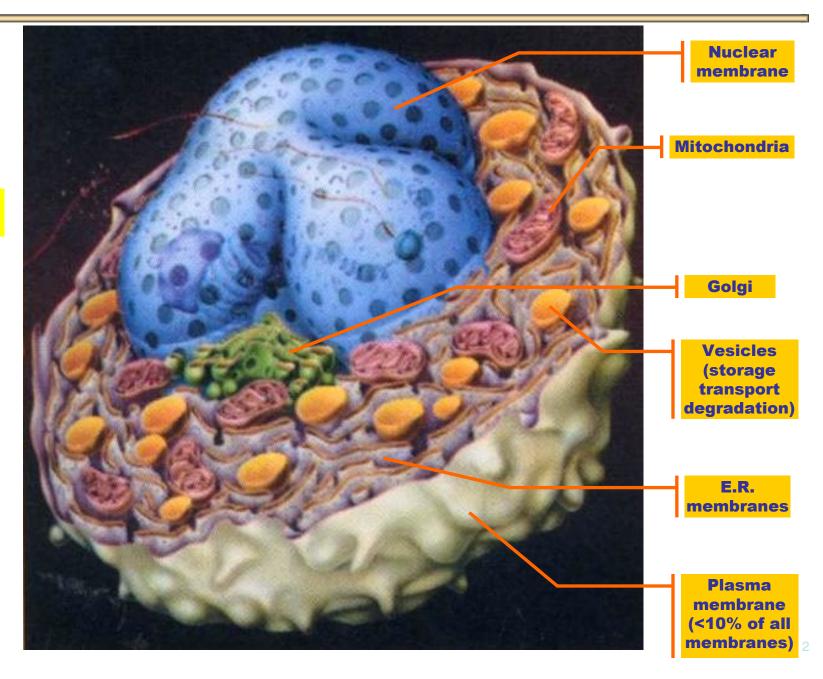
# Membrane Interactions Luca Cardelli

**Microsoft Research** 

Lisbon, 2003-11-12

http://www.luca.demon.co.uk

# **Eukaryotic Cell**

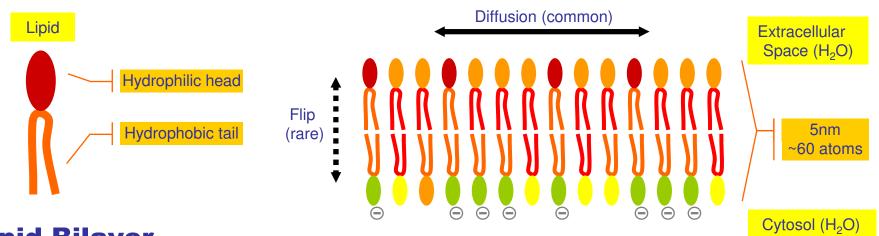


Membranes everywhere

# **Membrane-based Systems**

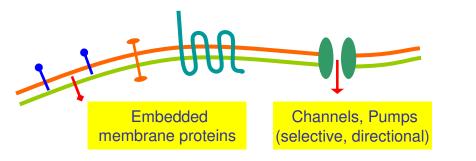
- Many cellular processes involve membranes.
   It's very far from a "chemical soup":
  - For a cell to function properly, each of its numerous proteins must be localized to the correct cellular membrane or aqueous compartment. [MCB p.675]
- What is the dynamics of these complex configurations of membranes?
- In modeling it, we *must* use abstractions, to avoid combinatorial explosion: 1 membrane  $\approx \infty$  molecules.
- Emerging area of Systems Biology
   (~ interdisciplinary study of relationships and interactions of biological components).

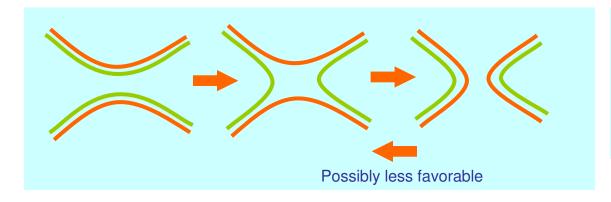
### **Membranes are Oriented 2D Surfaces**



### **Lipid Bilayer**

Self-assembling
Largely impermeable
Asymmetrical (in real cells)
Embedded proteins
A 2D fluid inside a 3D fluid!







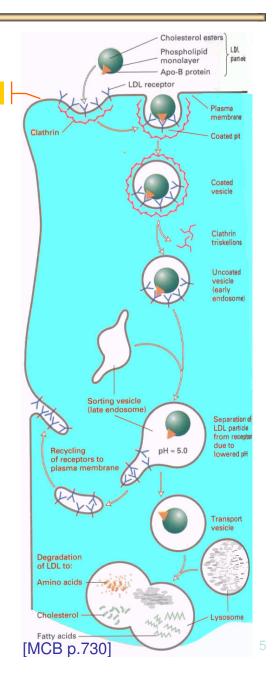
# **A Biological Algorithm**

Lipid bilaver

LDL-Cholesterol Degradation

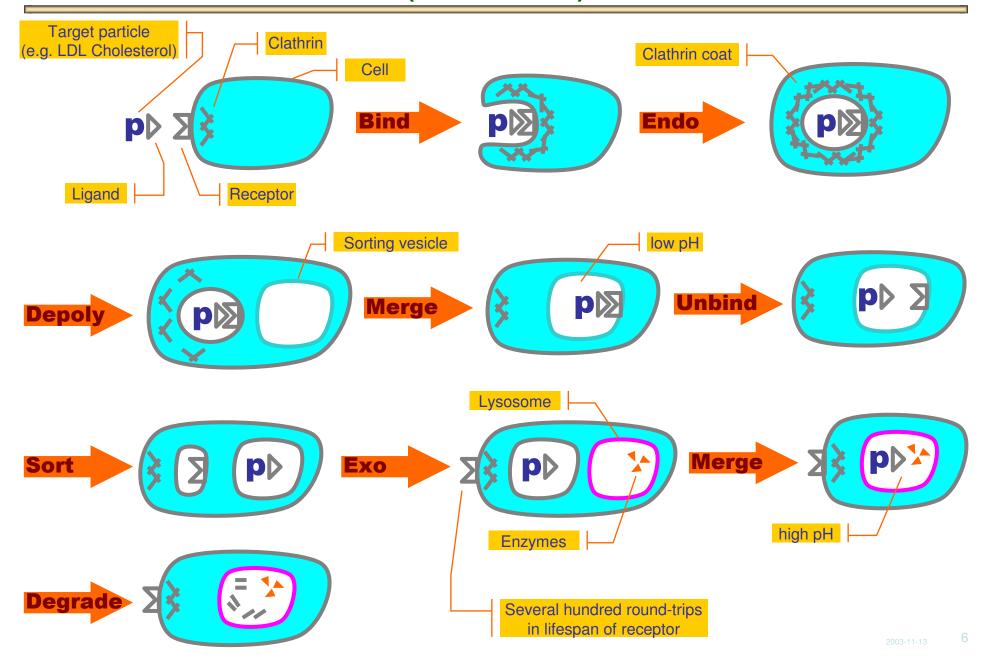
 A cast of many thousands (molecules) just to get one molecule from A to B.

- Membranes are key to the algorithm, we want to model *them*, not their individual molecules.
- How do people know all that?
  - They take pictures, see all stages of the algorithm in the same snapshot.
  - Stop genes, see what stages survive; build temporal sequence of stages.
  - Identify key molecules. Model them and play with them to see what they do.
  - Many steps still murky. Not possible to model them in detail even if wanted to.

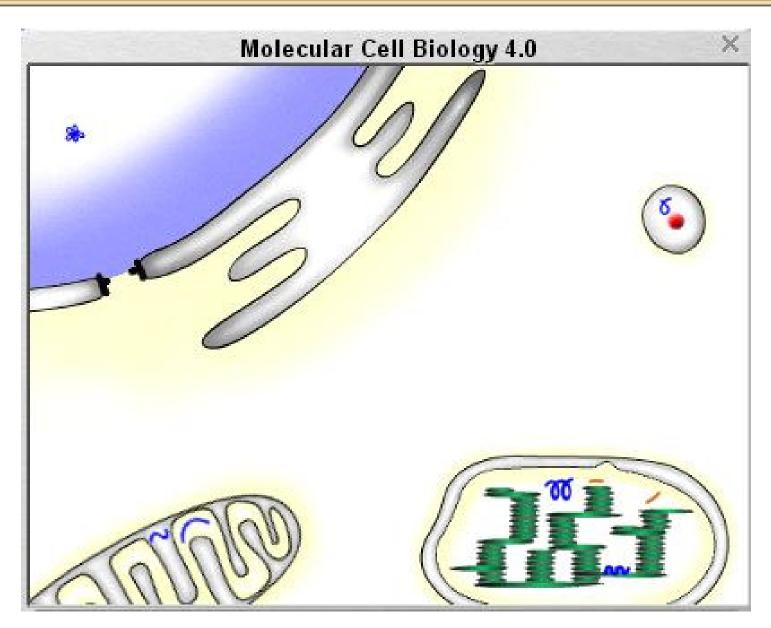


## **Receptor-Mediated Degradation Pathway**

(Abstract view)



# **Dynamic Compartments**



### **Aims**

- Describing biological processes
  - Avoid informal diagrams.
  - Write bioalgorithms in something close to a language.
- Abstraction options
  - Start too low ⇒ get lost in a mess of details.
  - Start too high  $\Rightarrow$  ignore too many details.
- Strategy (for now)
  - 1) Start too high (but learn basic gameplay).
  - 2) Move one or two levels down.
- Approaches considered here
  - (Whole-)Membrane Reactions (*Bitonal Reactions*)
  - Rewriting systems (BiGraphs, Gamma, P-Systems, etc.)
  - Patch Reactions (BioSPi, BioAmbients, Brane Calculi)
     Stochastic Simulation

### Part I

# **Bitonal Systems**

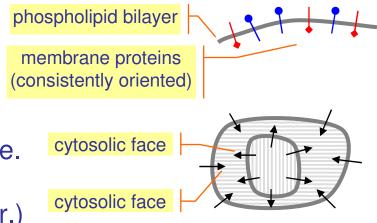
# **Systems of Oriented Membranes**

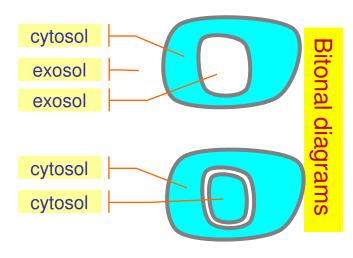
Membranes are closed non-intersecting curves, with an orientation<sup>(1)</sup>.

