

Complex Network Architecture: A cartoon guide

Application

Error/flow control

Global

Relay/MUX

E/F control

Local

Relay/MUX

John Doyle

John G. Braun Professor
Control and Dynamical Systems
BioEngineering, Electrical Engineering
Caltech

Physical

Reactions

Flow

Protein level

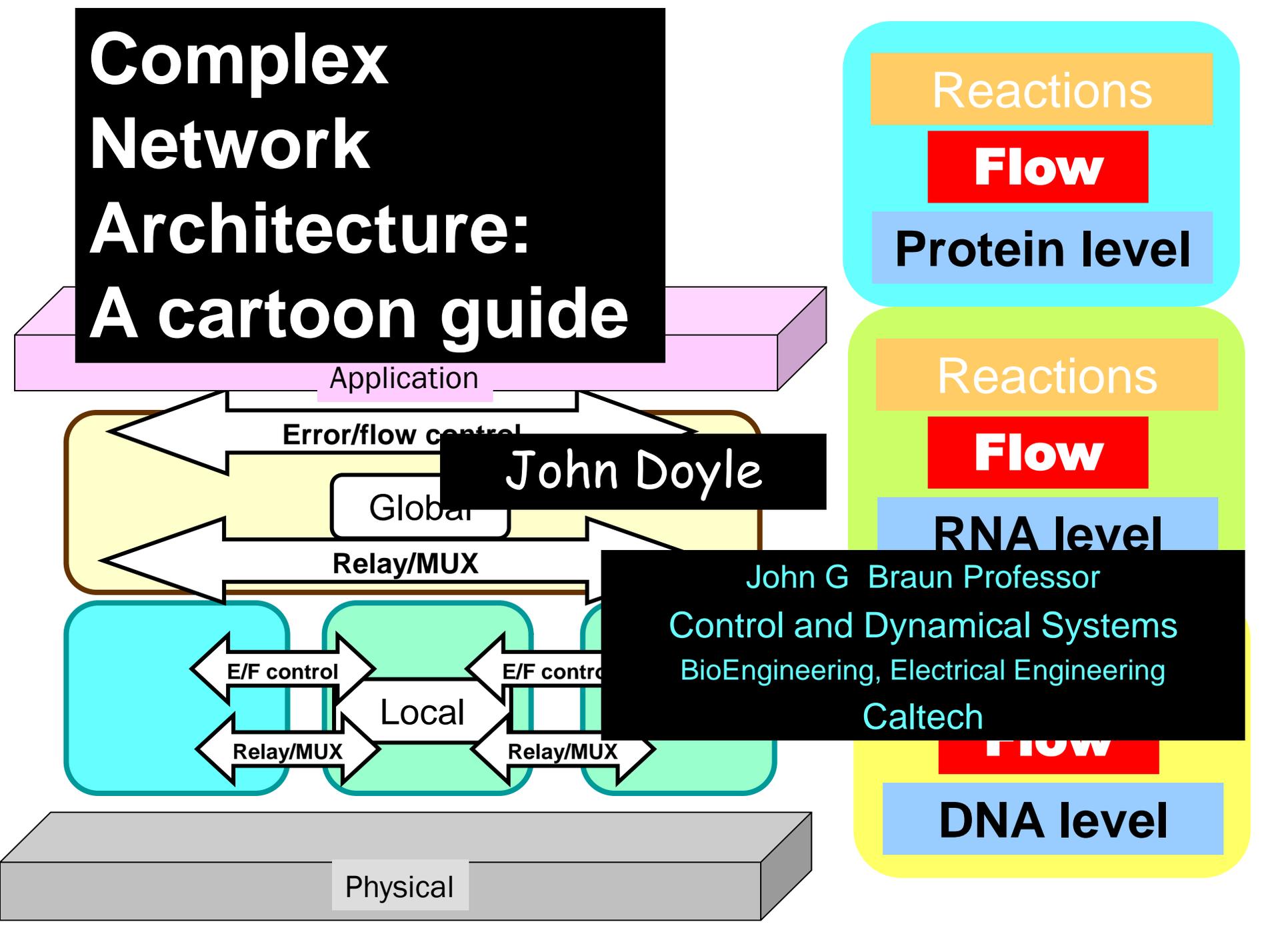
Reactions

Flow

RNA level

Flow

DNA level



Outline

- Not merely “complexity, networks, abstraction, recursion, modularity,…”
- But very specific forms of these.
- Formal methods have great potential

- Illustrate with case studies and cartoons:
Internet versus bacterial biosphere

- Implicitly: importance of formal methods, not merely modeling and simulation

Huge range of dynamics

- Spatial
- Temporal

Reactions

Flow

Protein level

Reactions

Flow

RNA level

Reactions

Flow

DNA level

Application

Error/flow control

Global

Relay/MUX

E/F control

Local

Relay/MUX

E/F c

Rela

Physical

Bewildering
w/out clear
grasp of
layered
architecture

Network Math and Engineering (NetME) Challenges

- Predictive modeling, simulation, and analysis of complex systems in technology and nature
- Theoretical foundation for design of network architectures
- Balance rigor/relevance, integrative/coherent
- Model/simulate is critical but limited
 - Predicting rare but catastrophic events
 - Design, not merely analysis
 - Managing complexity and uncertainty

“Architecture”

- Most persistent, ubiquitous, and global features of organization
- Constrains what is possible for good or bad
- Platform that enables (or prevents) innovation, sustainability, etc,
- Internet, biology, energy, manufacturing, transportation, water, food, waste, law, etc
- Existing architectures are unsustainable
- Theoretical foundation is fragmented, incoherent, incomplete

Stochastics in Biology

- Arkin, Gillespie, Petzold, Khammash, El-Samad, Munsky, Paulsson, Vinnicombe, many others...
- Noise in the cellular environment
 - Elowitz, van Oudenaarden, Collins, Swain, Xie, Elston, ...
- Stochastic Monte Carlo Simulation
 - Kurtz, Gibson, Bruck, Anderson, Rathinam, Cao, Salis, Kaznessis, ...
- Statistical moment computations
 - Hespanha, Singh, Verghese, Gomez-Uribe, Kimura
- Density function computations
 - McNamara, Sidje, ...
- Stochastic differential equation approximations
 - van Kampen, Kurtz, Elf, Ehrenberg,...
- Spatial stochastic models and tools
 - Elf, Iglesias,...

Very incomplete, idiosyncratic list

Other Influences

- **Internet** (Kelly/Low, Willinger, Clark, Wroclawski, Day, Chang, etc etc)
- **Biology/Medicine** (Savageau, G&K, Mattick, Csete, Arkin, Alon, Caporale, de Duve, Exerc Physio, Acute Care, etc etc...)
- **Architecture** (Alexander, Salingeros,...)
- **Aerospace** (many, Maier is a good book)
- **Philosophy/History** (Fox Keller, Jablonka&Lamb)
- **Physics/ecology** (Carlson)
- **Management** (Baldwin,...)
- **Resilience/Safety/Security Engineering/Economics** (Wood, Anderson, Leveson, ...)

Biology versus the Internet

Similarities

- Evolvable architecture
- Robust yet fragile
- Constraints/deconstrain
- Layering, modularity
- Hourglass with bowties
- Feedback
- Dynamic, stochastic
- Distributed/decentralized
- *Not* scale-free, edge-of-chaos, self-organized criticality, etc

Differences

- Metabolism
- Materials and energy
- Autocatalytic feedback
- Feedback complexity
- Development and regeneration
- >4B years of evolution
- How the parts work?

Biology versus the Internet

Similarities

- Evolvable architecture
- **Robust yet fragile**
- **Constraints/deconstrain**
- **Layering, modularity**
- **Hourglass with bowties**
- Feedback
- Dynamics
- Distributed/decentralized
- *Not* scale-free, edge-of-chaos, self-organized criticality, etc

Differences

- Metabolism
- Materials and energy
- **Autocatalytic feedback**
- Feedback complexity
- Development and regeneration
- >4B years of evolution

Focus on
bacterial biosphere

Question: Human complexity

Robust

- 😊 Efficient, flexible metabolism
- 😊 Regeneration & renewal
- 😊 Rich microbial symbionts
- 😊 Immune systems
- 📄 Complex societies
- 🏠 Advanced technologies

Yet Fragile

- ☹️ Obesity and diabetes
- ☹️ Cancer
- ☹️ Parasites, infection
- ☹️ Inflammation, Auto-Im.
- 💀 Epidemics, war, ...
- 💣 Catastrophic failures

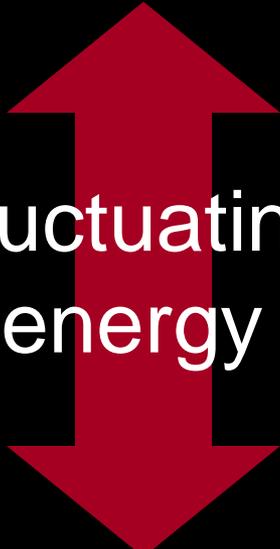
Mechanism?

Robust

- ☺ Efficient, flexible metabolism
- ☺ Regeneration & renewal
- ☺ Fat accumulation
- ☺ Insulin resistance
- ☺ Inflammation

Yet Fragile

- ☹ Obesity and diabetes
- ☹ Cancer
- ☹ Fat accumulation
- ☹ Insulin resistance
- ☹ Inflammation



Fluctuating
energy

Static
energy

Implications/

Generalizations

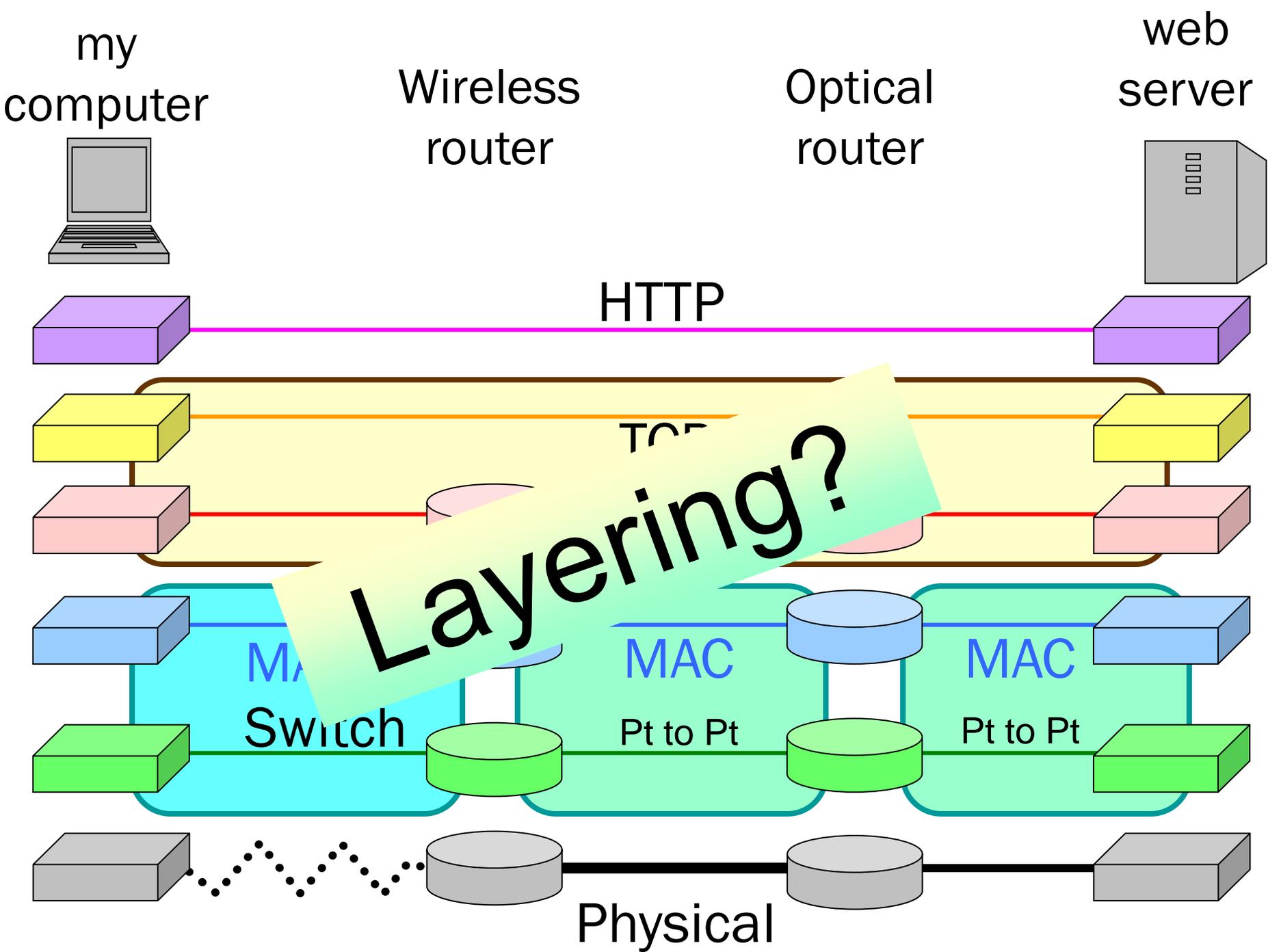
Robust

- ☺ Efficient, flexible metabolism
- ☺ Rich microbial symbionts
- ☺ Immune systems
- ☺ Regeneration & renewal
- 📄 Complex societies
- 🏠 Advanced technologies

Yet Fragile

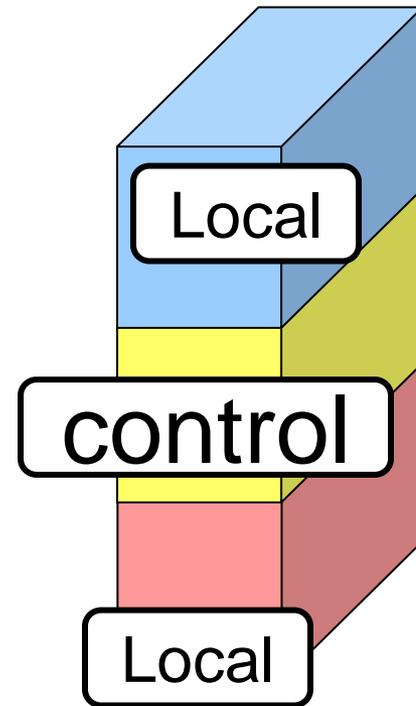
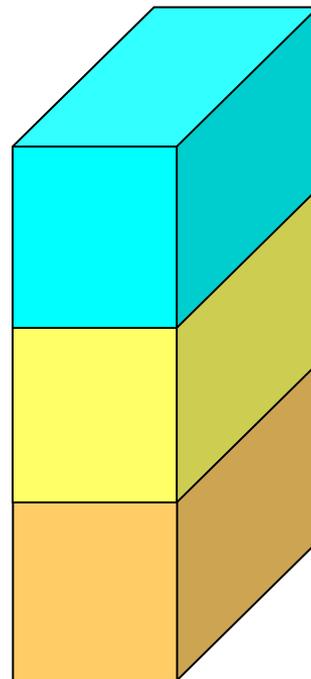
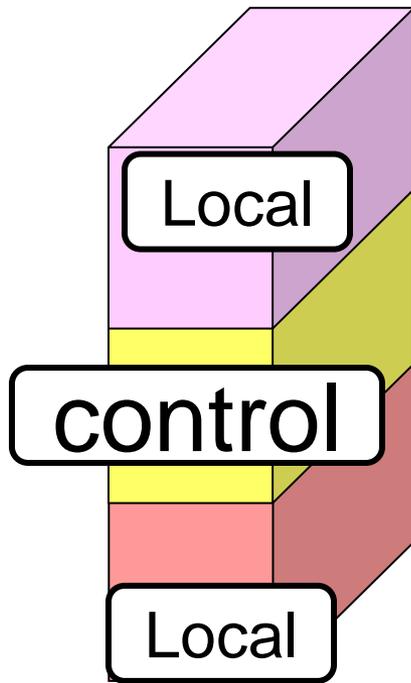
- ☹ Obesity and diabetes
- ☹ Parasites, infection
- ☹ Inflammation, Auto-Im.
- ☹ Cancer
- 💀 Epidemics, war, ...
- 💣 Catastrophic failures

- Fragility = Hijacking, side effects, unintended... of mechanisms evolved for robustness
- Complexity is driven by control, robust/fragile tradeoffs
- Math: New robust/fragile conservation laws



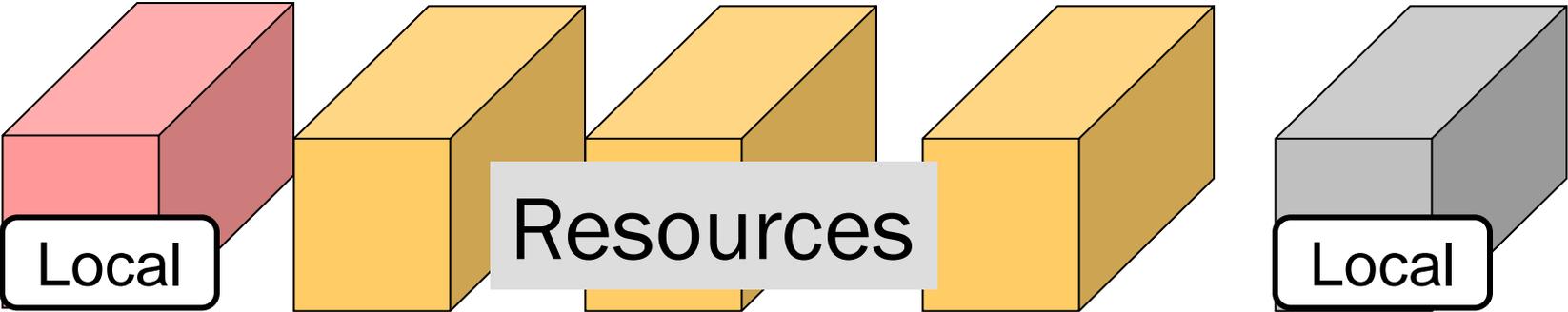
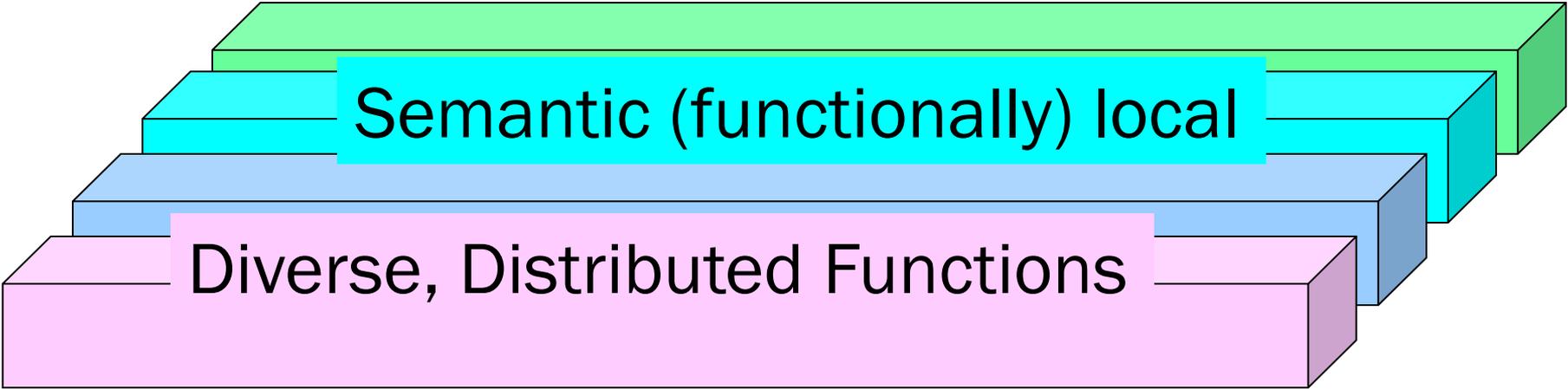
Non-networked Systems

