Courtesy of Justin Lo. Used with permission.

Natalie Kuldell

February 3rd, 2009

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.”

Photo of Freeman Dyson
removed due to copyright restrictions.

Quack? Genius?

2020: Futurists

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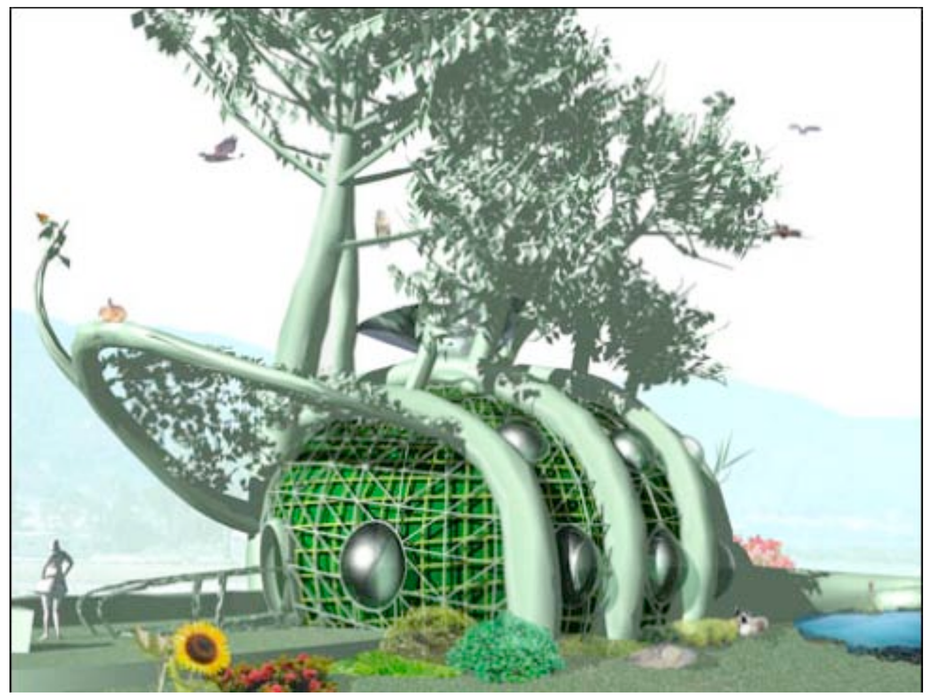


MIT Human Ecology Design team

2020: Historians

Image removed due to copyright restrictions.
Cover of Omni Magazine, Feburary 1980.
See http://www.physics.emory.edu/~weeks/sea/omni/800204.htm

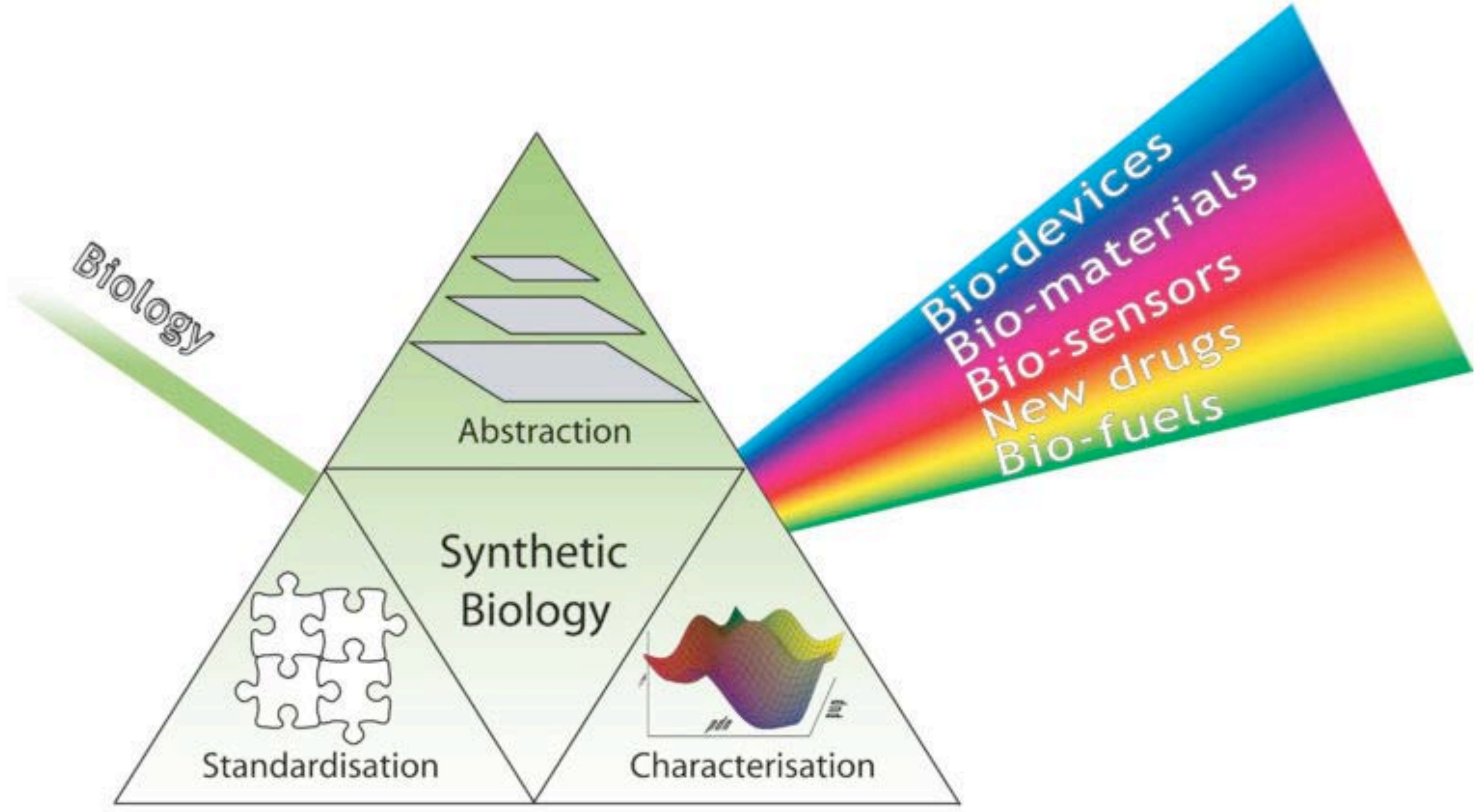
"a sophisticated computer at your fingertips"

