Synthetic biology: Engineering new functions, cells, and even life?

BCH394P/364C Systems Biology / Bioinformatics
Edward Marcotte, Univ of Texas at Austin

**Synthetic Biology** = design and engineering of biological systems that aren’t found in nature

**Why would we want to do this?**
- Want to understand natural systems. One of the best ways to understand a system is to change it or make new, related ones
- To fully “understand” a system, we should be able to predict the outcome when we change the system
- For molecular biology, this means:
  - designing new gene circuits and networks
  - modeling the designed systems & predicting their properties
  - making & testing the designs
  - updating our understanding from the model/test agreement
The Repressilator = engineered genetic circuit designed to make bacteria glow in an oscillatory fashion = “repressor” + “oscillator”

Transcriptional repressors

\[ \text{TetR} \]
\[ \lambda \text{ cl} \quad \text{Lacl} \]

Proteins per cell

Time (min)

Green fluorescent protein


The Repressilator = engineered genetic circuit designed to make bacteria glow in an oscillatory fashion

Repressilator

Reporter

\[ \text{TetR} \]
\[ \lambda \text{ cl} \quad \text{Lacl} \]

\[ \text{P}_{\lambda \text{cl-lite}} \quad \text{P}_{\text{lac01}} \quad \text{tetR-lite} \]

\[ \text{P}_{\text{tet01}} \]

\[ \lambda \text{P}_{R} \]

\[ \text{gfp-aav} \]

\[ \text{kan}^R \]

\[ \text{ColE1} \]

The repressilator in action...

![Graph and images related to the repressilator]


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**iGEM: A synthetic biology contest**

Can simple biological systems be built from standard, interchangeable parts and operated in living cells?

Or is biology too complicated to be engineered in this way?

**Broader goals include:**
- Enable systematic engineering of biology
- Promote open & transparent development of tools for engineering biology
- Help construct a society that can productively apply biological technology

(from iGEM's web site)
IGEM: A synthetic biology contest

2004: MIT, UT, Princeton, Boston University, Cornell
2005: 13 teams (the above + UK, Germany, more...)
2006: 32 teams, incl. Japan, Latin America, Korea, India, more Europe
54 teams in 2007, 112 in 2009, 165 in 2011, and 245 in 2013...
...now roughly 6,000 entrants / year

A little local history to illustrate the field:
UT’s 2004/2005 iGEM project – build bacterial edge detector

Projector

petri dish coated with bacteria

shine image onto cells

Original image

Cells luminesce along the light/dark boundaries

Adapted from Zack Simpson
How does edge detection work in principle?

A computer might visit each pixel in turn, and check to see if it is bordered by both black & white pixels. If yes, highlight the pixel.

Is this pixel part of an edge?

No   
No   
Yes

Bacterial photography

“Light cannon” developed by Aaron Chevalier, UT undergraduate


The first bacterial photograph (coliroid?)...

Escherichia darwinia

Image: Aaron Chevalier

On to the edge detector...

Tabor et al., Cell 137(7):1272-1281 (2009)
It works!

Projected Mask | Photo strain | Edge detector strain

Tabor et al., Cell 137(7):1272-1281 (2009)

A
Photography

B
Communication

C
Inverter

D
Edge Detector

Tabor et al., Cell 137(7):1272-1281 (2009)
One major success of synthetic biology is engineering artemisinic acid production from wormwood into yeast:

Normal source = sweet wormwood

![Diagram of artemisinic acid production](image)


Some other recent successes in this field:

**Synthetic Biology**

**Complete biosynthesis of opioids in yeast**

Eleanor Gilbert,* Sarah Dobson,* Caoileann Monaghan,† and Martha Milligan Colman*†

Complete biosynthesis of cannabinoids and their unnatural analogues in yeast

Who needs nature?
**Made-to-order, designer organisms**

We can now manufacture a complete genome from commodity chemicals

Therefore, we can program whatever changes we want, assuming we can get it into cells...
“We report the design, synthesis, and assembly of the 1.08–mega–base pair *Mycoplasma mycoides* JCVI-syn1.0 genome starting from digitized genome sequence information and its transplantation into a *M. capricolum* recipient cell to create new *M. mycoides* cells that are controlled only by the synthetic chromosome.”
"The only DNA in the cells is the designed synthetic DNA sequence, including “watermark” sequences and other designed gene deletions and polymorphisms, and mutations acquired during the building process. The new cells have expected phenotypic properties and are capable of continuous self-replication."

PCR of 4 engineered “watermarks”

But, wait! They only changed DNA, not the rest of the cell!

However...

In biology, *software encodes the hardware.*
Most (all?) of the cell is specified by the DNA.