Functions



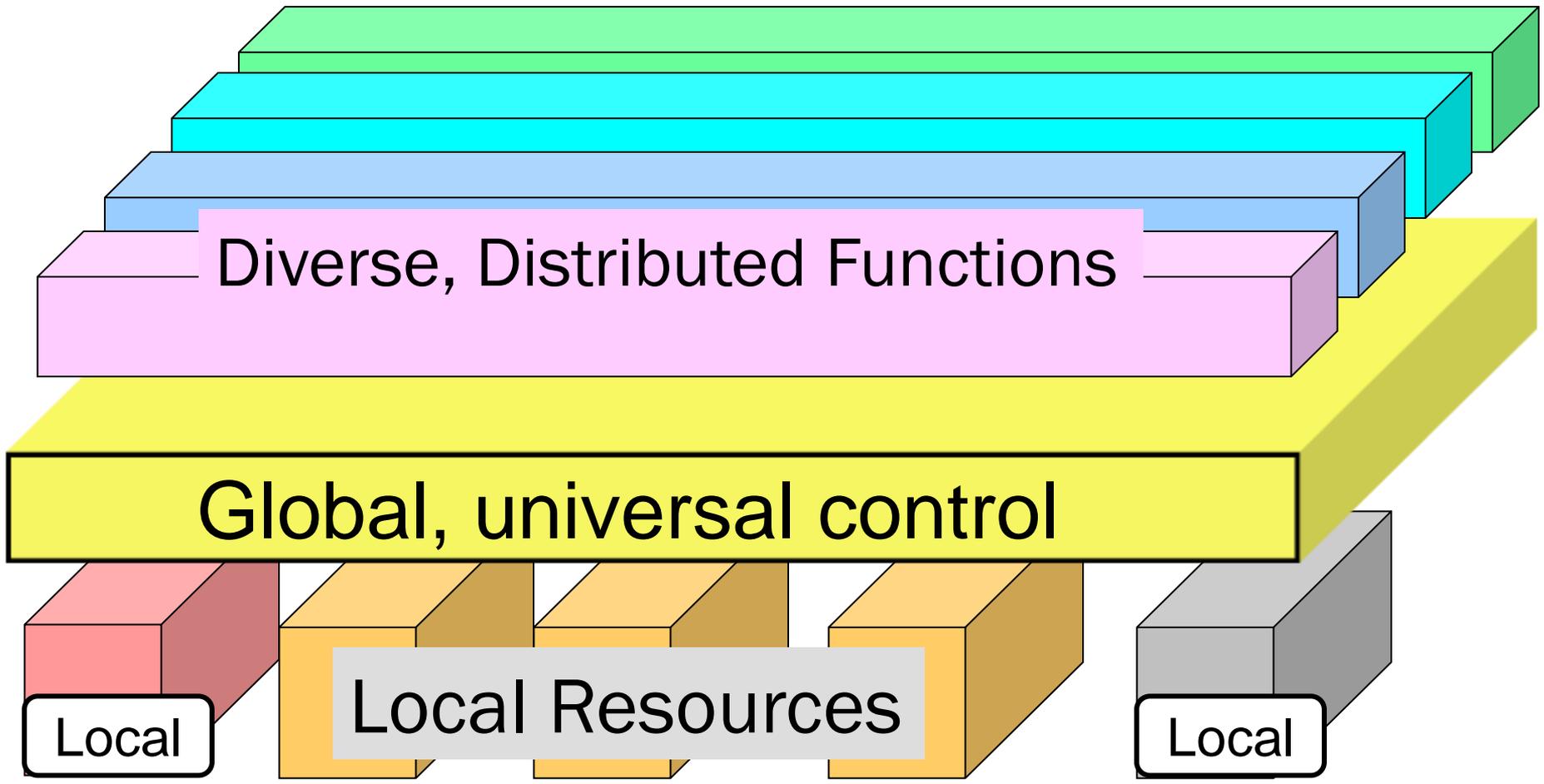
Resources

Network requirements



Geographically local

Layered solution



Diverse, Distributed Functions

Global, universal control

Local

Local Resources

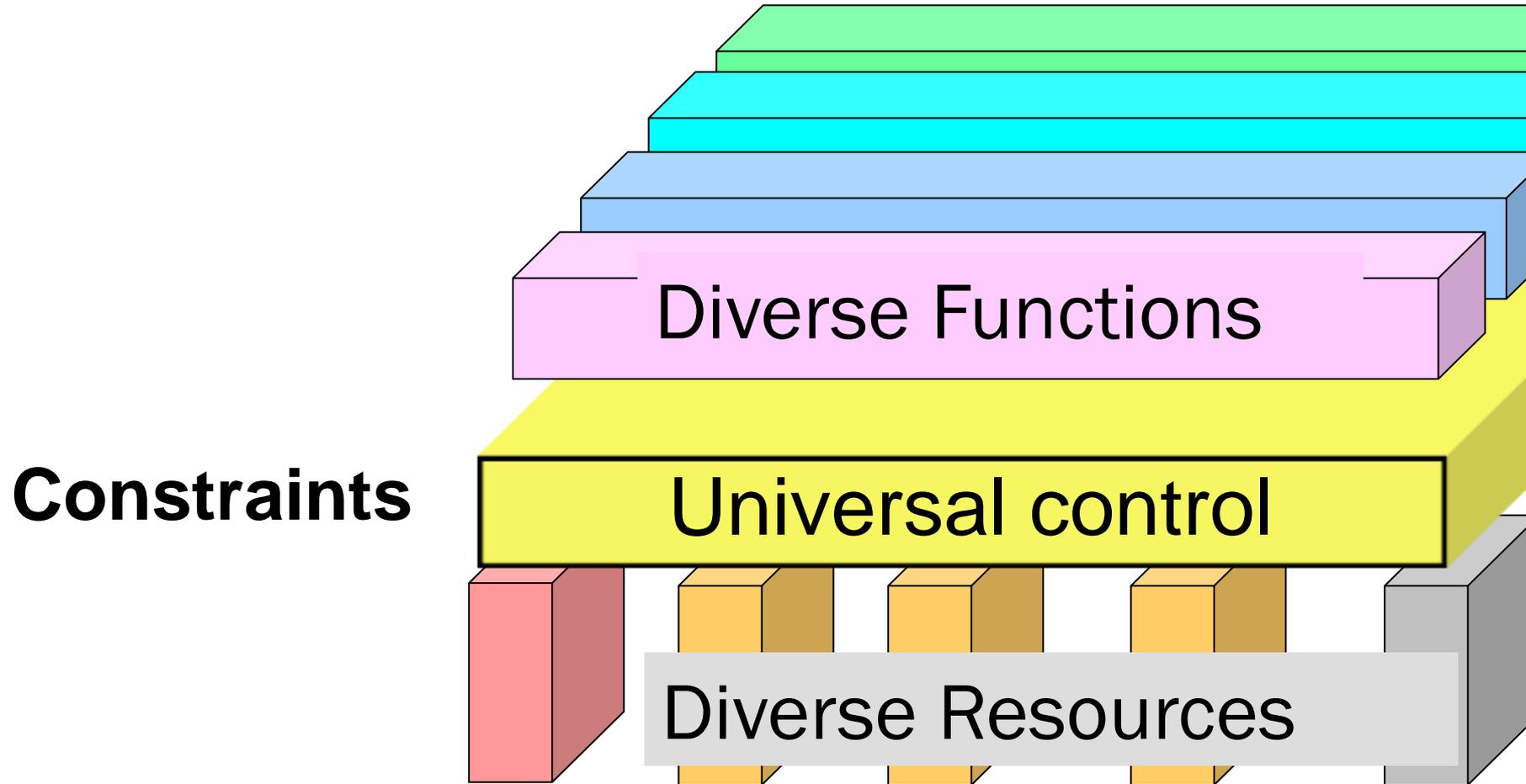
Local

Constraints



Universal control

That deconstrain



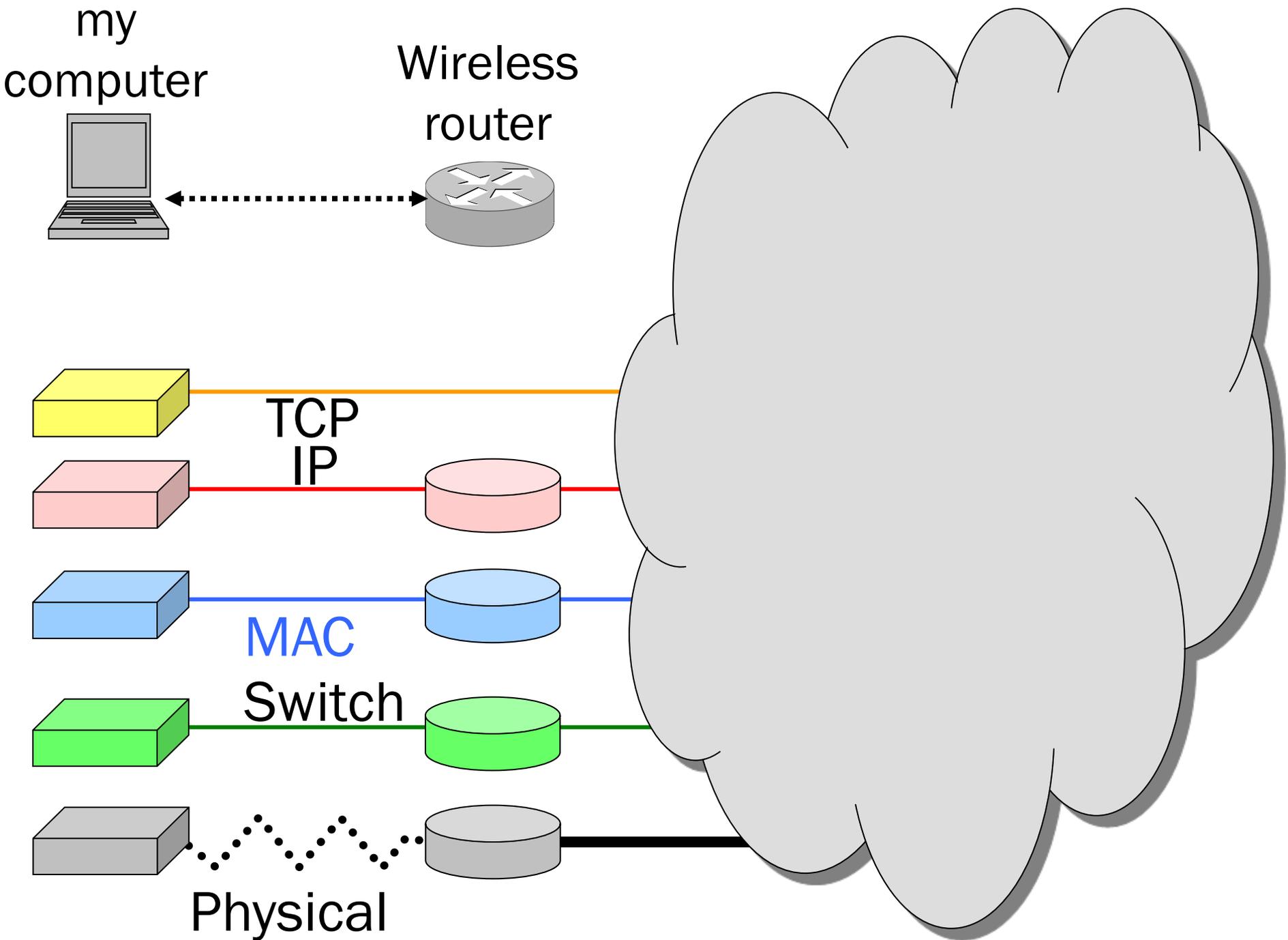
Constraints

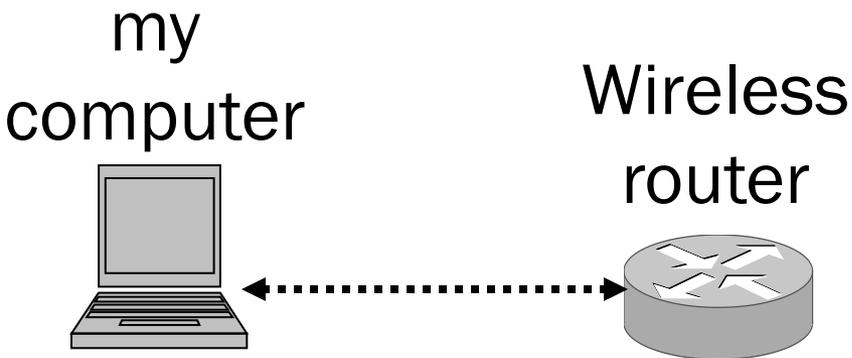
Diverse Functions

Universal control

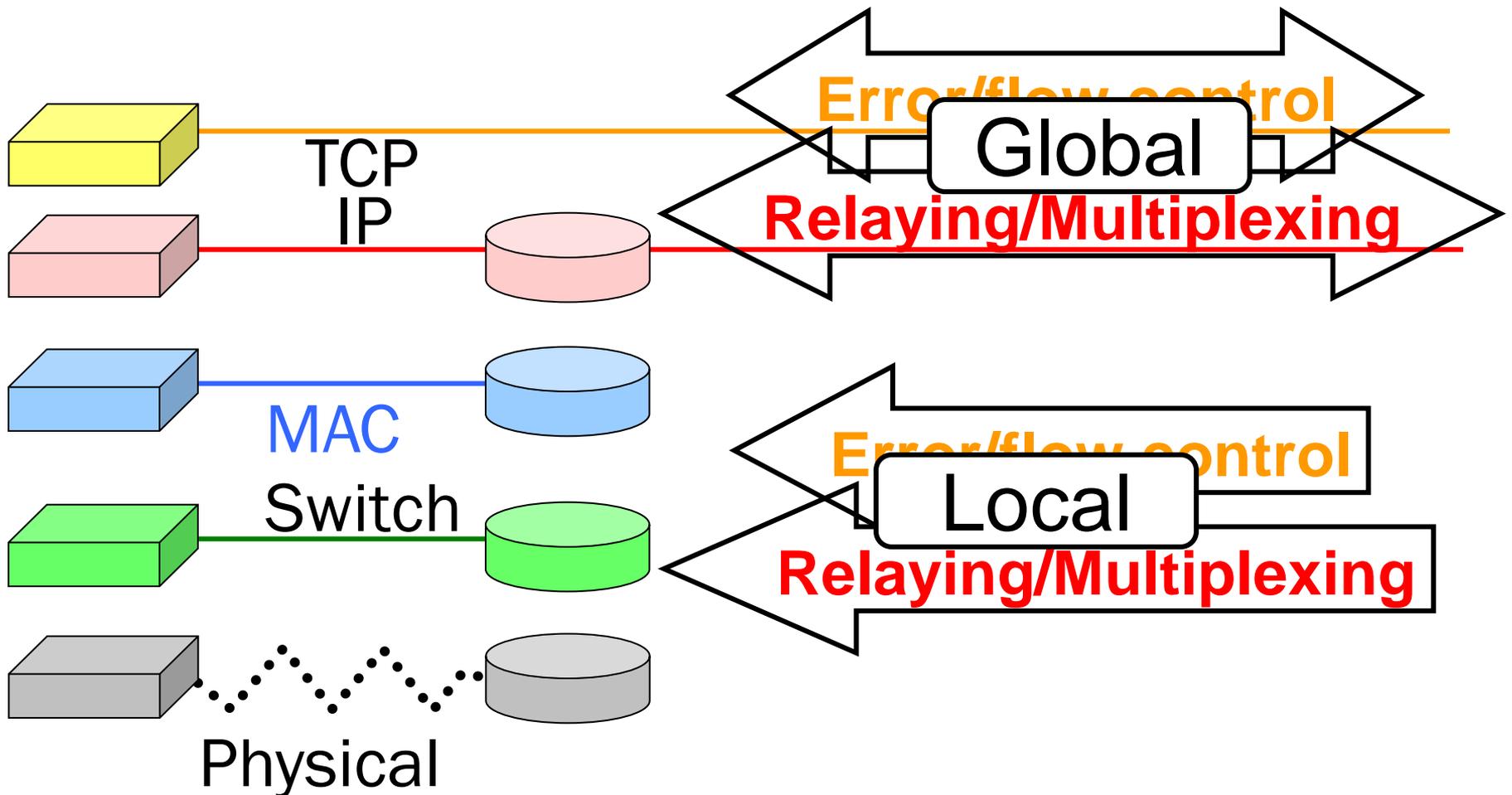
Diverse Resources

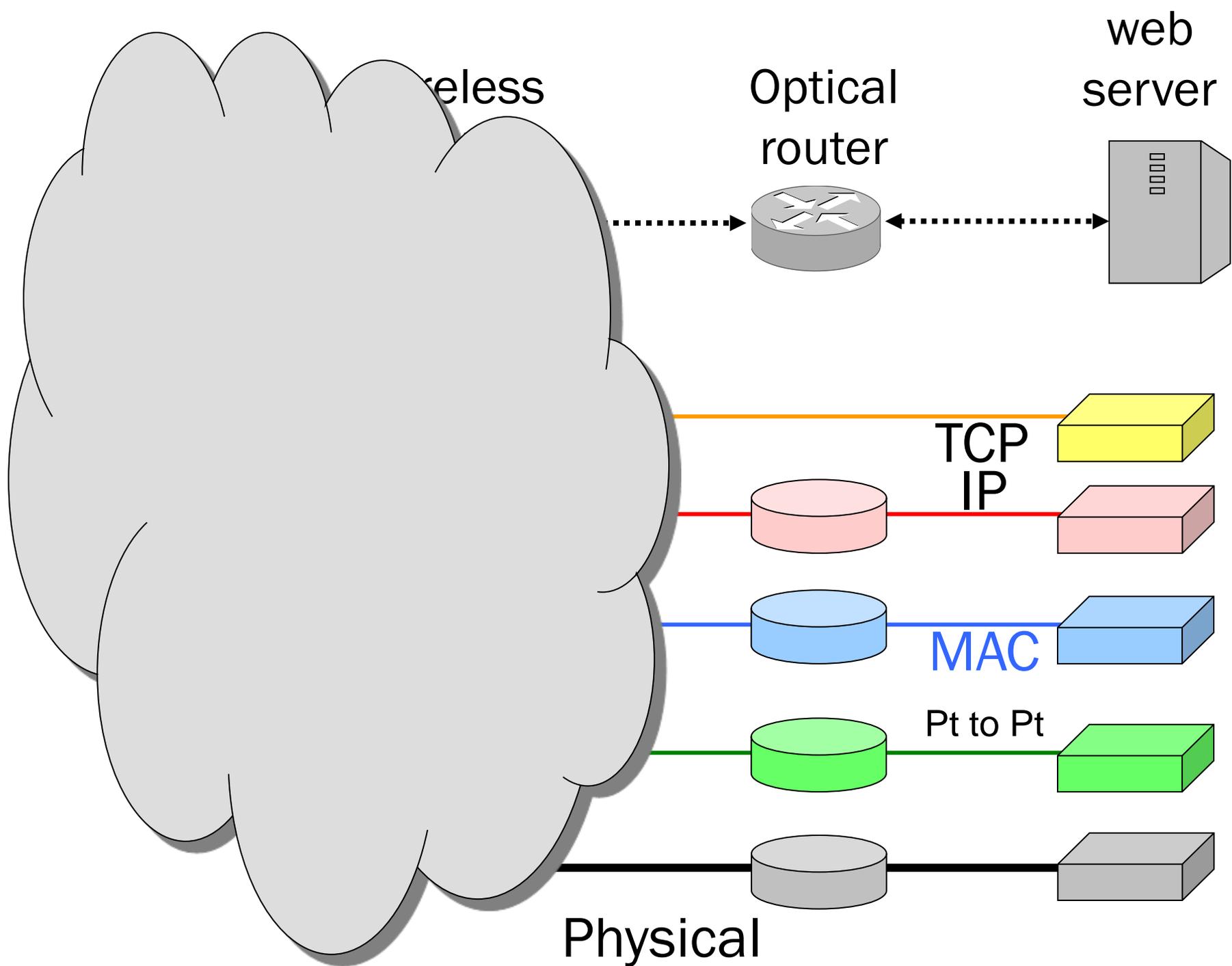
That deconstrain

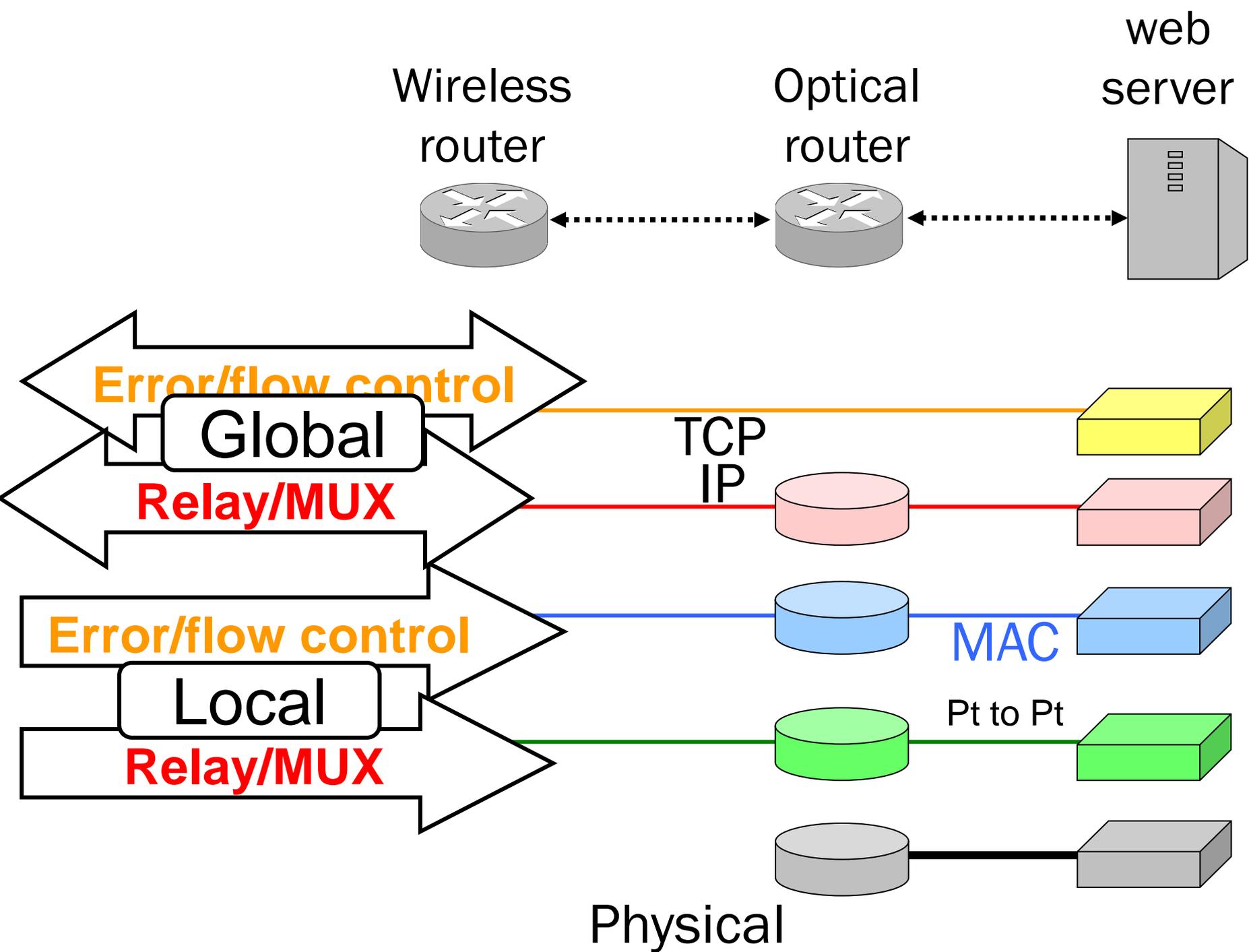


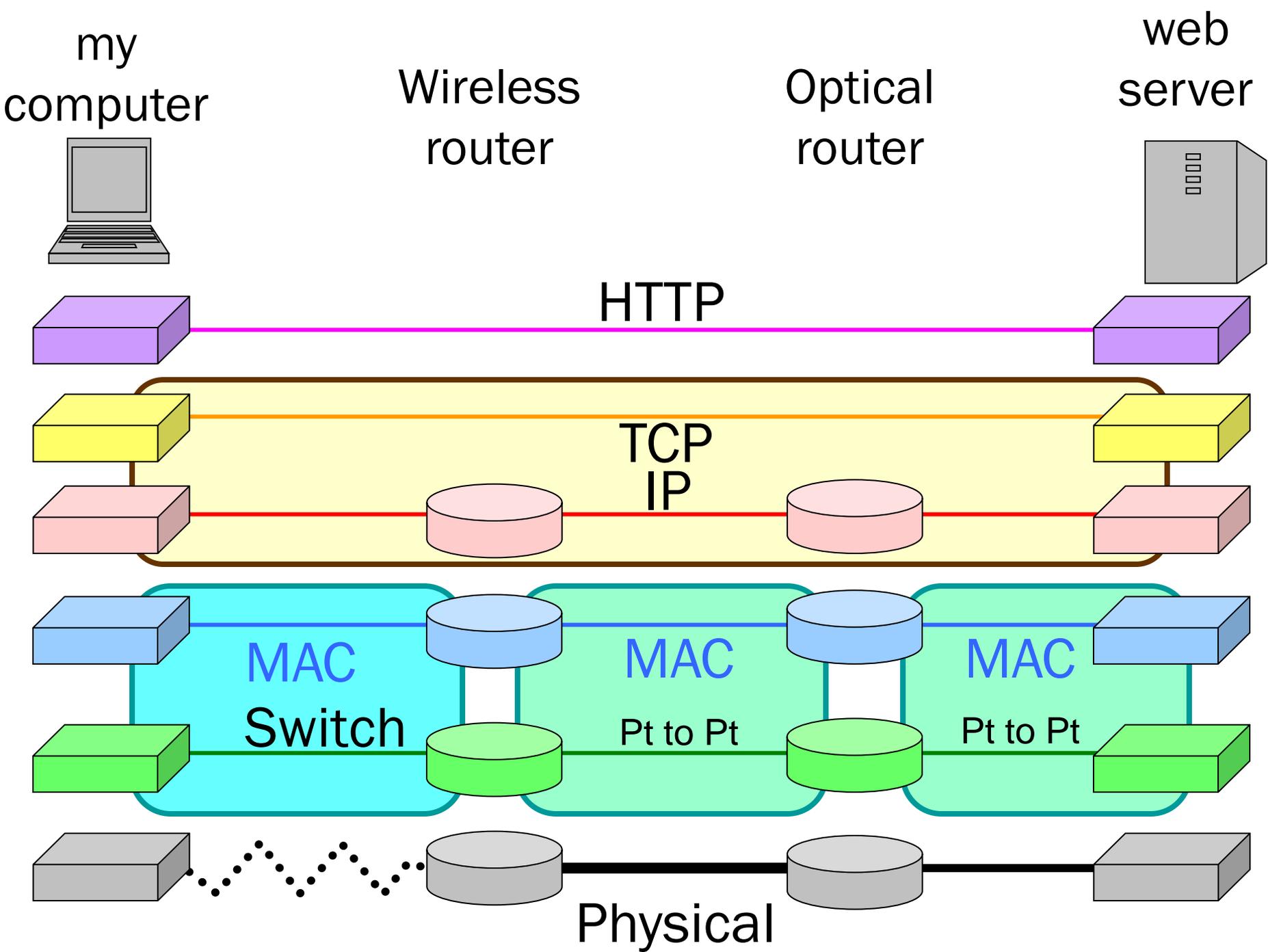


- Differ in
- Details
 - Scope

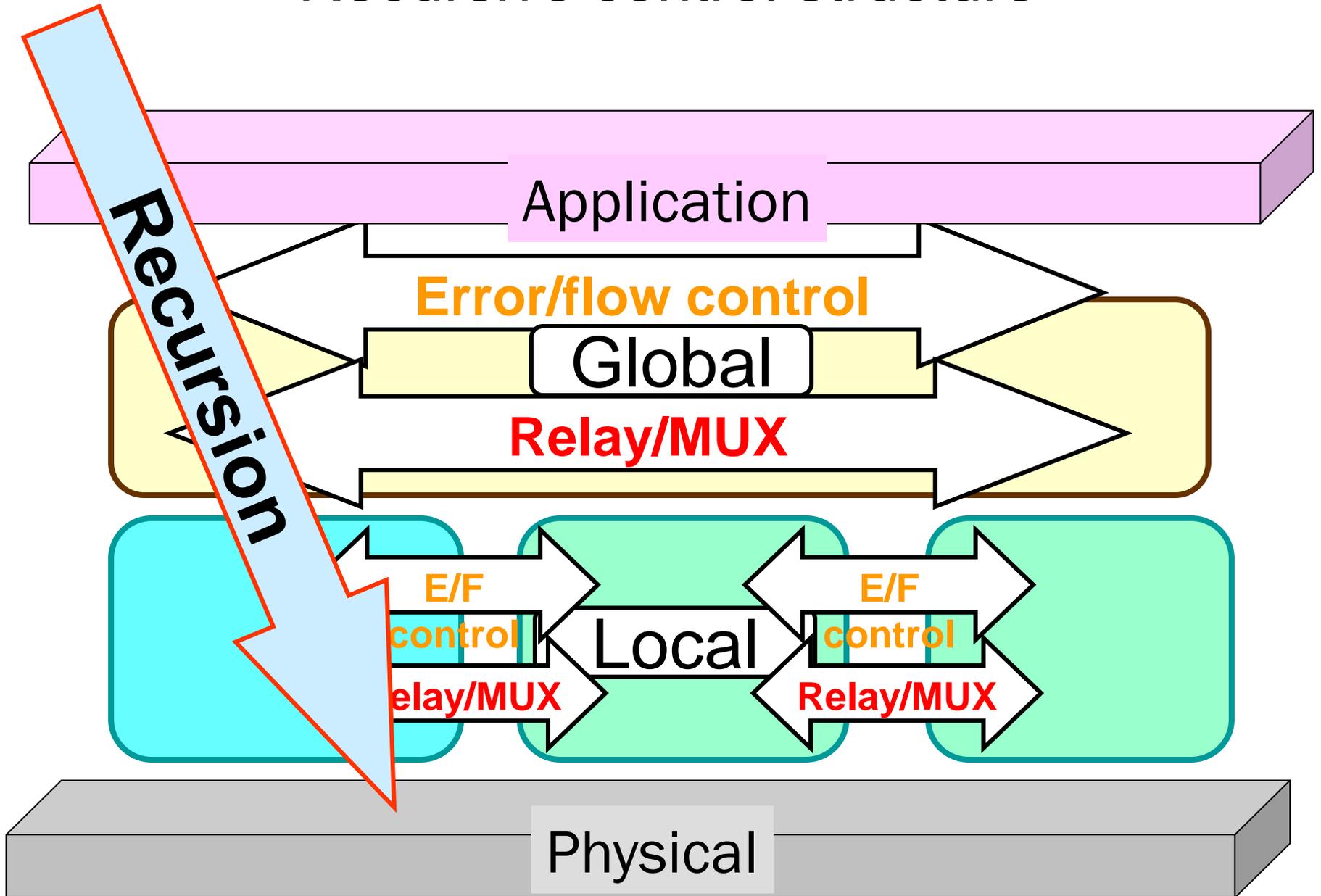


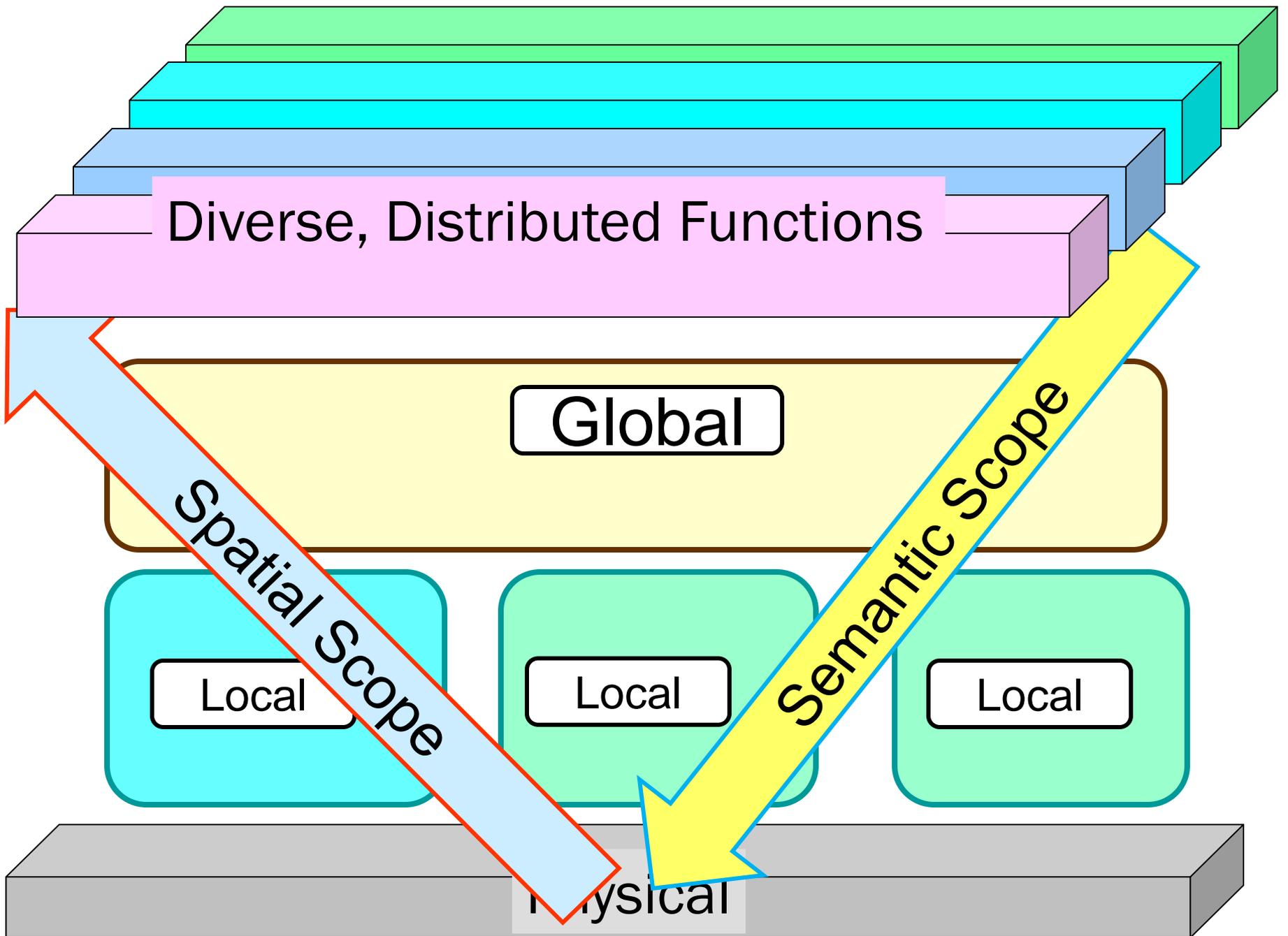






Recursive control structure





Diverse, Distributed Functions

Global

Local

Local

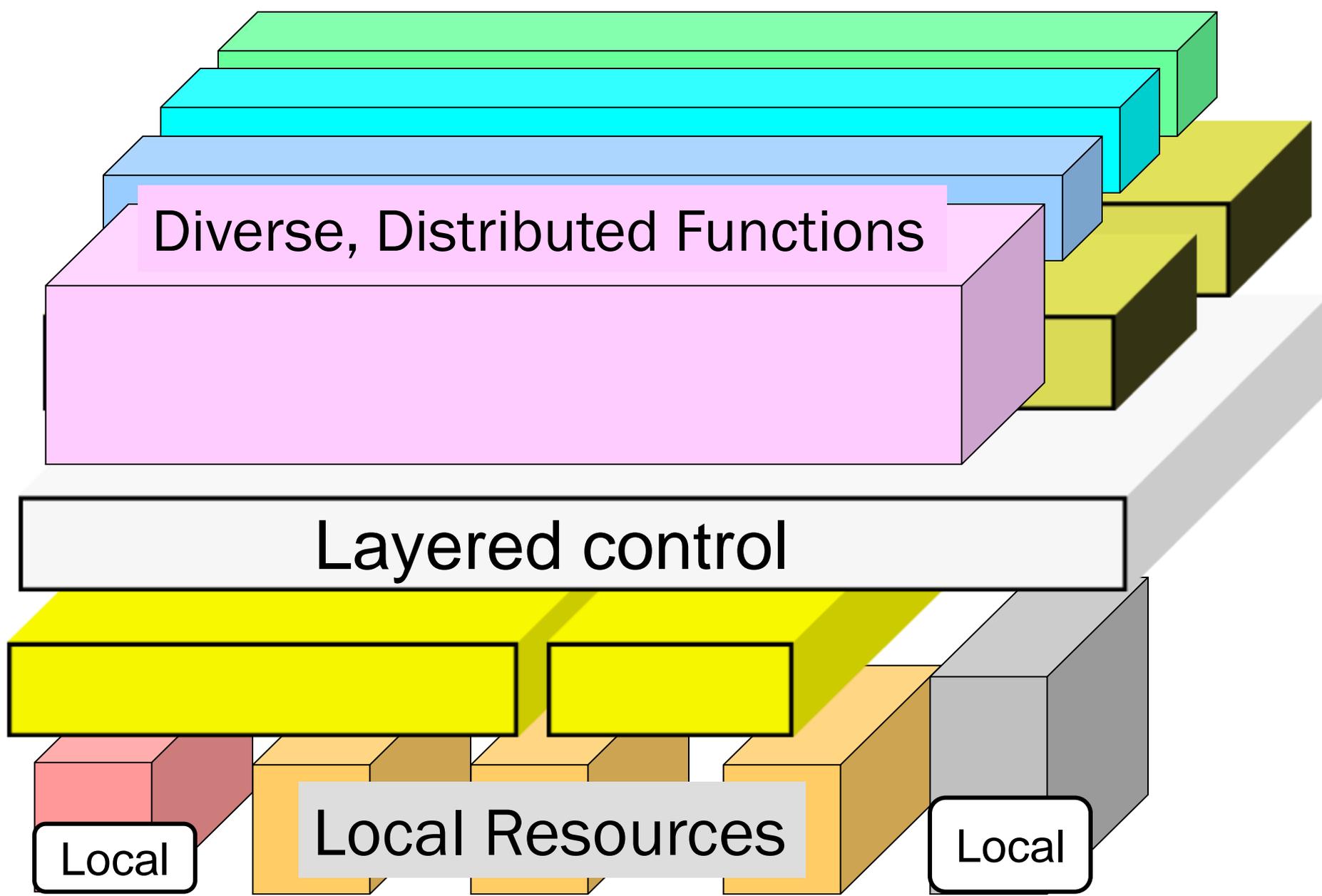
Local

Physical

Spatial Scope

Semantic Scope

Layered solution



Diverse, Distributed Functions

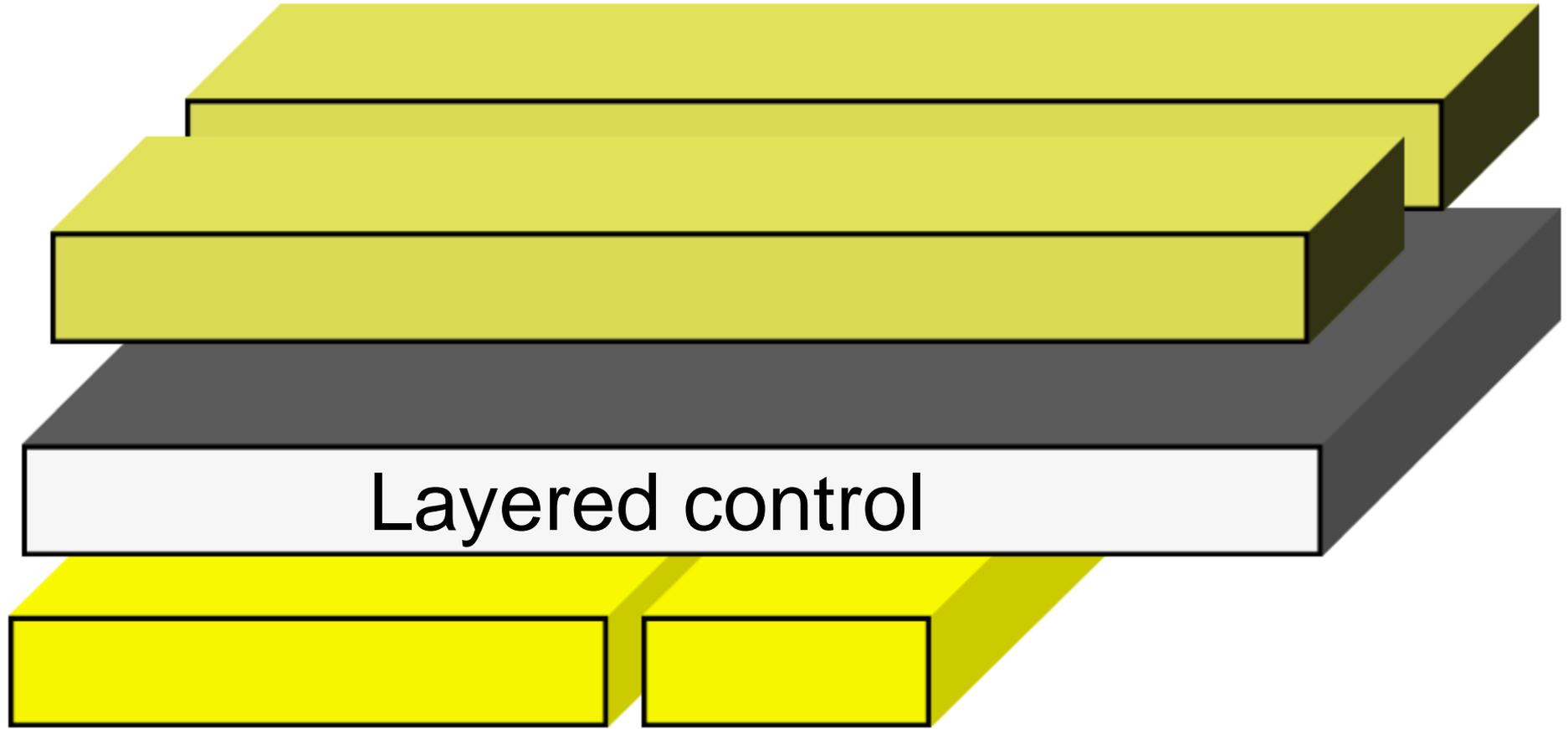
Layered control

Local

Local Resources

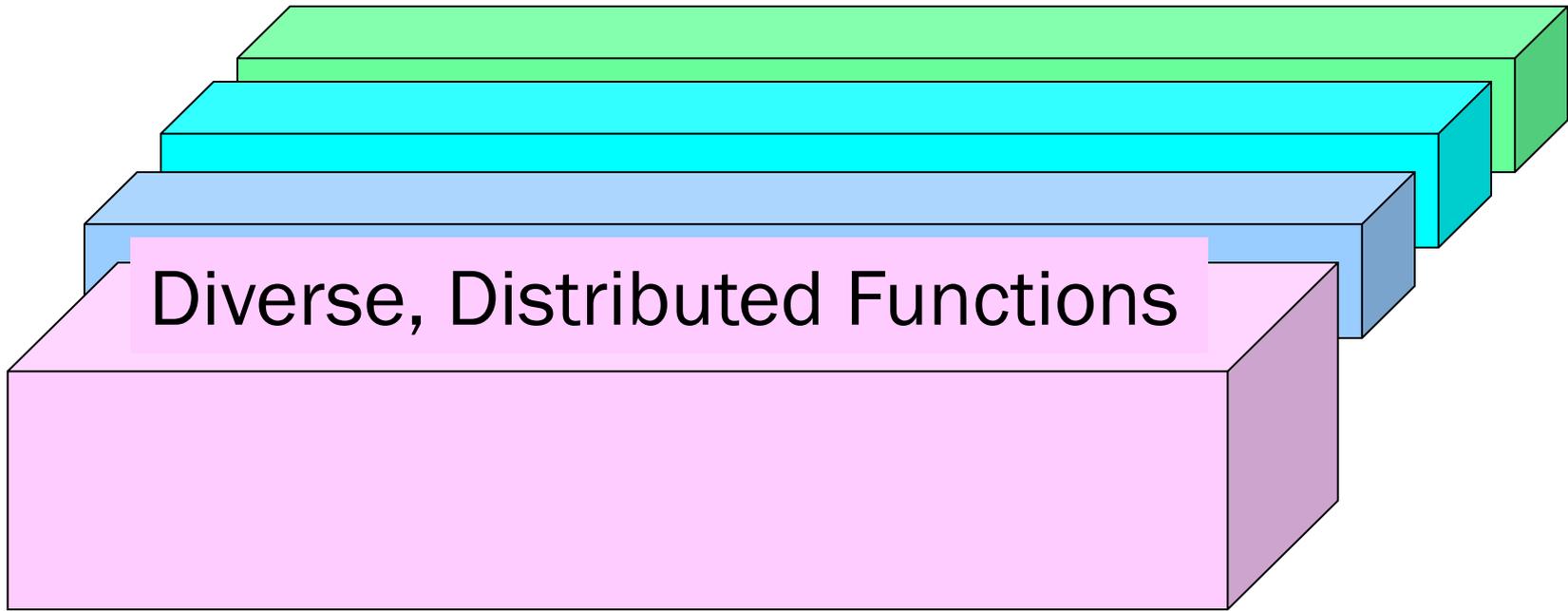
Local

How many layers are there?

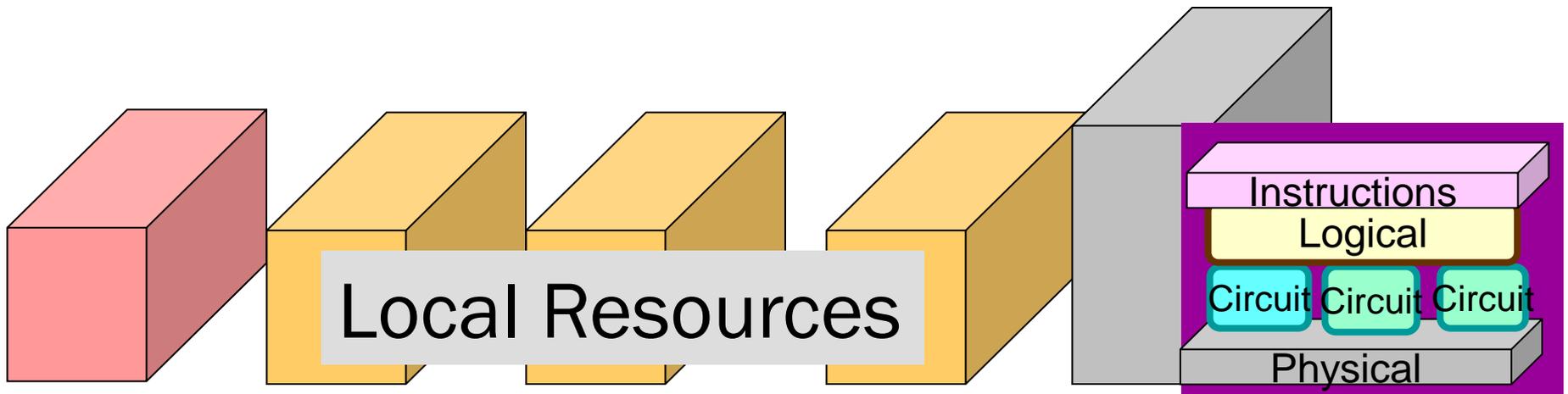


As many as you need.

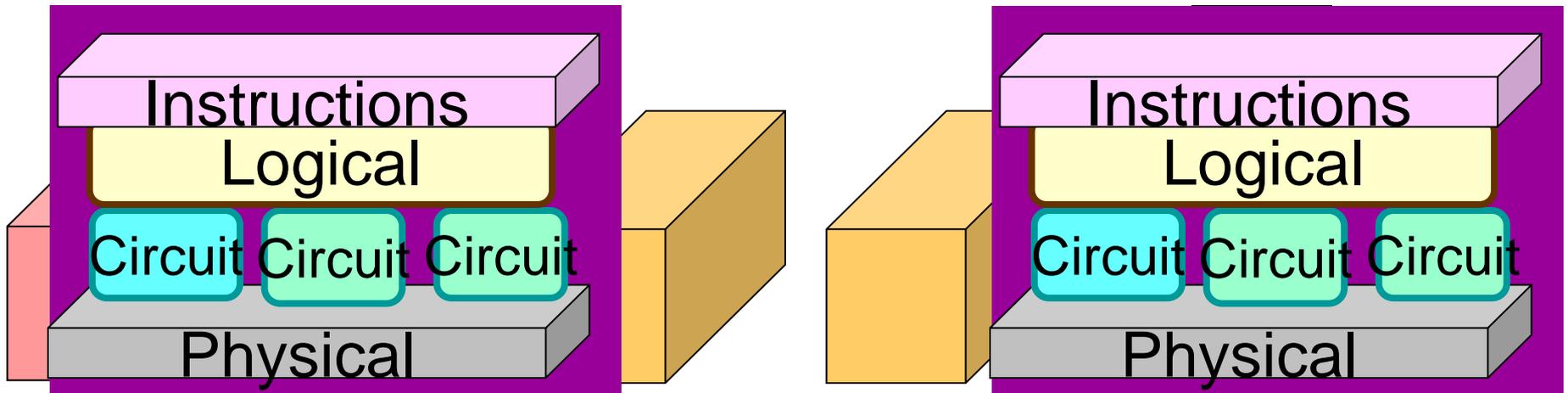
Layered solution



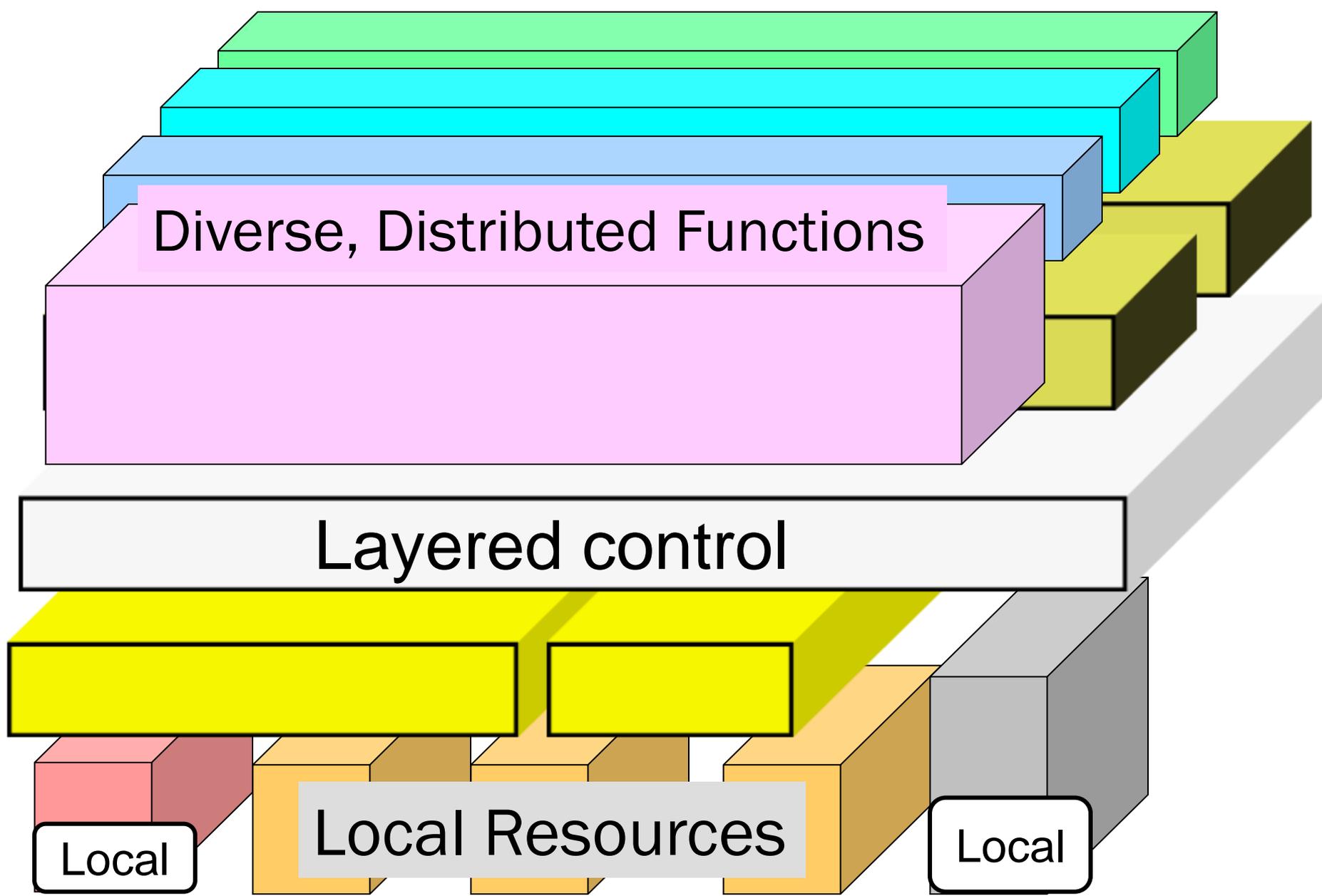
And layers have sublayers



And layers have sublayers



Layered solution



Diverse, Distributed Functions

Layered control

Local

Local Resources

Local

Diverse, Distributed Functions

Huge range of dynamics

- Spatial
- Temporal

Instructions

Logical

Circuit Circuit Circuit

Physical

Bewildering w/out
clear grasp of
layered architecture

telephony

telephony

Diverse applications

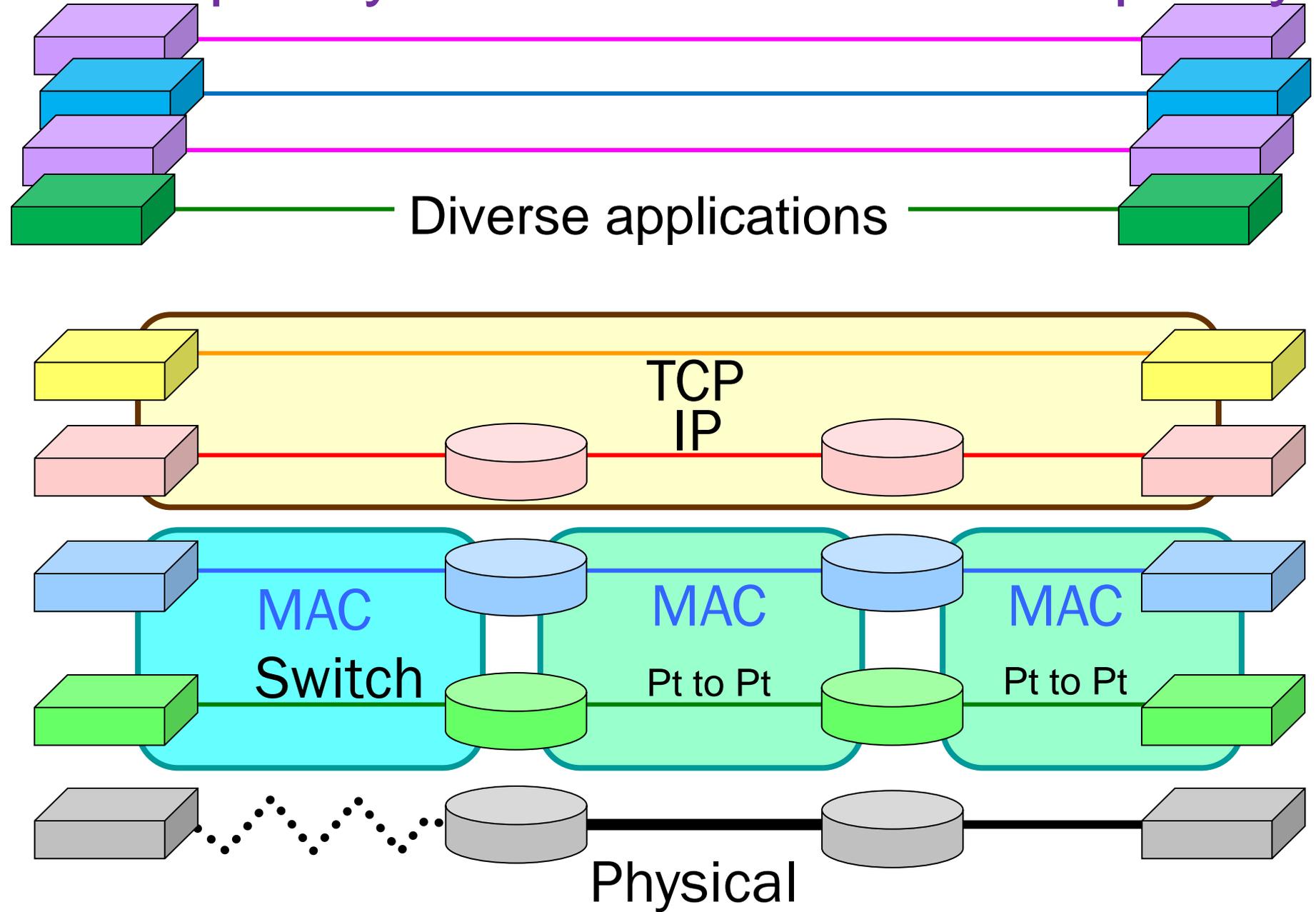
TCP
IP

MAC
Switch

MAC
Pt to Pt

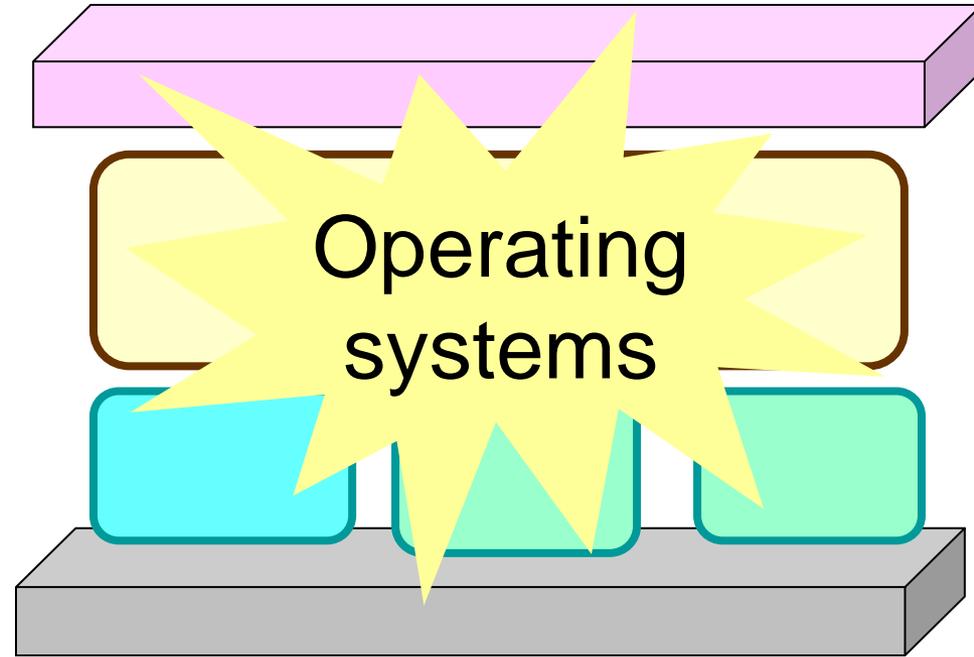
MAC
Pt to Pt

Physical

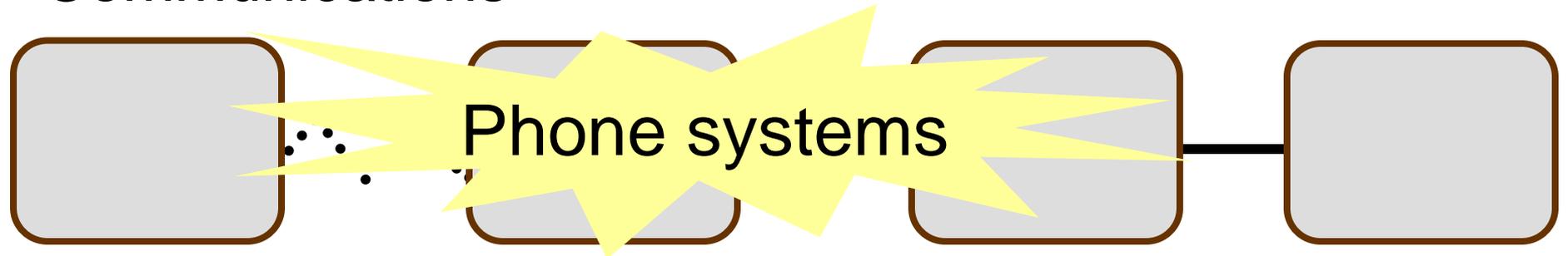


Ancient network architecture:
“Bell-heads versus Net-heads”

Layers (Net)
Computer



Pathways (Bell)
Communications



Cyber-Physical Theories

- Thermodynamics
- Communications
- Control
- Computation

Cyber

- Thermodynamics
- Communications
- Control
- Computation

Physical

- Thermodynamics
- Communications
- Control
- Computation

Internet

Bacteria

Case studies

Cyber

- Thermodynamics
- Communications
- Control
- Computation

Physical

- Thermodynamics
- Communications
- Control
- Computation

Promising unifications

Theoretical framework: Constraints that deconstrain

Applications Deconstrained

$$\min_{\mathbf{x}} \int \|\mathbf{R}\tilde{\mathbf{x}} - \mathbf{c}\|^2 + \|\mathbf{R}\mathbf{x} - \mathbf{c}\|^2 dt$$

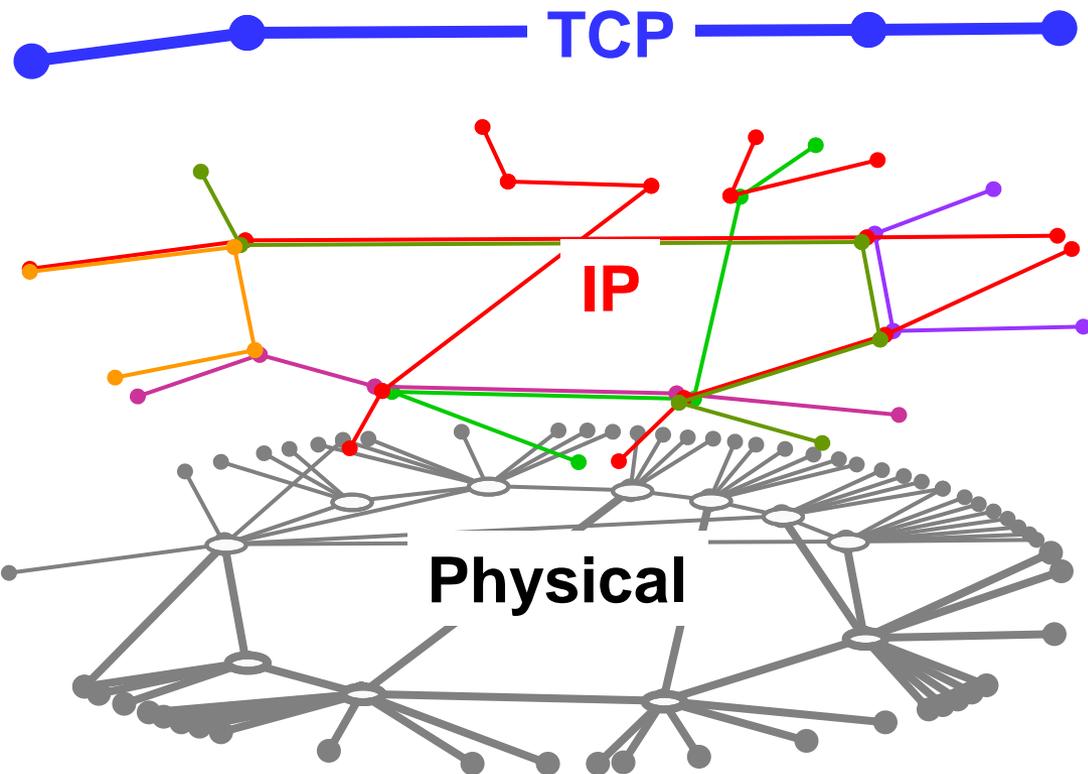
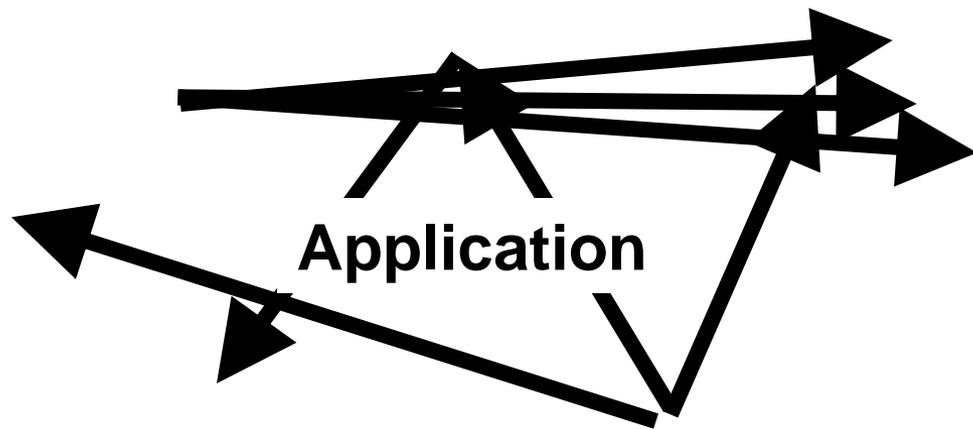
$$\left| \tilde{\mathbf{x}} = \arg \max_{\mathbf{v}} L(\mathbf{v}, \mathbf{p}), \quad \dot{\mathbf{p}} = \mathbf{R}\mathbf{x} - \mathbf{c} \right.$$

$$\Rightarrow x_s = \arg \max_{\mathbf{v}} L_s(\mathbf{v}, \mathbf{p})$$

Resources Deconstrained

- Optimization
- Optimal control
- Robust control
- Game theory
- Network coding

Architecture is *not* graph topology.



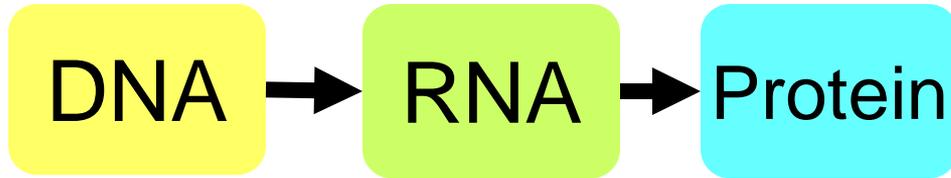
Architecture facilitates arbitrary graphs.

Biology versus the Internet

Similarities

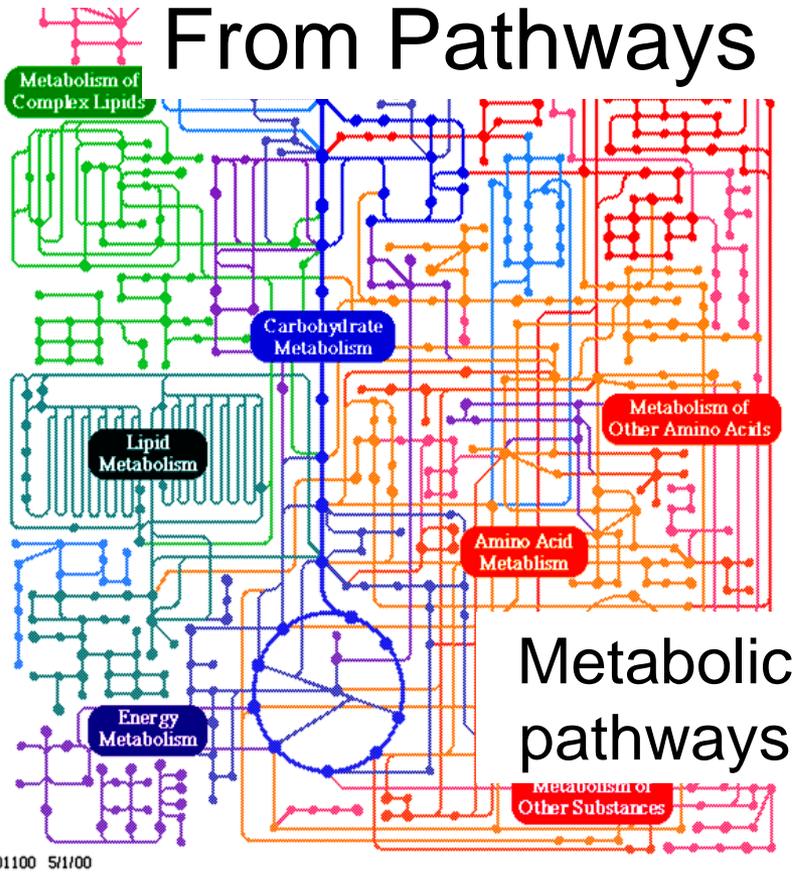
- Evolvable architecture
- Robust yet fragile
- Constraints/deconstrain
- Layering, modularity
- Hourglass with bowties
- Feedback
- Dynamics
- Distributed/decentralized
- *Not* scale-free, edge-of-chaos, self-organized criticality, etc

“Central dogma”

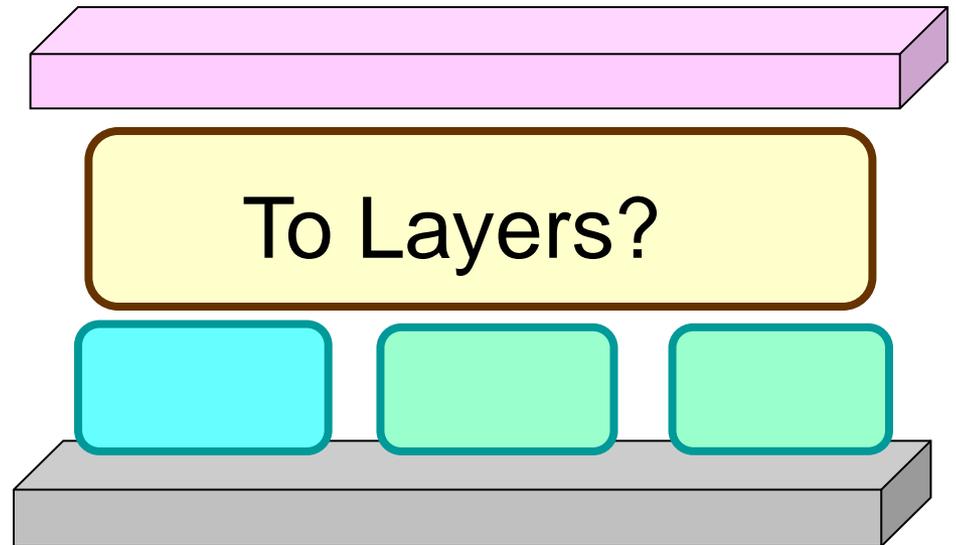


Network architecture?

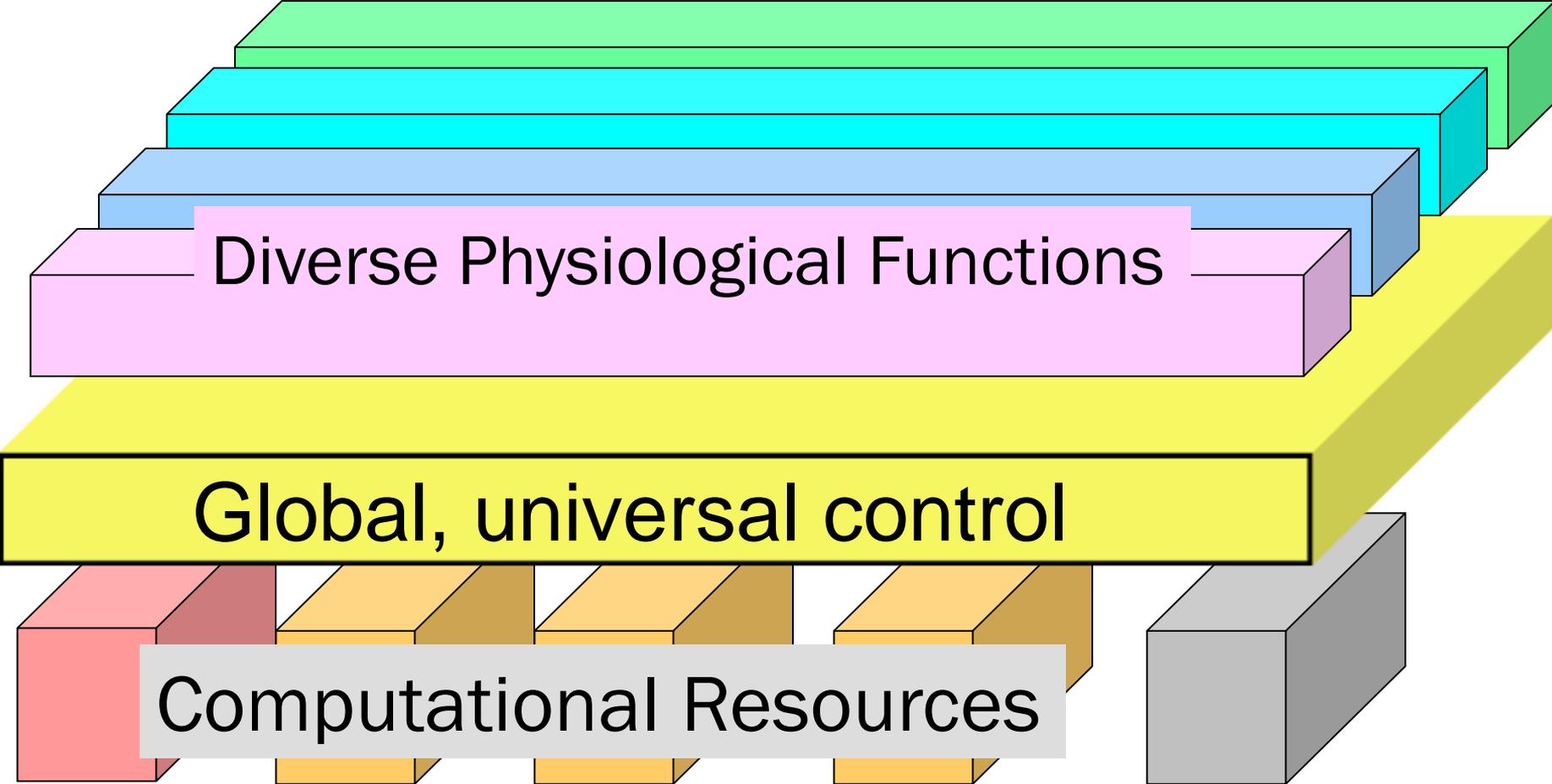
From Pathways



To Layers?



Layered Brain (Hawkins)?



Diverse Physiological Functions

Global, universal control

Computational Resources

Diverse Physiological Functions

Global, universal control

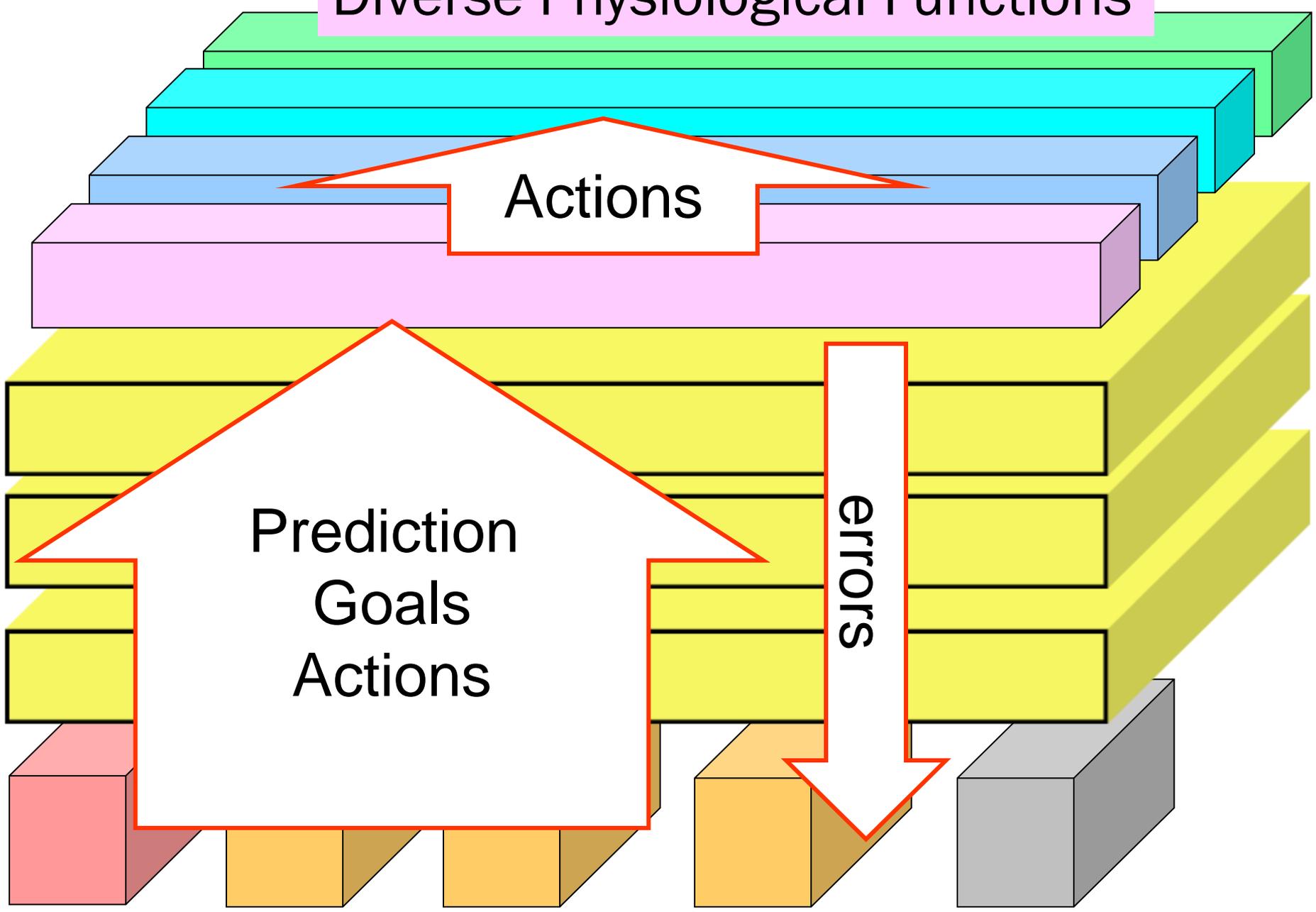
Computational Resources

Diverse Physiological Functions

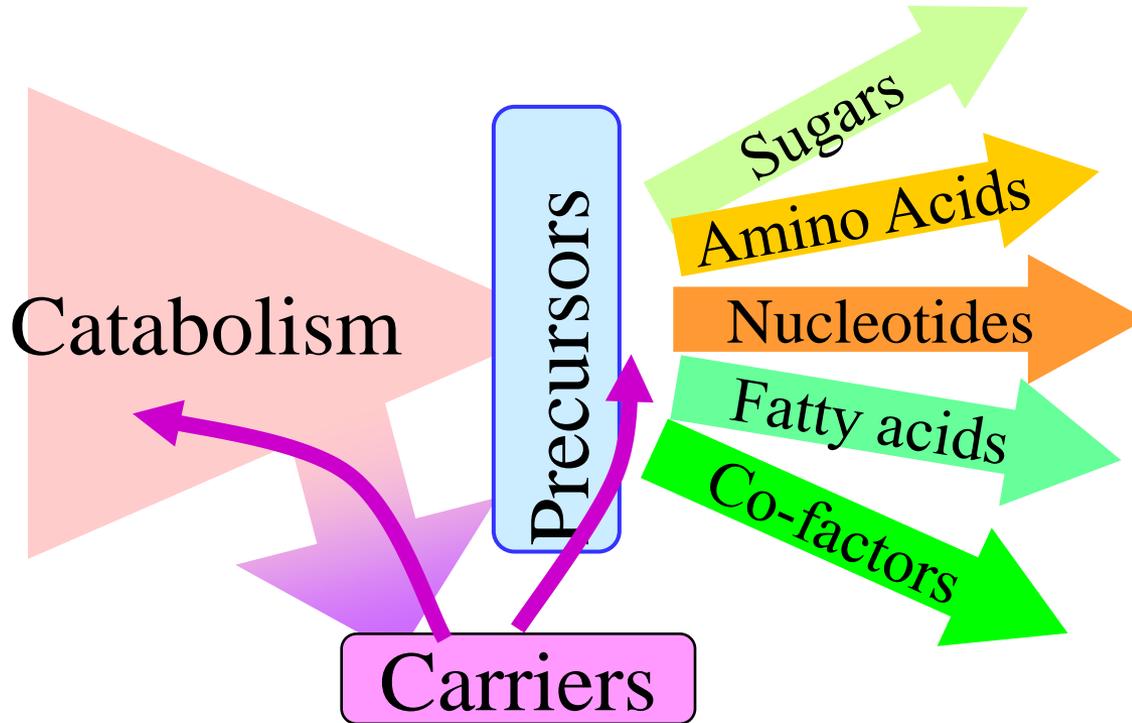
Actions

Prediction
Goals
Actions

errors



Inside every cell

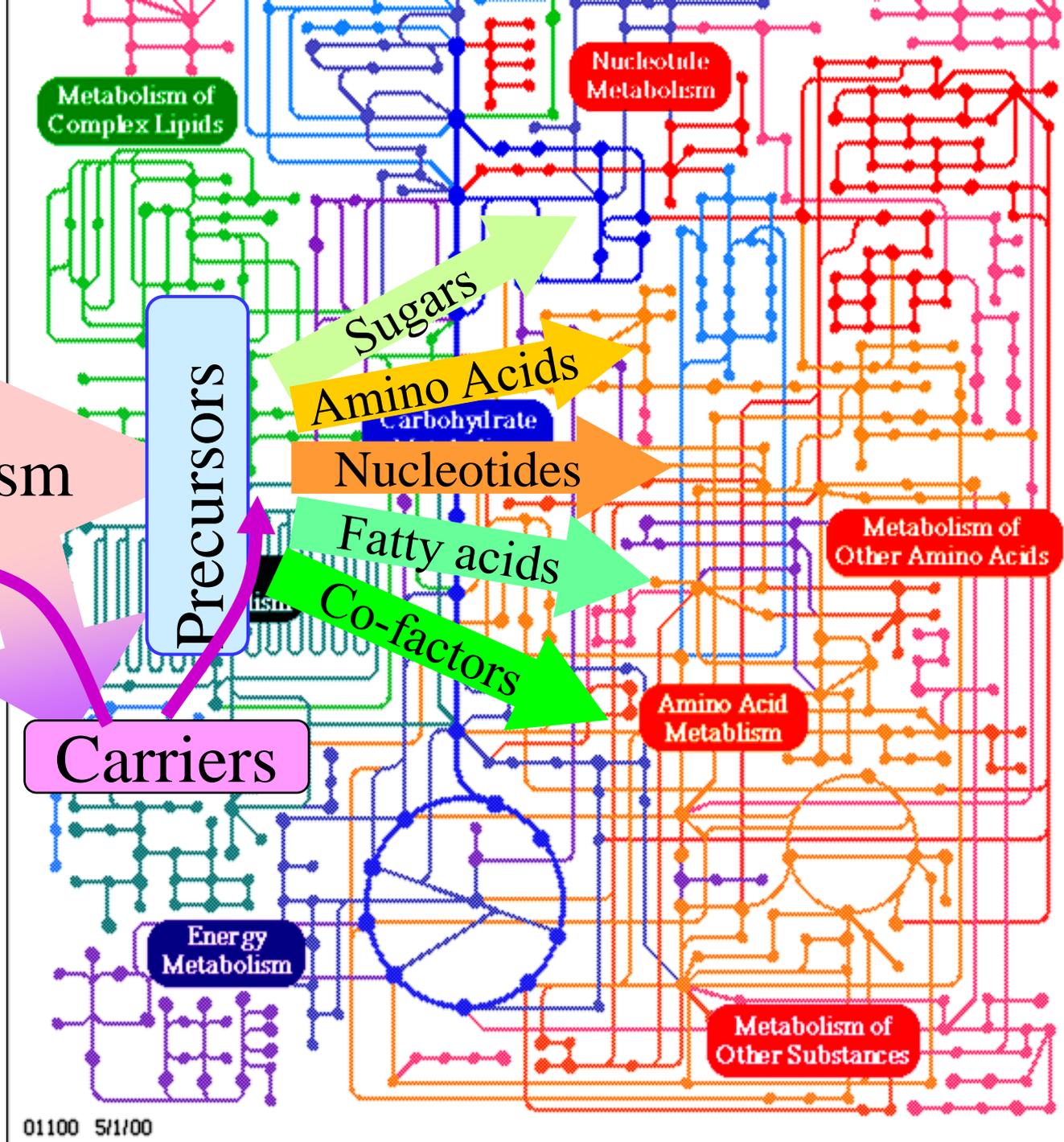


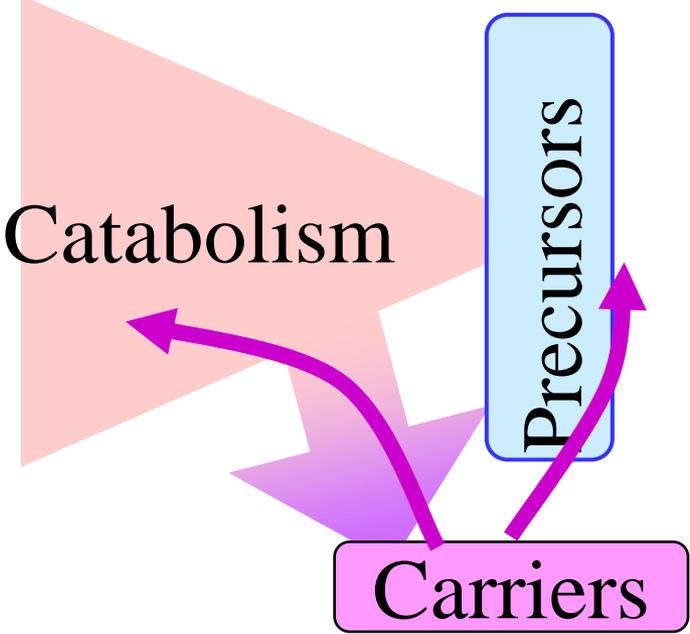
Core metabolic bowtie

Core
metabolism

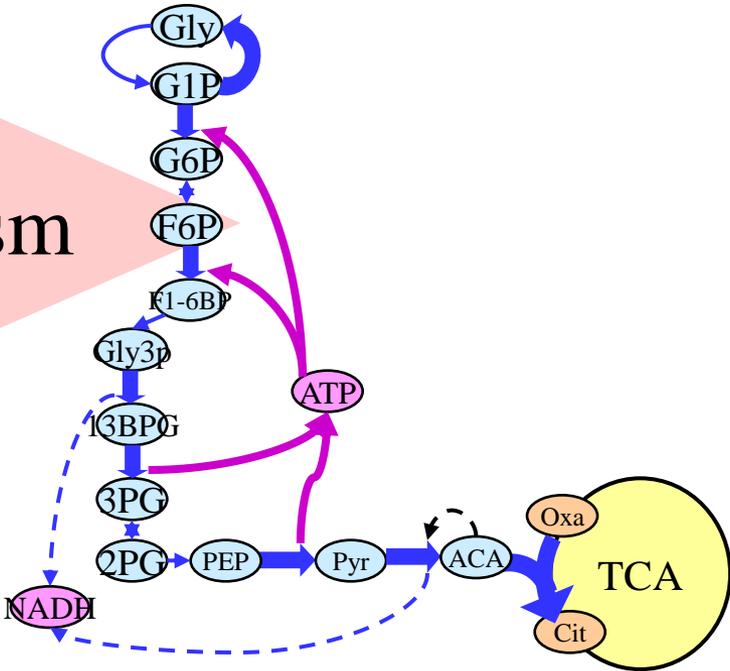
Catabolism

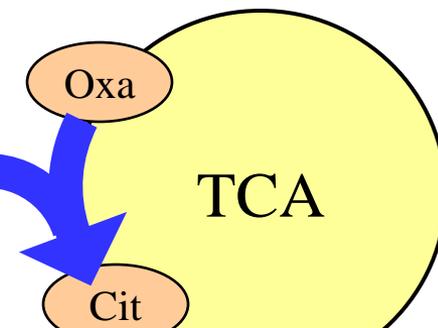
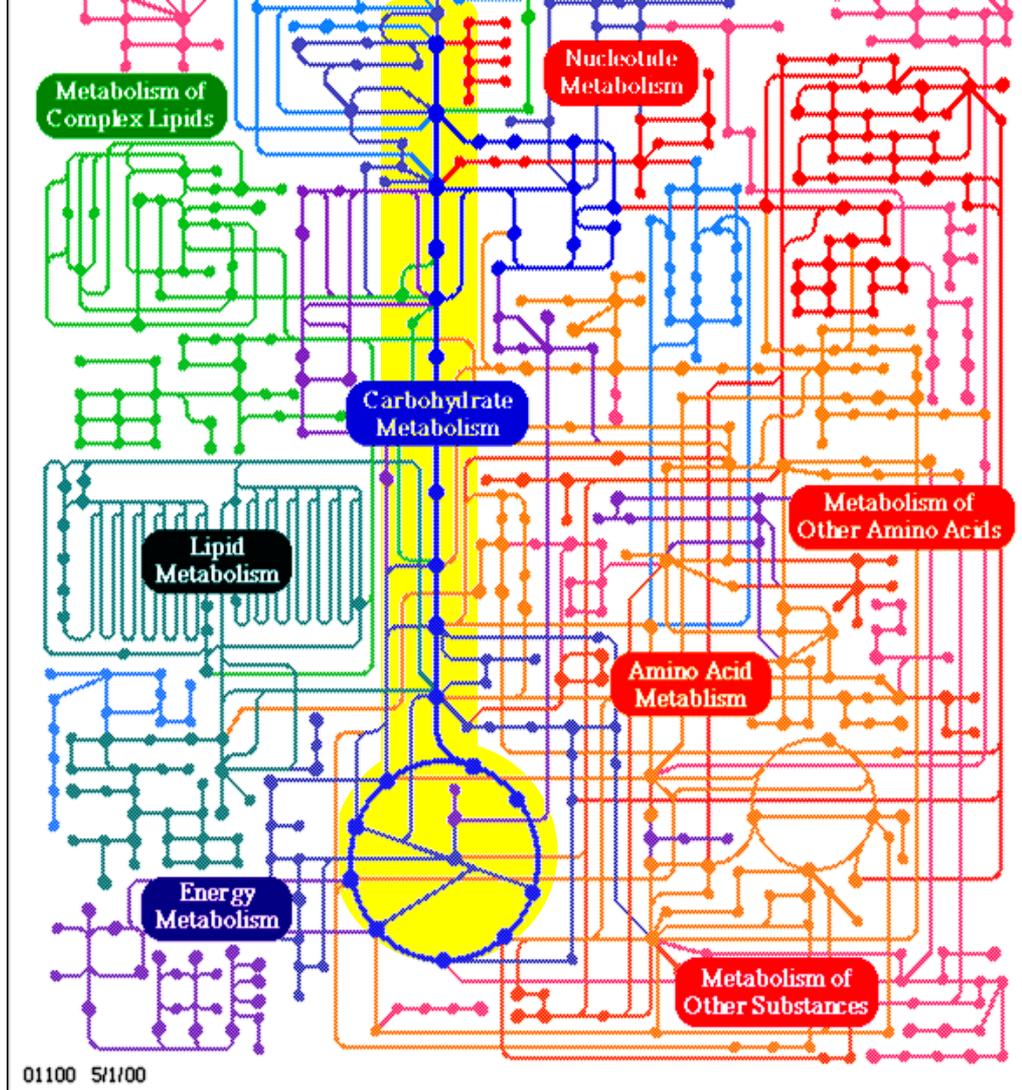
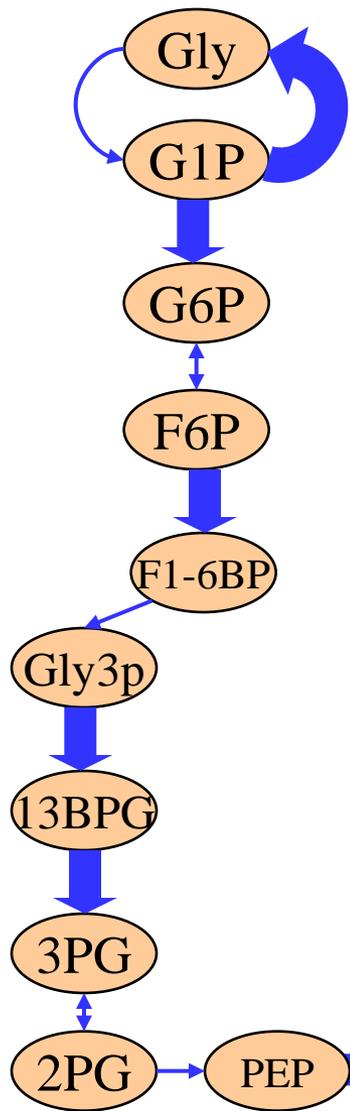
Inside every
cell ($\approx 10^{30}$)

