

Abstract Machines of Systems Biology

Luca Cardelli

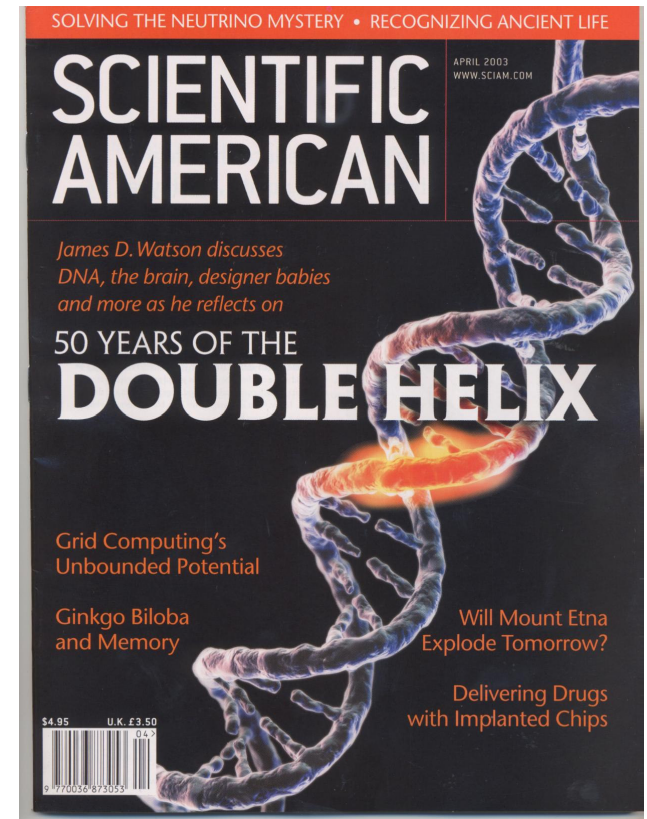
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50 Years of Molecular Cell Biology

- **Genes are made of DNA**
 - Store digital information as sequences of 4 different nucleotides
 - Direct protein assembly through RNA and the Genetic Code
- **Proteins (>10000) are made of amino acids**
 - Process signals
 - Activate genes
 - Move materials
 - Catalyze reactions to produce substances
 - Control energy production and consumption
- **Bootstrapping still a mystery**
 - DNA, RNA, proteins, membranes are today interdependent. Not clear who came first
 - Separation of tasks happened a long time ago
 - Not understood, not essential



Towards Systems Biology

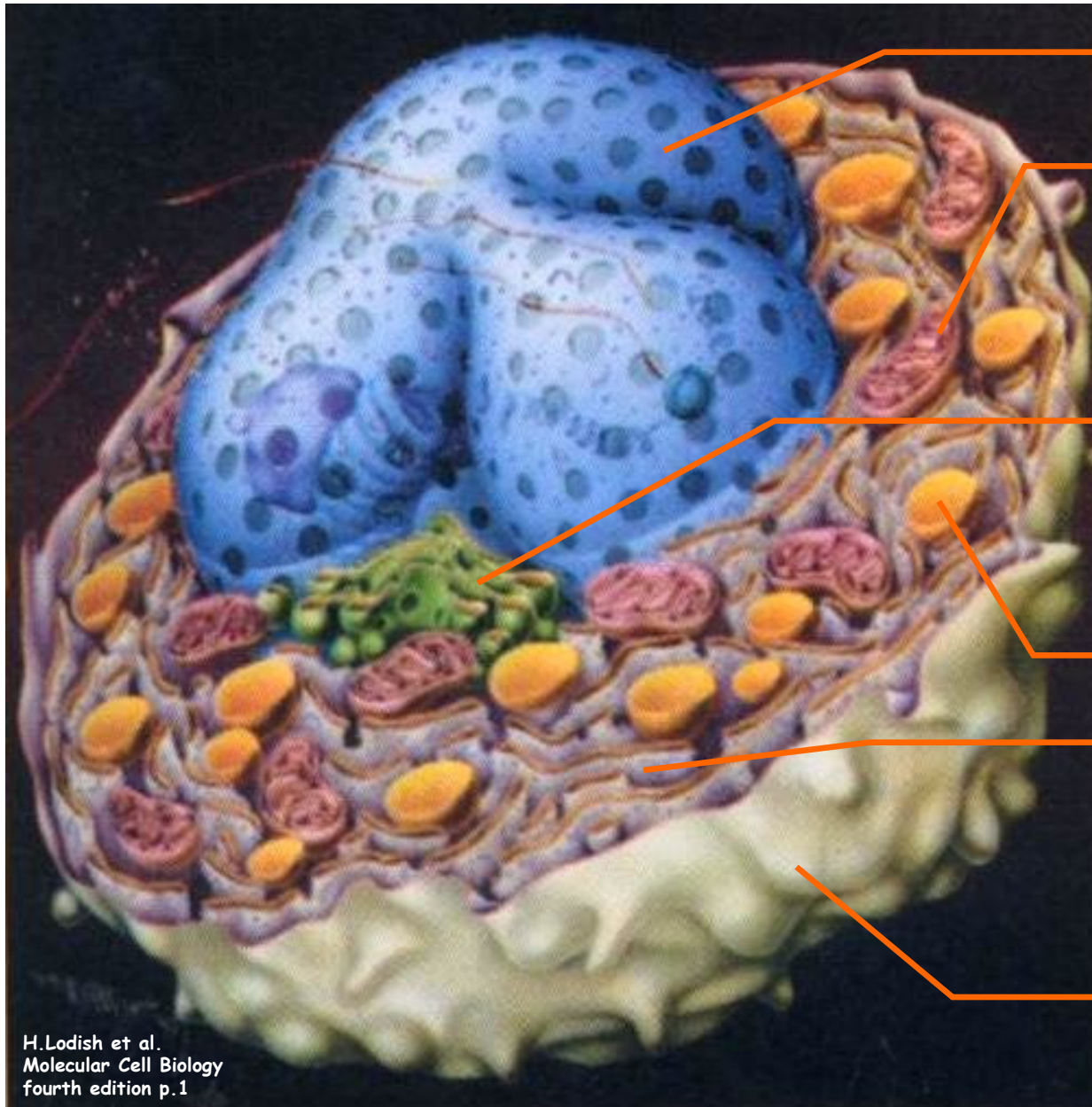
- Biologists now understand many of the cellular components
 - A whole team of biologists will typically study a single protein for years
 - When each component and each reaction is understood, the system is understood (?)
- But this has not led to understand how "the system" works
 - Behavior comes from complex chains of interactions between components
 - Predictive biology and pharmacology still rare
 - Synthetic biology still unreliable
- New approach: try to understand "the system"
 - Experimentally: massive data gathering and data mining (e.g. Genome projects)
 - Conceptually: modeling and analyzing networks (i.e. interactions) of components
- What kind of a system?
 - Just beyond the basic chemistry of energy and materials processing...
 - Built right out of digital information (DNA)
 - Based on information processing for both survival and evolution
- Can we fix it when it breaks?
 - The question really becomes: How is information structured and processed?

Structural Architecture

Eukaryotic Cell

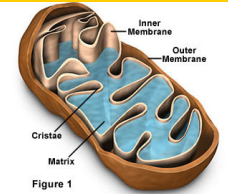
(10~100 trillion in human body)

Membranes everywhere

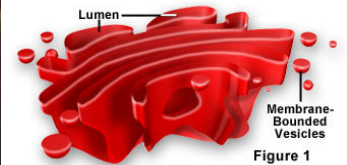


Nuclear membrane

Mitochondria

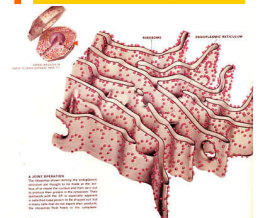


Golgi



Vesicles

E.R.



Plasma membrane (<10% of all membranes)

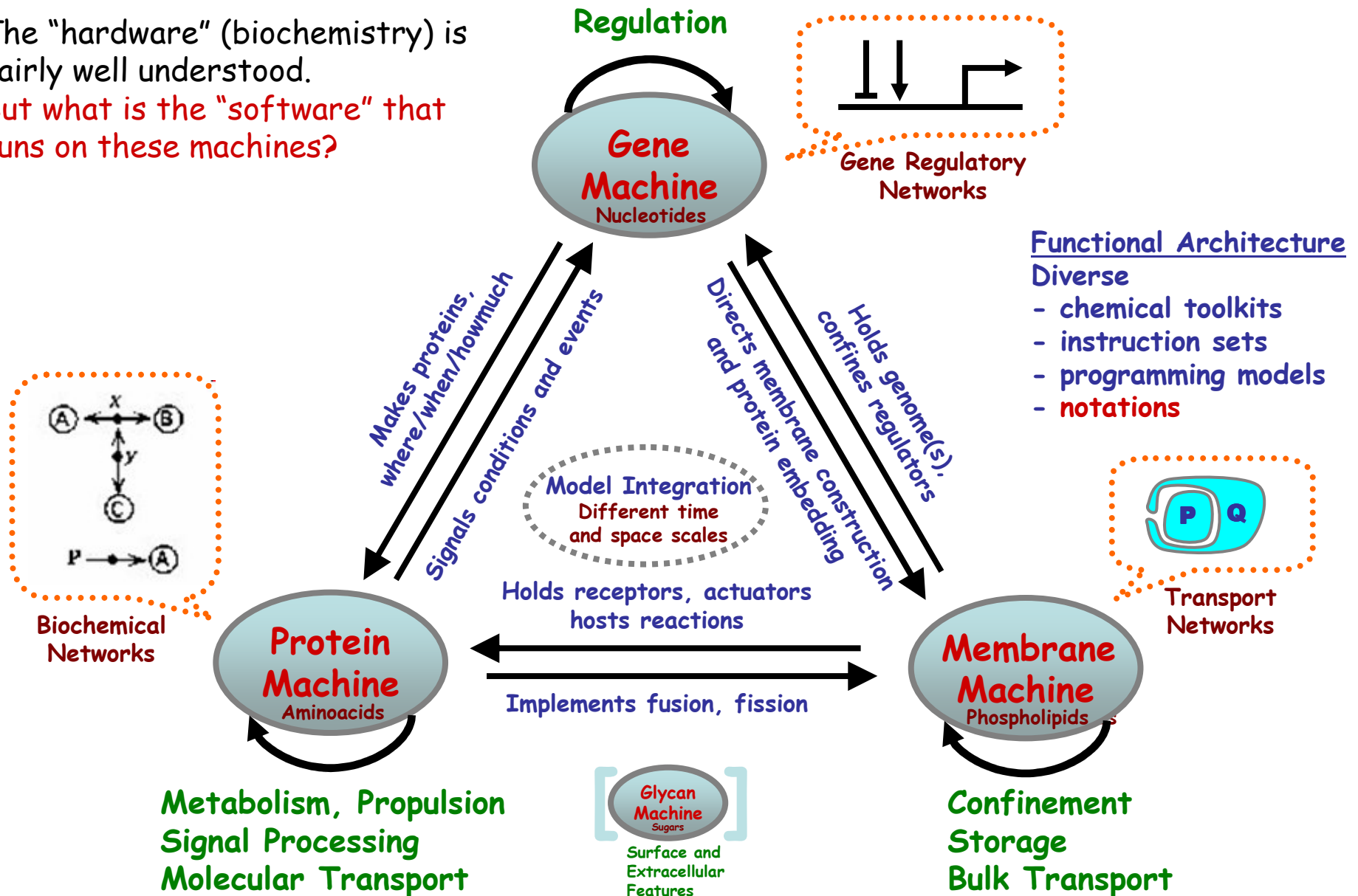


H.Lodish et al.
Molecular Cell Biology
fourth edition p.1

Abstract Machines of Systems Biology

The "hardware" (biochemistry) is fairly well understood.

But what is the "software" that runs on these machines?



Metabolism, Propulsion
Signal Processing
Molecular Transport

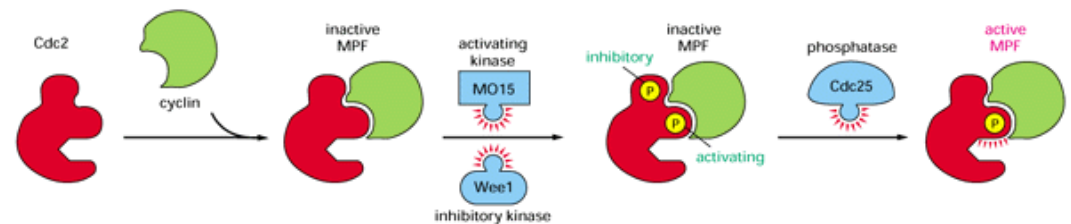
Confinement
Storage
Bulk Transport

Surface and Extracellular Features

1. The Protein Machine

Very close to the atoms.

- **Complex folded-up shapes that:**
 - Fit together, dock, undock.
 - Excite/unexcite, warp each other.
 - Bring together, catalyze, transform materials.
 - Form complex aggregates and networks.



- **Mapping out such networks:**
 - In principle, it's "just" a very large set of chemical equations.
 - Notations have been developed to summarize and abstract.

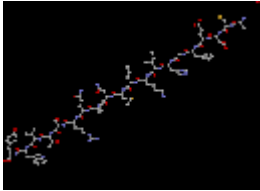


An actual molecular interaction network.

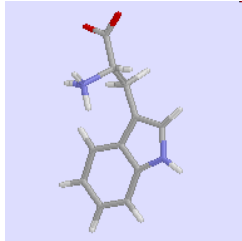
(Nodes are distinct protein kinds, arcs mean that two kinds of proteins interact.)

Protein Structure

Primary

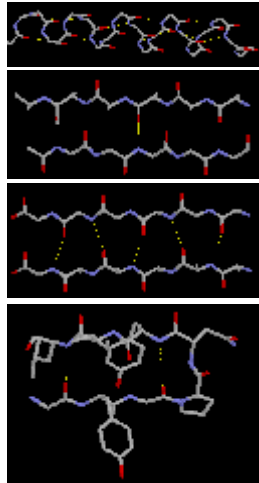


The 20 Aminoacids



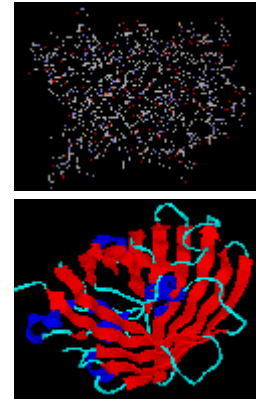
Tryptophan

Secondary



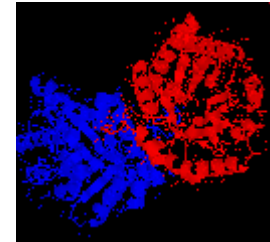
Alpha Helix, Beta Sheet

Tertiary



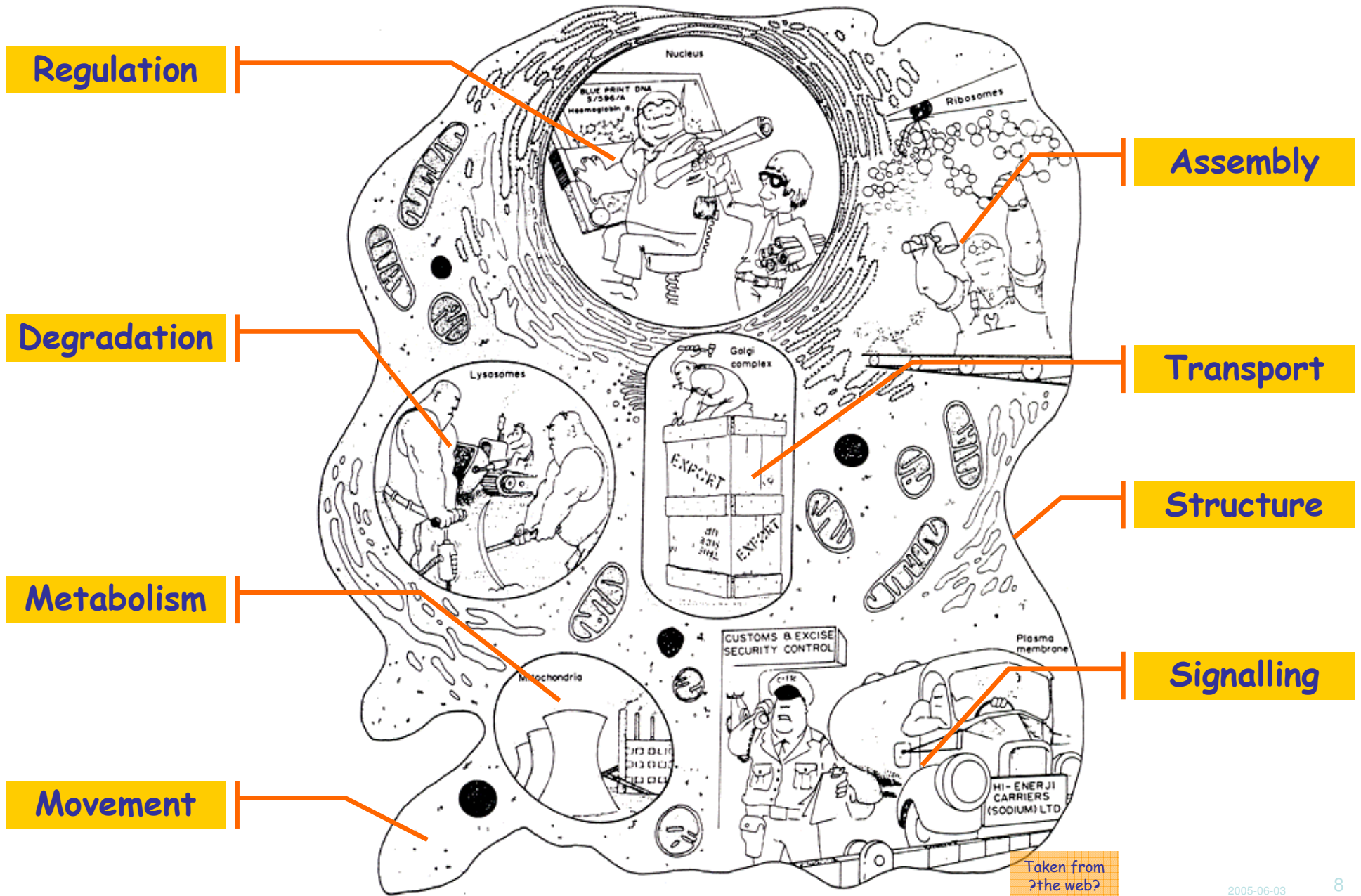
Green Fluorescent Protein

Quaternary



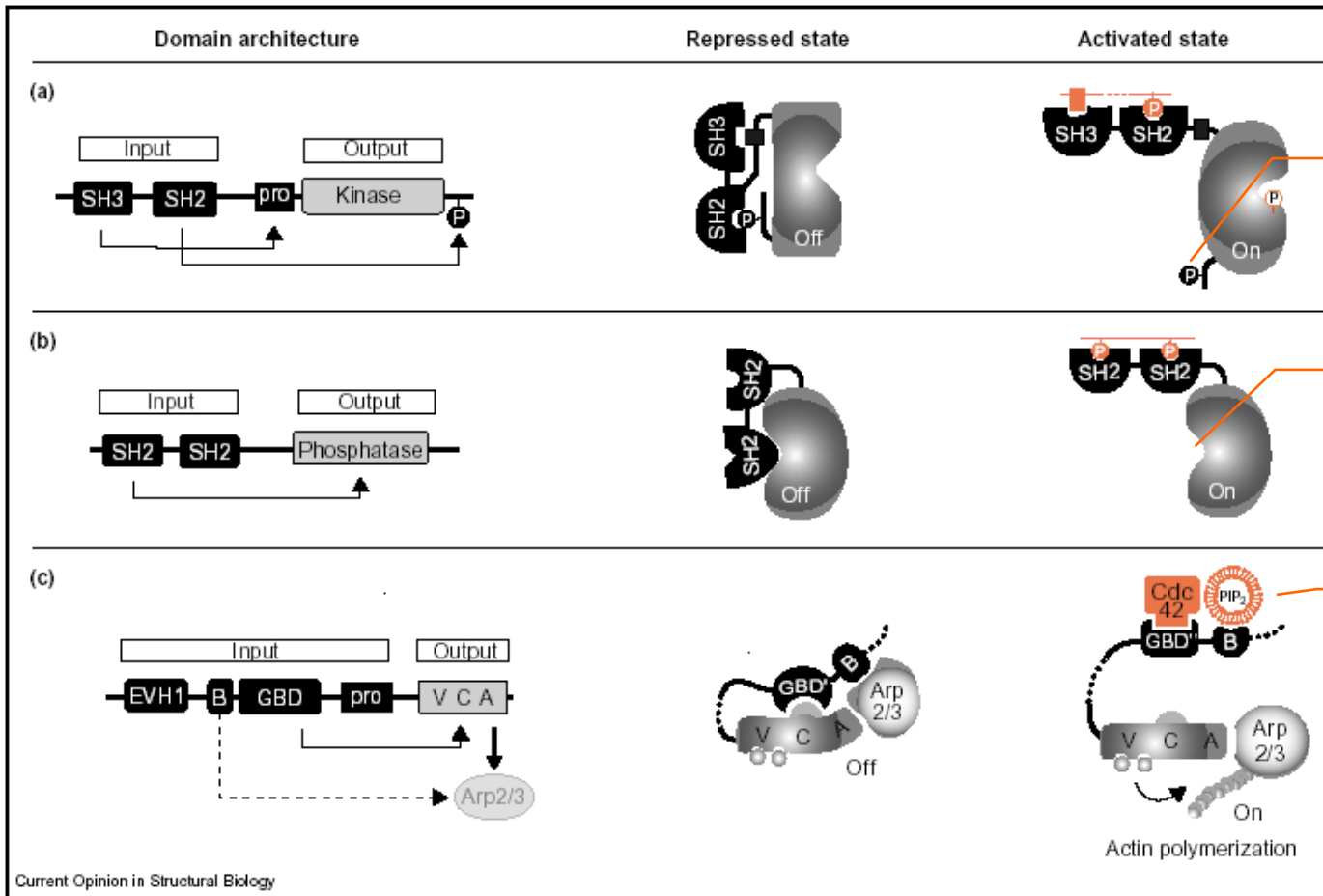
Triose Phosphate Isomerase

Protein Function



Taken from
?the web?

