

BioSolar Cells



A data integration and
visualization resource for the
metabolic network of
Synechocystis sp. PCC 6803

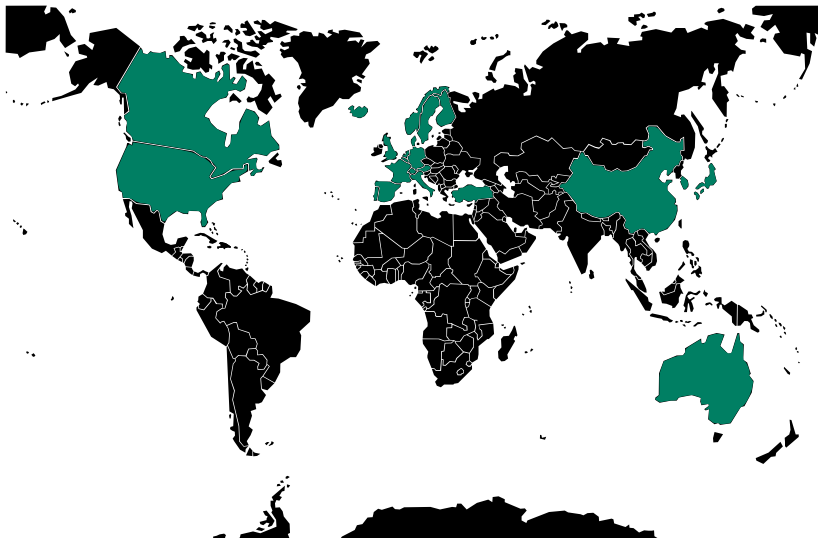
Timo Maarleveld, December 20th 2013

"The metabolic network"

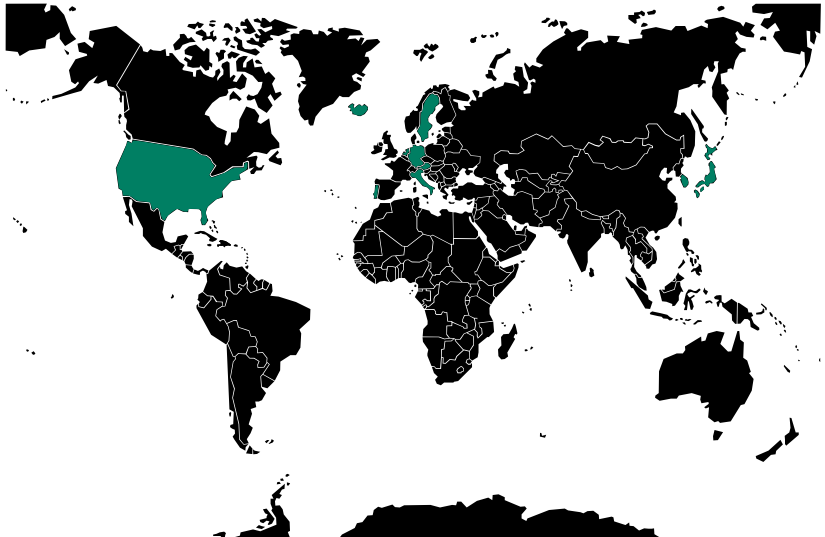
Genome-scale stoichiometric metabolic model

- Large models
- Links metabolic genes with metabolic reactions
- Only stoichiometry; no kinetics
- Steady-state flux distributions

