# SBOL 9: Workshop Newcastle, UK Draft Agenda

Date: April 24-26, 2013
Time: 9:00 - 5:00
Location: Newcastle University

**Remote Connection Information:** See end of this document

**Acknowledgements:**

# Agenda

### Day 1 - Wed, Apr 24th -- The State of SBOL
Location: Ground floor lecture theatre, Centre for Bacterial Cell Biology, Baddiley-Clark building.
9:00    Meet, greet & tea
9:30    Welcome and Introductions [Anil Wipat]
- i.    Organization of materials for the workshop [Matthew Pocock]
- ii.   Present (and revise) the Agenda

9:40    Matthew's State of the SBOL Union Address [Matthew]
10:00   SBOL in Action and Related Work [10 min Talk + 5 min Questions] [Chair: Matthew Pocock, Notes: TBD]
- ○    Jake Beal - BioCompiler
- ○    Larisa Soldotova - Ontology for Synthetic Biology

10:30   Coffee Break
10:45   [Continue] SBOL in Action and Related Work [10 min Talk + 5 min Questions] [Chair: Matthew Pocock, Notes: TBD]
- ○    Evan Appleton - Experimentally-Driven Algorithms for Optimized DNA Assembly
- ○    Michal Galdzicki - SBOL Designer demo
- ○    Nicholas Roehner - Genetic Technology Mapping with SBOL in iBioSim
- ○    Goksel Misirli
- ○    Robert Cox
- ○    Kirtan Dave

12:00   Lunch
1:00    Working Group Updates & Rechartering [20 min - 10 talk, 5 discuss, 5 vote] [Chair: Goksel, Notes: TBD]
- ○    Devices - Raik Grünberg (5 min, remote talk)
- ○    Modeling - Chris Myers
- ○    Visual - Jackie Quinn

- ○ Performance (characterisation) - Matthew Pocock
- ○ Regulatory - Ernst Oberortner, Matthew Pocock, Nicholas Roehner
- ○ Assembly - Ernst Oberortner

2:30 Coffee Break

2.45 [Continue] Working Group Updates & Rechartering [20 min - 10 talk, 5 discuss, 5 vote]
[Chair: Goksel Misirli, Notes: TBD]
- ○ Script - Ernst Oberortner
- ○ Compliance - Ernst Oberortner, Michal Galdzicki
- ○ Attribution - Michal Galdzicki
- ○ Host Context - Bryan Bartley (arriving 3pm). Michal Galdzicki
- ○ Vector Express Designer (10 min)

4:00 Governance [Chair: Herbert, Notes: TBD]
- ○ Editor Turnover
- ○ Funding
- ○ Joining other Groups
  - ■ "participating group" for sequence ontology?
  - ■ Open Source Bioinformatics Forum? http://www.open-bio.org/

5:00 Wrap up

7:00 Meal at the Marco Pierre White Steakhouse Bar & Grill
    Address: 2-8 Fenkle Street, Newcastle upon Tyne, NE 1 5XN


## Day 2 - Thu, Apr 25th -- Breakouts and Excursion

Location: Ground floor lecture theatre, Centre for Bacterial Cell Biology, Baddiley-Clark building.

8:30 Tea

9:00 Plan Breakout Sessions (make progress on specific tasks in small groups) [Chair: Chris Myers, Notes: TBD]
    Potential Topics:
- ○ SBOL Visual - Jackie Quinn
- ○ libSBOLj Hacking
- ○ Extension Method
- ○ IWBDA Abstracts
- ○ Technical Training (tutorials on Maven, GitHub)
- ○ Increasing Adoption
- ○ SBOL Primer - Jackie Quinn
- ○ Regulatory Elements - Robert Cox
- ○ SBOL Compliance - Michal Galdzicki
- ○ TBD - *Please send breakout session ideas to the Editors*

9:20 Talk by Ryan Cawood - Oxford Genetics provider of a catalogue of DNA components

9:30 Breakout Sessions

12:30 Wrap up / Lunch

1:00 Excursion

7:00    Meal at SIX at BALTIC Centre for Contemporary Art
    Address: SIX Restaurant, BALTIC Centre for Contemporary Art Gateshead Quays, South Shore Road, Gateshead, NE8 3BA


## Day 3 - Fri, Apr 26th -- Breakouts and the Road Ahead

Location: Room 701, School of Computing Science, Claremont Tower.
9:00    [Continue] Breakout Sessions
12:30  Lunch
1:30    Breakout Groups Report Back
2:00    Roadmapping Discussion - Ernst Oberortner
- Envisioning directions for SBOL
- Setting goals and priorities for the next six months
4:30    Wrap up

**Remote Connectivity**
We're using Skype for providing remote connectivity for the conference - I will be managing access to the call through Matt Pocock's Skype account.

