

Computing Life: Blue-print modelling and domino approach in design principle studies of Reactive Oxygen Species management

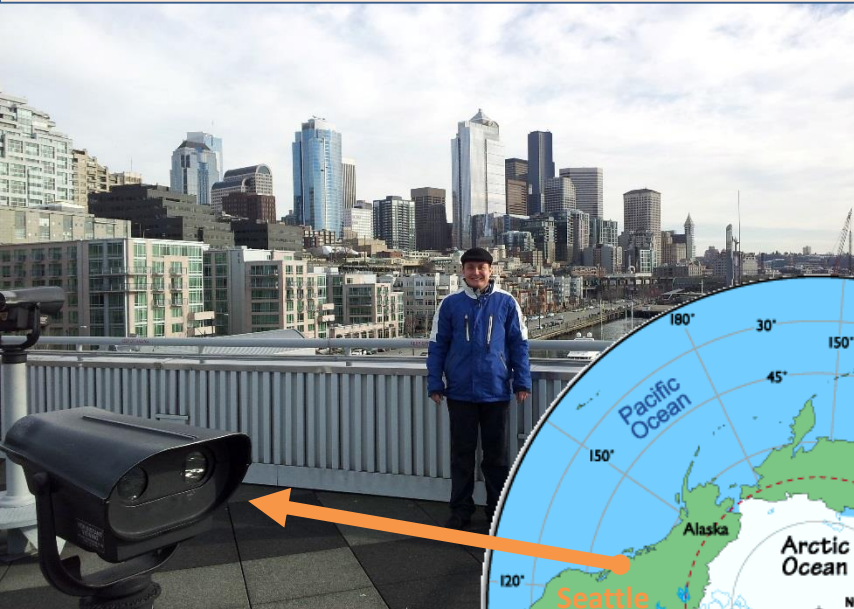
Dr. Alexey Kolodkin

Or:

Designing strategies to visualize Life

Seattle, USA

Knowledge Transfer in Systems Biomedicine



Irkutsk, Russia

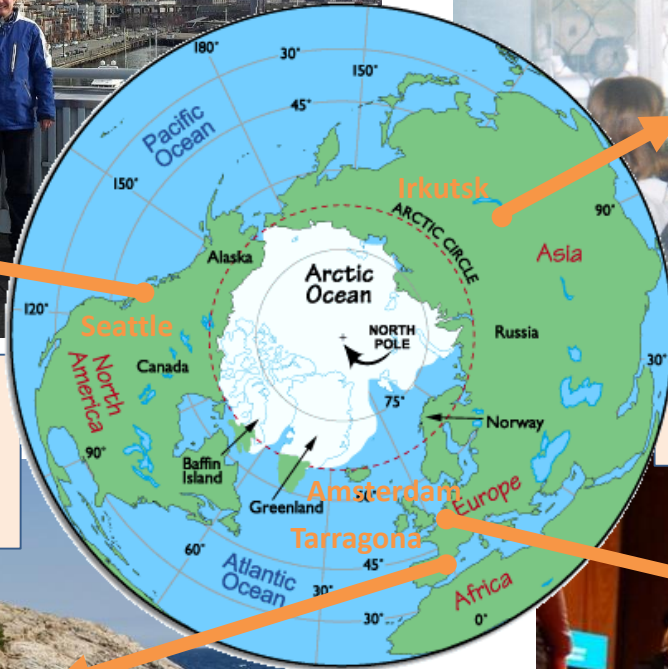
Physiology at Irkutsk State University (Diploma)



Tarragona, Spain
Chemical Engineering
(M.Sc)



Amsterdam, the Netherlands
Systems Biology (M.Sc and Ph.D)



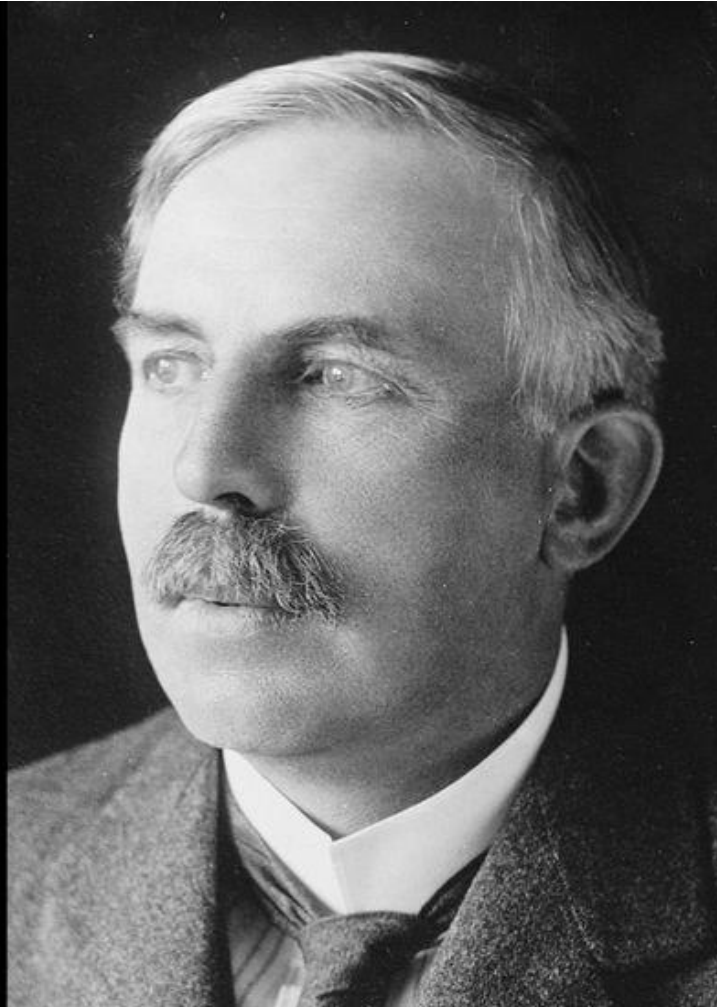
Luxembourg Centre for Systems Biomedicine



“All science is
either physics
or stamp
collecting.”

Ernest Rutherford, *physicist,*
born August 30, 1871

Dobson's Improbable Quote of the Day

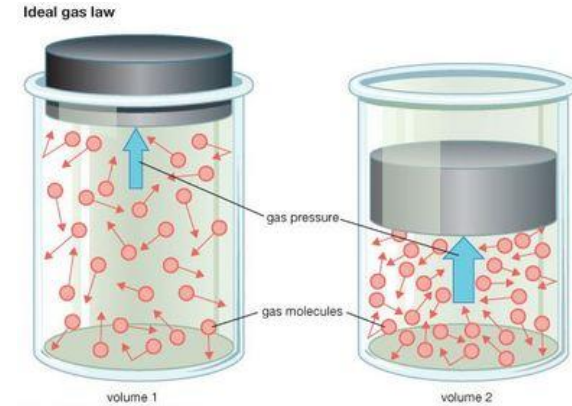


Physics

How emergent properties of system relate to each other:

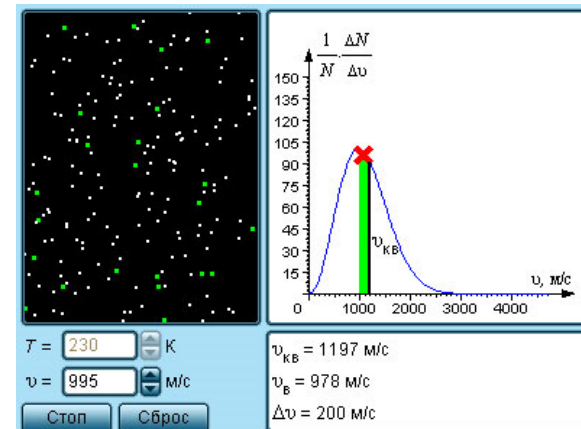
$$PV = nRT$$

Pressure (above P), Temperature (above T), Number of moles (above n), Volume (below V), Gas constant (below R)



How properties of system emerge:

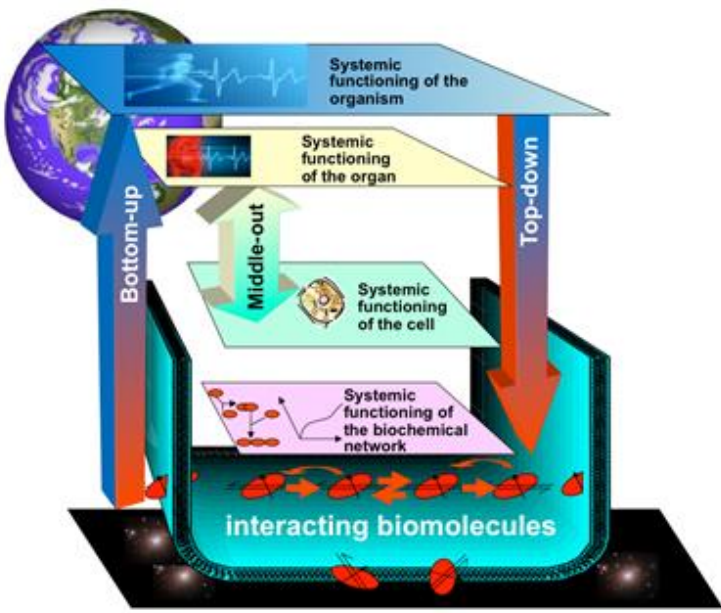
$$E_k = 3/2k*T$$



Stamp collecting



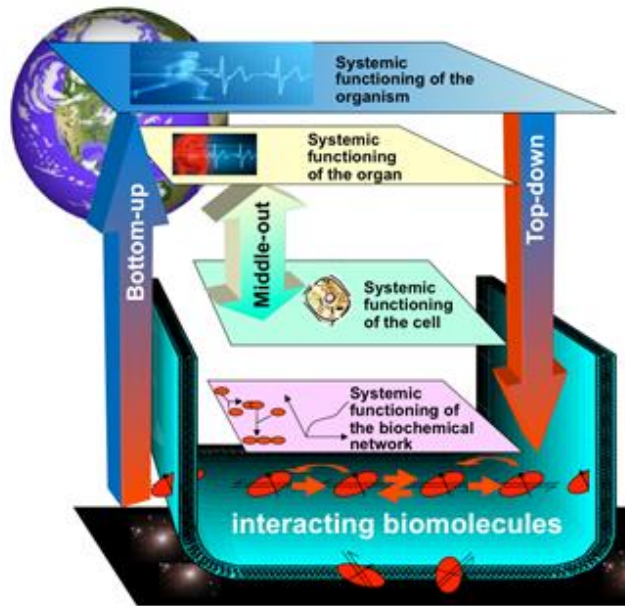
“Stamp collecting” in biology



List of genes associated with 6000 genetic diseases:

