EMERGENCE: A foundation for Synthetic Biology in Europe

WP1: General Networking activities

Fostering a community of knowledge

Vítor Martins dos Santos

Systems and Synthetic Biology Group
Division of Microbiology
Helmholtz Centre for Infection Research
Braunschweig, Germany

Consolidating the bases for a Synthetic Biology community

Foundations:

- Intellectual (concepts, abstraction, semantics…)
- Methodological (design, standardization, experimental / computational,…)
- Technological (IT, gene synthesis, microfluidics,…)

By:

- recruiting the required competences from (not so) neighboring disciplines;
- exploiting synergies (competences, expertise, complementarity...);
- fostering transnational/transcontinental communication & cooperation
- promoting education at various stages (school, undergraduate, ..)
- embedding early developments into a meaningful societal / economical context

WP1: General Networking Activities

Objectives:

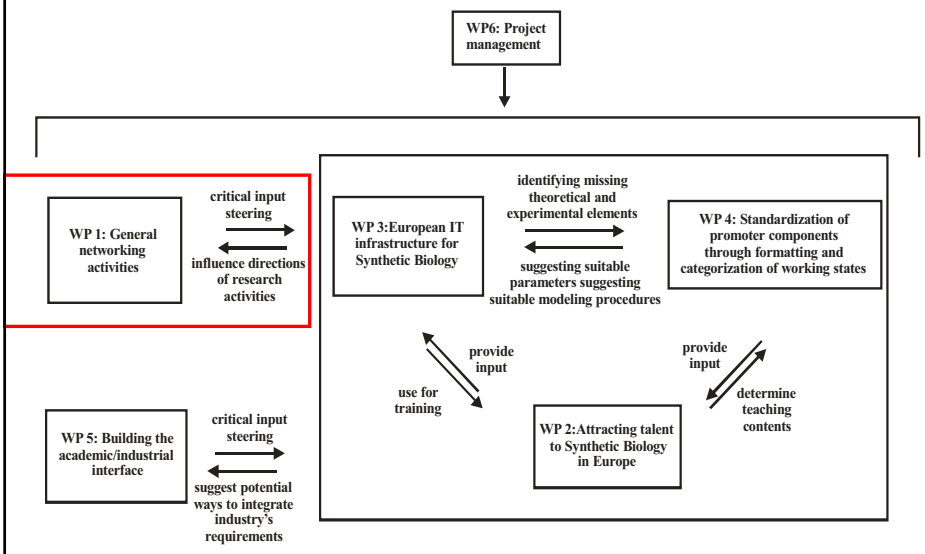
a) To establish a networking platform for current and future synthetic biology projects

b) To rapidly organize workshops for urgent issues in European synthetic biology

c) To implement a Europe-wide, cross-disciplinary framework for discussion on the possibilities, needs, limitations, and implications of synthetic biology.

d) To foster interactions with extra-European initiatives, with special emphasis on US, the Mid-East and Asia: Global knowledge space

Embeddding WP1 in EMERGENCE



Description of Tasks I

Task 1: ***Developing, maintaining, and evaluating a standardized meeting structure*** that allows efficient review and distribution of the conclusions obtained at individual meetings.

Overarching, jointly with WP Management

Task 2: ***Hosting workshops on development of the European IT infrastructure for synthetic biology, design tools for synthetic biology, and/or standardization of biological parts.***

Jointly with WP3 (IT infrastructure), WP4 (Design tools and Biological parts), Standardisation Issues (Overarching)

Description of Tasks II

Task 3: ***Establishment of study groups on specific subjects relevant to synthetic biology***

"Foundational" technologies, including e.g. high-throughput genome minimization,
DNA synthesis),
potential of genetic circuits, modularity in proteins, handling noise & error
propagation in biological systems,
robustness in biological systems,
transferability of engineering foundations
……...

Description of Tasks II

Task 4: ***Platform for organizing thematic workshops/courses/meetings, resulting from maturation of study groups into specific workshops***, courses, or small scientific meetings, or from initiatives from members of the advisory board or the steering committee.

Task 5: ***EMERGENCE will promote exchange and training visits between European and overseas participants***, in particular with the Middle East and Asia, including:

•invitations for a number of leading scientists in the field to participate in study groups;
•seeking actively to participate in similar initiatives in those countries; and inclusion of Middle Eastern/Asian researchers in the EMERGENCE
•communication and dissemination pipelines.
•The participation of senior European synthetic biology scientists in Asian meetings will be particularly encouraged.

Deliverables Month 1-18

D1.1: Material and rules for standardized meeting structure in place for the first time (month 3). Responsible: HZI

D1.2: Report on the first workshop on development of the European IT infrastructure for synthetic biology (month 8) Responsible: HZI

D1.3: Report on the first workshop for design tools for synthetic biology (month 4) Responsible: CNIO

D1.4. Report on recommendations of the intra-consortium expert group on suitable promoter standardization formats (month 12) Responsible: CNB

Deliverables 18-36 month

D1.5: Updated material for the appropriate section in the quarterly Synthetic Biology Newsletter regarding tasks 2, 3, and 4 (months 3, 6, 9, 12, etc): Responsible ETH

D1.6. Report on workshop on foundations of measurement statistics in synthetic biology (month 24)

D1.7. Document identifying “common European-Asian interests and ways to develop them” or similar document in place and signed by extra-European and European groups/organizations involved in synthetic biology (month 32)

Milestones and expected results

M1.1. **Recommendations for the European IT infrastructure for synthetic biology** are discussed and recommendations issued (month 3)

M1.2. **Recommendations for design tools on the IT infrastructure** are discussed and recommendations issued (month 4)

M1.3 **First experiences with the study group format** are reviewed by the steering committee after 6 months and by advisory board and steering committee after 12 months and the format is adapted, if necessary (month 6, 12)

M1.4. **Recommendations on standardization of biological parts** are discussed (month 11)

M1.5. **Recommendations on measurement systems in synthetic biology** are discussed (month 24)

M1.6. Steering committee and advisory board decide whether the **critical mass in Europe-Asian relations in synthetic biology** has been reached and drafting a “common interests” document is going to be useful (month 24)

D1.1 - Material and rules for standardized meeting structure

Web-based template document:

Definition of the theme and Scope

The need for the SynBio community and goals

Implementation plan (size, mode, participants

Timeline

Financing possibilities

Process:
Submission to Steering committee (WP-leaders, Coordinator)

Eg. IT: A. Valencia; Teaching: Sven P.; INdustry: L. Pasamontes

D1.1 - Material and rules for standardized meeting structure: examples themes

context-independent biological systems/modules

microfluidics technologies / single cell measurents

minimal genomes / minimal systems

what to measure / how to measure?

design concepts
how can we handle “systems“ (made of parts)?

D1.2 -Report on the first workshop on development of the European IT infrastructure for synthetic biology

Workshop Computational Infrastructure and Methods for Synthetic Biology

The Eighth Annual BioPathways Meeting

Vítor Martins dos Santos
Vincent Schachter
Vincent Danos
Joanne Luciano
Aviv Regev
Eric Neumann

July 19-20, 2007
Satellite Meeting ISMB-ECCB 2007
Vienna, Austria

7:30 – 8:45	Registration	
9:00-9:10	Vincent Schachter Genoscope, Evry & BioPathways Consortium	Opening remarks
Session 1: Computational Methods and Infrastructure for Synthetic Biology Chairman: Vítor Martins dos Santos		
9:10-09:30	Vitor Martins dos Santos, Helmholtz Center for Infection Research, Braunschweig	EMERGENCE: a Foundation for Synthetic Biology in Europe
9:30-10:00	Alfonso Valencia, CNIO, Madrid	Bioinformatics tools to help in the design of biological systems
10:00-10:30	Jörg Stelling, ETH, Zürich	Formal tools for Model-Based Synthetic Biology
10:30-11:00	Coffee Break	
11:00-11:30	Randy Rettberg, MIT, Cambridge	The MIT registry of parts and devices
11:30-12:00	Alfonso Jaramillo, Ecole Polytechnique, Paris	Model-based design of genetic circuitry
12:00-13:00	Lunch	
Session 2: Network Reconstruction & Analysis (part 1) Chairman: Vincent Schachter		
13:00-13:45	Florence d'Alche-Buc, University of Evry	Supervised Inference of Protein-Protein Interaction Networks
13:45-14:30	Jason Ernst, Carnegie Mellon University	Reconstructing Dynamic Regulatory Maps
14:30-14:50	Tijana Milenkovic and Natasa Przulj, Irvine, University of California	Uncovering Biological Network Function via Graphlet Degree Signatures
14:50-15:10	Kam Dahlquist, Loyola Marymount University	Mathematical Modeling of the Transcriptional Network Controlling the Environmental Stress Response in Saccharomyces cerevisiae
Session 3: Databases & Software Tools Chairman: Joanne Luciano		
15:10-15:30	Ozgun Babur, Bilkent University	PATIKAweb Components for Microarray Data Analysis & Advanced Graph-Theoretic Querying
15:30-16:00	Coffee Break	
16:00-16:20	Richard Adams, University of Edinburgh	The Edinburgh Pathway Editor
16:20-16:40	Esther Schmidt, EBI, Cambridge	Reactome - a knowledgebase of biological pathways
16:40-17:20	Eric Neumann, Teranode Corp.	A Genome - Phenome Integrated Approach for Mining Disease-Causal Genes using Semantic Web
Round Table Discussion		
17:20-18:30	IT Infrastructure & Computational Methods for Systems and Synthetic Biology	

Session 4 : Network Reconstruction & Analysis (part 2) Chairman: Eric Neumann		
9:00-9:45	Peter Karp, SRI International	Gene Regulation in EcoCyc and Pathway Tools
9:45-10:30	Jerzy Tiuryn, University of Warsaw	Identification of functional modules from ancestral protein-protein interactions
10:30-11:00	**Coffee Break**	
11:00-11:20	Rainer Koenig, DFKZ, Heidelberg	Using gene expression data and network topology to detect substantial pathways, clusters and switches
11:20-11:40	Hanif Khalak	Microarray-based Class Modeling and Prediction using Set-Enrichment Analysis
11:40-12:00	Sol Efroni, NIH/NCI	Identification of Key Processes underlying Cancer Phenotypes using Biologic Pathway Analysis
12:00-13:00	**Lunch**	
13:00-13:45	Eytan Ruppin, Tel-Aviv University	Genome Scale Studies of Robustness and Annotation of the Yeast Metabolic Network
13:45-14:30	Fengzhu Sun, University of Southern California	Network motif identification in stochastic networks
Session 5: Evolution of pathways and networks Chairman: Toni Gabaldón		
14:30-15:15	Simon Lovell	Protein-protein interactions and their networks: can they tell us about biology?
15:15-15:35	Natalia Maltsev	Co-evolutionary analysis of Metabolic Pathways and Enzymes in PUMA2 and Chisel systems
15:35-16:00	**Coffee Break**	
16:00-16:45	Toni Gabaldón	Evolution of metabolic systems: insights from comparative genomics
16:45-17:30	Philip Kim	Relating three-dimensional structures to protein networks provides evolutionary insights
Round Table Discussion		
17:30-18:30	**Network Reconstruction and Evolution**	
End of meeting		

D1.3 - Report on workshop for design tools for synthetic biology (CNB)

Satellite meeting to the ESF – EMBO on SynBio

November 2007

(Alfonso, Jörg, Randy, etc)

Report being drafted (CNIO)

D1.4 - Report on recommendations of the intra-consortium expert group on suitable promoter standardization formats (CNB)

VDL – Report in preparation

Silva-Rocha R, de Lorenzo V.
Mining logic gates in prokaryotic transcriptional regulation networks.
FEBS Lett. 2008 Apr 9;582(8):1237-44.

D1.4 -Updated material for the appropriate section in the quarterly Synthetic Biology Newsletter regarding tasks 2, 3, and 4

Frauke Greve / Sven Panke

Newsletters Dec 2006, June 2007, Dec 2008, June 2008

Includes list of conferences, research highlights, press releases, funding activities

Activities towards Task 4 (European Networking)

Activities towards Task 4 (European Networking)

Series of Workshops on different aspects of SynBio:

-Biofine (Tessy), Freiburg April 10, 2008
-Genopole (Jaramillo), 26-27 June, 2008
-IRGC Workshop Session on the Risk Governance of Synthetic Biology (26 & 27 June - Geneva, Switzerland)
-Stakeholder meeting Roadmap SynBio (Tessy), 10 June 2008
-ESF workshop on Minimal Systems (with A. Moya), in planning
Etc.....

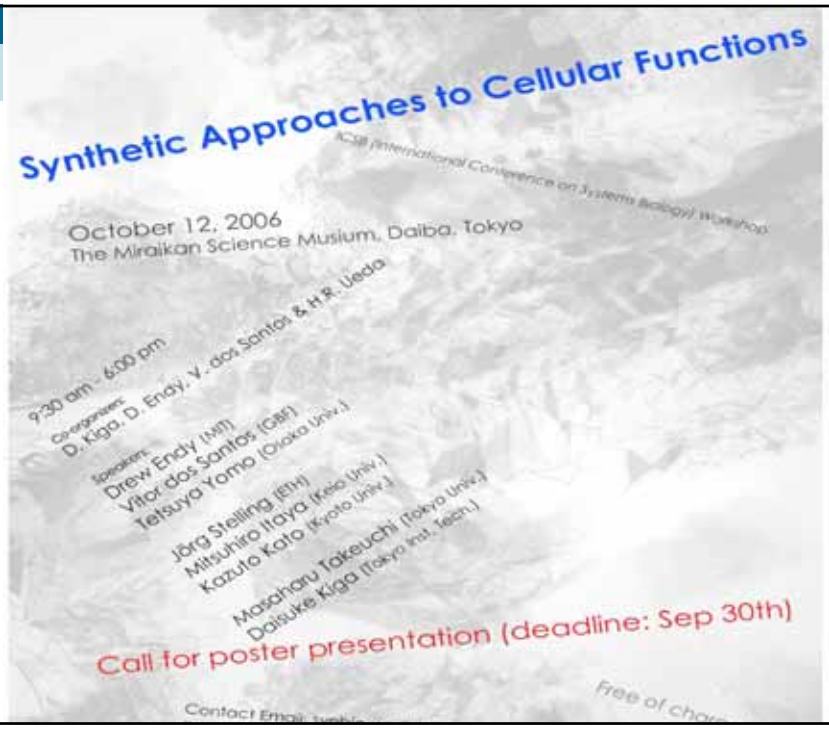
Activities towards Task 4 (Global Networking)

Workshop on:

Synthetic Aproaches to Cellular Functions, Tokyo, 13 October 2006

Organised jointly by D. Kige (JP), H. Ueda (JP), D. Endy (US), Martins dos Santos („EU“)

About 120 worldwide attendants, 50+ posters. NEST-PATHFINDER SB projects presented. Overwhelming reaction



Future networking activities Asia

Sino-German Exploratory Workshop on Synthetic Biology, Hangzhou, China, 2008. Couple to Probactys (EU) and perhaps other projects

To be organised jointly with Huanming Yang (Beijing Genome Institute, CN)

Exchange of students/ scientists:

- China (2 students 7 month each plus 2 scientists 1 week in 2007)
- India (2 Students 4 month each, plus scientist 1 week 2008)

Explorative project in Israel on digital evolving microbial communities

Indian - EU workshop on Synthetic Biology (January or September 2009)

ESF-JSPS Frontier Science Conference Series for Young Researchers (Synbio tentative for 2009)

How shall we proceed?

Report on the identification of scientific & infrastructure bottlenecks in SB (jointly WP4 & WP3)

Study groups: bottom-up, priorital themes?

Possible themes:

- context-independent biological systems/modules
- microfluidics technologies / single cell measurents
- minimal genomes / minimal systems
- what to measure / how to measure?
- design concepts
- how can we handle “systems“ (made of parts)?
- .....

Thematic Workshops: IT and Standardization. Time plan?

Exchange visits?

Future activities, other

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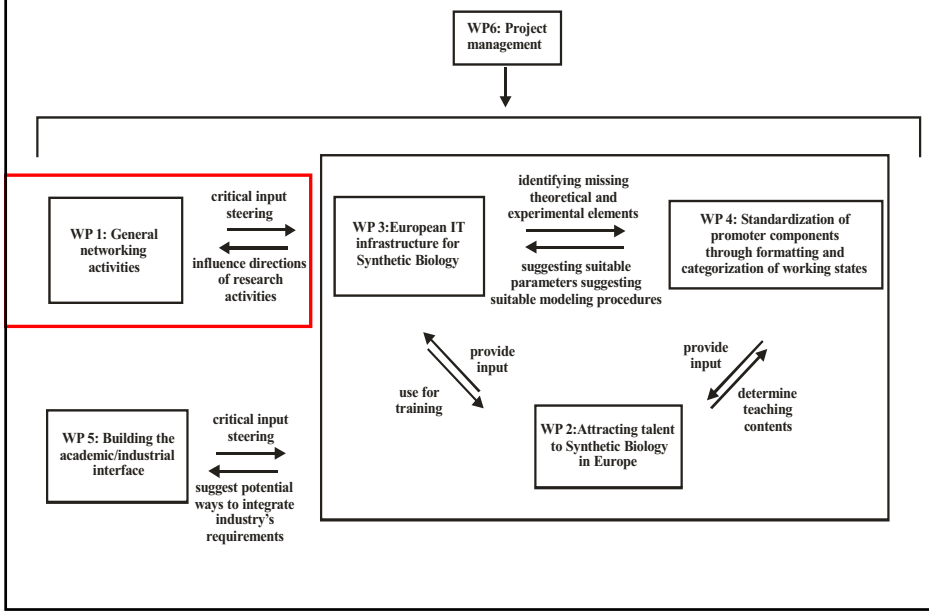
Project Structure



Emergence WP3
A European IT infrastructure for Synthetic Biology

M.A. Marchisio

Zurich, 28/05/08

Starting point: the *MIT Registry of Standard Biological Parts*
(http://partsregistry.org)

Goal: building a European mirror of the Registry containing computational tools

--> to retrieve biological information from other databases;

--> to design circuits made of the Standard Biological Parts.

Information integration

(CNIO – I. Cases, A. Valencia; MIT – R. Rettberg)

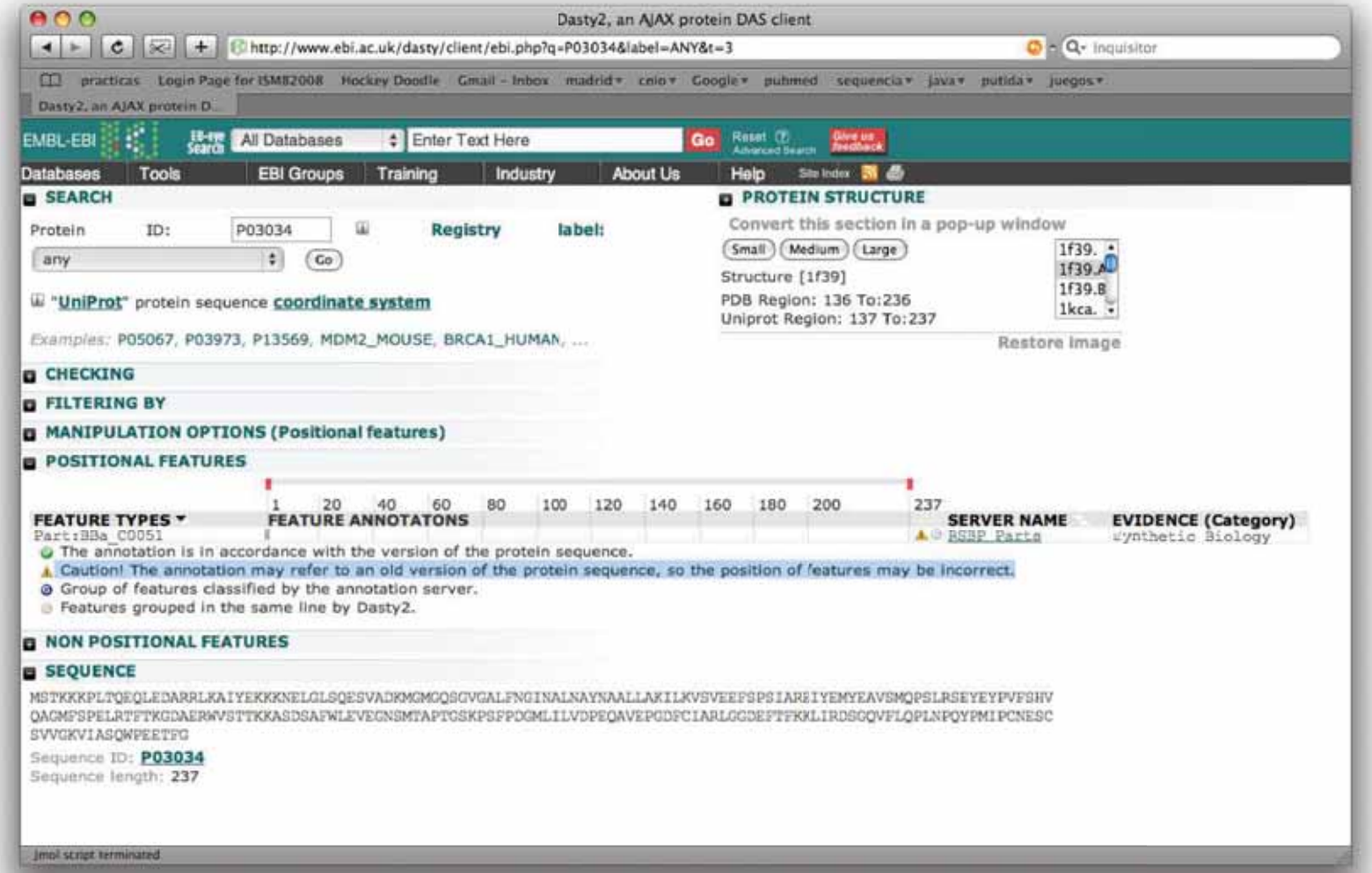
DAS (Distributed Annotation System) server solution:
- easier implementation;
- cooperation with other projects (Biosapiens NoE).

1st step: testing the Registry connectivity with other databases

Three prototype DAS servers implemented on the MIT site:
- reference (sequence and IDs);
- annotation1 (structure, functions, etc.);
- annotation2 (Uniprot as a reference server; gets Uniprot ID, returns part IDs).

Dasty2

(http://www.ebi.ac.uk/dasty/)



by courtesy of I. Cases

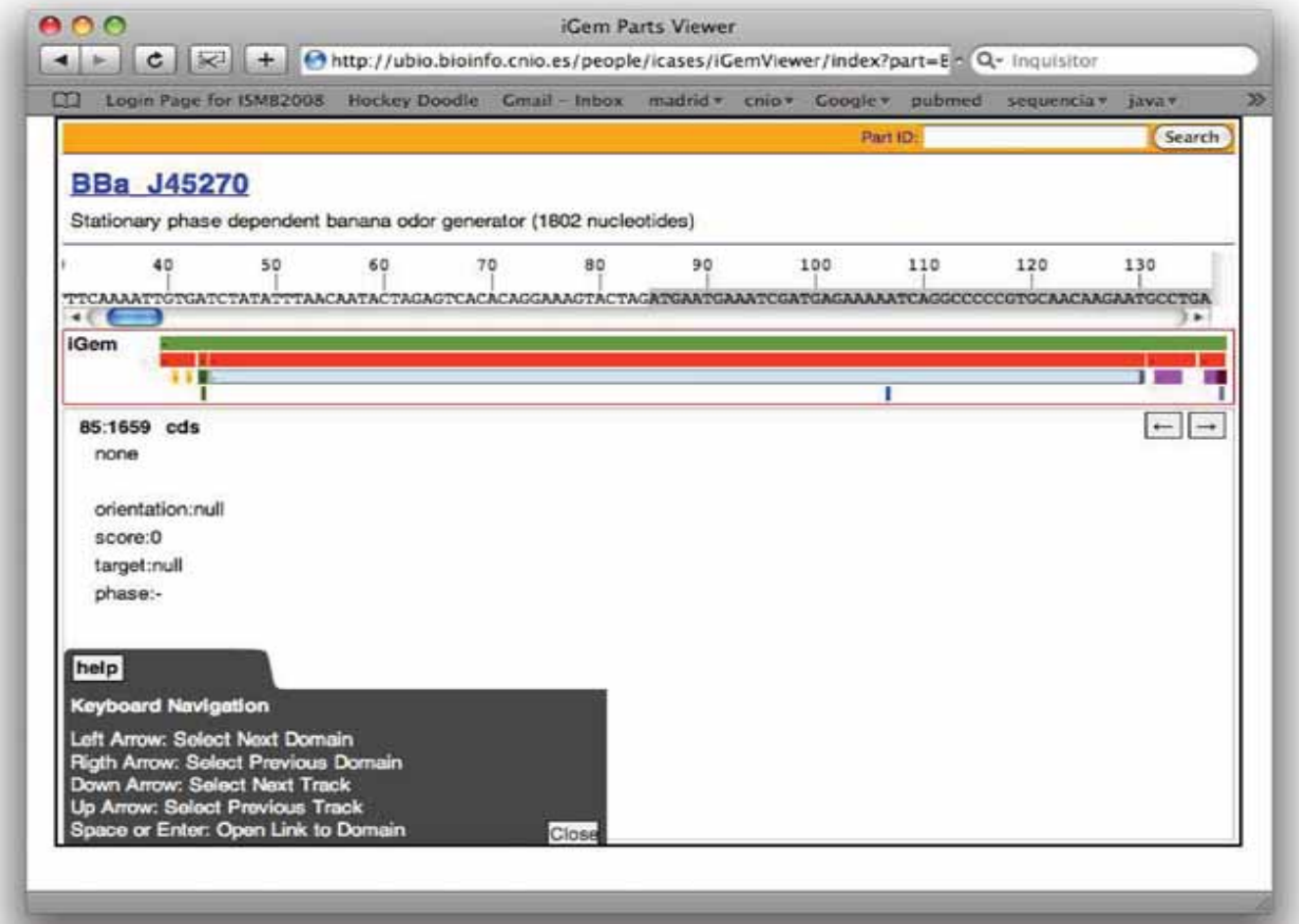
2nd step: development of new tools to access and visualize content of biological databases

(http://cargo2.bioinfo.cnio.es/)

CARGO (Cases et al., NAR 2007) extended to handle information from the three prototypes DAS installed on the MIT site.

