Natalie Kuldell

February 3rd, 2009

http://openwetware.org/wiki/20.20(S09)

2020: Futurists

Freeman Dyson writes:

"Biotechnology will become as domesticated as computer games and children and housewives will create their new animal and plant species at home."

Quack? Genius?

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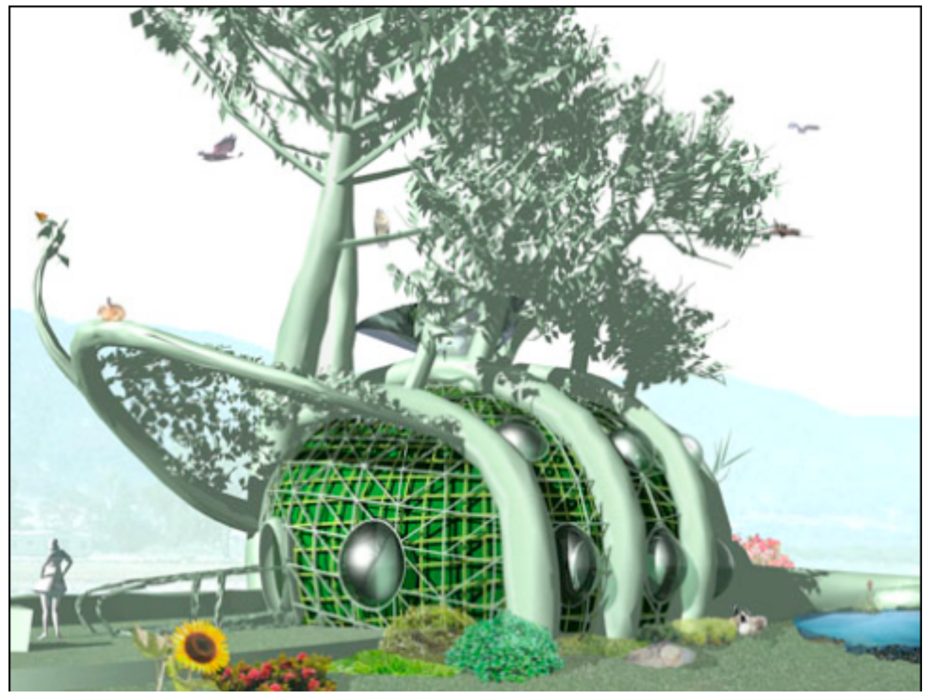
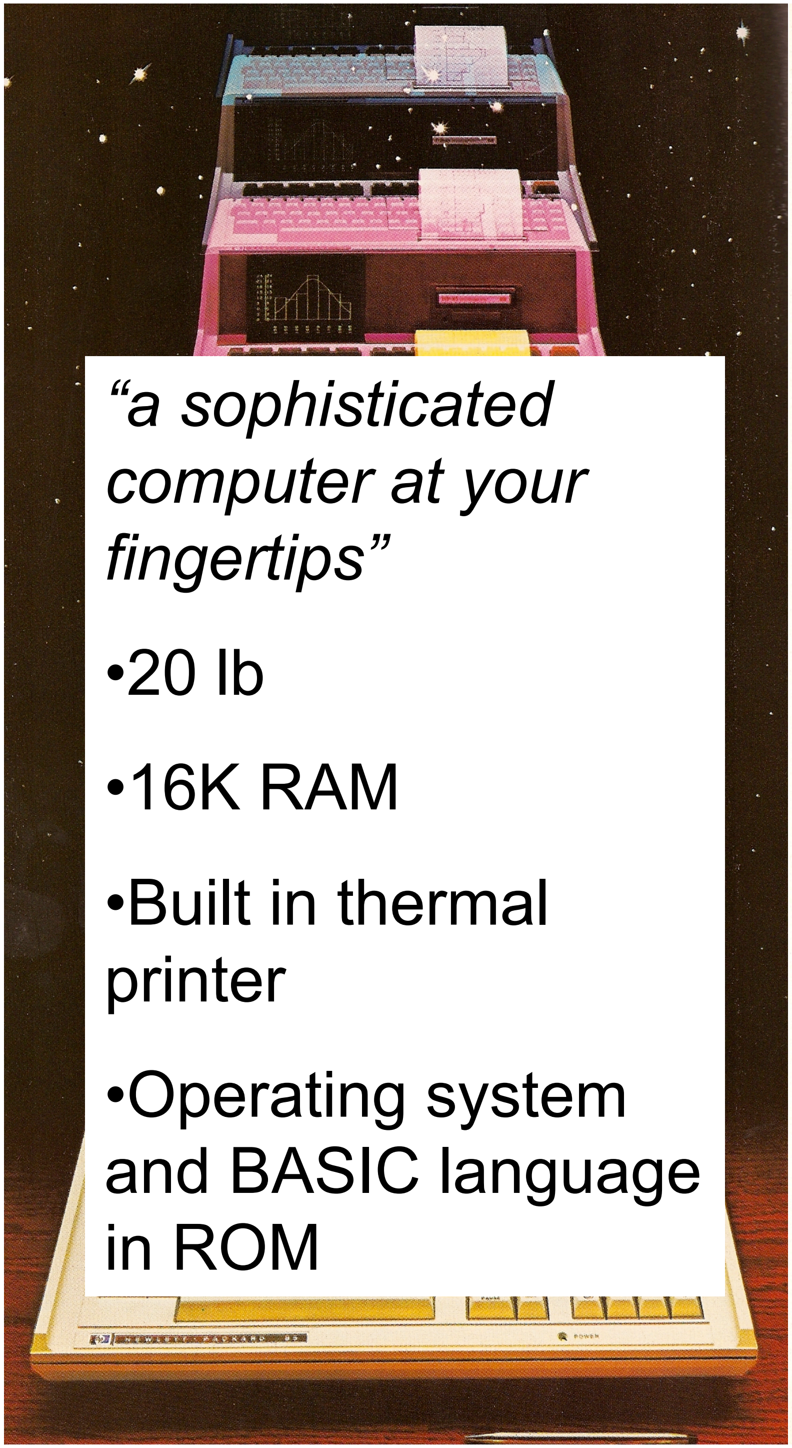


MIT Human Ecology Design team

2020: Historians



"a sophisticated computer at your fingertips"

- 20 lb
- 16K RAM
- Built in thermal printer
- Operating system and BASIC language in ROM

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A NEW WORLD OF PERSONAL-PROFESSIONAL COMPUTATION.

Imagine the new world that would unfold before you if you had a powerful, portable, completely integrated computer system at your personal disposal. And at an affordable price. That's exactly what Hewlett-Packard has just created.

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A COMPLETE COMPUTER SYSTEM IN ONE SMALL PACKAGE.

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Interactive graphics under keyboard control.

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Standard typewriter keyboard with separate numeric key pad and eight user-definable special function keys.

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Operating system and BASIC language, permanently stored in ROM.

A SOPHISTICATED COMPUTER AT YOUR FINGERTIPS.

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A key to this achievement is Hewlett-Packard's choice of BASIC for the HP-85's language. BASIC is easy to learn and lets you solve complex problems in an English-like, conversational style.

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The HP-85's versatility, expandability and sophisticated simplicity all grew out of Hewlett-Packard's underlying principle of excellence by design. Excellence by design means rigorous quality control and testing as well as a worldwide maintenance support network.

When you buy the HP-85, you're not just buying a computer system, you're buying the confidence that the Hewlett-Packard name brings and the knowledge that the HP-85 can expand with your changing needs.

For the address of your nearest HP dealer, CALL TOLL-FREE 800-648-4711 except from Alaska or Hawaii. In Nevada, 800-992-5710. For details on the HP-85, send the attached coupon, or write: Hewlett-Packard, 1000 N.E. Circle Blvd., Corvallis, OR 97330, Dept. 272C.

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619/20

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Please send details on HP-85.

