Aalto University
School of Chemical
Technology

Synthetic biology

(Course CHEM-E8125), spring 2022

Introduction

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Course outline

28.2. **Introduction** to synthetic biology and the course

7.3. **Standardization, biobricks and chassis**

14.3. **Artificial genomes: Yeast Sc2.0**

21.3. **Synbio as an enabler of applications in sustainable bioeconomy**

28.3. Homework presentations

4.4. **Modelling of metabolism and circuits**

25.4. Common modelling session

2.5. **Homework presentations based on articles**

9.5. **Homework presentations based on articles**

16.5. **Homework presentations based on articles**

23.5. **Ethics & safety, iGEM**

1.6. **Exam**

Synthetic biology -

Conceptually and technologically ”new” way of doing bio

- Synthetic Biology is the design and construction of new biological functionalities not found in Nature, and
- Use of novel tools and concepts that make biology engineerable

From repetitive trial-and-error biology to
design and a controlled way of building biological systems

Biotechnology is the key enabling technology
for our future, and
Synthetic Biology is its cutting edge.

Impact on all fields of biotech (industrial, medical, plant, bionanotech)

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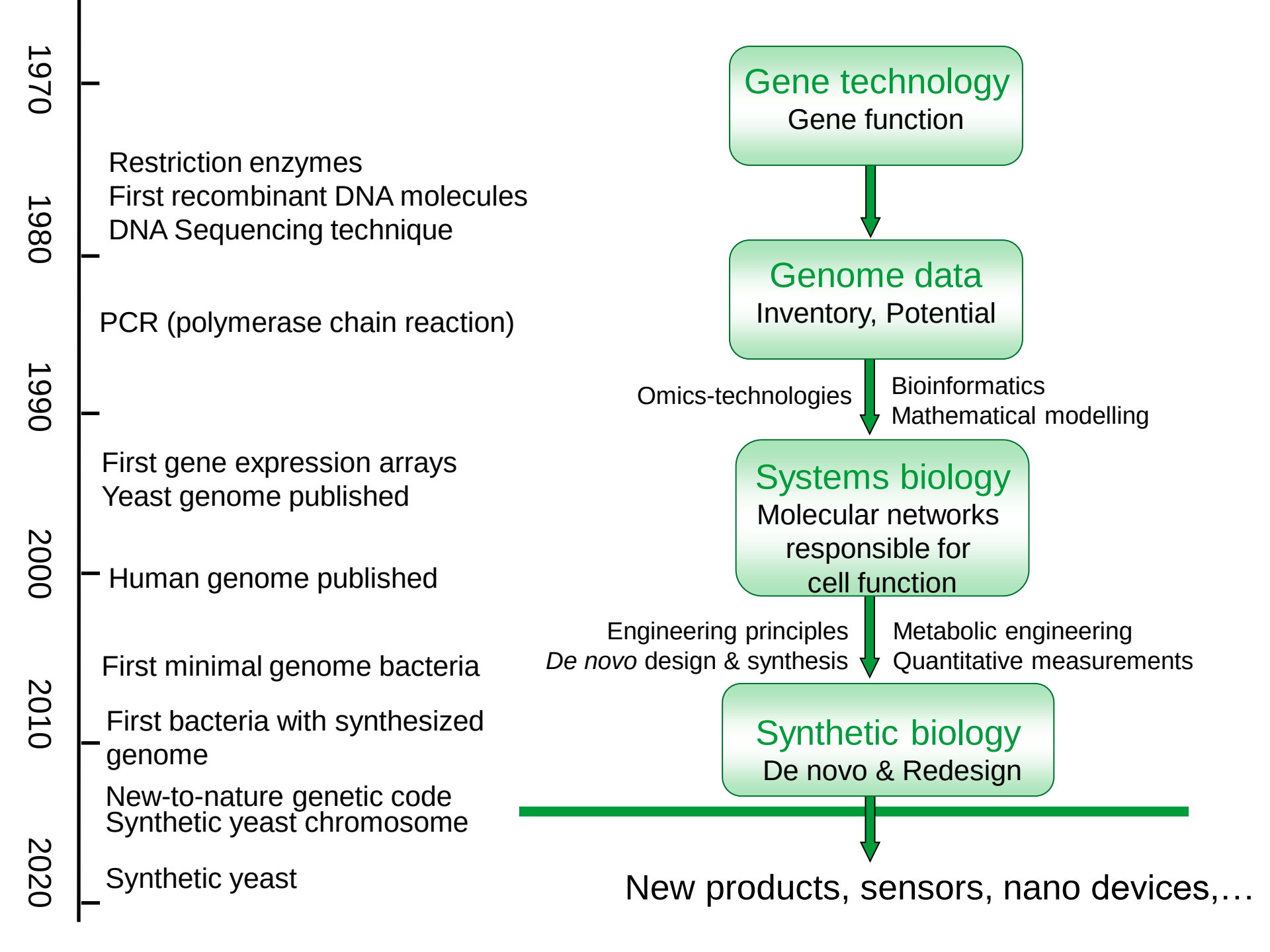
“Synthetic biology” term was introduced 1974
by the Polish geneticist Waclaw Szybalski


1970
1980
1990
2000
2010
2020
Restriction enzymes
First recombinant DNA molecules
DNA Sequencing technique
PCR (polymerase chain reaction)
First gene expression arrays
Yeast genome published
Human genome published
First minimal genome bacteria
First bacteria with synthesized genome
New-to-nature genetic code
Synthetic yeast chromosome
Synthetic yeast
Gene technology
Gene function
Genome data
Inventory, Potential
Omics-technologies
Bioinformatics
Mathematical modelling
Systems biology
Molecular networks responsible for cell function
Engineering principles
De novo design & synthesis
Metabolic engineering
Quantitative measurements
Synthetic biology
De novo & Redesign
New products, sensors, nano devices,…

Enablers of synbio

- Fast and cheap genome sequencing and DNA synthesis
- Computer-based design and automated cell construction
- Biology as an engineering science; engineering principles
- Genome-editing tools (CRISPR)

Human design of standardised modular biological parts and devices that can be assembled in desired combinations to functional controllable systems.

"What I can not create,
I can not understand"

