



STANDARDS AND
SPECIFICATIONS

IN SYNTHETIC
BIOLOGY

APRIL 26-27, 2008 • SEATTLE, WASHINGTON

**Funded by the Microsoft Computational
Challenges in Synthetic Biology Initiative.**

Welcome to Seattle! Enclosed in this book you will find maps to help navigate your way around Talaris, the surrounding area, University Village, Seattle Center, and downtown Seattle. Also included is a list of workshop participants, schedule, and abstracts with a space for writing notes next to each abstract. We hope you enjoy your stay and the workshop proceedings this weekend.

Sincerely,

Herbert Sauro

Sean Sleight

Deepak Chandran

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Schedule

Friday, April 25

- 5:30 - 6:00pm : Open bar (Talaris Dining Room)
- 6:00 - 8:00pm : Welcome dinner (Talaris Dining Room)

Saturday, April 26

- 8:00 - 9:00am : Breakfast (Cedar Foyer)

Opening: Overview (Cedar Room)

- 9:00 – 9:15am : Herbert Sauro, Welcome and Introduction
- 9:15 – 9:45am : Raik Grünberg, Summary of BioBrick technical standards and definitions
- 9:45 – 10:30am : Discussion
- 10:30 – 10:45am : Break

Session 1: Experimental standards (Cedar Room)

- 10:45 – 11:05am : Kim de Mora (speaking for Jason Kelly), Measurement kit for BioBrick promoters and ribosome binding sites
- 11:05 – 11:25am : John Cumbers, Dual Luciferase Assay for Promoters (DLAP)
- 11:25 – 11:45am : J. Christopher Anderson, A roadmap for quantitative standards
- 11:45 – 12:30pm : Discussion
- 12:30 – 1:30pm : Lunch (Dining Room)

Session 2: Organizing, storing, and sharing biological parts (Cedar Room)

- 1:30 – 1:50pm : Mac Cowell and Jason Morrison, Bricklet: An open software application for storing, sharing, and finding standardized biological parts
- 1:50 – 2:10pm : Raik Grünenberg, BrickIt: An open source solution for local BioBrick management
- 2:10 – 2:30pm : Jean Peccoud, From registries of biological parts to IDE of genetic systems
- 2:30 – 3:00pm : Discussion
- 3:00 – 3:15pm : Break

Session 3: Computer languages for modeling synthetic biology, Part 1 (Cedar Room)

- 3:15 – 3:35pm : Ralph Santos, PICA (Part Interaction and Composition Assertion): A proposal for a data model and annotation standard for biological parts
- 3:35 – 3:55pm : Andrew Miller, CellML for modeling synthetic biology
- 3:55 – 4:15pm : Michael Pedersen, LBS: A language of biological systems
- 4:15 – 4:35pm : Vincent Rouilly, Describing and simulating BioBrick assemblies with Petri Nets
- 4:35 – 5:05pm : Discussion
- 5:05 – 5:30pm : Registry Tools “Birds of a Feather” Session (organized by Mac Cowell and Jason Morrison)
- 5:30 – 6:30pm : Poster Session and Open Bar
- 6:30pm - ? : Dinner (Ram Brewery, U Village)

Sunday, April 27

- 7:30 – 8:30am : Breakfast (Cedar Foyer)

Session 4: Computer languages for modeling synthetic biology, Part 2 (Cedar Room)

- 8:30 – 8:50am : Mike Hucka, The SBML experience of developing a popular format
- 8:50 – 9:10am : Mike Hucka, Modular models in SBML Level 3: Update on progress
- 9:10 – 9:30am : Michael Blinov, Describing rule-based models
- 9:30 – 9:50am : Lucian Smith, Antimony: A human writable model definition language
- 9:50 – 10:20am : Discussion
- 10:20 – 10:35am : Break

Session 5: Software tools for synthetic biology (Cedar Room)

- 10:35 – 10:55am : Sarah Richardson, BioStudio: Computer assisted design of synthetic genomes
- 10:55 – 11:15am : Guillermo Rodrigo, Automatic design of biological networks using standardized biological model parts
- 11:15 – 11:35pm : Jonathan Goler, BioJade: A comprehensive, extensible design and simulation platform for synthetic biology
- 11:35 – 11:55pm : Deepak Chandran, Athena: a design tool for construction and simulation of modular biological systems
- 11:55 – 12:30pm : Discussion
- 12:30 – 1:30pm : Lunch (Dining Room)

Wrap-up (Cedar Room)

- 1:30 – 3:00pm : Discussion on Workshop Report
- 3:00 - 8:00pm : Day Trip to the Seattle Center to visit the Science Fiction Museum / Experience Music Project and/or Pacific Science Museum and Dinner

Overview Discussion Notes

Talk Abstracts

Session 1: Experimental standards

Jason Kelly

MIT

**Measurement kit for BioBrick promoters and
ribosome binding sites**

I will present a "measurement kit" for BioBrick promoters and ribosome binding sites that will be distributed to iGEM teams this year. I will describe the value shared physical reference standards had to earlier engineering fields, and explain how biological engineers can use such standards to speak in common units and to identify sources of variability inherent in our parts. I will also present results exploring the variability in part measurement across researchers at five institutions that characterized a set of promoters using the measurement kit.

