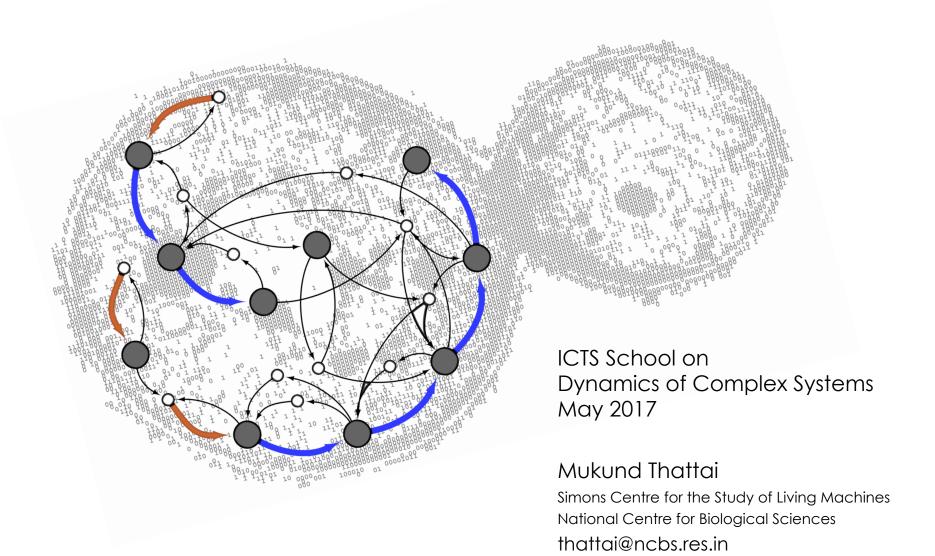
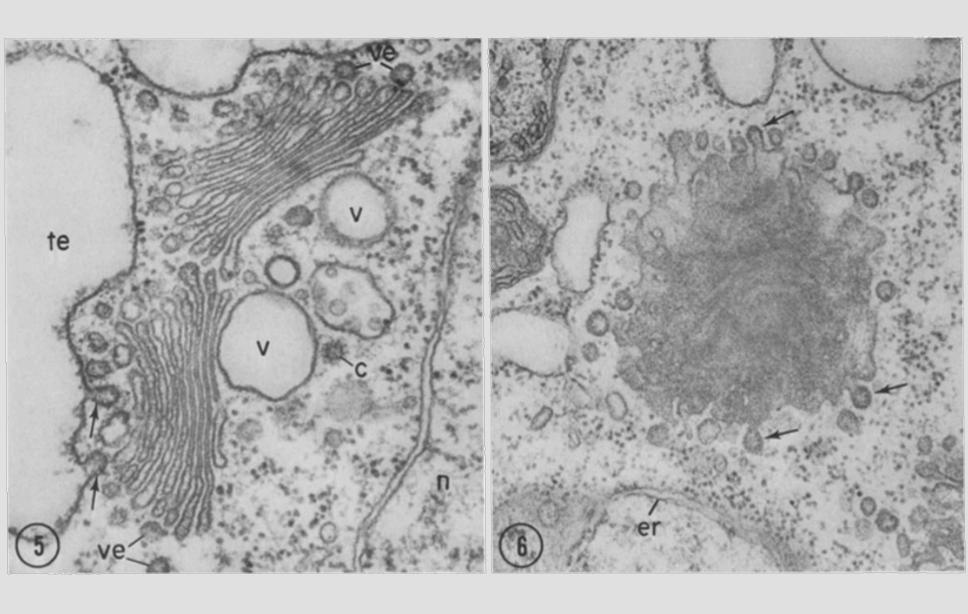
# Dynamical models of membrane traffic: toward "statistical cell biology"