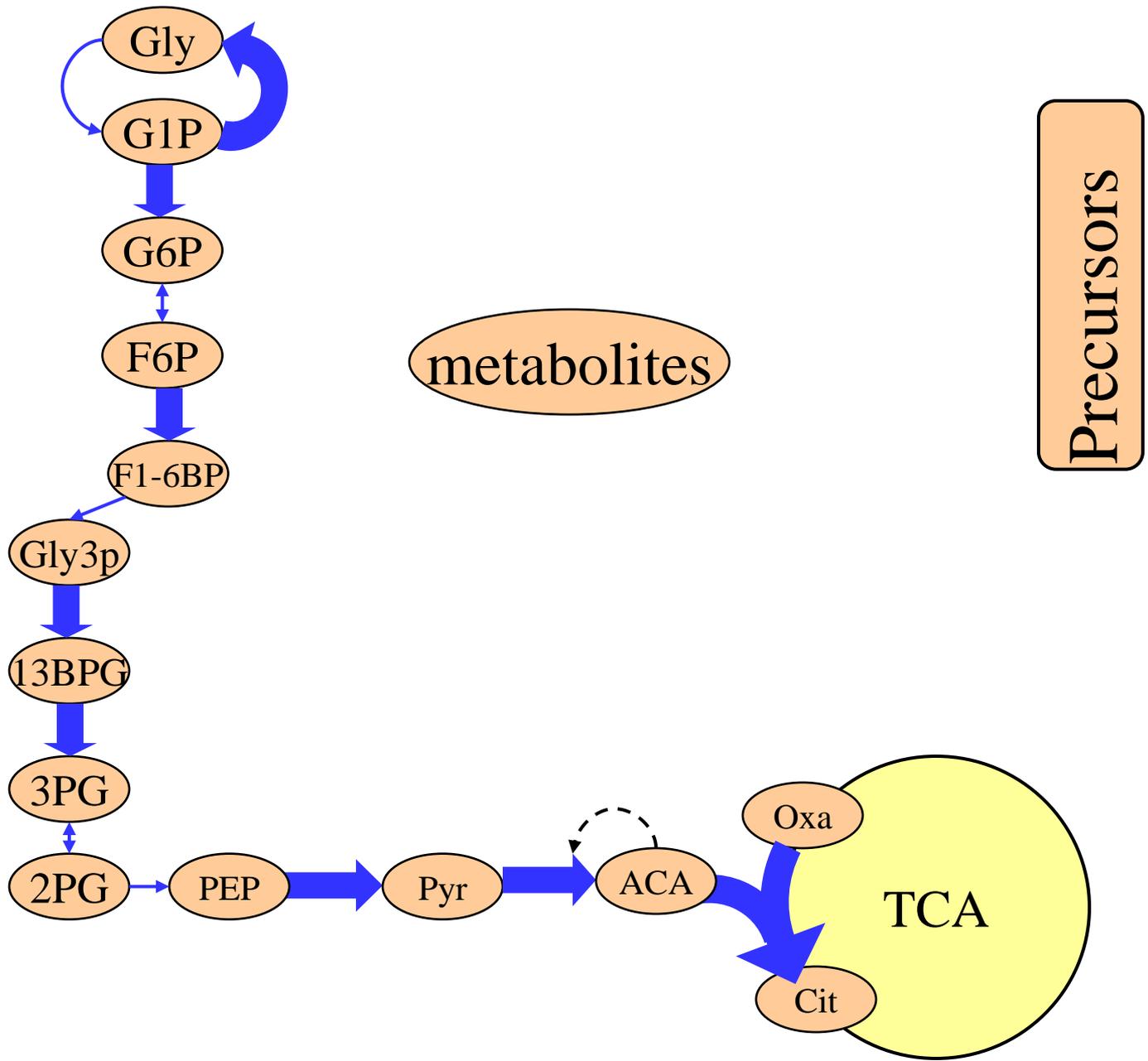


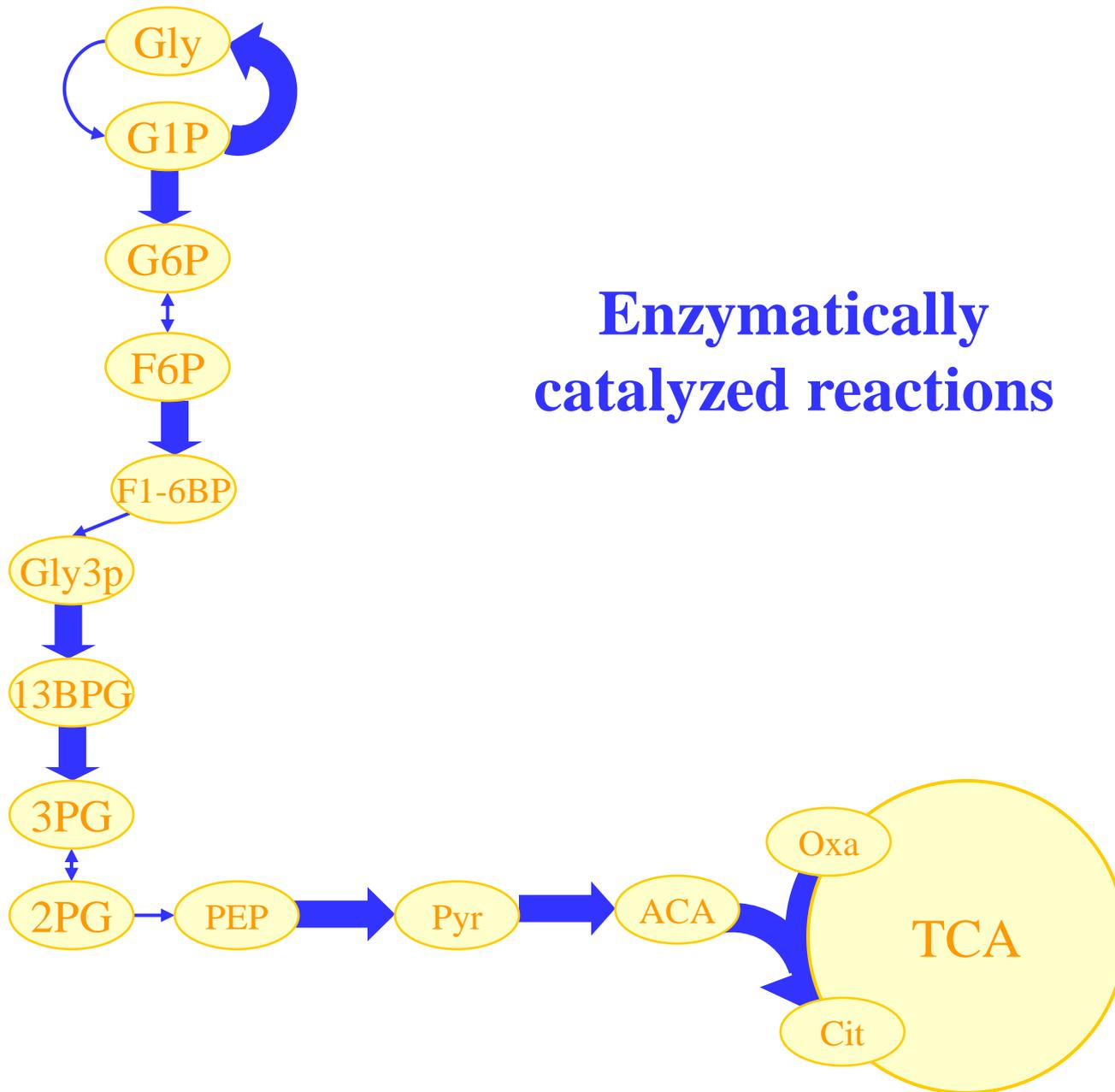


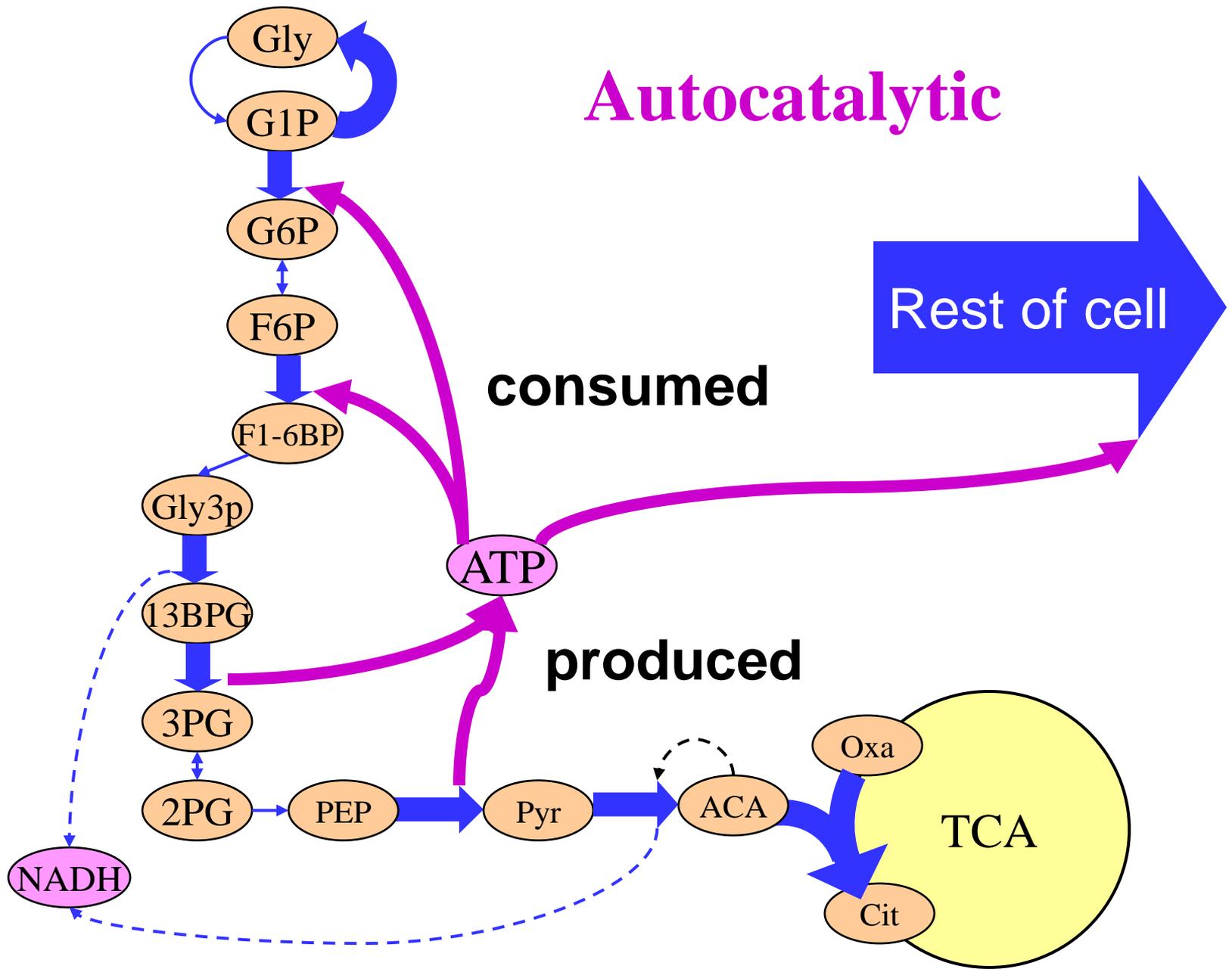
Catabolism

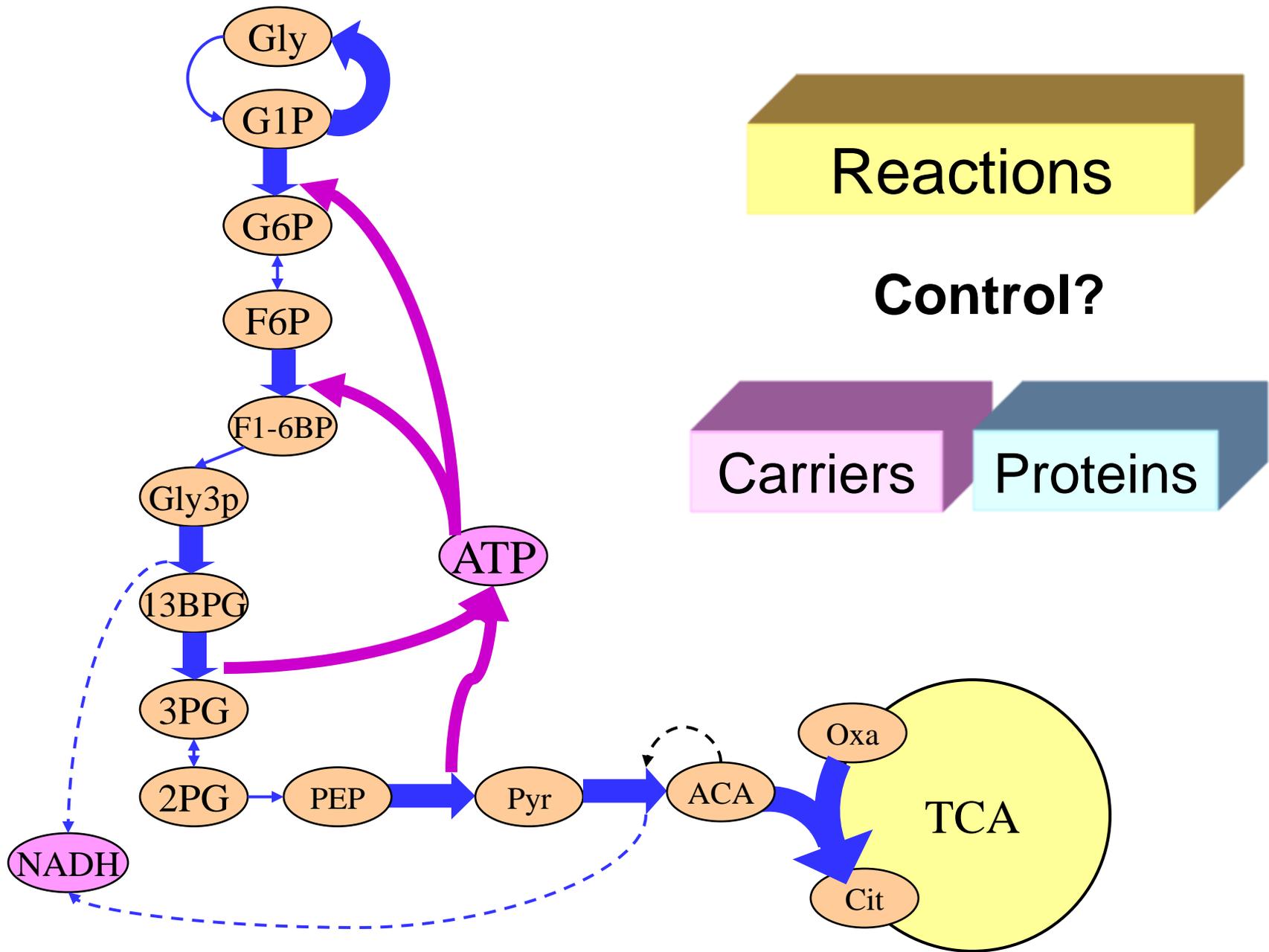


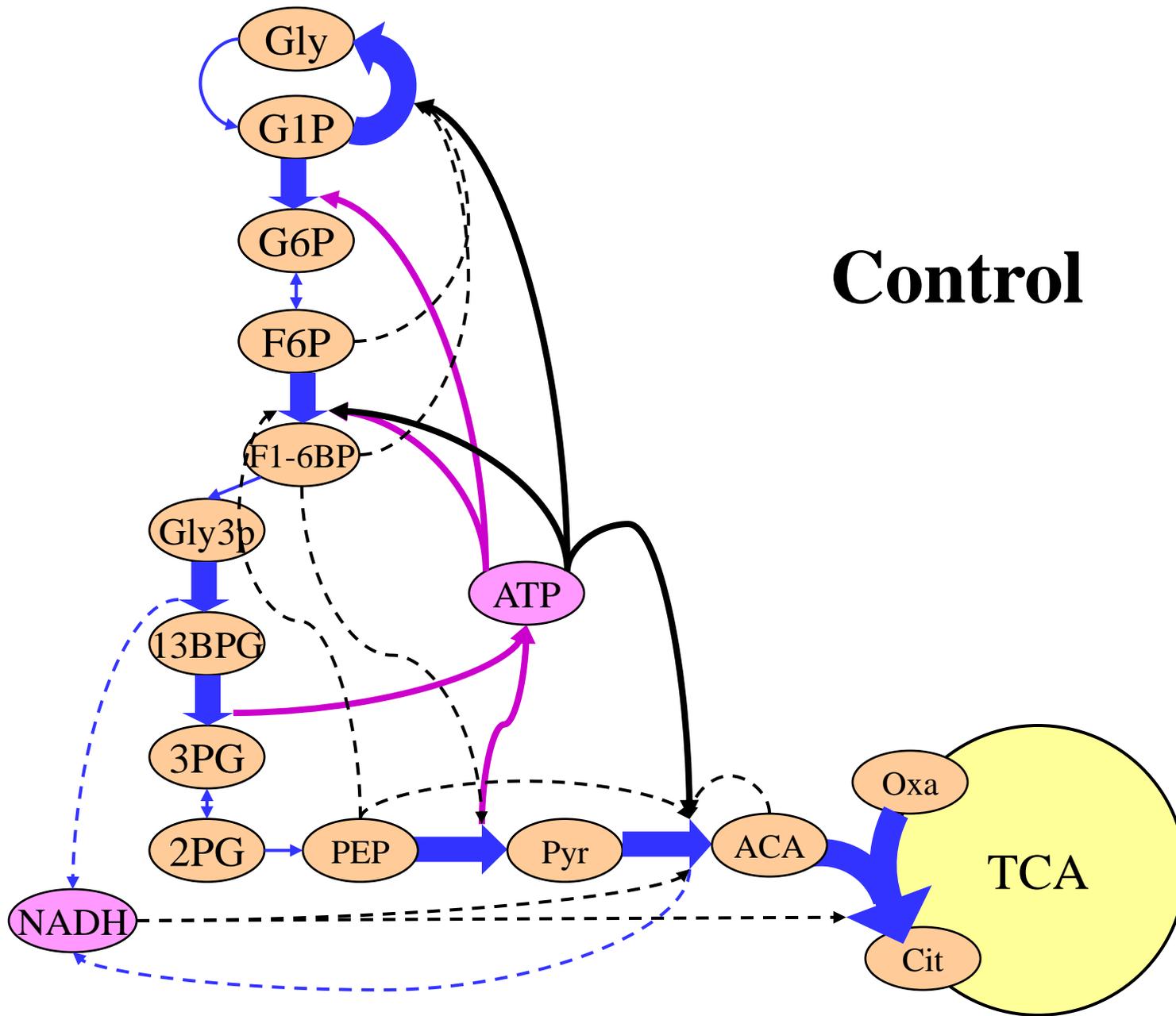


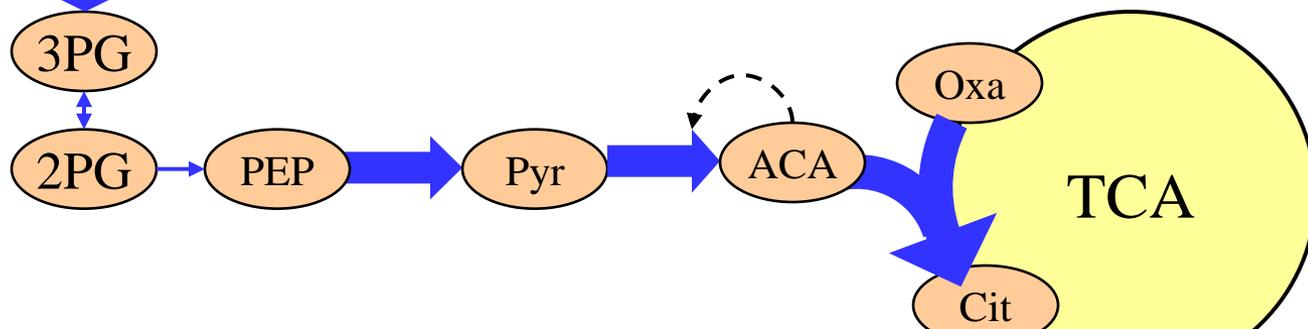
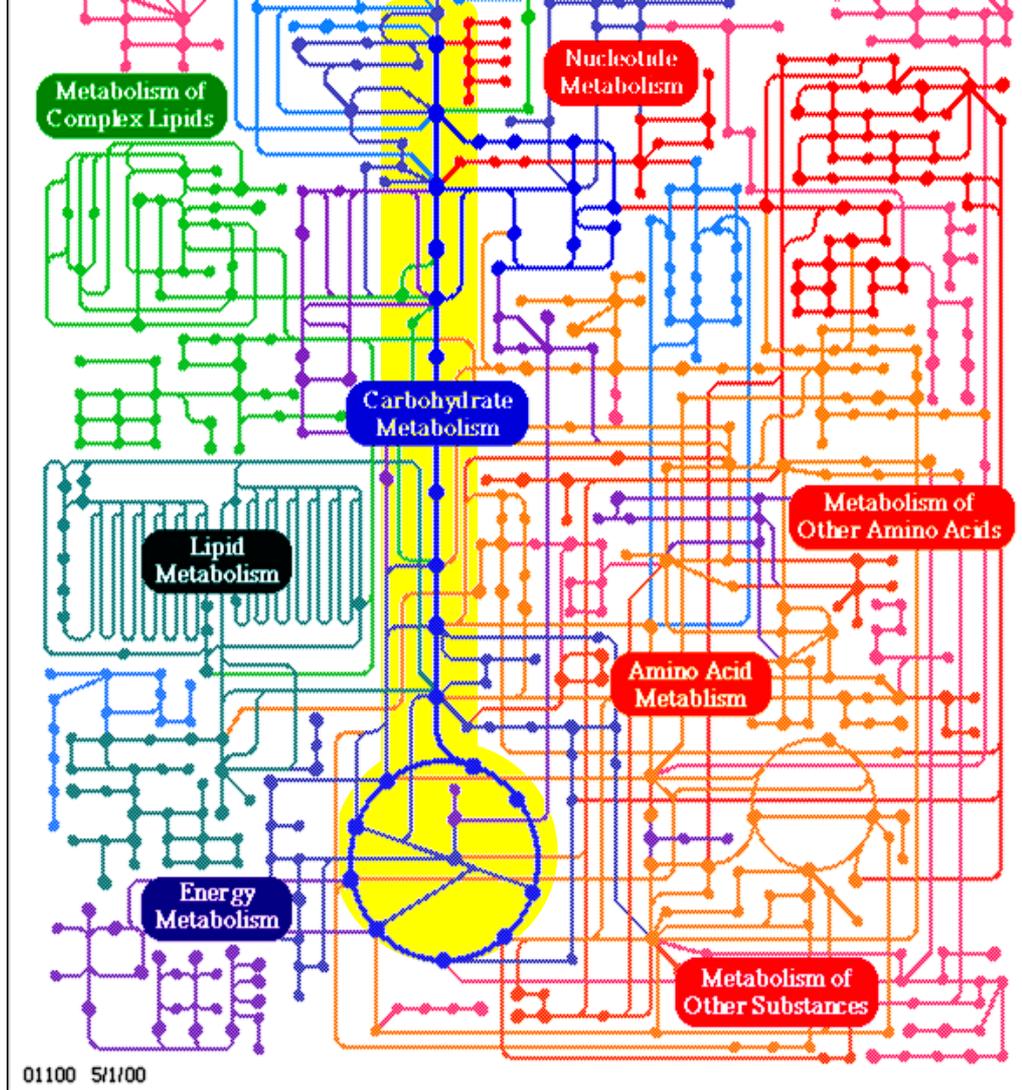
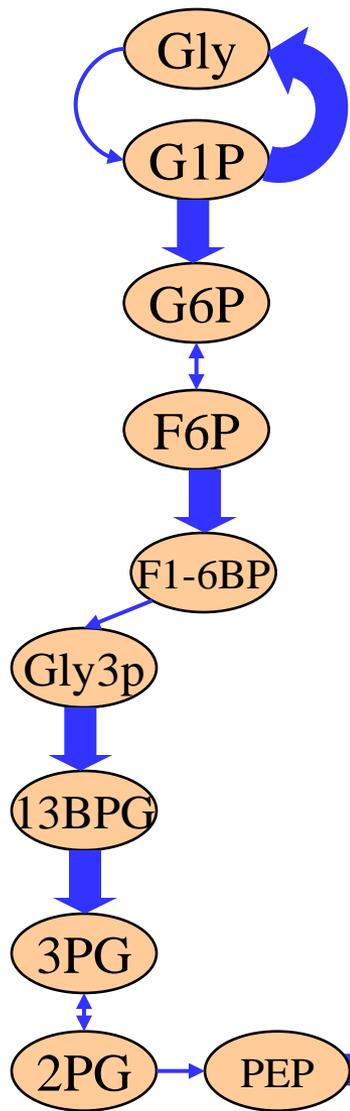




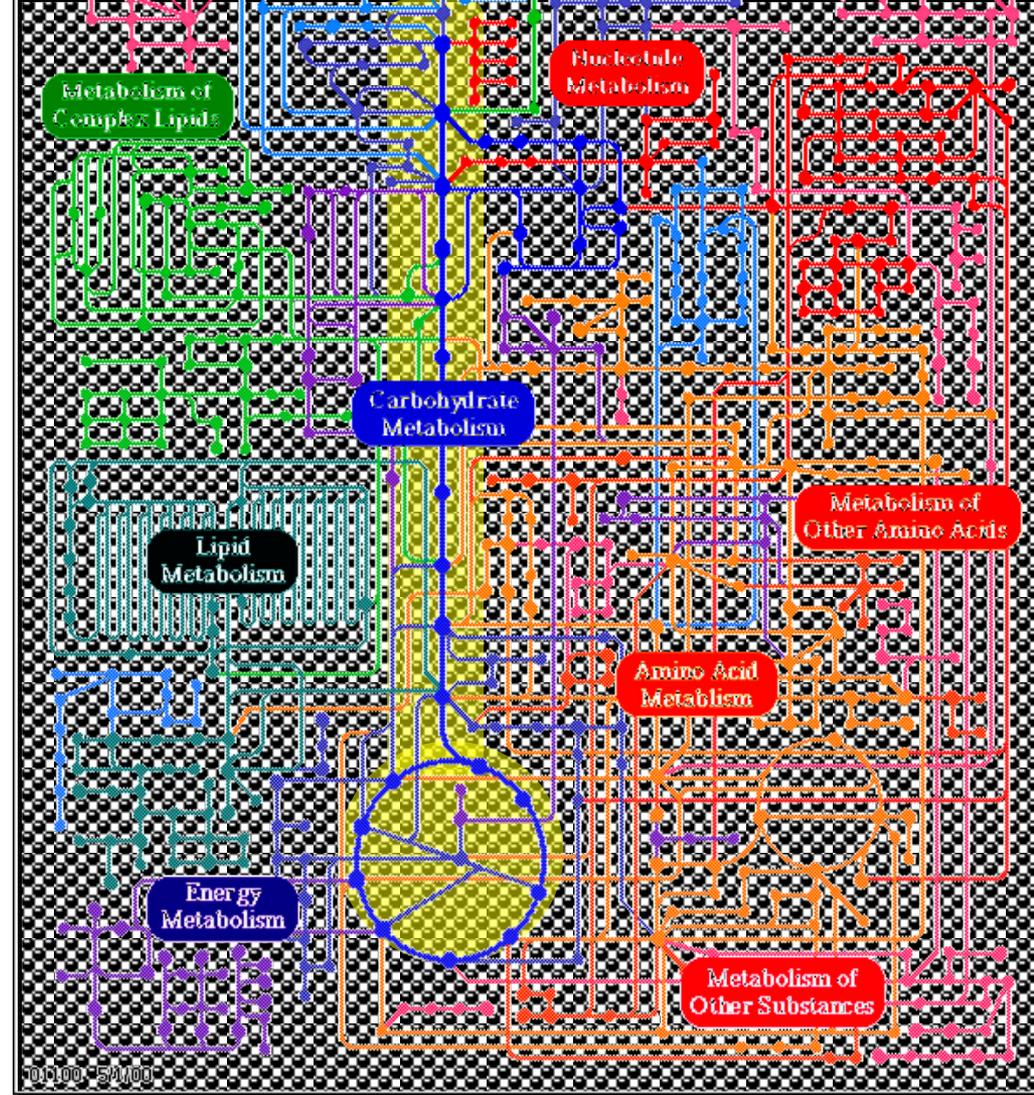
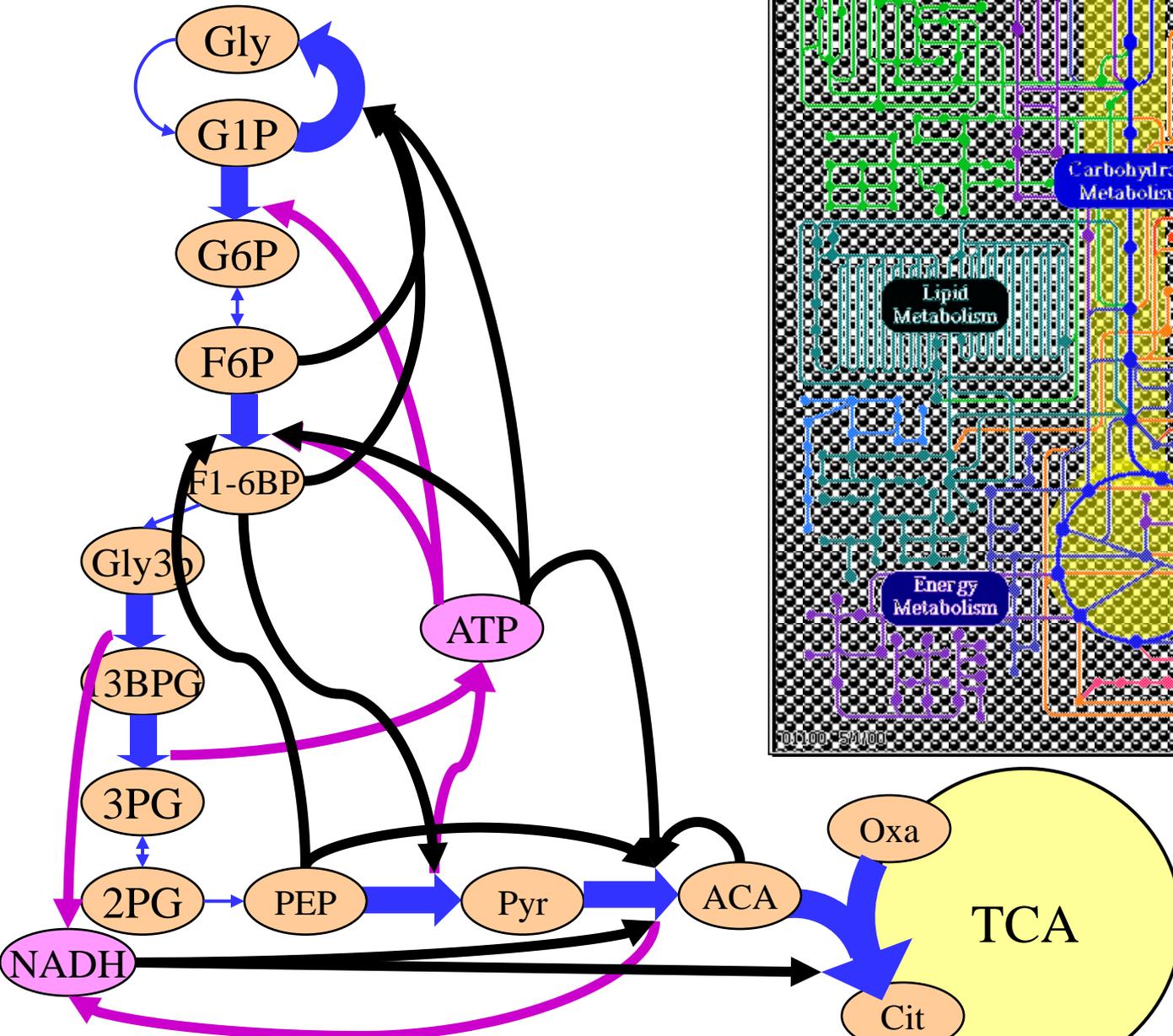


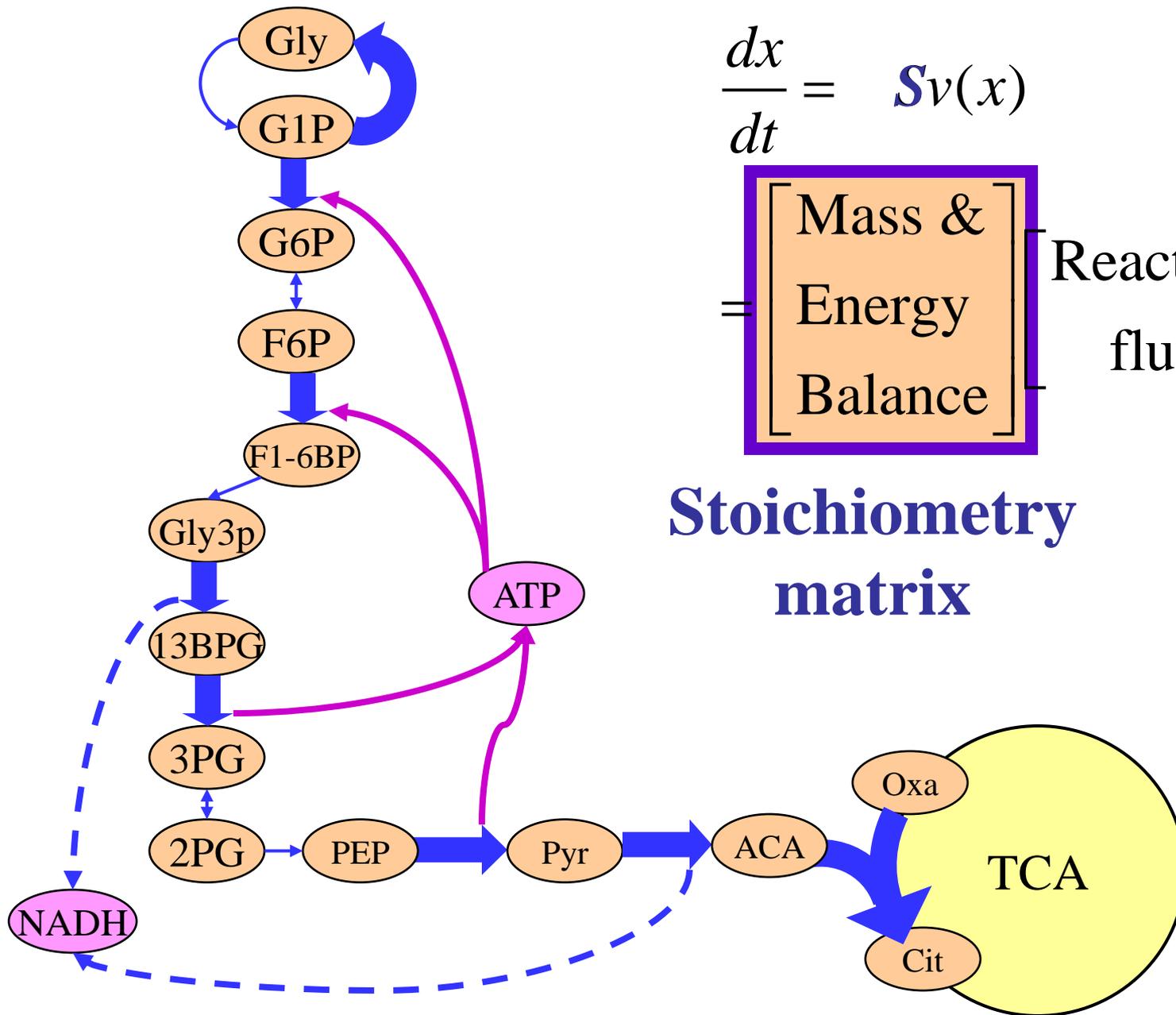






If we drew the feedback loops the diagram would be unreadable.

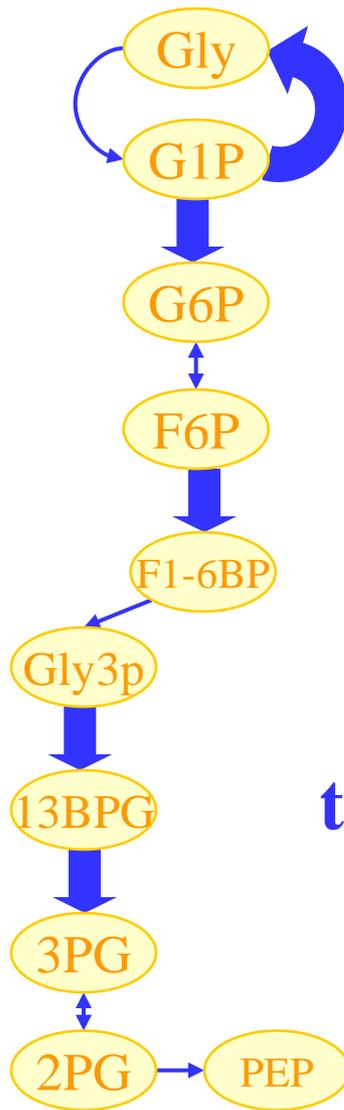




$$\frac{dx}{dt} = Sv(x)$$

$$= \begin{bmatrix} \text{Mass \& Energy Balance} \end{bmatrix} \begin{bmatrix} \text{Reaction flux} \end{bmatrix}$$

Stoichiometry matrix

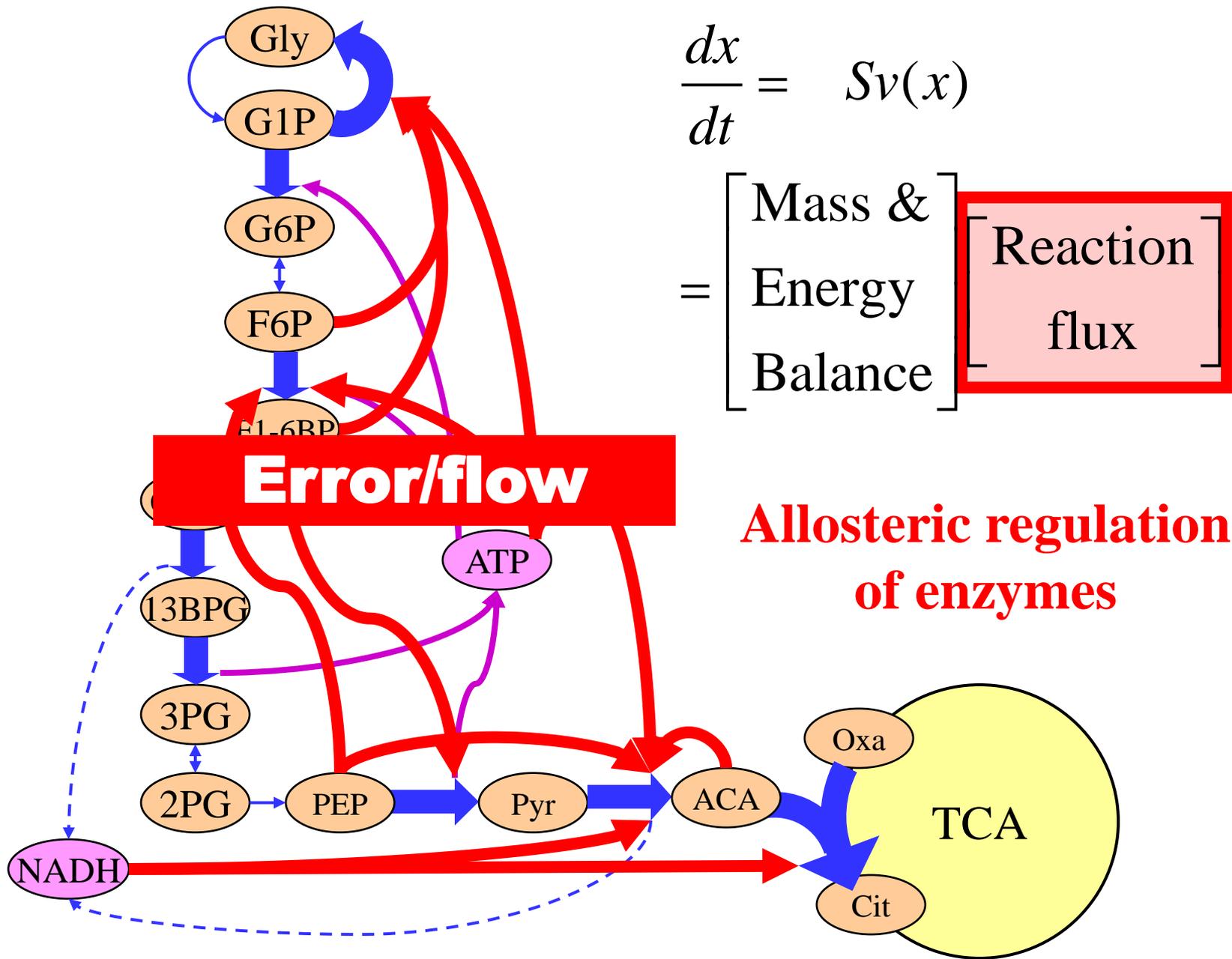


$$\frac{dx}{dt} = Sv(x)$$

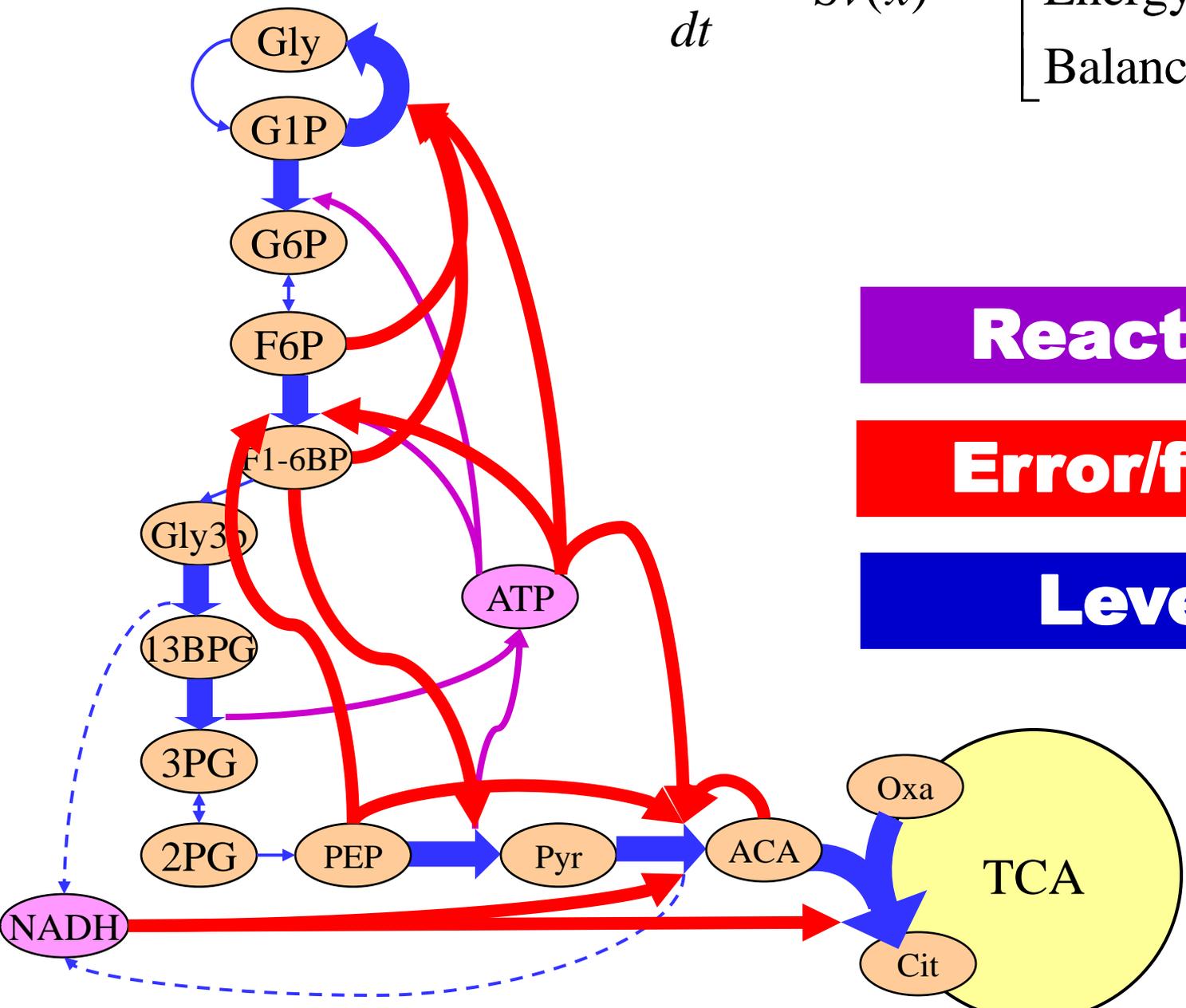
$$= \begin{bmatrix} \text{Mass \&} \\ \text{Energy} \\ \text{Balance} \end{bmatrix} \begin{bmatrix} \text{Reaction} \\ \text{flux} \end{bmatrix}$$

Regulation of enzyme levels by transcription/translation/degradation

level



$$\frac{dx}{dt} = Sv(x) = \begin{bmatrix} \text{Mass \&} \\ \text{Energy} \\ \text{Balance} \end{bmatrix} \begin{bmatrix} \text{Reaction} \\ \text{flux} \end{bmatrix}$$