Each membrane has two faces. A cytosolic (~inner) face and an exoplasmic (~outer) face. Nested membranes alternate orientation. (E.g. cytosolic faces always face each other.)

This alternation is illustrated by using two tones: blue (cytosol<sup>(2)</sup>) and white (exosol<sup>(3)</sup>). Bitonal diagrams.

Double membranes (e.g. the nuclear membrane) can be used for blue-in-blue components.





- (1) A membrane is built from a phospholipid bilayer that is asymmetrical. Moreover, all real membranes are heavily sprinkled with proteins: "each type of integral membrane protein has a single specific orientation with respect to the cytosolic and exoplasmic faces of a cellular membrane, and all molecules of any particular integral membrane protein share this orientation. This absolute asymmetry in protein orientation confers different properties on the two membrane faces." MCB p162.
- (2) Short for Cytoplasmic Solution. (3) Short for Exoplasmic Region (I am making this one up).

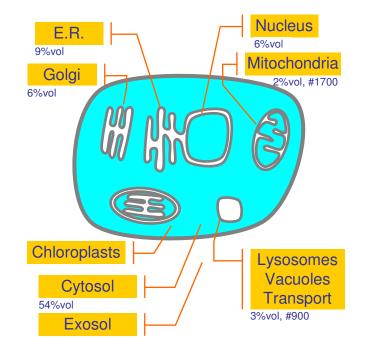
# **Bitonal Diagrams**

### **Bitonal Postulate**

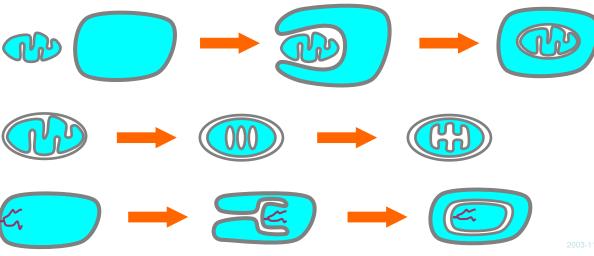
Blue and white areas alternate.

### **Bitonal Invariant**

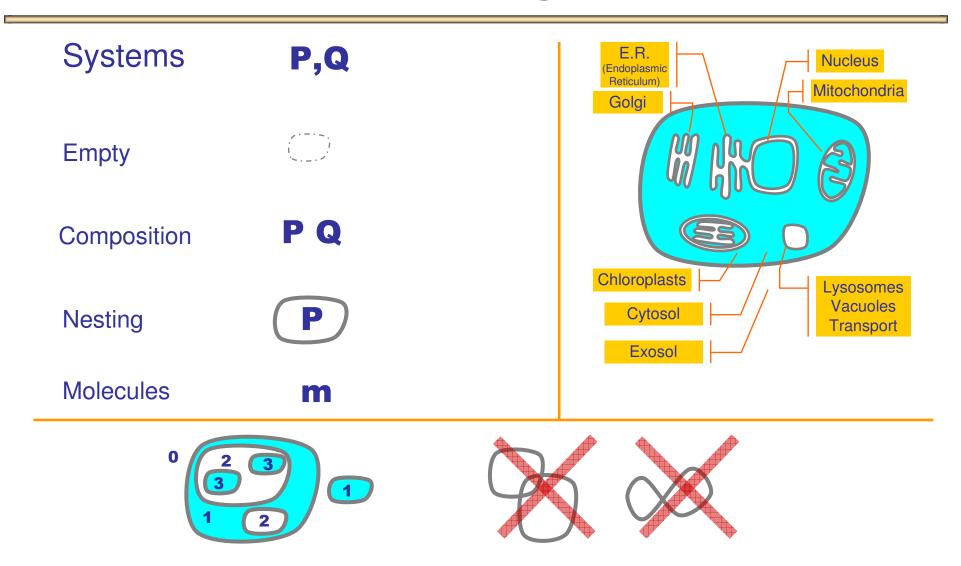
Bitonality is preserved by reactions (i.e. blue and white fluids never mix).



**Evolutionary** explanations of bitonality



# **Membrane Systems**



The *depth* of a point is the number of membranes that contain it. The *tonality* of a point is white/blue iff its depth is even/odd.

### Reactions

A *reaction* is a pair of membrane systems (before and after), but we are only interested in *gradual changes*; e.g.:



There are two ways to characterize gradual changes:

- Local interactions of membrane patches.
   (What really happens at the biochemical level.)
- Membrane reactions that preserve tonality "almost everywhere".
   (Matching biological terminology, e.g. mitosis, endocytosis.)
   These turn out to be equivalent!

### **Bitonal Reactions**

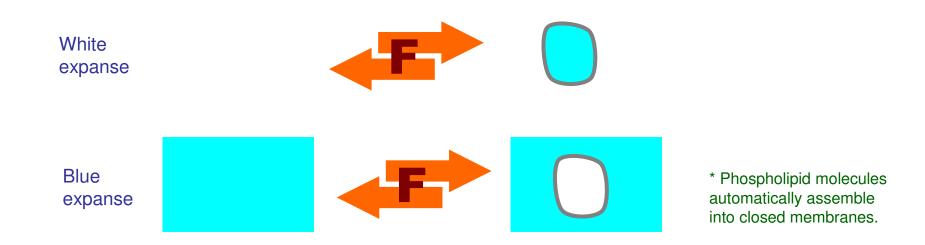
Are "local".

Do not mix "inside" and "outiside" fluids.

Preserve bitonal coloring.

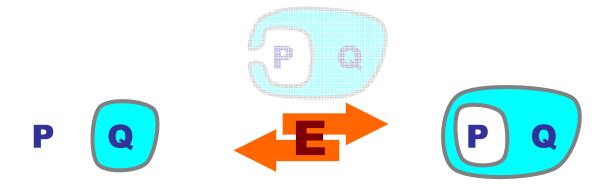
### √ Froth/Fizz Reaction

The spontaneous appearance/disappearance of empty bubbles (of the correct tonality).

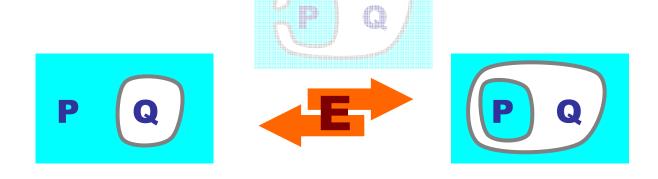


N.B. non-empty membranes should not "spontaneously" be created or deleted: usually only very deliberate processes cause that. However, spontaneous froth/fizz seems be harmless; it means that empty membranes are not observable.

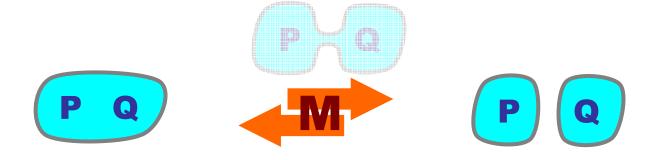
## ✓ Endo/Exo Reaction



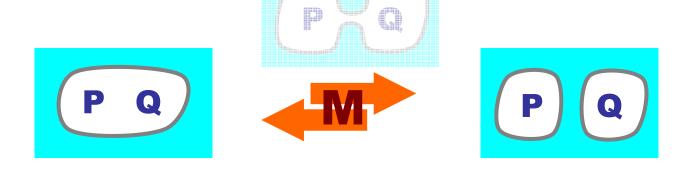
### Dual:



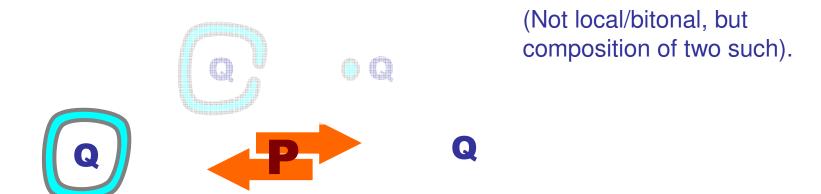
### ✓ Mito/Mate Reaction



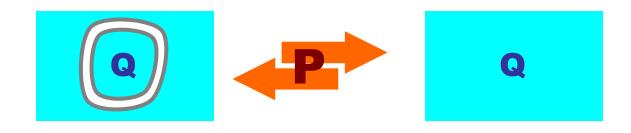
### Dual:



### ✓ Peel/Pad Transformation



### Dual:



### **×** Ambients





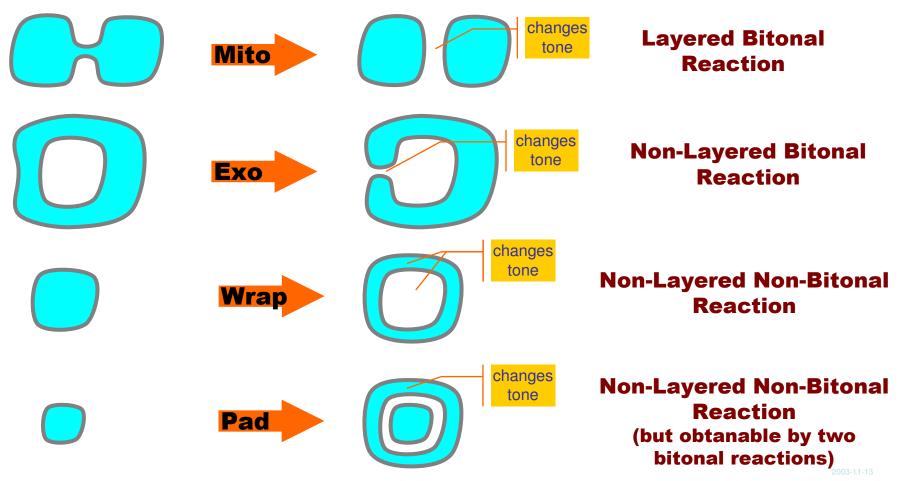


These abstract transformations are not bitonal (are not implementable by a finite and fixed sequence of abstract bitonal reactions); they invert the color of arbitrary subsystems which are in general not simply-connected.