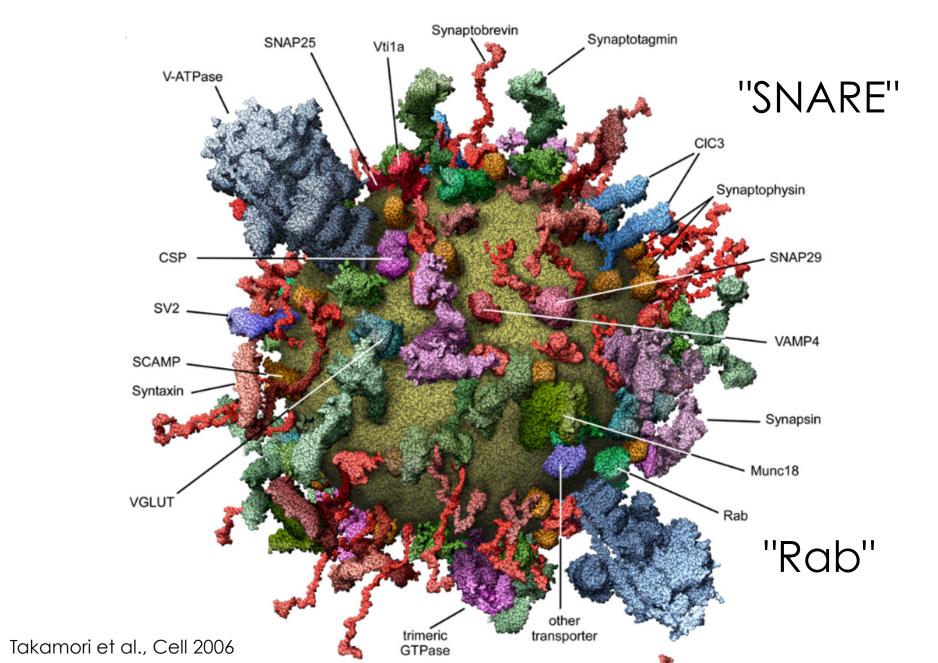




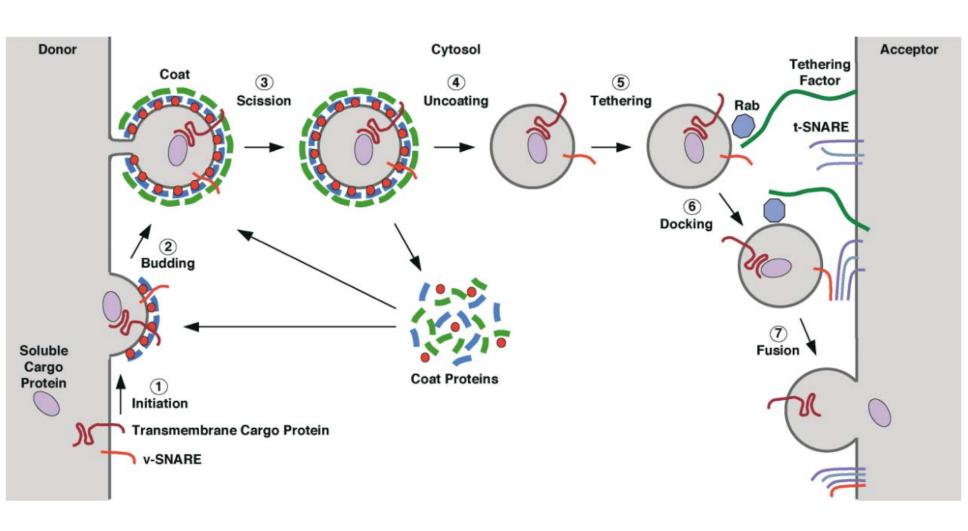


Farquhar & Palade, J Cell Biol 1981

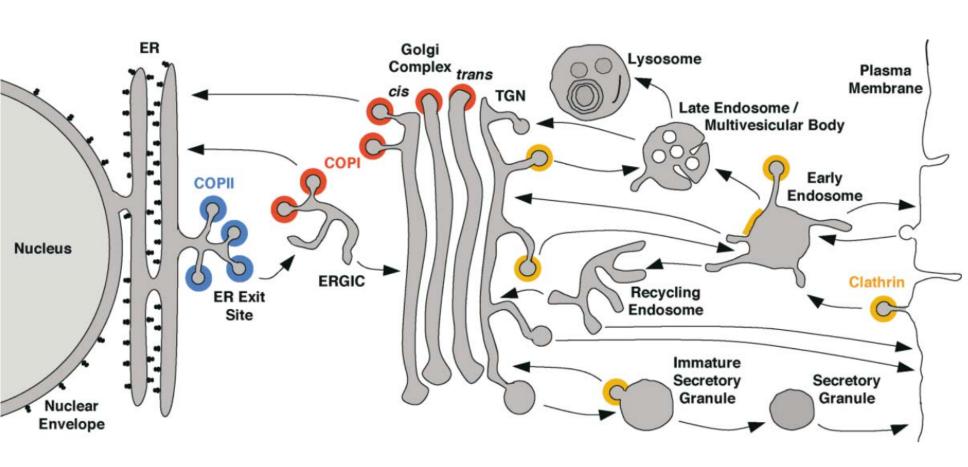
### A 40 nm transport vesicle



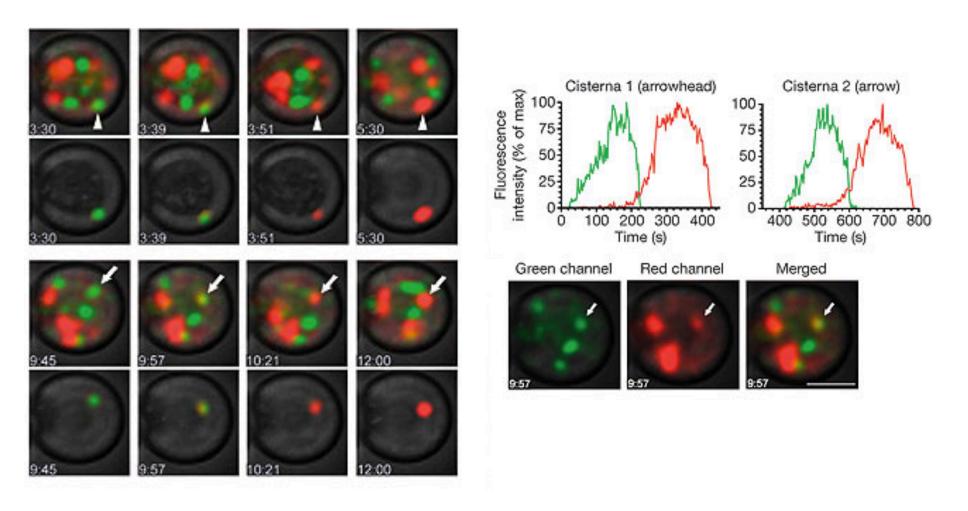
#### How do the transporters know where to go?



#### The dynamic membrane traffic system



#### Large cargo traverse the Golgi by "cisternal maturation"



#### Modelling cisternal maturation

$$x_{tot} = \sum_{x,y} n(x,y)x$$
,  $y_{tot} = \sum_{x,y} n(x,y)y$ .

$$n_X \equiv n(1,0), n_Y \equiv n(0,1)$$

#### Stochastic description

Two X vesicles fuse homotypically to create a compartment:

$$n_X \downarrow_2, n(2,0) \uparrow^1$$
