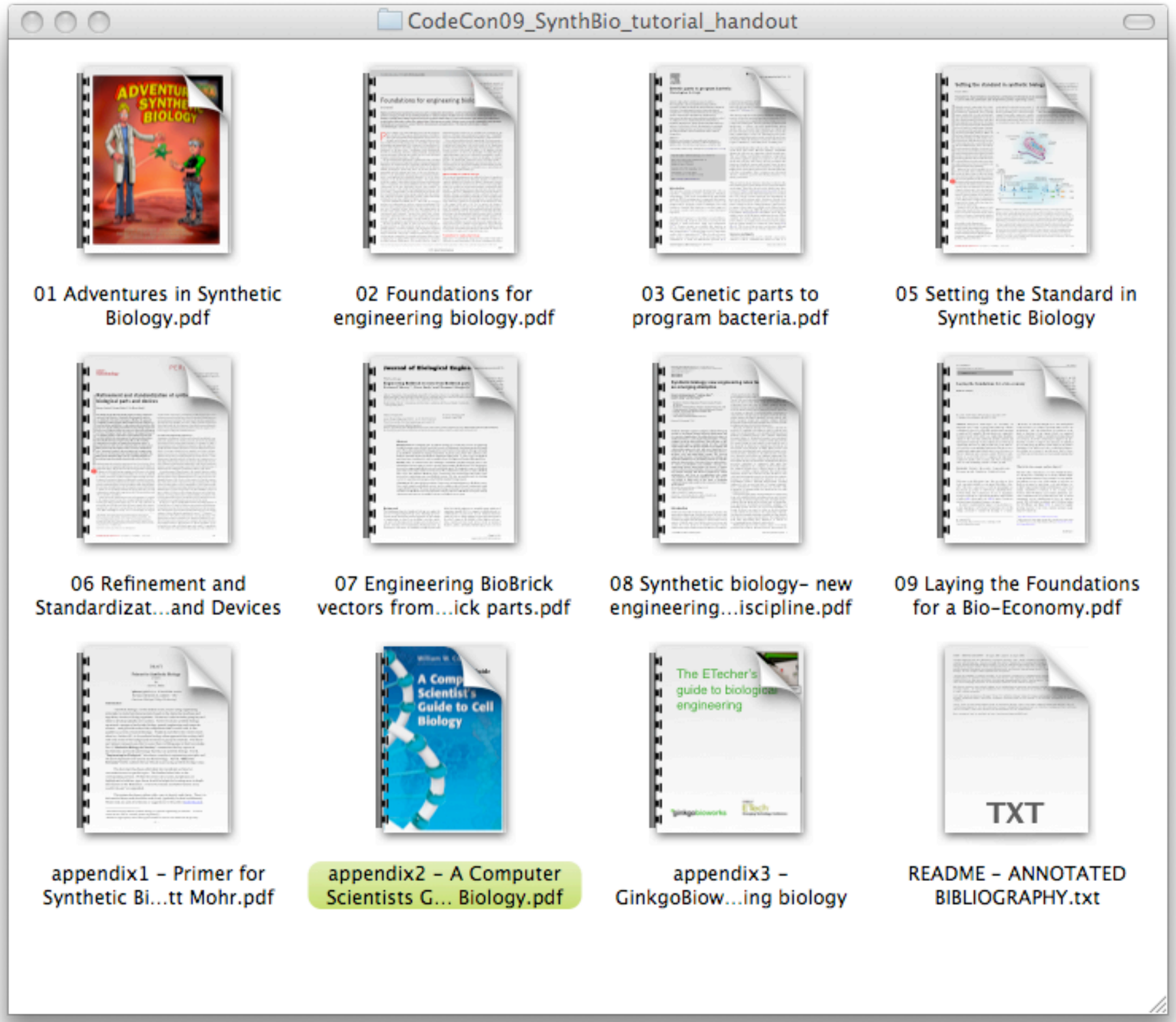
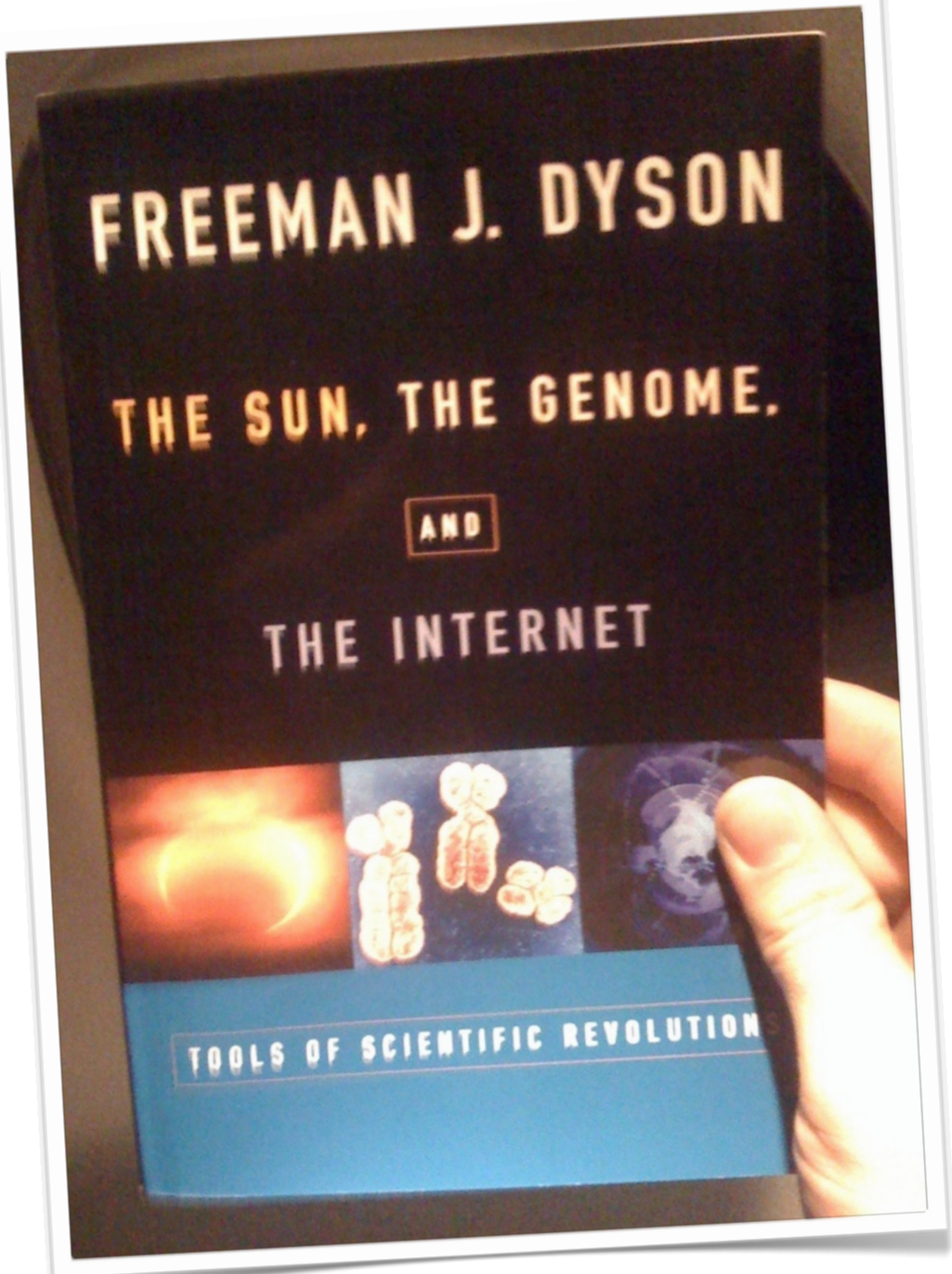
DIY Synthetic Biology @ Maker Revolution

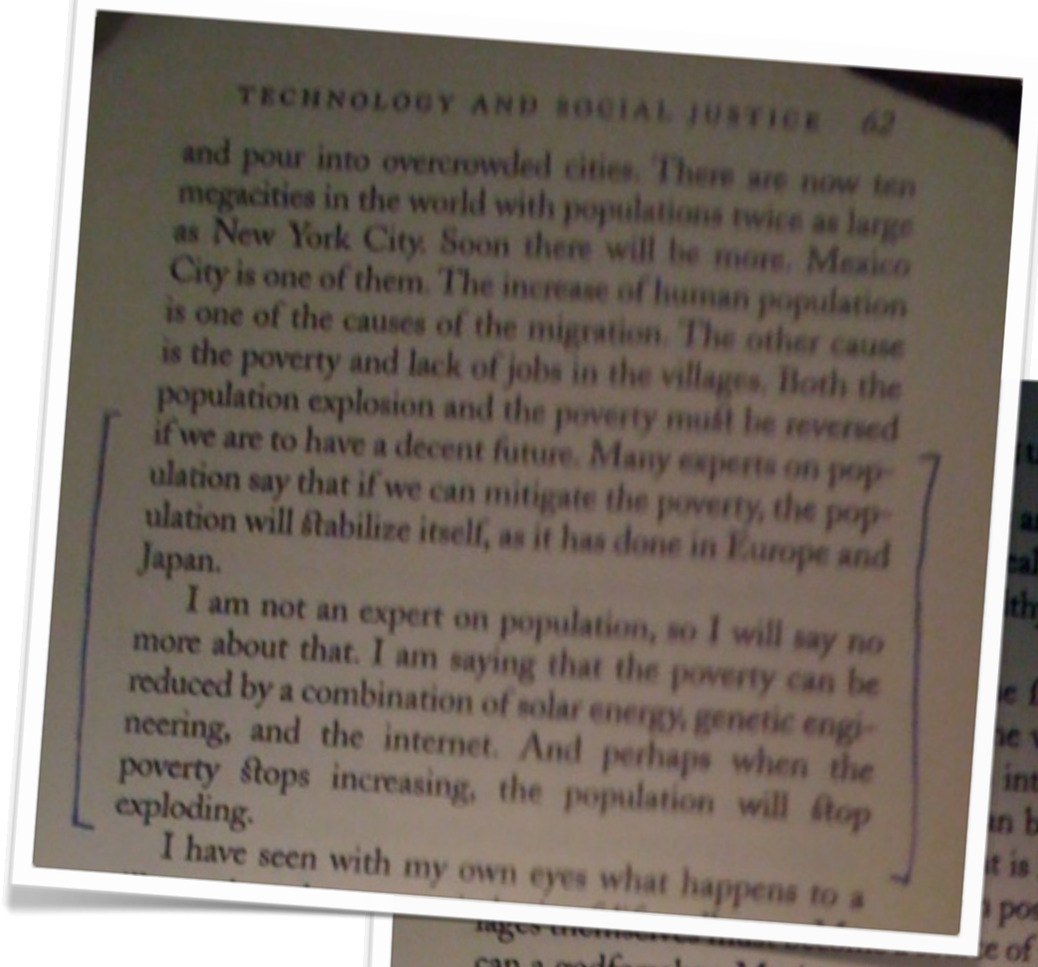
26 Apr 2009

http://digg.com/d1nuSY

http://bit.ly/diybiocc



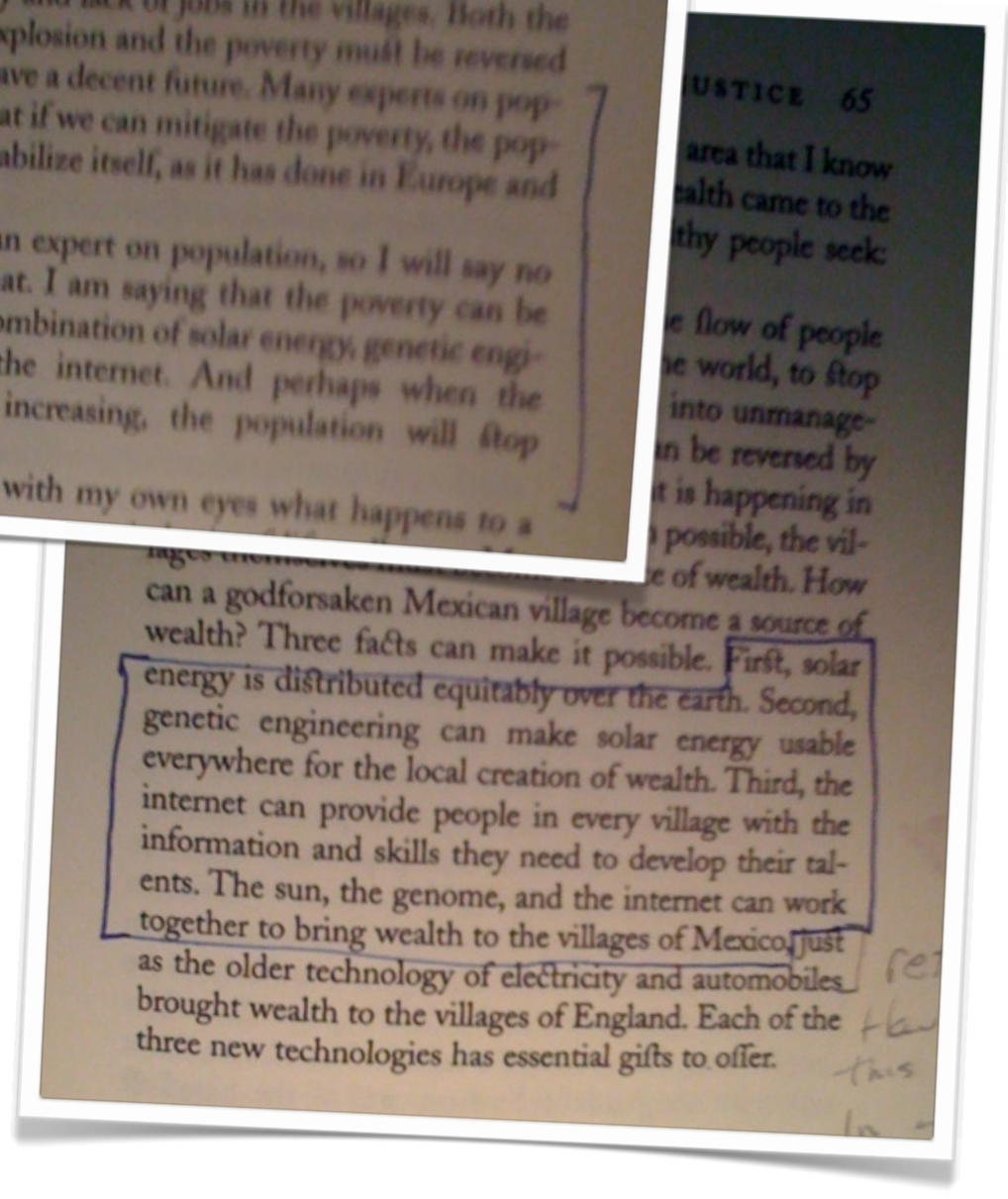




and pour into overcrowded cities. There are now ten megacities in the world with populations twice as large as New York City. Soon there will be more. Mexico City is one of them. The increase of human population is one of the causes of the migration. The other cause is the poverty and lack of jobs in the villages. Both the population explosion and the poverty must be reversed if we are to have a decent future. Many experts on population say that if we can mitigate the poverty, the population will stabilize itself, as it has done in Europe and Japan.

I am not an expert on population, so I will say no more about that. I am saying that the poverty can be reduced by a combination of solar energy, genetic engineering, and the internet. And perhaps when the poverty stops increasing, the population will stop exploding.

I have seen with my own eyes what happens to a



area that I know
alth came to the
thy people seek:

e flow of people
e world, to stop
into unmanage-
n be reversed by
t is happening in
possible, the vil-
e of wealth. How

can a godforsaken Mexican village become a source of wealth? Three facts can make it possible. First, solar energy is distributed equitably over the earth. Second, genetic engineering can make solar energy usable everywhere for the local creation of wealth. Third, the internet can provide people in every village with the information and skills they need to develop their talents. The sun, the genome, and the internet can work together to bring wealth to the villages of Mexico, just as the older technology of electricity and automobiles brought wealth to the villages of England. Each of the three new technologies has essential gifts to offer.

Towards a Biotech Society

BIOSECURITY AND BIOTERRORISM: BIODEFENSE STRATEGY, PRACTICE, AND SCIENCE
Volume 1, Number 3, 2003

The Pace and Proliferation of Biological Technologies

ROBERT CARLSON

THE ADVENT OF THE home molecular biology laboratory is not far off. While there is no *Star Trek* "Tricorder" in sight, the physical infrastructure of molecular biology is becoming more sophisticated and less expensive every day. Automated commercial instrumentation handles an increasing fraction of laboratory tasks that were once the sole province of doctoral level researchers, reducing labor costs and increasing productivity. This technology is gradually moving into the broader marketplace as laboratories upgrade to new equipment. Older, still very powerful instruments are finding their way into wide distribution, as any cursory tour of eBay will reveal.[1] These factors are contributing to a proliferation that will soon put highly capable tools in the hands of both professionals and amateurs worldwide. There are obvious short term risks from increased access to DNA synthesis and sequencing technologies, and the general improvement of technologies used in measuring and manipulating molecules will soon enable a broad and distributed enhancement in the ability to alter biological systems. The resulting potential for mischief or mistake causes understandable concern—there are already public calls by scientists and politicians alike to restrict access to certain technologies, to regulate the direction of biological research, and to censor publication of some new techniques and data. It is questionable, however, whether such efforts will increase security or benefit the public good. Proscription of information and artifacts generally leads directly to a black market that is difficult to monitor and therefore difficult to police. A superior alternative is the deliberate creation of an open and expansive research community, which may be better able to respond to crises and better able to keep track of research whether in the university or in the garage.

FACTORS DRIVING THE BIOTECH REVOLUTION

The development of powerful laboratory tools is enabling ever more sophisticated measurement of biology at the molecular level. Beyond its own experimental utility, every new measurement technique creates a new mode of interaction with biological systems. Moreover, new measurement techniques can swiftly become means to manipulate biological systems. Estimating the pace of improvement of representative technologies is one way to illustrate the rate at which our ability to interact with and manipulate biological systems is changing.

For example, chemically synthesized DNA fragments, or oligonucleotides, can be used in DNA computation, in the fabrication of gene expression arrays ("gene chips"), and to make larger constructs for genetic manipulation. Mail-order oligonucleotides were with much fanfare recently used to build a functional poliovirus genome from constituent molecules for the first time.[2] The rate at which DNA synthesis capacity is changing is thus a measure of the improvement in our ability to manipulate biological systems and biological information. Similarly, improvements in DNA sequencing capabilities are a measure of our ability to read biological information; in particular the ability to proofread the results of DNA synthesis. Here I refer to such technology, whether instrument or molecule, as "biological technology."

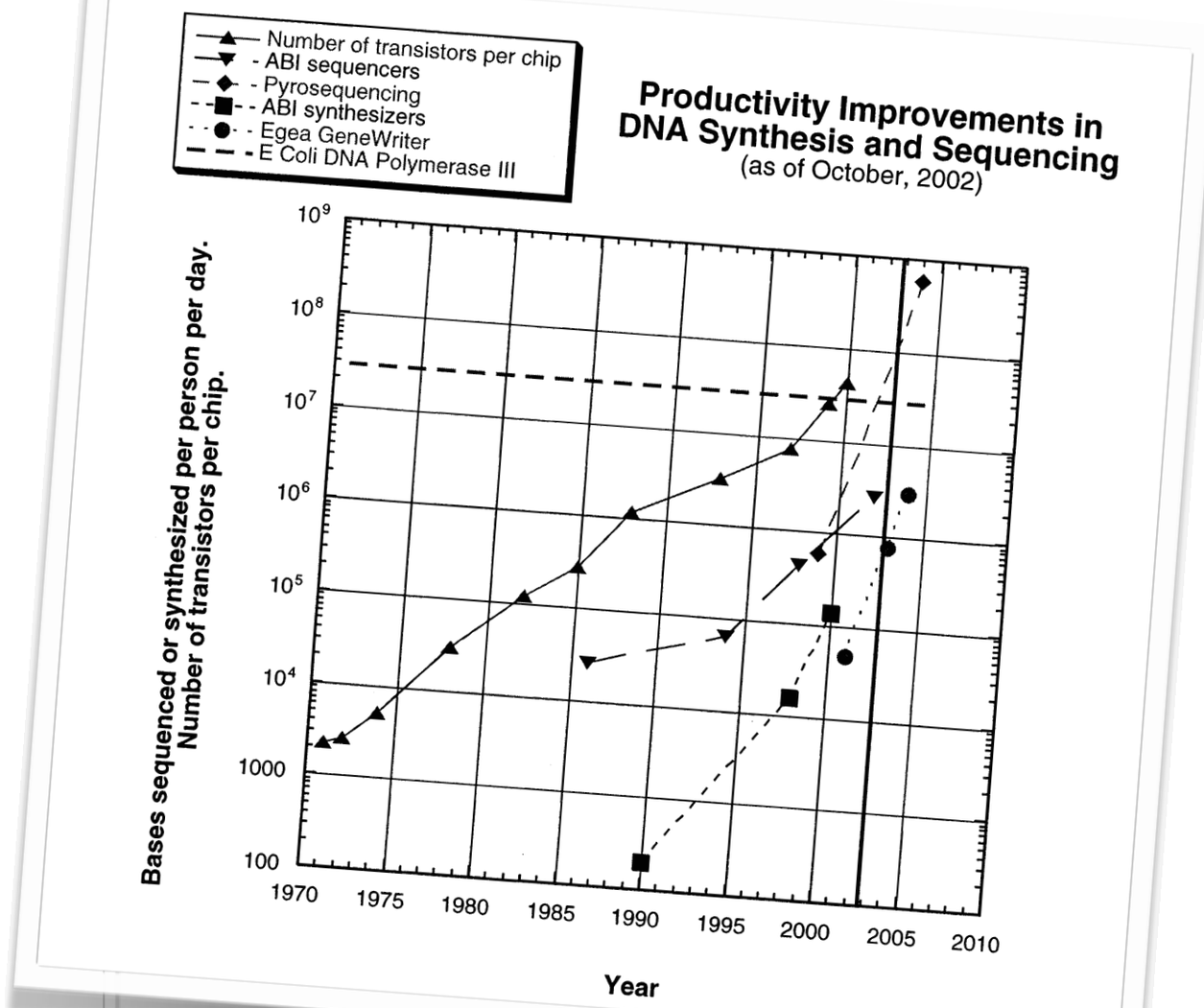
THE PACE OF TECHNOLOGICAL CHANGE THROUGH THE PRISM OF MOORE'S LAW

Figure 1 contains estimates of potential daily productivity of DNA synthesis and sequencing based on commercially available instruments, including the time necessary to prepare samples. There have been only a few generations of instruments—there is thus a limited amount of data for examination. These estimates are not intended to absolutely quantify a rate of change, but rather to capture the essence of the trends. Several tech-

[1]See http://listings.ebay.com/pool1/listings/list/all/category11811/index.html.

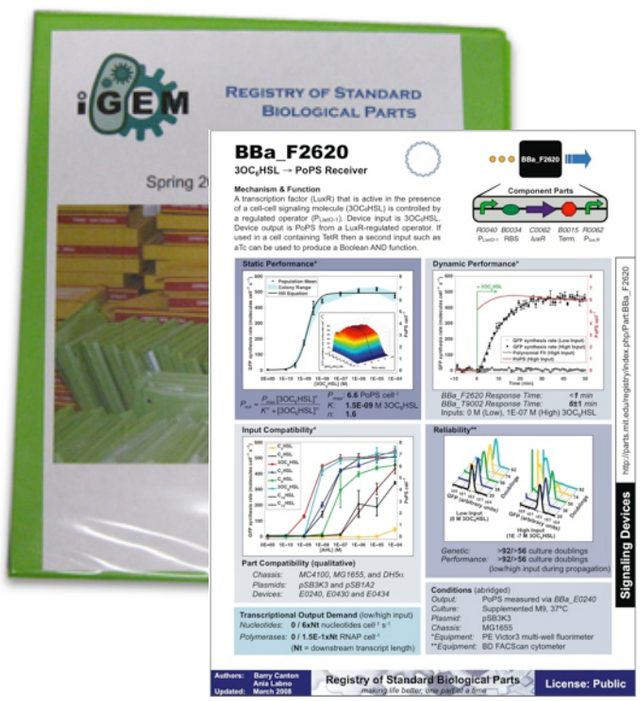
[2]Cello J, Paul AV, Wimmer E. Chemical Synthesis of Poliovirus cDNA: Generation of Infectious Virus in the Absence of Natural Template. Science 2002. 297(5583): p. 1016–1018.

Robert Carlson, PhD, is a Research Scientist in the Department of Electrical Engineering at the University of Washington and an Adjunct Research Fellow at the Molecular Sciences Institute in Berkeley, California.



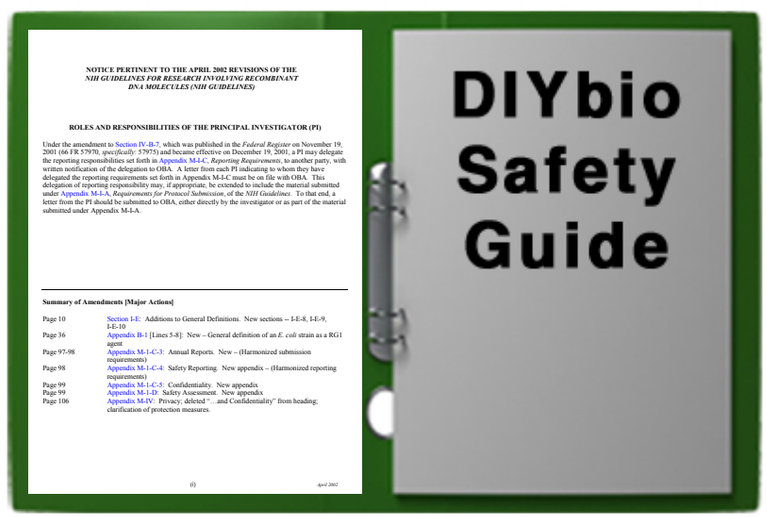
Long Tail Life Sciences

Standardization & abstraction; SB tools; Part Collections

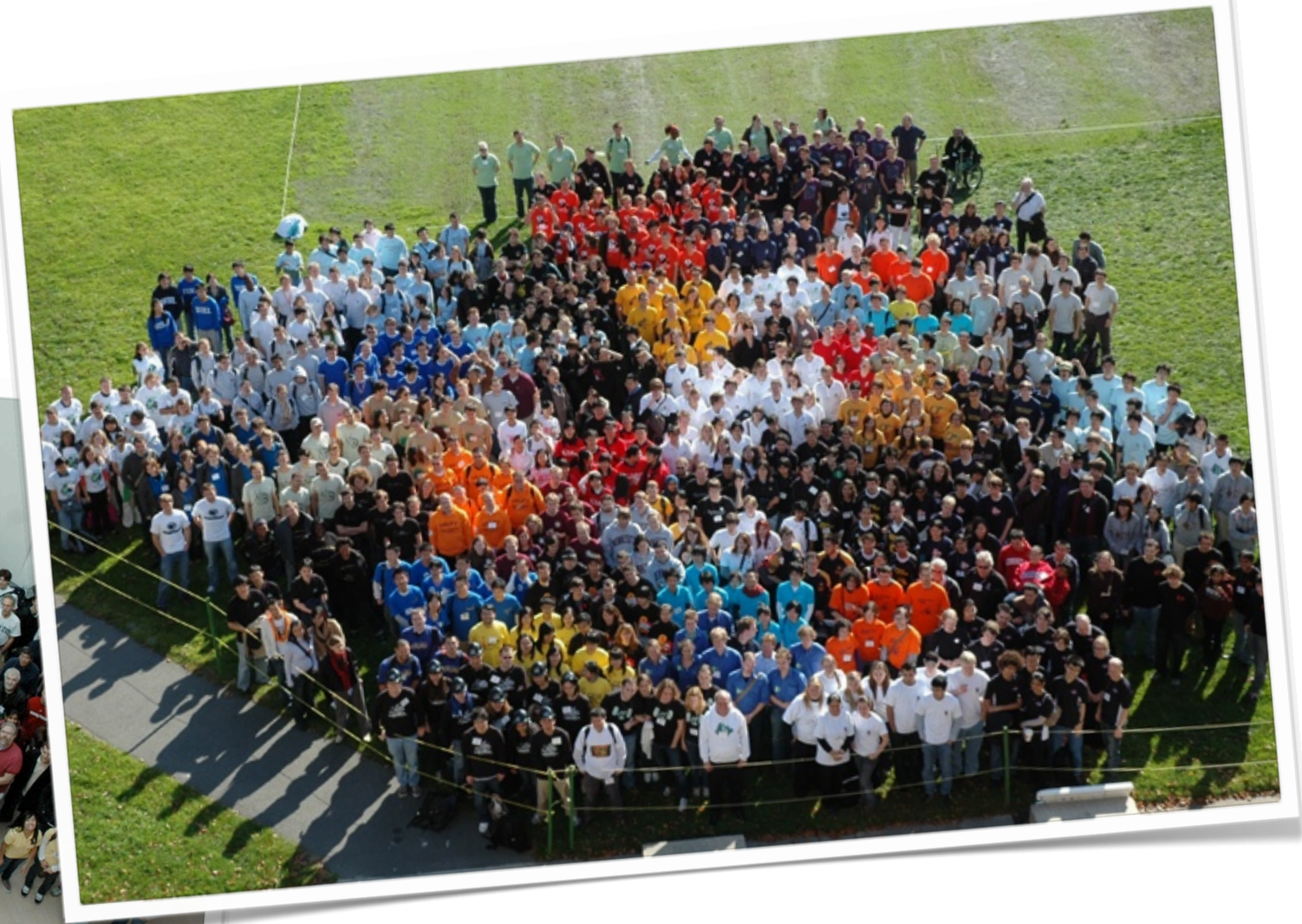


DIY and off-the-shelf equipment and services

framework that minimizes safety risks and repercussions for society and garge biohackers



international Genetically Engineered Machine Competition **2002 - 2008**



Users & Groups

non-wiki

Log in

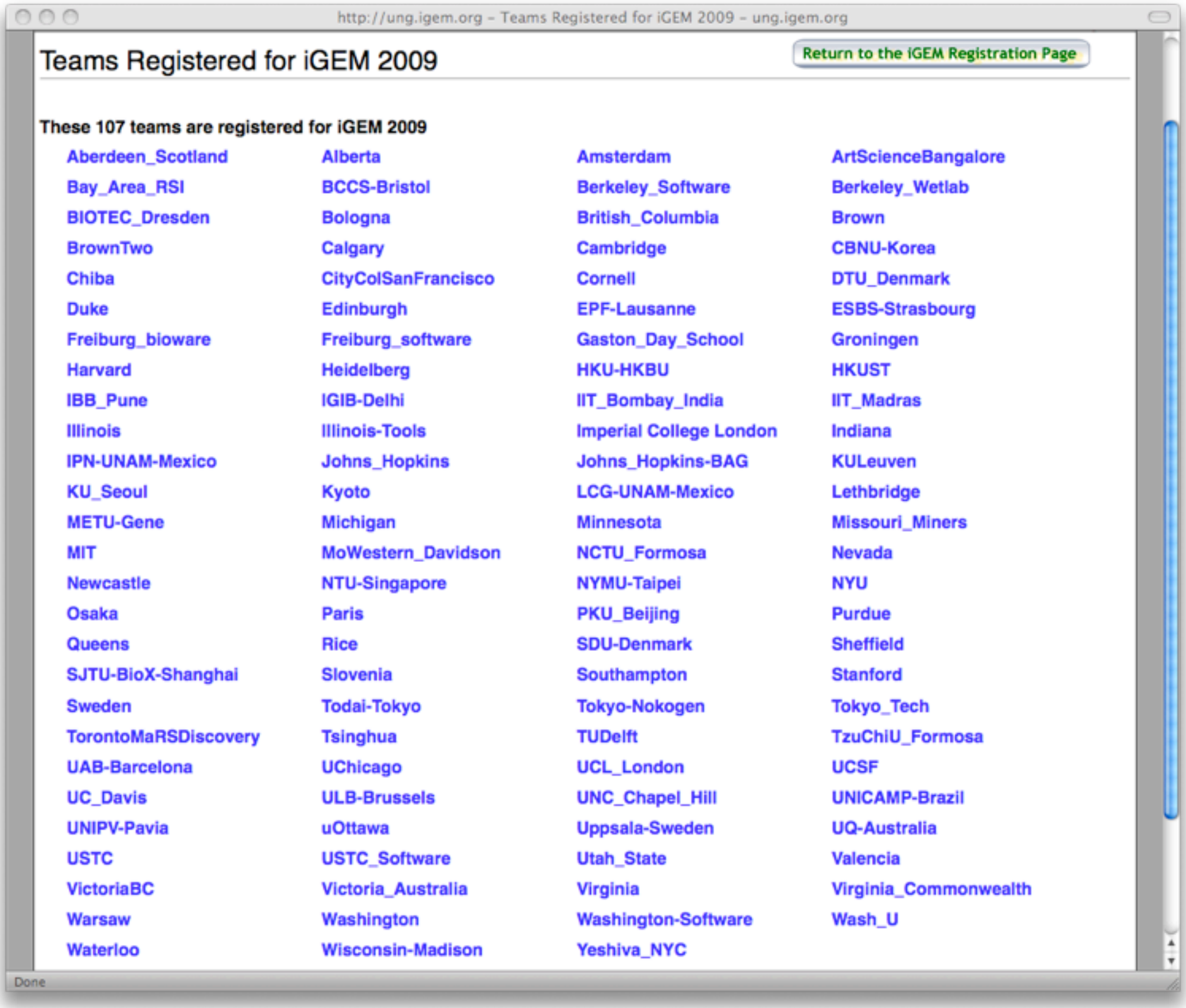
Teams Registered for iGEM 2008

Return to the iGEM Registration Page

These 85 teams are registered for iGEM 2008

Alberta_NINT	Bay_Area_RSI	BCCS-Bristol	Beijing_Normal
Bologna	Brown	BrownTwo	Calgary_Ethics
Calgary_Software	Calgary_Wetware	Caltech	Cambridge
Chiba	Colombia	CPU-NanJing	Davidson-Missouri_Western
Duke	Edinburgh	EPF-Lausanne	ESBS-Strasbourg
ETH_Zurich	Freiburg	Groningen	Guelph
Harvard	Hawaii	Heidelberg	HKUSTers
iHKU	IIT_Madras	Illinois	Imperial_College
Istanbul	Johns_Hopkins	KULeuven	Kyoto
LCG-UNAM-Mexico	Lethbridge_CCS	Melbourne	METU_Turkey
Mexico-UNAM-IPN	Michigan	Minnesota	Mississippi_State
Missouri_Miners	MIT	Montreal	Newcastle_University
NTU-Singapore	NYMU-Taipei	Paris	Peking_University
PennState	Peru	Prairie_View	Princeton
Purdue	Rensselaer	Rice_University	Slovenia
Tianjin	Tokyo_Tech	Toronto_Bluegenes	Tsinghua
TUDelft	TU_Munchen	UCSF	UC_Berkeley
UC_Berkeley_Tools	UNIPV-Pavia	University_of_Alberta	University_of_Chicago
University_of_Lethbridge	University_of_Ottawa	University_of_Sheffield	University_of_Washington
USTC	Utah_State	Valencia	Virginia
Warsaw	Waterloo	WEGO_Taipei	Wisconsin
Example			

