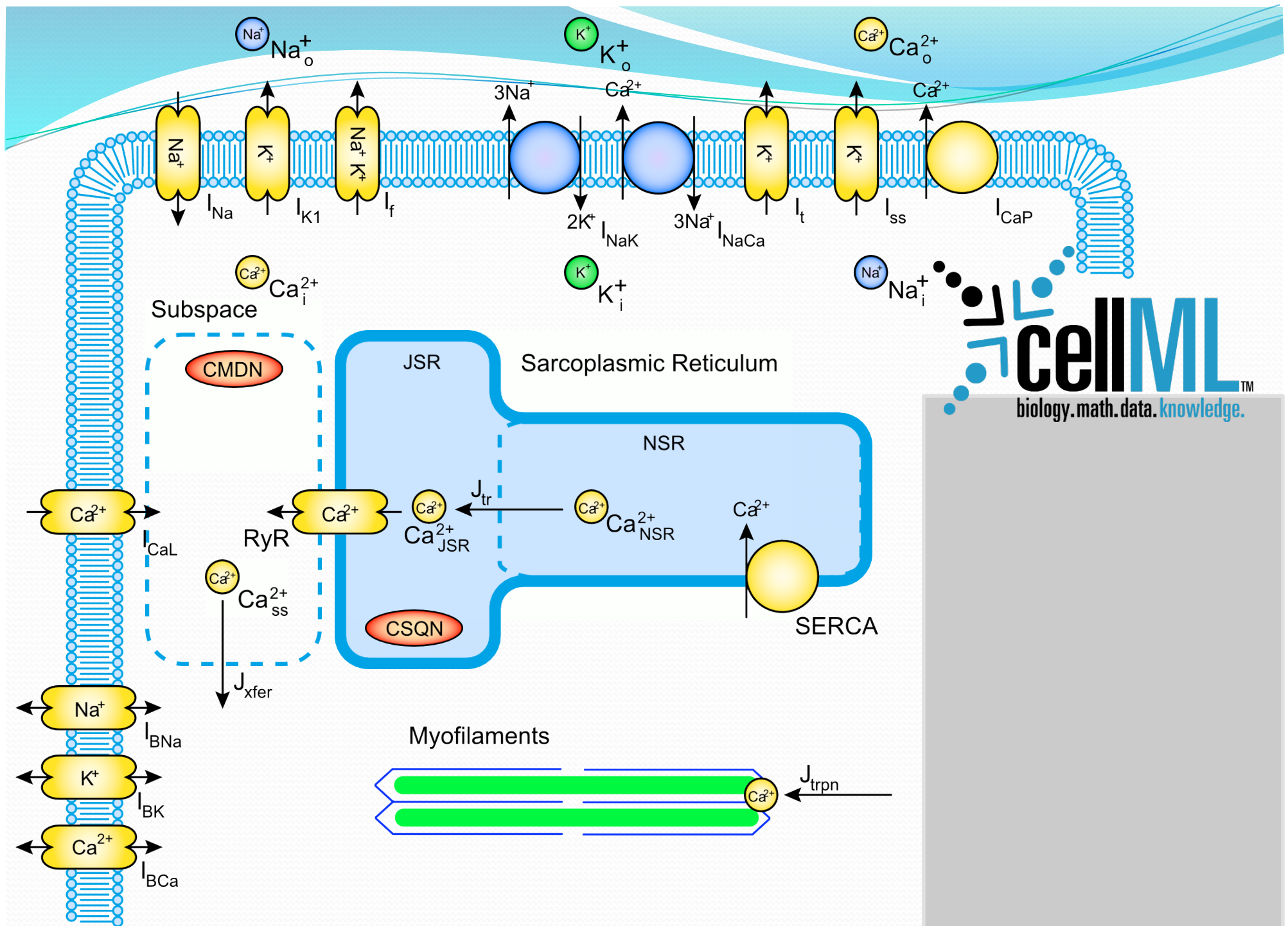


From model to models_

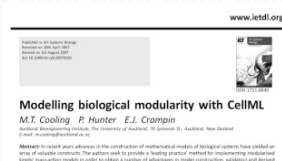
Constructing libraries of modular CellML models

Mike Cooling, February 2010
Auckland Bioengineering Institute



Modular Models

- Construction with recombination in mind
- Fine-grained reuse – mathematical equation level



biology

472

www.ietdl.org

Exp Physiol 94.5 pp 472–485

Experimental Physiology – Research Paper

Facilitating modularity and reuse: guidelines for structuring CellML 1.1 models by isolating common biophysical concepts

S. M. Wimalaratne, M. D. B. Halstead, C. M. Lloyd, M. T. Cooling, E. J. Crampin and P. F. Nielsen
Auckland Bioengineering Institute, The University of Auckland, 70 Symonds Street, Auckland, New Zealand