 rate  $An_X(n_X - 1)$ 

A compartment buds an X or Y vesicle:

$$n_X \uparrow^1 n(x,y) \downarrow_1, n(x-1,y) \uparrow^1$$
 rate  $Bx n(x,y)$ 

$$n_Y \uparrow^1 n(x,y) \downarrow_1, n(x,y-1) \uparrow^1$$
 rate  $Dy n(x,y)$ 

A compartment fuses to an *X* or *Y* vesicle :

$$n_X \downarrow_1 n(x,y) \downarrow_1, n(x+1,y) \uparrow^1$$
 rate  $A \frac{x^2}{(x+y)^2} n_X n(x,y)$ 

$$n_Y \downarrow_1 n(x,y) \downarrow_1, n(x,y+1) \uparrow^1$$
 rate  $Cx n_Y n(x,y)$ 

Deterministic description

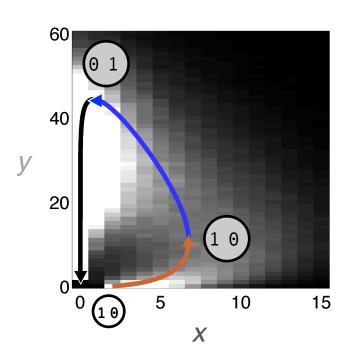
$$\frac{dx}{dt} = A\overline{n_X} \frac{x^2}{(x+y)^2} - Bx$$

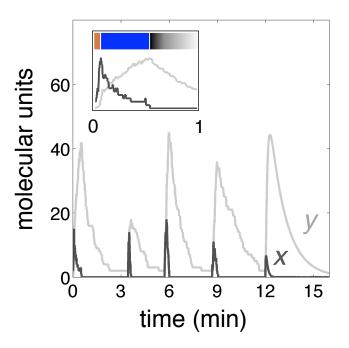
$$\frac{dy}{dt} = C\overline{n_Y}x - Dy$$

