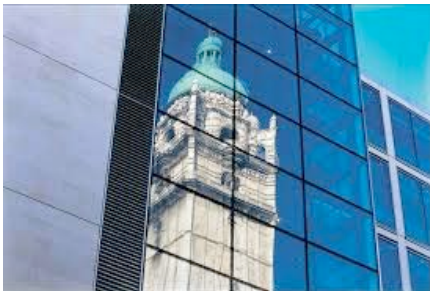
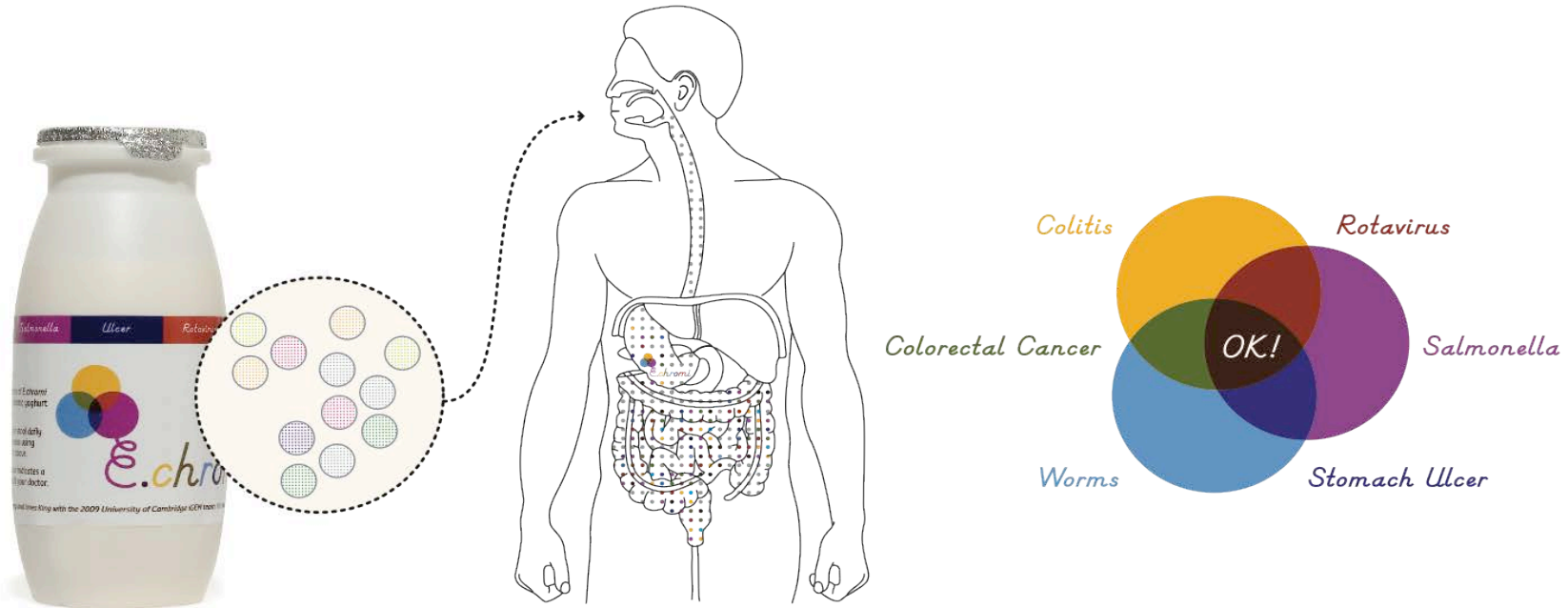


Synthetic Biology – Trends and Updates
EC WORKSHOP ON SYNTHETIC BIOLOGY -
FROM SCIENCE TO POLICY AND SOCIETAL CHALLENGES
Luxembourg 9th Dec 2015

Professor Paul Freemont @paulfreemont
Co-director and Co-founder EPSRC Centre for Synthetic Biology and Innovation
Co-director and Co-founder of UK National Innovation and Knowledge Centre
for Synthetic Biology Imperial College London, UK



WHAT IF ?



1. Drink

Synthetic *E. chromi* bacteria are ingested as a probiotic yoghurt.

2. Colonise

Colonising the gut, the *E. chromi* keep watch for the chemical markers of disease.

3. Monitor

If a disease is detected, the bacteria secrete an easily-read colour signal, visible in faeces.



E. chromi - cheap, personalised disease monitoring from the inside out.

E. chromi, 2009 University of Cambridge iGEM team



Programmable bacteria detect and record an environmental signal in the mammalian gut

Jonathan W. Kotula^{a,b,1}, S. Jordan Kerns^{a,b,1}, Lev A. Shaket^b, Layla Siraj^b, James J. Collins^{b,c,d}, Jeffrey C. Way^b, and Pamela A. Silver^{a,b,2}

^aDepartment of Systems Biology, Harvard Medical School, Boston, MA 02115; ^bWyss Institute for Biologically Inspired Engineering, Harvard University, Boston, MA 02115; ^cDepartments of Biomedical Engineering and Medicine, and Center of Synthetic Biology, Boston University, Boston, MA 02215; and ^dHoward Hughes Medical Institute

Edited* by Richard D. Koldner, Ludwig Institute for Cancer Research, La Jolla, CA, and approved February 19, 2014 (received for review November 25, 2013)

The mammalian gut is a dynamic community of symbiotic microbes that interact with the host to impact health, disease, and metabolism. We constructed engineered bacteria that survive in the mammalian gut and sense, remember, and report on their experiences. Based on previous genetic memory systems, we constructed a two-part system with a “trigger element” in which the lambda Cro gene is transcribed from a tetracycline-inducible promoter, and a “memory element” derived from the *ci*/Cro region of phage lambda. The memory element has an extremely stable *ci* state and a Cro state that is stable for many cell divisions. When *Escherichia coli* bearing the memory system are administered to mice treated with anhydrotetracycline, the recovered bacteria all have switched to the Cro state, whereas those administered to untreated mice remain in the *ci* state. The trigger and memory elements were transferred from *E. coli* K12 to a newly isolated murine *E. coli* strain; the stability and switching properties of the memory element were essentially identical in vitro and during passage through mice, but the engineered murine *E. coli* was more stably established in the mouse gut. This work lays a foundation for the use of synthetic genetic circuits as monitoring systems in complex, ill-defined environments, and may lead to the development of living diagnostics and therapeutics.

in which the lac repressor (*lacI*-) and *tetR*-encoded repressors inhibit the synthesis of the other protein, such that the system exists in two stable states that can be interchanged by environmental exposure to either isopropyl- β -D-thiogalactopyranoside or tetracycline. Ajo-Franklin et al. (21) developed a more general system in which a formally identified trigger element was separated from a bistable transcriptional memory element in yeast; in this way, a wide variety of input signals can be recorded using a single memory element with diverse trigger promoters. Burrill et al. (4) used this type of memory system to characterize gene-expression profiles in cells that responded differentially to a uniform exposure to DNA damaging agents. Thus, memory devices can be used in laboratory applications under controlled conditions.

Microbes carrying memory elements have potential for broad use as nondestructive environmental sensing systems. To realize this potential, such memory systems will need to be able to function in real-world environments beyond the controlled conditions of a laboratory. Thus, a memory device must be stable in either of two states for long periods of time, even in the presence of basal expression from a trigger element. DNA rearrangement systems may undergo an uninduced change of state resulting from leaky expression of a trigger element if the chances of a recombination event increase linearly with expression levels. T



RESEARCH ARTICLE | CANCER

Programmable probiotics for detection of cancer in urine

Tal Danino^{1,*}, Arthur Prindle^{2,*}, Gabriel A. Kwong^{1,†}, Matthew Skalak¹, Howard Li², Kaitlin Allen¹, Jeff Hasty^{2,3,4,‡} and Sangeeta N. Bhatia^{1,5,6,7,8,‡,§}

+ Author Affiliations

↔[§]Corresponding author. E-mail: sbhatia@mit.edu

↔* Equally contributing lead authors.

↔† Present address: Wallace H. Coulter Department of Biomedical Engineering, Georgia Tech and Emory School of Medicine, Atlanta, GA 30332, USA.

↔‡ Equally contributing senior authors.

Science Translational Medicine 27 May 2015:
Vol. 7, Issue 289, pp. 289ra84
DOI: 10.1126/scitranslmed.aaa3519

RESEARCH ARTICLE

A Forward-Design Approach to Increase the Production of Poly-3-Hydroxybutyrate in Genetically Engineered *Escherichia coli*

Richard Kelwick^{1,2*‡}, Margarita Kopniczky^{1,2‡}, Iain Bower^{1,3}, Wenqiang Chi^{1,4}, Matthew Ho Wai Chin^{1,4}, Sisi Fan^{1,3}, Jemma Pilcher^{1,3}, James Strutt^{1,3}, Alexander J. Webb^{1,2}, Kirsten Jensen^{1,2}, Guy-Bart Stan^{1,4}, Richard Kitney^{1,4*}, Paul Freemont^{1,2*}

1 Centre for Synthetic Biology and Innovation, South Kensington Campus, London, United Kingdom, **2** Department of Medicine, South Kensington Campus, London, United Kingdom, **3** Department of Life Sciences, South Kensington Campus, London, United Kingdom, **4** Department of Bioengineering, Imperial College London, South Kensington Campus, London, United Kingdom

‡ These authors are equal first authors on this work.

* p.freemont@imperial.ac.uk (PF); r.kitney@imperial.ac.uk (R. Kitney); r.kelwick@imperial.ac.uk (R. Kelwick)



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Citation: Kelwick R, Kopniczky M, Bower I, Chi W, Chin MHW, Fan S, et al. (2015) A Forward-Design Approach to Increase the Production of Poly-3-Hydroxybutyrate in Genetically Engineered

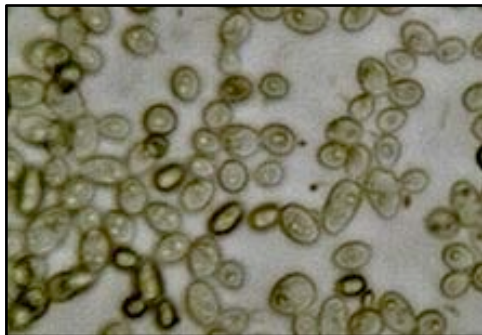
Abstract

Biopolymers, such as poly-3-hydroxybutyrate (P(3HB)) are produced as a carbon store in an array of organisms and exhibit characteristics which are similar to oil-derived plastics

WHAT IF ?



Gluconacetobacter xylinus



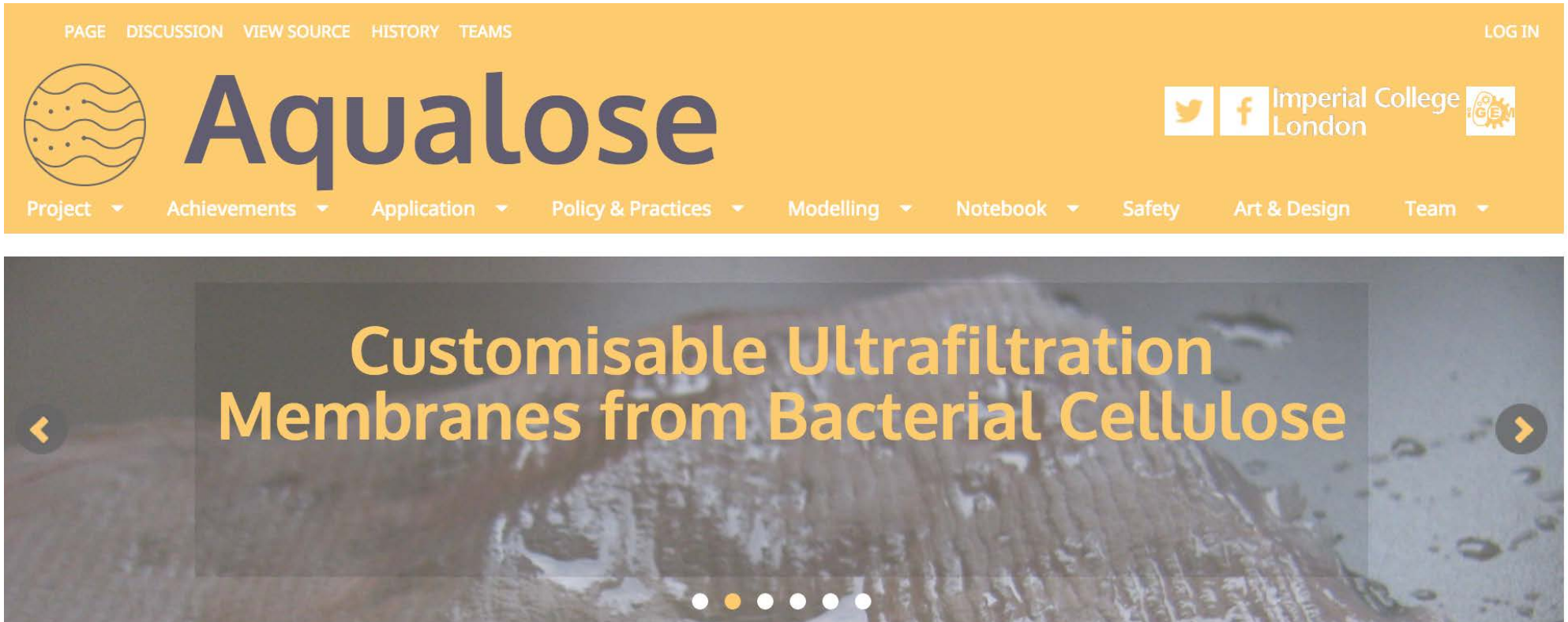
Gluconacetobacter xylinus + yeast



Suzanne Lee



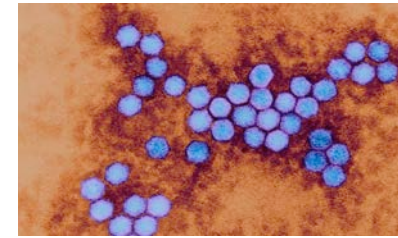
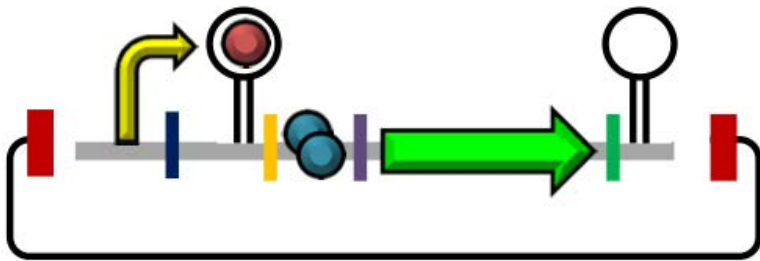
Imperial College IGEM 2014 Aqualose



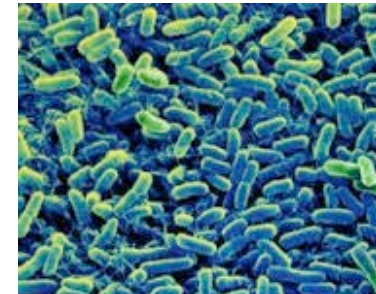
The image shows the top portion of a website. The header is orange and contains navigation links: PAGE, DISCUSSION, VIEW SOURCE, HISTORY, TEAMS, and LOGIN. The main title 'Aqualose' is in large blue font, accompanied by a circular logo with wavy lines and dots. To the right are social media icons for Twitter and Facebook, and the text 'Imperial College London' with an IGEM logo. Below the header is a navigation menu with dropdown arrows for Project, Achievements, Application, Policy & Practices, Modelling, Notebook, Safety, Art & Design, and Team. The main banner features a microscopic image of a membrane with the text 'Customisable Ultrafiltration Membranes from Bacterial Cellulose' in orange. Navigation arrows and a progress indicator are also visible.