Notes

John Cumbers

Brown University

Dual Luciferase Assay for Promoters (DLAP)

I will present an extension of the promoter RBS assay that Jason Kelly has previously developed. Whilst Jason Kelly used GFP as a reporter our assay uses the Dual Luciferase system from Promega. It should provide greater accuracy over the GFP signal because it has reduced background due to chemiluminescence reading rather than fluorescence. This should provide better results for lower level expression promoters. It also introduces an internal control into the assay by using the renilla luciferase that remains constant whilst the firefly luciferase is under the control of the promoter of interest. This work is based off of an original idea by Tom Knight.

Notes

**J. Christopher Anderson
UC Berkeley
A roadmap for quantitative standards**

An analogy to electronic circuits is frequently invoked when discussing synthetic biology particularly when discussing the quantitative standardization of genetic parts. The success and scalability of electronic circuits in part stems from the ubiquitous practice of standardization and measurement. However, it is in no small part due to a deep theoretical understanding of the underlying medium that encapsulates concrete descriptions for the measurements forming the basis of the standards. In synthetic biology we operate with a deep observational knowledge of our medium but with few predictive quantitative or physicochemical models. Coping with this lack of knowledge is likely to remain a limiting aspect of our field for years to come. I will discuss specific experimental examples to illustrate the problem at hand and describe some roadmaps for developing standards that allow us to operate despite this uncertainty.

Notes

Session 1 Discussion Notes

Session 2: Organizing, storing, and sharing biological parts

Mac Cowell and Jason Morrison

MIT

Bricklet: a simple, flexible, and open software application for storing, sharing, and finding standardized biological parts

Bricklet is a simple, flexible, and open software application for storing, sharing, and finding standardized biological parts. The system is a test implementation of a data specification for parts and their relationships, an architecture for sharing parts in a web of registries, and a user interface congruent with the most common registry use cases. We incorporate ideas both from the technical standards mailing list and from our discussions with synthetic biologists who are using existing software. Keeping the platform flexible enough to handle different part standards, and even different models for defining parts, was one of our main priorities. Our main goal was to build concrete implementations of some of the ideas that have come out of the community discussion, not to compete with any existing registry software.

In this talk, we will describe the decisions we have made, discuss the technical details of Bricklet, and share our thoughts on how this project fits into both the synthetic biology community and the ecology of synthetic biology software. We will illustrate the utility of decoupling data representation from user interface, and hope to discuss with you the future of open data formats in a web of synthetic biology part registries.

Notes

Raik Gruenberg

CRG

BrickIt: An open source solution for local BioBrick management

The BioBrick format for assembling and exchanging functional DNA fragments is still mainly used by iGEM teams. Even in the realm of Synthetic Biology, applications for "normal" research projects are the exception. At the CRG, we have recently started a initiative to create a local BioBrick user community around an institute-wide repository. The BioBrick format is attractive also to labs pursuing more classic rather than synthetic biology research. However, there are some practical issues to be considered. Foremost, the infrastructure provided by the parts registry at the MIT is geared towards iGEM users rather than day-to-day work in normal research laboratories. In order to fill this gap, I have developed a prototype Open Source solution for local BioBrick management (<http://brickit.sf.net>). BrickIt implements a database-backed django web server that can be installed in a lab or institute to share information about DNA samples and BioBricks that are under construction or available in-house. While the data are kept locally, improvements to BrickIt itself can be exchanged among a community of open source developers and are easily migrated to a running production system. BrickIt could thus also become a platform for developing and testing BioBrick data exchange strategies or new user interfaces. More generally, we need a joint effort for developing a community-wide open source software infrastructure that supports the use and exchange of BioBricks.

Notes

Jean Peccoud

Virginia Tech

From registries of biological parts to IDE of genetic systems

The design and construction of novel biological systems by combining basic "building blocks" represents a dominant paradigm in Synthetic Biology. Since 2000, the standardization of these basic parts has been regarded as crucial to the transition from the ad-hoc methods of traditional genetic engineering to the industrial-scale process being contemplated by engineers leading this emerging field. As synthetic constructs become more complex, it will become increasingly difficult to develop registries of biological parts for various applications, organisms, legal environments, etc. The development and maintenance of these resources create new computational and experimental challenges. These challenges will be articulated and a new framework will be proposed that could be used to develop future registries of biological parts.

Notes

Session 2 Discussion Notes

Session 3: Computer languages for modeling synthetic biology, Part 1

Ralph Santos

Lawrence Berkeley Labs

PICA (Part Interaction and Composition Assertion): A Proposal for a data model and annotation standard for biological parts

PICA establishes a baseline data model and framework to support data exchange of biological parts. Rather than attempting to provide a comprehensive solution to the part description problem, the strategy of the PICA framework is to establish as a primary product a simple core data model highly limited and specific in scope and then establish several extension mechanisms defined in the framework of an abstract language to allow outside developers several options to use and enhance the data model as well as the body of annotations. The basic data model and annotation standard focuses on describing parts using grammatically simple expressions anchored in open biological ontologies. The priority of the core data model is to prioritize breadth of application, ease of annotation, and limiting expressivity to simple but clearly defined relations rooted directly in the terms of the base ontologies. The latter limitation is specific and deliberate to encourage others in the community to develop model extensions for annotations to expand the range and specificity of annotations. The data model is built within the framework of a language partly to provide a logical model for organizing and validating annotations and partly so that data model

extensions and future revisions can be related to one another in a regularized and unified manner.

