Quantitative Assessment of Thermodynamics on the Solution Space of Genome-Scale Metabolic Models

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Outline



- 1 Introduction and Background
- 2 Incorporating Thermodynamics into Flux-Balance Analysis
- 3 Quantitative Assessment of Thermodynamics on the Solution Space
- 4 Conclusions

Constraint-Based Models



Why models?

- Understanding cellular behavior
- Contextualize high-throughput data

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- Contextualize high-throughput data

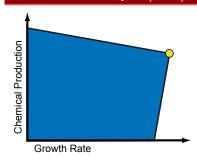
Flux distribution subject to

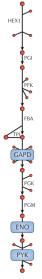
- Steady-state mass balance constraints
- · Limits on fluxes

And want to

Maximize growth

Flux Balance Analysis (FBA)





Why Thermodynamics?



Tighter Constraints on the Flux Space

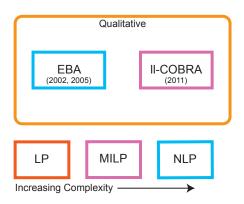
• Elimination of thermodynamically infeasible loops: $A \rightarrow B \rightarrow C \rightarrow A$

Insight into Cellular Metabolism

- Thermodynamic feasibility of cellular pathways
- Quantitative information on intracellular concentrations

Incorporating Thermodynamics



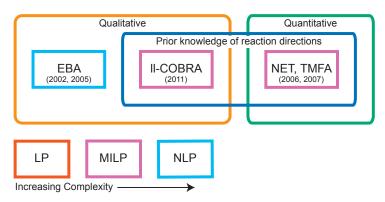


EBA: Beard, et al, *Biophys J* 2002. **II-COBRA**: Schellenberger, et al, *Biophys J* 2011.

NET: Kummel, et al, *Mol Syst Biol* 2006. **TMFA**: Henry, et al, *Biophys J* 2007.

Incorporating Thermodynamics





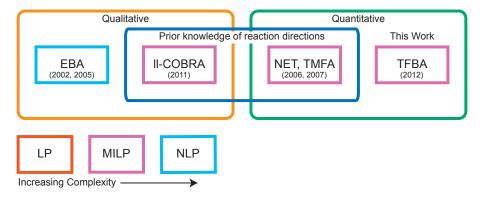
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Incorporating Thermodynamics



Thermodynamic flux-balance analysis (TFBA) enables a *quantitative* approach to thermodynamics without relying on prior knowledge of reaction directions



TFBA: Hamilton et al, under review.

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TFBA Formulation

max cellular growth

s.t. mass balance

all reactions bidirectional

 $\Delta_r G' \cdot v \leq 0$

 $\Delta_r G'$ calculation

 $\Delta_r G'^0$ definition

global concentration bounds

Transport: Henry, et al, *Biophys J* 2007.

GC Method: Jankoswki et al, Biophys J 2008.

TFBA: Hamilton, et al, under review.

TFBA: Thermodynamics Flux Balance Analysis



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MIP Formulation of $\Delta G_i \cdot v < 0$

$$\Delta_r G' < 0 \implies \delta_{fwd} = 1$$
 $v < 0 \implies \delta_{rev} = 1$

 $v > 0 \implies \delta_{fwd} = 1$

$$\Delta_r G' > 0 \implies \delta_{rev} = 1$$
 $\delta_{fwd} + \delta_{rev} < 1$

Transport: Henry, et al, *Biophys J* 2007.

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TFBA: Thermodynamics Flux Balance Analysis



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Calculating $\Delta_r G'$

$$\Delta_r G' = \Delta_r G'^0 + RT \sum S \ln C + \Delta_t G'^0$$

 $\Delta_r G^{\prime 0}$ by Group Contribution (GC)

$$\Delta_r G'^0 = \sum S \Delta_f G'^0$$

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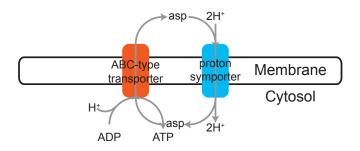


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Elimination of ATP-Generating Cycles



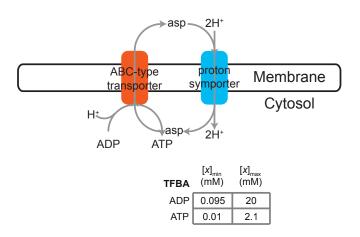
• TFBA predicts ATP-generating cycles



Elimination of ATP-Generating Cycles



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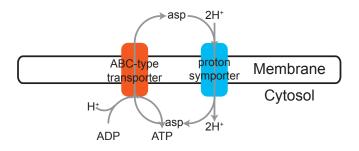


TFBA: Hamilton et al, under review.