It’s as though you bought a old Blackberry...

installed the Android operating system...

& your phone physically morphed into a Galaxy S10...
Some good quotes from the paper:

“If the methods described here can be generalized, design, synthesis, assembly, and transplantation of synthetic chromosomes will no longer be a barrier to the progress of synthetic biology.”

“We expect that the cost of DNA synthesis will follow what has happened with DNA sequencing and continue to exponentially decrease. Lower synthesis costs combined with automation will enable broad applications for synthetic genomics.”

“As synthetic genomic applications expand, we anticipate that this work will continue to raise philosophical issues that have broad societal and ethical implications.”

In 2016, Hutchison, Chuang, et al. reported making living mycoplasma after cutting the genome by ½ the genes.
JCVI-syn3.0 now makes for a remarkably compact, engineerable, free living cell “chassis” to study

...which now has a rich metabolic reconstruction...
...and highly defined composition, to the extent one can write its biomass reaction equation:

In parallel, methods were developed to edit genomes at many locations in parallel, e.g. reassigning all amber (TAG) stop codons in *E. coli* to ochre (TAA)
& now, “rebooting” yeast with synthetic chromosomes

Turns out chromosomes can be synthesized and replaced for yeast too...

& China is pushing for a completely synthetic yeast genome...

In 2017, the Synthetic Yeast Genome Project (Sc2.0) reported on five newly constructed synthetic yeast chromosomes:

How the cover was made: http://science.sciencemag.org/content/355/6329/eaan1126
Design of a synthetic yeast genome

Sarah M. Richardson,1,2,3 Leslie A. Mitchell,1,2,3 Giovanni Strappazzoni,1,4,5 Lan Yang,6,7,8 Jessica H. Drummond,7,8 James E. D. Carls,7,8 Deepak Lowe,1,5 Cheng Lin Victor Hang,2 Srinivasan Chandrasekaran,2 Yishai Cai,9,10 Joff D. Becker,9,11 Joel R. Beato12,13

We describe complete design of a synthetic eukaryotic genome, sc2.0, a highly modified Saccharomyces cerevisiae genome reduced in size by nearly 8%, with 1.1 megabases of the synthetic genome deleted, inserted, or altered. sc2.0 chromosome design was implemented with BioStudio, an open-source framework developed for eukaryotic genome design, which coordinates design modifications from nucleotide to genome scales and enhances version control to systematically track edits. To achieve complete sc2.0 genome synthesis.

Table 1. Design challenges and policies adopted. CDS, gene coding sequence; snoRNA, small nuclear RNA.

<table>
<thead>
<tr>
<th>Design challenge or amendment</th>
<th>Policy adopted by design team</th>
</tr>
</thead>
<tbody>
<tr>
<td>Subtelomeric repeats of varying copy number on multiple chromosomes</td>
<td>Delete and monitor for phenotypes as chromosomes are combined. Exceptions: vitamin biosynthesis genes retain one copy.</td>
</tr>
<tr>
<td>Dispersed repeated genes of high copy number, as well as high-copy CDS and serine/phenylalanine genes</td>
<td>Delete and monitor for phenotypes as chromosomes are combined.</td>
</tr>
<tr>
<td>Isosym sites &gt;300 bp apart when inserted algorithmically (not especially useful and more difficult to synthesize)</td>
<td>Isosym thinning to eliminate the isosym site closer to the centromere.</td>
</tr>
<tr>
<td>Stop codon overlaps a second CDS; insertion of isosym site would disrupt second CDS; also TAG reading to TAA could disrupt CDS</td>
<td>Favor preservation of “verified ORFs” over “dubious ORFs” and “uncharacterized ORFs”; always add isosym site to a verified ORF.</td>
</tr>
<tr>
<td>Tandem repeats inside CDSs (34)</td>
<td>In synthesis phase, permit 10% length variation for homopolymer tracts &gt;10 bp provided they are in a noncoding region.</td>
</tr>
<tr>
<td>Homopolymer tracts, including frequent A and T tracts, are difficult to synthesize</td>
<td>In synthesis phase, permit 10% length variation for homopolymer tracts &gt;10 bp provided they are in a noncoding region.</td>
</tr>
<tr>
<td>Introns</td>
<td>Delete pre-mRNA introns precisely, except from genes with evidence of a fitness defect caused by intron deletion (35, 36). The HAC2 intron, which uses separate splicing machinery and is known to play a critical role in regulation of the unfolded protein response, was not deleted (3). Delete all RNA introns precisely.</td>
</tr>
<tr>
<td>Intronically embedded snoRNAs</td>
<td>These are individually nonessential and were deleted with their host intron. They could be “refactored” by insertion into the array of snoRNAs on chr II.</td>
</tr>
</tbody>
</table>
Synthesis, cyclization, and characterization of synV

Table 3. Summary statistics for design of Sc2.0. WT, wild type; SYN, synthetic.