Some Allosteric Switches



Allosteric ("other shape") reactions modify accessibility.

Kinase

= donates phosphate P
= phosphorylates other proteins

Phosphatase

= accepts phosphate P
= dephosphorylates other proteins

Logical AND

at equal concentrations of the individual input stimuli, activation is much higher if both stimuli are present

"Phosphatase Kinase Kinase" = a kinase that activates a kinase that activates a phosphatase that deactivates a protein.

Domain architecture and autoinhibitory interactions in modular switch proteins. (a) Src family kinases contain N-terminal SH3 and SH2 domains, and a kinase domain flanked by intramolecular SH3-binding and SH2-binding sites (when the C-terminal motif tyrosine is phosphorylated by Csk). The crystal structures of several family members show that both intramolecular domain interactions function in concert to lock the kinase in an inactive conformation. Activating stimuli (red) include external SH2 or SH3 ligands. After initial activation, the kinase is maintained in an active state by autophosphorylation of its activation loop. (b) SHP-2 phosphatase contains two SH2 domains and a phosphatase domain. The crystal structure of the phosphatase

shows that the N-terminal SH2 domain participates in an autoinhibitory interaction that directly blocks the phosphatase active site. Binding of external SH2 ligands activates by disrupting the autoinhibitory interaction. (c) N-WASP contains an Enabled VASP homology 1 (EVH1) domain, a B motif, a GBD, a proline-rich segment (pro) and an output region (VCA) that alone binds the Arp2/3 complex and stimulates its actin nucleation activity. The B and GBD motifs are required to repress activity and, by current models, are thought to participate in intracomplex interactions (only the structure of the GBD intramolecular complex for WASP is known). GTP-bound Cdc42 and PIP₂ synergistically activate N-WASP.

Humans have the same number of modular protein domains (building blocks) as worms, but twice the number of multi-domain proteins.

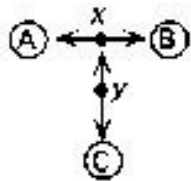
MIM: Molecular Interaction Maps (Kohn)



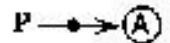
The double-headed line indicates that proteins **A** and **B** can bind to each other. The "node" placed on the line represents the **A:B** complex.



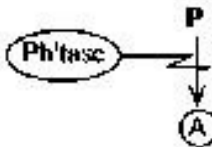
Asymmetric binding where protein **A** donates a peptide that binds to a receptor site or pocket on protein **B**.



Representation of multimolecular complexes: x is **A:B**; y is **(A:B):C**. This notation is extensible to any number of components in a complex.



Covalent modification of protein **A**. The single-headed line indicates that **A** can exist in a phosphorylated state. The node represents the phosphorylated species.



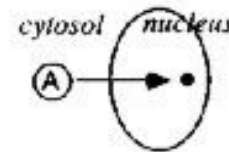
Cleavage of a covalent bond: dephosphorylation of **A** by a phosphatase.



Proteolytic cleavage at a specific site within a protein.



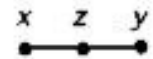
Stoichiometric conversion of **A** into **B**.



Transport of **A** from cytosol to nucleus. The node represents **A** after it has been transported into the nucleus.



Formation of a homodimer. Filled circle on the right represents another copy of **A**. The node on the line represents the homodimer **A:A**.



z is the combination of states defined by x and y .



Enzymatic stimulation of a reaction.



General symbol for stimulation.



A bar behind the arrowhead signifies necessity.



General symbol for inhibition.



Shorthand symbol for transcriptional activation.



Shorthand symbol for transcriptional inhibition.



Degradation products

Taken from
Kurt W. Kohn

Molecular Interaction Maps

<http://www.cds.caltech.edu/~hsauro/index.htm>

JDesigner

The p53-Mdm2 and DNA Repair Regulatory Network

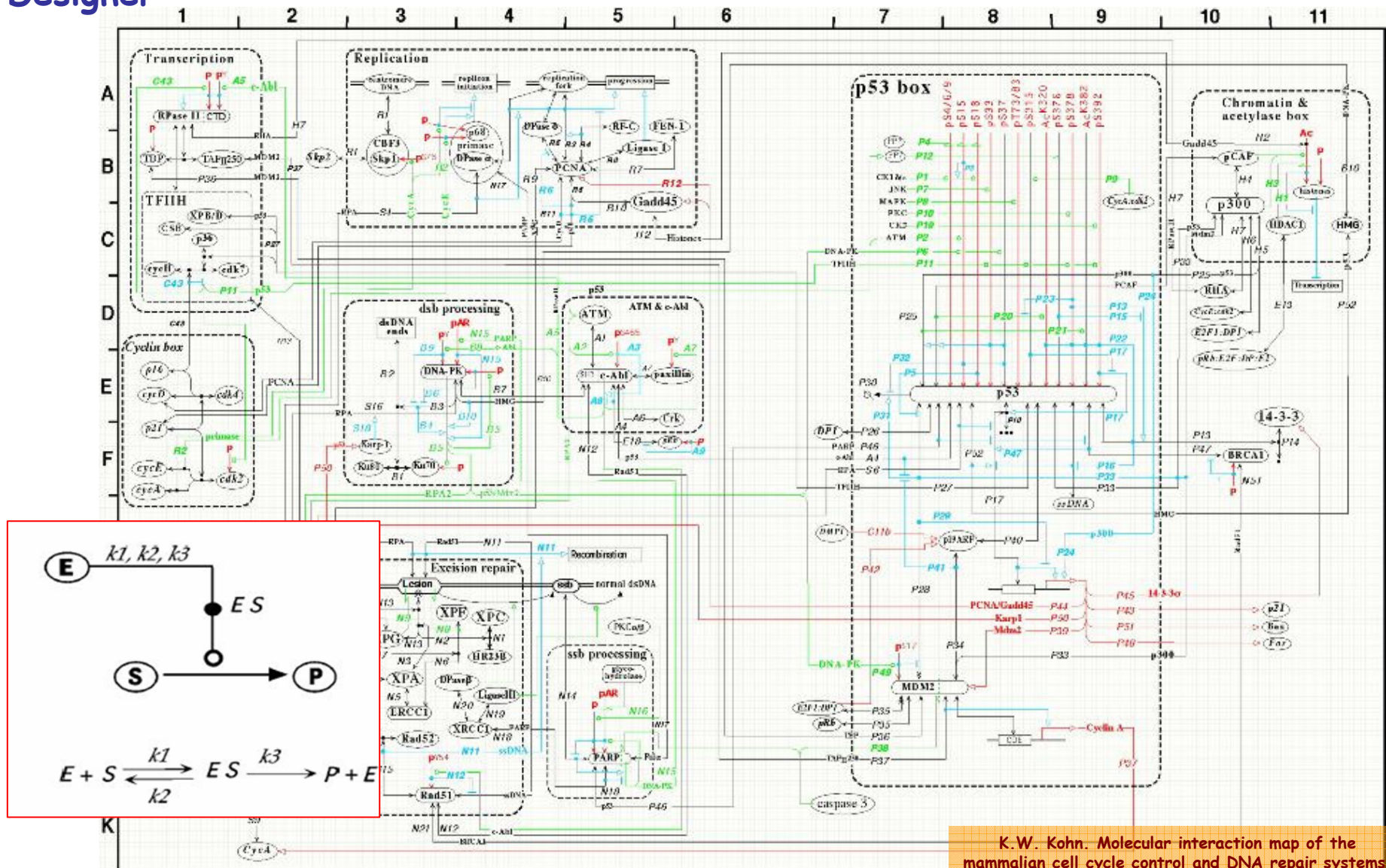
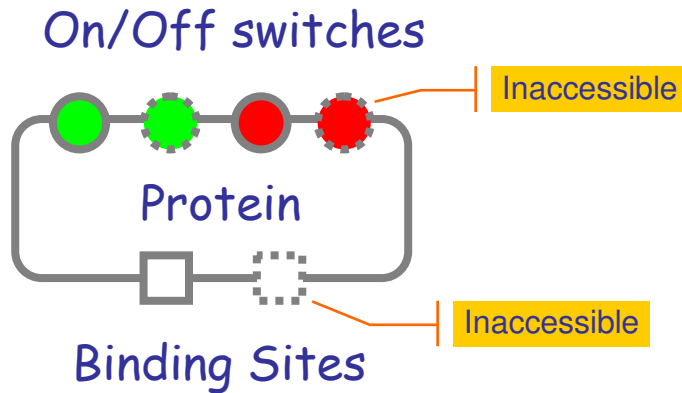


Figure 6B: The p53-Mdm2 and DNA repair regulatory network (version 2p - May 19, 1999)

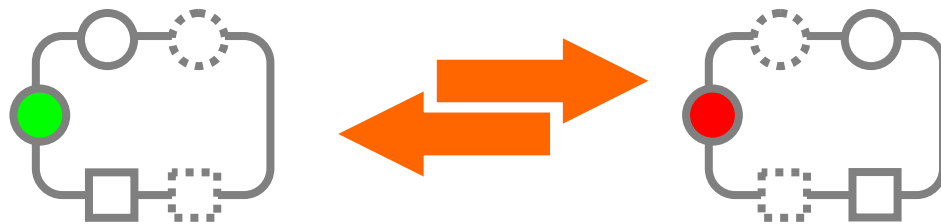
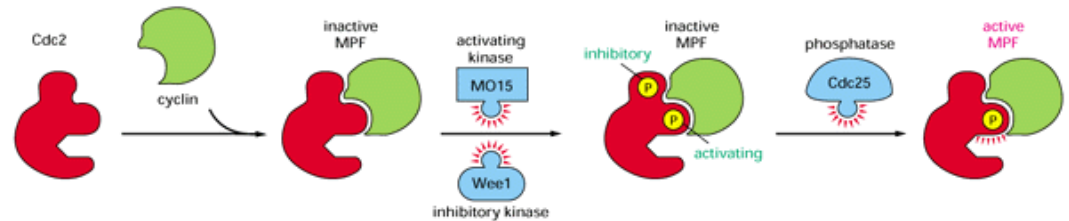
K.W. Kohn. Molecular interaction map of the mammalian cell cycle control and DNA repair systems. *Molecular Biology of the Cell* 10(8):2703-34, 1999.

The Protein Machine "Instruction Set"

cf. BioCalculus [Kitano&Nagasaki], κ -calculus [Danos&Laneve]

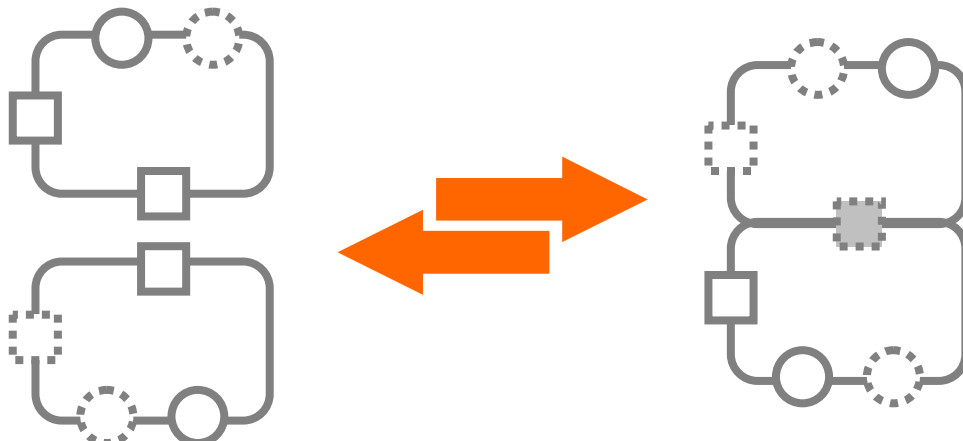


Each protein has a structure of binary switches and binding sites. But not all may be always *accessible*.



Switching of accessible switches.

- May cause other switches and binding sites to become (in)accessible.
- May be triggered or inhibited by nearby specific proteins in specific states.



Binding on accessible sites.

- May cause other switches and binding sites to become (in)accessible.
- May be triggered or inhibited by nearby specific proteins in specific states.

Notations for the Protein Machine

- **Stochastic π -Calculus**
 - Priami (following Hillston's PEPA) formalizes a stochastic version of p-calculus where channels have communication *rates*.
- **BioSPi**
 - Regev-Shapiro-Silverman propose modeling chemical interactions (exchange of electrons and small molecules) as "communication".
 - Standard stochastic simulation algorithms (Gillespie) can be used to run in-silico experiments.
 - Complex formation is encoded via p-restriction.
- **PEPA**
 - Calder Gilmore and Hillston model the ERK pathway.
- **k-calculus**
 - Danos and Laneve (following Kitano's BioCalculus) define a calculus where complex formation is primitive.
- **(Stochastic) Petri Nets**
 - S.Reddy'94 modeling pathways.
 - Srivastava Perterson and Bentley analyze and simulate E.coli stress response circuit.
- **Bio State Charts**
 - Harel uses State Charts to model biological interactions via a semi-graphical FSM notation.
- **Pathway Logic**
 - Talcott-Eker-Knapp-Lincoln use term-rewriting.
- **BioCham**
 - ChabrierRivier-Fages-Soliman use term-rewriting and CLT modelchecking.
- **Kohn Diagrams, Kitano Diagrams**
- **SBML (Systems Biology Markup Language)**
 - XML dialect for MIM's:
 - Compartments (statically nested)
 - Reagents with concentrations
 - Reactions with various rate laws
 - Read and written by many tools via the Systems Biology Workbench protocol

MAPK Cascade

Ultrasensitivity in the mitogen-activated protein cascade, Chi-Ying F. Huang and James E. Ferrell, Jr., 1996, *Proc. Natl. Acad. Sci. USA*, 93, 10078-10083.

Biochemistry: Huang and Ferrell

Proc. Natl. Acad. Sci. USA 93 (1996)

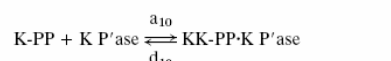
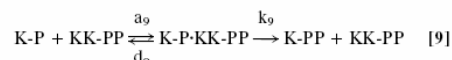
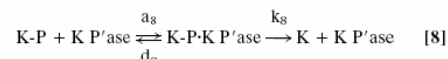
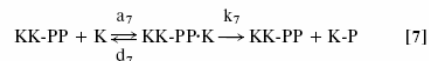
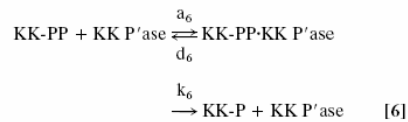
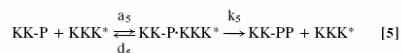
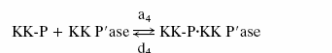
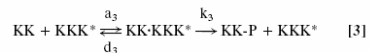
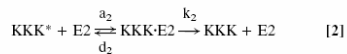
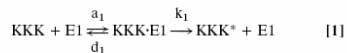
Table 2. Predicted Hill coefficients for MAP kinase cascade components: Varying the assumed K_m values

Reaction	Range of assumed K_m values	Range of effective Hill coefficients (nH) predicted for		
		MAPKKK	MAPKK	MAPK
1. MAPKKK → MAPKKK*	60–1500 nM	1.0	1.7	4.9
2. MAPKKK* → MAPKKK	60–1500 nM	1.0	1.7	4.9
3. MAPKK → MAPKK-P	60–1500 nM	1.0	1.3–2.3	4.0–5.1
4. MAPKK-P → MAPKK	60–1500 nM	1.0	1.5–1.9	3.6–6.7
5. MAPKK-P → MAPKK-PP	60–1500 nM	1.0	1.3–2.4	3.8–5.2
6. MAPKK-PP → MAPKK-P	60–1500 nM	1.0	1.7–1.8	4.1–6.4
7. MAPK → MAPK-P	60–1500 nM (300 nM [†])	1.0	1.7	3.7–6.2
8. MAPK-P → MAPK	60–1500 nM	1.0	1.7	4.3–5.2
9. MAPK-P → MAPK-PP	60–1500 nM	1.0	1.7	3.4–6.1
10. MAPK-PP → MAPK-P	60–1500 nM	1.0	1.7	4.7–5.1

The assumed K_m values for each reaction were individually varied over the ranges shown, with the assumed K_m values for the other nine reactions held constant. The effective Hill coefficients were calculated from the steepness of the predicted stimulus/response curves, as described in the text.

[†]The K_m value for reaction 7 has been measured to be 300 nM for the phosphorylation of a mammalian MAPK by a MAPKK (N. Ahn, personal communication). All of the other K_m values were initially assumed to be 300 nM as well.

Calculations. Eqs. 1–10 represent the reactions of the MAPK cascade, which are shown schematically in Fig. 1. We have used Goldbeter and Koshland's nomenclature for the rate constants—the letter a denotes association, d denotes dissociation without catalysis, and k denotes product formation (11). KKK denotes MAPKKK; KK denotes MAPKK; and K denotes MAPK.



10 chemical reactions

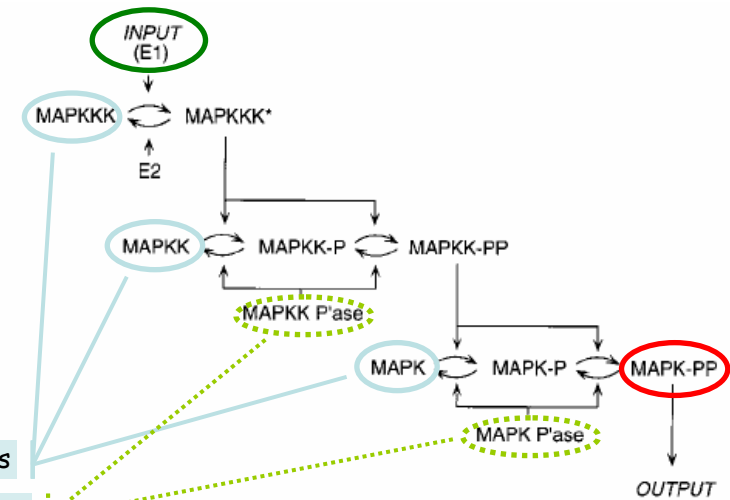


FIG. 1. Schematic view of the MAPK cascade. Activation of MAPK depends upon the phosphorylation of two conserved sites [Thr-183 and Tyr-185 in rat p42 MAPK/Erk2 (4, 5)]. Full activation of MAPKK also requires phosphorylation of two sites [Ser-218 and Ser-222 in mouse Mek-1/MKK1 (6–10)]. Detailed mechanisms for the activation of various MAPKKs (e.g., Raf-1, B-Raf, Mos) are not yet established; here we assume that MAPKKs are activated and inactivated by enzymes we denote E1 and E2. MAPKKK* denotes activated MAPKKK. MAPKK-P and MAPKK-PP denote singly and doubly phosphorylated MAPKK, respectively. MAPK-P and MAPK-PP denote singly and doubly phosphorylated MAPK. P'ase denotes phosphatase.