3rd step: realization of a pilot application.

IGEM Part Viewer: can visualize part content and return a possible link to Uniprot.



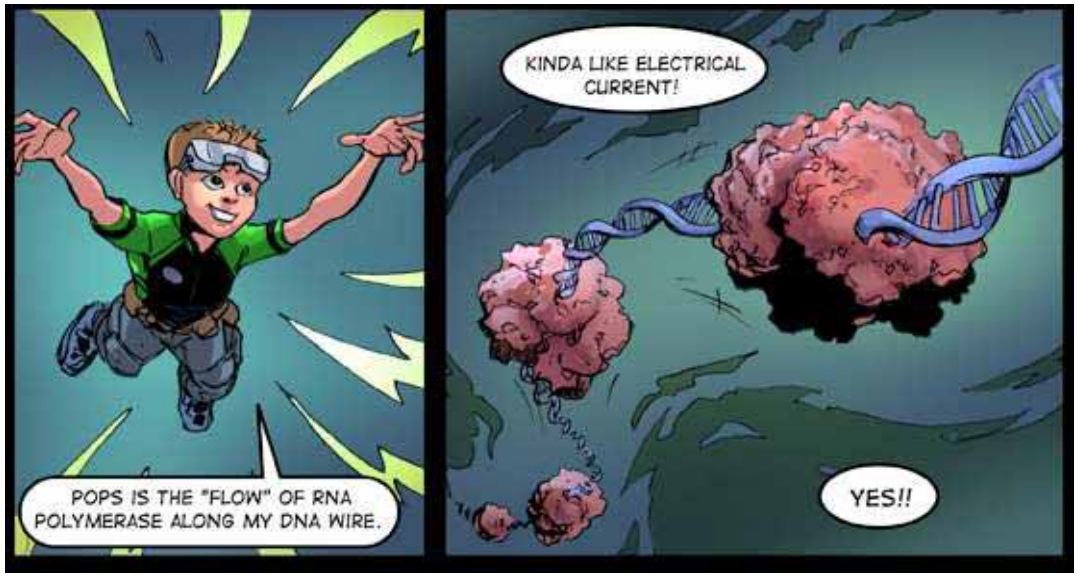
by courtesy of I. Cases

Circuit simulation

(ETHZ – M.A. Marchisio, J. Stelling)

Main activity: building of a ***"drag & drop"*** tool for circuit design

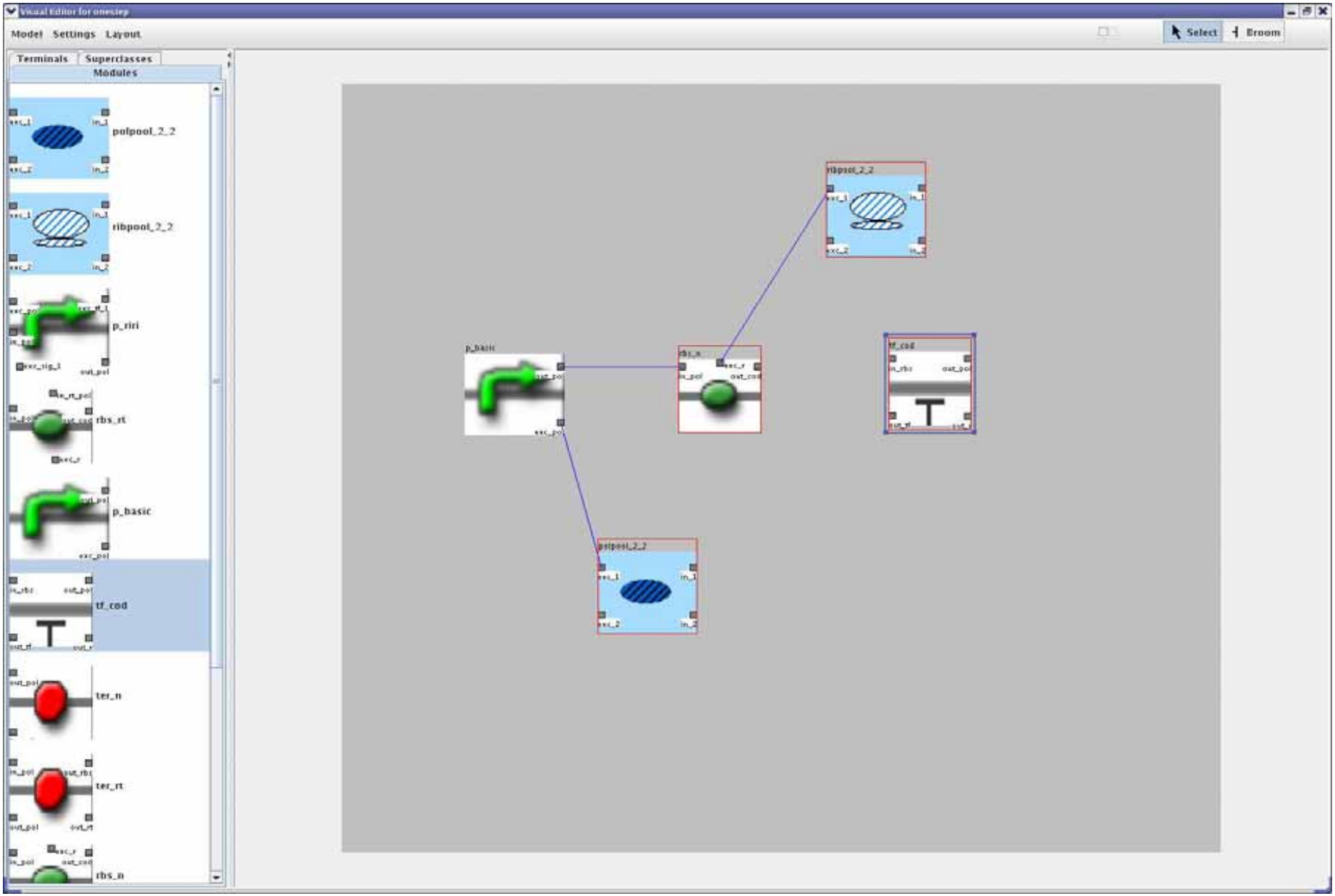
Main problem: composability of Registry parts
(common signal carriers definition)



Adventures in Synthetic Biology, Endy, D. *et al.*, appeared on *Nature* **438**, 449-453.

Canvas provided by **ProMoT**

(http://www.mpi-magdeburg.mpg.de/projects/promot/)



Model/tool features

ODE based model for every basic Registry parts.

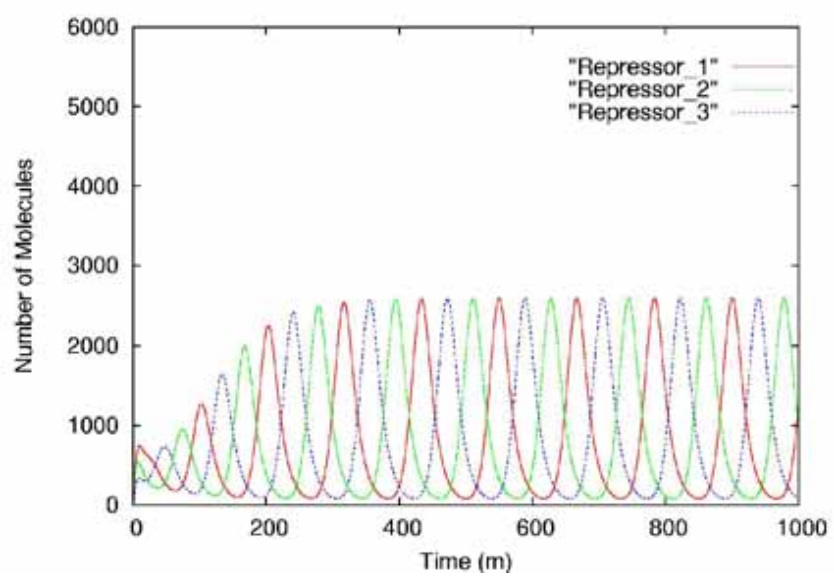
Set of Perl scripts to generalize parts' construction.

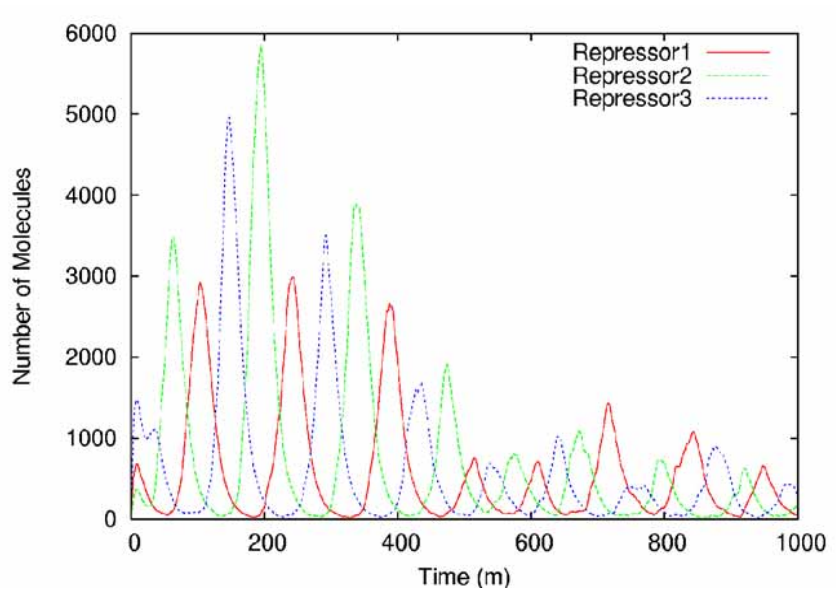
Devices (complex Registry part) realized by assembling basic parts.

Circuit files exportable into Matlab or SBML (level 1 or 2) format.

Possibility of running both deterministic and stochastic simulations.

Example: *the Repressilator*[*]





(*) Elowitz, M. B. and Leibler, S. (2000) *Nature* **403**, 335-338.

How to go on?

Definition of the European Registry mirror basic components.

They might be:

1) the part browser (CARGO + IGEM Part Viewer);
2) the access to different databases (CARGO + DAS servers);
3) the canvas for circuit design (ProMoT + part models).

Problems:

- necessity of a “source” of parameter values;
- integration of part generation and circuit design;
- putting together the information and the simulation side.

Biobrick Standardization

Synthetic Biology Concepts

- Standardization... transferable & predictable modules, conditions, methods
- Decoupling... separate complex design into simpler problems tackled independently
- Abstraction... hide detail behind standard interfaces and signal carriers
- Open exchange... organize specifications and methods

[D. Endy (2005) Foundations for engineering biology. Nature 438]

Content

1. BBF Standardization Process
2. from Pobol to a web of registries
3. BrickIt – open source biobrick management
4. A European web of registries project?

Standardization

Overview

http://openwetware.org/wiki/The_BioBricks_Foundation:Standards

article | talk | edit | history

The BioBricks Foundation:Standards

HOME | OUR GOALS | BOARD MEMBERS | FAQ | DONATIONS | CONTACT

Please visit:

- The BioBricks Foundation:Standards/Technical for the wiki notes from the BBF **Technical** Standards mailing list.
- The BioBricks Foundation:Legal for wiki notes from the BBF **Legal** Standards mailing list.
- The BioBricks Foundation:MailingLists to subscribe to BBF mailing lists, or browse the mailing list archives.

Standardization Process

1. two parties from different locations
2. demonstrate it's working
3. write it up
4. request RFC # on mailing list
5. others comment / revise
6. BBF enacts standard

Active Technical Standards Projects

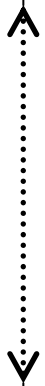
- Biobrick Formats (aka Physical Composition)
- Measurement standards
- Data exchange standards
- Technical Resources
- E.coli promoter standard

BBF Legal Working Group

- BBF Standards Mailing List
- BBF Standards Wiki

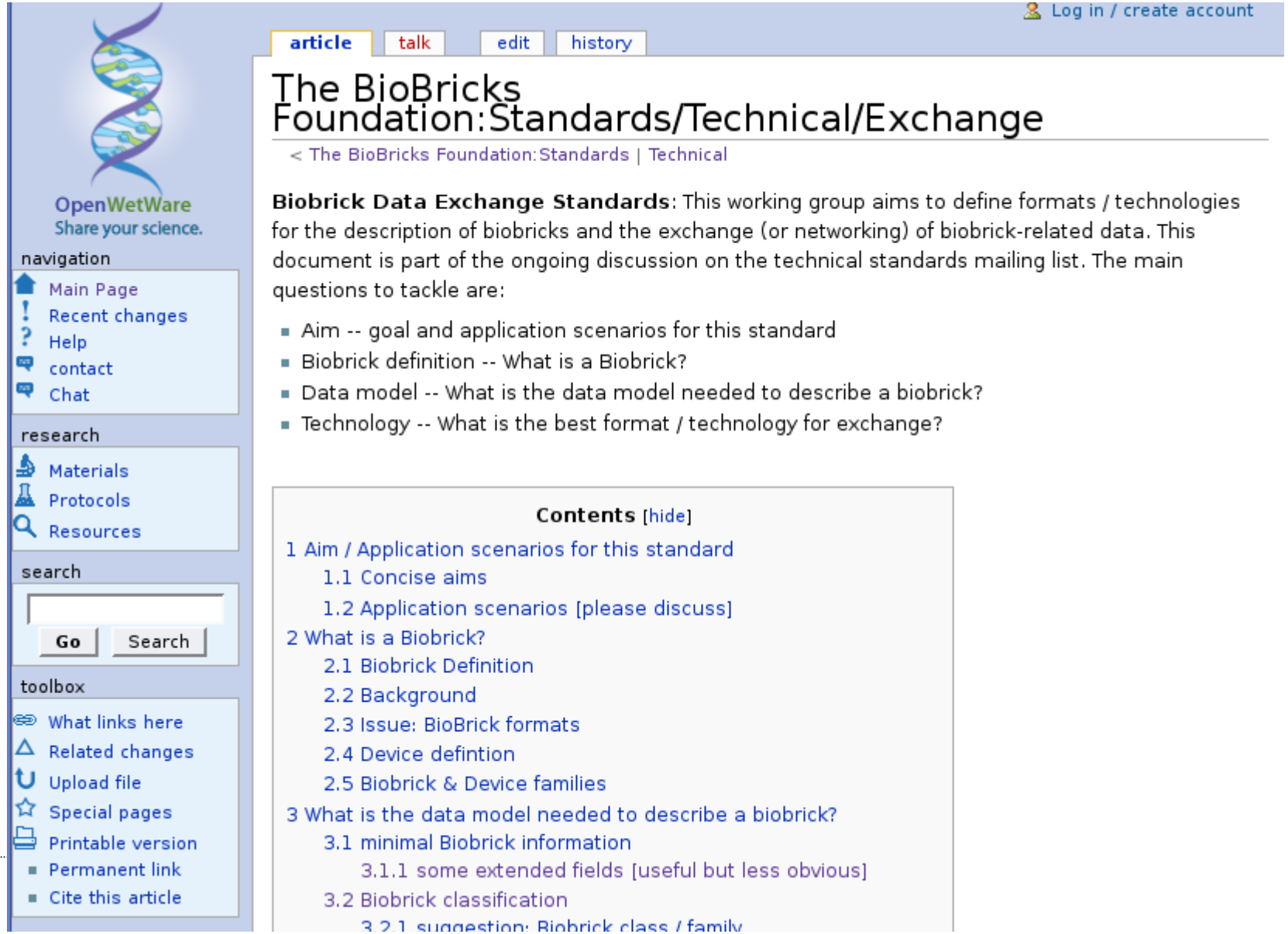
from PoBoL ...

... to a web of registries

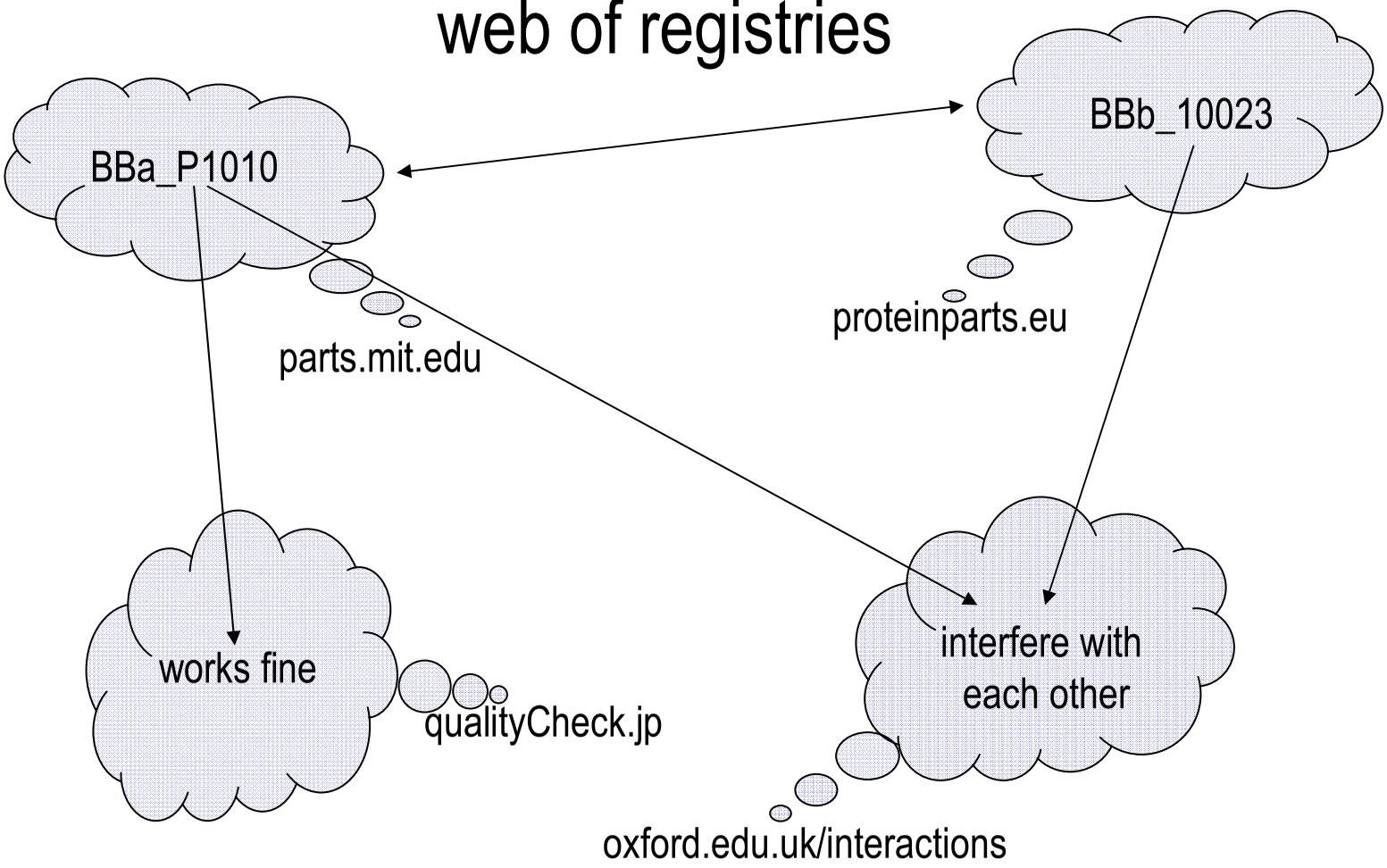


Data Exchange Wiki

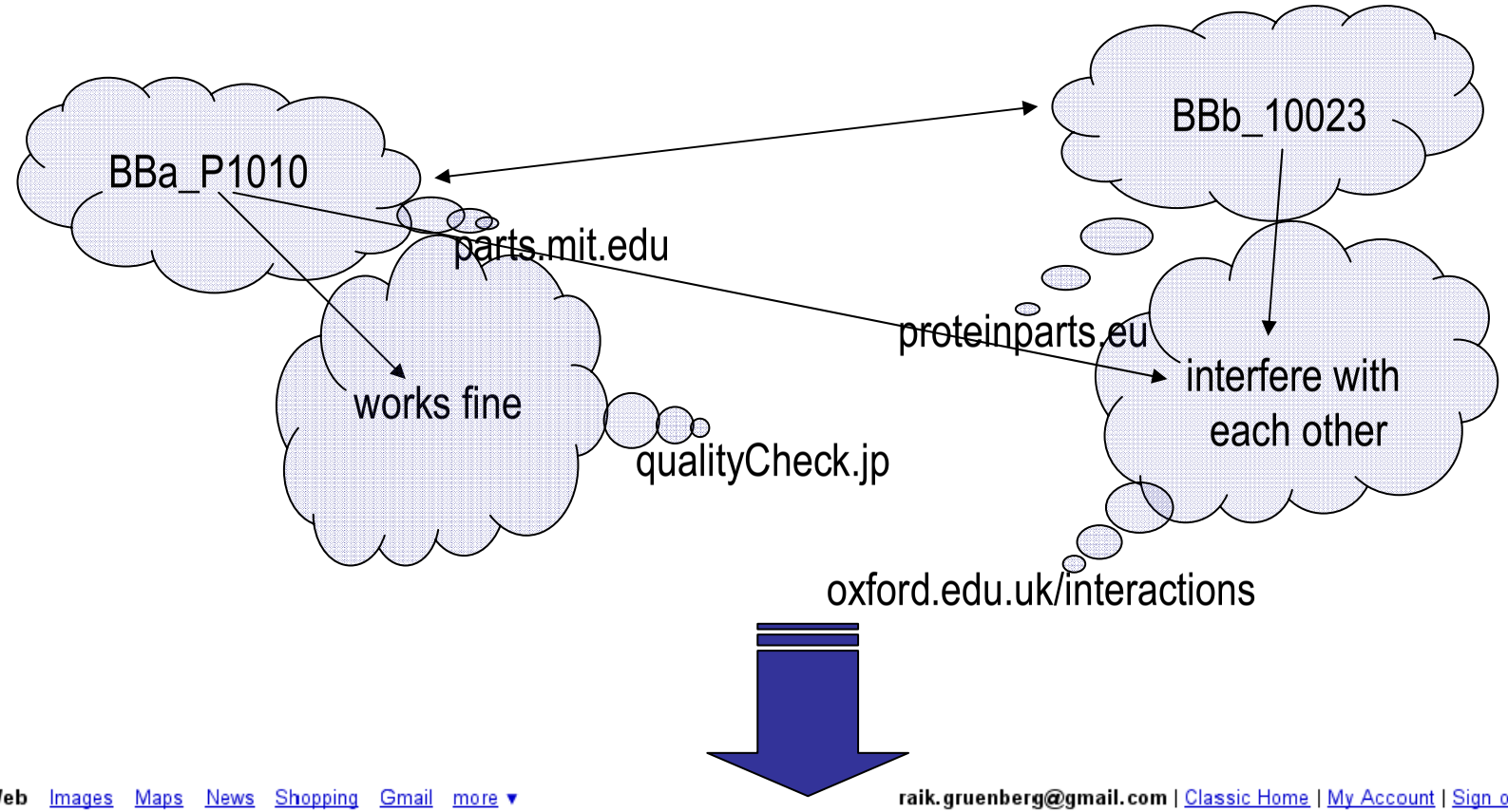
http://openwetware.org/wiki/The_BioBricks_Foundation:Standards/Technical/Exchange