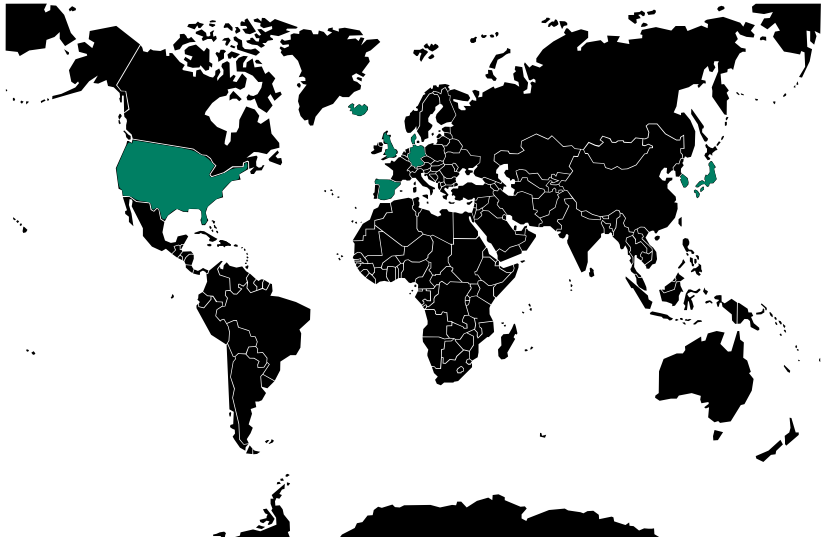
Published genome-scale models



Published tools

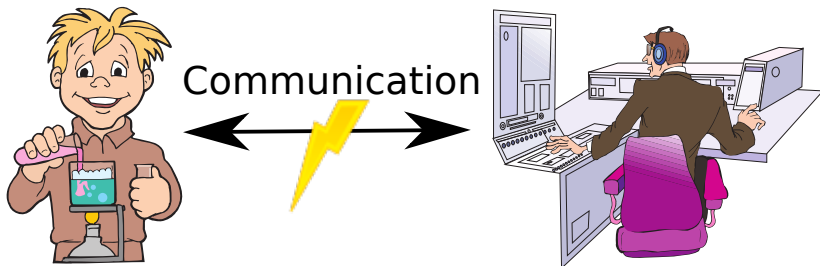


Published *Synechocystis* models

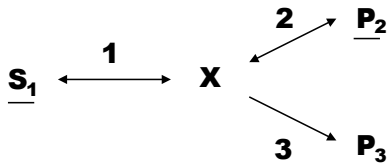


**However
But
Nevertheless**

Communication problem



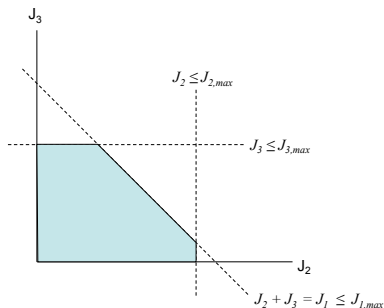
Flux Balance Analysis primer



- $J_1 = J_2 + J_3$
- $\mathbf{J} \geq 0$
- $J_1 \leq 10$, $J_2 \leq 8$, and $J_3 \leq 6$
- $\max Z = 0.5J_2 + 0.5J_3$

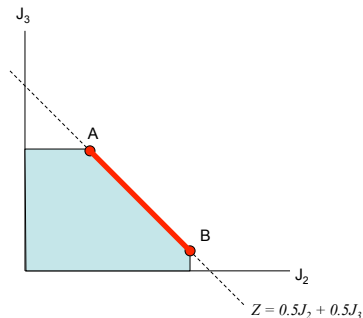
Example: The solution space

- Capacity constraints bound solution space
- $Z = 0.5J_2 + 0.5J_3 = [0 - 5]$
- $J_1 = J_2 + J_3 = [0 - 10]$



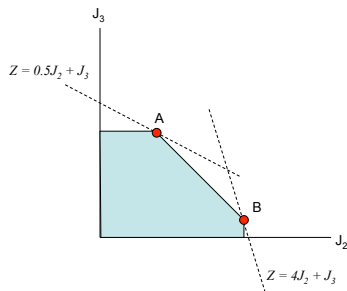
Example: Optimal solution space

- $Z = 0.5J_2 + 0.5J_3 = 5$
- $J_1 = J_2 + J_3 = 10$
- Optimal solution is not unique!