Moreover, these transformations are not "implementable": they imply either flipping orientation of membranes, or having membranes cross membranes, or destroying membranes (localized digestion excepted).

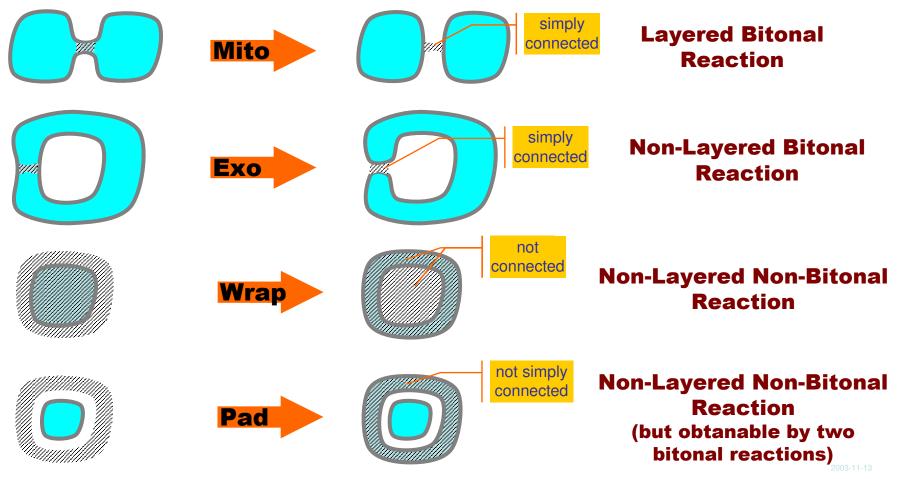
### **Bitonal Reactions**

 A bitonal (resp. layered) reaction is such that the points that change tone (resp. depth) form a simply-connected region (a region not separated by membranes).



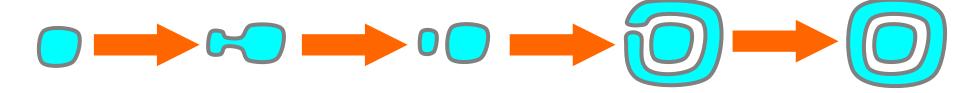
### **Bitonal Reactions**

• A bitonal (resp. layered) reaction is a pair of membrane systems <M,M'> such that the points that change tone (resp. depth) form a simply-connected region (a region not separated by membranes).



### **Bitonal Transformations**

- A *transformation* is a finite sequence of reactions. A *bitonal transformation* is a finite sequence of bitonal reactions.
- We want all "legal" transformations to be bitonal transformations (and hence "gradual" transformations). E.g.: padding:



 Some transformations are inherently nonbitonal.

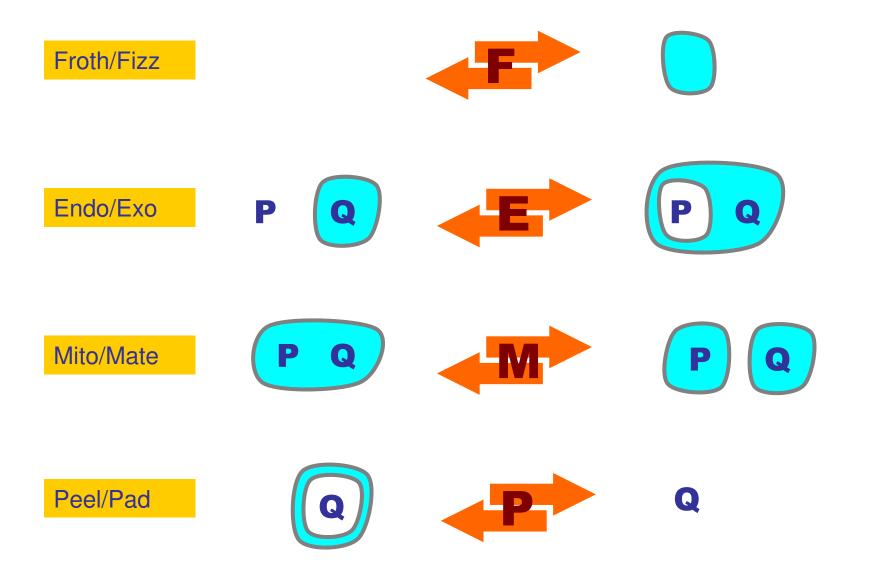
### **Abstract Transformations**

 An abstract reaction/transformation is a reaction/transformation where arbitrary subsystems (indicated by letters P,Q,...) are kept *fixed* on the plane, but other membranes can be changed.

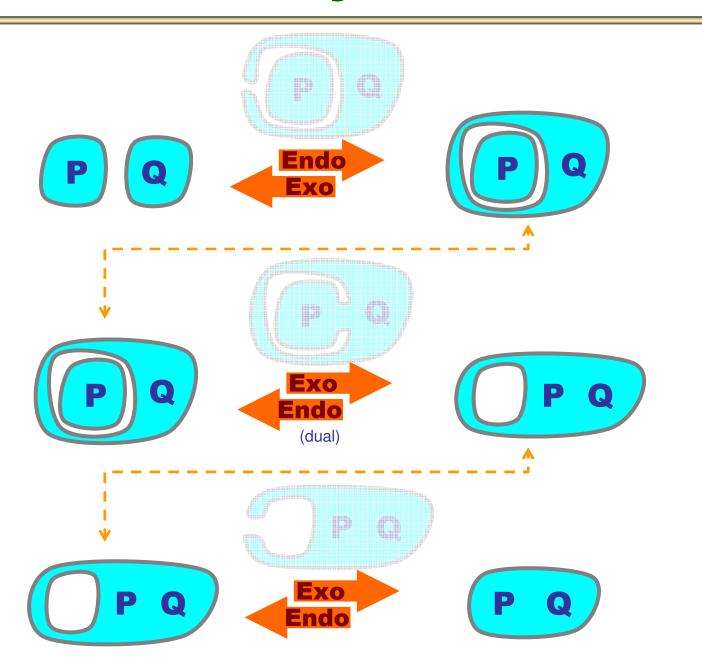


 An abstract transformation is bitonal if it is bitonal for arbitrary subsystems (with the same number of steps).

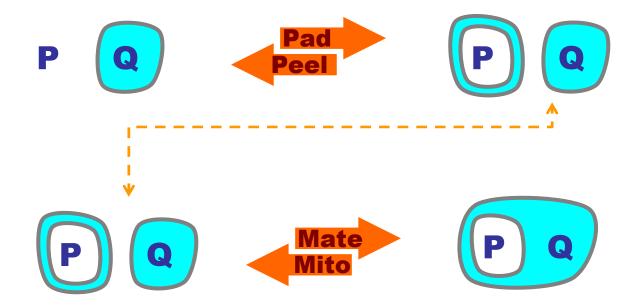
# **Summary: Four Good Transformations**



# Mito/Mate by 3 Endo/Exo

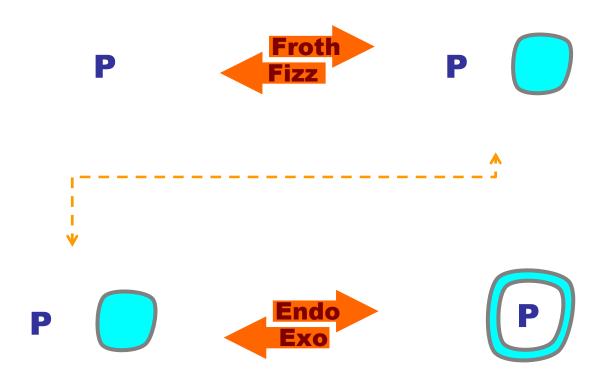


# **Endo/Exo by Mito/Mate and Peel/Pad**



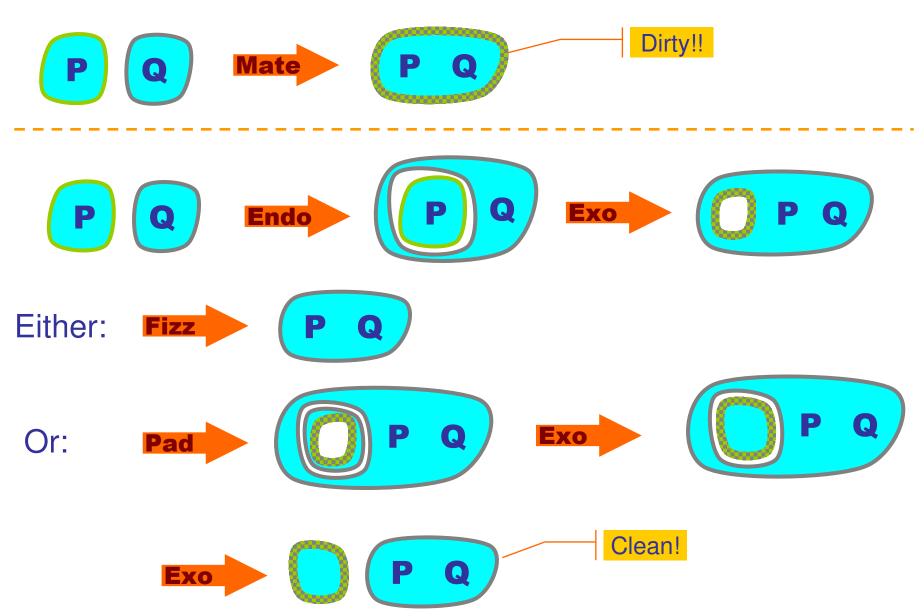
Endo/Exo from Mito/Mate only? No: depth of nesting is constant in Mito/Mate.