As 18 Ordinary Differential Equations Plus 7 conservation equations

$$\frac{d}{dt}[\text{KKK}] = -a_1[\text{KKK}][\text{E1}] + d_1[\text{KKK}\cdot\text{E1}] + k_2[\text{KKK}^*\cdot\text{E2}] \quad [111]$$

$$\frac{d}{dt}[\text{KKK}\cdot\text{E1}] = a_1[\text{KKK}][\text{E1}] - (d_1 + k_1)[\text{KKK}\cdot\text{E1}] \quad [112]$$

$$\frac{d}{dt}[\text{KKK}^*] = -a_2[\text{KKK}^*][\text{E2}] + d_2[\text{KKK}^*\cdot\text{E2}] + k_1[\text{KKK}\cdot\text{E1}] + (k_3 + d_3)[\text{KK}\cdot\text{KKK}^*] - a_3[\text{KKK}^*][\text{KK}] + (k_5 + d_5)[\text{KK}\cdot\text{P}\cdot\text{KKK}^*] - a_4[\text{KK}\cdot\text{P}][\text{KKK}^*] \quad [113]$$

$$\frac{d}{dt}[\text{KKK}^*\cdot\text{E2}] = a_2[\text{KKK}^*][\text{E2}] - (d_2 + k_2)[\text{KKK}^*\cdot\text{E2}] \quad [114]$$

$$\frac{d}{dt}[\text{KK}] = -a_3[\text{KK}][\text{KKK}^*] + d_3[\text{KK}\cdot\text{KKK}^*] + k_4[\text{KK}\cdot\text{P}\cdot\text{KK}\text{P}'ase] \quad [115]$$

$$\frac{d}{dt}[\text{KK}\cdot\text{KKK}^*] = a_3[\text{KK}][\text{KKK}^*] - (d_3 + k_3)[\text{KK}\cdot\text{KKK}^*] \quad [116]$$

$$\frac{d}{dt}[\text{KK}\cdot\text{P}] = -a_4[\text{KK}\cdot\text{P}][\text{KK}\text{P}'ase] + d_4[\text{KK}\cdot\text{P}\cdot\text{KK}\text{P}'ase] + k_5[\text{KK}\cdot\text{KKK}^*] + k_6[\text{KK}\cdot\text{PP}\cdot\text{KK}\text{P}'ase] + d_5[\text{KK}\cdot\text{P}\cdot\text{KKK}^*] - a_5[\text{KK}\cdot\text{P}][\text{KKK}^*] \quad [117]$$

$$+ d_6[\text{KK}\cdot\text{P}\cdot\text{KKK}^*] - a_6[\text{KK}\cdot\text{P}][\text{KKK}^*] \quad [117]$$

$$\frac{d}{dt}[\text{KK}\cdot\text{P}\cdot\text{KKK}^*] = a_4[\text{KK}\cdot\text{P}][\text{KKK}^*] - (d_4 + k_4)[\text{KK}\cdot\text{P}\cdot\text{KKK}^*] \quad [118]$$

$$\frac{d}{dt}[\text{KK}\cdot\text{P}\cdot\text{KKK}^*] = a_5[\text{KK}\cdot\text{P}][\text{KKK}^*] - (d_5 + k_5)[\text{KK}\cdot\text{P}\cdot\text{KKK}^*] \quad [119]$$

$$\frac{d}{dt}[\text{KK}\cdot\text{PP}] = k_7[\text{KK}\cdot\text{P}\cdot\text{KKK}^*] - a_6[\text{KK}\cdot\text{PP}][\text{KK}\text{P}'ase] + d_6[\text{KK}\cdot\text{PP}\cdot\text{KK}\text{P}'ase] - a_7[\text{KK}\cdot\text{PP}][\text{K}] + (d_7 + k_7)[\text{K}\cdot\text{KK}\cdot\text{PP}] + (d_9 + k_9)[\text{K}\cdot\text{P}\cdot\text{KK}\cdot\text{PP}] - a_8[\text{K}\cdot\text{P}][\text{KK}\cdot\text{PP}] \quad [120]$$

$$\frac{d}{dt}[\text{KK}\cdot\text{PP}\cdot\text{KK}\text{P}'ase] = a_6[\text{KK}\cdot\text{PP}][\text{KK}\text{P}'ase] - (d_6 + k_6)[\text{KK}\cdot\text{PP}\cdot\text{KK}\text{P}'ase] \quad [121]$$

$$\frac{d}{dt}[\text{K}] = -a_7[\text{K}][\text{KK}\cdot\text{PP}] + d_7[\text{K}\cdot\text{KK}\cdot\text{PP}] + k_8[\text{K}\cdot\text{P}\cdot\text{K}\text{P}'ase] \quad [122]$$

$$\frac{d}{dt}[\text{K}\cdot\text{KK}\cdot\text{PP}] = a_7[\text{K}][\text{KK}\cdot\text{PP}] - (d_7 + k_7)[\text{K}\cdot\text{KK}\cdot\text{PP}] \quad [123]$$

$$\frac{d}{dt}[\text{K}\cdot\text{P}] = k_7[\text{K}\cdot\text{KK}\cdot\text{PP}] - a_8[\text{K}\cdot\text{P}][\text{K}\text{P}'ase] + d_8[\text{K}\cdot\text{P}\cdot\text{K}\text{P}'ase] - a_9[\text{K}\cdot\text{P}][\text{KK}\cdot\text{PP}] + d_9[\text{K}\cdot\text{P}\cdot\text{KK}\cdot\text{PP}] + k_{10}[\text{K}\cdot\text{PP}\cdot\text{K}\text{P}'ase] \quad [124]$$

$$\frac{d}{dt}[\text{K}\cdot\text{P}\cdot\text{K}\text{P}'ase] = a_8[\text{K}\cdot\text{P}][\text{K}\text{P}'ase] - (d_8 + k_8)[\text{K}\cdot\text{P}\cdot\text{K}\text{P}'ase] \quad [125]$$

$$\frac{d}{dt}[\text{K}\cdot\text{P}\cdot\text{KK}\cdot\text{PP}] = a_9[\text{K}\cdot\text{P}][\text{KK}\cdot\text{PP}] - (d_9 + k_9)[\text{K}\cdot\text{P}\cdot\text{KK}\cdot\text{PP}] \quad [126]$$

$$\frac{d}{dt}[\text{K}\cdot\text{PP}] = -a_{10}[\text{K}\cdot\text{PP}][\text{K}\text{P}'ase] + d_{10}[\text{K}\cdot\text{PP}\cdot\text{K}\text{P}'ase] + k_9[\text{K}\cdot\text{P}\cdot\text{KK}\cdot\text{PP}] \quad [127]$$

$$\frac{d}{dt}[\text{K}\cdot\text{PP}\cdot\text{K}\text{P}'ase] = a_{10}[\text{K}\cdot\text{PP}][\text{K}\text{P}'ase] - (d_{10} + k_{10})[\text{K}\cdot\text{PP}\cdot\text{K}\text{P}'ase] \quad [128]$$

$$[\text{E1}_{\text{tot}}] = [\text{E1}] + [\text{KKK}\cdot\text{E1}] \quad [130]$$

$$[\text{E2}_{\text{tot}}] = [\text{E2}] + [\text{KKK}^*\cdot\text{E2}] \quad [131]$$

$$[\text{KK}_{\text{tot}}] = [\text{KK}] + [\text{KK}\cdot\text{P}] + [\text{KK}\cdot\text{PP}] + [\text{KK}\cdot\text{KKK}^*] + [\text{KK}\cdot\text{P}\cdot\text{KKK}^*] + [\text{KK}\cdot\text{P}\cdot\text{KK}\text{P}'ase] + [\text{KK}\cdot\text{PP}\cdot\text{K}] + [\text{KK}\cdot\text{PP}\cdot\text{K}\cdot\text{P}] \quad [132]$$

$$[\text{KK}\text{P}'ase_{\text{tot}}] = [\text{KK}\text{P}'ase] + [\text{KK}\text{P}'ase\cdot\text{KK}\cdot\text{P}] + [\text{KK}\text{P}'ase\cdot\text{KK}\cdot\text{PP}] \quad [133]$$

$$[\text{K}_{\text{tot}}] = [\text{K}] + [\text{K}\cdot\text{P}] + [\text{K}\cdot\text{PP}] + [\text{K}\cdot\text{KK}\cdot\text{PP}] + [\text{K}\cdot\text{PP}\cdot\text{K}\cdot\text{P}] + [\text{K}\cdot\text{P}\cdot\text{K}\text{P}'ase] + [\text{K}\cdot\text{PP}\cdot\text{K}\text{P}'ase] \quad [134]$$

$$[\text{K}\text{P}'ase_{\text{tot}}] = [\text{K}\text{P}'ase] + [\text{K}\cdot\text{P}\cdot\text{K}\text{P}'ase] + [\text{K}\cdot\text{PP}\cdot\text{K}\text{P}'ase] \quad [135]$$

These equations were solved numerically using the Runge-Kutta-based NDSolve algorithm in Mathematica (Wolfram Research, Champaign, IL). An annotated copy of the Mathematica code for the MAPK cascade rate equations can be obtained from J.E.F.

The 10 reactions described above give rise to 18 rate equations.

One equation for each species (8) and complex (10), but not for constant concentration enzymes (4)

In addition, there are seven conservation equations (Eqs. 29-35).

$$[\text{KKK}_{\text{tot}}] = [\text{KKK}] + [\text{KKK}^*] + [\text{KKK}\cdot\text{E1}] + [\text{KKK}^*\cdot\text{E2}] + [\text{KKK}^*\cdot\text{K}] + [\text{KKK}^*\cdot\text{K}\cdot\text{P}] \quad [29]$$

in exactly one state

Each molecule

As 12 processes (in SPiM)

```
let KKK() =
  (new u1@d1:Release
   !a1(u1); (do !u1;KKK() or !k1;KKKst()))
```

[1]substrate

```
and KKKst() =
  (new u2@d2:Release
   do !a2(u2); (do !u2;KKKst() or !k2;KKK())
   or ?a3(u3); (do ?u3;KKKst() or ?k3;KKKst())
   or ?a5(u5); (do ?u5;KKKst() or ?k5;KKKst()))
```

[2]substrate
[3]kinase
[5]kinase

KKK:E1 complex

```
let E1() =
  ?a1(u1); (do ?u1;E1() or ?k1;E1())
```

[1]enzyme

```
let E2() =
  ?a2(u2); (do ?u2;E2() or ?k2;E2())
```

[2]enzyme

E1:KKK complex

```
let KK() =
  (new u3@d3:Release
   !a3(u3); (do !u3;KK() or !k3;KK_PP()))
```

[3]substrate

```
and KK_PP() =
  (new u4@d4:Release new u5@d5:Release
   do !a4(u4); (do !u4;KK_PP() or !k4;KK())
   or !a5(u5); (do !u5;KK_PP() or !k5;KK_PP()))
```

[4]substrate
[5]substrate

```
and KK_PP() =
  (new u6@d6:Release
   do !a6(u6); (do !u6;KK_PP() or !k6;KK_PP())
   or ?a7(u7); (do ?u7;KK_PP() or ?k7;KK_PP())
   or ?a9(u9); (do ?u9;KK_PP() or ?k9;KK_PP()))
```

[6]substrate
[7]kinase
[9]kinase

One process for each component (12) including enzymes, but not for complexes.

```
and KKPse() =
  do ?a4(u4); (do ?u4;KKPse() or ?k4;KKPse())
  or ?a6(u6); (do ?u6;KKPse() or ?k6;KKPse())
```

[4]phtase
[6]phtase

```
let K() =
  (new u7@d7:Release
   !a7(u7); (do !u7;K() or !k7;K()))
```

[7]substrate

No need for conservation equations: implicit in "choice" operator in the calculus.

```
and K_PP() =
  (new u8@d8:Release new u9@d9:Release
   do !a8(u8); (do !u8;K_PP() or !k8;K())
   or !a9(u9); (do !u9;K_PP() or !k9;K_PP()))
```

[8]substrate
[9]substrate

```
and K_PP() =
  (new u10@d10:Release
   !a10(u10); (do !u10;K_PP() or !k10;K_PP()))
```

[10]substrate

```
and KPse() =
  do ?a8(u8); (do ?u8;KPse() or ?k8;KPse())
  or ?a10(u10); (do ?u10;KPse() or ?k10;KPse())
```

[8]phtase
[10]phtase

... and 20 Interaction Channels

```
type Release = chan()
type Bond = chan(Release)
type React = chan()
```

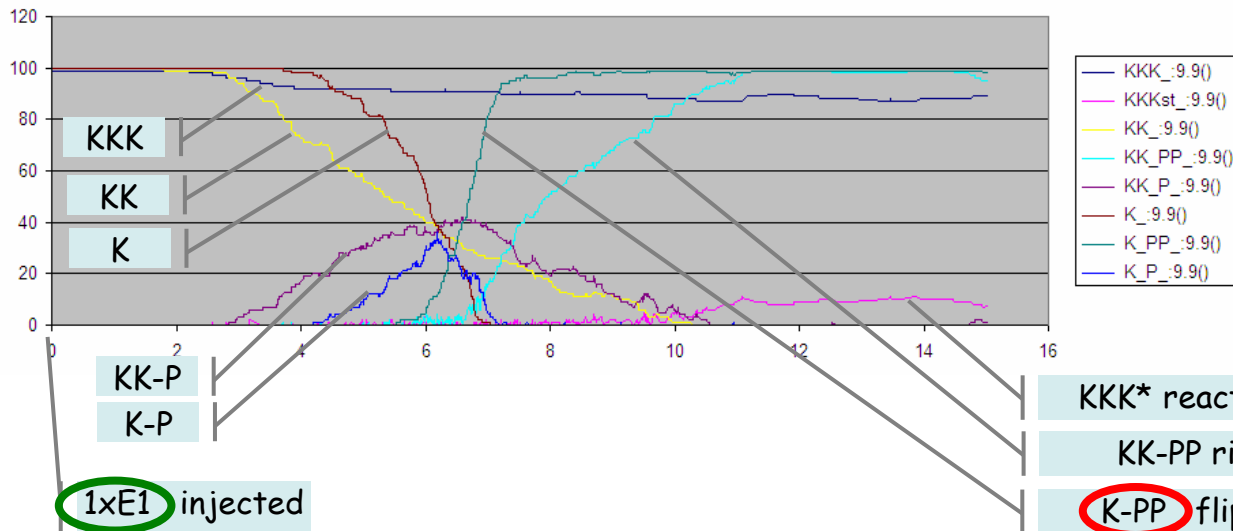
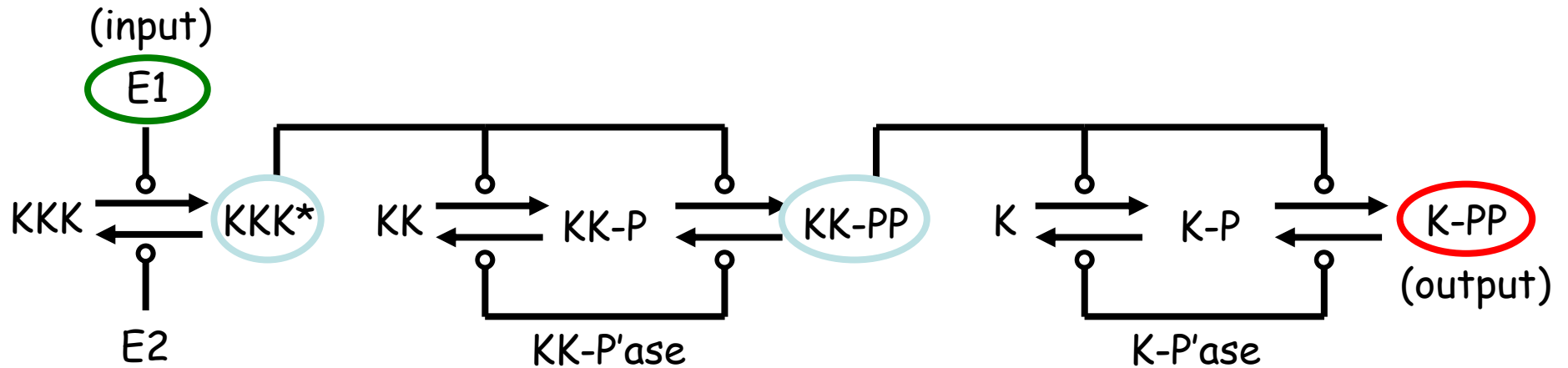
```
new a1@1.0:Bond val d1=1.0 new k1@1.0:React
new a2@1.0:Bond val d2=1.0 new k2@1.0:React
new a3@1.0:Bond val d3=1.0 new k3@1.0:React
new a4@1.0:Bond val d4=1.0 new k4@1.0:React
new a5@1.0:Bond val d5=1.0 new k5@1.0:React
new a6@1.0:Bond val d6=1.0 new k6@1.0:React
new a7@1.0:Bond val d7=1.0 new k7@1.0:React
new a8@1.0:Bond val d8=1.0 new k8@1.0:React
new a9@1.0:Bond val d9=1.0 new k9@1.0:React
new a10@1.0:Bond val d10=1.0 new k10@1.0:React
```

...

```
run 100 of KKK() run 100 of KK() run 100 of K()
run 1 of E2() run 1 of KKPse() run 1 of KPse()
run 1 of E1()
```

a_i, k_i : Two channels for each reversible chemical reaction of 2 molecules.
(No behavior attached to channels except interaction rate.)

MAPK Cascade Simulation in SPiM



All coefficients 1.0 !!!
 100xKKK, 100xKK, 100xK,
 1xE2, 1xKKPse, 1xKPse.

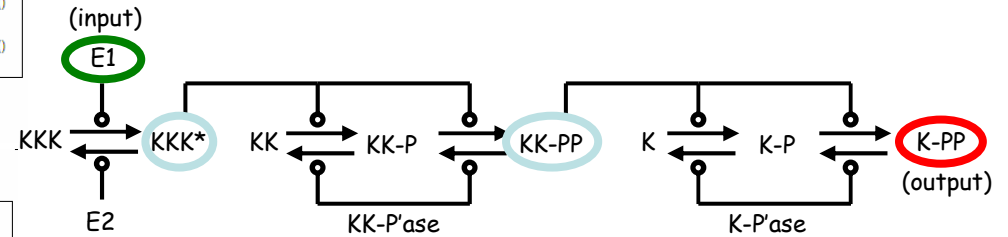
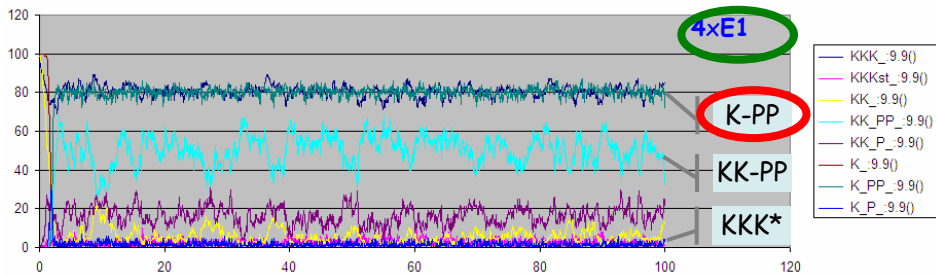
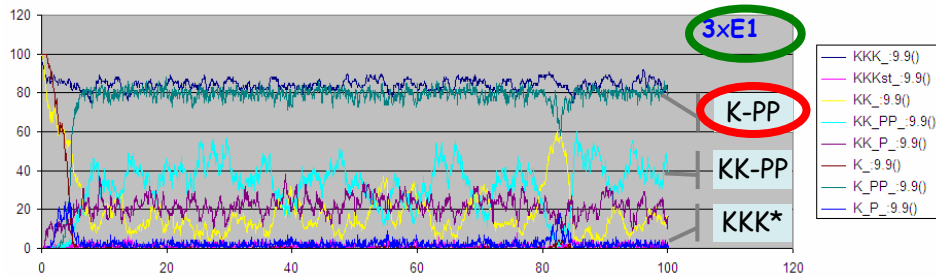
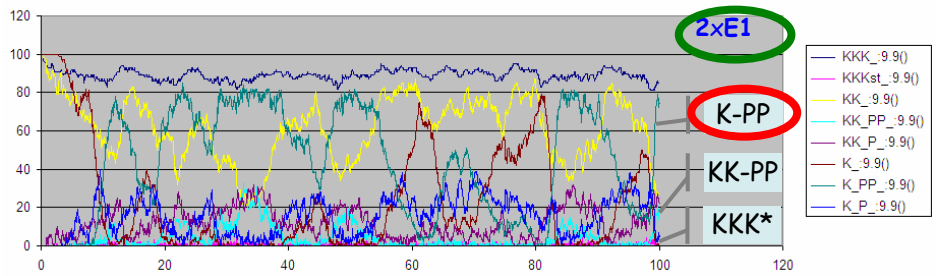
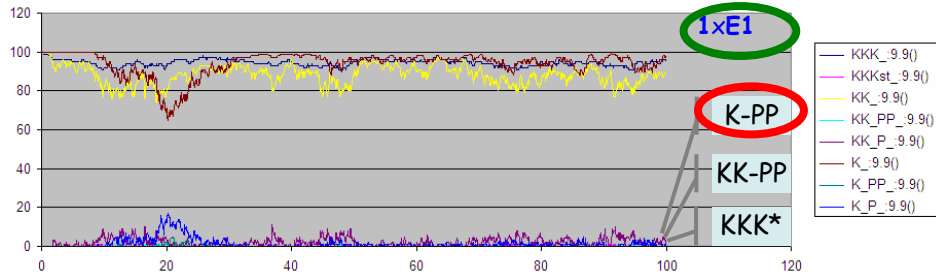
Input is 1xE1.
 Output is 100xK-PP (ultrasensitivity).

KKK* reacts mildly to E1

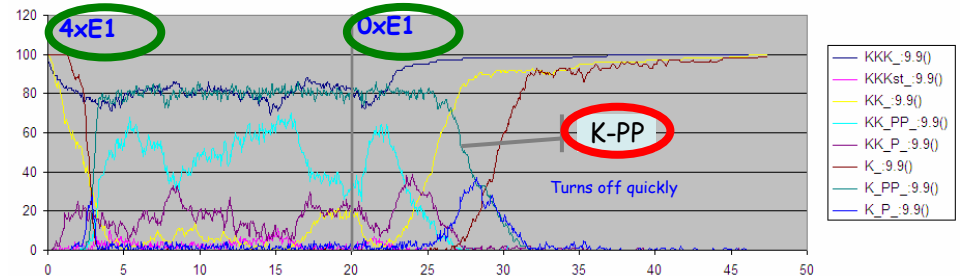
KK-PP rises quicker

K-PP flips up to 100!

MAPK Cascade Simulation in SPiM



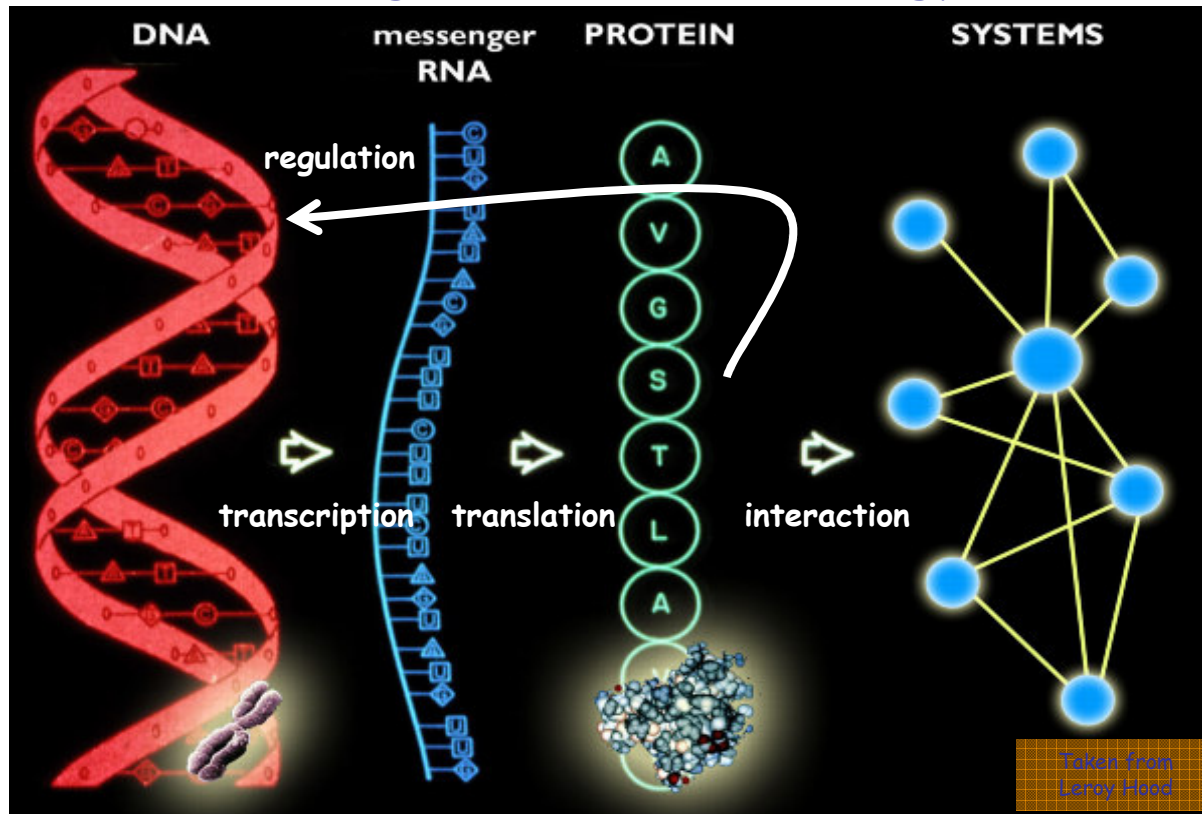
All coefficients 1.0 !!!
 100xKKK, 100xKK, 100xK,
 10xE2, 10xKKPse, 10xKPse.
 (so 1xE1 is no longer sufficient to produce an output)



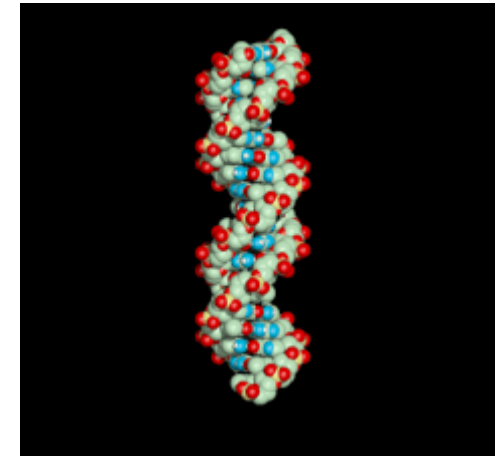
2. The Gene Machine

Pretty far from the atoms.