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

Image removed due to copyright restrictions.
Advertisement from same Omni Magazine issue (1980)
for the Hewlett-Packard HP-85 "personal-professional" computer.
See http://oldcomputers.net/ads/80s/hp-85.jpg

"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."

What's new: Application of engineering principles to biology



Postcards & snapshots so far

•genome re-engineering

See Chan, L. Y., S. Kosuri, and D. Endy. "Refactoring bacteriophage T7." Mol Syst Biol 1 (2005): 0018. PMCID: PMC1681472.

http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1681472/

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 to tolerate transposon insertions. Overlapping "cassettes" of 5 to 7 kilobases (kb), assembled from chemically synthesized oligonucleotides, were joined by in vitro recombination to produce intermediate assemblies of approximately 24 kb, 72 kb ("1/8 genome"), and 144 kb ("1/4 genome"), which were all cloned as bacterial artificial chromosomes in *Escherichia coli*. Most of these intermediate clones were sequenced, and clones of all four 1/4 genomes with the correct sequence were identified. The complete synthetic genome was assembled by transformation-associated recombination cloning in the yeast *Saccharomyces cerevisiae*, then isolated and sequenced. A clone with the correct sequence was identified. The methods described here will be generally useful for constructing large DNA molecules from chemically synthesized pieces and also from combinations of natural and synthetic DNA segments.

Science 319, no. 5867 (Feb 29, 2008): 1215-20.

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.

Science 310, no. 5475 (October 7, 2005): 77-80.

Postcards & snapshots so far

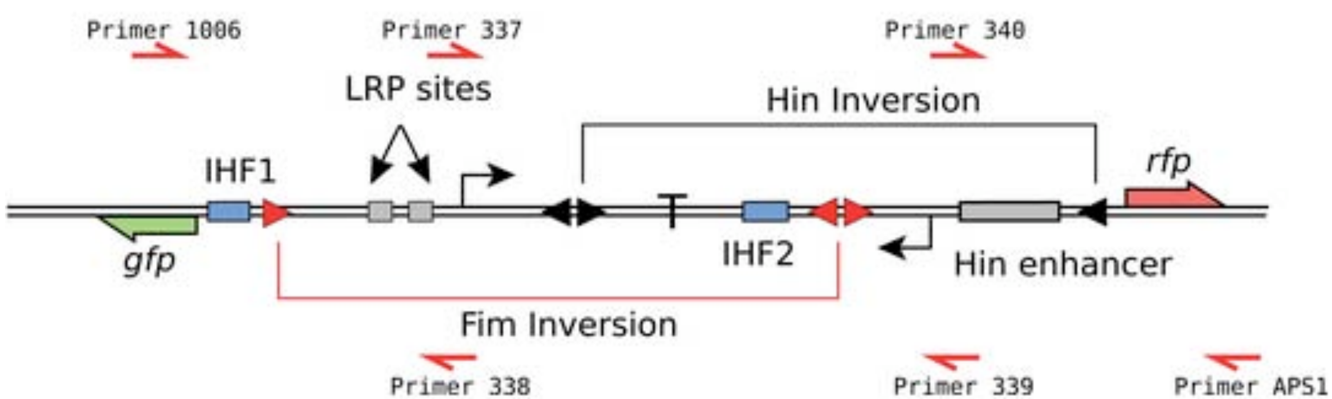
- •genome re-engineering
- •DNA based memory

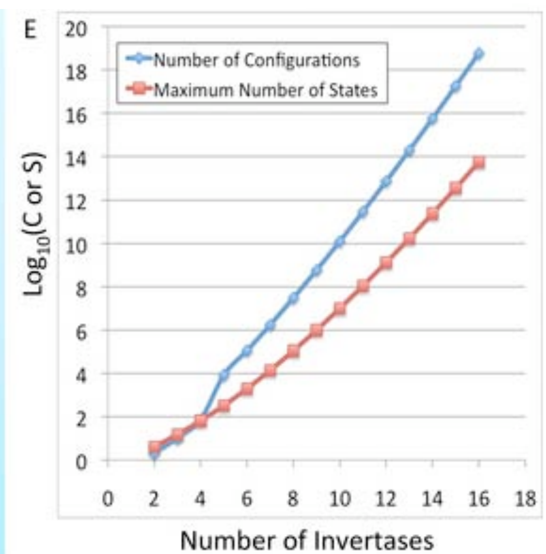
RESEARCH ARTICLE

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

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.