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TITLE ____________

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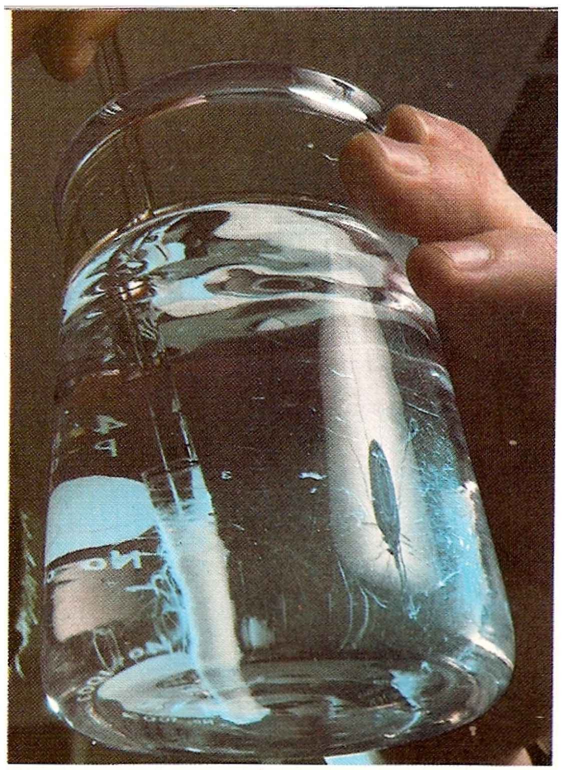
CITY ____________

STATE ________ ZIP ________

"a scientist clad in white spools threads of DNA onto a glass rod. He is about to treat it with enzymes, then insert it into E. coli, endowing the microbe with powers nature never gave it."



From a chilled beaker, a scientist clad in white gently spools spaghettilike threads of DNA onto a glass rod. He is about to treat it with enzymes that will clip away all but a chosen gene, then insert it into the genetic material of a bacterium called *Escherichia coli*, endowing the microbe with powers that nature never gave it.

Not long ago experiments with recombinant DNA stirred visions of strange, artificial diseases against which humanity would have no natural defense; such experiments provoked sharp controversy over whether scientists should be allowed to tamper with life itself. Today most of the fears have died down, and biotechnology is filling the heads of businessmen with visions of immense profits.

In the past ten years or so, dozens of new companies have begun to harness the life processes and put them to work in industry. Quietly, almost unnoticed in a world dazzled by innovative electronic products, these firms are fomenting a technological revolution that promises to shake the foundations of medicine, agriculture, food processing, energy production, and the chemical and pharmaceutical industries.

Already included among biotechnology's success stories are bacteria engineered to produce human insulin, drug-delivery systems that

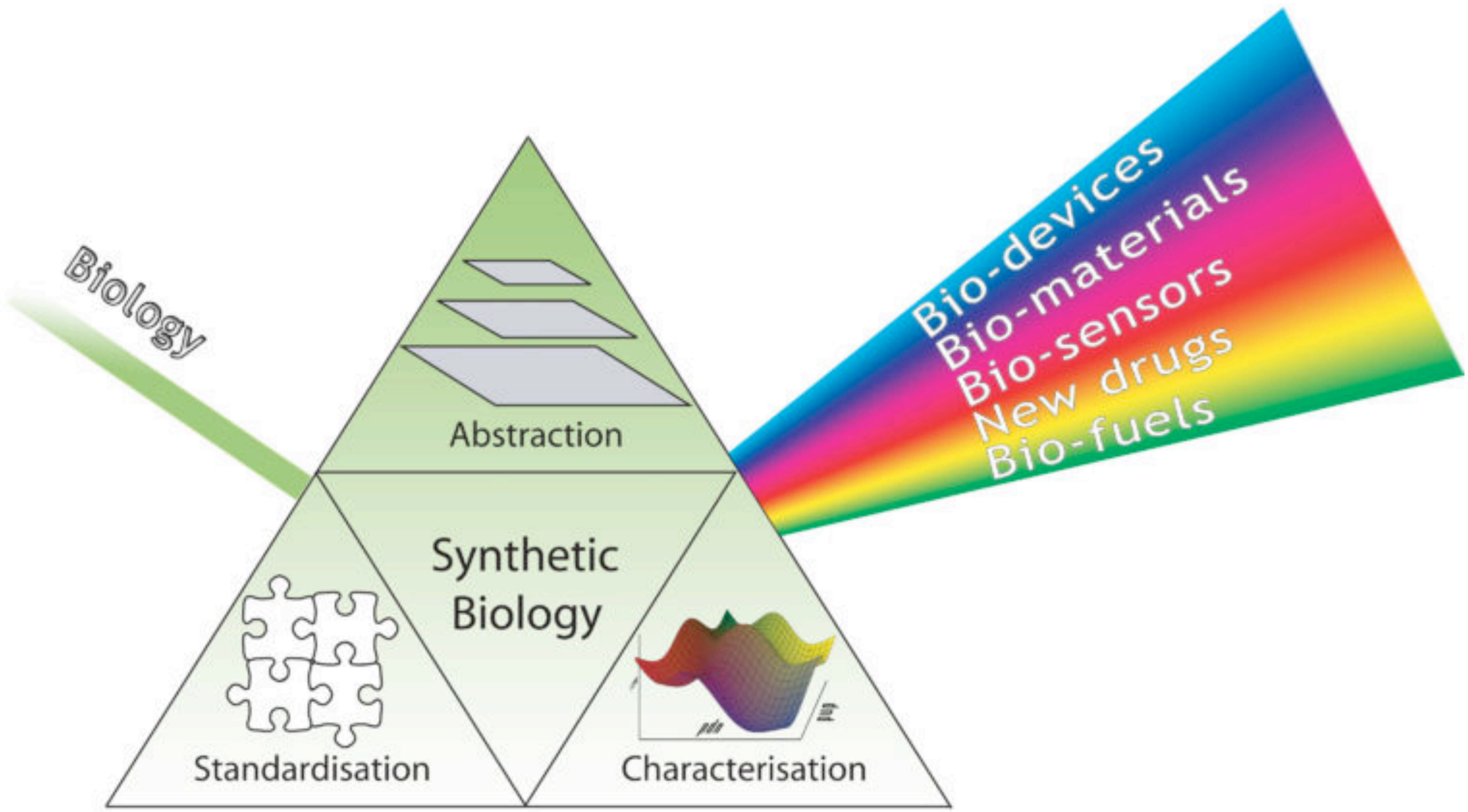
THE GENE TRUST

BY KATHLEEN AND SHARON McAULIFFE

Science and business join forces to exploit the machinery of life

PHOTOGRAPHS BY DOUGLAS KIRKLAND

What's new: Application of engineering principles to biology



Postcards & snapshots so far

•genome re-engineering

Molecular Systems Biology (2005) doi:10.1038/msb4100025

www.molecularsystemsbiology.com

molecular systems biology

Refactoring bacteriophage T7

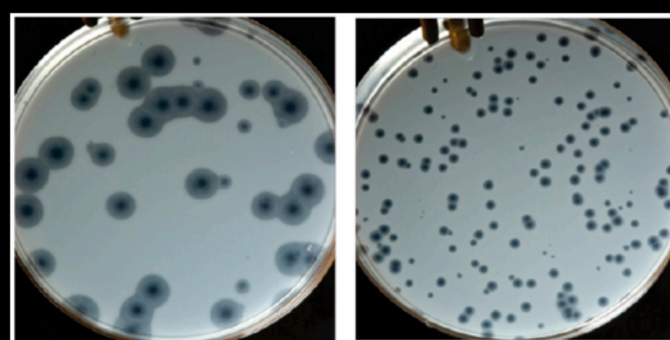
Leon Y Chan[1,3], Sriram Kosuri[2,3] and Drew Endy[2,*]

A Wild-type T7 *2.8–3* elements

```
----------------2.8----------------->
acgcaaaggggaggcgacatggcaggttacggcgctaaaggaatccgaaa
     <--3-RBS---><---------------3-------------
```

B T7.1 parts 28 and 29

```
acgcaaGggggagAcgacaCggcaggttacggcgctaaggatccggccgcaaaggggaggcgacatggcaggttacggcgctaaa
----------------2.8----------------><D28R|D29L><--3RBS------><--------------3----
```



Postcards & snapshots so far

•genome re-engineering

Complete Chemical Synthesis, Assembly, and Cloning of a *Mycoplasma genitalium* Genome

Daniel G. Gibson, Gwynedd A. Benders, Cynthia Andrews-Pfannkoch, Evgeniya A. Denisova, Holly Baden-Tillson, Jayshree Zaveri, Timothy B. Stockwell, Anushka Brownley, David W. Thomas, Mikkel A. Algire, Chuck Merryman, Lei Young, Vladimir N. Noskov, John I. Glass, J. Craig Venter, Clyde A. Hutchison III, Hamilton O. Smith*