Physicist Richard Feynman

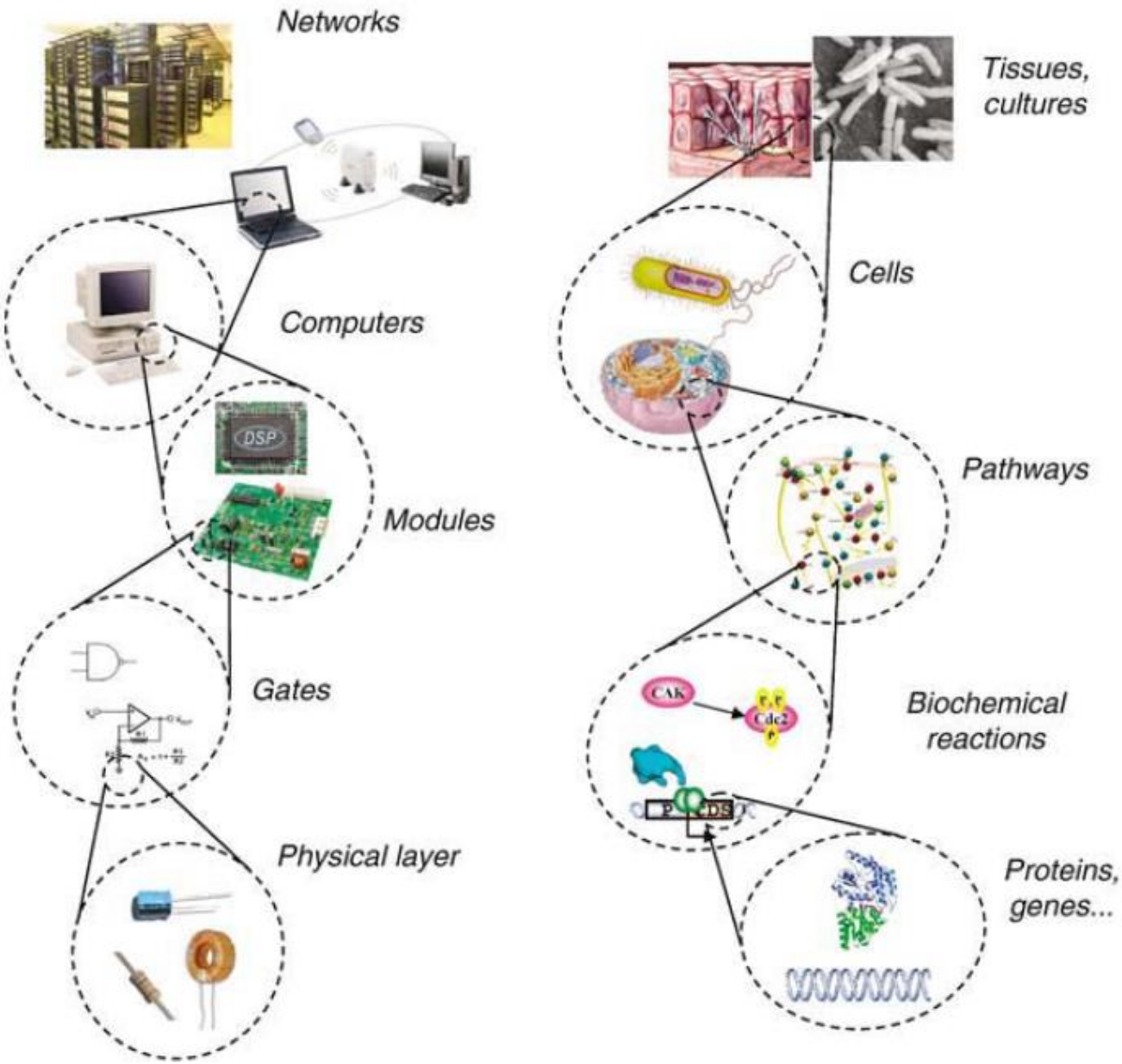
Synthetic biology

- Construction of designed biological operational units
  - model-based
  - quantifiable
  - programmable
  - standardized
  - orthogonal

- Synthetic genes, proteins, production pathways, intracellular control circuits, cell organelles, production hosts (chassis) …

- DNA as an engineering platform universal for life (as we know it)

Synthetic biology, analogy to electrical engineering

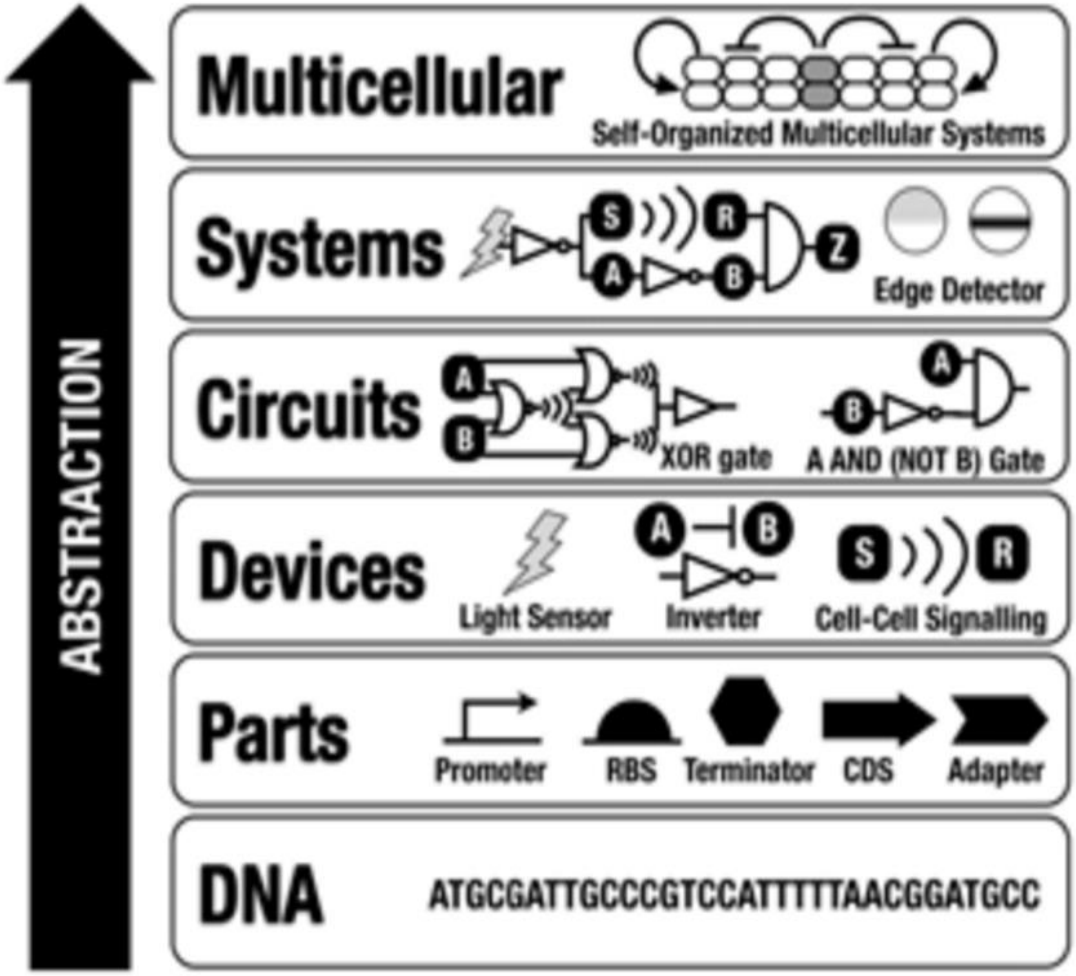


Human design of **standardised** modular biological parts and devices that can be assembled in desired combinations to functional controllable systems (BUT, does not need to be standardised only, e.g. laboratory evolution)

A mindset change needed & new interdisciplinary teaching

A practical definition of synthetic biology

Making biology easier to engineer: “Engineering of biology remains complex because we have never made it simple” (Thomas F Knight, MIT/Gingko Bioworks)

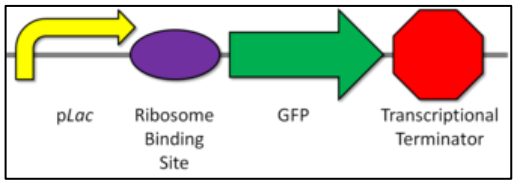


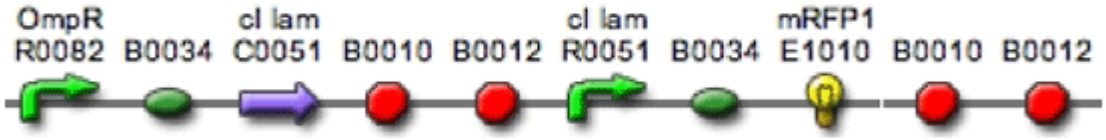
Biobricks

MIT & Berkeley & Harward & UCSF & Imperial College & ETH …

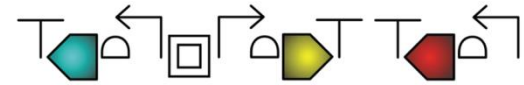
Register of standard biological parts – BioBricks™

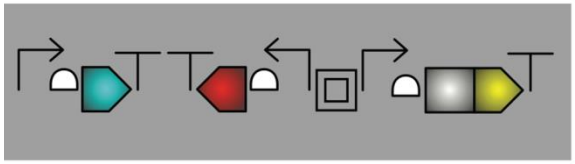
[Promoters](#)
[Ribosome Binding Sites](#)
[Protein domains](#)
[Protein coding sequences](#)
[Translational units](#)
[Terminators](#)
[DNA](#)
[Plasmid backbones](#)
[Primers](#)
[Protein generators](#)
[Reporters](#)
[Inverters](#)
[Receivers and senders](#)
[Measurement devices](#)
[Cell death](#): Parts involved in killing cells.
[Coliroid](#): Parts involved in taking a bacterial photograph.
[Chassis](#)
[Assembly standards](#)