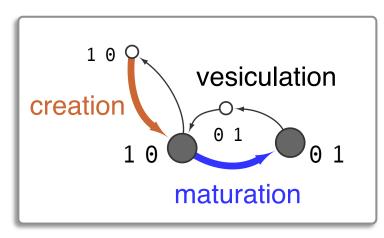
Hopf bifurcation

$$\frac{B}{B+D}\,\frac{C\overline{n_Y}}{C\overline{n_Y}+D}>\frac{1}{2}$$

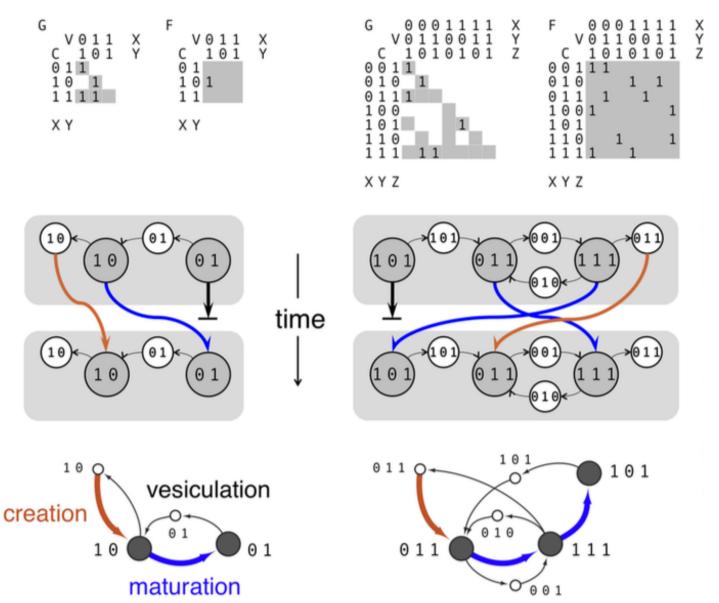
### Modelling cisternal maturation



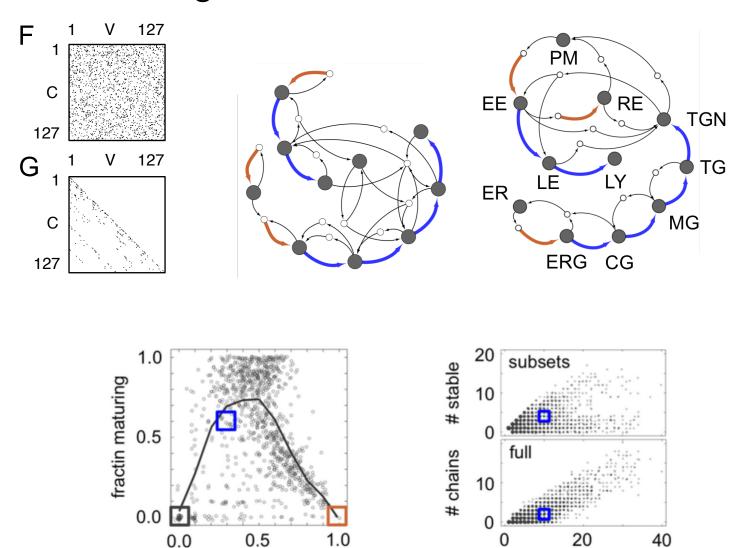




#### A Boolean model of vesicle traffic



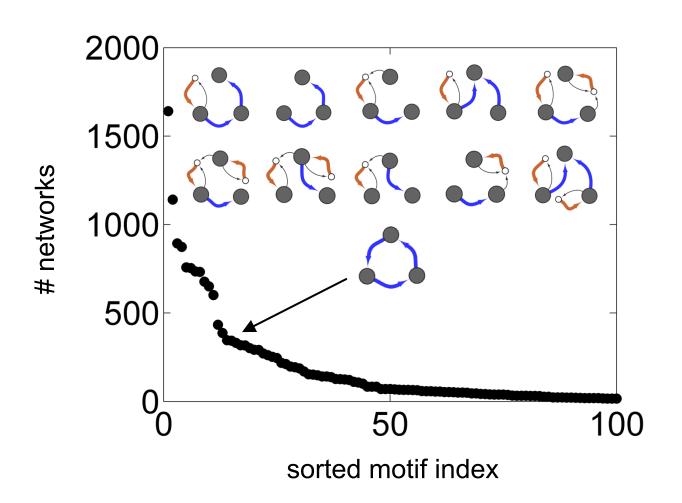
## Random budding and fusion rules generate cell-like networks