Applications for these 4 teams are pending approval by iGEM Headquarters


http://ung.igem.org - Teams Registered for iGEM 2009 - ung.igem.org
Teams Registered for iGEM 2009
Return to the iGEM Registration Page
These 107 teams are registered for iGEM 2009
Aberdeen_Scotland
Alberta
Amsterdam
ArtScienceBangalore
Bay_Area_RSI
BCCS-Bristol
Berkeley_Software
Berkeley_Wetlab
BIOTEC_Dresden
Bologna
British_Columbia
Brown
BrownTwo
Calgary
Cambridge
CBNU-Korea
Chiba
CityColSanFrancisco
Cornell
DTU_Denmark
Duke
Edinburgh
EPF-Lausanne
ESBS-Strasbourg
Freiburg_bioware
Freiburg_software
Gaston_Day_School
Groningen
Harvard
Heidelberg
HKU-HKBU
HKUST
IBB_Pune
IGIB-Delhi
IIT_Bombay_India
IIT_Madras
Illinois
Illinois-Tools
Imperial College London
Indiana
IPN-UNAM-Mexico
Johns_Hopkins
Johns_Hopkins-BAG
KULeuven
KU_Seoul
Kyoto
LCG-UNAM-Mexico
Lethbridge
METU-Gene
Michigan
Minnesota
Missouri_Miners
MIT
MoWestern_Davidson
NCTU_Formosa
Nevada
Newcastle
NTU-Singapore
NYMU-Taipei
NYU
Osaka
Paris
PKU_Beijing
Purdue
Queens
Rice
SDU-Denmark
Sheffield
SJTU-BioX-Shanghai
Slovenia
Southampton
Stanford
Sweden
Todai-Tokyo
Tokyo-Nokogen
Tokyo_Tech
TorontoMaRSDiscovery
Tsinghua
TUDelft
TzuChiU_Formosa
UAB-Barcelona
UChicago
UCL_London
UCSF
UC_Davis
ULB-Brussels
UNC_Chapel_Hill
UNICAMP-Brazil
UNIPV-Pavia
uOttawa
Uppsala-Sweden
UQ-Australia
USTC
USTC_Software
Utah_State
Valencia
VictoriaBC
Victoria_Australia
Virginia
Virginia_Commonwealth
Warsaw
Washington
Washington-Software
Wash_U
Waterloo
Wisconsin-Madison
Yeshiva_NYC
Done

iGEM

an existence proof for
small team-based biotech innovation

- Resveratrol Beer
- Bacterial Photography
- oderant synthesis (banana!)
- arsenic & lead biosensors
- H. pylori vaccine

Opportunity for DIYbio teams
to compete in 2010

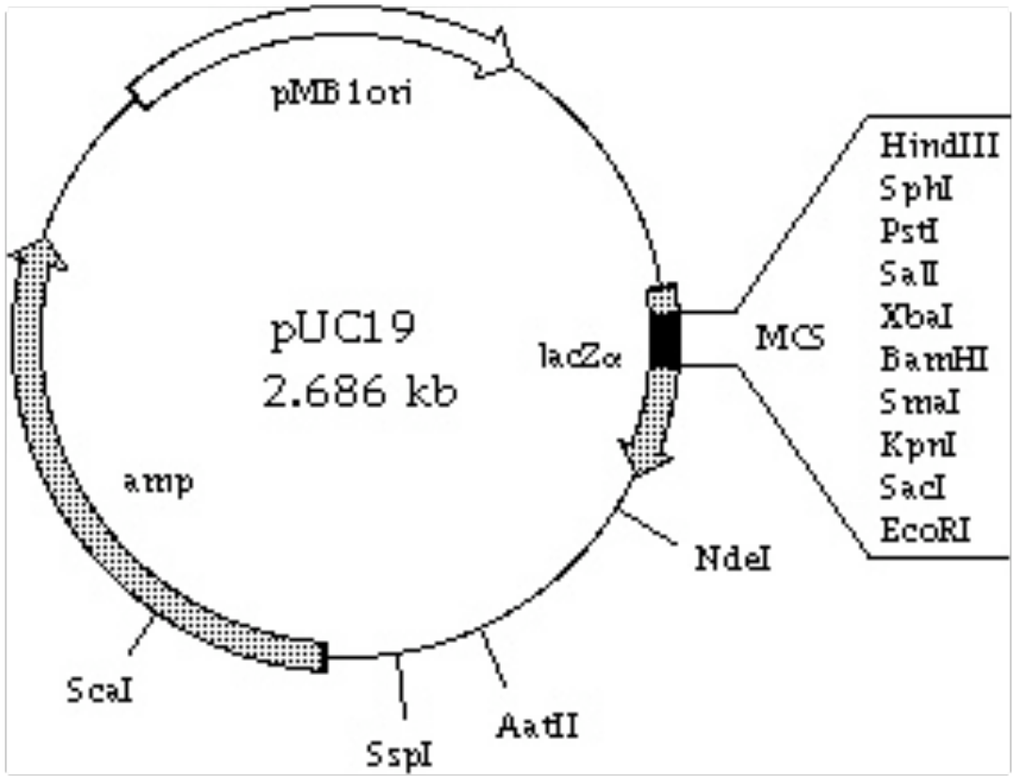

HMM... ARE YOU SURE YOU UNDERSTAND ENOUGH ABOUT WHAT YOU WANT TO DO?
YOU DON'T WANT TO MAKE THINGS WORSE.
WE'LL ONLY FIND OUT BY TRYING!
LET'S GRAB ONE!
HI THERE, BUDDY.

Case Study: pUC19

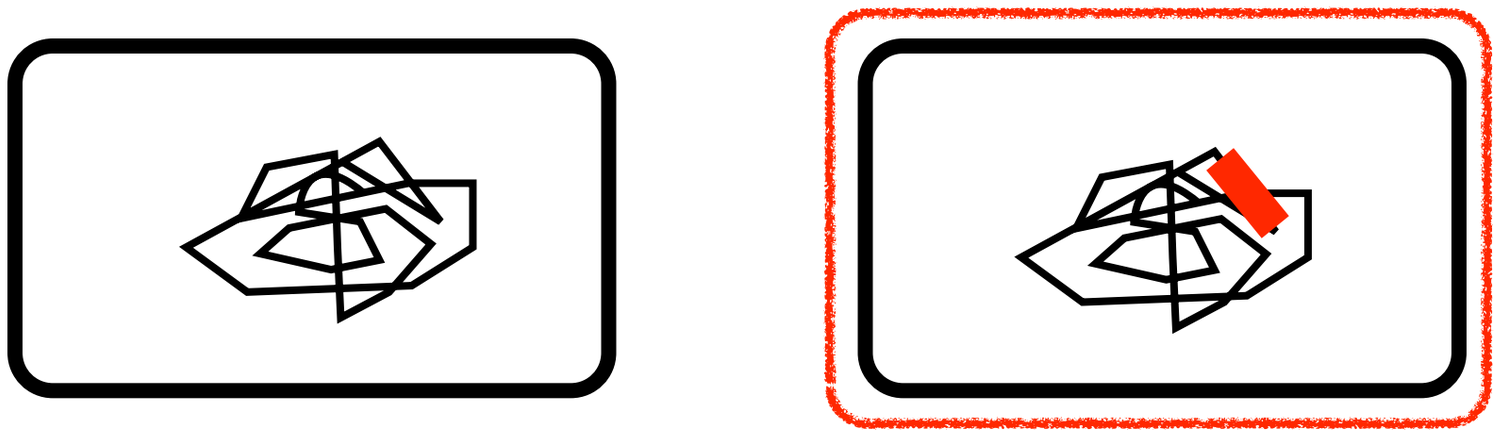
One of the most popular genetic engineering tools

It's a cloning vector - built to grab and carry DNA

Where did it come from?



Finding resistance genes



sensitive vs. resistant

live sensitive cells + resistant DNA = rare survivors

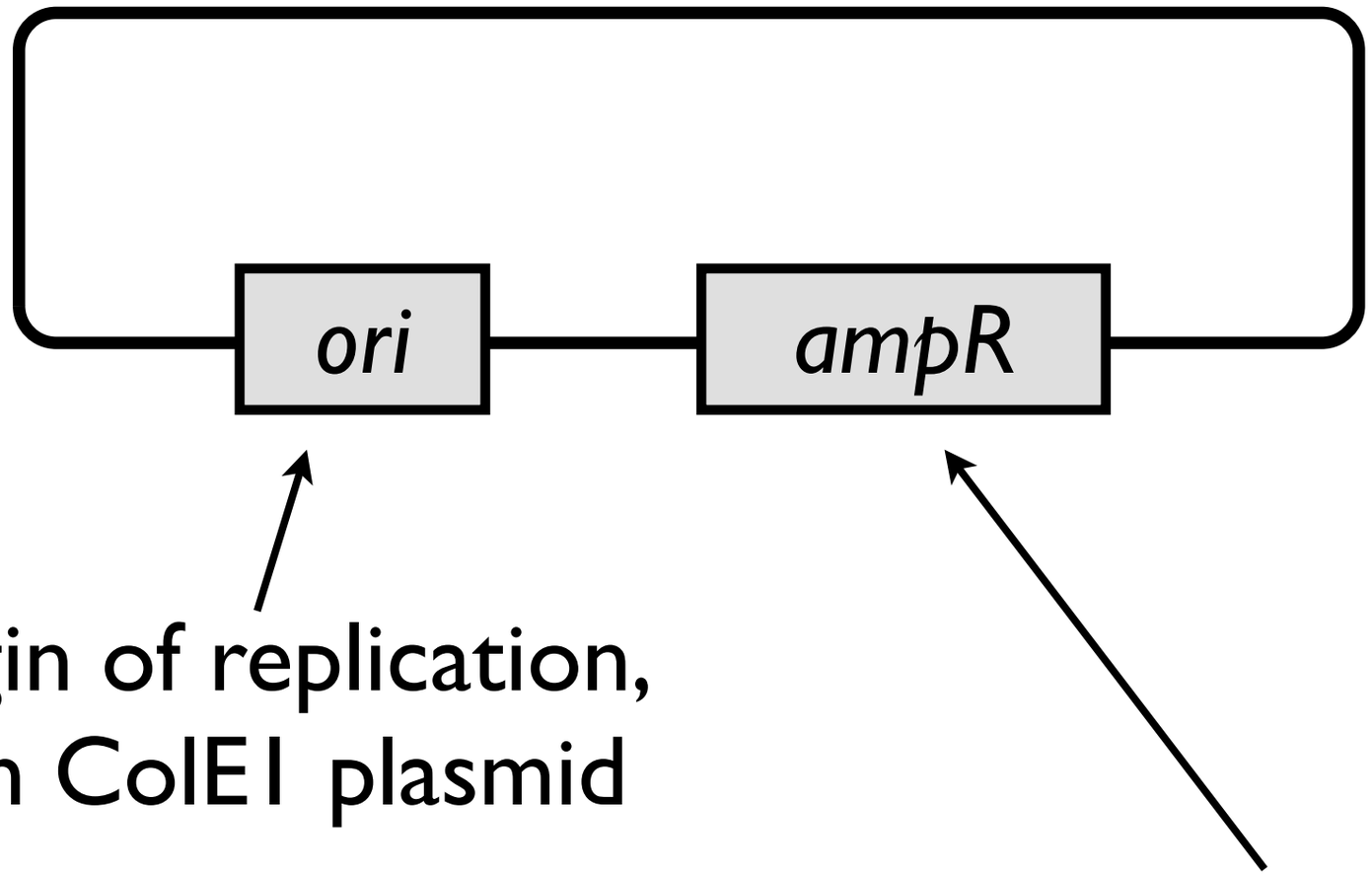
Mini-genomes as tools

How do I recover the DNA?

Put it on a plasmid - a small, self-replicating genetic device.

Modularity is your friend.

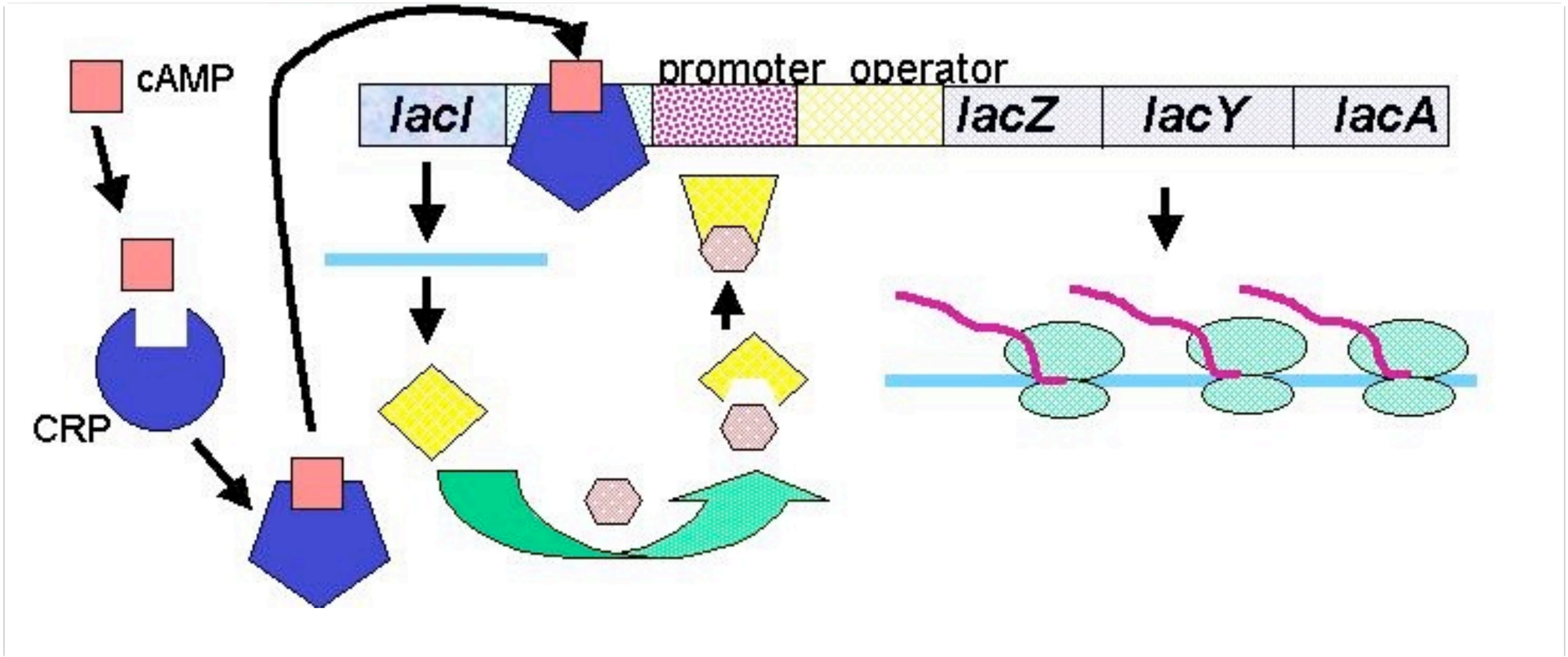
Synthetic resistance vector



Origin of replication,
from ColE1 plasmid

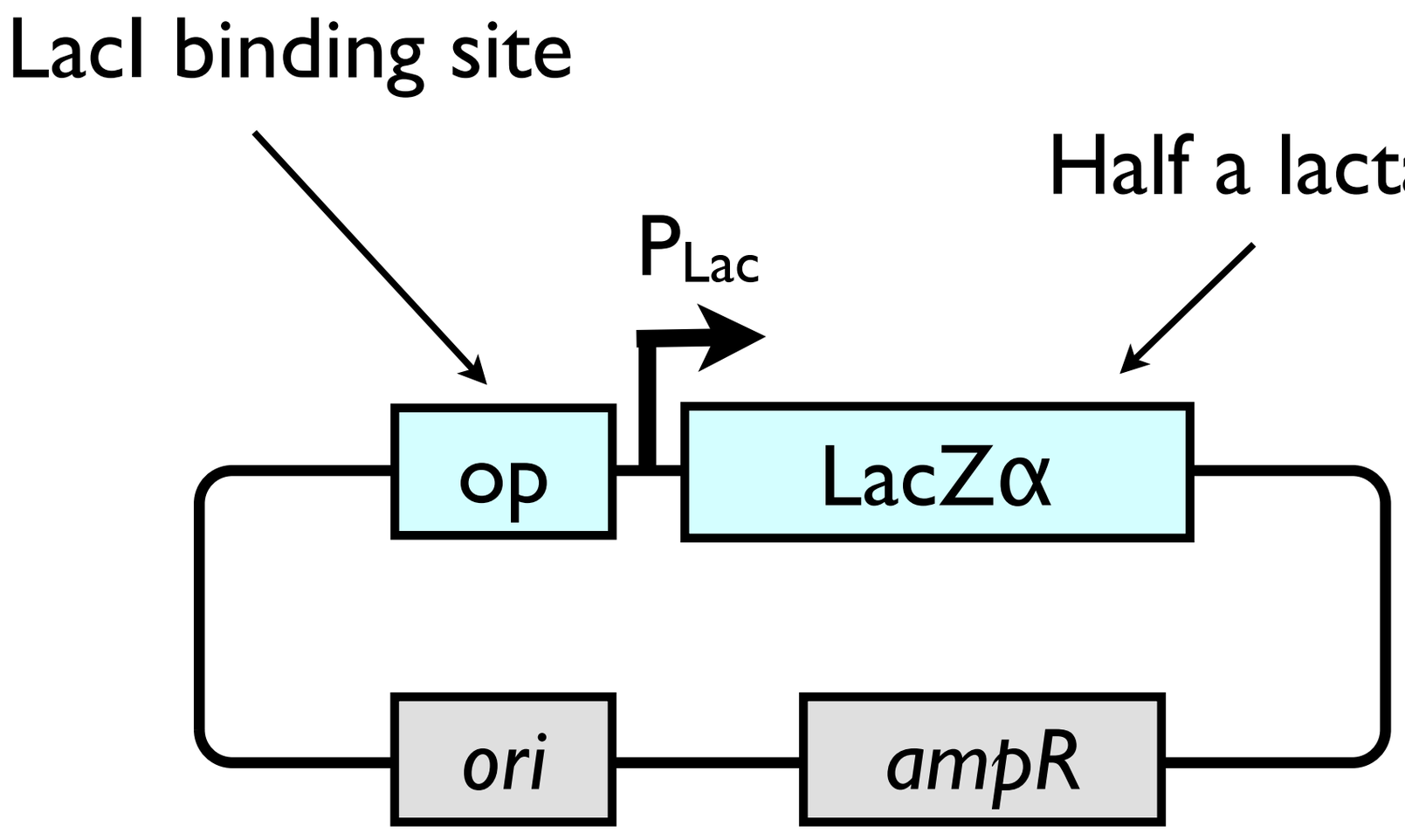
Gene for digesting
penicillin-like drugs

Lactose operon

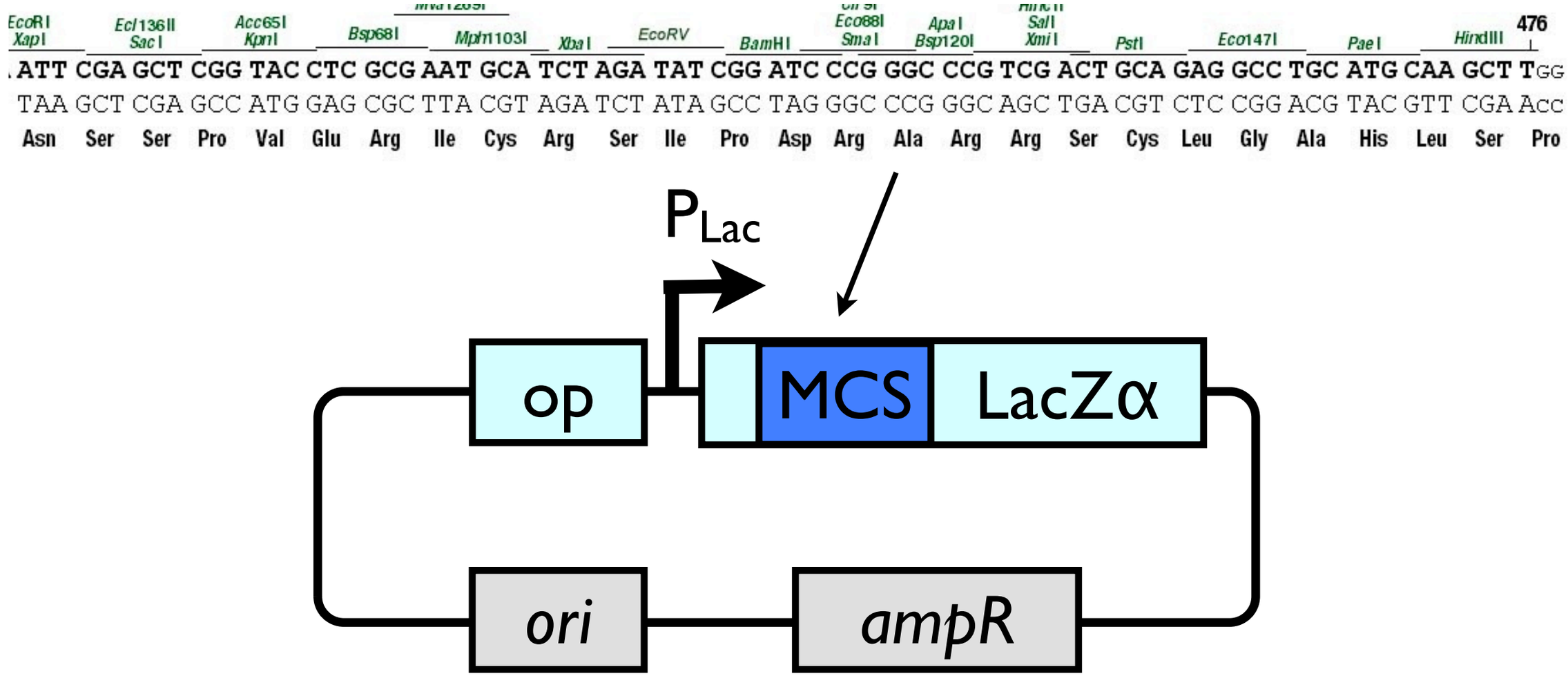


If lactose and no glucose...then eat lactose

Test kit for simplified *lac*



Hack it for cloning (add restriction sites)



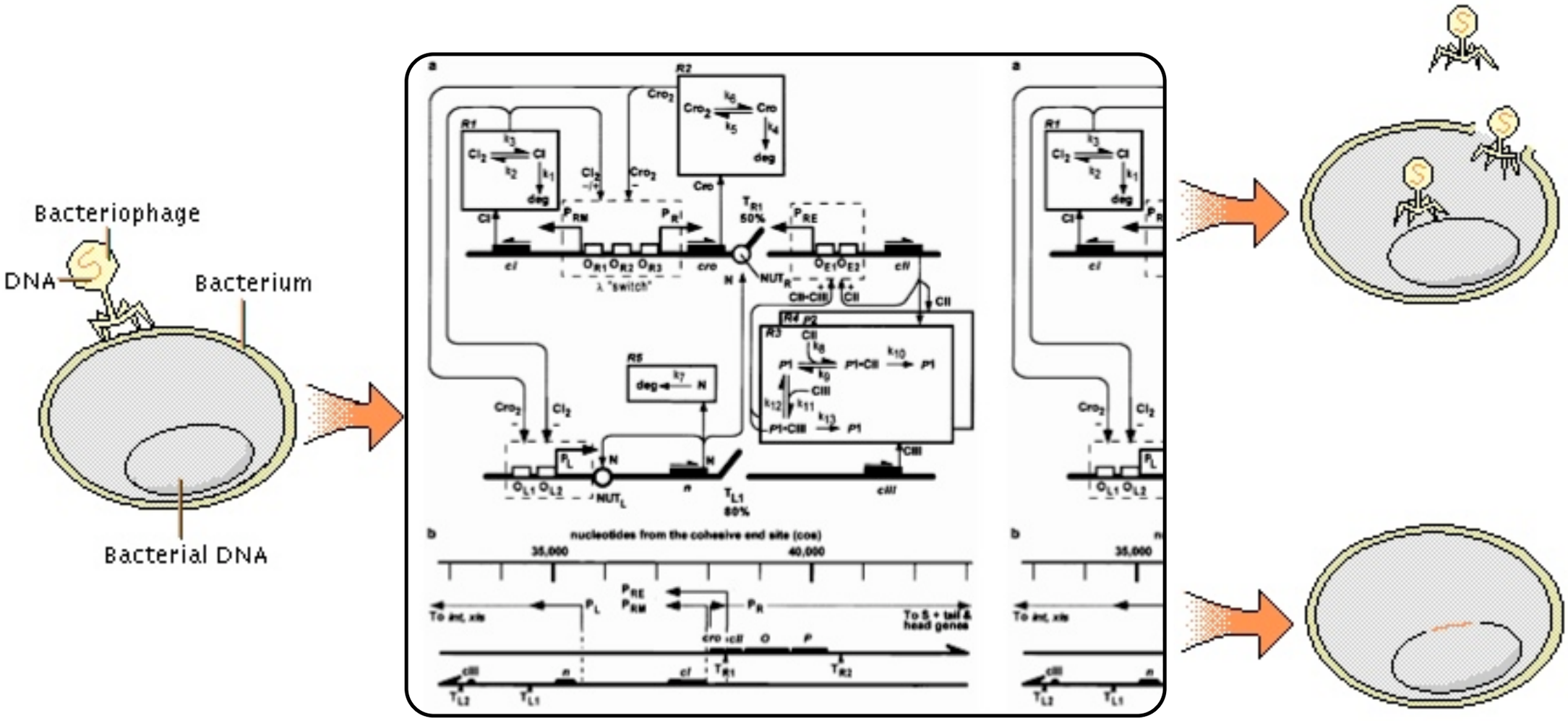
How can I reuse this?

We need abstractions.

And documentation.

Otherwise, we're stuck doing all that work again.

Phage λ: Inside the black box



A complicated regulatory pathway, which has kept scientists busy for half a century at least

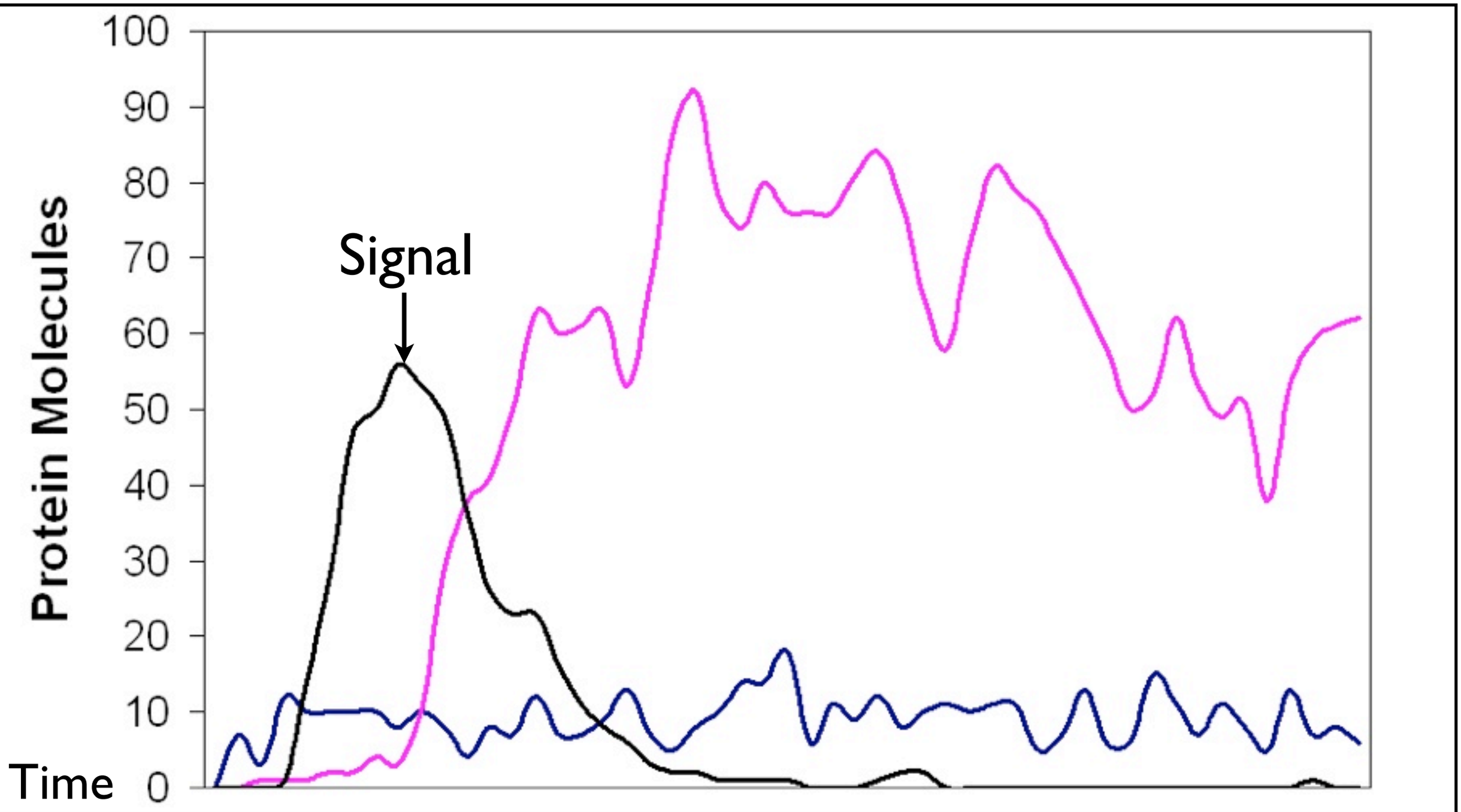
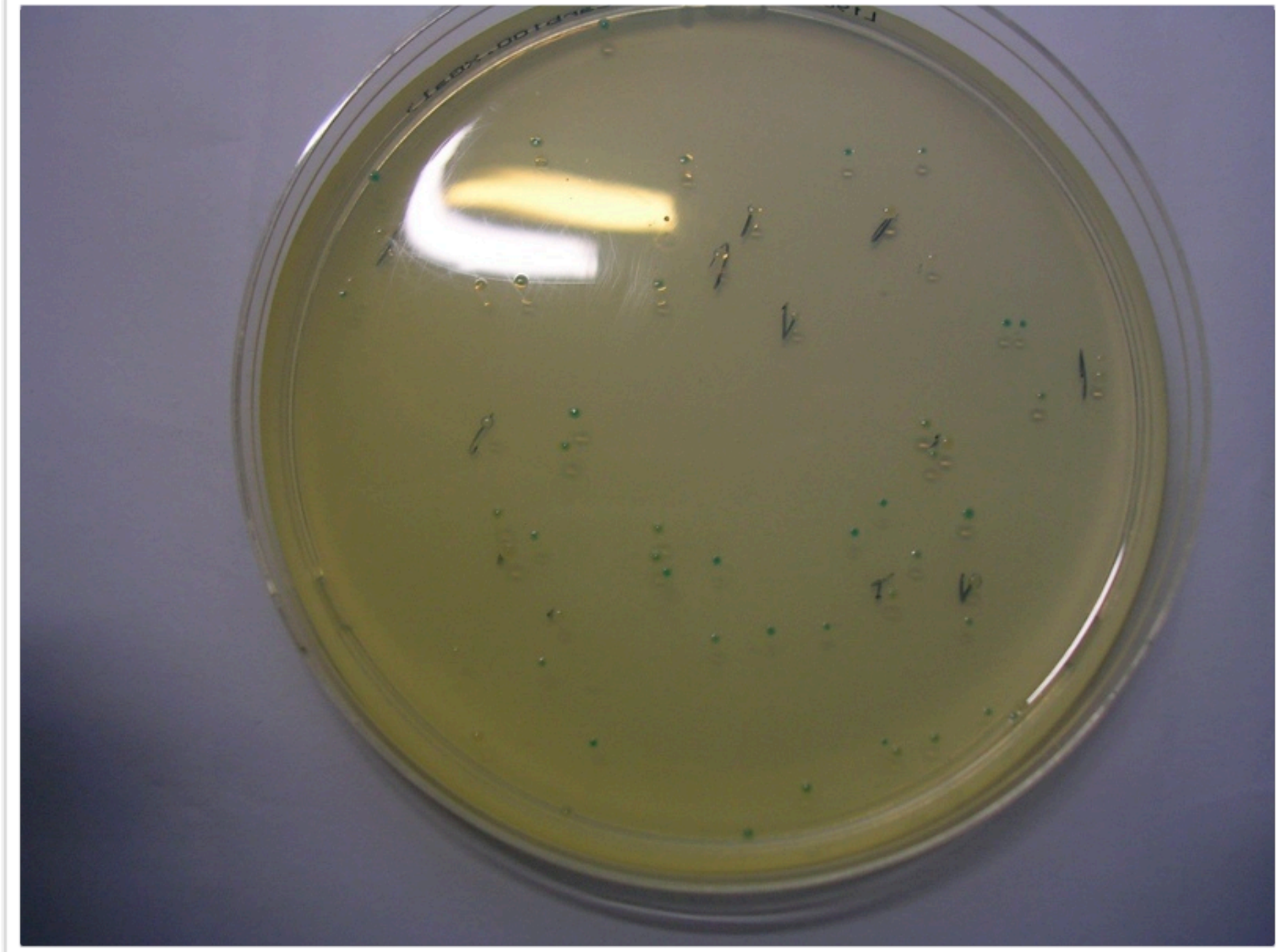


Figure 3. Bio-SPICE simulation of "carry" detection.
Blue line: CI activator. Purple line: Cro repressor. Black line: carry signal. Simulation was performed on a representation of the carry detector, using 15 mass action equations.

Actually not vaporware



Benchmarking: what *is* possible?

- One geek, one closet, one month's rent (and roughly two months' time)

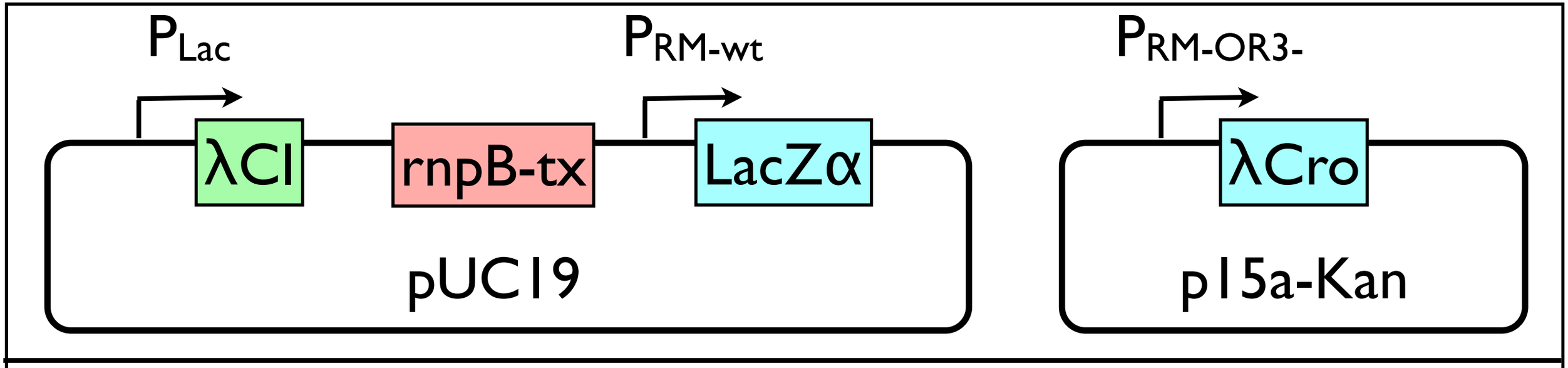


Figure 2a. Carry detection system: theory plus prototype.