Disease	Type of Inheritance	Gene Responsible
Phenylketonuria (PKU)	Autosomal recessive	Phenylalanine hydroxylase (<i>PAH</i>)
Cystic fibrosis	Autosomal recessive	Cystic fibrosis conductance transmembrane regulator (<i>CFTR</i>)
Sickle-cell anemia	Autosomal recessive	Beta hemoglobin (<i>HBB</i>)
Albinism, oculocutaneous, type II	Autosomal recessive	Oculocutaneous albinism II (<i>OCA2</i>)
Huntington's disease	Autosomal dominant	Huntingtin (<i>HTT</i>)
Myotonic dystrophy type 1	Autosomal dominant	Dystrophia myotonica-protein kinase (<i>DMPK</i>)
Hypercholesterolemia, autosomal dominant, type B	Autosomal dominant	Low-density lipoprotein receptor (<i>LDLR</i>); apolipoprotein B (<i>APOB</i>)
Neurofibromatosis, type 1	Autosomal dominant	Neurofibromin 1 (<i>NF1</i>)

“Physics” in Biology



Modularities

$$\mathcal{Q}(X, \mathbf{c}) = \frac{1}{2m} \sum_{\substack{\{i,j\} \\ i \neq j}} \left(X_{i,j} - \frac{k_i k_j}{2m} \right) \delta_{\mathbf{c}_i, \mathbf{c}_j}$$

$$\mathcal{Q}^M((X^{(g)})_g, \mathbf{c}) = \sum_g \mathcal{Q}(X^{(g)}, \mathbf{c})$$

$$= \sum_g \frac{1}{2m^g} \sum_{\substack{\{i,j\} \\ i \neq j}} \left(X_{i,j}^{(g)} - \frac{k_i^g k_j^g}{2m^g} \right) \delta_{\mathbf{c}_i, \mathbf{c}_j}$$

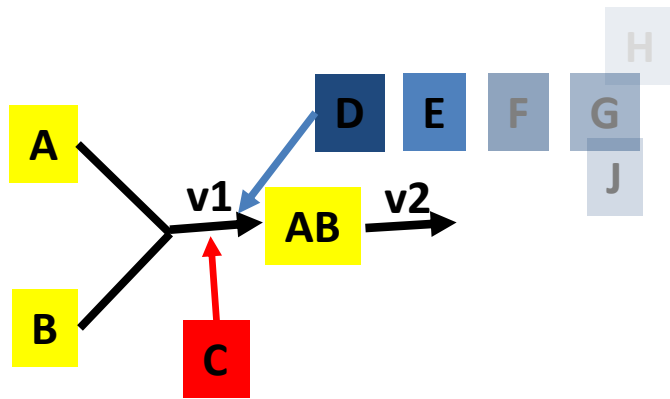
System of many equations, or, perhaps, one very complex equation?

picture by Jacky Snoep

Problems in computing the Life

High state-dependency of component properties E.g. interactions between proteins A and B depends on

- Other components (C,D,E,F...)
- Hysteresis
- Flow of mass and energy through the system
- Initial and boundary conditions, etc.



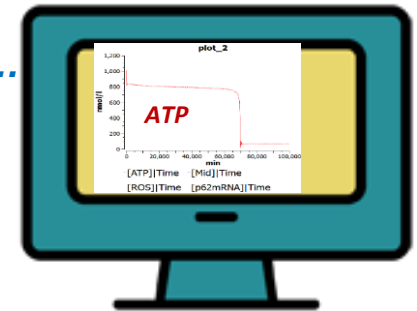
Solution through the systems biological approach:

Protein A + Protein B = Complex AB

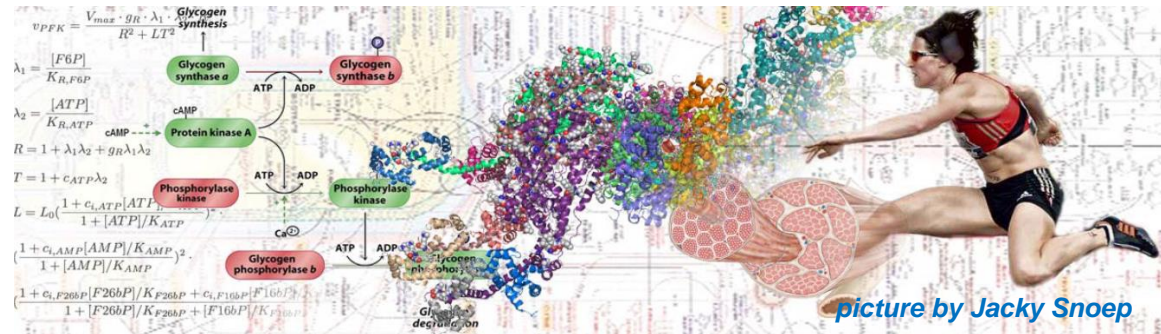
$$v1 = k_f[A][B][C] - k_b[AB]$$

$$v2 = \dots$$

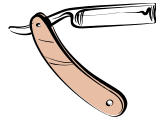
$$d[AB]/dt = v1 - v2 \dots$$



Systems Biology – reconstruction of biological emergence *in silico*



picture by Jacky Snoep



Occam's razor

William of Occam (1285-1349):

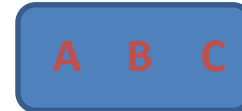
“One should not postulate (pose) more things without necessity” (*Pluralitas non est ponenda sine necessitate*)

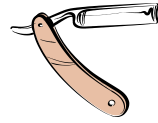
Which model is more likely to be correct?

more complicated model



simpler model





Occam's razor

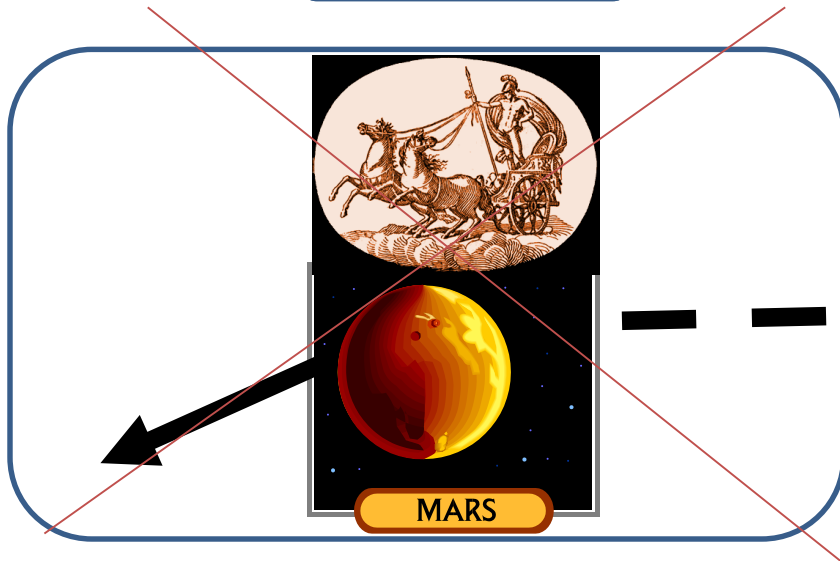
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Which model is more likely to be correct?

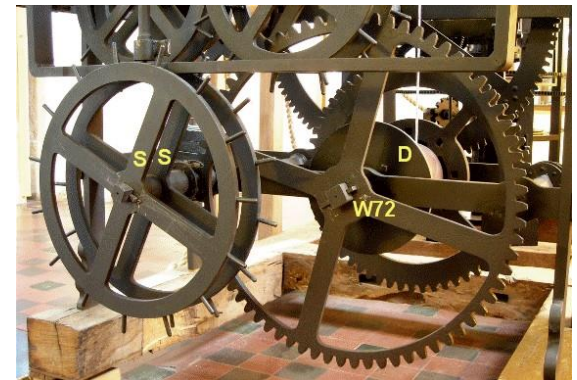
more complicated model

A B C D



simpler model

A B C

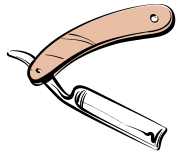




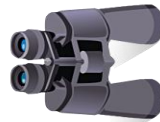
Systems Biology

Hans V. Westerhoff (at the begging of XXI century):
One should not remove things without necessity
(*Pluralitas non est eliminanda sine necessitate*)

