



Edinburgh Pathway Notation

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SBGN-1

**Edinburgh Centre for
Bioinformatics**





University of Edinburgh

- Scottish Centre for Genome Technology and Informatics (GTI)
 - Peter Ghazal
 - Stuart Moodie
- Edinburgh Centre for Bioinformatics
 - Igor Goryanin
 - Anatoly Sorokin



Interferon Pathway Biology Project

- Interferon response pathway in macrophage
- Have collated >200 components of pathway from literature
- 3 years of MSc students
- Each interaction has provenance info
- Developing scoring scheme



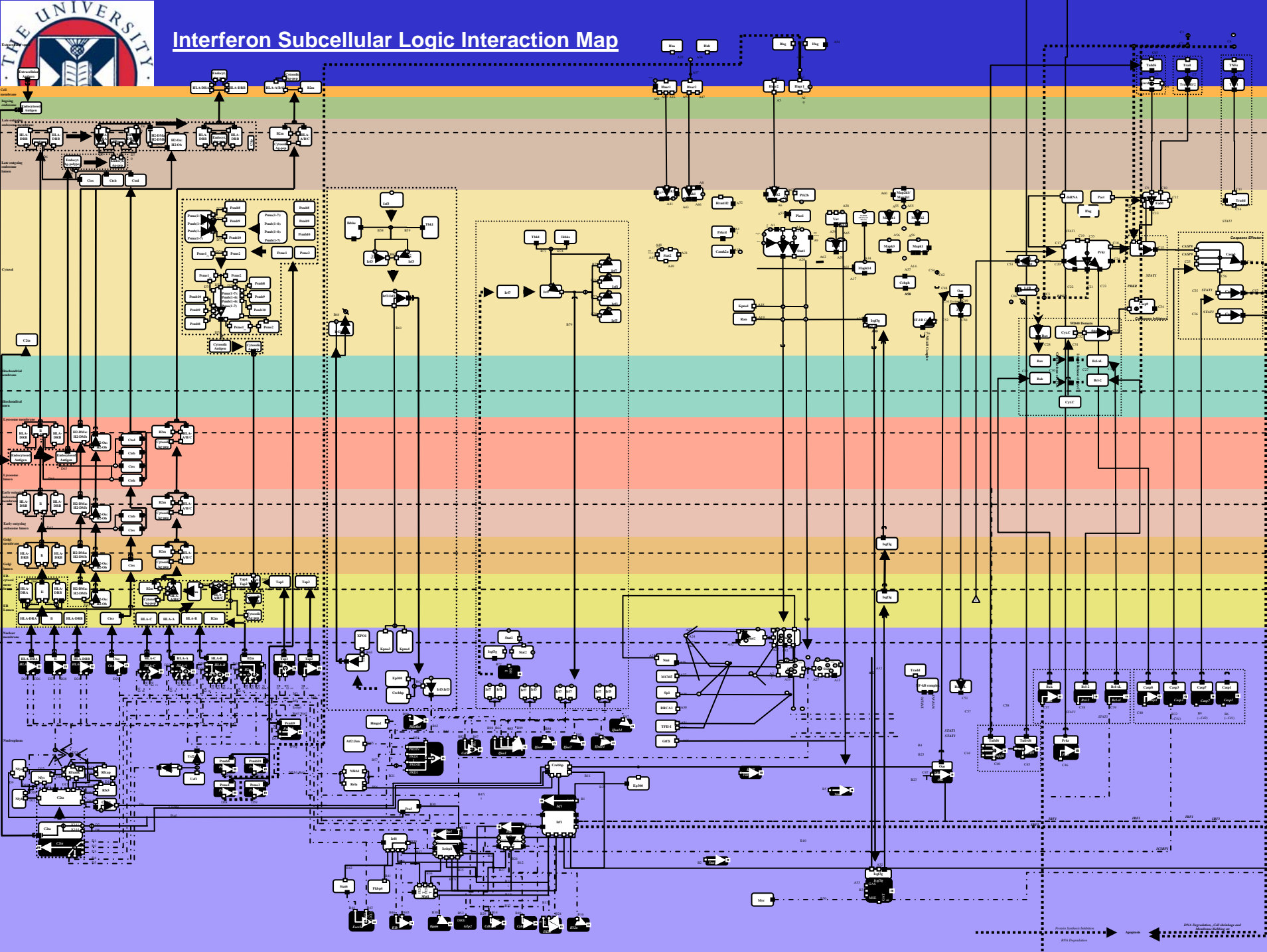
Objectives

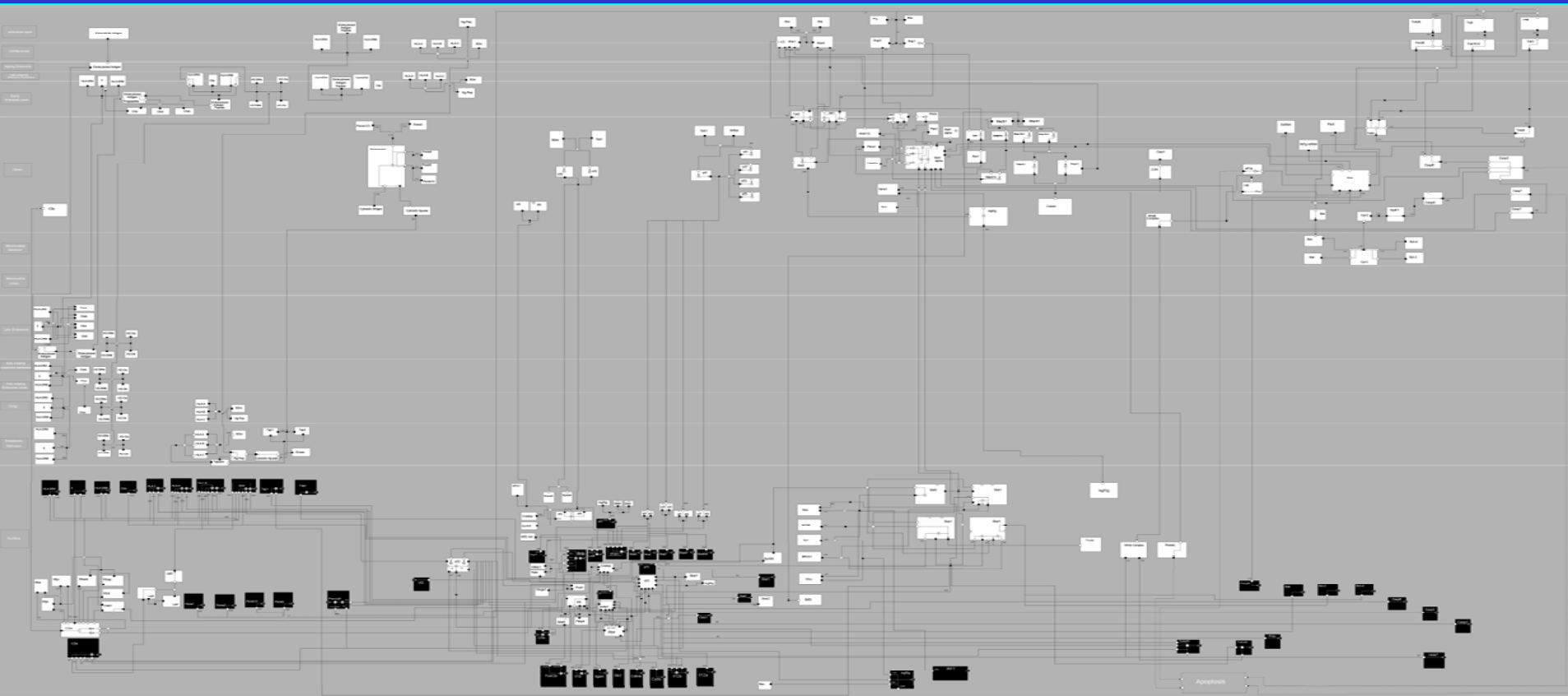
- To develop new approaches and understanding in Pathway Biology of infection and innate immunity
- Integration of HTP experimental data (high dimensional biology) with in silico pathway analysis
- Build a knowledge base using consensus pathway and logic interactions



Notation

- Use graphical representation of pathway
- Evolved a notation through use





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Aims of Notation

- Accessible to biologists
- Described logic of interactions
- Compact
- Showed subcellular localisation clearly
- Tolerant of incomplete knowledge
- Computable
 - Software tools
 - Maps to SBML



Design Principles

- Describe state of interacting species
 - Localisation, Complexes, Activation, Modification
- Minimise redundancy
- Minimise number of symbols and concepts to remember
- Focus on logic