Data Exchange Architecture

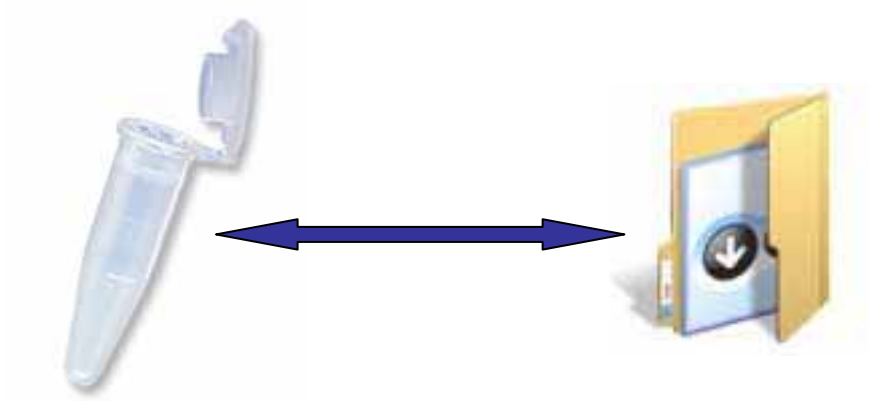


Data Exchange Architecture



Biobrick Definition

- A BioBrick is a standardized, continuous DNA encoding a basic biological function.
- A BioBrick has a unique DNA sequence.
- Basic Biobricks are defined by this DNA sequence.
- Composite Biobricks are defined as "sequence" of Basic BioBricks, along with intervening "scar" sequences.
- A Biobrick has a defined & standardized Format



PoBoL

PrOvisional Biobrick Ontology Language

minimal

extendable

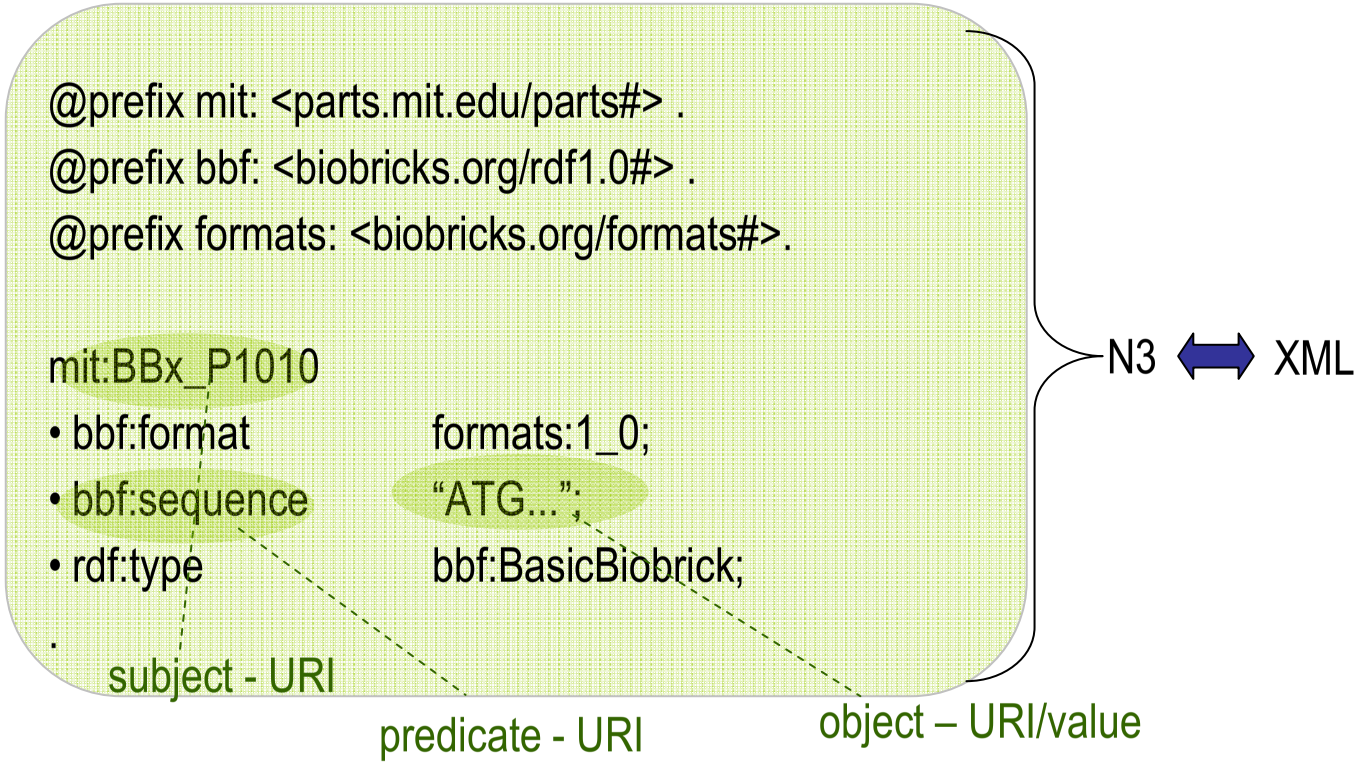
RDF / OWL / XML

- unique ID
- DNA sequence
- optional: sequence of basic building blocks + scars
- format [specifying: prefix, suffix, self_scar, name, description]
- short_description for humans
- long_description for humans
- author(s)
- reference(s) (web / literature) [pubmed ID?, isbn?, web-address?, doi? + comment?]

PoBOL – additional concepts

- BiobrickFamily
- BiobrickDevice
- BiobrickFormat
- Vector (Biobrick)
- CompositeBiobrick (Biobrick)
- BasicBiobrick (Biobrick)

PoBOL format: OWL / RDF / XML



BrickIt

open source Biobrick management

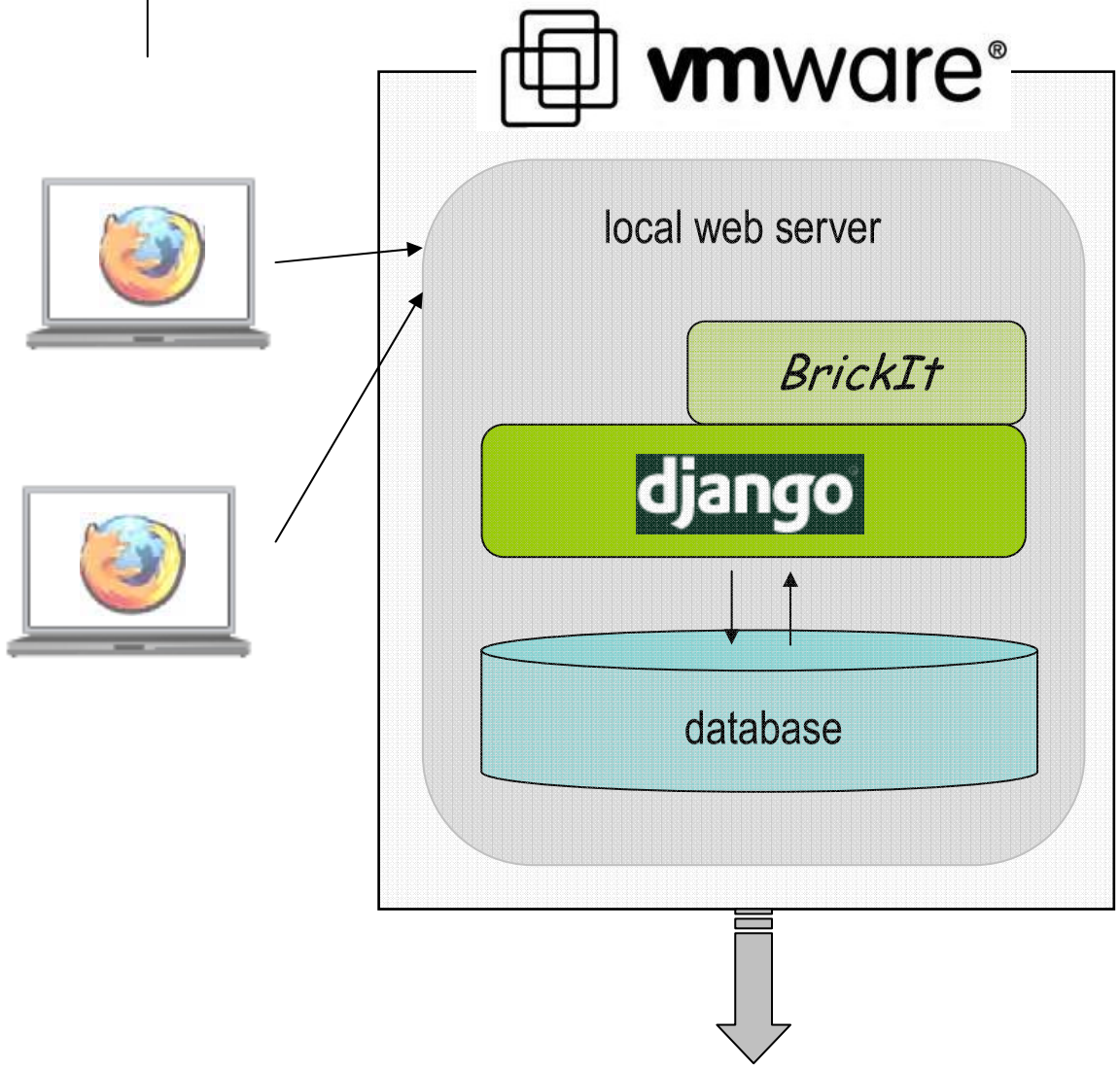
Registry of Standard Biological Parts

http://parts.mit.edu

Planning → Construction → Verification

- no tracking of your local samples
- no local modifications
- all openness is nice but…
- closed development

BrickIt architecture

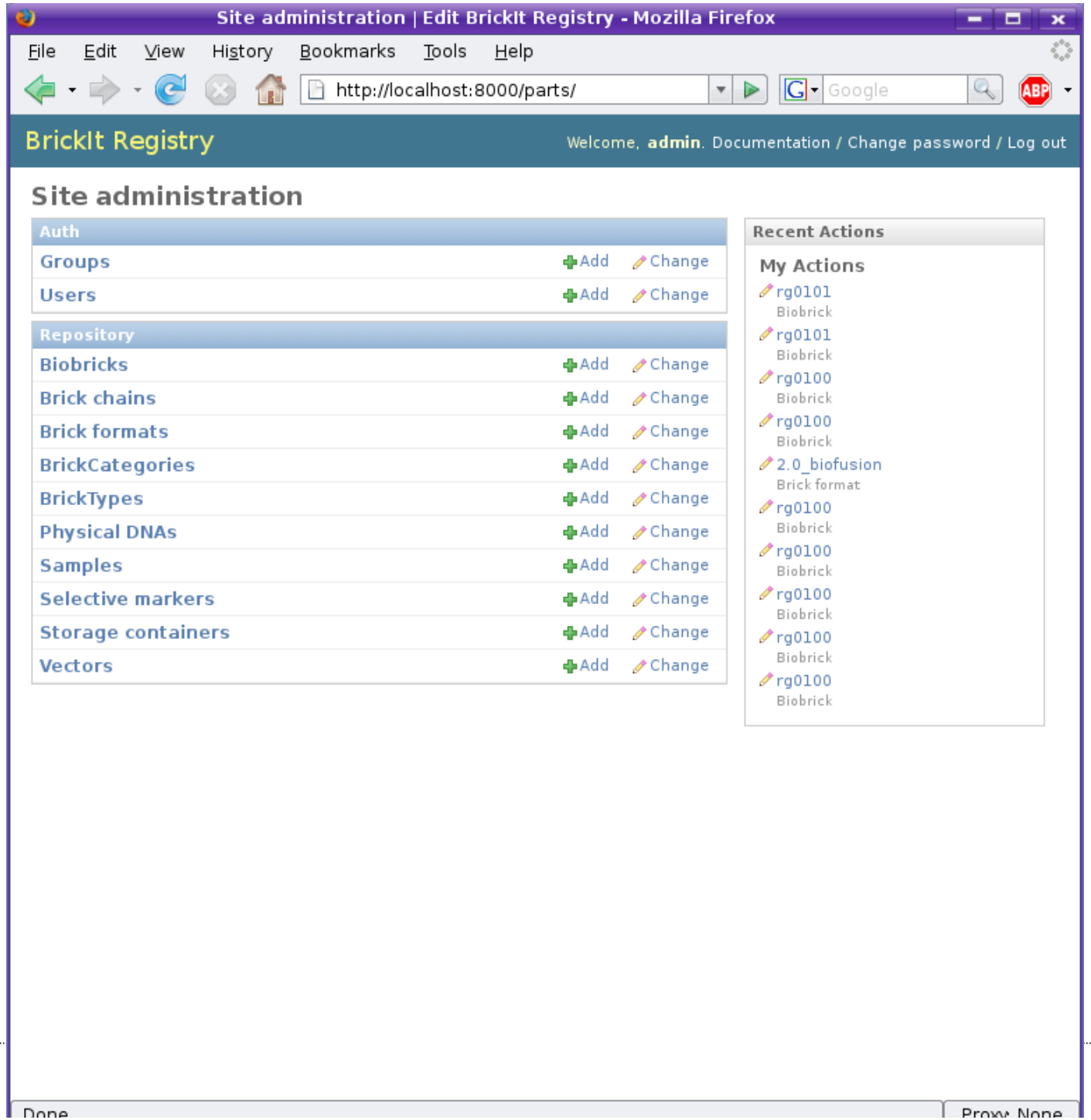


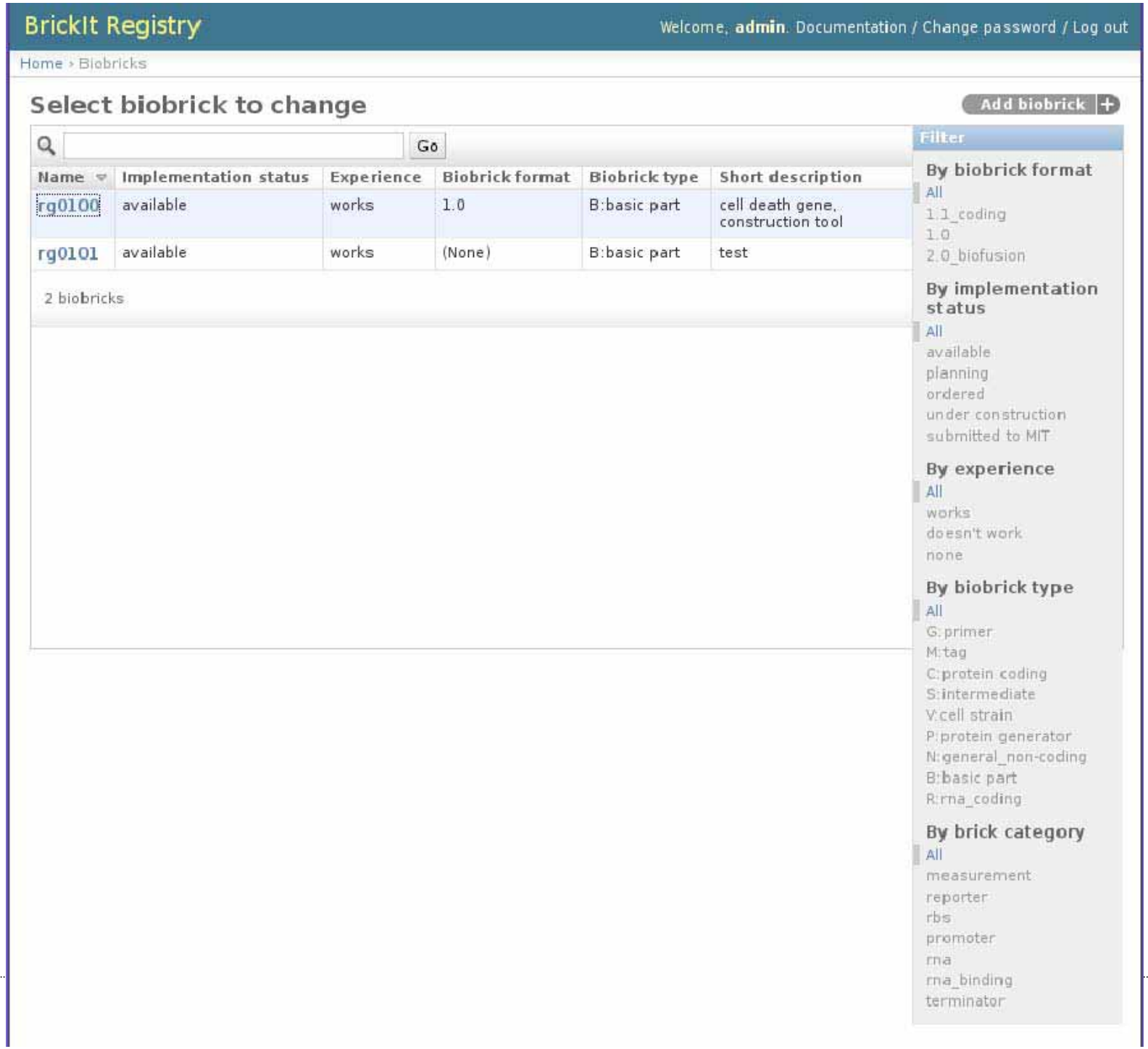
APACHE

python™

PostgreSQL

ubuntu
Server edition


Site administration | Edit BrickIt Registry - Mozilla Firefox
File Edit View History Bookmarks Tools Help
http://localhost:8000/parts/
Google
BrickIt Registry
Welcome, admin. Documentation / Change password / Log out
Site administration
Auth
Groups Add Change
Users Add Change
Repository
Biobricks Add Change
Brick chains Add Change
Brick formats Add Change
BrickCategories Add Change
BrickTypes Add Change
Physical DNAs Add Change
Samples Add Change
Selective markers Add Change
Storage containers Add Change
Vectors Add Change
Recent Actions
My Actions
rg0101 Biobrick
rg0101 Biobrick
rg0100 Biobrick
rg0100 Biobrick
2.0_biofusion Brick format
rg0100 Biobrick
rg0100 Biobrick
rg0100 Biobrick
rg0100 Biobrick
rg0100 Biobrick
Done
Proxy: None


BrickIt Registry
Welcome, admin. Documentation / Change password / Log out
Home › Biobricks
Select biobrick to change
Add biobrick
Go
Name
Implementation status
Experience
Biobrick format
Biobrick type
Short description
rg0100
available
works
1.0
B:basic part
cell death gene, construction tool
rg0101
available
works
(None)
B:basic part
test
2 biobricks
Filter
By biobrick format
All
1.1_coding
1.0
2.0_biofusion
By implementation status
All
available
planning
ordered
under construction
submitted to MIT
By experience
All
works
doesn't work
none
By biobrick type
All
G:primer
M:tag
C:protein coding
S:intermediate
V:cell strain
P:protein generator
N:general_non-coding
B:basic part
R:rna_coding
By brick category
All
measurement
reporter
rbs
promoter
rna
rna_binding
terminator

BrickIt Registry

Home › Biobricks › rg0100

Biobrick rg0100 / BBa_P1010

BBa_P1010 | History | Edit

Description

cell death gene, construction tool

The CcdB protein, constitutively expressed by P1010, is lethal to most of the BioBrick cell strains, only DB3.1 is resistant.

Use

P1010 is used when putting BioBrick parts into BioBrick plasmids. The part to be inserted and the plasmid are cut with BioBrick enzymes and mixed. The mixture will include both the original uncut or religated plasmid and the desired structure. However, because of CcdB, all of the cells containing the original plasmid die and the surviving colonies are the desired result.

Background

Most BioBrick plasmids are delivered with the P1010 insert see P1010 Physical DNA for the current list of plasmids that are available in this form. This particular Biobrick with its Plasmid backbone is considered a Construction Plasmid.

Comments

this entry is for testing purposes only

Sources & References

Source:

Source gene:

References

Sequence

Sequence without Prefix and Suffix

```
ACTGGCTGTGTATAAGGGAGCCTGACATTTATATTCCCCAGAACATCAGGTTAATGGCGTTTTTGATGTCATTTTCGCGG
TGGCTGAGATCAGCCACTTCTTCCCCGATAACGGAGACCGGCACACTGGCCATATCGGTGGTCATCATGCGCCAGCTTTC
ATCCCCGATATGCACCACCGGGTAAAGTTCACGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGGATCACCA
TCCGTCGCCCGGGCGTGTCAATAATATCACTCTGTACATCCACAAACAGACGATAACGGCTCTCTCTTTTATAGGTGTAA
ACCTTAAACTGCATTTCACCAGCCCCTGTTCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAACCGGGCGACCTCAGCCA
TCCCTTCCTGATTTTCCGCTTTCCAGCGTTCGGCACGCAGACGACGGGCTTCATTCTGCATGGTTGTGCTTACCAGACCG
GAGATATTGACATCATATATGCCTTGAGCAACTGATAGCTGTCGCTGTCAACTGTCACTGTAATACGCTGCTTCATAGCA
TACCTCTTTTTTGACATACTTCGGGTATACATATCAGTATATTCTTATACCGCAAAAATCAGCGCGCAAATACGCATAC
TGTTATCTGGCTTTTAGTAAGCCGGATCCACGCGT
```

Availability

This Biobrick can be found in the following Vectors and Samples:

Physical DNA	in Vector	in Container	Sample
rg0100_pBS	pBS	001: TestContainer	D_RG01 / rg01/01/08-1a
rg0100_pBS	pBS	001: TestContainer	D_RG01 / rg01/01/08-1b