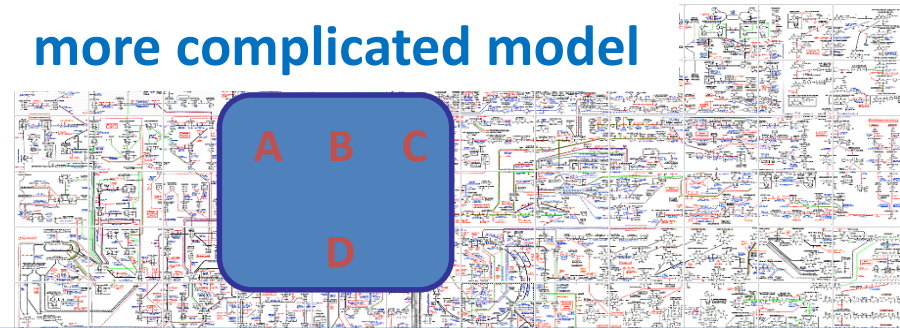
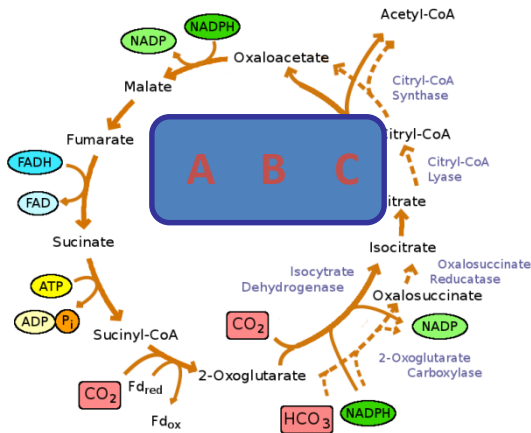
More likely to be correct



simpler model



more complicated model



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Original research

Computing life: Add *logos* to biology and *bios* to physics

Alexey Kolodkin^{a,b,*}, Evangelos Simeonidis^{a,b}, Hans V. Westerhoff^{c,d,e}

Vision and Strategy with flexible plans

Move forward:

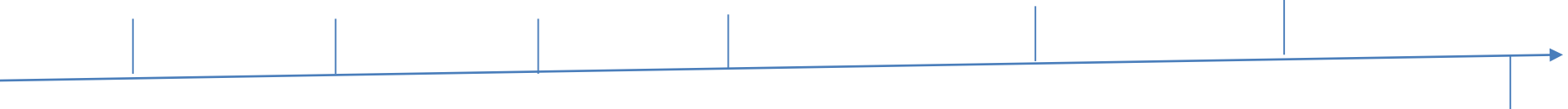


2000
Craig Venter's genome

Stiff plan



Step by step:

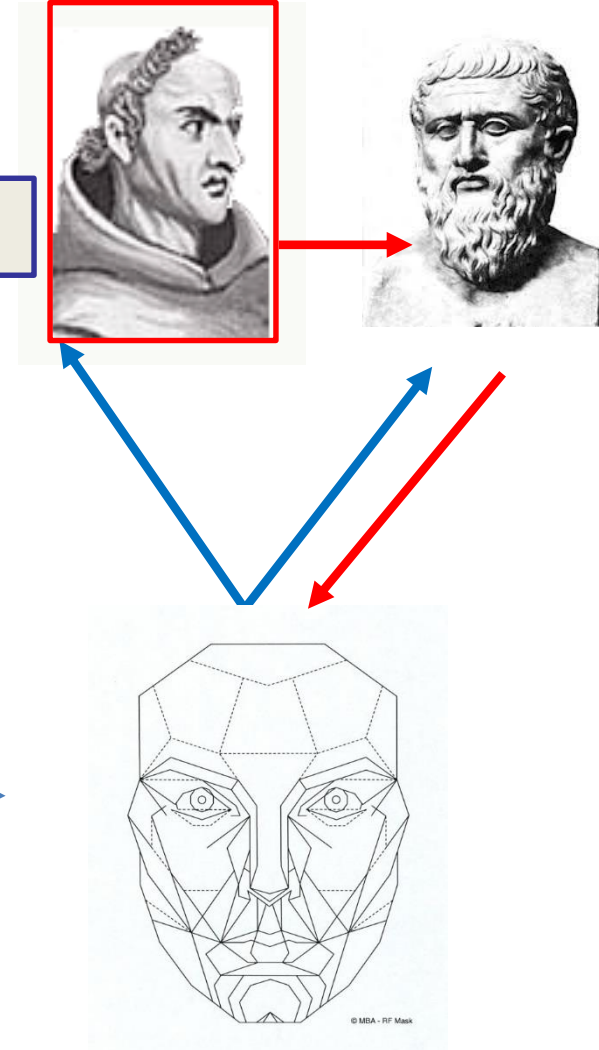


“Domino” approach

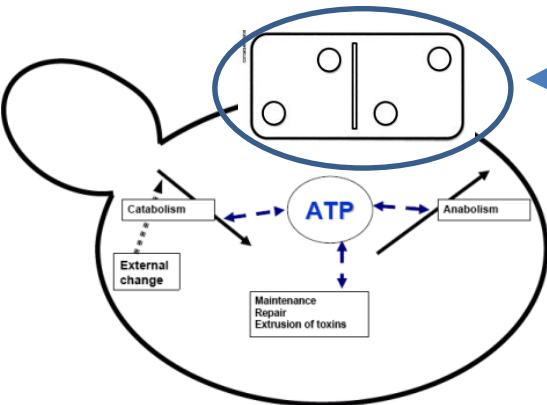
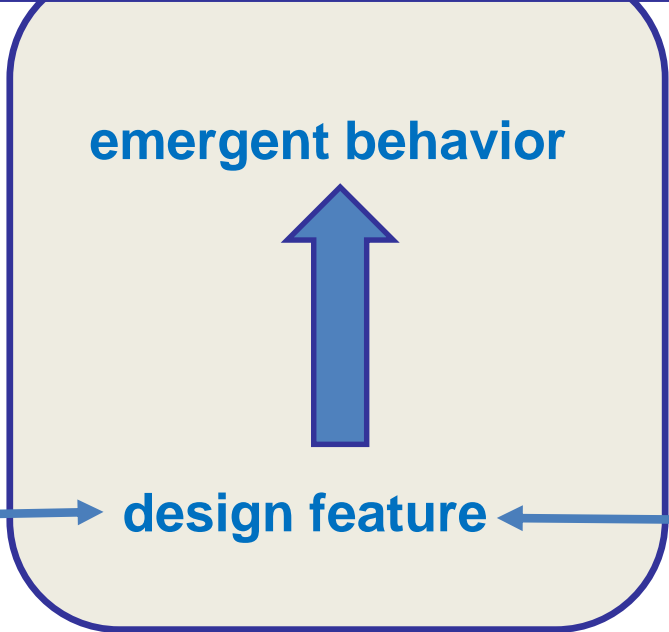


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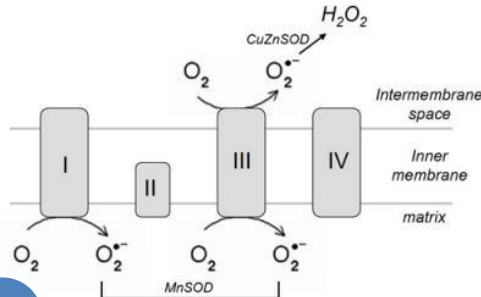
“Blue-print” modelling



