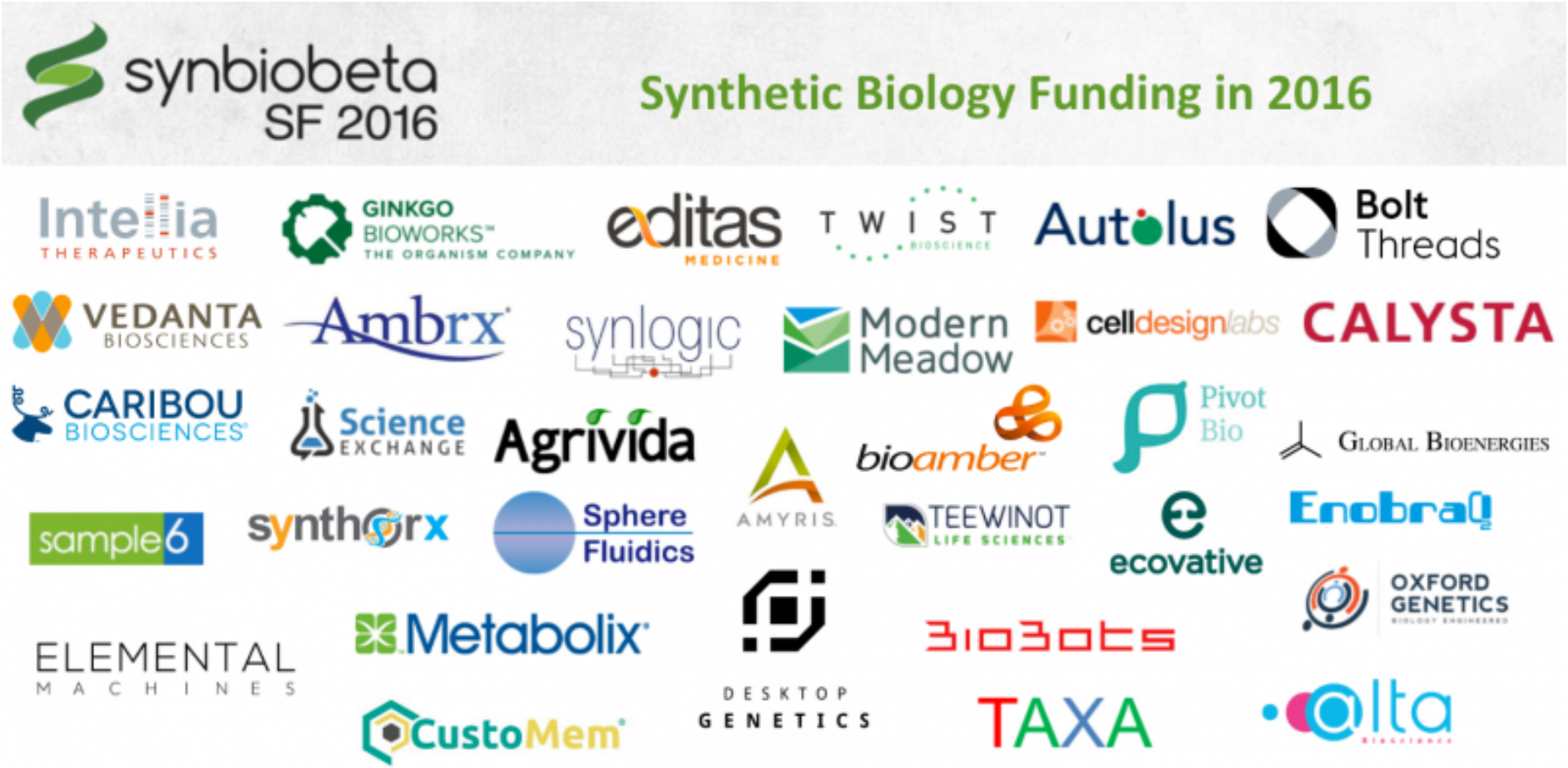
[#]ACS Synthetic Biology, American Chemical Society, Washington, D.C. 20036, United States

ABSTRACT: Research is communicated more effectively and reproducibly when articles depict genetic designs consistently and fully disclose the complete sequences of all reported constructs. *ACS Synthetic Biology* is now providing authors with updated guidance and piloting a new tool and publication workflow that facilitate compliance with these recommended practices and standards for visual representation and data exchange.