ADVENTURES IN SYNTHETIC BIOLOGY

STORY: DREW ENDY ISADORA DEESE
THE MIT SYNTHETIC BIOLOGY WORKING GROUP
ART: CHUCK WADEY www.CHUCKWADEY.COM

WANNA BET?

LL I NEED DO IS MAKE EM FORM A OSED FILM,-

FIRST YOU NEED TO ASSEMBLE THE DNA PARTS THAT ENCODE YOUR PROGRAM.

GET THEM FROM THE CATALOG.

ONE BALLOON-O-GENESIS-

-AND ONE GAS-O-MATIC MODULE.

COOL, HERE THEY ARE!

NOW WHAT?

LOAD THE DNA INTO OUR LITTLE FRIEND HERE.

WHAT DO YOU THINK, BUDDY?

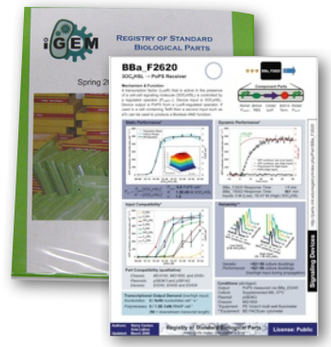
DNA'S READY TO GO.

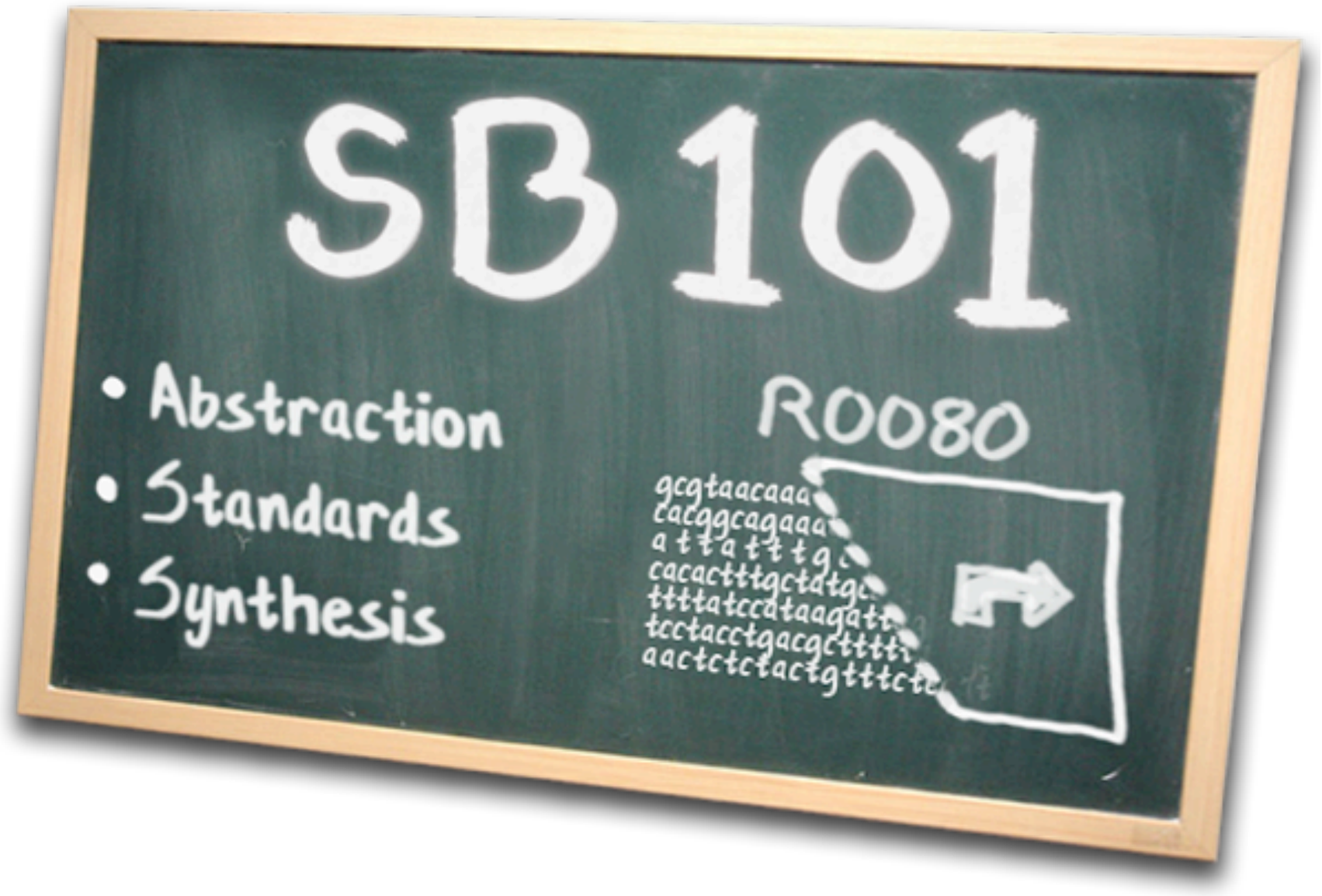
HELP ME CATCH HIM!

MEEP!

HE'S CHANGING!

POP POP


iGEM
Registry of Standard Biological Parts
BBa_F2620


SB101
• Abstraction
• Standards
• Synthesis
R0080

“A good device standard defines sufficient information about discrete parts to allow the design of predictable complex composite systems. It also provides guidelines for the minimal characterization and manufacturing tolerances of new elements.”

- Arkin, Setting the Standard.

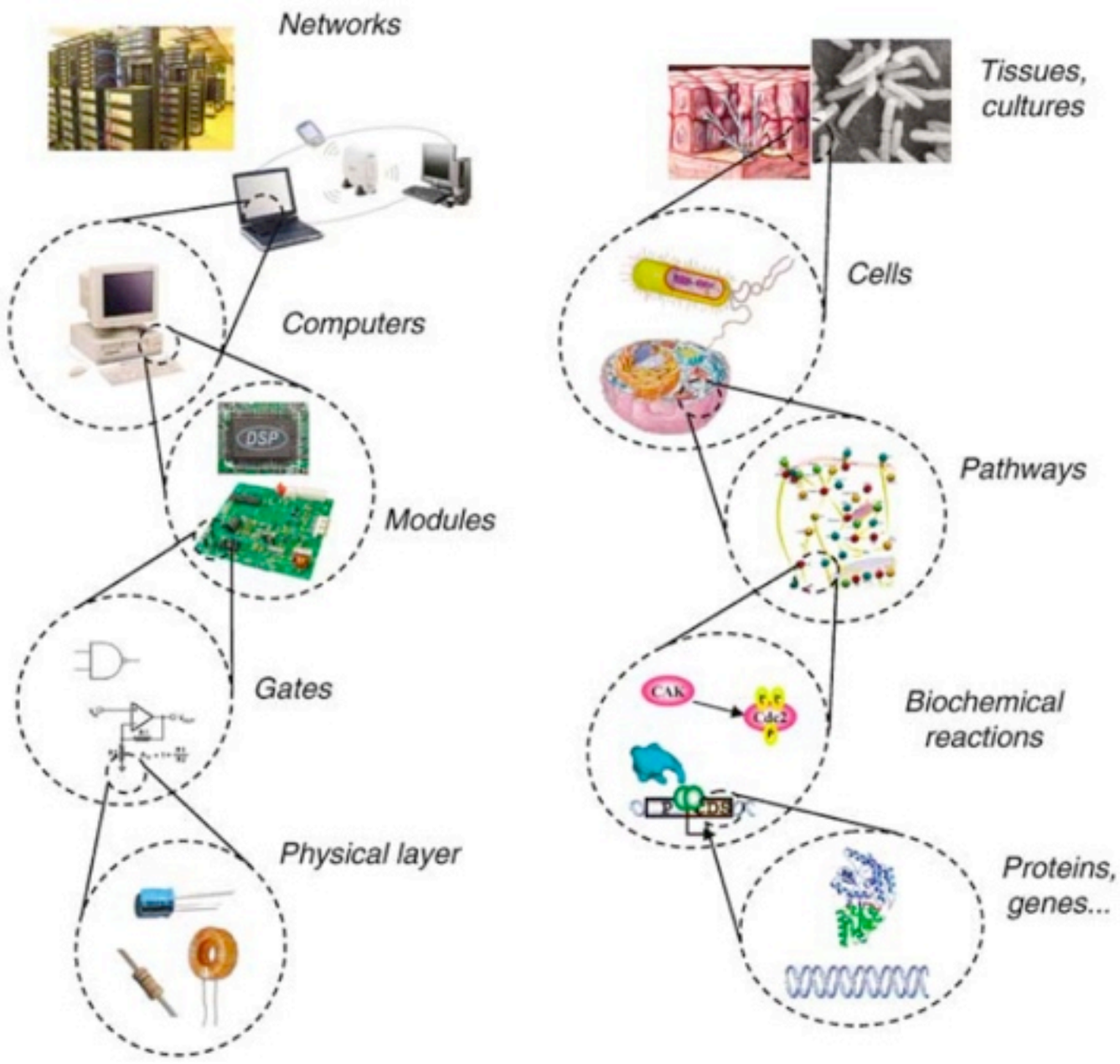
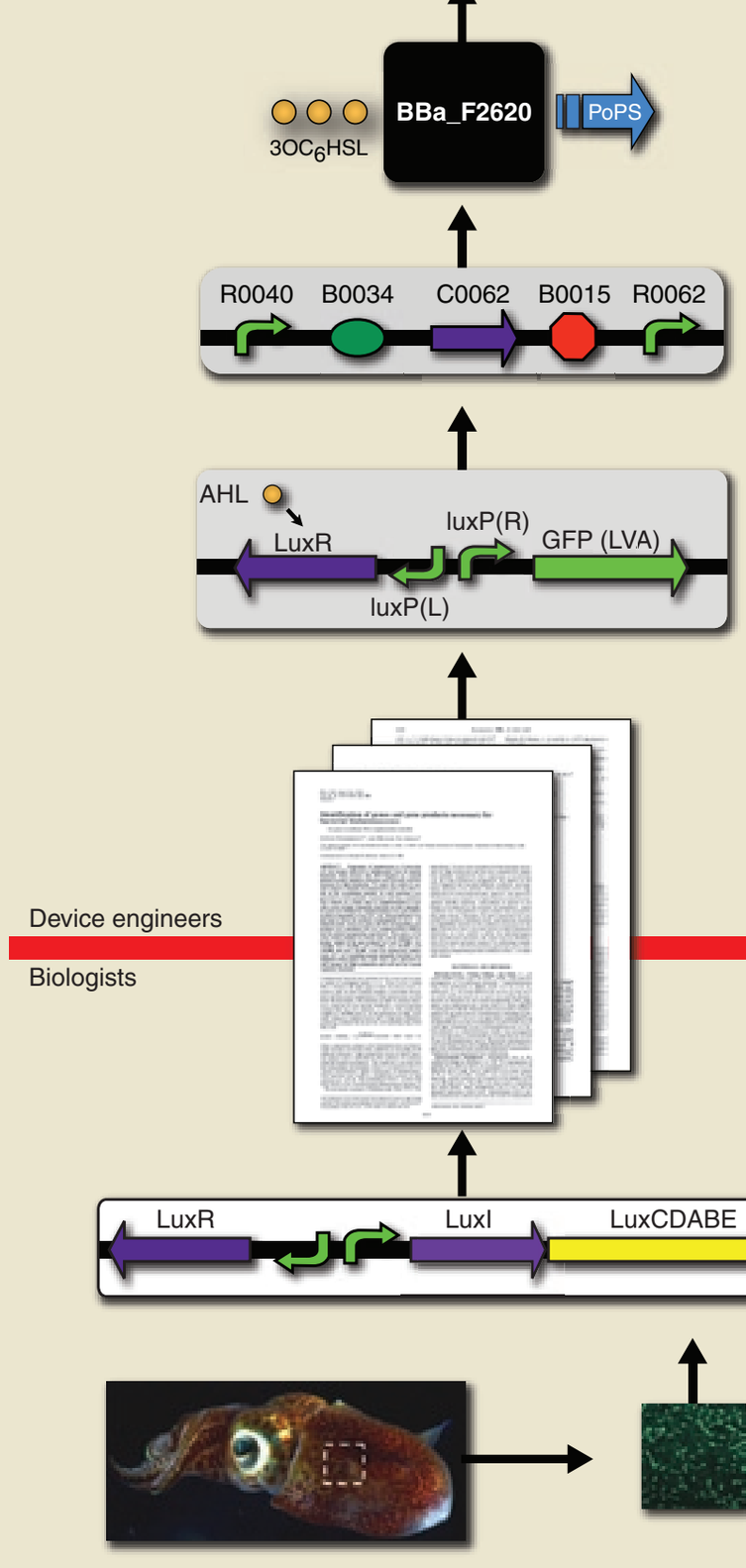


Figure 1 A possible hierarchy for synthetic biology is inspired by computer engineering.



6 Inputs and outputs to the device are defined and the component parts are no longer explicitly considered (this work).

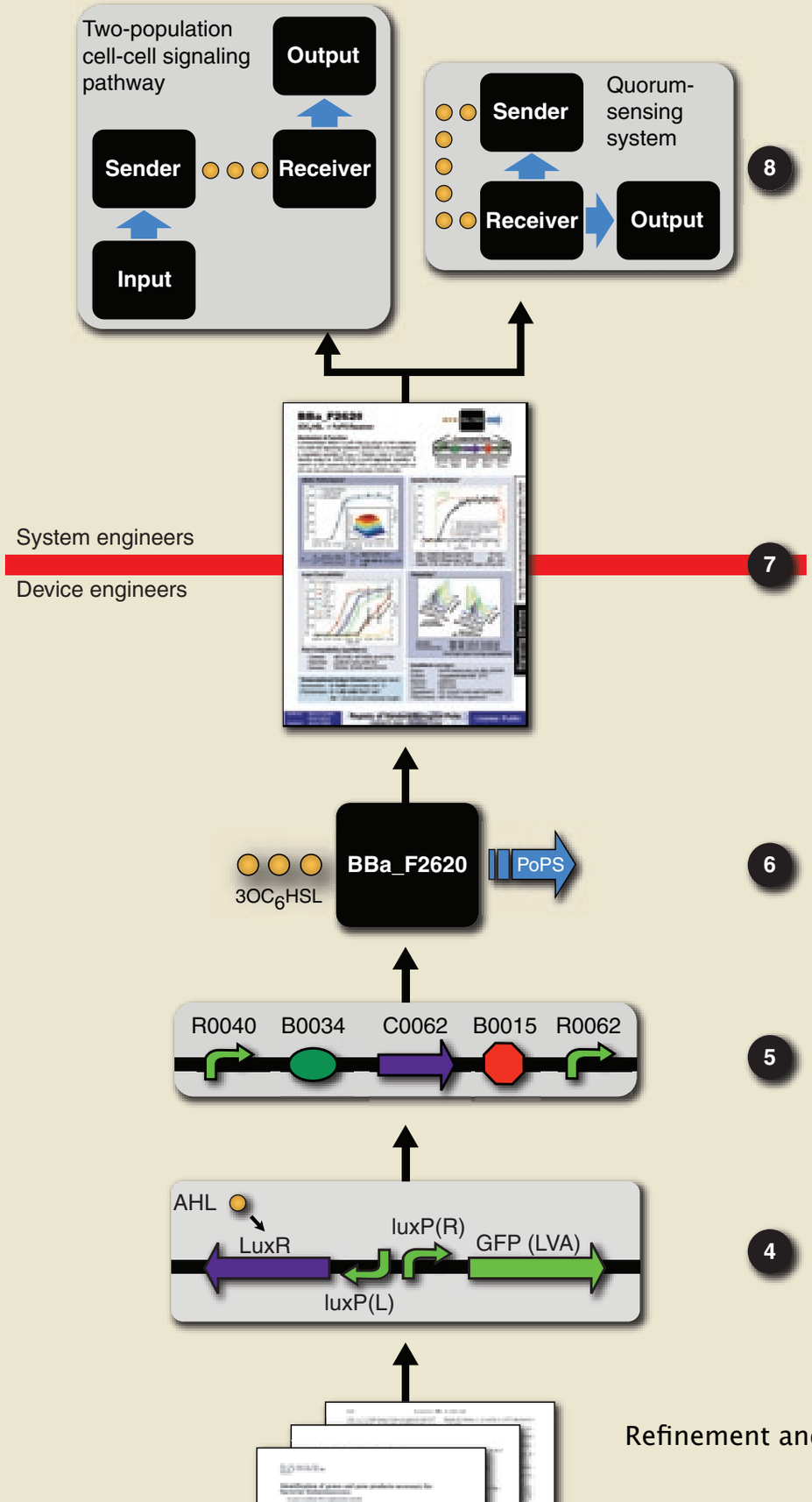
5 Engineers reimplement the receiver using BioBrick standard biological parts, thereby enabling ready reuse of the device (this work).

4 Engineers construct a proof-of-principle device using a subset of the natural quorum-sensing regulatory elements[14,15,25–29].

3 The mechanisms and genetic sequences necessary for bacterial quorum-sensing are shared via peer-reviewed publications. Such publications are currently the major channel of communication between biologists and device engineers[22–24].

2 Biologists elucidate the minimal set of genetic elements encoding quorum-sensing regulated bioluminescence (the lux genes of *V. fischeri*)[24].

1 Scientists identify a bioluminescent bacteria (*Vibrio fischeri*) that colonizes the light organ of a squid (*Euprymna scolopes*)[22]. Bioluminescence is regulated via quorum-sensing (cell-cell communication) between individual *V. fischeri* bacteria[23].



The receiver is used in systems in which the device characteristics fulfill the system specification (http://partsregistry.org/).

The behavior of the receiver is characterized to produce a device datasheet. The datasheet forms the interface between device and system engineers, eliminating the need for extensive interaction between the two groups (this work).

6 Inputs and outputs to the device are defined and the component parts are no longer explicitly considered (this work).

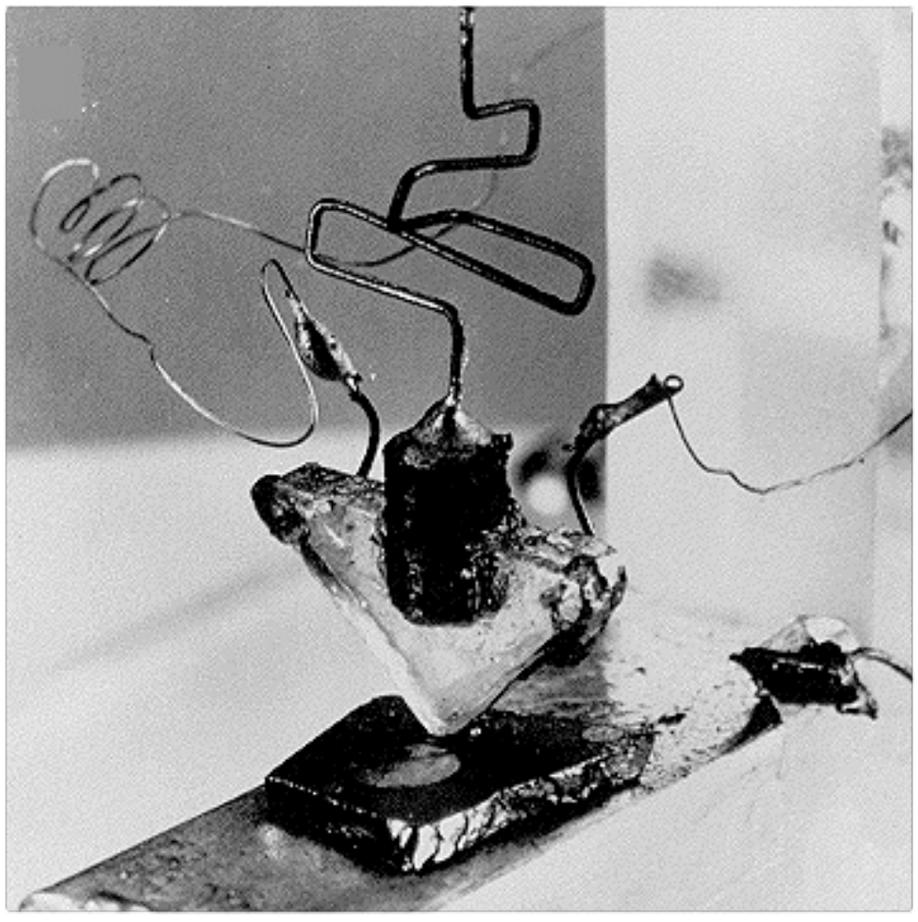
5 Engineers reimplement the receiver using BioBrick standard biological parts, thereby enabling ready reuse of the device (this work).

4 Engineers construct a proof-of-principle device using a subset of the natural quorum-sensing regulatory elements[14,15,25–29].

Refinement and Standardization of Synthetic Biological Parts and Devices, Canton et al. 2008

The Problem

We Build This



*transistor, **v1***

We Expect This

MOSPEC

NPN SILICON HIGH-VOLTAGE TRANSISTORS

... designed for use general-purpose, high voltage applications requiring high f_T

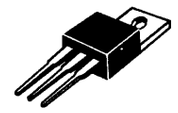
FEATURES:
*Collector-Emitter Sustaining Voltage-
$V_{CEO(sus)}$ = 350 V (Min)@ I_C=2.5 mA
* DC Current Gain-
hFE = 40 (Min.) @ I_C = 100 mA- MJE2361T
* Current Gain-Bandwidth Product
f_T=10 MHz (Typ) @ I_C =50 mA

NPN
MJE2360T
MJE2361T

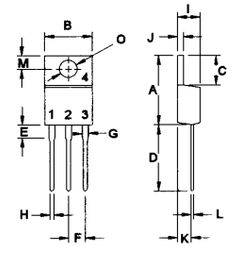
0.5 AMPERE
POWER
TRANASISTORS
350 VOLTS
30 WATTS

MAXIMUM RATINGS

Characteristic	Symbol	Rating	Unit
Collector-Emitter Voltage	V_{CEO}	350	V
Collector-Emitter Voltage	V_{CEV}	375	V
Emitter-Base Voltage	V_{EBO}	6.0	V
Collector Current - Continuous - Peak	I_C I_{CM}	0.5 1.0	A
Base current	I_B	0.25	A
Total Power Dissipation @T_C = 25°C Derate above 25°C	P_D	30 0.24	W W/°C
Operating and Storage Junction Temperature Range	T_J , T_{STG}	-65 to +150	°C



TO-220



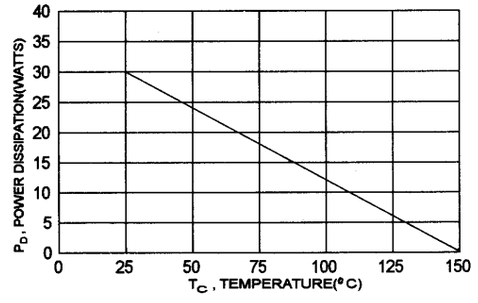
PIN 1.BASE
2.COLLECTOR
3.EMITTER
4.COLLECTOR(CASE)

DIM	MILLIMETERS	
	MIN	MAX
A	14.68	15.31
B	9.78	10.42
C	5.01	6.52
D	13.06	14.62
E	3.57	4.07
F	2.42	3.66
G	1.12	1.36
H	0.72	0.96
I	4.22	4.98
J	1.14	1.38
K	2.20	2.97
L	0.33	0.55
M	2.48	2.98
O	3.70	3.90

THERMAL CHARACTERISTICS

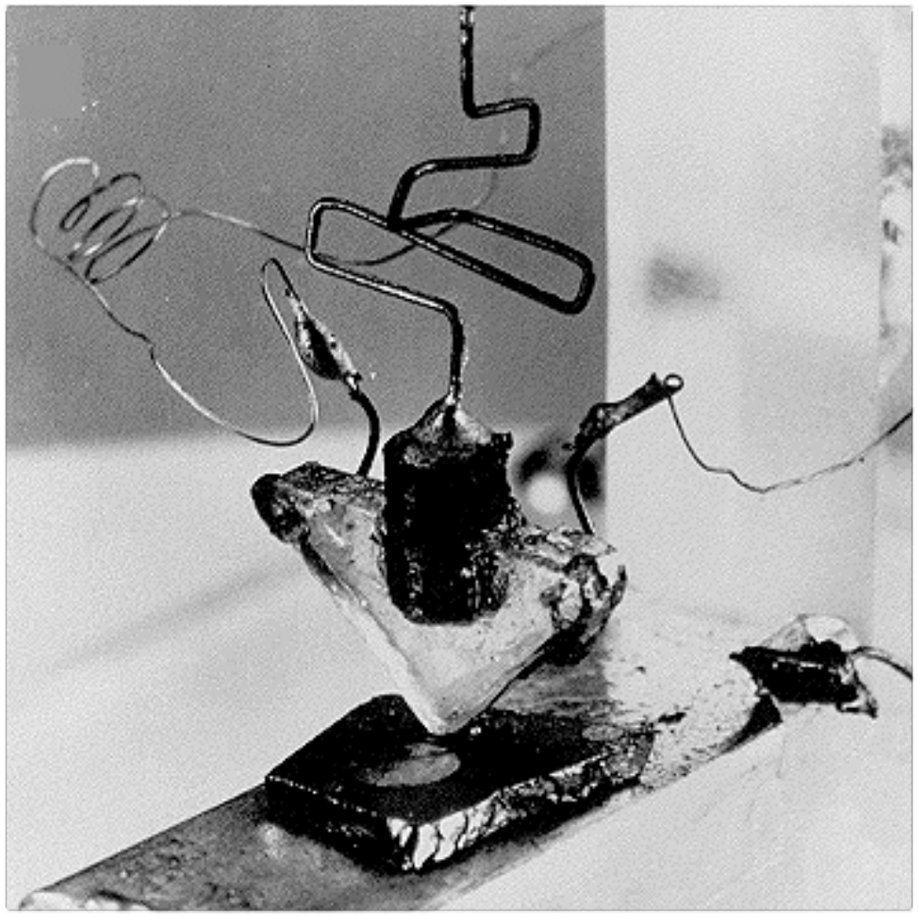
Characteristic	Symbol	Max	Unit
Thermal Resistance Junction to Case	Rθjc	4.167	°C/W

FIGURE -1 POWER DERATING



The Problem

We Build This



*transistor, **v1***

We Expect This

MOSPEC

NPN SILICON HIGH-VOLTAGE TRANSISTORS

... designed for use general-purpose, high voltage applications requiring high f_T

FEATURES:
*Collector-Emitter Sustaining Voltage-
$V_{CEO(SUS)}$ = 350 V (Min)@ I_C=2.5 mA
* DC Current Gain-
hFE = 40 (Min.) @ I_C = 100 mA- MJE2361T
* Current Gain-Bandwidth Product
f_T=10 MHz (Typ) @ I_C =50 mA

NPN
MJE2360T
MJE2361T

0.5 AMPERE
POWER
TRANASISTORS
350 VOLTS
30 WATTS

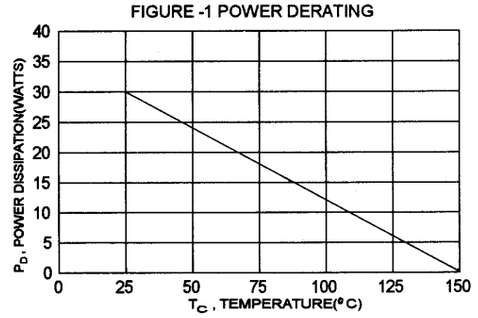
MAXIMUM RATINGS

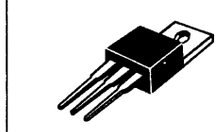
Characteristic	Symbol	Rating	Unit
Collector-Emitter Voltage	V_{CEO}	350	V
Collector-Emitter Voltage	V_{CEV}	375	V
Emitter-Base Voltage	V_{EBO}	6.0	V
Collector Current - Continuous - Peak	I_C I_{CM}	0.5 1.0	A
Base current	I_B	0.25	A
Total Power Dissipation @T_C = 25°C Derate above 25°C	P_D	30 0.24	W W/°C
Operating and Storage Junction Temperature Range	T_J , T_{STG}	-65 to +150	°C

THERMAL CHARACTERISTICS

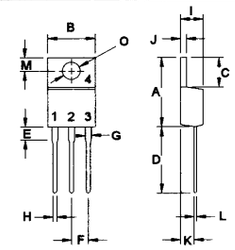
Characteristic	Symbol	Max	Unit
Thermal Resistance Junction to Case	Rθjc	4.167	°C/W

FIGURE -1 POWER DERATING





TO-220

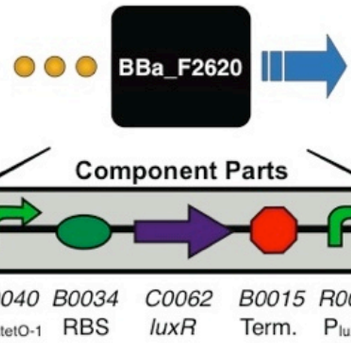


PIN 1.BASE
2.COLLECTOR
3.EMITTER
4.COLLECTOR(CASE)

DIM	MILLIMETERS	
	MIN	MAX
A	14.68	15.31
B	9.78	10.42
C	5.01	6.52
D	13.06	14.62
E	3.57	4.07
F	2.42	3.66
G	1.12	1.36
H	0.72	0.96
I	4.22	4.98
J	1.14	1.38
K	2.20	2.97
L	0.33	0.55
M	2.48	2.98
O	3.70	3.90

BBa_F2620

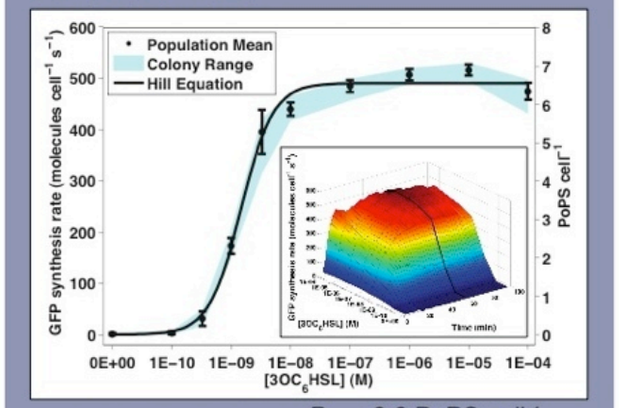
3OC$_6$HSL → PoPS Receiver



Mechanism & Function

A transcription factor (LuxR) that is active in the presence of a cell-cell signaling molecule (3OC$_6$HSL) is controlled by a regulated operator ($P_{LtetO-1}$). Device input is 3OC$_6$HSL. Device output is PoPS from a LuxR-regulated operator. If used in a cell containing TetR then a second input such as aTc can be used to produce a Boolean AND function.

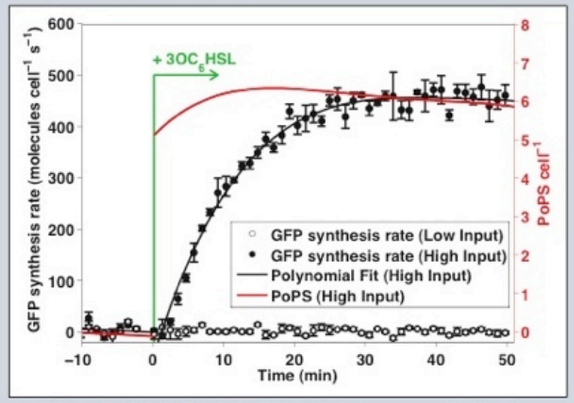
Static Performance*



$$P_{out} = \frac{P_{max}[3OC_6HSL]^n}{K^n + [3OC_6HSL]^n}$$

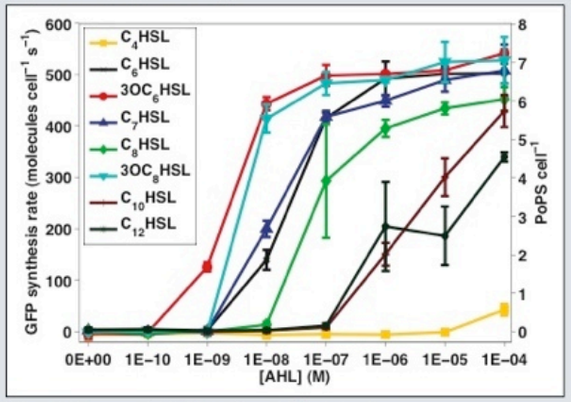
P_{max}: **6.6** PoPS cell^{-1}
K: **1.5E-09** M 3OC$_6$HSL
n: **1.6**

Dynamic Performance*

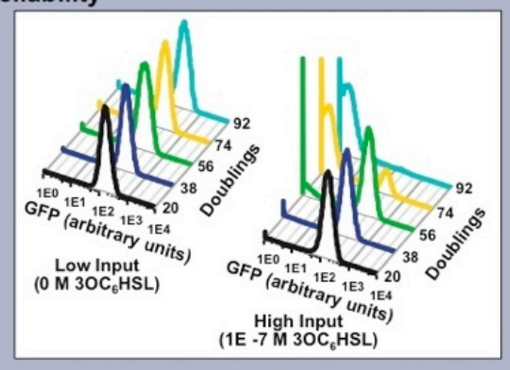


BBa_F2620 Response Time: ***<1** min*
BBa_T9002 Response Time: ***6±1** min*
Inputs: 0 M (Low), 1E-07 M (High) 3OC$_6$HSL

Input Compatibility*



Reliability**



Genetic: **>92/>56** culture doublings
Performance: **>92/>56** culture doublings
(low/high input during propagation)

Part Compatibility (qualitative)

Chassis: *MC4100*, *MG1655*, and *DH5α*
Plasmids: *pSB3K3* and *pSB1A2*
Devices: *E0240*, *E0430* and *E0434*

Transcriptional Output Demand (low/high input)

Nucleotides: **0 / 6xNt** nucleotides cell^{-1} s^{-1}
Polymerases: **0 / 1.5E-1xNt** RNAP cell^{-1}
(**Nt** = downstream transcript length)

Conditions (abridged)

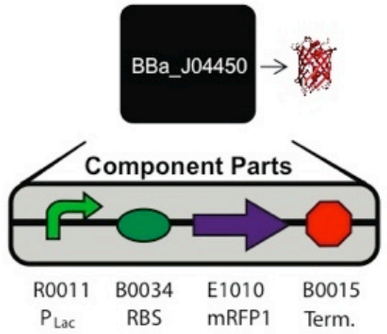
Output: PoPS measured via *BBa_E0240*
Culture: Supplemented M9, 37°C
Plasmid: pSB3K3
Chassis: MG1655
**Equipment:* PE Victor3 multi-well fluorimeter
***Equipment:* BD FACScan cytometer

Authors: Barry Canton
Ania Labno
Updated: March 2008

BBa_J04450

Red Fluorescent Protein Generator

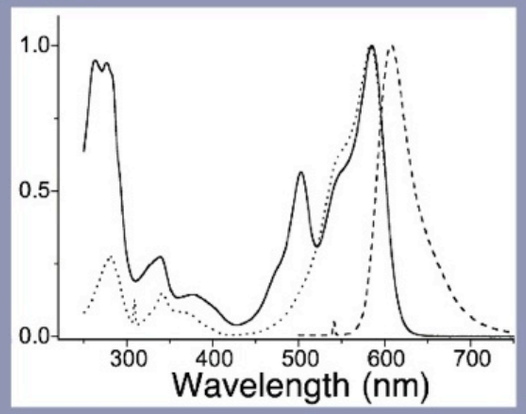
DNA



Mechanism & Function

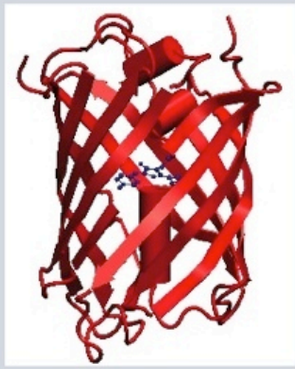
The expression of the gene for mRFP1 is controlled by a regulated operator (PLac). If used in a cell containing lac repressor (LacI) then an input such as IPTG can be used to modulate the expression of mRFP1.