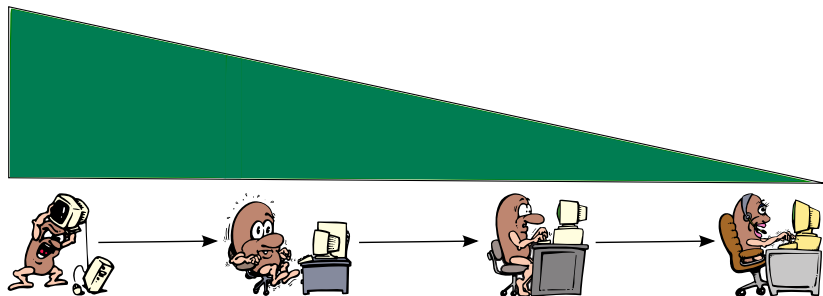


Example: Optimal solution space with unequal weights

- **A:** $Z = 0.5J_2 + J_3 = 8$
- **B:** $Z = 4J_2 + J_3 = 34$
- $J_1 = J_2 + J_3 = 10$
- Optimal solution is unique



The typical situation



The common tool

```
cplx_constructLPfromFBA time: 0.1383


cplx_analyzeModel FBA --> LP time: 0.1400

Parallel mode: deterministic, using up to 2 threads for concurrent optimization.
Tried aggregator 1 time.
LP Presolve eliminated 264 rows and 251 columns.
Aggregator did 335 substitutions.
Reduced LP has 218 rows, 320 columns, and 2227 nonzeros.
Initializing dual step norms . . .

Iteration log . . .
Iteration:    1    Dual objective      =      999999.000000
Iteration:   62    Dual objective      =     124837.892600
Iteration:  124    Dual objective      =         0.118388
Reinitializing dual norms . . .

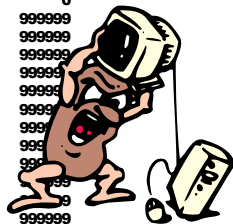
Dual simplex solved model.

INFO: Model is optimal: 1
Solution status = 1 : optimal
Solution method = 2 : dual
Objective value = 0.0906484648094 ←
Status: Model is optimal
LPS_OPT
Model is optimal
```

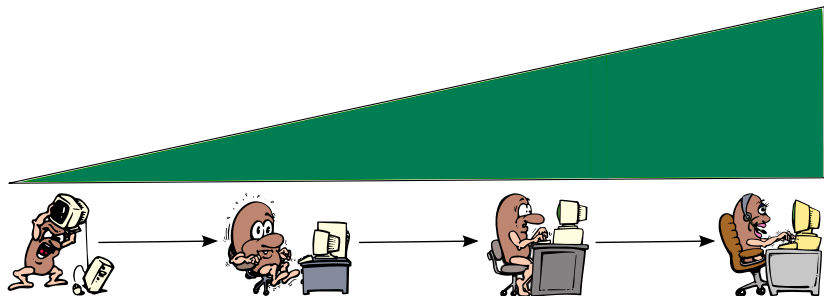
A cartoon character with a large head, wearing a white cap and glasses, holding a camera up to its eye. It is standing next to a small white box with a black dot on it.

The general FBA output

Number	Reaction	Flux value	LowerBound	UpperBound
1	R_ETOHtp	0	-999999	999999
2	R_MPBQ	2.4537E-005	-999999	999999
3	R_CTPS2	0	0	999999
4	R_CTPS1	0.013087102	0	999999
5	R_TMK	0	0	999999
6	R_UGLT	0	-999999	999999
7	R_PPTGS_Syn	0.002228983	0	999999
8	R_HPROb	0	-999999	0
9	R_HPROa	0	-999999	0
10	R_HEMEAS	1.9703E-005	0	999999
11	R_IPMD	0.046386488	0	999999
12	R_ADCS	0.000078867	0	999999
890	R_EX_glcglyc_e	0	0	999999
891	R_EAR80y	0.036720195	0	999999
892	R_MG2tex	0.002541428	-999999	999999
893	R_EX_mal_L_e	0	0	999999
894	R_G6PBDH	0	0	999999
895	R_SQD2_183_6_9_12	2.2305E-005	0	999999
896	R_3OAS141	0.001936926	0	999999
897	R_3OAS140	0.034783269	0	999999
898	R_ACLDC	0	-999999	999999
899	R_DXPRii	0.015816506	0	999999
900	R_GARFT	0	-999999	999999
901	R_G3PAT180	0.000108846	0	999999
902	R_CBFcu	13.66789315	0	999999
903	R_PRATPP	0.007567392	0	999999
904	R_PRAIS	0.028631283	0	999999
905	R_DM_cyanphy	0	0	999999
906	R_CPPPGO2	0	0	999999