Different Views

Logical

Edinburgh Process Notation

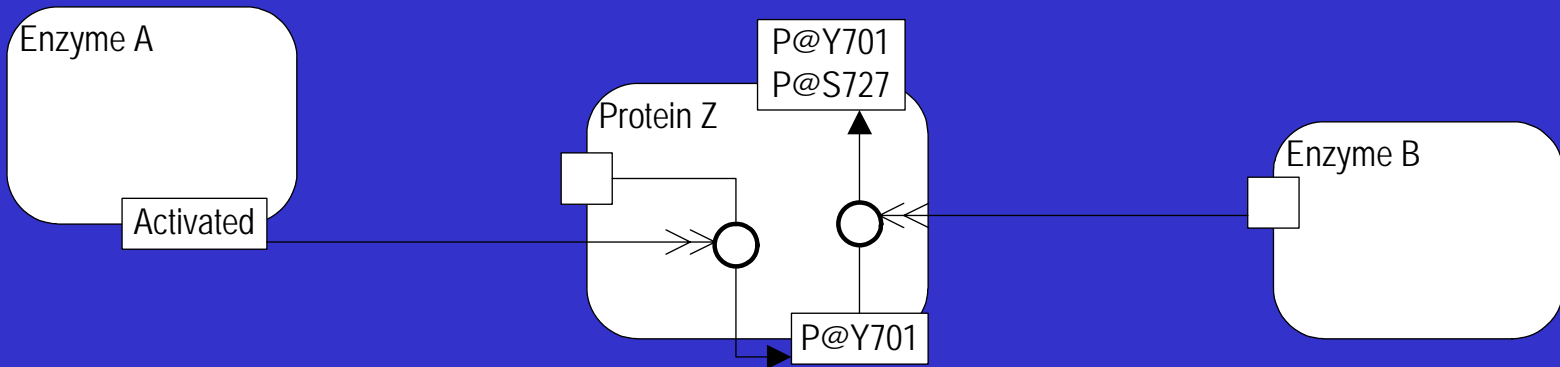
Biochemical

Kitano/MIM

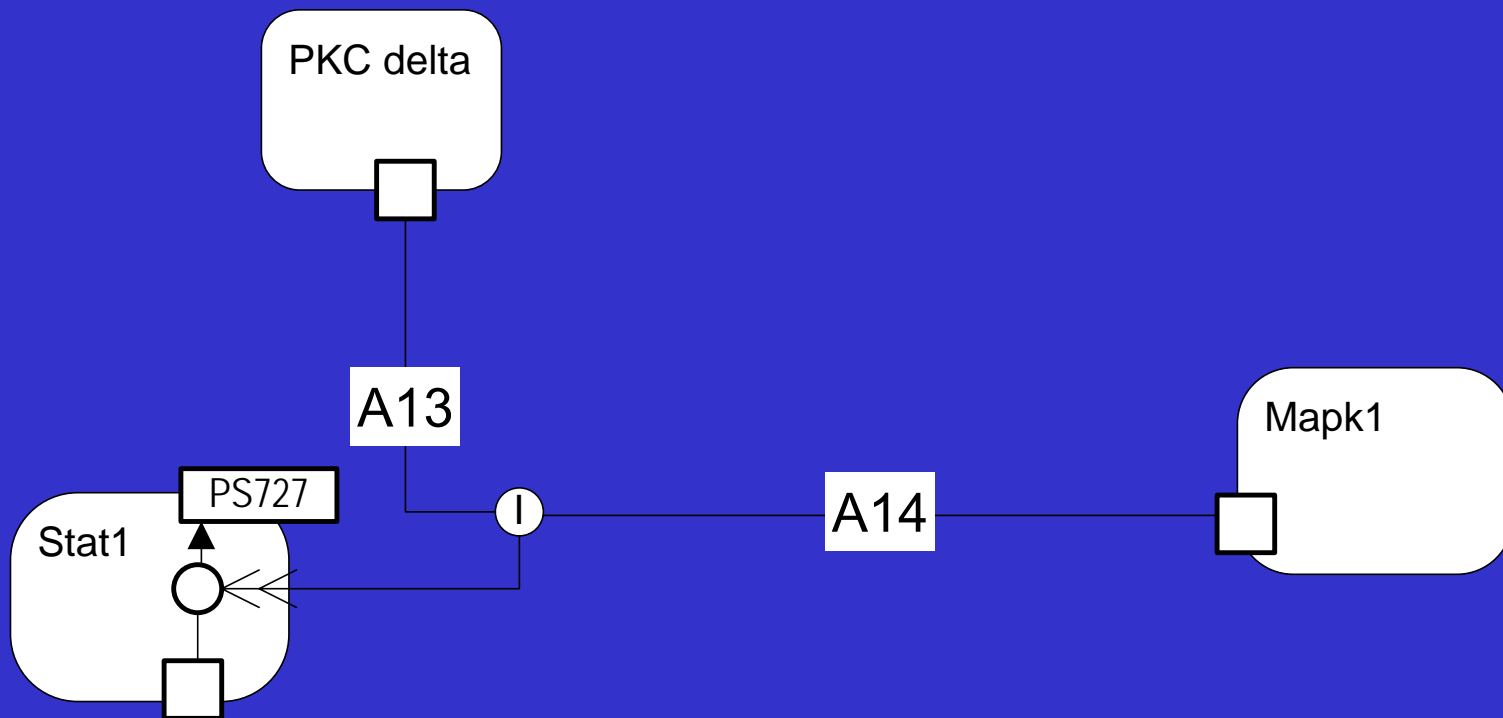
Metabolic



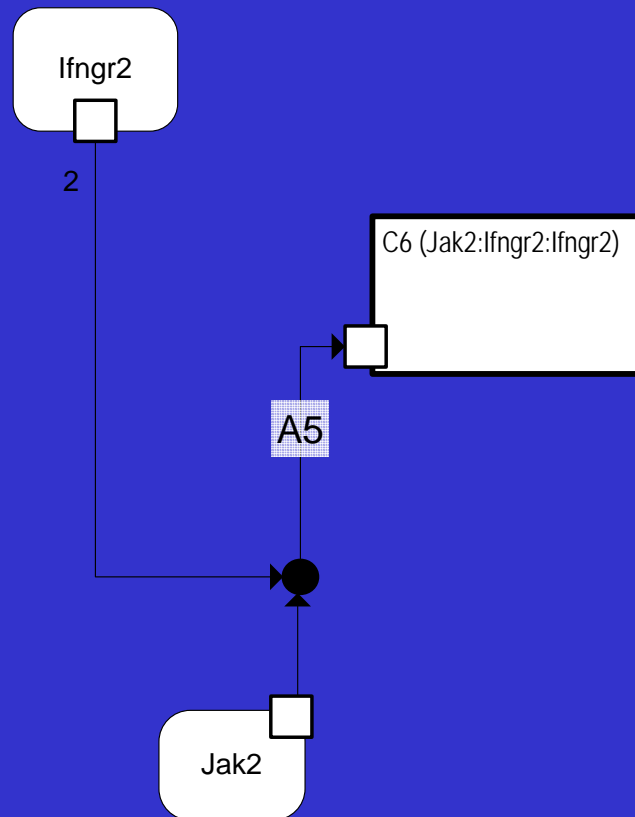