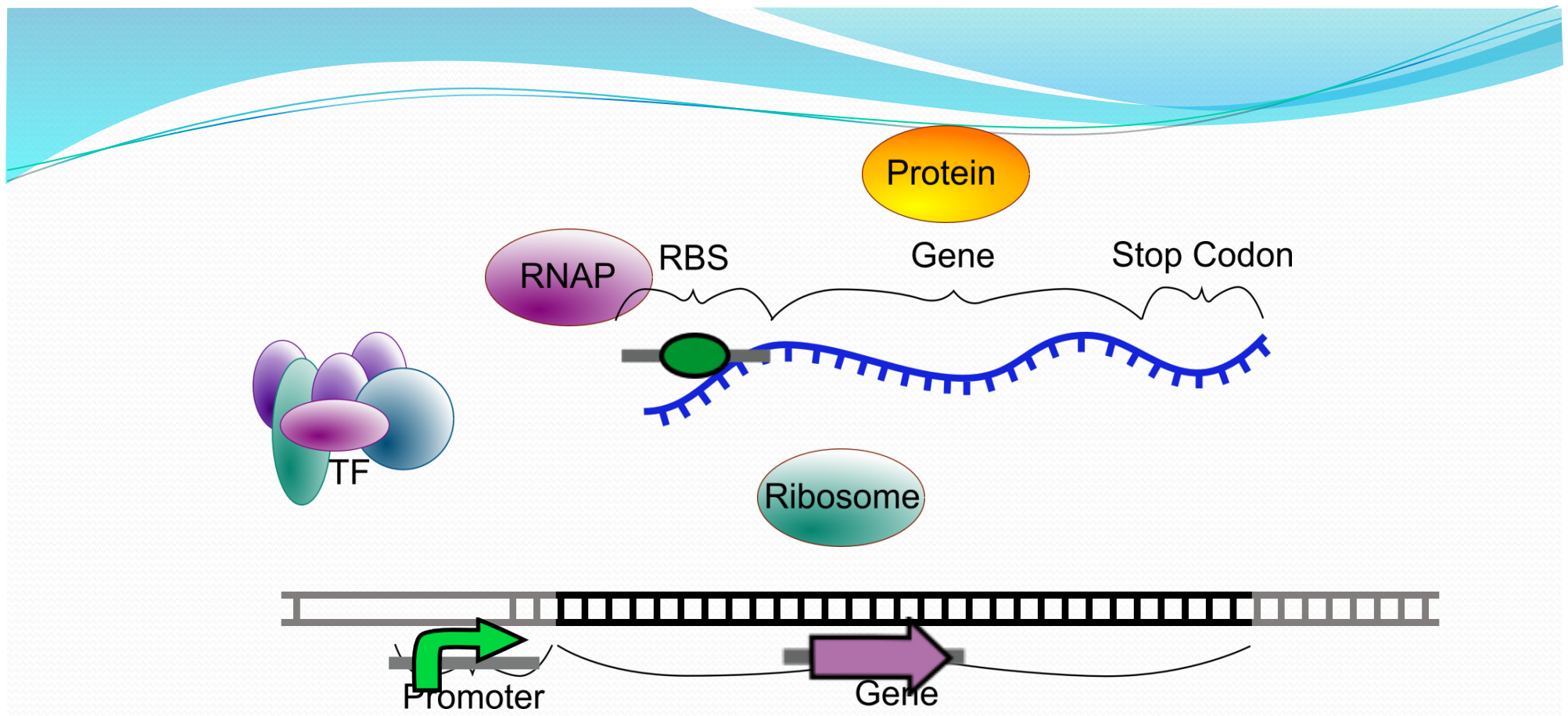
The CellML language was developed in response to the need for a high-level language to represent and exchange mathematical models of biological processes. The flexible structure of CellML allows modellers to construct mathematical models of the same biological system in many different ways. However, some modelling styles do not naturally lead to clear abstractions of the biophysical concepts and produce CellML models that are hard to understand and from which it is difficult to isolate parts that may be useful for constructing other models. In this article, we advocate building CellML models which isolate common biophysical concepts and, using

standardization of biological parts presents an opportunity to devel-

CellML: A Repository of Modular Model-Biology

Lawson¹, T. Yu¹, J. Hallinan² and A. Wipat²
¹Auckland Bioengineering Institute, The University of Auckland, Auckland, New Zealand
²Imperial College London, Biomedical Engineering Department, St Mary's Hospital, London NW6 7RU, United Kingdom

principles such as abstraction, standardization, and characterization to biology [Endy, 2005]. These concepts have proven to be crucial in other engineering disciplines in order to mature from 'dedicated craftsmanship' to successful industrial solutions. Arguably, to date in synthetic biology the best example of such an approach is the



Registry of Standard Parts

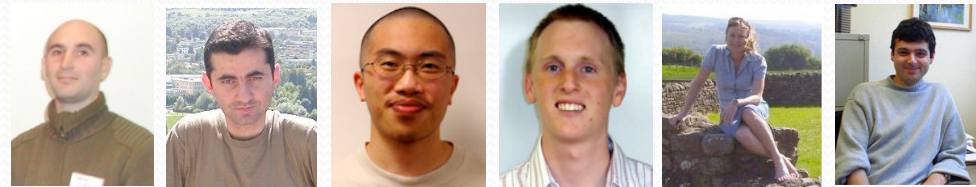
Constitutive *E. coli* σ^{70} promoters

This section lists promoters that are recognized by *E. coli* σ^{70} RNAP. σ^{70} is the major *E. coli* sigma factor so there should be RNAP present to transcribe these promoters under most growth conditions (although maximally during exponential growth).