# Peel/Pad by Froth/Fizz and Endo/Exo



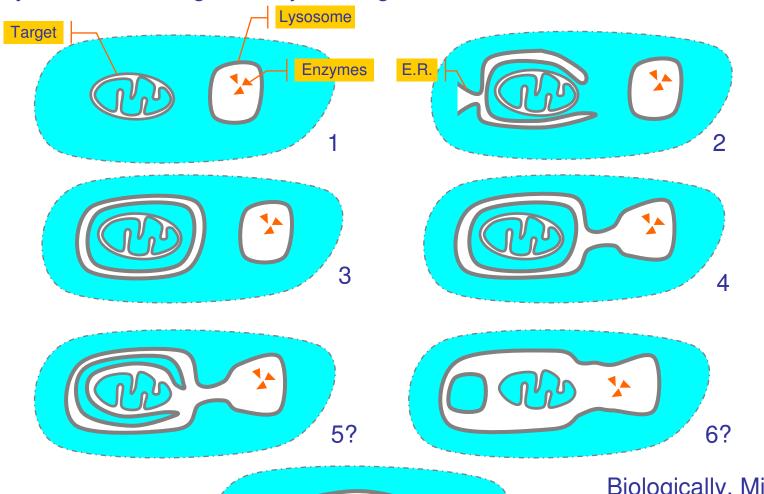
# **Ex: Clean Eating**

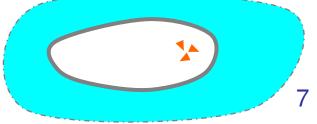
(why Endo/Exo is "healthier" than Mito/Mate)



# (Real) Ex: Autophagic Process

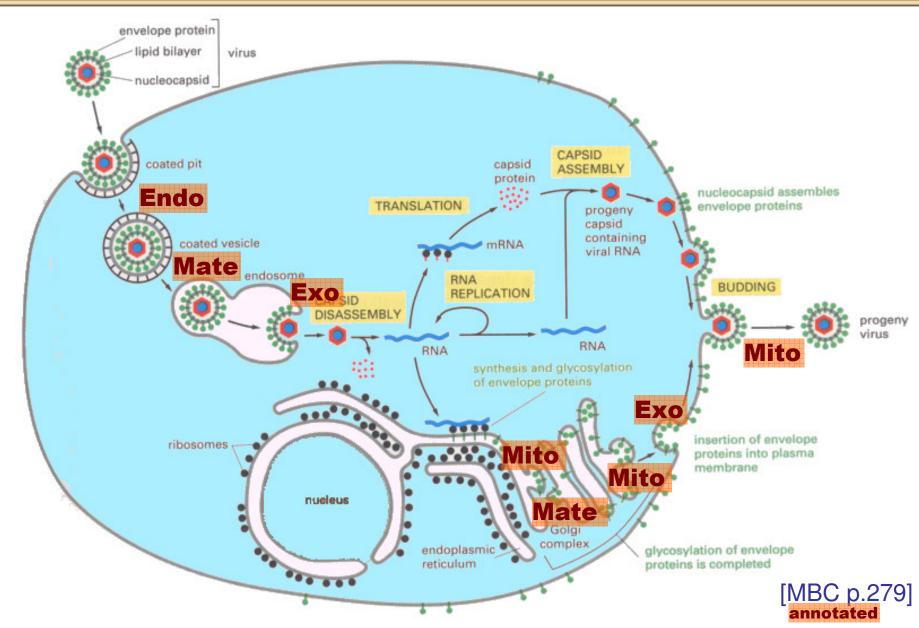
Lysosome and target don't just merge.





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

# (Real) Ex: Viral Reproduction



### **Bitonal Calculus**

$$X := \Diamond \mid X \circ X \mid (X)$$

We look at this calculus as a preliminary abstraction of more detailed process calculi one may devise.

### **Axioms**

♦ O is a comm. monoid

$$E/E: X \circ (Y) = ((X) \circ Y)$$

**Facts** 

(without using commutativity)

M/M:

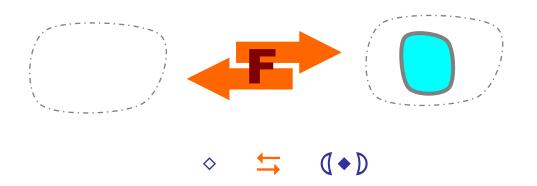
P/P:

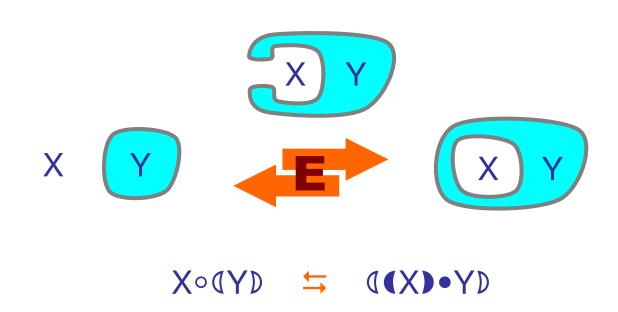
$$X \leftrightarrows X \circ \diamond \leftrightarrows X \circ (\diamond)$$

$$\leftrightarrows ((X)) \circ \diamond () \leftrightarrows ((X))$$

It is possible to define a simple "type system" that consistently colors brackets and operators with appropriate tones:

# **Axioms Illustrated**





### **Bitonal Calculus v2**

$$X := \Diamond \mid X \Diamond X \mid (X)$$

### **Axioms**

♦ o is a comm. monoid

M/M:  $(X \circ X') = (X') \circ (X)$ 

### Facts

E/E:

F/F:

$$X \circ QYD \Rightarrow QQXDD \circ QYD \Rightarrow QQXD \circ YD$$

$$( \diamond ) \ \leftrightarrows \ \diamond \circ ( \diamond ) \ \leftrightarrows \ ( ( \diamond ) \circ \diamond ) \ \leftrightarrows \ ( ( \diamond ) ) \ \leftrightarrows \ \diamond$$

### **Ex: Viral Infection**

```
(capsidD∘((endosome)•cytosolD → Endo
(((capsidD)•(endosome)•cytosolD → Mate
(((capsidD∘endosome)•cytosolD → Exo
((endosome)•capsid•cytosolD → ...
```

But what causes these reactions to happen (and in one direction only)?

To explain what "really happens" a bit better, we need to move to a lower level of abstraction.

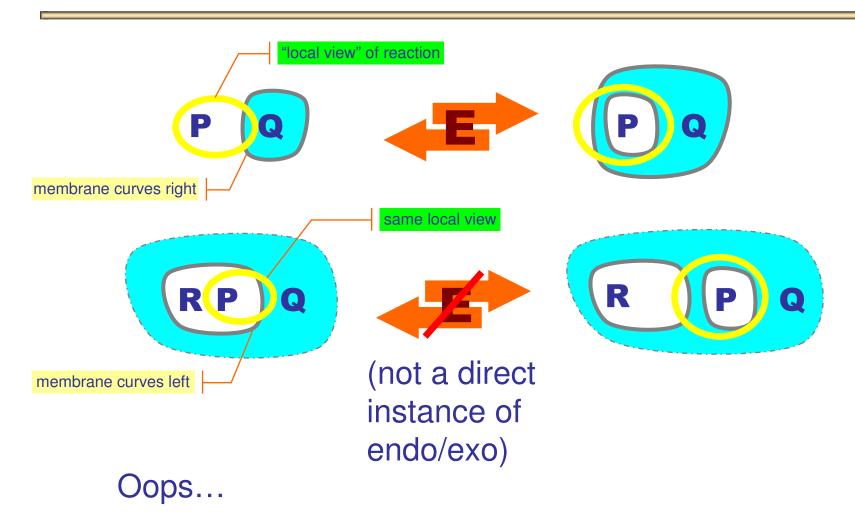
# **A Note About Locality**

### **Locality Postulate**

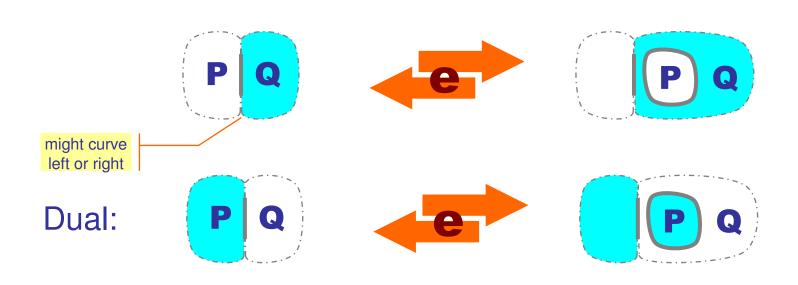
Interactions should be local to small membrane patches.