Spectra



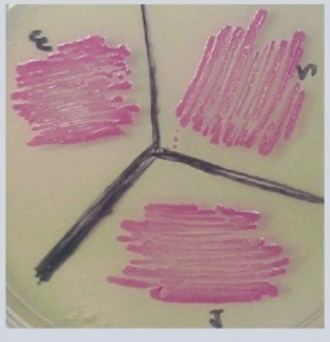
solid: absorpotion, dotted: excitation, dashed: emission

Structure



Protein structure for mRFP1 with the chromophore chemical structure shown in blue.

Usage



Cells expressing mRFP1 are visibly red under white light and for optimal fluorescence detection should be excited at ~584nm and detected with a 600nm long pass filter.

Origin

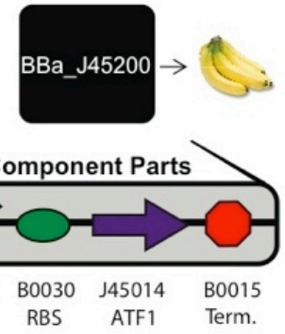
mRFP1 is an engineered variant of dsRED fluorescent protein originally isolated in *Discosoma sp.* (Mushroom Coral)

Reporter Devices

BBa_J45200

Banana Odor Generator

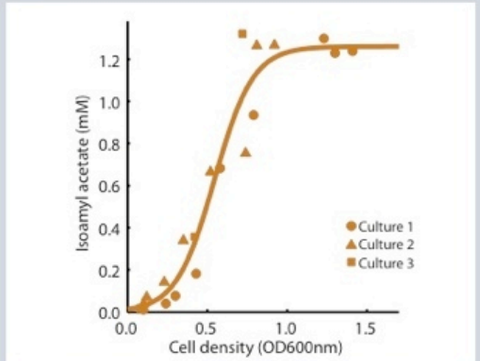
DNA



Mechanism & Function

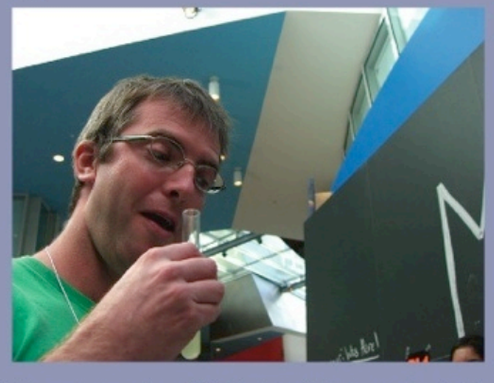
The banana odor generator (BBa_J45200) catalyzes the conversion of the precursor isoamyl alcohol to the odor isoamyl acetate that has a banana smell. The biosynthetic device is composed of two transcriptional devices: a constitutive transcription source (BBa_R0040) and an odor enzyme generator (BBa_J45199). Odor enzyme generators produce as output an enzyme that catalyzes production of an odor from a chemical precursor.

Activity



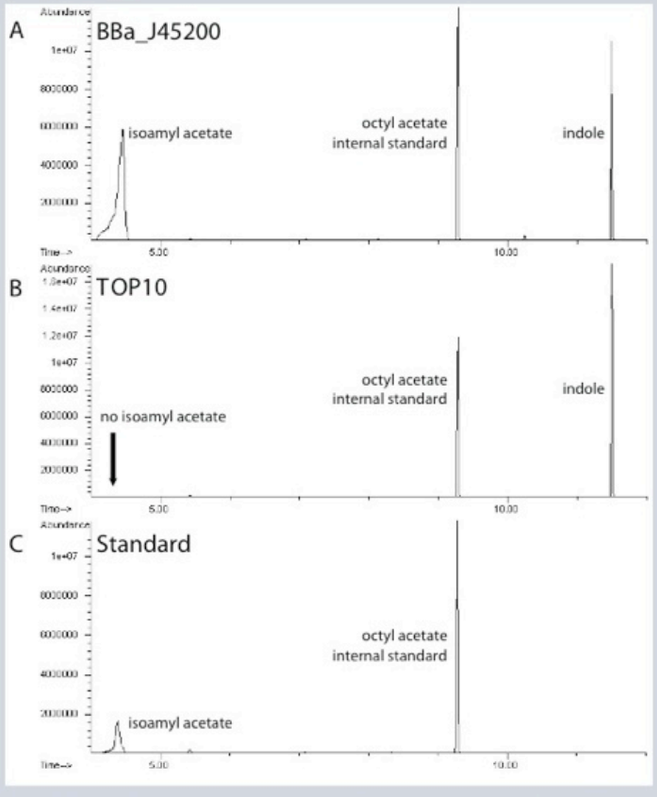
Isoamyl acetate concentration increases with cell density

Usage



Cells expressing ATF1 should be grown in the presence of isoamyl alcohol (5mM).

Chromatography

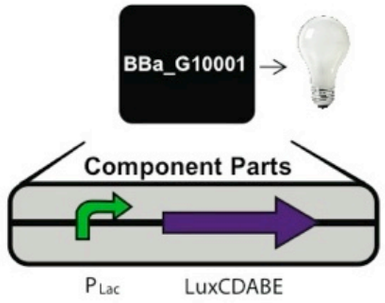


High levels of isoamyl acetate are produced when the precursor isoamyl alcohol is added to the culture medium (A), unless the cellular chassis (E. coli strain TOP10) does not contain J45200 (B). The retention time of the isoamyl acetate peak from J45200 is identical to that of the pure isoamyl acetate standard (C). Most E. coli strains produce indole. Octyl acetate was used as an internal standard for all samples containing isoamyl acetate

BBa_G10001

Visible Light Generator

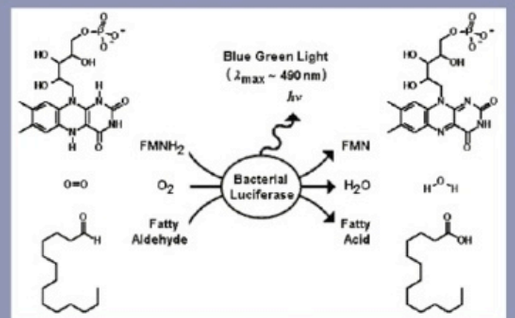
DNA



Mechanism & Function

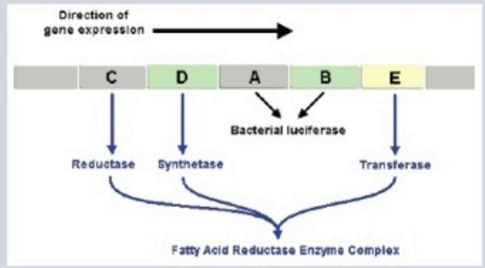
The expression of the Lux operon is controlled by a regulated operator (PLac). If used in a cell containing lac repressor (LacI) then an input such as IPTG can be used to modulate the expression of the Lux operon. When expressed this operon produces the necessary enzymes to generate the fatty aldehyde substrates as well as the luciferase enzyme that converts luciferin to visible light.

Reaction Mechanism



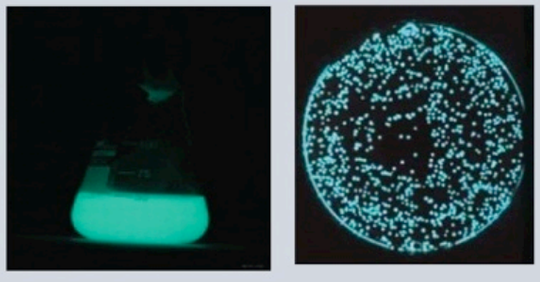
Bacterial luciferin is a reduced riboflavin phosphate (FMNH2, above) which is oxidized in association with a long-chain aldehyde, oxygen, and a luciferase to produce visible light.

Lux Operon



The fatty acid reductase enzyme complex is needed to recycle the fatty aldehyde substrate in the reaction and luciferase is required to catalyze the reaction. No other exogenous enzymes are necessary since FMNH2 is provided by the native electron transport chain in *E. coli*.

Usage

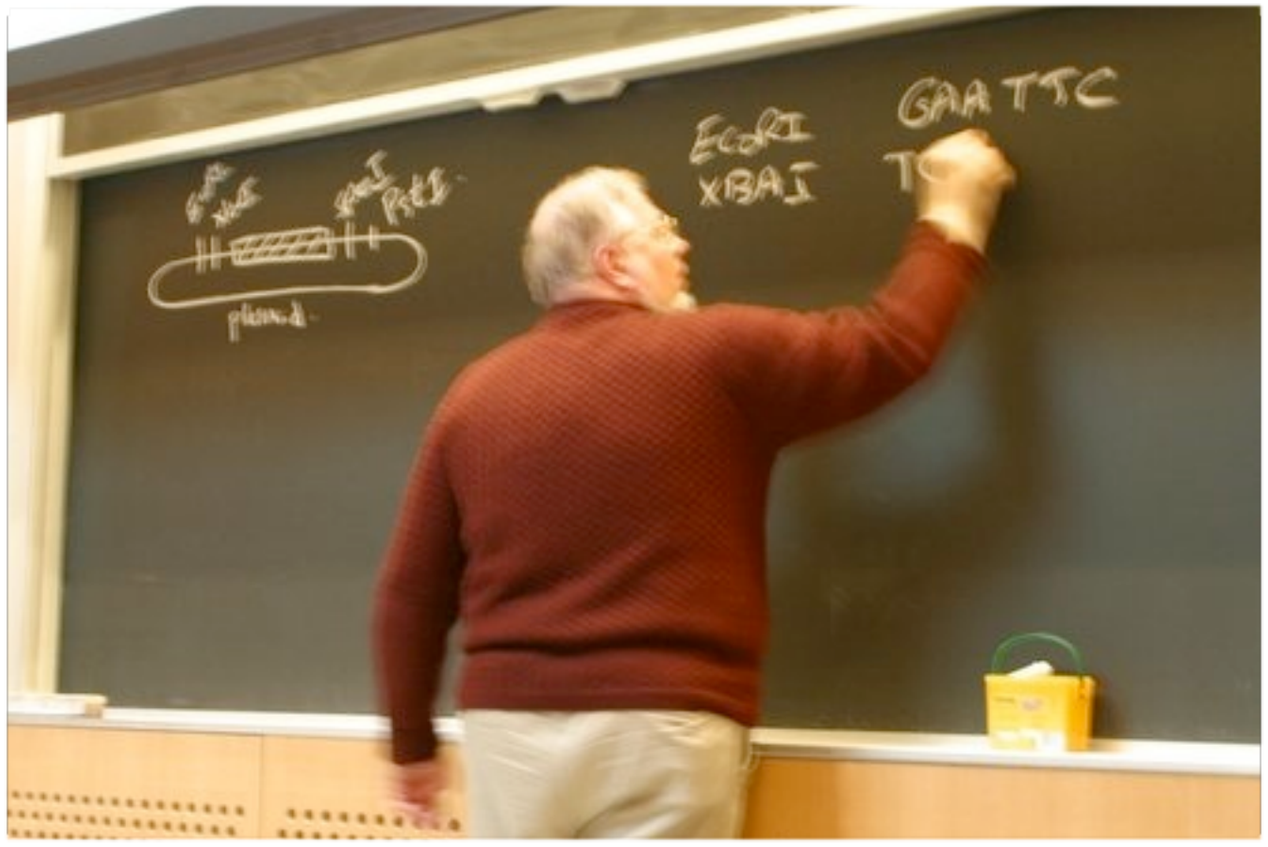


Cells expressing the lux operon are visible in low light in liquid culture or as colonies.

Origin

The Lux operon was isolated from *Vibrio fischeri* a bacteria found predominantly in symbiosis with marine animals such as the bobtail squid (above).

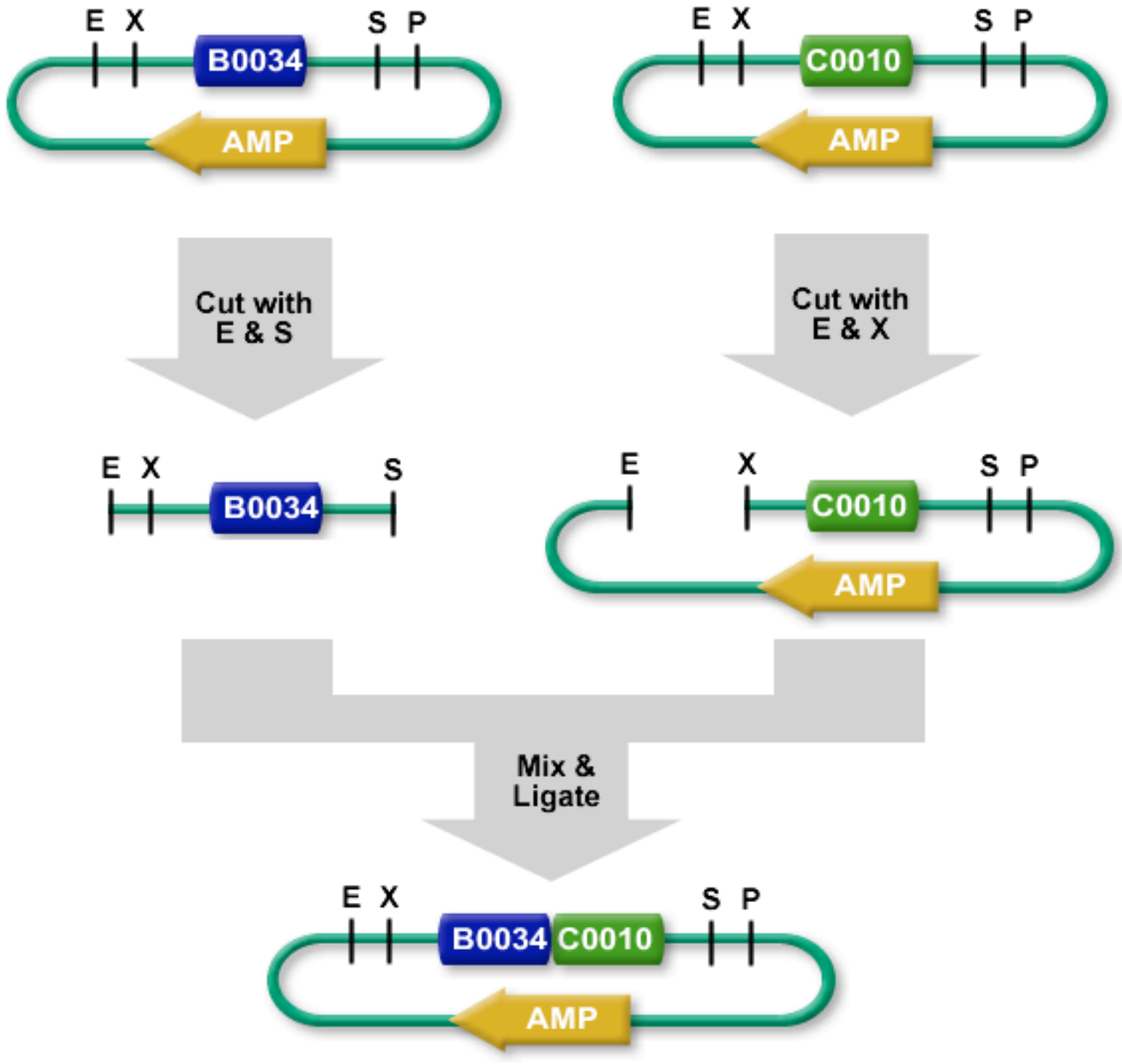
BioBricks



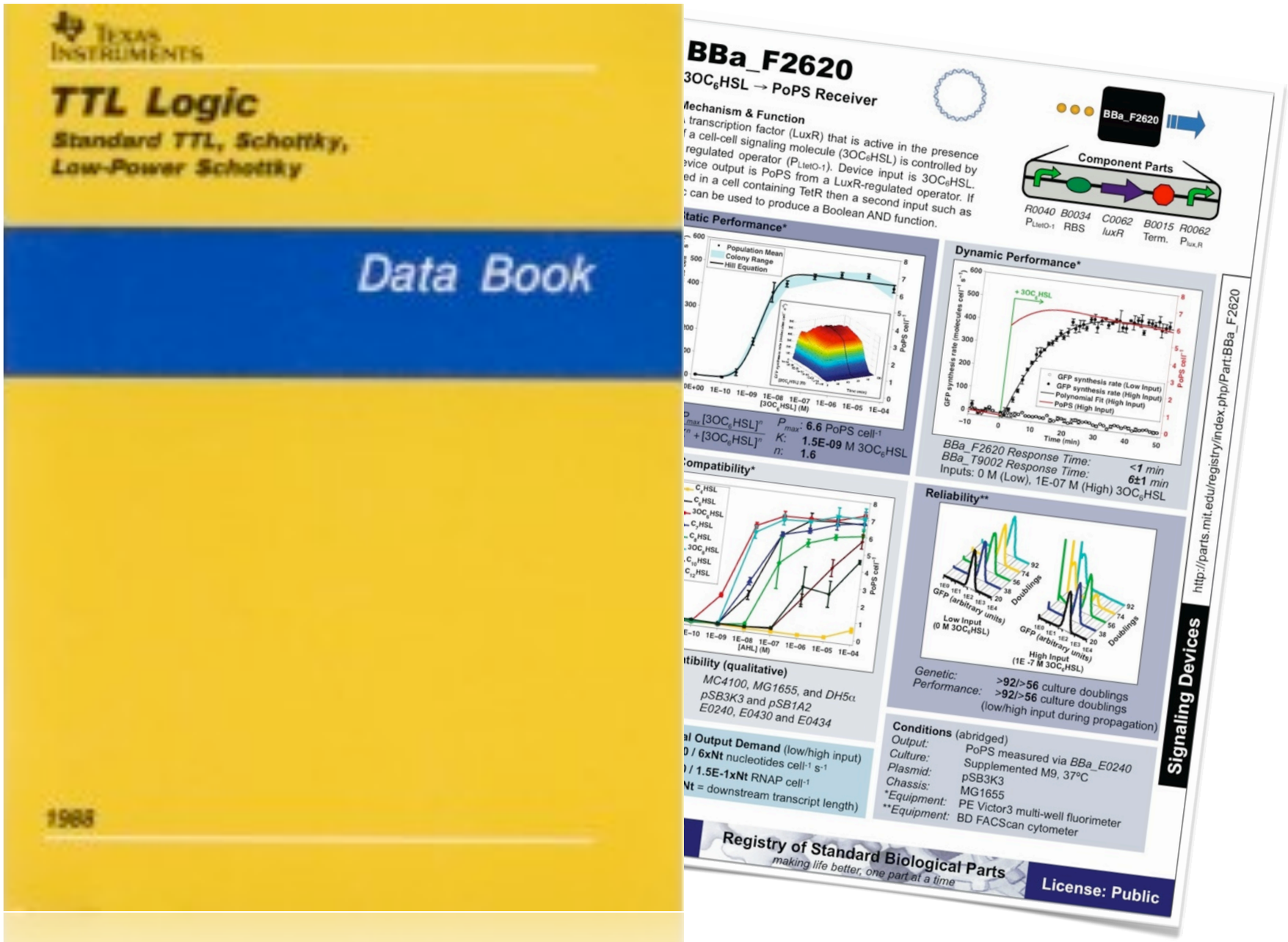
"I was surprised to find that molecular biologists were spending something like 50% of their time at the bench just on manipulating DNA to build particular constructs" *-Tom Knight*

BioBrick Standard Assembly

(BBa)



A Catalog


Texas Instruments
TTL Logic
Standard TTL, Schottky,
Low-Power Schottky
Data Book
1988
BBa_F2620
3OC6HSL → PoPS Receiver
Mechanism & Function
Component Parts
R0040 B0034 C0062 B0015 R0062
Static Performance*
Dynamic Performance*
Compatibility*
Reliability**
Conditions (abridged)
Signaling Devices
http://parts.mit.edu/registry/index.php/Part:BBa_F2620
Registry of Standard Biological Parts
making life better, one part at a time
License: Public

Part Types - partsregistry.org

http://partsregistry.org/Part_Types

Registry of Standard Biological Parts

page discussion view source history

Part Types

Browse parts by projects:

iGEM 2007 | iGEM 2006 | iGEM 2005 | Labs | Courses | Featured Parts

Or browse parts by part categories:

Systems

- Measurement
- Measurement (Under Development)
- Projects(empty)

Devices

- Reporters
- Inverters
- Signalling
- Protein Generator
- Composite Devices
- Measurement

Parts

- Ribosome Binding Sites
- Regulatory
- RNA
- DNA
- Protein Coding
- Terminators
- Conjugation

Chassis

- E.coli Strains
- Cell-Free Systems

Mammalian

Vectors

- Plasmids

Other

- Yeast Parts
- Construction Intermediate
- PCR Primer
- Tags
- Other
- Deleted
- Bacteriophage T7

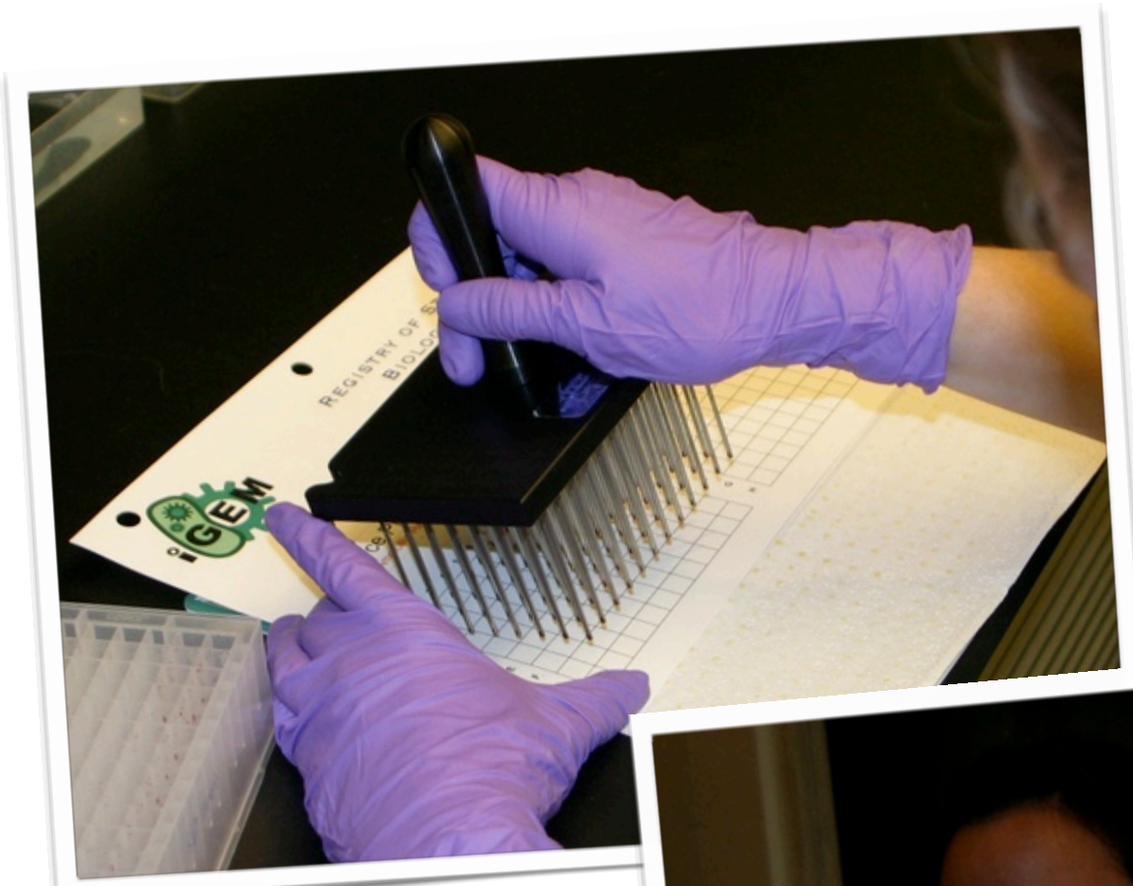
- For more information on each part type, click the ? for help documentation next to the category name.
- To discuss how to measure the functions of these parts visit Characterization of Parts

Recent changes What links here Related changes Upload file Special pages
Printable version Permanent link Privacy policy Disclaimers

- 6491 parts defined
- 1880 physically available

-July 2008

Parts Registry kits



NEWSLETTER

Homebrew Computer Club

Robert Reiling, Editor ☐ Post Office Box 626, Mountain View, CA 94042 ☐ **Joel Miller**, Staff Writer

Typesetting, graphics and editorial services donated by **Laurel Publications**, 17235 Laurel Rd., Los Gatos, CA 95030 (408) 353-3609

RANDOM DATA

By Robert Reiling

Computer clubs continue to form around the country...E. Brooner would like to have material to help him get started with the "Flathead Computer Society" in the Kalispell area. His Address is P.O. Box 236, Lakeside, Montana 59922.

Did you see the SOL terminal demonstrated by Bob Marsh at the Sept. 1st meeting? An excellent design that will interest hobbyists and commercial users alike. It's available from Processor Technology, 6200 Hollis St., Emeryville, CA 94608. Write them for prices and specifications.

The OSI Systems Journal has been sent to all OSI customers (free—at least for the time being). It's a bi-monthly magazine with plans to go monthly in the future. There are 28 pages in the first issue (August 1976, Vol. 1, No. 1) with a hardware feature covering the OSI 440 Video Graphics System and software, features concerning Tiny BASIC for the 6800 and a Graphics Editor for the 6502. It also includes OSI product and software catalog data. The BASIC is, of course, the 2K Tiny BASIC developed by Tom Pittman. Many of you have met Tom at the Homebrew computer Club meetings. The OSI Systems Journal is a good way to learn more about the OSI computer hardware and software along with helpful user information. The contact address is: The OSI Systems Journal, P.O. Box 134, Hiram, Ohio 44234.

KIM-1 users now have a newsletter. Eric Rehnke is producing the newsletter every 5-8 weeks, MOS Technology, Inc. helped get it started by sending copies to all known KIM owners. The user group, however, is independent of MOS Technology, Inc. The newsletter is devoted to KIM-1 support. Subscriptions are $5.00 for the next six issues. Contact "KIM-1 User Notes," c/o Eric C. Rehnke, Apt. 207, 7656 Broadview Rd., Parma, Ohio 44134.

The BAMUG club has a new contact address. It is BAMUG, c/o Timothy O'Hare, 1211 Santa Clara Ave., Alameda, CA 94501. Write Timothy for club information. I suggest you include a stamped, self-addressed envelope.

Beware of board snatchers! Glenn Ewing reports 11 boards were taken out of his IMSAI computer. The boards are: MPU, 4 RAM-4's, SIO-2, P10-4, PIC-8, PROM-4, IFM and FIB. Glenn suggests you consider providing good security for your computer and associated equipment. In his case the computer was in a locked office which was burglarized. In the event you have information on the above boards, write Lt. Glenn Ewing, Code 62EI, Naval Post Graduate School, Monterey, CA 93940.

For family and friends of people who always wanted to know about computers, but didn't want to ask them, four easy-going classes are available starting Oct. 19th on Tuesdays from 7 to 9 p.m. You can learn how computers work and what they can and can't do. You will also have some of the jargon deciphered, see what you can do with a computer, play some games and learn to program. The cost is $25. Contact the Community Computer Center, 1919 Menalto Ave., Menlo Park, CA 94025, phone (415) 325-4444.

A call for papers in personal computing has been issued by the 1977 National Computer Conference. The conference is scheduled for June 13-16, 1977. I have a few copies of the guidlines if you would like to submit a paper.

The First West Coast Computer Faire will be held April 16 and 17, 1977 at the San Francisco Civic Auditorium. This faire is shaping up rapidly. If you would like to lead a conference or participate in a conference session, please contact me. More information about the Faire is in the accompanying article.☐

THE FIRST WEST COAST COMPUTER FAIRE

A Call For Papers And Participation

The San Francisco Bay Area is finally going to have a major conference and exhibition exclusively concerned with personal and home computing—The First West Coast Computer Faire. And, it promises to be a massive one! It will take place in the largest convention facility in Northern California: The Civic Auditorium in San Francisco. It will be a two-and-a-half day affair, starting on Friday evening and running through Sunday evening, April 15-17.

It is being sponsored by a number of local and regional hobbyist clubs, educational organizations and professional groups. These include:

- The two largest amateur computer organizations in the United States—the Homebrew Computer Club and the Southern California Computer Society
- Both of the Bay Area chapters of the Association Of Computing Machinery—the San Francisco Chapter and the Golden Gate Chapter
- Stanford University's Electrical Engineering Department

DIYbio » Local Groups

http://diybio.org/local/

Google

as seen online!

search

DIYbio

Blog Home Local Groups Mailing List & Event Calendar Press Projects FriendFeed

Local Groups

There are DIYbioers all over the globe! See if there is a meetup near you on the map below. If there is not, add your location and your contact information to the map, so others can get in touch with you - just don't forget to update it once you start a regular meetup!

View a larger map, or to add yourself or your group to the map. You'll need to sign into your Google account in order to add a new point. It's a little unclear, so here's a screenshot of adding a new point

about us

DIYbio is an organization that aims to help make biology a worthwhile pursuit for citizen scientists, amateur biologists, and DIY biological engineers who value openness and safety. This will require mechanisms for amateurs to increase their knowledge and skills, access to a community of experts, the development of a code of ethics, responsible oversight, and leadership on issues that are unique to doing biology outside of traditional professional settings.

recent comments

Ana (Quo): Hola Fernando, Soy una redactora de la revista Quo y estoy ...

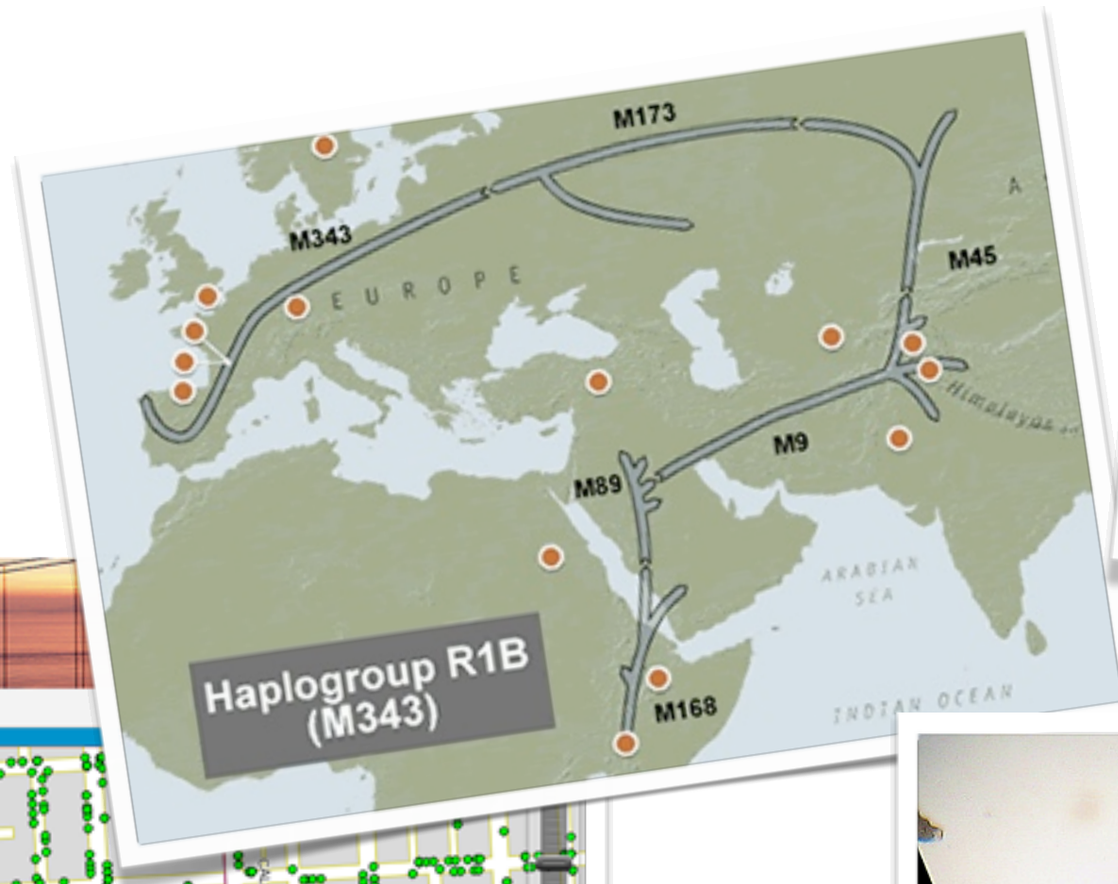
Nick See Weinberg: Would someone please add CodeCon to the DIYbio G-Cal? Thanks...

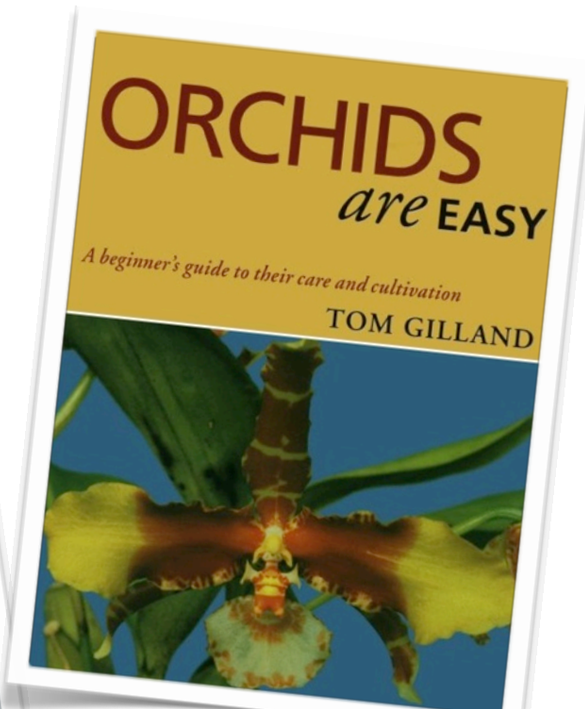
Charles Stone: Hey everyone!