State Transition/Activation



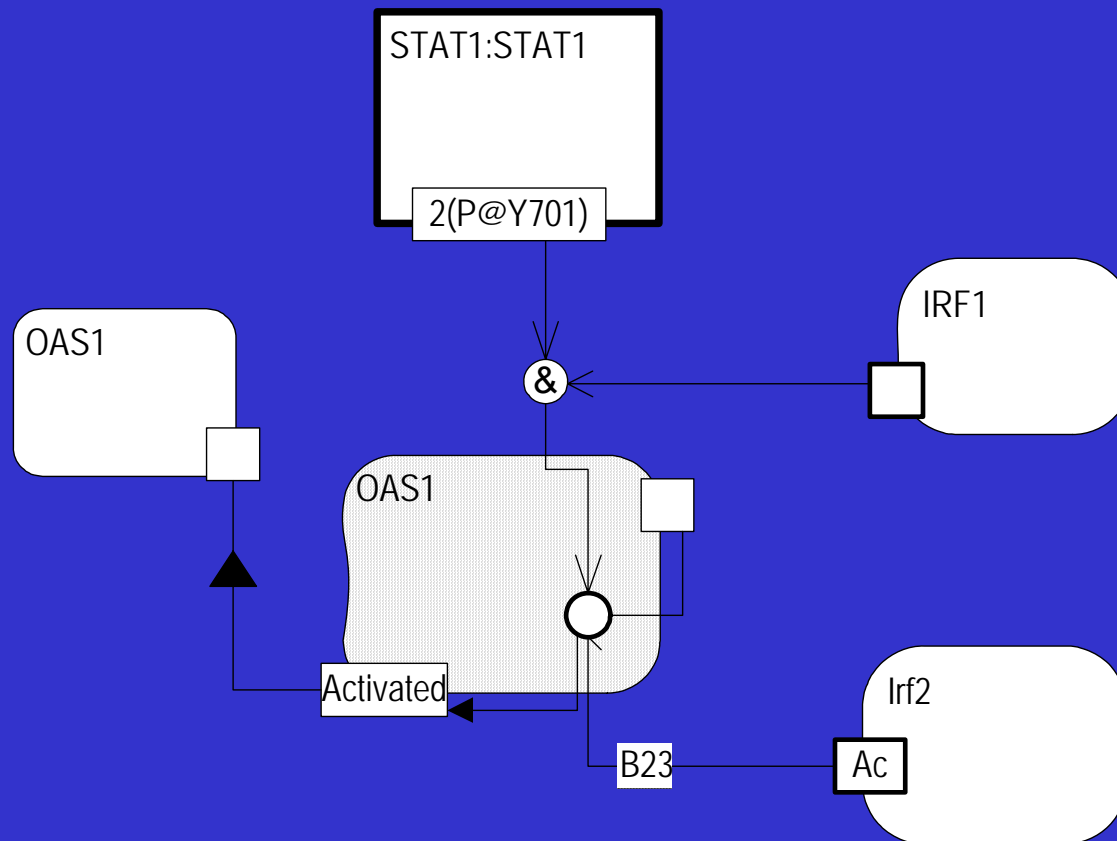
Logic Gates



Complex Formation

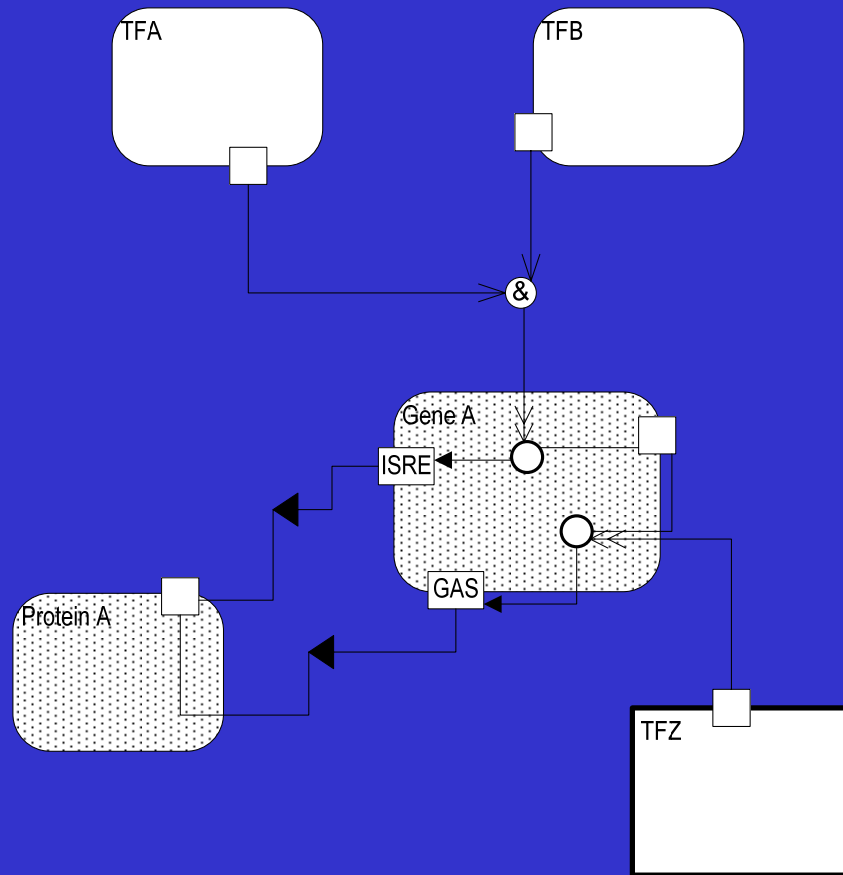


Gene Regulation