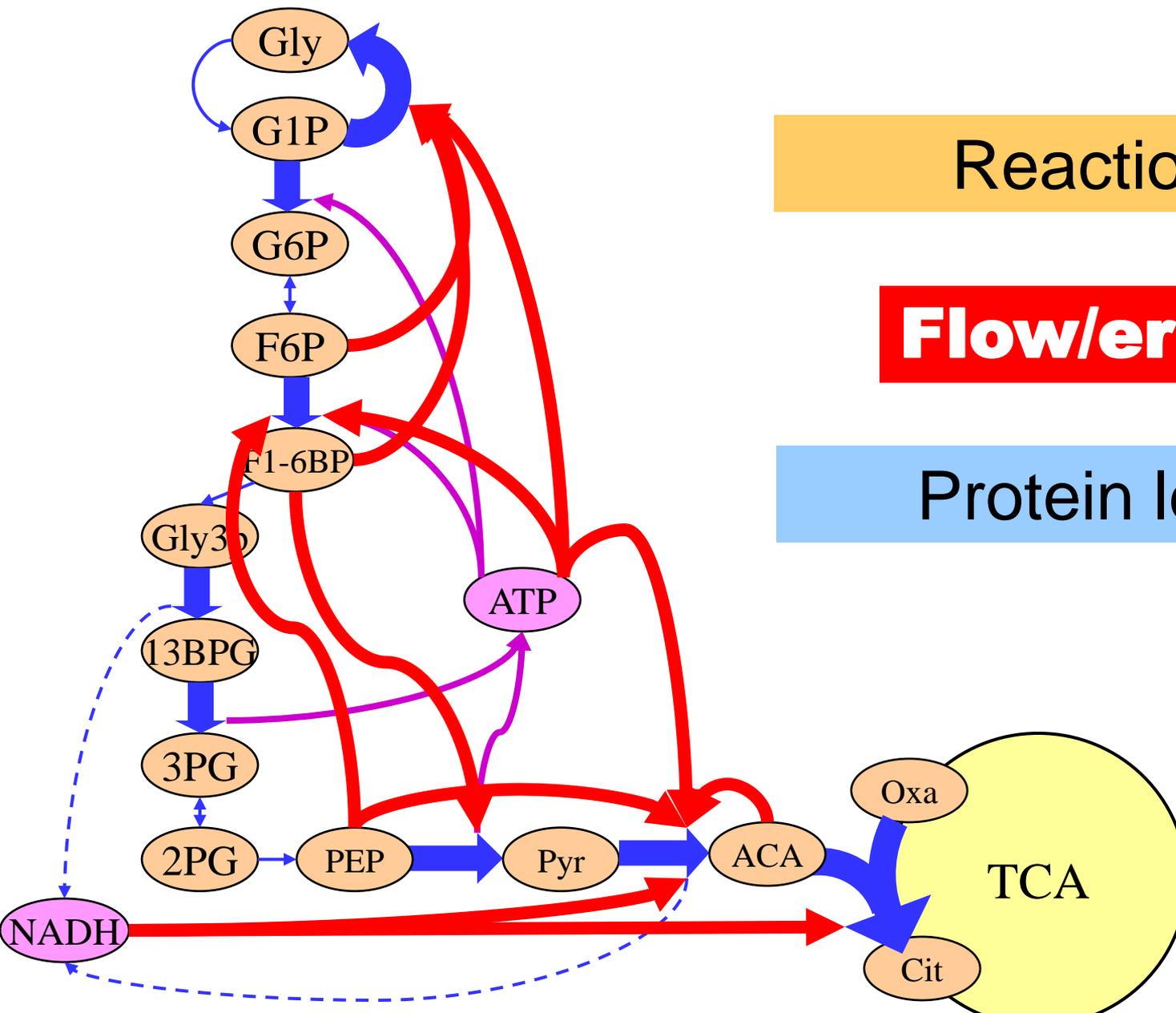


Reaction

Error/flow

Level

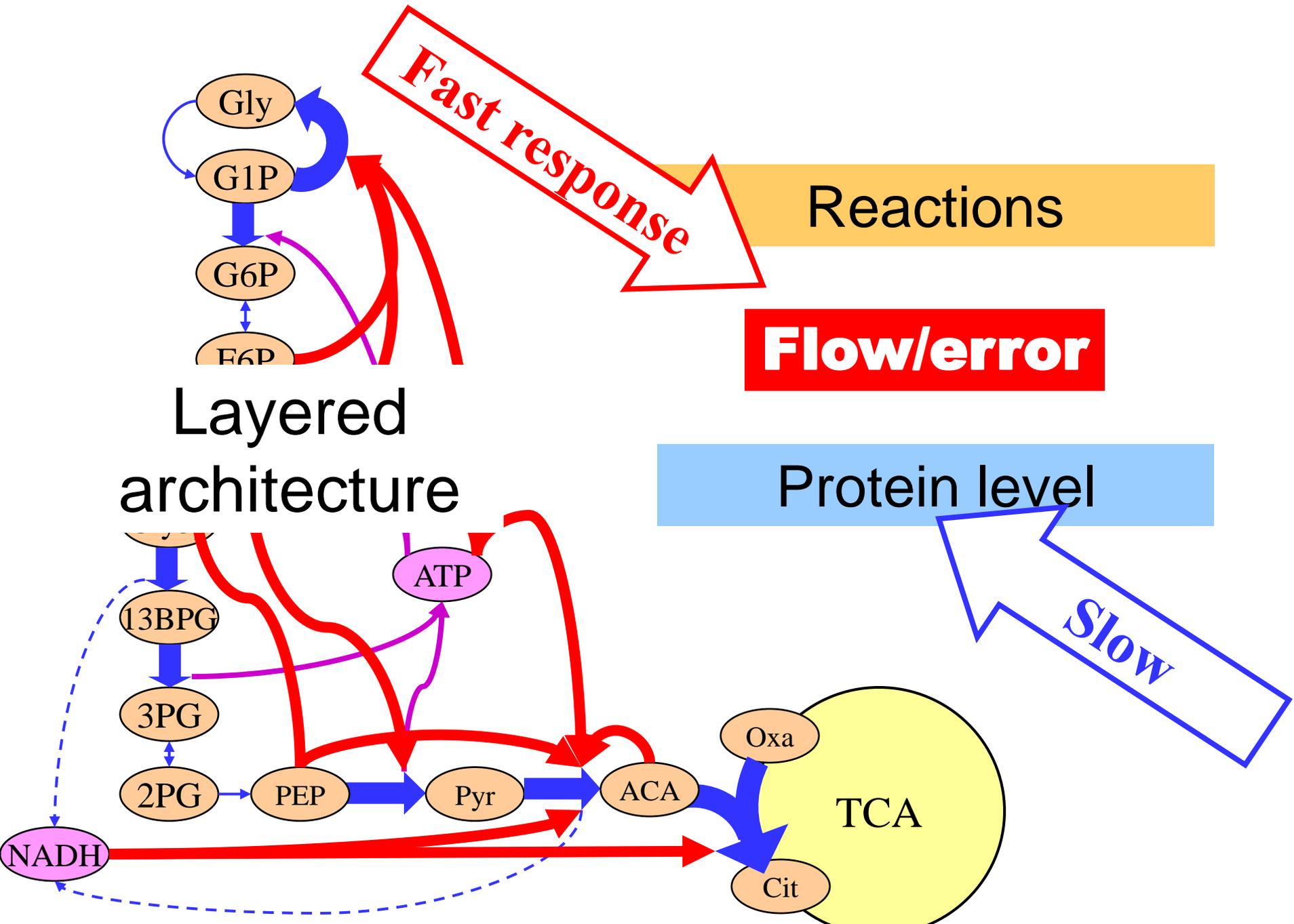
TCA



Reactions

Flow/error

Protein level



Reactions

Flow/error

Macromolecules

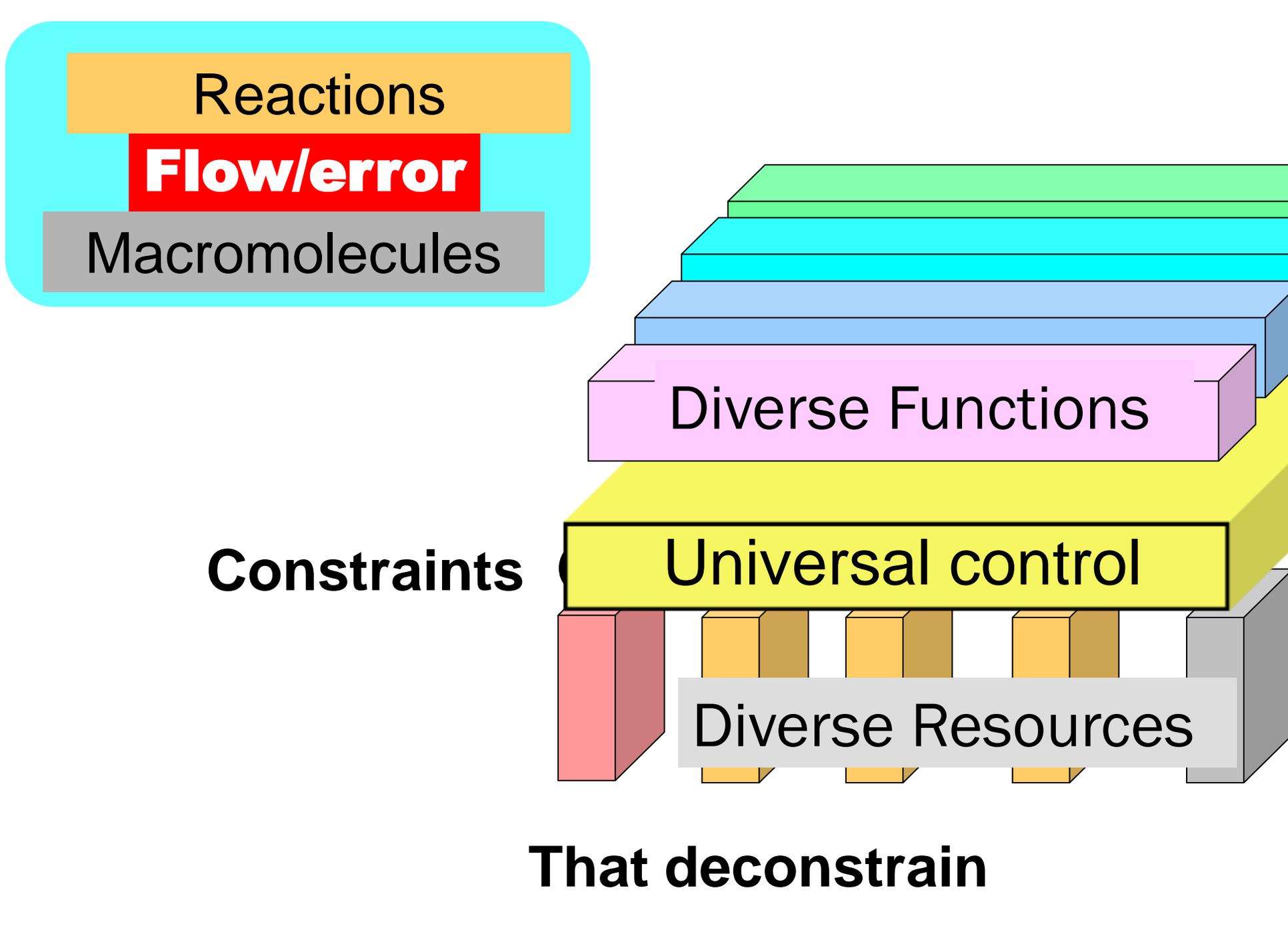
Diverse Functions

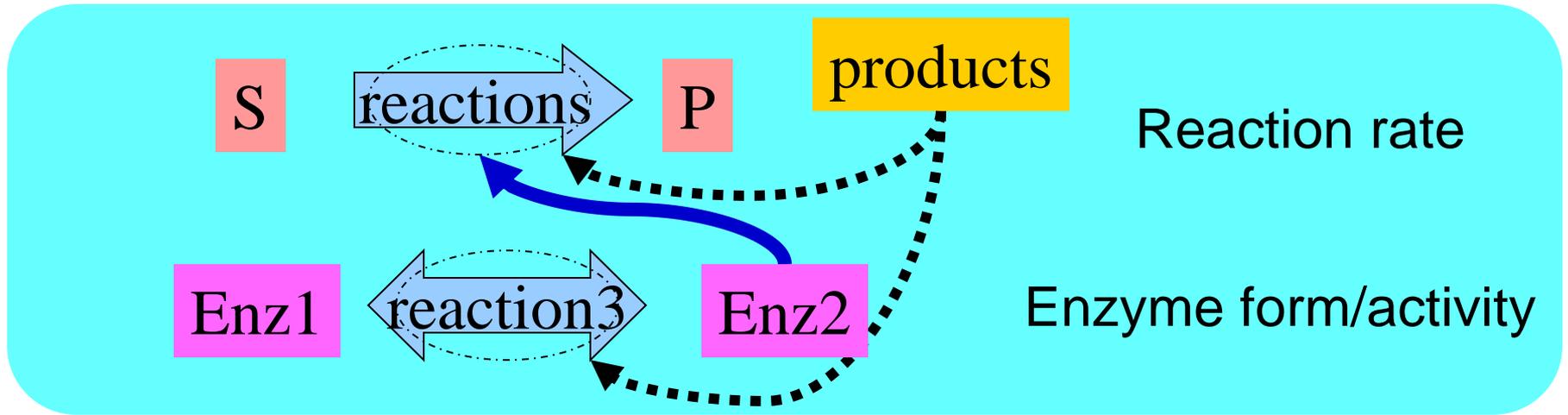
Universal control

Diverse Resources

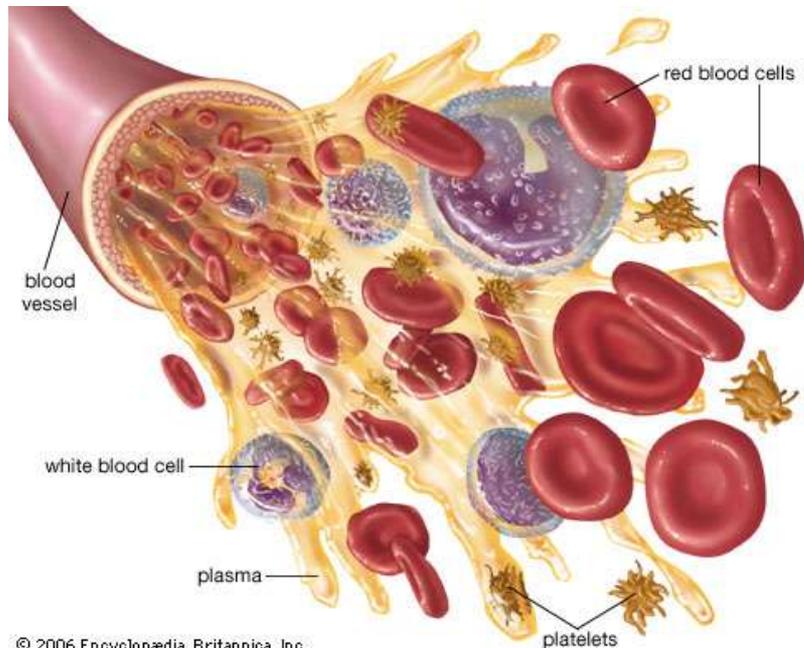
Constraints

That deconstrain





Running only the top layers



Mature red blood cells live 120 days

“metabolism first”
origins of life?

Reactions

Flow/error

Protein level

Reactions

Flow/error

RNA level

Reactions

Flow/error

DNA level

Protein

Reactions

Flow/error

Protein level

RNA

Translation

Flow/error

RNA level

DNA

Transcription

Flow/error

DNA level

Reactions

Flow/error

Protein level

Translation

Flow/error

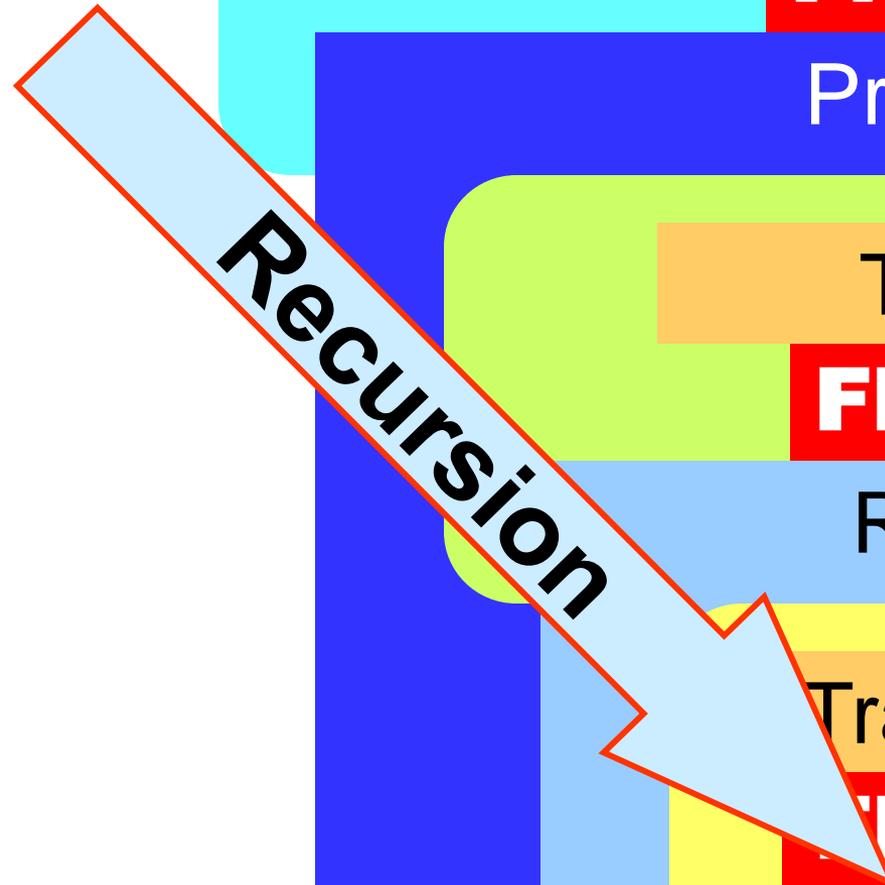
RNA level

Transcription

Flow/error

DNA level

Recursion



Diverse Reactions

Flow/error

Protein level

Conserved
core
control

Reactions

Translation
RNA level

Transcription

Flow/error

DNA

DNA

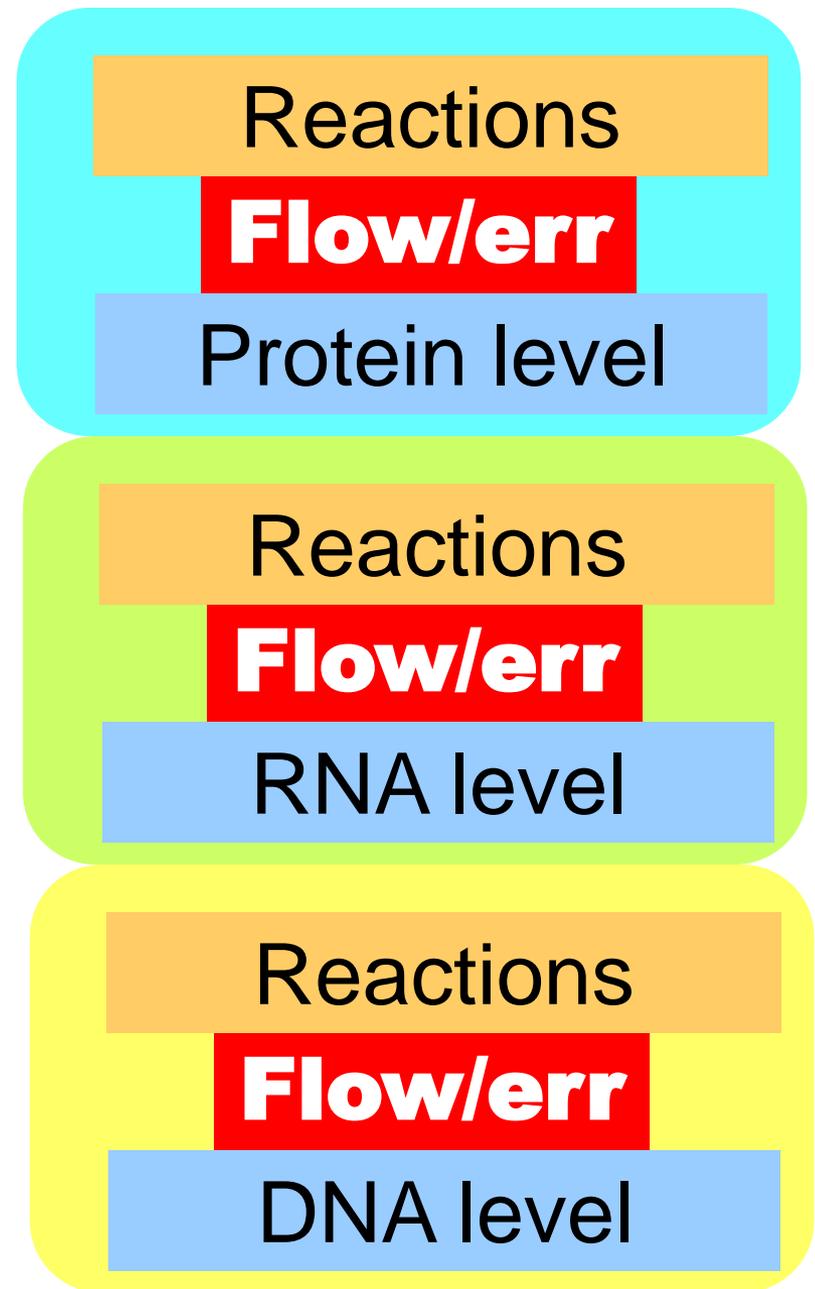
DNA

Diverse Genomes

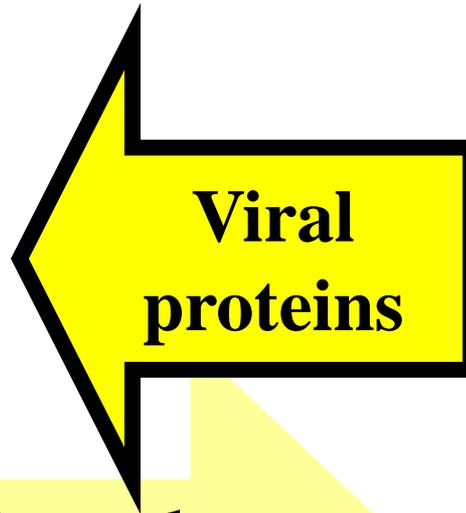
Top to bottom

- Metabolically costly but fast to cheap but slow
- Special enzymes to general polymerases
- Allostery to regulated recruitment
- Analog to digital
- High molecule count to low (noise)

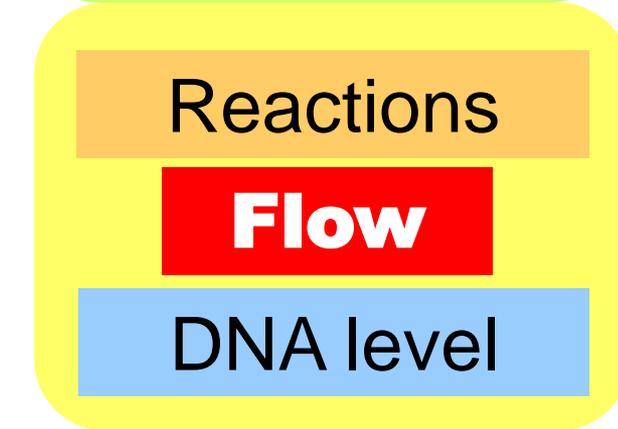
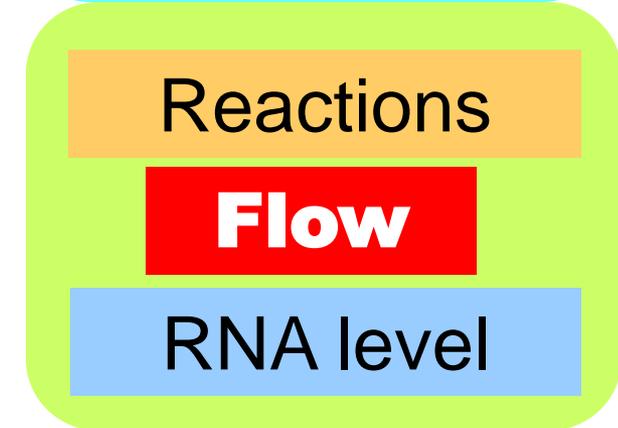
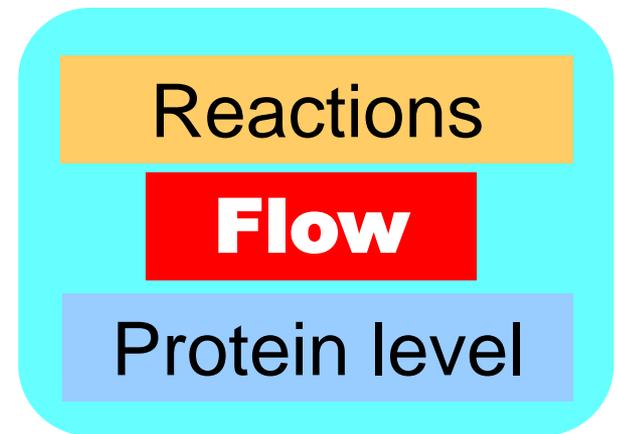
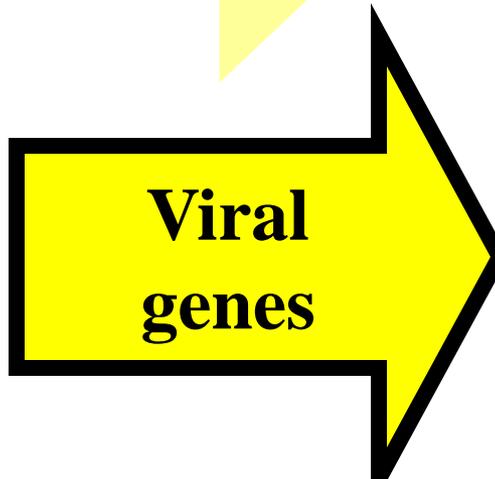
Rich Tradeoffs



Fragility example: Viruses



Viruses exploit the universal bowtie/hourglass structure to hijack the cell machinery.



Biology versus the Internet

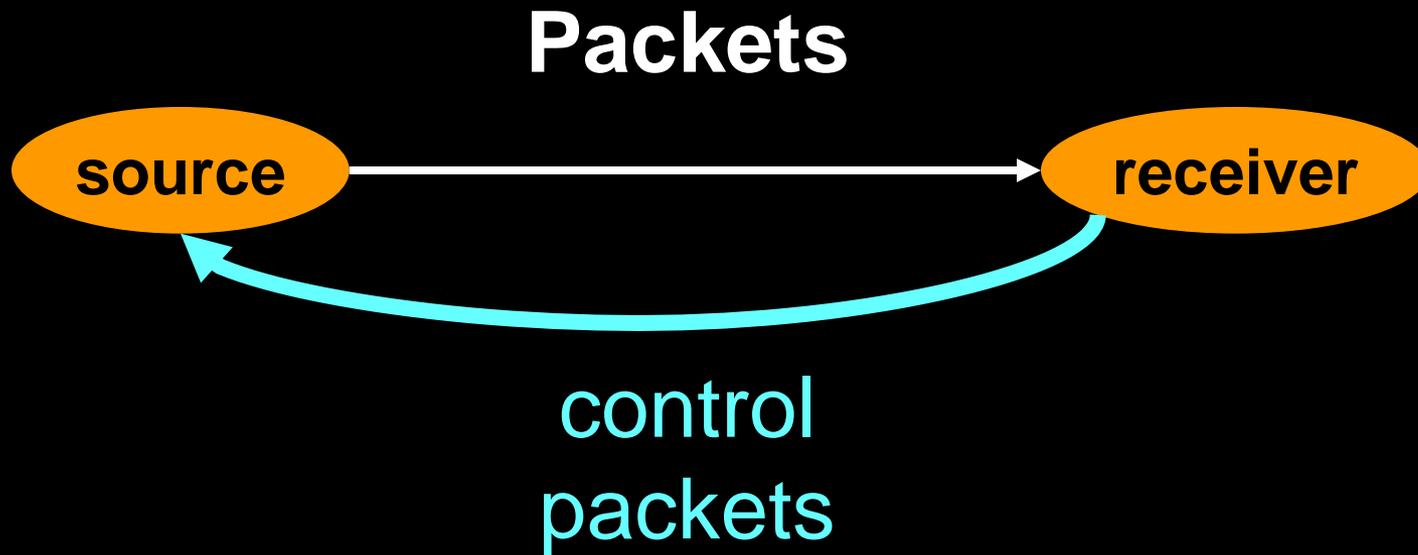
Similarities

- Evolvable architecture
- Robust yet fragile
- **Constraints/deconstrain**
- **Layering, modularity**
- **Hourglass with bowties**
- Feedback
- Dynamics
- Distributed/decentralized
- *Not* scale-free, edge-of-chaos, self-organized criticality, etc

Differences

- Metabolism
- Materials and energy
- **Autocatalytic feedback**
- Feedback complexity
- Development and regeneration
- >4B years of evolution

Control of the Internet

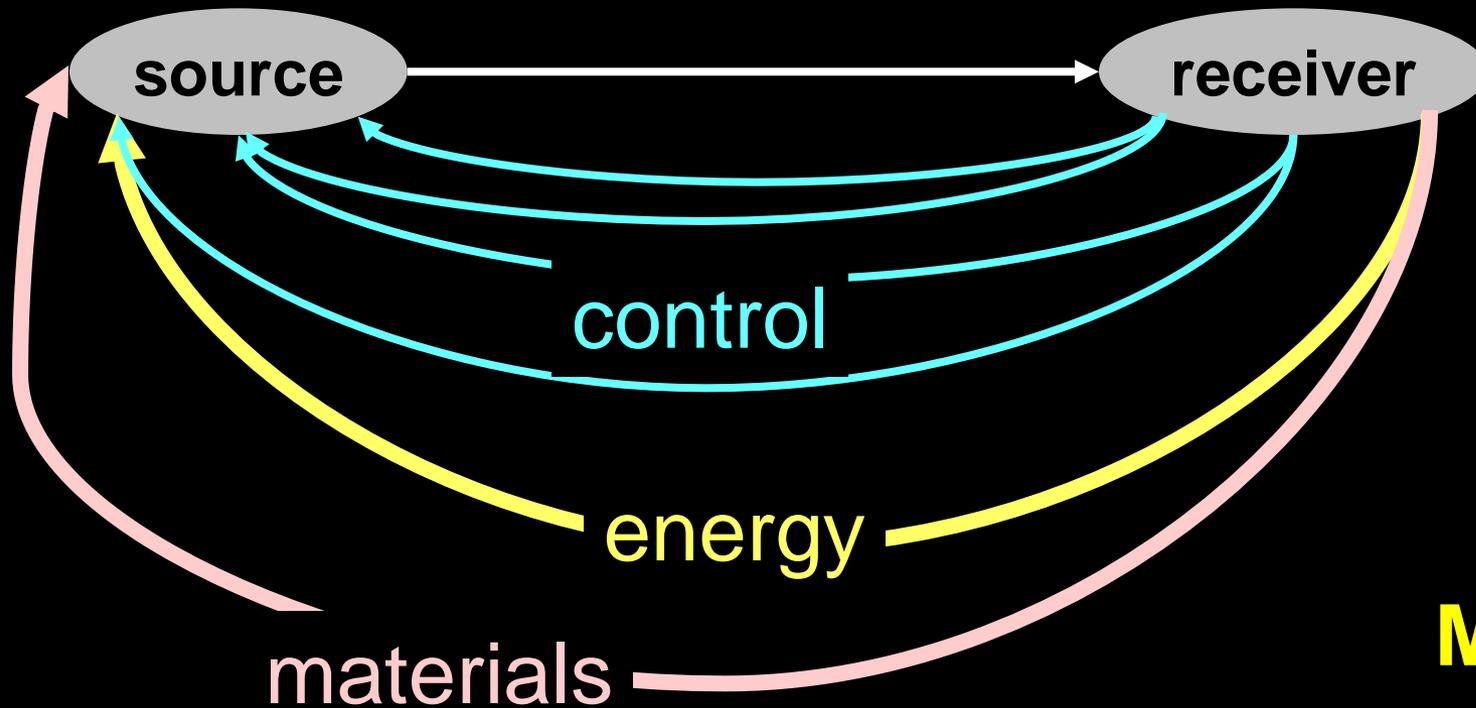


signaling
gene expression
metabolism
lineage

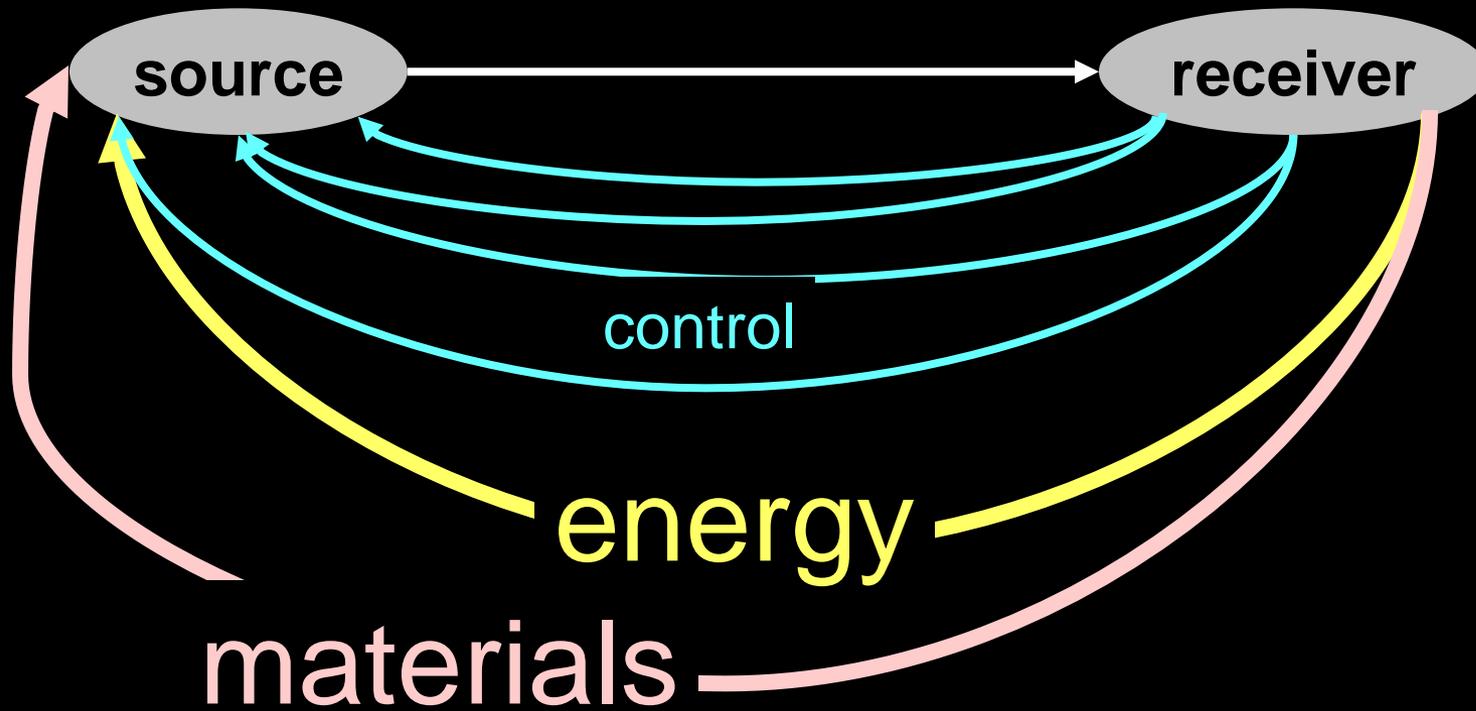


**Biological
pathways**

signaling
gene expression
metabolism
lineage

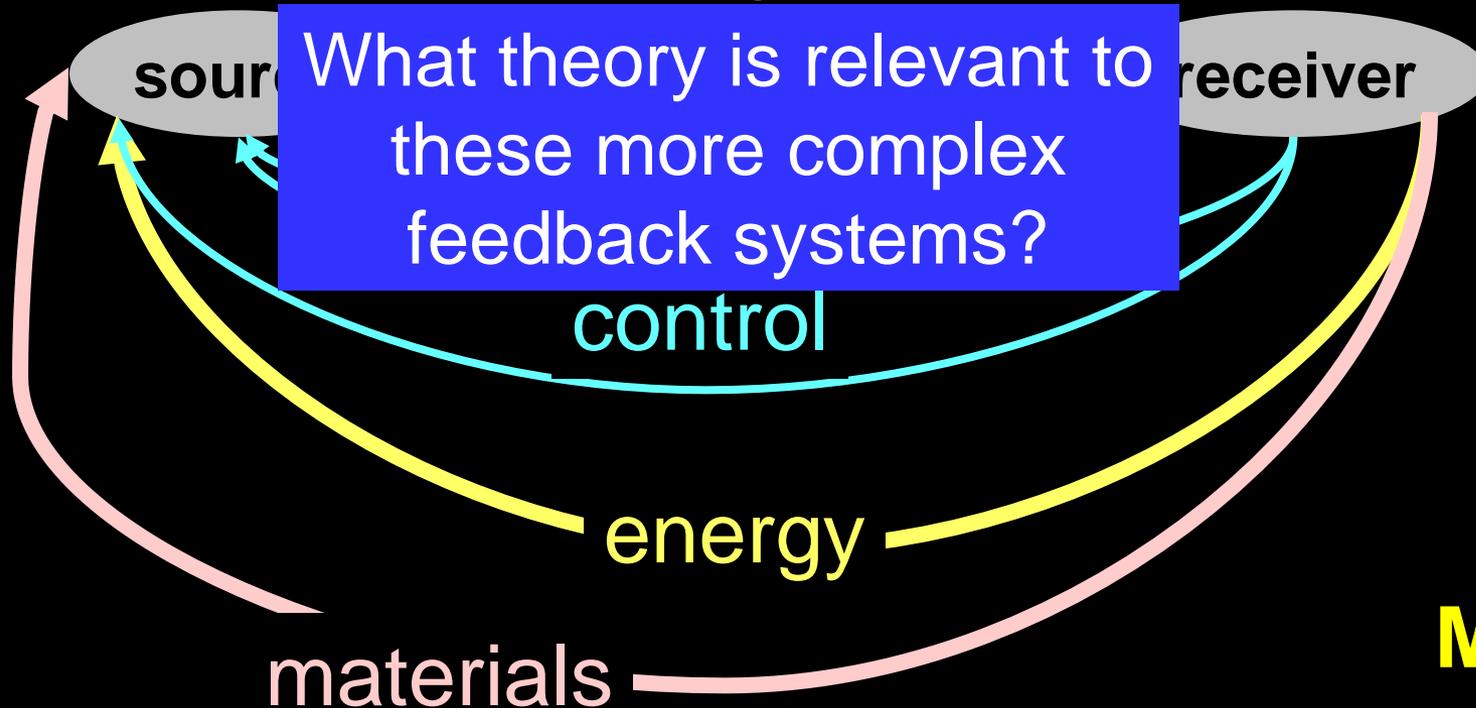


**More
complex
feedback**



Autocatalytic feedback

signaling
gene expression
metabolism
lineage

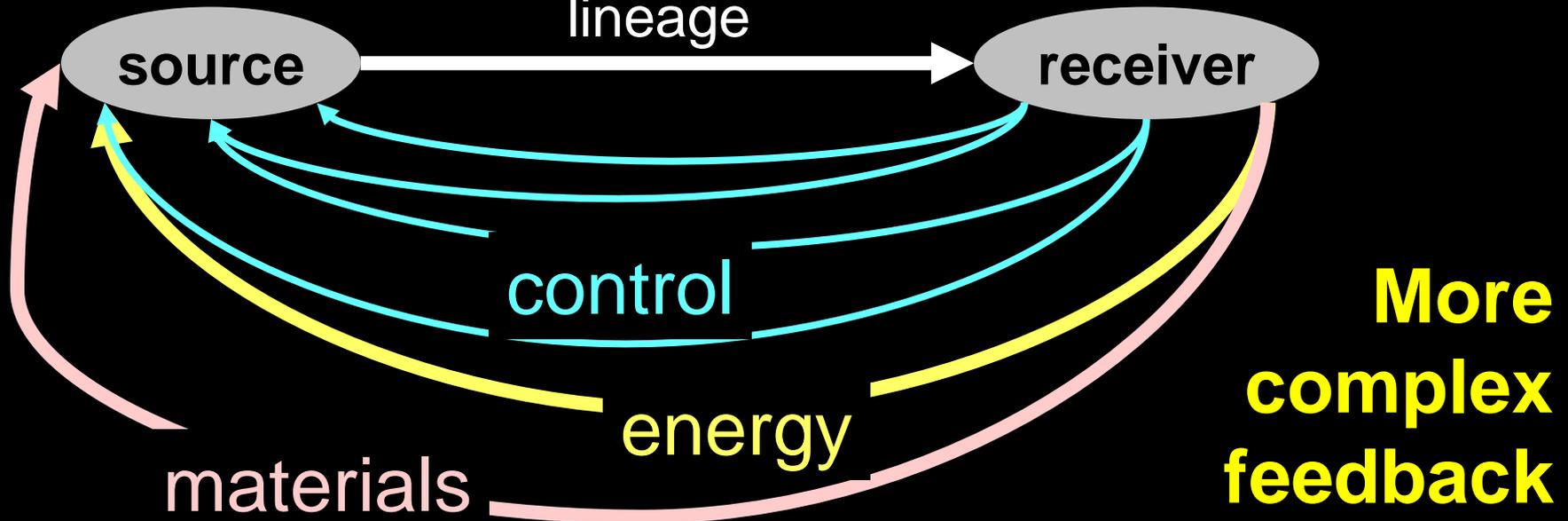


**More
complex
feedback**

What theory is relevant to these more complex feedback systems?

$$\frac{1}{\pi} \int_0^{\infty} \ln |S(j\omega)| \frac{z}{z^2 + \omega^2} d\omega \geq \ln \left| \frac{z+p}{z-p} \right|$$

metabolism
lineage



The diagram illustrates the flow of metabolic intermediates. At the bottom, a pink box labeled 'Carriers' has two purple arrows: one pointing left towards a pink triangle labeled 'Catabolism', and one pointing up towards a blue vertical box labeled 'Precursors'. From the 'Precursors' box, five colored arrows point rightwards to various products: a light green arrow for 'Sugars', a yellow arrow for 'Amino Acids', an orange arrow for 'Nucleotides', a teal arrow for 'Fatty acids', and a bright green arrow for 'Co-factors'. The entire diagram is set against a light yellow background within a cyan rounded rectangle.

Catabolism

Precursors

Sugars

Amino Acids

Nucleotides

Fatty acids

Co-factors

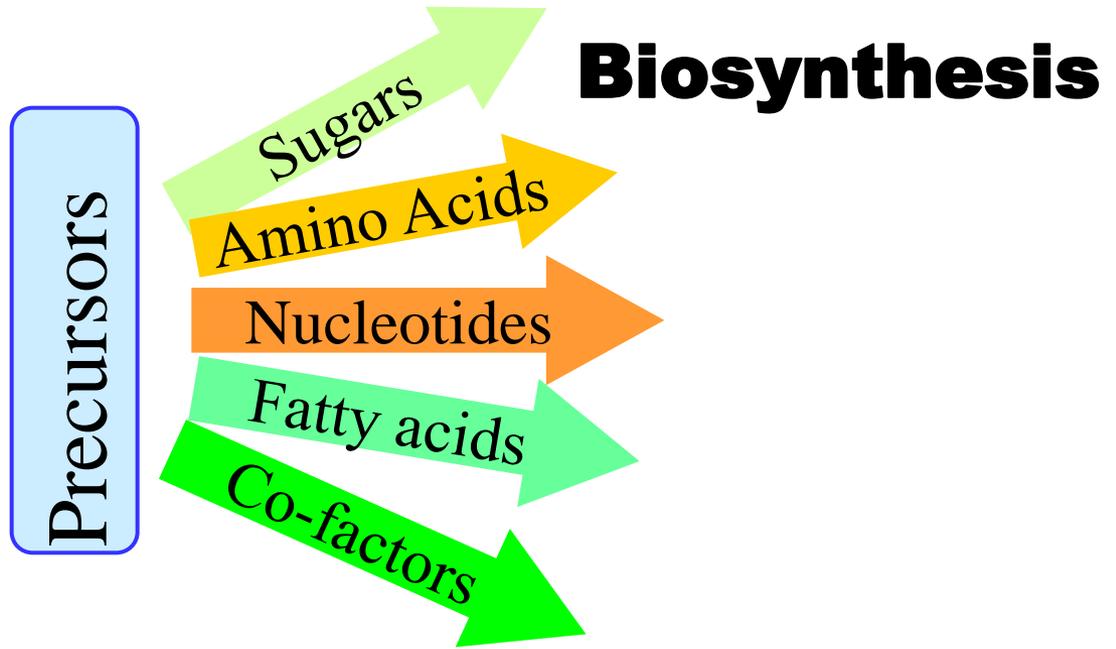
Carriers

Flow/error

Protein level

RNA

DNA



RNA

DNA

Biosynthesis

Precursors

Sugars

Fatty acids

Co-factors

Amino Acids

Nucleotides

RNA

Transc.

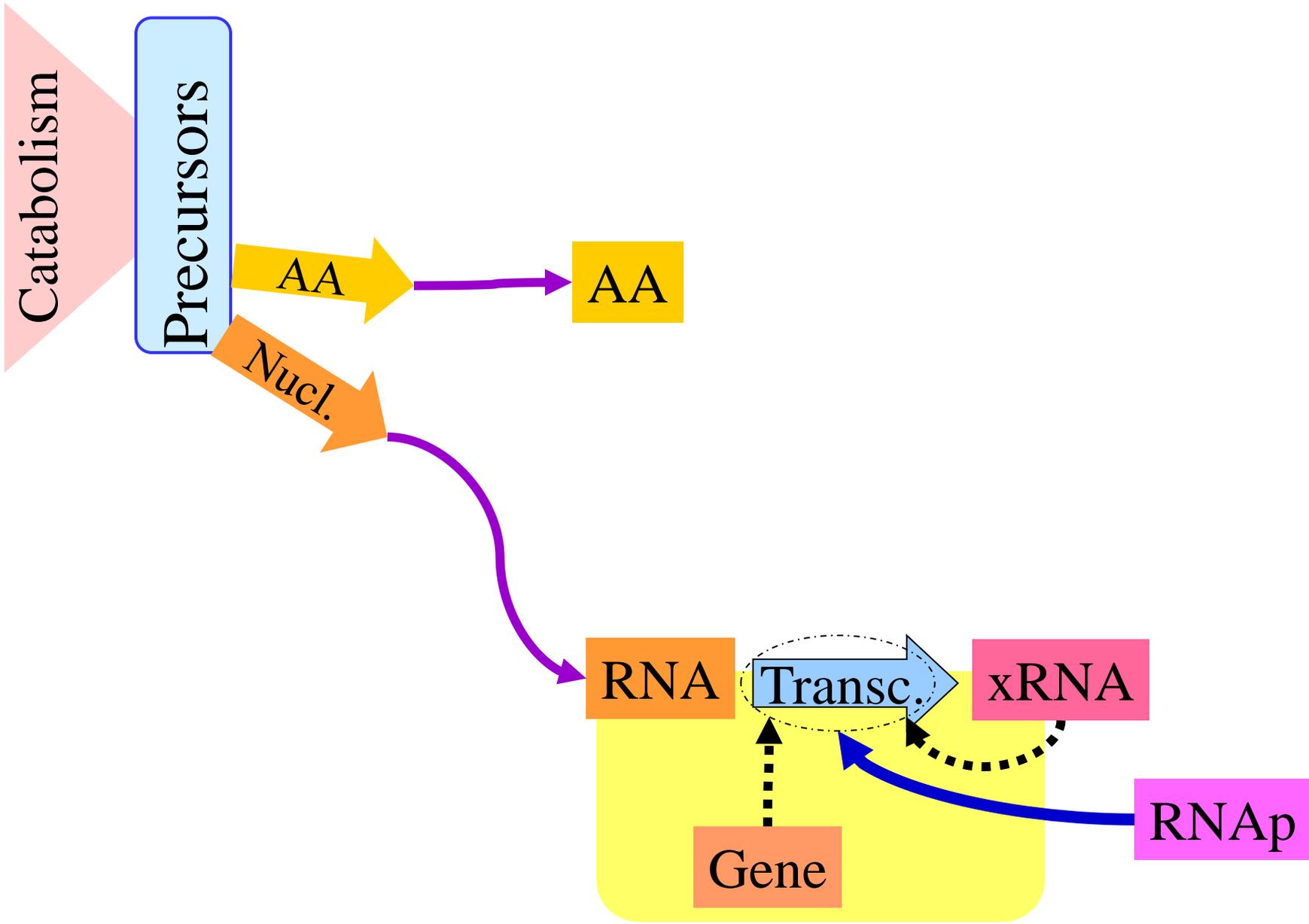
xRNA

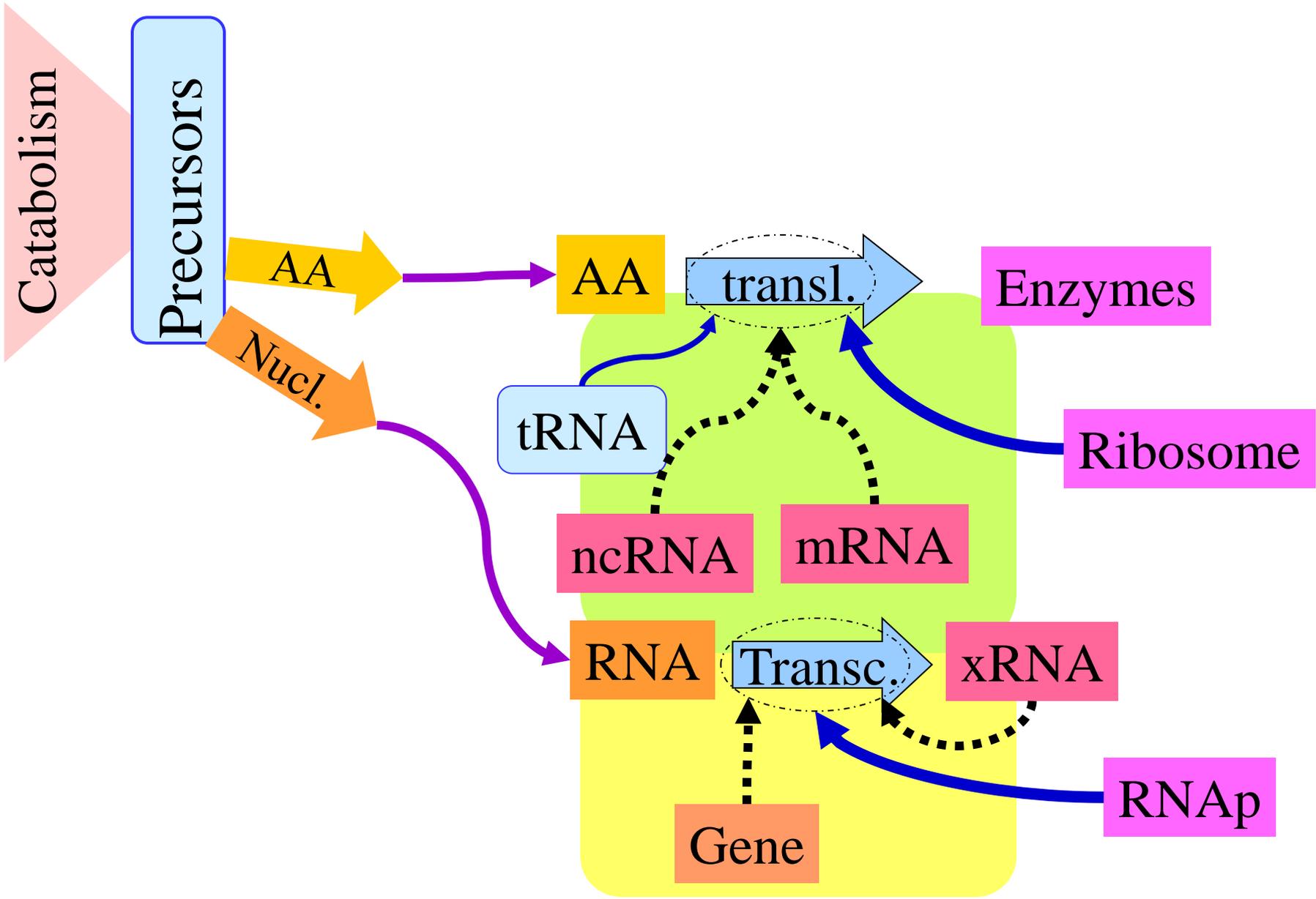
RNA level/
Transcription rate

RNAP

Gene

DNA level





“Central dogma”

Protein

Transl.

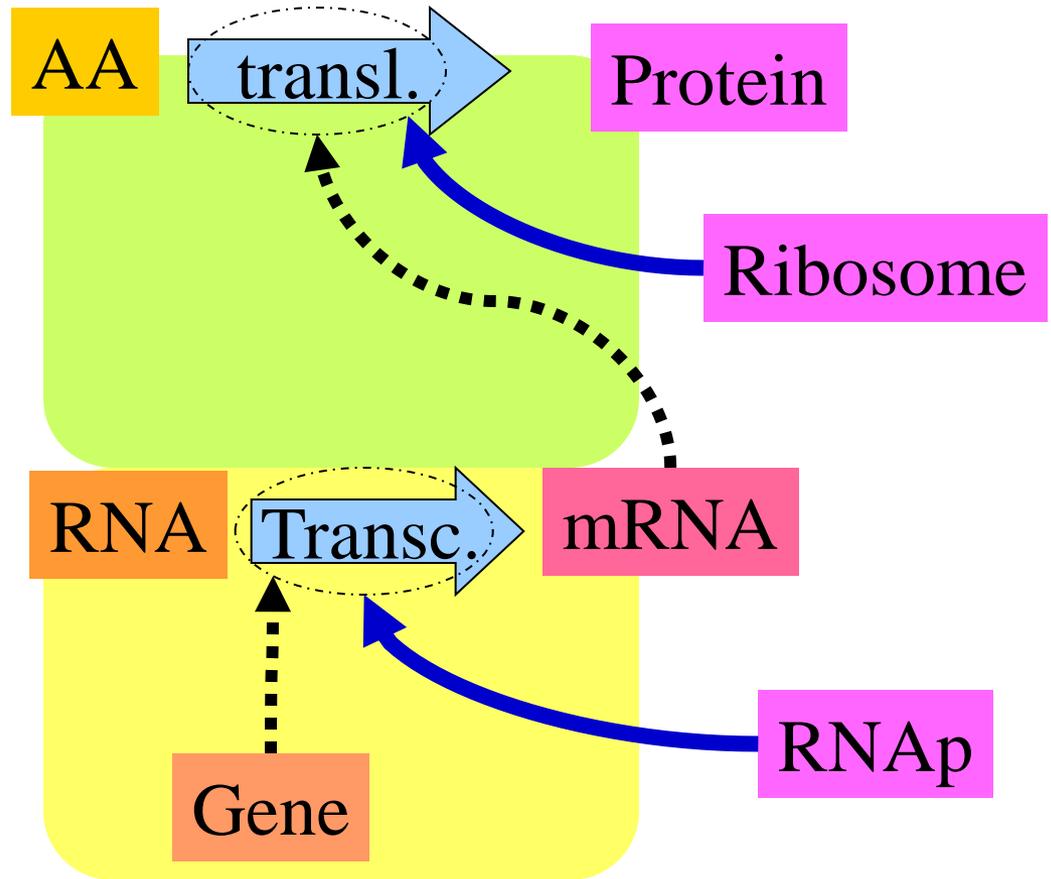
Flow

RNA

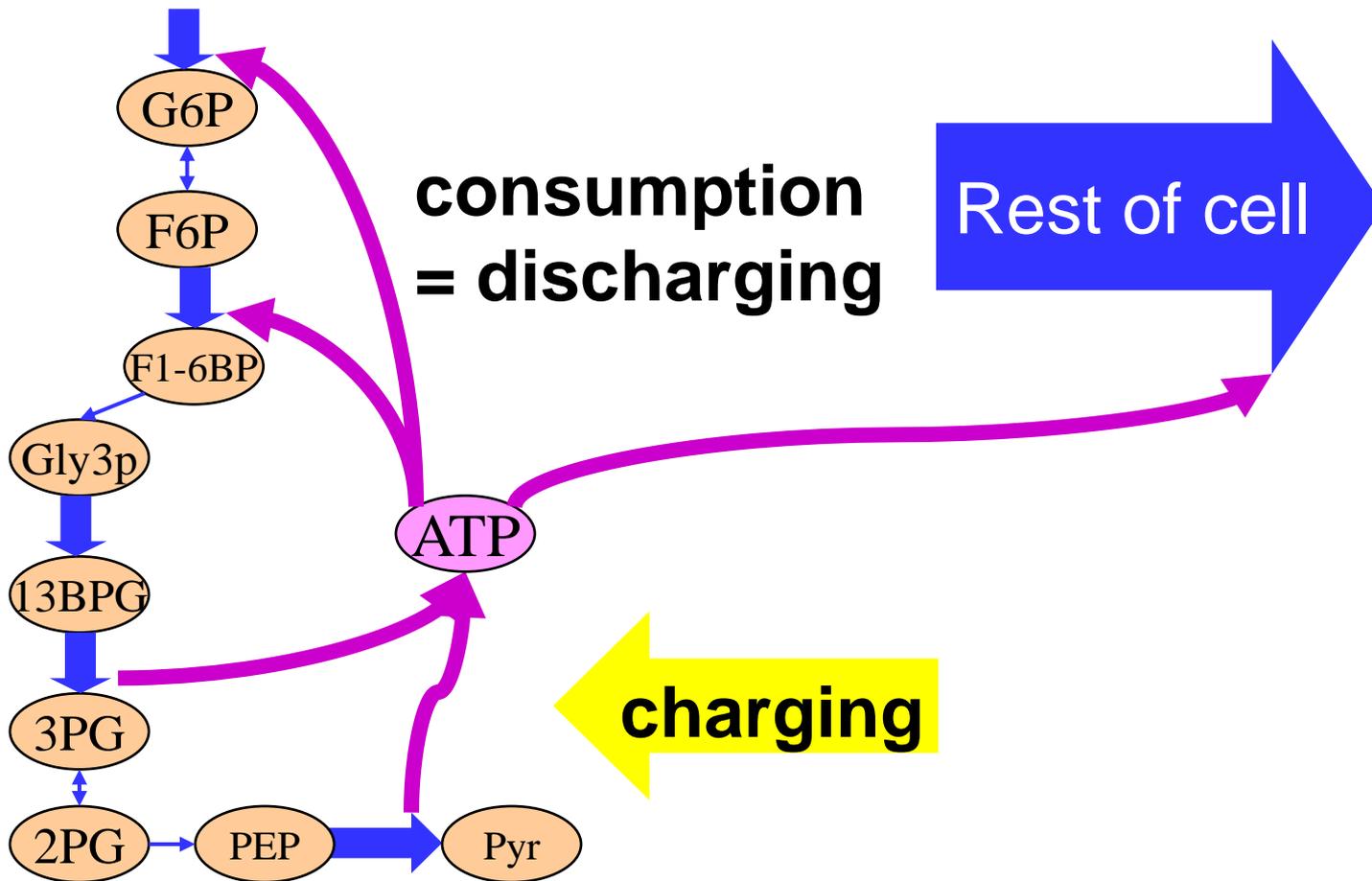
Transc.