Tomorrow (we will start broadcasting between 9.00-9.30am GMT):

* Add matthew.pocock as a contact.
* When you are ready to connect to the call, send a short message requesting access.

I will then connect you to the conference call, which will provide you access to a video feed of the presentation, and the presentation itself through a shared desktop.

# Workshop Notes

## Notes by Jackie Quinn

### Jake Beal - BioCompiler

- High-level program -> Optimize GRN design
- Generates
    - GraphViz to generate SBOLv diagrams
        - Add to SBOL Visual software list
    - Matlab ODE files
        - One particular ODE model
    - SBOL-ish XML (limitations on libSBOLc, written in C++)
        - What is needed to make it SBOL XML compliant?
        - Focuses on regulatory relationships
- Diagrams (XOR) demonstrate need for visualization of regulation (software to lay out diagrams...)
- Reduces tendency of humans to screw up repressor-based logic
- Is the current level of abstraction well suited to these diagrams? Is there a way to do better?
- Might stick another front end (python or C?) as command language
- Currently supported: boolean logic computation.
    - Don't have confidence in analog computation from high level to low level.
- Would like to generate/translate to SBML
- Strong need for regulatory extension, for example to transfer structure to SBML generating tools

### Larisa Soldatova - Ontology for Synthetic Biology

- Centre of Systems and Synthetic Biology  (www.brunel.ac.uk/research/centres/cssb)
    - knowledge representation in biomodelling, multi-scale modelling of behaviour, biofiuels, software systems
- Ontology driven Biological Models
- How to get tools to support Systems/Synthetic Biology (as opposed to the traditional biomedical applications
- Goals:
    - Integration of existing technology, sources of data into biomodelling platform
    - Ontology for SB based on OBI
- Currently working on Synthetic Biology Lexicon, to populate OBM and support text mining for SB

### Evan Appleton

- Modeling DNA Assembly pipelines/algorithms
    - biobricks, moclo, gibson

- Steps
    - Generate Part Junctions
    - Optimize cloning steps
- Heuristics - # stages, # steps, efficiency (sp. to method, rxn conditions)
- Getting input from experimentalists
    - Variations on output for testing intermediates, getting stuck in assembly
    - Can force/forbid intermediates/part junctions, manually or via Eugene
    - Efficiency parameters/measurements inputted by user
- Generating SBOL Visual through Pigeon, not using SBOL Data Model (putting parts, sequences, in DB)
- Generates instructions for liquid handling robots

## Michal Galdzicki - Version Control in SBOL Designer
- Work in collab. with Clark & Parsia, built in Java
- Demo
    - retrieve DNA components from repositories
    - version control for syn bio
    - nested components
- Reproduce CMY circuits in SBOL Designer w/ multiple agents
- Demo Notes
    - Generic components for C, M, Y, and created repo and committed
    - created template for C (pro, rbs, cds, ter)
    - traverse layers (composition of components), display in thumbnails on right hand panel
    - use sparql to find parts and assign to components in design, discards substructure for subcomponents
    - Generic symbol looks similar to operator

## Nic Roehner - DAG-based tech mapping of genetic circuits (iBioSim)
- SBML-to-SBOL Library Construction
- Inspired by EE - partitioning, decomposition, matching, covering
- Example: And-Or-Invert in iBioSim, written in SBML
- Matching process assigns each element in DAG to DNA component
- Covering - exponential run time (preventing cross-talk)
- Future Work
    - Cyclic regulatory graphs (feedback)
    - Alt methods for decomposition
- Note: use of color coding with SBOL Visual

## Goksel Misirli - Representing Biological Systems for the Flowers Consortium
- Flowers Consortium - UK wide consortium for syn bio, commercialization of research
- Develop platform technology, model based approach
- Develop Model repository

- - model, genetic description, context, environment/host
  - Extensions on modelling, regulation, etc would be valuable
  - Representation of biological *systems* (as opposed to constructs)
    - DNA component as a part of "Genetic Incorporation"
  - Web based system for retrieving Systems, in json

### Kirtan Dave
  - SBOL Plugin to connect SBML and SBOL
  - JSBML?
  - Objective - create metabolic reaction equations in SBML (starting from SBOL)

### Robert Sidney Cox - Synthetic Promoter Designs
  - "Kick-ass promoters," things to consider:
    - Transcription factor interactions (see slides for list)
      - bacterial, 6-8 interactions
  - Combinatorial promoter assembly, went with random assembly of operators with screening


## Notes by Mike
  - Add graphviz to list of software
  - need libSBOLc update/ maintenance
  - Guy interested in trying out SBOL Designer
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