Specs

Format:
1.0

Status:
available

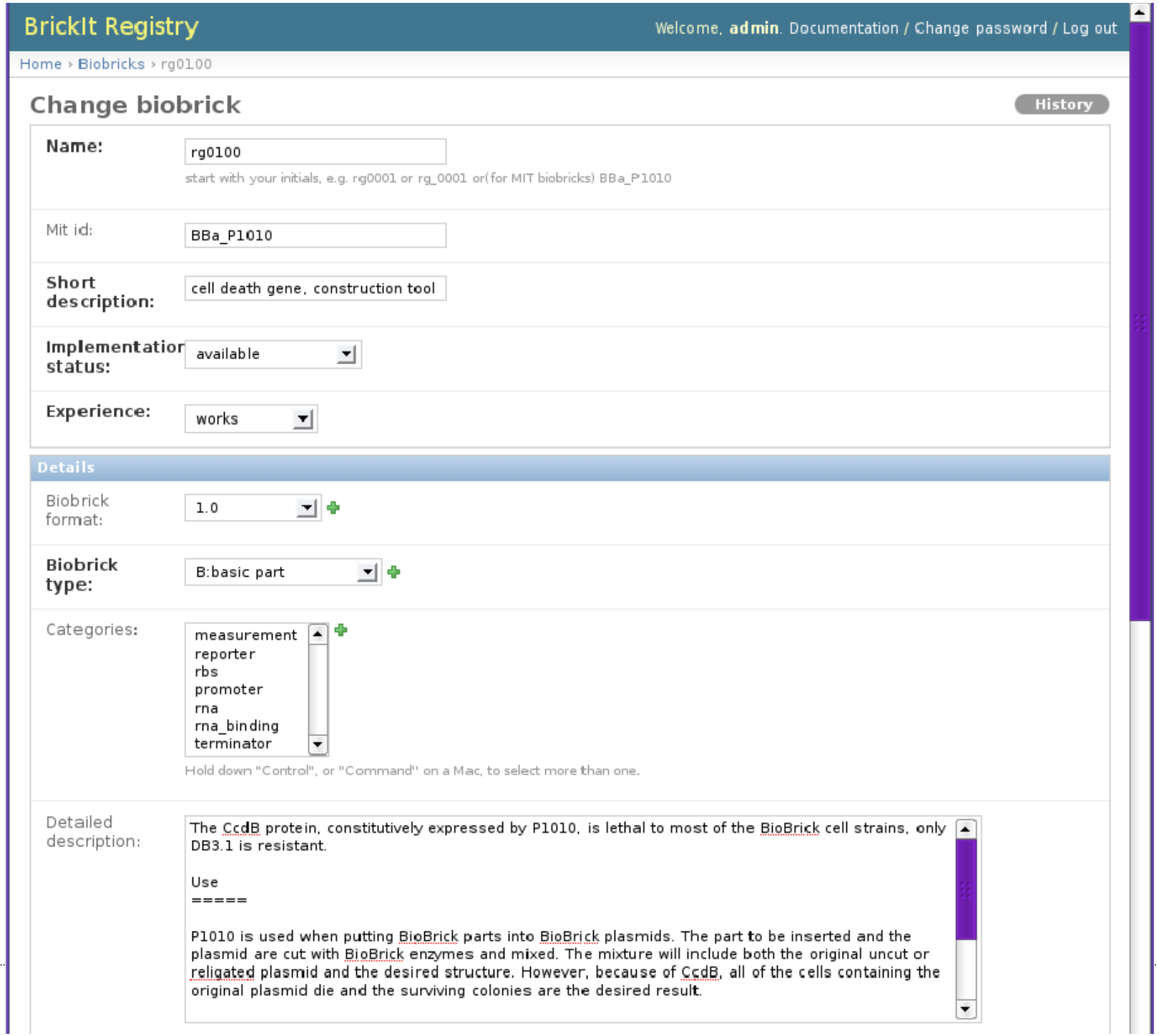
Experience:
works

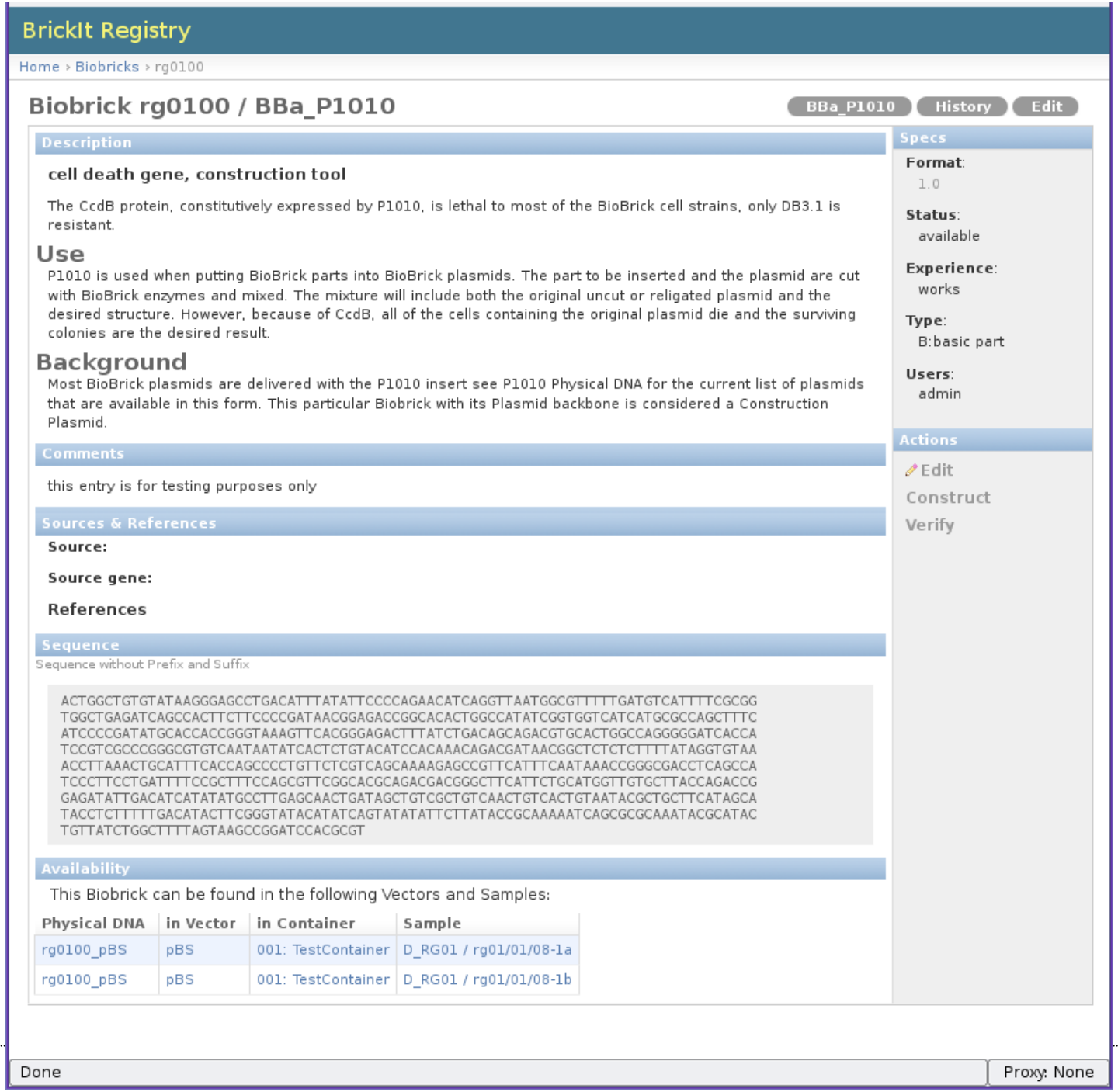
Type:
B:basic part

Users:
admin

Actions

Edit
Construct
Verify


BrickIt Registry
Welcome, admin. Documentation / Change password / Log out
Home › Biobricks › rg0100
Change biobrick
History
Name:
rg0100
start with your initials, e.g. rg0001 or rg_0001 or(for MIT biobricks) BBa_P1010
Mit id:
BBa_P1010
Short description:
cell death gene, construction tool
Implementation status:
available
Experience:
works
Details
Biobrick format:
1.0
Biobrick type:
B:basic part
Categories:
measurement
reporter
rbs
promoter
rna
rna_binding
terminator
Hold down "Control", or "Command" on a Mac, to select more than one.
Detailed description:
The CcdB protein, constitutively expressed by P1010, is lethal to most of the BioBrick cell strains, only DB3.1 is resistant.
Use
=====
P1010 is used when putting BioBrick parts into BioBrick plasmids. The part to be inserted and the plasmid are cut with BioBrick enzymes and mixed. The mixture will include both the original uncut or religated plasmid and the desired structure. However, because of CcdB, all of the cells containing the original plasmid die and the surviving colonies are the desired result.


BrickIt Registry
Home › Biobricks › rg0100
Biobrick rg0100 / BBa_P1010
BBa_P1010
History
Edit
Description
cell death gene, construction tool
The CcdB protein, constitutively expressed by P1010, is lethal to most of the BioBrick cell strains, only DB3.1 is resistant.
Use
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Comments
this entry is for testing purposes only
Sources & References
Source:
Source gene:
References
Sequence
Sequence without Prefix and Suffix
ACTGGCTGTGTATAAGGGAGCCTGACATTTATATTCCCCAGAACATCAGGTTAATGGCGTTTTTGATGTCATTTTCGCGG
TGGCTGAGATCAGCCACTTCTTCCCCGATAACGGAGACCGGCACACTGGCCATATCGGTGGTCATCATGCGCCAGCTTTC
ATCCCCGATATGCACCACCGGGTAAAGTTCACGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGGATCACCA
TCCGTCGCCCGGGCGTGTCAATAATATCACTCTGTACATCCACAAACAGACGATAACGGCTCTCTCTTTTATAGGTGTAA
ACCTTAAACTGCATTTCACCAGCCCCTGTTCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAACCGGGCGACCTCAGCCA
TCCCTTCCTGATTTTCCGCTTTCCAGCGTTCGGCACGCAGACGACGGGCTTCATTCTGCATGGTTGTGCTTACCAGACCG
GAGATATTGACATCATATATGCCTTGAGCAACTGATAGCTGTCGCTGTCAACTGTCACTGTAATACGCTGCTTCATAGCA
TACCTCTTTTTGACATACTTCGGGTATACATATCAGTATATATTCTTATACCGCAAAAATCAGCGCGCAAATACGCATAC
TGTTATCTGGCTTTTAGTAAGCCGGATCCACGCGT
Availability
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in Vector
in Container
Sample
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pBS
001: TestContainer
D_RG01 / rg01/01/08-1a
rg0100_pBS
pBS
001: TestContainer
D_RG01 / rg01/01/08-1b
Specs
Format:
1.0
Status:
available
Experience:
works
Type:
B:basic part
Users:
admin
Actions
Edit
Construct
Verify
Done
Proxy: None

File Edit View History Bookmarks Tools Help

http://parts.mit.edu/registry/index.php/Part:BBa_P1010

Google

Create an account or log in

article | discussion | edit | history

Part:BBa_P1010

DNA Available
Experience: Works

Designed by Leon Chan

Entered: 2004-07-28

cell death gene, construction tool

The CcdB protein, constitutively expressed by P1010, is lethal to most of the BioBrick cell strains , only DB3.1 is resistant.

P1010 is used when putting BioBrick parts into BioBrick plasmids. The part to be inserted and the plasmid are cut with BioBrick enzymes and mixed. The mixture will include both the original uncut or religated plasmid and the desired structure. However, because of CcdB, all of the cells containing the original plasmid die and the surviving colonies are the desired result.

BioBrick Construction Plasmids Containing This Part

[edit]

Most BioBrick plasmids are delivered with the P1010 insert see P1010 Physical DNA for the current list of plasmids that are available in this form. This particular Biobrick with its Plasmid backbone is considered a Construction Plasmid.

Usage and Biology

[edit]

For more information on how to use this brick, visit its Featured Parts:Cell Death page

jump to part

BBa_

BBa_P1010

- Part Main Page
- Part Design
- Experience
- Hard Information
- Physical DNA

navigation

- Main Page
- Browse Part Types
- iGEM 2007 Wiki
- Community portal
- Recent changes
- Recent part changes

resources

- User Accounts
- Add a Part
- Part Searches
- DNA Repositories
- Sequence Analysis
- Assembly Tool
- Help

search

Go | Search

toolbox

- What links here
- Related changes
- Upload file
- Special pages
- Printable version

BrickIt Registry

Home › Biobricks › rg0100

Biobrick rg0100 / BBa_P1010

BBa_P1010 | History | Edit

Description

cell death gene, construction tool

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TGGCTGAGATCAGCCACTTCTTCCCCGATAACGGAGACCGGCACACTGGCCATATCGGTGGTCATCATGCGCCAGCTTTC
ATCCCCGATATGCACCACCGGGTAAAGTTCACGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGGATCACCA
TCCGTCGCCCGGGCGTGTCAATAATATCACTCTGTACATCCACAAACAGACGATAACGGCTCTCTCTTTTATAGGTGTAA
ACCTTAAACTGCATTTCACCAGCCCCTGTTCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAACCGGGCGACCTCAGCCA
TCCCTTCCTGATTTTCCGCTTTCCAGCGTTCGGCACGCAGACGACGGGCTTCATTCTGCATGGTTGTGCTTACCAGACCG
GAGATATTGACATCATATATGCCTTGAGCAACTGATAGCTGTCGCTGTCAACTGTCACTGTAATACGCTGCTTCATAGCA
TACCTCTTTTTTGACATACTTCGGGTATACATATCAGTATATTCTTATACCGCAAAAATCAGCGCGCAAATACGCATAC
TGTTATCTGGCTTTTAGTAAGCCGGATCCACGCGT
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rg0100_pBS	pBS	001: TestContainer	D_RG01 / rg01/01/08-1b

Specs

Format:
1.0

Status:
available

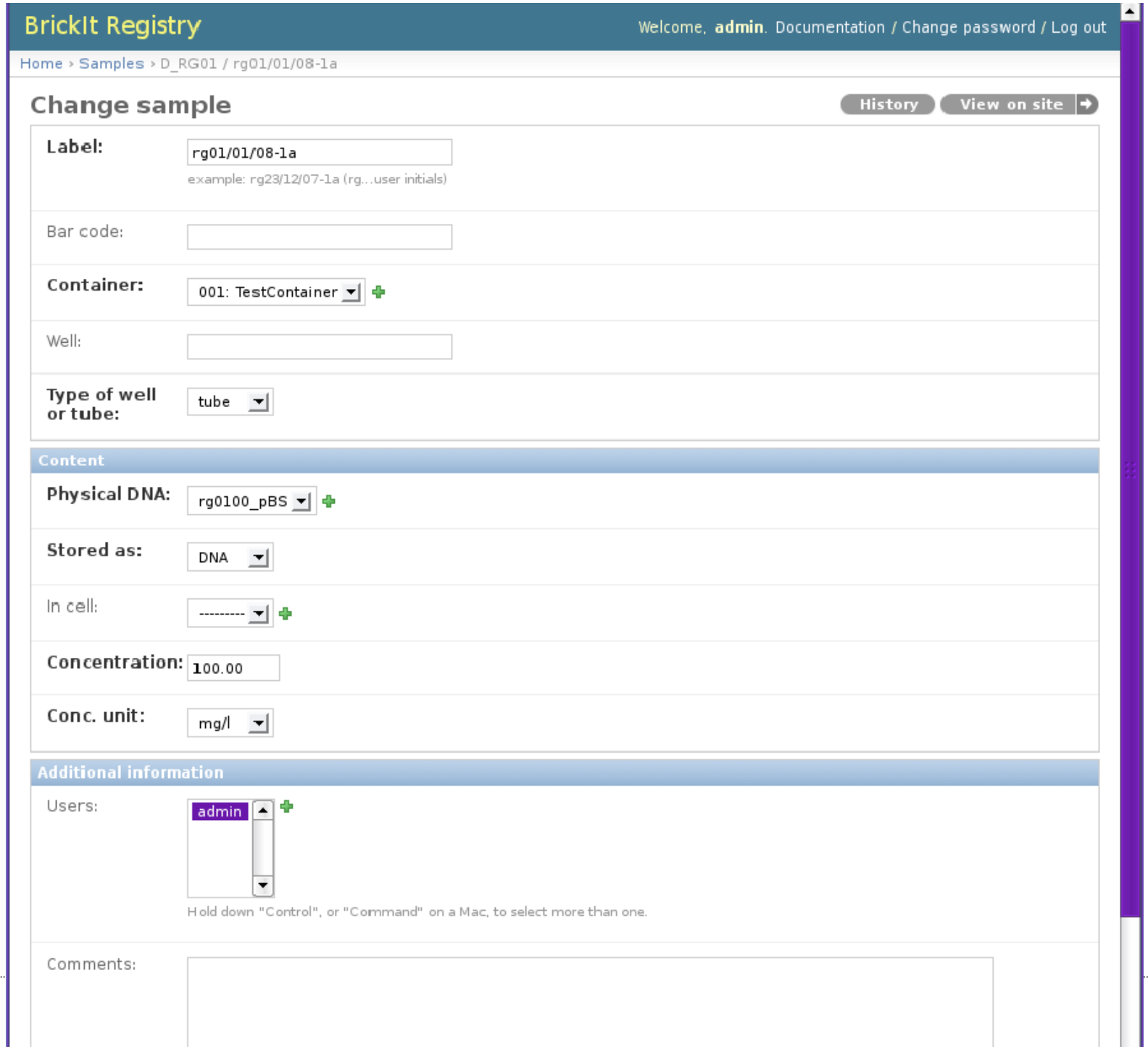
Experience:
works

Type:
B:basic part

Users:
admin

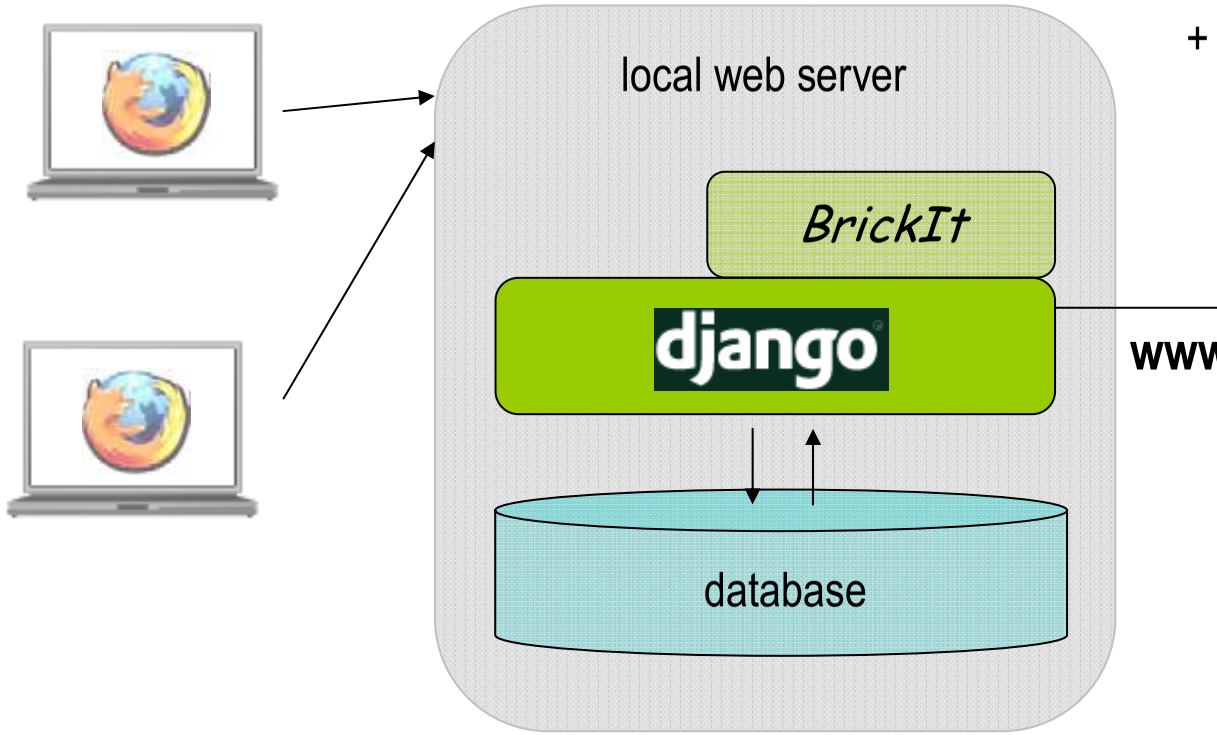
Actions

Edit
Construct
Verify


BrickIt Registry
Welcome, admin. Documentation / Change password / Log out
Home › Samples › D_RG01 / rg01/01/08-1a
Change sample
History
View on site
Label:
rg01/01/08-1a
example: rg23/12/07-1a (rg...user initials)
Bar code:
Container:
001: TestContainer
Well:
Type of well or tube:
tube
Content
Physical DNA:
rg0100_pBS
Stored as:
DNA
In cell:

Concentration:
100.00
Conc. unit:
mg/l
Additional information
Users:
admin
Hold down "Control", or "Command" on a Mac, to select more than one.
Comments:

BrickIt architecture



+ rapid development

+ clean yet pragmatic design

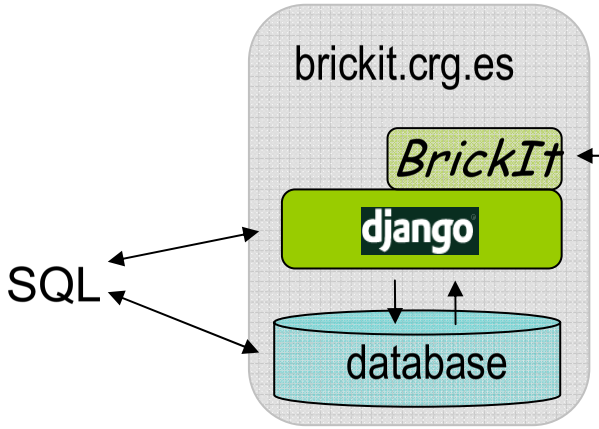
+ data models defined in Python

+ well documented & supported

www.djangoproject.com

The Web framework for perfectionists with deadlines.
Django makes it easier to build better Web apps more quickly and with less code.

Flexible



huge reservoir of Python libraries,
Biopython, numpy, SciPy…

python™

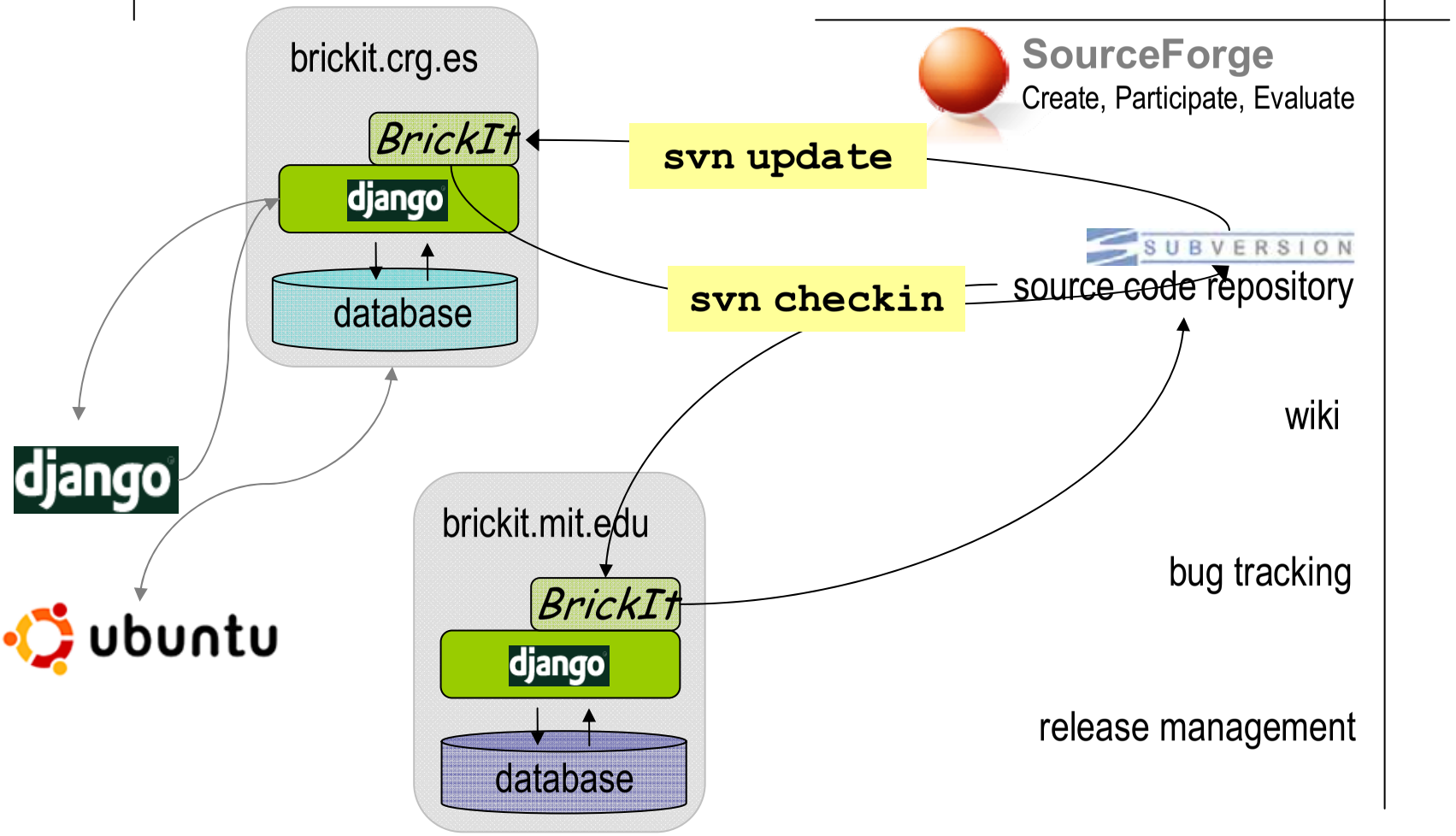
Simple, powerful object API

```
from djbrickit.repository.models import Vector, SelectiveMarker

amp = SelectiveMarker( name='amp', short_description='AmpR' )
amp.save()

pBS = Vector.objects().get(name='pBS')
pBS.marker = amp
pBS.save()
```

Shared development



divided data but shared infrastructure & development

E.U. project proposal?

In conclusion, ...

- ...check out the BBF Standardization process!
- ...PoBOL = minimal Biobrick description language
- ...BrickIt = open source development platform for custom part registries
- ... weaving a web of registries
- ... lobby for an E.U. project?

Corner stones

- extension of standards
- open source developer community
- registry platform
- design tools
- aggregation / data mining tools
- ...