We have synthesized a 582,970–base pair *Mycoplasma genitalium* genome. This synthetic genome, named *M. genitalium* JCVI-1.0, contains all the genes of wild-type *M. genitalium* G37 except MG408, which was disrupted by an antibiotic marker to block pathogenicity and to allow for selection. To identify the genome as synthetic, we inserted "watermarks" at intergenic sites known

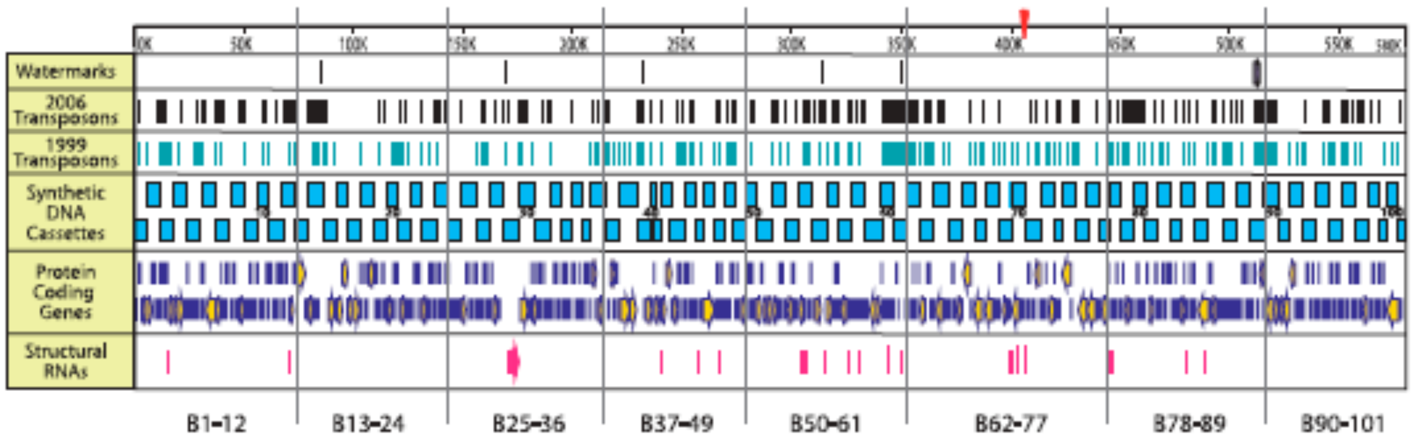


Fig. 1. Linear GenomBench (Invitrogen) representation of the circular 582,970-bp *M. genitalium* JCVI-1.0 genome. Features shown include locations of watermarks and the aminoglycoside resistance marker, viable Tn4001 transposon insertions determined in our 1999 and 2006 studies (3, 4), overlapping synthetic DNA cassettes that comprise the whole genome sequence, 485 *M. genitalium* protein-coding genes, 43 *M. genitalium* rRNA, tRNA, and structural RNA genes, and B-series assemblies (Fig. 2). The red dagger on the genome coordinates line shows the location of the yeast/*E. coli* shuttle vector insertion. Table S1 lists cassette coordinates; table S2 has FASTA files for all 101 cassettes; table S3 lists watermark coordinates; table S4 lists the sequences of the watermarks.

www.sciencemag.org SCIENCE VOL 319 29 FEBRUARY 2008

Postcards & snapshots so far

- genome re-engineering

Characterization of the Reconstructed 1918 Spanish Influenza Pandemic Virus

Terrence M. Tumpey,[1*] Christopher F. Basler,[2] Patricia V. Aguilar,[2] Hui Zeng,[1] Alicia Solórzano,[2] David E. Swayne,[4] Nancy J. Cox,[1] Jacqueline M. Katz,[1] Jeffery K. Taubenberger,[3] Peter Palese,[2] Adolfo García-Sastre[2]

The pandemic influenza virus of 1918–1919 killed an estimated 20 to 50 million people worldwide. With the recent availability of the complete 1918 influenza virus coding sequence, we used reverse genetics to generate an influenza virus bearing all eight gene segments of the pandemic virus to study the properties associated with its extraordinary virulence. In stark contrast to contemporary human influenza H1N1 viruses, the 1918 pandemic virus had the ability to replicate in the absence of trypsin, caused death in mice and embryonated chicken eggs, and displayed a high-growth phenotype in human bronchial epithelial cells. Moreover, the coordinated expression of the 1918 virus genes most certainly confers the unique high-virulence phenotype observed with this pandemic virus.

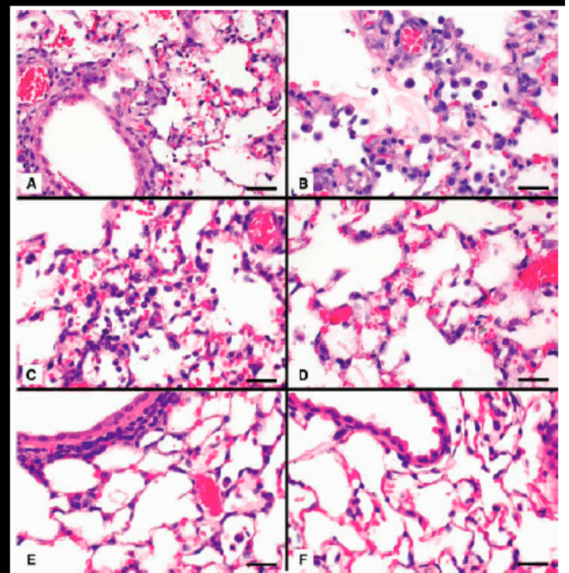


Fig. 2. Photomicrographs of hematoxylin and eosin–stained lung sections. (A to C), lungs from mice infected with the 1918 influenza virus: (A) necrotizing bronchiolitis and severe alveolitis, (B) severe alveolar edema and histiocytic alveolitis with scattered neutrophils, and (C) alveolitis, predominantly neutrophilic, and associated hemorrhage. (D) Moderate alveolitis and edema in lungs from a mouse infected with 1918 HA/NA/M/NP/NS:Tx/91 virus. (E) Mild peribronchial inflammation with adjacent minimal alveolitis in a mouse infected with Tx/91 HA:1918 virus. (F) Lung tissue from a Tx/91-infected mouse showing the paucity of lesions. Scale bars, 25 µm (A) and 15 µm (B to F).

Postcards & snapshots so far

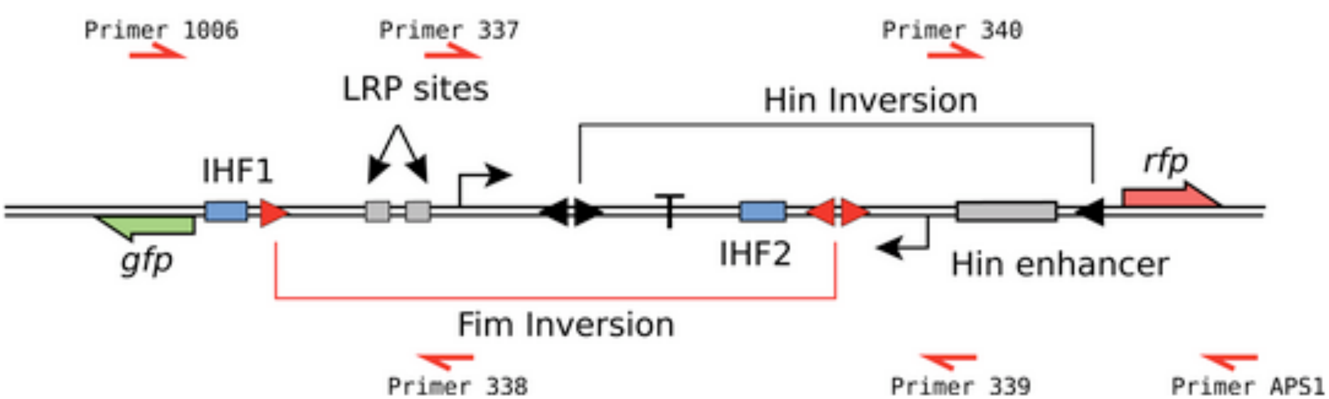
- •genome re-engineering
- •DNA based memory