[More...](#)

-?-	Name	Description	Promoter Sequence	Positive Regulators	Negative Regulators
1★	BBa_I14018	P(Bla)	...gtttatacatagcgagtagctctgttatgg		
1★	BBa_I14033	P(Cat)	...agagggtccaacttcaccataatgaaca		
1★	BBa_I14034	P(Kat)	...taacaactaacggacaattctacctaaca		
	BBa_I732021	Template for Building Primer Family Member	...acatcaagccaaattaacaggattaacac		
	BBa_I742126	Reverse lambda cl-regulated promoter	...gaggtaaaatagtaacacgcacgggtgta		

Our goal



- Registry of Standard *Virtual* Parts to complement the Registry of Standard Biological Parts

[home](#) | [journals A-Z](#) | [subject areas](#) | [advanced search](#) | [authors](#) | [reviewers](#) | [libraries](#) | [about](#) | [my BioMed Central](#)

This article is part of the supplement: [BioSysBio 2007: Systems Biology, Bioinformatics, Synthetic Biology](#).

Poster presentation

Registry of BioBricks models using CellML

Vincent Rouilly¹ ✉, **Barry Canton²**, **Poul Nielsen³** and **Richard Kitney¹**

¹ Department of Bioengineering, Imperial College, London, SW7 2AZ, UK
² Division of Bioengineering, MIT, Cambridge, MA 02139, USA
³ Bioengineering Institute, University of Auckland, Auckland, New Zealand, 92019

✉ author email ✉ corresponding author email

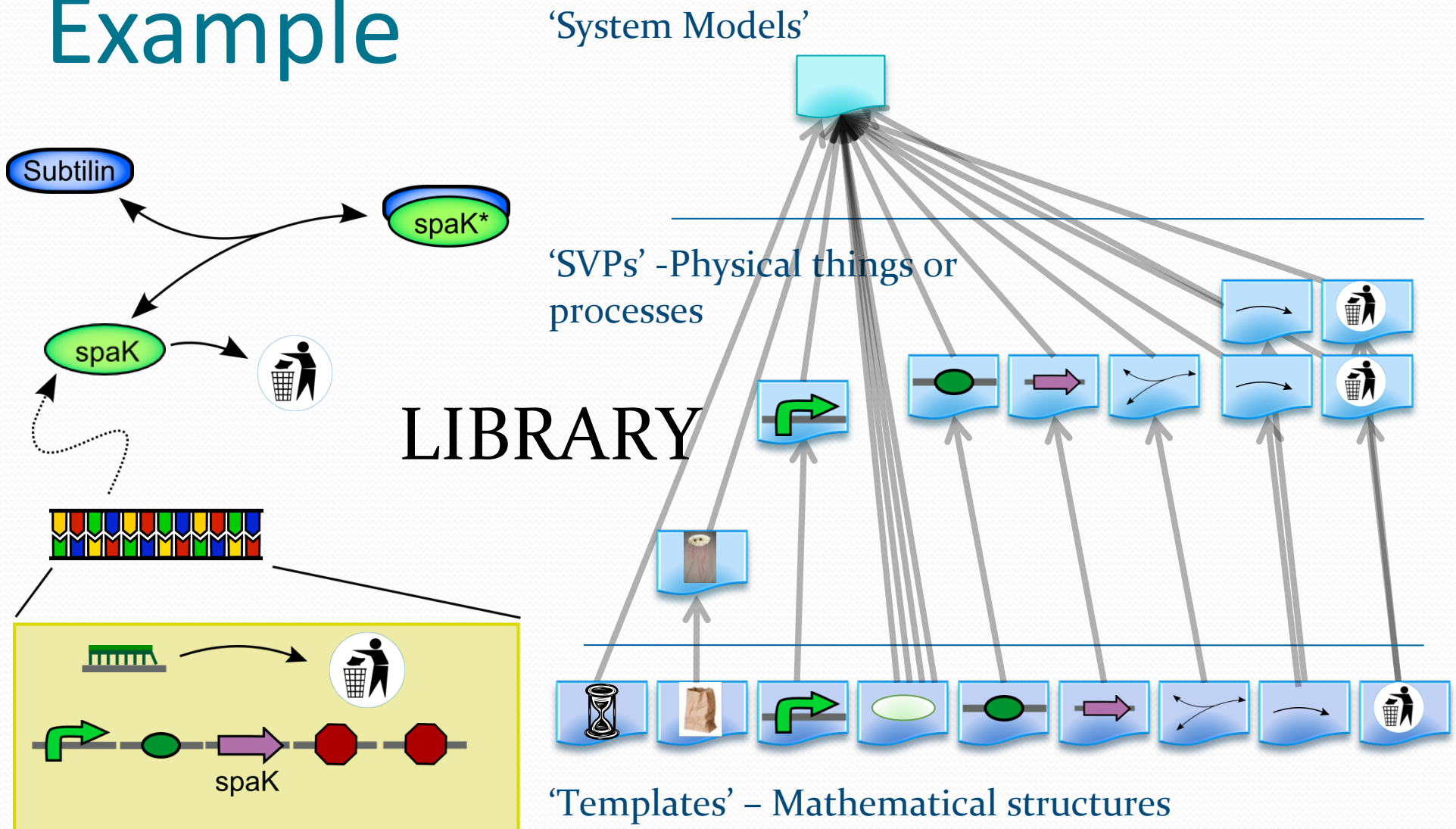
from BioSysBio 2007: Systems Biology, Bioinformatics and Synthetic Biology
Manchester, UK. 11–13 January 2007