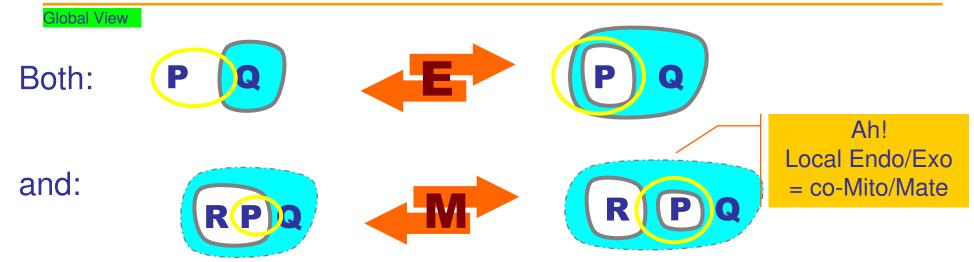
E.g., independent of global membrane properties such as overall curvature.

# **Endo/Exo Violates Locality**

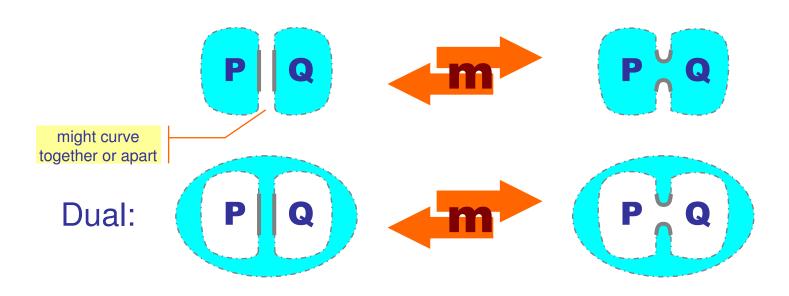


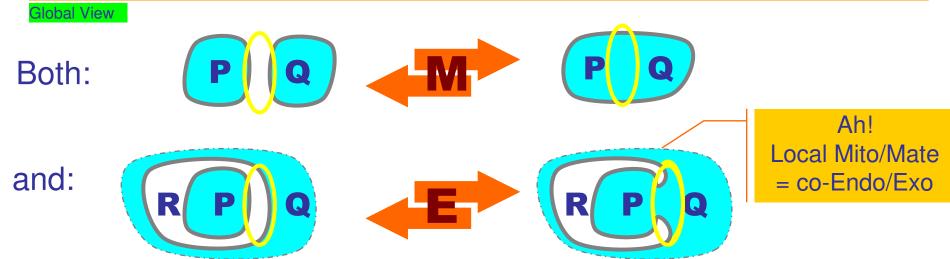
### ✓ Local-view Endo/Exo Reaction





## ✓ Local-view Mito/Mate Reaction





## **Locality is Not Violated**

- Hence, even though Endo/Exo and Mito/Mate strictly violate locality, locality is indirectly preserved in a bigger system that includes them both and their duals.
- This needs to be somewhat justified (L.Cardelli: "Bitonal Systems") after which we can forget about local-view reactions.
- Problem: how to formally represent the localview reactions?

#### **Assessment**

- High-level: Membrane Interactions
  - Abstraction level still too high; we want to talk about "different sorts" of membranes.
  - We need to be a bit more deterministic.
- Mid-level: Graph Rewriting
  - Abstractly talk about the "sort" of a membrane, and how it changes into other abstract sorts.
- Lower-Level: Patch Interactions
  - Model individual membrane proteins.

## Part II (short)

# Different Kinds of Membranes

#### **Sorted Membranes**

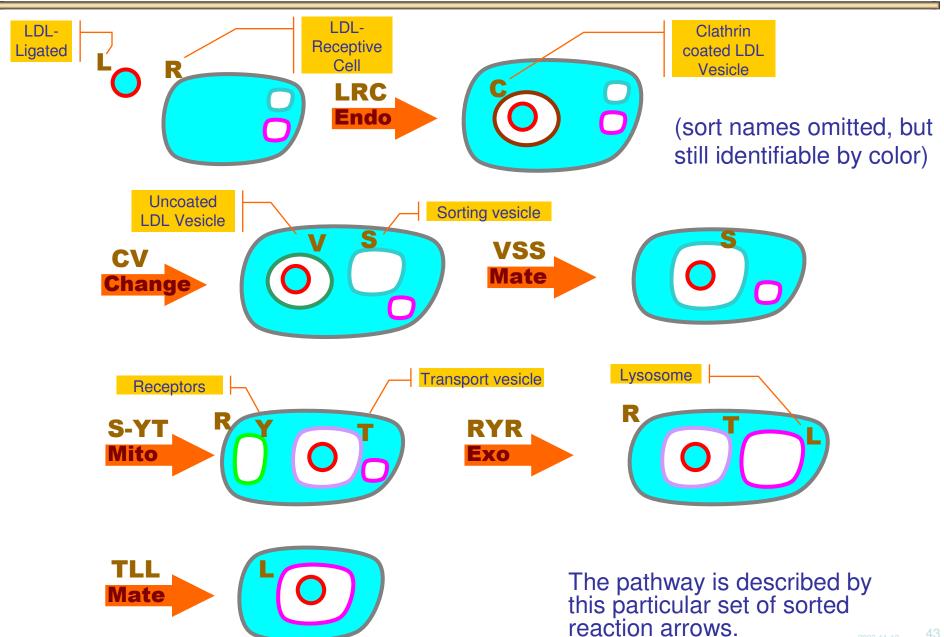
- Different kinds of membranes.
  - Lipid bilayer is universal. All membranes can in principle merge, but the lipid compositions vary.
  - The set of proteins bound to a membrane confer unique characteristics to it and its contents.
- Each membrane is uniform.
  - Membrane proteins diffuse rapidly through the surface of a membrane; they are not localized (unless held together).
- Hence: sorts of membranes.
  - A single name will characterize the collection of features of a membrane; its sort.
  - Each sort is meant to be "implemented" by lower level mechanisms.

#### **Sorted Membrane Rewrites**

## Rewriting systems

- We can describe sorted membrane reactions as labeled rewrites (such as labeled versions of endo/exo).
- E.g. as a special case of Milner's BiGraphs, where the "sort" is the "control". This is possible because each node in a bigraph has a single control.

## **Receptor-Mediated Degradation Pathway**



#### **Part III**

## **Brane Calculi**

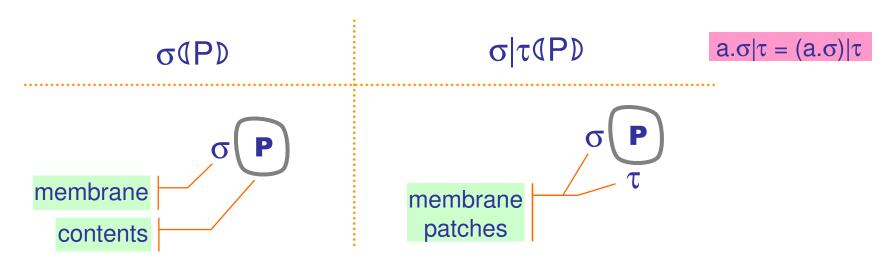
## What makes Endo happen?

- Moving down a level, to explain "why" certain reactions like endo/exo happen: they do not happen magically.
- Describe membranes as composed of independently active "patches" or membrane proteins (not characterized by a single sort).
- Can be formalized pretty much as action/coaction interactions in process calculi.
- But with actions "on" the membranes, not "inside" them!

#### **Brane Calculi**

systems 
$$P,Q ::= \diamond |P \circ Q| !P |\sigma (P)$$
 nests of membranes branes  $\sigma,\tau ::= 0 |\sigma|\tau |!\sigma| a.\sigma$  combinations of actions  $a ::= 1 | \dots$  (a great variety of possibilities)

### 1D fluids ( $\sigma$ ) inside a 2D fluid (P)



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

## **Structural Congruences**

$$P \circ Q \equiv Q \circ P$$

$$P \circ (Q \circ R) \equiv (P \circ Q) \circ R$$

$$P \circ \diamond \equiv P$$

$$!P \equiv P \circ !P$$
 etc.

$$0 ( \diamond ) \equiv \diamond$$

$$P \equiv Q \Rightarrow P \circ R \equiv Q \circ R$$

$$P \equiv Q \Rightarrow !P \equiv !Q$$

$$P \equiv Q \land \sigma \equiv \tau \Rightarrow \sigma (P) \equiv \tau (Q)$$

$$\sigma | \tau \equiv \tau | \sigma$$

$$\sigma|(\tau|\rho) \equiv (\sigma|\tau)|\rho$$

$$\sigma | 0 \equiv \sigma$$

$$|\sigma \equiv \sigma| |\sigma|$$
 etc.

$$1.\sigma \equiv \sigma$$

$$\sigma \equiv \tau \Rightarrow \sigma | \rho \equiv \tau | \rho$$

$$\sigma \equiv \tau \Rightarrow !\sigma \equiv !\tau$$

$$\sigma \equiv \tau \Rightarrow a.\sigma \equiv a.\tau$$

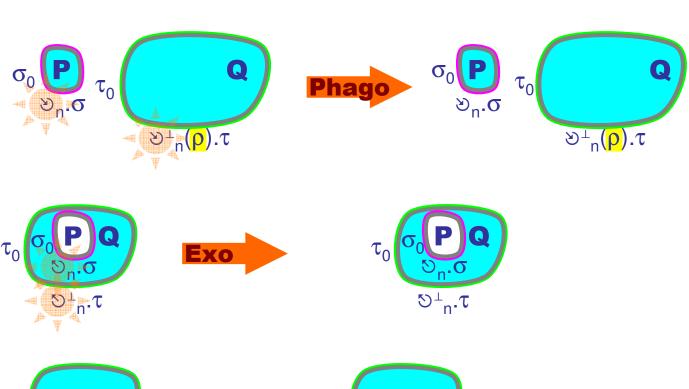
$$P \equiv P' \land P' \longrightarrow Q' \land Q' \equiv Q \Rightarrow P \longrightarrow Q$$