Elimination of ATP-Generating Cycles



- TFBA predicts ATP-generating cycles
- Adding concentration constraints eliminates cycles



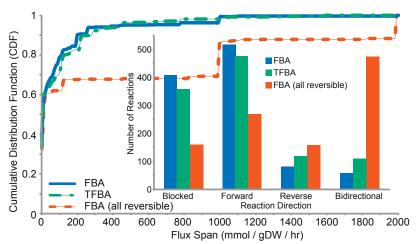
TFBA	[x] _{min} (mM)	[x] _{max} (mM)	[x] _{meas} (mM)
ADP	0.095	20	0.56
ATP	0.01	2.1	9.6

TFBA: Hamilton et al, under review.

Effect of Thermodynamics on the Flux Space



- TFBA assumes all reactions can be bidirectional
- Thermodynamic interactions shrink the flux space



TFBA: Hamilton et al, under review.

Using TFBA to Predict Growth Phenotypes



- CONGA identifies single-gene deletions for which TFBA and FBA give different predictions (Growth vs. No Growth)
- Better prediction in 7 cases: TFBA predicts a reversible reaction which FBA does not
- Worse prediction in 12 cases: TFBA predicts a reversible reaction which is physiologically irreversible
- Synthetic Lethal (SL) Finder identifies the reaction responsible for the phenotype difference

CONGA: Hamilton and Reed, *PLoS ONE* 2011. TFBA: Hamilton, et al., *under review*.

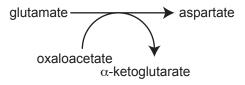
Exp. Data: Baba, et al, Mol Syst Biol 2006. SL Finder: Suthers, et al, Mol Syst Biol 2009.

Analyzing Better Predictions

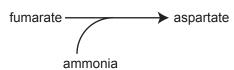


- ΔaspC predicted to be rescued by aspA
- Constructed $\triangle aspC\triangle aspA$ mutant

aspC: aspartate aminotransferase



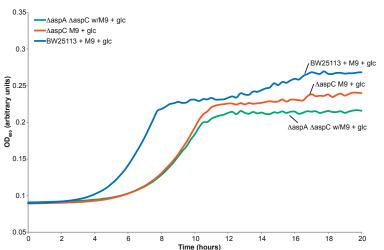
aspA: aspartate-ammonia lyase



Analyzing Better Predictions



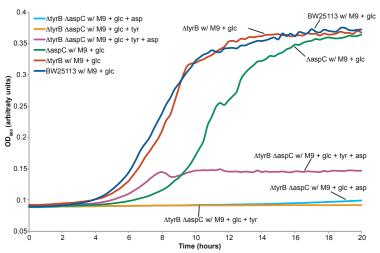
- $\triangle aspC\triangle aspA$ mutant proved viable
- Sequence similarity suggested tyrB as an isoform for aspC



Analyzing Better Predictions



- ΔaspCΔtyrB mutant proved nonviable tyrB is an isoform for aspC
- Constrain the direction of aspC







Batch Culture						
	Uncons.	Cons.	Total			
Overlap	46	33	79			
No Over.	9	19	28			
No Data	409	96	505			
Total	474	138	612			

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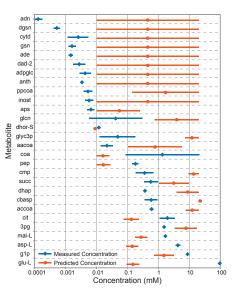
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Using TFBA to Predict Metabolite Concentrations



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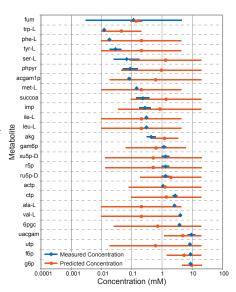
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- · Identify measurements which are most useful

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- Predicted concentration measurements remain large
- Incorporate physiochemical correlations or kinetic constraints

Acknowledgements



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 - Vivek Dwivedi
 - Mink Arunrattanamook
 - John de Friel





Questions?



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