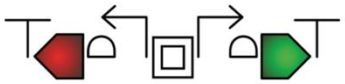




SBOL, synthetic biology open language



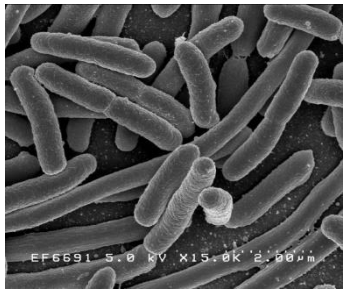




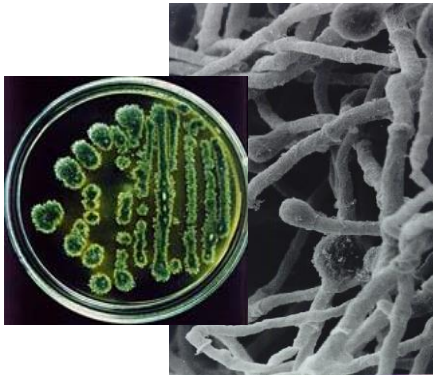
promoter	primer binding site
cds	restriction site
ribosome entry site	blunt restriction site
terminator	5′ sticky restriction site
operator	3′ sticky restriction site
insulator	5′ overhang
ribonuclease site	3′ overhang
rna stability element	assembly scar
protease site	signature
protein stability element	user defined
origin of replication	

Chassis

Bacterium
Escherichia coli

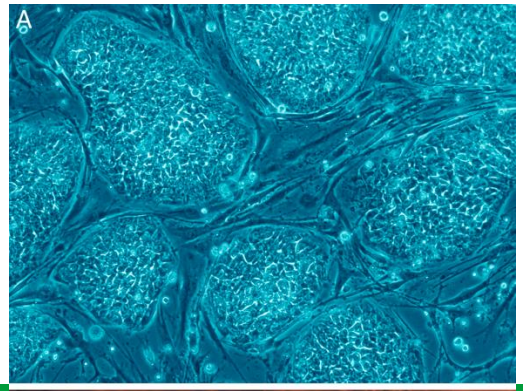


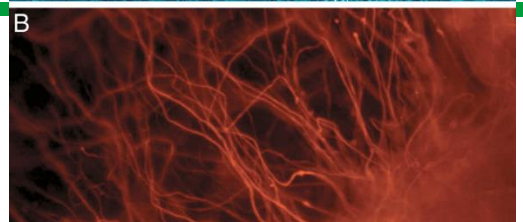
Yeast
Saccharomyces cerevisiae



Filamentous fungus
Trichoderma reesei

Human embryonic stem cells





Human nerve cells

Cyanobacterium
Synechocystis

Plant
Arabidopsis thaliana

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Synthetic biology is revolutionising Biotechnology
and is needed for sustainable breakthroughs in Bioeconomy

Gene technology → Systems biology → **Synthetic biology**

1st generation
Cell factories

Raw materials and sugars naturally used by the microbe (e.g. starch, glucose, lactose)

- Use of natural organisms, no genetic engineering
- Strain improvement by random mutagenesis with chemicals and radiation

Organism specific products e.g.
- alcohol and flavour compounds with wine yeasts
- mixture of acetone, butanol and ethanol (ABE) with bacteria

2nd generation
Cell factories

Broadened substrate range (e.g. (hemi)cellulose, xylose)

- Transfer of combination of genes found in nature to the production organism
- Strain improvement by targeted gene expression and inactivation

New traits/products in old hosts e.g.
- human insulin with yeast
- high levels of industrial enzymes with fungi
- 2nd generation bioethanol (C5 fermenting *Saccharomyces* yeast)

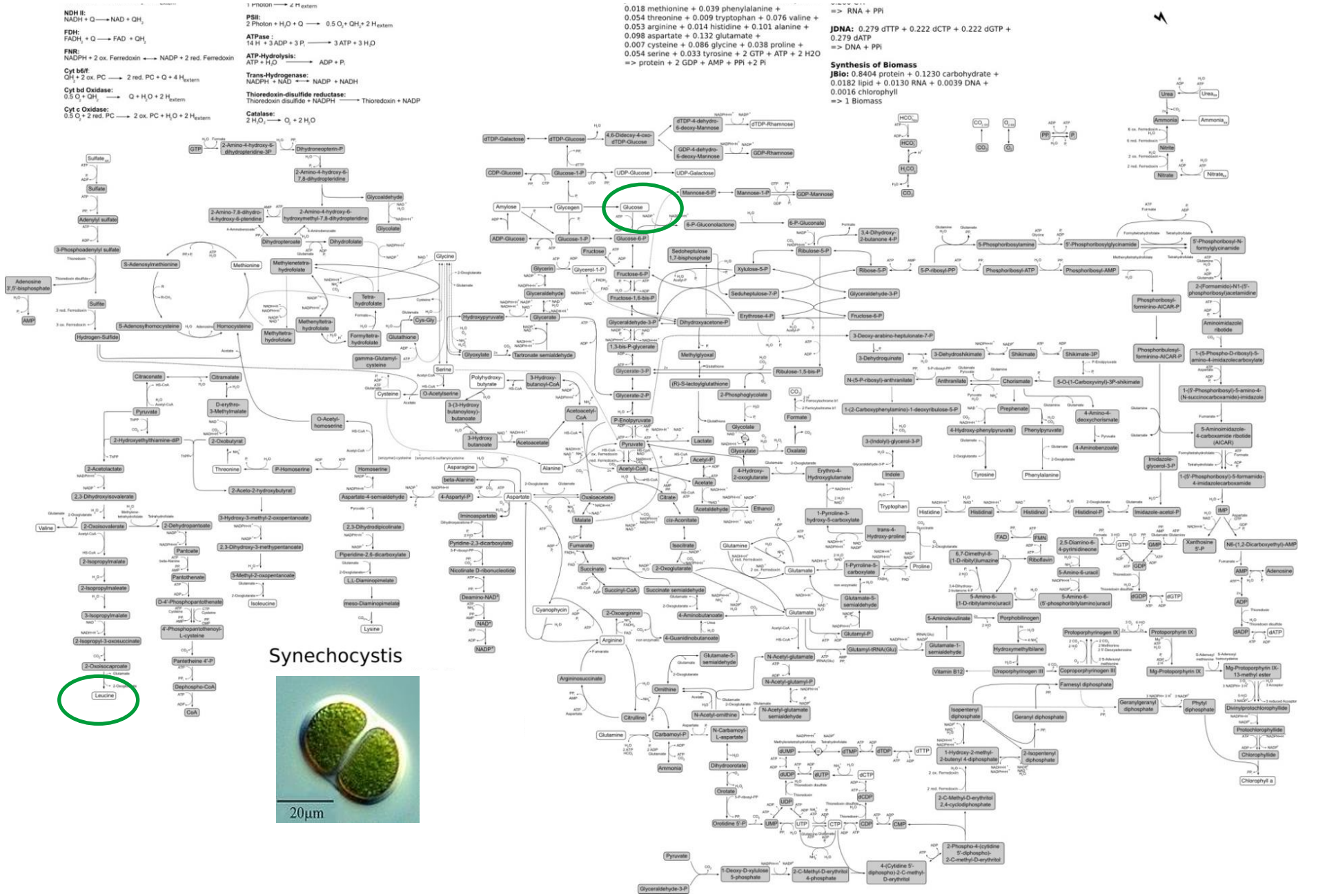
3rd generation
Cell factories

Tailor-made carbon and energy use (e.g. waste CO_2, methanol, glycerol)

- Design of new-to-nature genes, gene combinations and synthetic metabolic reaction pathways, and ultimately entire cells
- Strain improvement by rapid automated gene assembly and transformation, combined with very high-through-put screening

Novel products in tailor-made hosts e.g.
- biotech production of current petrochemicals
- novel jet fuels produced with yeast
- engineered spider silk for superior materials