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 build an oscillating network, termed

NATURE | VOL 403 | 20 JANUARY 2000 | www.nature.com

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

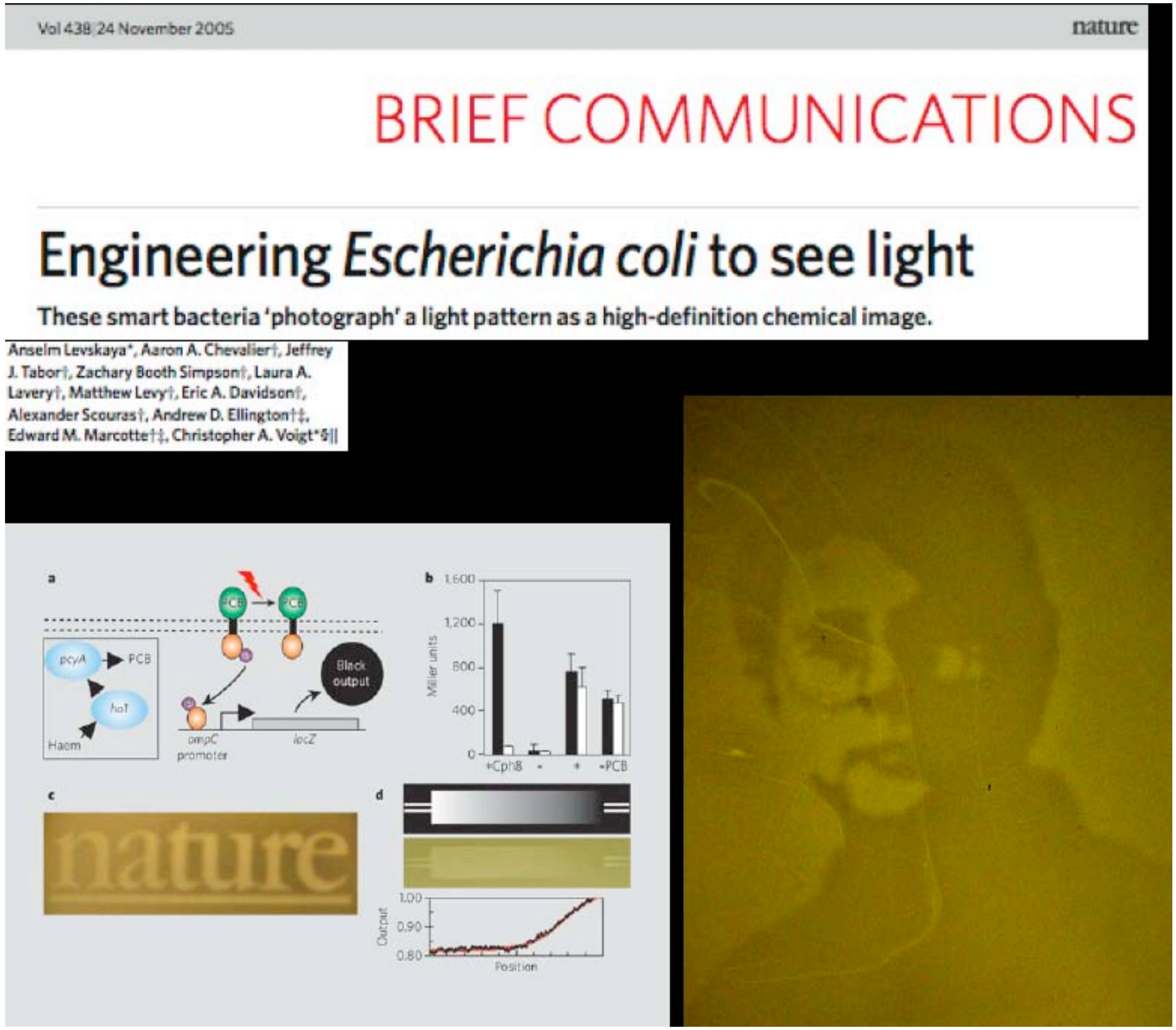
Vincent JJ Martin[1,2,3], Douglas J Pitera[1,3], Sydnor T Withers[1], Jack D Newman[1] & Jay D Keasling[1]

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.

Source: *Nature Biotechnology* 21 (2003): 796-802.

Postcards & snapshots so far

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



Courtesy of Christopher A. Voigt. Used with permission.