The overall standard proposal package defines extension mechanisms intended to support development both within and external to the definition of a single standard. To extend the data model the PICA framework is defined as a set of modules to support incremental additions to the data model and language. The framework supports both private extension of the language outside any standards process or submission of modules to the community to publicly extend the standard. To encourage opportunities for interoperation with and among different technologies the standard package also includes a module describing a kernel within the language to be reserved for external references. This language subset is established for the benefit of outside developers with the intent of it being managed with special concern for stability and extensibility. Additionally, the standard proposes an elementary identification scheme for identifying and characterizing language modules in terms of an abstract hierarchy to support decentralized development of language extensions.

Initially a broad view of some of the problems to be addressed with a data exchange standard shall be considered along with considerations for particular needs of particular user groups within the overall user community. Then the minimal data model is presented followed by a discussion of the factors that influenced its formation. The extension mechanisms included in the proposal package are described along with the description of several optional modules to illustrate their use. Finally the packaging of the model

into a proposal standard for the BioBricks Foundation is presented.

Notes

Andrew Miller
Auckland Bioengineering Institute
CellML for modeling synthetic biology

CellML is an XML based markup language for the representation of mathematical models. Because it declares the equations making up a system (rather than defining the procedure for solving the system), and cleanly separates all domain-specific information from the model as metadata, it is a good model exchange format for a wide range of problem types.

The latest stable version, CellML 1.1, has a number of features which make it well suited for modelling synthetic biology problems. In particular, the import functionality allows models to be broken up into re-usable components, which can be placed in separate files to form part of a library of components.

Work is already underway on the next version of CellML 1.2. Many proposals which would simplify the representation of synthetic biology models, or expand the types of models that can be represented, have been made for CellML 1.2.

Notes

Michael Pedersen
University of Edinburgh
LBS: A language of biological systems

Abstract: LBS is a textual language for modelling biological systems. Its aim is to match the domain of biology and provide support for modular abstraction while still having a formally defined meaning. In this talk I will first show how LBS can express common biological notions such as modification sites, complexes and compartments. I will then demonstrate how parameterised modules can be built and discuss some of the challenges of obtaining truly general and reusable modules. This is joint work with Gordon Plotkin.

Notes

Vincent Rouilly

Imperial College London

**Describing and simulating BioBrick assemblies
with Petri Nets**

The Petri Nets formalism has been introduced in the 60's in order to represent, analyse, and simulate concurrent systems. Many of its applications can be found in fields related to manufacturing, networking, or electronic chip design. During the last 15 years, a growing literature presents the use of Petri Net to model biological systems. Petri nets can be seen as a computational graph structure, allowing a natural and modular description of biological processes, as well as a powerful analytical framework to explore the dynamical properties of biological networks. The standard and modular description language, offered by the Petri net formalism, appears to be worth exploring when it comes to represent BioBrick assemblies.

In this short talk, we aim at briefly presenting the Petri net formalism, with its different flavours (deterministic, stochastic, or hybrid). We will also demonstrate the use of the Petri nets to support the description, and the stochastic simulation, of transcriptional networks.

Notes

Ranjit Randhawa
Virginia Tech
Model composition and aggregation in
macromolecular regulatory networks

Models of regulatory networks become more difficult to construct and understand as they grow in size and complexity. Large models are usually built up from smaller models, representing subsets of reactions within the larger network. This dissertation focuses on novel model construction techniques that extend the ability of modelers to construct larger models by supplying them with tools for decomposing models and using the resulting components to construct larger models.

Over the last 20 years, molecular biologists have amassed a great deal of information about the genes and proteins that carry out fundamental biological processes within living cells --- processes such as growth and reproduction, movement, signal reception and response, and programmed cell death. The full complexity of these macromolecular regulatory networks is too great to tackle mathematically at the present time. Nonetheless, modelers have had success building dynamical models of restricted parts of the network. Systems biologists need tools now to support composing 'submodels' into more comprehensive models of integrated regulatory networks.

Modeling languages and tools help modelers construct their models by providing a computational environment that minimizes the amount of human error during the construction step. While modelers are currently able to construct small and

medium-sized models by hand, the process is simplified by using computational tools that decrease the time taken to input a model and provide error-testing services along the way. We have identified and developed four novel processes (model fusion, composition, flattening, and aggregation) whose purpose is to support the construction of larger models.

Notes

Session 3 Discussion Notes

Session 4: Computer languages for modeling synthetic biology, Part 2

Mike Hucka

Cal Tech

The SBML experience of developing a popular format

The Systems Biology Markup Language (SBML) is an XML-based exchange format for computational models in systems biology. Although it started as a small effort involving a limited number of collaborators, it grew to become a de facto standard format that today is being developed by an international community of interested developers and users. Both SBML and its development process are far from perfect, yet they seem to address the community's needs well enough to have reached this point. In this presentation, I will summarize some of SBML's history and offer a few personal opinions about the reasons behind SBML's success.

Notes

Mike Hucka

Cal Tech

Modular models in SBML Level 3: Update on progress

The next generation of SBML (Level 3) is set to consist of modular extensions layered on top of a core set of language features. One of the language extensions being planned is support for "model composition", that is, the ability to create models that contain or reference other models (either parts or whole models). Not only does this capability promise to help support the growing complexity and size of today's computational models; it will be a critical feature needed to support models of biological circuits stored in BioBricks-type parts libraries. In this presentation, I will summarize the current state of development in this area of SBML.