Flow

DNA

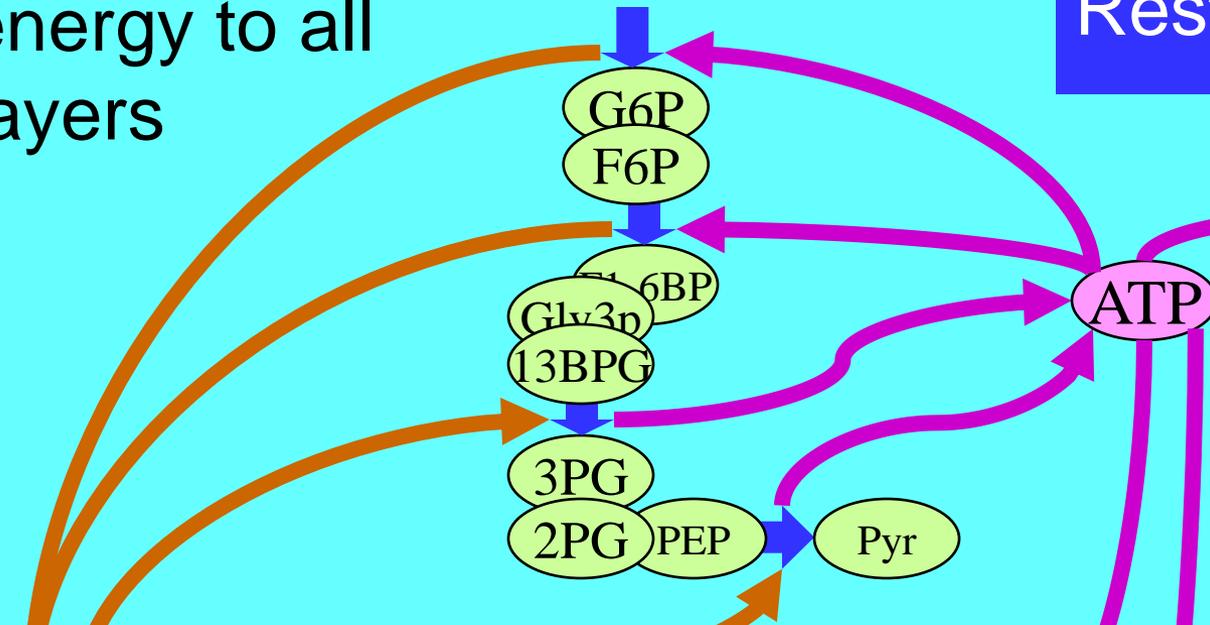


This is just charging and discharging



ATP supplies energy to all layers

Rest of cell



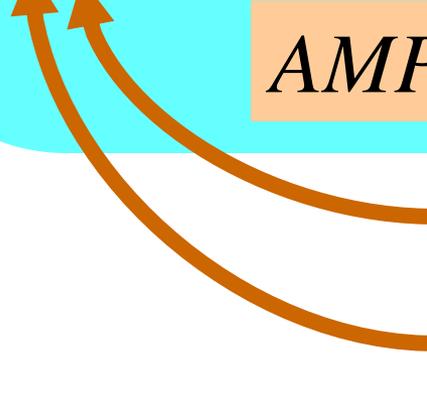
Flow/error

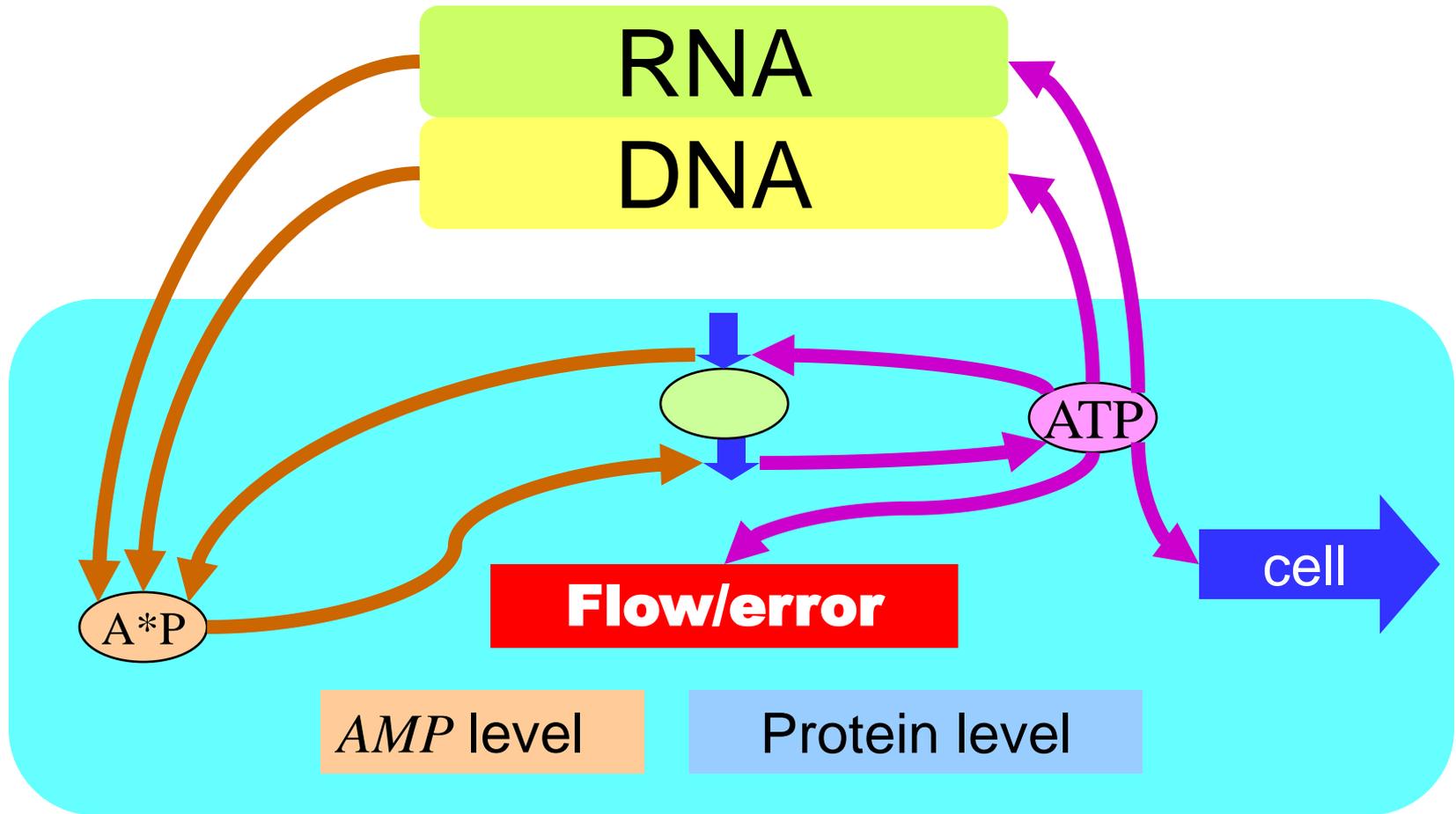
AMP level

Protein level

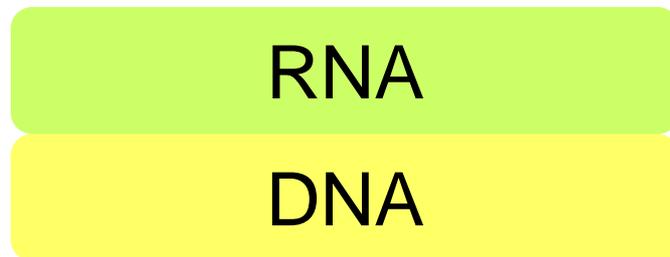
RNA
DNA

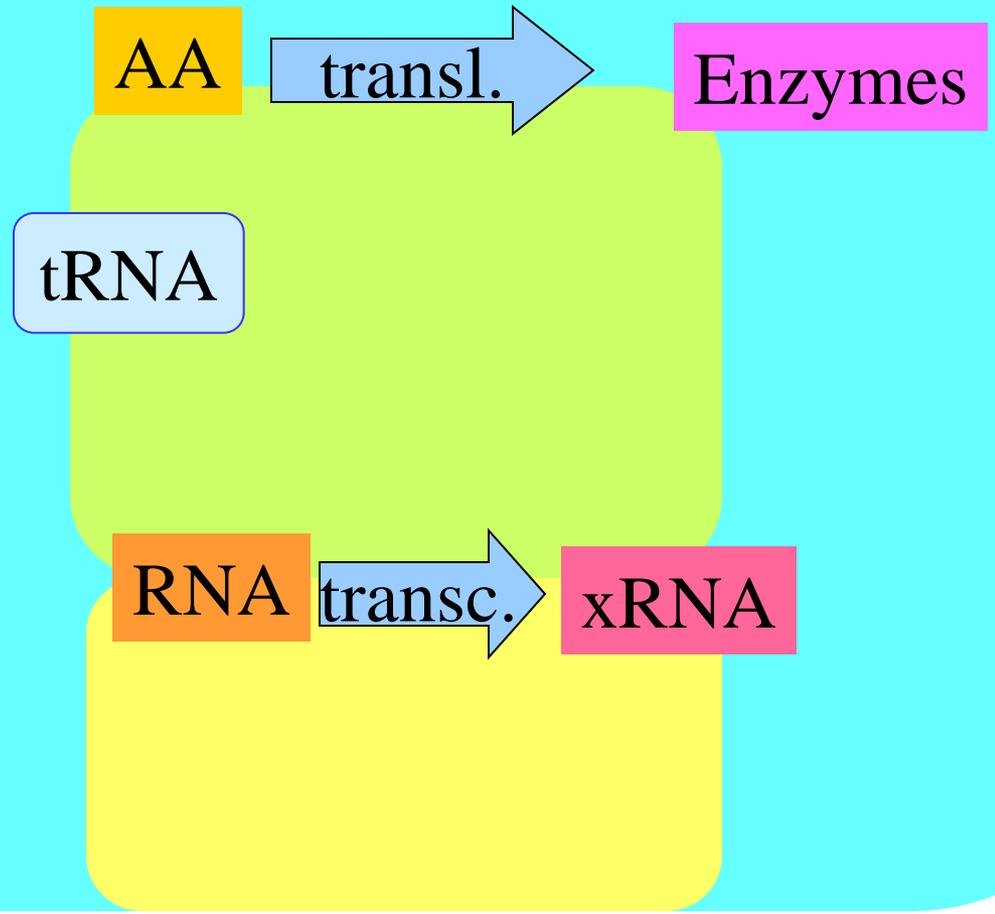
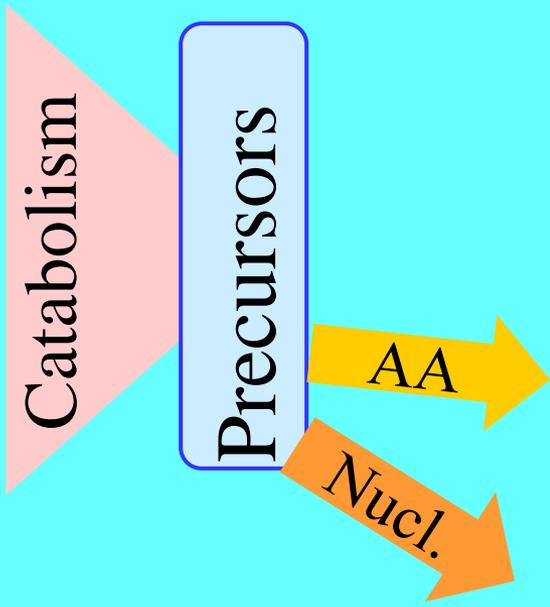
A*P



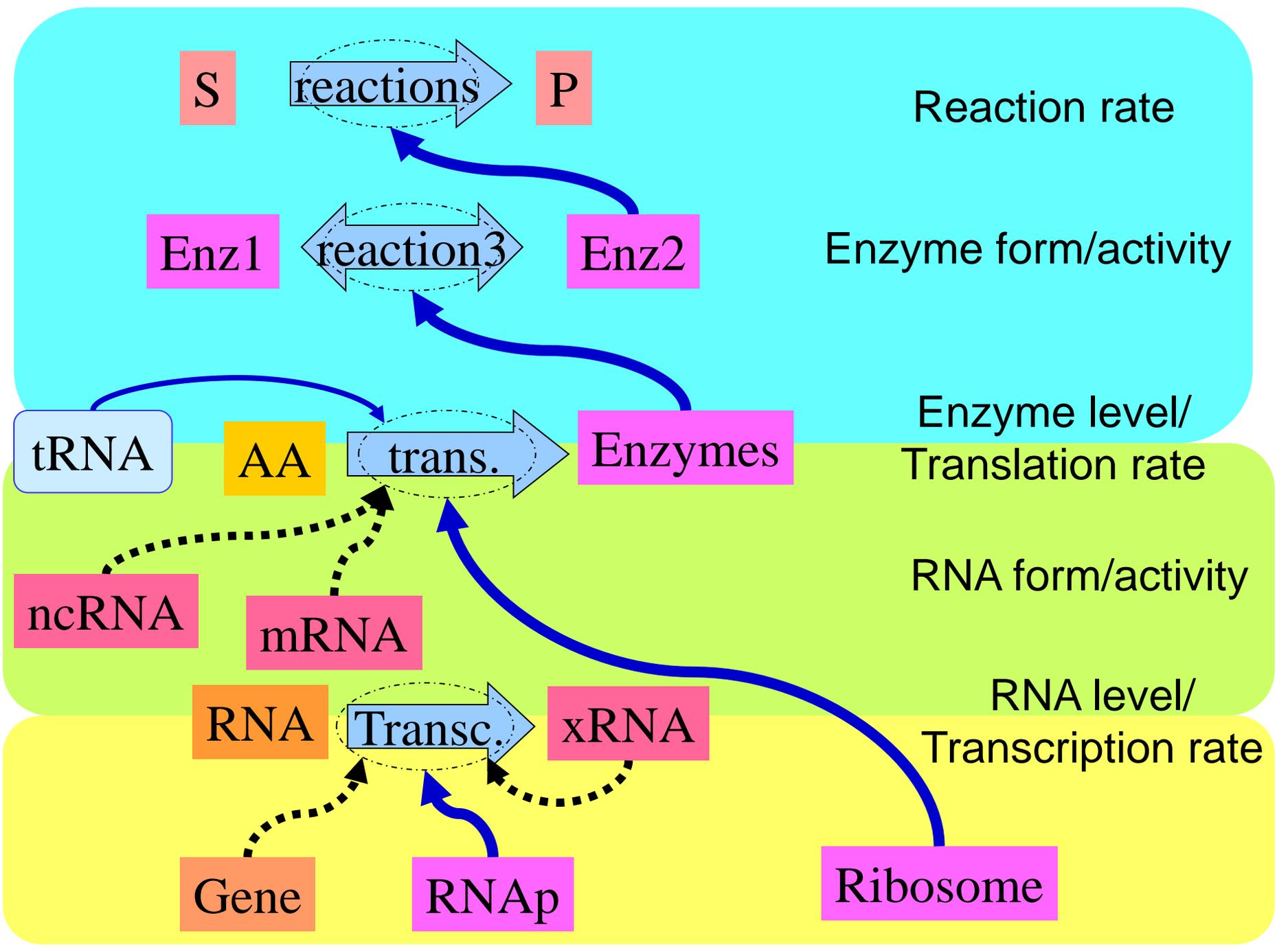


Lots of ways to draw this.

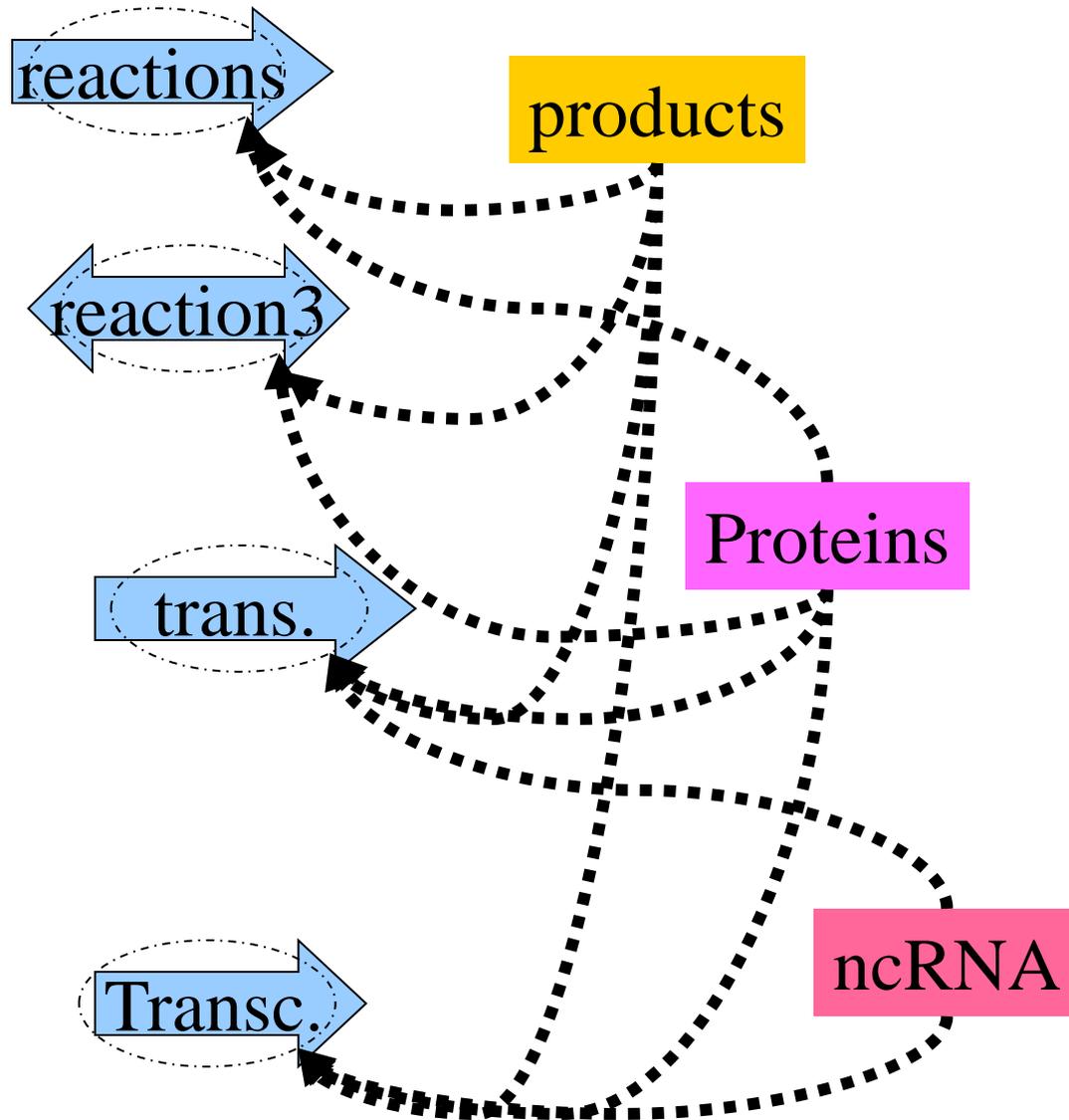




Layered

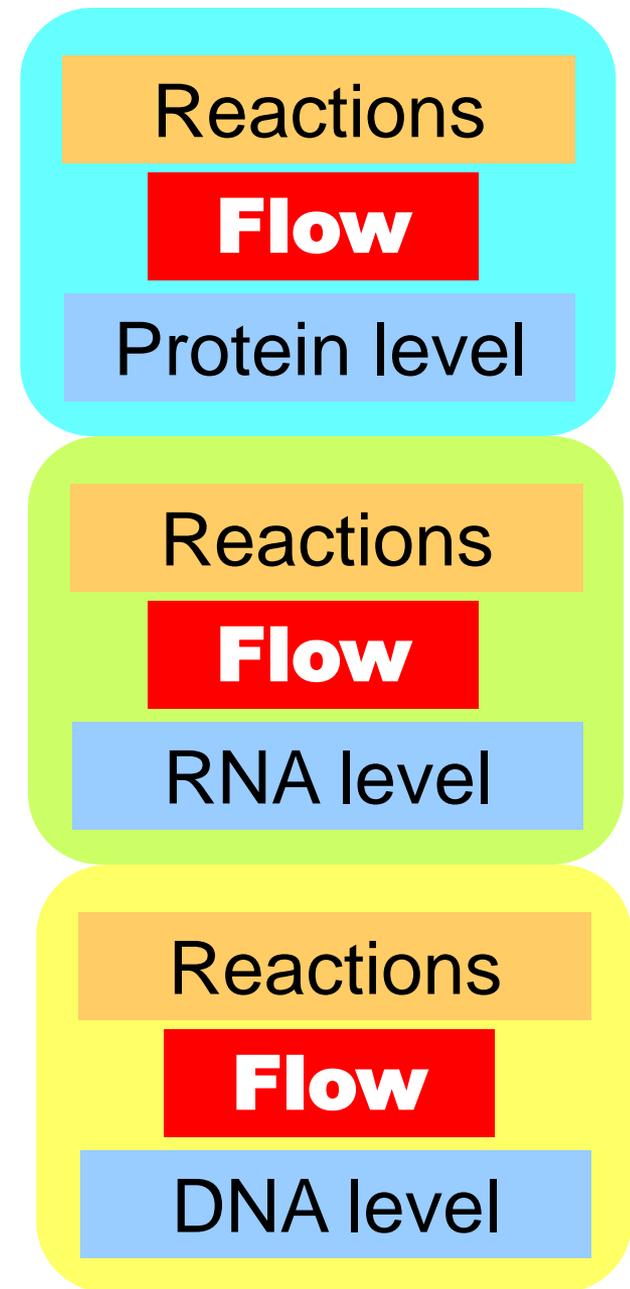
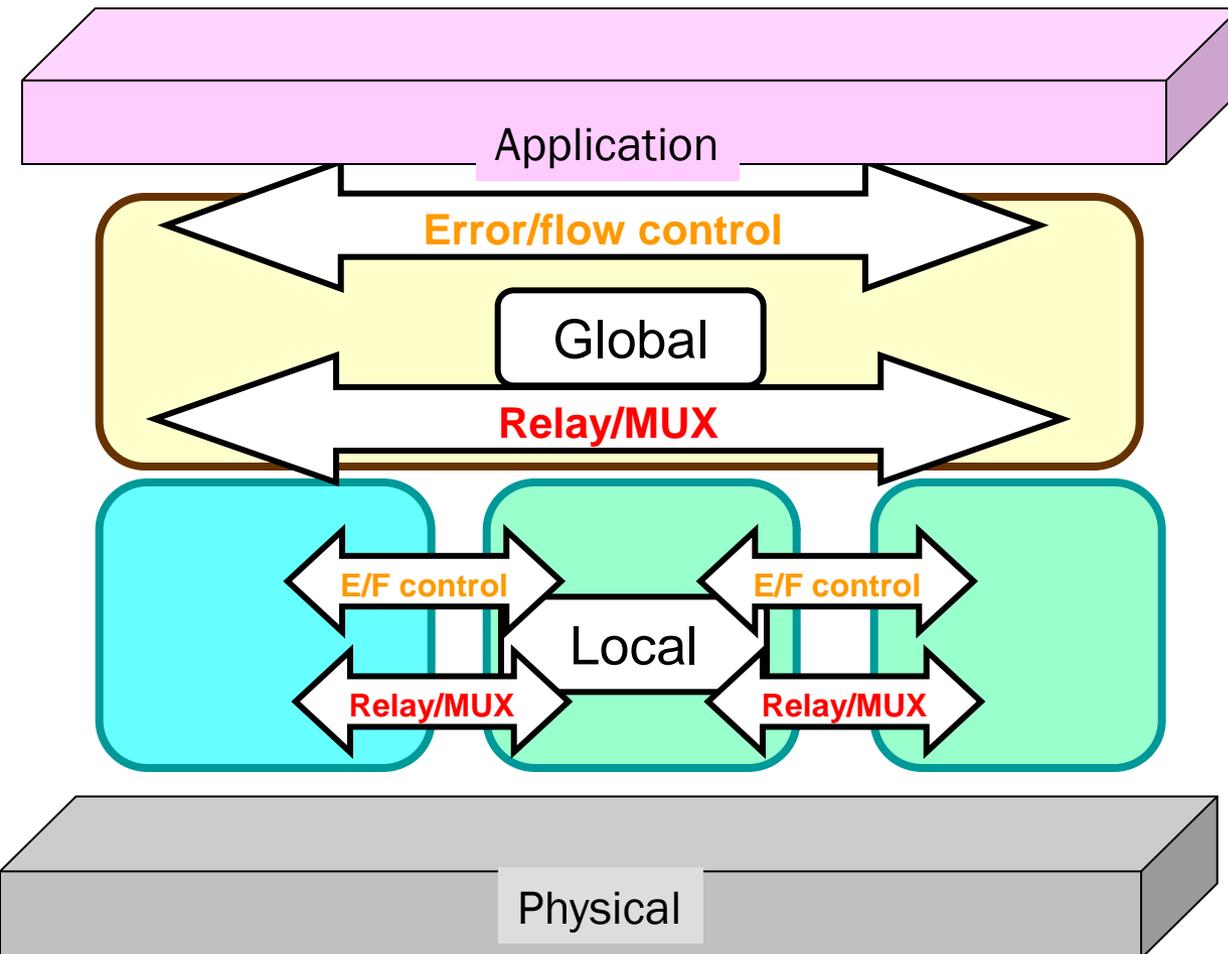


Control?



All products
feedback everywhere

Recursive control structure



Recursive control structure

Reactions

Flow

Protein level

Reactions

Flow

RNA level

Reactions

Huge range of dynamics

- Spatial
- Temporal

Relay/MUX

E/F control

E/F control

Local

Relay/MUX

Relay/MUX

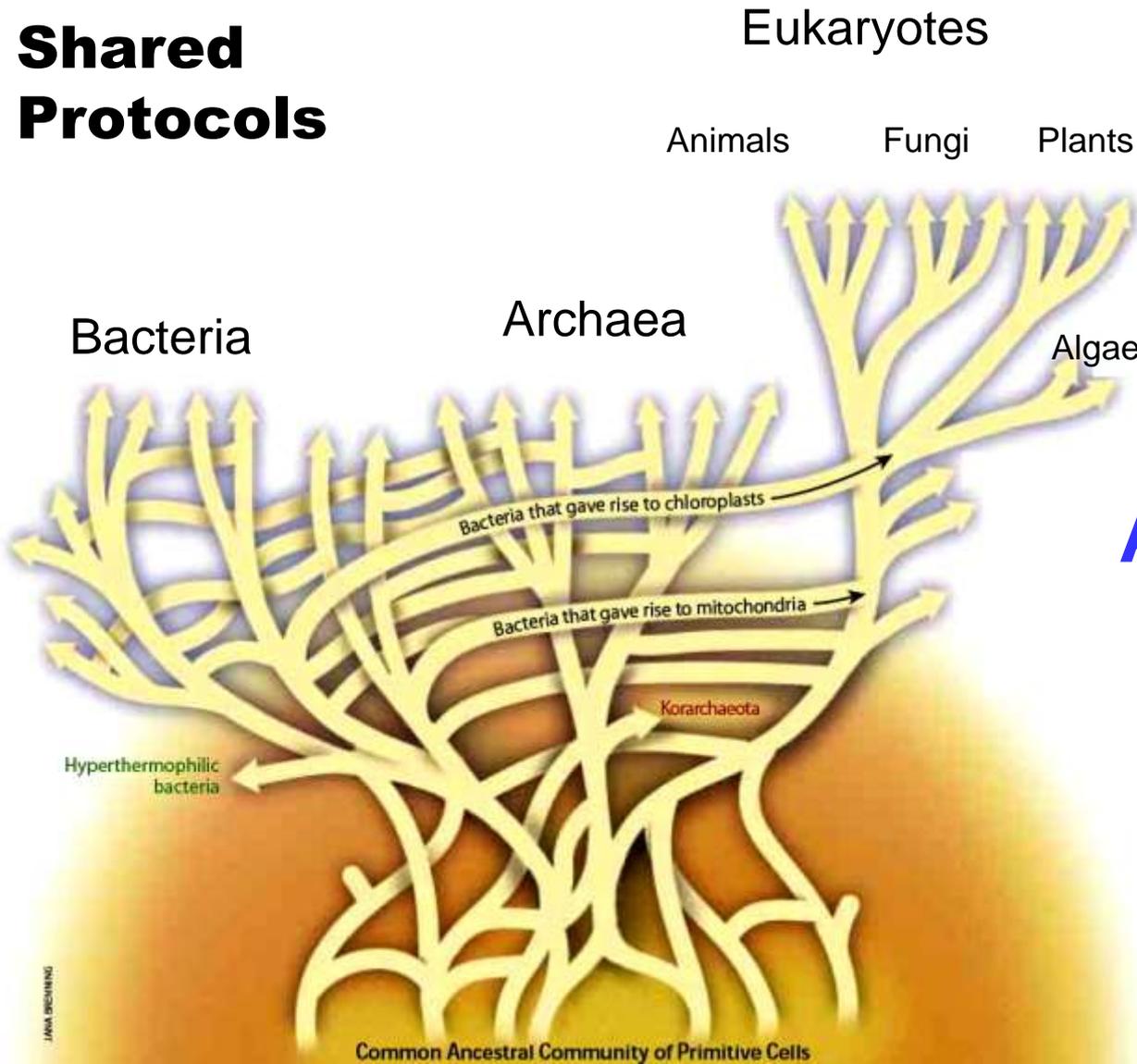
Physical

Bewildering w/out clear grasp of layered architecture

Horizontal gene transfer

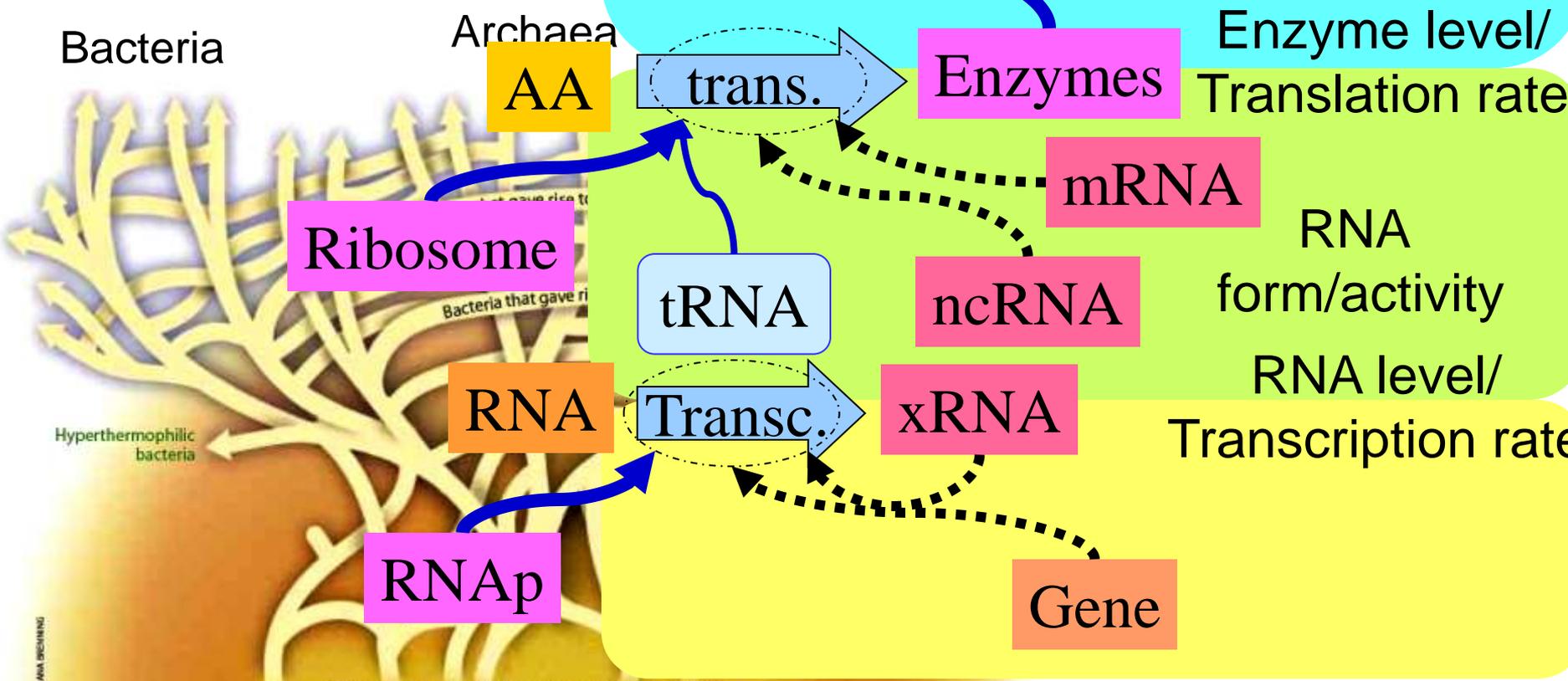
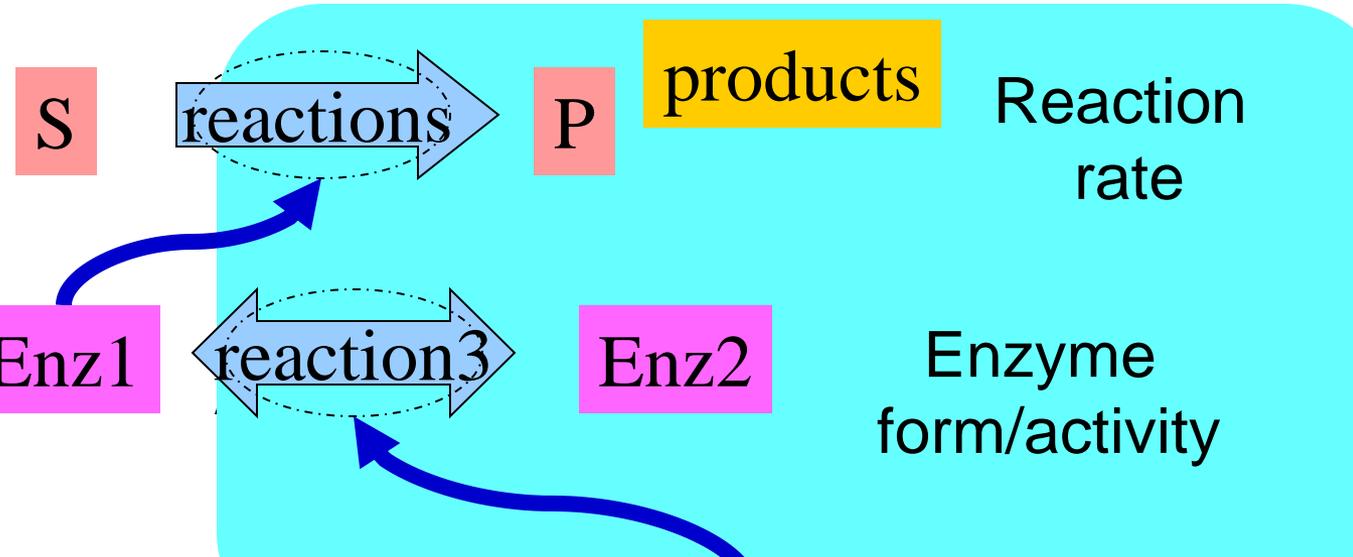
HGT and Shared Protocols

What is locus of early evolution?



Architecture!?!

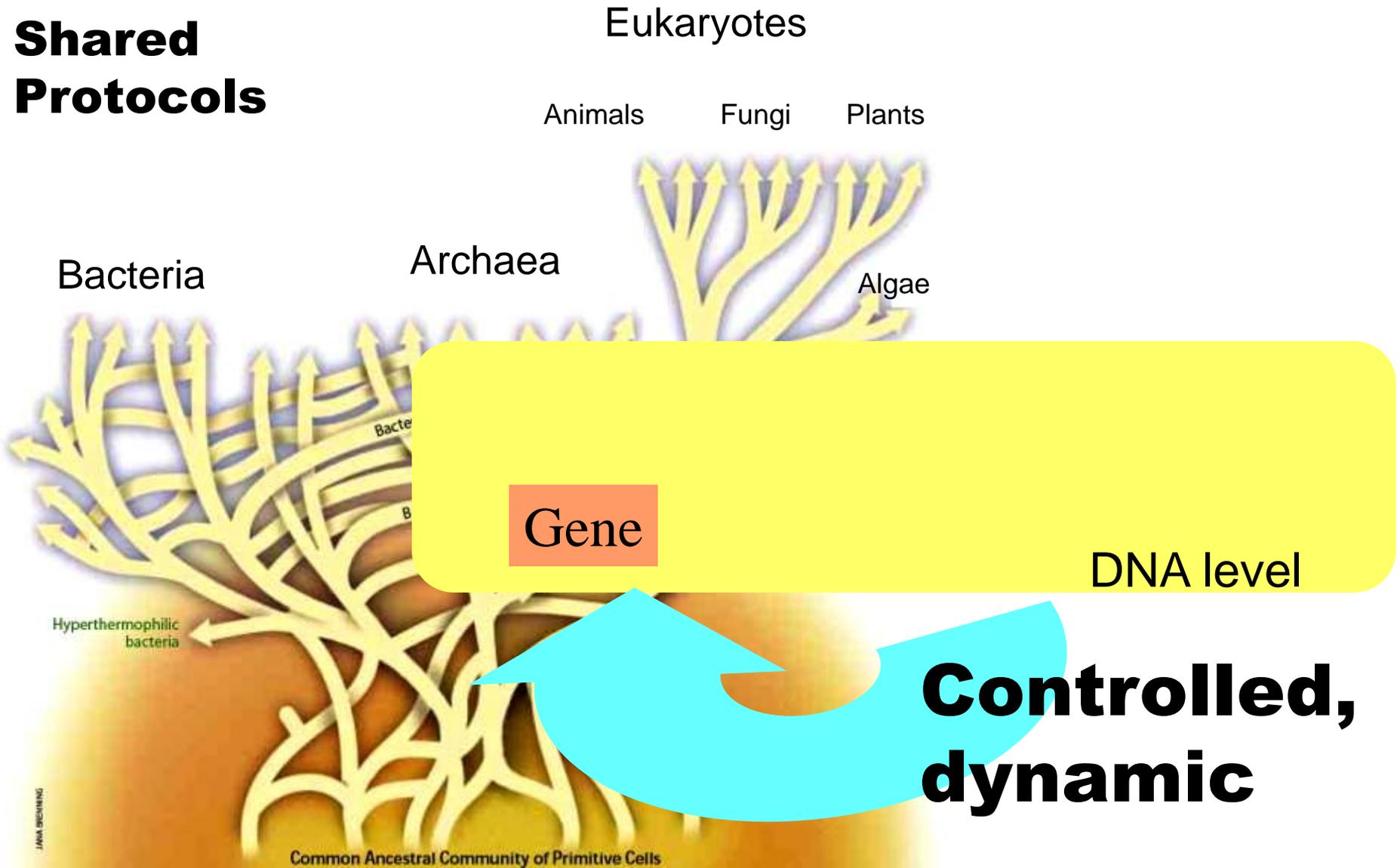
HGT and Shared Protocols

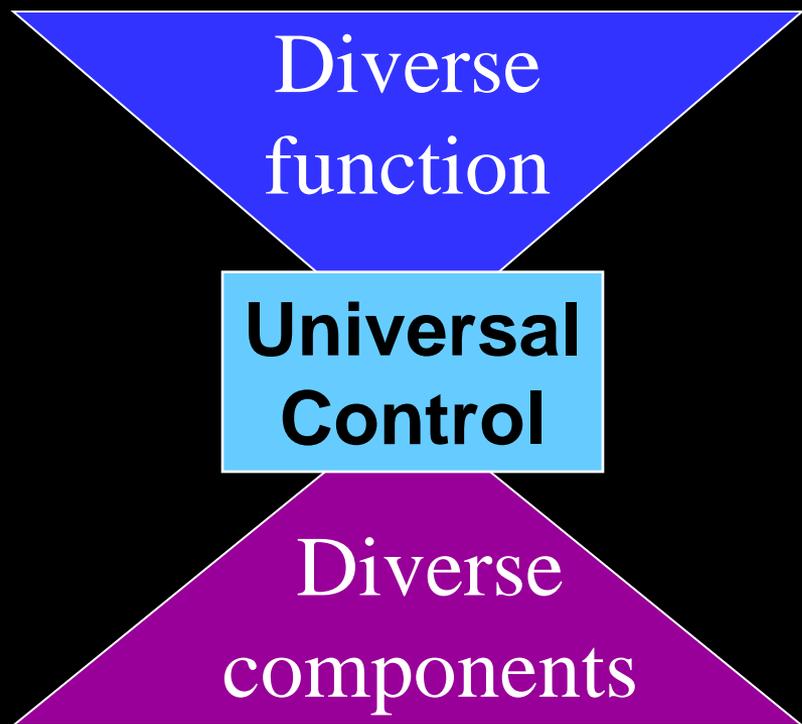
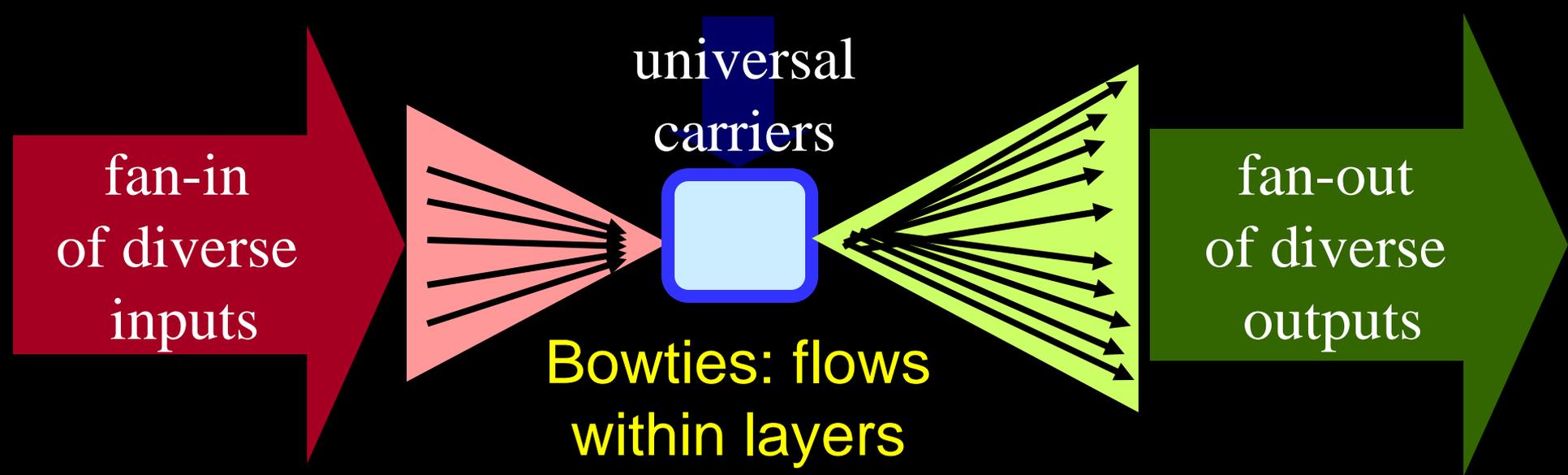


Horizontal gene transfer

- Not a static database
- Not only point mutations

HGT and Shared Protocols





Essential ideas

Robust
yet
fragile

Constraints
that
deconstrain

fan-in
of diverse
inputs

fan-out
of diverse
outputs

Diverse
function

Diverse
components

Highly robust

- Diverse
- Evolvable
- Deconstrained

Robust
yet fragile

Constraints that
deconstrain

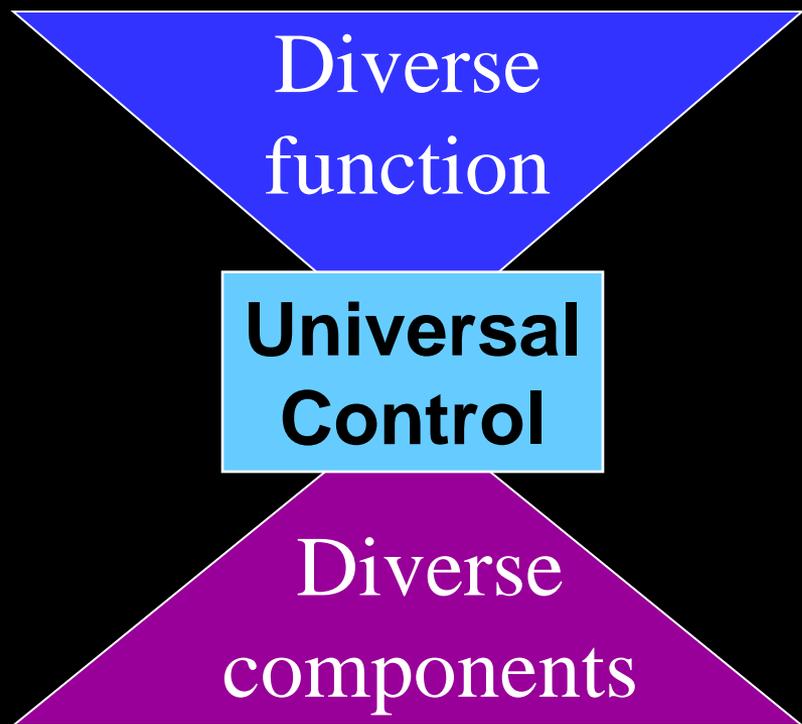
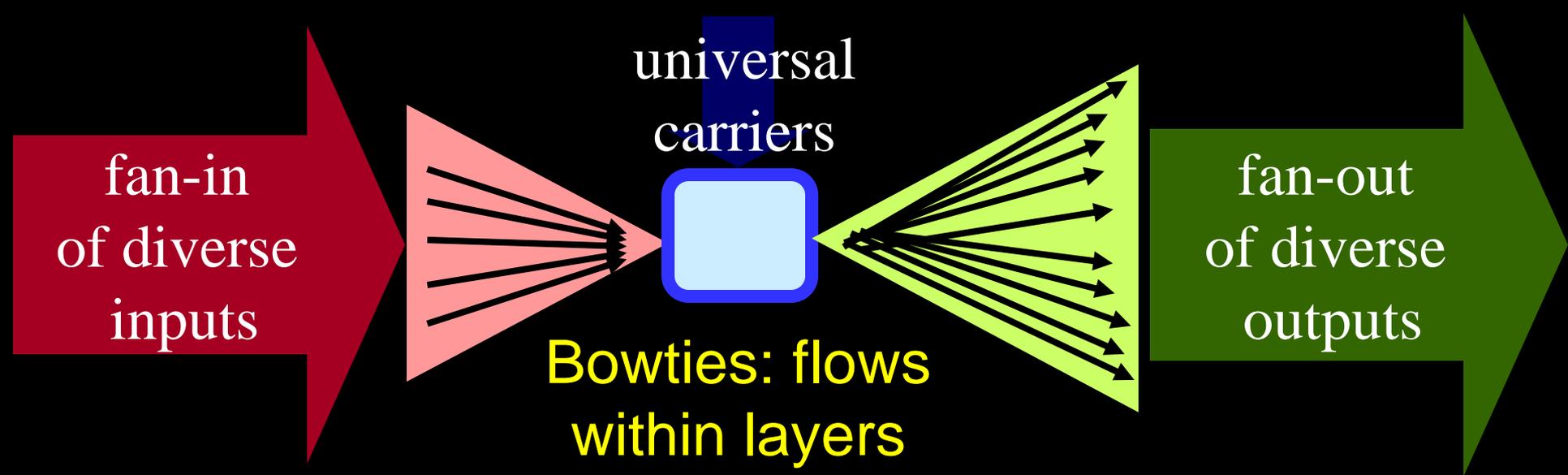
universal
carriers



Highly fragile

- Universal
- Frozen
- Constrained
- Hijacking

**Universal
Control**



Essential ideas

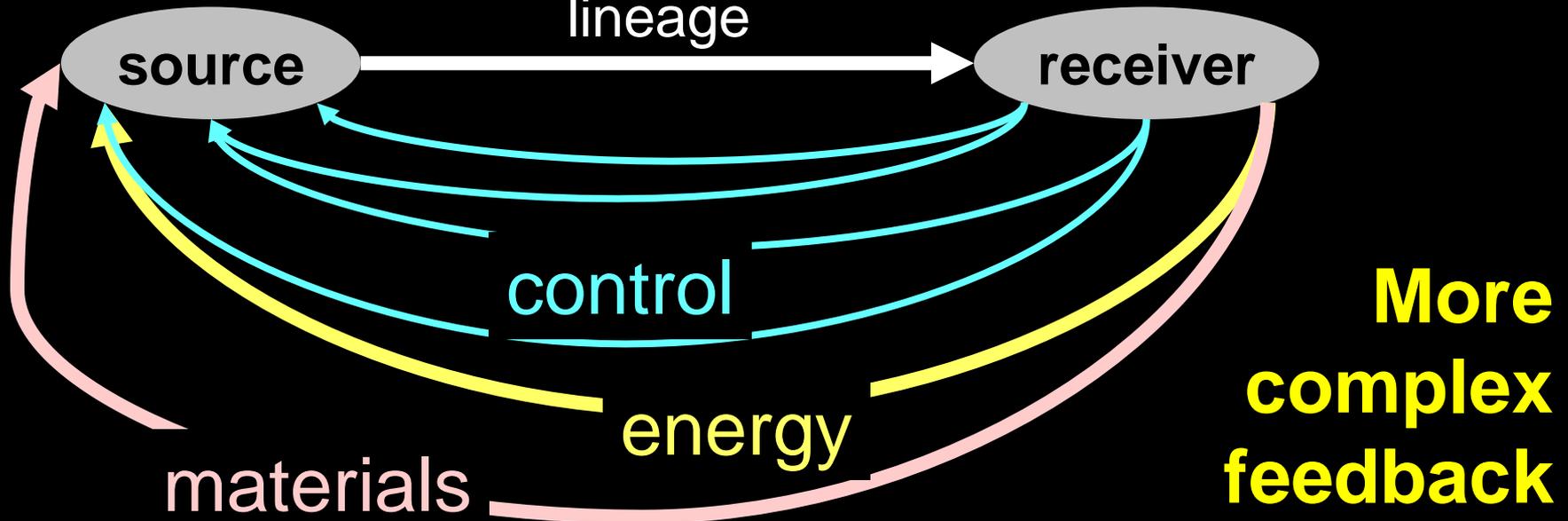
Robust
yet
fragile

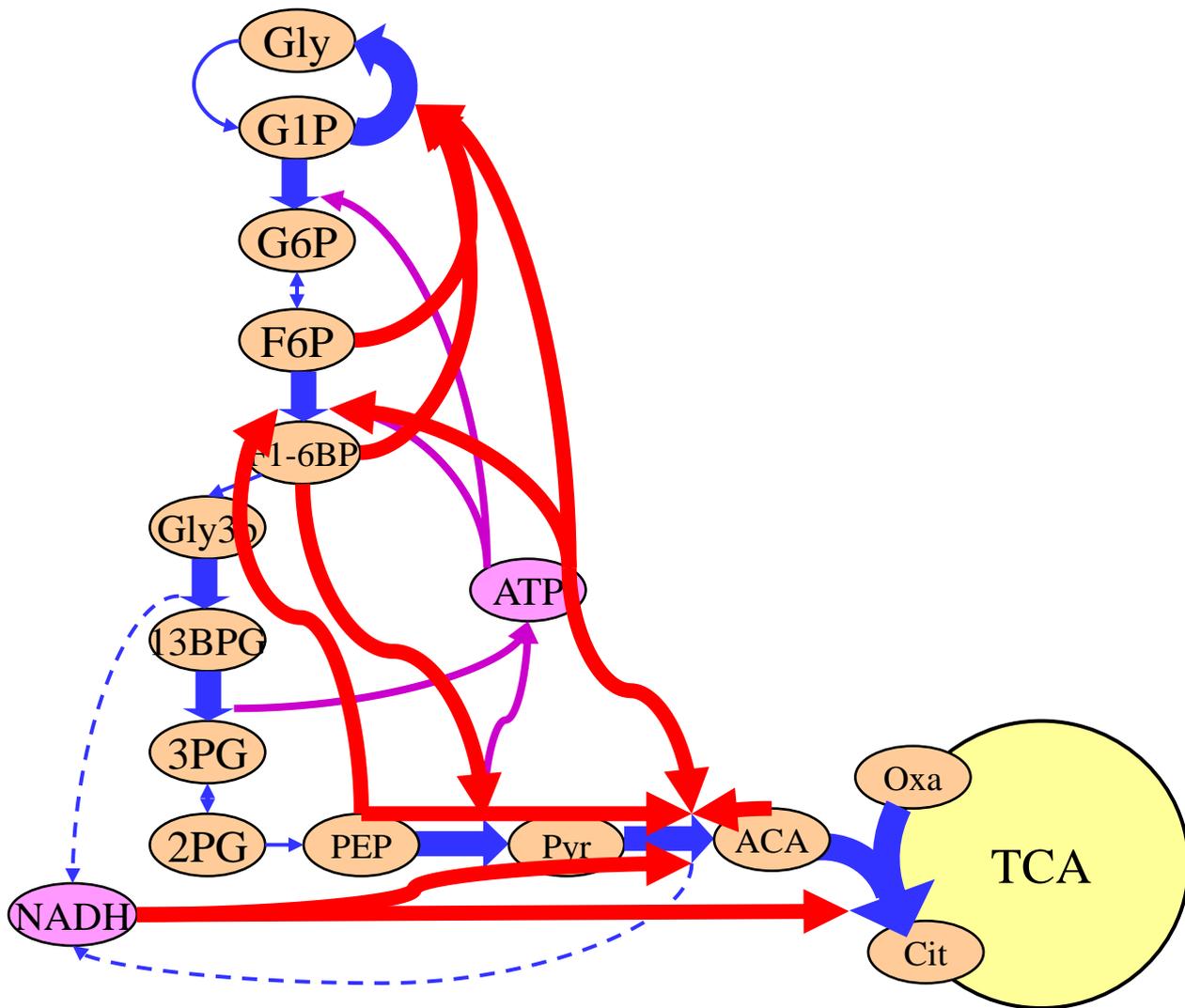
Constraints
that
deconstrain

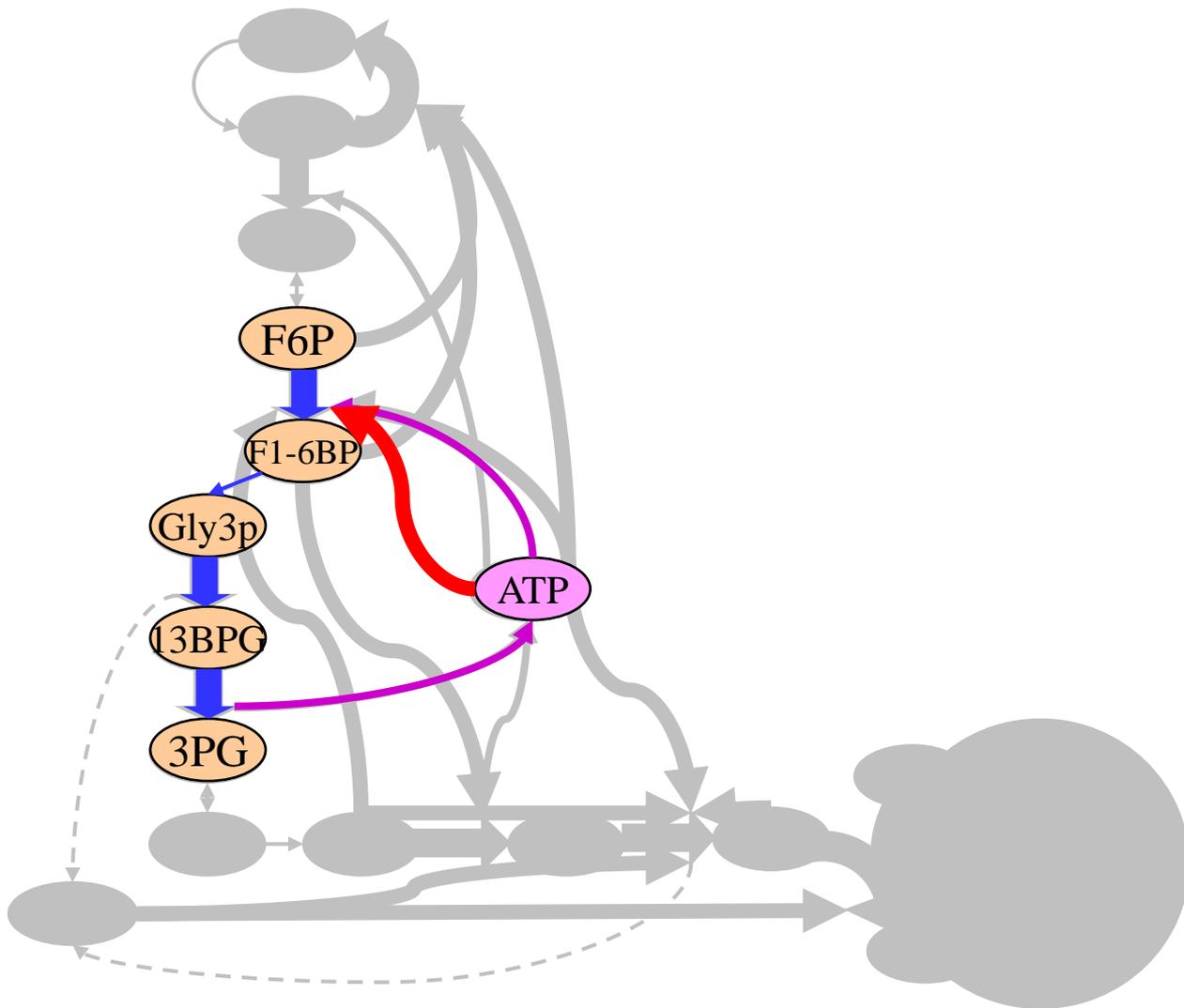
What theory is relevant to these more complex feedback systems?