Genetic engineering of the cellulose-producing bacterium
Komagataeibacter rhaeticus for production of novel biomaterials.
Florea et al 2015 in press

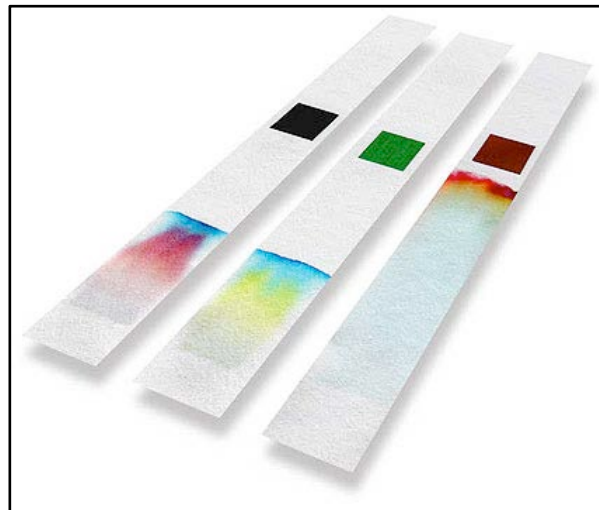
WHAT IF ?



viruses



bacteria



parasites

Paper-Based Synthetic Gene Networks

Keith Pardee,^{1,2} Alexander A. Green,^{1,2} Tom Ferrante,¹ D. Ewen Cameron,^{2,3} Ajay DaleyKeyser,¹ Peng Yin,¹ and James J. Collins^{1,2,3,*}

¹Wyss Institute for Biological Inspired Engineering, Harvard University, Boston, MA 02115, USA

²Department of Biomedical Engineering and Center of Synthetic Biology, Boston University, Boston, MA 02215, USA

³Howard Hughes Medical Institute, Chevy Chase, MD 20815, USA

*Correspondence: jcollins@bu.edu


<http://dx.doi.org/10.1016/j.cell.2014.10.004>

SUMMARY


Synthetic gene networks have wide-ranging uses in reprogramming and rewiring organisms. To date, there has not been a way to harness the vast potential of these networks beyond the constraints of a laboratory or in vivo environment. Here, we present an in vitro paper-based platform that provides an alternate, versatile venue for synthetic biologists to operate and a much-needed medium for the safe deployment of engineered gene circuits beyond the lab. Commercially available cell-free systems are freeze dried onto paper, enabling the inexpensive, sterile

Earlier studies in the area of in vitro synthetic biology and cell-free systems have made important contributions to our understanding of fundamental molecular biology and biochemistry and, more recently, in the study of molecular switch dynamics and complex gene circuits (Hong et al., 2014; Karzbrun et al., 2014; Sun et al., 2014; Takahashi et al., 2014). These efforts, however, have focused on solution-phase reactions using fresh from frozen cell-free systems and often in liposomes with the goal of assembling artificial cells (Kuruma et al., 2009; Kobori et al., 2013). These solution-phase reactions are not stable or practical for handling outside of the lab and therefore miss the opportunity to leverage the abiotic and sterile nature of these systems.


WHAT IF ?



petroleum

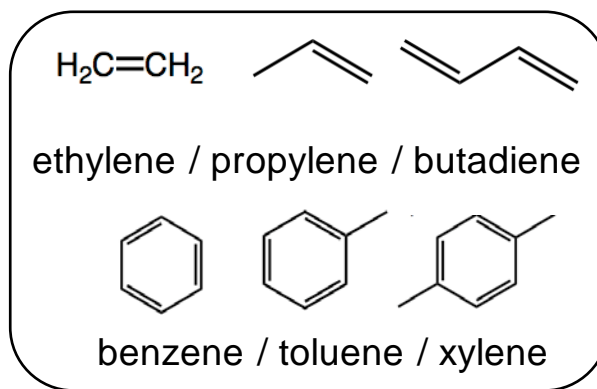


coal

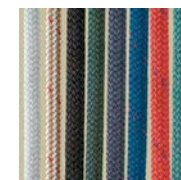


natural gas

Carbon feedstocks

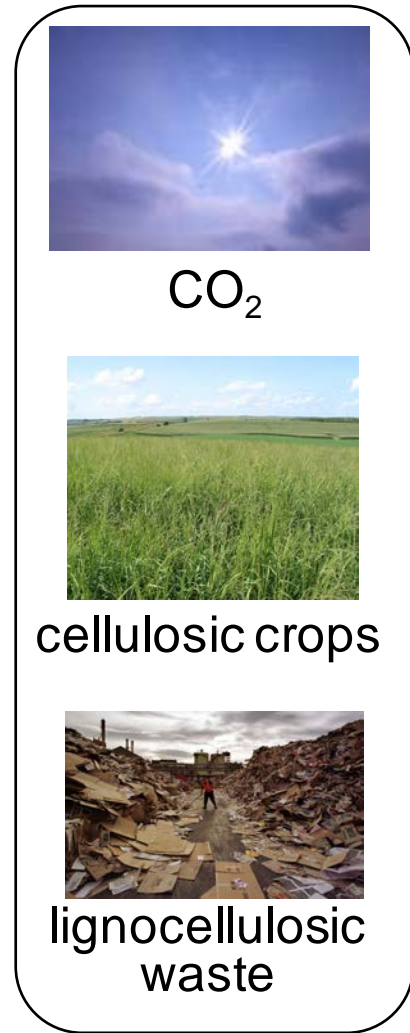


Building blocks



Value - added chemicals

WHAT IF ?



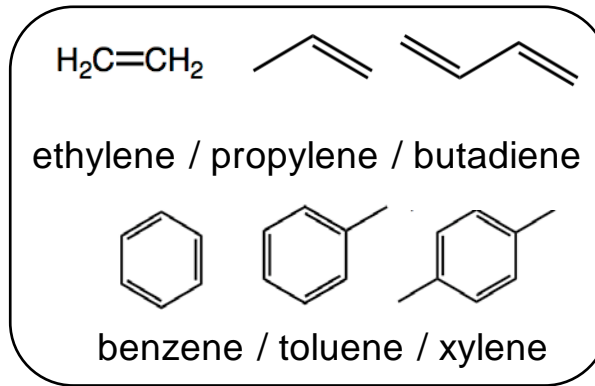
A vertical rounded rectangle containing three images. The top image shows a bright sun in a blue sky with the text CO_2 below it. The middle image shows a field of green crops with the text "cellulosic crops" below it. The bottom image shows a pile of brown waste with the text "lignocellulosic waste" below it.

CO_2

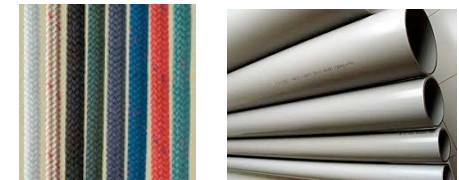
cellulosic crops

lignocellulosic waste

Biomass feedstocks

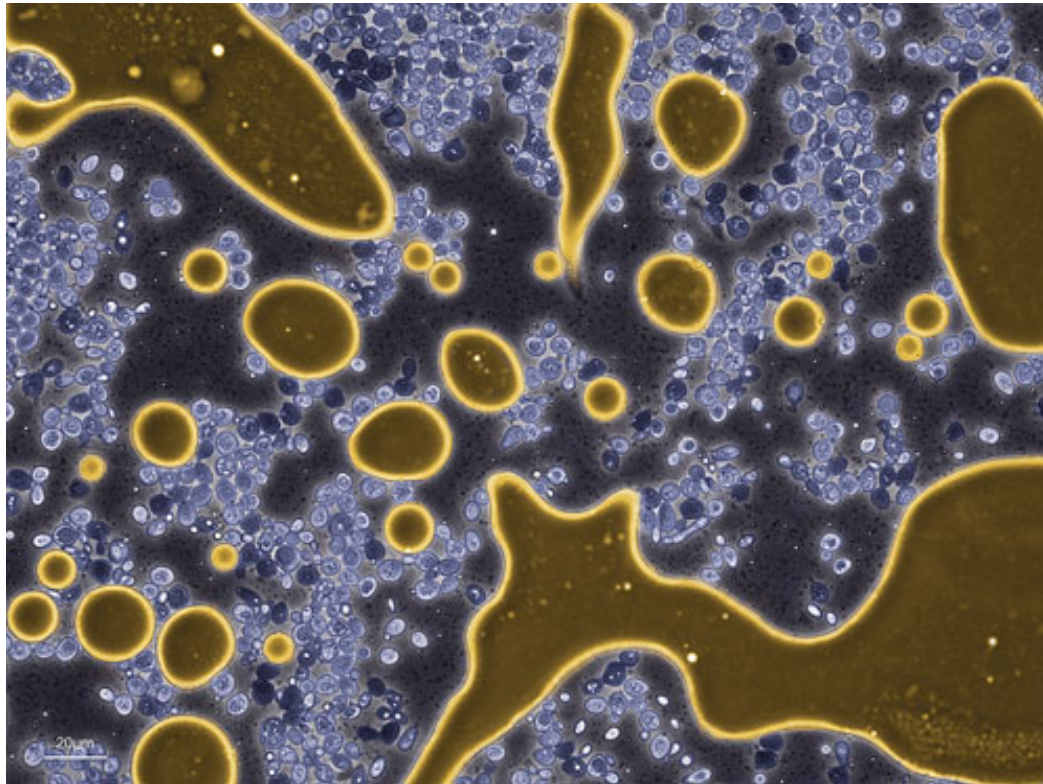


Building blocks



Value - added chemicals

S. cerevisiae secreting farnesene/biodiesel



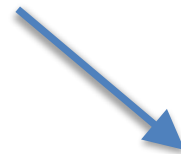
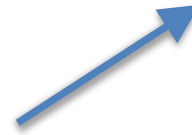
~112K bases added
~41K bases removed
~450 single nucleotide changes

~1.25% of the genome!



DNA as a programmable material

WHAT IF ?



DIY-Bio, Biohackers and the Growth of Community Labs

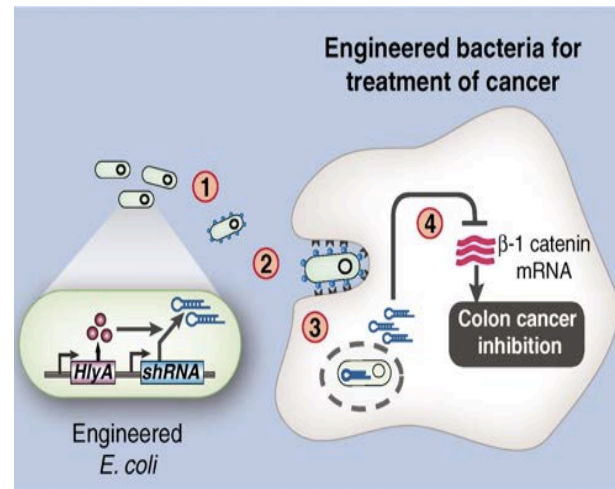
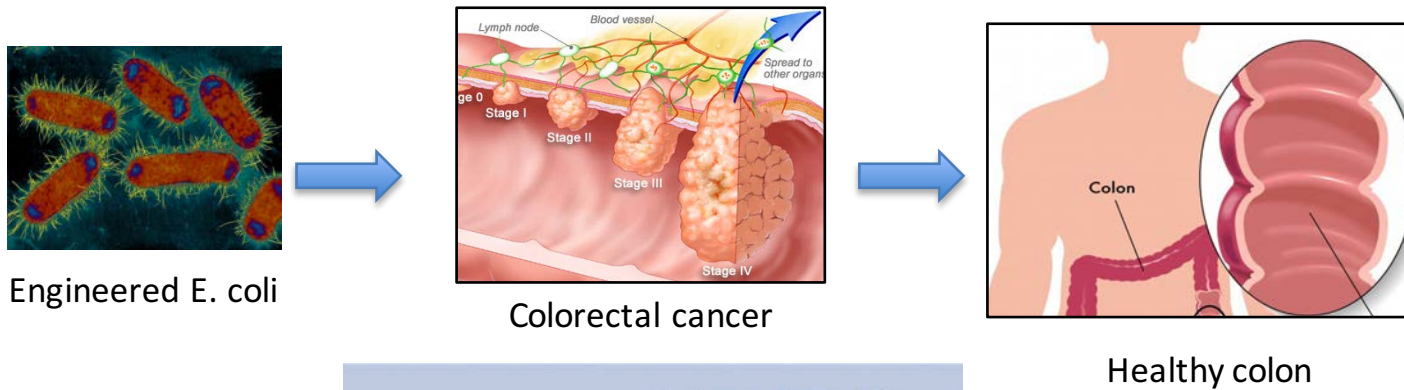


London BioHackspace
Biohacking / DIYBio in London

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WHAT IF ?

Engineered bacteria to detect and kill cancer cells



(adapted from *Science* 333: 6047 (2011); <http://www.wisegEEK.com/what-are-cold-forceps.htm>); <http://www.webMD.com/colorectal-cancer/ss/slideshow-colorectal-cancer-overview>)



Journal of Molecular Biology

Volume 355, Issue 4, 27 January 2006, Pages 619–627



Environmentally Controlled Invasion of Cancer Cells by Engineered Bacteria

J. Christopher Anderson^{a, c}, Elizabeth J. Clarke^c, Adam P. Arkin^{a, b},  , Christopher A. Voigt^{b, c}

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Letter

Nature Biotechnology 24, 697 - 702 (2006)
Published online: 14 May 2006 | doi:10.1038/nbt1211

Short hairpin RNA-expressing bacteria elicit RNA interference in mammals

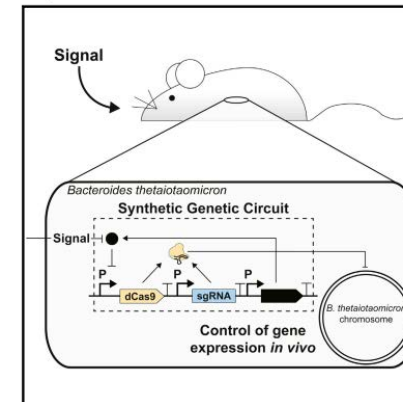
Shuanglin Xiang^{1,2}, Johannes Fruehauf^{1,2} & Chiang J Li¹

Cell Systems

Article

Programming a Human Commensal Bacterium, *Bacteroides thetaiotaomicron*, to Sense and Respond to Stimuli in the Murine Gut Microbiota

Graphical Abstract



Authors

Mark Mimee, Alex C. Tucker, Christopher A. Voigt, Timothy K. Lu

Correspondence

timlu@mit.edu

In Brief

The development of genetic parts to precisely program the human commensal gut bacterium *Bacteroides thetaiotaomicron* lays the foundation for microbiome engineering.