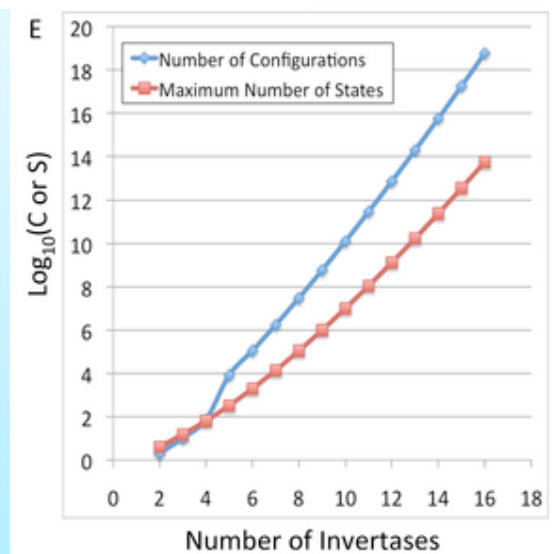
RESEARCH ARTICLE

Design and Construction of a Double Inversion Recombination Switch for Heritable Sequential Genetic Memory

Timothy S. Ham[1], Sung K. Lee[2], Jay D. Keasling[1,2,3], Adam P. Arkin[1,2*]

Citation: Ham TS, Lee SK, Keasling JD, Arkin AP (2008) Design and Construction of a Double Inversion Recombination Switch for Heritable Sequential Genetic Memory. PLoS ONE 3(7): e2815. doi:10.1371/journal.pone.0002815





Postcards & snapshots so far

- genome re-engineering
- DNA based memory
- logic engineering

Science 17 October 2008:
Vol. 322. no. 5900, pp. 456 – 460
DOI: 10.1126/science.1160311

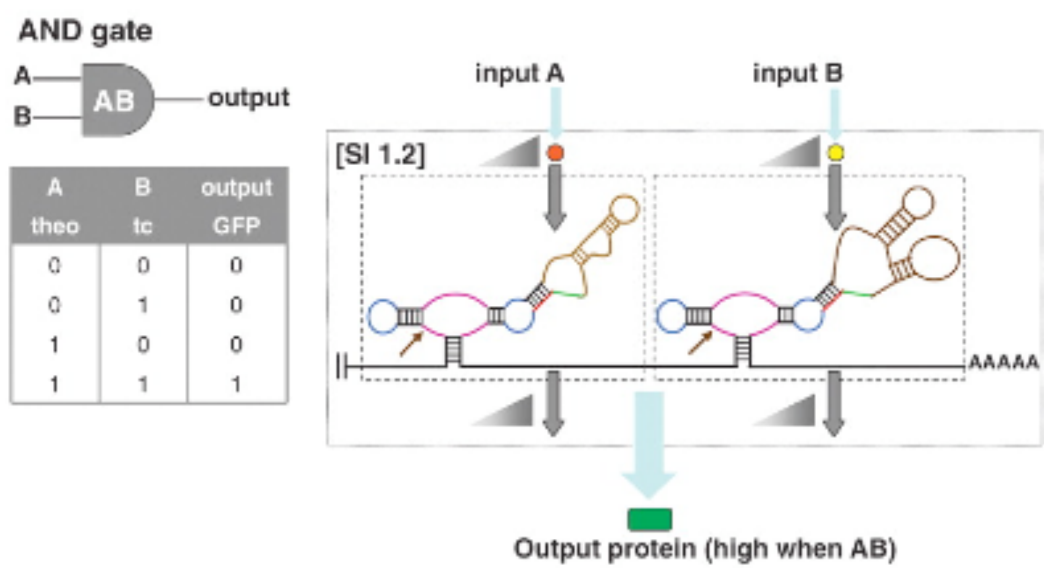
‹ Prev | Table of Contents | Next ›

REPORTS

Higher-Order Cellular Information Processing with Synthetic RNA Devices

Maung Nyan Win and Christina D. Smolke*

The engineering of biological systems is anticipated to provide effective solutions to challenges that include energy and food production, environmental quality, and health and medicine. Our ability to transmit information to and from living systems, and to process and act on information inside cells, is critical to advancing the scale and complexity at which we can engineer, manipulate, and probe biological systems. We developed a general approach for assembling RNA devices that can execute higher-order cellular information processing operations from standard components. The engineered devices can function as logic gates (AND, NOR, NAND, or OR gates) and signal filters, and exhibit cooperativity. RNA devices process and transmit molecular inputs to targeted protein outputs, linking computation to gene expression and thus the potential to control cellular function.



A theo	B tc	output GFP
0	0	0
0	1	0
1	0	0
1	1	1

Postcards & snapshots so far

- •genome re-engineering
- •DNA based memory
- •logic engineering
- •circuit engineering

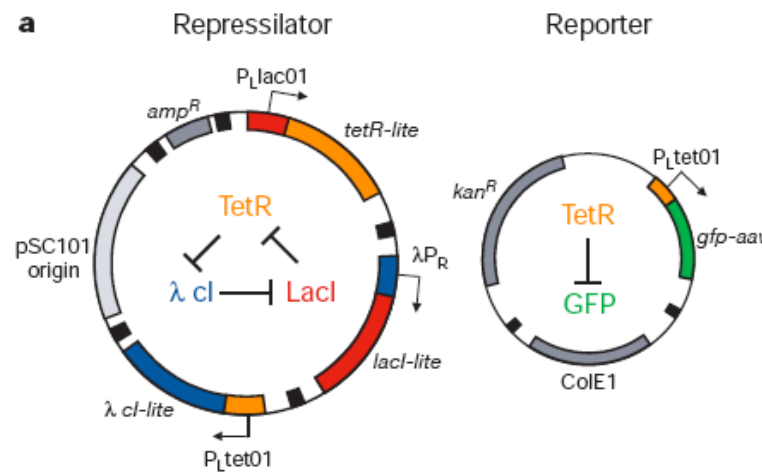
A synthetic oscillatory network of transcriptional regulators

Michael B. Elowitz & Stanislas Leibler

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

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[3–5] to buil

NATURE | VOL 403 | 20 JANUARY 2000 | www



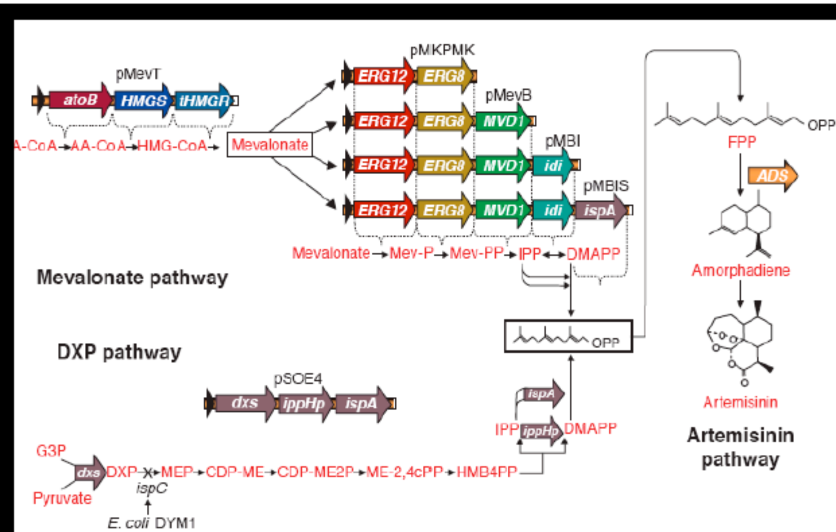
Postcards & snapshots so far

- •genome re-engineering
- •DNA based memory
- •logic engineering
- •circuit engineering

Engineering a mevalonate pathway in *Escherichia coli* for production of terpenoids