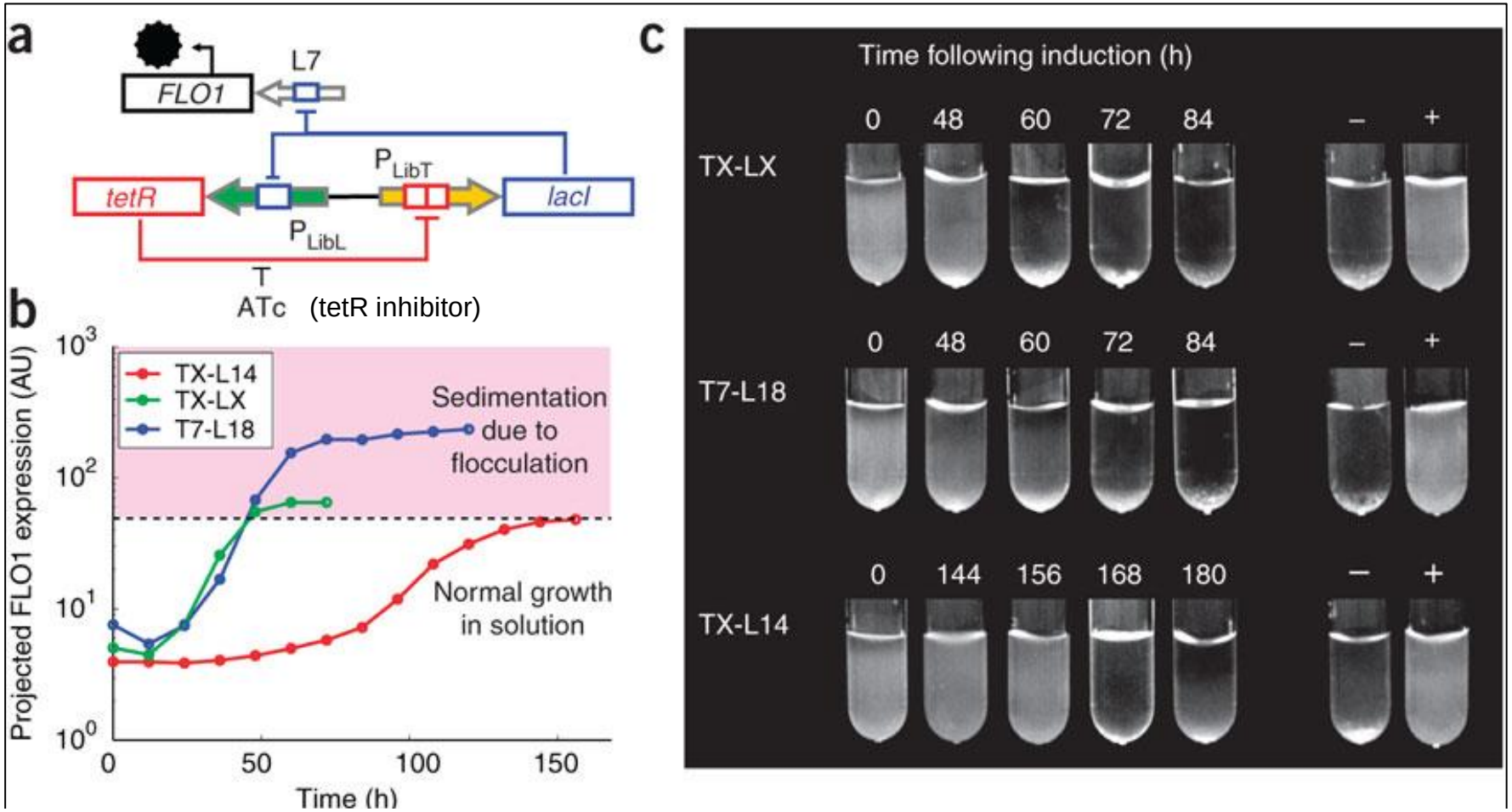
Mathematical models of cellular metabolism



Control circuits

- inputs, outputs, receivers, transmitters
- standardisation, reproducibility
- quantification & measurements
- mathematical modelling

Ellis et al. Nat Biotechnol. 2009; 27(5): 465–471. doi:10.1038/nbt.1536.



Control of yeast sedimentation (flocculation) with anhydrotetracycline (ATc) controllable expression circuit after product formation to aid product recovery and cell removal

Some examples of synthetic biology

- Technology: *In vitro* synthesis of designed DNA/genes & genome editing
- New genetic codes
- Unnatural aminoacids
- Synthesis of mirrow image polymers

- Novel enzyme catalysts
- Novel chemicals

- Molecular motors
- Nanorobots
- Energy generation (redesign of photosynthesis, biofuel cells)

- Virus assembly *in vitro* from parts
- Synthetic organelles
- Microbes for monitoring (odours, toxins etc, signal transmission)

- Minimalistic cells for production – chassis* (e.g. ~ 473 essential genes in *Mycoplasma*)
  - Assembly from parts and desired genes – novel genomes
  - Omittment of unnecessary reactions (->standard chassis) -> Addition of wanted ones

- ”Normal” metabolic engineering

* asennuspohja

Vol 464|18 March 2010|doi:10.1038/nature08817

nature

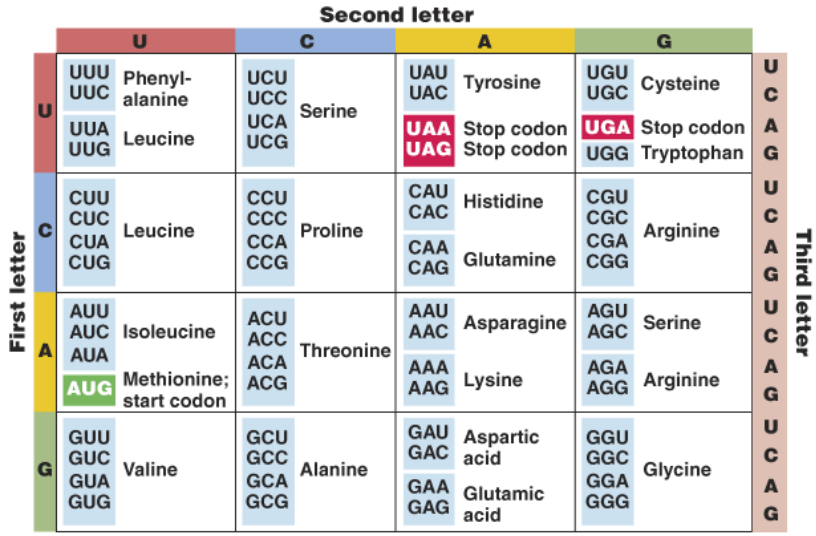
LETTERS

Encoding multiple unnatural amino acids via evolution of a quadruplet-decoding ribosome

Heinz Neumann[1]*, Kaihang Wang[1]*, Lloyd Davis[1], Maria Garcia-Alai[1] & Jason W. Chin[1]

- Normally 61 codons (triplets of nucleotides) code for the 20 common amino acids (+ 3 codons for stop).
- Engineering of an orthogonal ribosome that reads quadrupled codons.
- Enables simultaneous incorporation of numerous (over 200) unnatural amino acids to proteins

-> novel properties – numerous applications.