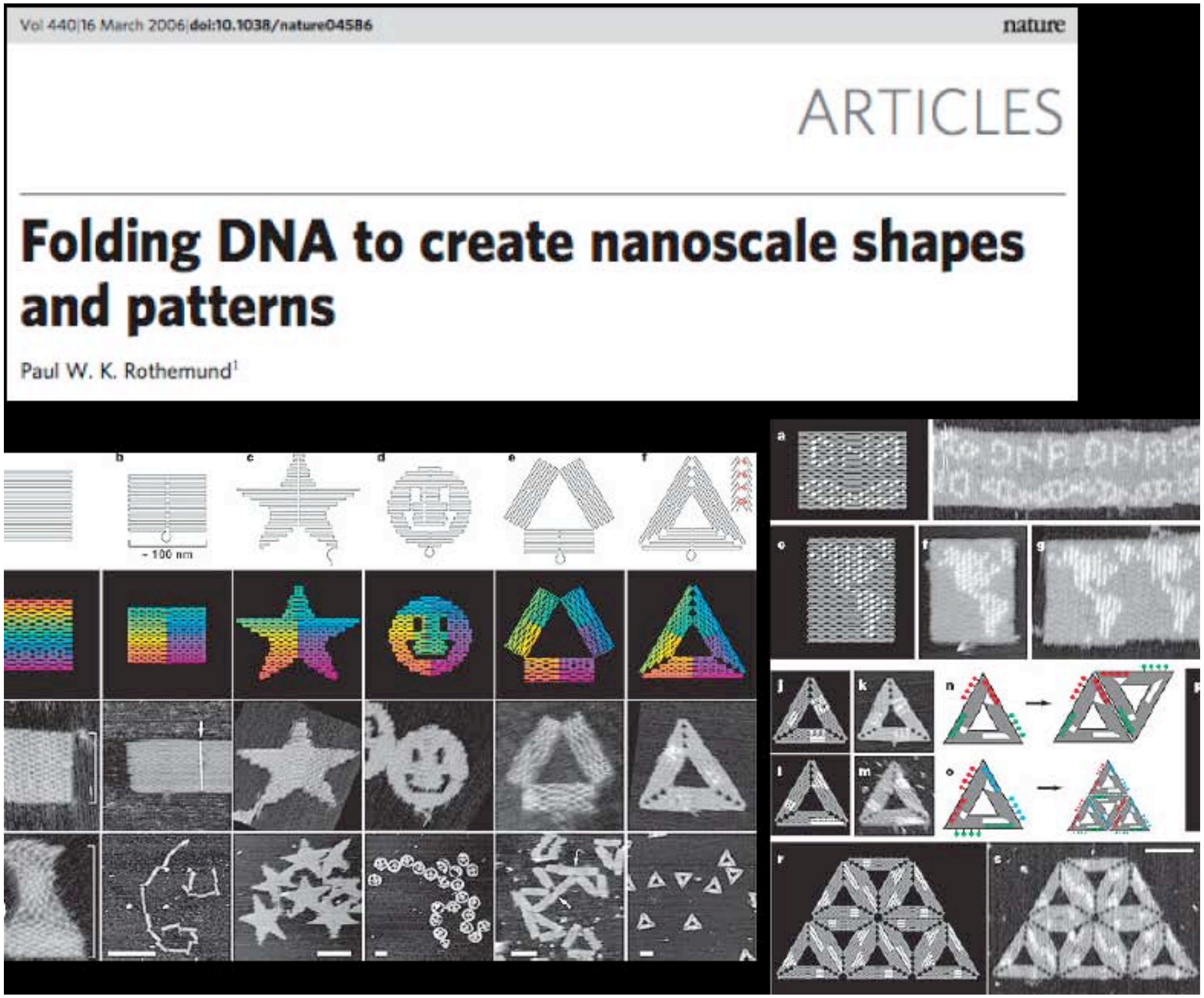
Postcards & snapshots so far

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

Image removed due to copyright restrictions.
See: http://www.technologyreview.com/tr35/Profile.aspx?TRID=601

Postcards & snapshots so far

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



Courtesy of Paul W. K. Rothemund. Used with permission.

Postcards & snapshots so far

- genome re-engineering
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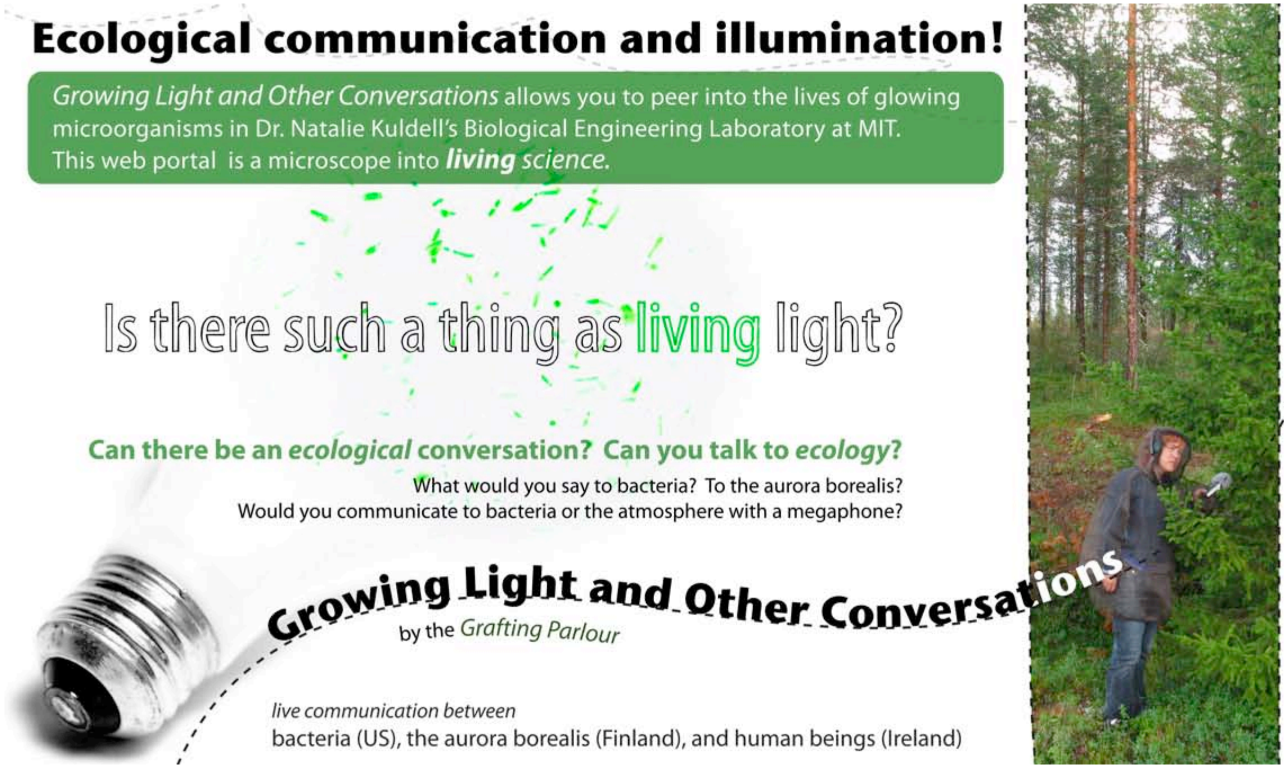


Courtesy of the League of Imaginary Scientists. Used with permission.