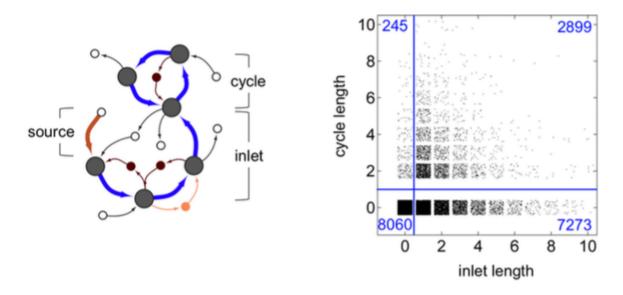
fraction homotypically fusing

# compartments

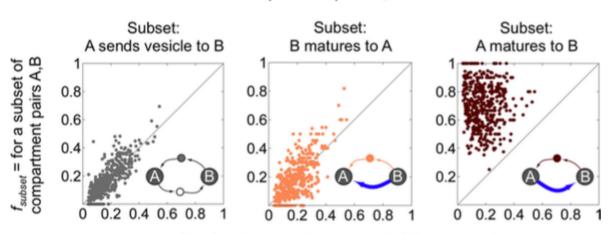
### Enriched motifs in vesicle traffic networks with random budding and fusion rules



#### The "maturation chain" motif

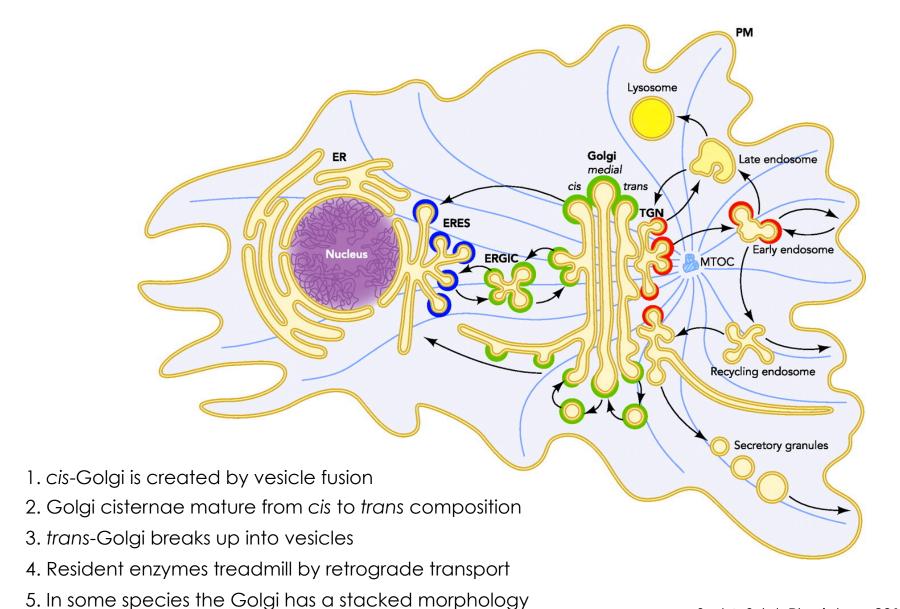


f = Fraction of compartment pairs A,B with a B-to-A vesicle



 $f_{all}$  = for all compartment pairs A,B in a network

#### Retrograde vesicles drive maturation in real cells!





# Many evolutionary innovations are non-adaptive

The spandrels of San Marco and the Panglossian paradigm: a critique of the adaptationist programme

By S. J. GOULD AND R. C. LEWONTIN

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An adaptationist programme has dominated evolutionary thought in England and the United States during the past 40 years. It is based on faith in the power of natural selection as an optimizing agent. It proceeds by breaking an organism into unitary 'traits' and proposing an adaptive story for each considered separately. Trade-offs among competing selective demands exert the only brake upon perfection; non-optimality is thereby rendered as a result of adaptation as well. We criticize this approach and attempt to reassert a competing notion (long popular in continental Europe) that organisms must be analysed as integrated wholes, with Baupläne so constrained by phyletic heritage, pathways of development and general architecture that the constraints themselves become more interesting and more important in delimiting pathways of change than the selective force that may mediate change when it occurs.



Brodsky, Thattai & Mayor, Nat Cell Biol 2012 Ramadas & Thattai, Biophys J 2013 Purkanti & Thattai, PNAS 2015 Mani & Thattai, Mol Biochem Parasitol 2016 Dey, Thattai & Baum, Trends Cell Biol 2016 Mani & Thattai, eLife 2016 Shukla et al, PLoS ONE 2017 (in rev.)

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