Highlights

- We develop sets of genetic parts for a human commensal bacterium
- Promoter and RBS libraries control gene expression over a 10,000-fold dynamic range
- Orthogonal, inducible sensors enable synthetic genetic memory and CRISPRi
- Genetic circuits respond to stimuli in a complex mouse gut microbiota

Mimee et al., 2015, Cell Systems 1, 62–71
July 29, 2015 ©2015 Elsevier Inc.
<http://dx.doi.org/10.1016/j.cels.2015.06.001>



CellPress

WHAT IF ?

Engineered phage and bacteria to target pathogens



bacteriophage



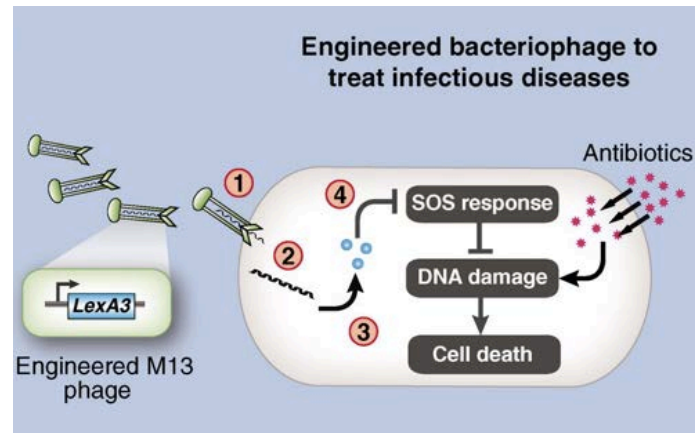
Attacking bacterium



Bacteria cell lyses and dies



Engineered E. coli



(adapted from Science 333: 6047 (2011); <http://www.sciencephoto.com/>)

Engineered bacteriophage targeting gene networks as adjuvants for antibiotic therapy

Timothy K. Lu^{a,b} and James J. Collins^{b,1}

^aHarvard-Massachusetts Institute of Technology Division of Health Sciences and Technology, Cambridge, MA 02139; and ^bHoward Hughes Medical Institute, Center for BioDynamics and Department of Biomedical Engineering, Boston University, Boston, MA 02215

Edited by Arnold L. Demain, Drew University, Madison, NJ, and approved February 3, 2009 (received for review January 16, 2008)

Antimicrobial drug development is increasingly lagging behind the evolution of antibiotic resistance, and as a result, there is a pressing need for new antibacterial therapies that can be readily designed and implemented. In this work, we engineered bacteriophage to overexpress proteins and attack gene networks that are not directly targeted by antibiotics. We show that suppressing the SOS network in *Escherichia coli* with engineered bacteriophage enhances killing by quinolones by several orders of magnitude in vitro and significantly increases survival of infected mice in vivo. In addition, we demonstrate that engineered bacteriophage can enhance the killing of antibiotic-resistant bacteria, persister cells, and biofilm cells, reduce the number of antibiotic-resistant bacteria that arise from an antibiotic-treated population, and act as a strong adjuvant for other bactericidal antibiotics (e.g., aminoglycosides and β -lactams). Furthermore, we show that engineering bacteriophage to target non-SOS gene networks and to overexpress multiple factors also can produce effective antibiotic adjuvants. This work establishes a synthetic biology platform for the rapid translation and integration of identified targets into effective antibiotic adjuvants.

antibiotic adjuvants | antibiotic resistance | bacterial persistence | bacteriophage therapy | synthetic biology

ary pressures. Instead of overexpressing lethal genes, our design targets nonessential genes and the networks they regulate that are not directly attacked by antibiotics. Combination therapy with different antibiotics, different bacteriophage, or antibiotic plus phage may reduce the incidence of phage resistance and/or antibiotic resistance (16–20). Therefore, by using a combination of engineered antibiotic-enhancing phage and antibiotics, we hoped to reduce the incidence of antibiotic resistance and enhance bacterial killing.

Results

Targeting the SOS DNA Repair System. Bactericidal antibiotics (e.g., quinolones such as ofloxacin) induce hydroxyl radical formation that leads to DNA, protein, and lipid damage and ultimately to cell death (8). DNA damage induces the SOS response (21, 22) which results in DNA repair (Fig. 1A). It has been shown that bacterial killing by bactericidal antibiotics can be enhanced by knocking out *recA* and disabling the SOS response (8). Here we took an alternative approach and engineered M13mp18 phage to overexpress *lexA3*, a repressor of the SOS response (23). Overexpression of *lexA3* to suppress the SOS system has been demonstrated to inhibit the emergence of antibiotic resistance (24). We used M13mp18, a modified version of M13 phage, as our

Molecular Systems Biology 7, Article number 521; doi:10.1038/msb.2011.55
Citation: Molecular Systems Biology 7:521
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www.molecularsystemsbiology.com

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systems
biology

Engineering microbes to sense and eradicate *Pseudomonas aeruginosa*, a human pathogen

Yamin Saedi¹, Choon Kit Wong¹, Tat-Ming Lo, Hung Xuan Nguyen², Hua Ling, Susanna Su Jan Leong, Chueh Loo Poh³ and Matthew Wook Chang^{4*}

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doi:10.1038/msb.2011.55; accepted 30.6.11

NANO LETTERS

Letter

pubs.acs.org/NanoLett

Engineered Phagemids for Nonlytic, Targeted Antibacterial Therapies

Russell J. Krom,^{†,‡,||,⊥} Prema Bhargava,^{†,§,||,¶} Michael A. Lobritz,^{†,§,||,¶} and James J. Collins^{*,†,‡,§,||}

[†]Institute for Medical Engineering and Science, Department of Biological Engineering, and Synthetic Biology Center, Massachusetts Institute of Technology, Cambridge, Massachusetts 02139, United States

[‡]Harvard-MIT Program in Health Sciences and Technology, Cambridge, Massachusetts 02139, United States

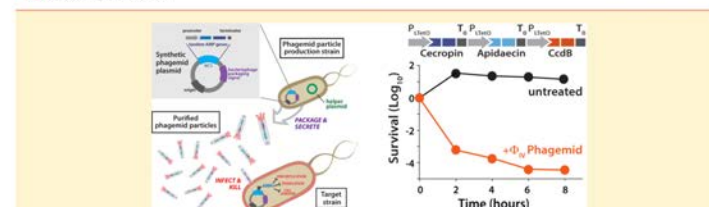
[§]Broad Institute of MIT and Harvard, Cambridge, Massachusetts 02142, United States

[¶]Wyss Institute for Biologically Inspired Engineering, Harvard University, Boston, Massachusetts 02115, United States

[⊥]Department of Molecular and Translational Medicine, Boston University, Boston, Massachusetts 02215, United States

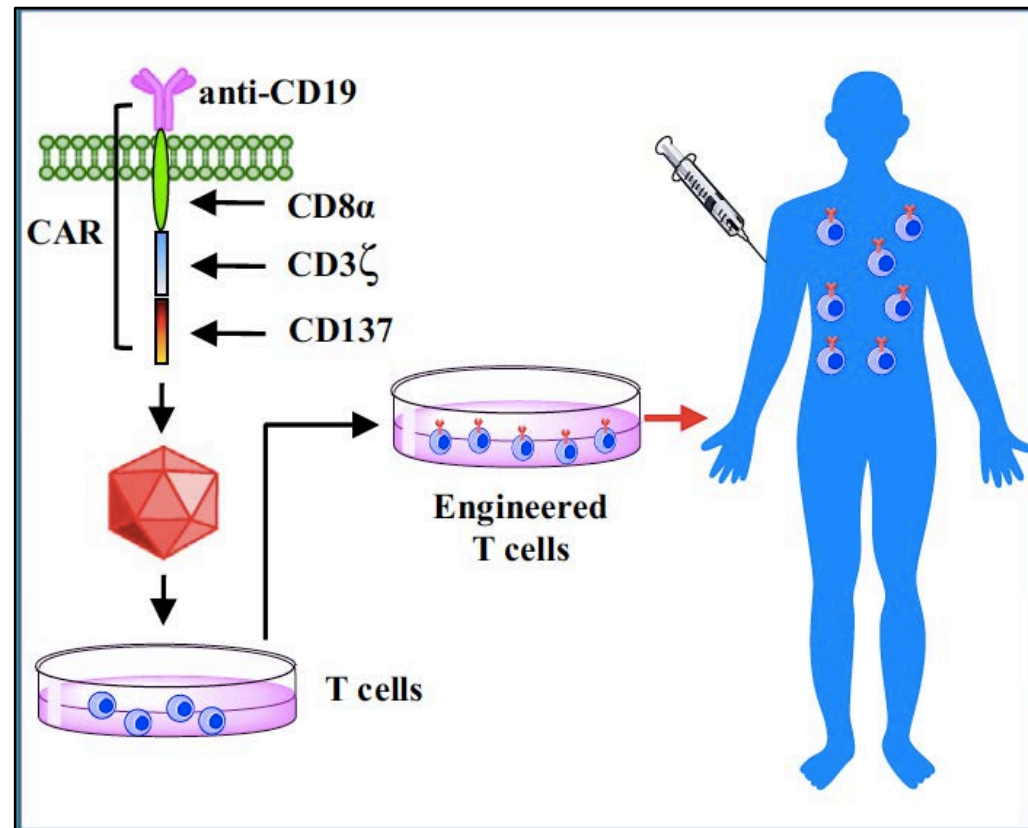
^{||}Division of Infectious Diseases, Massachusetts General Hospital, Boston, Massachusetts 02114, United States

Supporting Information



WHAT IF ?

Engineered T-cells to target cancer



T cell engineering

< Previous Article

Volume 39, Issue 1, p49–60, 25 July 2013

Review

Switch to Standard View

Adoptive T Cell Transfer for Cancer Immunotherapy in the Era of Synthetic Biology

Michael Kalos^{1,2}, Carl H. June^{1,2,3}

Open Archive

DOI: <http://dx.doi.org/10.1016/j.immuni.2013.07.002> |  CrossMark

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Review

Cite this article: June CH, Levine BL. 2015
T cell engineering as therapy for cancer and
HIV: our synthetic future. *Phil. Trans. R. Soc. B*
370: 20140374.
<http://dx.doi.org/10.1098/rstb.2014.0374>

Accepted: 3 July 2015

One contribution of 13 to a discussion meeting
issue 'Cells: from Robert Hooke to cell
therapy—a 350 year journey'.

T cell engineering as therapy for cancer and HIV: our synthetic future

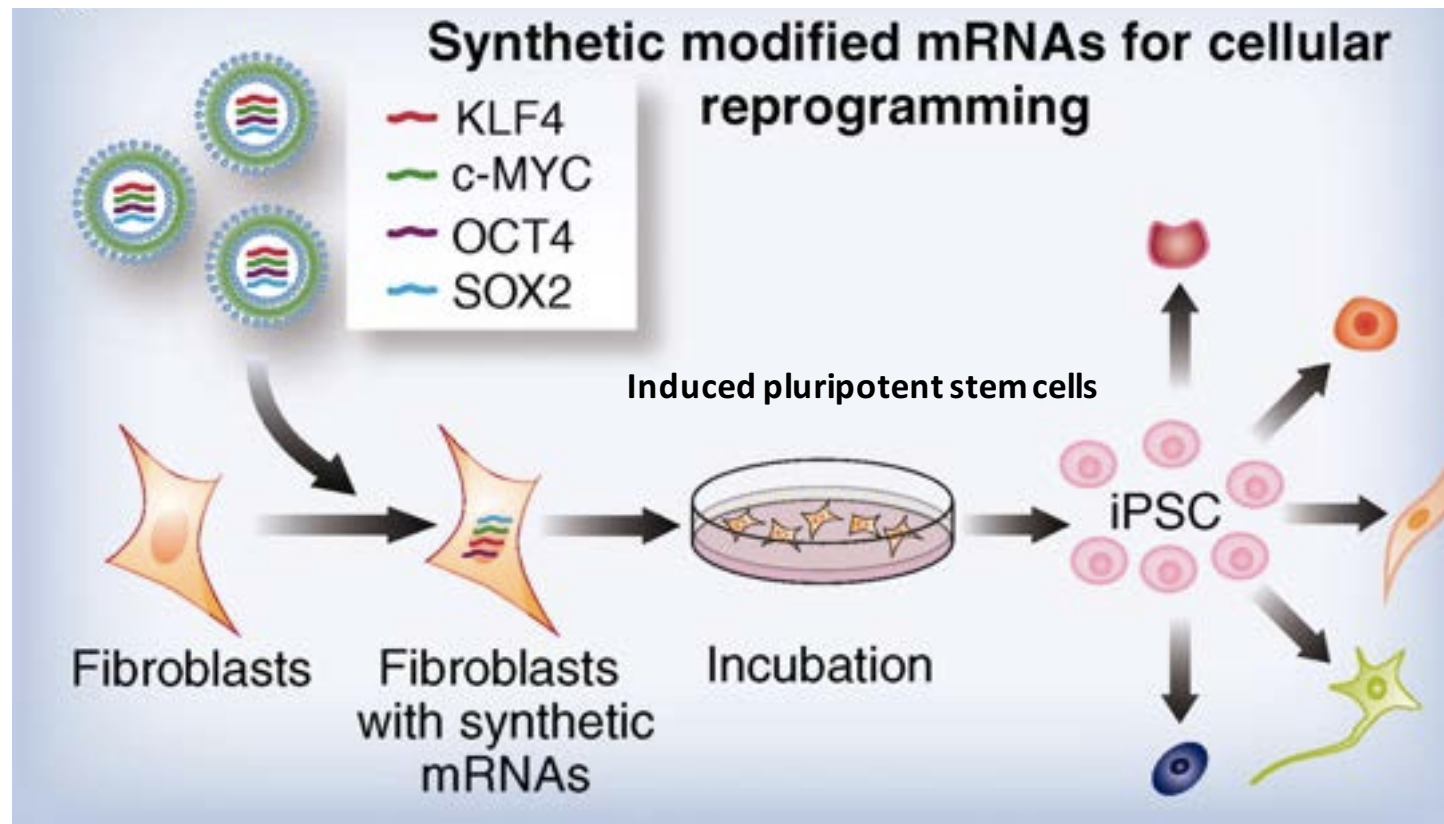
Carl H. June^{1,2,3} and Bruce L. Levine^{2,3}

¹Abramson Family Cancer Research Institute, ²Center for Cellular Immunotherapies, and ³Department of Pathology and Laboratory Medicine, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA 19104-5156, USA

It is now well established that the immune system can control and eliminate cancer cells. Adoptive T cell transfer has the potential to overcome the significant limitations associated with vaccine-based strategies in patients who are often immune compromised. Application of the emerging discipline of synthetic biology to cancer, which combines elements of genetic engineering and molecular biology to create new biological structures with enhanced functionalities, is the subject of this overview. Various chimeric antigen receptor designs, manufacturing processes and study populations, among other variables, have been tested and reported in recent clinical trials. Many questions remain in the field of engineered T cells, but the encouraging response rates pave a wide road for future investigation into fields as diverse as cancer and chronic infections.