Funding for:

- programming sprints
- people
- web servers / infrastructure
- travel for outside participants
- outreach / teaching / iGem

Acknowledgements

BBF Standards mailing list

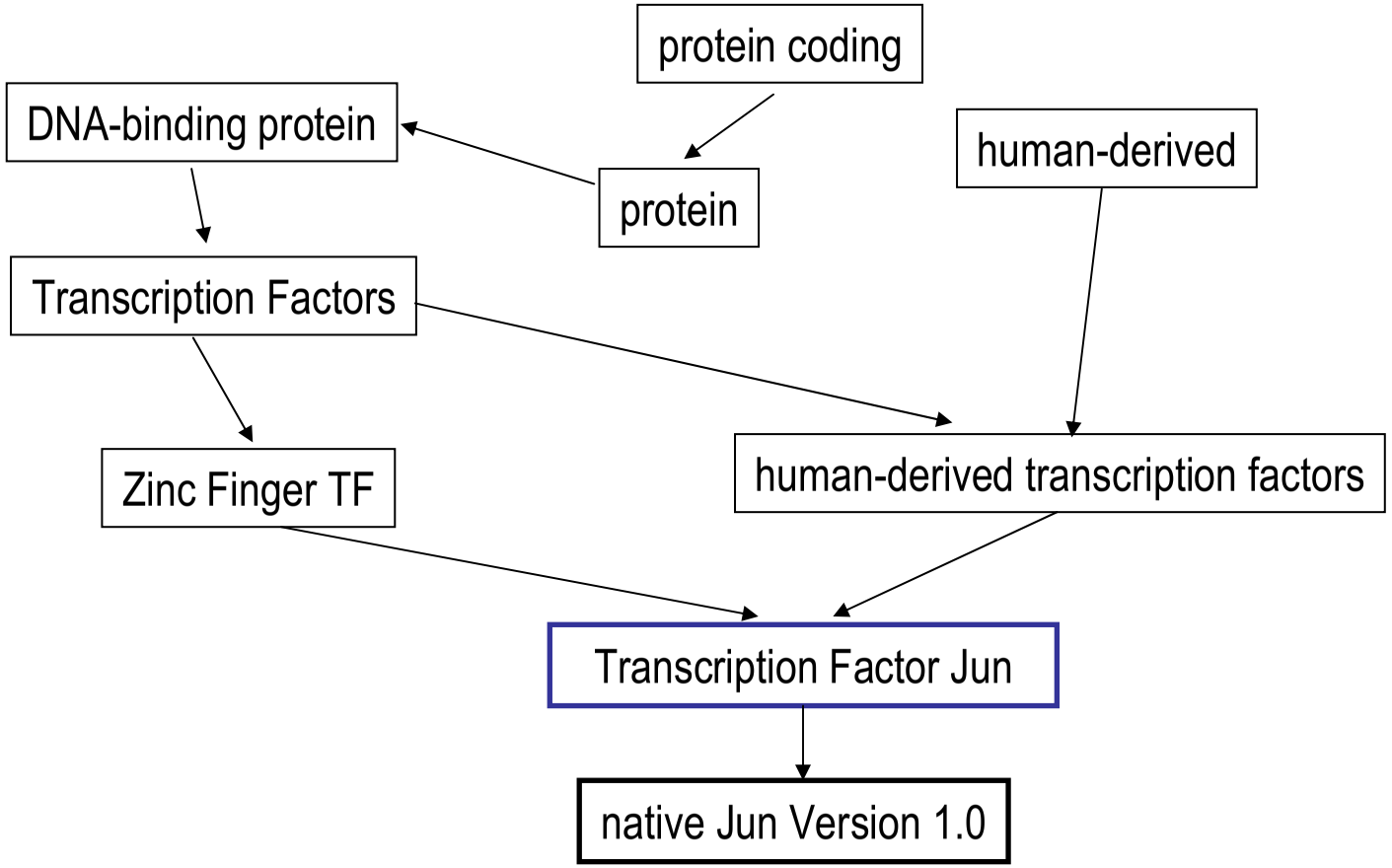
CRG Centre de Regulació Genòmica

Luis Serrano

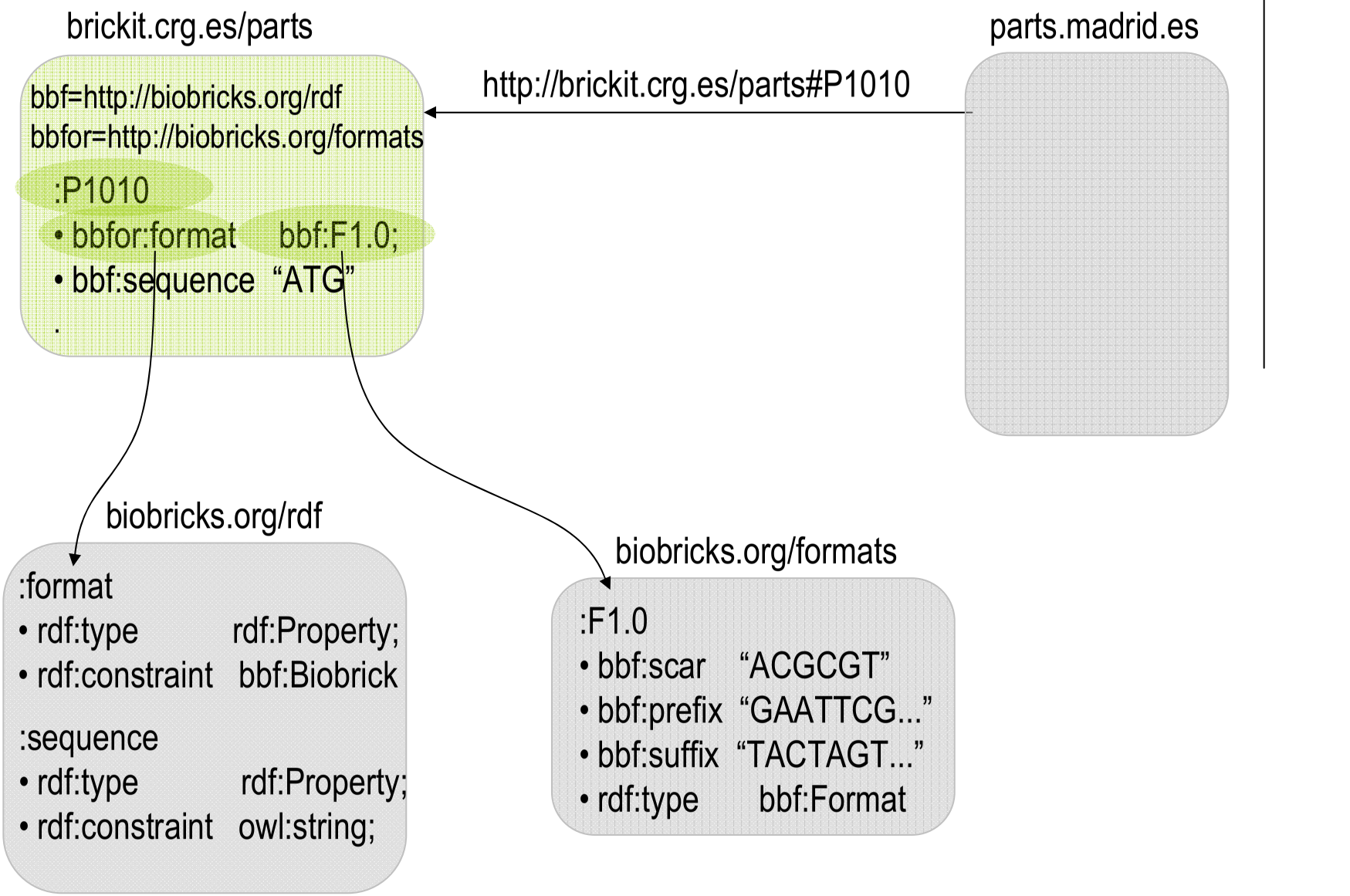
HFSP Human Frontier Science Program

Biobrick Classification

- Biobricks are grouped into Families
- Each Family can have many sub- and many parent families



Data Exchange: REST / RDF+OWL



EMERGENCE WP4

Towards a consensus language for SB:

Conceptual and hermeneutical tools for

Formatting and categorization of Transcriptional Working States

P2 (CSIC), P4 (CRG), P7 (UCL)

The central question:

How to

- describe
- de-construct
- re-construct

Biological complexity?

Hermeneutics

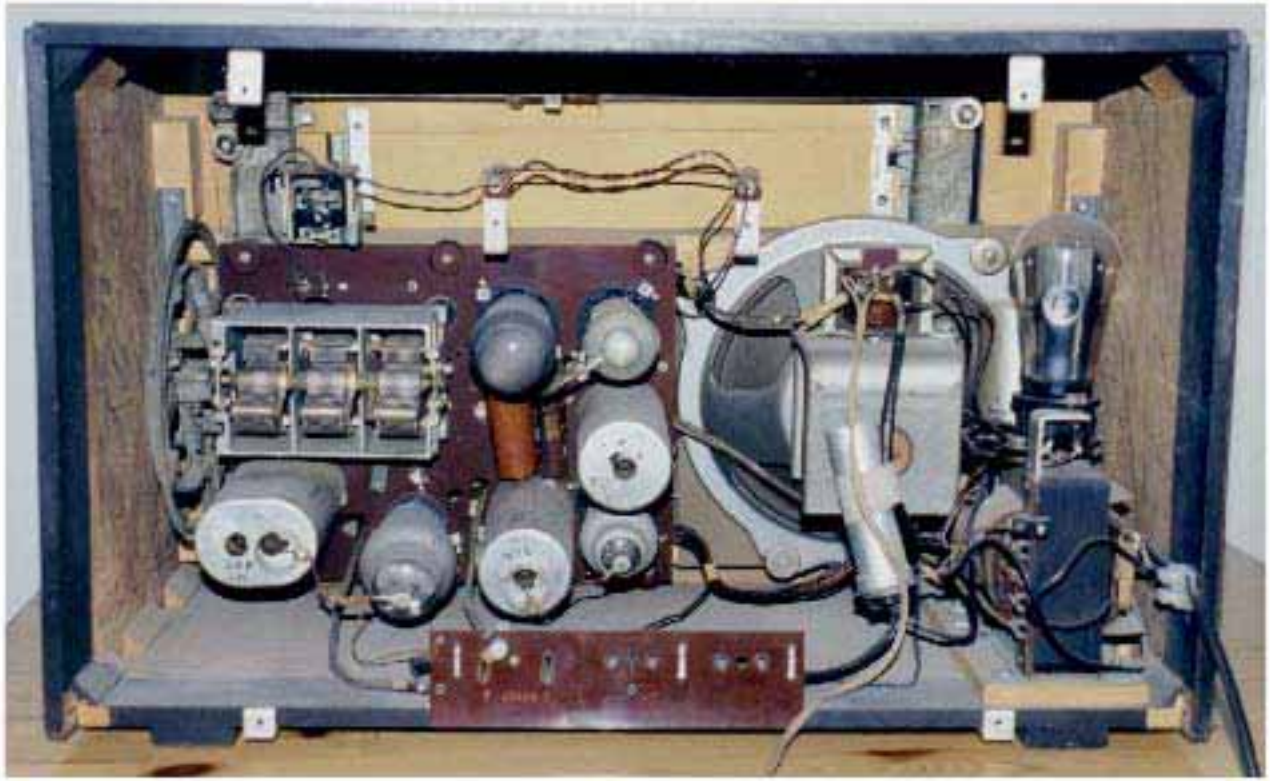
The development of interpretation tools and understanding of texts and systems of meaning. The concept of "text" is here extended beyond written documents to any number of objects subject to interpretation.

The hermeneutical problem:

- All languages for describing reality are metaphoric
- Understanding complex systems relies on suitable metaphores
- No descriptive language is neutral, they all have an agenda

Metaphor #1: The radio

Building a radio with parts

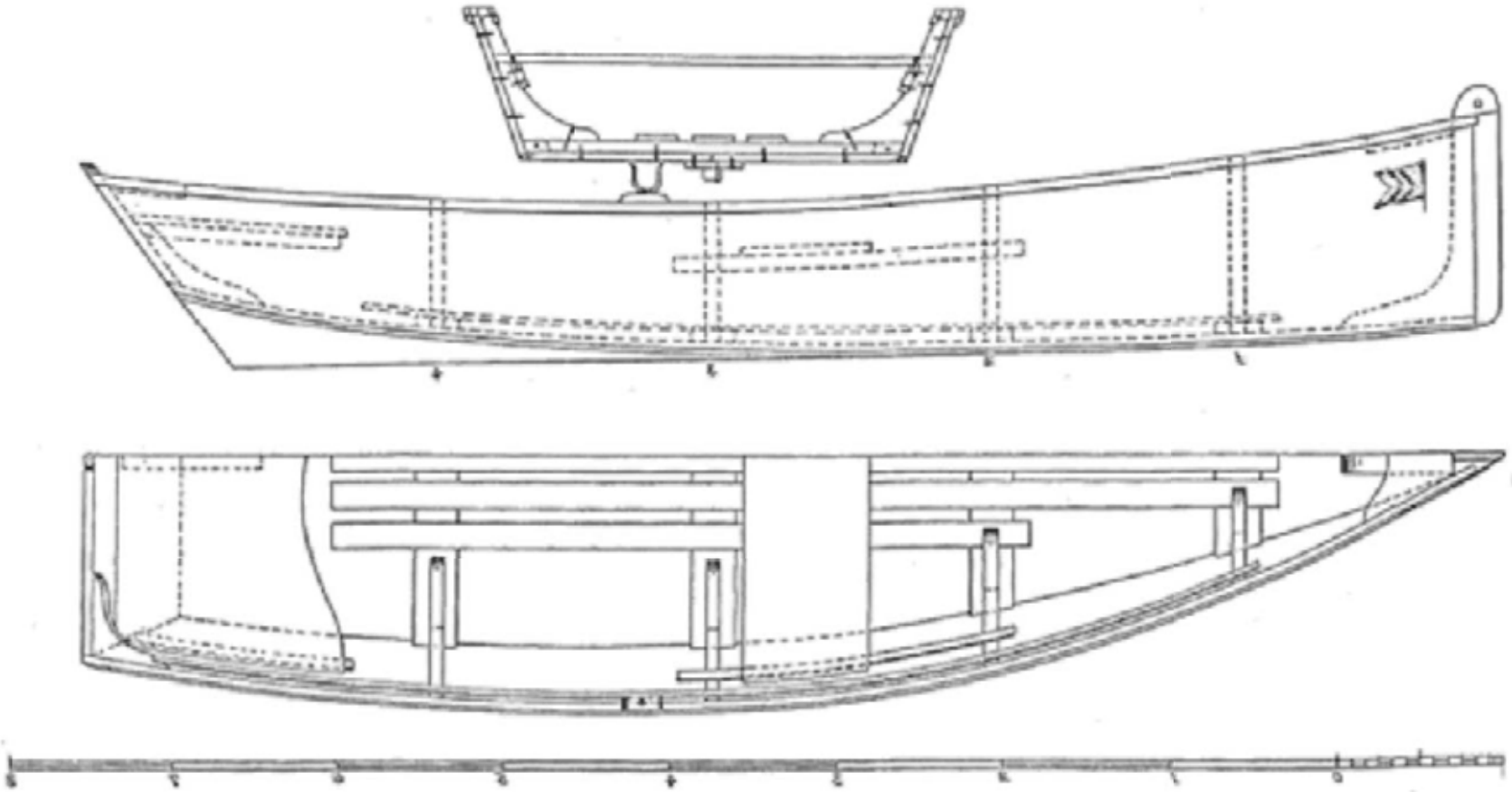


J. Keasling

Metaphor #2: The chassis (iGEM favourite!)

D. Endy

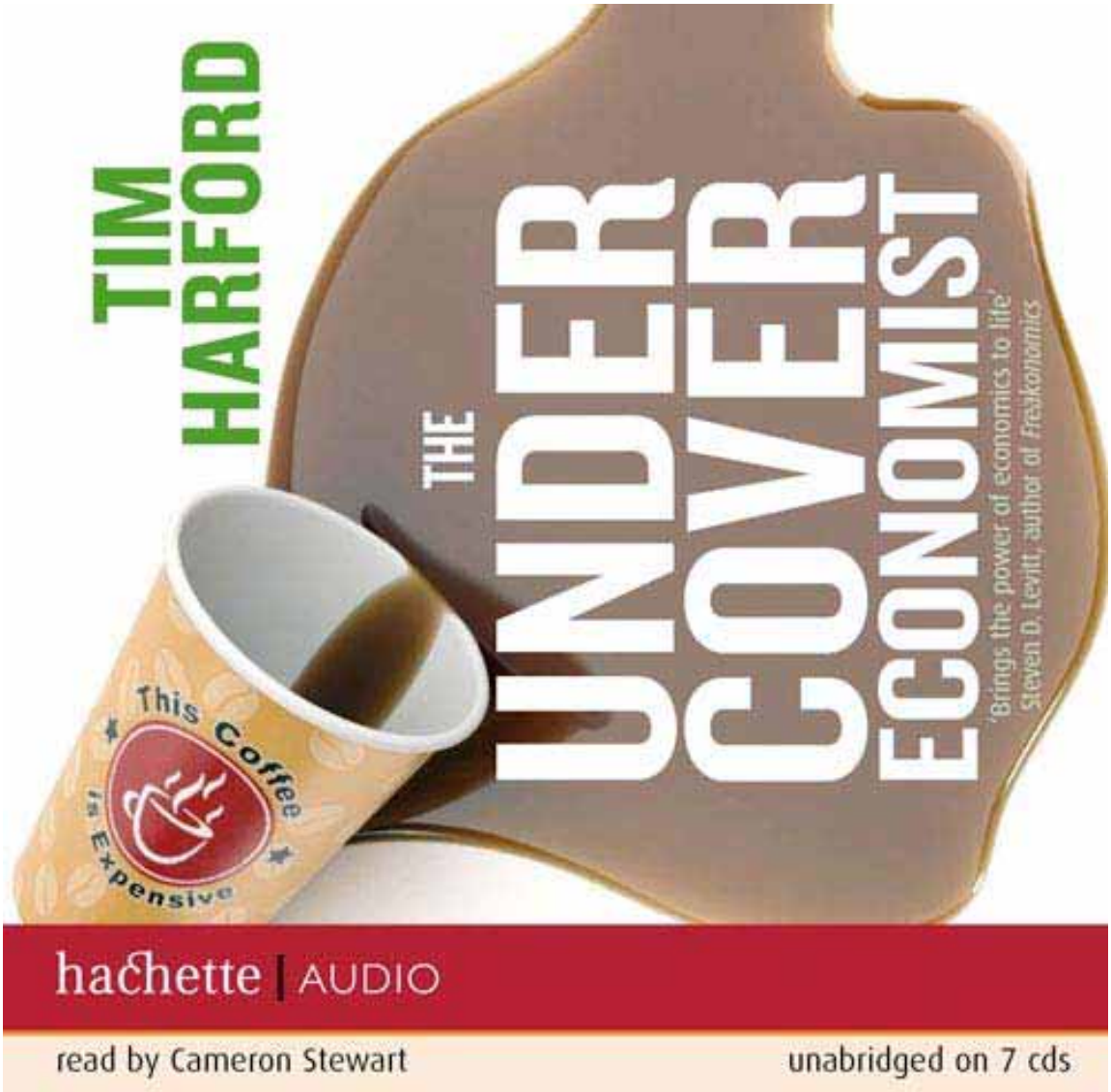
Metaphor #3: The Delphic boat



A. Danchin

Metaphor #4: The Company

JA Ranea

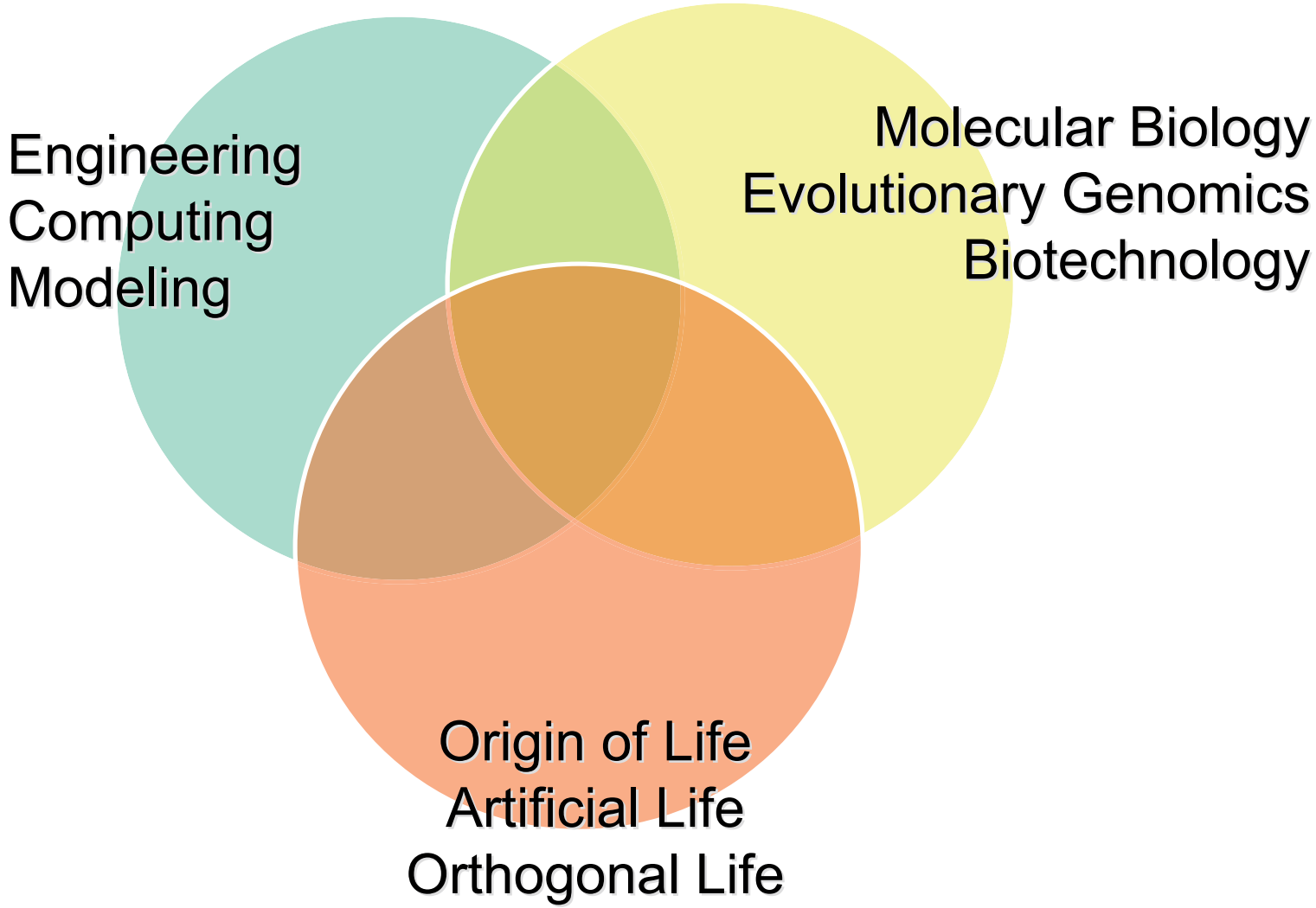


hachette | AUDIO

read by Cameron Stewart

unabridged on 7 cds

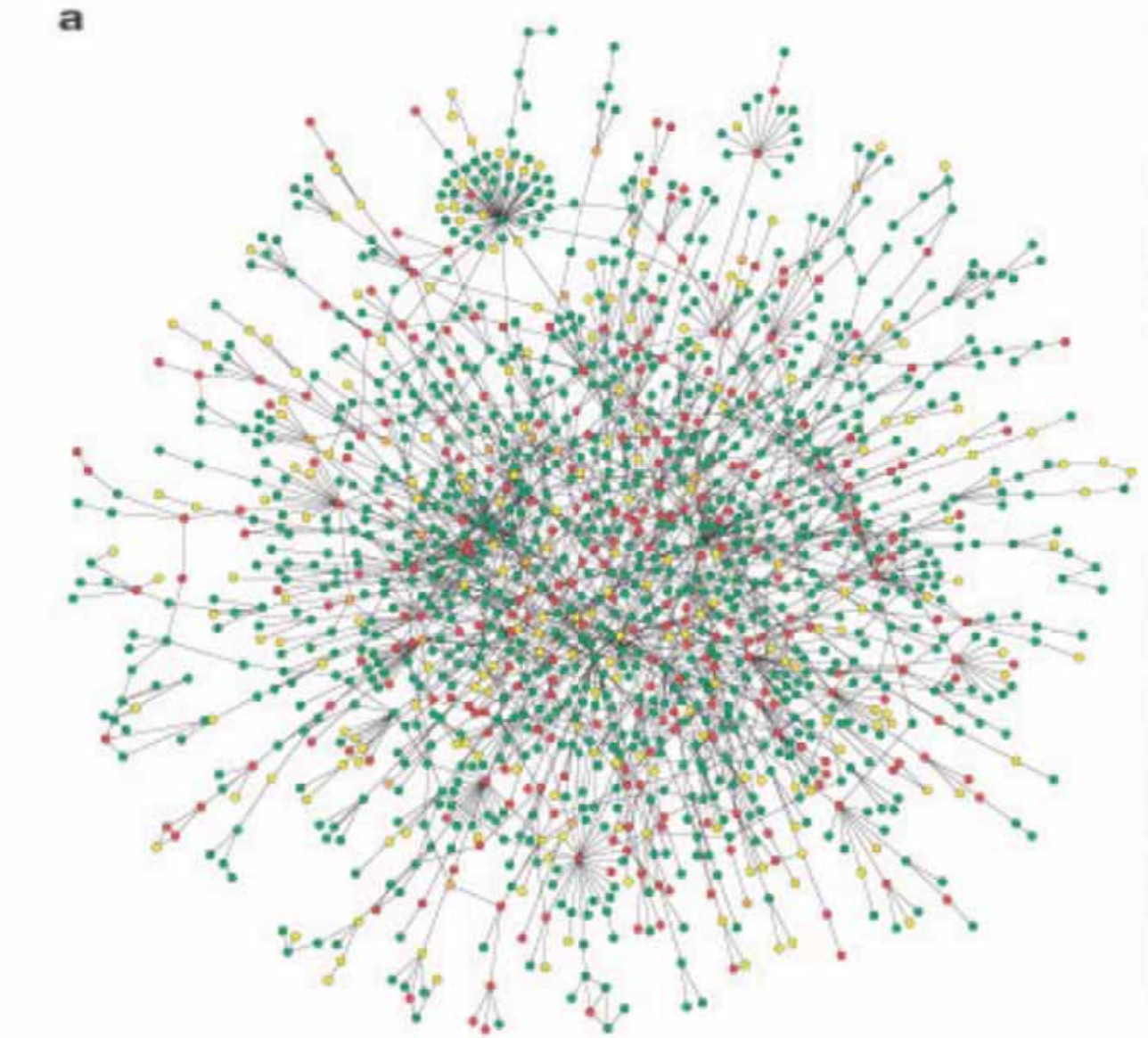
The 3 agendas/stakeholders of SB in Europe