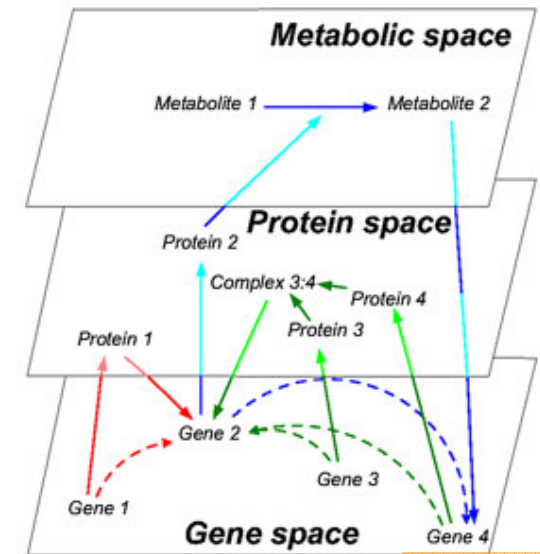
The "Central Dogma" of Molecular Biology



4-letter digital code 4-letter digital code 20-letter digital code 50.000(?) shapes

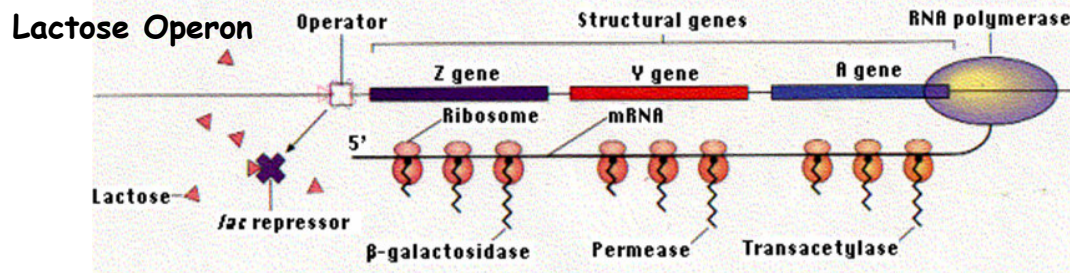


[DNA Tutorial](#)



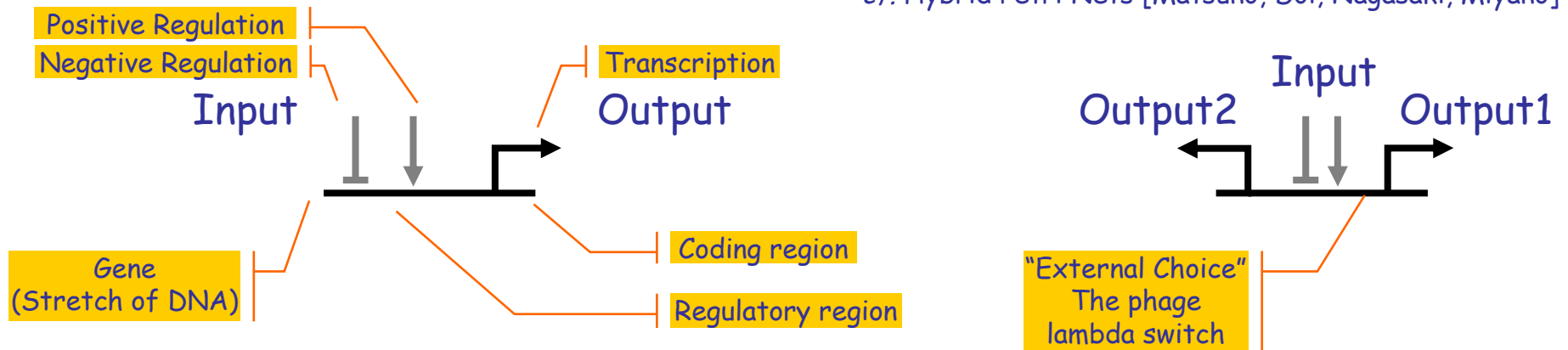
Taken from Pedro Mendes

2005-06-03



The Gene Machine "Instruction Set"

cf. Hybrid Petri Nets [Matsuno, Doi, Nagasaki, Miyano]



Regulation of a gene (positive and negative) influences transcription. The regulatory region has precise DNA sequences, but not meant for coding proteins: meant for binding regulators.

Transcription produces molecules (RNA or, through RNA, proteins) that bind to regulatory region of other genes (or that are end-products).

Human (and mammalian) Genome Size

3Gbp (Giga base pairs) 750MB @ 4bp/Byte (CD)

Non-repetitive: 1Gbp 250MB

In genes: 320Mbp 80MB

Coding: 160Mbp 40MB

Protein-coding genes: 30,000-40,000

M.Genitalium (smallest true organism)

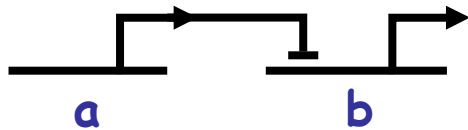
580,073bp 145KB (eBook)

E.Coli (bacteria): 4Mbp 1MB (floppy)

Yeast (eukarya): 12Mbp 3MB (MP3 song)

Wheat 17Gbp 4.25GB (DVD)

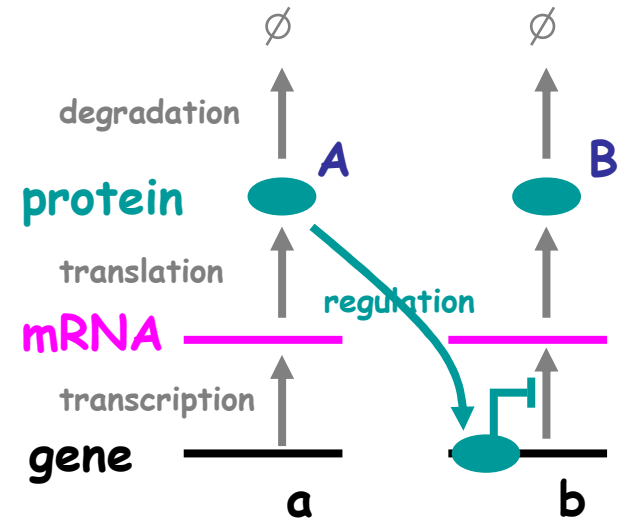
Gene Composition



Is a shorthand for:

Under the assumptions [Kim & Tidor]

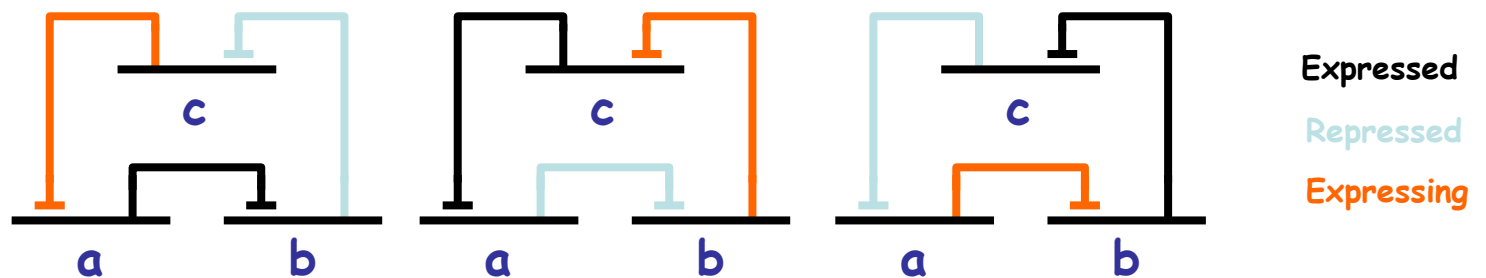
- 1) The solution is well-stirred
(no spatial dependence on concentrations or rates).
- 2) There is no regulation cross-talk.
- 3) Control of expression is at transcription level only
(no RNA-RNA or RNA-protein effects)
- 4) Transcriptions and translation rates monotonically affect mRNA and protein concentrations resp.



Ex: Bistable Switch

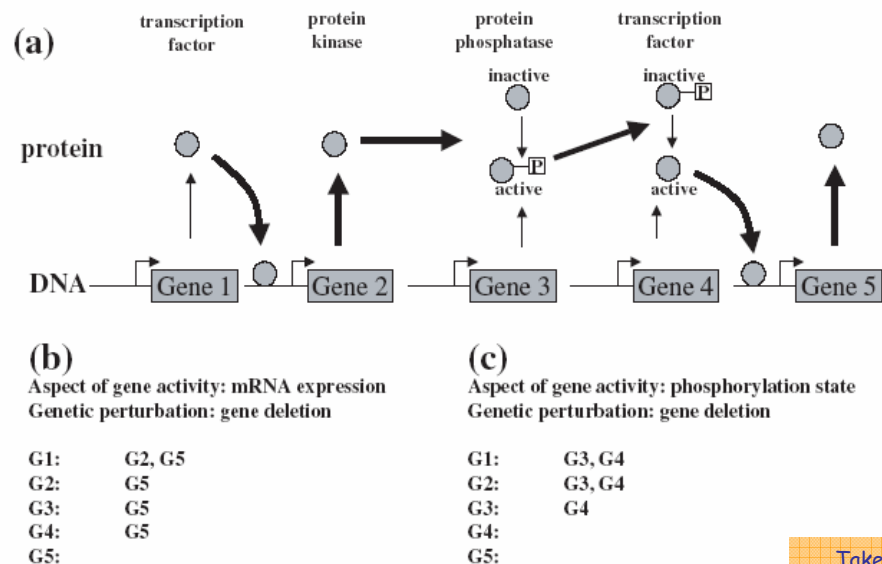


Ex: Oscillator



Indirect Gene Effects

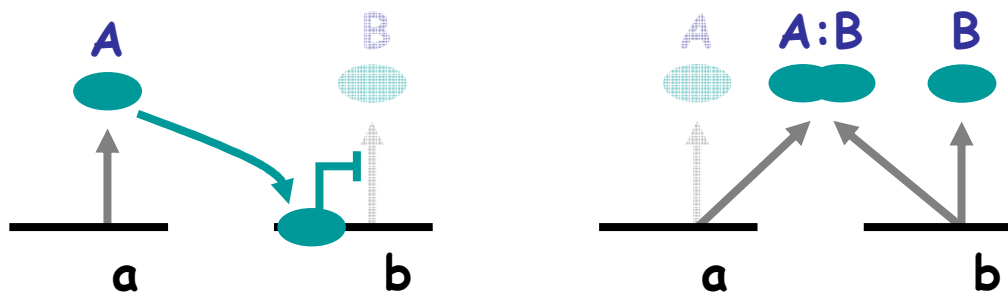
No combination of standard high-throughput experiments can reconstruct an a-priori known gene/protein network [Wagner].



Taken from
Andreas Wagner

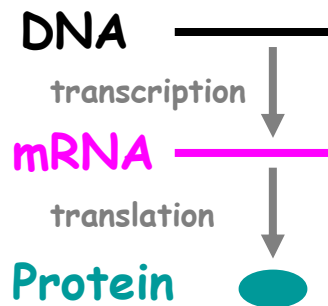
Fig. 1. The importance of specifying gene activity when reconstructing genetic networks. (a) A hypothetical biochemical pathway involving two transcription factors, a protein kinase, and a protein phosphatase, as well as the genes encoding them. See text for details. (b) Shown is a list of perturbation effects for each of the five genes in (a), when perturbing individual genes by deleting them, and when using mRNA expression level as an indicator of gene activity. The left-most symbol in each line stands for the perturbed gene. To the right of each colon is a list of genes whose activity is affected by the perturbation. (c) Analogous to (b) but for a different notion of gene activity (phosphorylation state).

One of many bistable switches that cannot be described by pure gene regulatory networks [Francois & Hakim].



Structure of the Coding Region

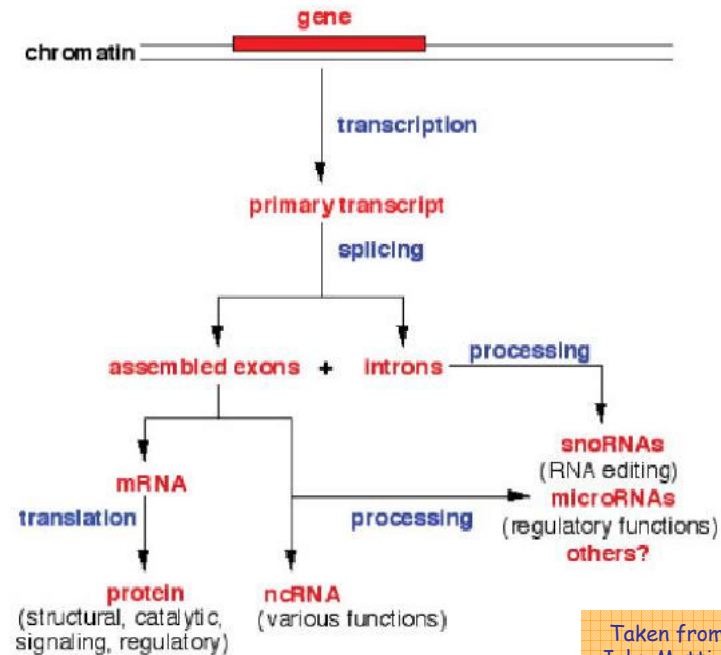
The Central Dogma



RNA is not just an intermediary; it can:

- Fold-up like a protein
- Act like an enzyme
- Regulate other transcribed RNA
- Direct protein editing
- ...

Challenging the Dogma (in higher organisms)



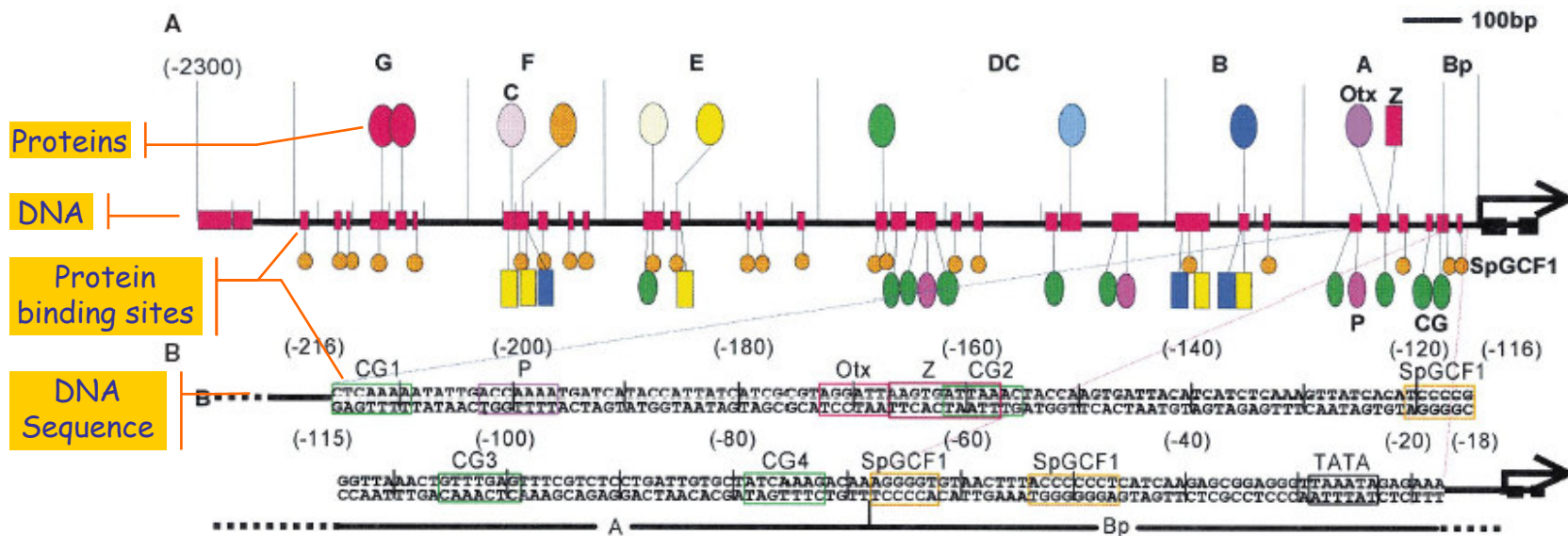
Taken from
John Mattick

97-98% of the transcriptional output of the human genome is non-protein-coding RNA.

30-40,000 "protein genes" (1.5% of genome)

60-100,000 "transcription units" (>30% of genome is transcribed)

Structure of a Regulatory Region



2300bp!
 > average protein

C Module A functions:

Vegetal plate expression in early development:

Synergism with modules B and G enhancing endoderm expression in later development:

Repression in ectoderm (modules E and F) and skeletogenic mesenchyme (module DC):

Modules E, F and DC with LiCl treatment:

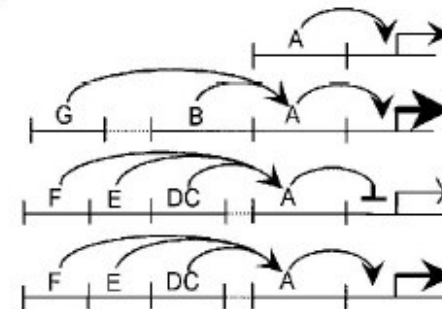
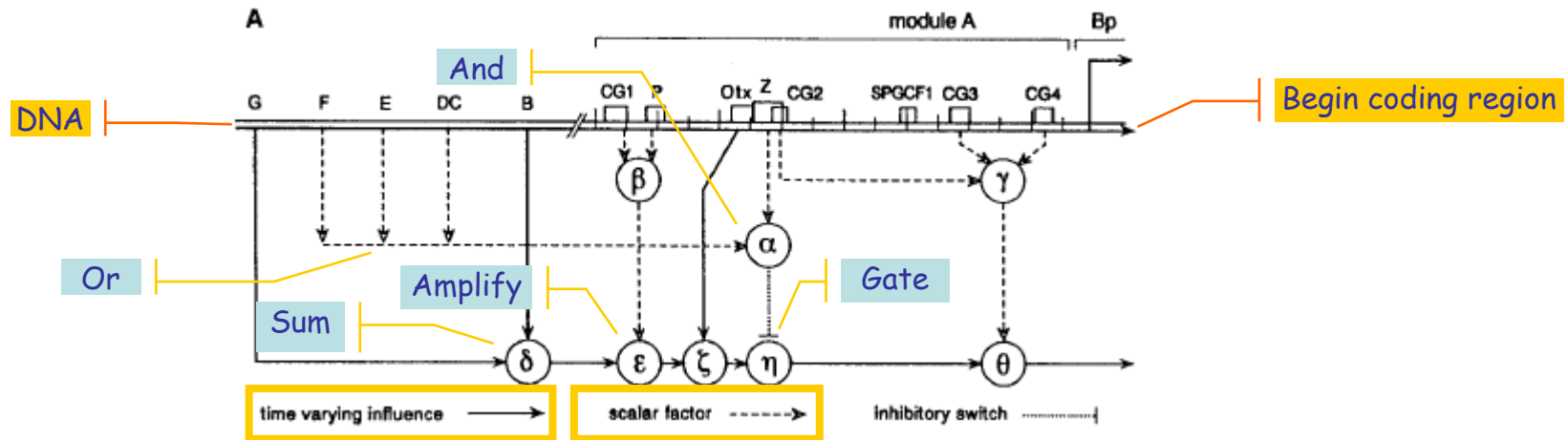


Fig. 1. *Endo16* cis-regulatory system and interactive roles of module A. (A) Diversity of protein binding sites and organization into modular subregions [modified from (7)]. Specific DNA binding sites are indicated as red blocks; modular subregions are denoted by letters G to A (Bp, basal promoter). Proteins binding at the target sites considered in this work are indicated: Otx, SpOtx-1 (12); SpGCF1 (14); the proteins CG, Z, and P, which are not yet cloned; and protein C [a CREB family protein (18)] in subregion F. Proteins for which sites occur in multiple regions of the DNA sequence (indicated by the black line) are shown beneath. (B) Sequence of module A and location of protein binding sites. Sites are indicated in the same colors as in (A). A fragment containing CG₃ and CG₄ sites as well as Bp has no endoderm-

specific activity and services other upstream cis-regulatory systems promiscuously; similarly, the *Endo16* cis-regulatory system functions specifically with heterologous promoters substituted for Bp (5, 8, 19). Boxed sequences indicate conserved core elements of the target sites (7, 12, 14), not the complete target site sequences. (C) Integrative and interactive functions of module A (5, 8). Module A communicates the output of all upstream modules to the basal transcription apparatus. It also initiates endoderm expression, increases the output of modules B and G, and is required for functions of the upstream modules F, E, and DC. These functions are repression of expression in nonendodermal domains and enhancement of expression in response to LiCl.