Notes

Michael Blinov
University of Connecticut
Describing rule-based models

Most computable descriptions of biological systems, such as a current version of Systems Biology Markup Language (SBML), specify each and every species and reaction. However, because of combinatorial complexity (a protein that contains n sites at which phosphate can be added can occupy 2^n different states), this approach is limited in scope and often unscalable. An alternative approach is a rule-based description, whether rules specify main features of biomolecules or their activities and interactions. A biological system is described by (1) molecules and their attributes (domain specification, including conformational states and binding sites, and locations); (2) initial state of the system, defined by seed species; (3) specification of possible changes in attributes (interactions, activities, and modifications of the domains) and formation of chemical bonds between binding sites of interacting molecules, including limitations on the contexts in which reactions are possible; and (4) specified model outputs, which may correspond to individual or multiple microscopic molecular species (e.g., the sum of concentrations of molecular species that contain a protein in a certain phosphorylated form). Using this description, an automated engine can either generate a network of species and reactions that is complete for the scope of specified inputs, or perform on-the fly simulation that generates only the network of populated species. I will describe BioNetGen scripting language (BNGL) that is a Perl-like computer-readable language for rule-based description of biological systems. If time permits, I'll describe how BNGL can be used for rule-

based extension of SBML (Level 3).

References:

1. Blinov ML, Yang J, Faeder JR, Hlavacek WS. (2006) Graph theory for rule-based modeling of biochemical networks. *Lect. Notes Comput. Sci.* **4230**, 89-106.
2. Hlavacek WS, Faeder JR, Blinov ML, Posner RG, Hucka M, Fontana W. (2006) Rules for modeling signal-transduction systems. *Sci. STKE* **2006**, re6.
3. Blinov ML, Faeder JR, Yang J, Goldstein B, Hlavacek WS. (2005) 'On-the-fly' or 'generate-first' modeling? *Nat. Biotechnol.* **23**, 1344-1345.
4. Blinov ML, Faeder JR, Goldstein B, Hlavacek WS. (2004) BioNetGen: software for rule-based modeling of signal transduction based on the interactions of molecular domains. *Bioinformatics* **20**, 3289-3291.

Notes

Lucian Smith

University of Washington

Antimony: A human writable model definition language

Taking a cue from Jarnac's model definition language, Antimony is a modular model definition language that strives to allow scientists to define and use reaction networks in a modular manner. It is designed not only to be human-readable, but human-writable, in a way that XML-style languages are not. We have identified several design parameters we have incorporated into this language we believe to be helpful for modular reaction network languages, including: the ability to 'flatten' a model to make it suitable for export to non-modular systems; the ability to expose species and reactions in submodels to the models that contain them; and the ability to leave aspects of a submodel undefined, in order to more fully define them in the including model.

Notes

Session 4 Discussion Notes

Session 5: Software tools for synthetic biology

Sarah Richardson

Johns Hopkins University

BioStudio: Computer assisted design of synthetic genomes

Sarah Richardson, Jef Boeke, and Joel Bader

The execution of a synthetic genome project entails solving three major logistical problems. First, manipulations that are simple enough to be accomplished by manual editing at gene-scale become unreasonably involved if done by hand at genome-scale. Computational assistance will be required for large and bulky genomes, but most biologists balk at using command-line tools. Second, as the project progresses there will be many versions of the synthetic genome, which must be carefully annotated and tracked to allow a “roll-back” in the case of lethal modifications. Finally, any project on a genome-scale involves many people from different technical backgrounds whose communication must be clear and whose efforts must be coordinated without redundancy. Concerned and interested members of the scientific community will also wish to suggest directions for the project, or monitor it for ethical reasons. Here we present progress towards solving all three problems with the development of BioStudio – a visual, open source platform for the computer-assisted multiscale design of synthetic genomes. BioStudio is both an integrated development environment and a genome version control system, with the ability to modify nucleotide sequences

automatically or manually at multiple resolutions. It uses a user-friendly genome browser-like format and is currently able to locate and manipulate potential and existing restriction enzyme recognition sites, identify and incorporate unique sequences for PCR identification of wildtype and synthetic sequence, edit existing genome features, and create and annotate user-created genome features. Each version of the genome is encoded in a Gene Feature Format (GFF) file, which is then displayed by the open source annotation viewer GBrowse and stored in a branching version control system. Collaboration and transparency is accomplished through the use of a wiki. Each feature in a GFF file has a corresponding “article” in the wiki, where registered users can actively discuss its treatment. To ensure that BioStudio actually meets the needs of synthetic biologists, it is under development alongside the design of a synthetic *Saccharomyces cerevisiae* genome, SC2.0.

Notes

**Guillermo Rodrigo
École Polytechnique**

**Automatic design of biological networks using
standardized biological model parts**

Guillermo Rodrigo¹, Javier Carrera¹, and Alfonso Jaramillo²

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Recent works on Synthetic Biology consist of designing functional genetic networks in order to reprogram cells using rational design techniques. We will present an automated procedure based on optimization techniques to design biological networks. We apply our methodology to design several logic gates, oscillators and memory devices. However, the *in vivo* implementation of such designs could pose unbridgeable problems or reveal new specifications to be included in the model. We have extended our algorithm to design networks by assembling biological part models. The models contain data obtained from part characterizations, which in the future will be taken from future database of model parts. We evolve such circuits by replacing model parts to reach the imposed design specifications. In addition, we incorporate the effect of the chassis by including the interaction with the cellular resources, which allowed us to model the effects on growth rate when expressing a heterologous system. Thus, the use of

the chassis as a generalized model part will be crucial in the development of a model-based design in Synthetic Biology.