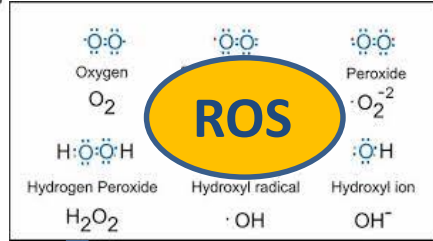
Design principles study



Reactive Oxygen Species (ROS) management



mitochondria,
ER,
cytoplasm



Cell differentiation

Immune response

Cell damage

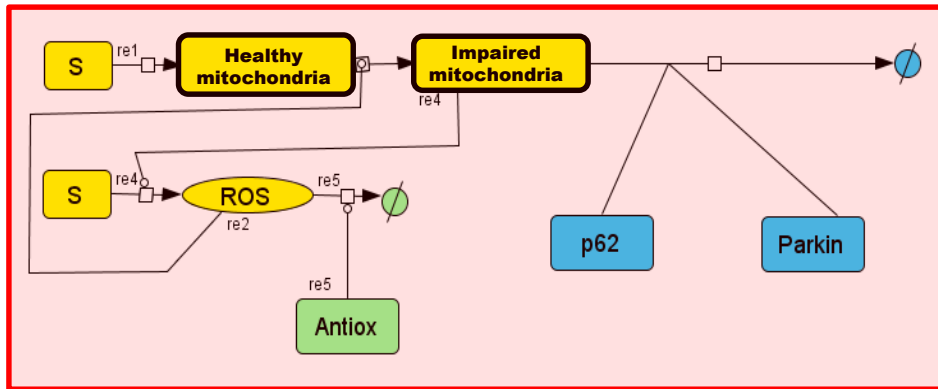
ROS regulatory network

Parkinson's disease



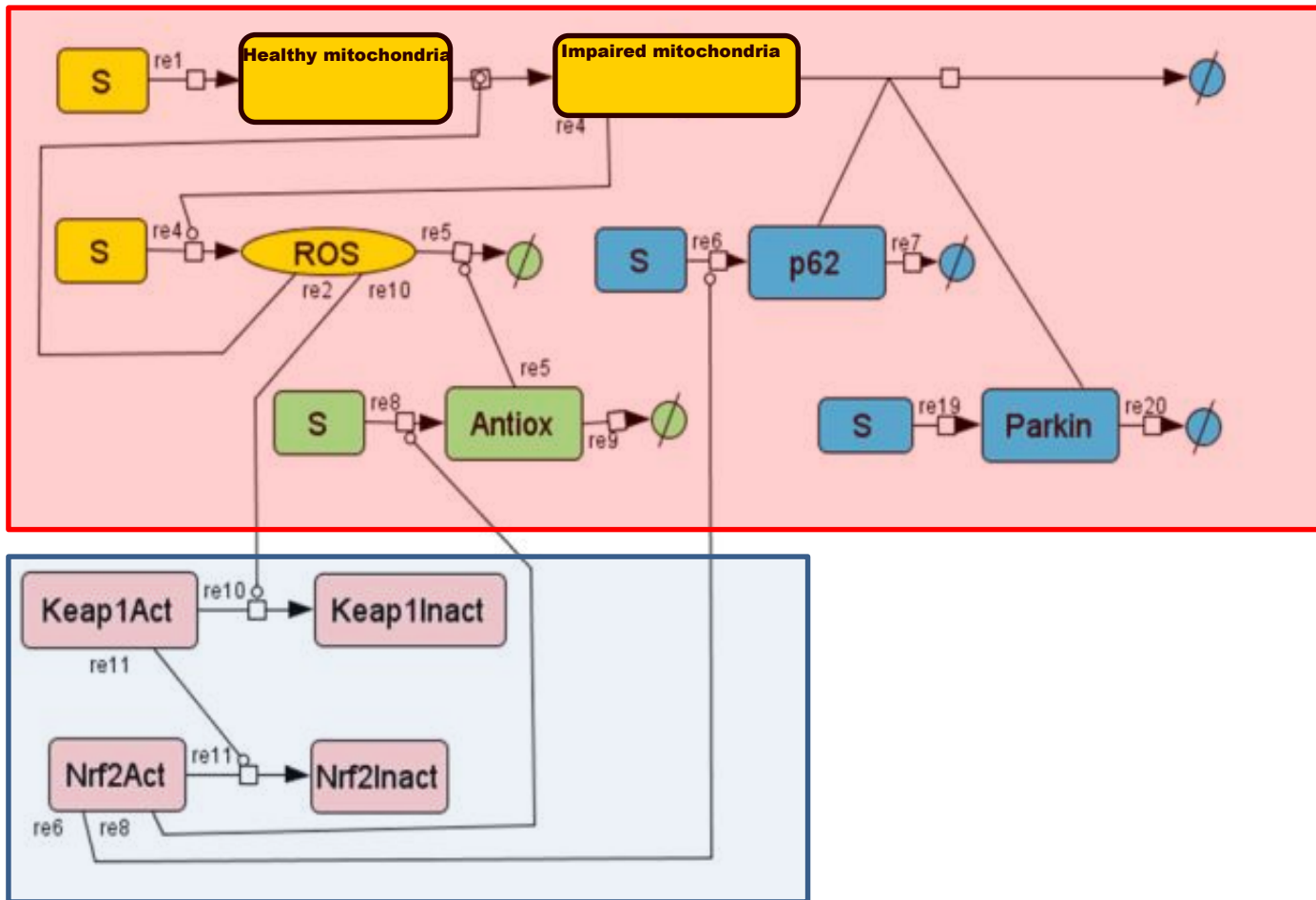
Cancer

Model 1



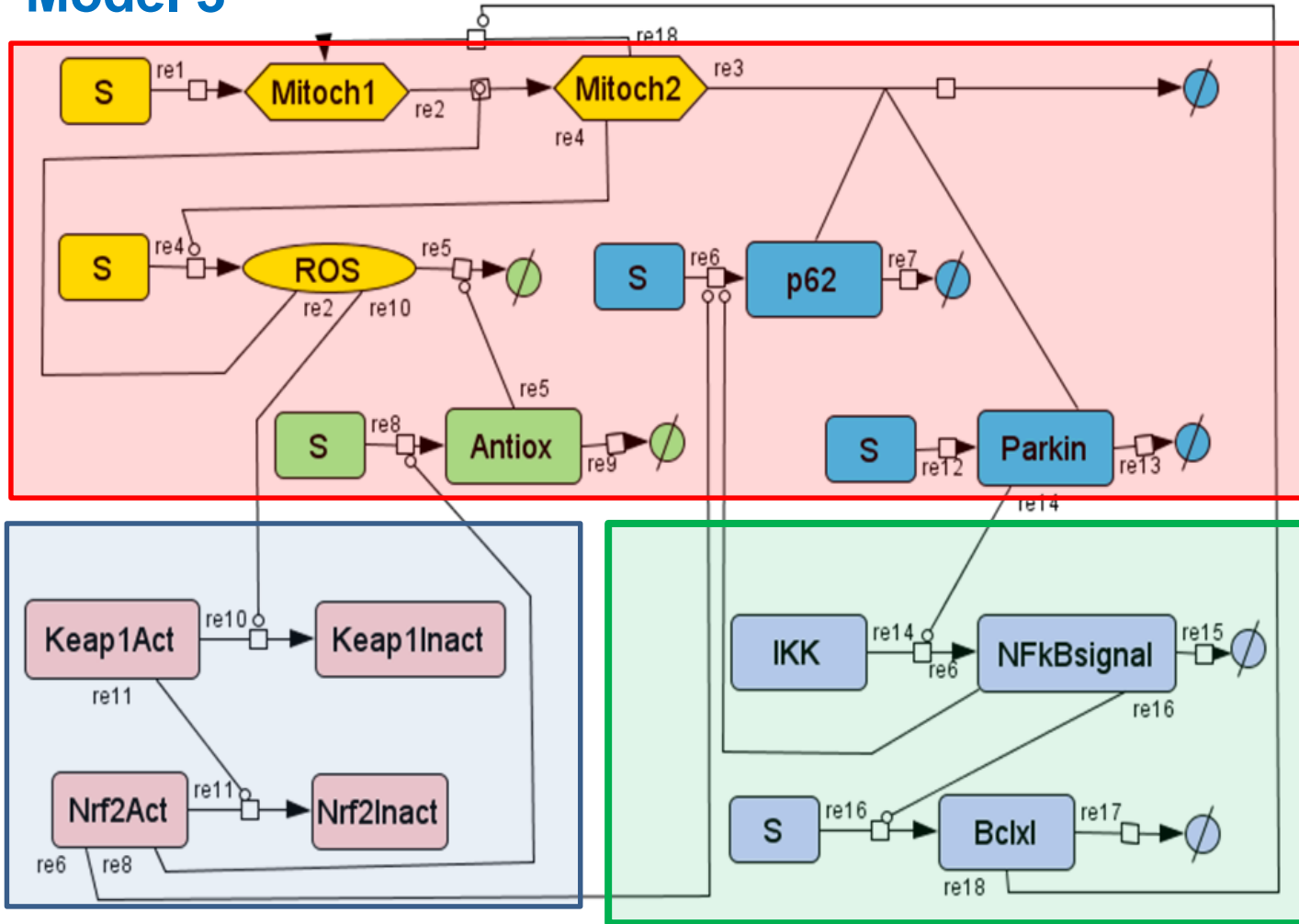
We add nrf2-keap1 system (regulation of p62 and antioxidants)

Model 2



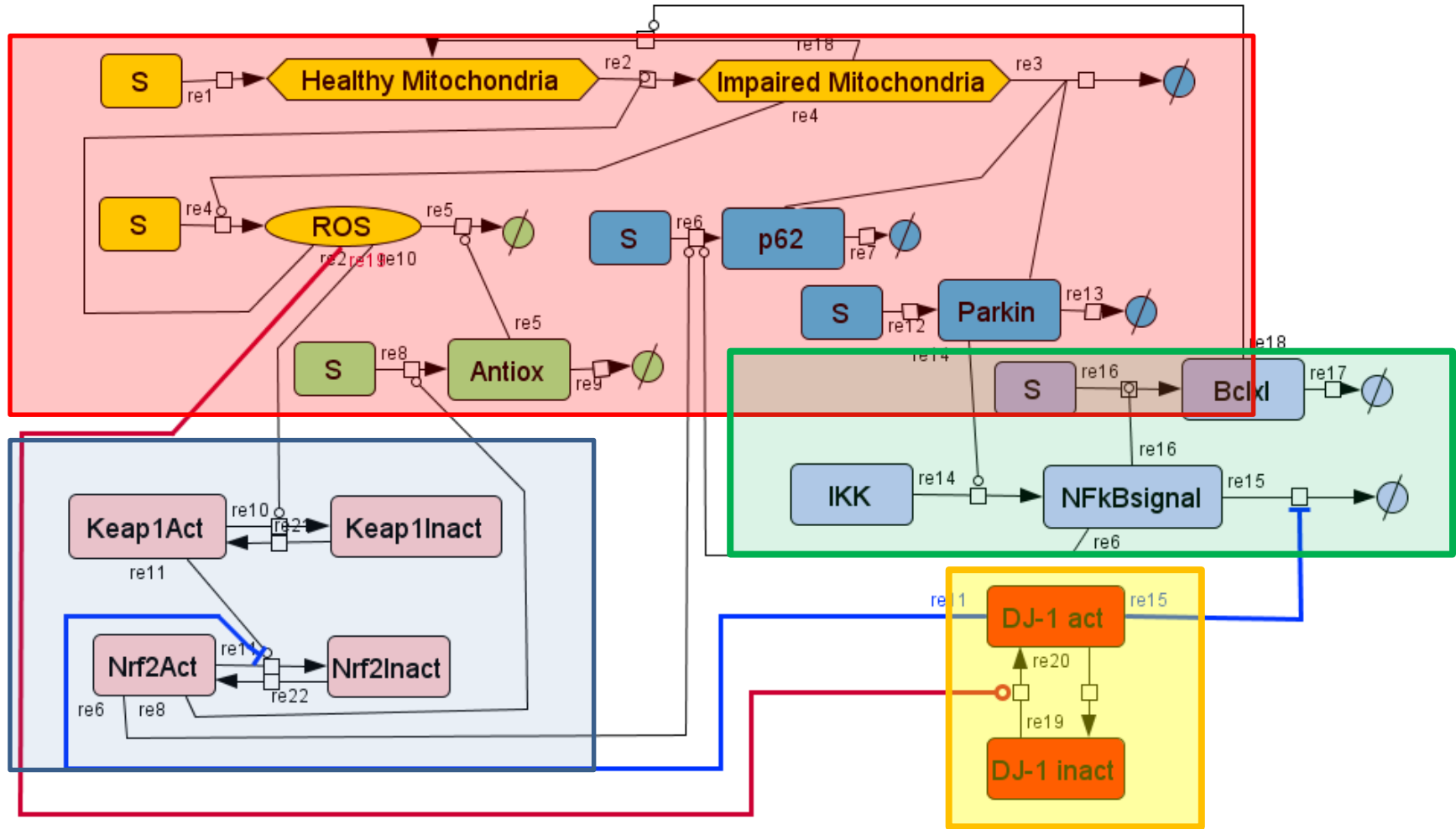
We add NFkB signalling (“recovery” of mitochondria)