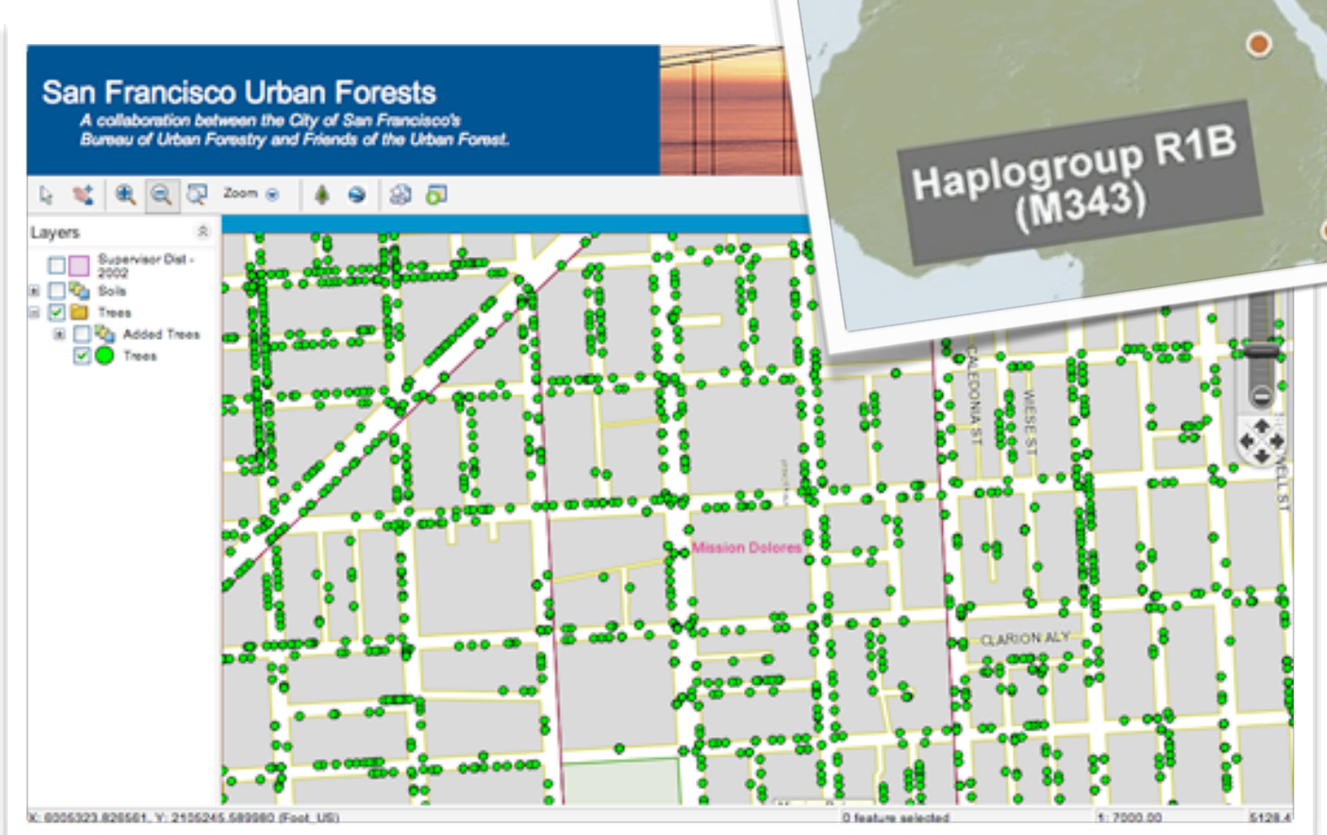
Transferring data from maps.google.com...

diybio is naturalism

macroscopic
to
microscopic







tardigrade

diybio is engineering

- graft a hybrid cranberry-apple tree

or

- add resveratrol production to yeast (healthier beer!)

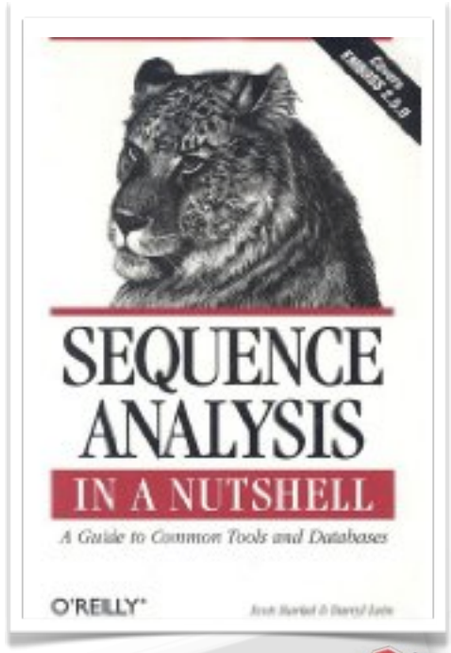
Ben Harris-Roxis / Flickr

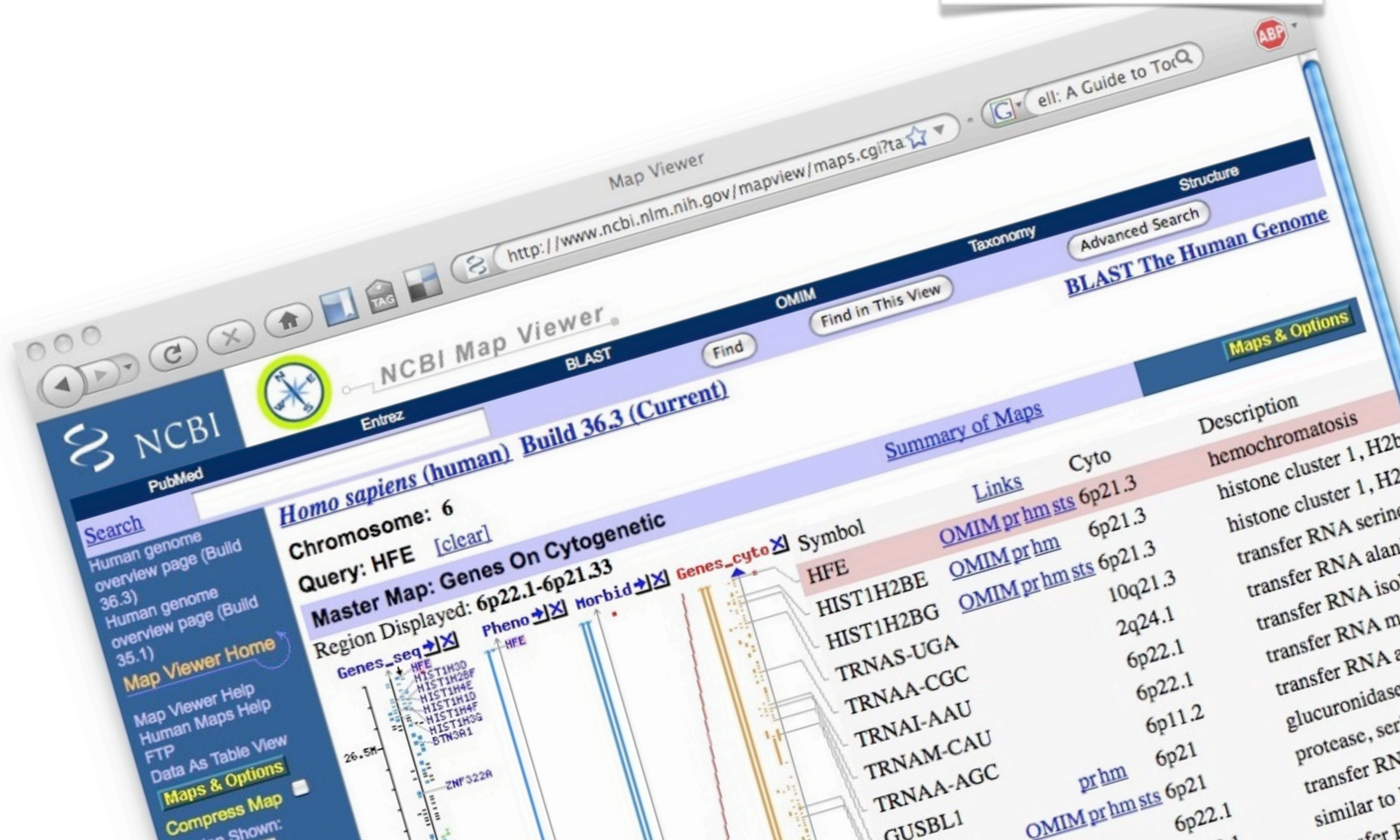
diybio is more

working on the SmartLab table, Dec 08

Alba, the fluorescent bunny (Eduardo Kac, 2000)

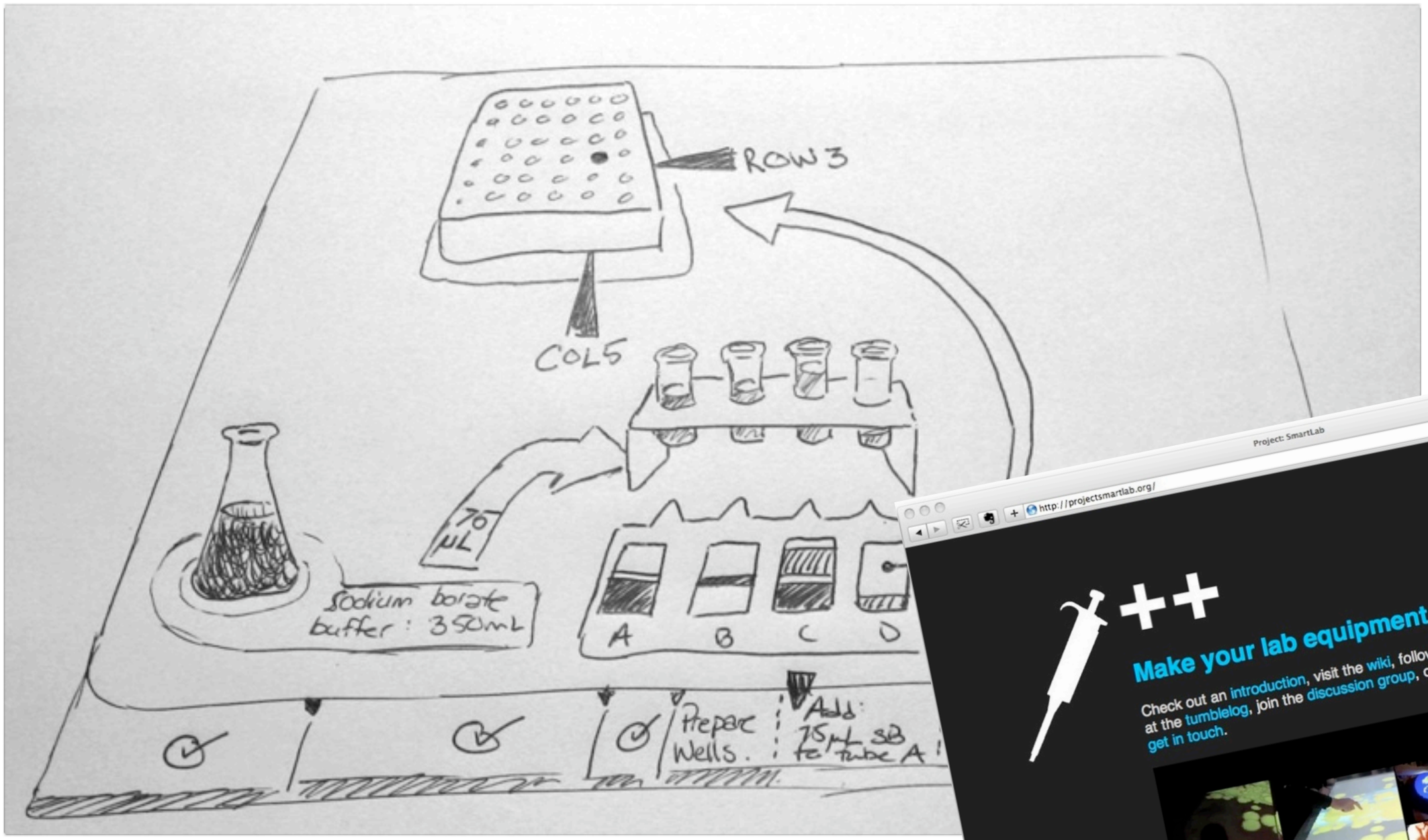
- hardware
- informatics
- art





SmartLab Project

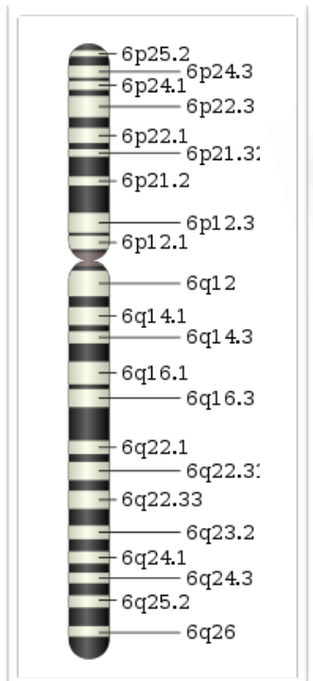
multitouch augmented reality lab bench for recording and teaching molecular biology

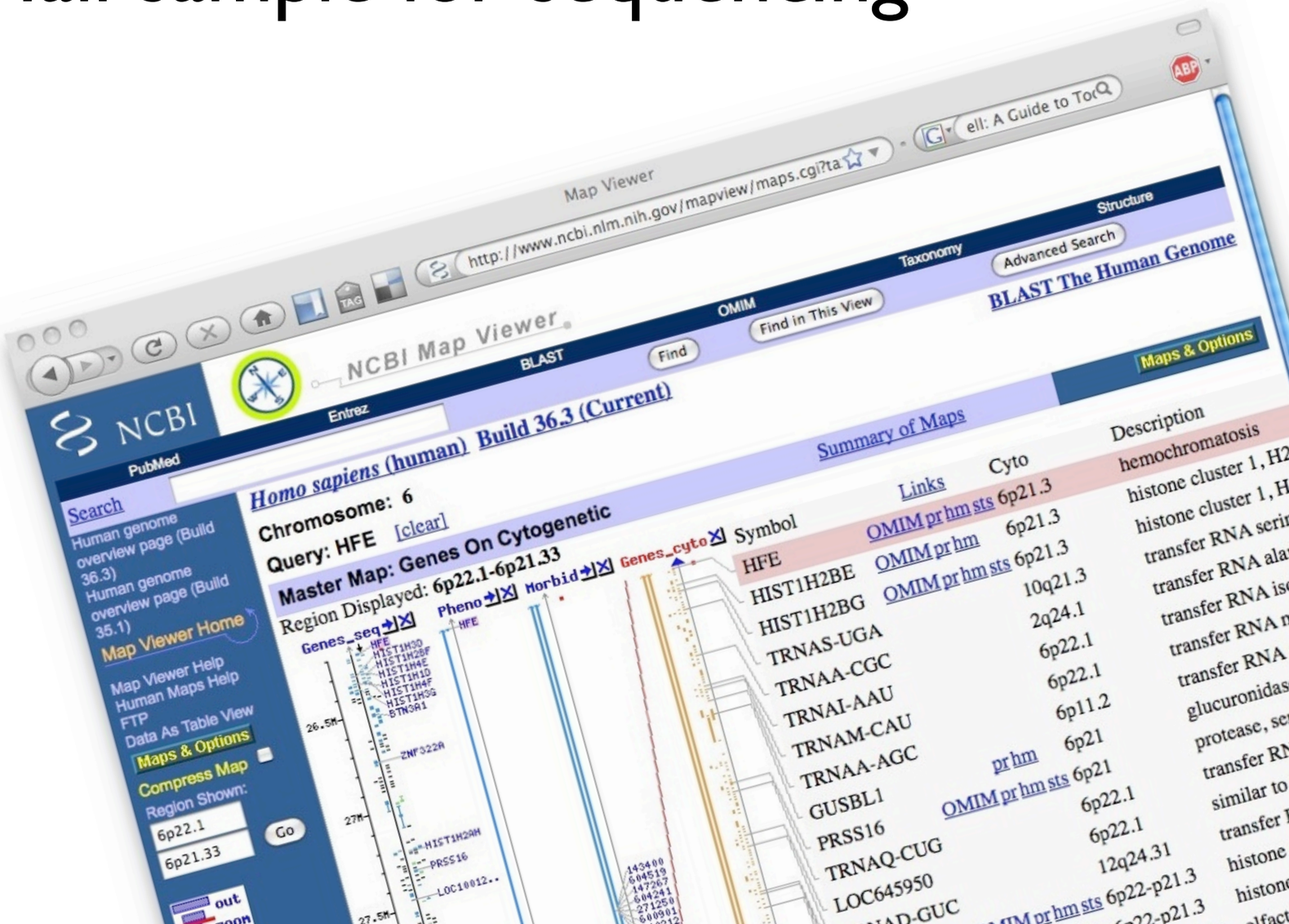


self-genotyping

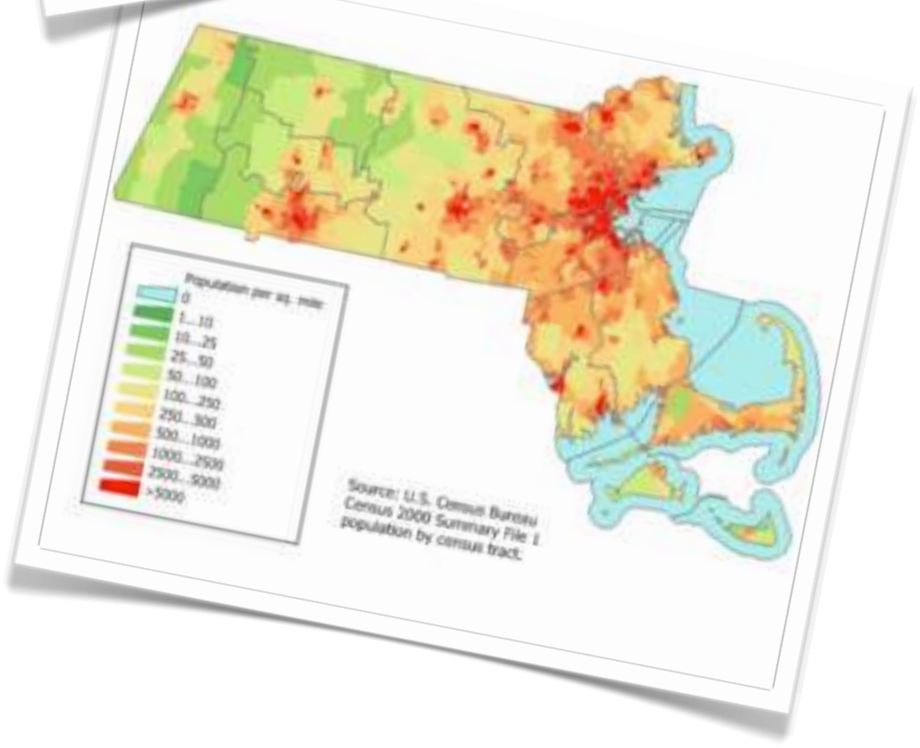
Is Kay a carrier of hemochromotosis on her 6th chromosome?

1. Allele-specific PCR at home
2. Mail sample for sequencing

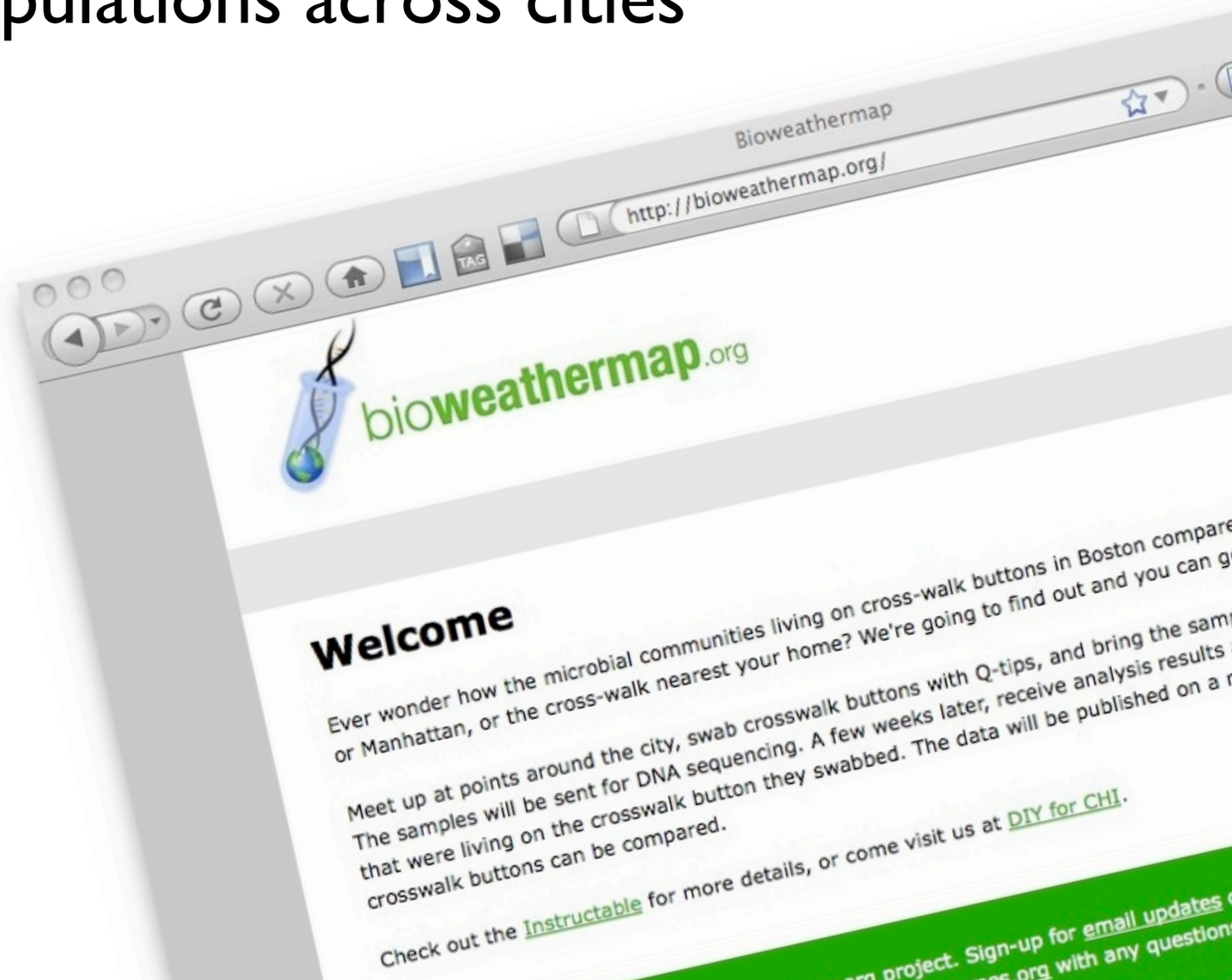




bioweathermaps



flashmob + science =
distributing tracking of bacterial populations across cities

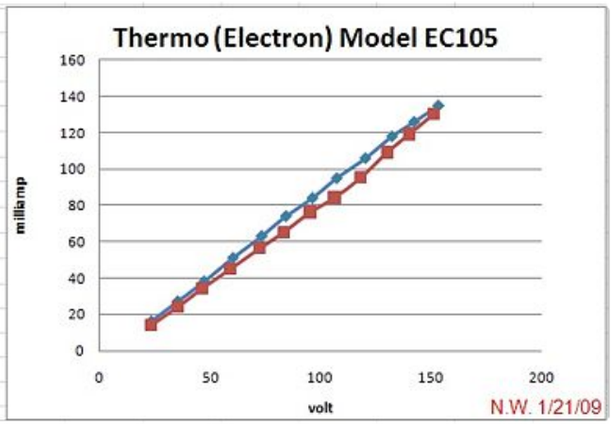


Gel Box 2.0

for sorting dna by size

the best commercial boxes cost > $1200.
build an open source alternative for ~$100

1x TAE		1x TAE + 1.2% Gel	
V	mA	V	mA
23	16	23	14
35	27	35	24
47	38	46	34
60	51	59	45
73	63	72	56
84	74	83	65
96	84	95	76
107	95	106	84
120	106	118	95
132	118	130	109
142	126	140	119
153	135	151	130



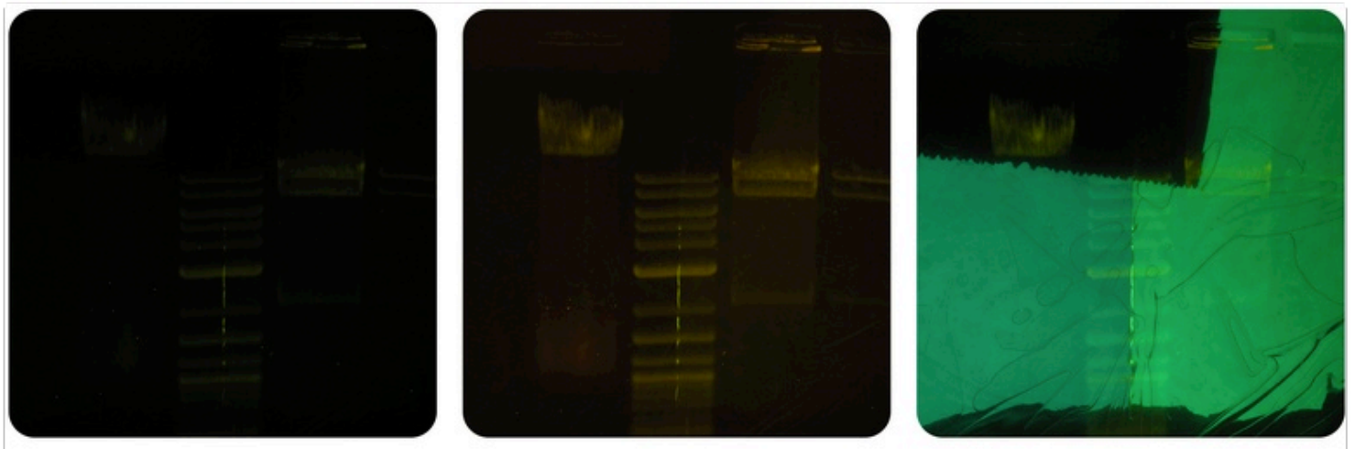
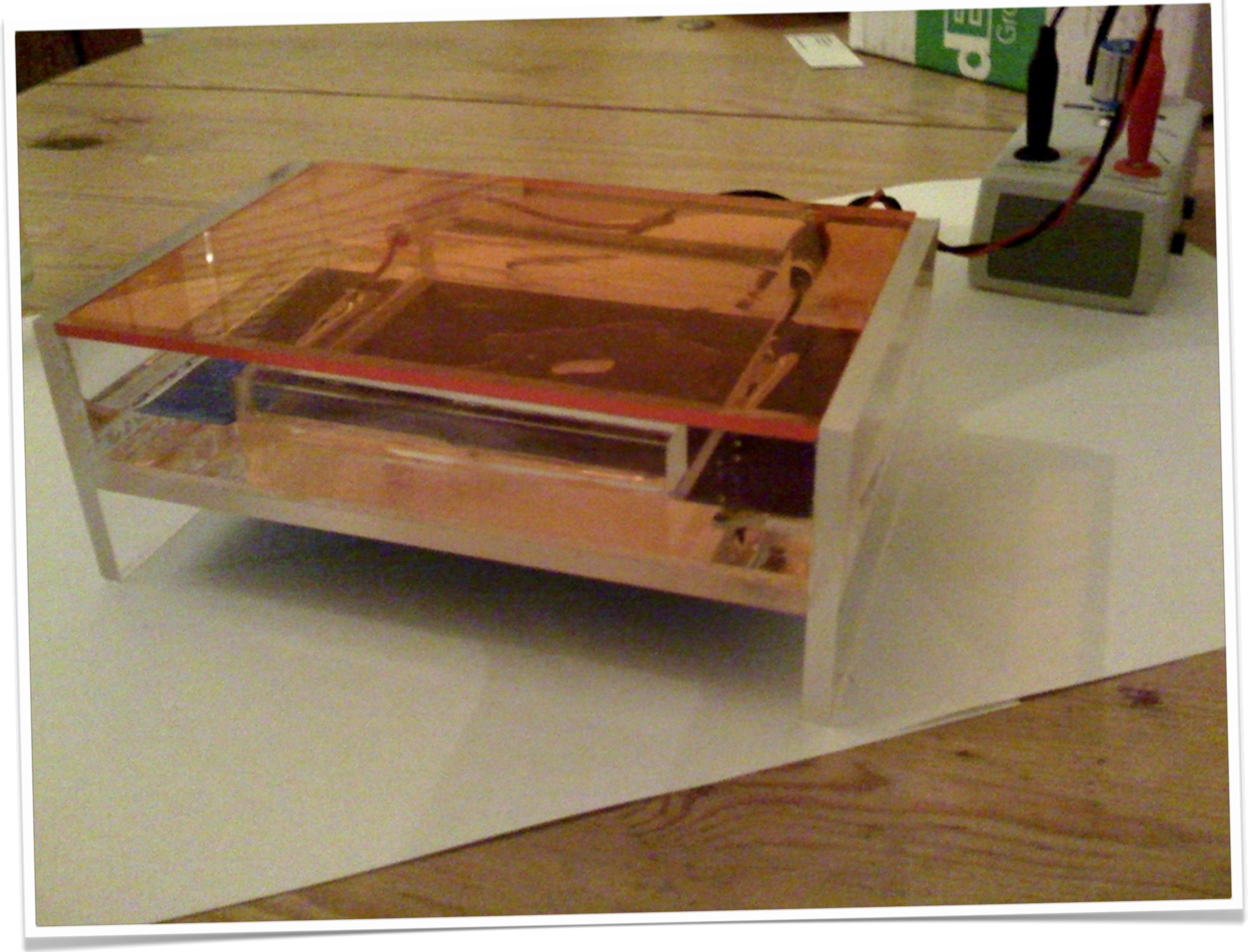


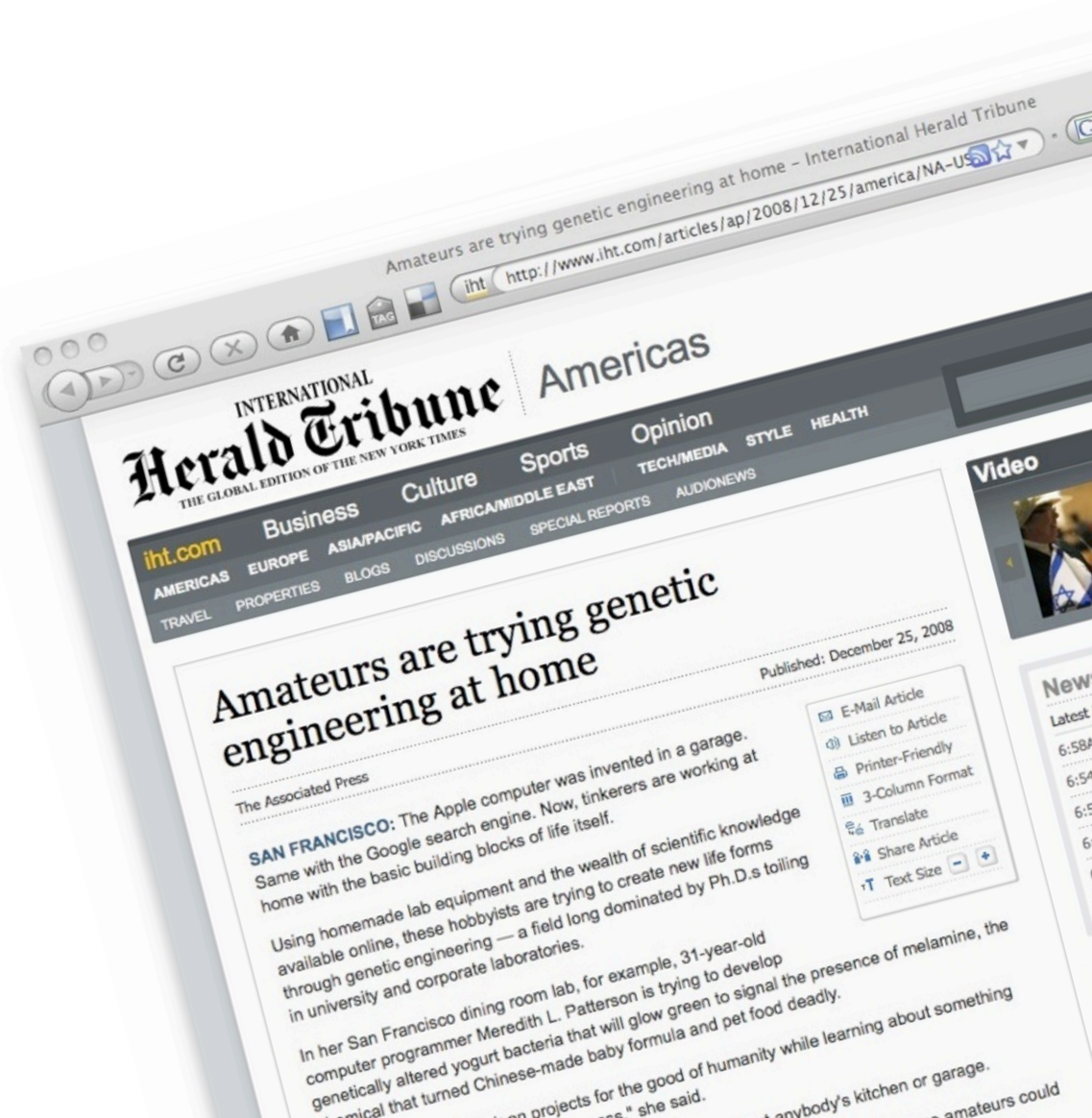
Image: Norman Wang - http://bit.ly/GelBox2-transilluminator_image

Gel Box 2.0 v0.1 circa feb 09 ($150)