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.

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.

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

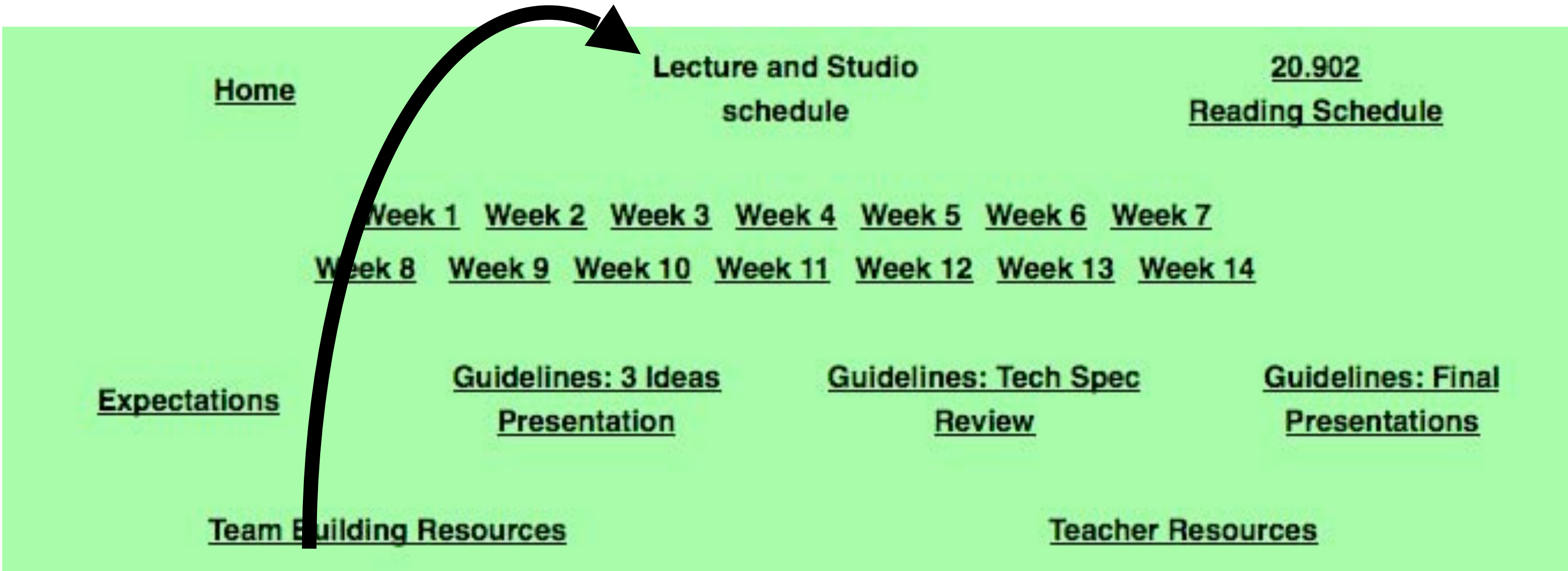
Guidelines: 3 Ideas Presentation

Guidelines: Tech Spec Review

Guidelines: Final Presentations

Team Building Resources

Teacher Resources


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

Tuesdays/Thursdays

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?