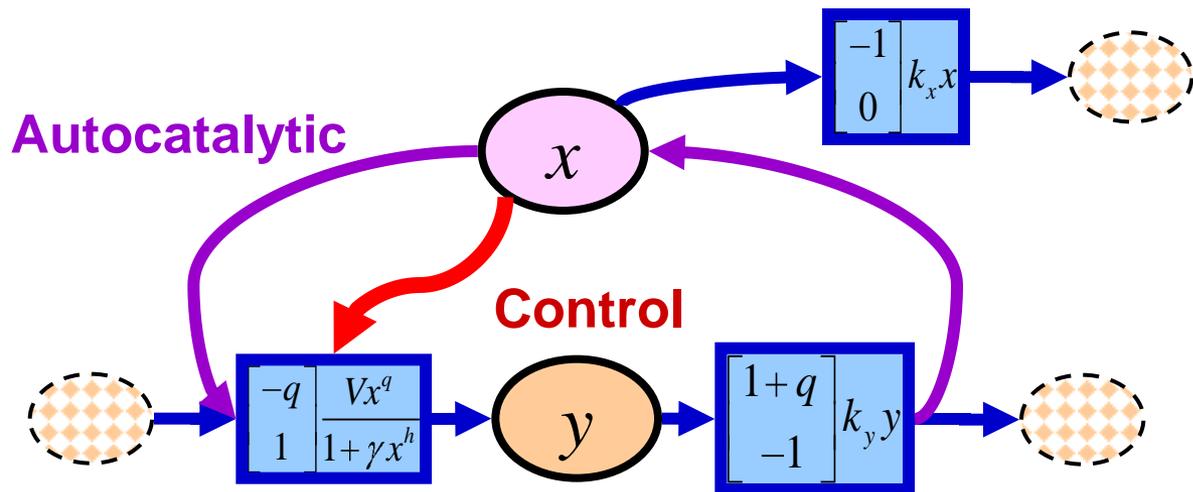
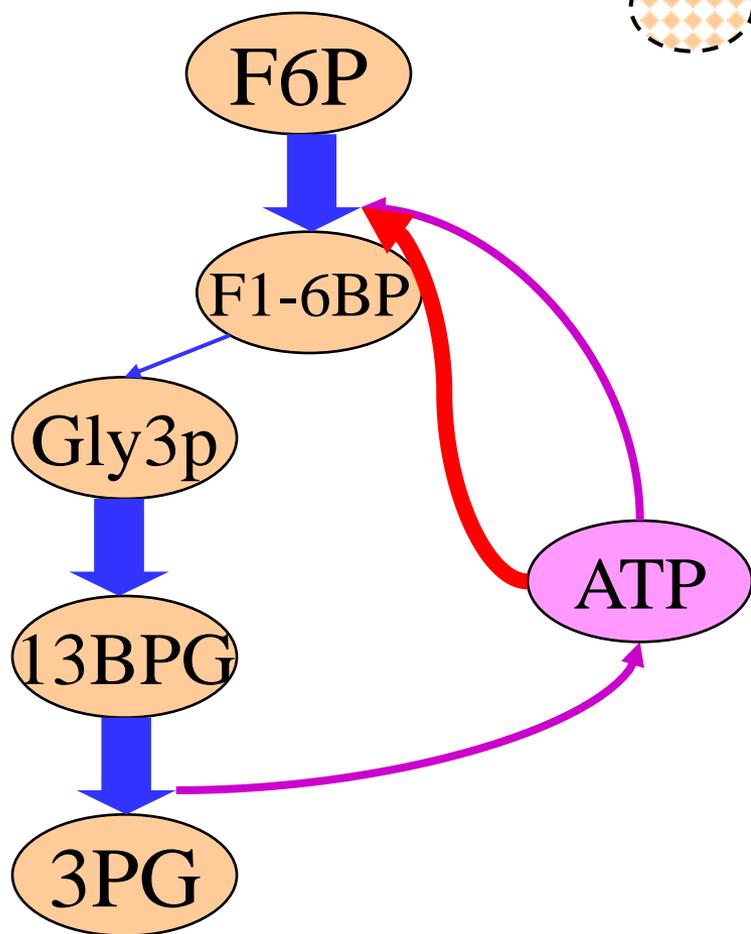
$$\frac{1}{\pi} \int_0^{\infty} \ln |S(j\omega)| \frac{z}{z^2 + \omega^2} d\omega \geq \ln \left| \frac{z+p}{z-p} \right|$$

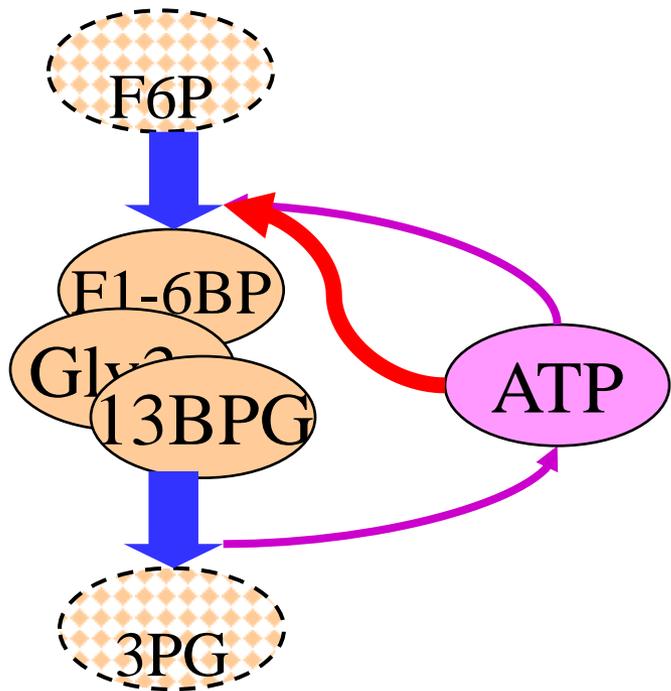
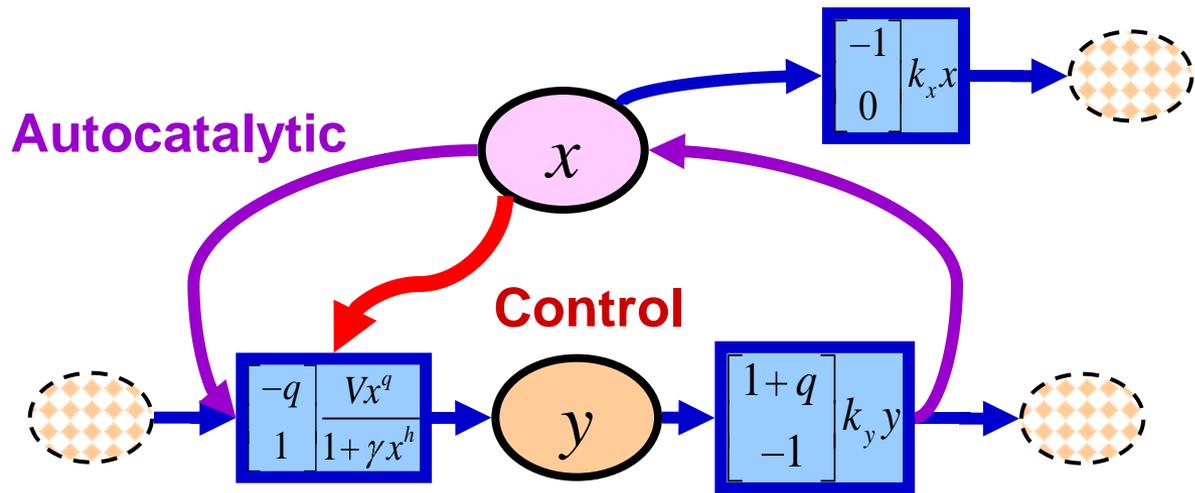
metabolism
lineage

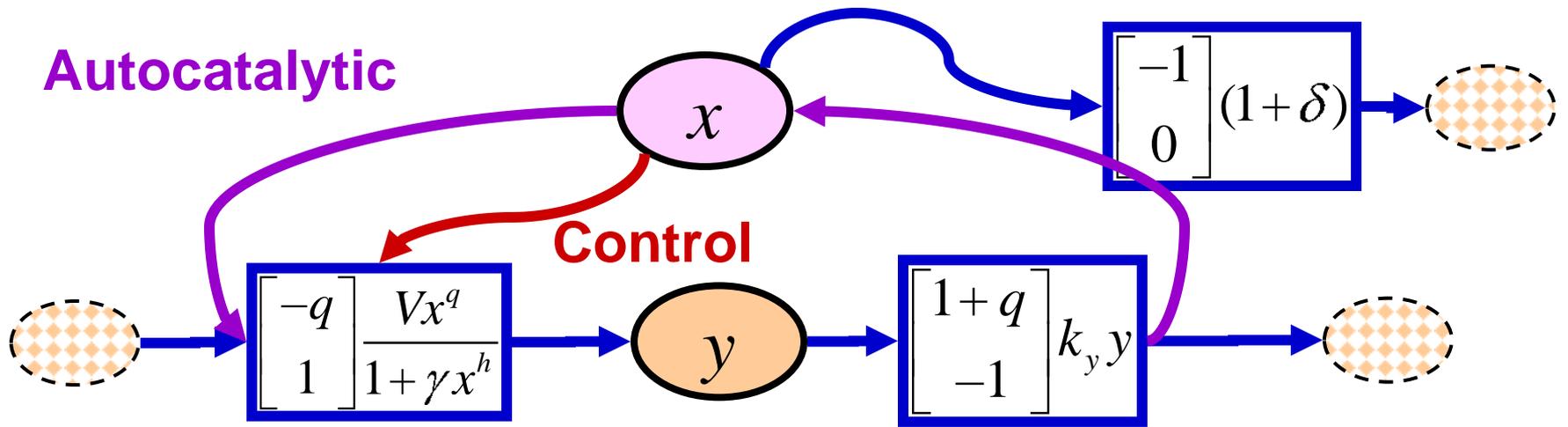












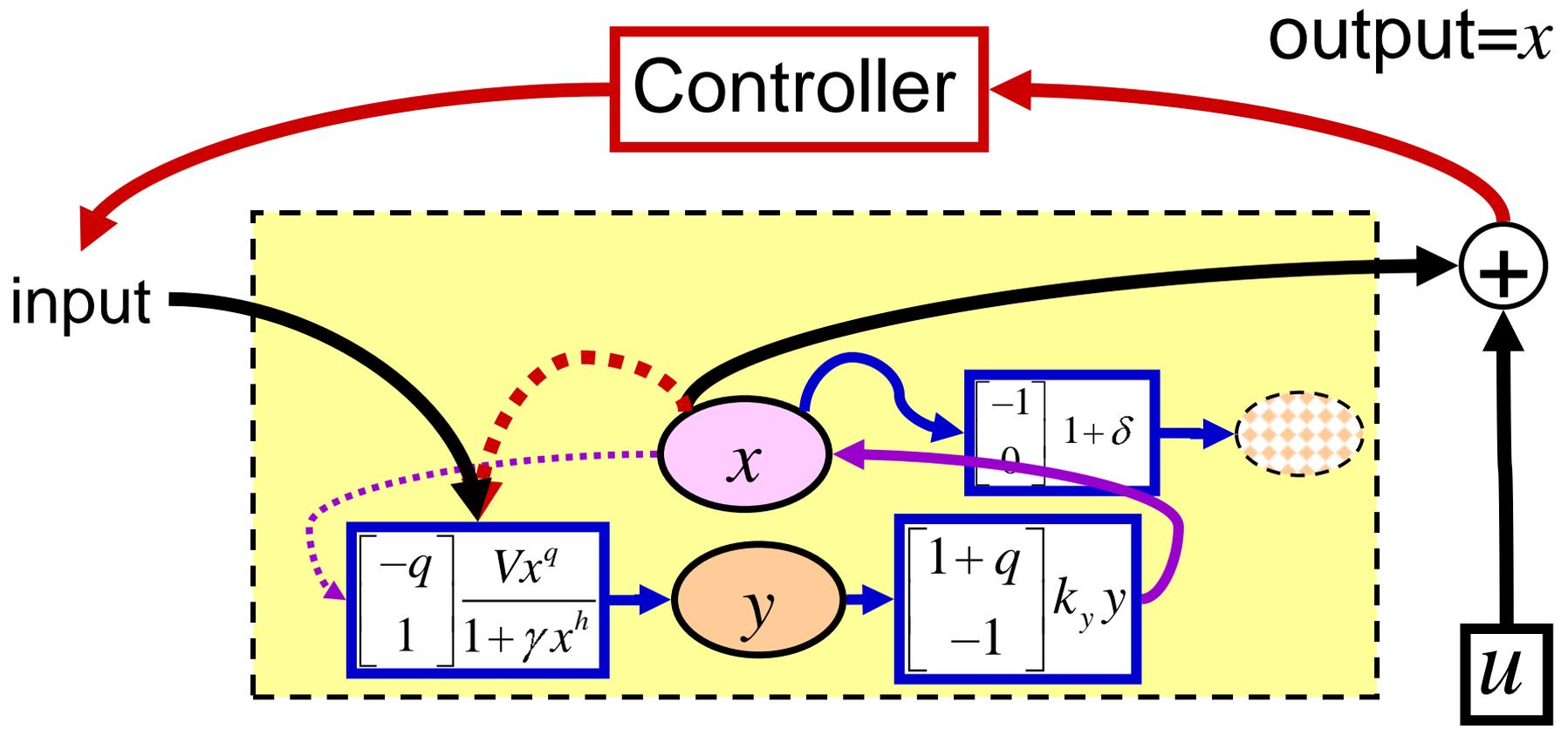
Autocatalytic

$$\begin{bmatrix} \dot{x} \\ \dot{y} \end{bmatrix} = \begin{bmatrix} -q \\ 1 \end{bmatrix} \left(\frac{Vx^q}{1+\gamma x^h} \right) + \begin{bmatrix} 1+q \\ -1 \end{bmatrix} ky + \begin{bmatrix} -1 \\ 0 \end{bmatrix} (1+\delta)$$

Control

Control theory cartoon

$$S \quad j\omega = \frac{x}{u}$$



Caution: mixed cartoon

$$S(j\omega) = \frac{X(j\omega)}{U(j\omega)}$$

Hard limits

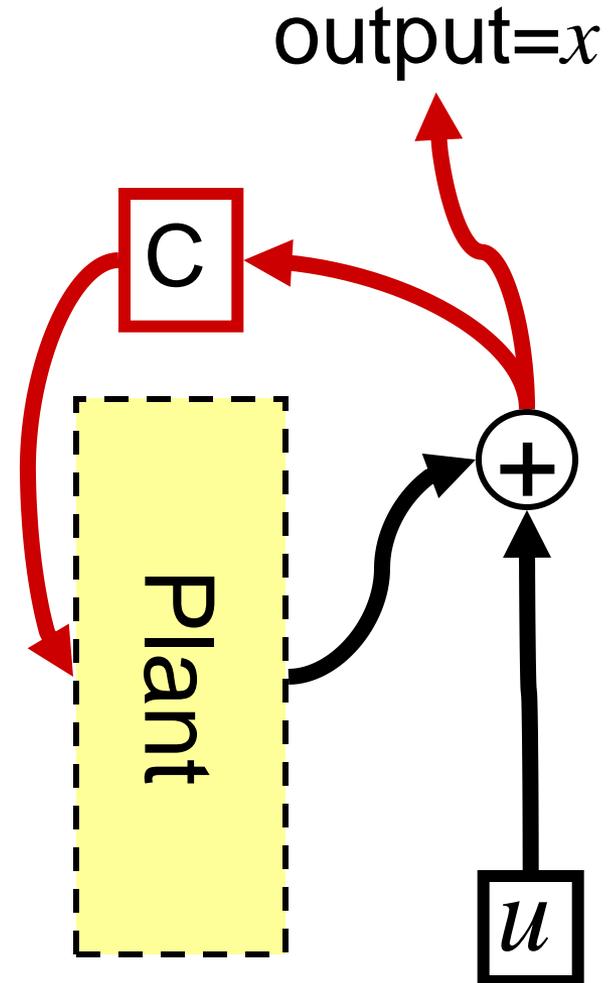
$$\frac{1}{\pi} \int_0^{\infty} \ln |S(j\omega)| d\omega \geq 0$$

$$\int_{-\infty}^{\infty} \ln |S(j\omega)| d\omega = \int_{-\infty}^{\infty} \ln \left| \frac{X(j\omega)}{U(j\omega)} \right| d\omega$$

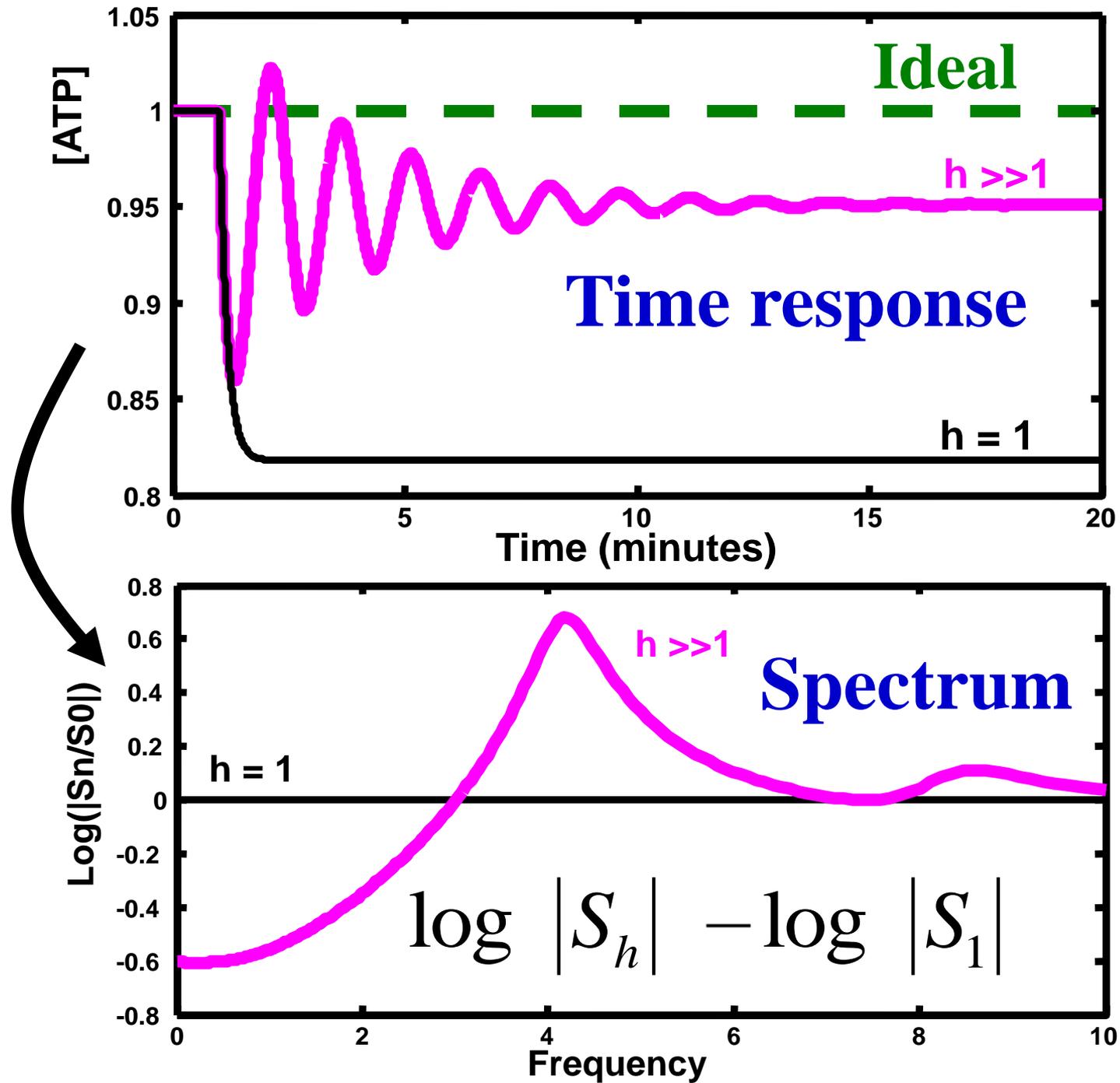
$$= \int_{-\infty}^{\infty} \ln |X(j\omega)| d\omega - \int_{-\infty}^{\infty} \ln |U(j\omega)| d\omega$$



Entropy rates

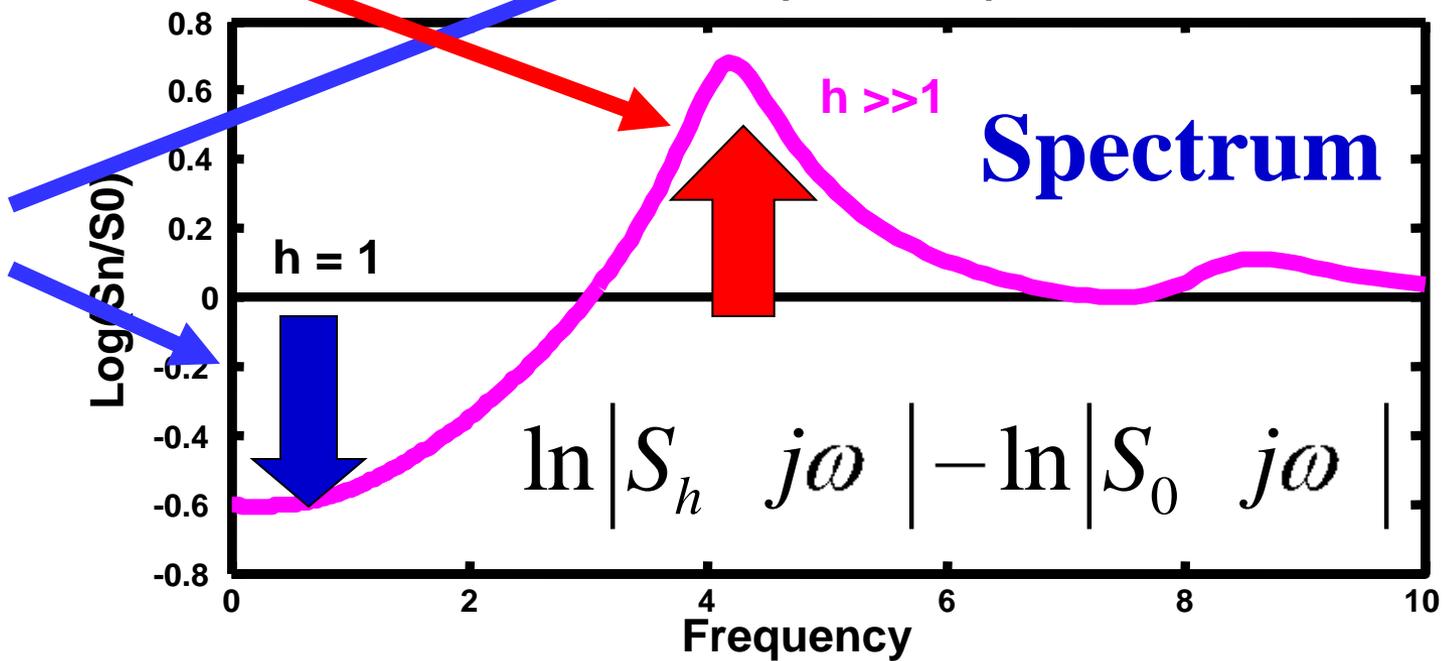
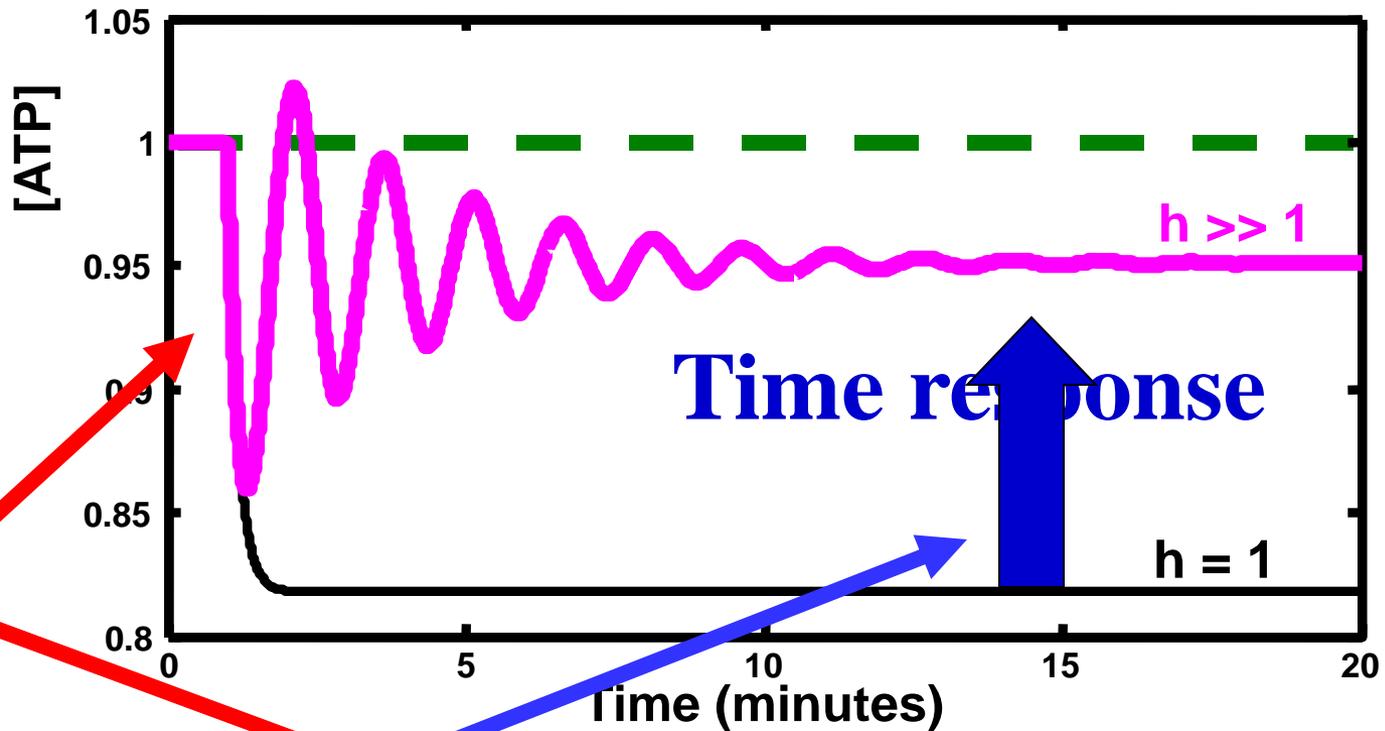


$S_h = F(x)|_h$
Fourier
Transform
of error



Yet fragile

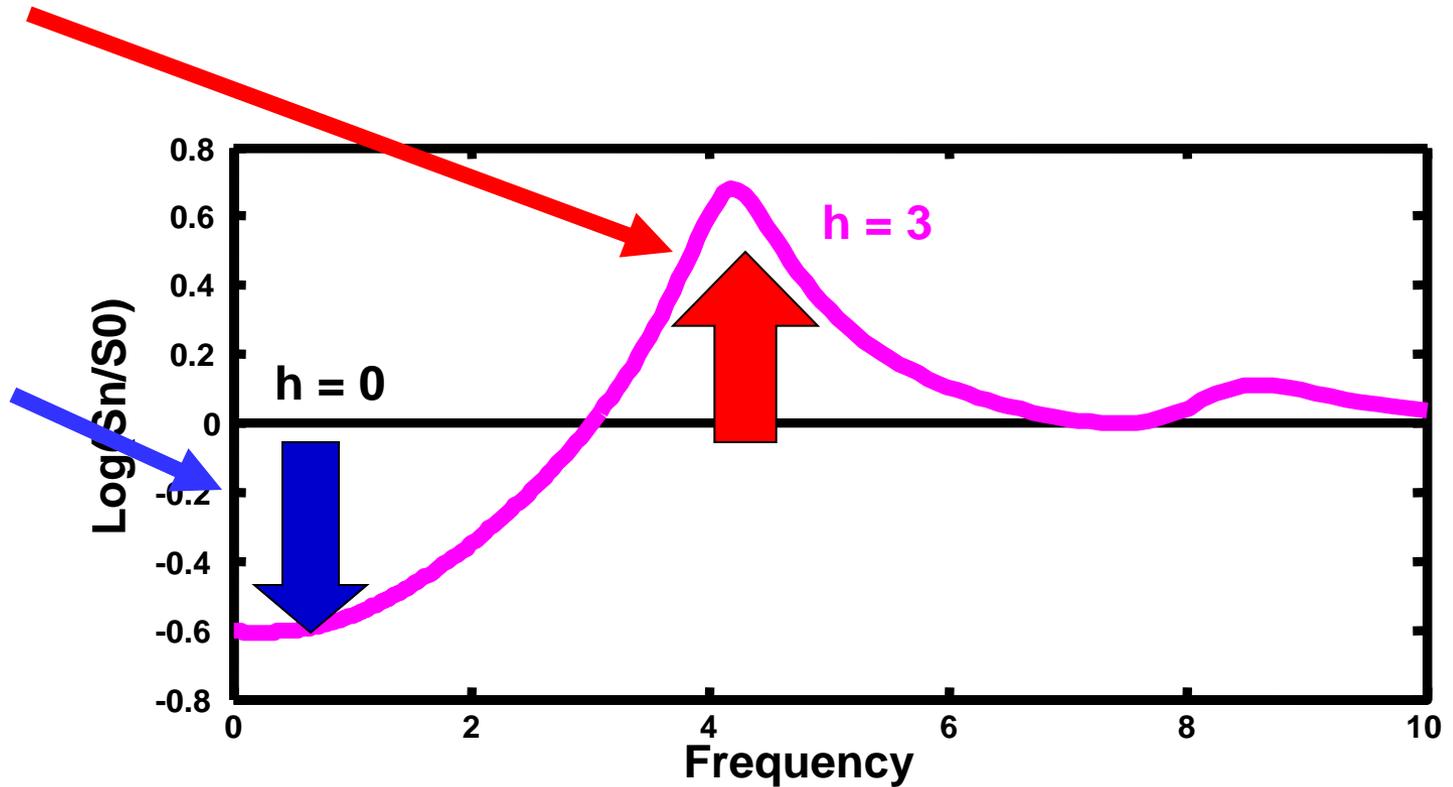
Robust



$$\int_0^{\infty} \Delta \ln |S(j\omega)| d\omega = 0$$

**Yet
fragile**

Robust

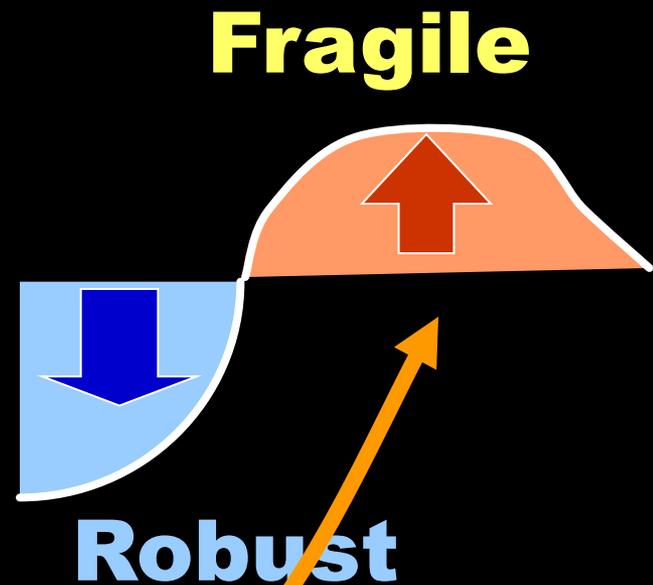


[a system] can have
[a property] *robust* for
[a set of perturbations]

Yet be *fragile for*

[a different property]

Or [a different perturbation]



Robust yet fragile = fragile robustness

$$S(j\omega) = \frac{X(j\omega)}{U(j\omega)}$$

Hard limits

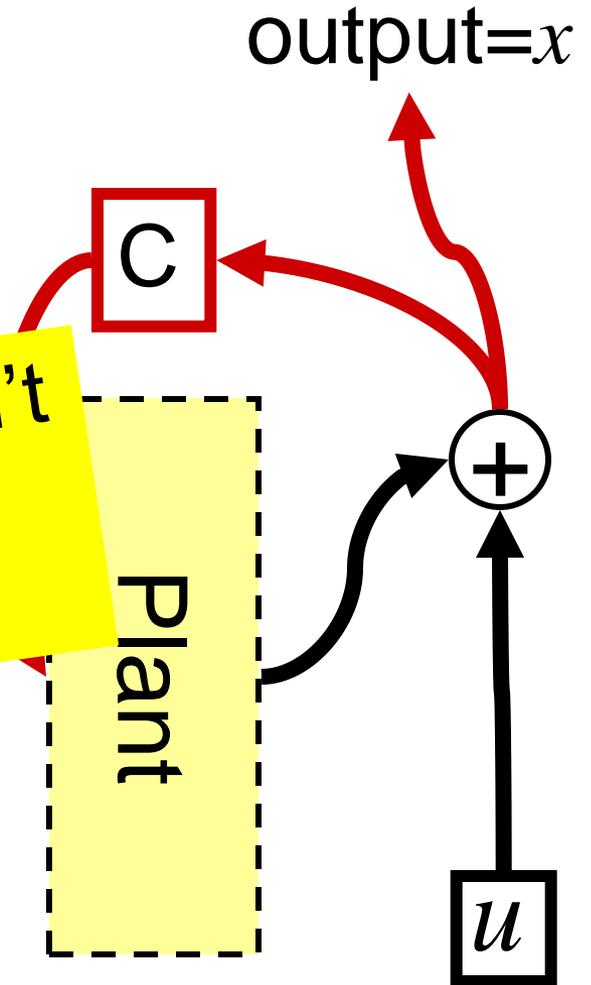
$$\frac{1}{\pi} \int_0^{\infty} \ln |S(j\omega)| d\omega \geq 0$$

$$\int_{-\infty}^{\infty} \ln |S(j\omega)| d\omega$$

$$= \int_{-\infty}^{\infty} \ln |X(j\omega)| d\omega - \int_{-\infty}^{\infty} \ln |U(j\omega)| d\omega$$

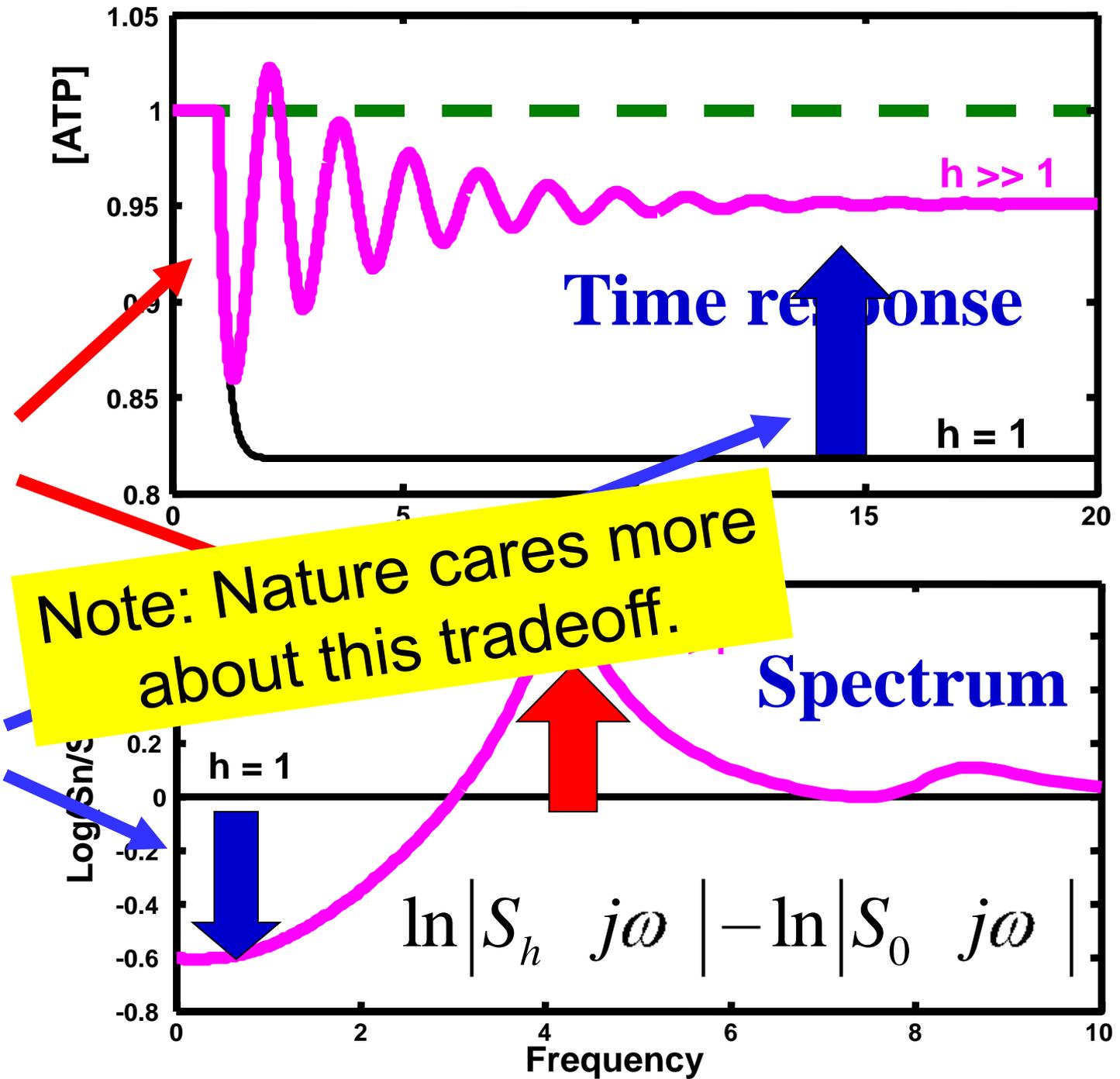
Entropy rates

Note: Nature doesn't care much about entropy rates.



Yet fragile

Robust

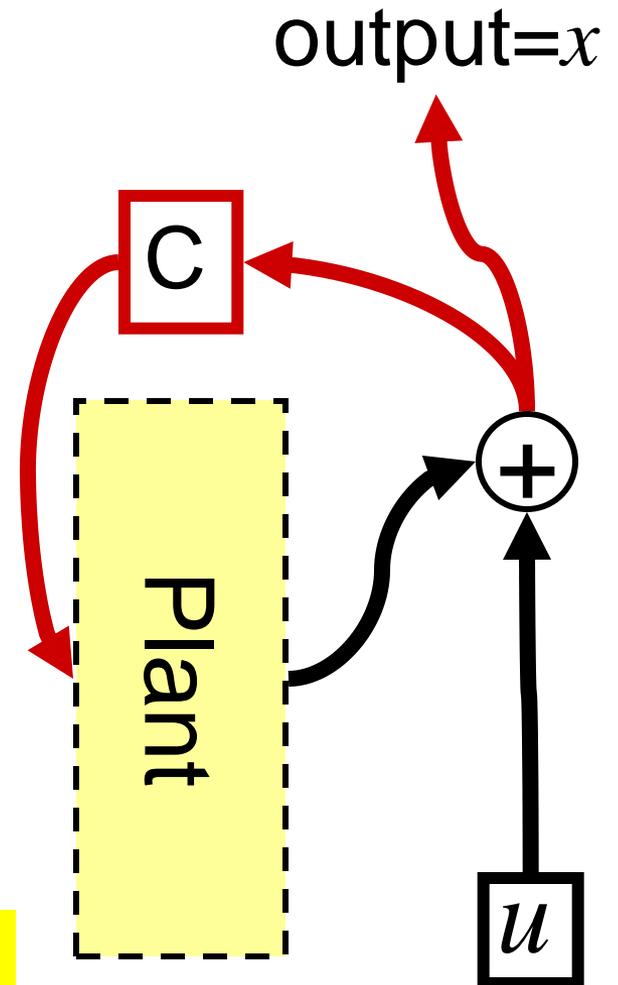


$$S(j\omega) = \frac{X(j\omega)}{U(j\omega)}$$

$$\frac{1}{\pi} \int_0^{\infty} \ln |S(j\omega)| d\omega \geq 0$$

$$\frac{1}{\pi} \int_0^{\infty} \ln |S(j\omega)| \left| \frac{z}{z^2 + \omega^2} \right| d\omega \geq \ln \left| \frac{z+p}{z-p} \right|$$

The plant can make this tradeoff worse.



$$S(j\omega) = \frac{X(j\omega)}{U(j\omega)}$$

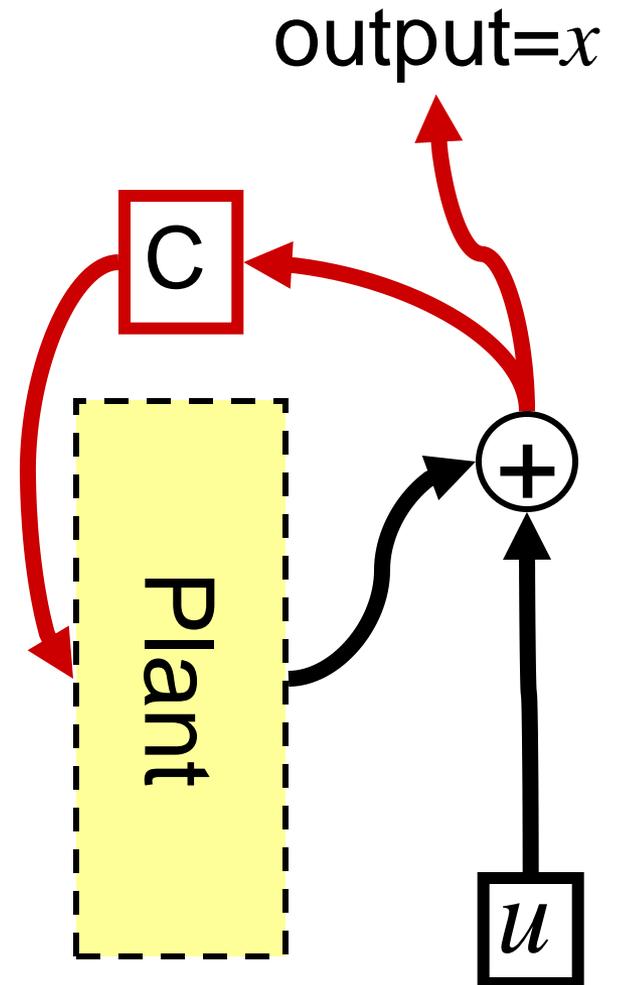
$$\frac{1}{\pi} \int_0^{\infty} \ln |S(j\omega)| d\omega \geq 0$$

$$\frac{1}{\pi} \int_0^{\infty} \ln |S(j\omega)| \frac{z}{z^2 + \omega^2} d\omega \geq \ln \left| \frac{z+p}{z-p} \right|$$

All controllers: \geq

Biological cells: $=$

$$z = \frac{k}{q} \quad p = \text{RHP zero } s^2 + q\alpha + k \quad s - \alpha k$$

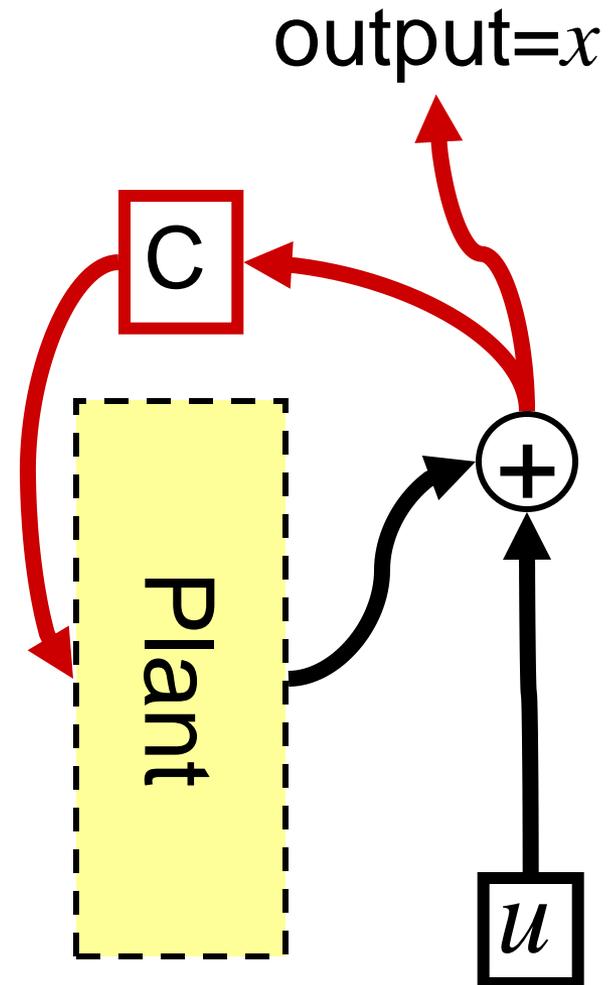


$$S(j\omega) = \frac{X(j\omega)}{U(j\omega)}$$

$$\frac{1}{\pi} \int_0^{\infty} \ln |S(j\omega)| d\omega \geq 0$$

$$\frac{1}{\pi} \int_0^{\infty} \ln |S(j\omega)| \frac{z}{z^2 + \omega^2} d\omega \geq \ln \left| \frac{z+p}{z-p} \right|$$

Small z is bad.



$$z = \frac{k}{q}$$

$$p = \text{RHP zero } s^2 + q\alpha + k s - \alpha k$$

Small z is *bad* (oscillations and crashes)

$$\frac{1}{\pi} \int_0^{\infty} \ln |S(j\omega)| \frac{z}{z^2 + \omega^2} d\omega \geq \ln \left| \frac{z+p}{z-p} \right|$$

Small z =

- small k and/or
- large q

Efficiency =

- small k and/or
- large q



$$z = \frac{k}{q}$$

Correctly predicts conditions
with “glycolytic oscillations”

$$S(j\omega) = \frac{X(j\omega)}{U(j\omega)}$$

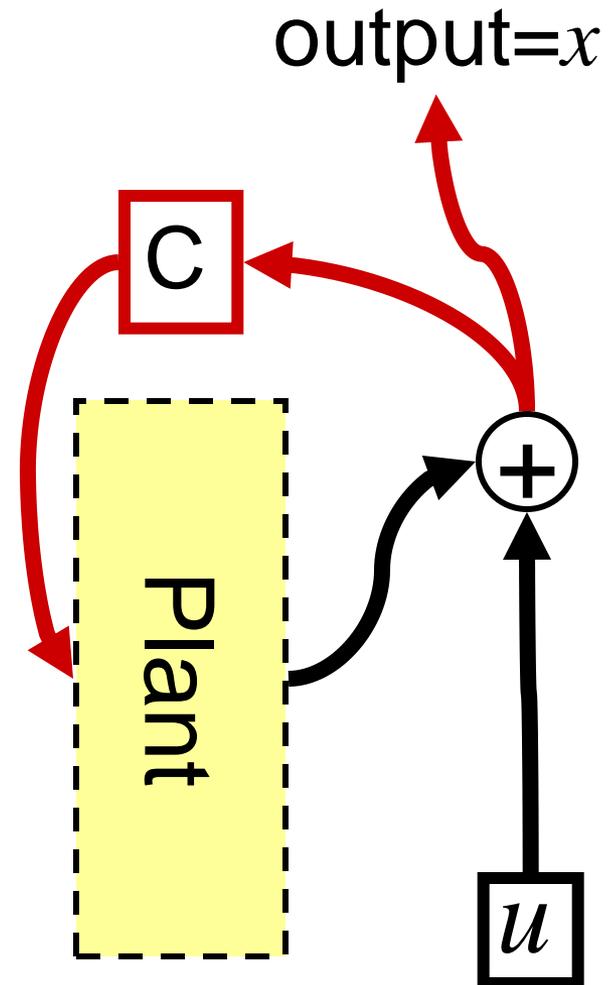
Hard limits

$$\frac{1}{\pi} \int_0^{\infty} \ln |S(j\omega)| d\omega \geq 0$$

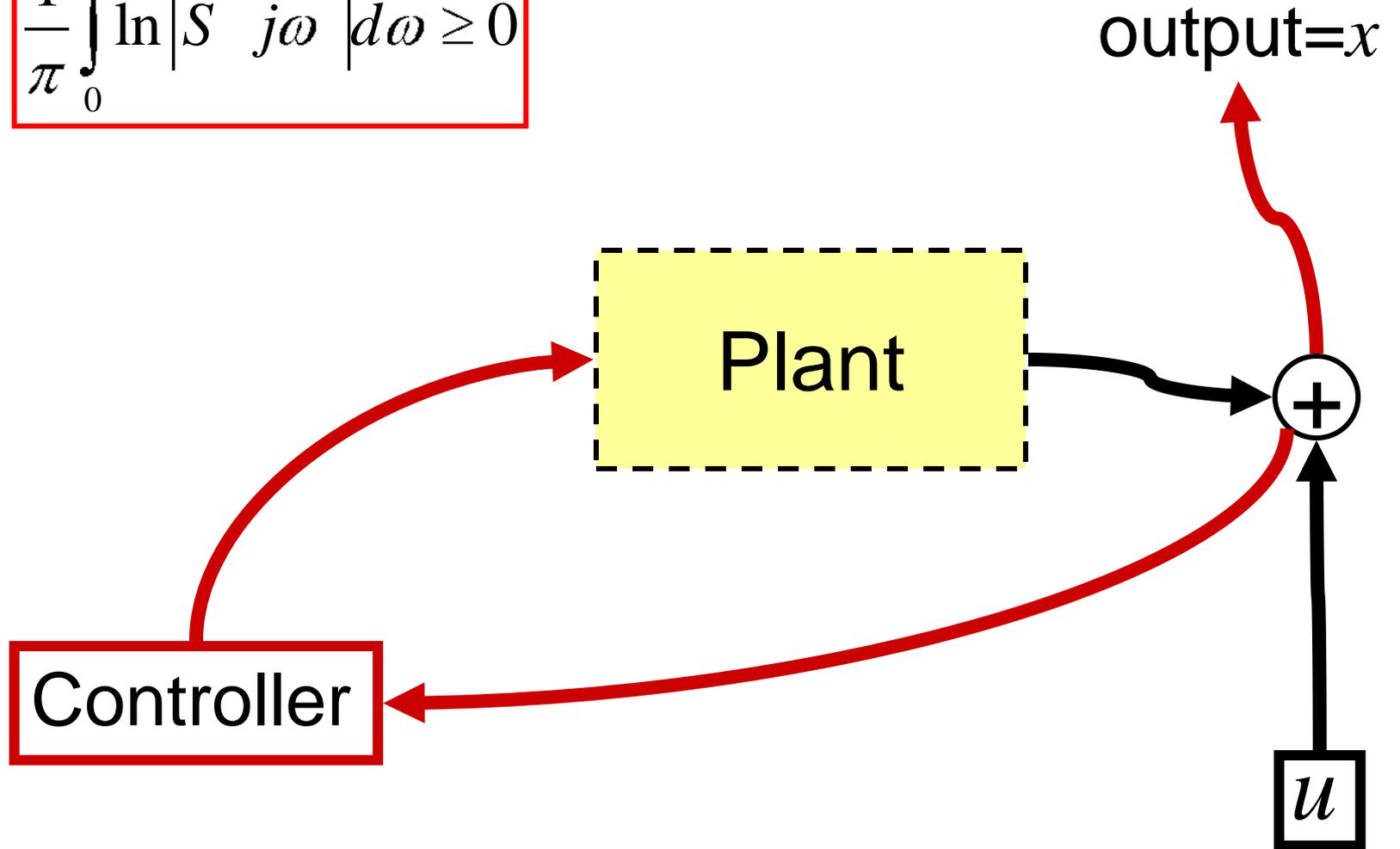
$$\int_{-\infty}^{\infty} \ln |S(j\omega)| d\omega = \int_{-\infty}^{\infty} \ln \left| \frac{X(j\omega)}{U(j\omega)} \right| d\omega$$

$$= \int_{-\infty}^{\infty} \ln |X(j\omega)| d\omega - \int_{-\infty}^{\infty} \ln |U(j\omega)| d\omega$$