GloGurt & Melaminometer

lactobacillus "hello world" +
biosensing melamine



$3000 lab

at a boston-based coworking space

testing diy hardware

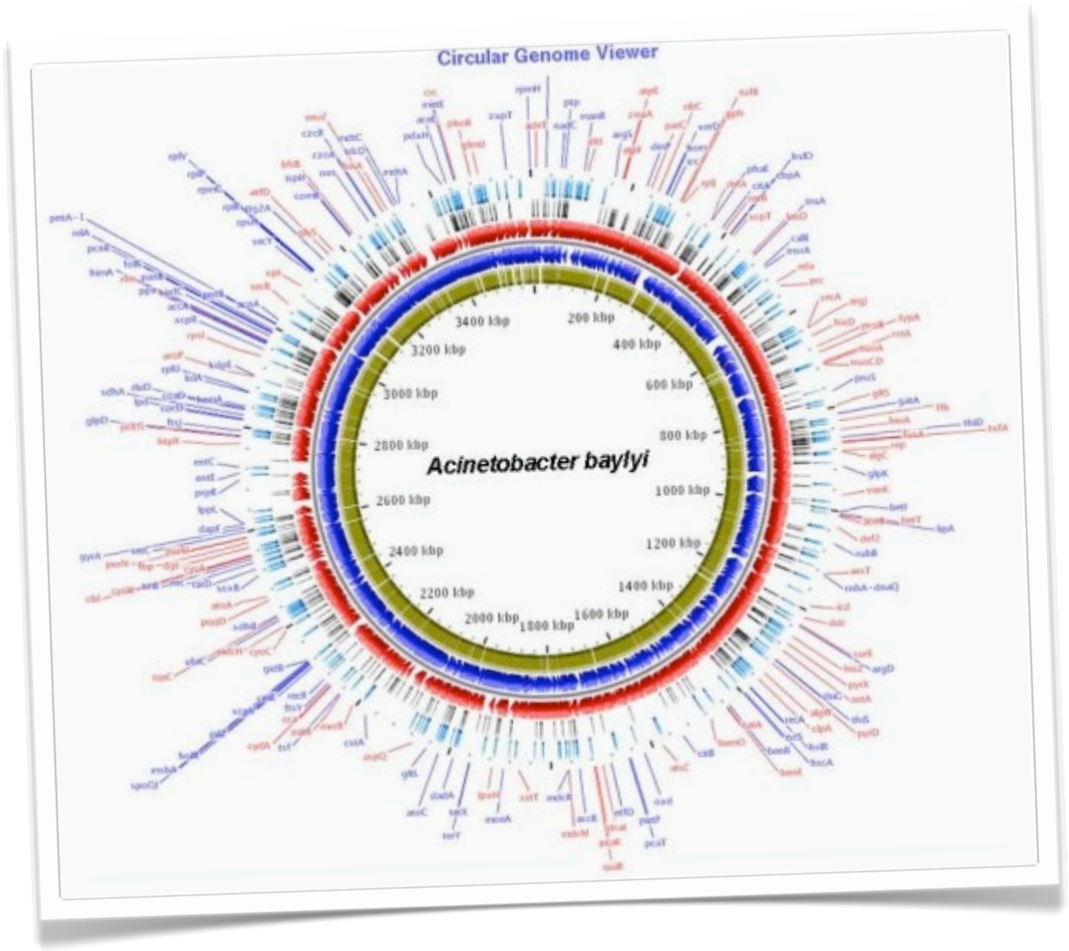
testing diy protocols

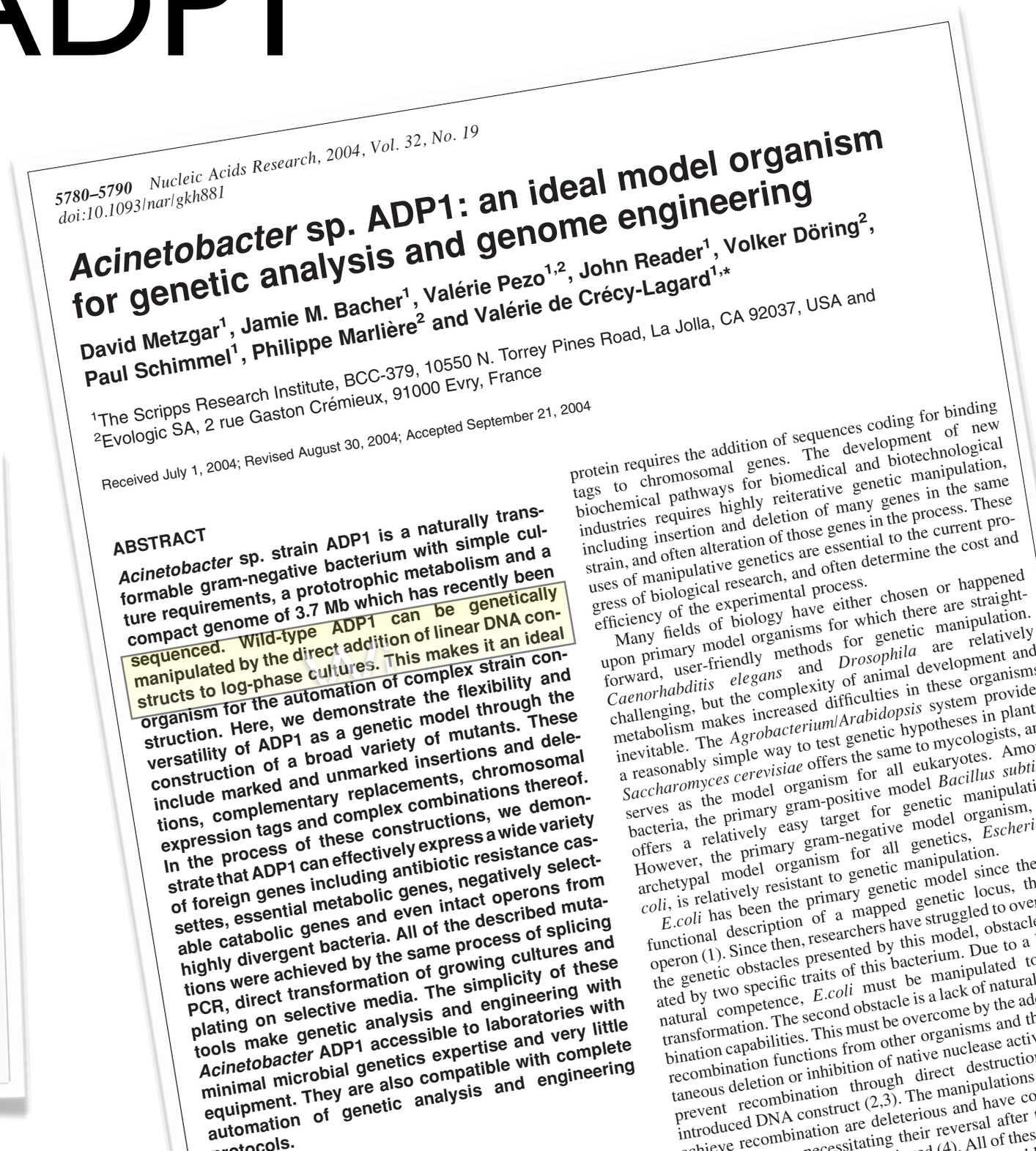
(DNA extraction, transformation, culturing, gels, PCR

demonstrating it works

Acinetobacter Baylyi ADP1

- gram-negative
- genome sequenced
- naturally competent!





5780–5790 *Nucleic Acids Research*, 2004, Vol. 32, No. 19
doi:10.1093/nar/gkh881

Acinetobacter sp. ADP1: an ideal model organism for genetic analysis and genome engineering

David Metzgar[1], Jamie M. Bacher[1], Valérie Pezo[1,2], John Reader[1], Volker Döring[2], Paul Schimmel[1], Philippe Marlière[2] and Valérie de Crécy-Lagard[1,*]

[1]The Scripps Research Institute, BCC-379, 10550 N. Torrey Pines Road, La Jolla, CA 92037, USA and
[2]Evologic SA, 2 rue Gaston Crémieux, 91000 Evry, France

Received July 1, 2004; Revised August 30, 2004; Accepted September 21, 2004

ABSTRACT

***Acinetobacter* sp. strain ADP1 is a naturally transformable gram-negative bacterium with simple culture requirements, a prototrophic metabolism and a compact genome of 3.7 Mb which has recently been sequenced. Wild-type ADP1 can be genetically manipulated by the direct addition of linear DNA constructs to log-phase cultures. This makes it an ideal organism for the automation of complex strain construction. Here, we demonstrate the flexibility and versatility of ADP1 as a genetic model through the construction of a broad variety of mutants. These include marked and unmarked insertions and deletions, complementary replacements, chromosomal expression tags and complex combinations thereof. In the process of these constructions, we demonstrate that ADP1 can effectively express a wide variety of foreign genes including antibiotic resistance cassettes, essential metabolic genes, negatively selectable catabolic genes and even intact operons from highly divergent bacteria. All of the described mutations were achieved by the same process of splicing PCR, direct transformation of growing cultures and plating on selective media. The simplicity of these tools make genetic analysis and engineering with *Acinetobacter* ADP1 accessible to laboratories with minimal microbial genetics expertise and very little equipment. They are also compatible with complete automation of genetic analysis and engineering protocols.**

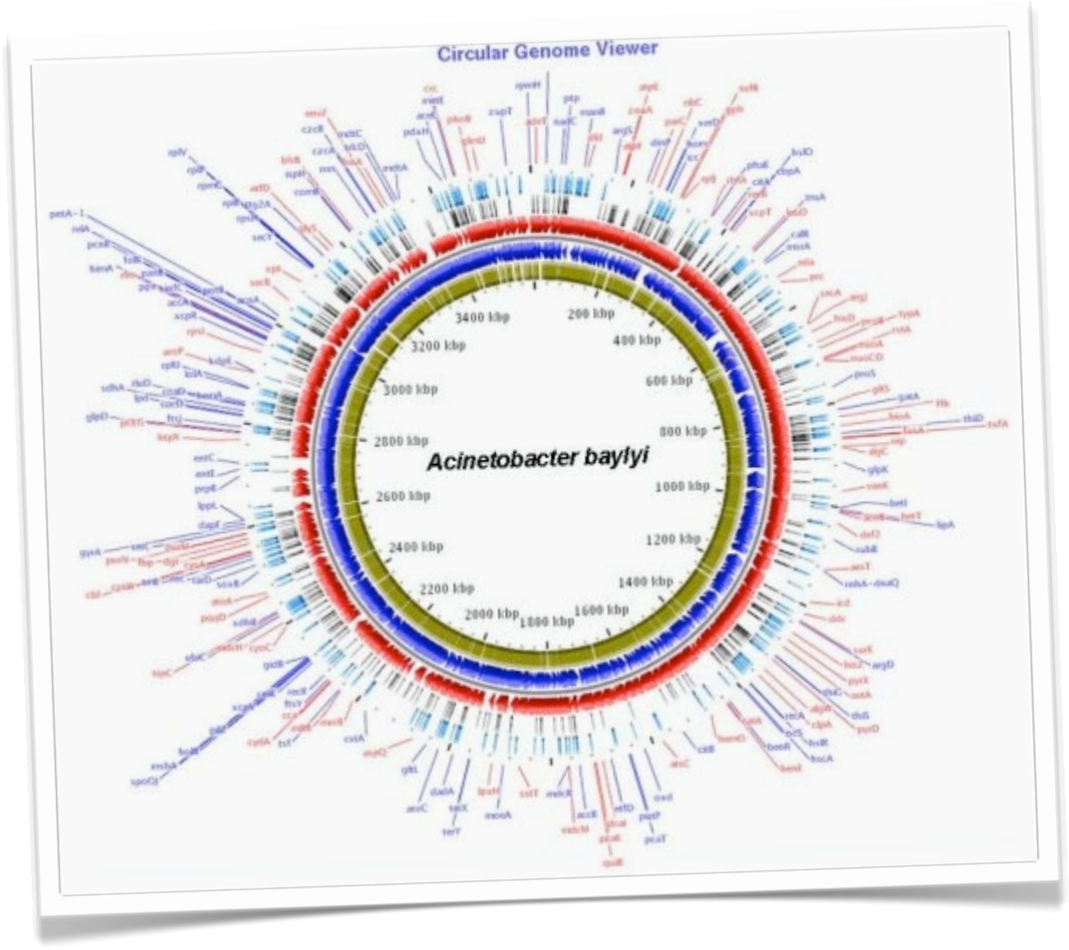
protein requires the addition of sequences coding for binding tags to chromosomal genes. The development of new biochemical pathways for biomedical and biotechnological industries requires highly reiterative genetic manipulation, including insertion and deletion of many genes in the same strain, and often alteration of those genes in the process. These uses of manipulative genetics are essential to the current progress of biological research, and often determine the cost and efficiency of the experimental process.

Many fields of biology have either chosen or happened upon primary model organisms for which there are straightforward, user-friendly methods for genetic manipulation. *Caenorhabditis elegans* and *Drosophila* are relatively challenging, but the complexity of animal development and metabolism makes increased difficulties in these organisms inevitable. The *Agrobacterium*/*Arabidopsis* system provides a reasonably simple way to test genetic hypotheses in plants. *Saccharomyces cerevisiae* offers the same to mycologists, and serves as the model organism for all eukaryotes. Among bacteria, the primary gram-positive model *Bacillus subtilus* offers a relatively easy target for genetic manipulation. However, the primary gram-negative model organism, the archetypal model organism for all genetics, *Escherichia coli*, is relatively resistant to genetic manipulation.

E.coli has been the primary genetic model since the first functional description of a mapped genetic locus, the lac operon (1). Since then, researchers have struggled to overcom the genetic obstacles presented by this model, obstacles cre ated by two specific traits of this bacterium. Due to a lack natural competence, *E.coli* must be manipulated to allo transformation. The second obstacle is a lack of natural reco bination capabilities. This must be overcome by the addition recombination functions from other organisms and the sim taneous deletion or inhibition of native nuclease activities prevent recombination through direct destruction of introduced DNA construct (2,3). The manipulations need achieve recombination are deleterious and have conside epistatic effects, necessitating their reversal after the d have been achieved (4). All of these ste

Acinetobacter Baylyi ADP1

- gram-negative
- genome sequenced
- naturally competent!



5780–5790 *Nucleic Acids Research*, 2004, Vol. 32, No. 19
doi:10.1093/nar/gkh881

Acinetobacter sp. ADP1: an ideal model organism for genetic analysis and genome engineering

David Metzgar[1], Jamie M. Bacher[1], Valérie Pezo[1,2], John Reader[1], Volker Döring[2], Paul Schimmel[1], Philippe Marlière[2] and Valérie de Crécy-Lagard[1,*]

[1]The Scripps Research Institute, BCC-379, 10550 N. Torrey Pines Road, La Jolla,
[2]Evologic SA, 2 rue Gaston Crémieux, 91000 Evry, France

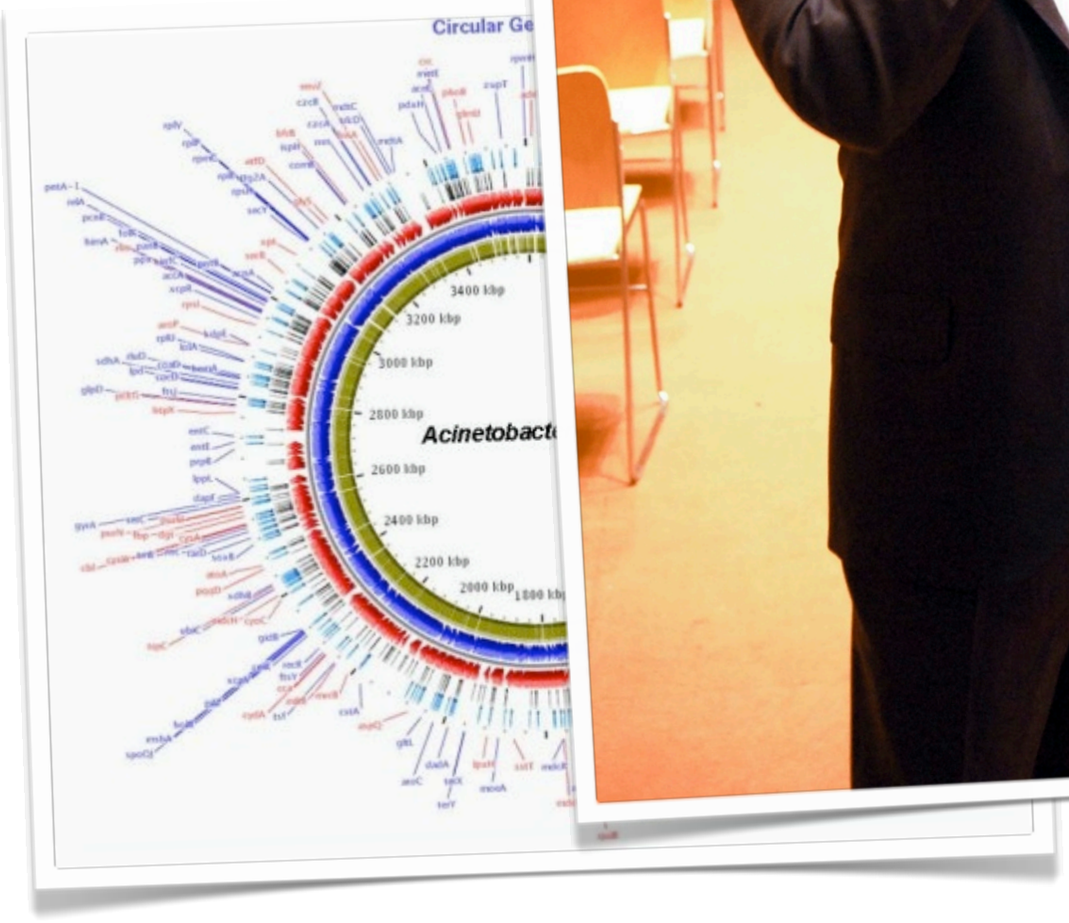
Received July 1, 2004; Revised August 30, 2004; Accepted September 21, 2004

ABSTRACT

Acinetobacter **sp. strain ADP1 is a naturally transformable gram-negative bacterium with simple culture requirements, a prototrophic metabolism and a compact genome of 3.7 Mb which has recently been sequenced. Wild-type ADP1 can be genetically manipulated by the direct addition of linear DNA constructs to log-phase cultures. This makes it an ideal organism for the automation of complex strain construction. Here, we demonstrate the flexibility and versatility of ADP1 as a genetic model through the construction of a broad variety of mutants. These include marked and unmarked insertions and deletions, complementary replacements, chromosomal expression tags and complex combinations thereof. In the process of these constructions, we demonstrate that ADP1 can effectively express a wide variety of foreign genes including antibiotic resistance cassettes, essential metabolic genes, negatively selectable catabolic genes and even intact operons from highly divergent bacteria. All of the described mutations were achieved by the same process of splicing PCR, direct transformation of growing cultures and plating on selective media. The simplicity of these tools make genetic analysis and engineering with** ***Acinetobacter*** **ADP1 accessible to laboratories with minimal microbial genetics expertise and very little equipment. They are also compatible with complete automation of genetic analysis and engineering protocols.**

Ac Baylyi

- gram-negati
- genome seq
- naturally co



an ideal model organism
genome engineering

e Pezo[1,2], John Reader[1], Volker Döring[2],
alérie de Crécy-Lagard[1,*]

. Torrey Pines Road, La Jolla,
France

tember 21, 2004

protein requires the a
tags to chromosom
biochemical pathwa
industries requires
including insertion
strain, and often alt
uses of manipulati
gress of biological
efficiency of the

Many fields o
upon primary m
forward, user-fr
Caenorhabditis
challenging, bu
metabolism ma
inevitable. The
a reasonably s
Saccharomyce
serves as the
bacteria, the
offers a rel
However, t
archetypal
coli, is rela
E.coli h
functional
operon (1
the genet
ated by t
natural
transfor
binatio
recomb
taneou
prev
introd

trans-
e cul-
and a
y been
etically
IA con-
an ideal
ain con-
lity and
ugh the
s. These
nd dele-
mosomal
s thereof.
e demon-
de variety
tance cas-
ely select-
erons from
ibed muta-
of splicing
ultures and
ity of these
neering with
ratories with

Acinetobacter ADP1 accessible t
minimal microbial genetics expertise and very little
equipment. They are also compatible with complete
automation of genetic analysis and engineering
protocols.

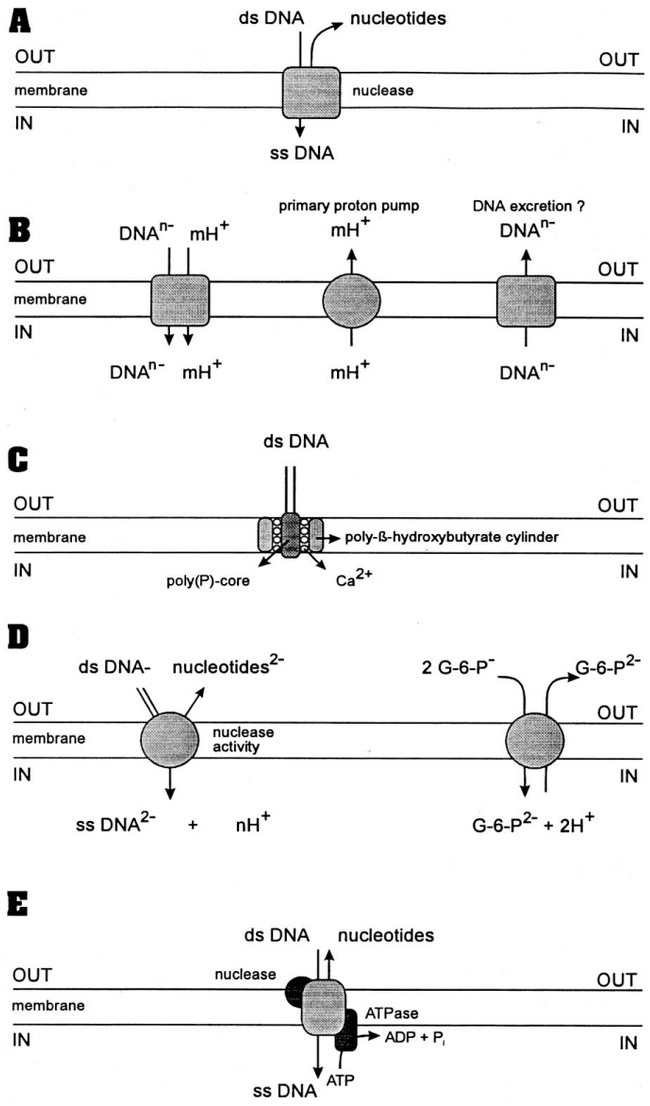


Fig. 2. Schematic representation of different models proposed to explain the mechanism and/or energisation of DNA uptake. (**A**) The hydrolysis of one strand provides the energy to drive the uptake of the complementary strand. (**B**) DNA is taken up electroneutrally in symport with protons and is thus driven by the transmembrane pH gradient. Hypothetically, DNA may be excreted electrogenically using the existing transmembrane electrical potential. (**C**) A pHB cylinder filled with a polyphosphate core [poly(P)-core] and stabilised by Ca^{2+} may constitute a DNA transporter. The DNA is bound to the polyphosphate core, which is subsequently degraded allowing the DNA to be internalised. (**D**) Analogous to glucose-6-phosphate (G-6-P) transport by the *E. coli* UhpT transporter, negatively charged ds DNA is transported towards the cytoplasm, encouters an endonuclease and is hydrolysed, resulting in monovalent negatively charged ss DNA and nt. The monovalently charged ss DNA and nt liberate a proton into the more alkaline cytoplasm and the now divalent negatively charged nt are expelled. This results in an anion exchange reaction dependent on proton cycling. (**E**) ds DNA is hydrolysed by an endonuclease, the nt are liberated, and the ss DNA is internalised via an ATP-dependent uptake system.

5780–5790 Nucleic Acids Research, 2004, Vol. 32, No. 19
doi:10.1093/nar/gkh881

Acinetobacter sp. ADP1: an ideal model organism for
genetic analysis and genome engineering

Davi
Pau
[1]The
[2]Ev
Rec

expression of the *tdk* gene, together with supplemental thymidine, is essential in the absence of *thyA* activity as *Acinetobacter* ADP1 does not contain an endogenous *tdk* allele.

DISCUSSION

Acinetobacter ADP1 provides a remarkably simple, inexpensive and robust model system for genetic manipulation. Most of the existing antibiotics and antibiotic resistance cassettes tested here were functional in ADP1. These markers were used to build positive/negative selection cassettes, which were in turn used to efficiently construct a wide variety of mutations including gene disruptions and deletions, expressed chromosomal insertions, tagged chromosomal genes and various combinations of these types of mutations. Moving mutations from one strain to another was as straightforward as amplifying the mutation from the donor strain and inoculating a growing culture of the recipient strain with the raw PCR product, or even simply transforming with purified genomic DNA from the donor strain. All constructions shown here utilized approximately 1 kb flanking regions to specifically integrate constructs into the ADP1 genome. Attempts to use shorter flanks were generally unsuccessful. Splicing PCRs with shorter flanks resulted in high yields of product, but no transformants were recovered in selection. This limitation may be due to the minimal volume of our transformations.

The techniques used in this paper were reiterative and highly similar. All manipulations aside from the initial cassette constructions were performed using splicing PCR and selective plating only. Primers were chosen using very simple rules based on melting temperature, GC content, potential interprimer misextension and position with regard to the affected ORF. All PCRs were performed in identical conditions. Furthermore, all direct manipulations of ADP1 cells were performed in minimal volumes similar to those found in standard 96-well plate formats. The high rate of success under these conditions suggests that this system could be readily adapted to an automated platform, allowing for all steps to be achieved robotically. Similarly, the simplicity of the ADP1 genetic engineering protocols developed here should allow this system to be adopted by both training institutions and laboratories that have a need for an inexpensive and user-friendly method for generating genetically manipulated strains. The *Acinetobacter* constructions described here required only a PCR machine, incubators and access to oligonucleotide synthesis. It is notable that the majority of all constructions, including the cassette constructions, antibiotic tests, resistance allele tests and associated design efforts, were achieved by one researcher (D.Metzgar), with very little previous genetic manipulation experience in the course of one year. Attempts by other researchers to use the same system were generally equally successful, but it was noted that success was dependent on careful and consistent choice of primer sequences (see Materials and Methods).

Together, the paired traits of natural competence and recombination allow for rapid production of genetically engineered strains. Replacement of existing genetic models with *Acinetobacter* ADP1 should be straightforward, as ADP1 presented no particular challenges with respect to culturing conditions, bioinformatic prediction of metabolic pathways, or mutational stability in culture, even in conditions that were optimized for *E.coli* rather than *Acinetobacter*. In the short time during which this model has been under development in our laboratory, it has allowed us to test a number of biological questions (27) in a much more efficient manner than would have been possible with previously utilized model organisms.

ACKNOWLEDGEMENTS

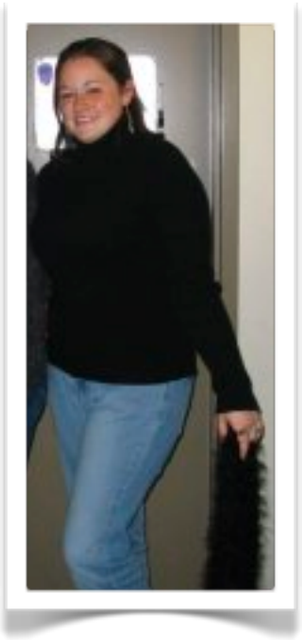
We thank L. Nicholas Ornston for critical reading of this work, and Integrated Genomics for access to ERGO. This work was supported by National Institute of Health Grant GM23562, National Science Foundation Grant MCB-0128901 and a fellowship from the National Foundation for Cancer Research.

REFERENCES

1. Beckwith,J.R. (1967) Regulation of the lac operon. Recent studies on the regulation of lactose metabolism in *Escherichia coli* support the operon model. *Science*, **156**, 597–604.
2. Murphy,K.C. (1998) Use of bacteriophage lambda recombination functions to promote gene replacement in *Escherichia coli*. *J. Bacteriol.*, **180**, 2063–2071.
3. Zhang,Y., Buchholz,F., Muyrers,J.P. and Stewart,A.F. (1998) A new logic for DNA engineering using recombination in *Escherichia coli*. *Nature Genet.*, **20**, 123–128.
4. Court,D.L., Sawitzke,J.A. and Thomason,L.C. (2002) Genetic engineering using homologous recombination. *Annu. Rev. Genet.*, **36**, 361–388.
5. Miller,J.H. (1972) *Experiments in Molecular Genetics*. Cold Spring Harbor Laboratory, Cold Spring Harbor, NY.
6. Barbe,V., Vallenet,D., Fonknechten,N., Kreimeyer,A., Oztas,S., Labarre,L., Cruveiller,S., Robert,C., Duprat,S., Wincker,P. *et al*. (2004) Unique features revealed by the genome sequence of *Acinetobacter* sp. ADP1, a versatile and naturally transformation competent bacterium. *Nucleic Acids Res.*, **32**, 5766–5779.
7. Kok,R.G., van Thor,J.J., Nugteren-Roodzant,I.M., Vosman,B. and Hellingwerf,K.J. (1995) Characterization of lipase-deficient mutants of *Acinetobacter calcoaceticus* BD413: identification of a periplasmic lipase chaperone essential for the production of extracellular lipase. *J. Bacteriol.*, **177**, 3295–3307.
8. Palmen,R. and Hellingwerf,K.J. (1997) Uptake and processing of DNA by *Acinetobacter calcoaceticus*—a review. *Gene*, **192**, 179–190.
9. Porstendorfer,D., Gohl,O., Mayer,F. and Averhoff,B. (2000) ComP, a pilin-like protein essential for natural competence in *Acinetobacter* sp. Strain BD413: regulation, modification, and cellular localization. *J. Bacteriol.*, **182**, 3673–3680.
10. de Vries,J. and Wackernagel,W. (2002) Integration of foreign DNA during natural transformation of *Acinetobacter* sp. by homology-facilitated illegitimate recombination. *Proc. Natl Acad. Sci. USA*, **99**, 2094–2099.
11. Lamb,D.C., Kelly,D.E., Masaphy,S., Jones,G.L. and Kelly,S.L. (2000) Engineering of heterologous cytochrome P450 in *Acinetobacter* sp.: application for pollutant degradation. *Biochem. Biophys. Res. Commun.*, **276**, 797–802.
12. Murphy,K.C., Campellone,K.G. and Poteete,A.R. (2000) PCR-mediated gene replacement in *Escherichia coli*. *Gene*, **246**, 321–330.
13. Jones,R.M. and Williams,P.A. (2003) Mutational analysis of the critical bases involved in activation of the AreR-regulated sigma54-dependent promoter in *Acinetobacter* sp. strain ADP1. *Appl. Environ. Microbiol.*, **69**, 5627–5635.
14. Richaud,C., Mengin-Lecreulx,D., Pochet,S., Johnson,E.J., Cohen,G.N. and Marlière,P. (1993) Directed evolution of biosynthetic pathways. Recruitment of cysteine thioethers for constructing the cell wall of *Escherichia coli*. *J. Biol. Chem.*, **268**, 26827–26835.
15. Blondelet-Rouault,M.H., Weiser,J., Lebrihi,A., Branny,P. and Pernodet,J.L. (1997) Antibiotic resistance gene cassettes derived from the omega interposon for use in *E. coli* and *Streptomyces*. *Gene*, **190**, 315–317.

ADP1:

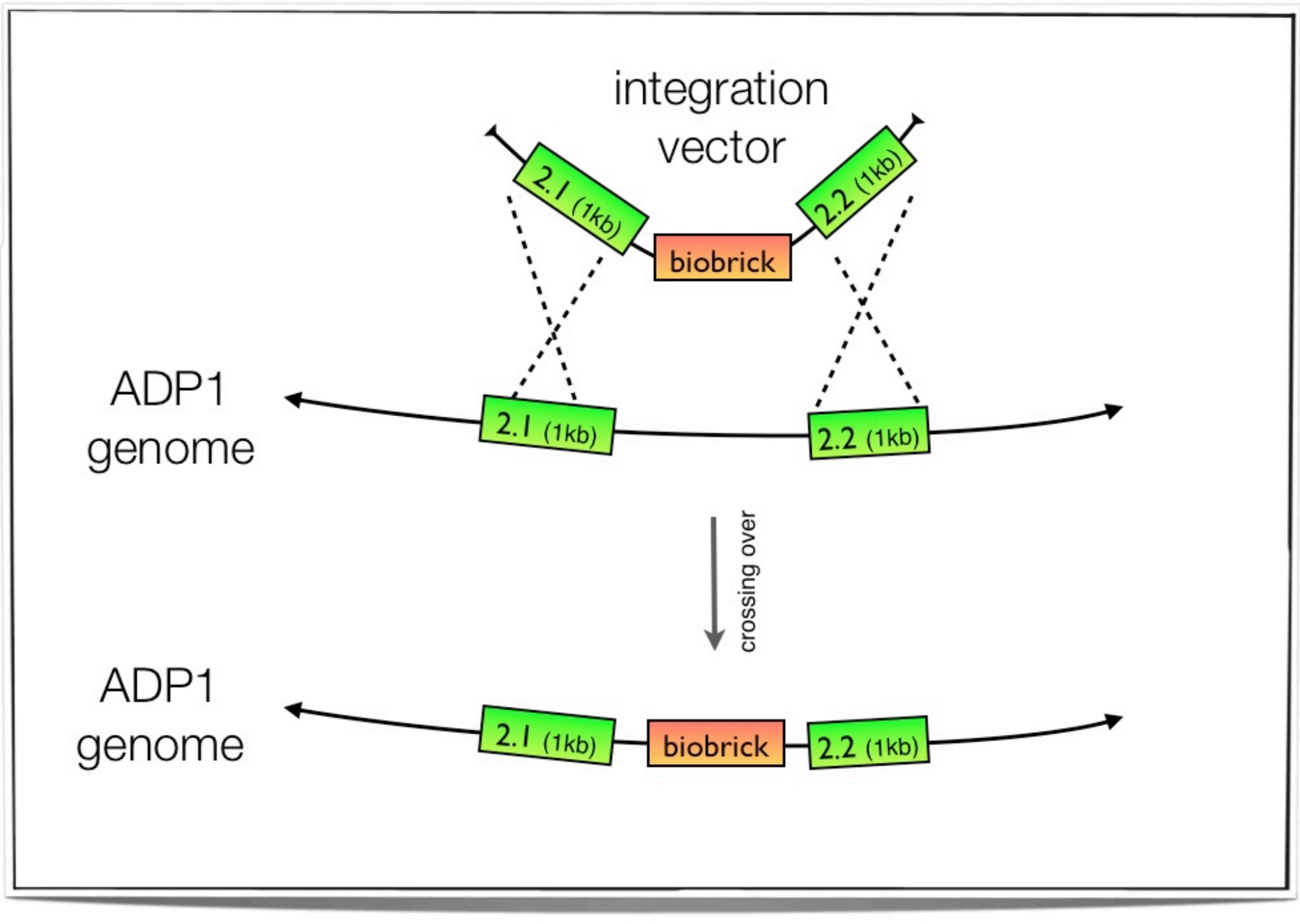
- simple, inexpensive, robust model system
- transfering parts is easy:
  - amplify donor genome, add to growing culture
- Techniques are reiterative and pseudo-idempotent; good for automation
- Equipment needed:
  - PCR
  - incubators
  - oligo synthesis
- All accomplished by one researcher over one year with minimal prior experience w/ genetic engineering



Samantha Burke

- 2.1 - j04550 - 2.2: fail (RFP)
- 2.1 - p1003 - 2.2 : worked (Kan resistance)

not all E. coli promoters
compatible?



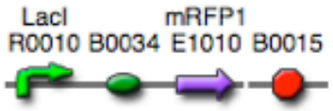
Part:BBa_J04450

DNA Available
Experience: Works

Designed by Tamar Odle Group: iGEM_Davidson

Entered: 2005-06-09

RFP Coding Device switched on by IPTG

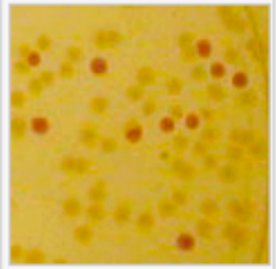


Constitutive RFP device. The colonies are clearly red in color under natural light after about 18 hours. Smaller colonies are visibly red under UV. The RFP part does not contain a degradation tag and the RBS is strong.

Pictures

BBa_J04450 visualized under non-UV lightbox

BBa_J04450 visualized under 254nm wavelength UV lightbox



BBa_J04450 Colonies

Registry of Standard Biological Parts

Go Search

page discussion view source history Log in / create account

BBa P1003 Main Page Part Design Physical DNA Hard Information Experience

Part:BBa_P1003

DNA Available
Experience: Works

Designed by Reshma Shetty Group: Knight Lab, MIT

Entered: 2006-01-23

kanamycin resistance cassette

Kanamycin resistance cassette including promoter and coding sequence. It lacks a terminator.