First letter	Second letter: U	Second letter: C	Second letter: A	Second letter: G	Third letter
U	UUU, UUC Phenylalanine	UCU, UCC, UCA, UCG Serine	UAU, UAC Tyrosine	UGU, UGC Cysteine	U, C
	UUA, UUG Leucine		UAA, UAG Stop codon	UGA Stop codon	A
				UGG Tryptophan	G
C	CUU, CUC, CUA, CUG Leucine	CCU, CCC, CCA, CCG Proline	CAU, CAC Histidine	CGU, CGC, CGA, CGG Arginine	U, C, A, G
			CAA, CAG Glutamine		
A	AUU, AUC, AUA Isoleucine	ACU, ACC, ACA, ACG Threonine	AAU, AAC Asparagine	AGU, AGC Serine	U, C
	AUG Methionine; start codon		AAA, AAG Lysine	AGA, AGG Arginine	A, G
G	GUU, GUC, GUA, GUG Valine	GCU, GCC, GCA, GCG Alanine	GAU, GAC Aspartic acid	GGU, GGC, GGA, GGG Glycine	U, C, A, G
			GAA, GAG Glutamic acid		

Natural RNA code

A=adenine, C=cytosine, G=guanine, U=uracil (T=thymine in DNA)

Nature Vol 464| 18 March 2010| doi:10.1038/nature08817

The in vivo, genetically programmed incorporation of designer amino acids allows the properties of proteins to be tailored with molecular precision. The Methanococcus jannaschii tyrosyltransfer-RNA synthetase–tRNACUA (MjTyrRS–tRNACUA) and the Methanosarcina barkeri pyrrolysyl-tRNA synthetase–tRNACUA (MbPylRS–tRNACUA) orthogonal pairs have been evolved to incorporate a range of unnatural amino acids in response to the amber codon in Escherichia coli. However, the potential of synthetic genetic code expansion is generally limited to the low efficiency incorporation of a single type of unnatural amino acid at a time, because every triplet codon in the universal genetic code is used in encoding the synthesis of the proteome. To encode efficiently many distinct unnatural amino acids into proteins we require blank codons and mutually orthogonal aminoacyl-tRNA synthetase–tRNA pairs that recognize unnatural amino acids and decode the new codons. Here we synthetically evolve an orthogonal ribosome (ribo-Q1) that efficiently decodes a series of quadruplet codons and the amber codon, providing several blank codons on an orthogonal messenger RNA, which it specifically translates. By creating mutually orthogonal aminoacyl-tRNA synthetase–tRNA pairs and combining them with ribo-Q1 we direct the incorporation of distinct unnatural amino acids in response to two of the new blank codons on the orthogonal mRNA. Using this code, we genetically direct the formation of a specific, redox-insensitive, nanoscale protein cross-link by the bio-orthogonal cycloaddition of encoded azide- and alkyne-containing amino acids. Because the synthetase–tRNA pairs used have been evolved to incorporate numerous unnatural amino acids, it will be possible to encode more than 200 unnatural amino acid combinations using this approach. As ribo-Q1 independently decodes a series of quadruplet codons, this work provides foundational technologies for the encoded synthesis and synthetic evolution of unnatural polymers in cells.

Science 329:52- (2010)

Creation of a Bacterial Cell Controlled by a Chemically Synthesized Genome

Daniel G. Gibson,[1] John I. Glass,[1] Carole Lartigue,[1] Vladimir N. Noskov,[1] Ray-Yuan Chuang,[1] Mikkel A. Algire,[1] Gwynedd A. Benders,[2] Michael G. Montague,[1] Li Ma,[1] Monzia M. Moodie,[1] Chuck Merryman,[1] Sanjay Vashee,[1] Radha Krishnakumar,[1] Nacyra Assad-Garcia,[1] Cynthia Andrews-Pfannkoch,[1] Evgeniya A. Denisova,[1] Lei Young,[1] Zhi-Qing Qi,[1] Thomas H. Segall-Shapiro,[1] Christopher H. Calvey,[1] Prashanth P. Parmar,[1] Clyde A. Hutchison III,[2] Hamilton O. Smith,[2] J. Craig Venter[1,2]*

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.

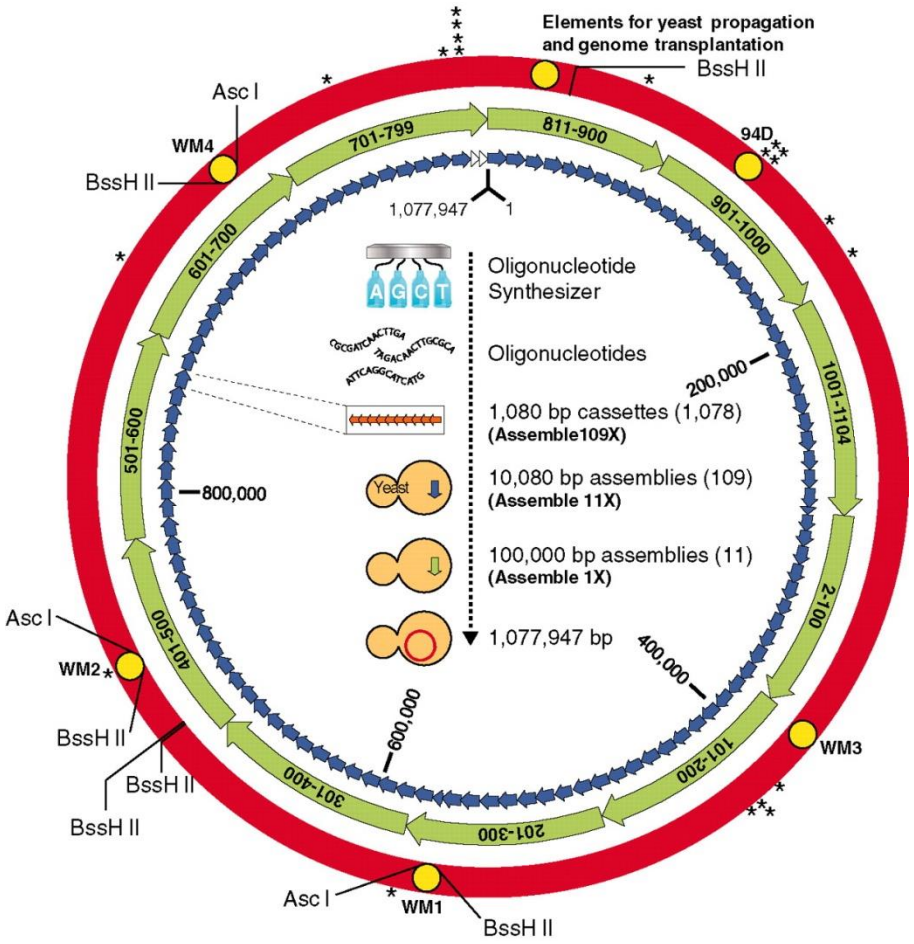
crude *M. mycoides* or *M. capricolum* extracts, or by simply disrupting the recipient cell's restriction system (*8*).

We now have combined all of our previously established procedures and report the synthesis, assembly, cloning, and successful transplantation of the 1.08-Mbp *M. mycoides* JCVI-syn1.0 genome, to create a new cell controlled by this synthetic genome.

Synthetic genome design. Design of the *M. mycoides* JCVI-syn1.0 genome was based on the highly accurate finished genome sequences of two laboratory strains of *M. mycoides* subspecies *capri* GM12 (*8*, *9*, *11*). One was the genome donor used by Lartigue *et al.* [GenBank accession CP001621] (*10*). The other was a strain created by transplantation of a genome that had been cloned and engineered in yeast, YCpMmyc1.1-Δ*typeIIIres* [GenBank accession CP001668] (*8*). This project was critically dependent on the accuracy of these sequences. Although we believe that both finished *M. mycoides* genome sequences are reli-

- Changing *Mycoplasma capricolum* cells to *M. genitalium* JCVI syn1.0 genome.
- A species changed into another with the use of a synthetic genome – "Synthetic cell".
- One single nucleotide mistake (deletion in dnaA-DNA replication) caused a severe problem for the project.

Gibson et al. Science 329:52- (2010)



The assembly of a synthetic M. mycoides genome in yeast. A synthetic M. mycoides genome was assembled from 1078 overlapping DNA cassettes in three steps. In the first step, 1080-bp cassettes (orange arrows), produced from overlapping synthetic oligonucleotides, were recombined in sets of 10 to produce 109 ~10-kb assemblies (blue arrows). These were then recombined in sets of 10 to produce 11 ~100-kb assemblies (green arrows). In the final stage of assembly, these 11 fragments were recombined into the complete genome (red circle). With the exception of two constructs that were enzymatically pieced together in vitro (27) (white arrows), assemblies were carried out by in vivo homologous recombination in yeast. Major variations from the natural genome are shown as yellow circles. These include four watermarked regions (WM1 to WM4), a 4-kb region that was intentionally deleted (94D), and elements for growth in yeast and genome transplantation. In addition, there are 20 locations with nucleotide polymorphisms (asterisks). Coordinates of the genome are relative to the first nucleotide of the natural M. mycoides sequence. The designed sequence is 1,077,947 bp. The locations of the Asc I and BssH II restriction sites are shown. Cassettes 1 and 800-810 were unnecessary and removed from the assembly strategy (11). Cassette 2 overlaps cassette 1104, and cassette 799 overlaps cassette 811.