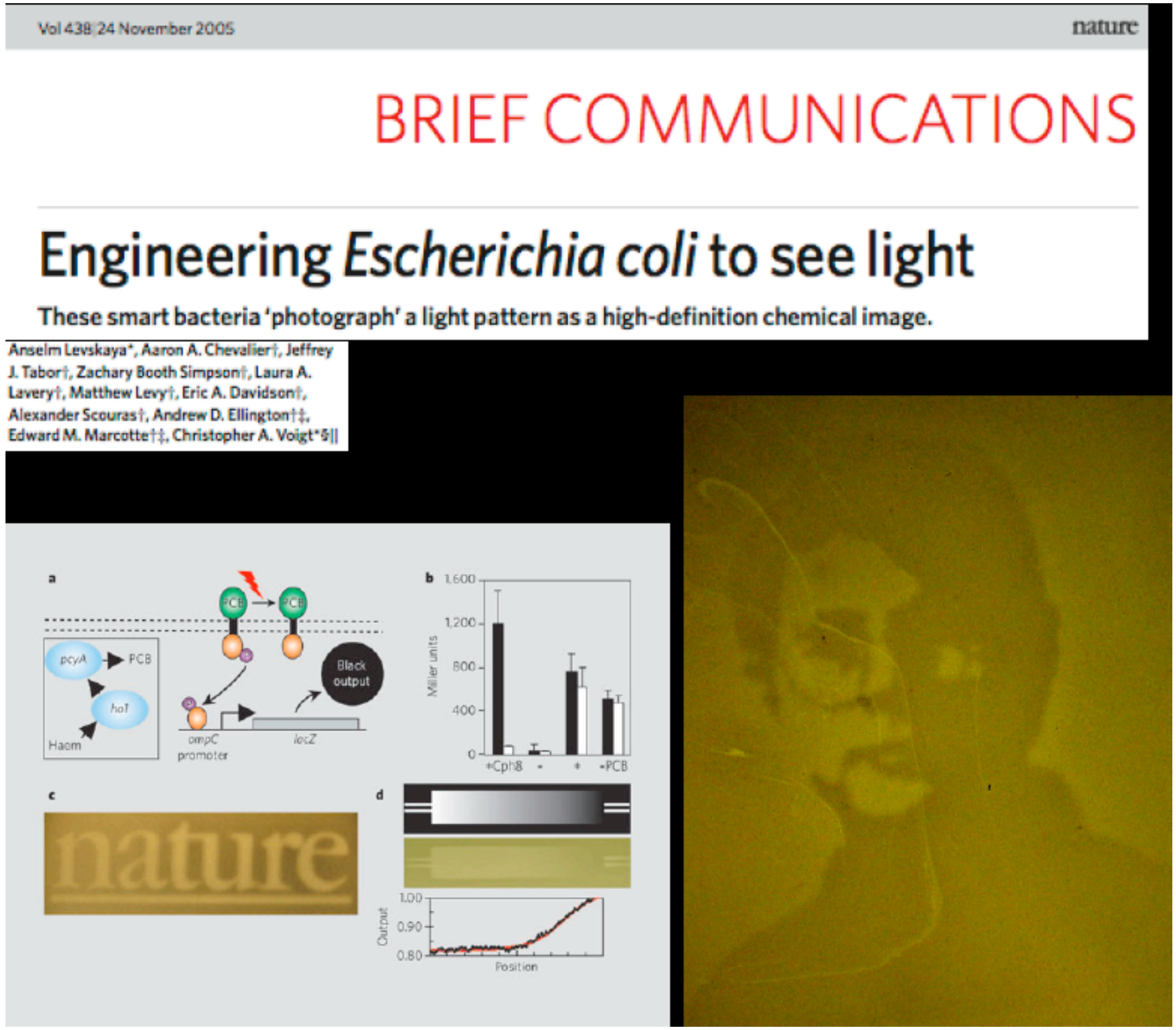
Vincent JJ Martin[1,2,3], Douglas J Pitera[1,3], Sydnor T Withers[1], Jack D Newman[1] & Jay D Keasling[1]

Isoprenoids are the most numerous and structurally diverse family of natural products. Terpenoids, a class of isoprenoids often isolated from plants, are used as commercial flavor and fragrance compounds and antimalarial or anticancer drugs. Because plant tissue extractions typically yield low terpenoid concentrations, we sought an alternative method to produce high-value terpenoid compounds, such as the antimalarial drug artemisinin, in a microbial host. We engineered the expression of a synthetic amorpha-4,11-diene synthase gene and the mevalonate isoprenoid pathway from *Saccharomyces cerevisiae* in *Escherichia coli*. Concentrations of amorphadiene, the sesquiterpene olefin precursor to artemisinin, reached 24 µg caryophyllene equivalent/ml. Because isopentenyl and dimethylallyl pyrophosphates are the universal precursors to all isoprenoids, the strains developed in this study can serve as platform hosts for the production of any terpenoid compound for which a terpene synthase gene is available.



Postcards & snapshots so far

- •genome re-engineering
- •DNA based memory
- •logic engineering
- •circuit engineering
- •system engineering


Vol 438|24 November 2005

nature

BRIEF COMMUNICATIONS

Engineering *Escherichia coli* to see light

These smart bacteria 'photograph' a light pattern as a high-definition chemical image.

Anselm Levskaya*, Aaron A. Chevalier†, Jeffrey J. Tabor†, Zachary Booth Simpson†, Laura A. Lavery†, Matthew Levy†, Eric A. Davidson†, Alexander Scouras†, Andrew D. Ellington†‡, Edward M. Marcotte†‡, Christopher A. Voigt*§||

Postcards & snapshots so far

- •genome re-engineering
- •DNA based memory
- •logic engineering
- •circuit engineering
- •system engineering

doi:10.1016/j.jmb.2005.10.076

J. Mol. Biol. (2006) **355**, 619–627

JMB

Available online at www.sciencedirect.com

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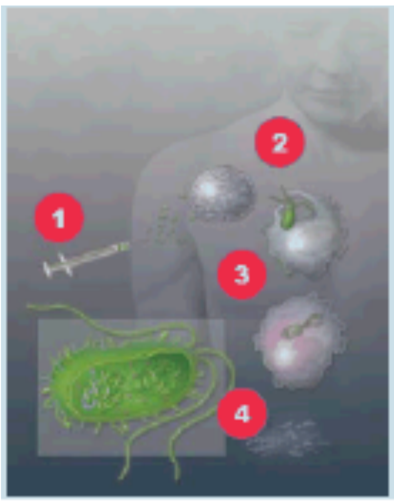
ELSEVIER

Environmentally Controlled Invasion of Cancer Cells by Engineered Bacteria

J. Christopher Anderson[1,3], Elizabeth J. Clarke[3], Adam P. Arkin[1,2]* and Christopher A. Voigt[2,3]



Tumor-killing bacteria

1. Engineered bacteria are injected into the bloodstream; polysaccharide molecules on their surfaces allow them to evade the immune system

2. When they detect the low-oxygen environment of a tumor, the bacteria produce invasion, a protein that allows them to infiltrate the cancer cells

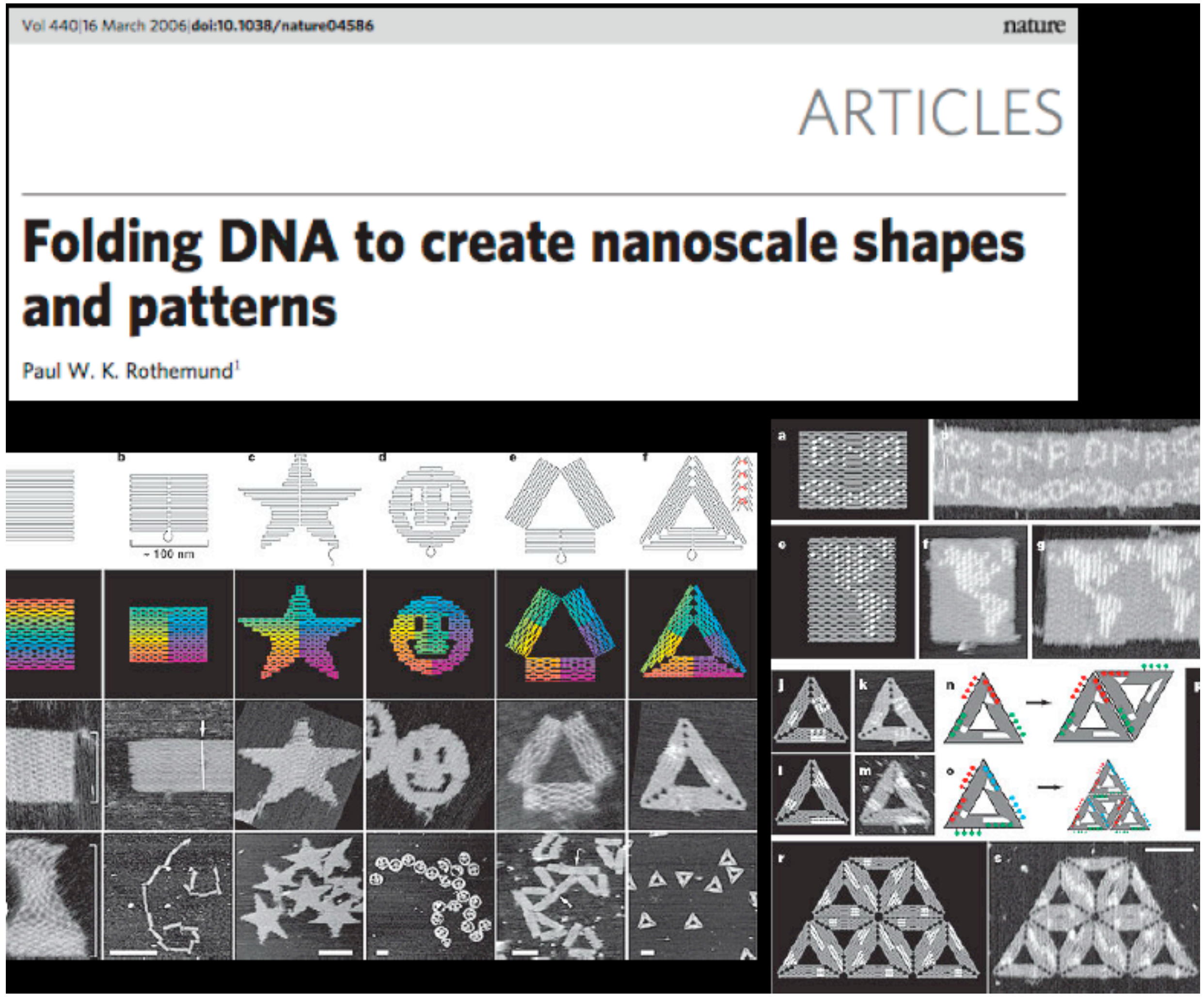
3. The invasion binds to the cancer cells, prompting the cells to engulf the bacteria