Notes

Jonathan Goler

UC Berkeley

BioJade: a comprehensive, extensible design and simulation platform for synthetic biology

The next generations of both biological engineering and computer engineering demand that control be exerted at the molecular level. Creating, characterizing and controlling synthetic biological systems may provide us with the ability to build cells that are capable of a plethora of activities, from computation to synthesizing nanostructures. To develop these systems, we must have a set of tools not only for synthesizing systems, but also designing and simulating them. The BioJADE project provides a comprehensive, extensible design and simulation platform for synthetic biology. BioJADE is a graphical design tool built in Java, utilizing a database back end, and supports a range of simulations using an XML communication protocol. BioJADE currently supports a library of over 100 parts with which it can compile designs into actual DNA, and then generate synthesis instructions to build the physical parts. The BioJADE project contributes several tools to Synthetic Biology. BioJADE in itself is a powerful tool for synthetic biology designers. Additionally, we developed and now make use of a centralized BioBricks repository, which enables the sharing of BioBrick components between researchers, and vastly reduces the barriers to entry for aspiring Synthetic Biologists.

Notes

Deepak Chandran

University of Washington

Athena: a design tool for construction and simulation of modular biological systems

The field of synthetic biology is the attempt to bring engineering principles to biology. While classical biology is generally done solely in the lab, this new perspective will require modeling and analysis of designs before building them. The software Athena has been developed in hopes to fill this need. In contrast to most biological simulation softwares, Athena has a greater focus on synthetic biology, with features that allow users to assemble "parts" such as genes and promoters and specify their Polymerase Per Second rate (PoPS). Parts can also be loaded from the RegulonDB database, allowing users to find transcription factors that fit a particular design. Designing regulatory networks has been made easier by providing tools that automatically generate transcription rate formulas for the user. The sequence for all the parts is also included in the model, allowing complete design of a plasmid. While adding these capabilities, the software does not sacrifice the ability to simulate metabolic and signaling models such as SBML models. A unique feature to Athena is the ability to realize "modules", or models that can be connected to one another without disturbing the individual models. Any model constructed in Athena can be saved as a module and reused inside other modules. Modules can then be analyzed separately or together. Analysis includes basic stochastic and ODE simulations as well as all the tools from the Systems Biology Workbench. The statistical package R is also integrated into the software, allowing various types of statistical analysis on the modules. In summary,

Athena allows design of modular biological systems and provides the necessary tools for analyzing the modules and constructing the final plasmid.

Notes

Session 5 Discussion Notes

Poster abstracts

Javier Carrera

École Polytechnique

Standards for automated design in synthetic biology

Instituto de Biología Molecular y Celular de Plantas,
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We propose a methodology to design gene regulatory networks with targeted dynamics based on combinatorial optimisation. We use genetic programming techniques to evolve from scratch a transcriptional circuit with unconstrained number of genes that works as a digital device or as an oscillator. For that, we use predefined models of genetic parts stored in SBML, which will allow using them in a standardised registry of part models, to assemble them in a functional genetic network. Our designed genetic circuits are composed of predefined models of genetic parts, having a desired time-response and a degree of robustness under stochastic perturbation of the parameters. Our optimisation procedure will allow the engineering of new genetic devices with desired transfer functions and robustness that could be synthesised and tested experimentally. Our procedure could be viewed as a genome evolution where a given genome would acquire mutations at the promoter, ribosome binding site or coding regions. This amounts to explore the space of all possible transcriptional regulation networks, where at each step we would add/subtract

new interactions or modify kinetic parameters, to find the optimal circuit with specified system behaviour. We apply our methodology to the design of genetic devices having a desired switching or oscillatory behaviour.

Notes

Andrew Miller
Auckland Bioengineering Institute
The physiome CellML environment

CellML is an XML based markup language for the representation of mathematical models. One key aspect for the success of a model exchange format is the availability of generic, reliable and portable software libraries and end-user tools for the manipulation, validation, transformation, and simulation of models.

The CellML API is a well-documented interface definition for CellML processing libraries. The API has been implemented in C++, but bridges can be generated to allow access from other languages. Additional optional modules to simplify common tasks such as units processing, translation of models to procedural programming languages, and simulation, are also available. The API also has comprehensive test coverage of the interfaces.

A number of CellML-aware tools are available. One such tool, called the Physiome CellML Environment, is intended to be a comprehensive CellML Environment, and allows models to be visually edited and simulated (with graphical display of results).

In addition, to these tools, the Physiome Model Repository software provides a web based solution for creating repositories of CellML models and associated documentation. This software is used to operate the public CellML Model Repository.

Notes

Vincent Rouilly

Imperial College London

Registry of BioBricks models using CellML

One of the main goals in Synthetic Biology is to assess the feasibility of building novel biological systems from interchangeable and standardized parts. In order to collect and share parts, a Registry of standardized DNA BioBricks

<http://parts.mit.edu/registry> website has been established at the MIT. BioBricks can be assembled to form devices and systems to operate in living cells. Design of reliable devices and systems would benefit from accurate models of system function. To predict the function of systems built from many parts, we need to have accurate models for the parts and mechanisms to easily compose those part models into a system model. Therefore, in parallel to increasing the number of parts available and characterising them experimentally, a logical extension to the Registry would be to build a Registry of BioBrick models to complement the physical parts. A key aspect in this effort is the use of a description language able to describe and support the BioBrick concepts of modularity and abstraction. In this article, we demonstrate that such Registry of BioBrick Models is achievable. A mock-up is provided based on the great flexibility and modularity offered by the CellML Language.