Genome editing - CRISPR

A Programmable Dual-RNA–Guided DNA Endonuclease in Adaptive Bacterial Immunity

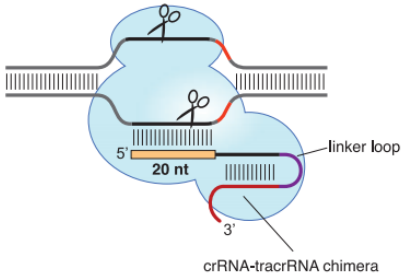
Martin Jinek,[1,2]* Krzysztof Chylinski,[3,4]* Ines Fonfara,[4] Michael Hauer,[2]† Jennifer A. Doudna,[1,2,5,6]‡ Emmanuelle Charpentier[4]‡

Clustered regularly interspaced short palindromic repeats (CRISPR)/CRISPR-associated (Cas) systems provide bacteria and archaea with adaptive immunity against viruses and plasmids by using CRISPR RNAs (crRNAs) to guide the silencing of invading nucleic acids. We show here that in a subset of these systems, the mature crRNA that is base-paired to trans-activating crRNA (tracrRNA) forms a two-RNA structure that directs the CRISPR-associated protein Cas9 to introduce double-stranded (ds) breaks in target DNA. At sites complementary to the crRNA-guide sequence, the Cas9 HNH nuclease domain cleaves the complementary strand, whereas the Cas9 RuvC-like domain cleaves the noncomplementary strand. The dual-tracrRNA:crRNA, when engineered as a single RNA chimera, also directs sequence-specific Cas9 dsDNA cleavage. Our study reveals a family of endonucleases that use dual-RNAs for site-specific DNA cleavage and highlights the potential to exploit the system for RNA-programmable genome editing.

17 AUGUST 2012 VOL 337 SCIENCE

— tracrRNA

Cas9 programmed by single chimeric RNA



www.sciencemag.org SCIENCE VOL 339 15 FEBRUARY 2013

RNA-Guided Human Genome Engineering via Cas9

Prashant Mali,[1]* Luhan Yang,[1,3]* Kevin M. Esvelt,[2] John Aach,[1] Marc Guell,[1] James E. DiCarlo,[4] Julie E. Norville,[1] George M. Church[1,2]†

www.sciencemag.org SCIENCE VOL 339 15 FEBRUARY 2013

Multiplex Genome Engineering Using CRISPR/Cas Systems

Le Cong,[1,2]* F. Ann Ran,[1,4]* David Cox,[1,3] Shuailiang Lin,[1,5] Robert Barretto,[6] Naomi Habib,[1] Patrick D. Hsu,[1,4] Xuebing Wu,[7] Wenyan Jiang,[8] Luciano A. Marraffini,[8] Feng Zhang[1]†

Cell Stem Cell

Brief Report

Functional Repair of CFTR by CRISPR/Cas9 in Intestinal Stem Cell Organoids of Cystic Fibrosis Patients

Gerald Schwank,[1,2,7] Bon-Kyoung Koo,[1,2,7,8] Valentina Sasselli,[1,2] Johanna F. Dekkers,[3,4] Inha Heo,[1,2] Turan Demircan,[1] Nobuo Sasaki,[1,2] Sander Boymans,[1] Edwin Cuppen,[1,6] Cornelis K. van der Ent,[3] Edward E.S. Nieuwenhuis,[5] Jeffrey M. Beekman,[5,6] and Hans Clevers[1,2,*]

Cell Research (2015) 25:67-79.

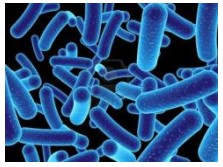
www.nature.com/cr

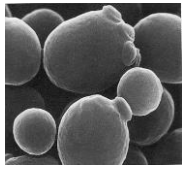
ORIGINAL ARTICLE

Correction of a genetic disease by CRISPR-Cas9-mediated gene editing in mouse spermatogonial stem cells

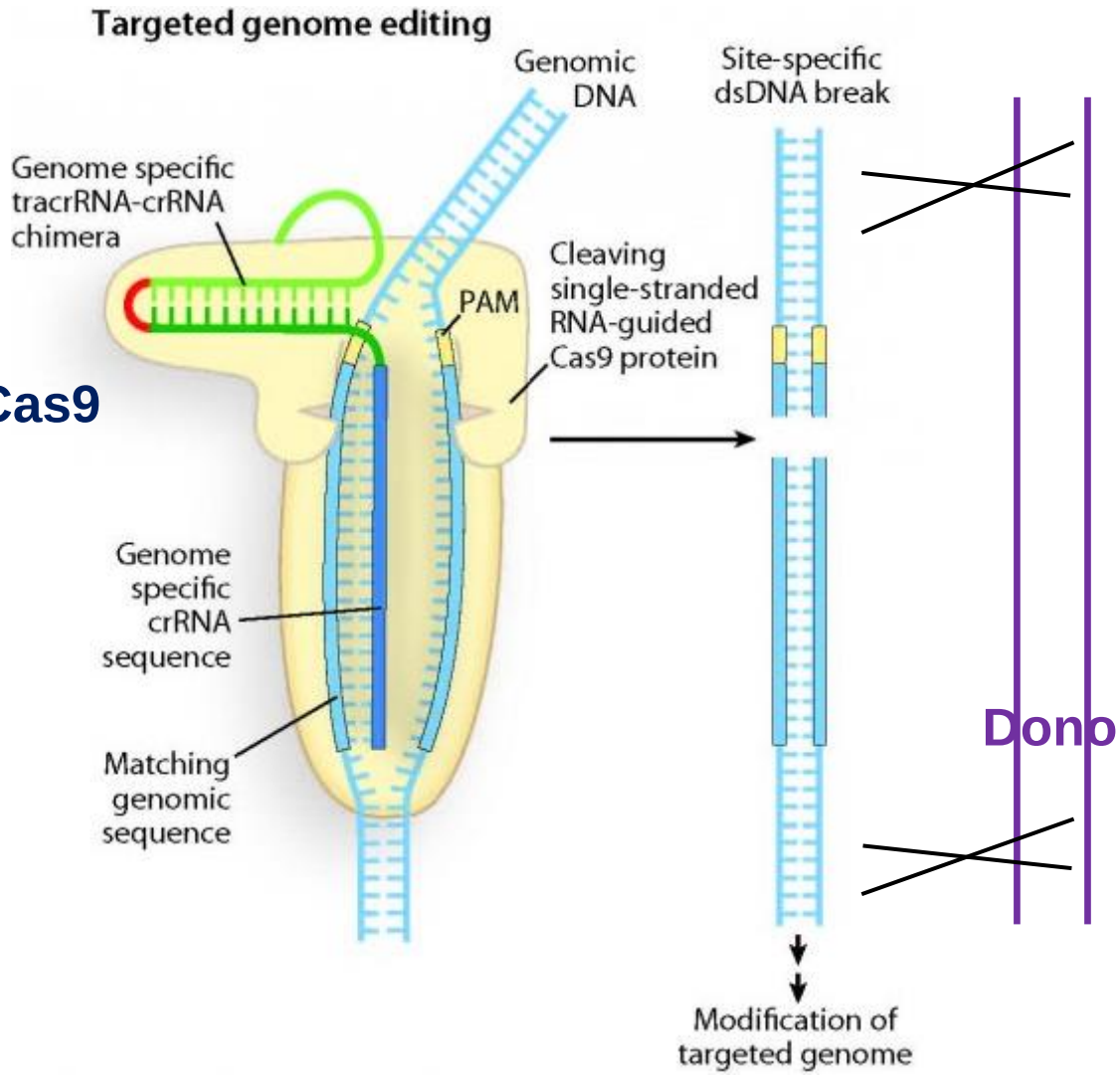
Yuxuan Wu[1,2,*], Hai Zhou[1,2,3,*], Xiaoying Fan[4,*], Ying Zhang[2,5,*], Man Zhang[1,2,*], Yinghua Wang[1,2], Zhenfei Xie[1,2], Meizhu Bai[1,2,6], Qi Yin[1,2], Dan Liang[1,2], Wei Tang[7], Jiaoyang Liao[1,2], Chikai Zhou[1,2], Wujuan Liu[1,2], Ping Zhu[4], Hongshan Guo[4], Hong Pan[1,2], Chunlian Wu[3], Huijuan Shi[8], Ligang Wu[2,5], Fuchou Tang[4], Jinsong Li[1,2,6]