Model 3

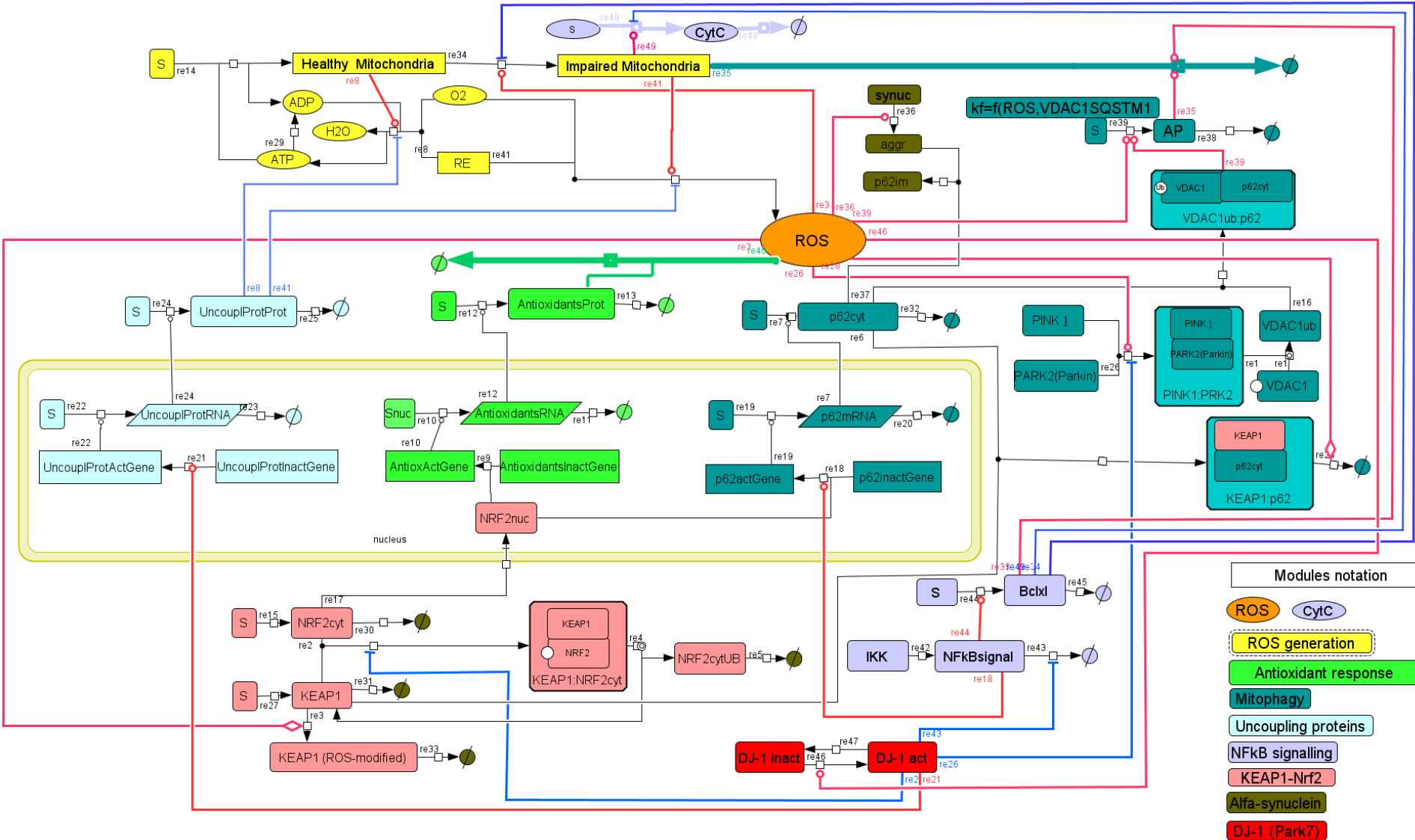


DJ-1 is a regulator of regulators

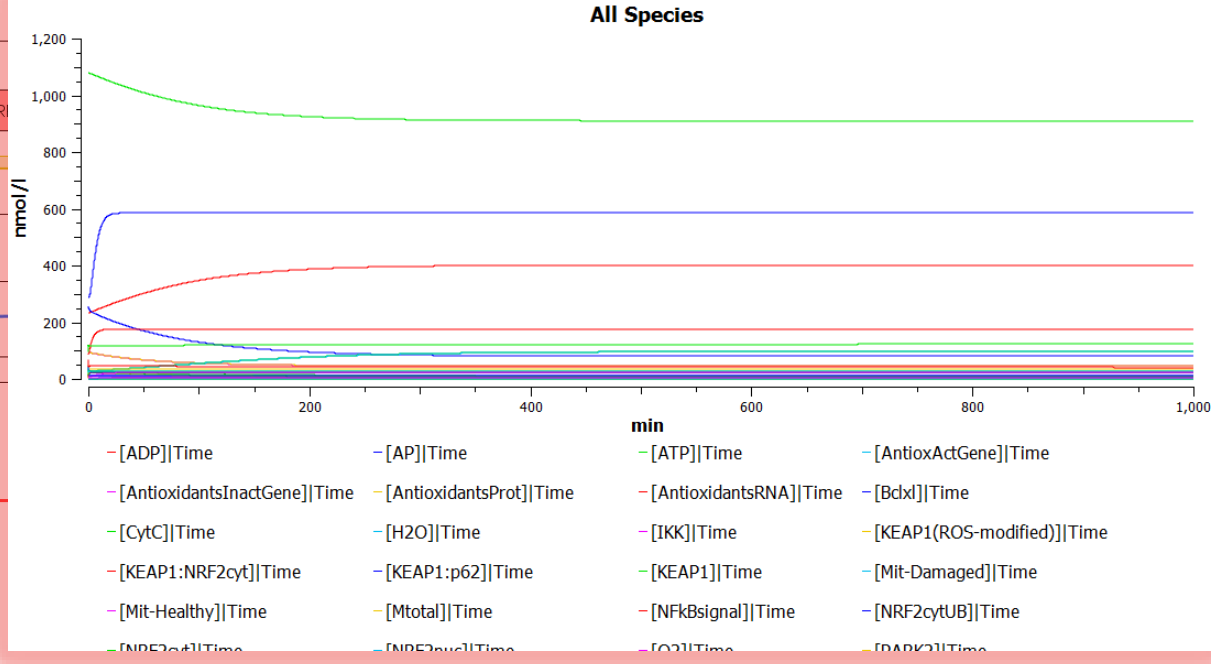
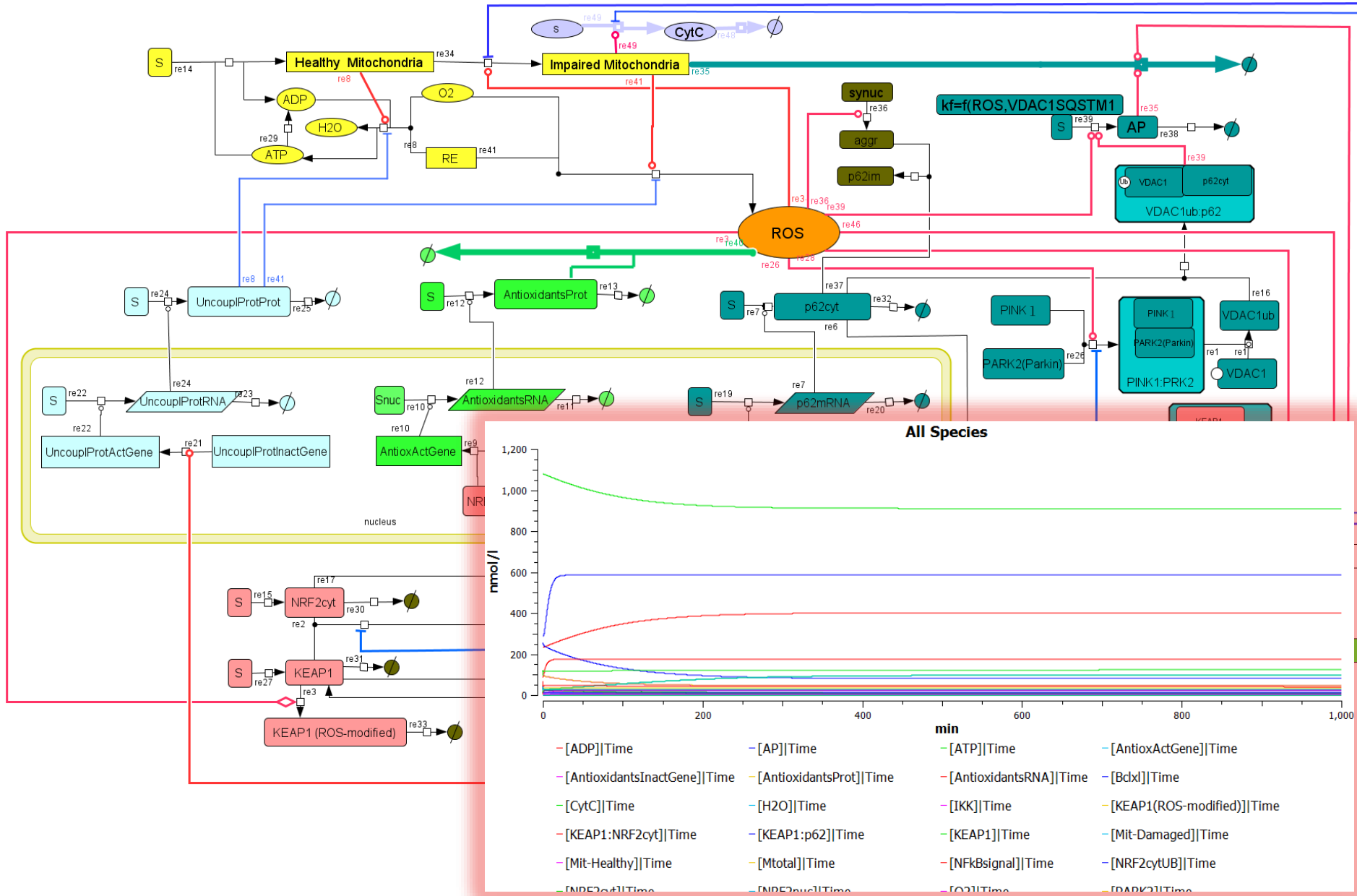
Model 4