A Brief History of Synthetic Biology

iGEM 2016: 300 teams, 4432 participants

A Brief History of Synthetic Biology



These 33 Synthetic Biology Companies Raised More Than $900 Million in 2016

A Brief History of Synthetic Biology

A Brief History of Synthetic Biology

A Brief History of Synthetic Biology

A Brief History of Synthetic Biology

iGEM 2017: 310 teams with nearly 5400 participants from 44 countries.

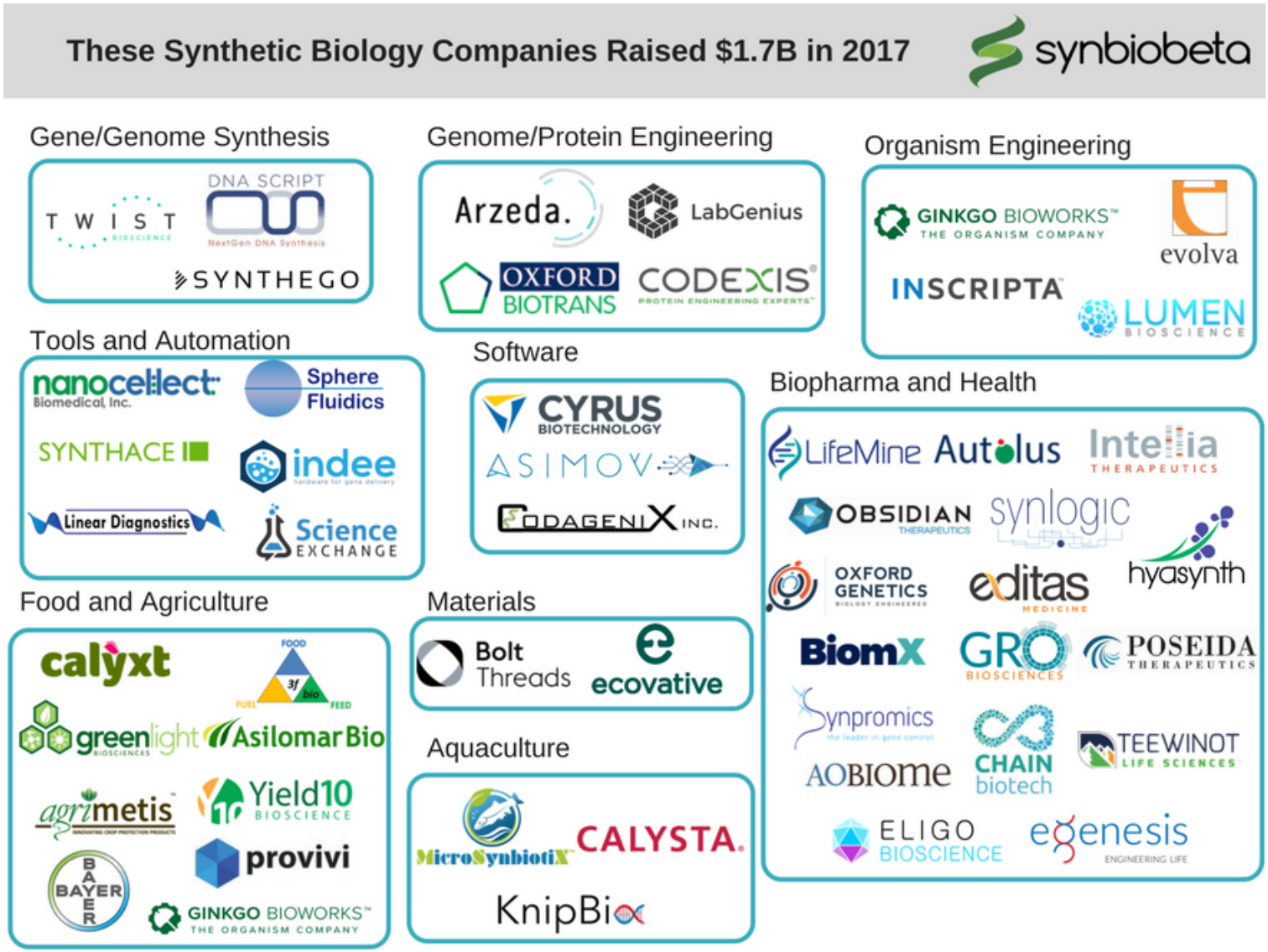
A Brief History of Synthetic Biology

iGEM 2017: 310 teams with nearly 5400 participants from 44 countries.