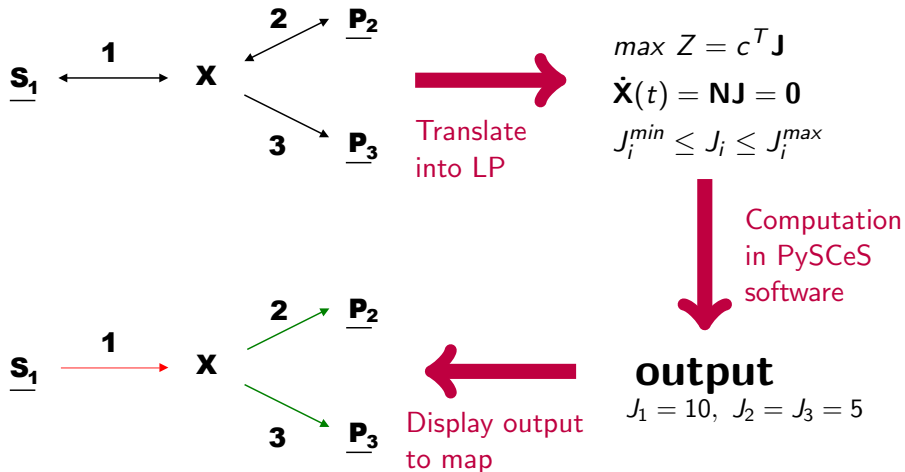
Goal



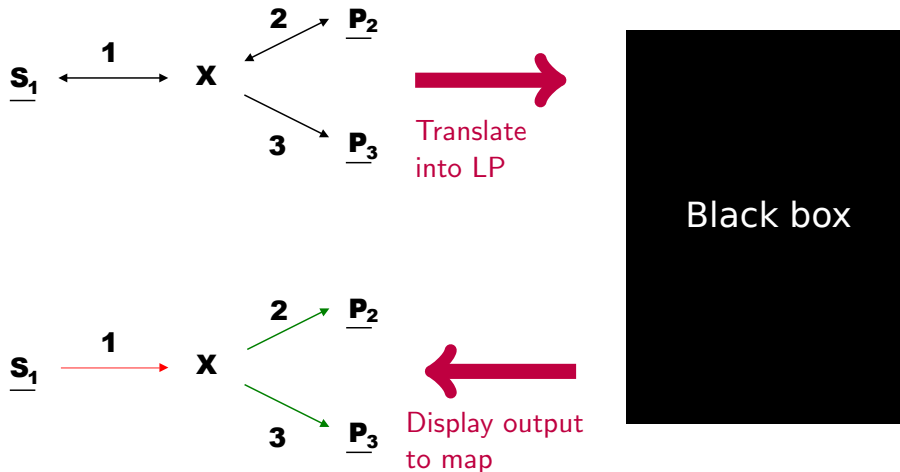
But what if



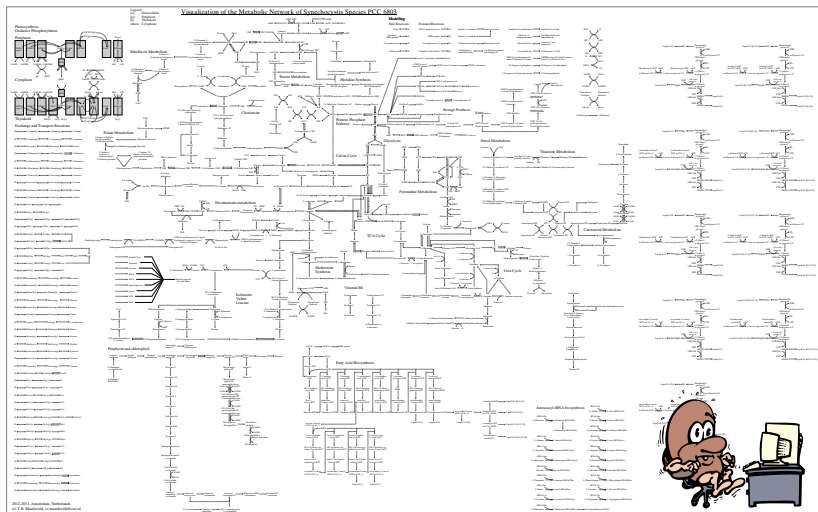
Basic idea