WHAT IF ?

Systematic cellular reprogramming



Cell therapy and regenerative medicine

Highly Efficient Reprogramming to Pluripotency and Directed Differentiation of Human Cells with Synthetic Modified mRNA

Luigi Warren,^{1,17} Phillip D. Manos,^{2,4,17} Tim Ahfeldt,^{4,6,7,18} Yui-Han Loh,^{8,9,18} Hu Li,^{11,12,18} Frank Lau,^{4,13} Wataru Ebina,¹ Pankaj K. Mandal,¹ Zachary D. Smith,^{1,4} Alexander Meissner,^{4,5,14} George Q. Daley,^{2,3,4,5,8,15,16} Andrew S. Brack,^{5,6} James J. Collins,^{11,12,16} Chad Cowan,^{4,5,6,13} Thorsten M. Schlaeger,^{2,8} and Derrick J. Rossi^{1,2,5,10,*}

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²Stem Cell Program

³Manton Center for Orphan Disease Research
Children's Hospital Boston, Boston, MA 02115, USA

⁴Department of Stem Cell and Regenerative Biology

⁵Harvard Stem Cell Institute

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⁶Center of Regenerative Medicine, Massachusetts General Hospital, 185 Cambridge Street, Boston, MA 02114-2790, USA

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⁹Department of Biological Chemistry and Molecular Pharmacology

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¹²Wyss Institute for Biologically Inspired Engineering, Harvard University, Boston, MA 021

¹³Stowers Medical Institute, 185 Cambridge Street, Boston, MA 02114, USA

¹⁴Broad Institute of MIT and Harvard, Cambridge, MA 02142, USA

¹⁵Howard Hughes Medical Institute

¹⁶Division of Hematology/Oncology, Brigham and Women's Hospital, Boston, MA 02115,

¹⁷These authors contributed equally to this work

¹⁸These authors contributed equally to this work

*Correspondence: rossi@idi.harvard.edu

DOI 10.1016/j.stem.2010.08.012

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NATURE REVIEWS MOLECULAR CELL BIOLOGY | REVIEW

Synthetic biology in mammalian cells: next generation research tools and therapeutics

Florian Lienert, Jason J. Lohmueller, Abhishek Garg & Pamela A. Silver

[Affiliations](#) | [Corresponding author](#)

Nature Reviews Molecular Cell Biology 15, 95–107 (2014) | doi:10.1038/nrm3738

online 17 January 2014

NATURE METHODS | BRIEF COMMUNICATION

Cas9 gRNA engineering for genome editing, activation and repression

Samira Kiani, Alejandro Chavez, Marcelle Tuttle, Richard N Hall, Raj Chari, Dmitry Ter-Ovanesyan, Jason Qian, Benjamin W Pruitt, Jacob Beal, Suhani Vora, Joanna Buchthal, Emma J K Kowal, Mohammad R Ebrahimkhani, James J Collins, Ron Weiss & George Church

[Affiliations](#) | [Contributions](#) | [Corresponding authors](#)

Nature Methods (2015) | doi:10.1038/nmeth.3580

Received 12 April 2015 | Accepted 10 August 2015 | Published online 07 September 2015

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We demonstrate that by altering the length of Cas9-associated guide RNA (gRNA) we were able to control Cas9 nuclease activity and simultaneously perform genome editing and transcriptional regulation with a single Cas9 protein. We exploited these principles to engineer mammalian synthetic circuits with combined transcriptional regulation and kill functions governed by a single multifunctional Cas9 protein.

October 2015

Gerontology Online First

Section title: Regenerative and Technological Section /
Viewpoint

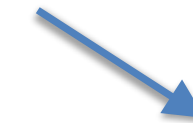
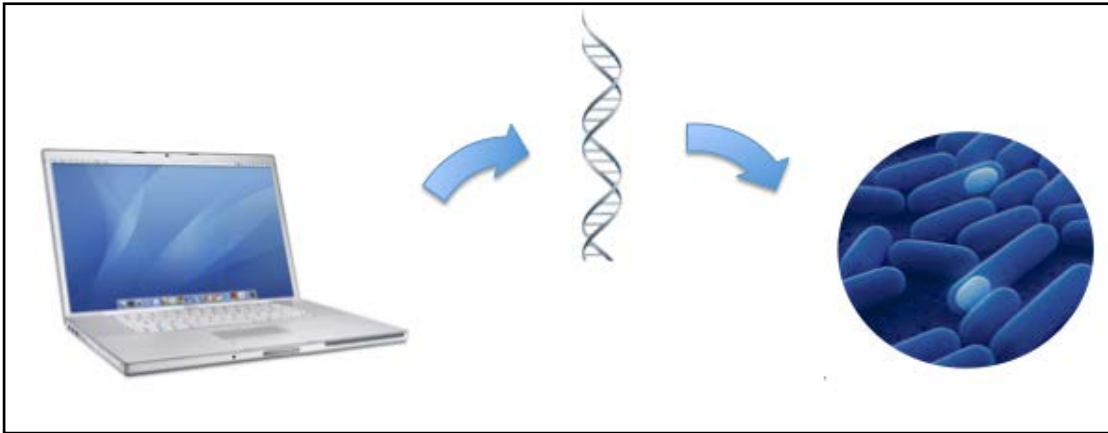
Gerontology
(DOI:10.1159/000440721)

Synthetic Biology: Rational Pathway Design for Regenerative Medicine

Davies J.A.

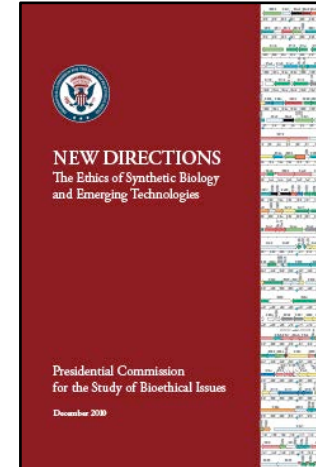
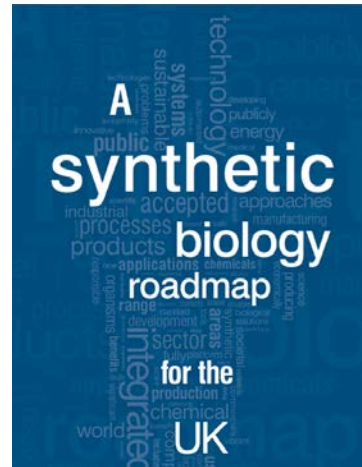
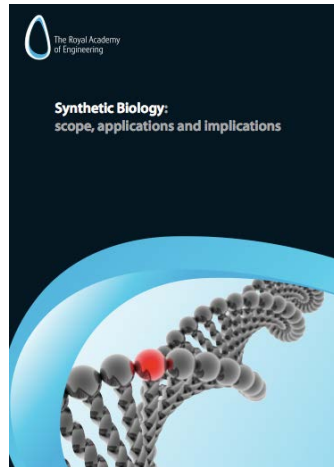
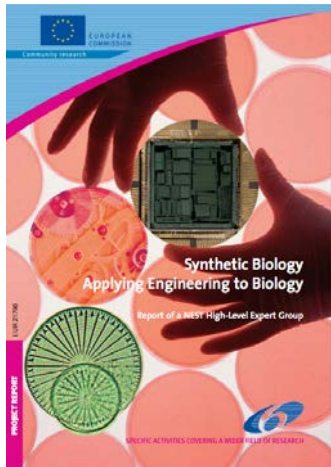
Centre for Integrative Physiology, University of Edinburgh, Edinburgh, UK

WHAT IF ?



So why is synthetic biology causing such a big fuss?

“Synthetic biology aims to design and engineer biologically based parts, novel devices and systems as well as redesigning existing, natural biological systems”



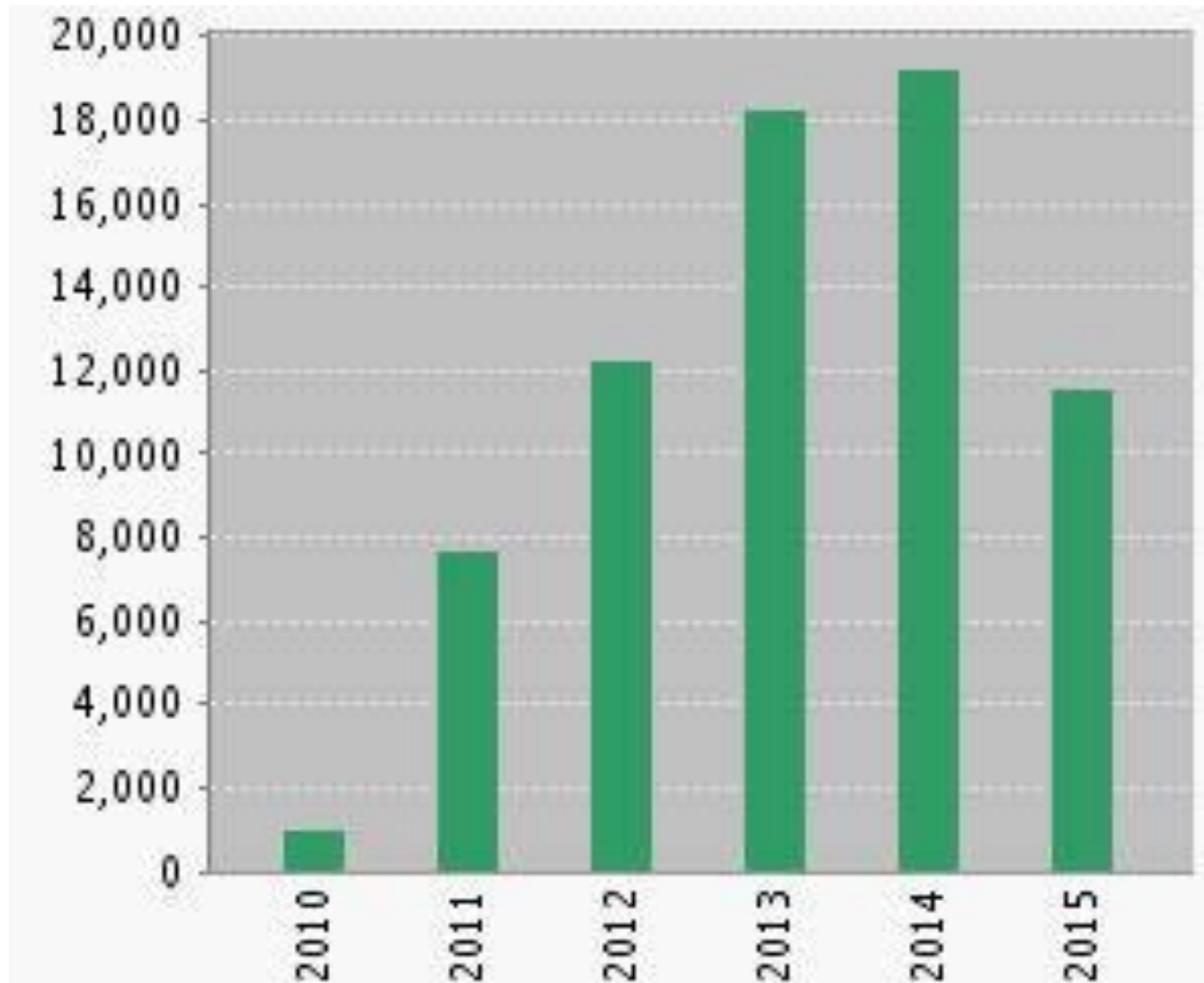
SCHER, SCENIHR, SCCS

operational definition for Synthetic Biology

“SynBio is the application of science, technology and engineering to facilitate and accelerate the design, manufacture and/or modification of genetic materials in living organisms.”



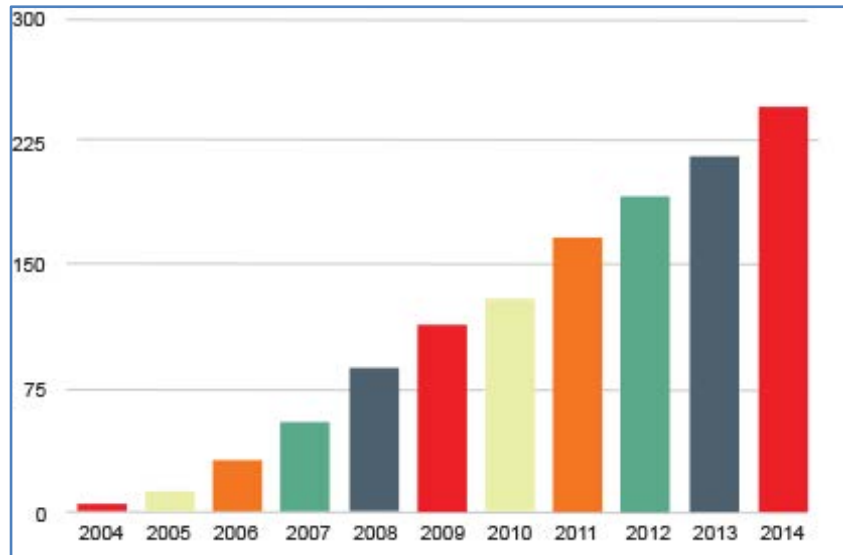
Synthetic Biology is a rapidly growing field



Citations of papers containing key works synthetic biology **70256 - 47,000 papers since 2001**

A growing community of student researchers – growth of iGEM

International Genetically Engineered Machine Competition



280 teams are registered for 2015
259 teams at the Jamboree
~15,000 iGEM alumni



Synthetic Biology has a powerful vision for merging engineering design practice into the construction of biology systems and cells at the genetic level

An engineering design framework for Synthetic Biology

- (1) *System control* (feed-back/ feed-forward biological control networks)
- (2) *Redundancy* (gene duplication/ multiple regulatory pathways)
- (3) *Modular design* (evolutionary robust / multi-functional / compartmental)
- (4) *Structural stability* (homeostasis)

Hypothesis – Are these also intrinsic features of complex natural living systems?

A systematic engineering framework for biological systems aims to test the hypothesis

Can we use Biology to Build new Biology?

Can we learn about biology through design and construction?

- Biological systems are modular
- Biological function is primarily encoded in DNA
- Large knowledge base of genome sequences
- Large diversity of biological parts (genes/regulatory)
- Increased understanding of molecular / cell biology
- New technologies to synthesize and assemble DNA

However.....

Standardising biology poses challenges

- Biology is not fully 'plug and play'
 - Context dependency
 - Evolution, adaptation and natural selection
 - Non-predictive stochastic behaviour
 - Self assembly and emergent properties
 - Non-linear dynamical processes
 - Multi-scale interactions



- Living cells have constrained volumes and high concentrations of biochemical components

One approach to overcome
biological complexity in
engineering biology is the use
of **Systematic Design**

What is Systematic Design ?