Notes

Workshop Report Discussion Notes

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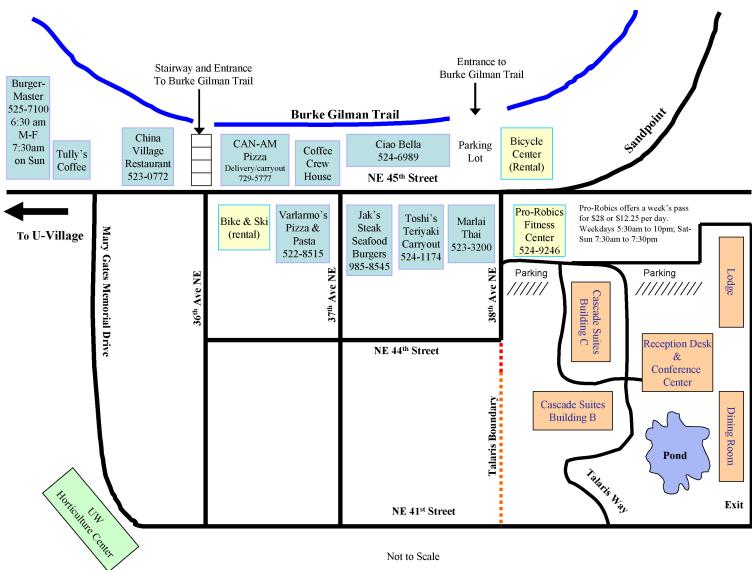
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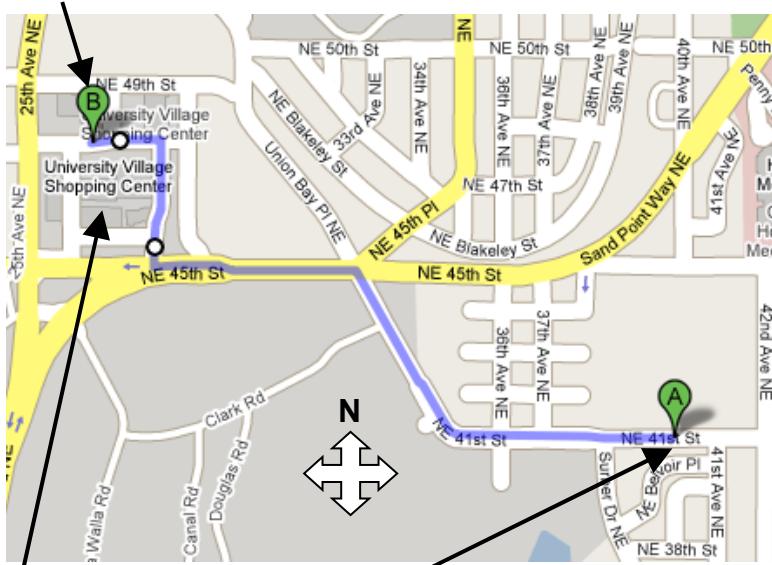
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Restaurants and Shops Near Talaris



Directions to University Village and Ram Brewery

Ram Restaurant and Brewery

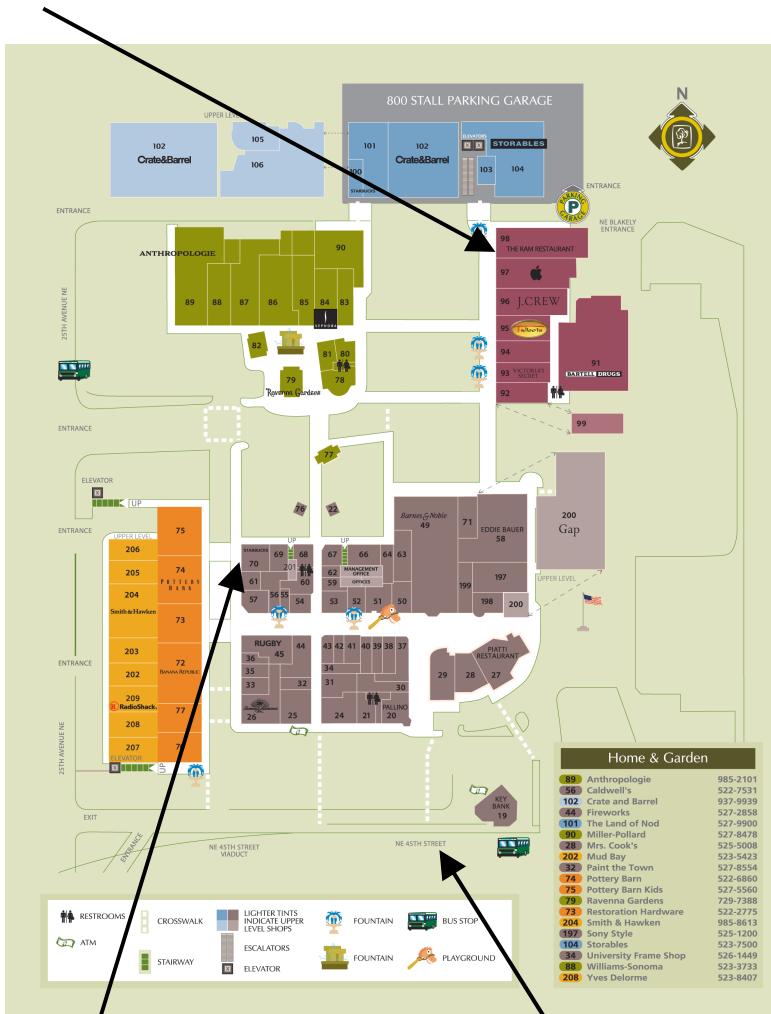


University Village

Talaris Conference Center

University Village

Ram Restaurant and Brewery



Starbucks Coffee

NE 45th St.