Function of a Regulatory Region



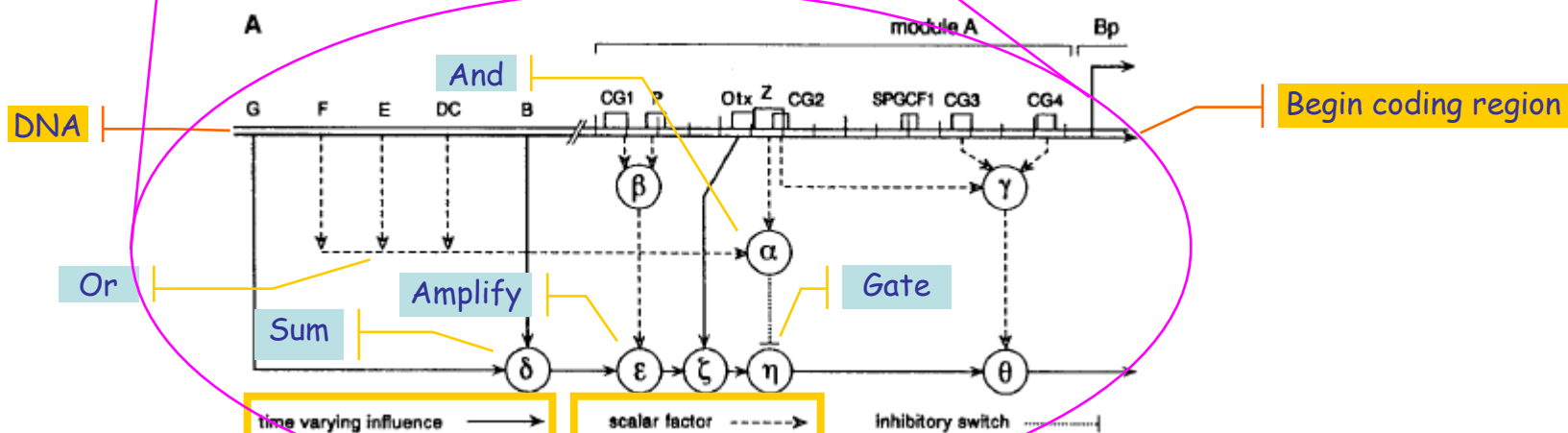
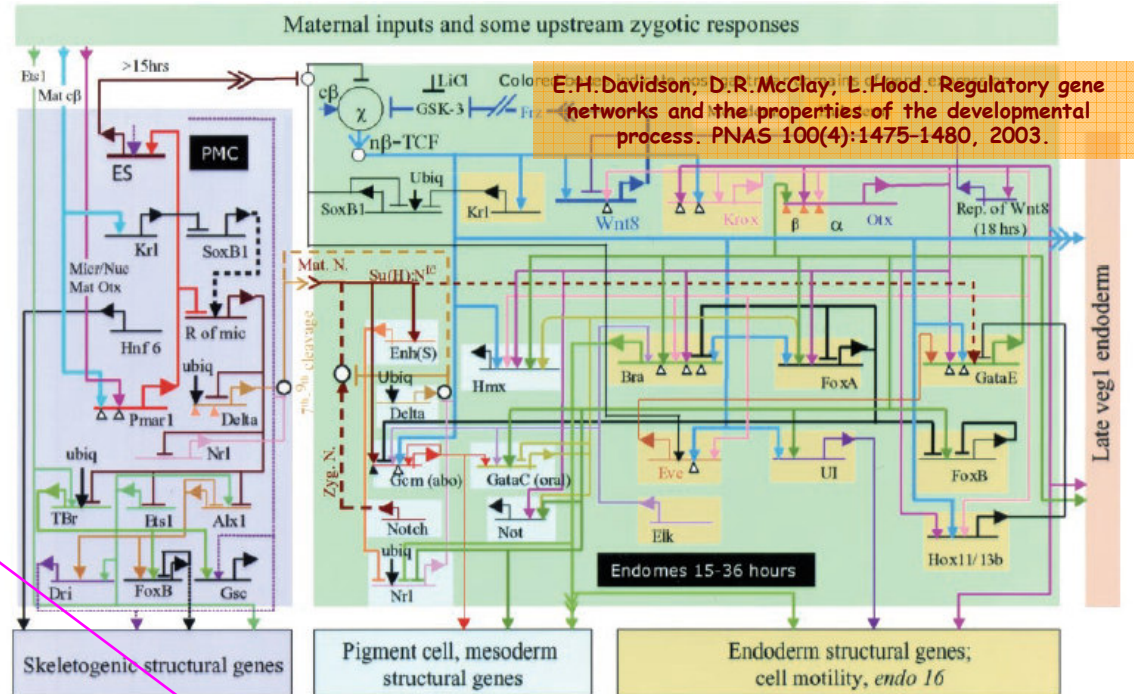
B

if (F = 1 or E = 1 or CD = 1) and (Z = 1) Repression functions of modules F, E, and DC mediated by Z site
 $\alpha = 1$
 else $\alpha = 0$
 if (P = 1 and CG₁ = 1) Both P and CG₁, needed for synergistic link with module B
 $\beta = 2$
 else $\beta = 0$
 if (CG₂ = 1 and CG₃ = 1 and CG₄ = 1) Final step up of system output
 $\gamma = 2$
 else $\gamma = 1$
 $\delta(t) = B(t) + G(t)$ Positive input from modules B and G
 $\epsilon(t) = \beta * \delta(t)$ Synergistic amplification of module B output by CG₁-P subsystem
 if ($\epsilon(t) = 0$) Switch determining whether Otx site in module A, or upstream modules (i.e., mainly module B), will control level of activity
 $\zeta(t) = Otx(t)$
 else $\zeta(t) = \epsilon(t)$
 if ($\alpha = 1$) Repression function inoperative in endoderm but blocks activity elsewhere
 $\eta(t) = 0$
 else $\eta(t) = \zeta(t)$
 $\theta(t) = \gamma * \eta(t)$ Final output communicated to BTA

Gene Regulatory Networks

<http://strc.herts.ac.uk/bio/maria/NetBuilder/>

NetBuilder



C-H. Yuh, H. Bolouri, E.H. Davidson. Genomic Cis-Regulatory Logic: Experimental and Computational Analysis of a Sea Urchin Gene. Science 279:1896-1902, 1998

The Programming Model

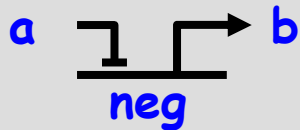
- **Strange facts about genetic networks:**
 - **Not an operator algebra.** The output of each gate is fixed and pre-determined; it is never a function of the input!
 - **Not term-rewriting, nor Petri nets.** Inhibition is widespread.
 - **Not Communicating Sequential Processes.** Feedback is widespread: asynchronous communication needed to avoid immediate self-deadlocks. Even the simplest gates cannot be modeled as a single synchronous automata.
 - **Not Message-Passing between genes.** Messages themselves have behavior (e.g., they stochastically decay and combine), hence messages are processes as well.
 - **Not Data-Flow.** Any attempt to use data-flow-style modeling seems doomed because of widespread loops that lead to deadlocks or unbounded queues. Data-flow tokens do not "decay" like proteins.
- **How can it possibly work?**
 - **Stochastic broadcasting.** The apparently crude idea of broadcasting a whole bunch of asynchronous decaying messages to activate a future gate, means there are never any "pipeline full" deadlocks, even in presence of abundant feedback loops.
 - **Stochastic degradation.** Degradation is fundamental for system stability, and at the same time can lead to sudden instability and detection of concentration levels.

Notations for the Gene Machine

- Many of the same techniques as for the Protein Machine apply.
 - Process Calculi, Petri Nets, Term-Rewriting Systems...
- But the “programming model” is different.
 - Asynchronous stochastic control.
 - Biologically poorly understood.
 - Network “motifs” are being analyzed.
- Specific techniques:
 - Hybrid Petri Nets
 - [Matsuno, Doi, Nagasaki, Miyano] Gene Regulation
 - Genomic Object Net www.genomicobject.net
- Gene Regulation Diagrams
- Mixed Gene-Protein Diagrams

Gene Gates and Circuits

A gene gate

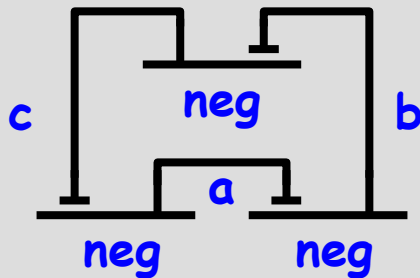


$$\text{neg}(a,b) \triangleq$$

$$\begin{aligned} & ?a_r; \tau_\eta; \text{neg}(a,b) + \\ & \tau_\varepsilon; (\text{tr}(b) \mid \text{neg}(a,b)) \end{aligned}$$

$$\text{tr}(p) \triangleq (!p_r; \text{tr}(p)) + \tau_\delta$$

A genetic circuit (engineered in E.Coli)



$$\begin{aligned} & \text{neg}(a,b) \mid \\ & \text{neg}(b,c) \mid \\ & \text{neg}(c,a) \end{aligned}$$

The stochastic- π program

```
val dk = 0.001    (* Decay rate *)
val inh = 0.001  (* Inhibition rate *)
val cst = 0.1    (* Constitutive rate *)
```

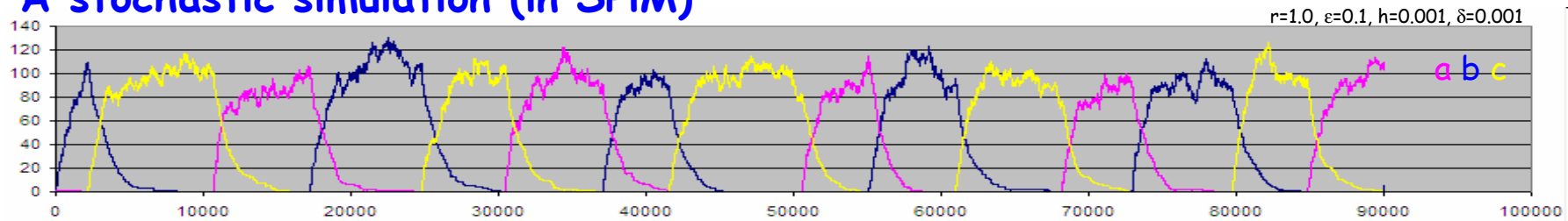
```
let tr(p:chan()) =
  do !p; tr(p) or delay@dk
```

```
let neg(a:chan(), b:chan()) =
  do ?a; delay@inh; neg(a,b)
  or delay@cst; (tr(b) | neg(a,b))
```

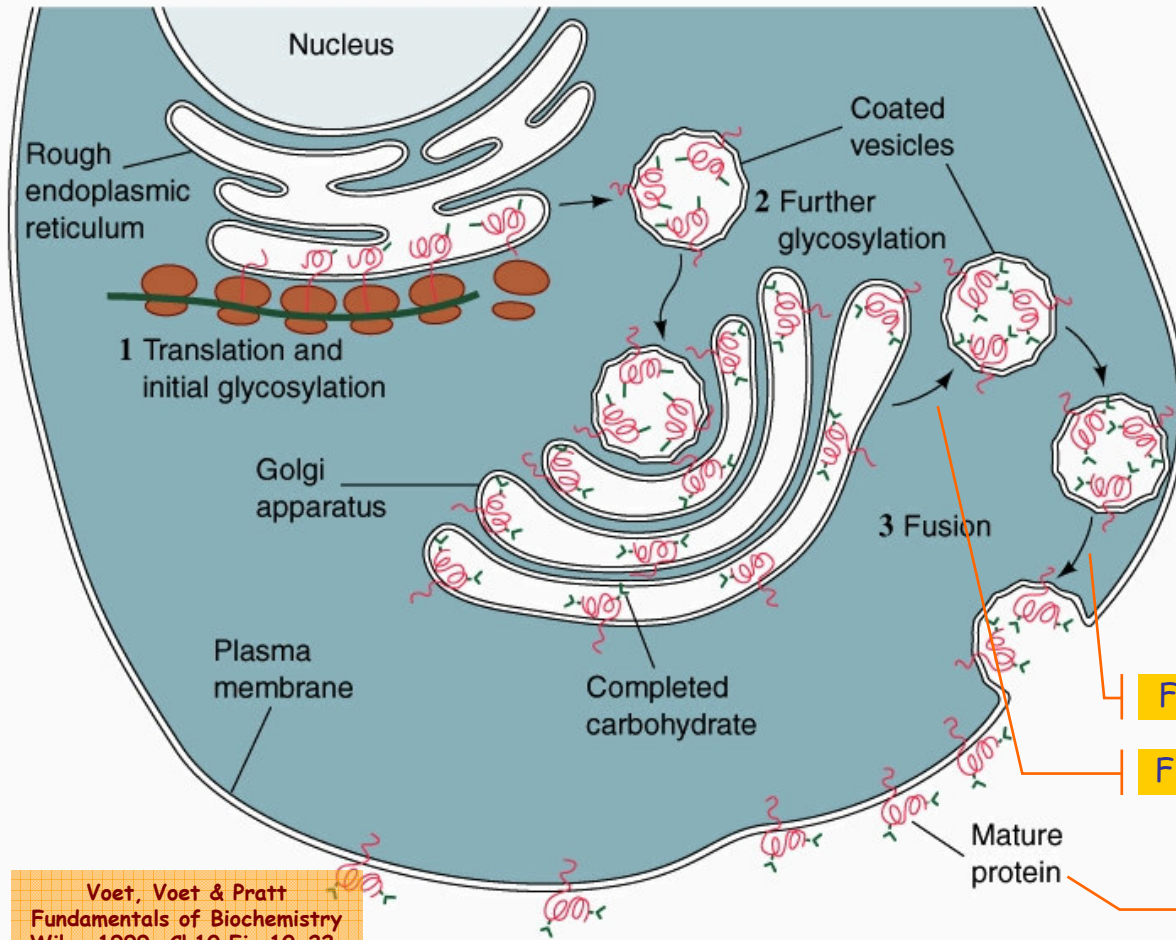
```
(* The circuit *)
```

```
val bnd = 1.0    (* Protein binding rate *)
new a@bnd:chan() new b@bnd:chan() new c@bnd:chan()
run (neg(c,a) | neg(a,b) | neg(b,c))
```

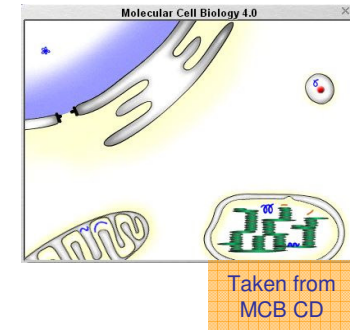
A stochastic simulation (in SPiM)



3. The Membrane Machine *Very far from the atoms.*



Molecular transport and transformation through dynamic compartment **fusion and fission**.



Fusion

Fission

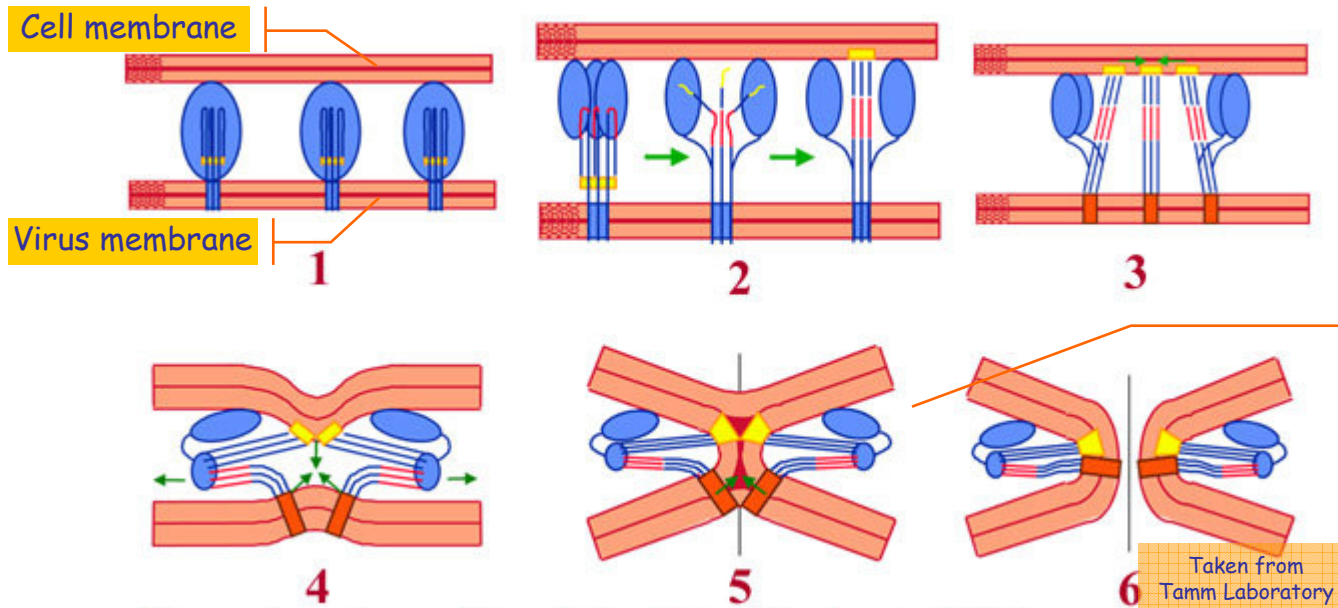
} The Instruction Set

Voet, Voet & Pratt
Fundamentals of Biochemistry
Wiley 1999. Ch10 Fig 10-22.
Copyright 1999 John Wiley and Sons, Inc. All rights reserved.

Well, what is all that for?
"Given the complicated pathways that have evolved to synthesize them, it seems likely that these [modified proteins] have important functions, but for the most part these functions are not known" [MBC p.609]

Membrane Fusion

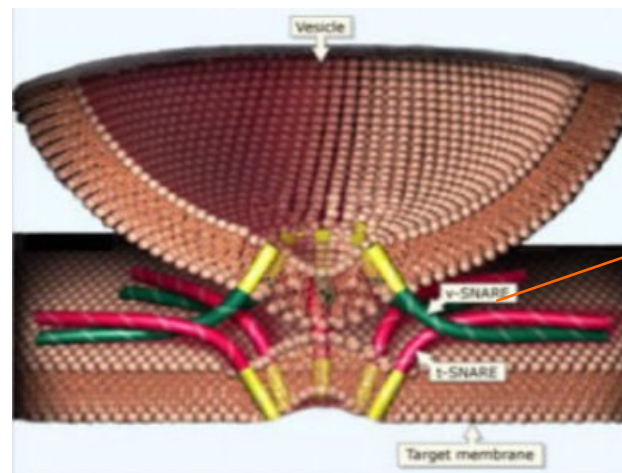
Positive curvature to
Negative curvature
transition in 3D



**Aggressive fusion
(virus)**

By unknown mechanisms,
the exoplasmic leaflets
of the two membranes
fuse" [MCB p745]

Proposed sequence of events in pH sensitive hemagglutinin membrane fusion

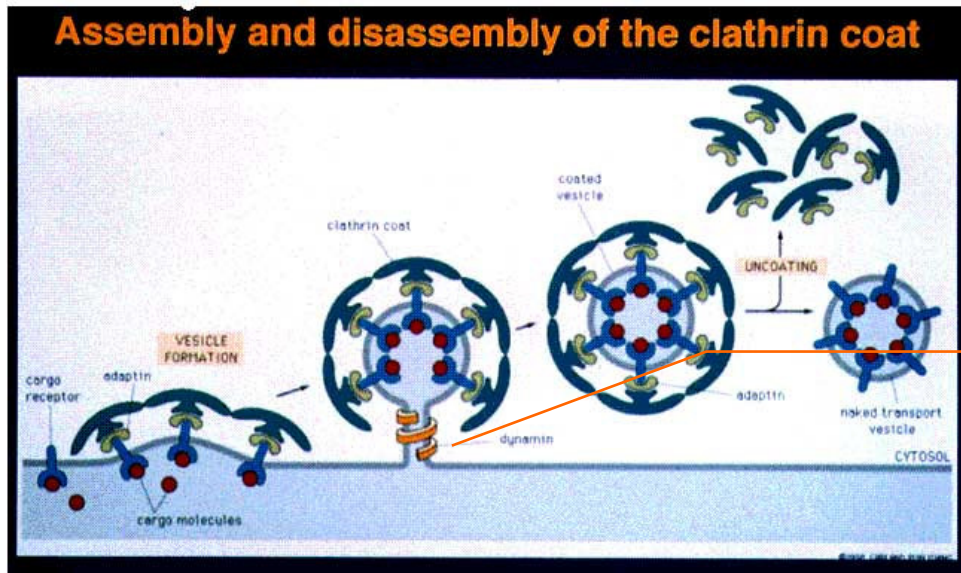


**Cooperative fusion
(vesicle)**

"Fusion of the two
membranes immediately
follows prefusion, but
precisely how this occurs is
not known" [MCB p742]