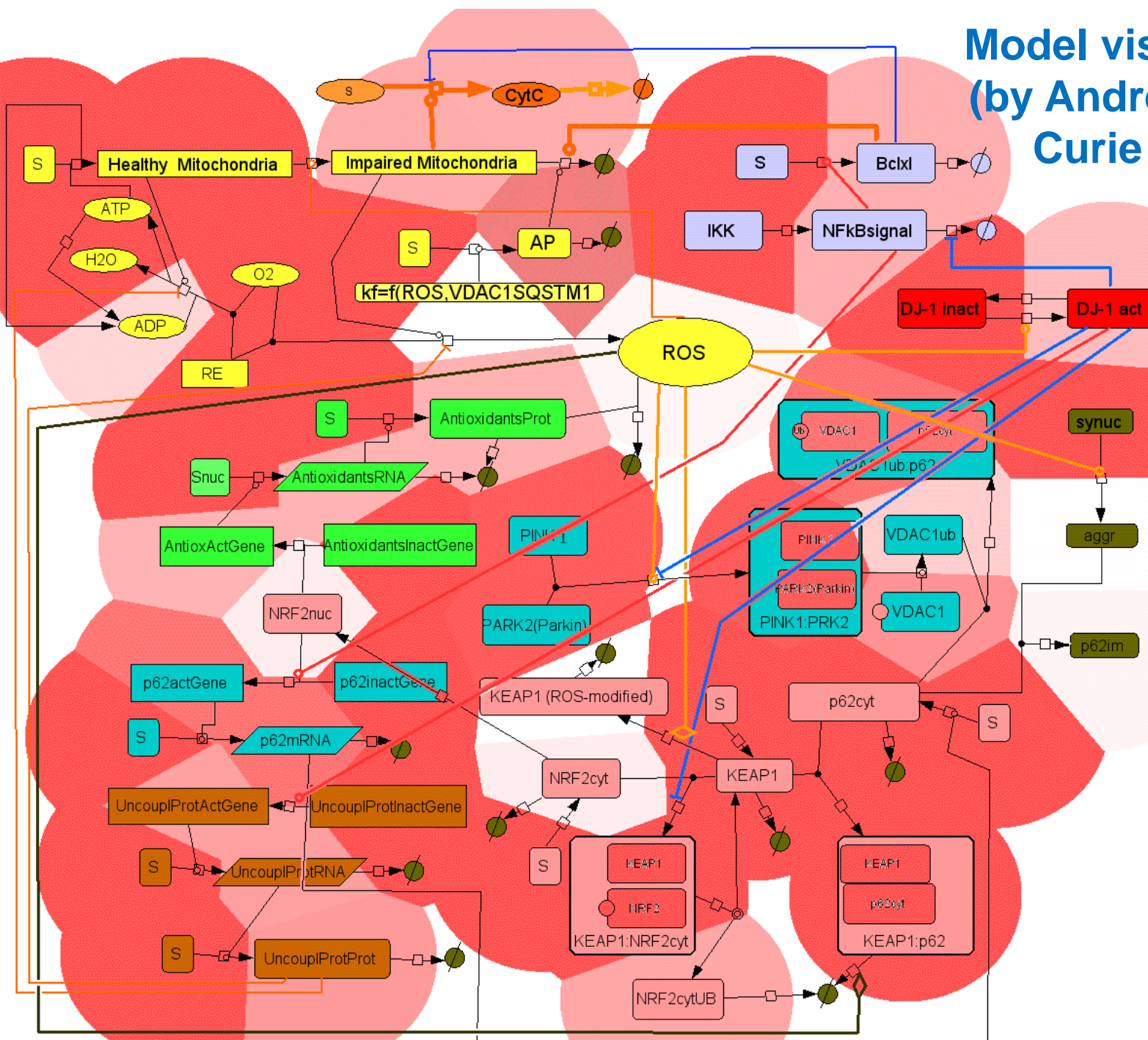
Detailed model of ROS management



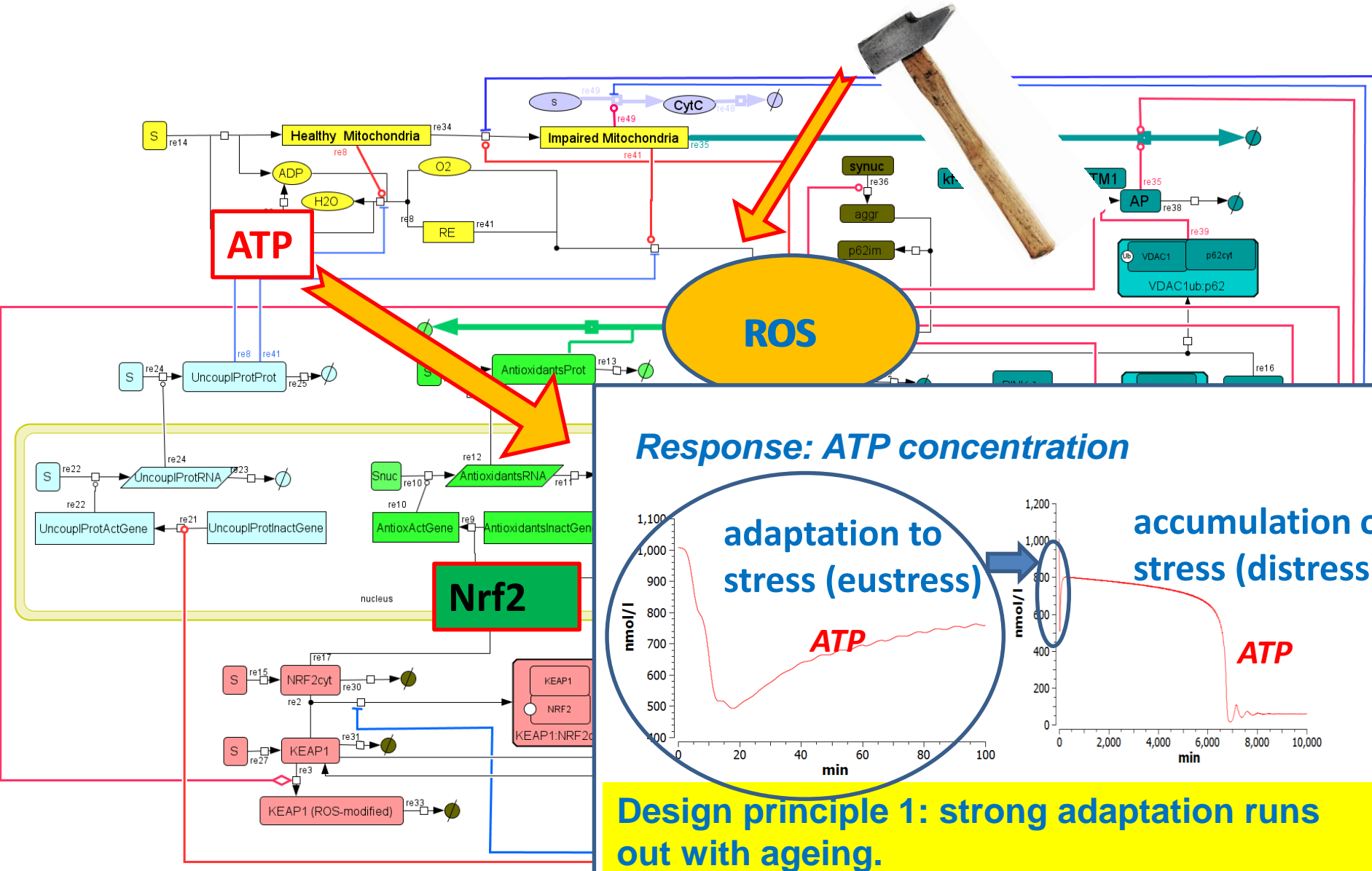
Model visualizes Life



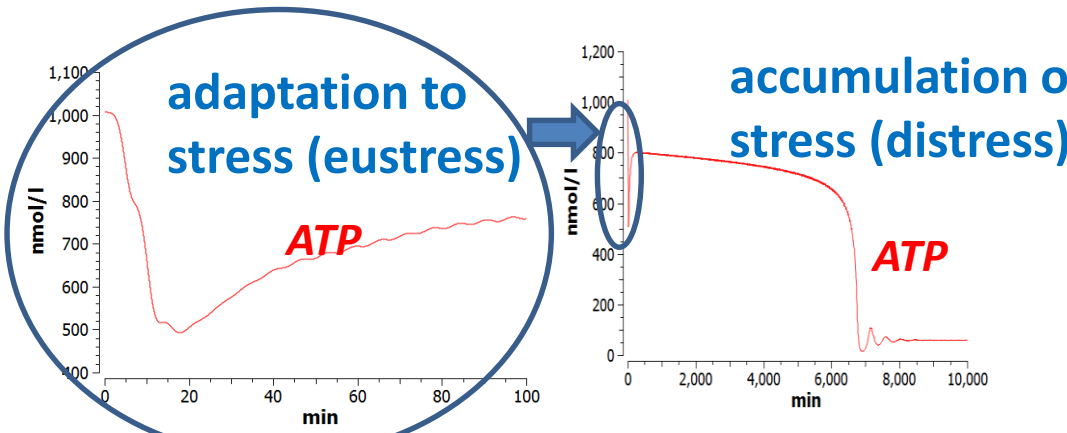
Model visualizes Life (by Andrei Zinovyev, Curie Institute)



Simulation of emergent behavior: stress and distress



Response: ATP concentration

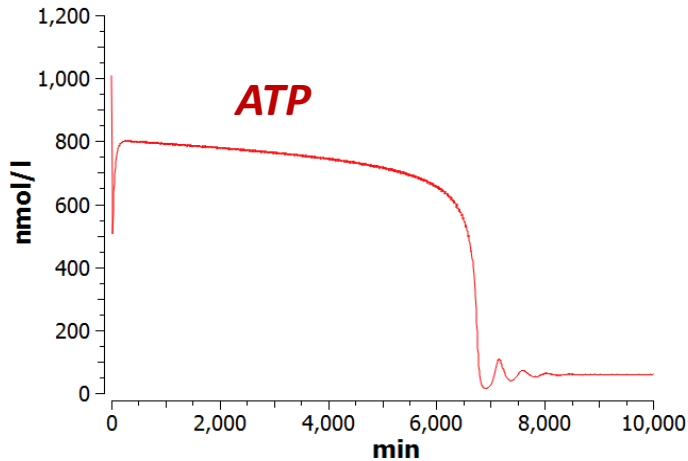


Design principle 1: strong adaptation runs out with ageing.