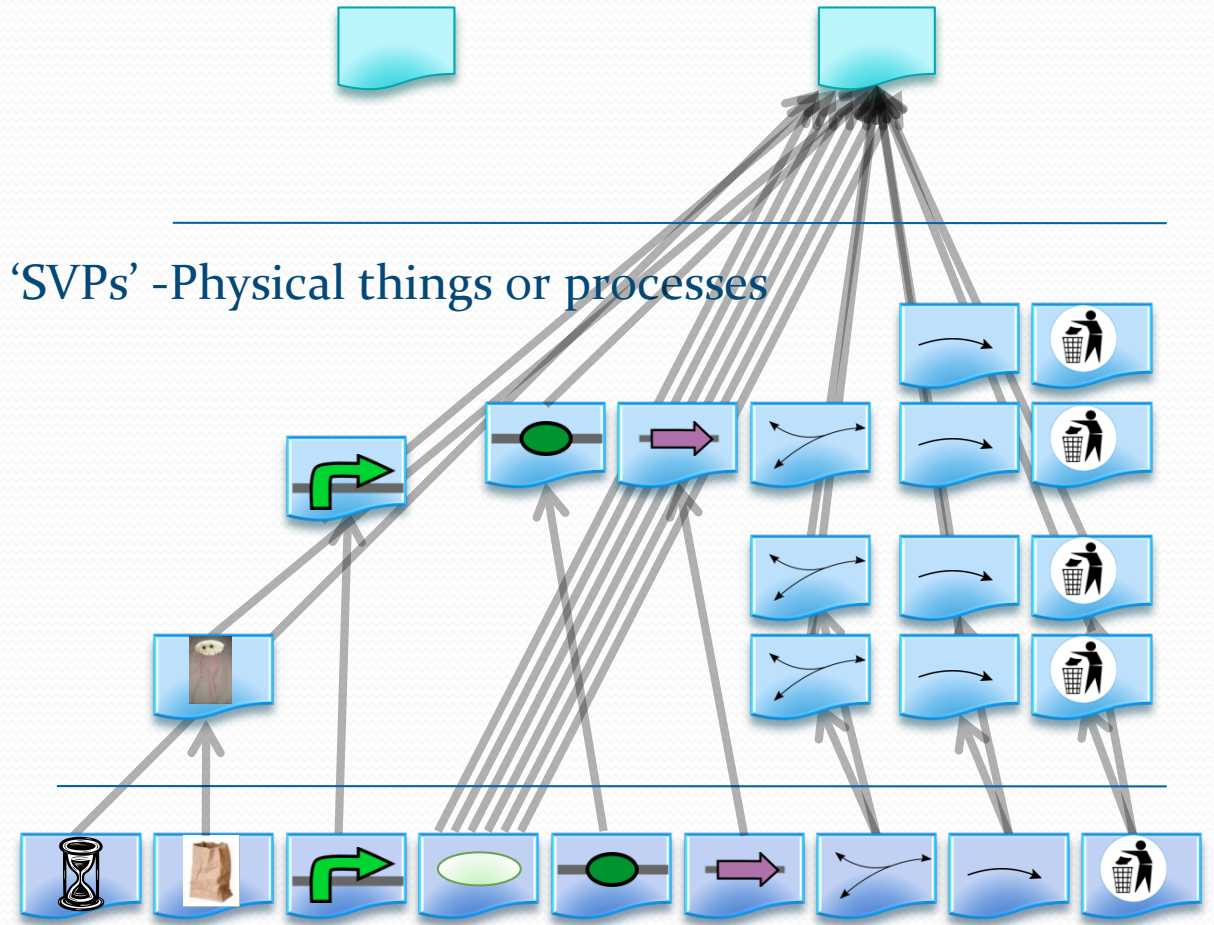
BMC Systems Biology 2007, **1**(Suppl 1):P79 doi:10.1186/1752-0509-1-S1-P79