Membrane Fission

Negative curvature to Positive curvature transition in 3D

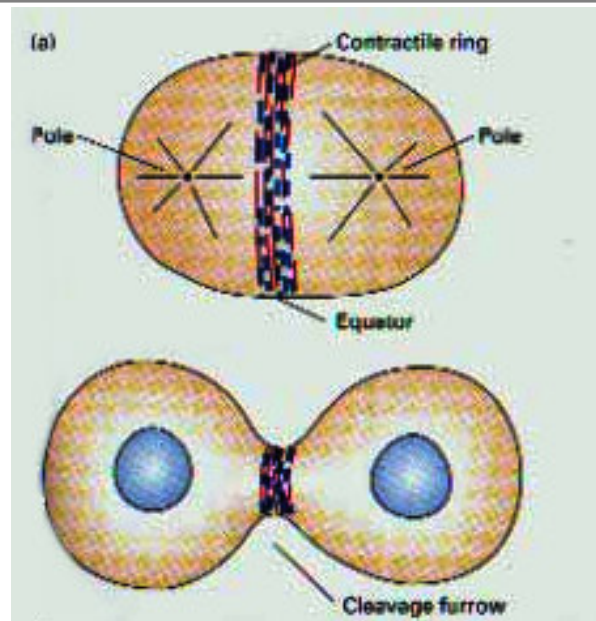


Vesicle Formation



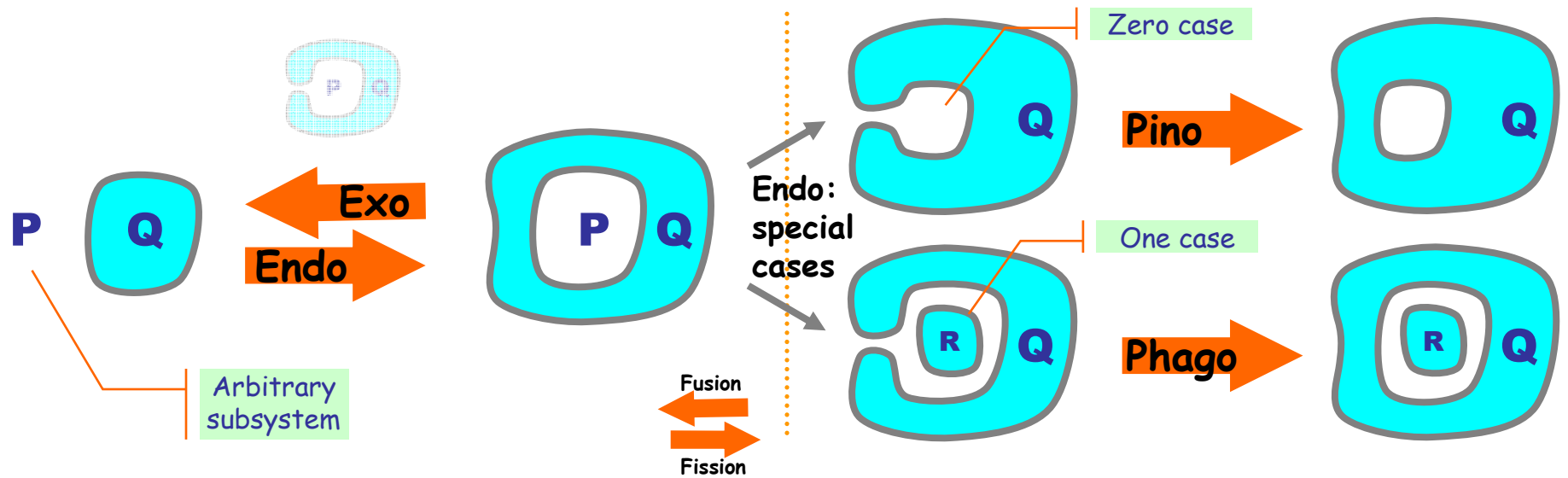
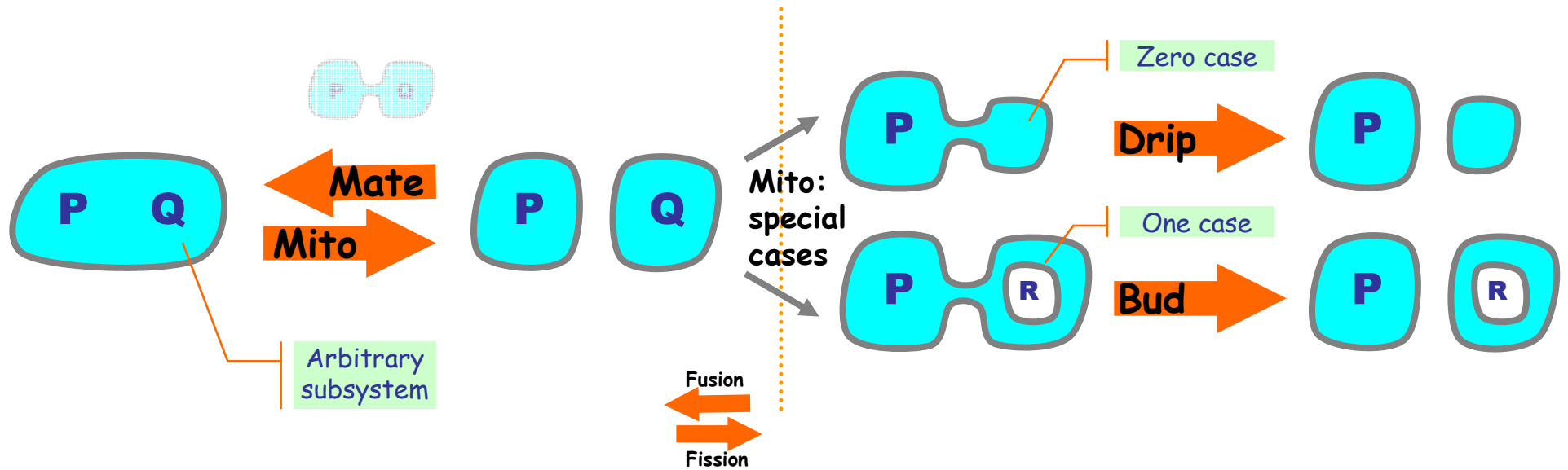
Movie by Allison Bruce

"Nonetheless, the actual process whereby a segment of phospholipid bilayer is 'pinched off' to form a pit and eventually a new vesicle is still not understood" [MCB p.746]

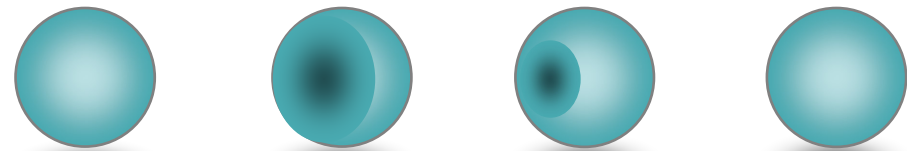


Cytokinesis (Mitosis)

The Membrane Machine "Instruction Set"



... in 3D



S-Exo

Fusion

S-Endo



T-Exo

Fission

T-Endo



S-Mito

Fission

S-Mate



T-Mito

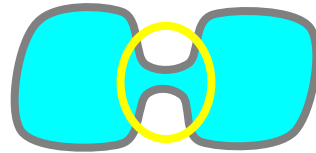
Fusion

T-Mate

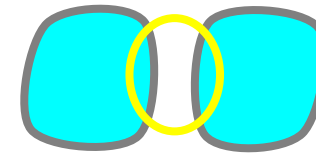


Locally Implementable!

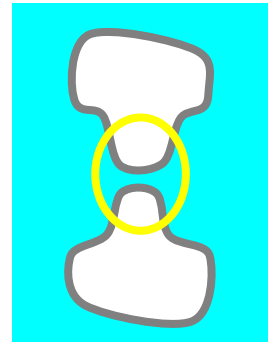
Global Views



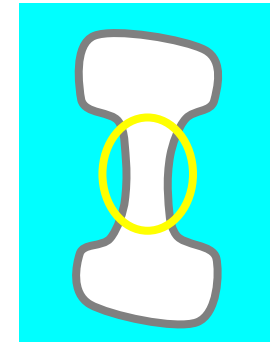
Mito →



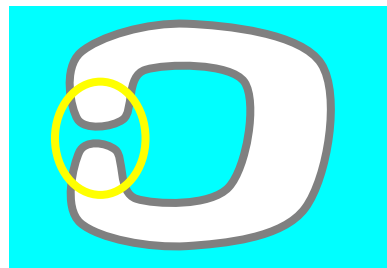
(Fission)



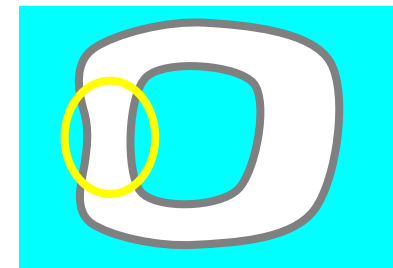
Mate →



(Fusion)



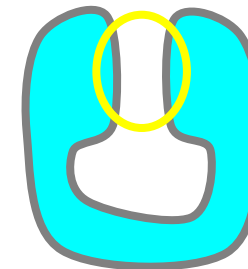
Endo →



(Fission)



Exo →

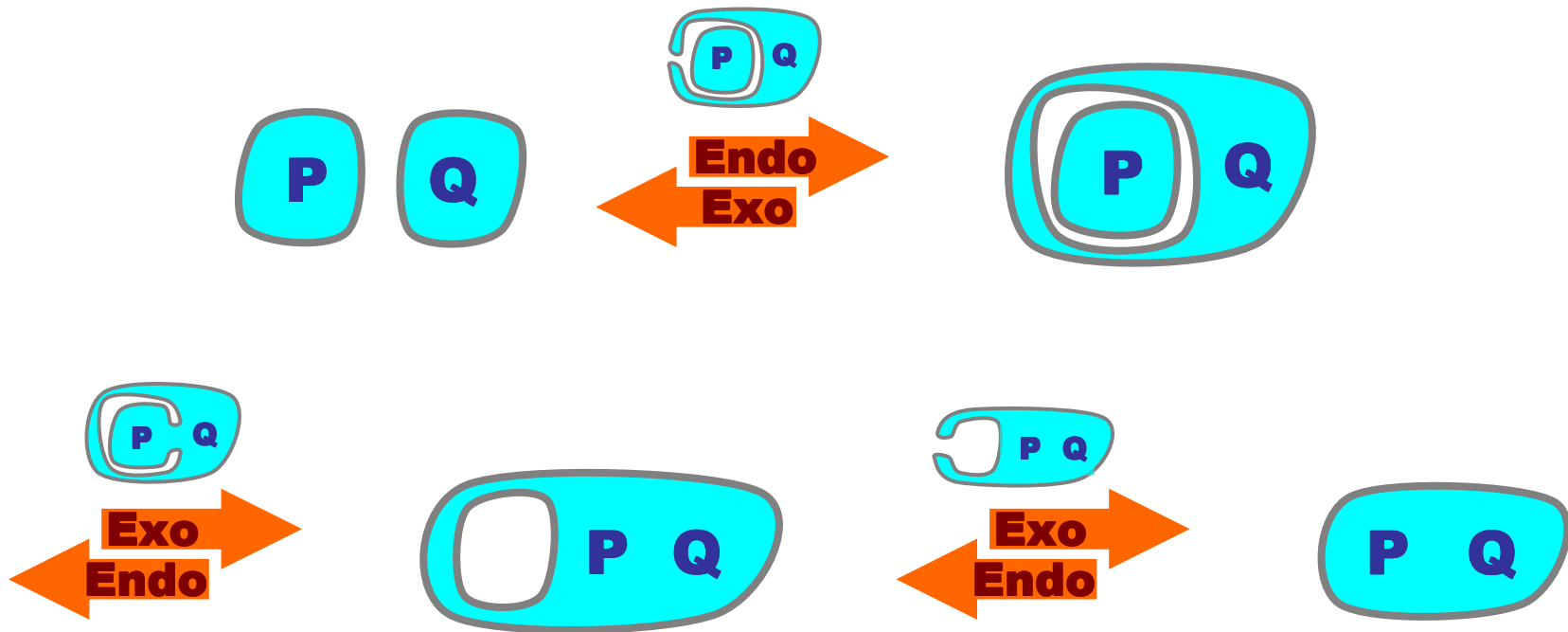


(Fusion)



Same
Local
View!

Mito/Mate by 3 Endo/Exo

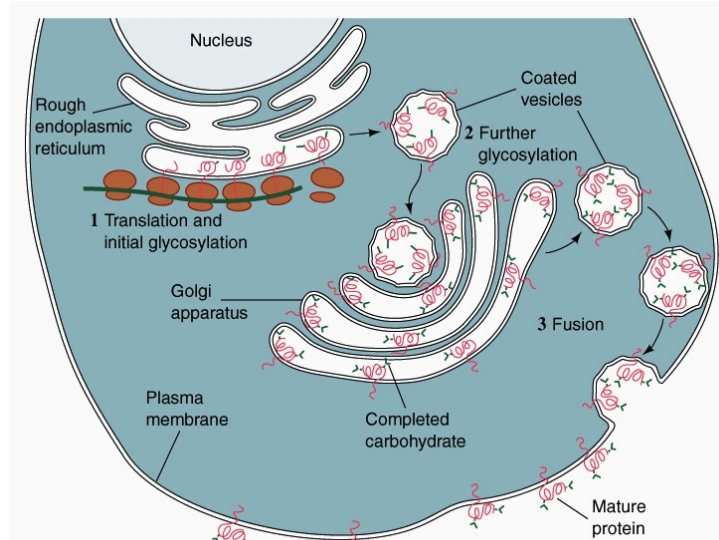


Notations for the Membrane Machine

- "Snapshot" diagrams
 - In biology literature.
- P-Systems
 - G.Paun uses ideas from the theory of grammars and formal languages to model "Membrane Computing" (book 2002).
<http://psystems.disco.unimib.it/>.
- BioAmbients
 - An extension of BioSPI along Ambient Calculus lines (with more bio-relevant mobility primitives) to model dynamic compartments.
- Brane Calculi
 - Computation *on* the membrane...

Membrane Algorithms

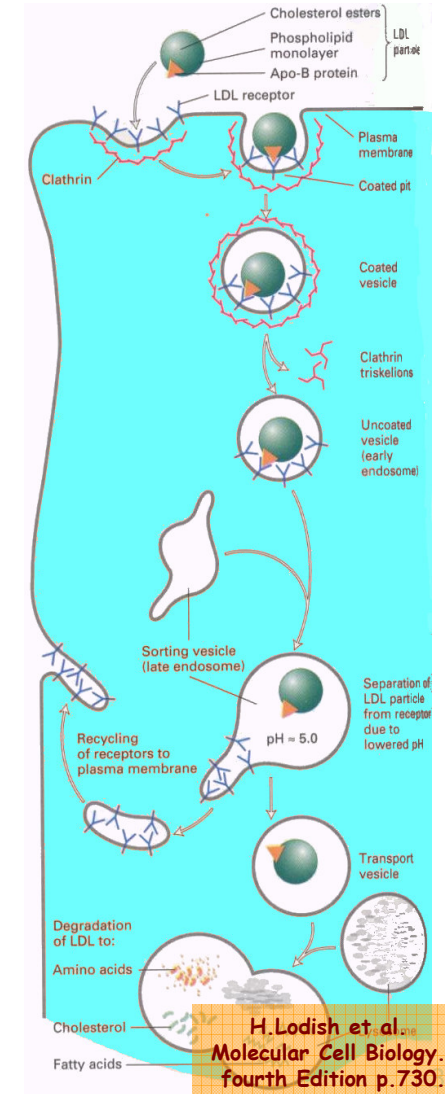
Protein Production and Secretion



Copyright 1999 John Wiley and Sons, Inc. All rights reserved.

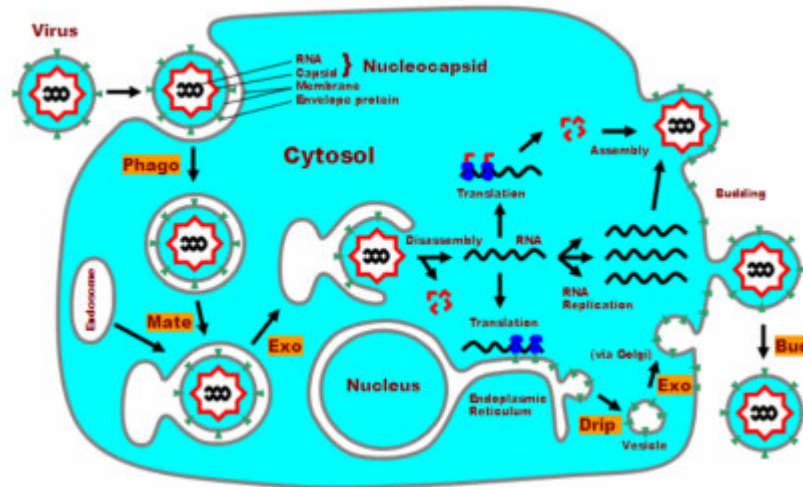
Voet, Voet & Pratt
Fundamentals of Biochemistry
Wiley 1999. Ch10 Fig 10-22.

LDL-Cholesterol Degradation



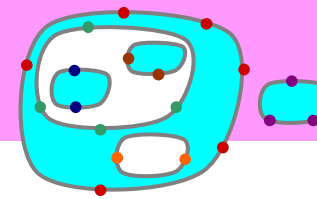
H. Lodish et al.
Molecular Cell Biology.
fourth Edition p.730.

Viral Replication



Adapted from: B. Alberts et al.
Molecular Biology of the Cell
third edition p.279.

Brane Calculi



systems $P, Q ::= \diamond \mid P \circ Q \mid !P \mid \sigma(P)$

nests of membranes

branes $\sigma, \tau ::= 0 \mid \sigma \mid \tau \mid !\sigma \mid a.\sigma$

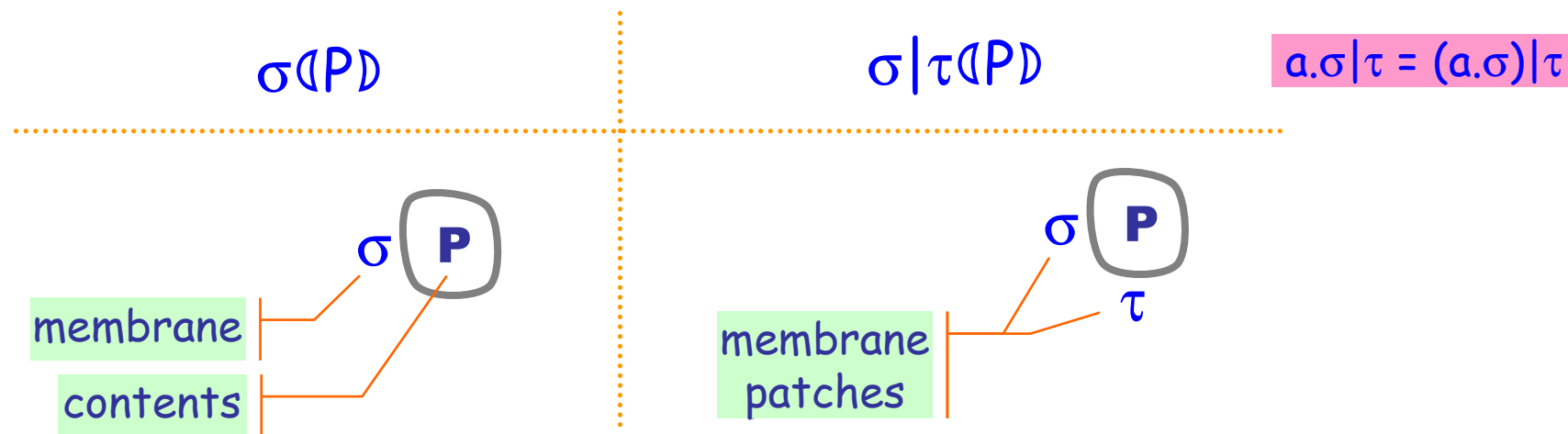
combinations of actions

actions $a ::= 1 \mid \dots$

(fill in as needed)

1D fluids (σ) inside a 2D fluid (P)

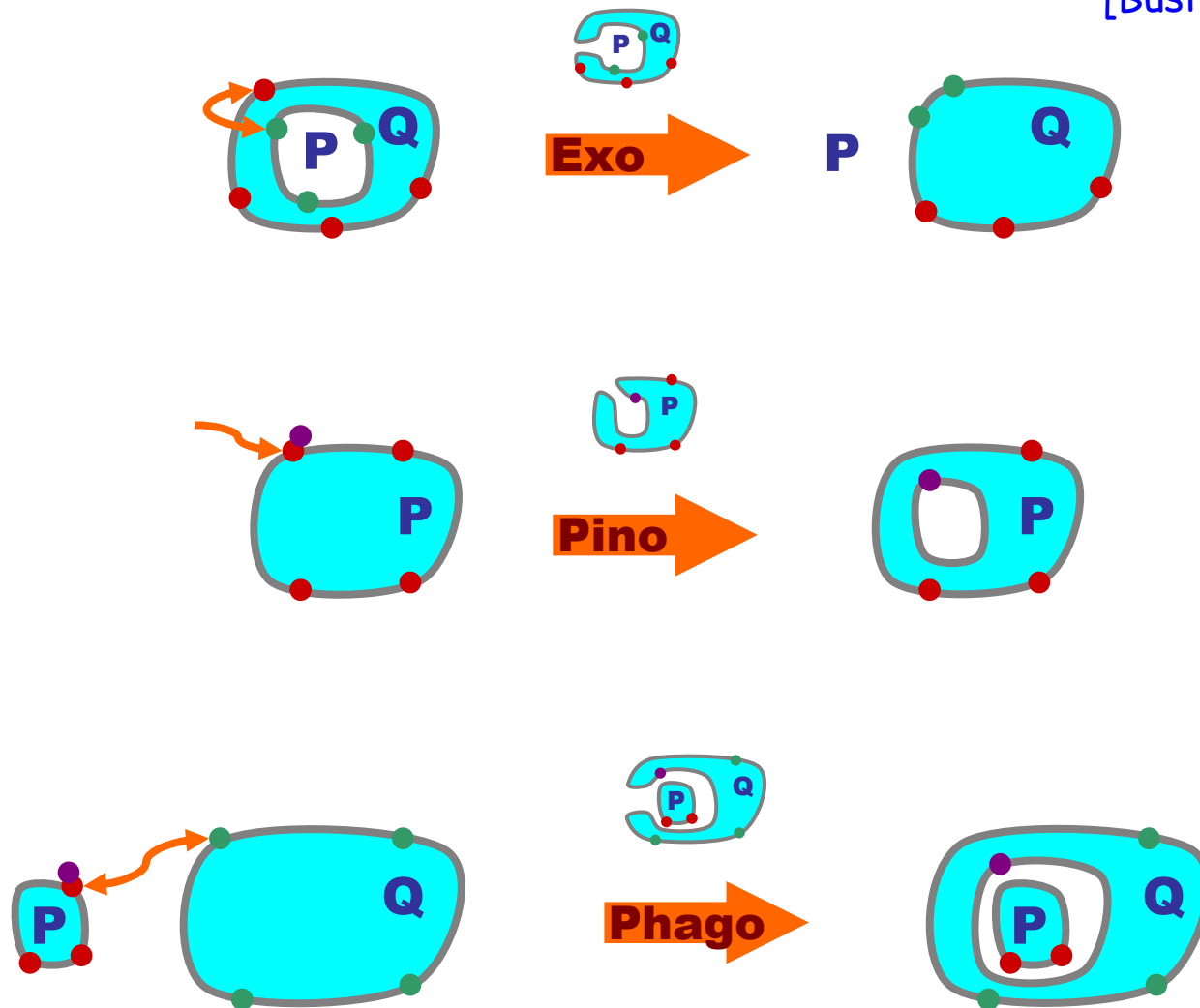
TWO commutative monoids instead of ONE of normal process calculi



N.B. Restriction (νn) could be added to both systems and branes. It usually would originate in branes, but would extrude to whole systems.