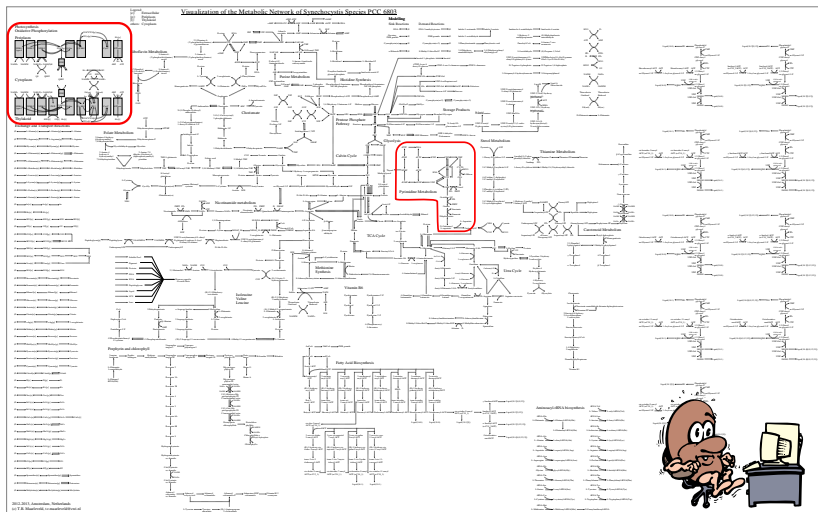
Basic idea



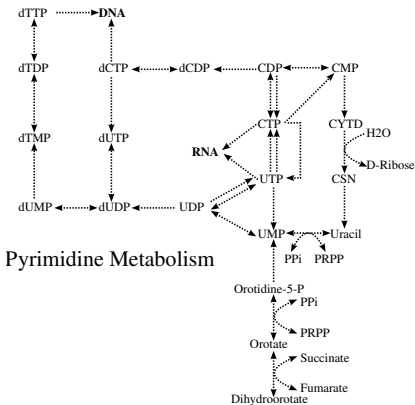
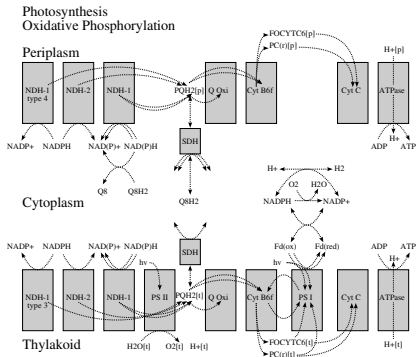
Interactive map of *Synechocystis* metabolism