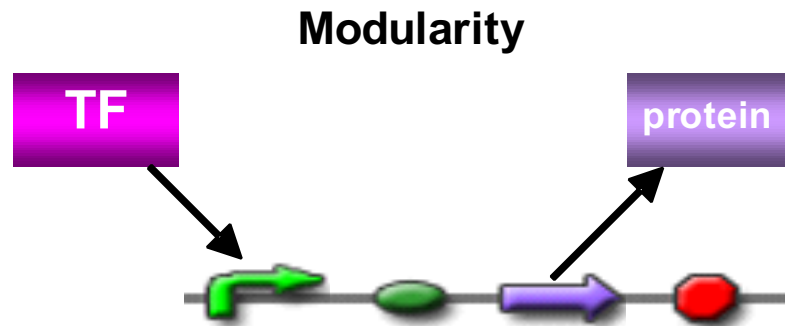
Systematic design is founded on the following engineering principles

- Modularisation – interchangeable modules
- Standardisation – standard parts and processes
- Abstraction – reducing complexity

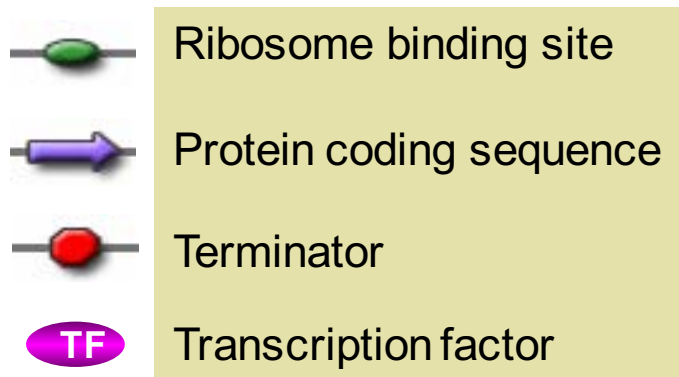
Systematic design aims to achieve
Robustness and Reproducibility

Key requirement is interoperability

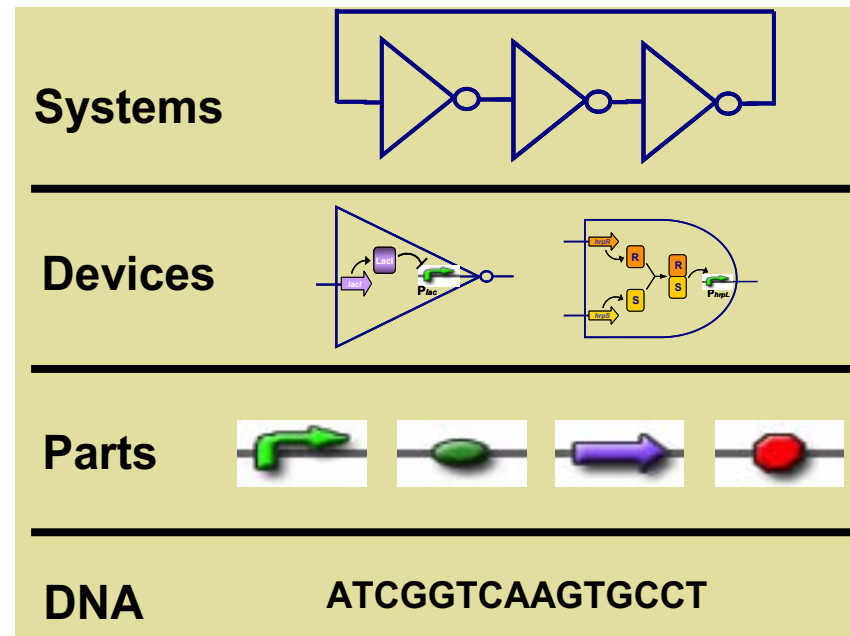
A systematic design framework using genetic parts that encode biological function



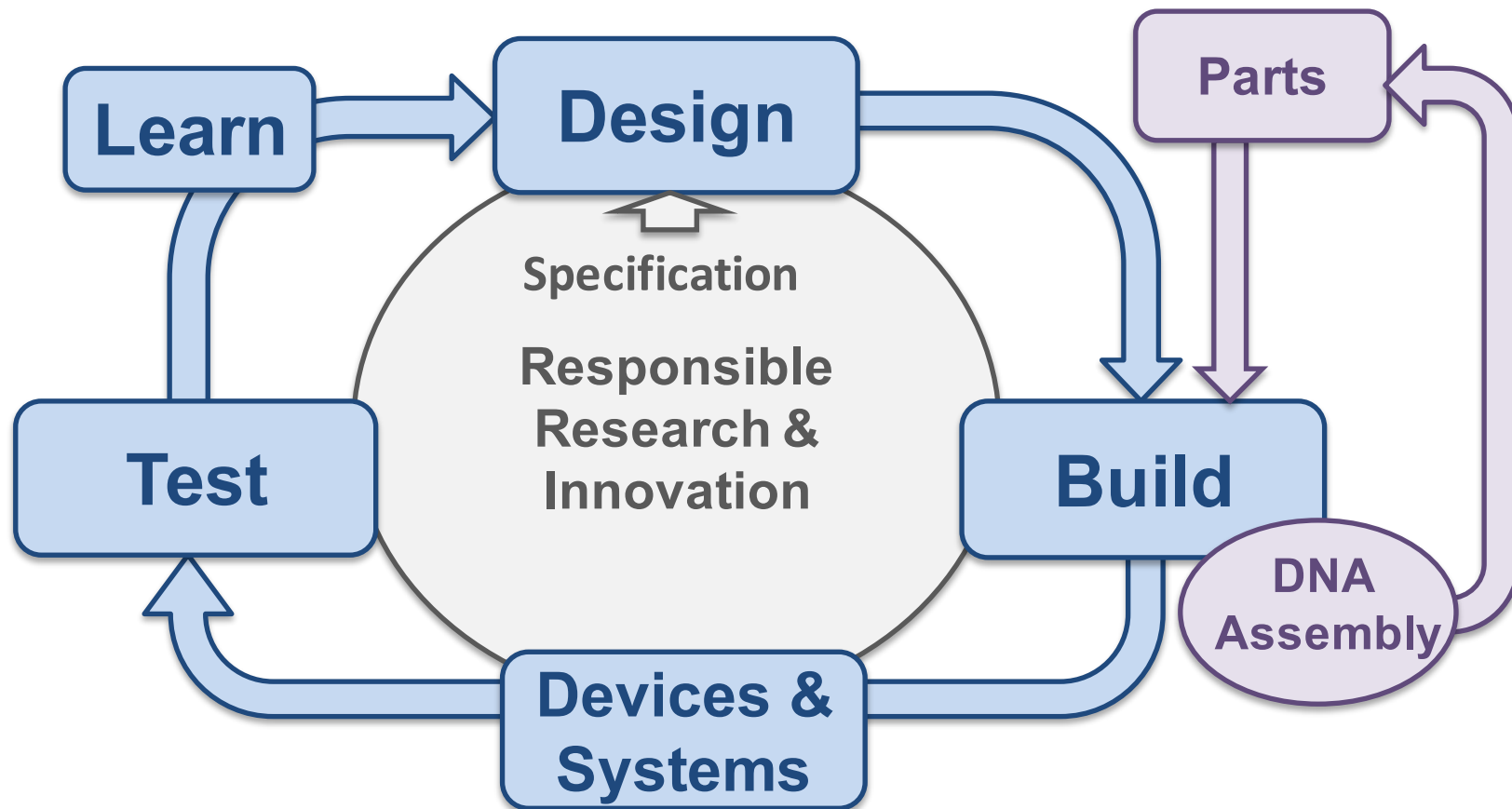
Typical gene transcription module



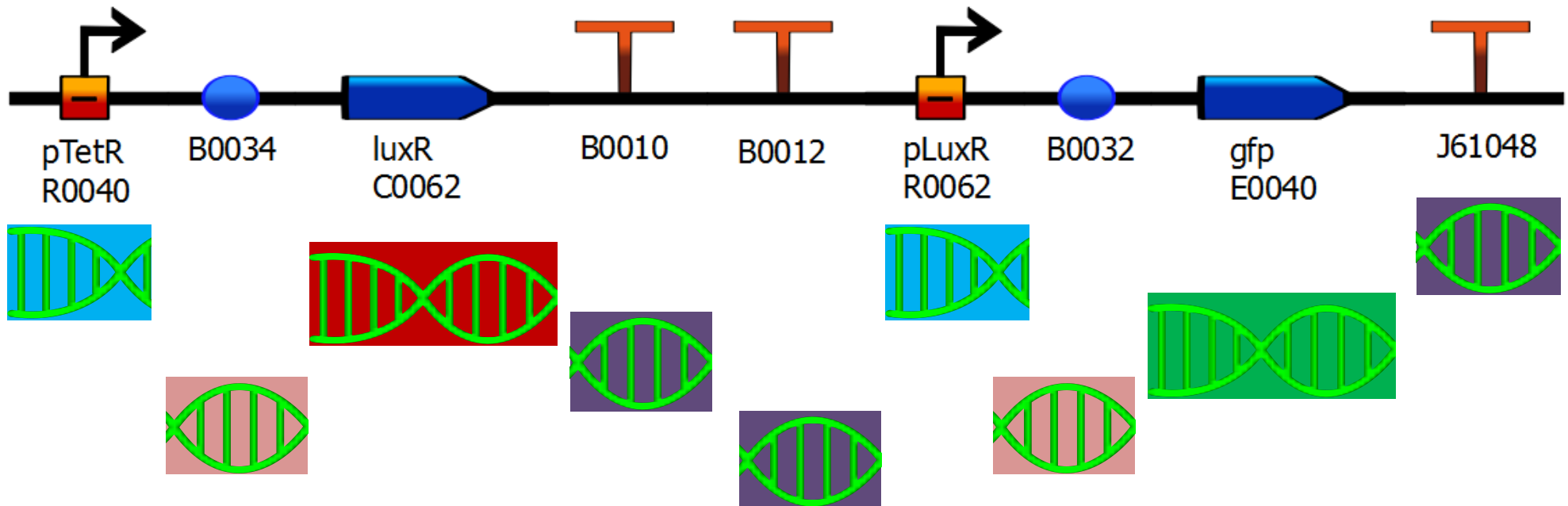
Abstraction hierarchy



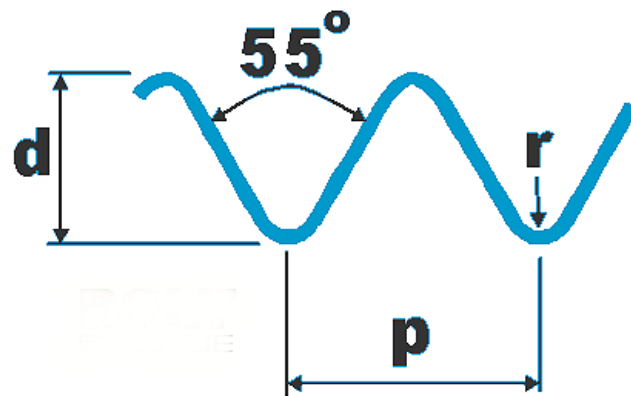
A systematic **DESIGN CYCLE** for Synthetic Biology



Can we build new biological systems with standardised DNA Parts?

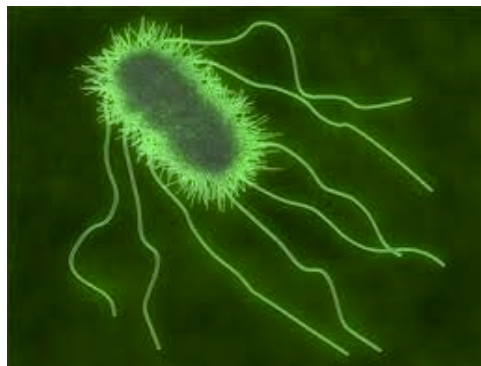
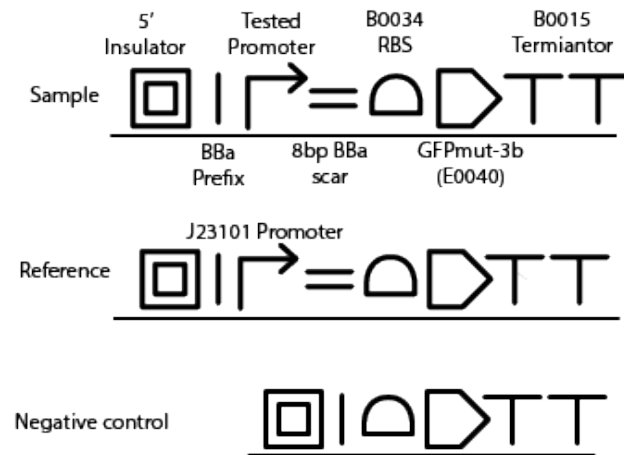


To enable forward engineering the synthetic biology field needs to develop standards



The first standard thread Sir Joseph Whitworth 1841

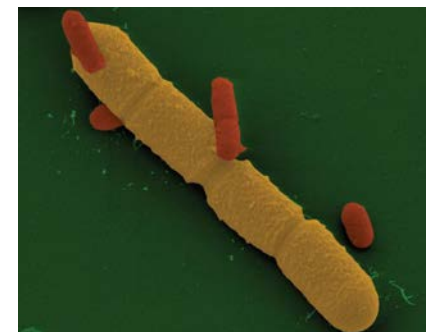
How do we standardise the construction of living matter?