#### **Bitonal Reactions**

actions

a ::= ... 
$$| \mathfrak{D}_{n} | \mathfrak{D}^{\perp}_{n}(\rho) | \mathfrak{D}_{n} | \mathfrak{D}^{\perp}_{n} | \mathfrak{D}(\rho)$$

phago ୬, exo ୭, pino ⊚





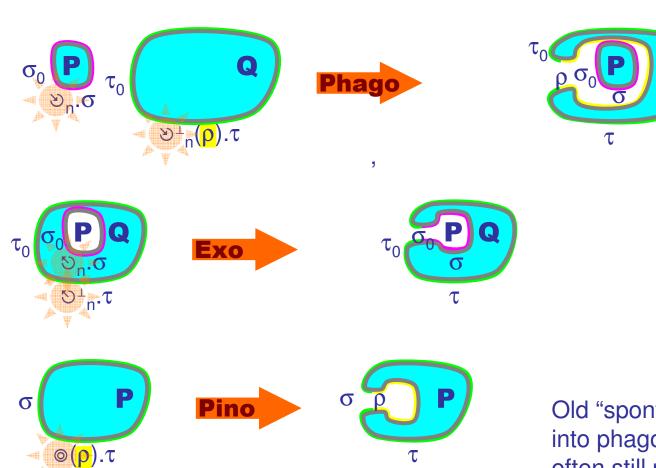
Old "spontaneous" endo splits into phagocytosis (phago, often still pronounced endo) and pinocytosis (pino).2003-11-13

#### **Bitonal Reactions**

actions

a ::= ... 
$$| \mathfrak{D}_{n} | \mathfrak{D}^{\perp}_{n}(\rho) | \mathfrak{D}_{n} | \mathfrak{D}^{\perp}_{n} | \mathfrak{D}(\rho)$$

phago ୬, exo ୭, pino ⊚



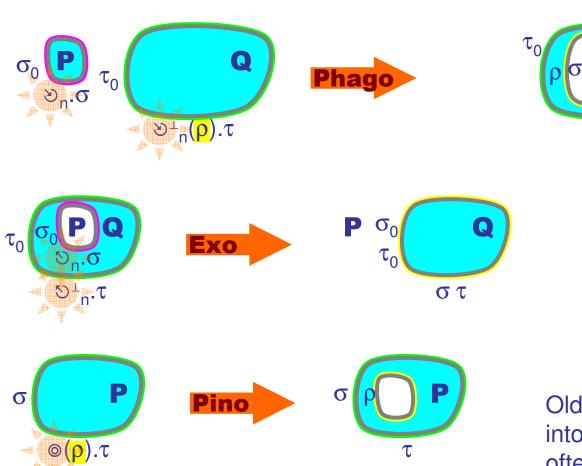
Old "spontaneous" endo splits into phagocytosis (phago, often still pronounced endo) and pinocytosis (pino). 2003-11-13

#### **Bitonal Reactions**

actions

a ::= ... 
$$| \mathfrak{D}_{n} | \mathfrak{D}^{\perp}_{n}(\rho) | \mathfrak{D}_{n} | \mathfrak{D}^{\perp}_{n} | \mathfrak{D}(\rho)$$

phago ୬, exo ୭, pino ⊚



Old "spontaneous" endo splits into phagocytosis (phago, often still pronounced endo) and pinocytosis (pino). 2003-11-13

$$\begin{aligned} & \text{Phago P}_{\mathbf{n}}.\sigma|\sigma_{0}\text{(PD o)}.\tau|\tau_{0}\text{(QD } \longrightarrow \tau|\tau_{0}\text{(p)}\sigma_{0}\text{(PDD oQD)} \\ & \text{Exo } & \text{Pino}.\tau|\tau_{0}\text{(PD o)}.\sigma|\sigma_{0}\text{(PD oQD)} \longrightarrow P \circ \sigma|\sigma_{0}|\tau|\tau_{0}\text{(QD)} \\ & \text{Pino } & \text{O(p)}.\sigma|\sigma_{0}\text{(PD } \longrightarrow \sigma|\sigma_{0}\text{(p)}\circ\text{PD)} \end{aligned}$$

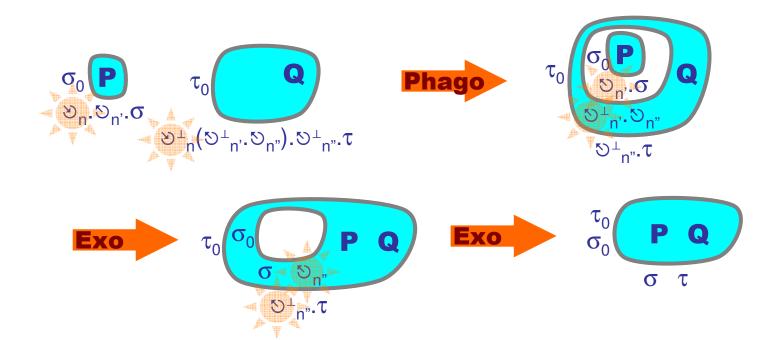
N.B.: the parity of nesting of P and Q is preserved; this makes the reactions preserve bitonality.

N.B.: in Phago (and Pino), one could perhaps require  $\rho$  to be, conservatively, a piece of  $\tau$ , by a non-linear rewrite:

#### **Abbreviations: Mate**

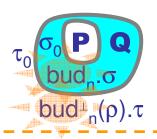
Mate 
$$mate_n.\sigma = \mathfrak{D}_n.\mathfrak{D}_{n'}.\sigma$$
  
 $mate_n.\tau = \mathfrak{D}_n^{\perp}(\mathfrak{D}_{n'}^{\perp}.\mathfrak{D}_{n''}^{\perp}).\mathfrak{D}_{n''}^{\perp}.\tau$ 



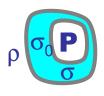


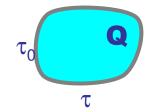
#### **Abbreviations: Bud**

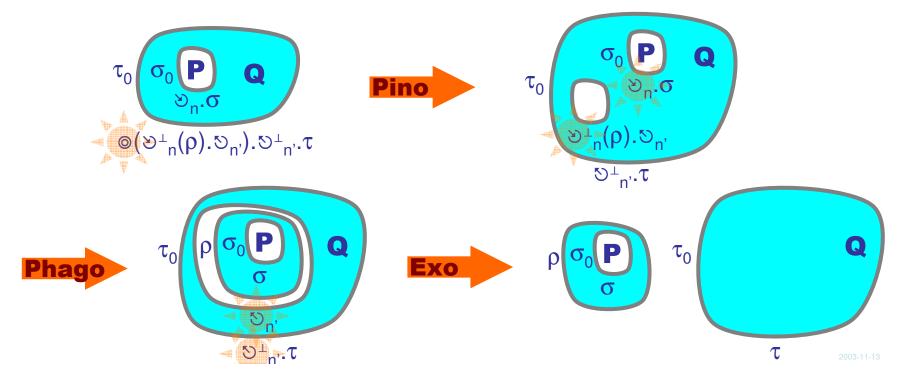
Bud  $\mathsf{bud}_{\mathsf{n}}.\sigma = \mathfrak{D}_{\mathsf{n}}.\sigma$  $\mathsf{bud}^{\perp}_{\mathsf{n}}(\rho).\tau = \mathfrak{D}(\mathfrak{D}^{\perp}_{\mathsf{n}}(\rho).\mathfrak{D}_{\mathsf{n}}).\mathfrak{D}^{\perp}_{\mathsf{n}}.\tau$  A budding version of old "spontaneous" mito, to avoid arbitrary splits. Follows the pattern of inverse-mate.









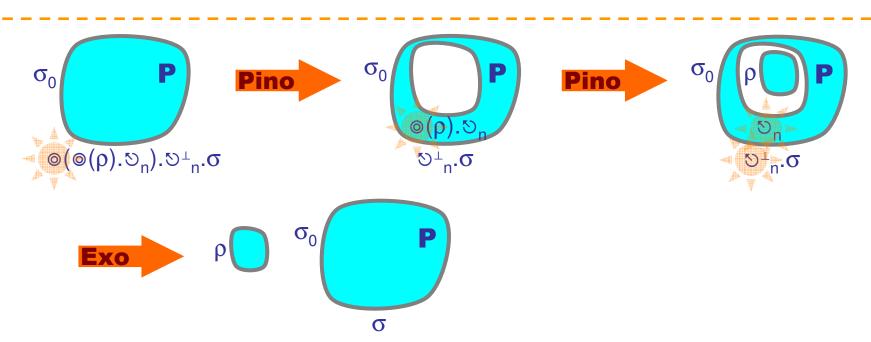


## **Abbreviations: Drip**

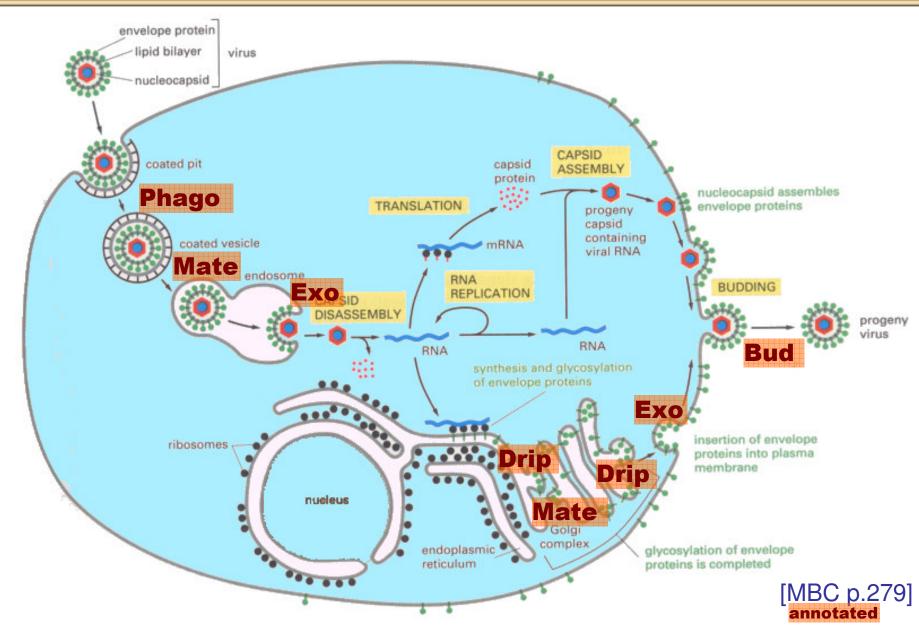
**Drip** 
$$drip_n(\rho).\sigma = \otimes(\otimes(\rho).\otimes_n).\otimes_{n}^{\perp}.\sigma$$

A zero-expelled-membranes version of old "spontaneous" mito, to avoid arbitrary splits. Follows the pattern of inverse-mate.