<table>
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<tr>
<th>chr</th>
<th>WT size</th>
<th>SYN size</th>
<th>No. of stop codon swaps</th>
<th>No. of loxP sites added</th>
<th>bp of PCRTag recoded</th>
<th>bp of RE sites recoded</th>
<th>No. of tRNA deleted</th>
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</table>
Inevitably (!), the human synthetic genome project:

First major project: Recoding human codons (~200K edits?) to create virus-resistant cells

Let’s end the lectures on a fun note, with some speculative near-future synthetic biology experiments

Science fiction? or not? You be the judge!
“De-extincting” extinct species

Remember Dolly, the cloned sheep?

What if the cells being cloned came from an extinct animal and were put into a surrogate mother? Would that resurrect the species?

This was tried in 2009 for the Pyrenean ibex, and almost worked...

But now there’s another way!

- We can sequence a genome in a few days for a few $K
- We can synthesize or alter big pieces of the DNA
- We can (almost) “reboot” cells with this DNA
- We can convert cells to stem cells to embryos
- We can in vitro fertilize animals

So why not just “edit” the genomes of the closest living animals to be like their extinct relatives?

Sound familiar?
Besides the genome engineering, this hinges on iPS:

From embryonic stem cells, we can grow an entire organism or any cells/tissues in it

& thanks to Yamanaka, we can convert skin cells back into stem cells

Shinya Yamanaka
Nobel Prize, 2012

There’s a serious proposal to resurrect the woolly mammoth. Here’s the process:

✓ Mammoth genome sequence
➢ Make ~100K DNA changes in elephant skin cells to convert elephant skin cells → mammoth skin cells
✓ Convert skin cells to stem cells
✓ Convert stem cells to embryos
➢ *In vitro* fertilize elephants

This might be a hard step.
Using a DNA editing tool called CRISPR, the scientists spliced genes for the mammoths’ small ears, subcutaneous fat, and hair length and color into the DNA of elephant skin cells. The tissue cultures represent the first time woolly mammoth genes have been functional since the species went extinct around 4,000 years ago.

The research has not yet been peer-reviewed or published in a scientific journal “because there is more work to do,” Church told the U.K.’s *Sunday Times*, “but we plan to do so.”


In fact, they’re hiring!

**Woolly Mammoth Revival Fellowship Announcement**

**Description of the Opportunity**

Revive & Restore is pleased to announce a post-doctoral fellowship opportunity for well-qualified individuals interested in a full-time appointment researching the science underlying Woolly Mammoth de-extinction in the laboratory of Dr. George Church at Harvard Medical School. This fellowship is fully supported by Revive & Restore, the leading non-profit organization working to bring biotechnologies to wildlife conservation. The fellowship will...

The Woolly Mammoth has emerged as a leading candidate for this work. It can be attempted because a close relative of the mammoth is still living—the Asian elephant. Thanks to the similarity of their genomes, the genes of woolly mammoth traits can be edited into the Asian elephant genome, and the combination brought to life as an elephant cousin, once again adapted to the conditions of the far north.

The ultimate goal of Woolly Mammoth Revival is to bring back this extinct species so that healthy herds may one-day re-populate vast tracts of tundra and boreal forest in Eurasia and North America. The intent is not to make perfect copies of extinct Woolly Mammoths, but to focus on the mammoth adaptations needed for Asian elephants to thrive in the cold climate of the Arctic. The milestones along the way range from developing elephant tissue cultures to genome editing and most importantly, developing insights that help with Asian elephant conservation.

https://genetics.hms.harvard.edu/about-us/departmental-employment-opportunities
Although the race is on as other groups try to resurrect frozen mammoth cells:

Which animal would you resurrect?

The dodo?

The quagga?

Sabertoothed tiger?

In principle, only need the DNA sequence (so, no dinosaurs)

Aurochs?
I vote for some crazy Australasian animals:

The 12’ tall moa

& of, course, the marsupial Tasmanian tiger

>90° !!!

The moa-eating Haast’s eagle

Actual scale!

What about neanderthal?
It’s achievable. But should we do it?

- Human and neanderthal genome sequence
- Edit DNA in human skin cells to convert convert human skin cells → neanderthal skin cells → I give this step 10 years max before we can do this
- Convert skin cells to stem cells
- Convert stem cells to embryos
- In vitro fertilize a surrogate mother

So many ethical questions! Where to start?