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Lecture and Studio schedule

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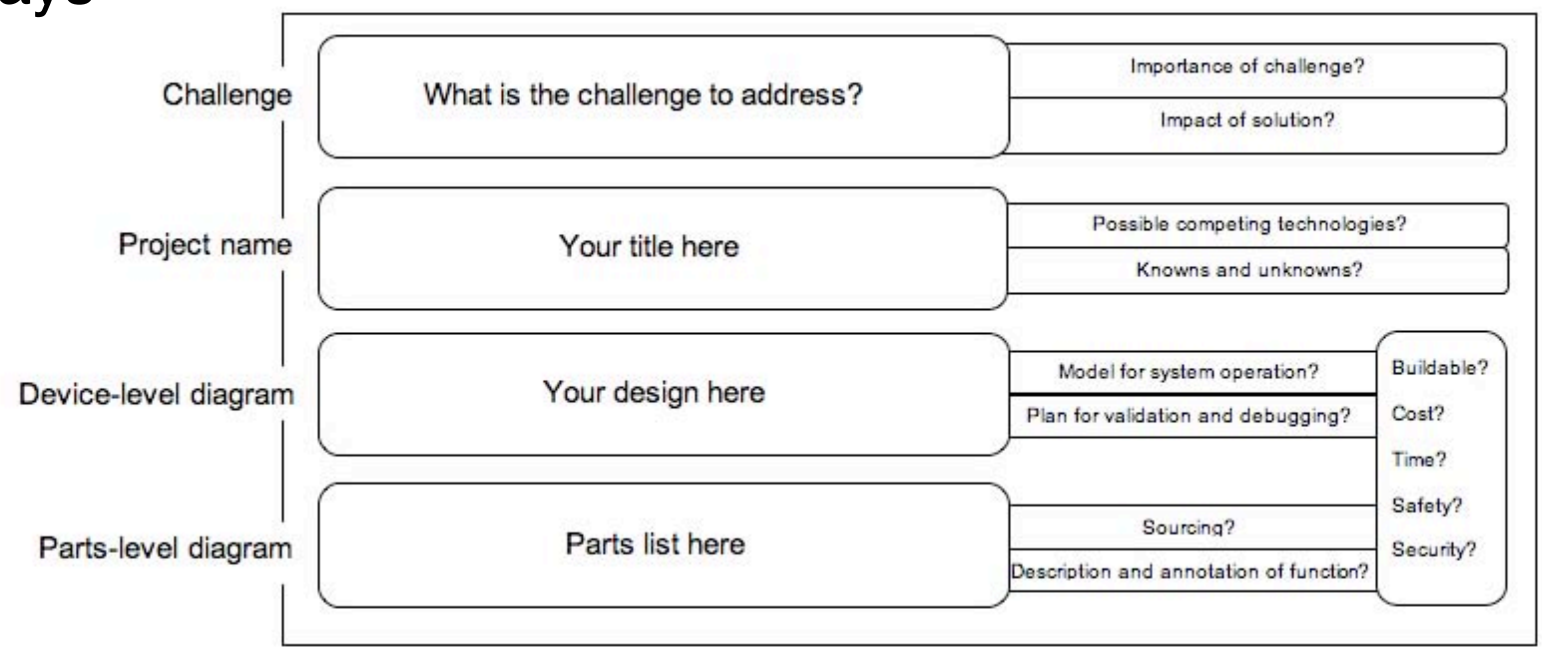
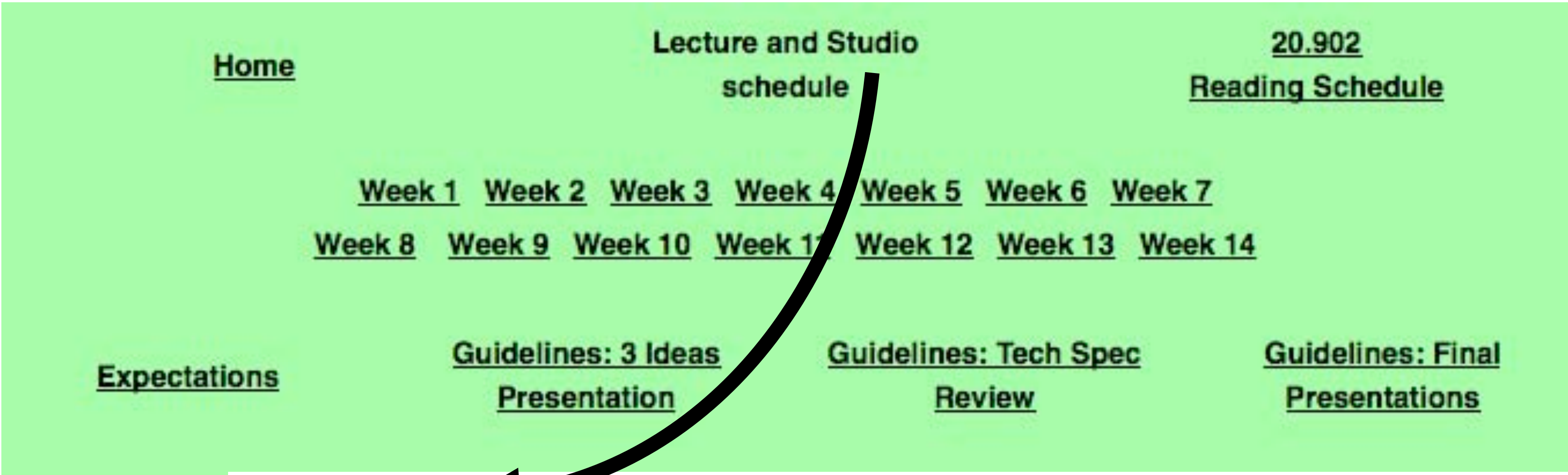
Wednesdays