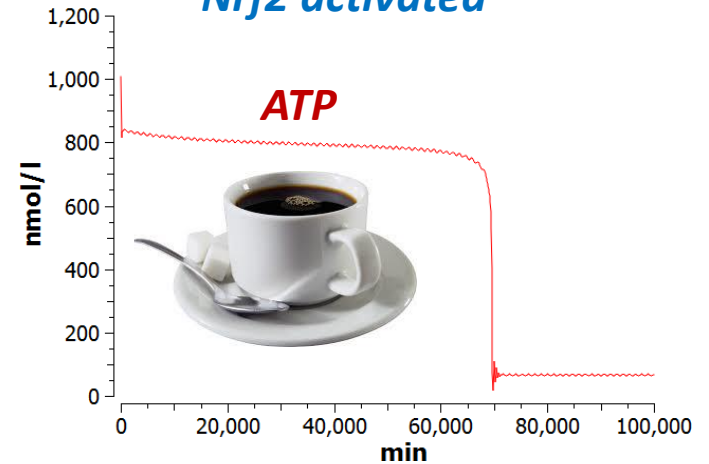
Simulation of treatment

Nrf2 may be activated by many drugs and biologically active compounds, e.g. caffeine and save neurons.

Without treatment



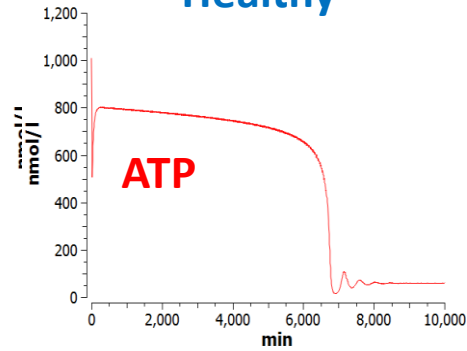
Nrf2 activated



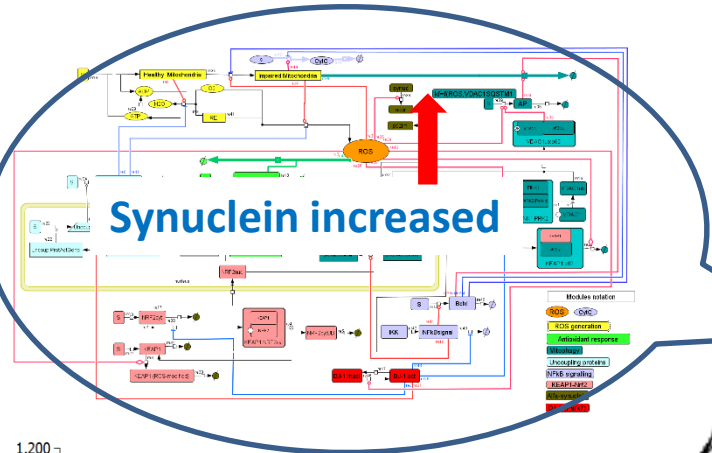
Design principle 2: Nrf2 activation might help.

Two mutations of Parkinson's Disease. No stress:

Healthy

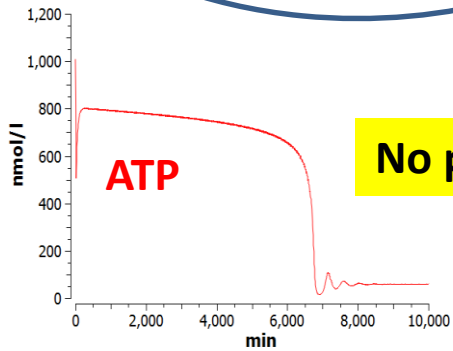
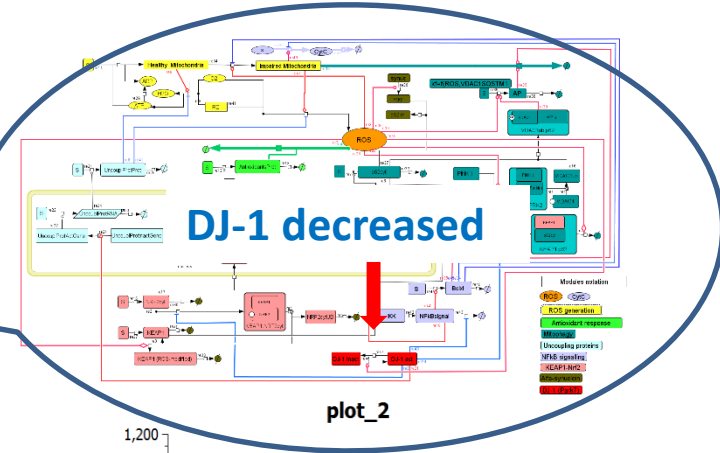


-[ATP]|Time -[Mid]|Time
-[ROS]|Time -[p62mRNA]|Time



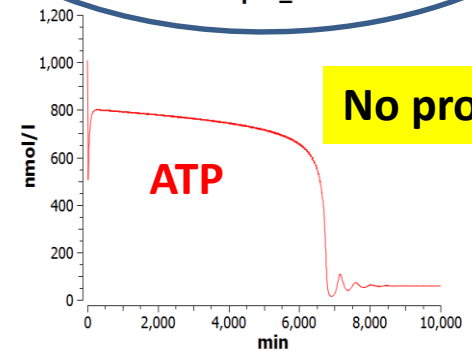
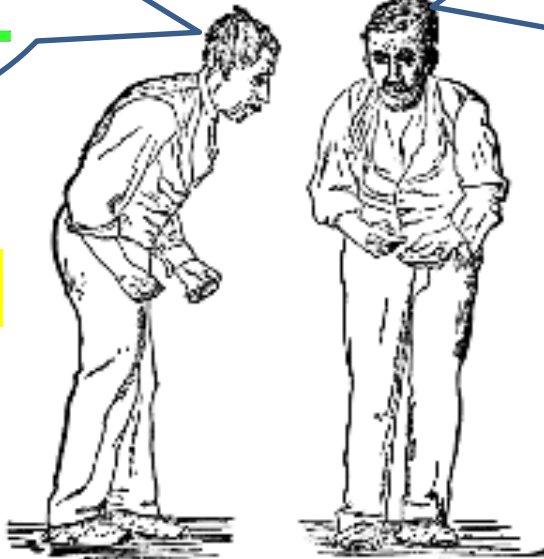
PD1