Genome editing - CRISPR

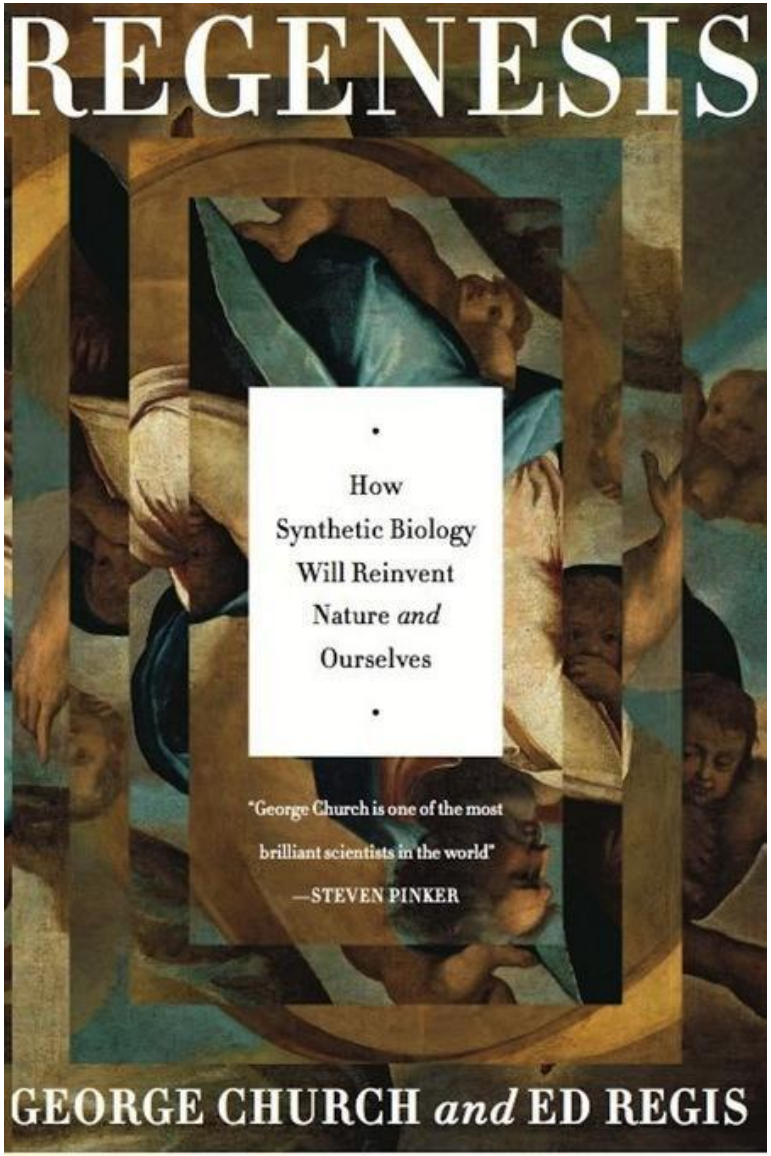


CRISPR/Cas9

- **Gene knockouts**
- **Gene insertions**
- **Gene regulation**
- **Genome editing**

Donor DNA

The CRISPR-Cas components consist of a **Cas9 endonuclease** and a designer genome targeting CRISPR **guide RNA (gRNA),** thereby resulting in **a simple and versatile RNA-directed system to generate dsDNA breaks for genome targeting and editing.**



Gene-editing record smashed in pigs

Researchers modify more than 60 genes in effort to enable organ transplants into humans.

Sara Reardon

06 October 2015 *NATURE* | NEWS

Geneticist George Church has co-founded a company that is developing genetically modified pigs to grow organs for human transplant

Biological organisms are excellent engineers

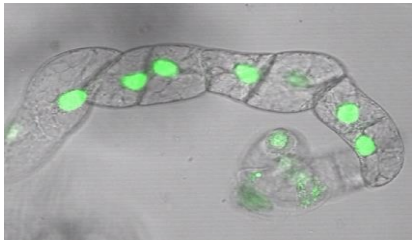
- Many functions manifest at single cell level
- The functions can be engineered and transferred to other organisms
- Cells have intrinsic synthesis power and the power of evolution – unlike in any other discipline

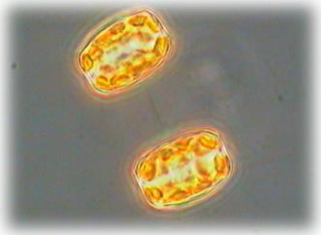
Fire fly

Lacewing fly's jump mechanism

Heart cell

Cellulose forming plant cells

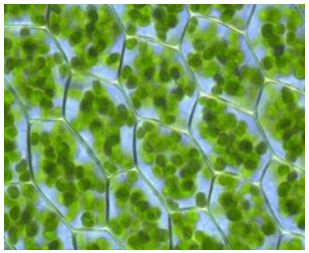




Fatty algal cells

Bacterial magnets

Spider silk



Light energy capturing chloroplasts

Single cell organisms can have very ”sophisticated” and varied functions

YEAST can e.g.