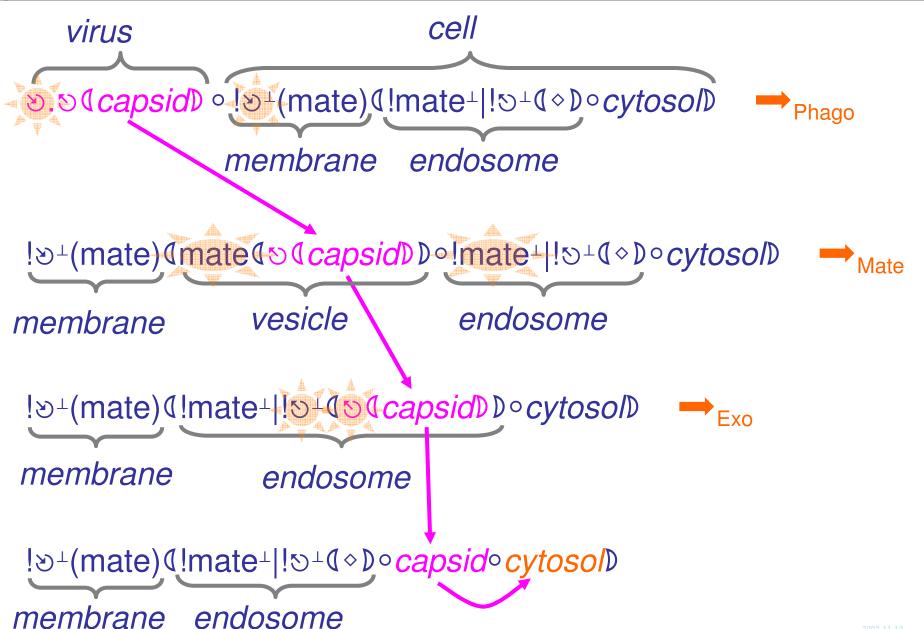




## (Real) Ex: Viral Reproduction

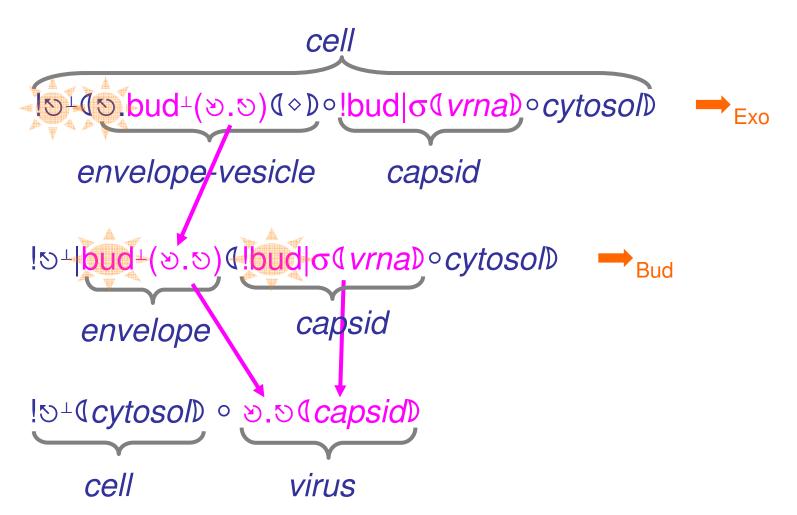


### **Ex: Viral Infection**



## **Ex: Viral Progeny**

capsid ∘ cytosol → → !envelope-vesicle ∘ !capsid ∘ cytosol by available cellular machinery



## **Ex: LDL Degradation Pathway**

```
LigatedLdl = LdlLigand(LDL)

Cell = CellBrane(!Lysosome • !SortingVesicle)

Lysosome = LysoBrane (LysoBody)

SortingVesicle = SortingBrane(•)
```

Compartments Membranes

LdlLigand =  $\mathfrak{D}_{IdlReceptor}$ .bud<sub>xferVesicle</sub>

CellBrane = !න<sup>⊥</sup><sub>IdlReceptor</sub>(VesicleBrane) | !න<sup>⊥</sup><sub>recycle</sub>

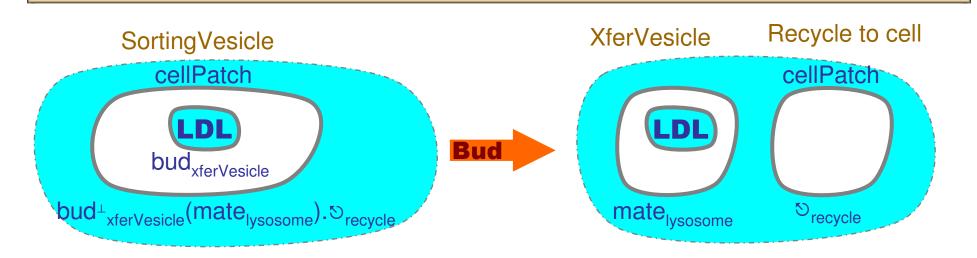
VesicleBrane = mate<sub>sortingVesicle</sub> | cellPatch<sup>(1)</sup>

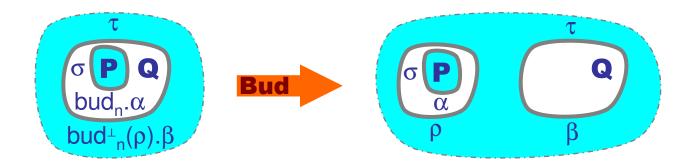
SortingBrane = mate<sup>⊥</sup><sub>sortingVesicle</sub>. bud<sup>⊥</sup><sub>xferVesicle</sub>(XferBrane). ⊗<sub>recycle</sub>

XferBrane = mate<sub>lysosome</sub> LysoBrane = !mate<sub>lysosome</sub>

<sup>(1)</sup>whatever gets dragged by phago from the cell membrane, e.g. more LDL receptors.

## ... the critical Bud step





## Ex: LDL Degradation Pathway in BioAmbients

Compartments Processes

```
LigatedLdI = [LdlLigand | LDL]

Cell = [CellBrane • !Lysosome • !SortingVesicle]

Vesicle(n) = [VesicleBrane(n)]

SortingVesicle = [SortingBrane | XferVesicle]

XferVesicle = [XferBrane]

Lysosome = [LysoBrane | LysoBody]
```

```
 \begin{array}{l} LdlLigand = s2s_{ldlBind}{}^{\bot}(n).in_{n}.in_{n}.merge_{xferVesicle} \\ LdlReceptor = (vn) \ s2s_{ldlBind}(n).in_{n}^{\bot} \mid Vesicle(n) \\ CellBrane = !LdlReceptor \mid !pop_{recycle}^{\bot}(1) \\ VesicleBrane(n) = in_{n}^{\bot}.merge_{sortingVesicle} \mid cellPatch^{(2)} \\ SortingBrane = merge_{sortingVesicle}^{\bot}.out_{bud}^{\bot}.pop_{recycle} \\ XferBrane = merge_{xferVesicle}^{\bot}.out_{bud}^{\bot}.merge_{lysosome} \\ LysoBrane = !merge_{lysosome}^{\bot}. \end{array}
```

<sup>(1)</sup>pop is out + merge. (2)cellPatch is cell membrane to be recycled

#### **Molecular Actions**

systems 
$$P,Q ::= ... \mid m \qquad m \in M \quad molecules$$
  
 $p,q ::= m_1 \circ ... \circ m_k \quad molecule \quad multisets$ 

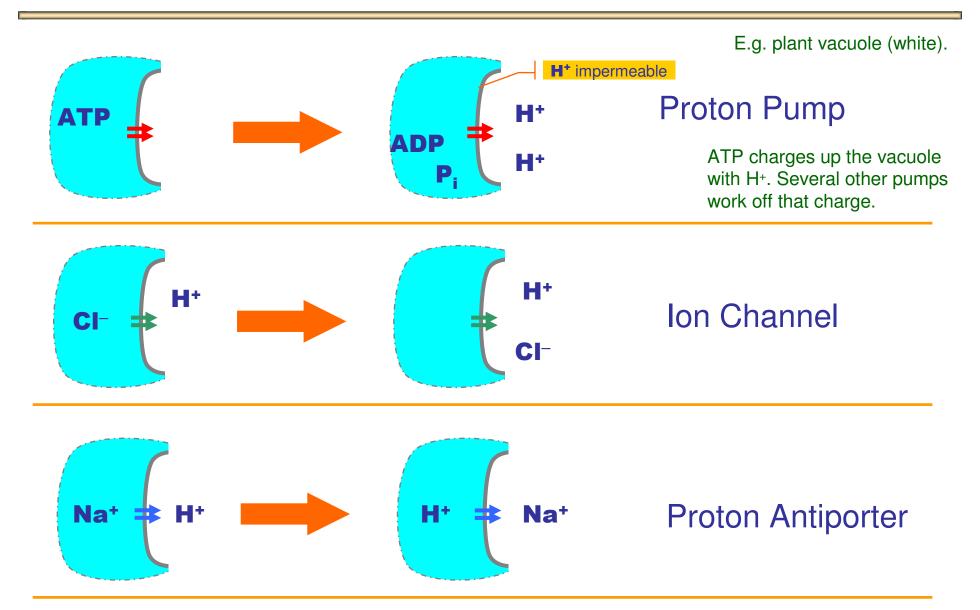
actions a ::= ... 
$$|p_1(p_2)| \Rightarrow q_1(q_2)$$
 bind&release