4. The cancer cell bursts the bacterium, releasing an enzyme that is toxic to the cancer cell

Image courtesy Tami Tolpa

Postcards & snapshots so far

- •genome re-engineering
- •DNA based memory
- •logic engineering
- •circuit engineering
- •system engineering
- •biomaterials engineering



Postcards & snapshots so far

- genome re-engineering
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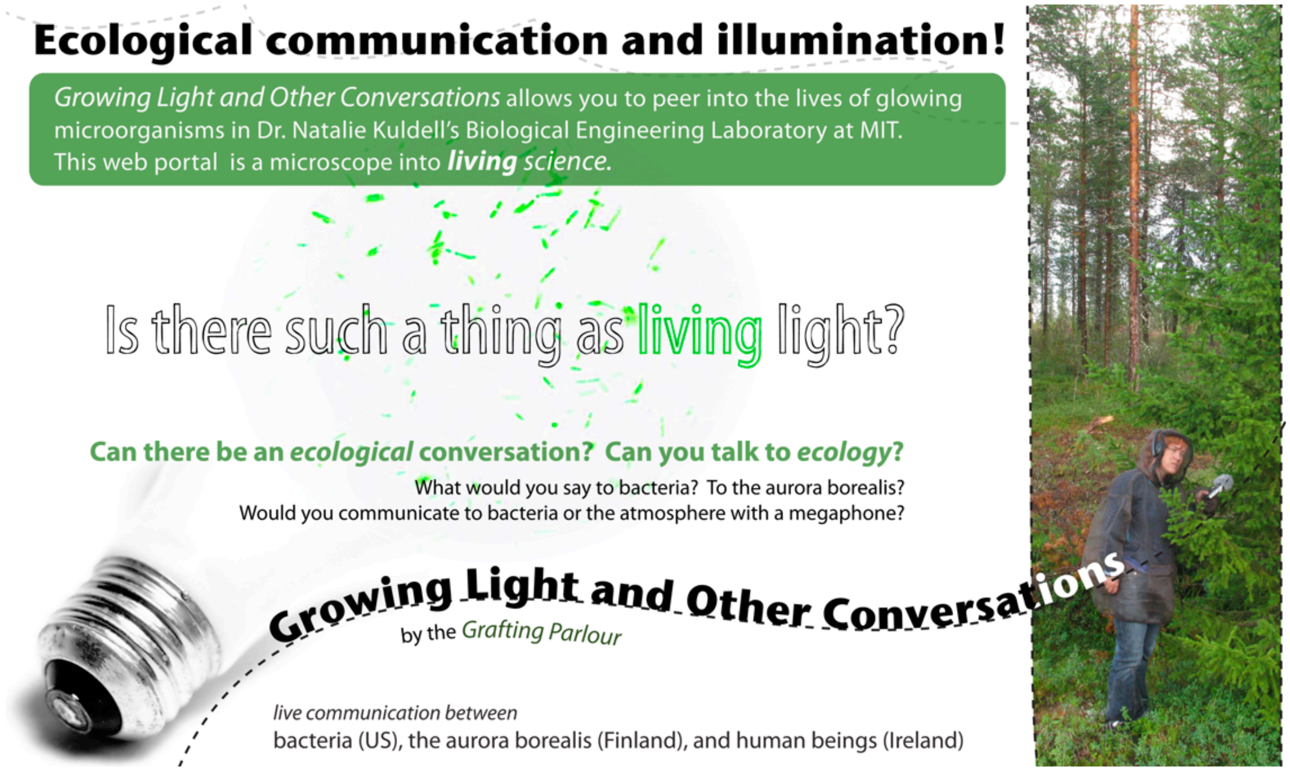
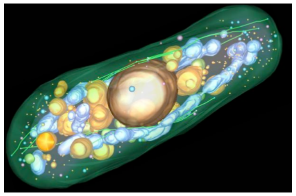
- system engineering
- biomaterials engineering



What you'll work on…

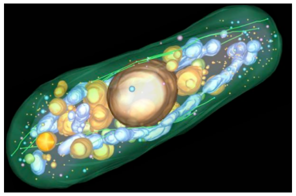
1. design a plausible and compelling synthetic biological system
2. develop a detailed design plan and construction roadmap
3. evaluate ownership, commercial, ethical aspects of the project

What you'll learn (I think)…



Understand the operation of genetic programs in prokaryotes and eukaryotes.

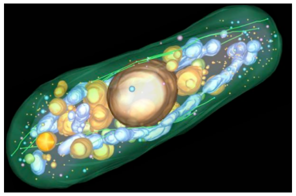
What you'll learn (I think)…



Understand the operation of genetic programs in prokaryotes and eukaryotes.

Describe key enabling technologies that support the engineering of biology, including synthesis, abstraction and standardization.

What you'll learn (I think)…

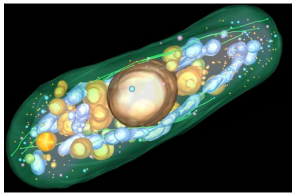


Understand the operation of genetic programs in prokaryotes and eukaryotes.

Describe key enabling technologies that support the engineering of biology, including synthesis, abstraction and standardization.

Develop awareness of issues of human practice that impact & result from the development and application of biological technologies.

What you'll learn (I think)…



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Home	Lecture and Studio schedule	20.902 Reading Schedule

Week 1 Week 2 Week 3 Week 4 Week 5 Week 6 Week 7
Week 8 Week 9 Week 10 Week 11 Week 12 Week 13 Week 14

Expectations	Guidelines: 3 Ideas Presentation	Guidelines: Tech Spec Review	Guidelines: Final Presentations

Team Building Resources Teacher Resources

http://openwetware.org/wiki/20.20(S09)

Home

Lecture and Studio schedule

20.902 Reading Schedule

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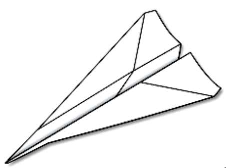
Team Building Resources