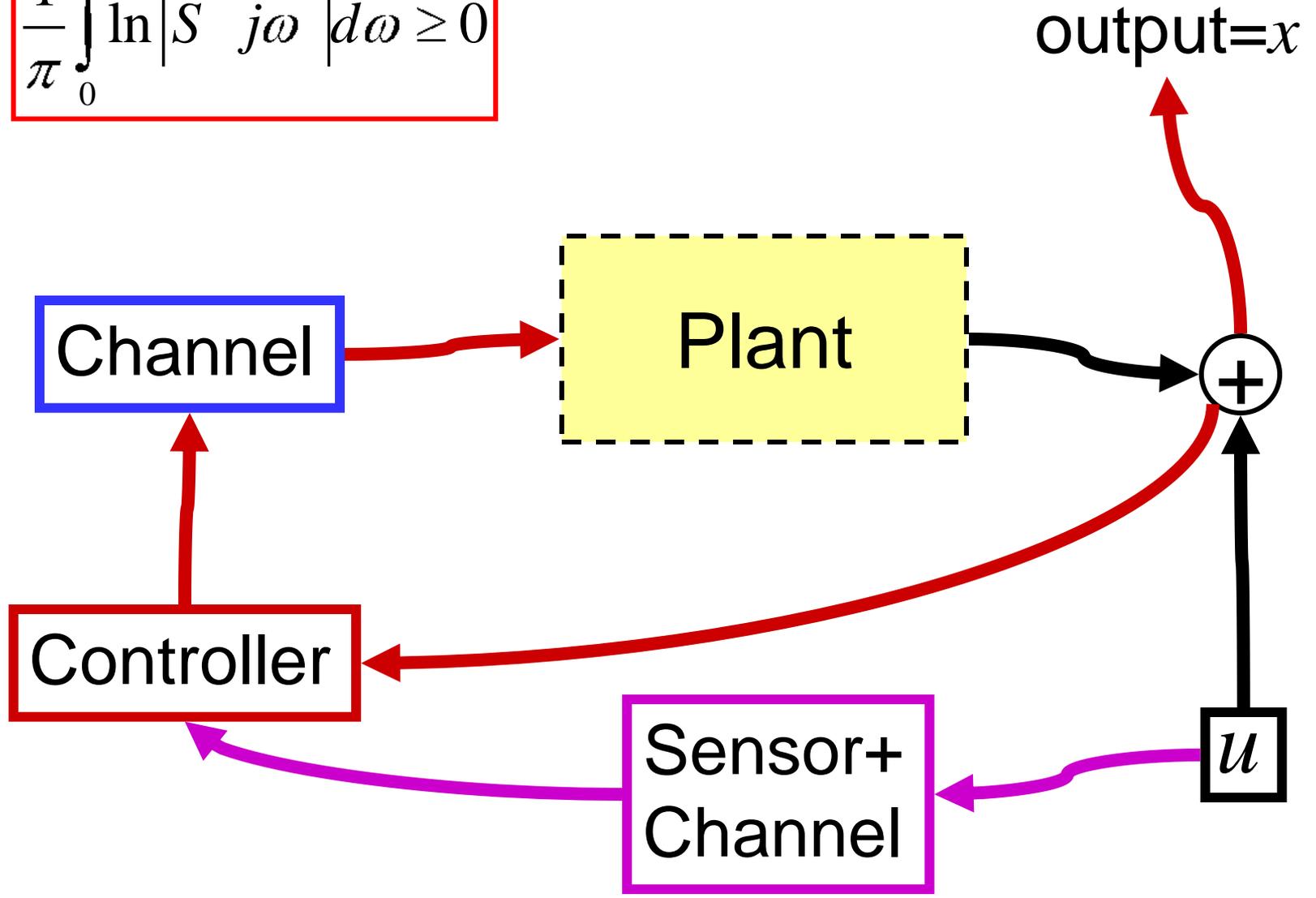
Entropy rates



$$\frac{1}{\pi} \int_0^{\infty} \ln |S(j\omega)| d\omega \geq 0$$



$$\frac{1}{\pi} \int_0^{\infty} \ln |S(j\omega)| d\omega \geq 0$$

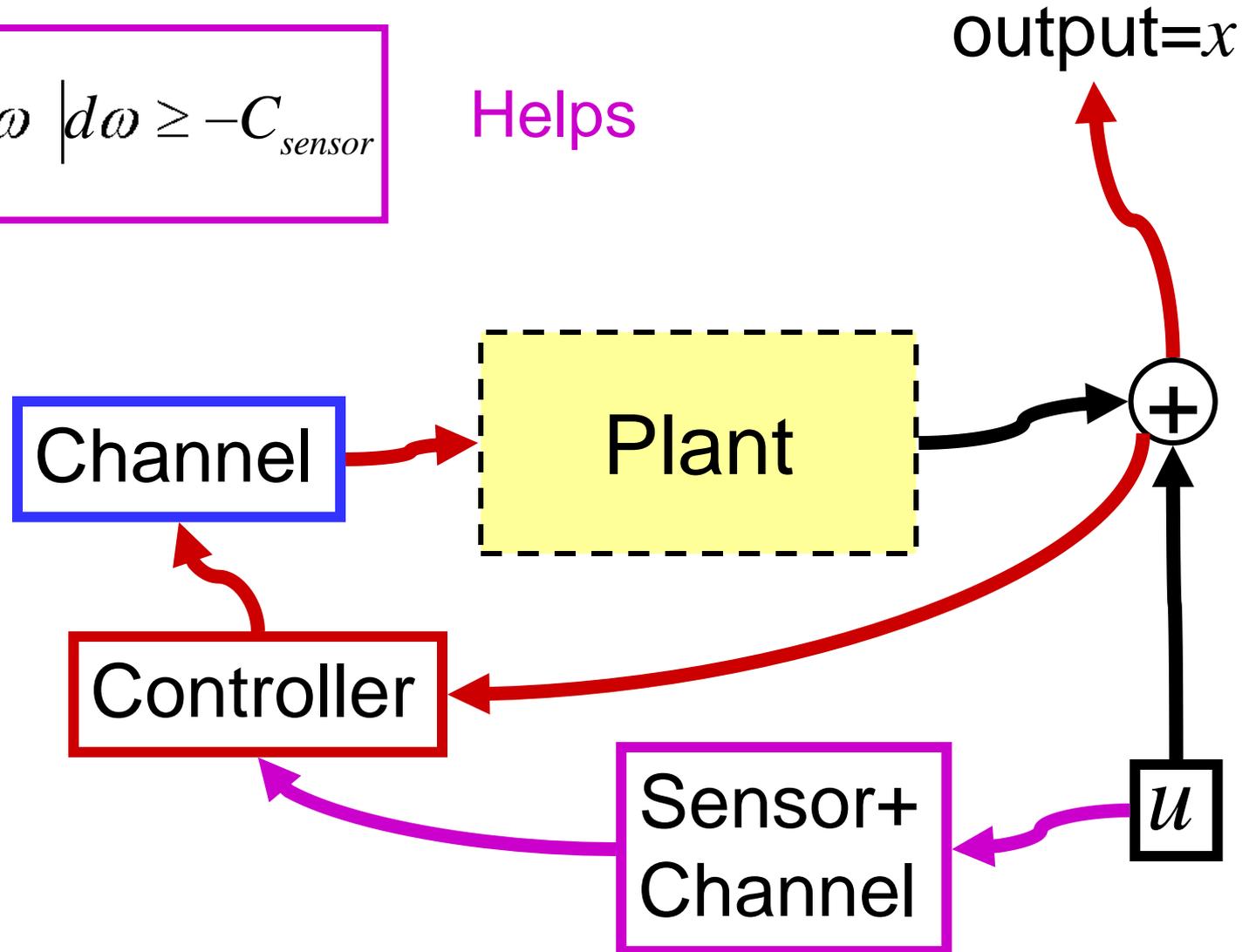


$$\frac{1}{\pi} \int_0^{\infty} \ln |S(j\omega)| d\omega \geq -C_{FB}$$

Hurts

$$\frac{1}{\pi} \int_0^{\infty} \ln |S(j\omega)| d\omega \geq -C_{sensor}$$

Helps



Reactions

Flow/error

Protein level

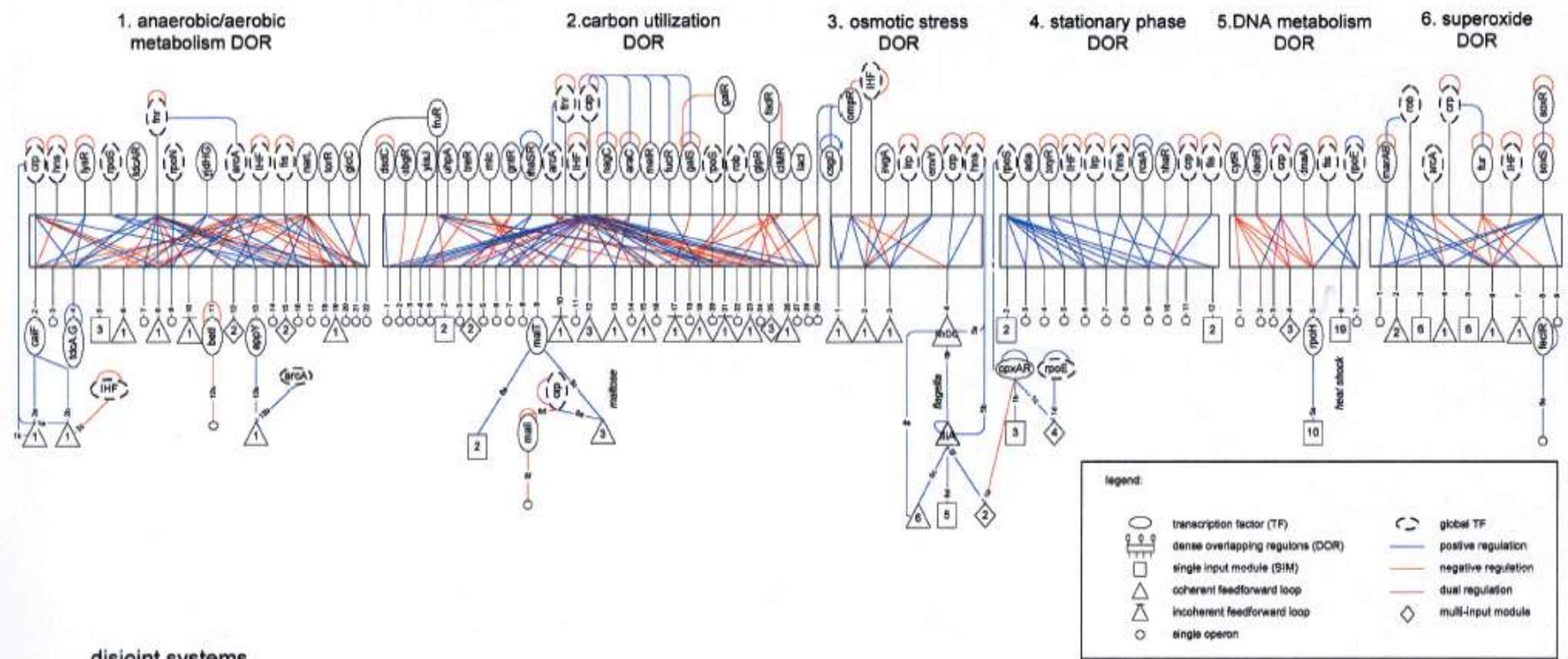
Trans*

Flow/error

*NA level

Network motifs in the transcriptional regulation network of *Escherichia coli*

Shai S. Shen-Orr¹, Ron Milo², Shmoolik Mangan¹ & Uri Alon^{1,2}



disjoint systems

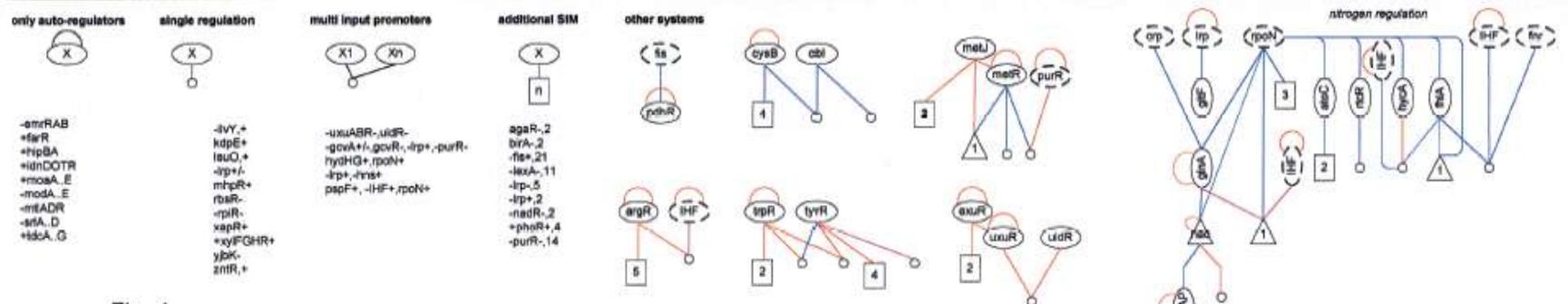
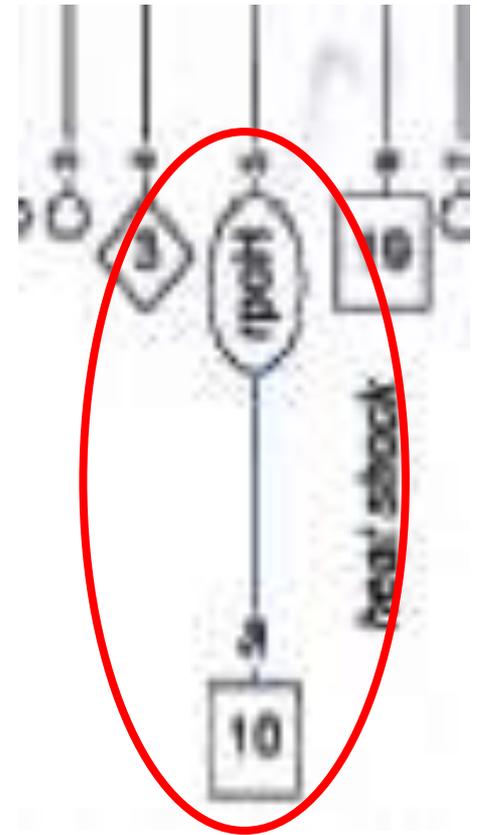
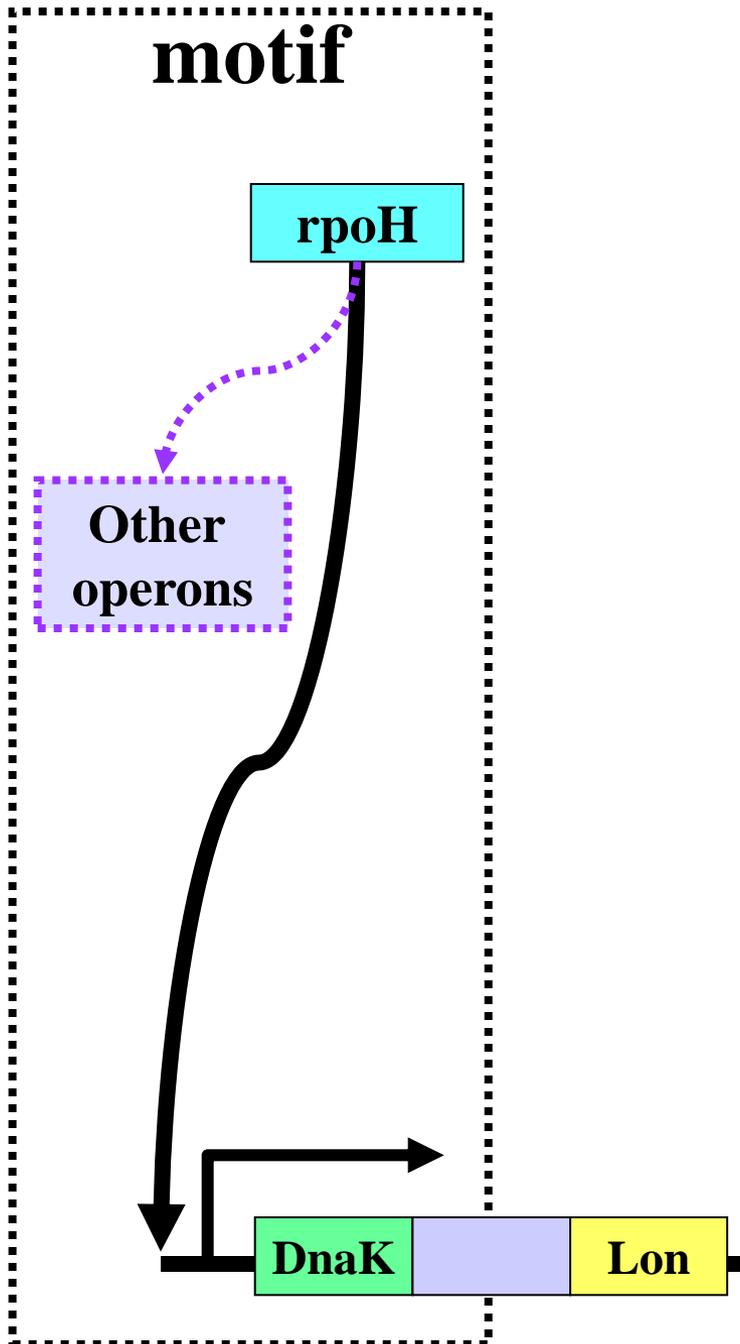


Fig. 4



See El-Samad, Kurata, et al...
PNAS, PLOS CompBio

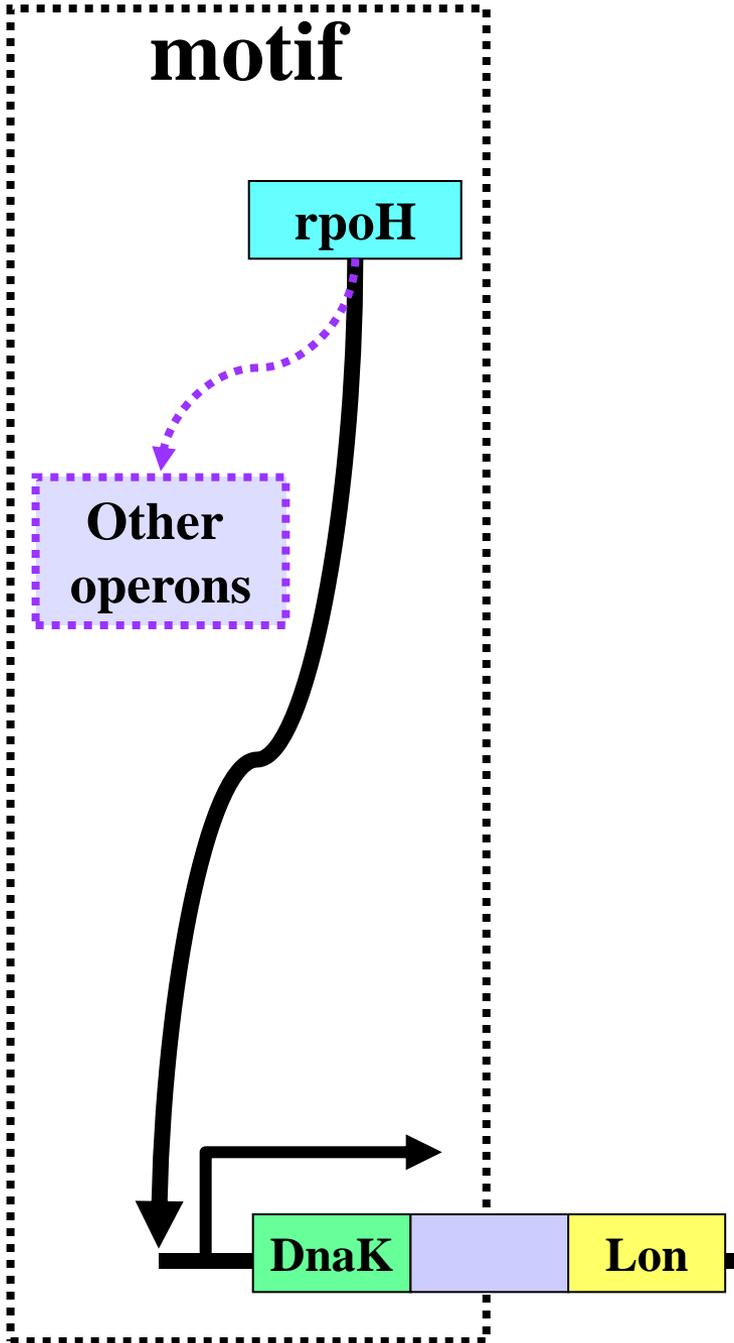
motif

rpoH

**Other
operons**

DnaK

Lon



Where are these layers?

Protein

RNA

DNA

Reactions

Flow/error

Protein level

Translation

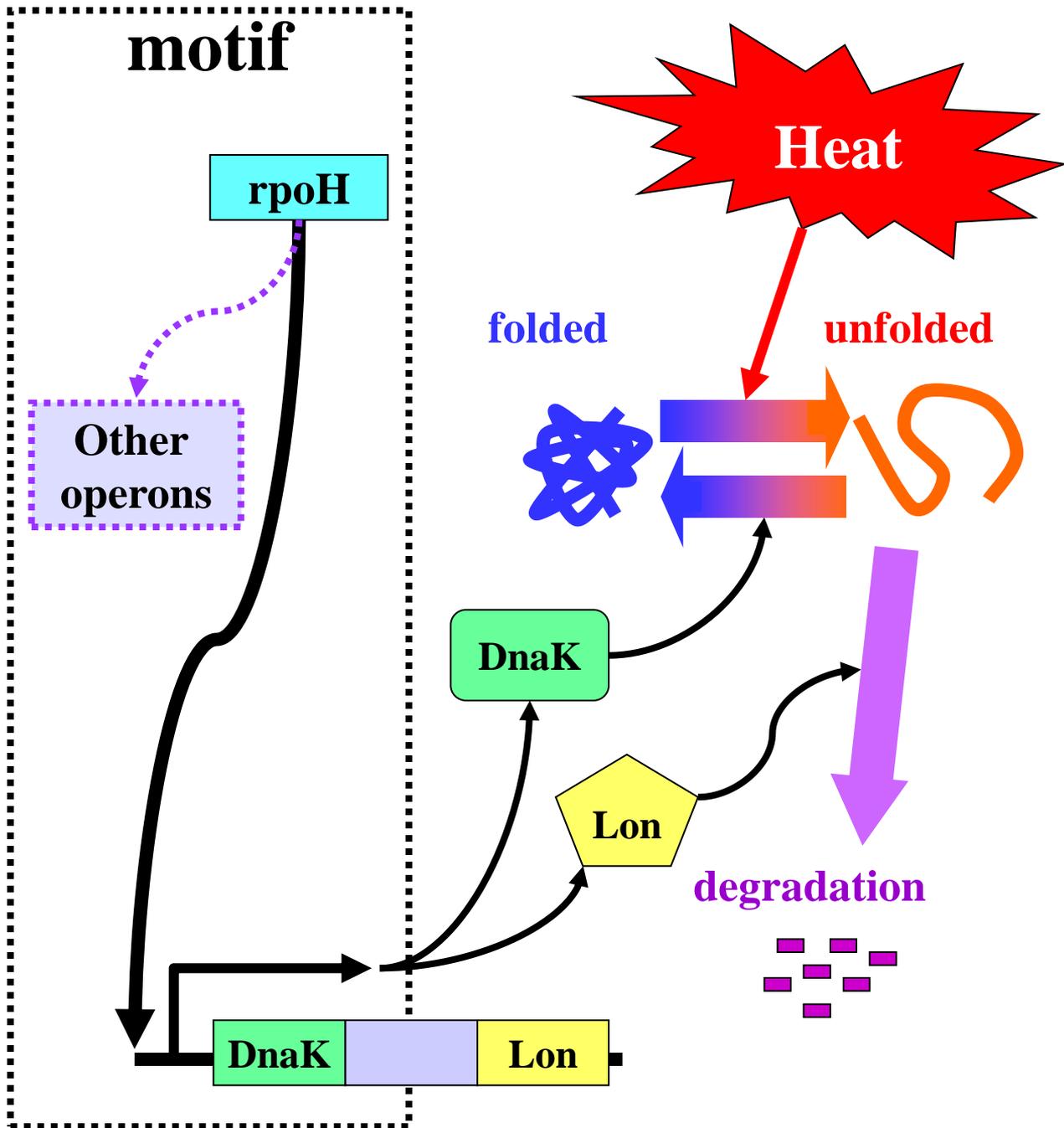
Flow/error

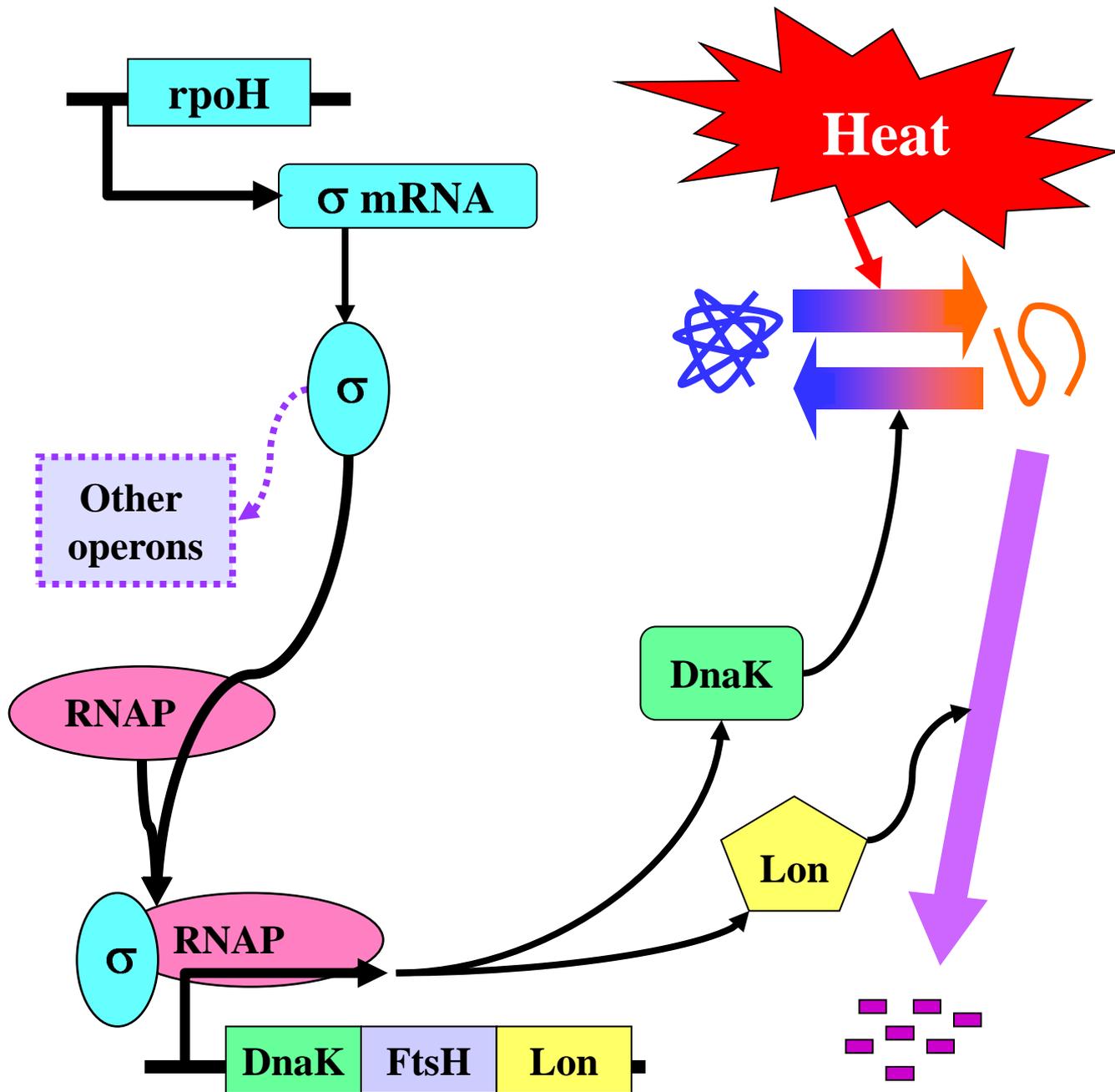
RNA level

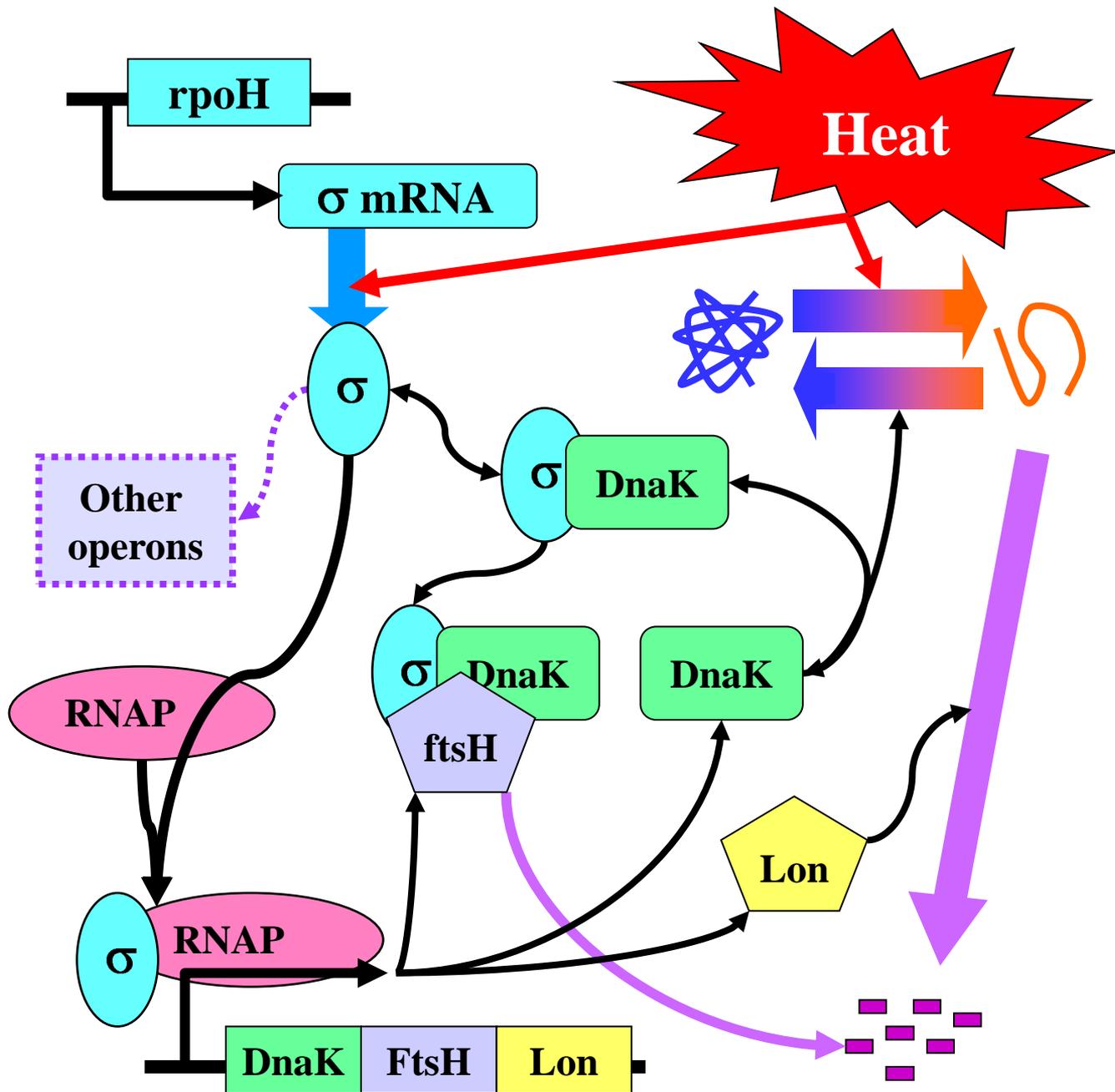
Transcription

Flow/error

DNA level







Where are these layers?

Protein

RNA

DNA

Reactions

Flow/error

Protein level

Translation

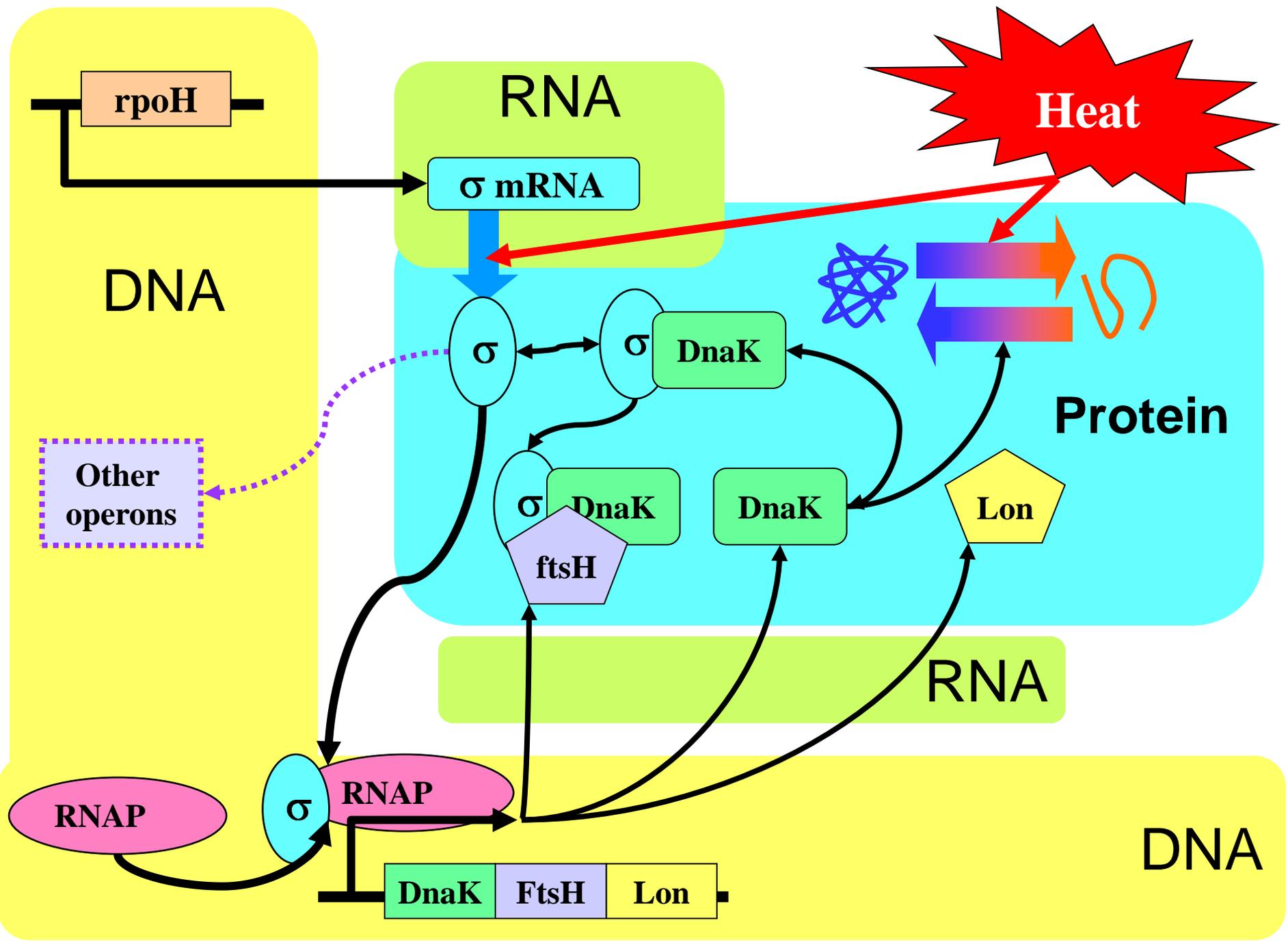
Flow/error

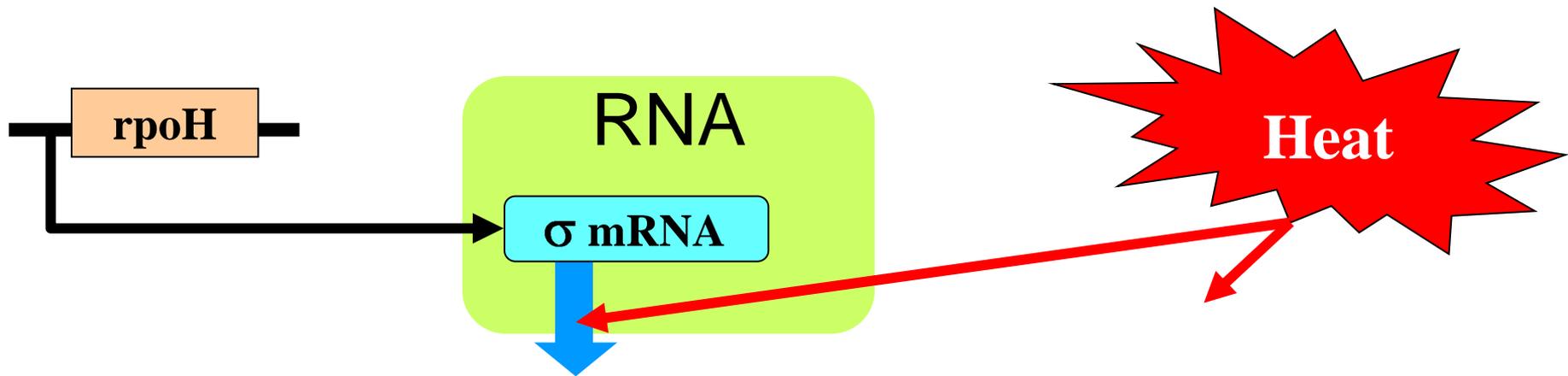
RNA level

Transcription

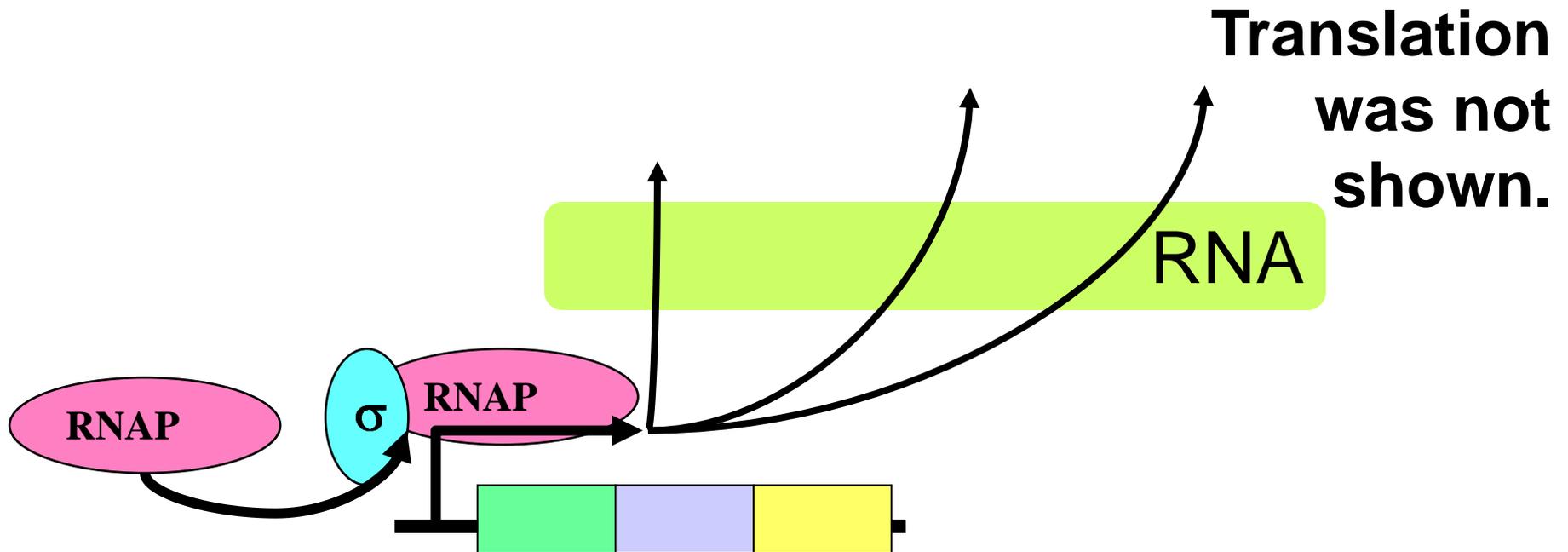
Flow/error

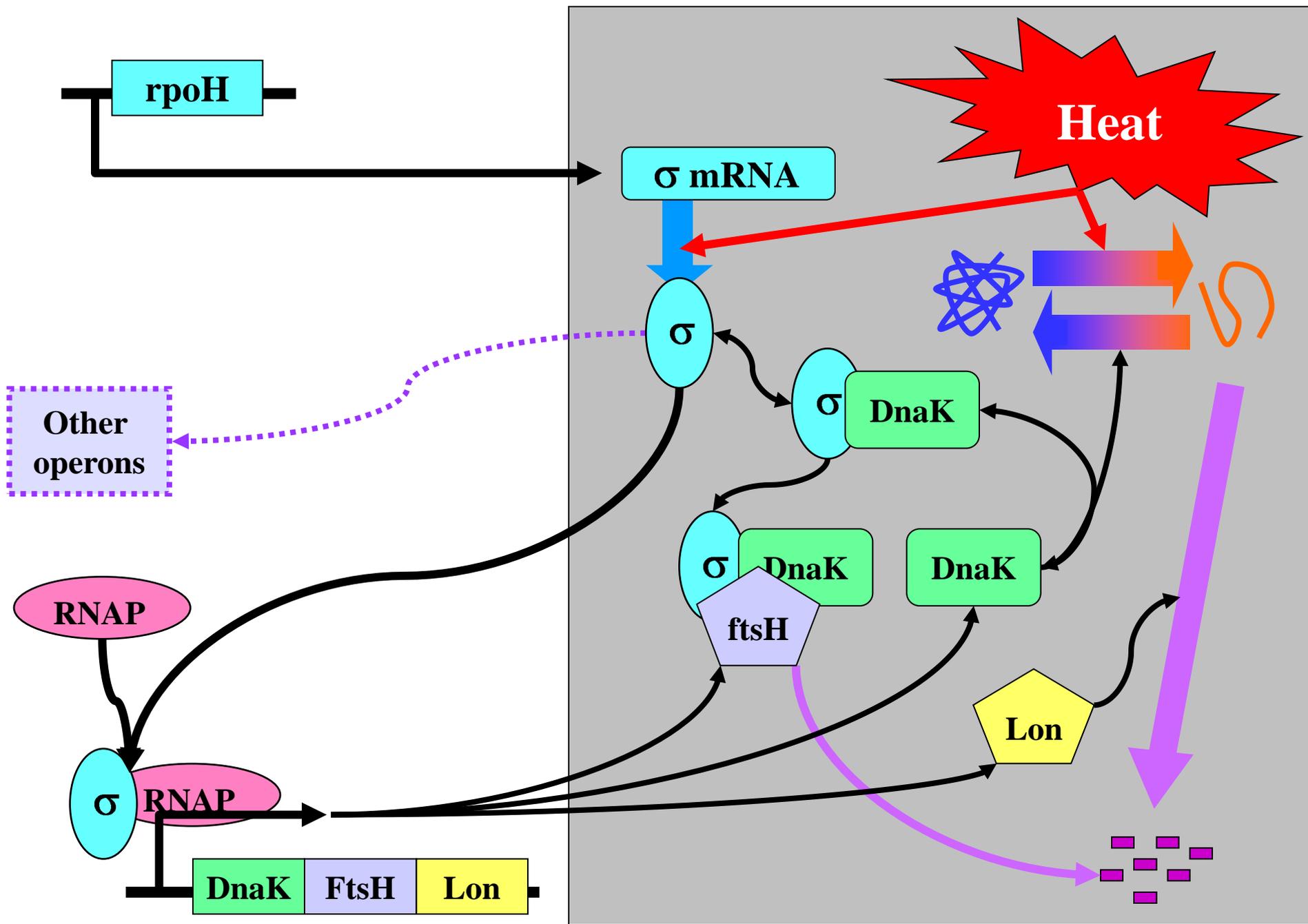
DNA level

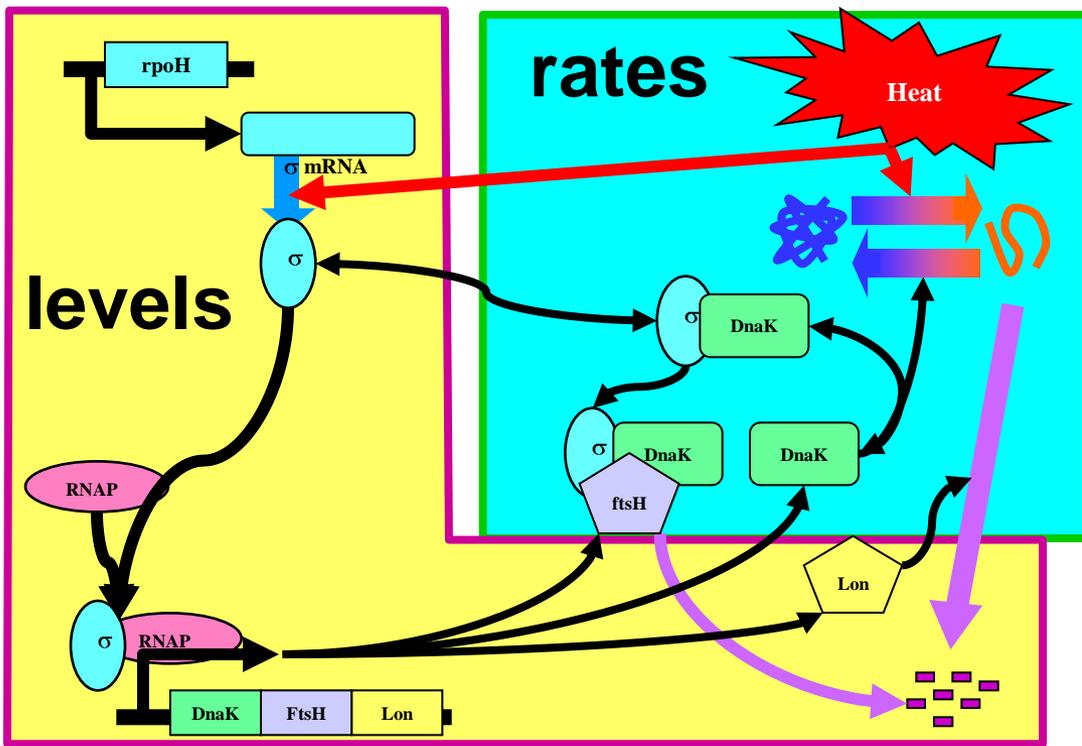




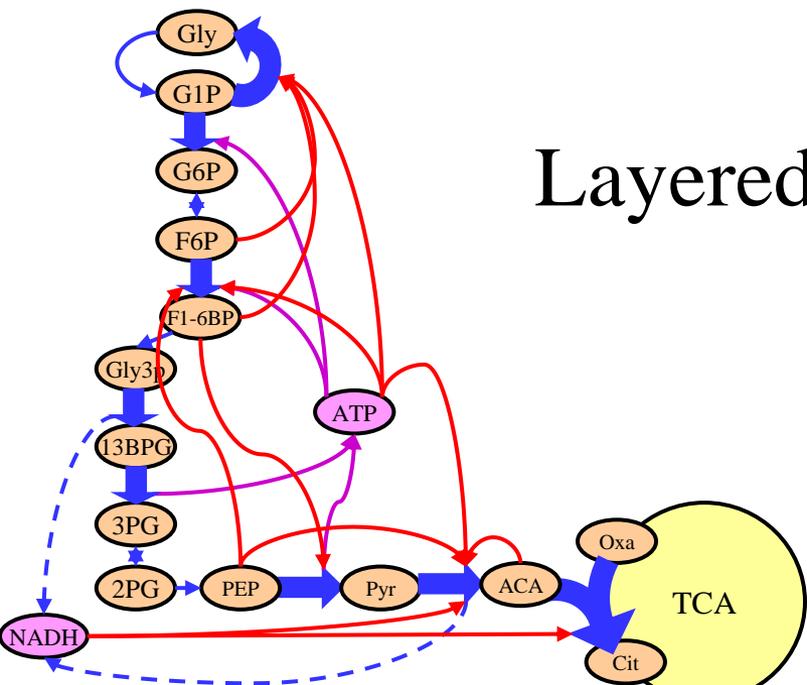
mRNA activity is actively controlled.







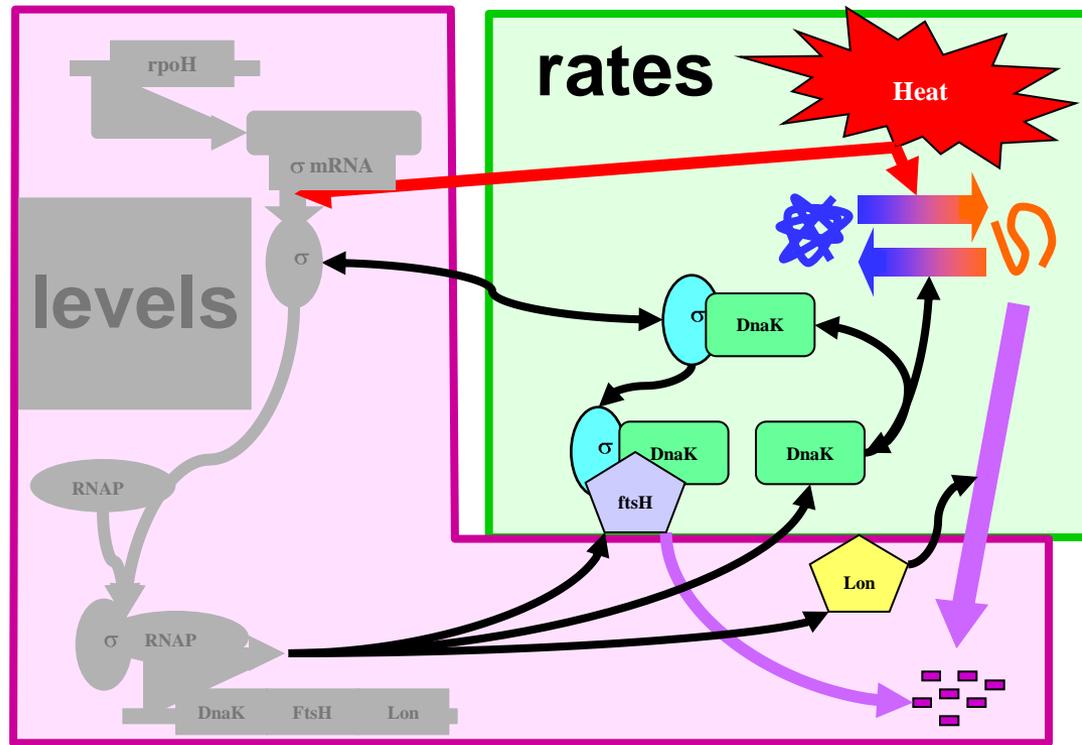
Layered control architectures



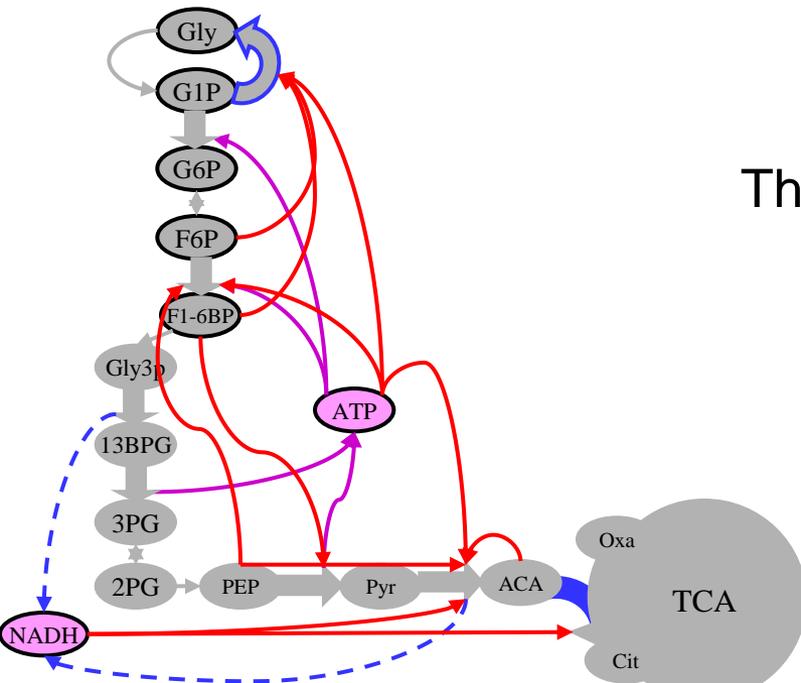
Allosteric

Trans*

The greatest complexity here is primarily in the control of *rates*

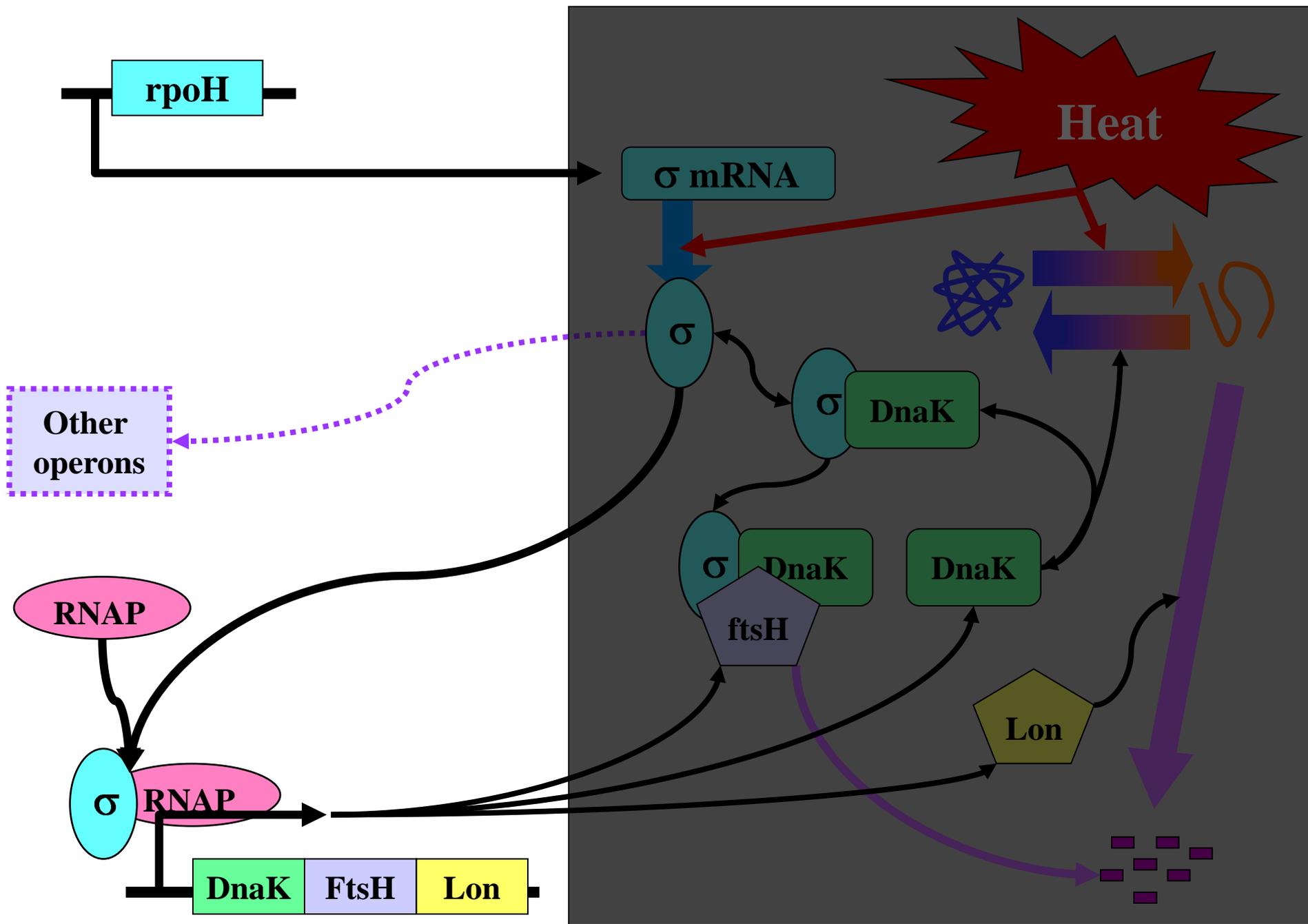


That is not always the case.