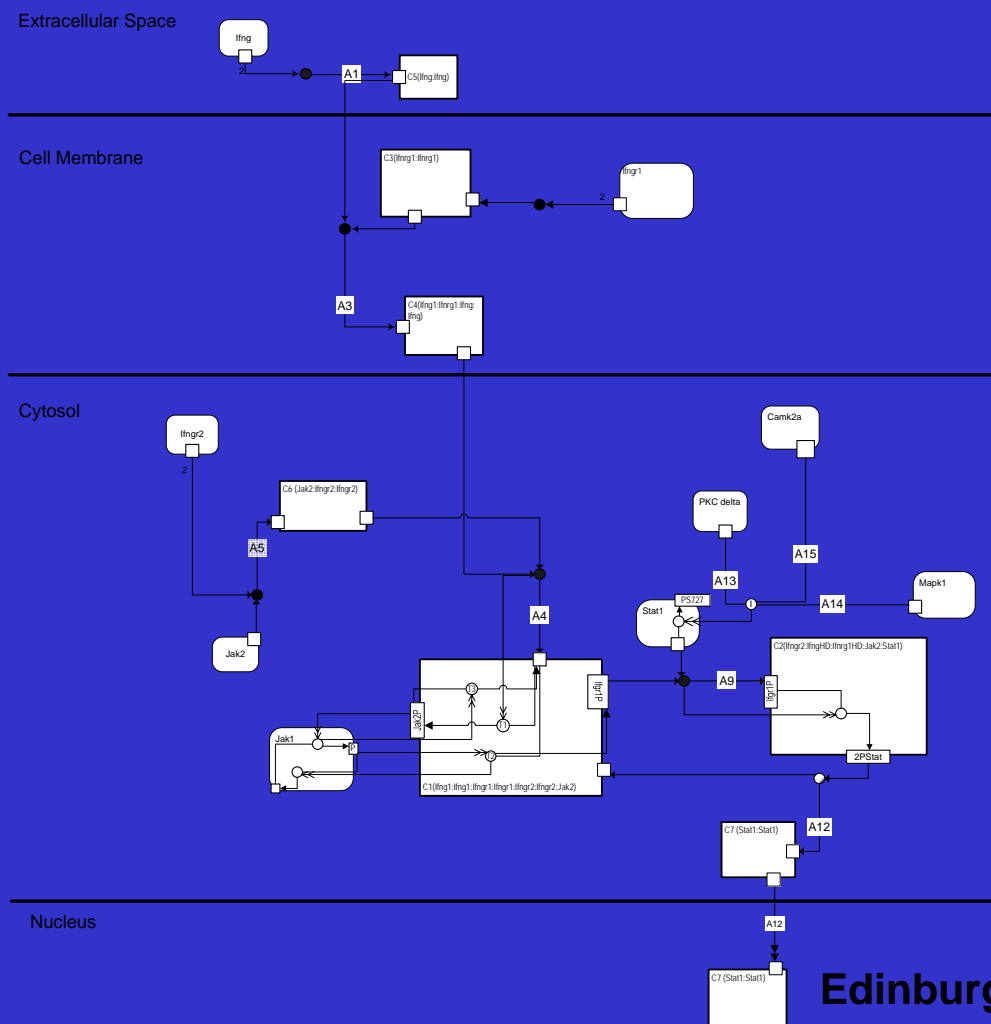




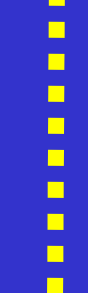
Gene Regulation: Multiple States



Localisation

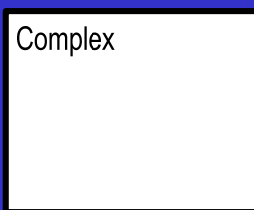
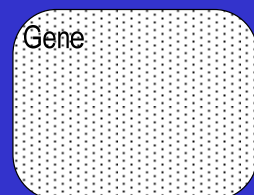