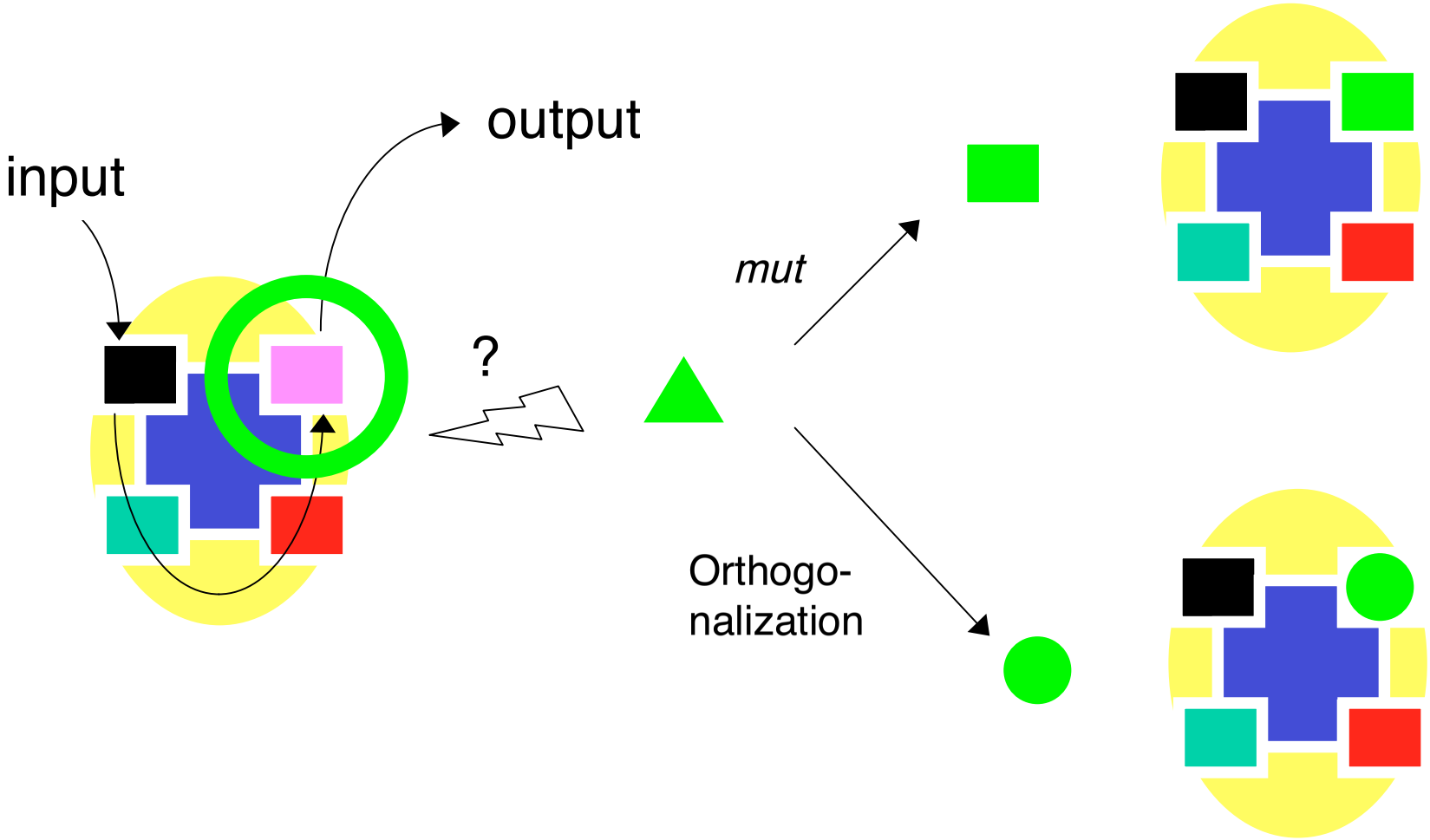
"... Engineers hate complexity. I hate emergent properties.
I like simplicity. I don't want the plane I take tomorrow
to have some emergent properties while it is flying..."

(www.edge.org; Engineering Biology:
a talk with Drew Endy, 2008)

Implantation of circuits in a pre-existing network?



Resistance to implantation of new functions in a *celular hyperstructure*



What to do under WP4?

- Early assembly of an expert group on standarization and connectivity of minimal functions.

- Text-mining on quantitative data relevant to promoter functioning (link to WP3) & production of a database

- Modelization of 4 types of prokaryotic promoters as the standard components of choice for building complex regulatory circuits.

- In silico analysis of the data collected for developing a concept aimed at reaching a transatlantic consensus.

Minimal *parts vs.* minimal *functions*

• A better conceptual frame is badly needed here to grasp what

minimal engineer-able biological building blocks

are. Just calling them Biobricks™ and make them equal to singular biological components (as is the case in the MIT-run catalogue of biological parts) can give the perception that the issue is already solved!

Finding the right descriptive terms….

Minimal parts *vs.* minimal functions

• The cell as an *automaton processing information* in an algorithmic fashion: the program and the machine.

• The quest for a minimal set of functions for a self-maintaining system is not exclusive of Synthetic Biology…

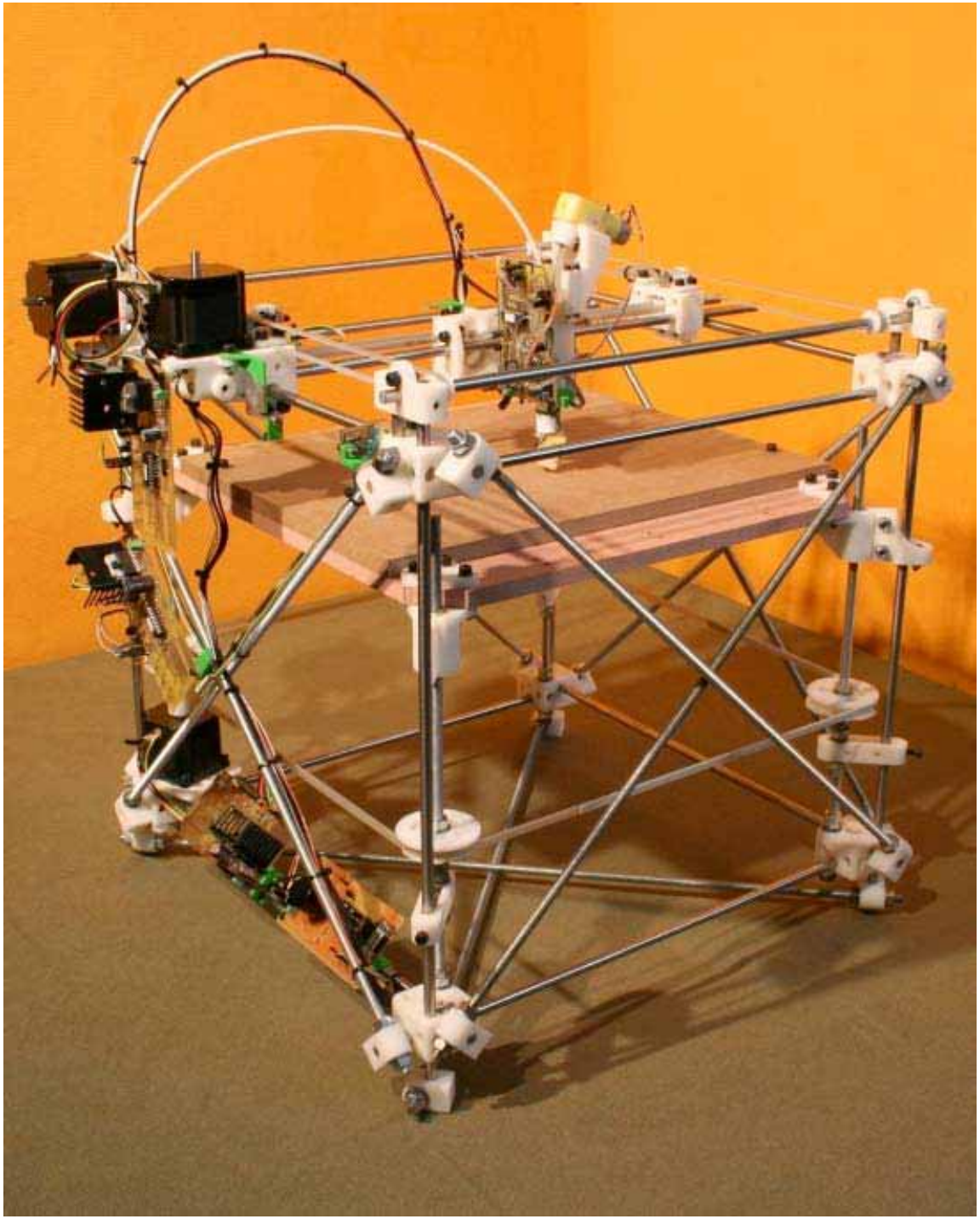
3D Printer: The RepRap Community Project

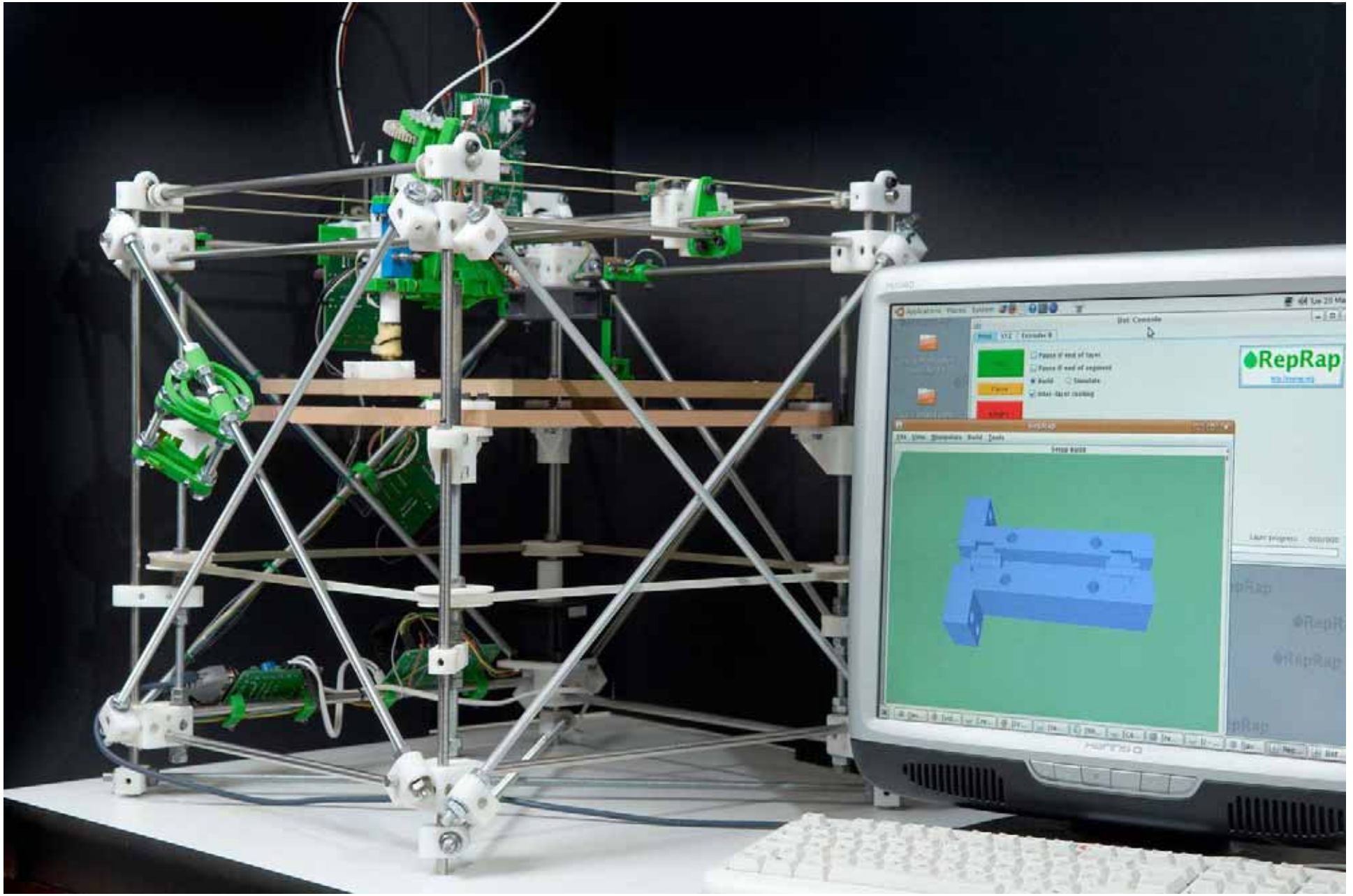
http://www.reprap.org

RepRap 1.0 "Darwin" is a rapid prototyping machine that is capable of making the majority of its own component parts.

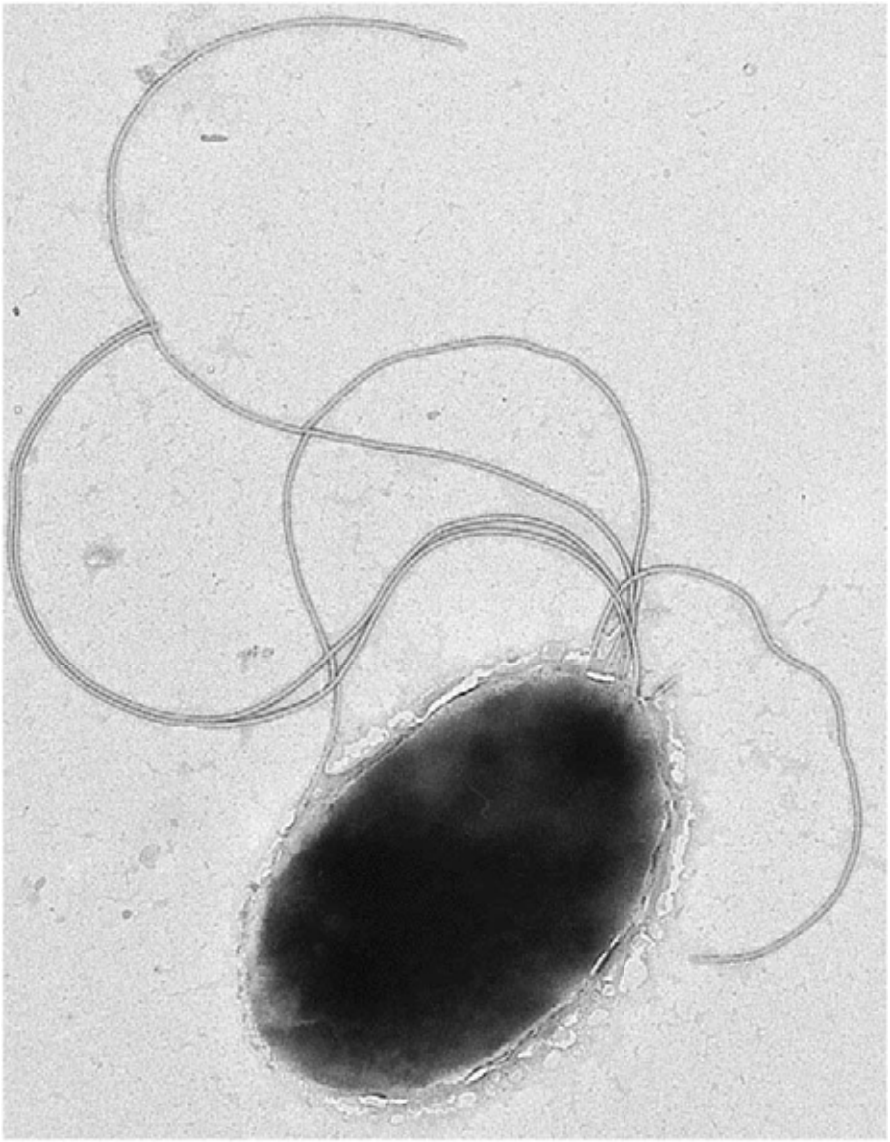
Darwin consists of a frame made from rods and printed parts. A flat build platform moves vertically in that frame, driven on screw threads by a stepper motor. At the top of the frame there are two write heads that move horizontally (driven by toothed belts and two more steppers) extruding a thin stream of molten plastic to form new layers on the build base.

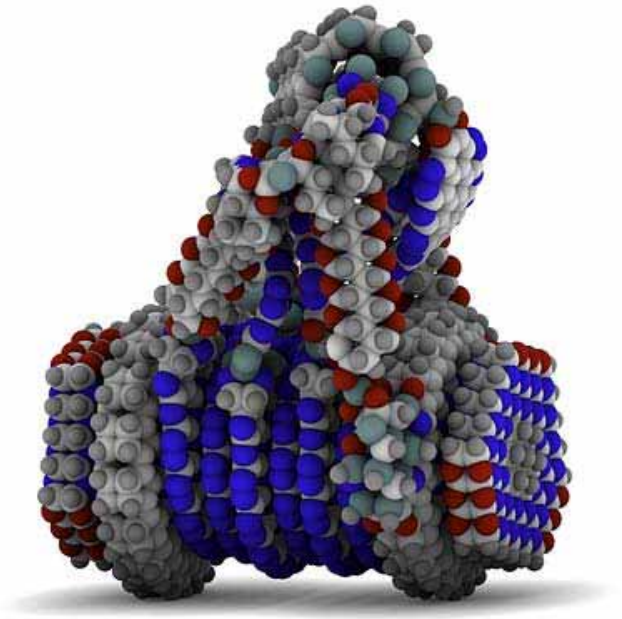
The machine prints layer by layer to form a solid object. The build base then moves one increment down, the second layer is extruded, and so on. There are two heads to allow a filler material to be laid down as well as the plastic. This filler is used to support overhanging parts of the objects being built, and is removed when the process is finished.

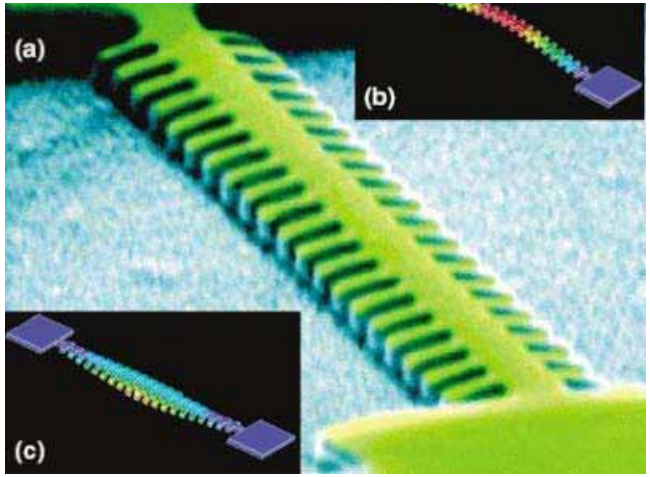



RepRap

The cell as a machine built on nanomachines







2 remarkable features of the Minimal self-replicating 3D printer:

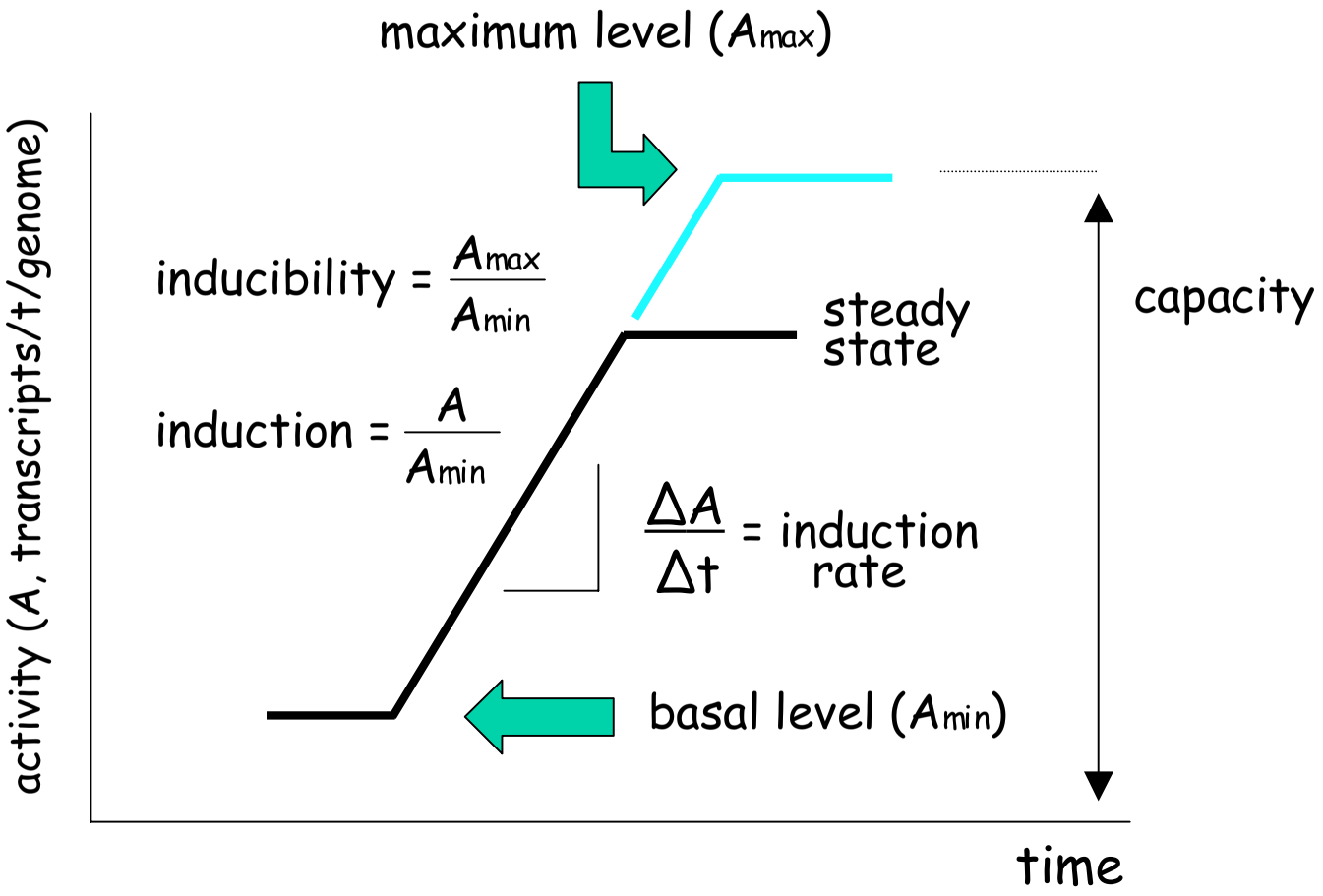
- Very little regulation needed
- Lubricants are essential!