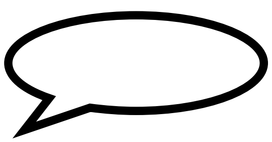
Teacher Resources

Tuesdays/Thursdays

11:30-1

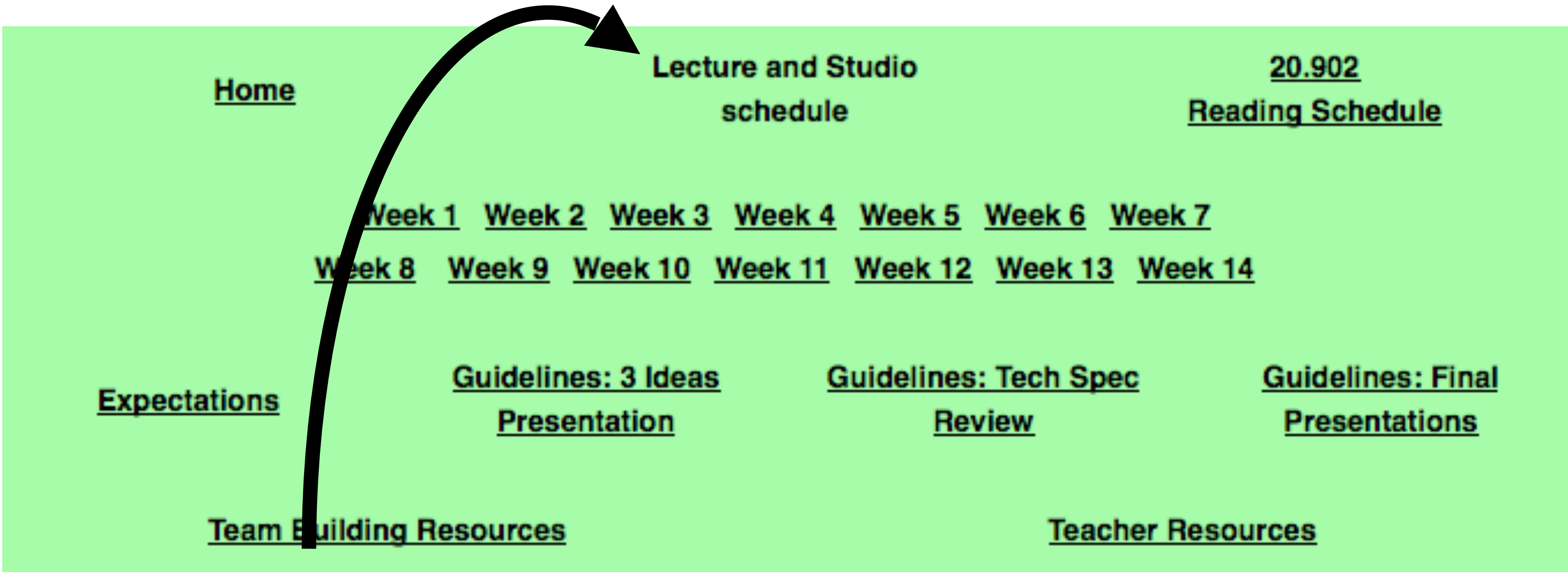


Start with challenge/puzzle/activity



Follow-up with group discussion

Occasional homework



- How can biology be made easier to engineer?
- What are the consequences of success?
- How has nature solved physical challenges?
- In what ways does nature innovate?

Home

Lecture and Studio schedule

20.902 Reading Schedule

Week 1 Week 2 Week 3 Week 4 Week 5 Week 6 Week 7

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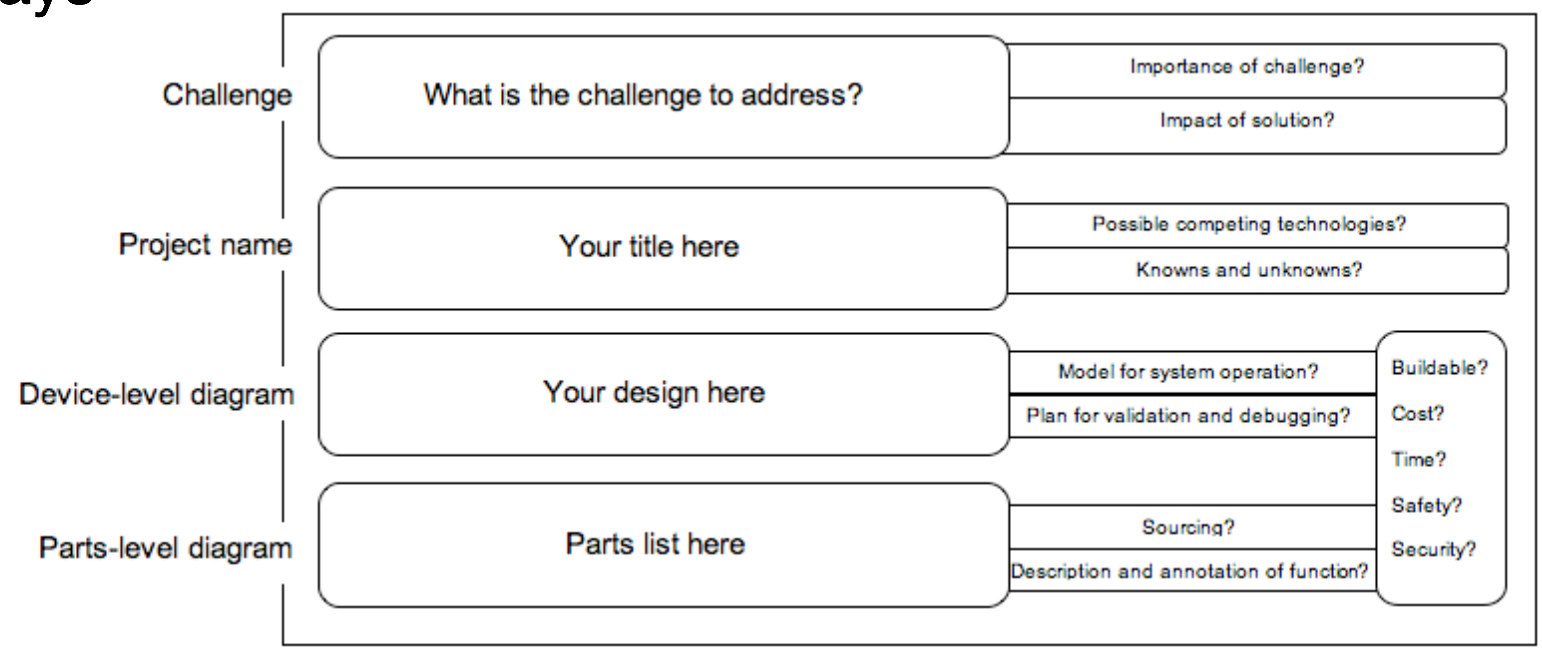
Wednesdays

2-5



Home

Lecture and Studio schedule

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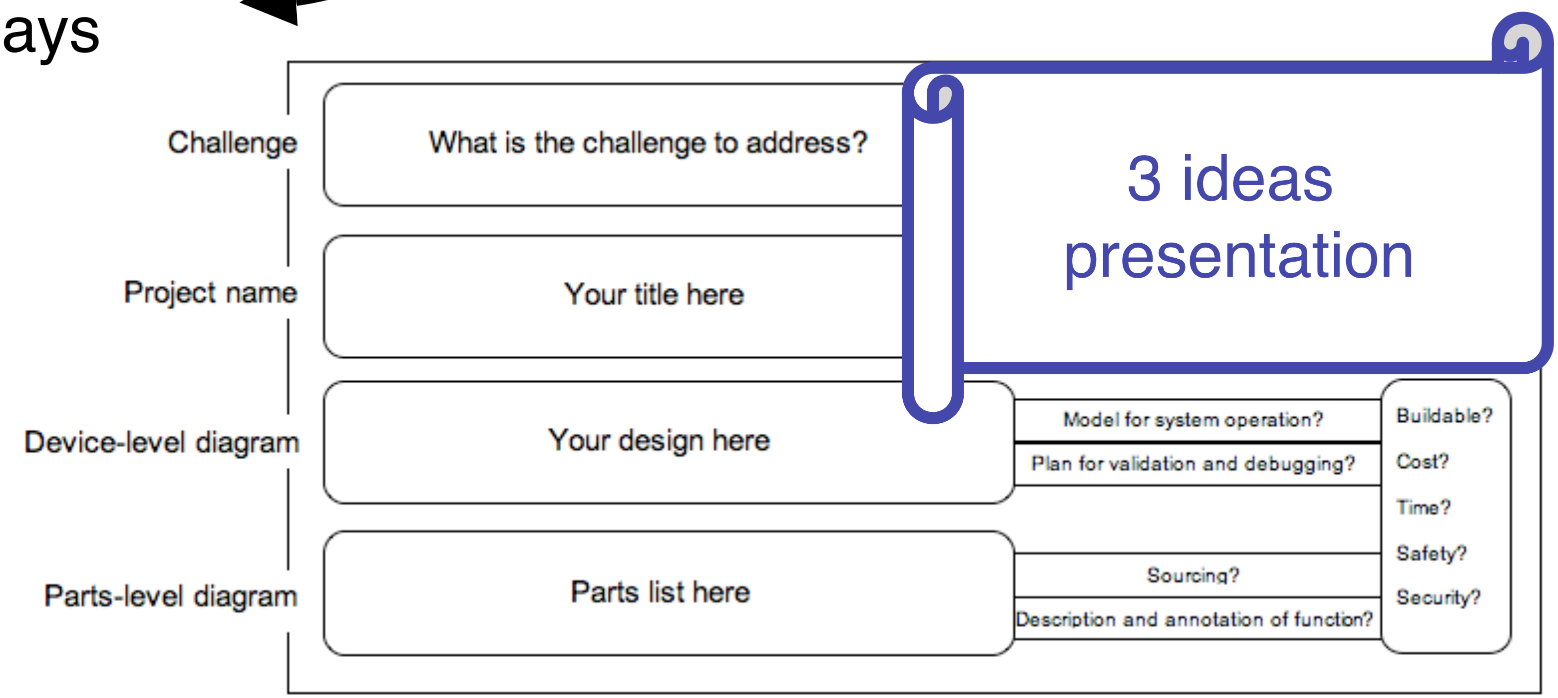