Women's Apparel

86	Ann Taylor	729-1132
89	Anthropologie	985-2101
72	Banana Republic	525-5560
54	Bryn Walker	525-0698
56	Caldwell's	522-7531
37	Chico's	729-7099
40	Coastal Collection	525-5675
77	Cole Haan	527-3069
58	Eddie Bauer	527-2646
35	Eileen Fisher	525-0046
200	Gap	525-1559
87	H&M	Open fall
96	J. Crew	523-0666
31	Louie Permelia	522-4722
85	Lucky Brand Dungarees	529-8104
81	Lucy	522-8008
66	Lululemon Athletica	524-6025
94	Mercer	388-0329
53	Nine West	985-2210
45	Rugby Ralph Lauren	526-2626
41	Rouge	985-8977
199	The North Face	525-8500
95	Talbots	523-0627
26	Tommy Bahama's	826-8030
93	Victoria's Secret	524-0477
68	Village Maternity	523-5167
36	Zovo Lingerie	525-9686

Men's Apparel

72	Banana Republic	525-5560
77	Cole Haan	527-3069
58	Eddie Bauer	527-2646
200	Gap	525-1559
87	H&M	Open fall
96	J. Crew	523-0666
85	Lucky Brand Dungarees	527-8104
66	Lululemon Athletica	524-6025
45	Rugby Ralph Lauren	526-2626
199	The North Face	525-8500
26	Tommy Bahama's	826-8030

Children's Apparel & Home

200	Gap Kids and Baby Gap	525-2146
38	Hanna Andersson	729-1099
51	Kid's Club	524-2553
85	Lucky Brand Dungarees	527-8104
101	The Land of Nod	527-9900
75	Pottery Barn Kids	527-5560
43	Sole Food Shoes	526-7184
68	Village Maternity	523-5167

Shoes & Accessories

52	Brighton Collectibles	524-4585
92	Coach	729-5908
40	Coastal Collection	525-5675
77	Cole Haan	527-3069
53	Nine West	985-2210
43	Sole Food Shoes	526-7184

Dining

29	Atlas Foods	522-6025
76	Blue C Sushi	525-4601
64	Delfino's Pizzeria	522-3466
71	Johnny Rockets	522-4483
20	Pallino Pastaria	522-8617
27	Piatti Restaurant	524-9088
98	Ram Restaurant & Brewery	525-3565
24	Sonrisa Modern Mex	524-2242
78	Zao Noodle Bar	529-8278

Cafes & Gourmet Specialties

49	Barnes & Noble Café	517-4107
77	Ben & Jerry's	526-0607
33	The Confectionery	523-1443
80	Fran's Chocolates	528-9969
103	Jamba Juice	522-3063
57	Pasta & Co.	523-8594
198	Specialty's Cafe & Bakery	524-4784
70	Starbucks Coffee	522-5228
100	Starbucks Coffee	522-6410
50	World Wrapps	522-7873

Books, Cards & Specialty Items

49	Barnes & Noble	517-4107
55	Buster & Sullivan	524-6825
56	Caldwell's	522-7531
44	Fireworks	527-2858
42	Impress Rubber Stamps	526-5818
32	Paint the Town	527-8554
67	Papyrus	523-0055

Beauty & Fitness

83	Aveda	526-2610
206	Beauty Works	527-2171
201	Calidora	522-2613
106	Gene Juarez	Open fall
60	Headlines Salon	527-2400
63	InSpa	985-7033
69	Kiehl's Since 1851	985-4414
39	L'Occitane en Provence	529-0801
81	Lucy	522-8008
66	Lululemon Athletica	524-6025
61	MAC Cosmetics	522-5986
105	Metropolitan Pilates	525-9900
51	The Salon at Kid's Club	524-2553
207	Seattle Sun Tan	525-5733
84	Sephora	526-9110