Usage and Biology

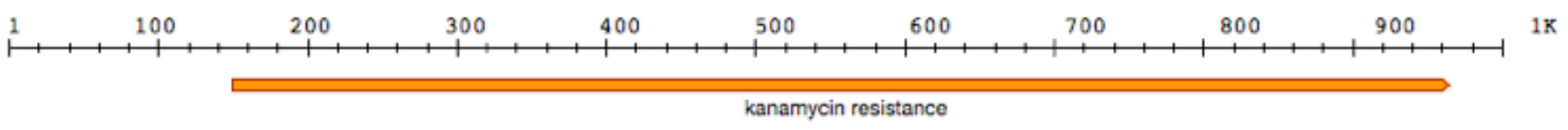
- Used for modular BioBrick vector construction using BioBrick base vector BBa_I51020.

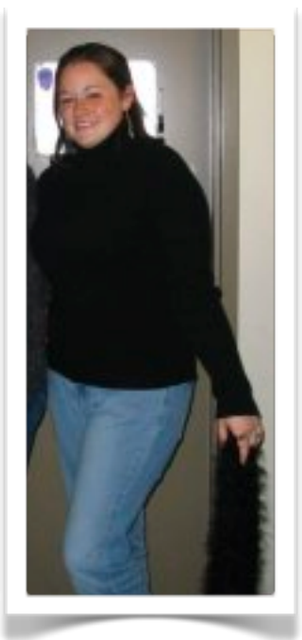
References

Engineering BioBrick vectors from BioBrick parts
Journal of Biological Engineering, 2008 Apr 14;2:5
Reshma Shetty, Drew Endy, Tom Knight
URL
GenBank EU496093

Sequence and Features

Format: Subparts | Ruler | SS | DS Search: Length: 967 bp Context: Part only Get selected sequence





Samantha Burke

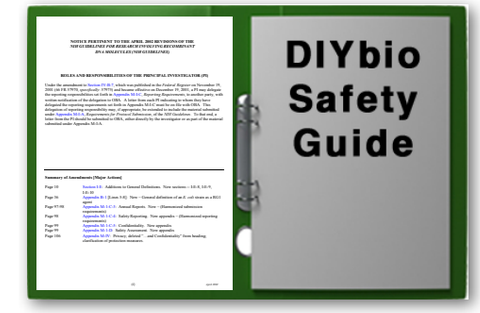
- 2.1 - j04550 - 2.2: fail (RFP)
- 2.1 - p1003 - 2.2 : worked (Kan resistance)

Genes work;
Promoters didn't?

NEXT

- RFP ADP1 !
- ID promoters that work in ADP1
- minimize 2.1 & 2.2
  - 1000bp -> 100bp
- or find ways of using plasmids
  - don't integrate into genome
  - circular, not linear
  - easier to isolate (miniprep)

Safety



“

Dear DIY bio people,
Do you think people might be receptive to some measure of absolute prohibition, along the lines of:

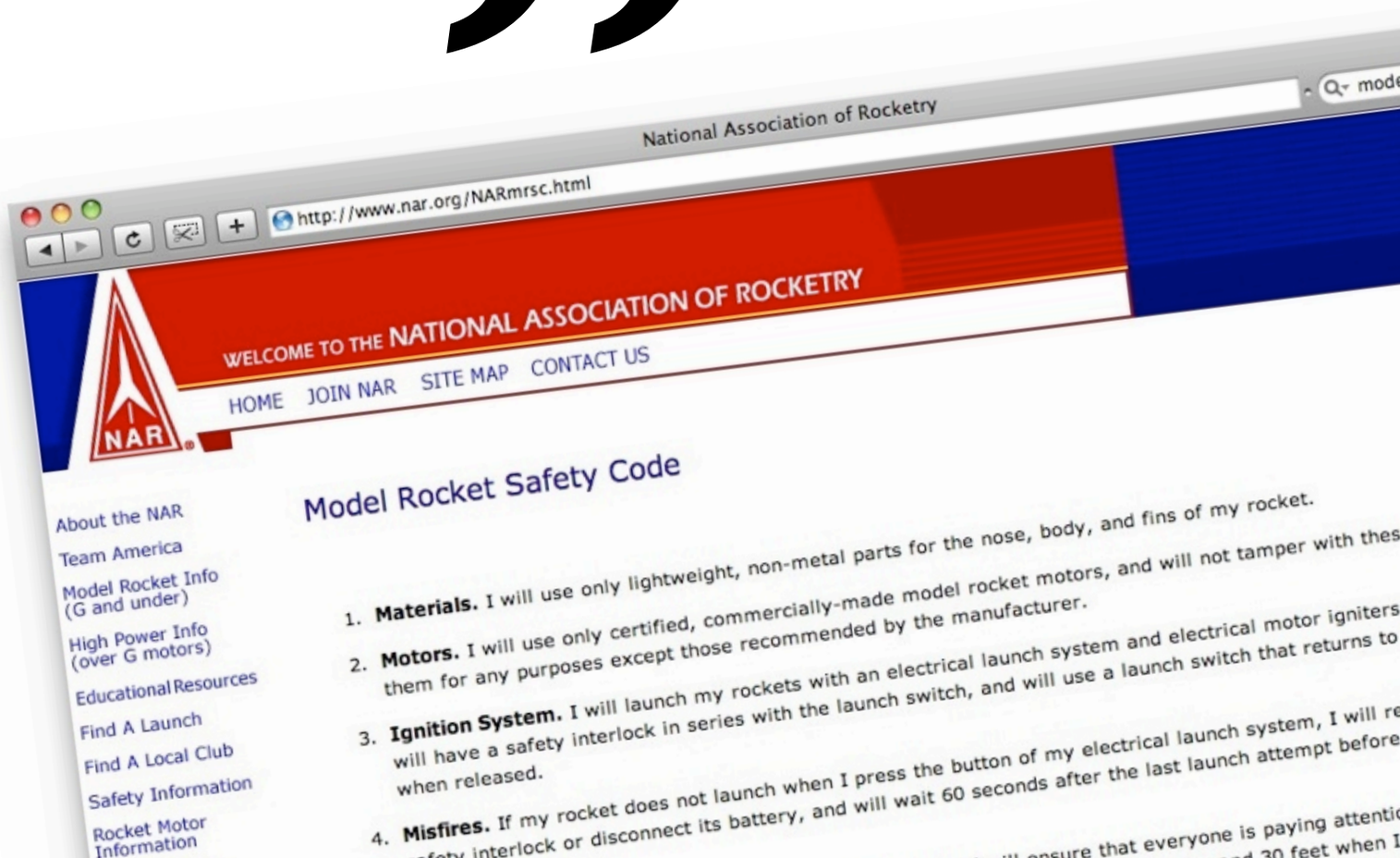
"Thou shalt not design, nor build, nor isolate, nor modify, nor grow, nor release any self replicating organism, with the intent of causing harm?"

”

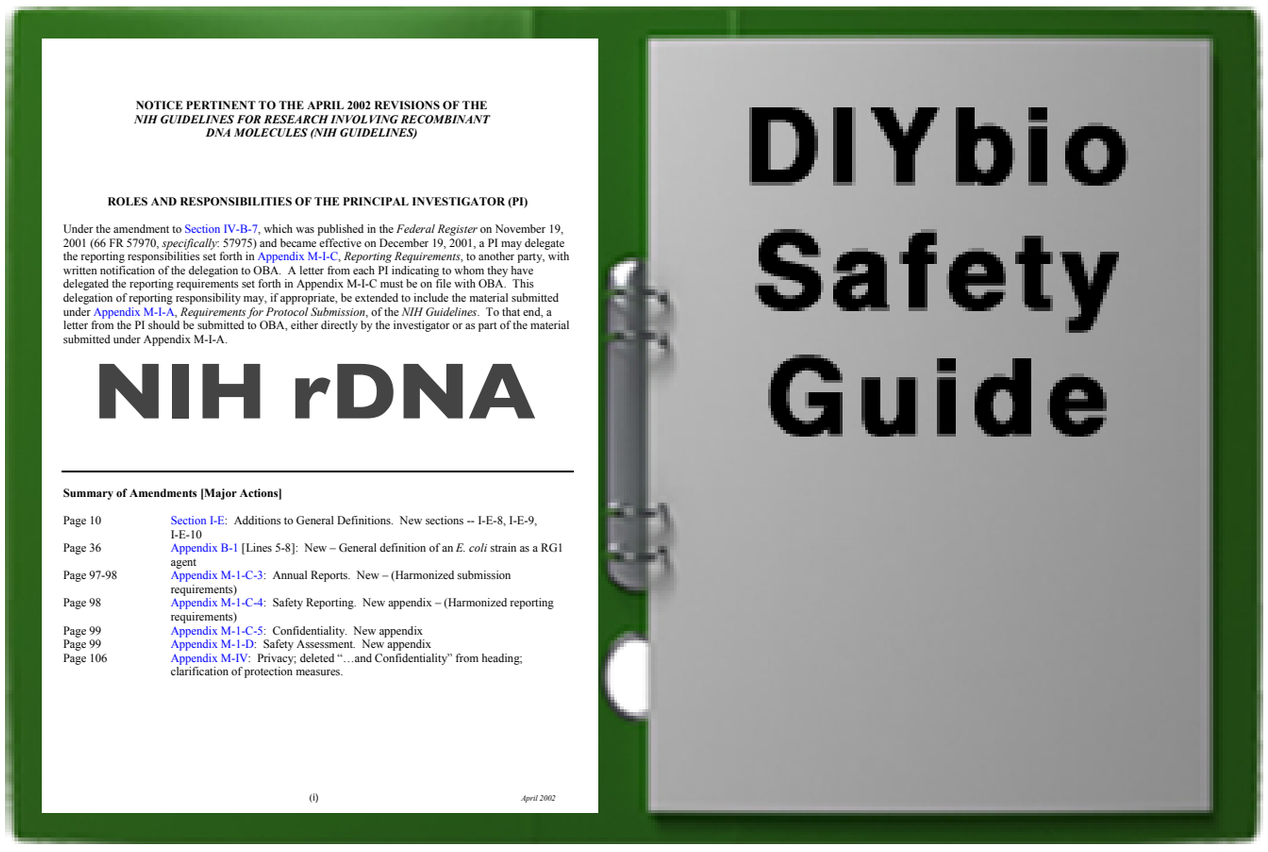
-Roger Brent

DIYbio creed:

Safe as an undergrad lab
or better:
safe enough to eat



safety@diybio.org



Need safety norms before we can expect broad-scale innovation must preempt stupidity

social hack: what is the 1-5 year strategy for DIYbio as a movement to be successful?

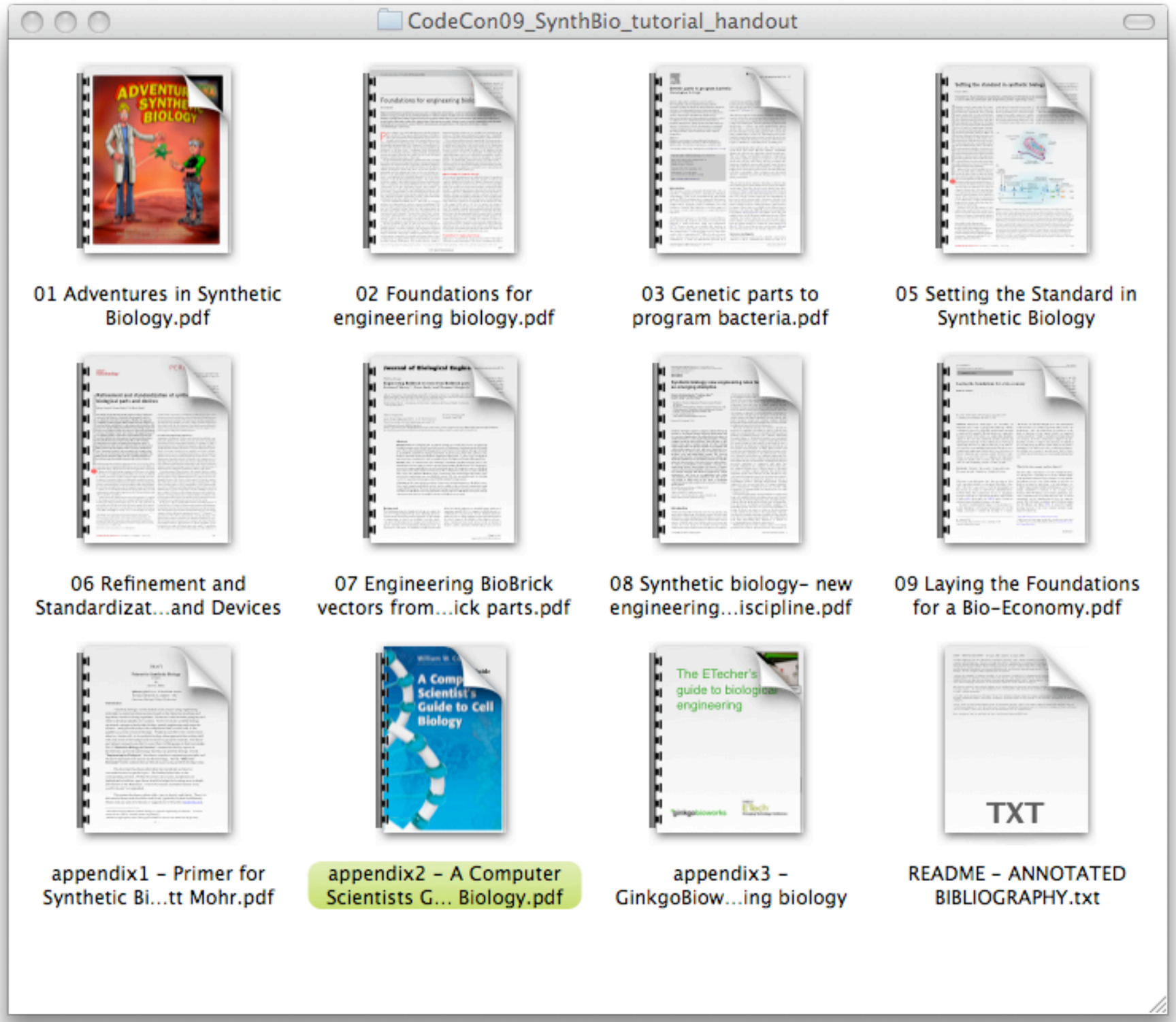
safety working group: safety@diybio.org

get involved?

Periodic meetups in San Francisco, Boston, NYC, Seattle and Chicago - email **diybio@googlegroups.com**

visit diybio.org for more info

http://bit.ly/diybiocc



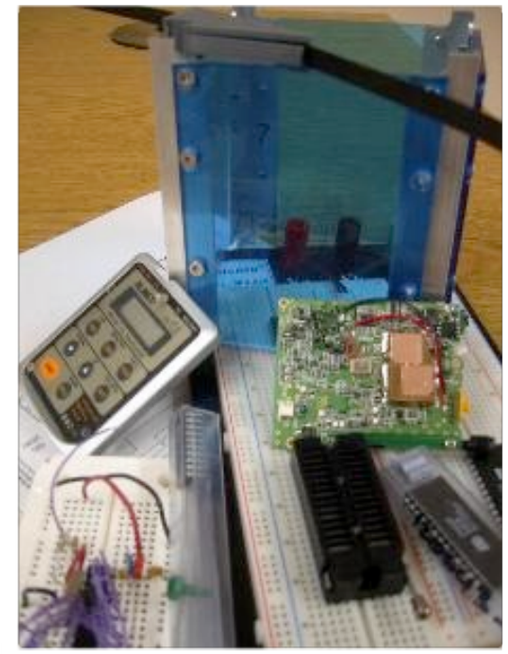
5-min dna extraction in a shot glass

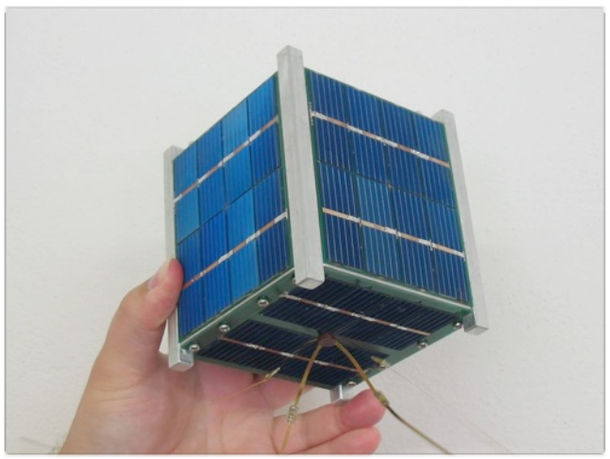
just add:
saliva + soap + salt +
160 proof rum

DIYbio in space

Eric Stackpole

- $1000 DIY cubesat
- launching in 6 mo
- altoids-size DIYbio payload
- 100-200g
- 5v, 100 mA
- -80c to 100c
- DTMF downlink





http://bit.ly/ReadySatGo

Software interchange formats for libraries and modeling.

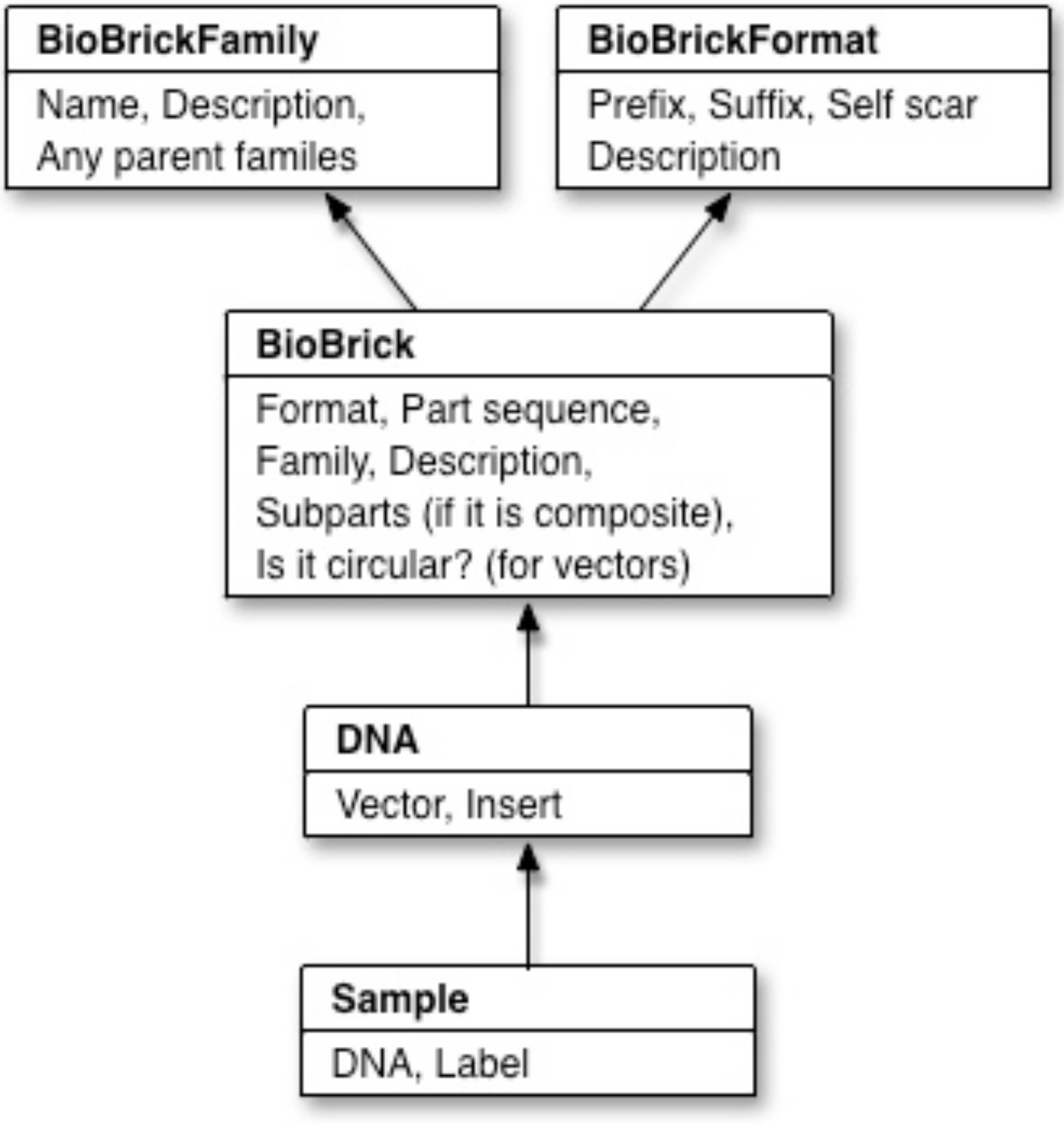
pobol

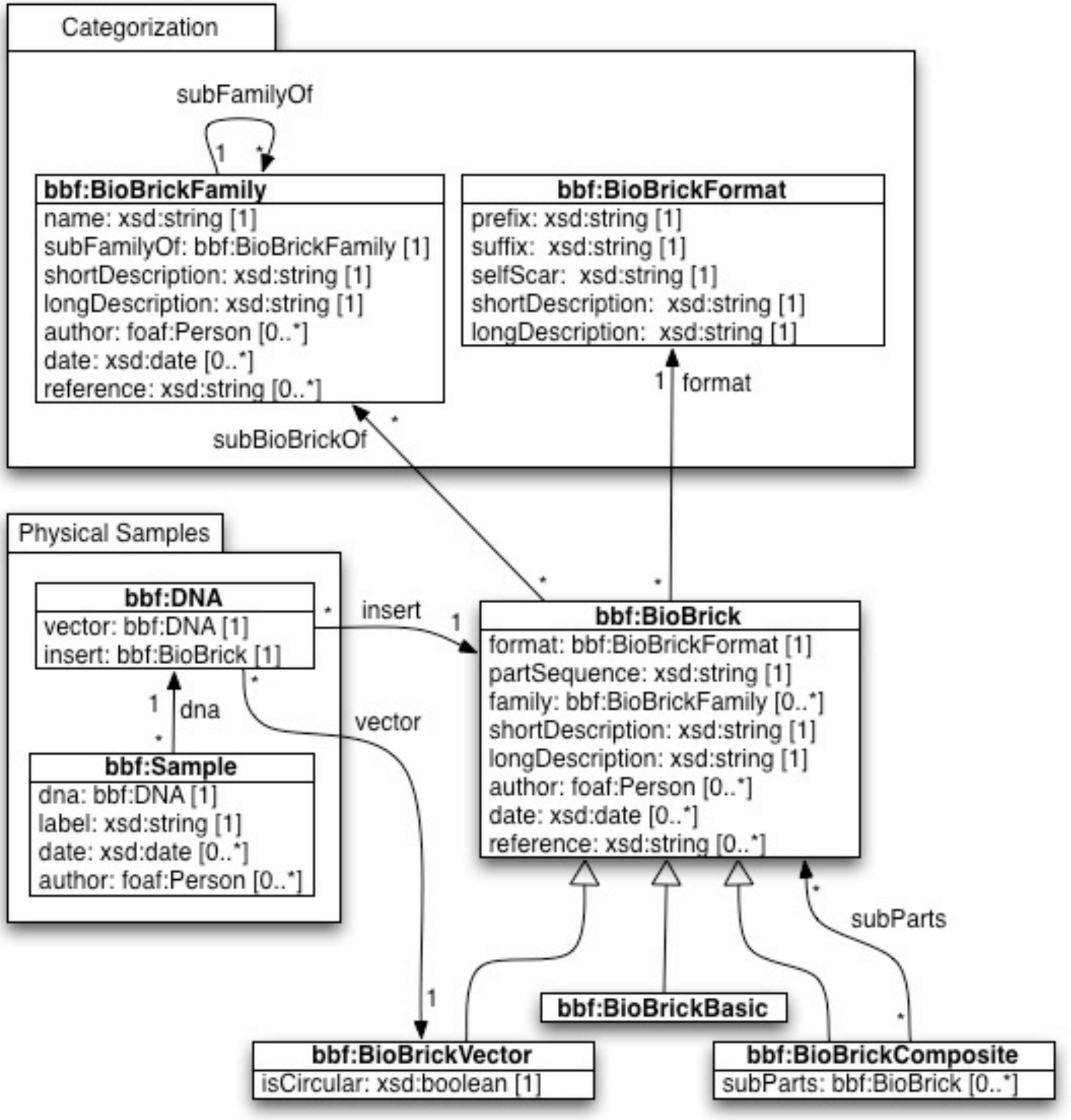
The PoBoL project aims to define an RDF-based data exchange standard for standard biological parts, BioBricks. The goals are to:

- Capture the minimal information needed to describe a BioBrick.
- Allow the connection of additional data to BioBricks.
- Remain open for extension and interlinking.

"PoBoL" stands for Provisional BioBrick Language. "Pobol" is also Welsh for "people", which reflects our desire for a community-driven format. Find out more at our:

- OpenWetWare Wiki page
- Google Group for discussion
- Google Code project for specifications and code

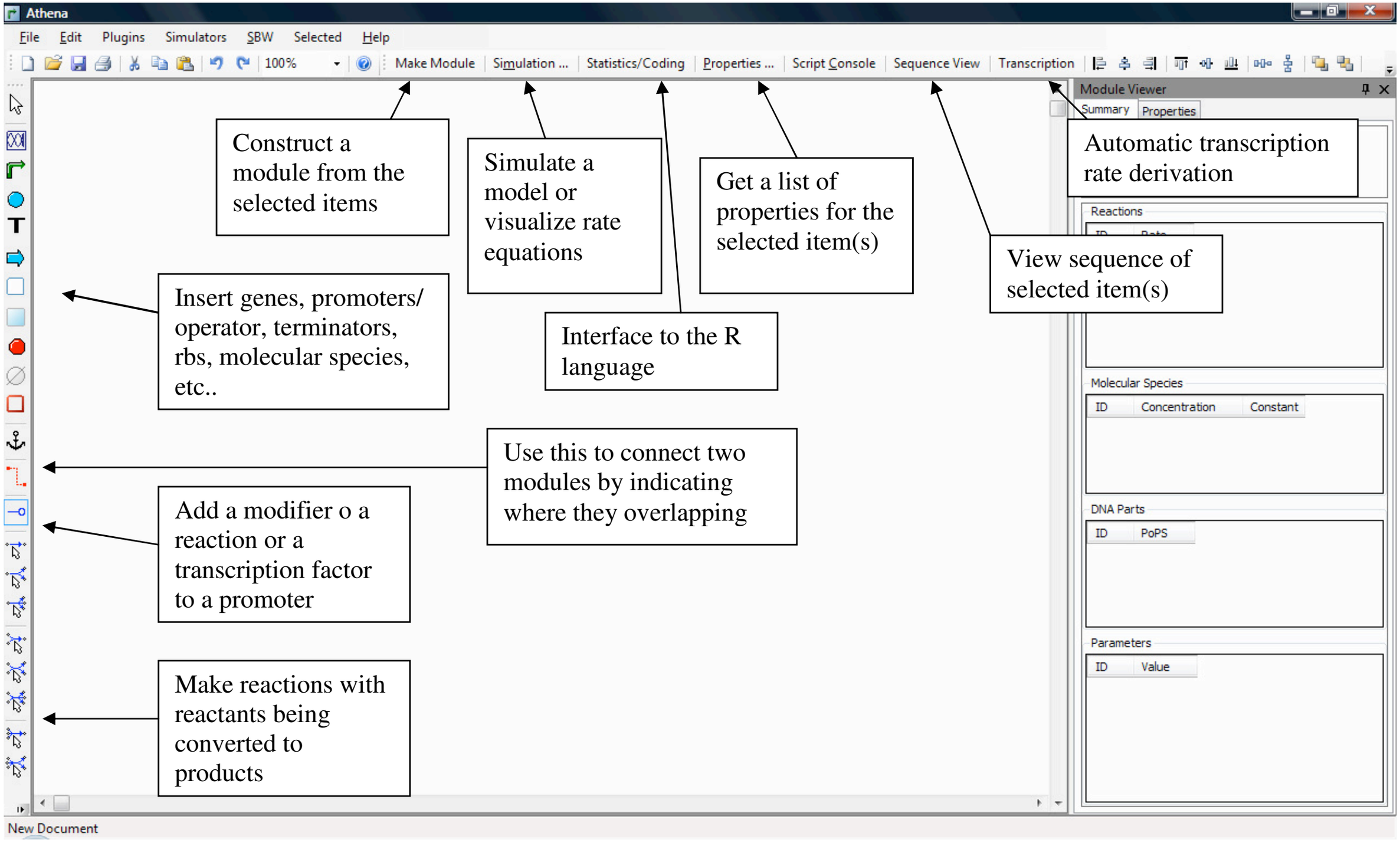

BioBrickFamily
Name, Description,
Any parent familes
BioBrickFormat
Prefix, Suffix, Self scar
Description
BioBrick
Format, Part sequence,
Family, Description,
Subparts (if it is composite),
Is it circular? (for vectors)
DNA
Vector, Insert
Sample
DNA, Label


Categorization
subFamilyOf
1
*
bbf:BioBrickFamily
name: xsd:string [1]
subFamilyOf: bbf:BioBrickFamily [1]
shortDescription: xsd:string [1]
longDescription: xsd:string [1]
author: foaf:Person [0..*]
date: xsd:date [0..*]
reference: xsd:string [0..*]
bbf:BioBrickFormat
prefix: xsd:string [1]
suffix: xsd:string [1]
selfScar: xsd:string [1]
shortDescription: xsd:string [1]
longDescription: xsd:string [1]
1
format
*
subBioBrickOf
*
*
Physical Samples
bbf:DNA
vector: bbf:DNA [1]
insert: bbf:BioBrick [1]
*
insert
1
bbf:BioBrick
format: bbf:BioBrickFormat [1]
partSequence: xsd:string [1]
family: bbf:BioBrickFamily [0..*]
shortDescription: xsd:string [1]
longDescription: xsd:string [1]
author: foaf:Person [0..*]
date: xsd:date [0..*]
reference: xsd:string [0..*]
*
1
dna
*
vector
bbf:Sample
dna: bbf:DNA [1]
label: xsd:string [1]
date: xsd:date [0..*]
author: foaf:Person [0..*]
*
subParts
1
bbf:BioBrickBasic
bbf:BioBrickVector
isCircular: xsd:boolean [1]
bbf:BioBrickComposite
subParts: bbf:BioBrick [0..*]

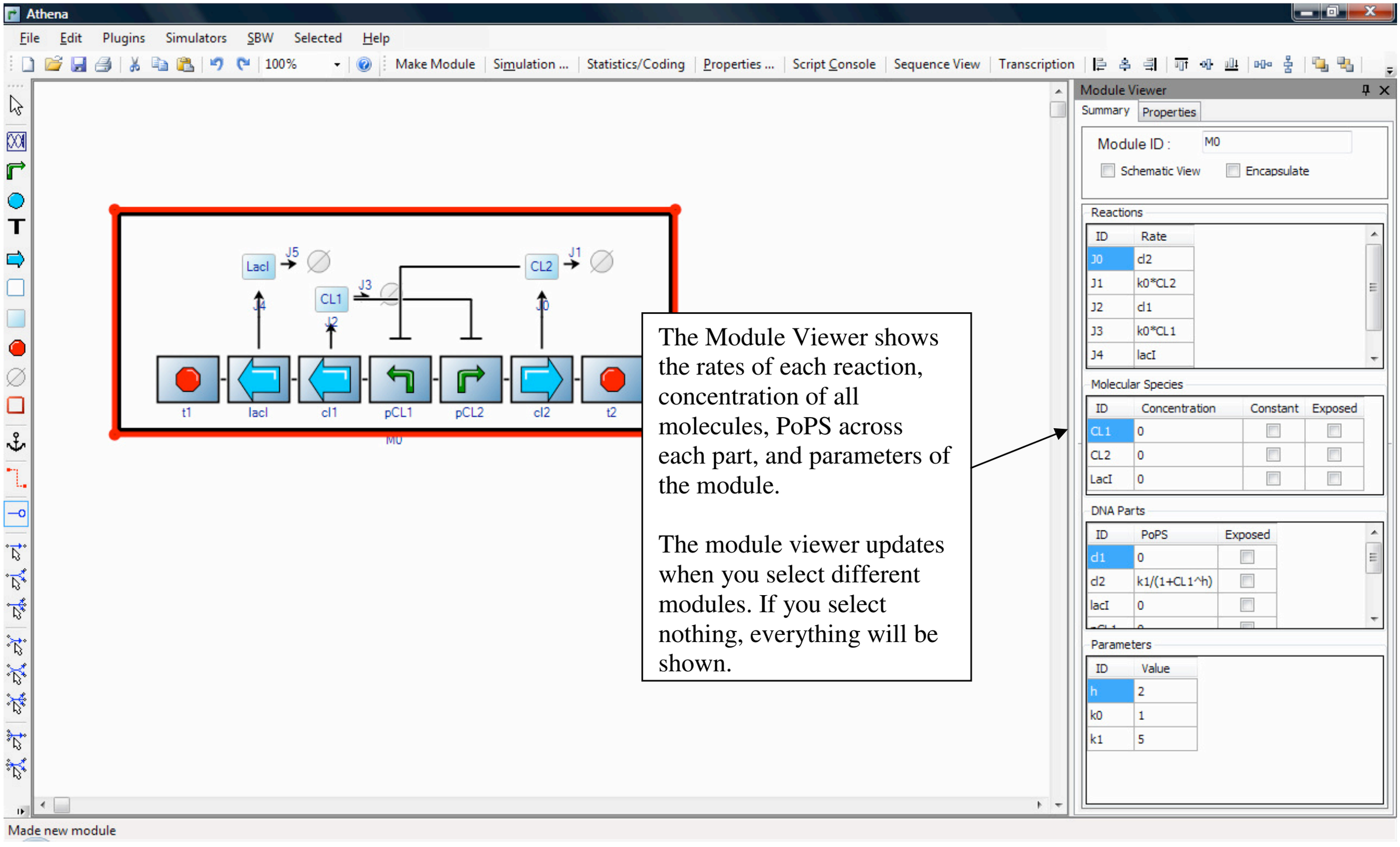
```
@prefix xsd:     <http://www.w3.org/2001/XMLSchema#> .
@prefix rdfs:    <http://www.w3.org/2000/01/rdf-schema#> .
@prefix rdf:     <http://www.w3.org/1999/02/22-rdf-syntax-ns#> .
@prefix owl:     <http://www.w3.org/2002/07/owl#> .
@prefix foaf:    <http://xmlns.com/foaf/0.1#> .
@prefix bbf:     <http://www.biobricks.org/rdf/0.1#> .
@prefix bbx:     <http://www.biobricks.org/rdf/formats#> .
@prefix usr:     <http://www.partsregistry.org/users#> .

:BBa_P1010
    rdf:type bbf:BiobrickBasic ;
    bbf:author usr:Leon_Chan ;
    bbf:date "2008-05-31"^^xsd:date ;
    bbf:format bbx:BBa ;
    bbf:longDescription "negative selection marker for construction
      plasmids. Only certain E.coli strains (DB3.1) can survive
      the expression of this marker."^^xsd:string ;
    bbf:partSequence "actggctgtgtata.......atccacgcgt"^^xsd:string ;
    bbf:shortDescription "cccdB death casette"^^xsd:string .
```