Outside



Inside

Symbols



State

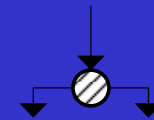
State
Transition

OR

AND

XOR

NOT



Absolute
Activation

Activation

Inhibition

Gene
Expression

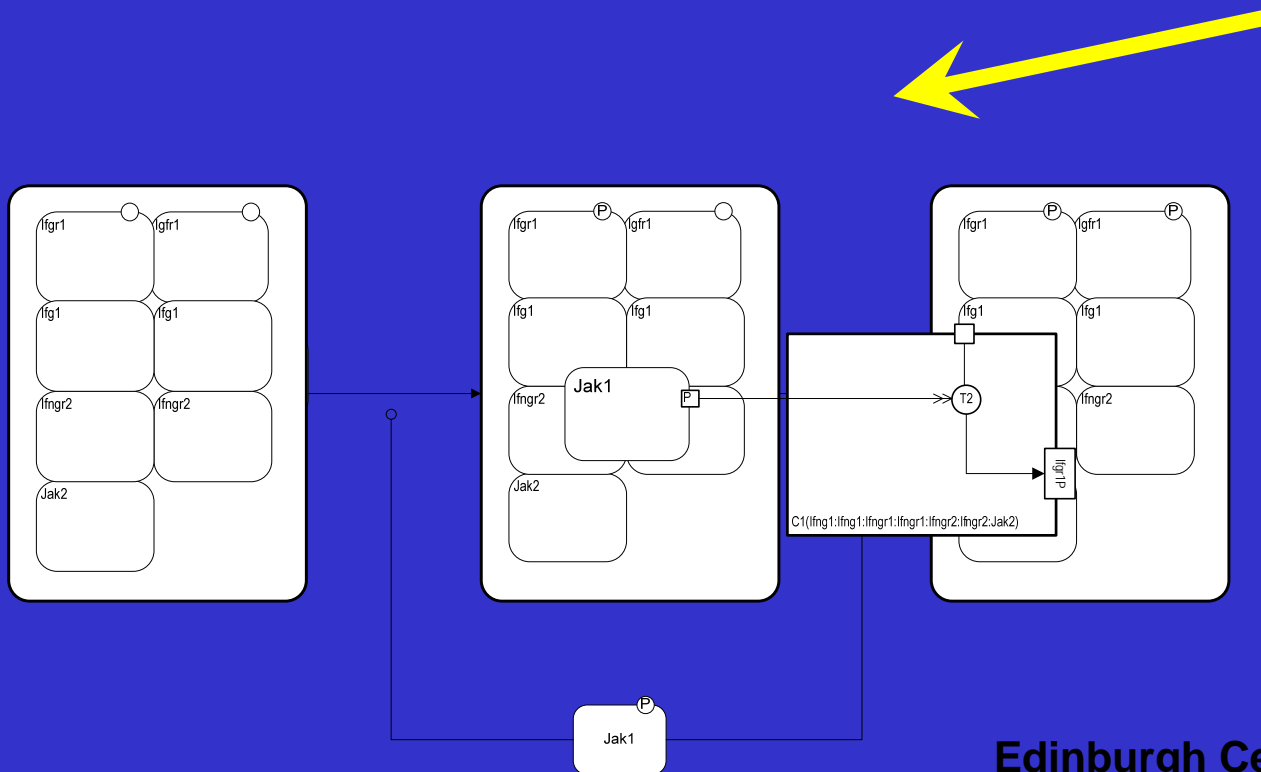
Complex
Formation

Dissociation

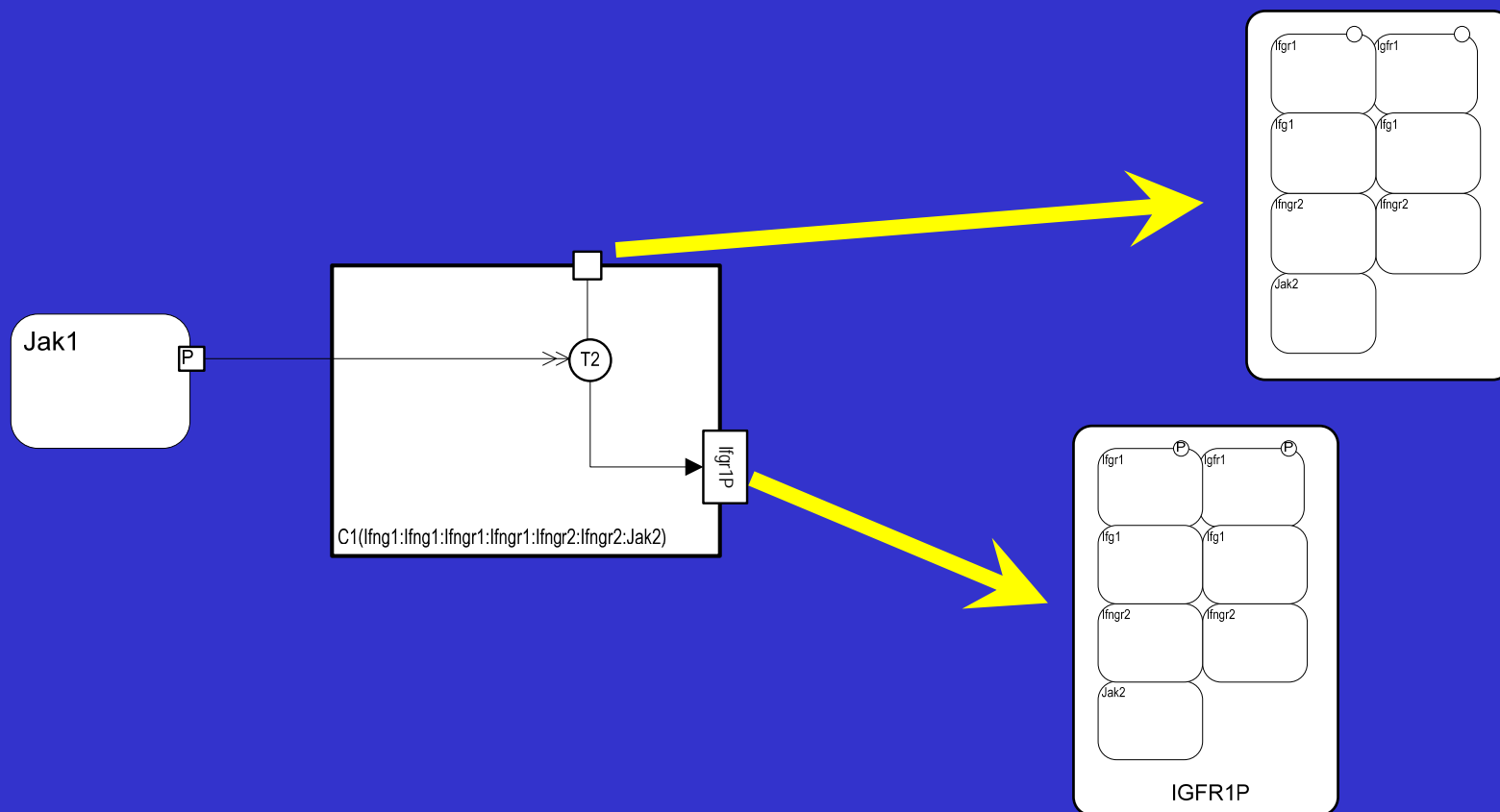
Translocation

State transition: the hidden details