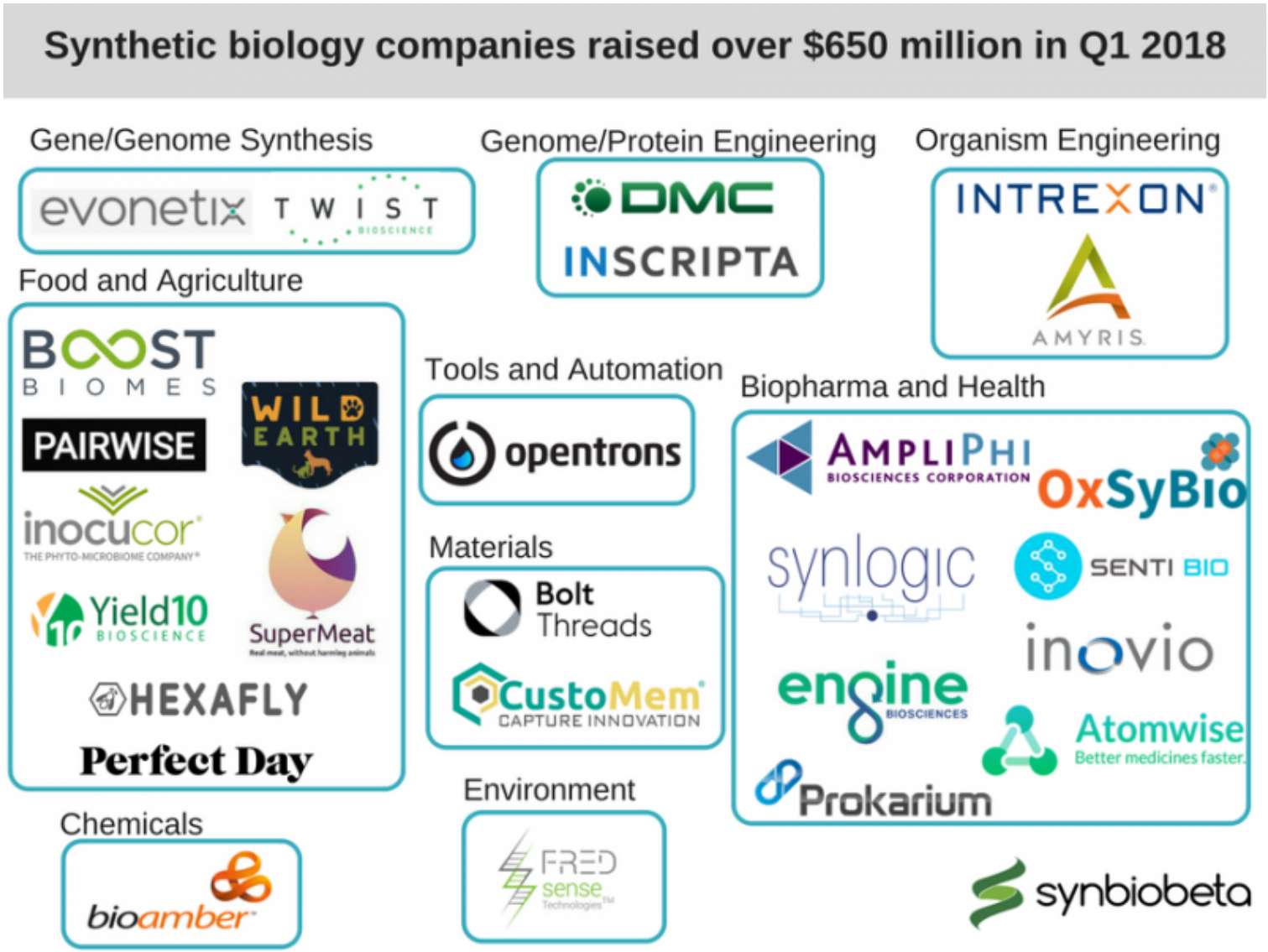
A Brief History of Synthetic Biology

iGEM 2017: 310 teams with nearly 5400 participants from 44 countries.