EMERGENT ISSUE

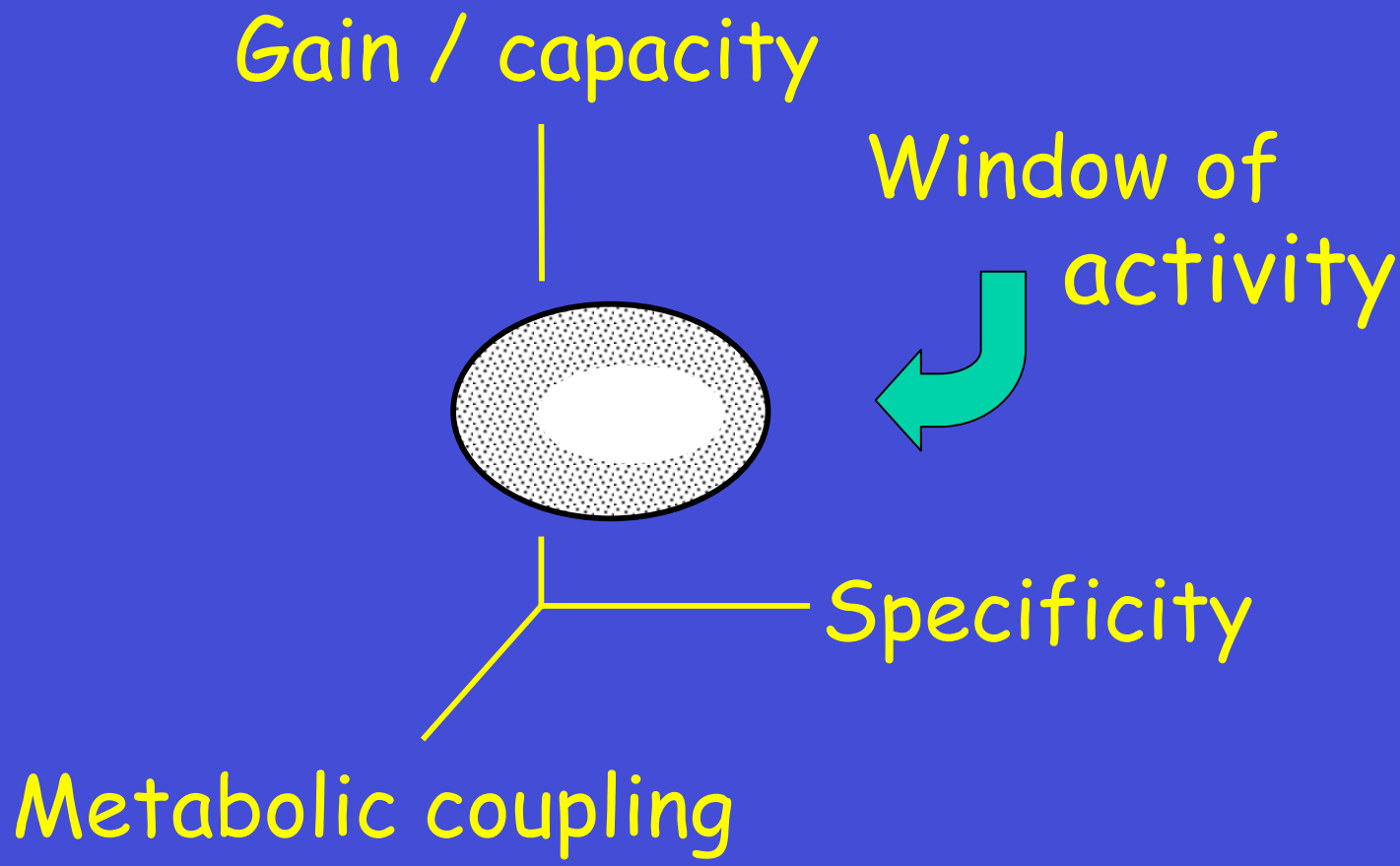
Metabolic transactions impose a permanent chemical and energetic frame to the cells, a sort of background economy.

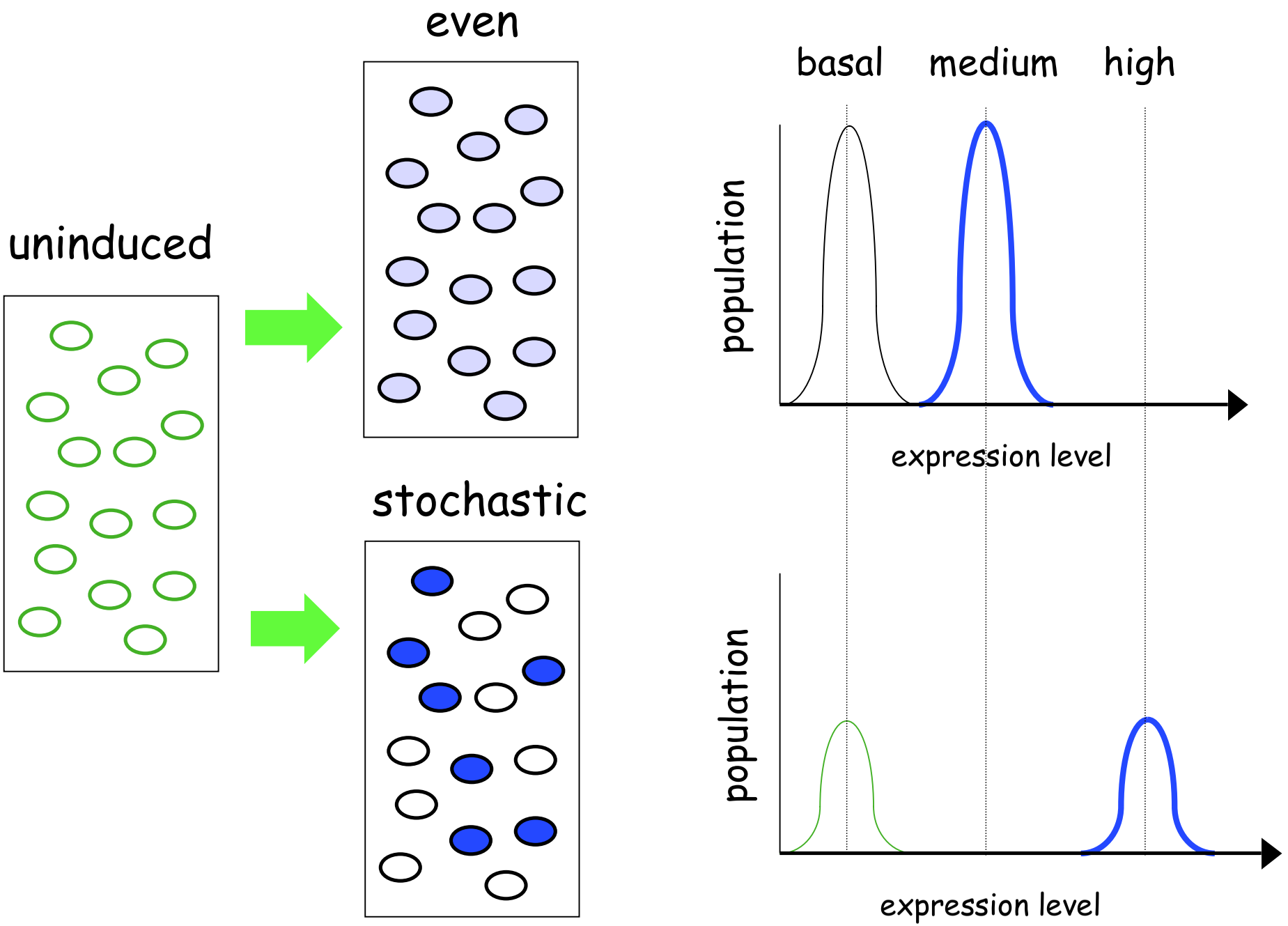
While the link between translation of mRNA and the ribosome is straightforward, the organization of metabolism is much less so.

Promoter parameters

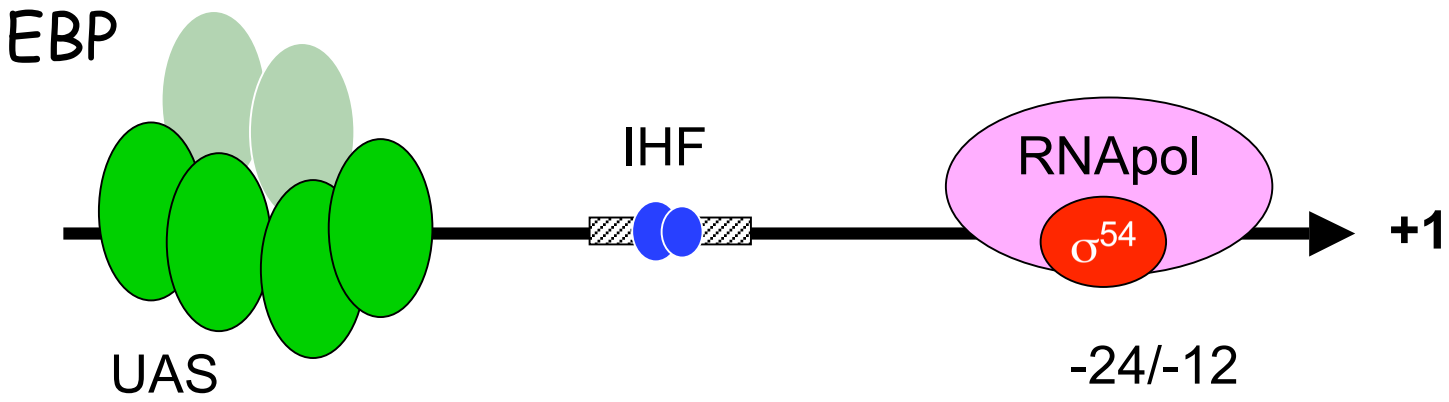


Definition of promoter activities *in vivo*

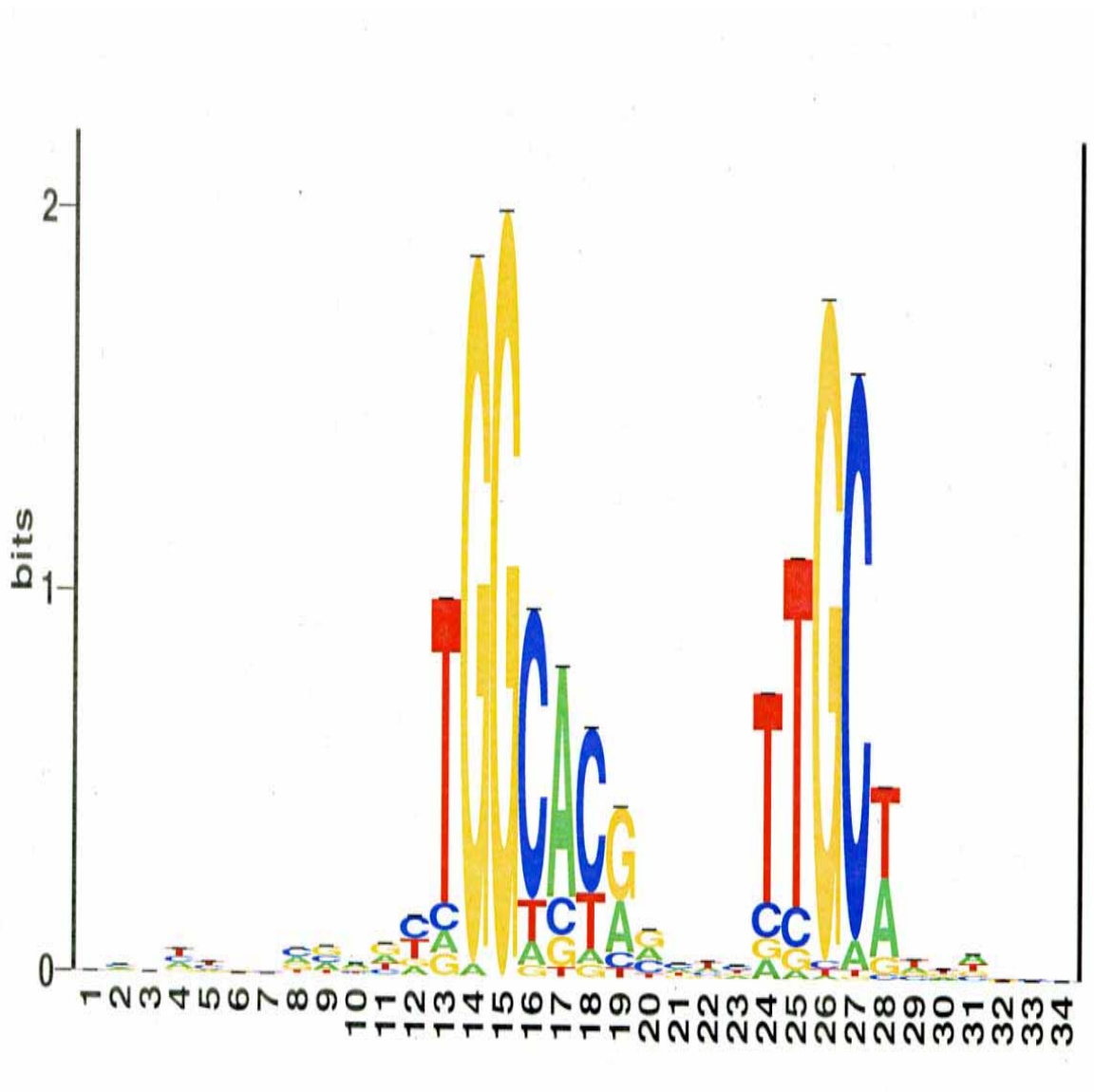



even
uninduced
stochastic
basal
medium
high
population
expression level
population
expression level