Published: 8 May 2007

- Composition of models to provide *in silico* simulations

Example

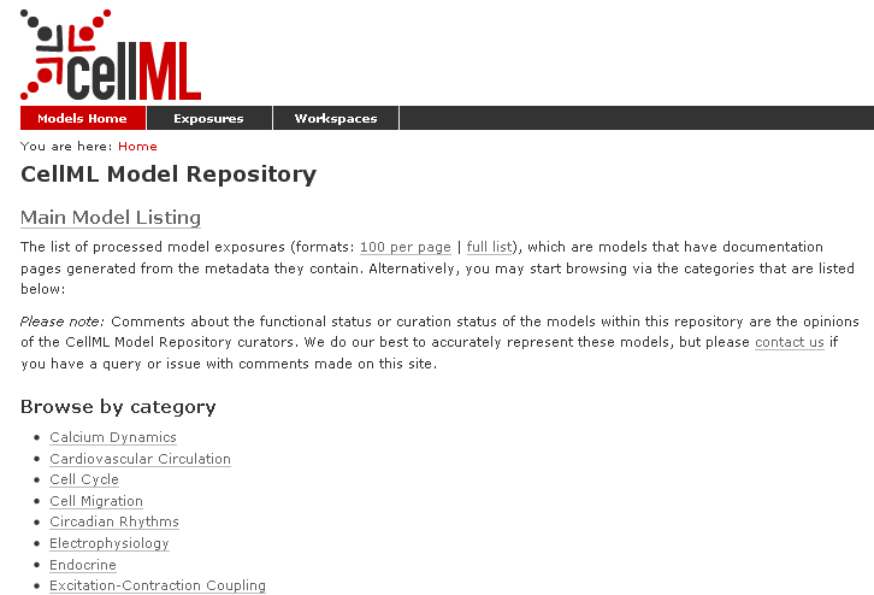




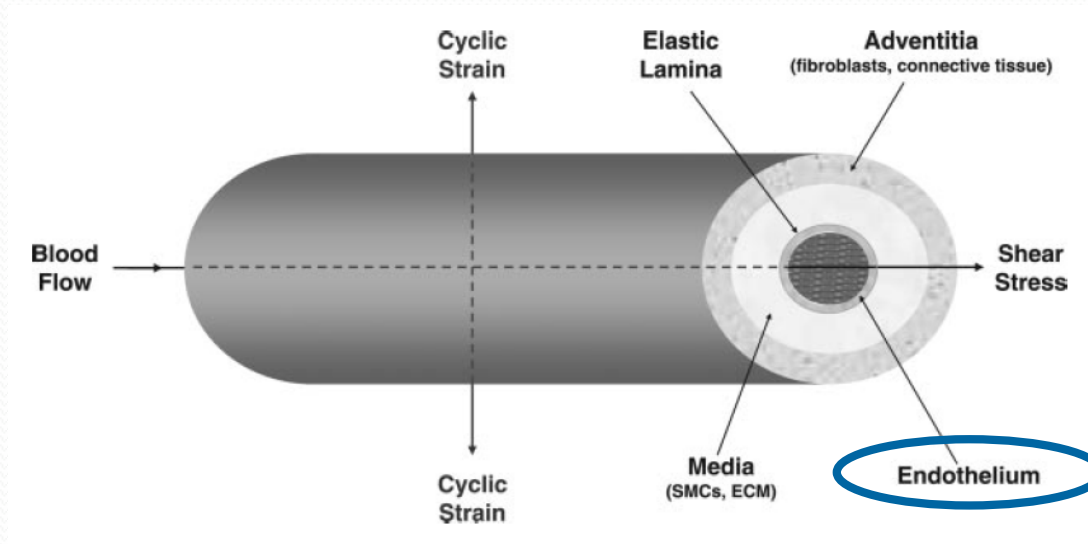
'Templates' – Mathematical structures

http://models.cellml.org

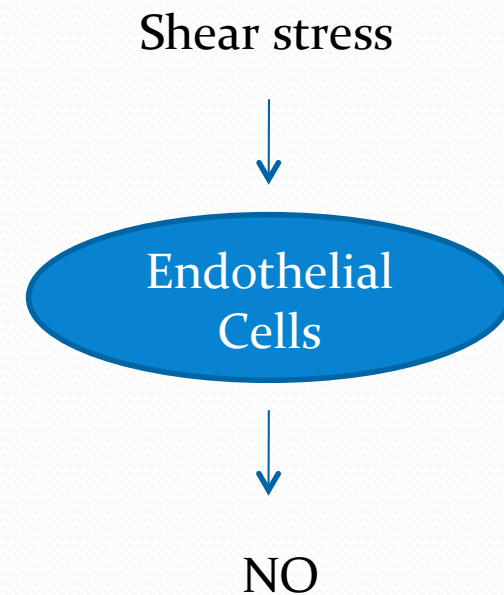
- Support for v1.1 models (multi-file, imports)
- ‘Sharing’ of models between projects through ‘embedded workspaces’
- Collaborative options
- (Distributed) version control