(multiset rewriting, inside and outside membranes)

Special cases: "\(\dip(\dip)\)" is omitted

$$m(\diamond) \rightrightarrows$$
 bind out  $\rightrightarrows m(\diamond)$  release out  $\diamond (m) \rightrightarrows$  bind in  $\rightrightarrows \diamond (m)$  release in

## **Ex: A Specialized Membrane**



A membrane of sort "PlantVacuole" has all those things on it.

```
ProtonPump = ! ATP(\diamond) \Rightarrow ADP\circP<sub>i</sub>(H+\circH+)
IonChannel = ! Cl-(H+) \Rightarrow \diamond(H+\circCl-)
ProtonAntiporter = ! Na+(H+) \Rightarrow H+(Na+)
```

PlantVacuole =
ProtonPump | IonChannel | ProtonAntiporter ( > )

## **Encoding Brane Calculi?**

$$\sigma(P)^{\dagger} \triangleq s[\sigma^{\dagger} | P^{\dagger}]$$
?

This encoding confuses membrane with contents, so that the exo encoding is problematic:

Exo 
$$\mathfrak{D}^{\perp}_{n}.\beta|\tau\mathfrak{Q}\mathfrak{D}_{n}.\alpha|\sigma\mathfrak{Q}\mathfrak{D}\mathfrak{D}\mathfrak{D} \longrightarrow \mathfrak{P} \circ \alpha|\sigma|\beta|\tau\mathfrak{Q}\mathfrak{D}$$

That is, find other encodings such that:

$$s[\mathfrak{S}_{n}^{\perp},\beta \mid s[\mathfrak{S}_{n}^{\dagger},\alpha \mid \sigma \mid P] \mid \tau \mid Q] \longrightarrow P \mid s[\alpha \mid \sigma \mid \beta \mid \tau \mid Q]$$

but the split  $\sigma \mid P$  is *arbitrary* here: some reactions could not be reflected back to legal brane calculus reactions  $(P^{\dagger} \rightarrow Q \Rightarrow \exists R. \ P \rightarrow R \land Q \rightarrow^* R^{\dagger})$ , and it would be in any case difficult to define  $\mathfrak{D}^{\dagger}$  so that it splits  $\sigma$  from P.

One cannot easily represent the Exo reaction in (Bio)Ambients, nor can one easily add it as a new primitive!

For exo at least, we need to explicitly identify the membrane.

either 
$$\sigma(P)^{\dagger} \triangleq s[m[\sigma^{\dagger}] | P^{\dagger}]$$
  
or  $\sigma(P)^{\dagger} \triangleq s[\sigma^{\dagger} | c[P^{\dagger}]]$ 

The second option should be chosen to avoid crossing 4 brackets in s2s reactions, so:

But this emulation interferes badly with concurrent Phago's (emulated by at least two "in" steps because of the double bracketing): neither emulations is atomic.

One cannot easily emulate atomic Phago/Exo in (Bio)Ambients.

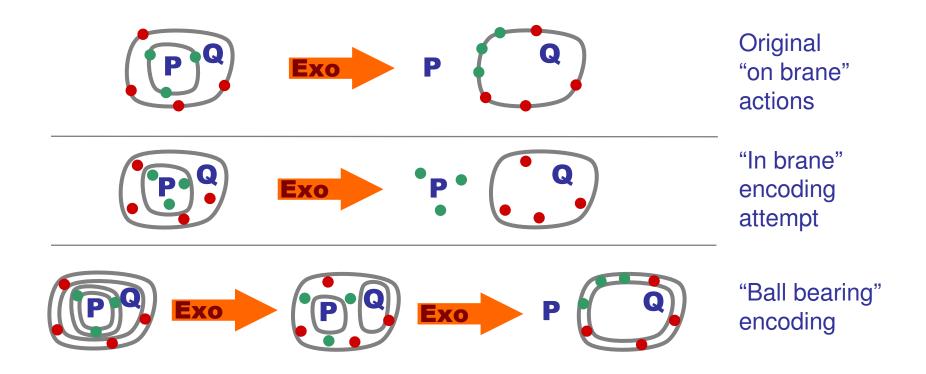
Conversely, in (Bio)Ambients one can use an action to create a whole new filled-in membrane:

$$a.s[\sigma \mid P] = a.(\sigma (P))$$

this is not allowed, nor easily representable, in brane calculi.

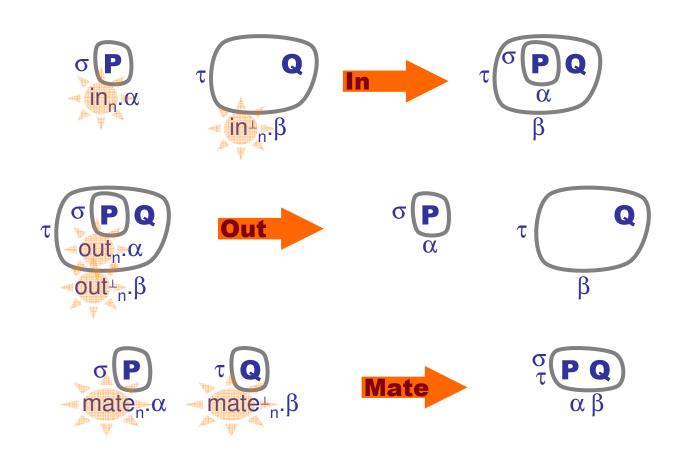
This is a power that real membranes do not seem to have.

## **Exo Encodings**



## **BioAmbients-like Mobility Actions**

actions  $a := ... | in_n | in_n^{\perp} | out_n | out_n^{\perp} | mate_n^{\perp} | mate_n^{\perp}$ 



In 
$$n_n \cdot \alpha | \sigma(PD \circ n_n \cdot \beta | \tau(QD \longrightarrow \beta | \tau(\alpha | \sigma(PD \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(PD \circ \beta | \tau(QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(PD \circ \beta | \tau(QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(\beta | \tau(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(\beta | \tau(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(\beta | \tau(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(\beta | \tau(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(\beta | \tau(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(\beta | \tau(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(\beta | \tau(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(\beta | \tau(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD \bigcirc n_n \cdot \beta | \tau(QD \longrightarrow \alpha | \sigma(P \circ QD ) ))))$$

N.B.: out + mate gives a "melt" primitive that is a good membrane-preserving approximation of "open":

$$melt_{n}.\beta|\tau (melt_{n}.\alpha|\sigma (PD \circ QD \longrightarrow \alpha|\sigma|\beta|\tau (P \circ QD ))$$

## Diffusion (CCS-like channels)

actions  $a := ... | df_n(m) | df_n(m)$  diffusion (within membrane)

$$\mathbf{df}_{n}(m).\alpha + \mathbf{df}_{n}(p).\beta \mid \sigma(P) \longrightarrow \alpha \mid \beta\{p \leftarrow m\} \mid \sigma(P)$$

### **BioAmbients-like Channels**

actions 
$$a ::= ... | s2s_n(m) | s2s_n^{\perp}(m) |$$
  
 $| p2c_n(m) | p2c_n^{\perp}(m) |$   
 $| c2p_n(m) | c2p_n^{\perp}(m)$ 

sibling to sibling parent to child to parent

$$\begin{array}{c} \mathbf{s2s_n(m).\alpha|\sigma(PD \circ s2s_n(p).\beta|\tau(QD))} \\ \rightarrow \alpha|\sigma(PD \circ \beta\{p\leftarrow m\}|\tau(QD)) \end{array}$$

$$\begin{array}{c} \mathbf{p2c_n(m).\alpha|\sigma (p2c_n^{\perp}(p).\beta|\tau (QD \circ PD)} \\ \rightarrow \alpha|\sigma (\beta\{p\leftarrow m\}|\tau (QD \circ PD) \end{array}$$

$$c2p^{\perp}_{n}(p).\beta|\tau(c2p_{n}(m).\alpha|\sigma(QD \circ PD)$$

$$\rightarrow \beta\{p\leftarrow m\}|\tau(\alpha|\sigma(QD \circ PD))$$

## Implementabilty?

- An implementable "instruction set" could consist of:
  - Bitonal mobility operators, including bud/mate (possibly restricting the  $\rho$  in  $\mathfrak{D}^{\perp}_{\mathsf{n}}(\rho)$  and  $\mathfrak{D}(\rho)$ ).
  - Selected bind&release pumps.
  - Selected s2s/p2c/c2p operators.
- N.B. BioAmbients in/out do not seem as likely to be directly implementable.

#### **Conclusions**

- What's different about "bio"-calculi?
  - Orientability and bitonality invariants inspire new, and possibly more bio-realistic, operators.
  - Low-dimensional fluids inside high-dimensional fluids: two commutative monoids.
  - Computing on the membrane, not inside of it.

### Papers

- Bitonal Systems: membrane reactions and their connections to "local" patch reactions.
- Brane Calculi: a class of process calculi with computation "on" the membranes, not inside them.

http://www.luca.demon.co.uk

#### References

[MCB] Molecular Cell Biology, Freeman. [MBC] Molecular Biology of the Cell, Garland.