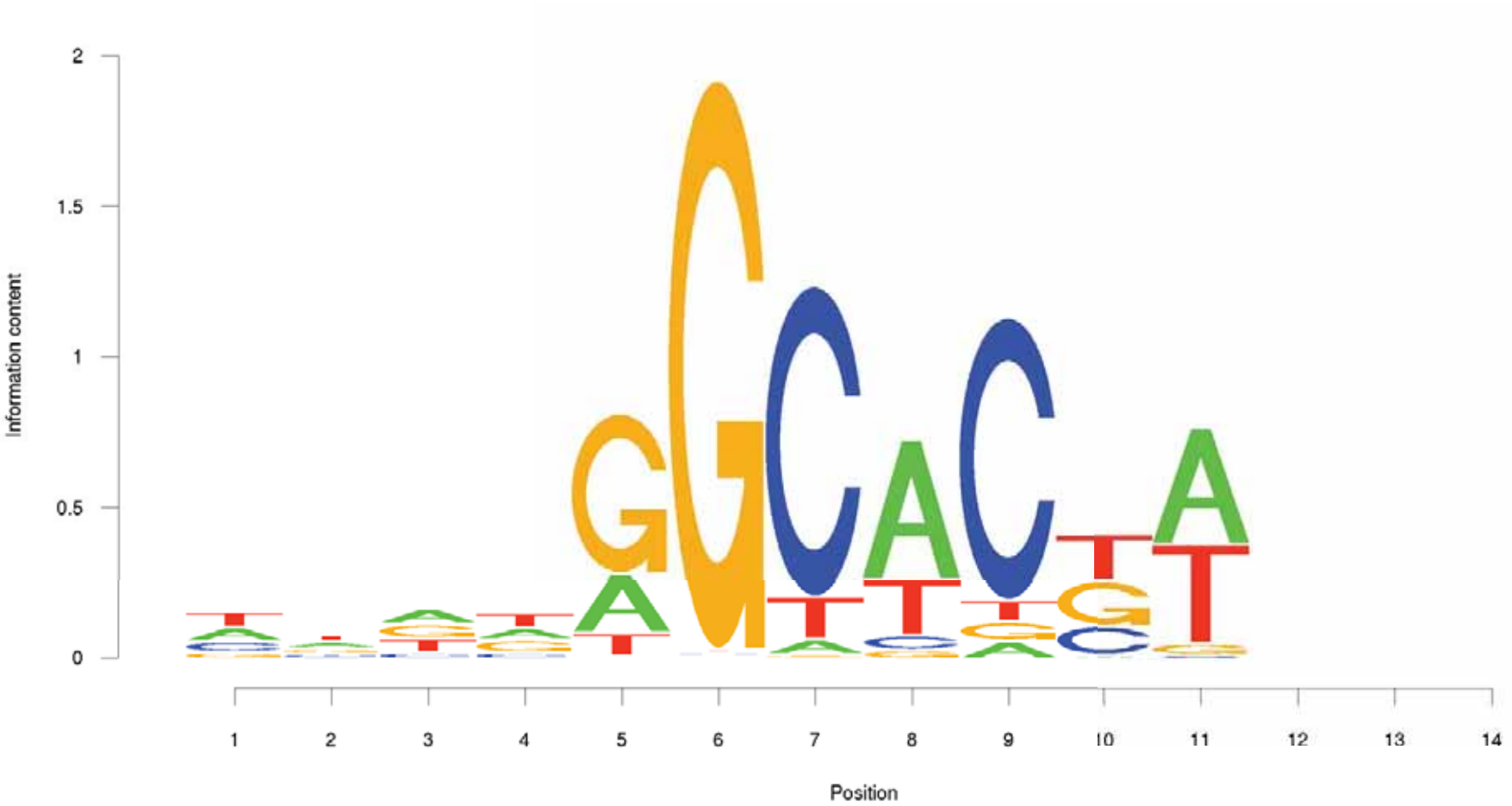
Sigma 54 (RpoN) dependent promoters



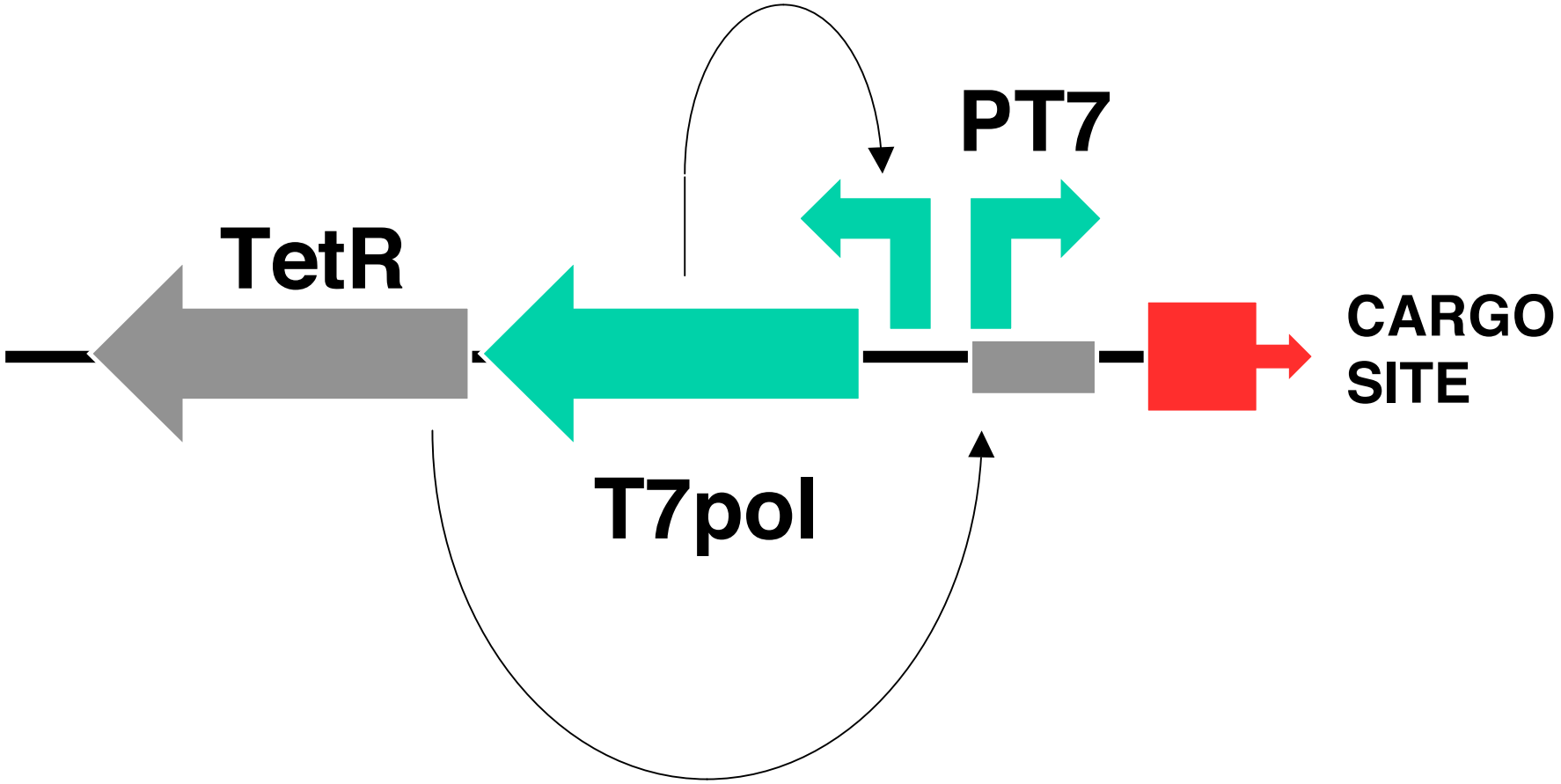
The -12/-24 site



Bases relevant for RpoN-DNA recognition

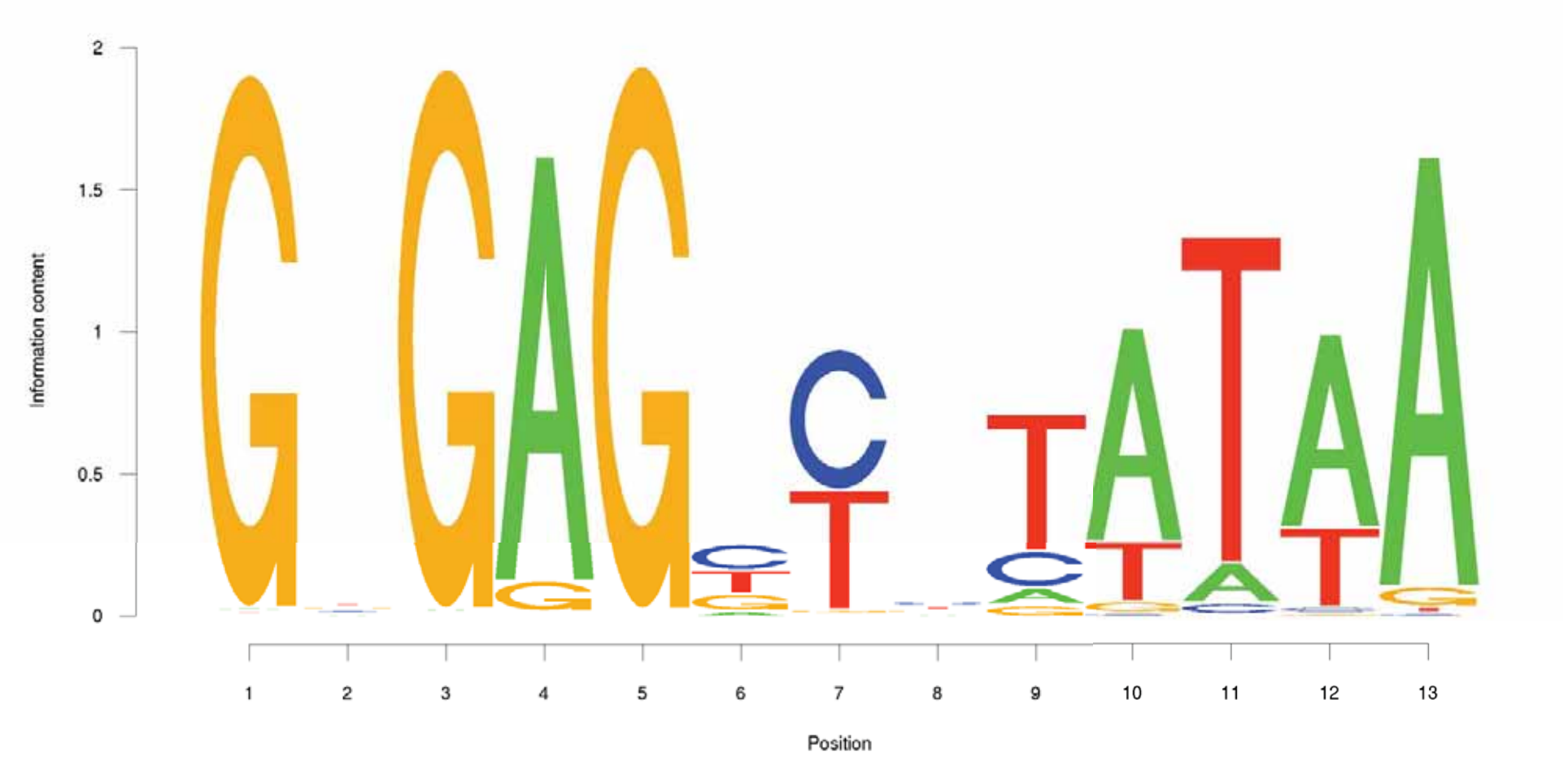


Towards a *bona fide* orthogonal regulatable promoter system

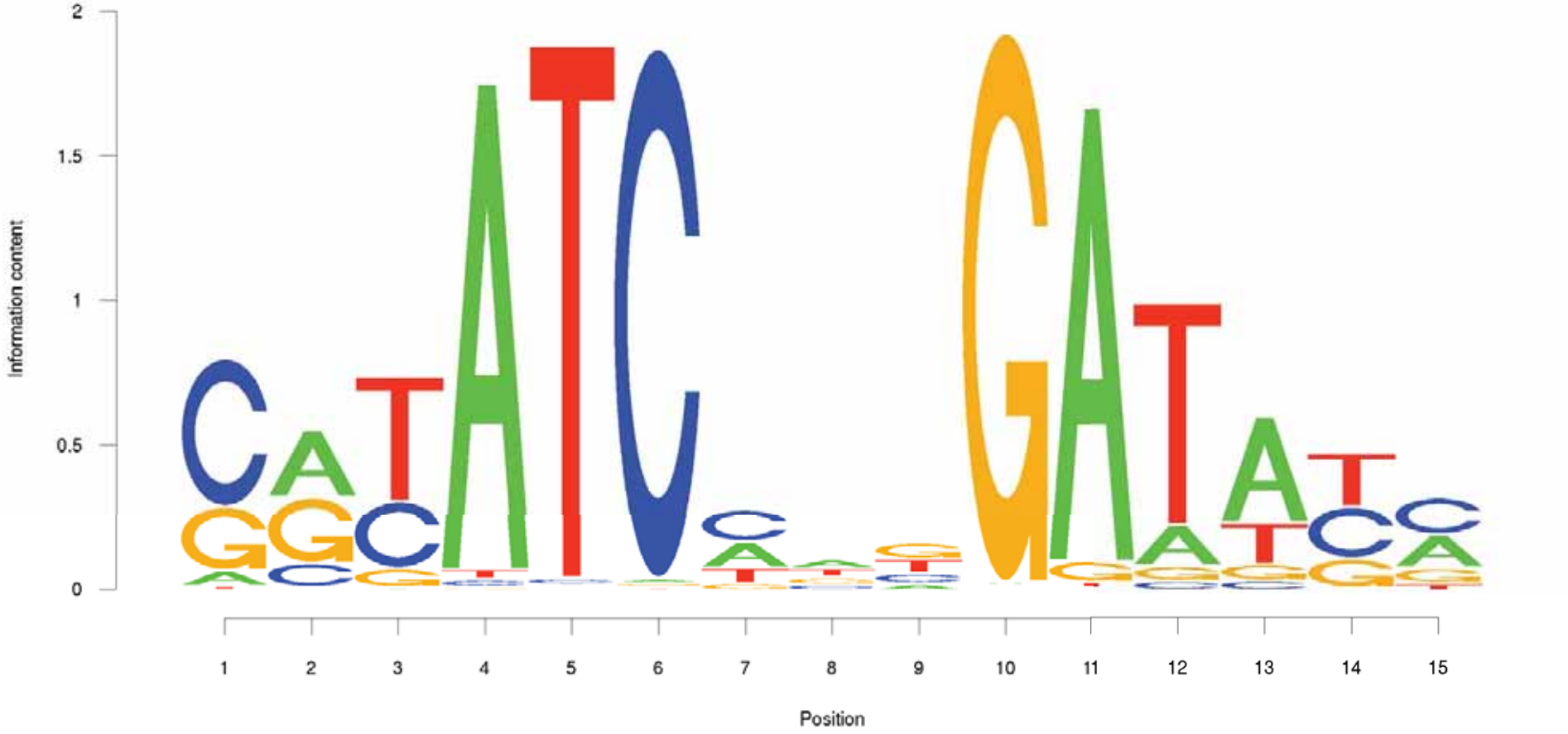


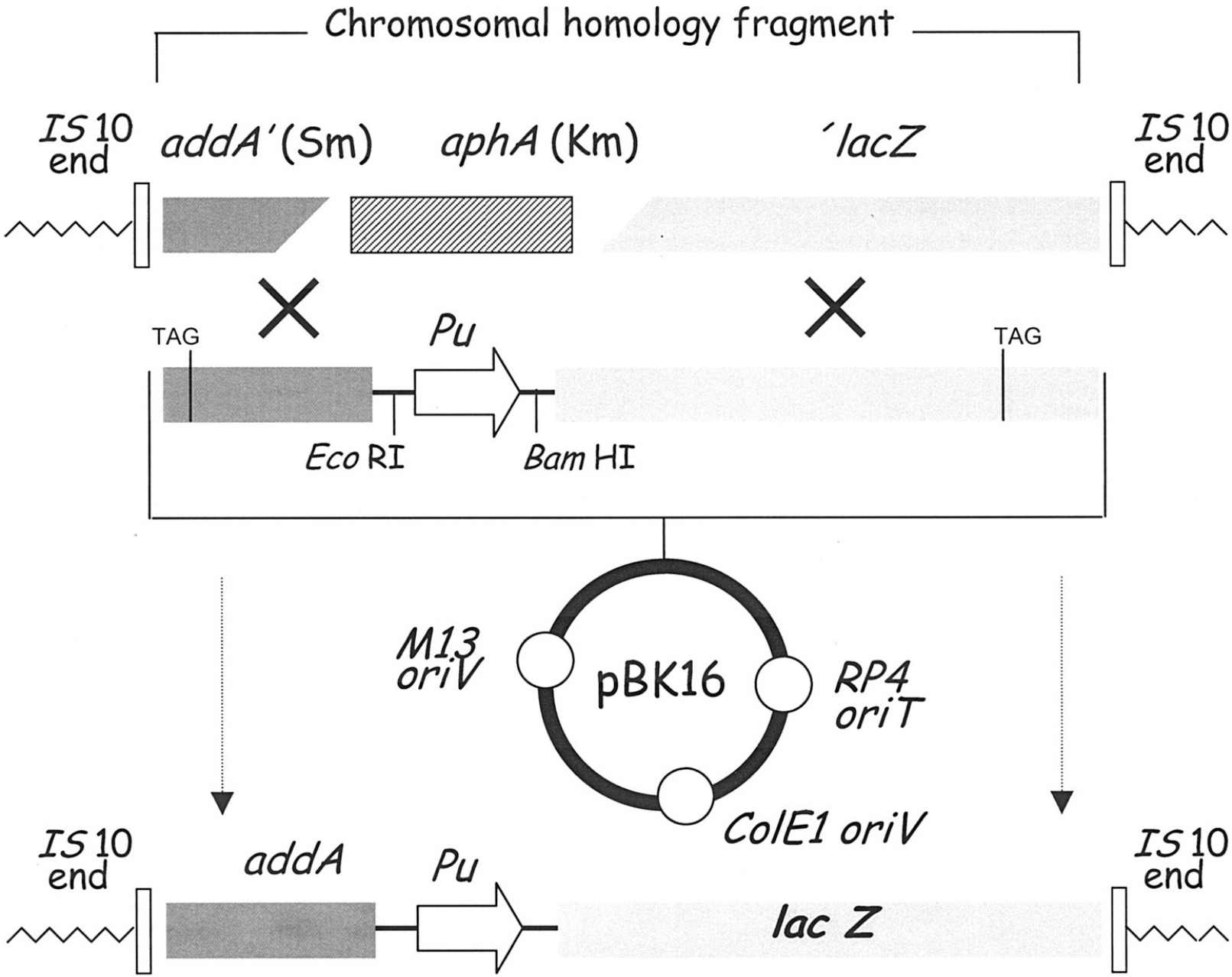
Collaboration with Alejandro & Andreu (CRG)

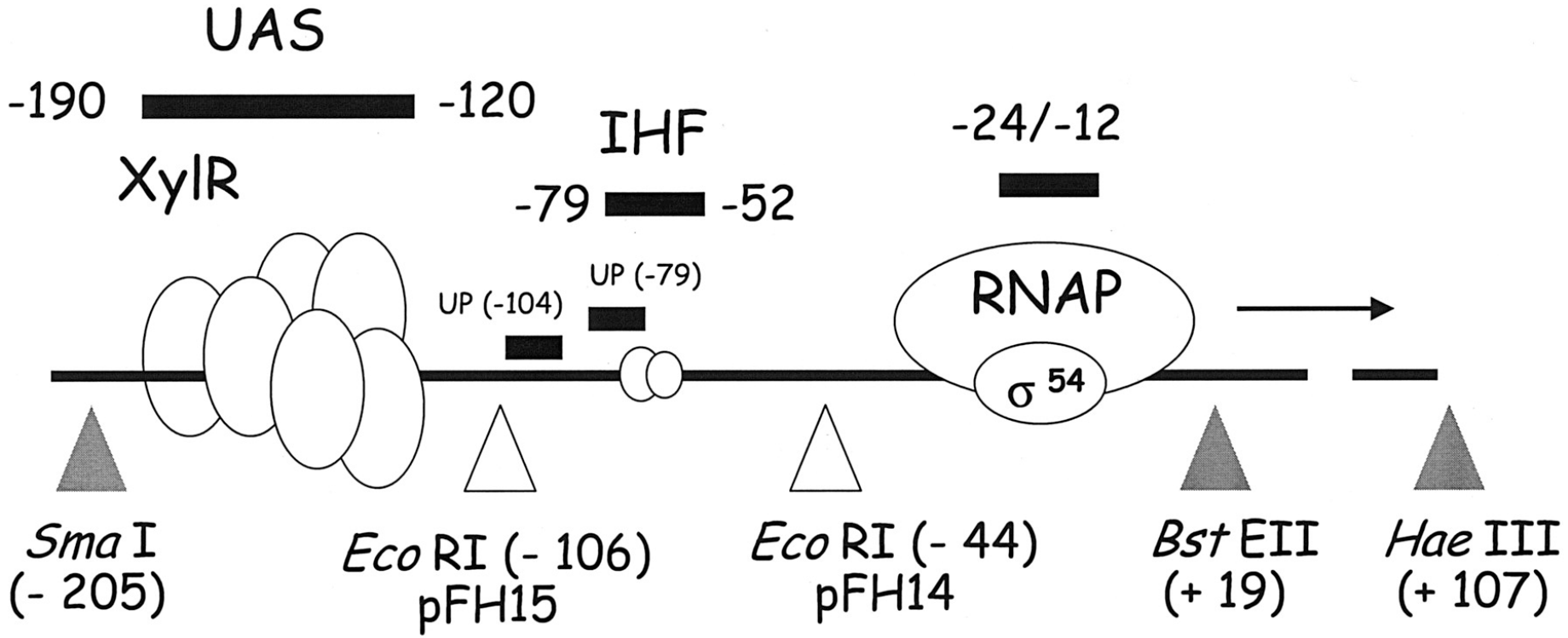
Bases relevant in T7Pol-DNA complex



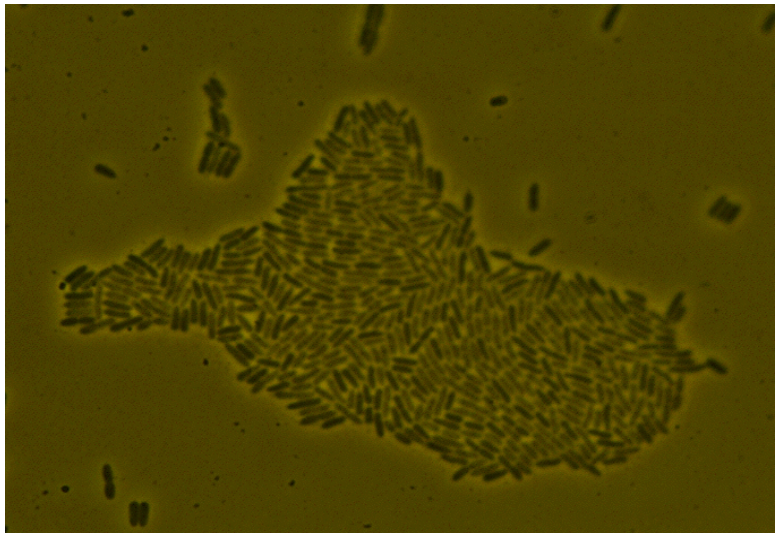
Bases relevant for TerR-DNA complex

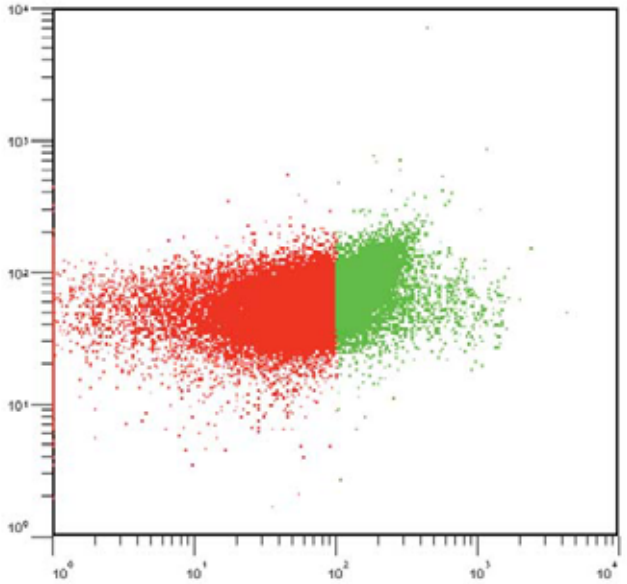


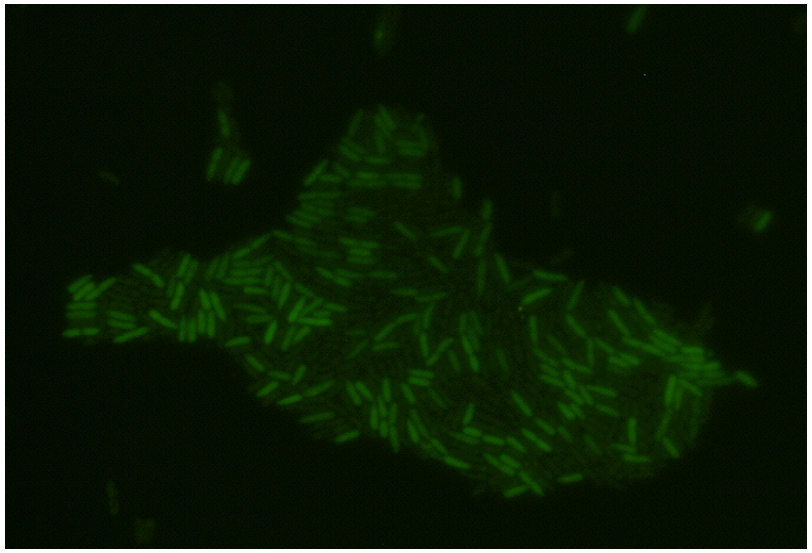

Chromosomal homology fragment
IS 10 end
addA'(Sm)
aphA (Km)
'lacZ
IS 10 end
TAG
Pu
TAG
Eco RI
Bam HI
M13 oriV
pBK16
RP4 oriT
ColE1 oriV
IS 10 end
addA
Pu
lac Z
IS 10 end

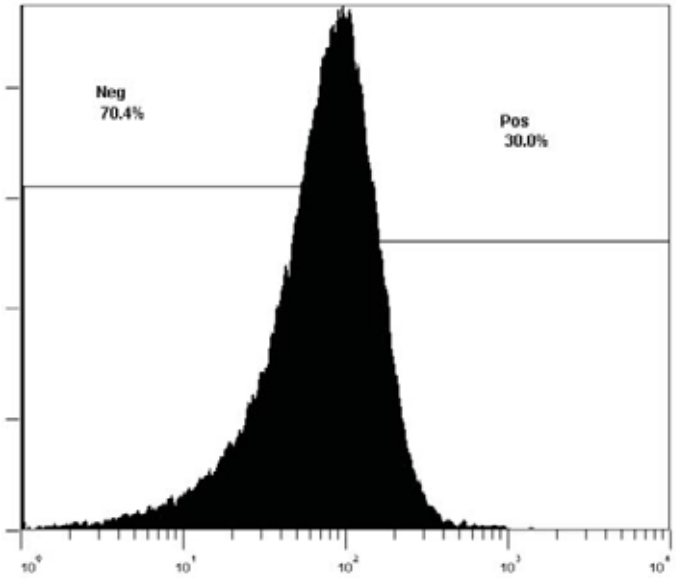

UAS
-190
-120
XylR
IHF
-79
-52
-24/-12
UP (-104)
UP (-79)
RNAP
σ 54
Sma I
(- 205)
Eco RI (- 106)
pFH15
Eco RI (- 44)
pFH14
Bst EII
(+ 19)
Hae III
(+ 107)

“Digital” response of XylR/*Pu*→ *GFP* to *m*-xylene exposure









Deliverables

D1.4. Report on reccomendations of the intra-consortium expert group on suitable promoter standarization formats

D4.1. Database on quantitative prokaryotic promoter performance

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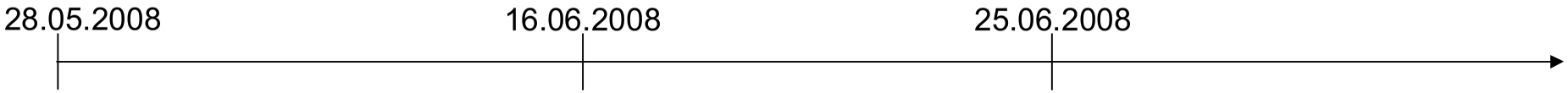
EMERGENCE Meeting Zürich May 2008

Workpackage 5: Building the Academia-Industry interface

Frank Notka, Ralf Wagner, May 2008

Status & Time lines

Contribution to different Workpackages



Annual Emergence meeting
Status update Workpackages

WP3: IT/MolBiol solutions in GS

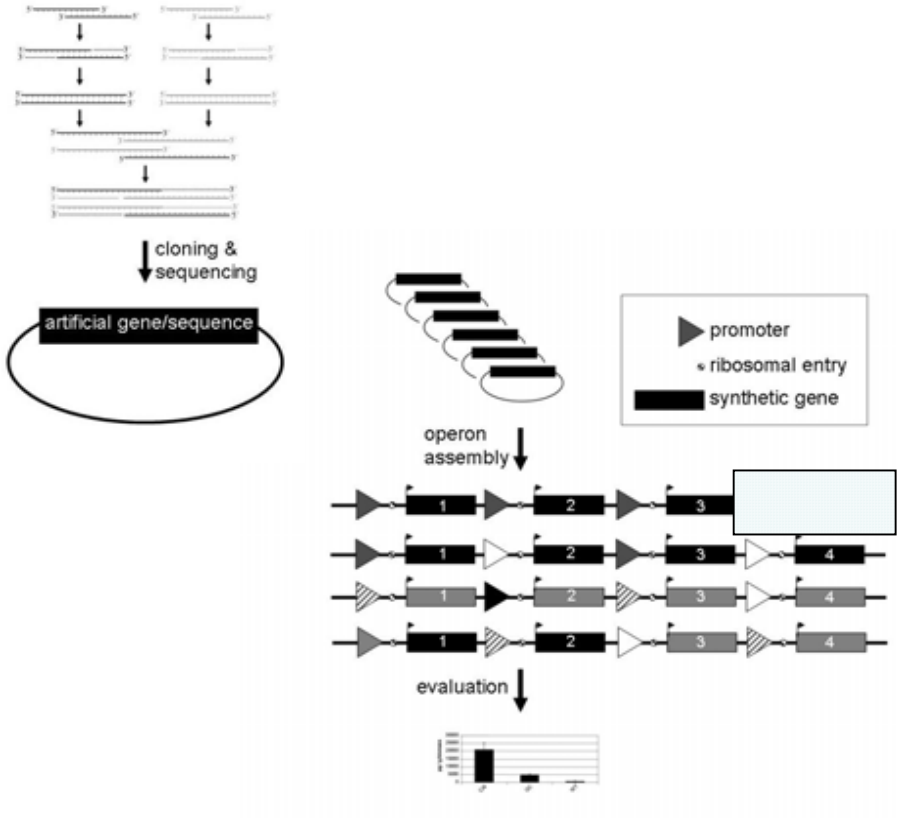
WP5: Academia/Industry Interface

IP Workshop WP5
- Discuss open source policy
- Provide a basis for discussion in Industry WS

Industry Workshop WP 5
- Definition SB
- Attract Industry to European SB
- Link Academia & Industry
- Accelerate progress in SB
- Address IP issues

Strategies and tools for gene synthesis and assembly:

Gene sized segments can be assembled from synthetic oligonucleotides allowing maximum freedom for rational operon design. Differently designed elements in operons can be evaluated and optimized.:



I) Design ☑
- adaptation to host
- interchangeable parts
- high flexibility

II) Synthesis capacities ☑
- up to 2 mio bp/month
- expanding automation platform
- introduction of Laboratory Information Management System (LIMS)

III) Variants of CDR/regulatory elements ☑
- epigenetic control
- metabolic control

IV) Functional circuit design ☐
- cooperative task

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Strategies and tools for gene synthesis and assembly:

Providing tools to effectively manage the complex and integrative process in genesynthesis to meet an expected increasing demand

Laboratory Information Management System (LIMS):

Operation level:

1. Order process
2. Gene optimization and design
3. Definition of oligonucleotides
4. Production and post-processing of oligos
5. *Gene assembly and cloning*
6. *Quality control*
7. *Export*

Information level:

1. Process steering
2. Process monitoring
3. Production parameters
4. Innovation management
5. Cost controlling
6. Customer support
7. Statistics

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Strategies and tools for gene synthesis and assembly:

Provide a strategy to evaluate parts in regard of biosecurity in order to avoid miss-use

BioInformatics @ Geneart: Providing highest biosecurity level

Initial check of gene synthesis:

(1) Country of customer (K-List, Embargo states)
(2) Nature of customer (HADDEX List)
(3) Nature of sequence (Internal data-base, blast)

Involvement of regulatory authorities/guidelines (BAFA and Australian group)

Check for associated pathogenicity/toxicity (dual-use components)

Based on these information a Go/No-Go decision is made

Workpackage 5
WS Define needs and interests of Industry

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Objectives:

- To introduce Synthetic Biology and defining the industrial expectations, priorities and concerns
- To discuss topics regarding regulation, collaboration, and business challenges
- To link the actual development of Synthetic Biology in Europe with major projects, funding and network options

➡ **Promote the Integration of Industry into the European SB development**

Invited Participants (http://spreadsheets.google.com/ccc?key=pMuMDXic0bDYn66S-6rJHAw&hl=en):

Experts from leading European industries covering:

- Chemistry (Lonza, **BASF**, Novozymes, Henkel)
- Pharma (**AstraZeneca**, **Roche**, Novartis)
- Environment/Biomaterials (**Metabolix**, BASF)
- Energy (Shell, Butalco)
- Biotechnology (**Lifewizz**, Brain, Cellectis) and

European academic Synthetic Biology exponents (DKFZ)

Workpackage 5
WS Define needs and interests of Industry

WS date: 25.06.2008 from 10 a.m. – 5 p.m.

Venue: Airport Munich
Hotel Kempinski

Welcome Address and Introduction

11:00 – 11:10	**Ralf Wagner,** GENEART AG
11:10 – 11:30	**Sven Panke,** ETH Zurich
11:30 – 12:00	Showcase by **Luis Serrano,** Centre for Genomic Regulation (CRG)

Topic I, SB and Chemical Manufacturing

12:00 – 13:00	Overview by **Sven Panke,** ETH Zurich & Discussion
13:00 – 14:00	Lunch

Topic II, SB and Pharma Research

14:00 – 15:00	Showcase by **Martin Fussenegger,** ETH Zurich & Discussion

Topic III, SB and IP Landscape

15:00 – 16:00	Open discussion
16:00	**Final discussion & Closing remarks**

Workpackage 5
WS on IP issues

WS date: 16.06.2008 from 10 a.m. – 2 p.m.

Venue: Munich
to be announced

Participants: Sven, Joachim Henkel, Berthold Rutz, DSM and Geneart

Main Goal: To develop a satisfactory and sustainable concept to regulate patent issues between participants, e.g. while dealing within a Registry network

Specific Objectives:
- Start an European IP discussion (provide a basis for the Industry WS)
- Is there a specific European aspect that we can contribute to the IP issue?
- Link the different perceptions of the academic and the industrial R&D processes (accelerated development vs. exploration of IP rights)

Proposed Agenda:

a)	Sven Panke (ETH):	MIT Registry and IP
b)	Jo Henkel (TUM):	SynBio and open source?
c)	Berthold Rutz (EPO):	Scenarios for Synthetic Biology IP solutions
d)	DSM/Geneart:	The industrial perspective
e)	Discussion:	What is a realistic goal for a registry-related IP strategy? Will a (European?) registry drown in IP problems

Workpackages 3 and 5: Deliverables

Deliverable		Month	Progress
3.4	Document describing the proof-of-concept study exploiting the integrated workflow for genetic circuit design	12/09	In progress
5.1	Reports on two industry workshops - to define the priorities of the European industry in the field of synthetic biology, and - to evaluate the fit of the European synthetic biology projects with the industry needs	06/07 & 06/08	Delay (involvement in 10/07) 1. WS fixed, registration i.p.
5.2	Reports on two workshops (associated to industry-relevant scientific conferences) to teach the industry in synthetic biology concepts and tools	12/07 & 12/08	Dependent on 5.1
5.3	Position paper on the priorities of the European industry in the field of synthetic biology, evaluation of fit with current EU synthetic biology projects, and decision on how to address the potential gaps	12/08	In progress
5.4	Intermediate and final report on status of discussion regarding IP strategy in the field of synthetic biology, originating from company internal assessments and summarizing the ideas on IP-management (same workshops as in D5.1)	12/07 & 12/09	Delay (involvement in 10/07) 1. WS fixed