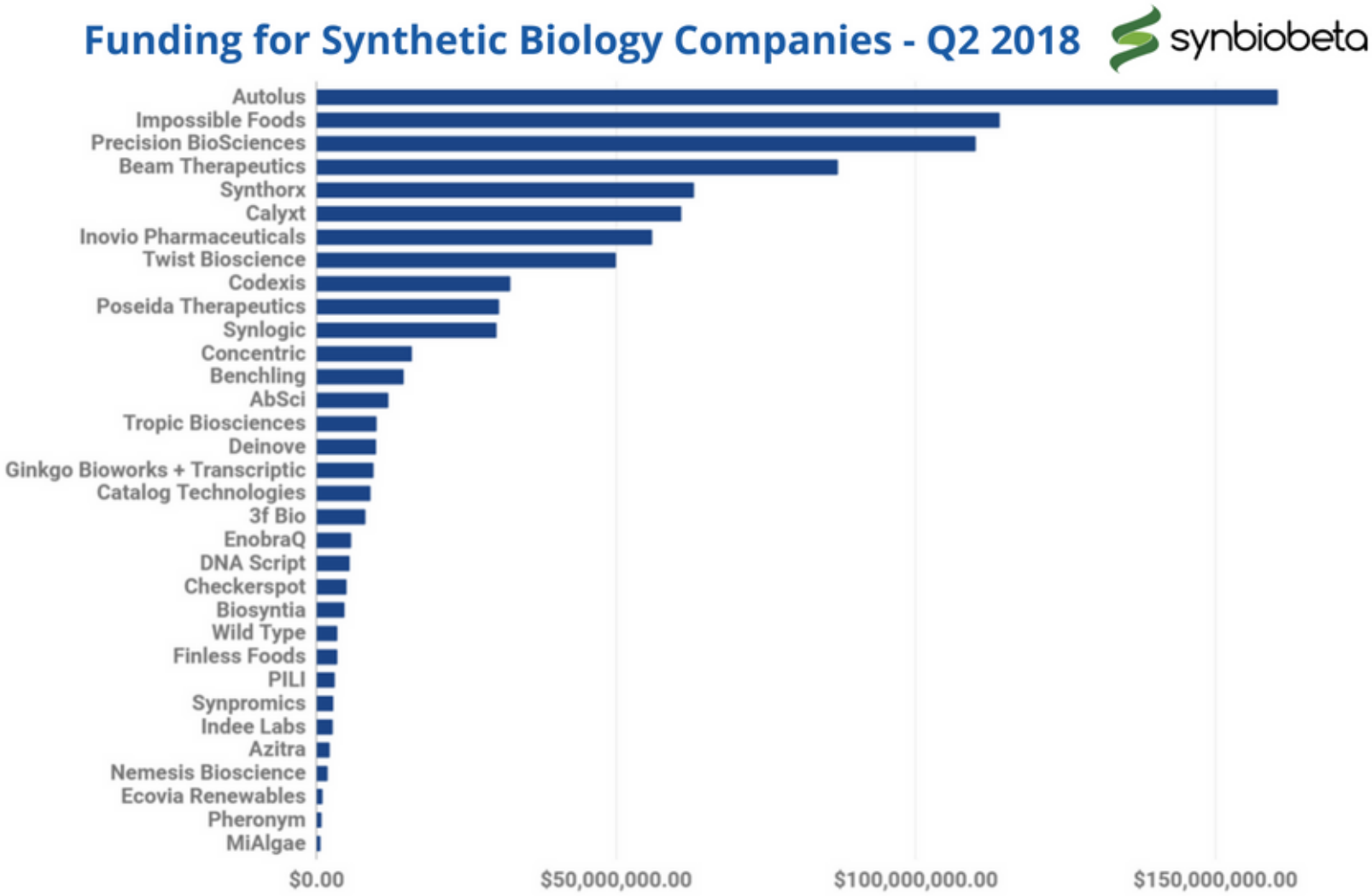
A Brief History of Synthetic Biology



A Brief History of Synthetic Biology

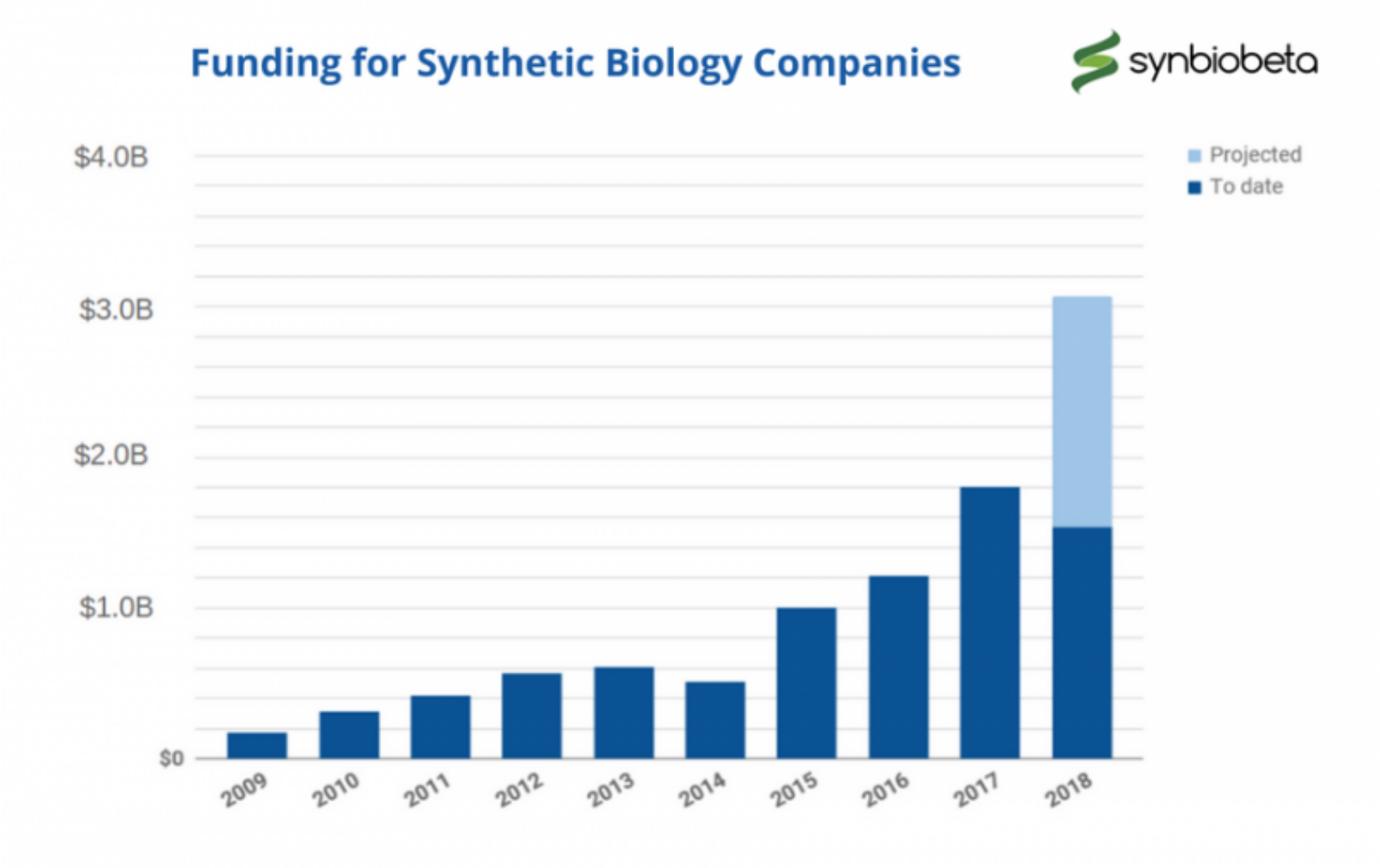


A Brief History of Synthetic Biology



These 33 Synthetic Biology Companies Raised $925 Million in 2018 Q2