Athena

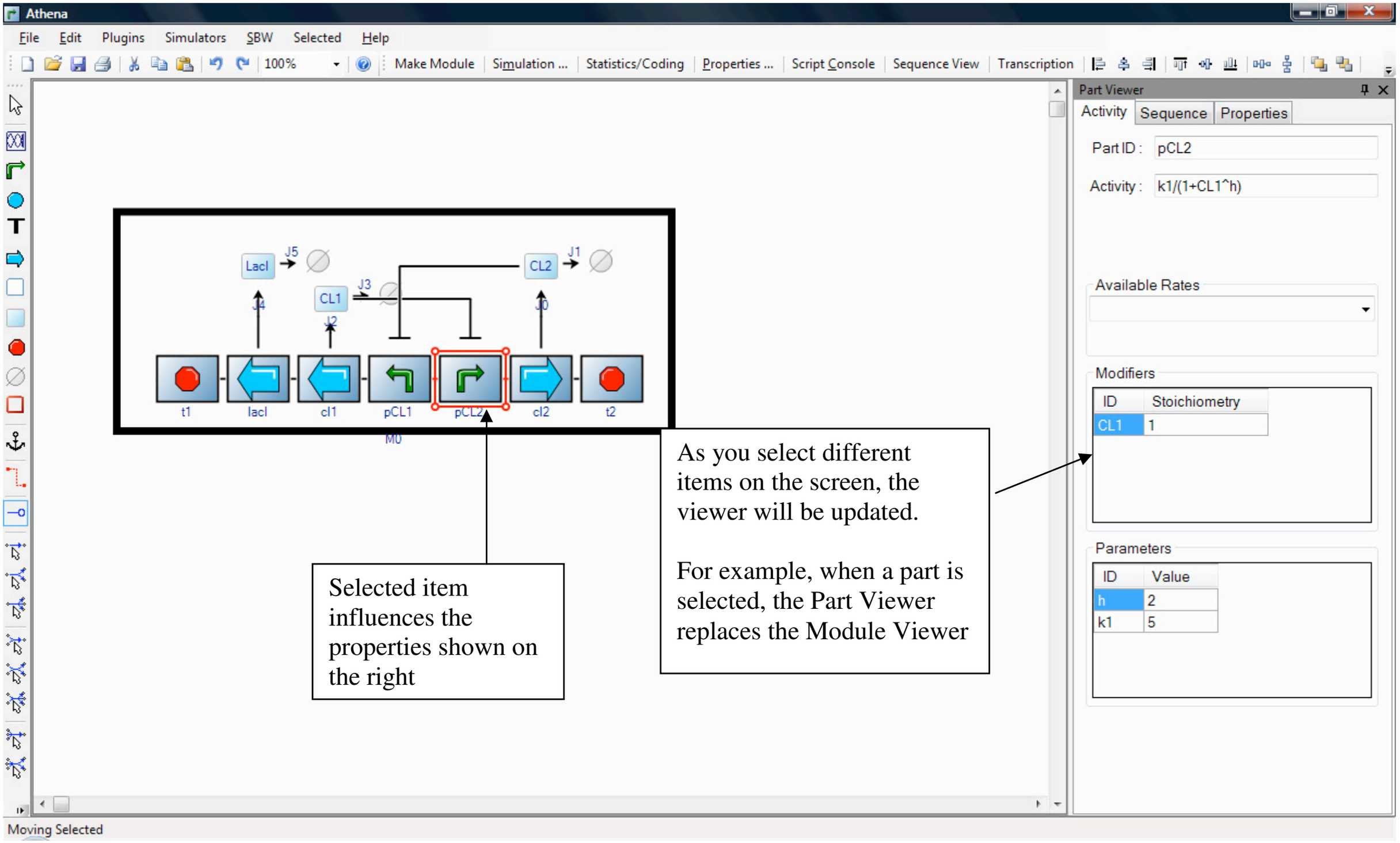
Basic Features



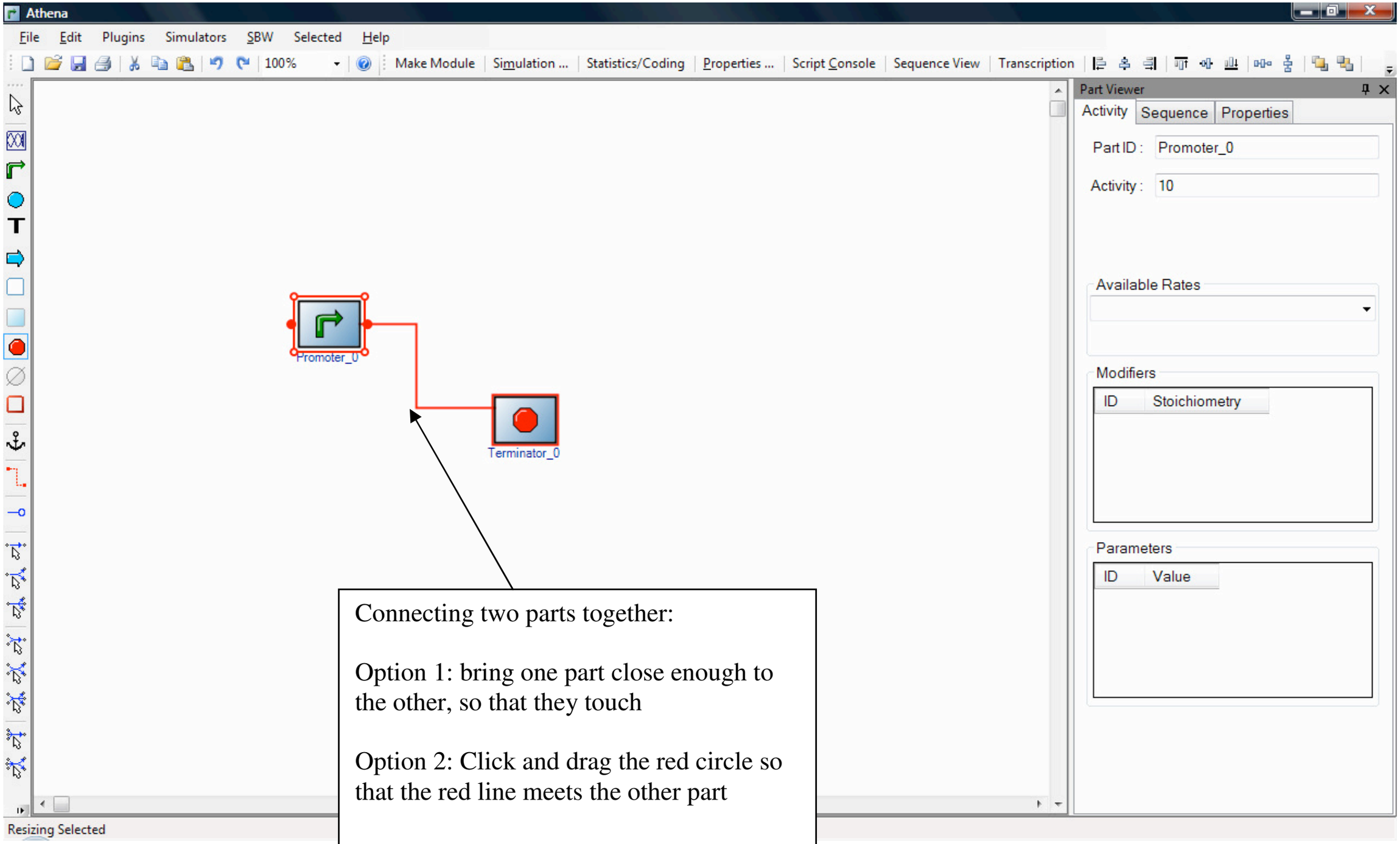
Looking at the complete model



Property Viewers



Connecting Parts (DNA stands)

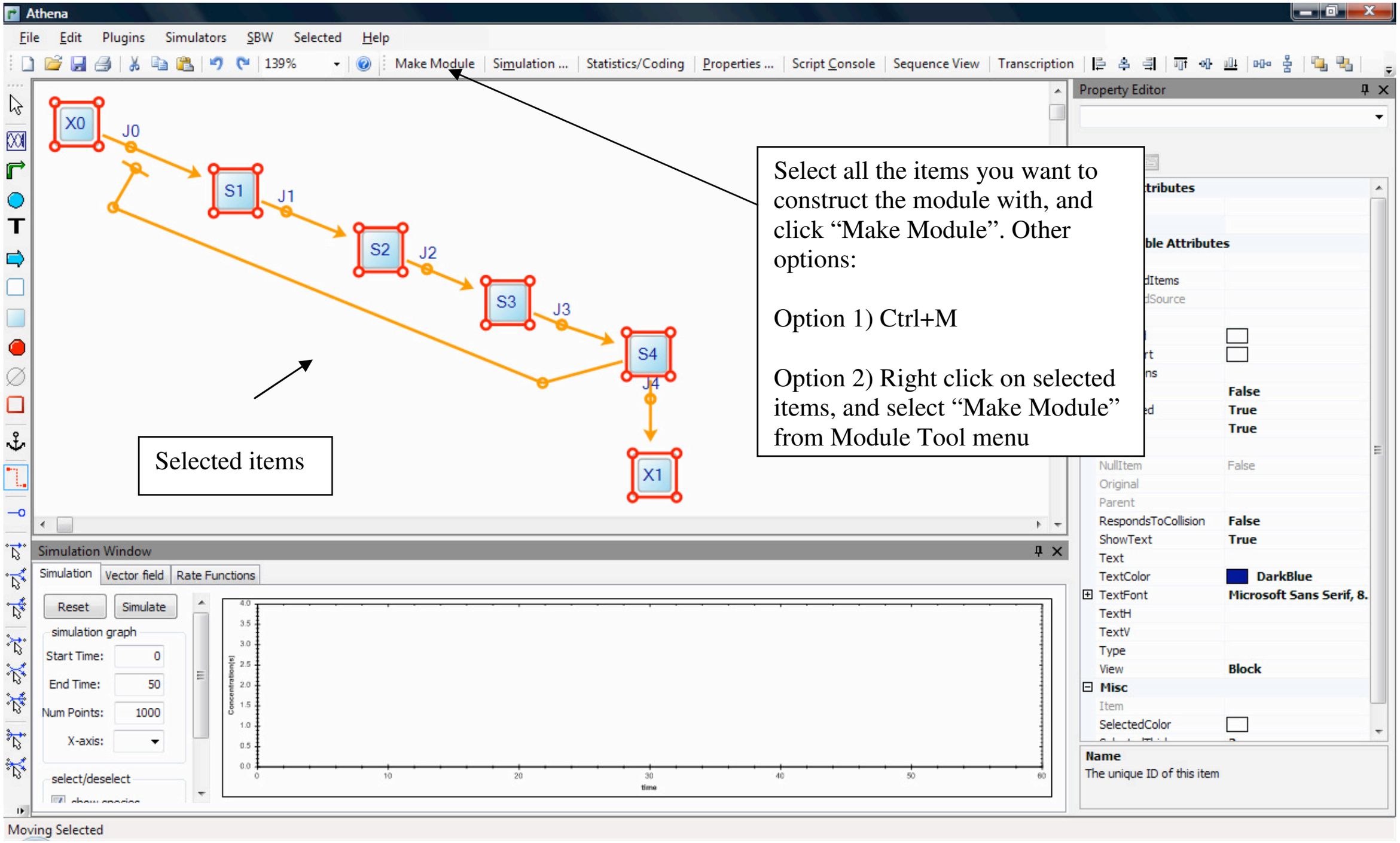


Connecting two parts together:

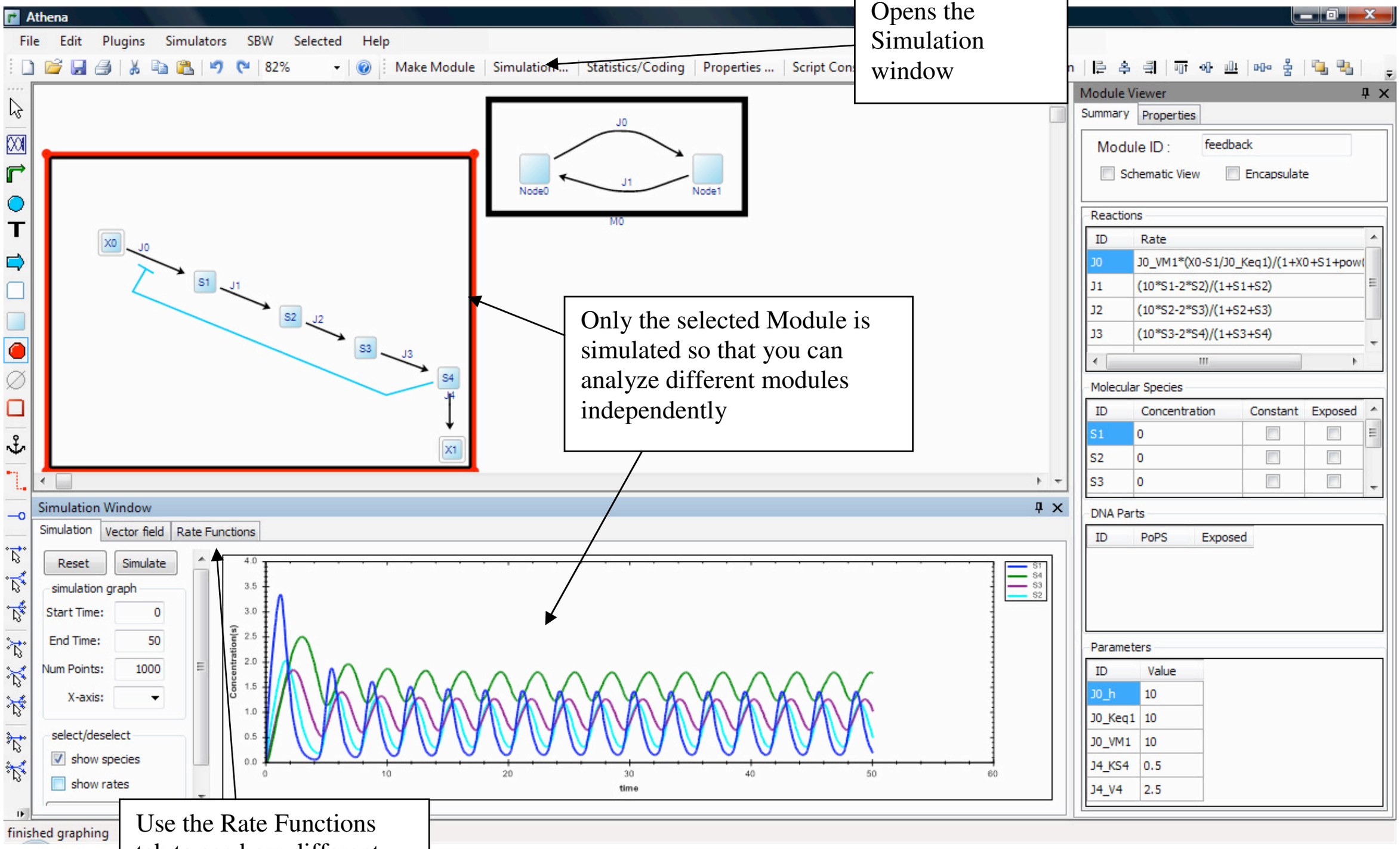
Option 1: bring one part close enough to the other, so that they touch

Option 2: Click and drag the red circle so that the red line meets the other part

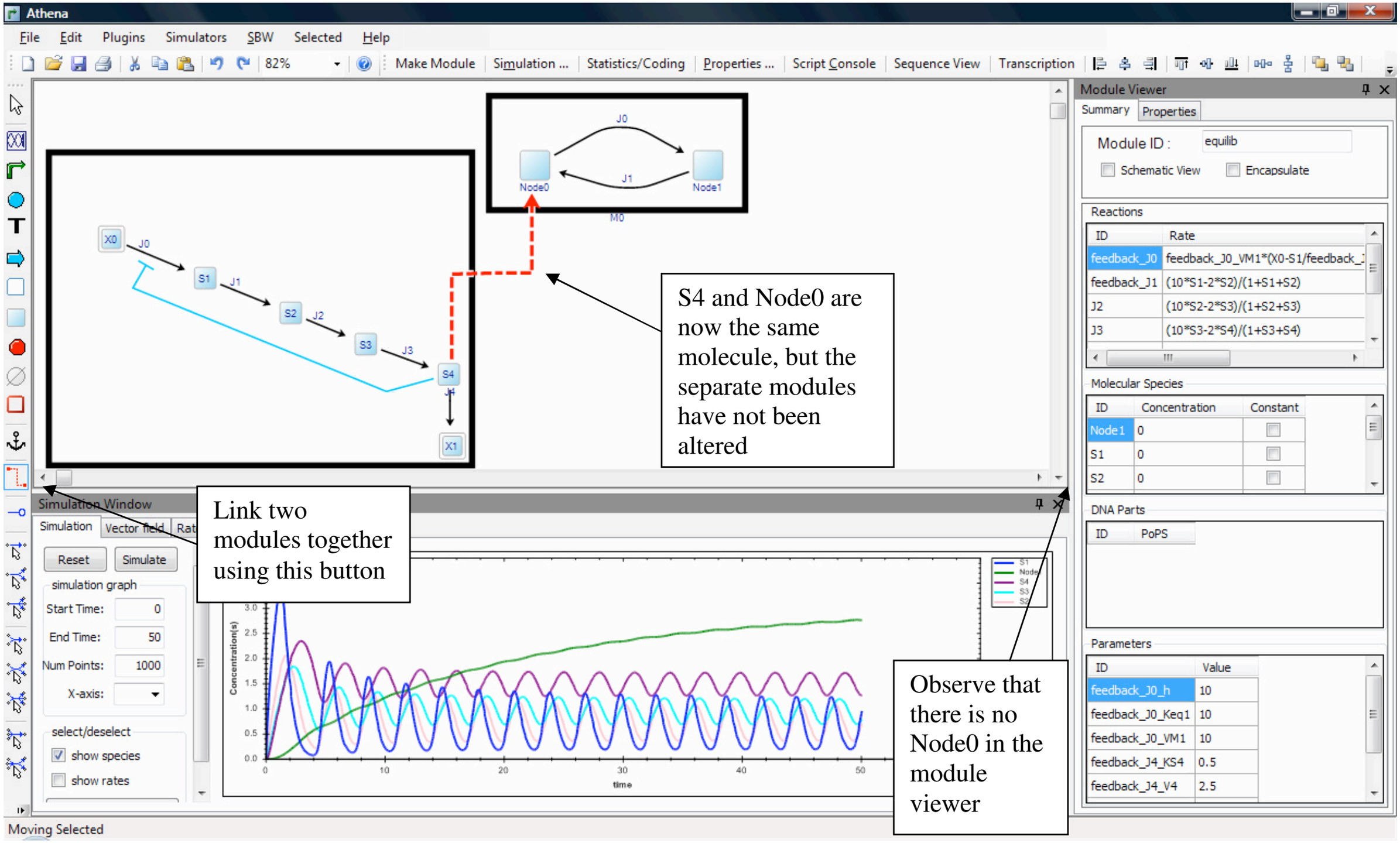
Making a Module



Simulating a Module



Connecting two or more modules



BioJADE

BioJADE

File BioBrick DB Settings Help

Library default Part BBa_9999 Aspects: Schematic FunctionalNetwork DNA Simulation Icon

Select Stamp Wire Cut Copy Paste Zoom In Zoom Out Save Revert Optimize Compile

Wire

Templates

nand2

not

reporter

source

or2

sender

Endy.1

Reverse Terminators

BBa_C0082

not: null

not: null

not: null

Used Parts

Help!

Wire Mode: Click mouse to start a wire. Click again to stop the wire, or ALT-click to set a waypoint. CTL-Click on terminals and press w to automatically wire together terminals.

Part Information

Part Type : Other

Designer : Jonathan Goler

Description : demo repressilator

Notes :

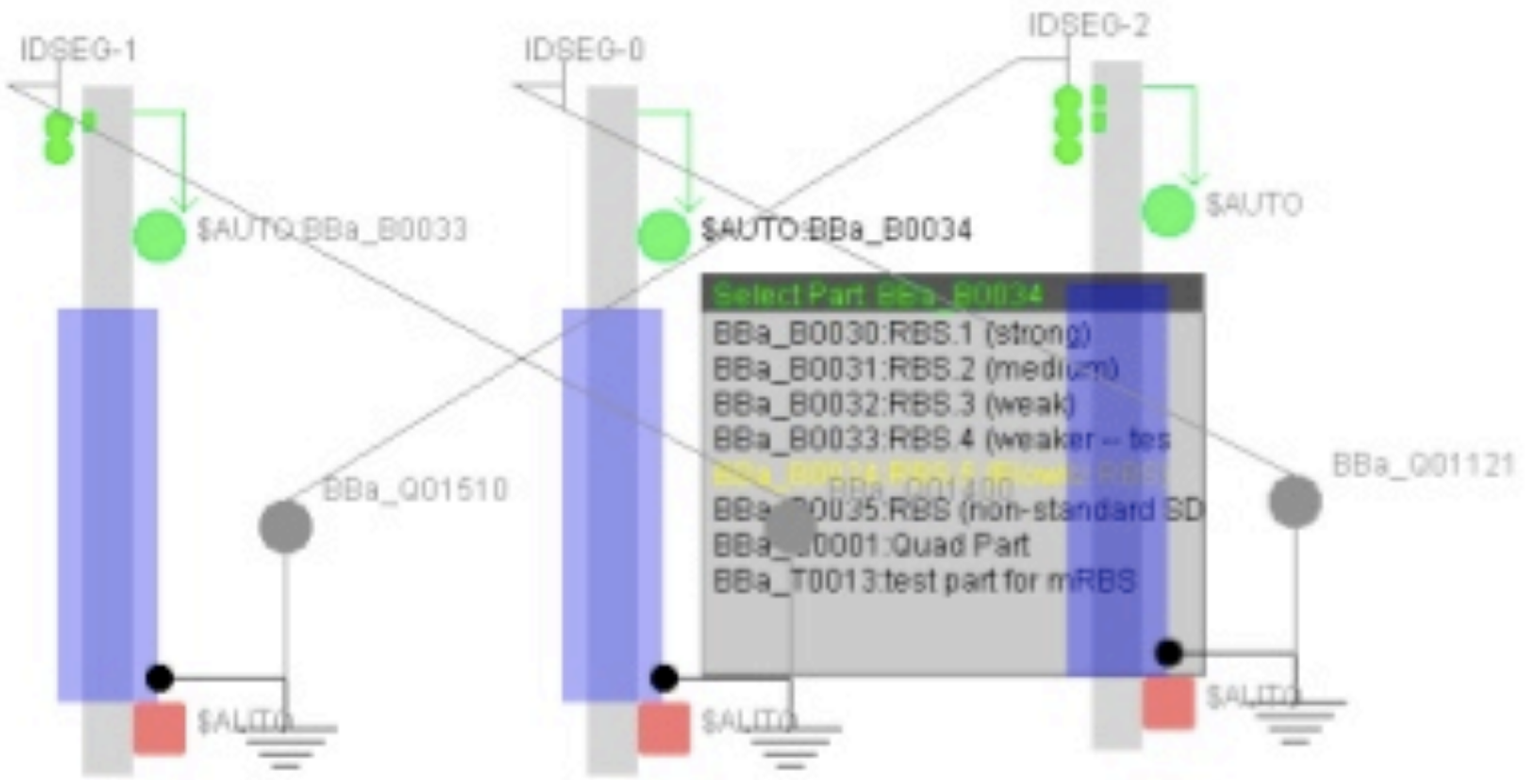
BioJADE

File BioBrick DB Settings Help

Library default Part BBa_9999 Aspects Schematic FunctionalNetwork DNA Simulation Icon

BBa_9999

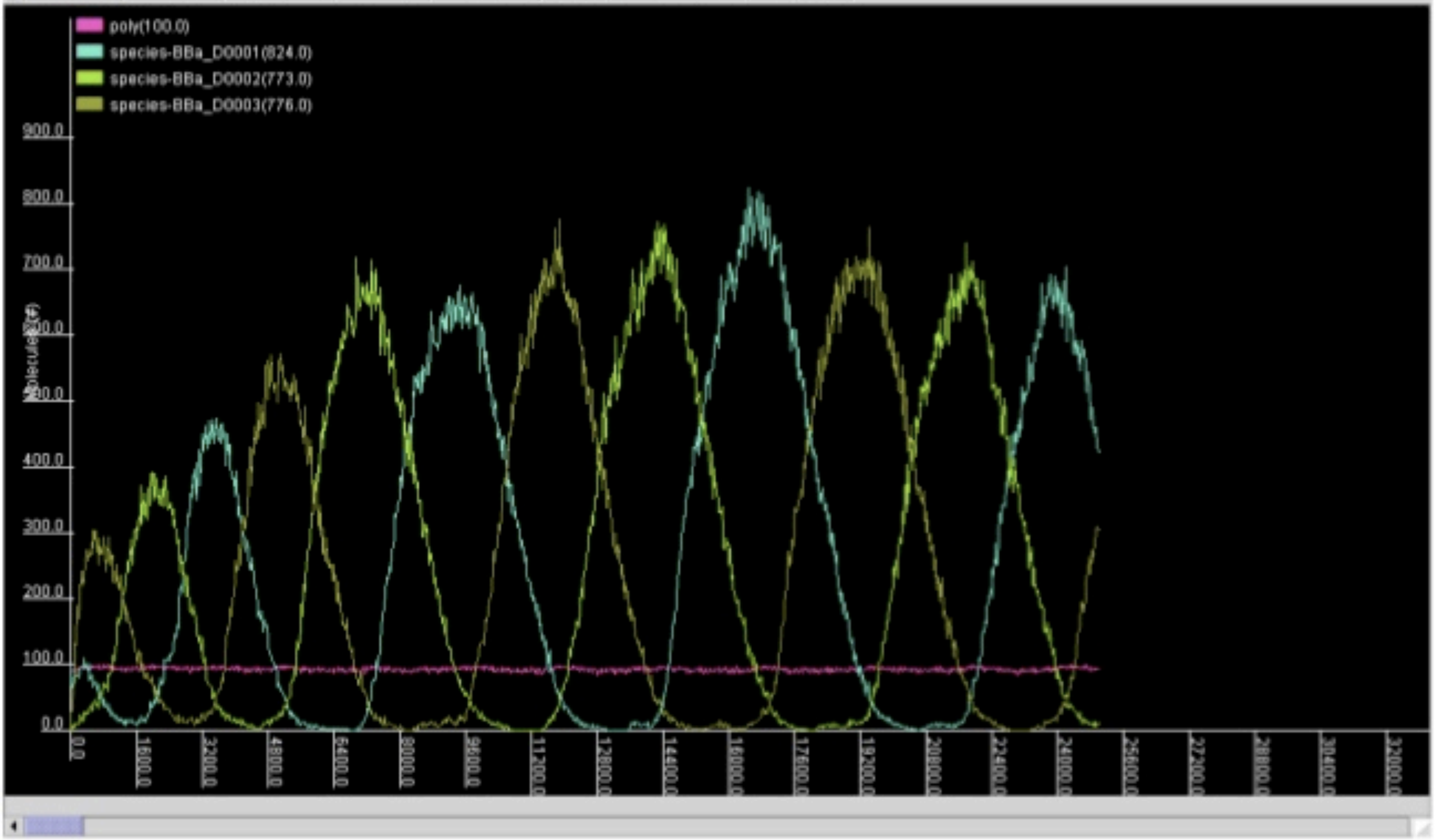
Re-Import Sequence Parameters Add Species Add Rxn Hide Rxns Save - Zoom +

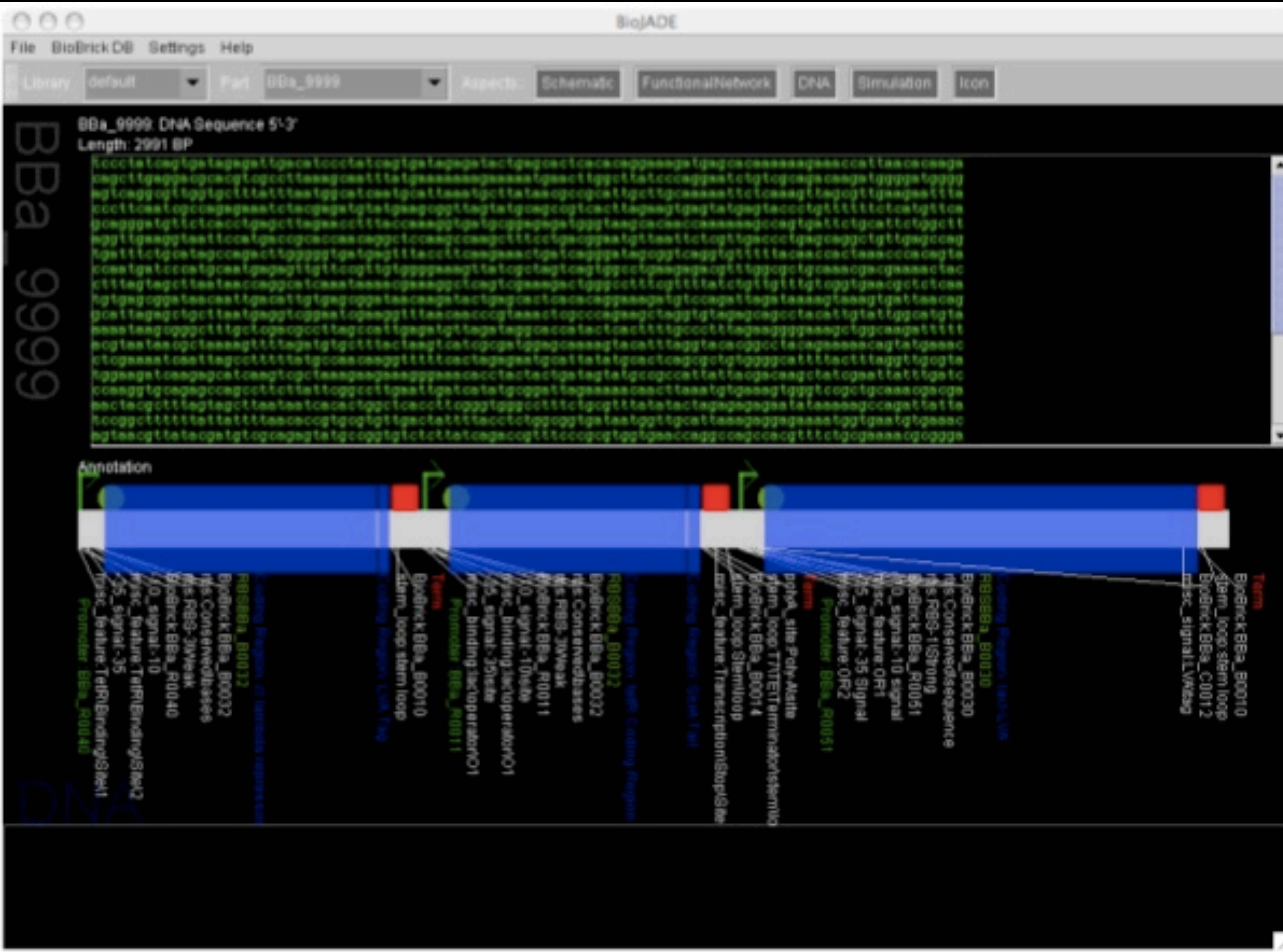


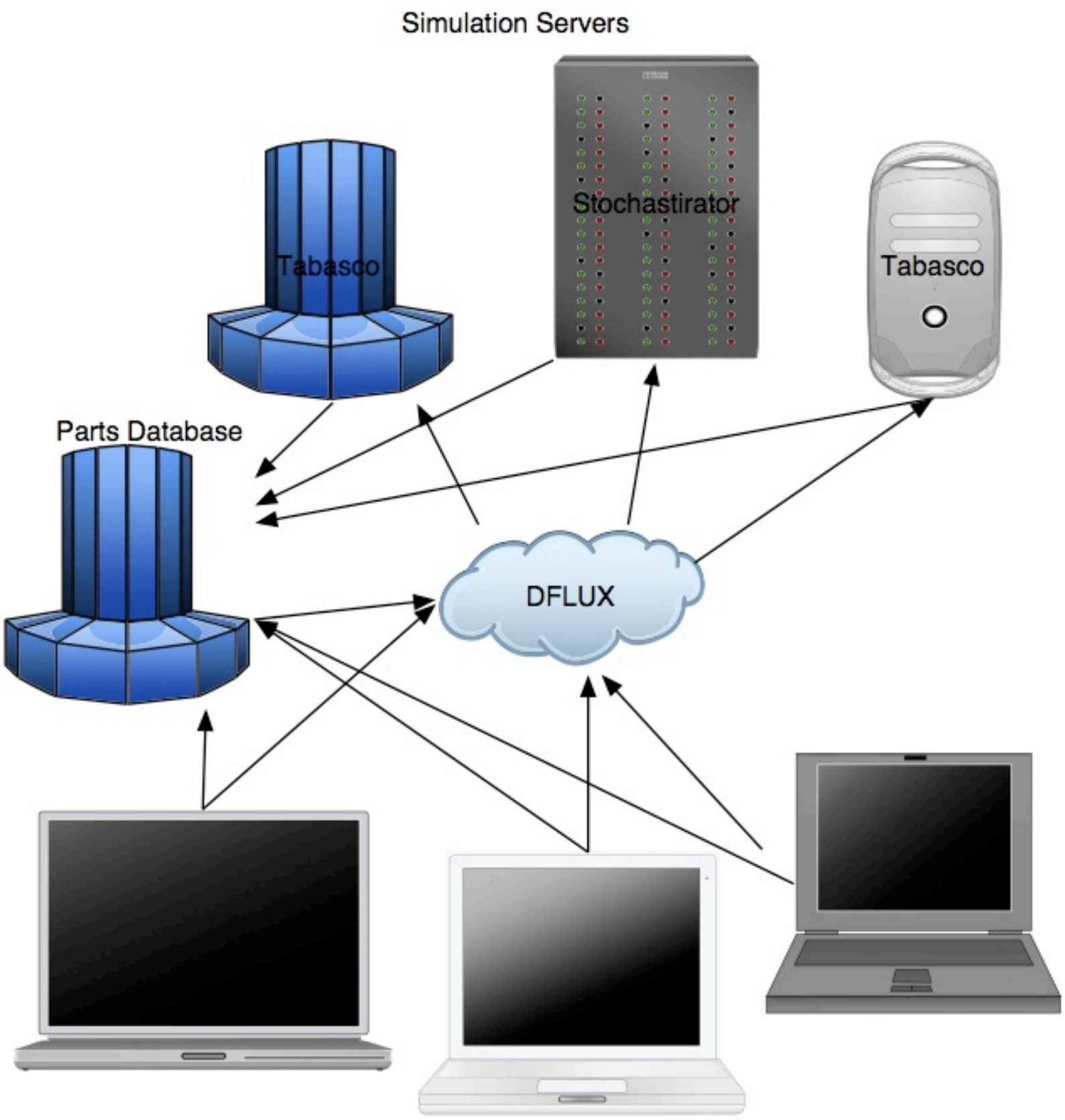
FunctionalNetwork

BioJADE/DFLUX Simulation Results : stoch-126.out1.out

Data Points | Zoom In (X) | Zoom Out (X) | Zoom In (Y) | Zoom Out (Y) | Colors | View Parameters | Print | Close




BioJADE
File
BioBrick DB
Settings
Help
Schematic
FunctionalNetwork
DNA
Simulation
Icon
BBa_9999: DNA Sequence 5'-3'
Length: 2991 BP
Annotation


Simulation Servers
Stochastirator
Tabasco
Tabasco
Parts Database
DFLUX
BioJADE Clients

http://genocad.org