Breath

O_2

CO_2

Eat

Sugar

Ethanol
Flavours

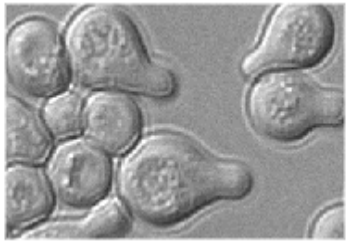
Respond to
cold and heat

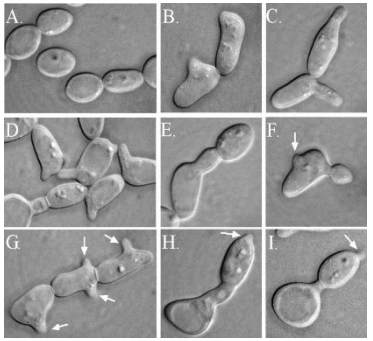
Respond to
pressure

Keep a
distance

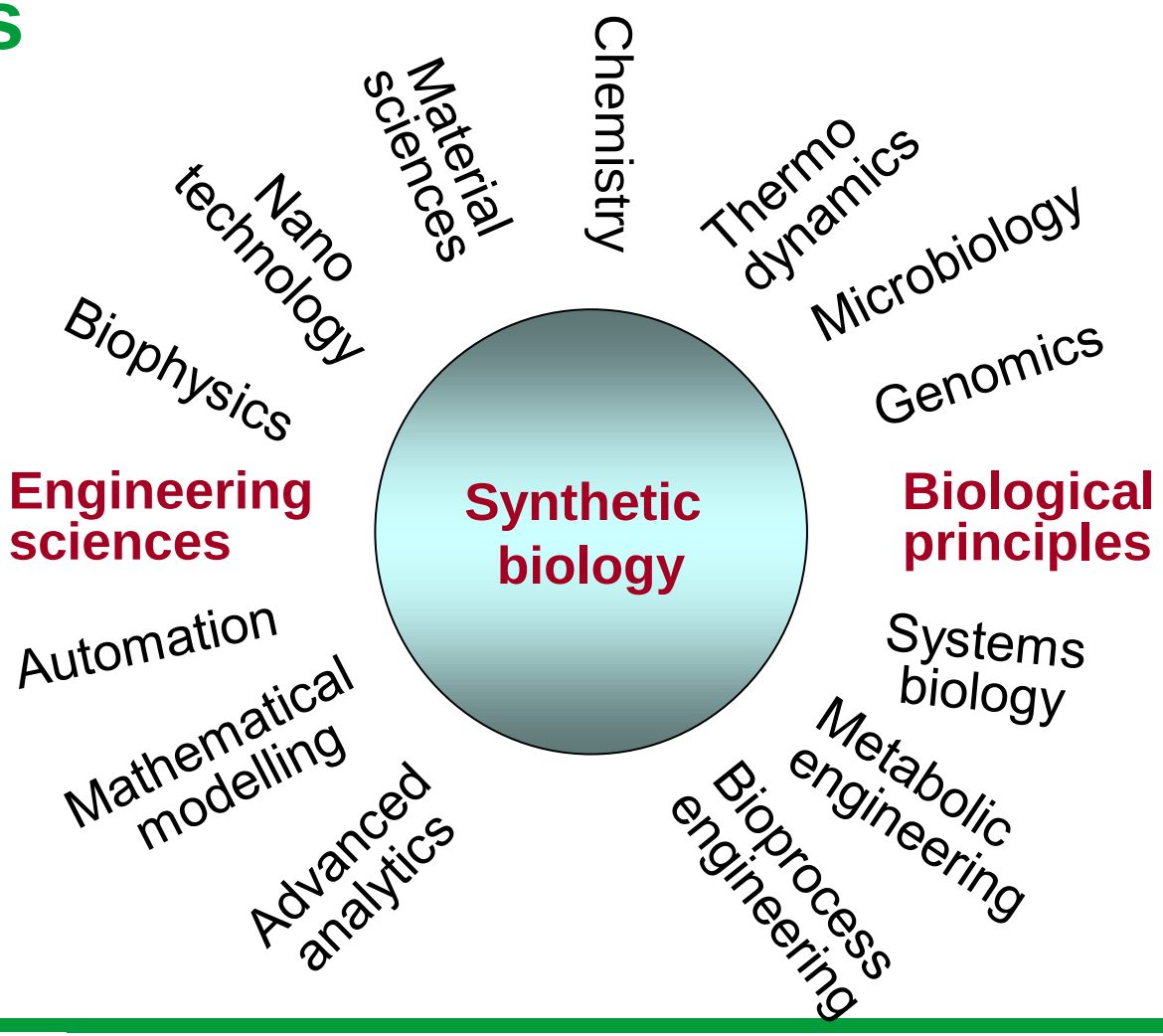
Mate

Shmoo cells





Synthetic biology relies on many disciplines



Arts Philosophy Ethics

Synbio interests many

Scientists

- Interests many scientific fields, including physics, chemistry, nanosciences
- A dream job for a natural scientists (combination of biology and engineering sciences)

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- Garage biology (like ICT), activity in USA and Europe including associations

Croudfunded in Biocurious: Glowing plants

BioCurious is the Hackerspace for Bio, Built in the Heart of Silicon Valley.
We are a community of scientists, technologists, entrepreneurs, and amateurs who believe that innovations in biology should be accessible, affordable, and open to everyone.
Located in Sunnyvale, CA, our co-working laboratory space and shared equipment is ideal for entrepreneurs, citizen scientists, hobbyists, and students.

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Philosophers

- How we do science is changing, ”from reading to writing”, from examination of existing reality to design
- What is life? Natural?

Ethicists

- How far can we go? Can we engineer humans?
- Safety and need for new regulations?

Artists

- Experimenting with (conceptual) limits
- Biological living systems as art medium

Synbio interests many

Laura Cinti: The Cactus Project (2001) is a living artwork of cacti expressing human hair. The work explores a reproductive paradox in genetic engineering - the inherent sterility of transformation processes.

The work makes use of agrobacterium-mediated gene transfer to introduce hair keratin genes into cells of cacti. Transformed cells were regenerated as engineered transgenic cacti. The aim was to have human keratins expressed in cacti cells morphologically similar to hair and for these to be produced externally.

"[W]hy should we still call this hair human? Doesn't it belong now to the cactus and not in a trivial sense either? Or better still, doesn't it become just a standard biological part, to use a revealing phrase from the biological engineering laboratory at MIT? In this case, as in so many others, what makes it standard is not its elemental composition but its technical transmissibility: the apotheosis of Fordism put into service as an organizing principle for life?"

Paul Lewis, The Edge Effect: Art, Science, and Ecology in a Deleuzian Century *in* An [Un]Likely Alliance: Thinking Environment[s] with Deleuze/Guattari

Can you judge if this is real or not?

Artists

- Experimenting with (conceptual) limits
- Biological living systems as art medium

iGEM Jamboree Boston 2014

BioGarage

- Community creation
- Open inspiring laboratory space
- Low-threshold bioengineering
- Interdisciplinarity
- Linking with international garages
- Science pitches, Bio-Slush, etc
- BD mentoring & support

"Guided tours for politicians"

"We would like to learn more in the lab"

"Normal people cloning would make them understand GMOs"

"A realistic option for start-ups"

"Proper place where biohazardous waste is treated correctly"

Opening event at Design Factory 27.9.2019
iGEM team demonstrating DNA isolation

Jenny and Antti Wihuri Foundation support for the Centre of Young Synbio Scientists (Prof. Merja Penttilä)

Contact BioGarage manager
james.evans@aalto.fi

Course outline

28.2.	**Introduction** to synthetic biology and the course
7.3.	**Standardization, biobricks and chassis**
14.3.	**Artificial genomes: Yeast Sc2.0**
21.3.	**Synbio as an enabler of applications in sustainable bioeconomy**
28.3.	Homework presentations
4.4.	**Modelling of circuits, oscillations and metabolism**
25.4.	Common modelling session
2.5.	**Homework presentations based on articles**
9.5.	**Homework presentations based on articles**
16.5.	**Homework presentations based on articles**
23.5.	**Ethics & safety, iGEM**
1.6.	**Exam**

Homework, evaluation

For inspiration: BioBuilder.org

Home work and oral presentations 28.3.

Select one of the two topics shown below. Prepare a ppt-slide set for a 15 min presentation. Send the slides to Merja by noon 25.3. the latest. 2-3 presentations of both topics will be randomly selected to be presented on 28.3.

1. Theme: Standardization, biobricks and chassis

Design a sensor system based on standard parts for inputs and outputs + variations, using the iGEM registry for standard parts and their assembly strategies. http://parts.igem.org/Main_Page

2. Theme: Artificial Yeast Sc2.0

Design a specific synthetic part of the yeast genome according to the rules laid out by the Sc2.0 consortium. Add your own ideas, discuss problems etc. http://syntheticyeast.org/

Homework based on articles 2.5., 9.5. & 16.5.

Select one article form the provided list. Form teams and make a 20 min presentation.

Course evaluation

All homeworks & hands-on need to be done (pass).

Exam: Show what you have learned! All topics matter for getting a good score. Learn concepts, possibilities. Think what is synthetic biology.

Group work - BioBricks

- Design a sensor based on standard parts for input and parts for outputs (+ circuit variations) using the iGEM registry for standard parts.
- Describe the idea of what kind of a sensor you want to build and why. Identify the selected parts (iGEM code numbers), how they work, how you assemble them (assembly standard) and how the system works in the off/on state. Show the design in the way you have seen in the course lectures. Give the truth table of your circuit design.
- Send the presentations to merja.penttila@vtt.fi by noon the 25.3. the latest.
- Max 15min for presentation, followed by discussion. Present as a group. Be clear, speak slowly.

Group work – Yeast 2.0

Prepare together a **15 min presentation** that contains:

A synthetic design of a ~30-50kb region (”megachunk”) of a selected *Saccharomyces cerevisiae* chromosome, following the same design and construction rules as used for creation of Sc2.0 (slides 18, 19).

- Why did you choose this region?
- Tell what is in the selected region (genes, introns etc). What would you include or omit from the design? (No need to go for a single nucleotide level). Illustrate as in slide 20.
- Which computer programs would you use/need?
- Brief explanation of the wet lab construction procedure

Answers to the questions:

- Explain the Scramble mechanism
- What is the significance and impact of the yeast 2.0?
- What would you use the yeast for or develop further? How?

You may also point out the possible problems you encounted in your group work.

Send the slides to merja.penttila@vtt.fi by noon the 25.3. the latest.
Present as a group. Speak clearly and slowly.