Jewelry

59	Something Silver	523-7545
62	Studio Porter Jensen	522-7050

Computers & Electronics

97	Apple Store	524-8100
205	AT&T	729-7184
209	Radio Shack	523-0534
197	Sony Style	525-1200
21	Tall's Camera	522-6566

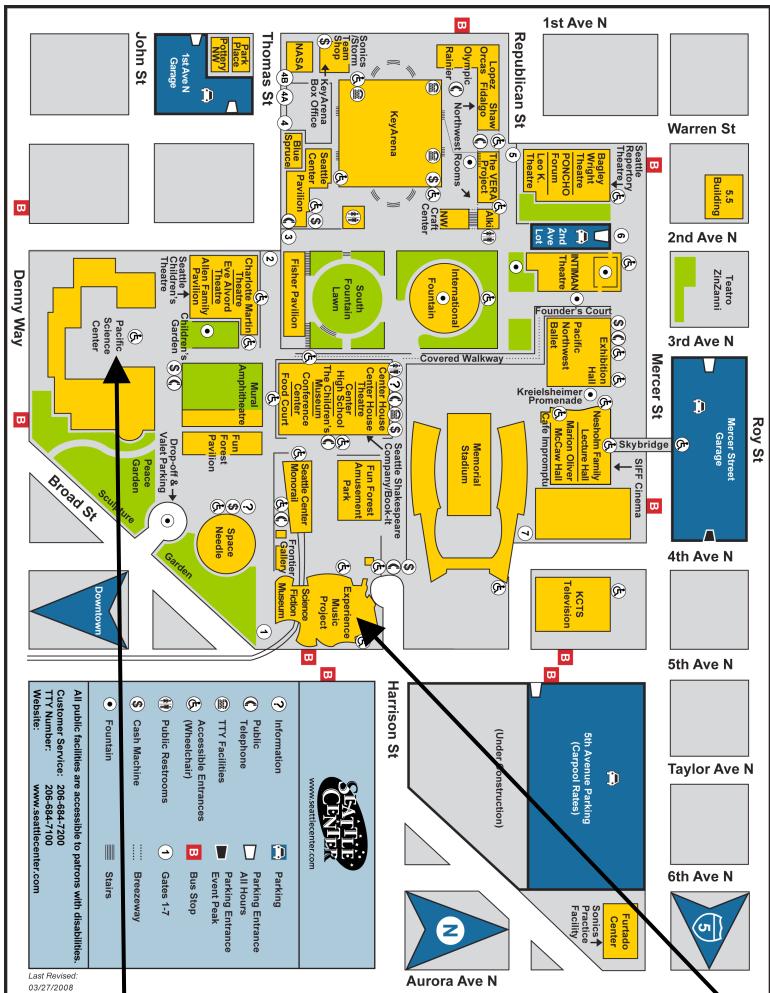
Services

205	AT&T	729-7184
25	Bank of America	585-4791
91	Bartell Drugs	525-0601
99	Bright Horizons Child Care	525-6291
82	Pamela J. Bingham, Optometrist	522-9323
19	Key Bank	447-5744
76	Lee's Keys	522-8840
82	Market Optical	522-9323
24	Tall's Camera	522-6566
203	The UPS Store	524-2558
22	Village Shoe Repair	525-0808

Offices (Upper Level)

Offices	Benchmark Associates	838-8700
Offices	Kumon	524-0915
Offices	Village Management Office	523-0622

Experience Music Project / Science Fiction Museum



Pacific Science Center

Downtown Seattle

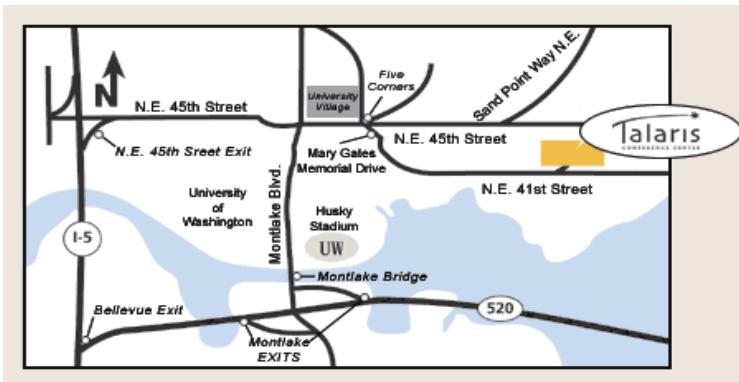


Talaris

CONFERENCE CENTER

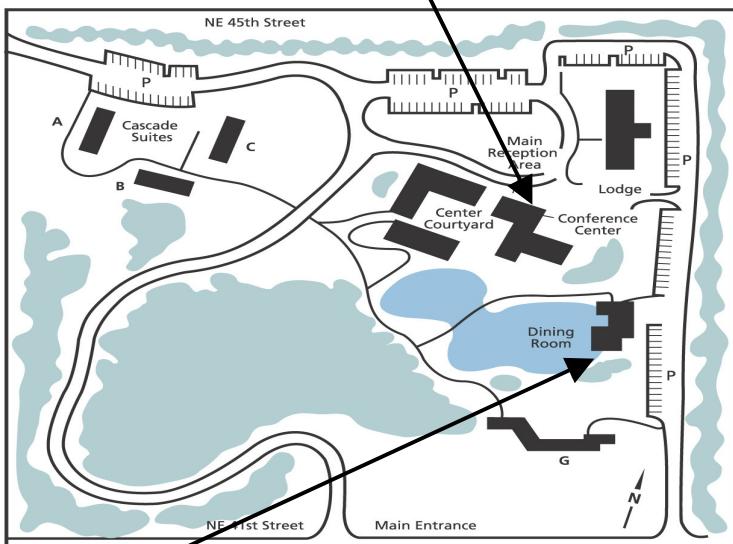


4000 NE 41st Street • Seattle, WA 98105-5428
tel: 206-268-7000 • fax: 206-268-7001
talarisconferencecenter.com



Talaris Conference Center is located to the east of the University District in Seattle; approximately ten minutes north of downtown and approximately 30 minutes from Sea-Tac Airport.

Main building where Cedar Room and Cedar Foyer rooms are located.



Dining room where welcome dinner and lunches will be held.

Park in any area marked with a "P".