E. coli



B. subtilis



Bacillus megaterium

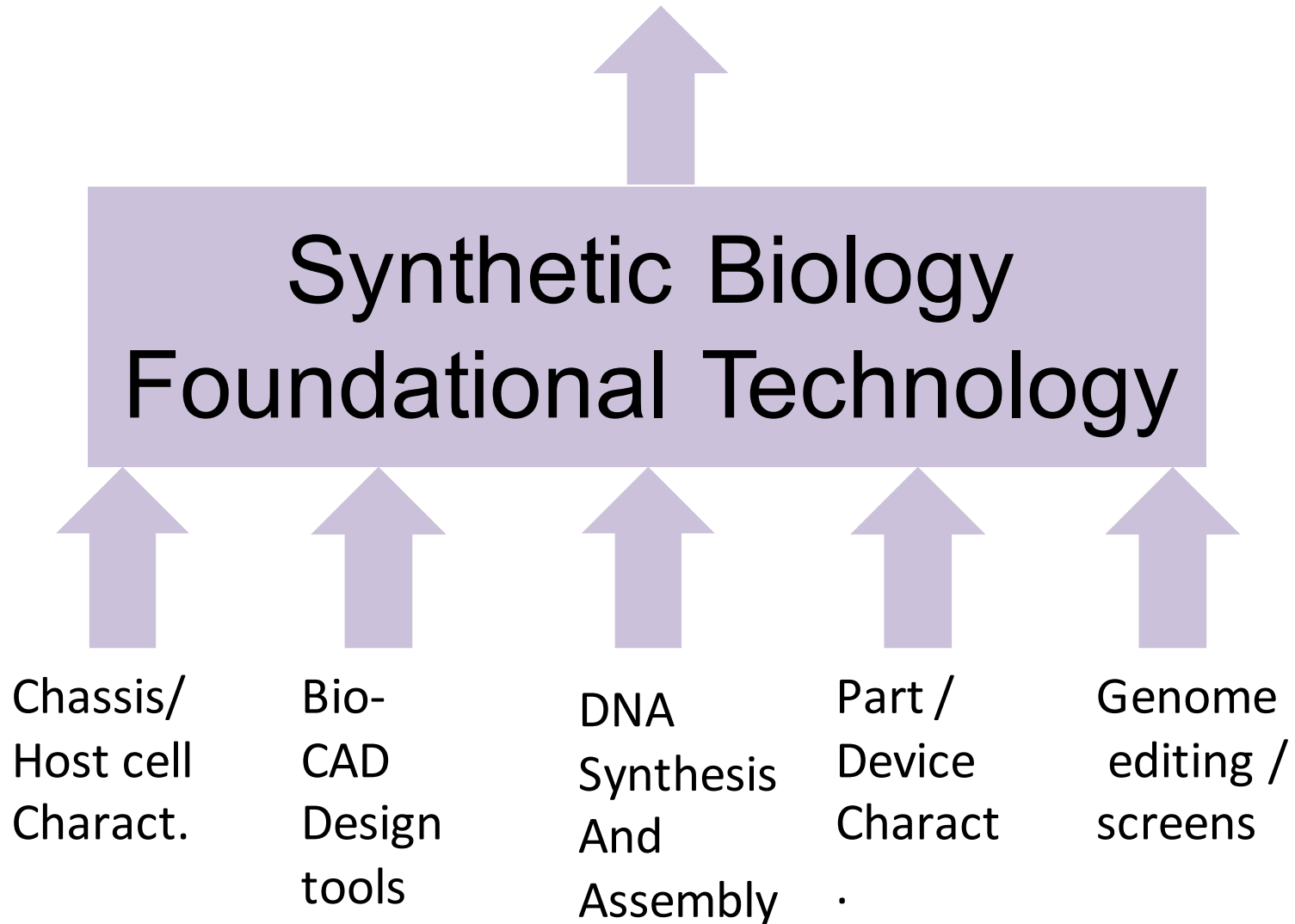
Standards development in synthetic biology

- Standard interchangeable biological parts



- Physical standards (DNA)
 - Assembly standards (may not be needed with increasing DNA synthesis)
- Functional standards
 - Standard culture conditions (media/temp/volume)
 - Standard measurements (e.g. Flow cytometry)
 - Standard strains of cell hosts or chassis
- Digital Information standards
 - SBOL
 - SBML
 - DICOM-SB

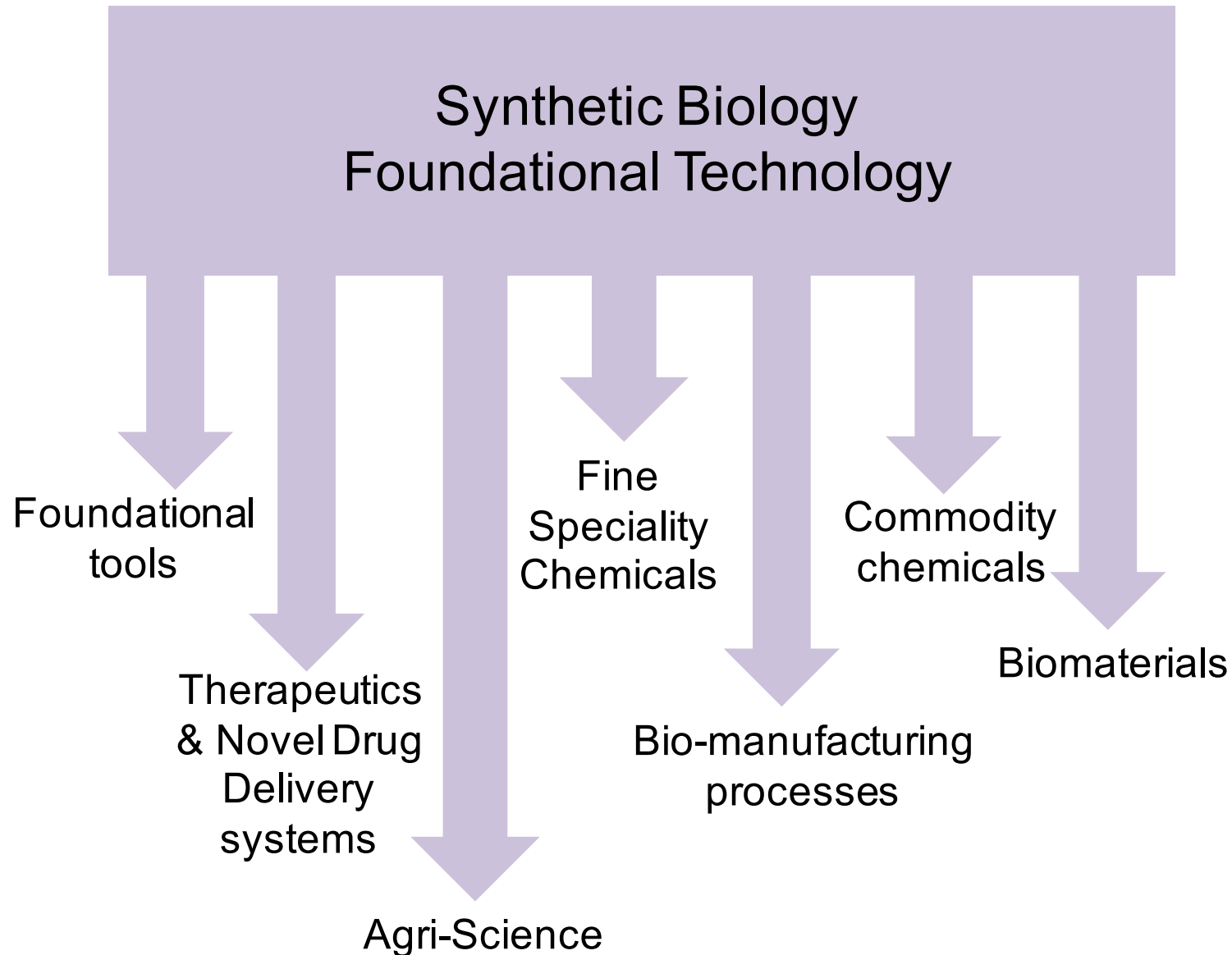
Different applications



Current Synthetic Biology research trends

- Engineering of biological systems
 - Refactoring and Redesigning
 - Genome editing
 - Genome construction
 - Automation, standards and tools
 - Deskillling and open source
- Creating alternative biological systems
 - exobiology/XNA
 - Artificial cell and Cell free systems

Synthetic Biology application trends



DESIGN



Available Bio-Design Tools

Pathway and circuit design

MATLAB: Simbiology <http://www.mathworks.co.uk/products/simbiology/>

OptCom <http://maranas.che.psu.edu/software.htm>

Genetic Engineering of Cells (GEC) <http://research.microsoft.com/en-us/projects/gec/>

Cell designer <http://www.celldesigner.org/>

ProMoT <http://www.mpi-magdeburg.mpg.de/projects/promot/>

GenoCAD <http://www.genocad.org/>

Operon calculator https://salis.psu.edu/software/OperonCalculator_EvaluateMode

Biopart design

Rosetta. <http://maranas.che.psu.edu/software.htm>

Cadnano. <http://cadnano.org/>

NUPAC <http://www.nupack.org/>

RNA Designer <http://www.rnasoft.ca/cgi-bin/RNAsoft/RNAdesigner/rnadesign.pl>

mfold/UNAFold <http://mfold.rna.albany.edu/>

RBS Calculator <https://salis.psu.edu/software>

RBS Designer <http://rbs.kaist.ac.kr>

UTR designer http://sbi.postech.ac.kr/utr_designer

Miscellaneous

R2oDNA Designer <http://r2odna.com/>

SBOL <http://www.sbolstandard.org/>

SBOLv <http://www.sbolstandard.org/visual>

Part registries worldwide

CSynBI
Centre for Synthetic Biology and Innovation

Promoter Database

Search Upload Home

Upload Data

Search

Feedback

The CSynBI Database team can be reached at csynbiob@gmail.com. We would be grateful to you if you could report what issues you have encountered. We are also very interested in any suggestions you may have on how to improve the current version database and on how to expand its scope in the next versions.

Welcome to the Csynbi Database (Version beta)

The Csynbi database has been created and designed so the Synthetic Biology community could easily store and share the results of characterisation experiments of promoters. Version beta of the database only deals with constitutive promoters; later versions will support a wider range of biobricks.

To upload new data, simply select the 'upload' option, enter the details of the characterisation experiment and finally upload the data. To download data, select the 'search' option, enter the search criteria and download the datasets of interest.

Navigation

Both upload and search functions of the database can be accessed at any point by clicking on the quick navigation buttons in the top panel.



Registry of Standard Biological Parts

Go Search

page discussion view source history Log in / create account


Welcome to the Registry of Standard Biological Parts.


The Registry is a **continuously growing** collection of genetic parts that can be mixed and matched to build synthetic biology devices and systems. Founded in 2003 at MIT, the Registry is part of the Synthetic Biology community's efforts to make biology easier to engineer. It provides a resource of available genetic parts to **IGEM** teams and academic labs. You can [register a new lab here](#).


The Registry is based on the principle of "get some, give some". Registry users benefit from using the parts and information available from the Registry in designing their engineered biological systems. In exchange, the expectation is that Registry users will, in turn, contribute back information and data on existing parts and new parts that they make to grow and improve this community resource.


Registry tools


- Search parts (?)
- Add a part
- Request a part
- Send parts to the Registry
- Sequence analysis

 [Catalog of parts & devices](#)

 [Help](#)

 [Users & groups](#)


 [DNA repositories](#)



search

Search this site: Search

home about projects services people data software





Joint BioEnergy Institute

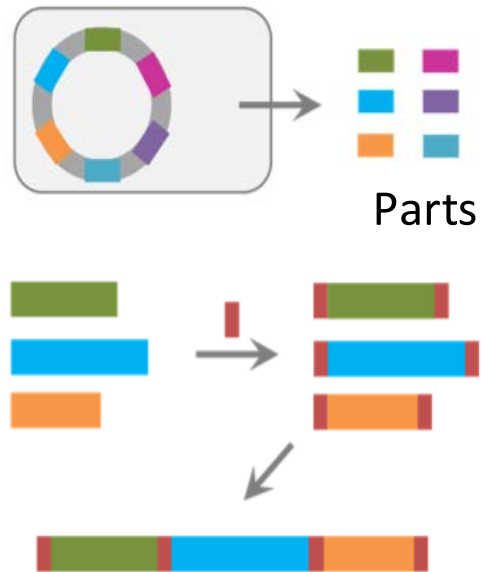


U.S. DEPARTMENT OF ENERGY

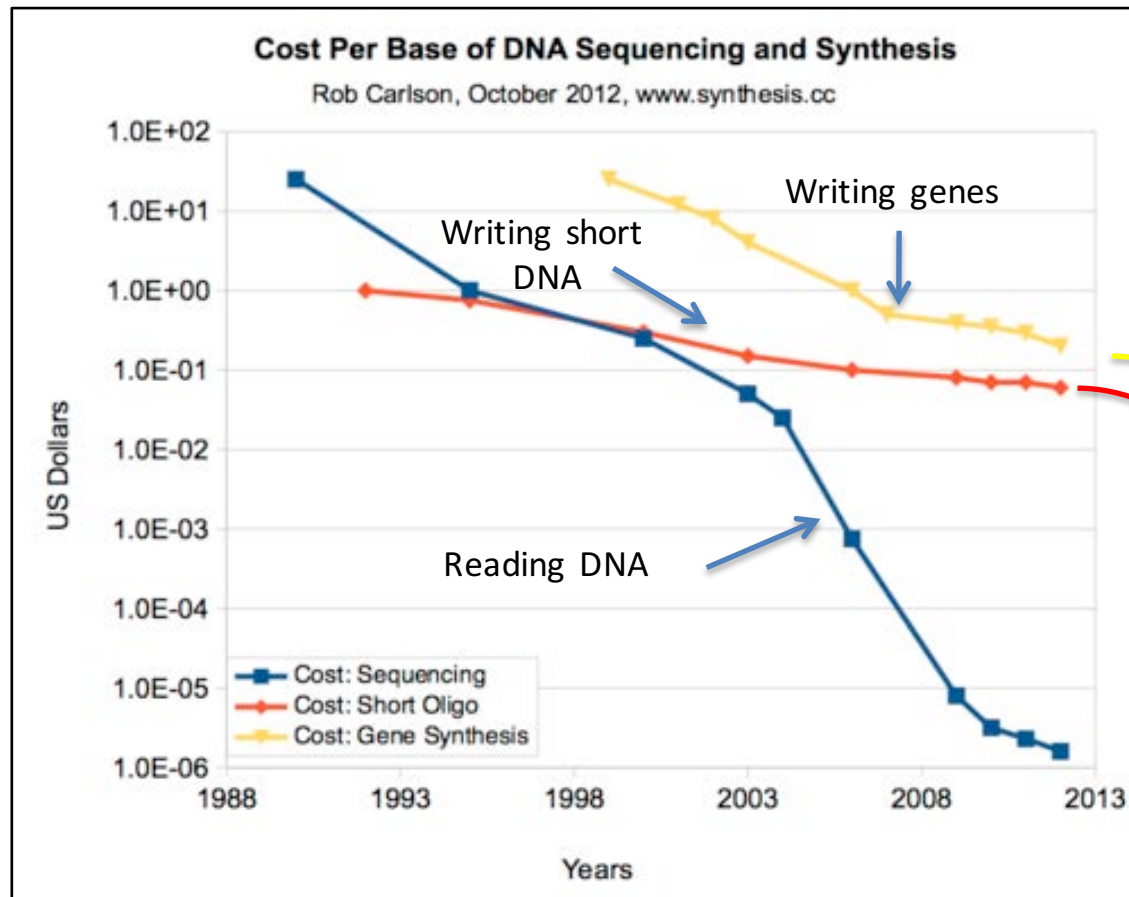
Search

ABOUT RESEARCH PEOPLE NEWS INDUSTRY

BUILD



Costs of DNA synthesis is driving the field



Cost per base

- sequencing ~ 0.000001 \$
- synthesis $\sim 0.10 - 0.28$ \$

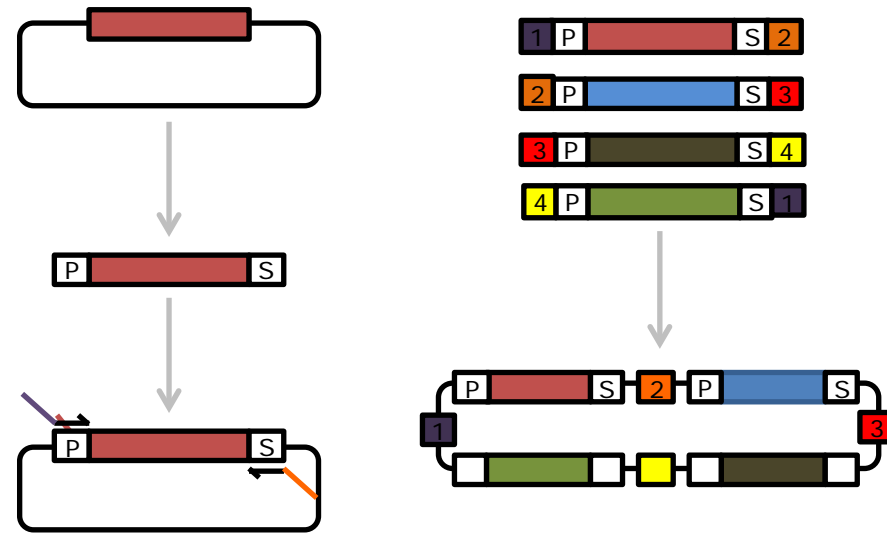
DNA assembly Standards

Tom Ellis, Geoff Baldwin

Interoperability

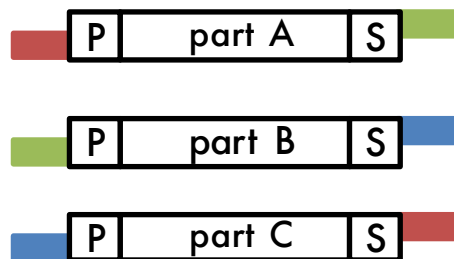
MODAL – Modular Overlap Directed Assembly with Linkers