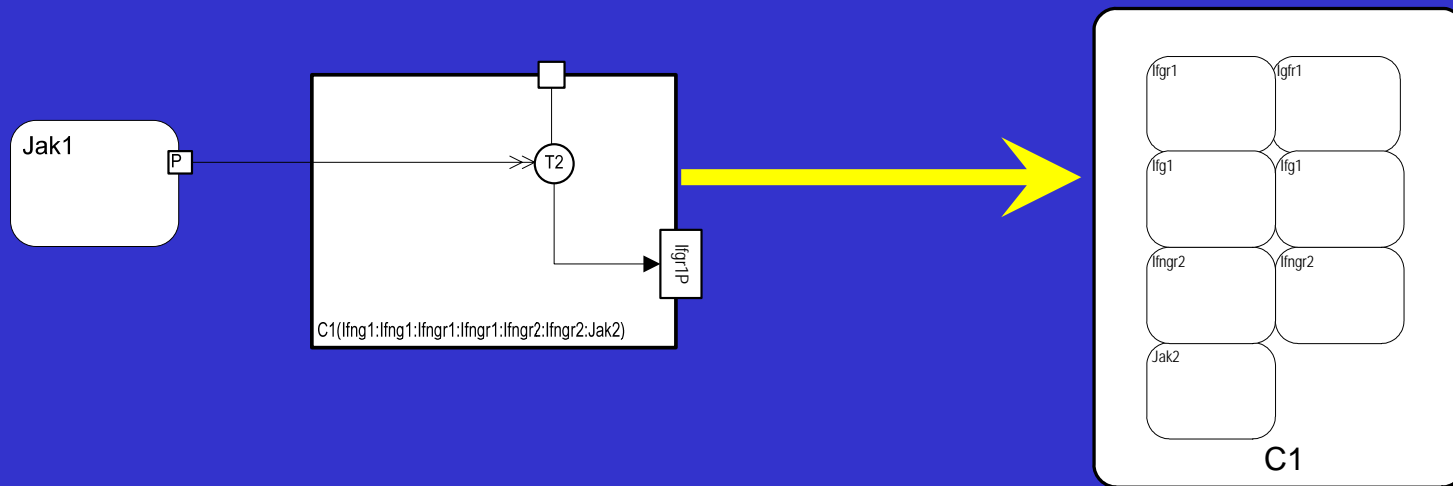
- Kitano process notation



State Details



Complex Details

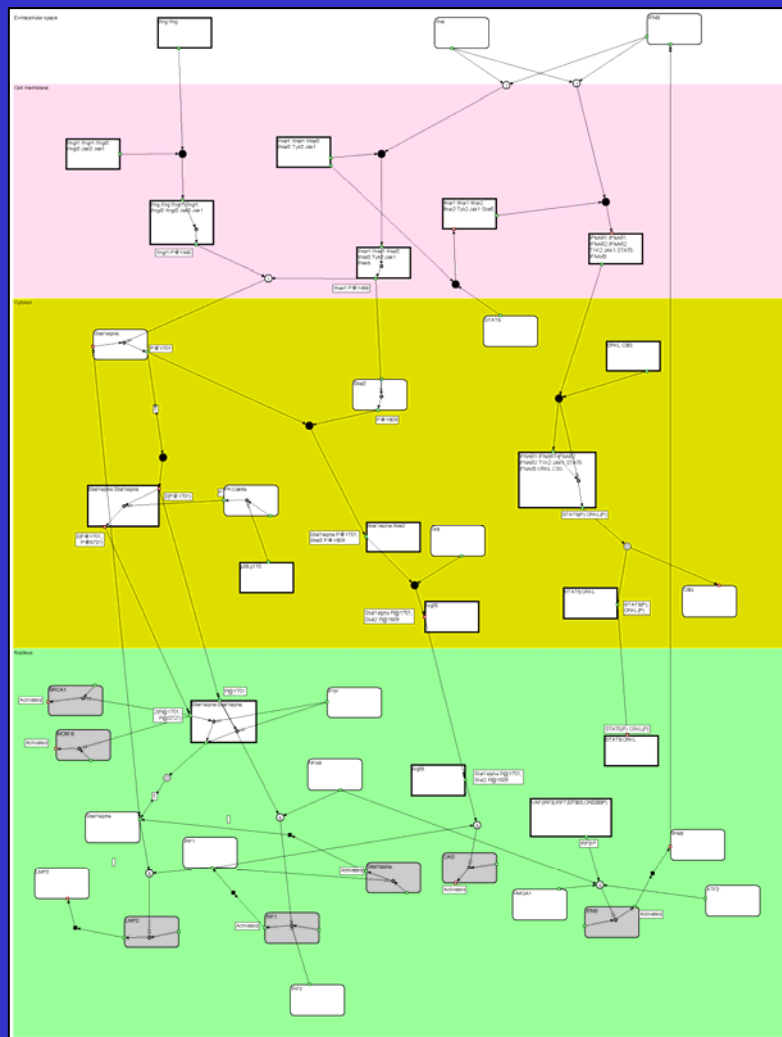




Tool Support: EPE

- Supports full notation
- Supports Kitano notation
- Hyperlinks to sub-diagrams
- Generates SBML map of notation

Jak/Stat





Benefits

- Simple
- Compact
- Quick to draw large maps
- Enables hierarchical organisation
- Links to biochemical notation
- Software support



Future Work

- Continue “Field test” notation
- Metabolic pathways
- mRNA regulation (miRNA)
- Pathway “modules”



Acknowledgements

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Questions?

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