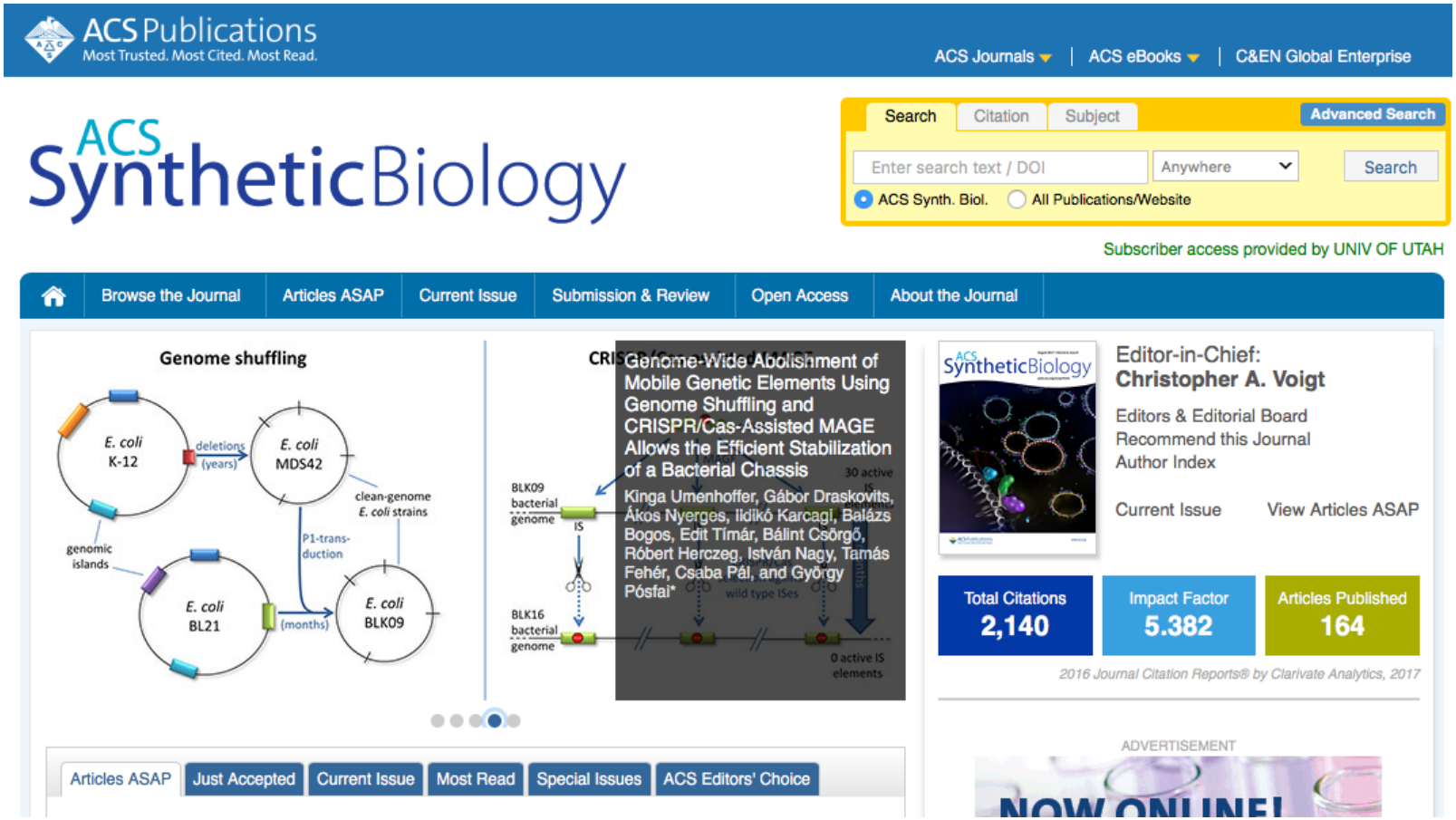
A Brief History of Synthetic Biology



Course Topics

- An Engineer's Guide to Genetic Circuits
- Genetic Parts, Devices, and their Construction
- Modeling of Genetic Circuits
- Analysis of Genetic Circuits
- Design of Genetic Circuits

Assignment #0



Select a paper from ACS Synthetic Biology describing a genetic circuit design. During the assignments for this course you will reproduce this design *in silico*. Each student must select a unique genetic circuit design.

Email me your selection before the end of the week (8/24).