Allosteric

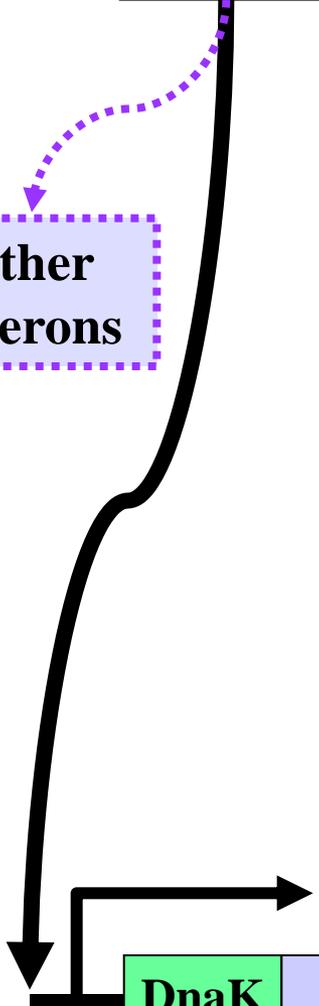
Trans*



motif

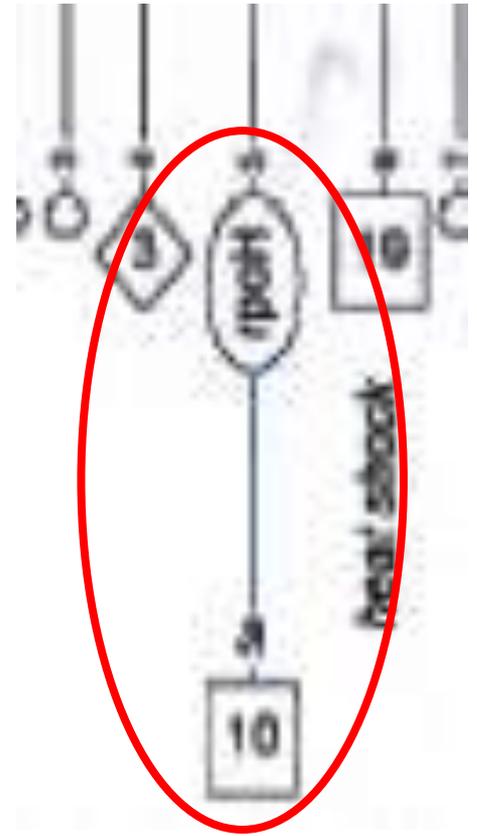
rpoH

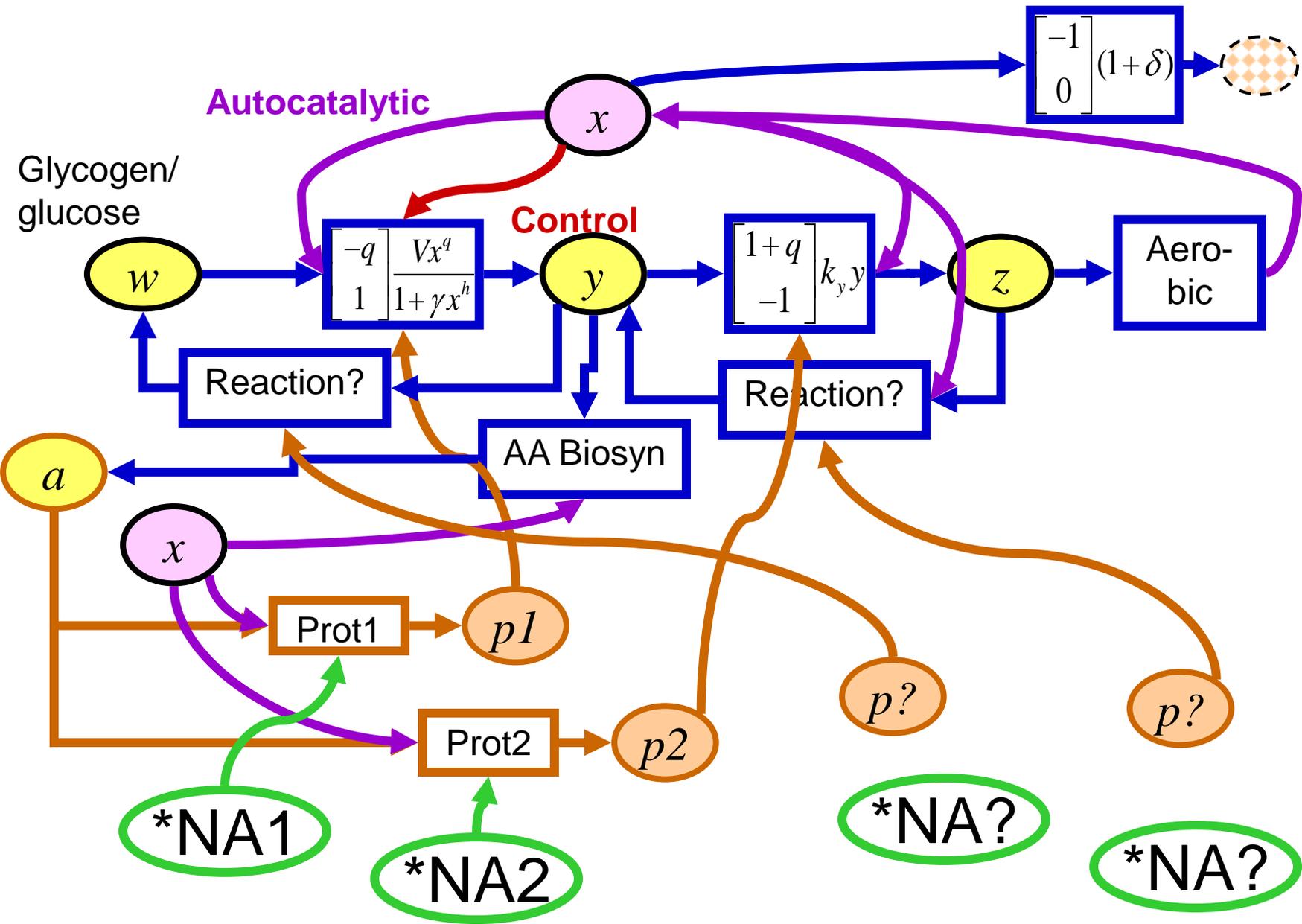
Other operons



DnaK

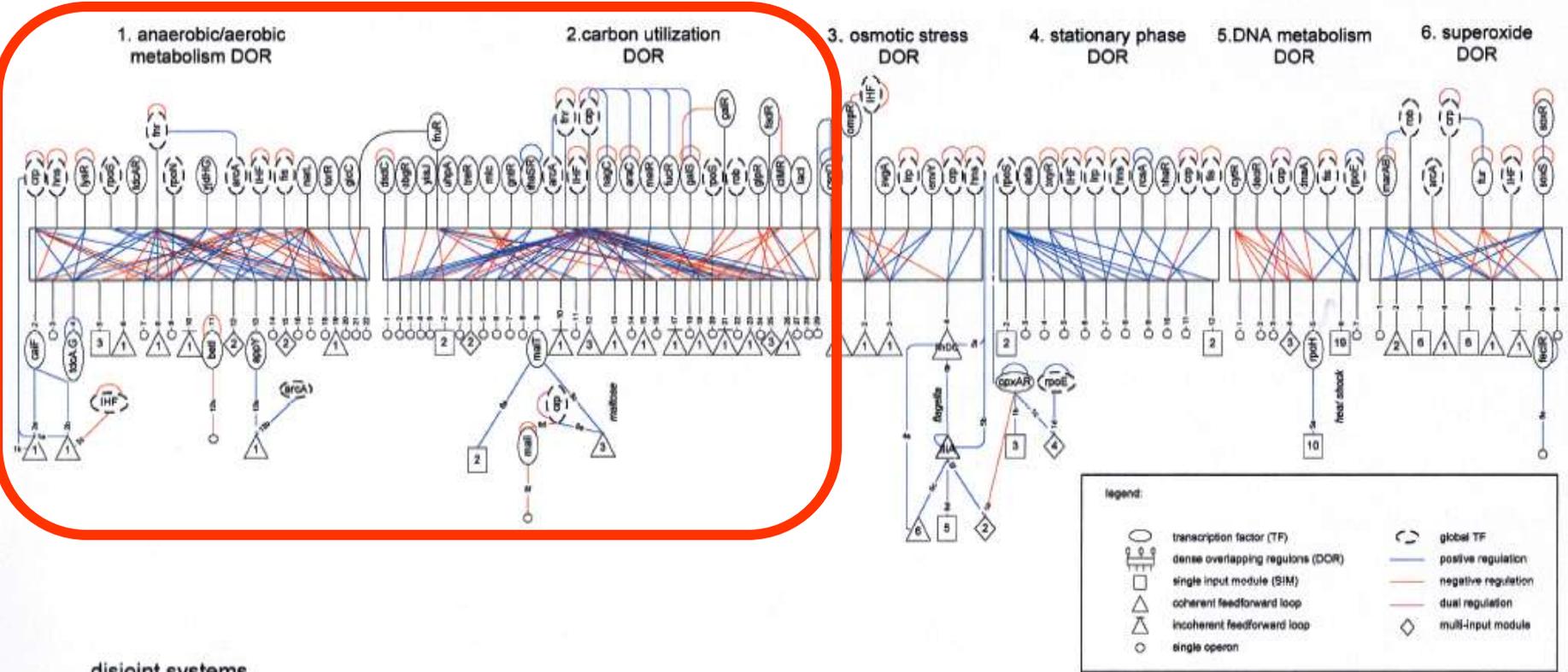
Lon





Network motifs in the transcriptional regulation network of *Escherichia coli*

Shai S. Shen-Orr¹, Ron Milo², Shmoolik Mangan¹ & Uri Alon^{1,2}



disjoint systems

only auto-regulators



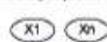
-smrRAB
+hrpR
+hspBA
+hndDTR
+modA_E
-modA_E
-meADR
-sfa_D
+tdcA_G

single regulation



-lvy_+
+kdpE+
+lsuO_+
-ltp+/-
+mhpR+
+rbsR-
-pflR-
+xapR+
+xyfFGHR+
+ybk-
+znrR_+

multi input promoters



-uxuABR_-uidR-
-gcvA+/-gcvR_-ltp+_-purR-
+hydHG+ +rhoN+
-ltp+_-ltns+
+pspF+_-lhf+ +rhoN+

additional SIM



+agaR_-2
+braA_-2
-fleA_-21
-lexA_-11
-ltp_-5
-ltp_-2
+nadR_-2
+phoR+_-4
-purR_-14

other systems



+argR
-lhf



+ltpR
+tyrR



+omrR
+uuuR
+uidR

nitrogen regulation

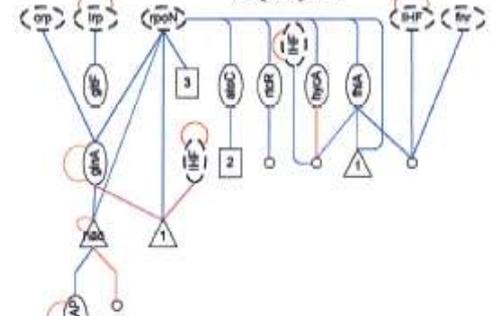
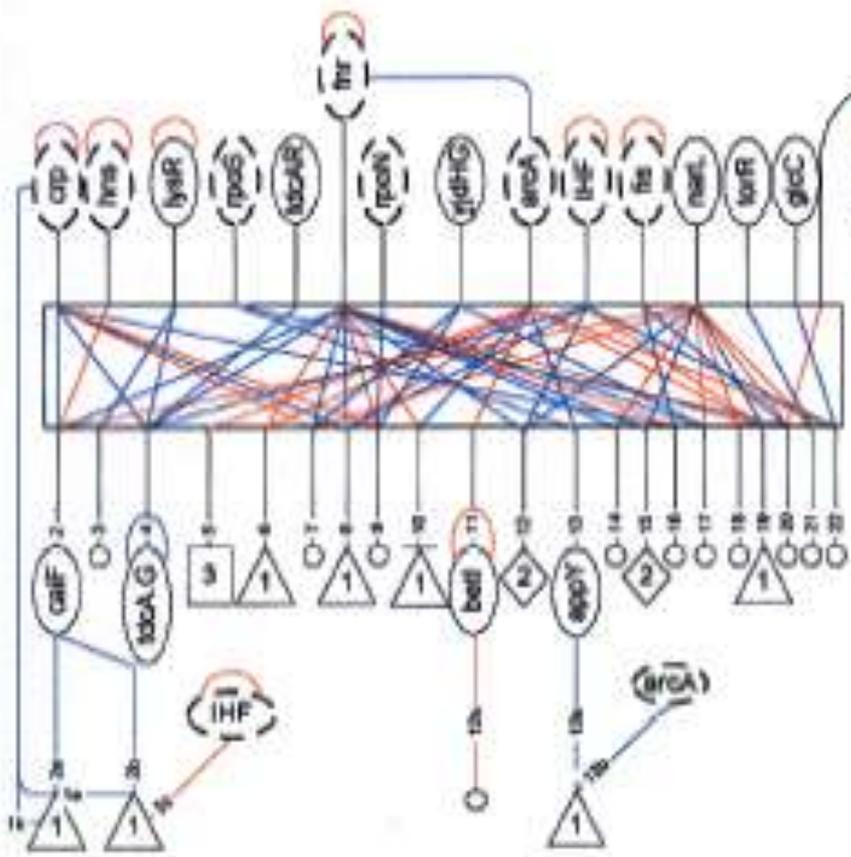
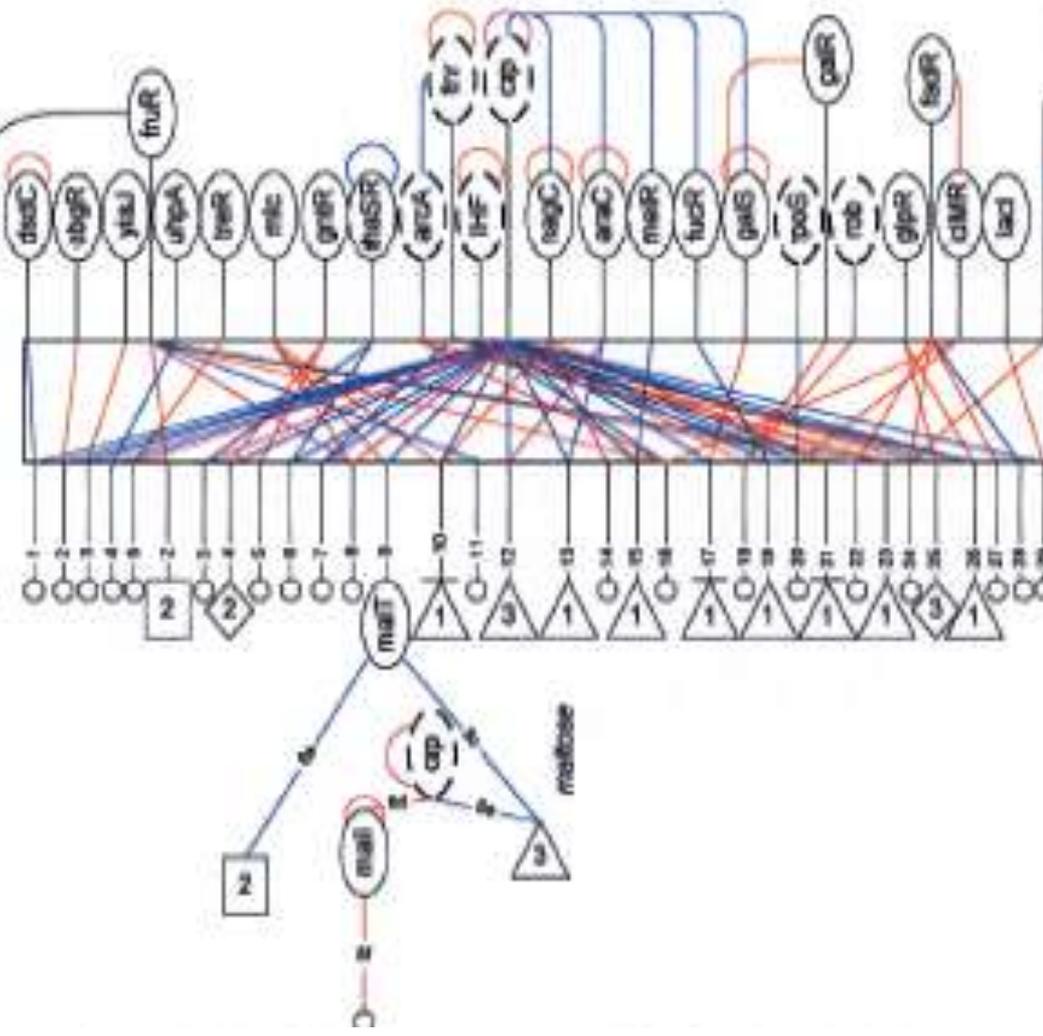


Fig. 4

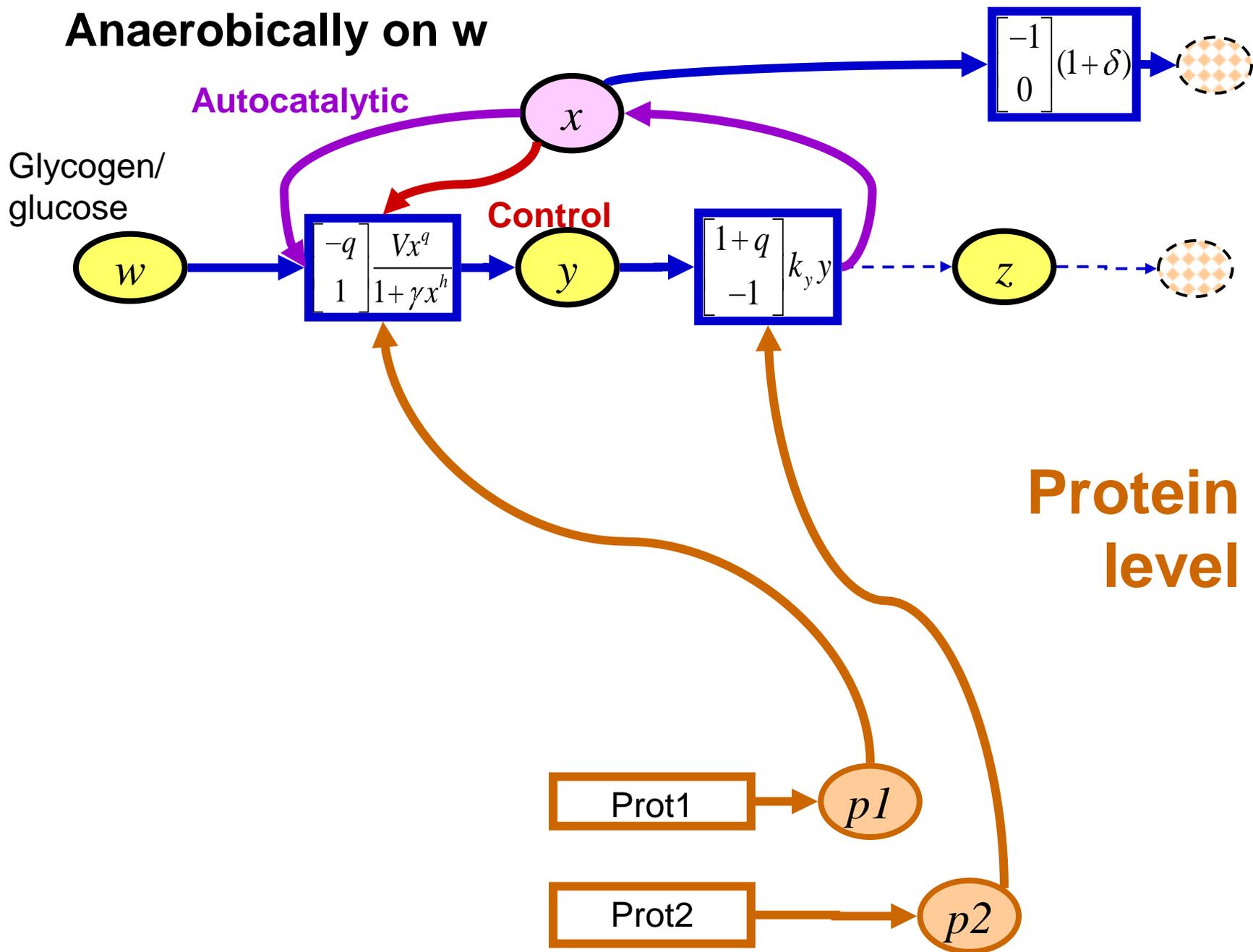
1. anaerobic/aerobic metabolism DOR



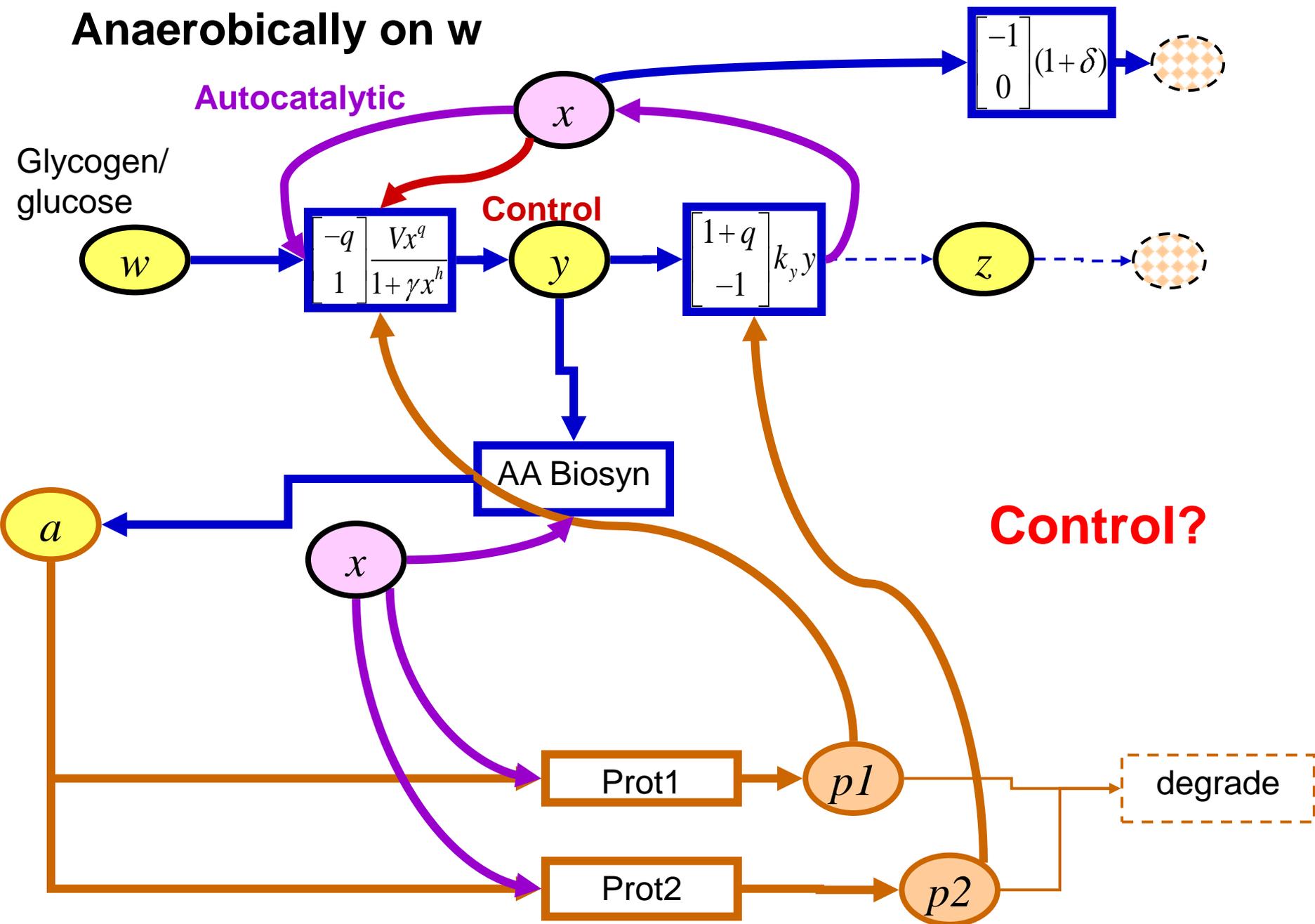
2. carbon utilization DOR

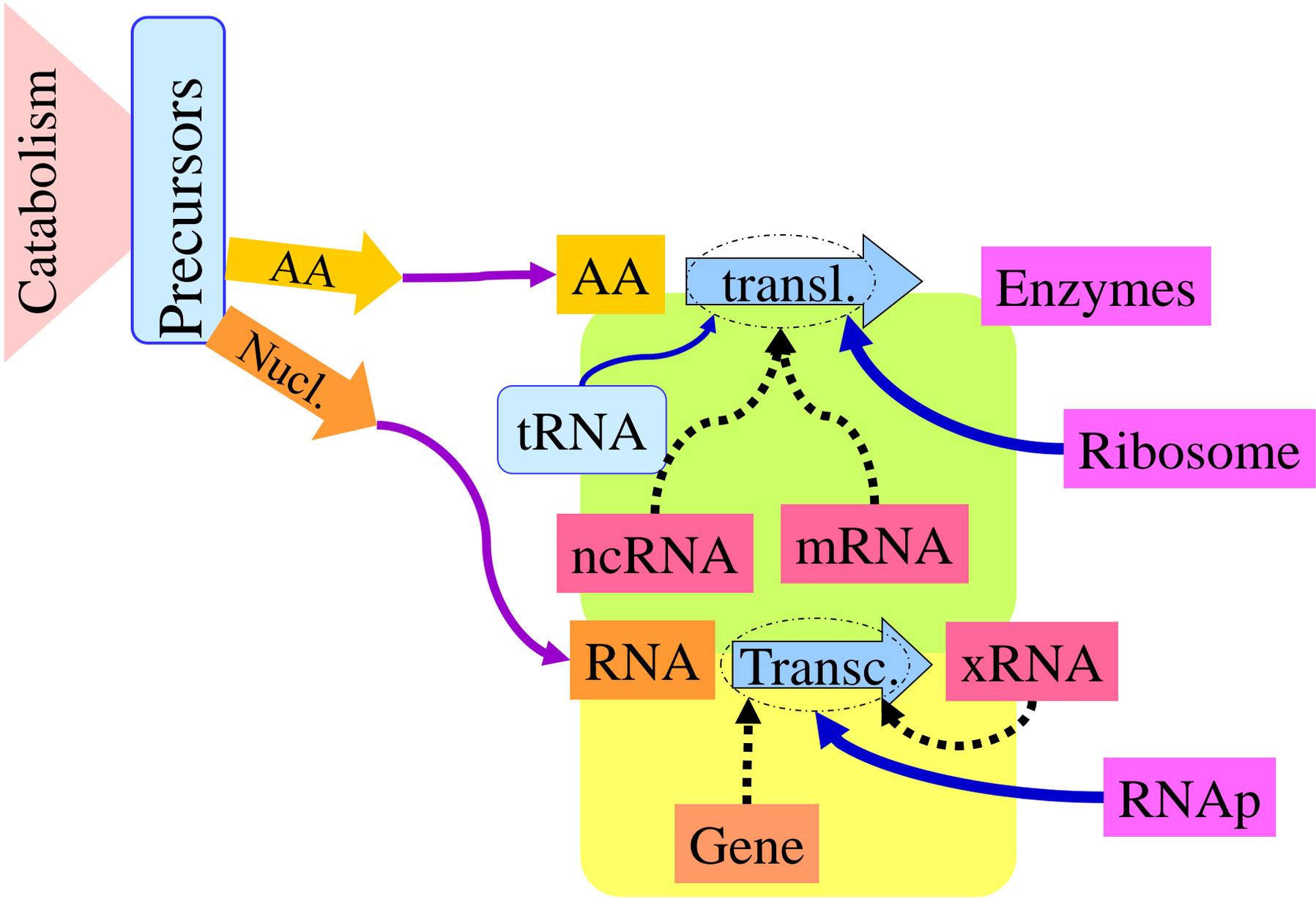


Anaerobically on w

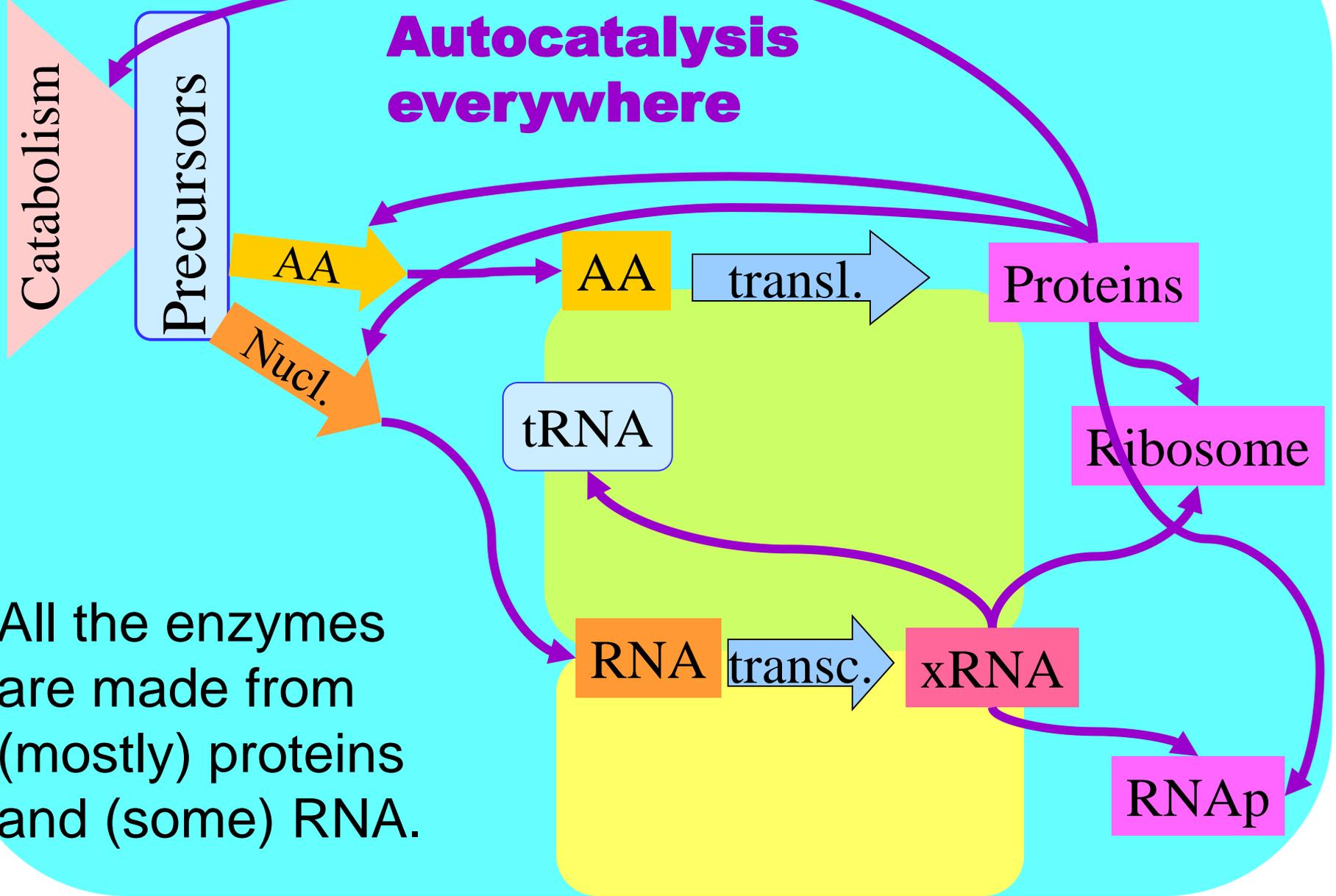


Anaerobically on w





Autocatalysis everywhere

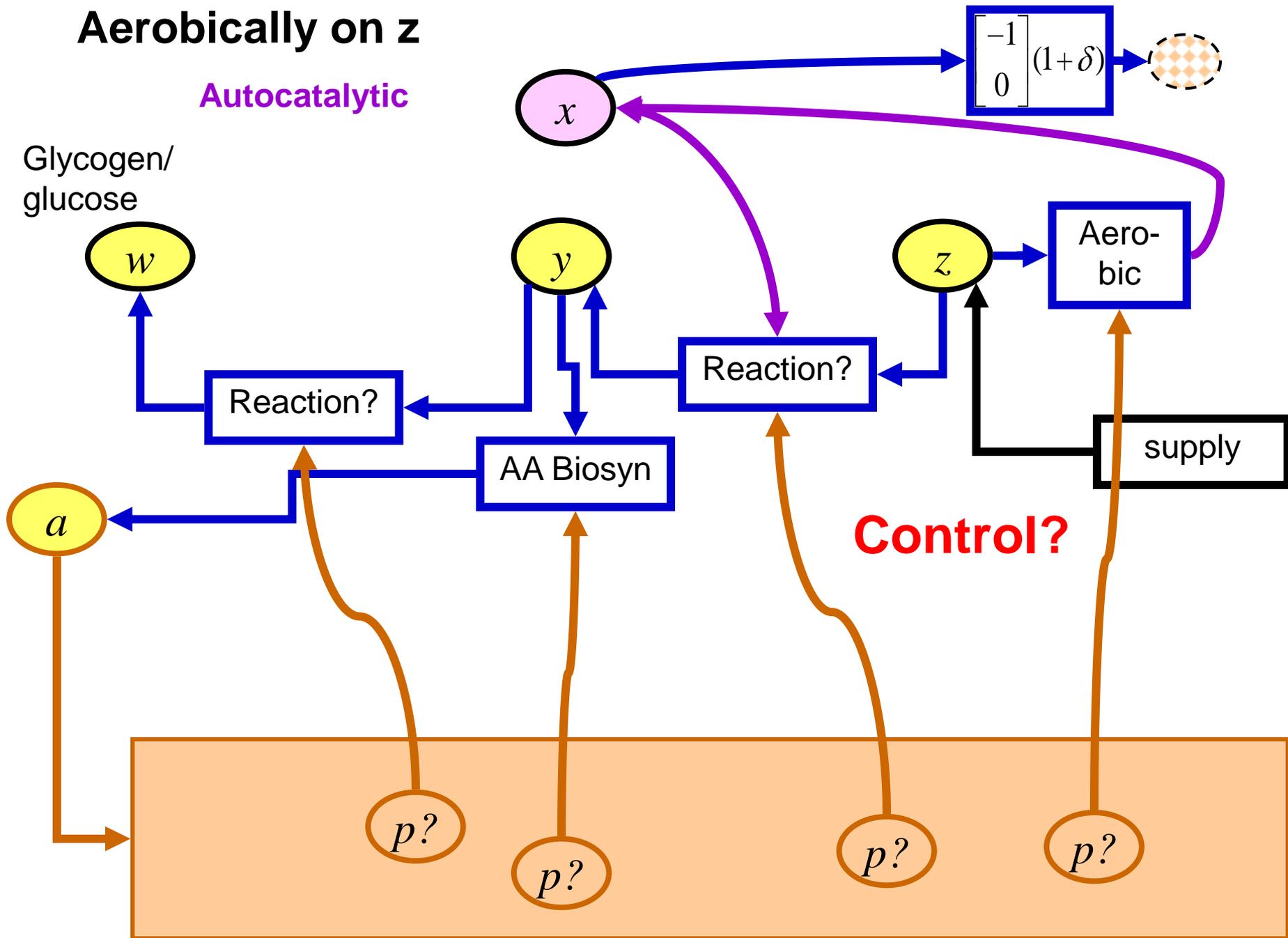


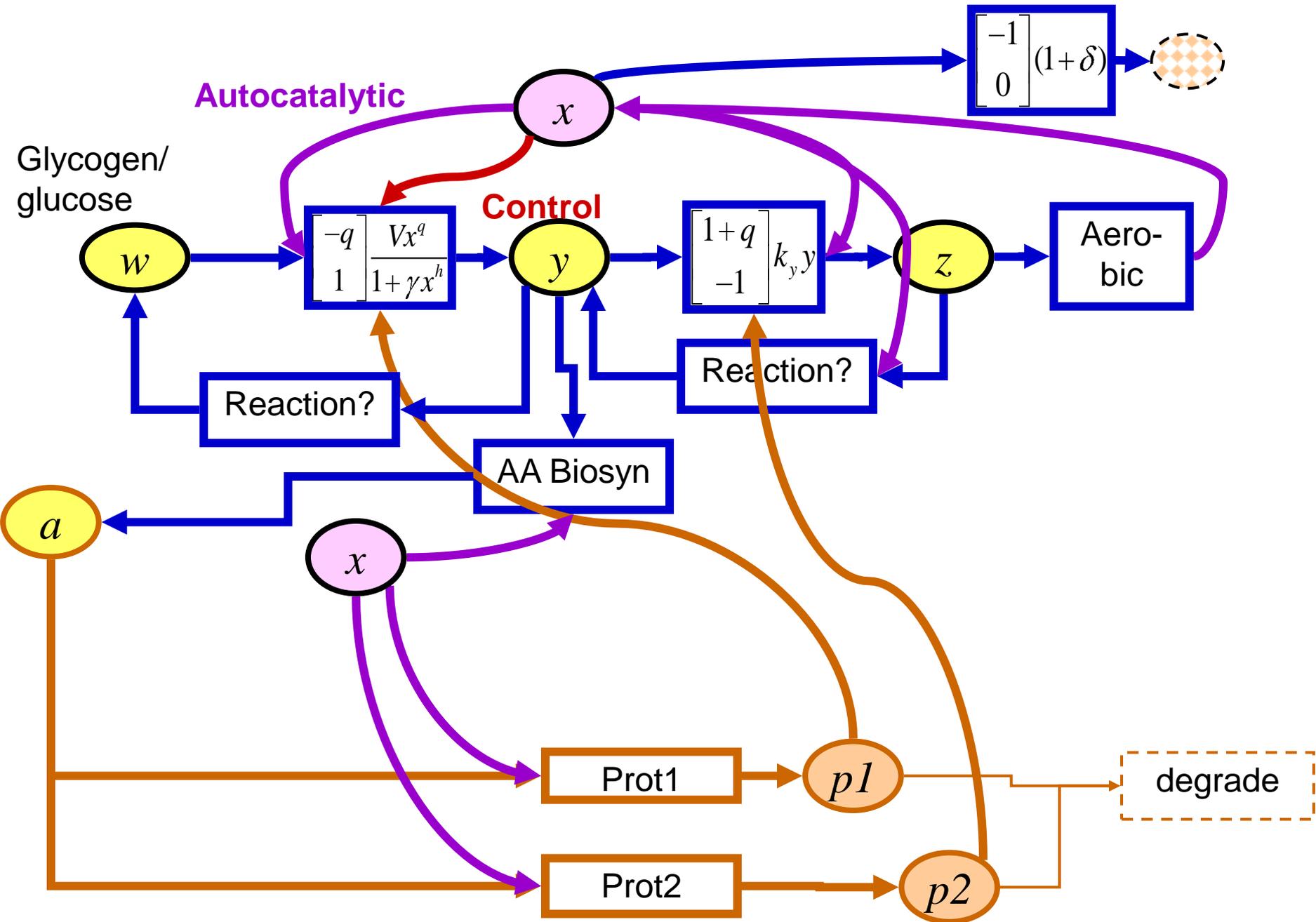
All the enzymes are made from (mostly) proteins and (some) RNA.

Aerobically on z

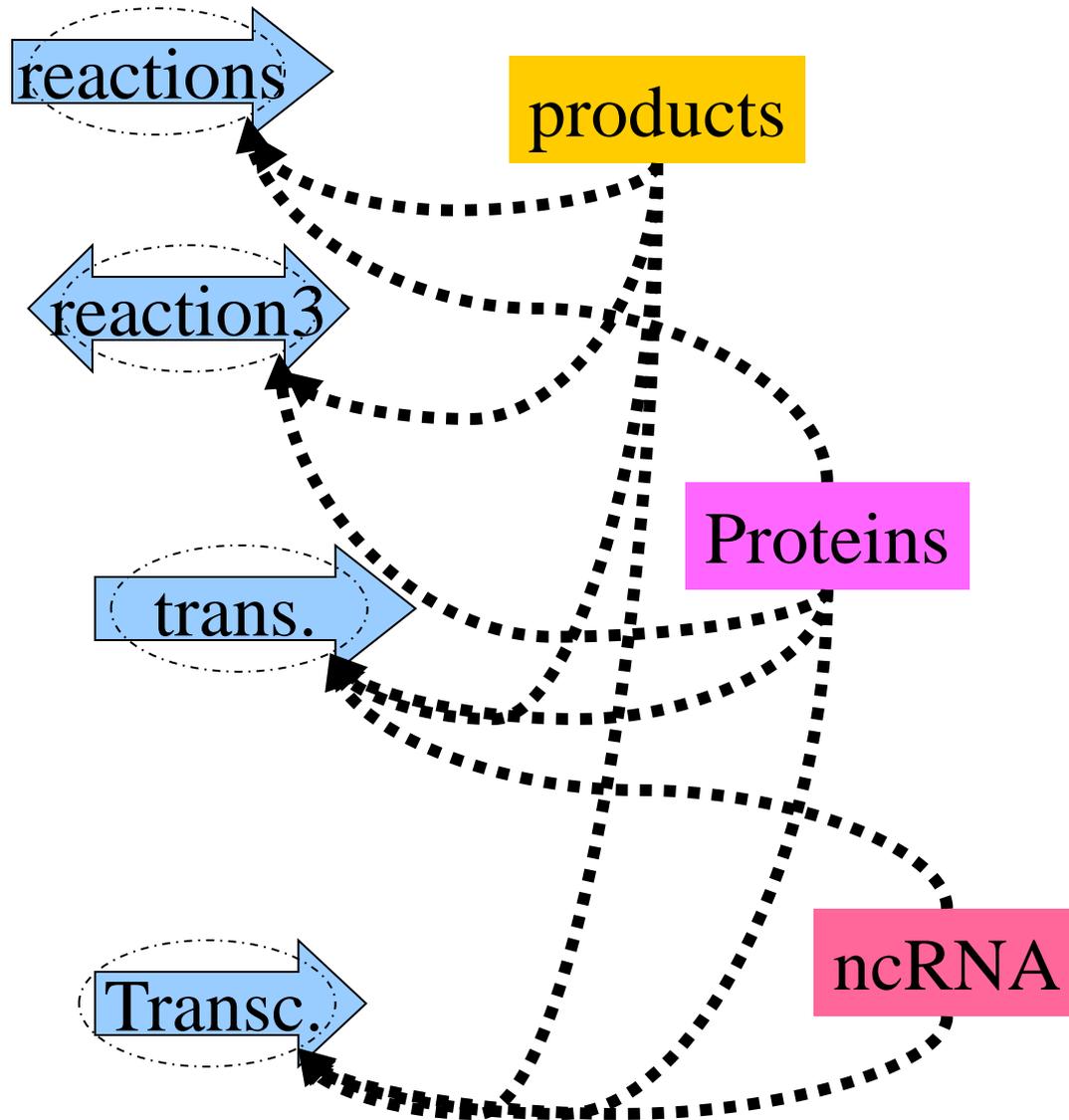
Autocatalytic

Glycogen/
glucose



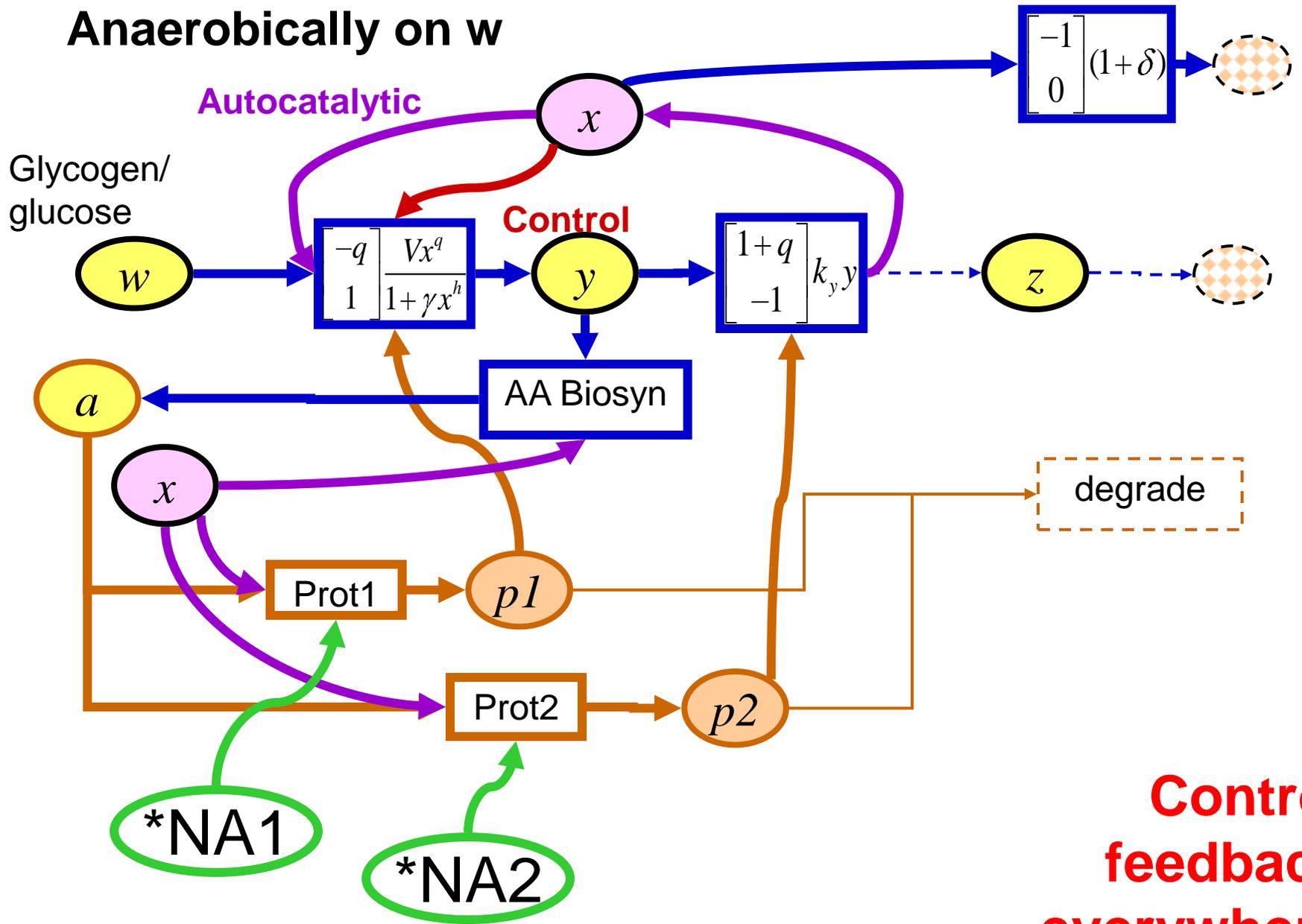


Control?

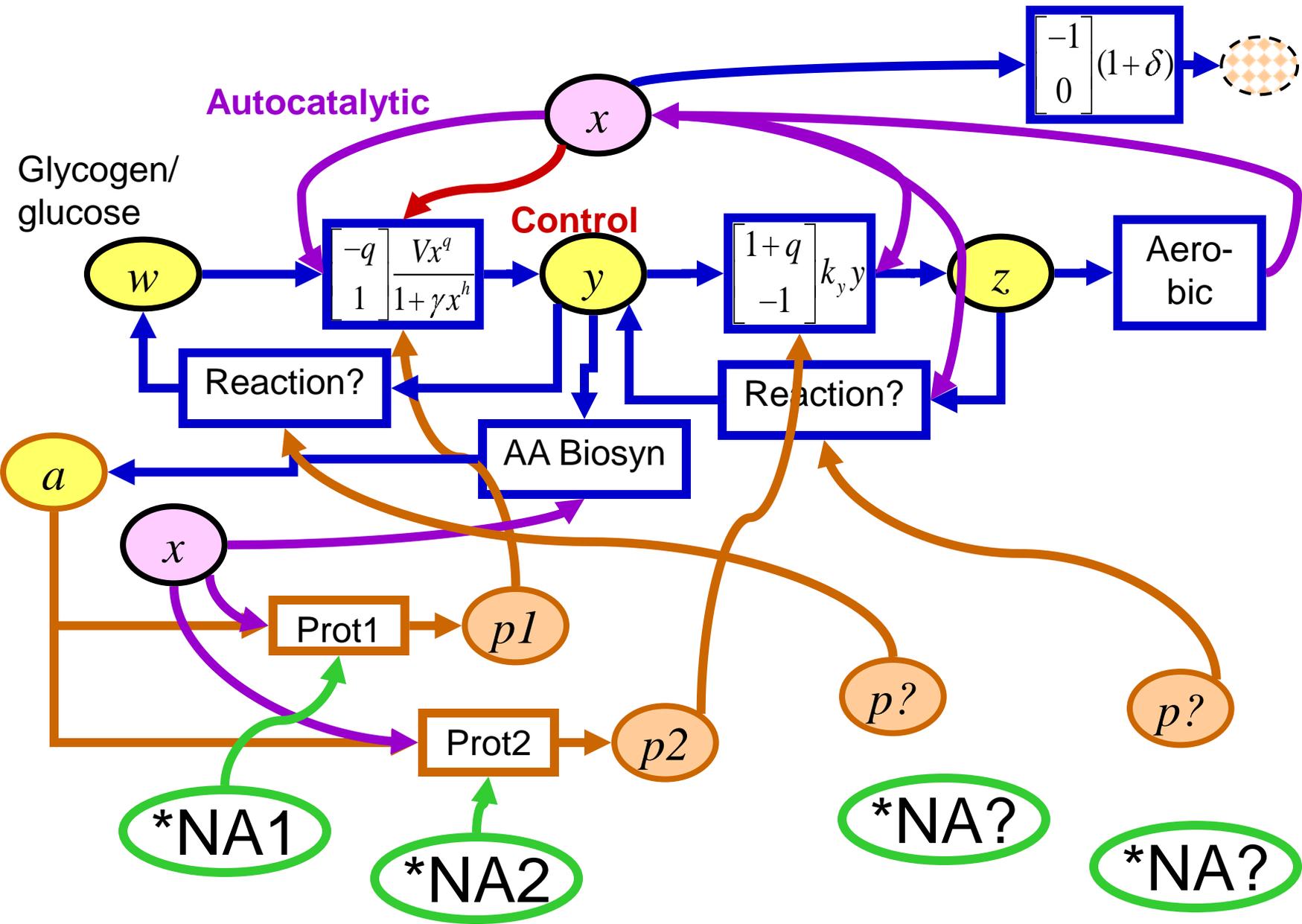


All products
feedback everywhere

Anaerobically on w



**Control
feedback
everywhere**



Anaerobically on w