Home

Lecture and Studio schedule

20.902 Reading Schedule

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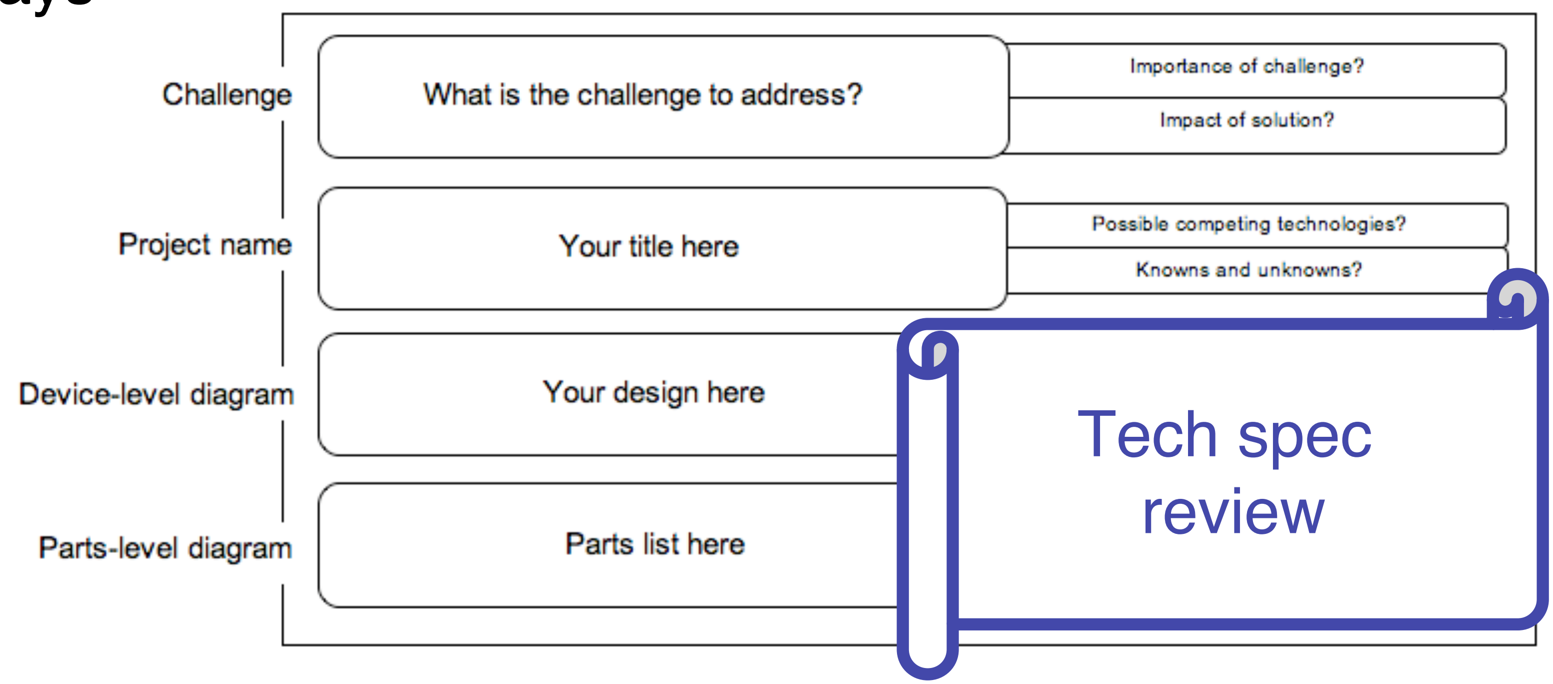


Home

Lecture and Studio schedule

20.902
Reading Schedule

Week 1 Week 2 Week 3 Week 4 Week 5 Week 6 Week 7
Week 8 Week 9 Week 10 Week 11 Week 12 Week 13 Week 14

Expectations

Guidelines: 3 Ideas Presentation

Guidelines: Tech Spec Review

Guidelines: Final Presentations

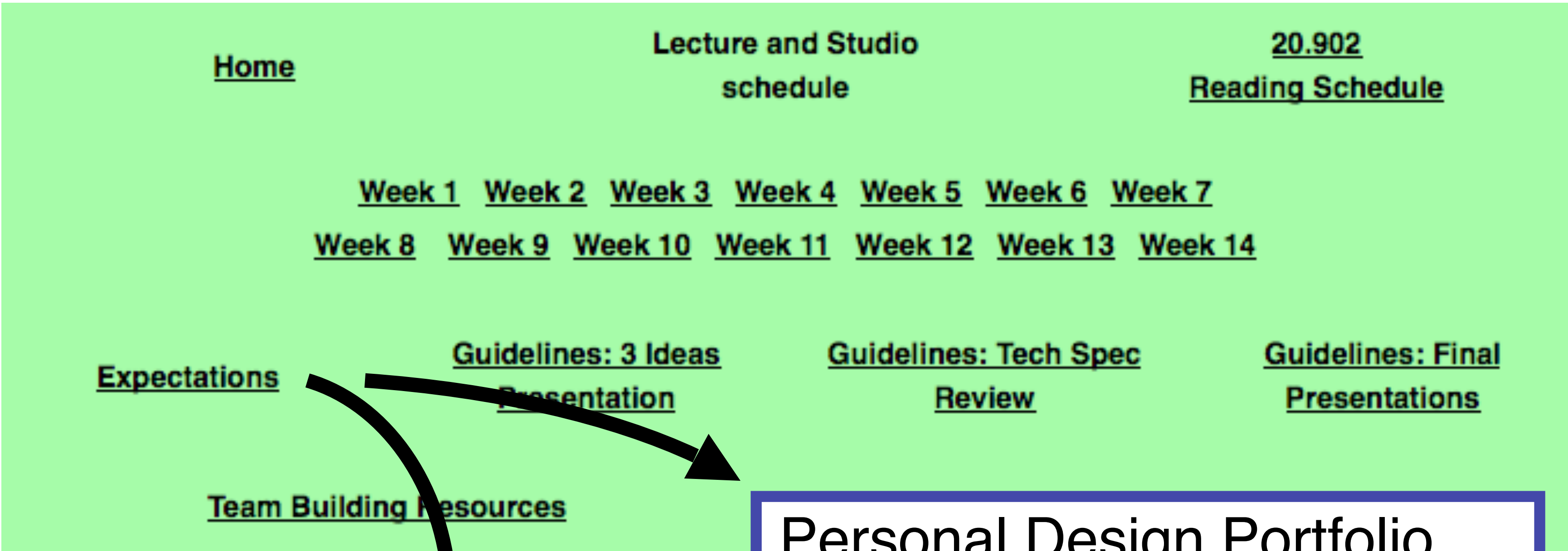
Team Building Resources

Teacher Resources

Project

- 3 ideas presentation
- Tech spec review
- Final presentation

60%, team grades



Project

- 3 ideas presentation
- Tech spec review
- Final presentation

60%, team grades

Personal Design Portfolio

25%, individual grades

Project Development Ntbk

10%, team grades

Instructor Leverage

5%, individual grades

Part 1: Readings

- Paper 1 (10%): presented with a partner
- Paper 2 (15%): presented solo
- Response record (25%): your thoughts about the papers you don't present.

Instructions for these assignment are here

Part 2: Team Mentoring

- Progress reports (15%): one page summaries of your freshman team's work
- Mentoring journal(15%): one page summary of your freshman team's dynamics
- Team's project average (15%): based on the grade for the 3 major assignments submitted by your freshman team
- Instructor Leverage (5%): discretionary adjustment by NK

Instructions for these assignments are here

Home	Lecture and Studio schedule	20.902 Reading Schedule

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Team Building Resources Teacher Resources

any ???s

Let's get building!!!

the end