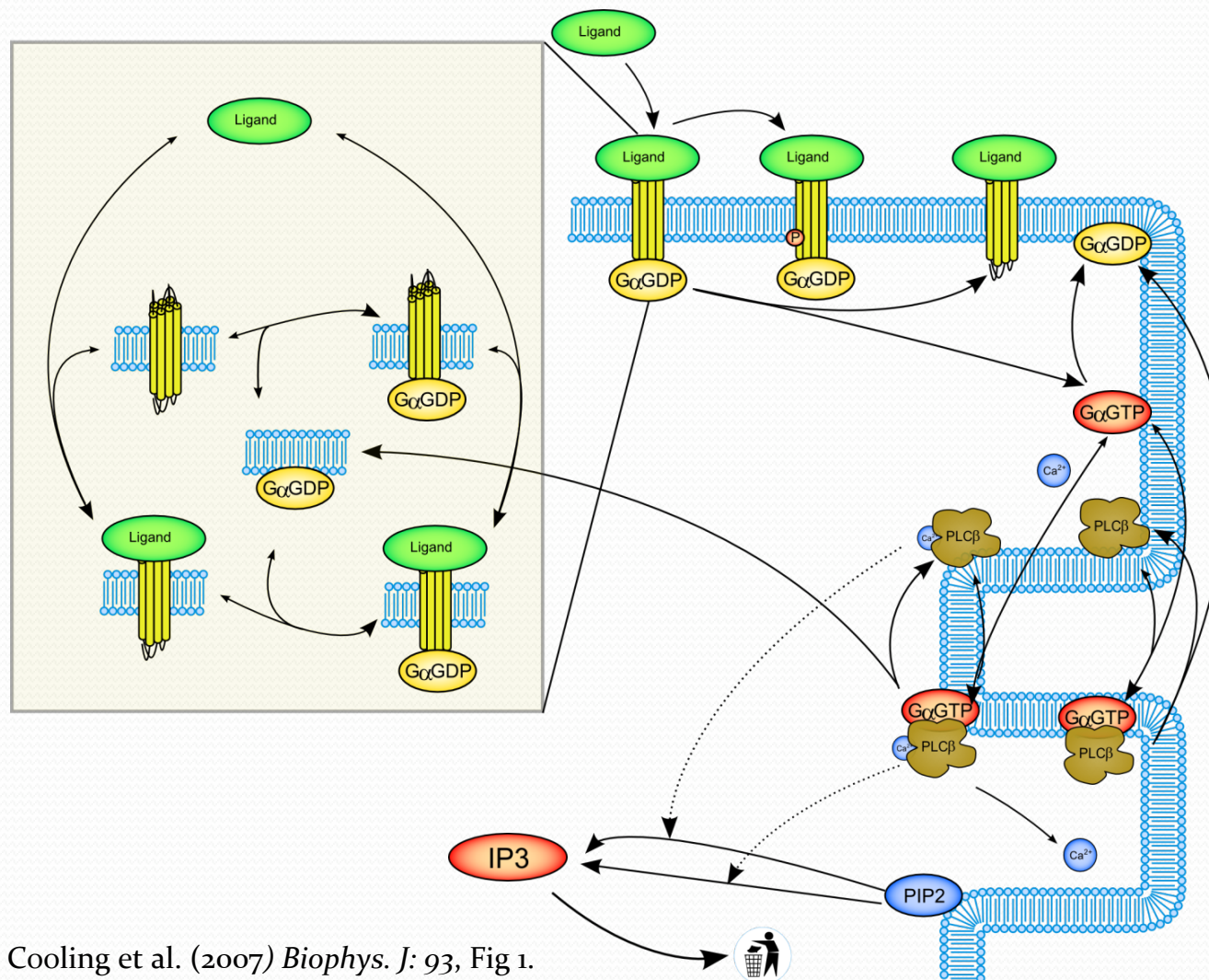
Next: Biomedical Applications

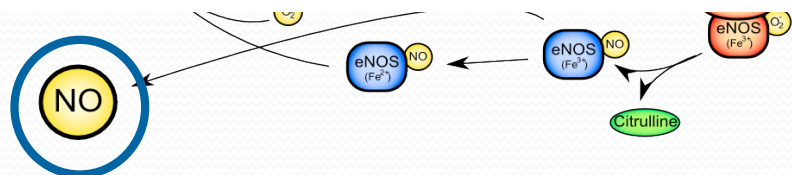


Cummins et al. (2007) *Am J Physiol Heart Circ Physiol*:292, Fig 1.

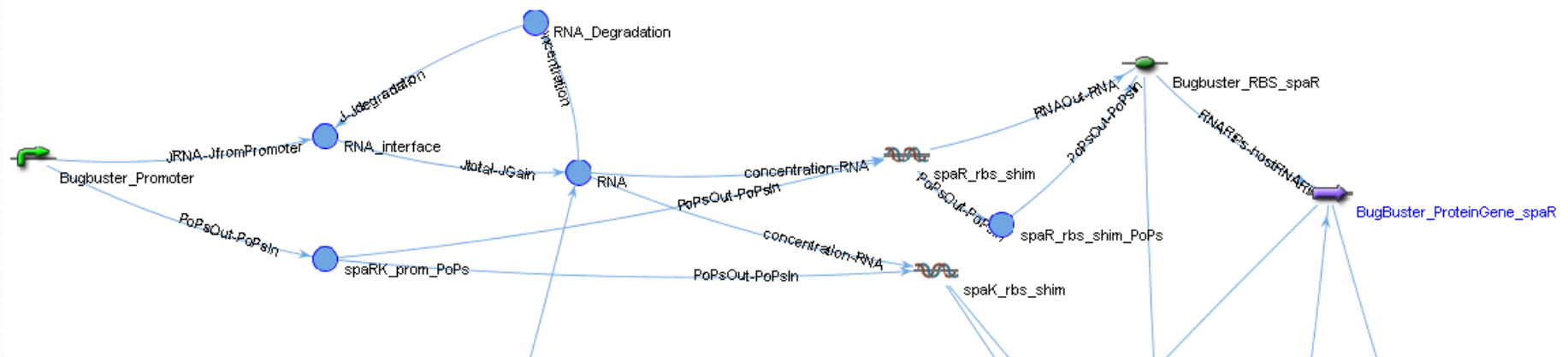
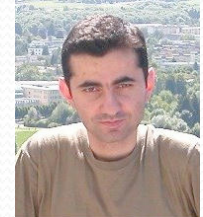


