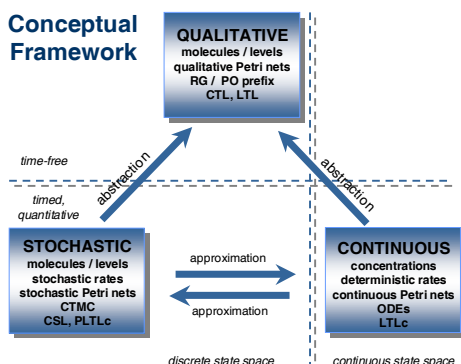
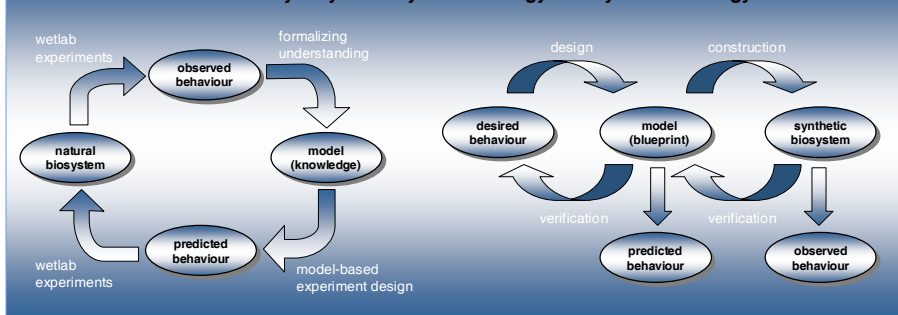


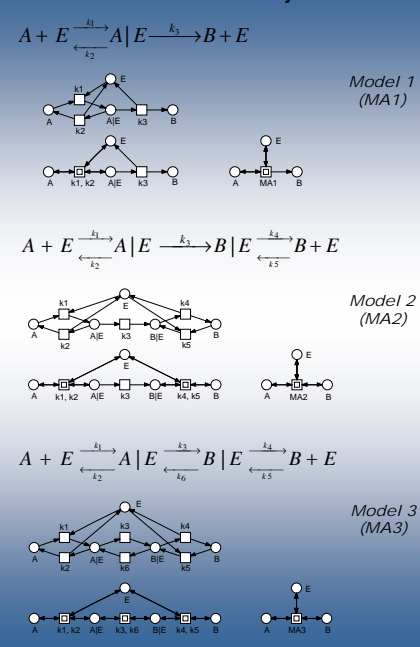
### Conceptual Framework



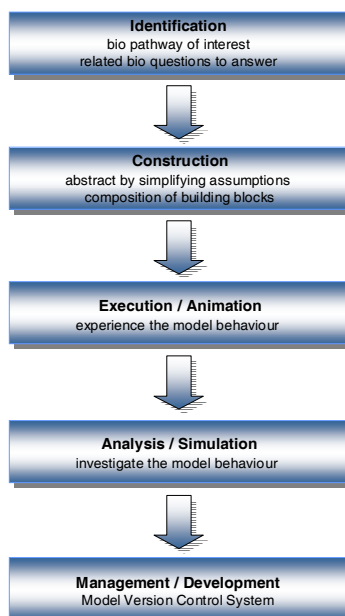
### Models as Key Players in Systems Biology and Synthetic Biology



### Mass / Action Patterns for Enzyme Reactions



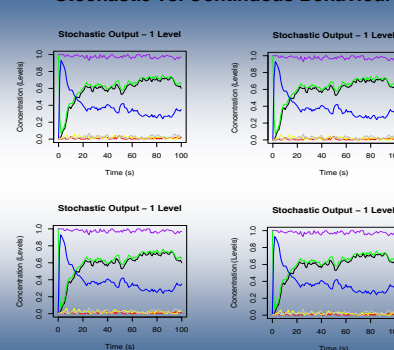
### Engineering Computational Models of Biological Systems



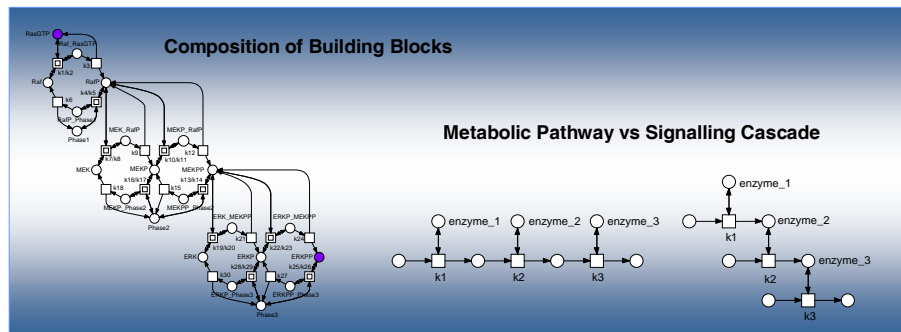
### STATIC ANALYSIS

place invariants (moieties)  
transition invariants (EMs / EPs)  
input / output relationships, pathway length, etc.  
modularisation / decomposition into subnetworks  
correlated subsets, flux-coupling assessment  
identification of bottlenecks / fragile nodes  
design of knockout experiments  
initial marking (state) construction  
semi-decision of general behavioural properties, etc.

### Stochastic vs. Continuous Behaviour



### Composition of Building Blocks



### Bio network model

### TL properties

behaviour description  
RG / CTMC  
simulation traces  
wetlab data

**MODEL CHECKERS**

**Exact / Simulative  
Behaviour Checking**

probability

### References

#### Methodology

- [1] R Breitling, D Gilbert, M Heiner, R Orton:  
A structured approach for the engineering of biochemical network models, illustrated for signalling pathways; Briefings in Bioinformatics 2008.
- [2] M Heiner, D Gilbert, R Donaldson:  
Petri Nets for Systems and Synthetic Biology; Springer LNCS 5016, 2008.

#### Case Studies

- [3] D Gilbert, M Heiner, S Rosser, R Fulton, X Gu, M Trybilo:  
A Case Study in Model-driven Synthetic Biology; IFIP WCC 2008/BICC, IFIP 2008.
- [4] D Gilbert, M Heiner, S Lehrack:  
A Unifying Framework for Modelling and Analysing Biochemical Pathways Using Petri Nets; Springer LNCS/LNBI 4695, 2007.
- [5] D Gilbert, M Heiner:  
From Petri Nets to Differential Equations - an Integrative Approach for Biochemical Network Analysis; Springer LNCS 4024, 2006.