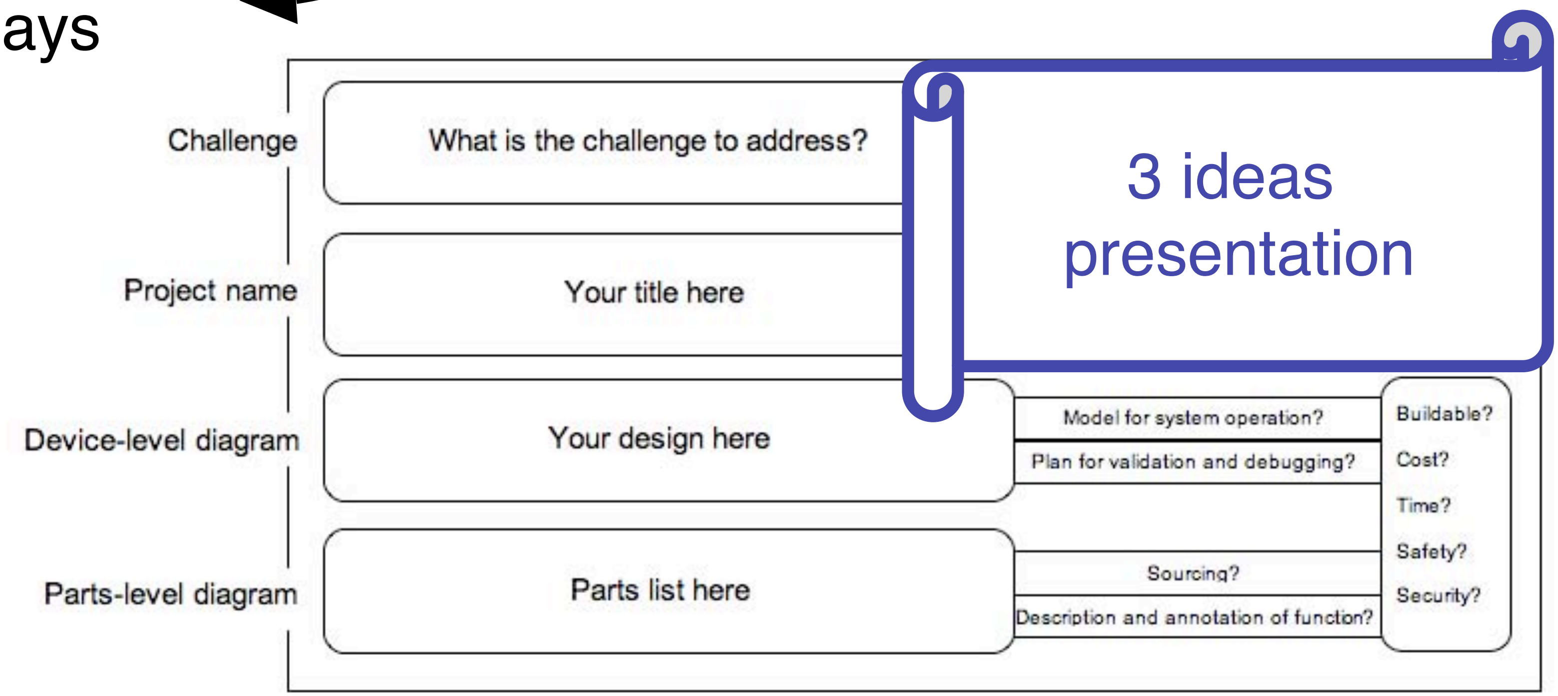
2-5

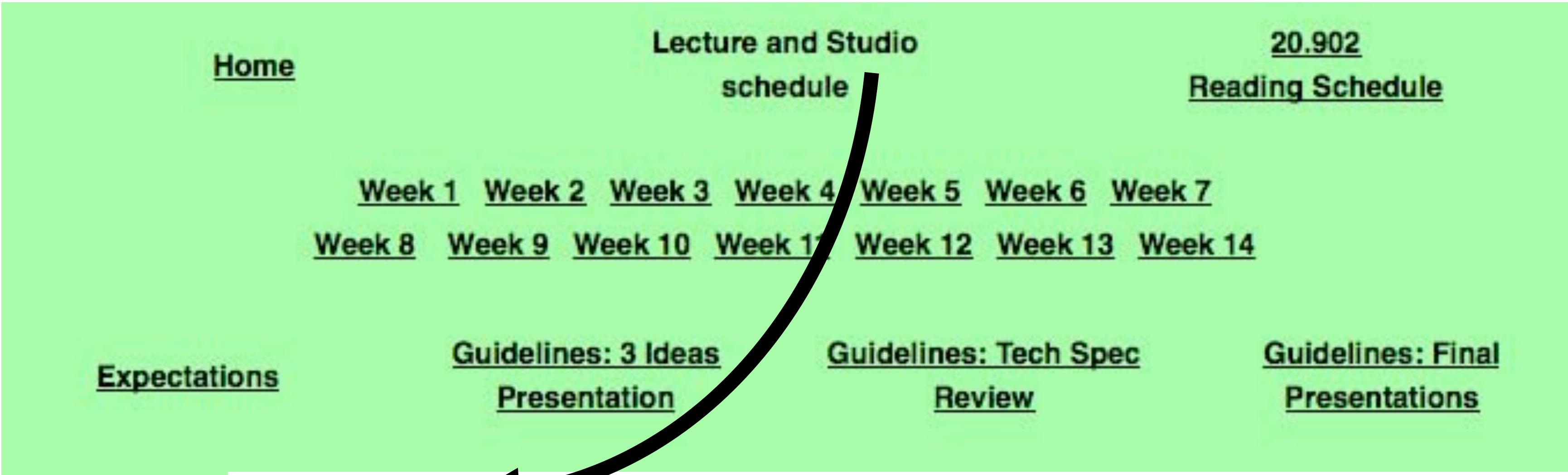




Wednesdays

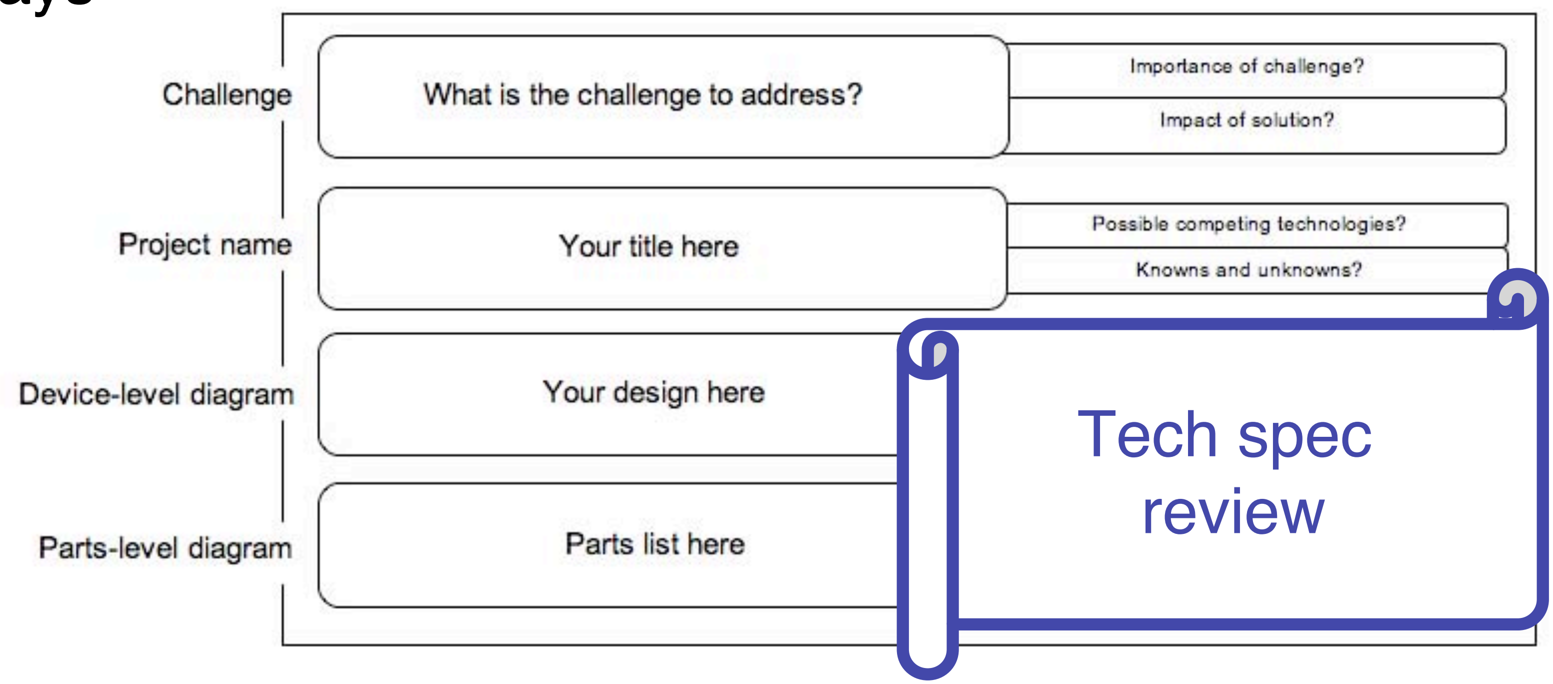
2-5

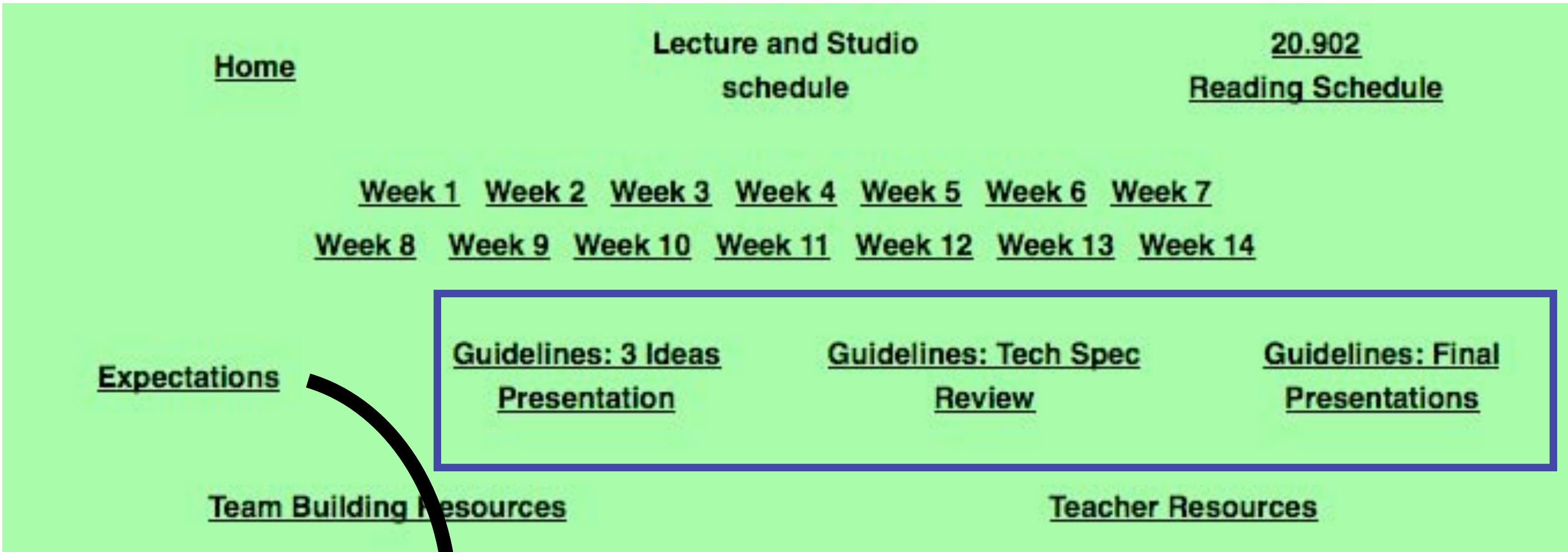




Wednesdays

2-5





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

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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

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Team Building Resources

Teacher Resources

any ???s

Let’s get building!!!

the end