Brane Reactions (Cartoons)

A Turing-Complete language
[Busi Gorrieri]



Brane-Molecule Reactions (Cartoons)

With *molecule multisets* \mathbf{p}, \mathbf{q} :



...

Phago $\Downarrow_n.\sigma|\sigma'(P) \circ \Downarrow_n^\perp(\rho).\tau|\tau'(Q) \Rightarrow \tau|\tau'(\rho(\sigma|\sigma'(P))) \circ Q$

Exo $\Downarrow_n^\perp.\tau|\tau'(\Downarrow_n.\sigma|\sigma'(P) \circ Q) \Rightarrow P \circ \sigma|\sigma'|\tau|\tau'(Q)$

Pino $\curvearrowright \odot(\rho).\sigma|\sigma'(P) \Rightarrow \sigma|\sigma'(\rho(\diamond) \circ P)$

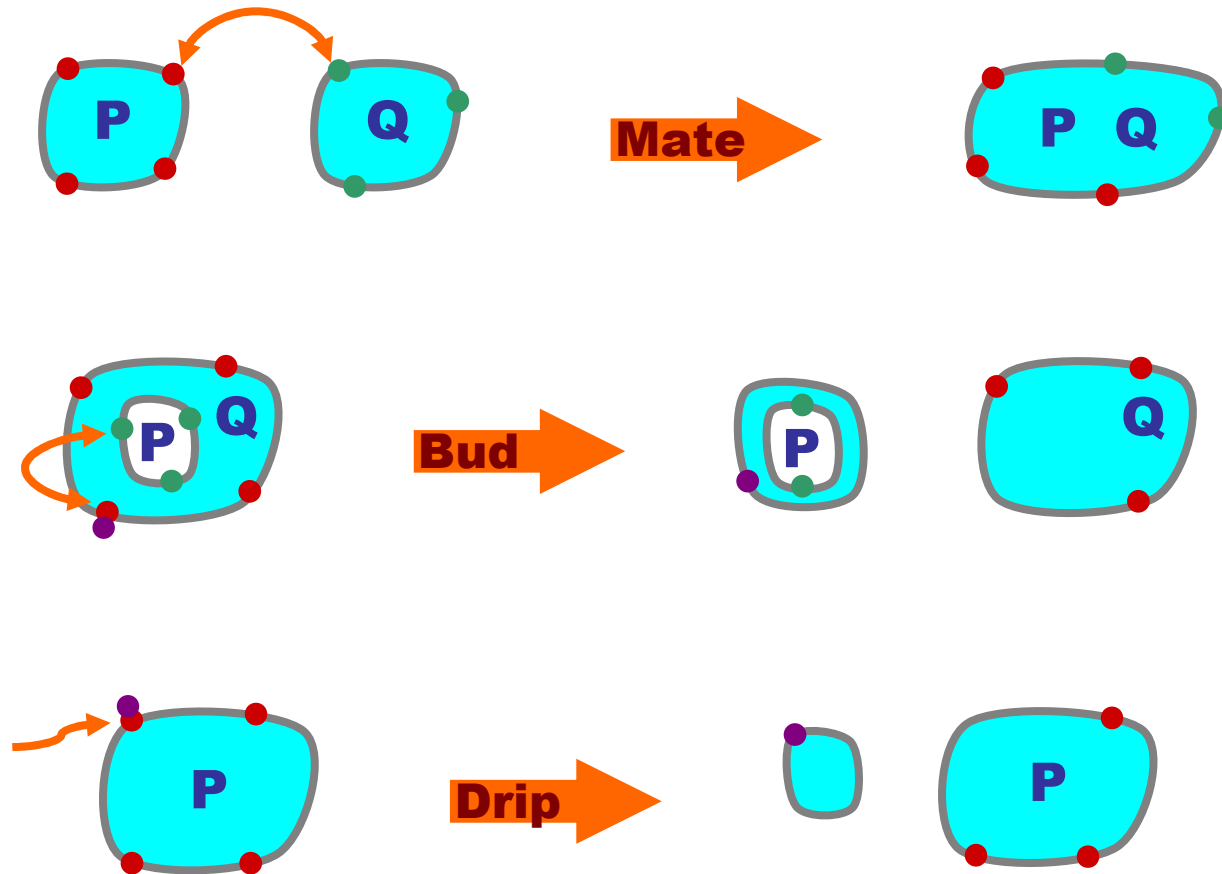
N.B.: the parity of nesting of P and Q is preserved;
this makes the reactions preserve bitonality.

B&R $p_1 \circ p_1(p_2) \Rightarrow q_1(q_2).\alpha|\sigma(p_2 \circ P) \Rightarrow q_1 \circ \alpha|\sigma(q_2 \circ P)$

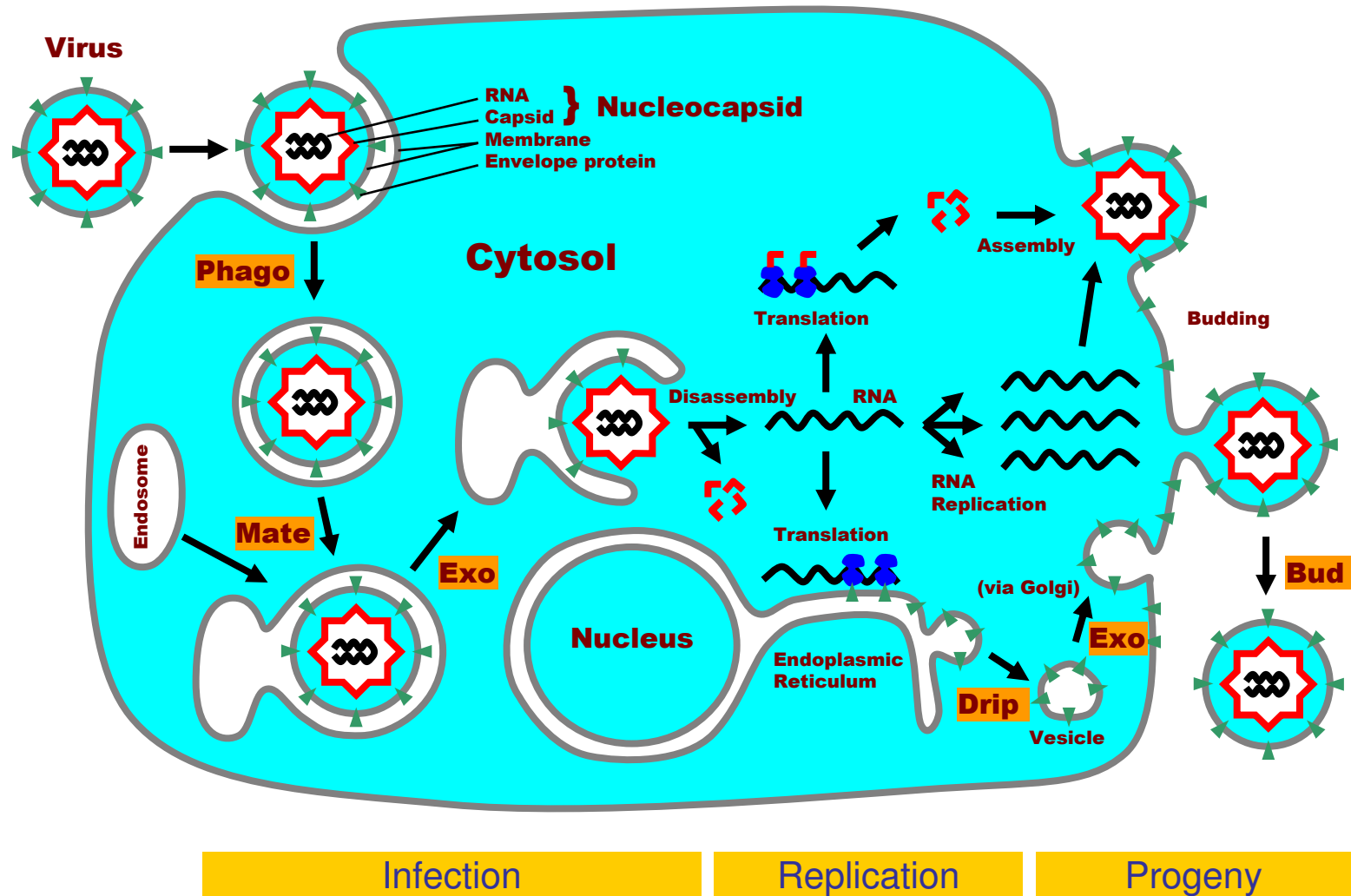
(multiset rewriting, inside and outside membranes)

Derivable Reactions (Cartoons)

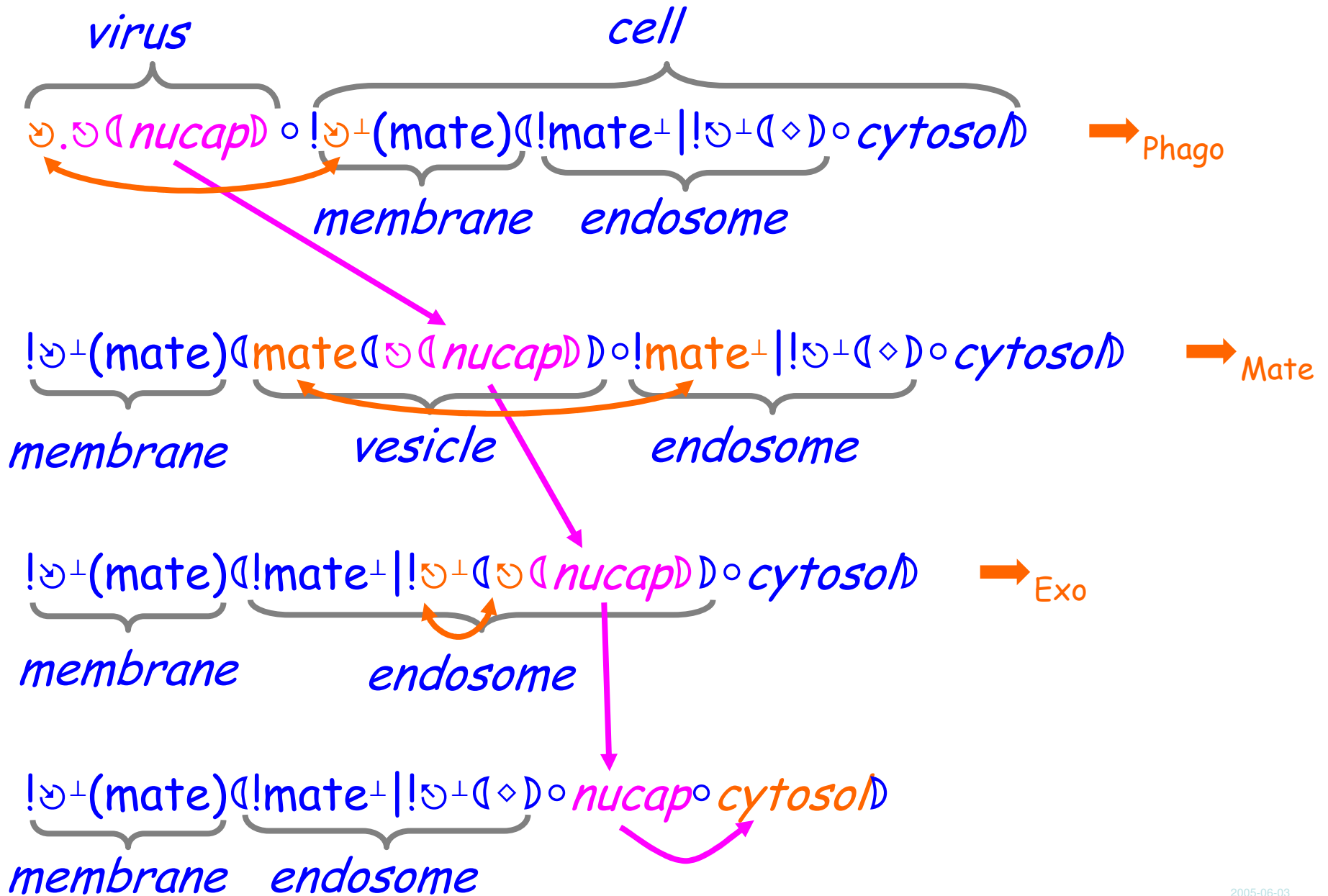
A Decidable-Termination language
[Busi Gorrieri]



Viral Reproduction



Ex: Viral Infection

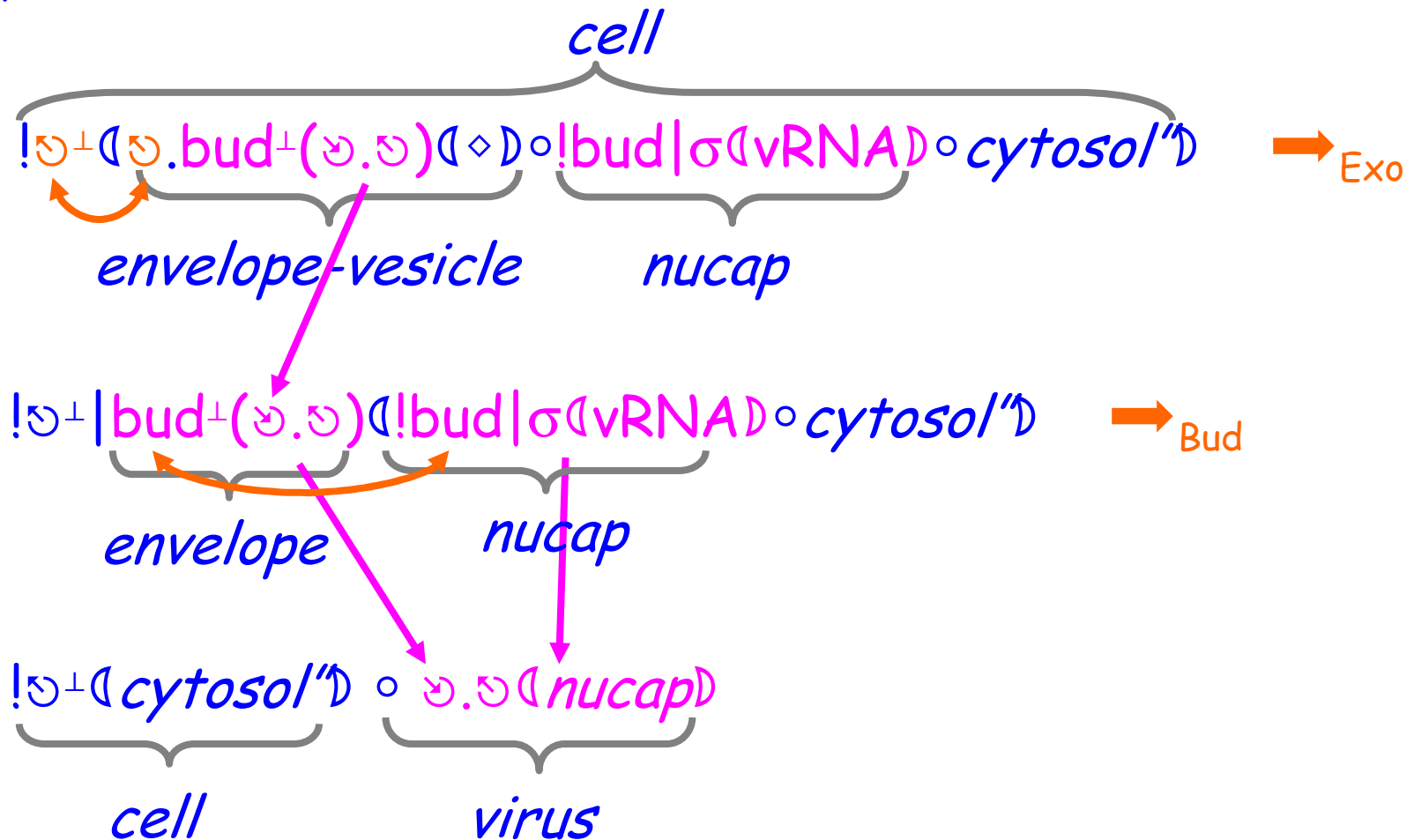


Ex: Viral Progeny

Assume:

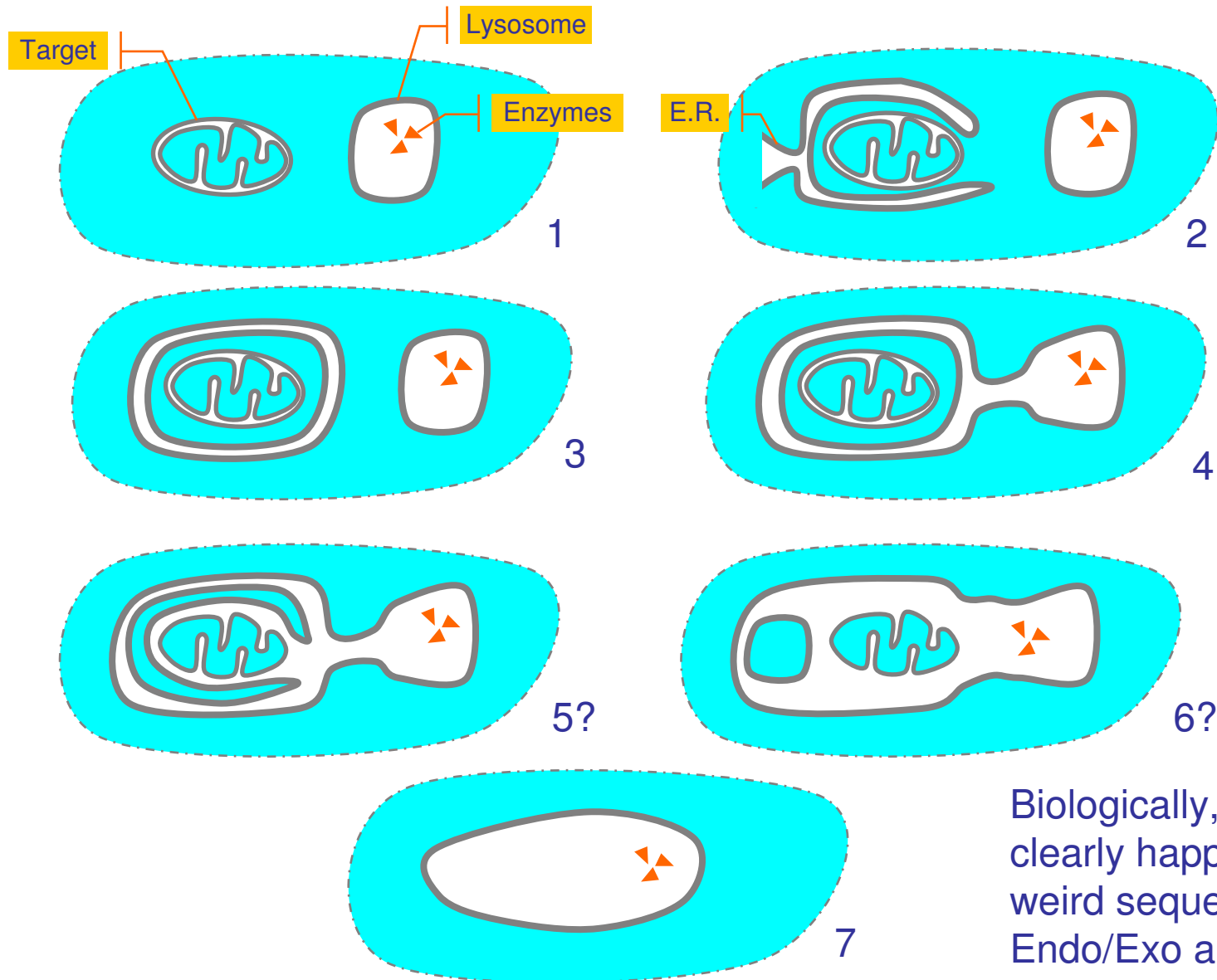
$nucap \circ cytosol \rightarrow \rightarrow nucap^n \circ envelope-vesicle^m \circ cytosol'$
 by available cellular machinery

Then:



Ex: Autophagic Process

Lysosome and target don't just merge.

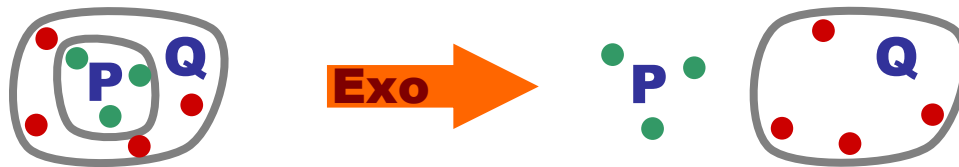


Biologically, Mito/Mate clearly happens. However, weird sequences of Endo/Exo are also common.