Modular Model Construction





Extensions - Annotations



....ccgcatgaaataaattcaggggtattgatgatgggttttgggtataatgtacaatcattgccagtctta
tatggtttagtaaatgggaagagatccgcatgaaataaattcaggggtattgatgatgggttttgggtat
aatatgtacaatcattgccagtcttatatggtttagtaaatgggaaggcagaaaaacgtttgaatagtatg
agggggccgatggcaaaaatccttgctgtcgatgatgaaaaagatattcttgtactgatacaaaatatttt
gcgccgtgaccagcatcaagttgacatttttagatcatgttcattggacagcctttttatttcattttgatagt
aaagaagtatttatcaataacaacaaactcaacctaacaaaaaatgaatataaaatctgtgaatttttag
ctcaacacaaaggggagaacttttt...

(Semi-Automated) Visualisation

BIOINFC

De
B
S.
ar
1A
70
Rex
Ach
Ass
—
AB

Database

Associate

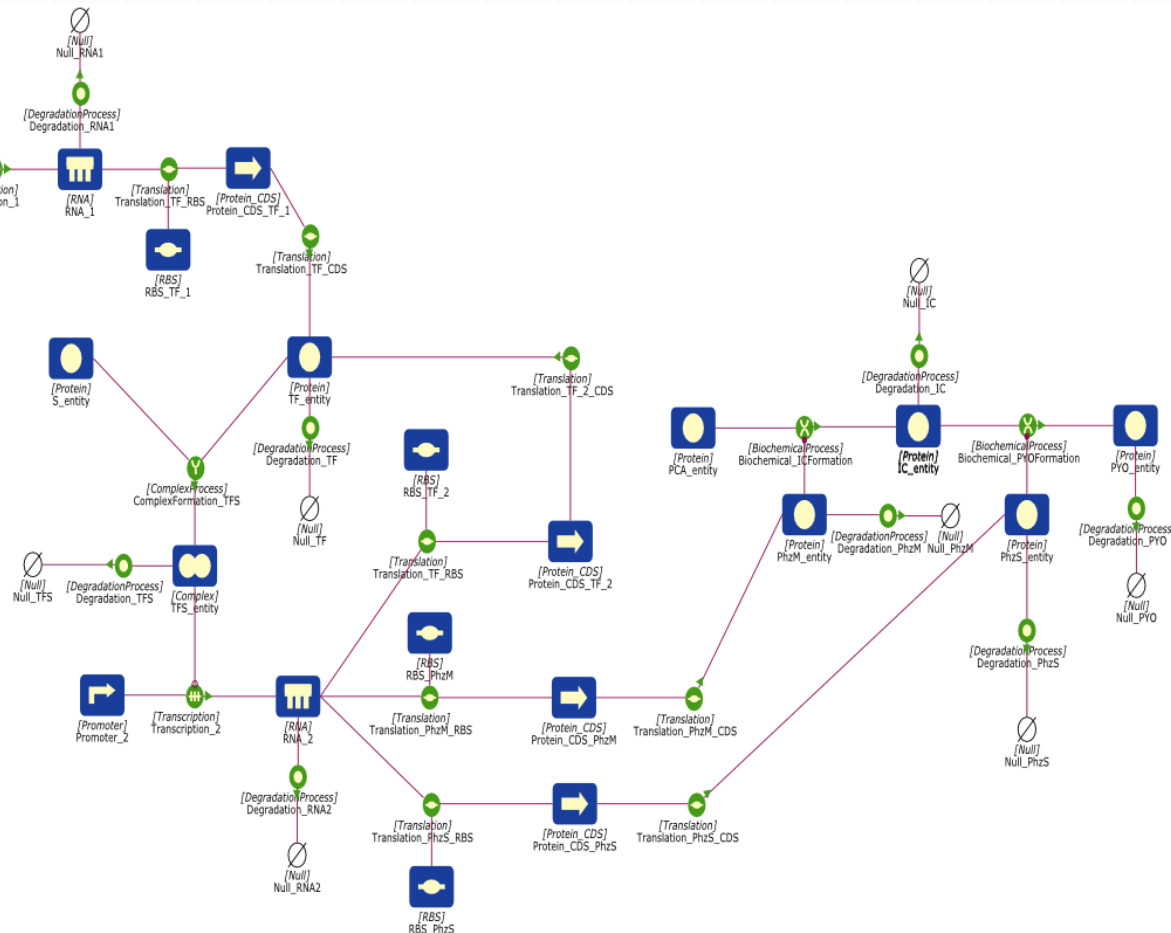
Wimala

Nielsen

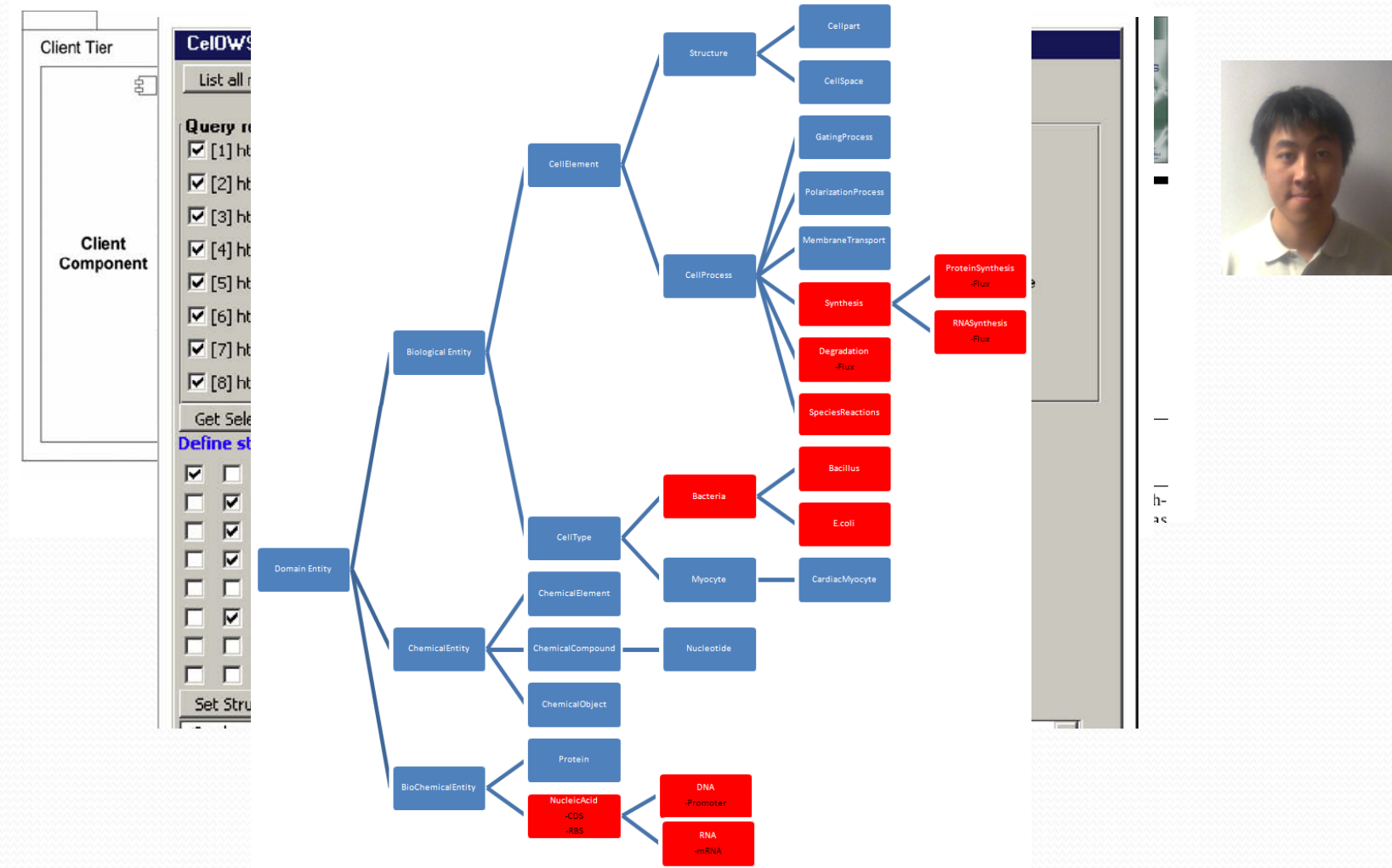
¹Auckland

²Department

Associate



(Semi-Automated) Composition





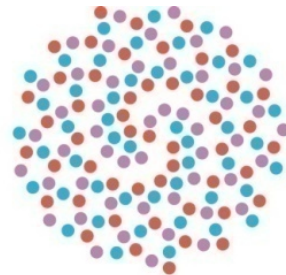
Summary

- Constructing libraries of modular reusable components in CellML
- Building larger models from those parts
- Goal: to make it easier to build and understand large models from reusable components.
 - Visualisation
 - Composition
 - Ontologies
 - Tools
- Practices not perfect....

Funding



wellcometrust



MAURICE WILKINS CENTRE
FOR MOLECULAR BIONICS



RESEARCH
COUNCILS UK