Interactive map of *Synechocystis* metabolism

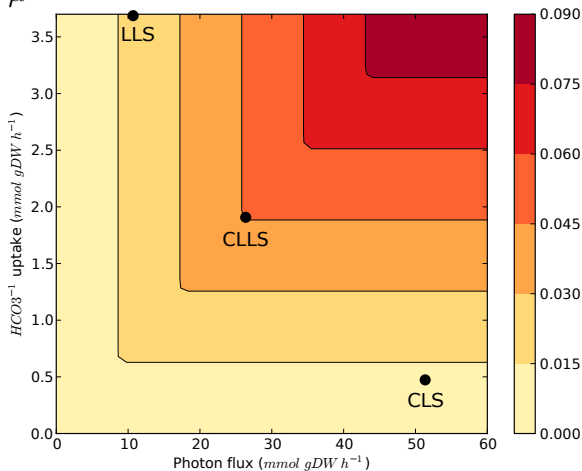


After zooming in

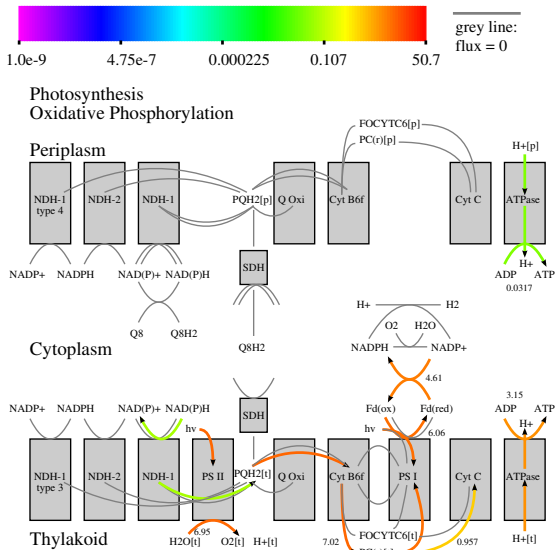


Exploring different scenario's

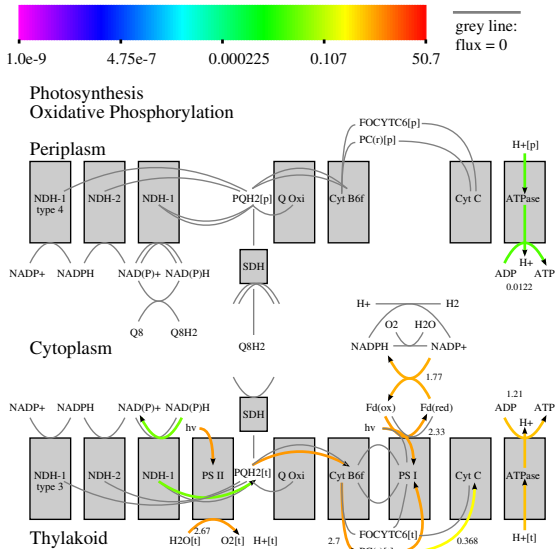
$$Z = \max \mu$$



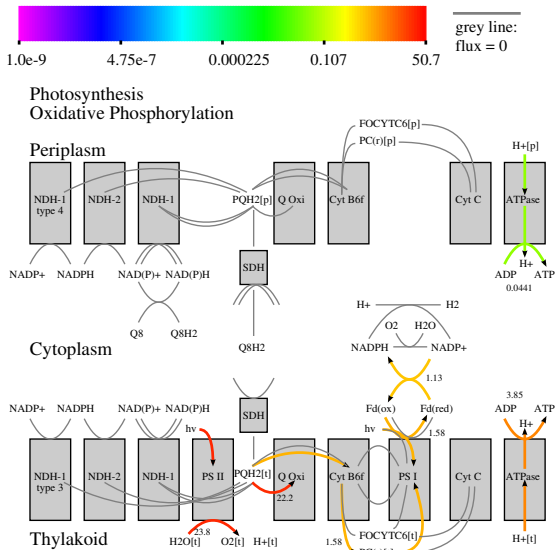
Carbon and Light Limiting State



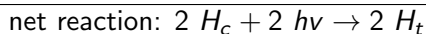
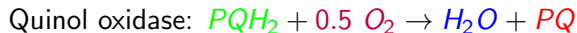
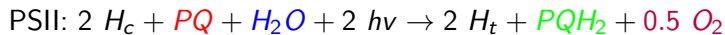
Light limiting state



Carbon Limiting State



Net effect



- net effect: ATP production!

How does this work??

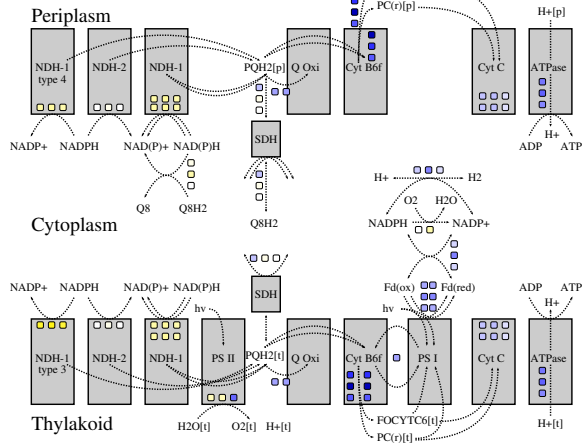


Demonstration

What else can we do?



Photosynthesis
Oxidative Phosphorylation



Conclusion

- Ready-to-use tool
- Data integration
- Modeling and visualization
- Repository



Acknowledgments



- Joost Boele
- Brett G. Olivier
- Frank J. Bruggeman
- Bas Teusink

Simulations and visualization can be done on-line at

<http://www.f-a-m-e.org/synechocystis>

Python package available for download from

<http://vonda.sf.net>

Contact information: t.r.maarleveld@cw.nl