(A. Casini et al NAR 2014a and 2014b)



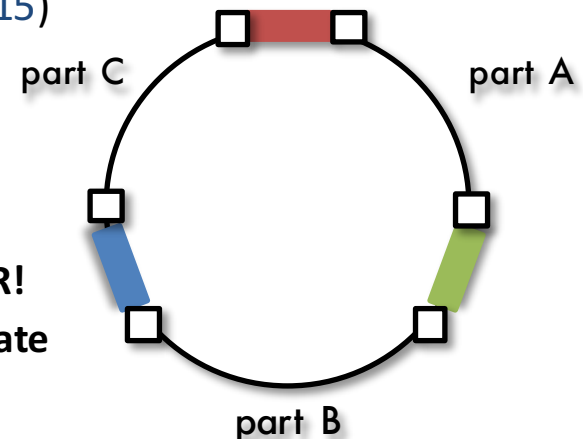
BASIC - Biopart Assembly Standard for Idempotent Cloning

M. Storch et al ACS Synbio 4 :791 (2015)



parts ligation

Long-overhang assembly No PCR!
Robust reactions easy to automate



Constructing Synthetic Yeast: Sc2.0

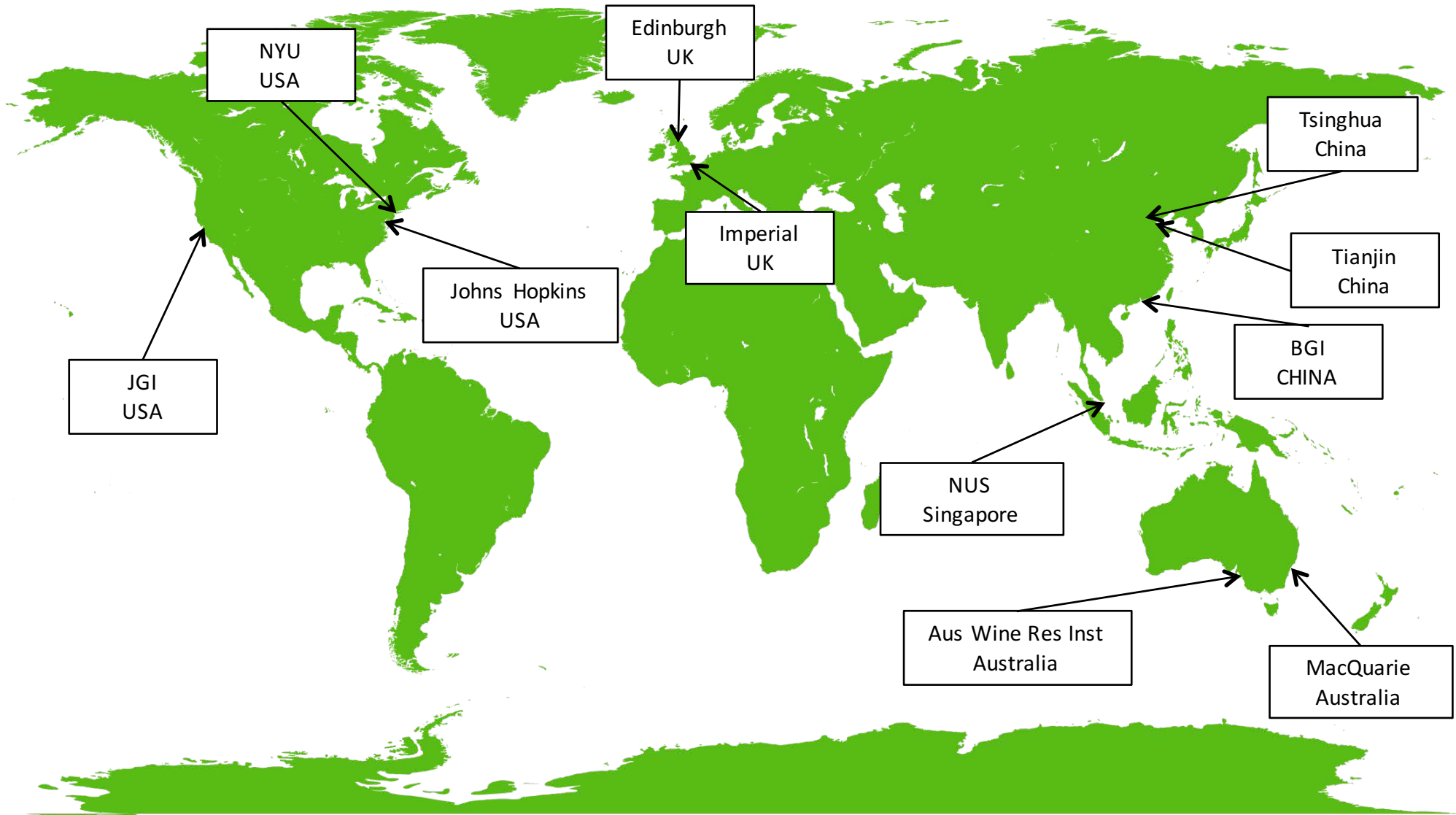
Design, Synthesise & Assemble a modified version of the *S. cerevisiae* genome 12 million bp and 16 chromosomes



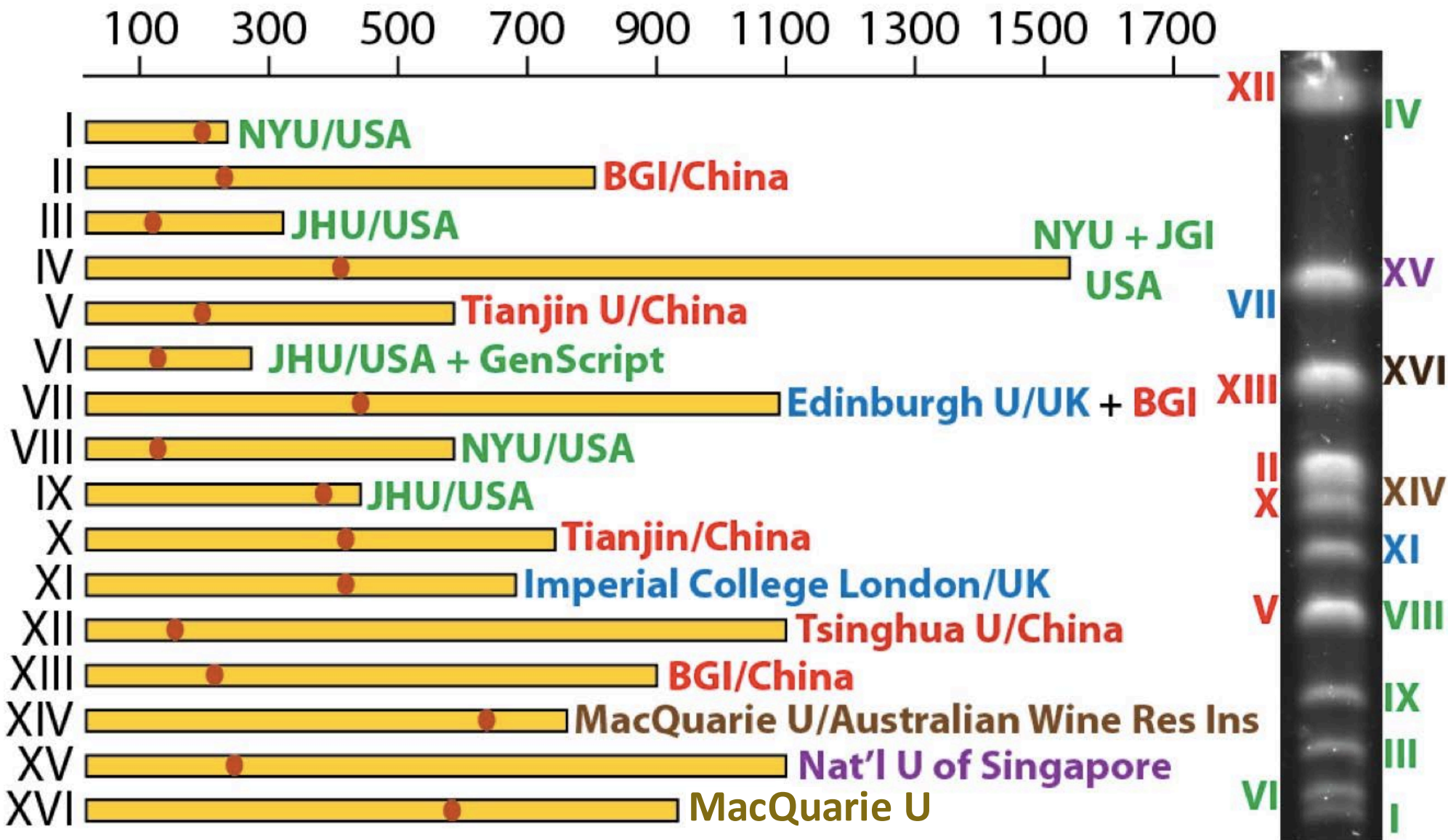
www.syntheticyeast.org
www.syntheticyeastresource.com

Jef Boeke (NY Medical School)

A global synthetic biology project



Sc2.0: 16 chromosomes, 12 million bp



2014 – Completed Syn Chromosome III

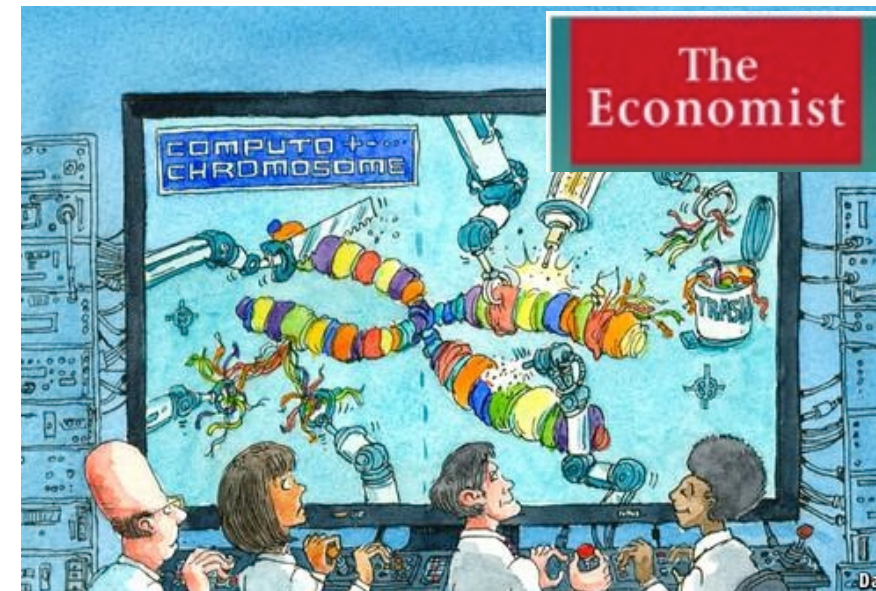
Scienceexpress

Research

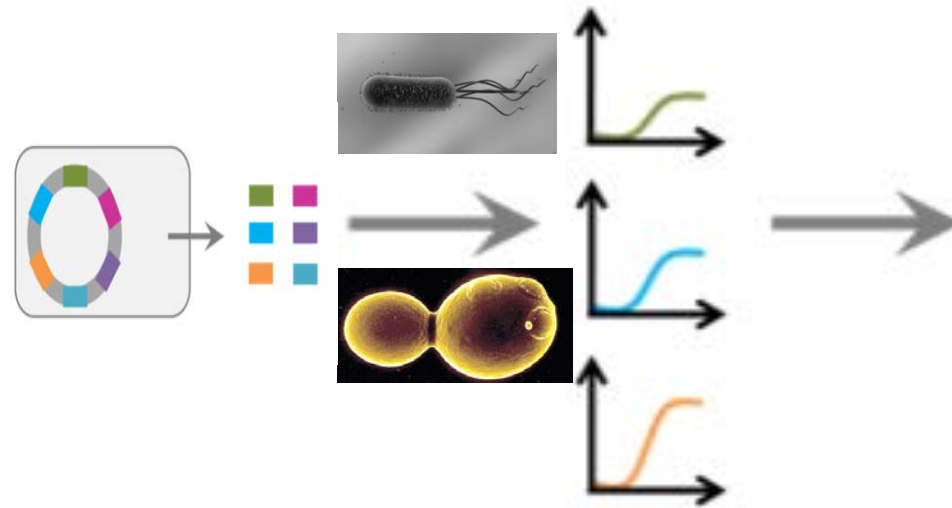
EMBARGOED UNTIL 2:00 PM US ET THURSDAY, 27 MARCH 2014