"On Brane" vs. "In Brane"



Original "on brane"
Exo of Brane Calculus



"In brane" encoding
(e.g. in BioAmbients
or SMBL) goes wrong



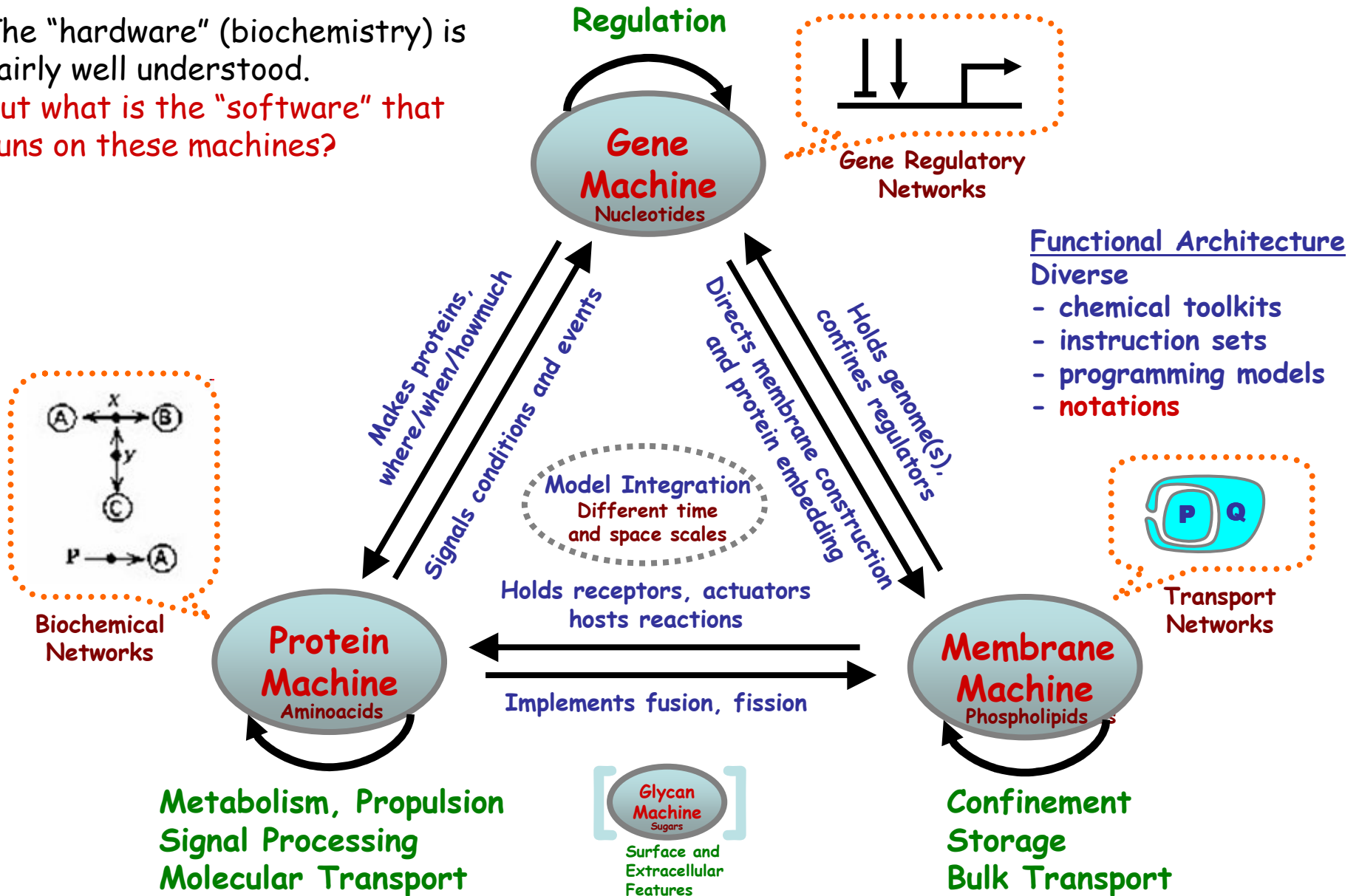
"Ball bearing"
encoding; best we can
do "in brane"

Awkward encoding. And all kinds of things can go wrong in the intermediate state.

- One cannot easily represent the Exo reaction in BioAmbients or any such compartment-based calculus, nor can one easily add it as a new primitive!
- But we can add BioAmbients-like In/Out out to Brane Calculi if we want to.

Abstract Machines of Systems Biology

The "hardware" (biochemistry) is fairly well understood.
 But what is the "software" that runs on these machines?



Metabolism, Propulsion
 Signal Processing
 Molecular Transport

Confinement
 Storage
 Bulk Transport

Surface and Extracellular Features

Importance of Stochastic Effects

- A **deterministic** system:
 - May get "stuck in a fixpoint".
 - And hence **never oscillate**.
- A similar **stochastic** system:
 - May be "thrown off the fixpoint" by stochastic noise, entering a long orbit that will later bring it back to the fixpoint.
 - And hence **oscillate**.

Surprisingly enough, we have found that parameter values that give rise to a stable steady state in the deterministic limit continue to produce reliable oscillations in the stochastic case, as shown in Fig. 5. Therefore, the presence of noise not only changes the behavior of the system by adding more disorder but can also lead to marked qualitative differences.

Mechanisms of noise-resistance in genetic oscillators

Jose´ M. G. Vilar, Hao Yuan Kueh, Naama Barkai, Stanislas Leibler
 PNAS April 30, 2002
 vol. 99 no. 9 p.5991

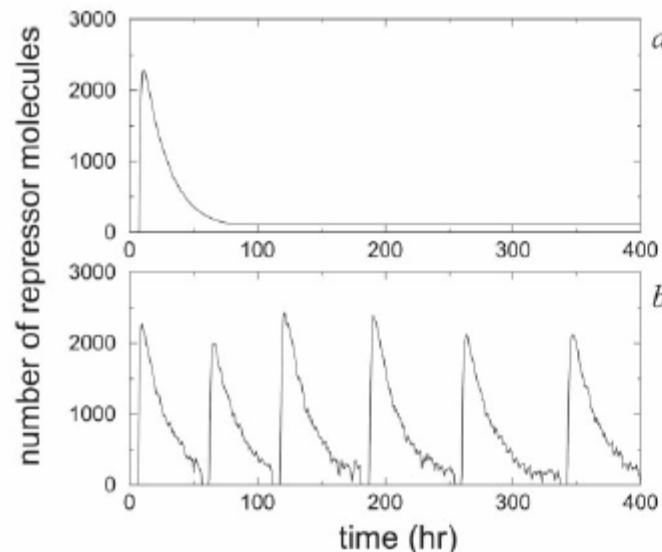


Fig. 5. Time evolution of R for the deterministic Eq. [1] (a) and stochastic (b) versions of the model. The values of the parameters are as in the caption of Fig. 1, except that now we set $\delta_R = 0.05 \text{ h}^{-1}$. For these parameter values, $\tau < 0$, so that the fixed point is stable.

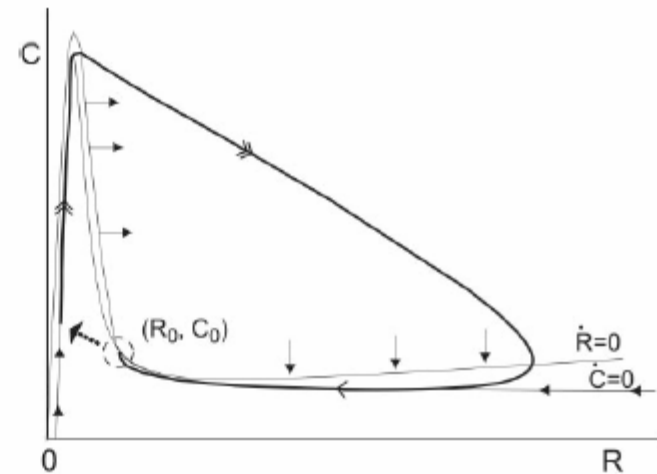


Fig. 6. Phase portrait as in Fig. 4 but for a situation in which the system falls into the stable fixed point (R_0, C_0) . The dotted arrow to the left of the fixed point illustrates a perturbation that would initiate a single sweep of the (former) oscillatory trajectory.

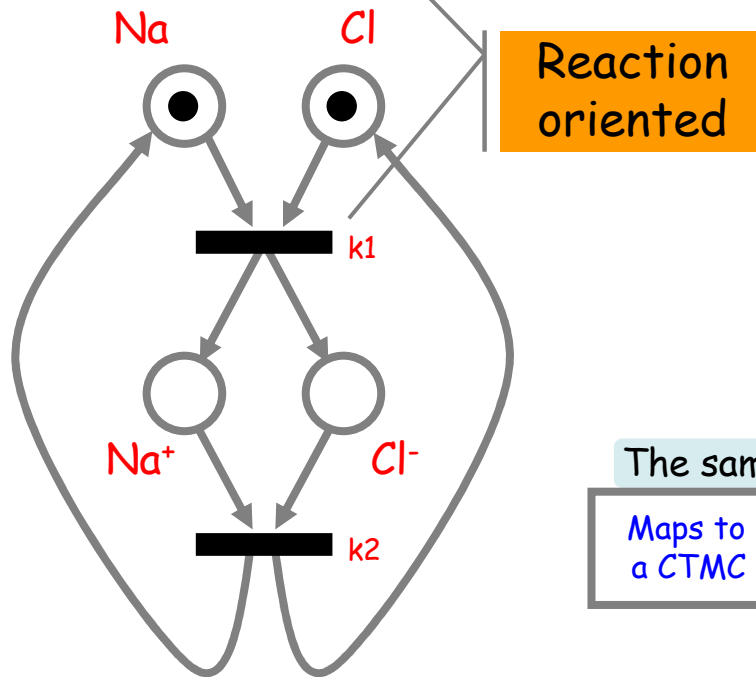
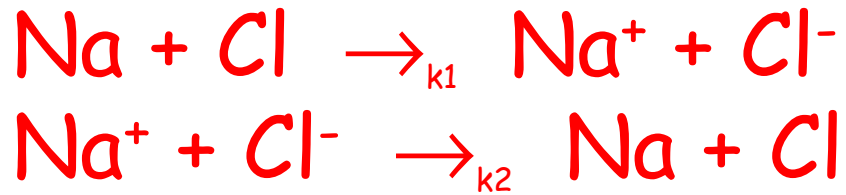
Model Construction and Validation

Reactive Systems

- **Modeling biological systems**
 - Not as continuous systems (often highly nonlinear)
 - But as discrete **reactive systems**; abstract machines with:
 - **States** represent situations
 - Event-driven **transitions** between states represent dynamics
 - The adequacy of describing (discrete) complex systems as reactive systems has been argued convincingly [Harel]
- **Many biological systems exhibit features of reactive systems:**
 - Deep layering of abstractions
 - Complex composition of simple components
 - Discrete transitions between states
 - Digital coding and processing of information
 - Reactive information-driven behavior
 - High degree of concurrency and nondeterminism
 - "Emergent behavior" not obvious from part list

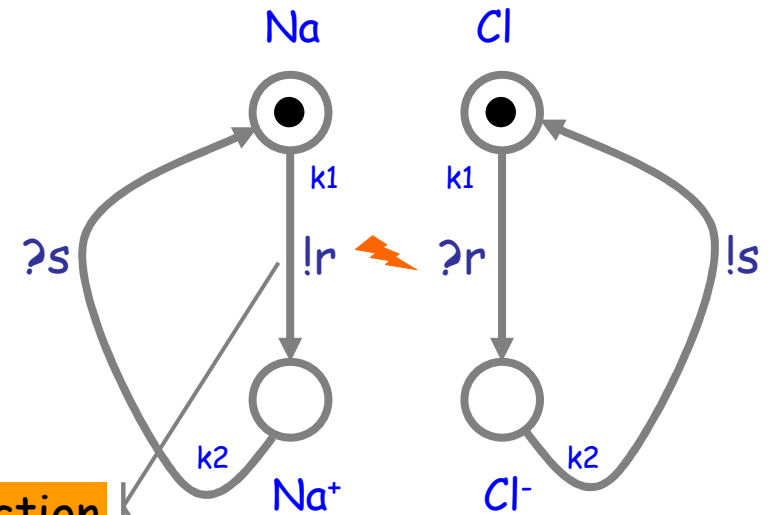
Chemistry vs. π -calculus

A process calculus (chemistry, or SBML)



This Petri-Net-like graphical representation degenerates into spaghetti diagrams: precise and dynamic, but not scalable, structured, or maintainable.

A compositional graphical representation, and the corresponding calculus.



Interaction oriented

The same "model"

Maps to a CTMC

Maps to a CTMC

$$\text{Na} = !r_{k_1}; ?s_{k_2}; \text{Na}$$

$$\text{Cl} = ?r_{k_1}; !s_{k_2}; \text{Cl}$$

A different process calculus (π)

Model Validation: Simulation

- **Basic stochastic algorithm: Gillespie**
 - Exact (i.e. based on physics) stochastic simulation of chemical kinetics.
 - Can compute concentrations and reaction times for biochemical networks.
- **Stochastic Process Calculi**
 - **BioSpi** [Shapiro, Regev, Priami, et. al.]
 - Stochastic process calculus based on Gillespie.
 - **BioAmbients** [Regev, Panina, Silverma, Cardelli, Shapiro]
 - Extension of BioSpi for membranes.
 - **Case study: Lymphocytes in Inflamed Blood Vessels** [Lecaa, Priami, Quaglia]
 - Original analysis of lymphocyte rolling in blood vessels of different diameters.
 - **Case study: Lambda Switch** [Celine Kuttler, IRI Lille]
 - Model of phage lambda genome (well-studied system).
 - **Case study: VICE** [U. Pisa]
 - Minimal prokaryote genome (180 genes) and metabolism of *whole* VIRTUAL CELL, in stochastic π -calculus, simulated under stable conditions for 40K transitions.
- **Hybrid approaches**
 - **Charon language** [UPenn]
 - Hybrid systems: continuous differential equations + discrete/stochastic mode switching.
 - Etc.

Model Validation: "Program" Analysis

- **Causality Analysis**

- *Biochemical pathways*, ("concurrent traces" such as the one here), are found in biology publications, summarizing known facts.
- This one, however, was automatically generated from a program written in BioSpi by comparing traces of all possible interactions. [Curti, Priami, Degano, Baldari]
- One can play with the program to investigate various hypotheses about the pathways.

- **Control Flow Analysis**

- Flow analysis techniques applied to process calculi.
- Overapproximation of behavior used to answer questions about what "cannot happen".
- Analysis of positive feedback transcription regulation in BioAmbients [Flemming Nielson].

- **Probabilistic Abstract Interpretation**

- [DiPierro Wicklicky].

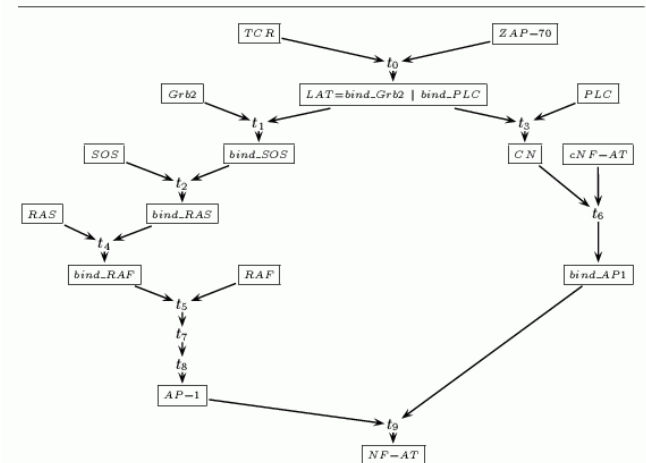


Fig.2. A computation of *Sys*. For readability, the processes, enclosed in boxes, have no address. Causality (both on transitions and processes) is represented by the (Hasse diagram resulting from the) arrows; their absence makes it explicit concurrent activities.

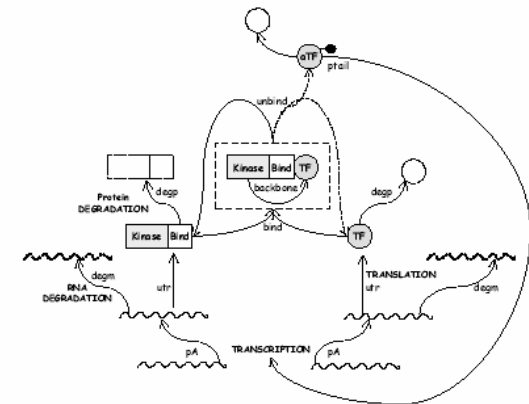


Fig. 1. Graphical presentation of Transcriptional Regulation by Positive Feedback [25].

Model Validation: Modelchecking

- **Temporal**

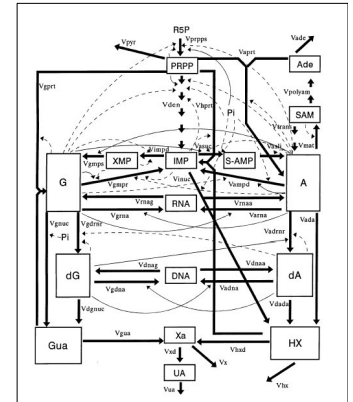
- Software verification of biomolecular systems (NA pump)
[Ciobanu]
- Analysis of mammalian cell cycle (after Kohn) in CTL.
[Chabrier-Rivier Chiaverini Danos Fages Schachter]
 - E.g. is state S_1 a necessary checkpoint for reaching state S_2 ?

- **Quantitative: Simpathica/xssys**

[Antioniotti Park Policriti Ugel Mishra]

- Quantitative temporal logic queries of human Purine metabolism model.

Eventually(Always (PRPP = 1.7 * PRPP1))
implies
steady_state()
and Eventually(Always(IMP < 2 * IMP1))
and Eventually(Always(hx_pool < 10*hx_pool1)))



- **Stochastic: Spring**

[Parker Normal Kwiatkowska]

- Designed for stochastic (computer) network analysis
 - Discrete and Continuous Markov Processes.
 - Process input language.
 - Modelchecking of probabilistic queries.

What Reactive Systems Do For Us

We can write things down precisely

- We can modularly describe high structural and combinatorial complexity ("do programming").

We can calculate and analyze

- Directly support simulation.
- Support analysis (e.g. control flow, causality, nondeterminism).
- Support state exploration (modelchecking).

We can visualize

- Automata-like presentations.
- Petri-Net-like presentations.
- State Charts, Live Sequence Charts [Harel]
 - Hierarchical automata.
 - Scenario composition.

We can reason

- Suitable equivalences on processes induce algebraic laws.
- We can relate different systems (e.g. equivalent behaviors).
- We can relate different abstraction levels.
- We can use equivalences for state minimization (symmetries).

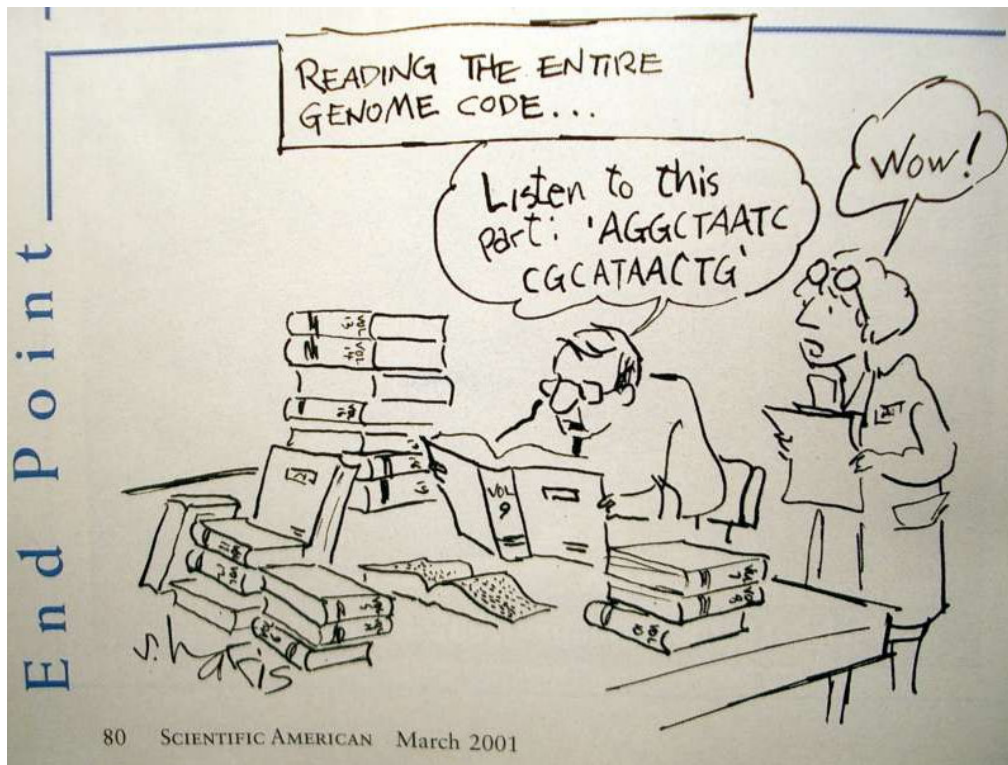
Disclaimers

- Some of these technologies are basically ready (medium-scale stochastic simulation and analysis, medium-scale nondeterministic and stochastic modelchecking).
- Others need to scale up significantly to be really useful. This is (has been) the challenge for computer scientists.

Many approaches, same basic philosophy, tools being built:

⇒ *Proc. Computational Methods in Systems Biology* [2003-2005]

Conclusions



Q: "The data are accumulating and the computers are humming, what we are lacking are **the words, the grammar and the syntax of a new language...**"

D. Bray (TIBS 22(9):325-326, 1997)

A: "The most advanced tools for computer process description seem to be also the best tools for the description of biomolecular systems."

E.Shapiro (Lecture Notes)

References

[MCB] Molecular Cell Biology, Freeman.

[MBC] Molecular Biology of the Cell, Garland.

[Ptashne] A Genetic Switch.

[Davidson] Genomic Regulatory Systems.

[Milner] Communicating and Mobile Systems: the Pi-Calculus.

[Regev] Computational Systems Biology: A Calculus for Biomolecular Knowledge (Ph.D. Thesis).

Papers

BioAmbients

a stochastic calculus with compartments.

Brane Calculi

process calculi with computation "on" the membranes, not inside them.

Bitonal Systems

membrane reactions and their connections to "local" patch reactions.

Abstract Machines of Systems Biology

the abstract machines implemented by biochemical toolkits.

www.luca.demon.co.uk/BioComputing.htm