PD2



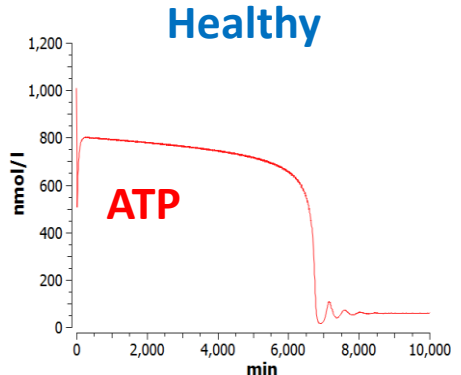
No problem

-[ATP]|Time -[Mid]|Time
-[ROS]|Time -[p62mRNA]|Time

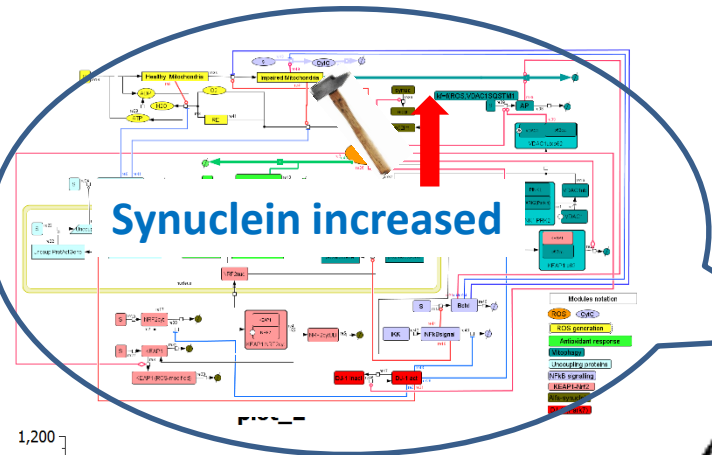


No problem

-[ATP]|Time -[Mid]|Time
-[ROS]|Time -[p62mRNA]|Time

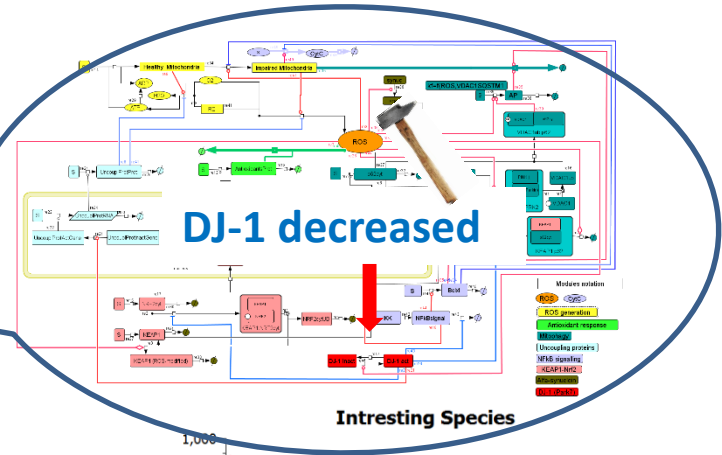


-[ATP]|Time -[Mid]|Time
 -[ROS]|Time -[p62mRNA]|Time

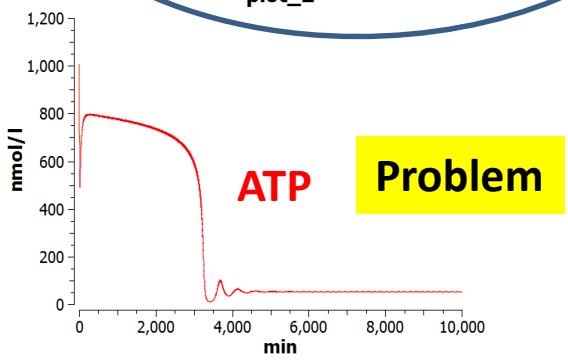


PD1

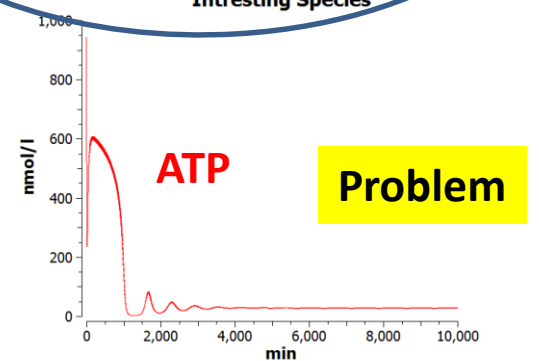
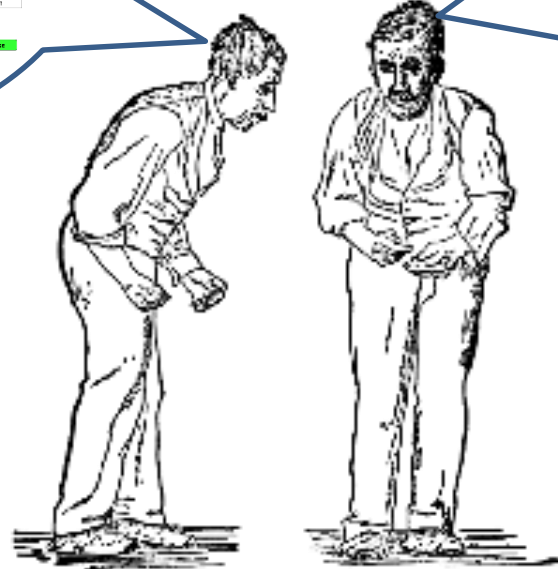
PD2



Intresting Species



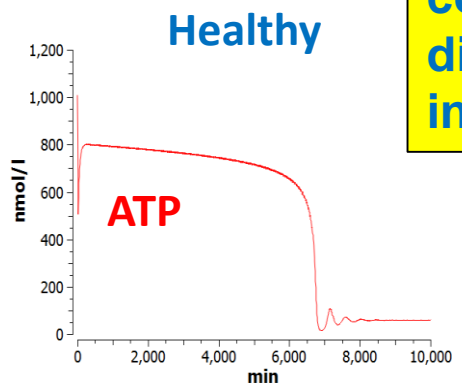
-[ATP]|Time -[Mid]|Time
 -[ROS]|Time -[p62mRNA]|Time



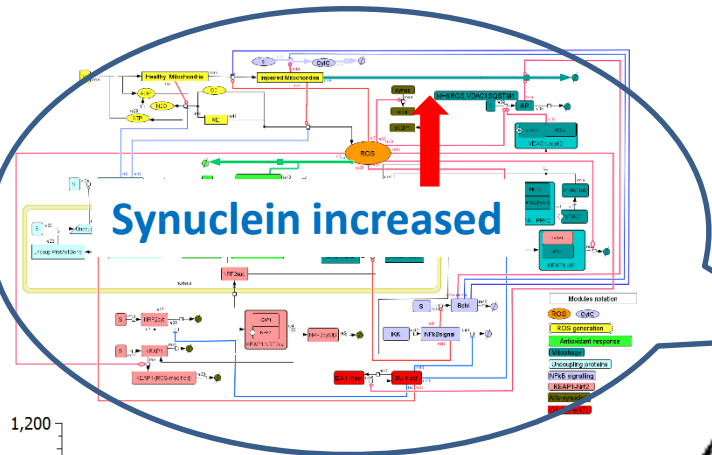
-[ATP]|Time -[CytC]|Time
 -[Mit-Damaged]|Time -[Mit-Healthy]|Time
 -[ROS]|Time -[p62cyt]|Time



Design principle 3: inter-individual variation in controllers may well cause disease variability between individuals.

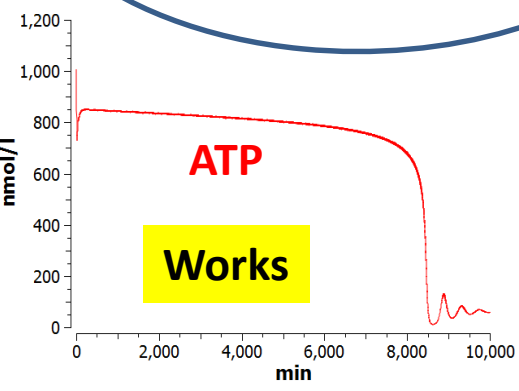
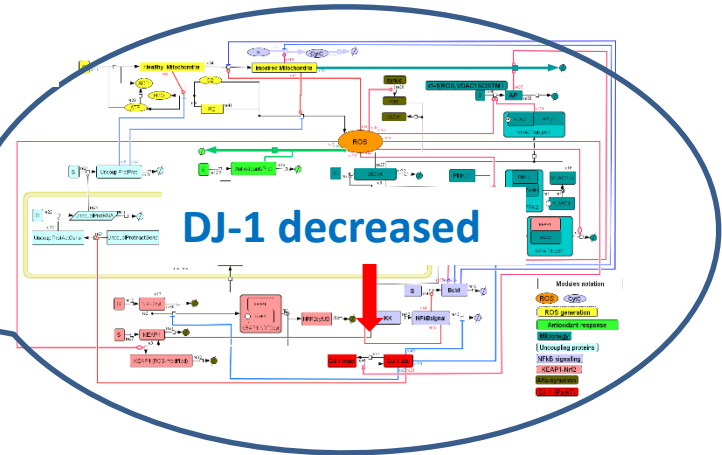


-[ATP]|Time -[Mid]|Time
-[ROS]|Time -[p62mRNA]|Time

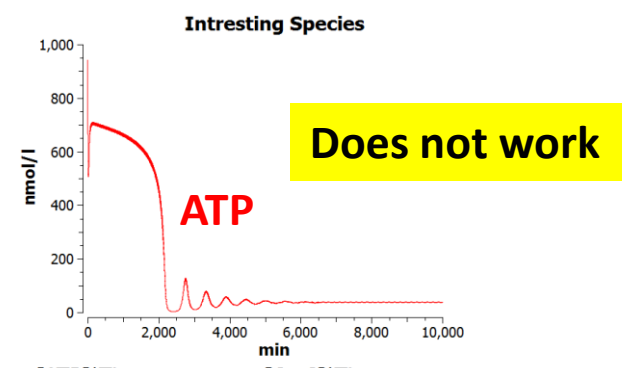
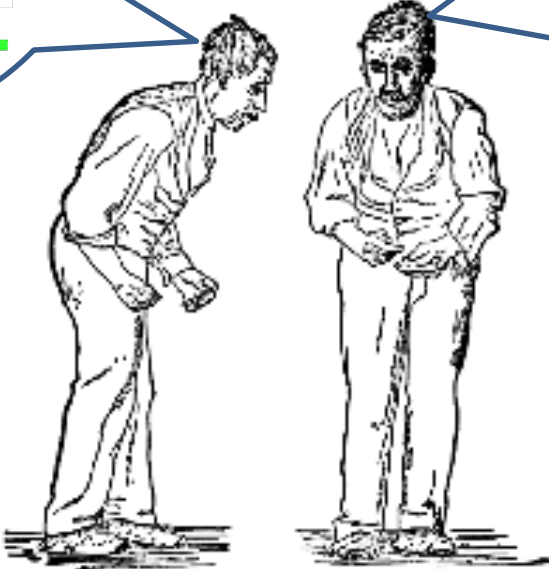


PD1

PD2



-[ATP]|Time -[Mid]|Time
-[ROS]|Time -[p62mRNA]|Time



-[ATP]|Time -[CytC]|Time
-[Mit-Damaged]|Time -[Mit-Healthy]|Time

Conclusions

- **A detailed, mechanistic, dynamic model of ROS management recapitulates ROS homeostasis and enlightens the functionality of this system in health and in Parkinson's disease**
- **PD-related increase of α -synuclein might be compensated by increased Nrf2 activation due to the individual's genome or behaviour (caffeine). However, Nrf2 activation does not help if PD is caused by various genetic deficiencies or mutations of DJ-1**
- **Inter-individual variation in controllers may well cause disease variability between individuals**

Acknowledgements

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Hans Westerhoff (Amsterdam)