Total Synthesis of a Functional Designer Eukaryotic Chromosome

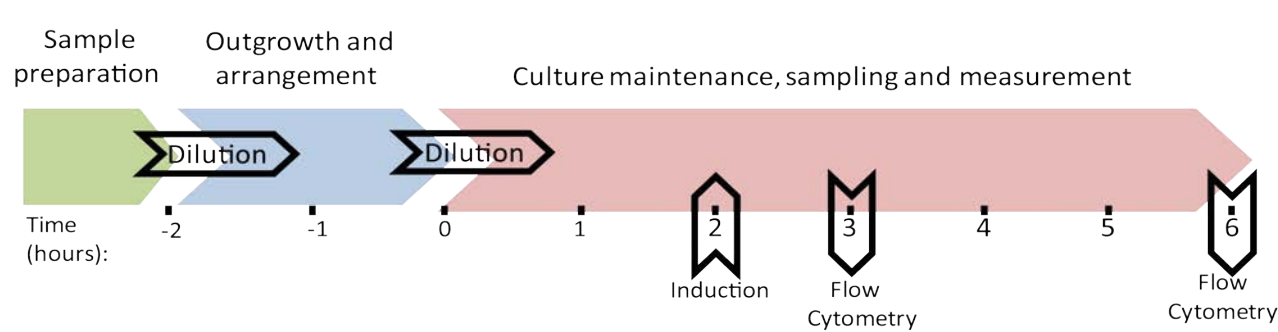
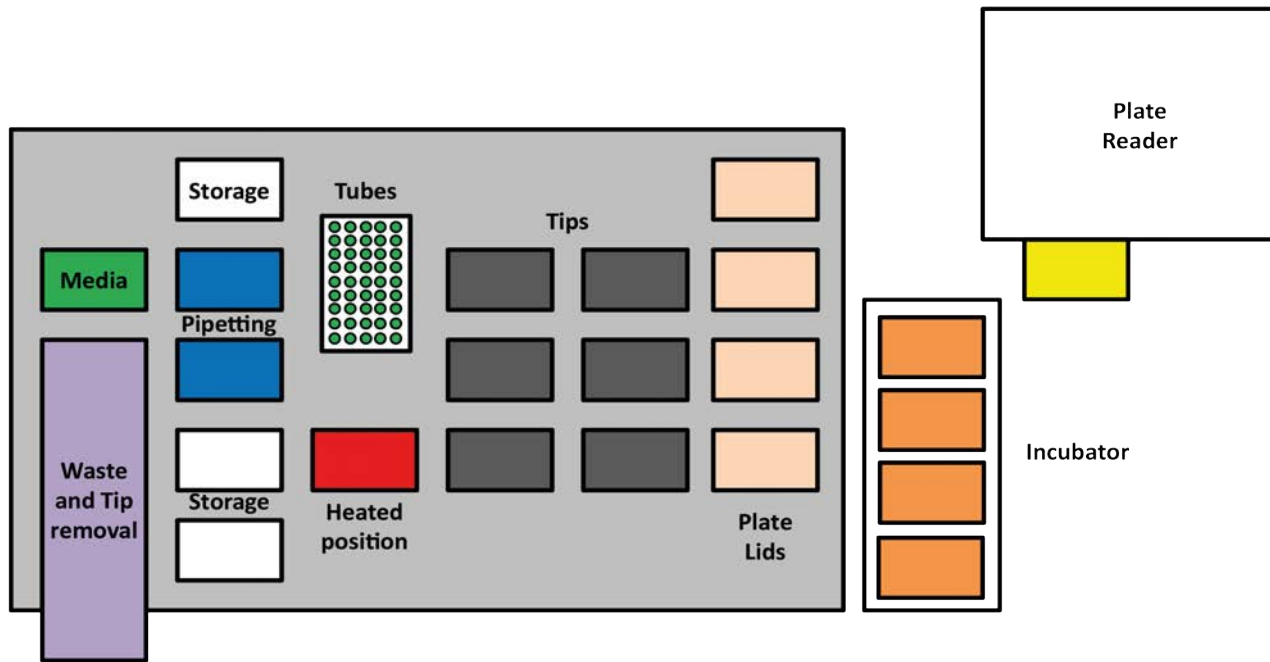
Narayana Annaluru,^{1*} Héloïse Muller,^{1,2,3,4*} Leslie A. Mitchell,² Sivaprakash Ramalingam,¹ Giovanni Stracquadanio,^{2,5} Sarah M. Richardson,⁵ Jessica S. Dymond,^{2,6} Zheng Kuang,² Lisa Z. Scheifele,^{2,7} Eric M. Cooper,² Yizhi Cai,^{2,8} Karen Zeller,² Neta Agmon,² Jeffrey S. Han,⁹ Michalis Hadjithomas,¹⁰ Jennifer Tullman,⁵ Katrina Caravelli,¹ Kimberly Cirelli,¹ Zheyuan Guo,¹ Viktoriya London,¹ Apurva Yeluru,¹ Sindurathy Murugan,⁵ Karthikeyan Kandavelou,^{1,11} Nicolas Agier,^{12,13} Gilles Fischer,^{12,13} Kun Yang,^{2,5} J. Andrew Martin,² Murat Bilgel,¹ Pavlo Bohutski,¹ Kristin M. Boulter,¹ Brian J. Capaldo,¹ Joy Chang,¹ Kristie Charoen,¹ Woo Jin Choi,¹ Peter Deng,¹ James E. DiCarlo,¹ Judy Doong,¹ Jessilyn Dunn,¹ Jason I. Feinberg,¹ Christopher Fernandez,¹ Charlotte E. Floria,¹ David Gladowski,¹ Pasha Hadidi,¹ Isabel Ishizuka,¹ Javaneh Jabbari,¹ Calvin Y. L. Lau,¹ Pablo A. Lee,¹ Sean Li,¹ Denise Lin,¹ Matthias E. Linder,¹ Jonathan Ling,¹ Jaime Liu,¹ Jonathan Liu,¹ Mariya London,¹ Henry Ma,¹ Jessica Mao,¹ Jessica E. McDade,¹ Alexandra McMillan,¹ Aaron M. Moore,¹ Won Chan Oh,¹ Yu Ouyang,¹ Ruchi Patel,¹ Marina Paul,¹ Laura C. Paulsen,¹ Judy Qiu,¹ Alex Rhee,¹ Matthew G. Rubashkin,¹ Ina Y. Soh,¹ Nathaniel E. Sotuyo,¹ Venkatesh Srinivas,¹ Allison Suarez,¹ Andy Wong,¹ Remus Wong,¹ Wei Rose Xie,¹ Yijie Xu,¹ Allen T. Yu,¹ Romain Koszul,^{3,4} Joel S. Bader,^{2,5} Jef D. Boeke,^{2,10,14} † Srinivasan Chandrasegaran¹ †



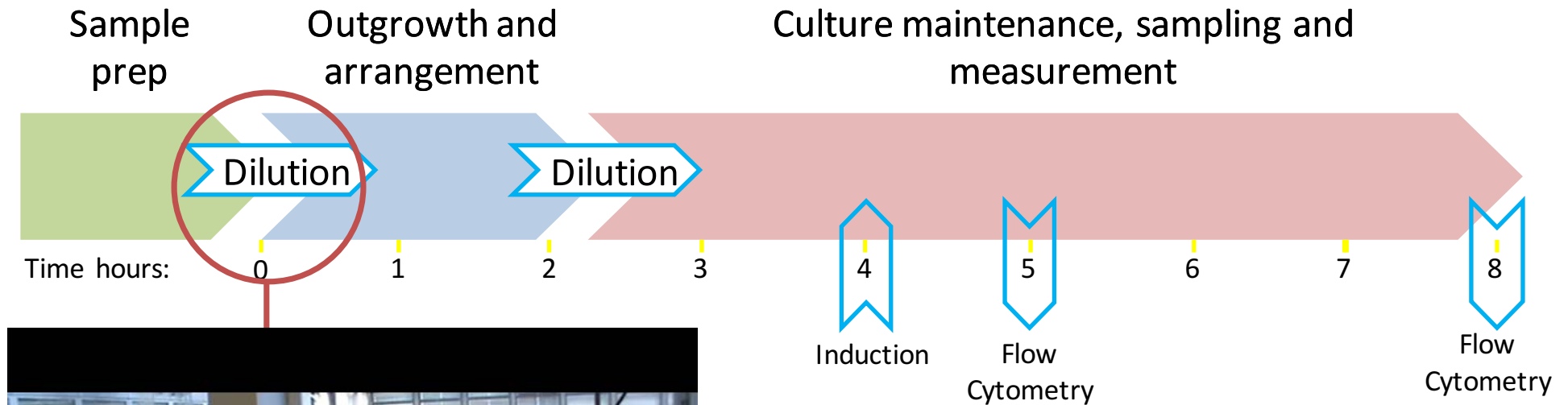
TEST



Automation characterisation platform v1.0



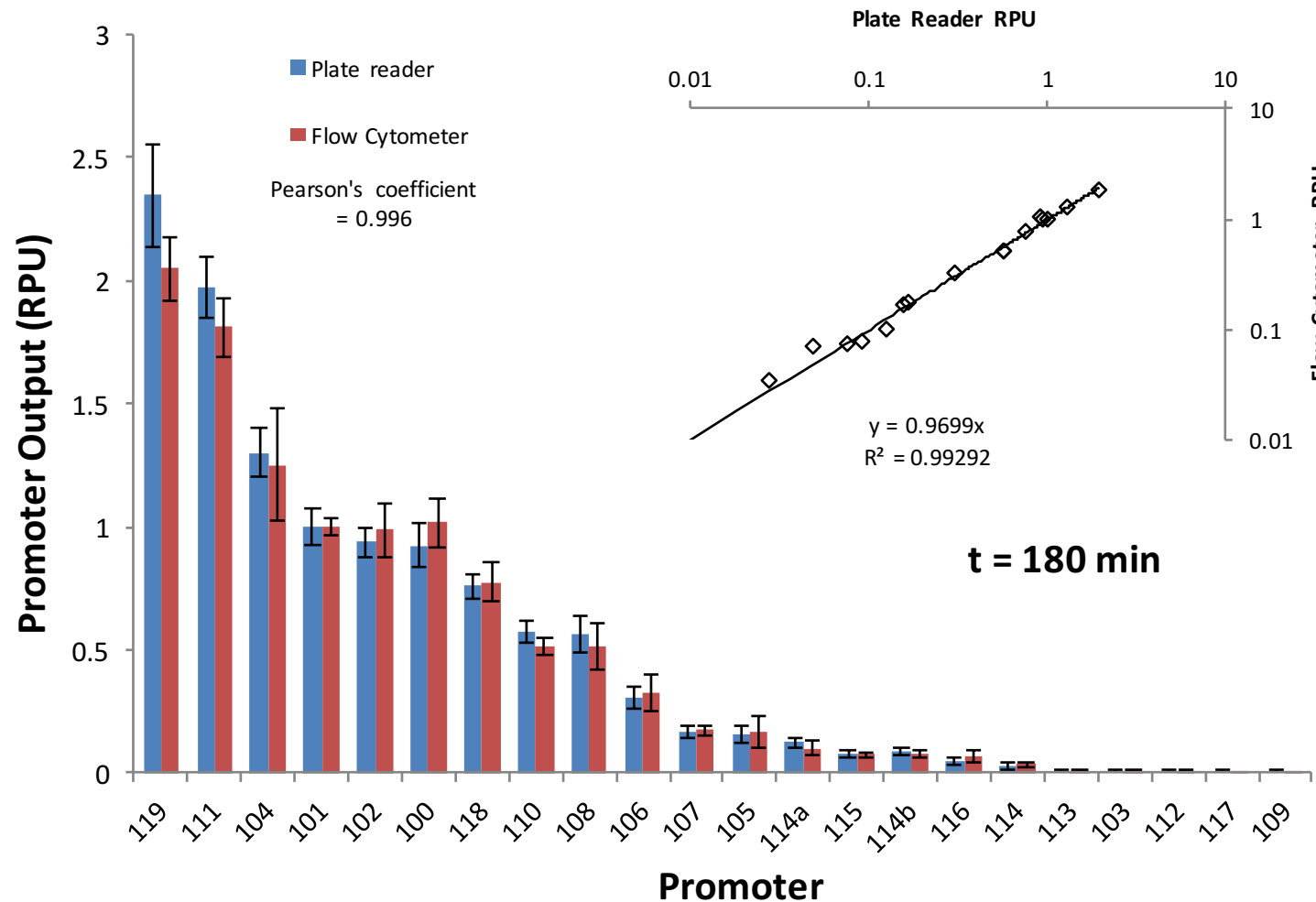
Automation characterisation platform v1.0



C. Hirst, R. Kitney, G. Baldwin

- Cells kept at similar phase of growth
 - Ensure high quality data
 - Ensures cells are at an appropriate population for assay
- Growth and measurement separated
 - Reduces noise in data
 - Greatly reduces evaporation

Anderson 22x promoter characterisation




Single cell versus population measurements show high degree of correlation

C. Hirst, R. Kitney, G. Baldwin

Data Sheets for Parts and SynBIS

Imperial College London **Bio-Part Data Sheet** **J23100** CSynBI Centre for Synthetic Biology and Innovation

Constitutive Promoter



J23100 Sequence

TTGACGGCTAGCTCAGTCC
TAGGTACAGTGCTAGC

Unregulated

E. coli DH10B

37°C O₂

Rich MOPS Glucose

P15a KnR

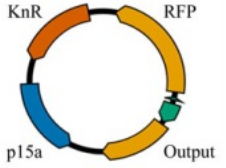
GFP mut3b


Main Results at 3 hours

Microplate Data		Flow Cytometry Data	
RPU (no units)	0.89 ± 0.19	RPU (no units)	0.88 ± 0.49
Synthesis Rate (GFP molecules /cell * hour)	29.2 ± 7.4	Fluorescence (arbitrary units)	1140 ± 820

Growth Data	Doubling Rate	318 ± 140 mins/doubling
	Doubling Rate Change	+20.5%

Genetic Context





Transcript: I13504 (B0034 Reference)

08/05/2013

Page 1 (Main)

Imperial College London **Bio-Part Data Sheet** **J23100** CSynBI Centre for Synthetic Biology and Innovation

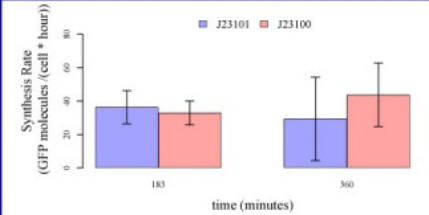
Context Summary

37°C O₂

Rich MOPS Glucose

Lag: 0 mins

Synthesis Rate



Data

9 Repeats

9 Controls

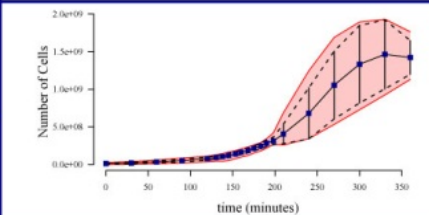
9 References

• Data Average

■ Envelope

⊥ Standard Deviation

Absorbance



Data

9 Repeats

9 Controls

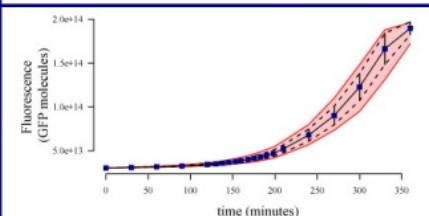
9 References

• Data Average

■ Envelope

⊥ Standard Deviation

Fluorescence



Page 2 (Plate Reader Results)

Bio-Part Data Sheet **J23100** CSynBI

Sequence: `ttgacggctagctcagtcc`

Context: Unregulated, Rich MOPS Glucose, P15a KnR, GFP mut3b, E-Coli DH10B, 37°C O₂

Main Results

Plate Reader	Medium	Flow Cytometry	Medium
RPU (no units)	0.9 ± 0.2	RPU (no units)	0.97 ± 0.16
Synthesis rate (GFP molecules /cell * hour)	7600 ± 500	Synthesis rate (GFP molecules /cell * hour)	7060 ± 500

Growth Data

Doubling Rate	173 ± 50 mins
Doubling Rate Change	-32.4 %

Genetic Context

Transcript: I13504 (B0034 Reference)

Copy Number: 1.00

Flowers Consortium
9-10 May 2013
Imperial College London

Automation characterisation platform v2.0 @Imperial College



CyBio

An Analytik Jena Company

Summary

- Automation and standardised metrology is accelerating the application of synthetic biology
- Data for part / device characterisation is being shared openly
- New chassis are being constructed e.g. Sc2.0
- Standards are being developed and shared
- Huge growth and interest by younger researchers
- Non-biologists are now doing synthetic biology e.g. Engineers
- Significant growth of community labs worldwide- see (www.biobuilder.org)