

Metabolic Modelling of *Acetobacterium woodii* for Biotechnological Purposes



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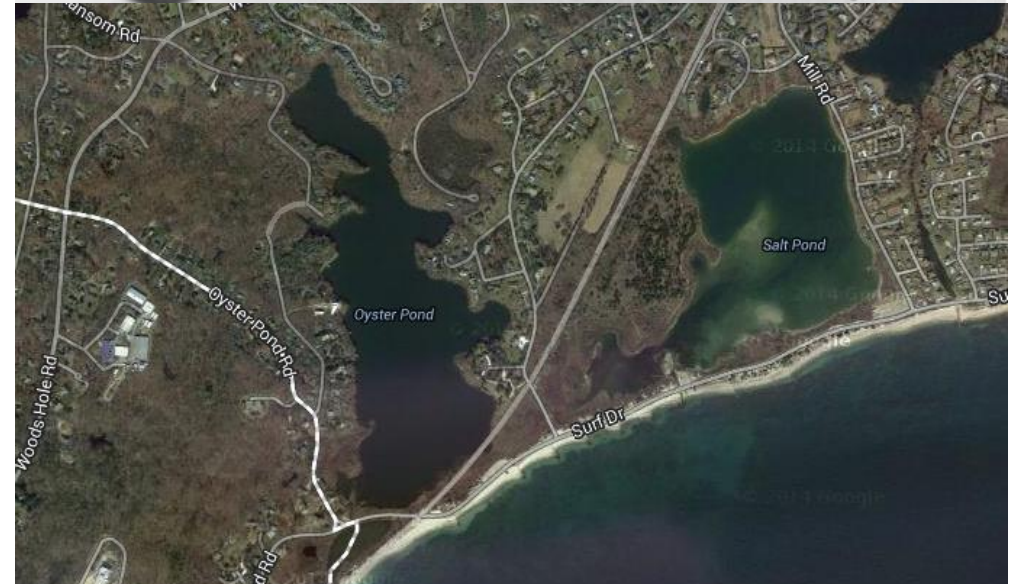
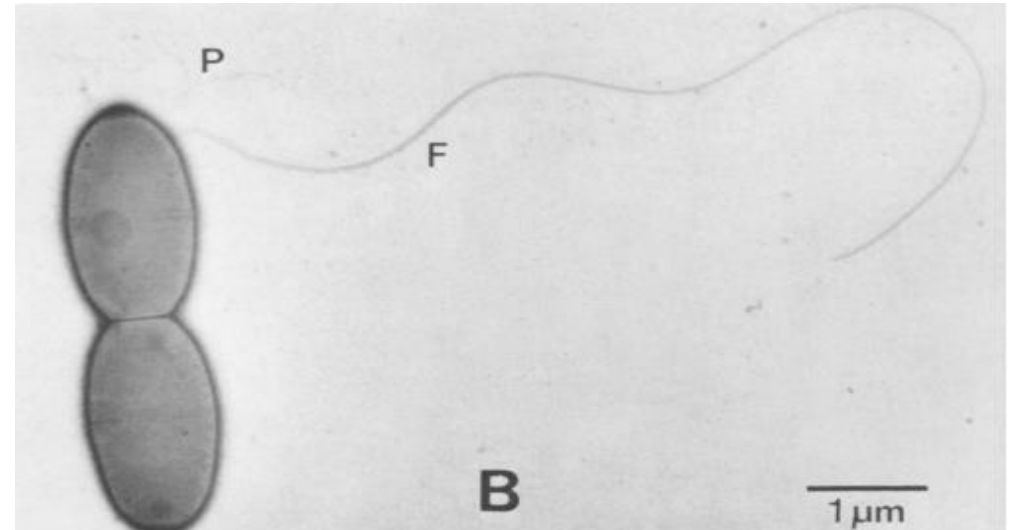
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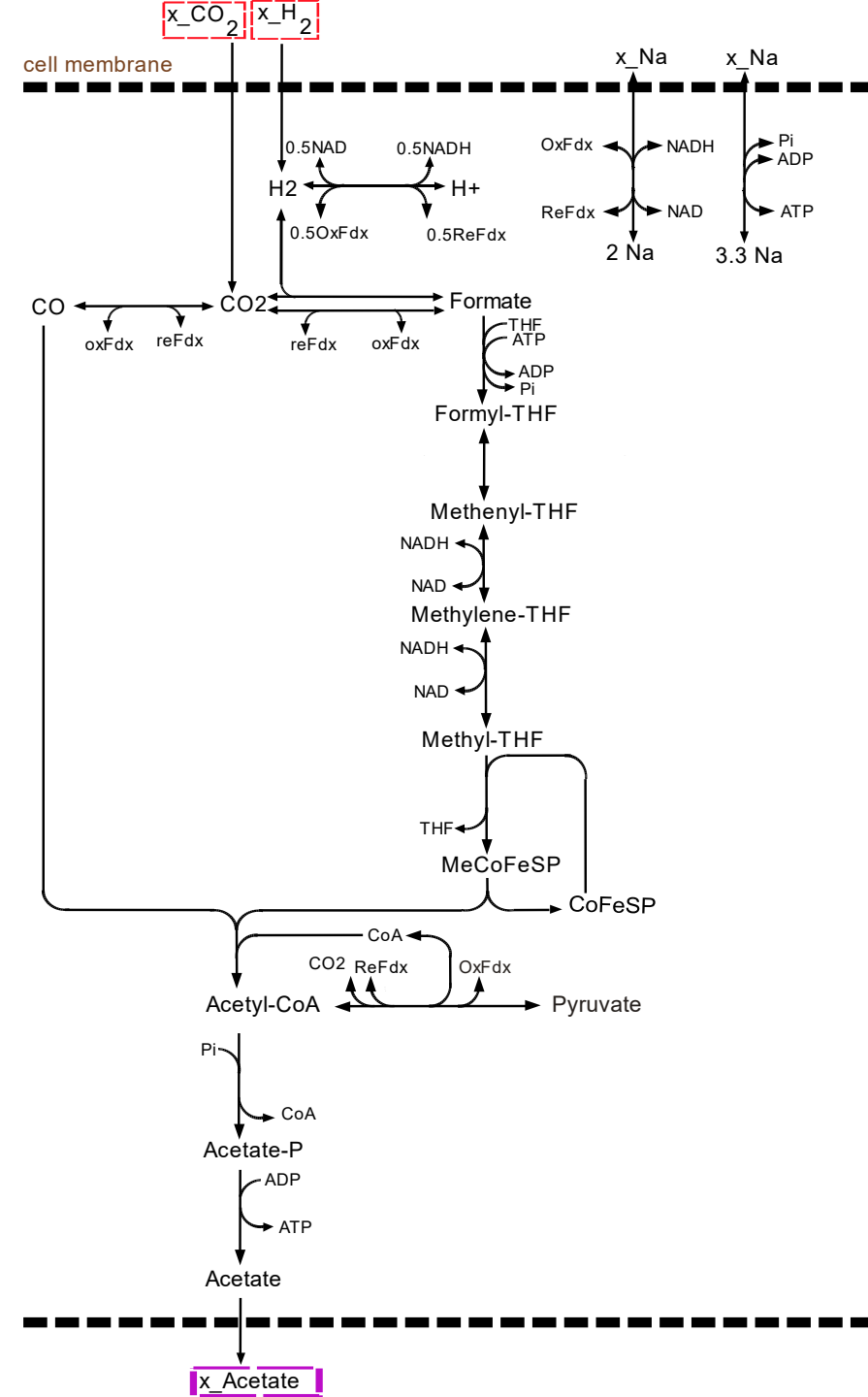
A. woodii Background

- Belongs to group of bacteria called acetogens, of which it is a model organism.
- All acetogens are able to fix CO₂ with H₂ for growth and energy purposes with the Woods-Ljungdahl Pathway (WLP).
- Much bioenergetic work done on *A. woodii* ; the only acetogen with all bioenergetically relevant reactions in WLP characterised.
- Categorised as a Rnf type Na⁺ dependant acetogen (along with *E. limosum*)



Balch, W. E., et al., 1977

Woods-Ljungdahl Pathway



Project aims

- Construct a genome-scale metabolic model of *A.woodii* using a sequenced strain (Poehlin, 2012)
- Gain insights into *A.woodii* metabolism using metabolic modelling.
- *In silico* strain engineering to contribute to the effort in producing an industrially relevant *A.woodii*.

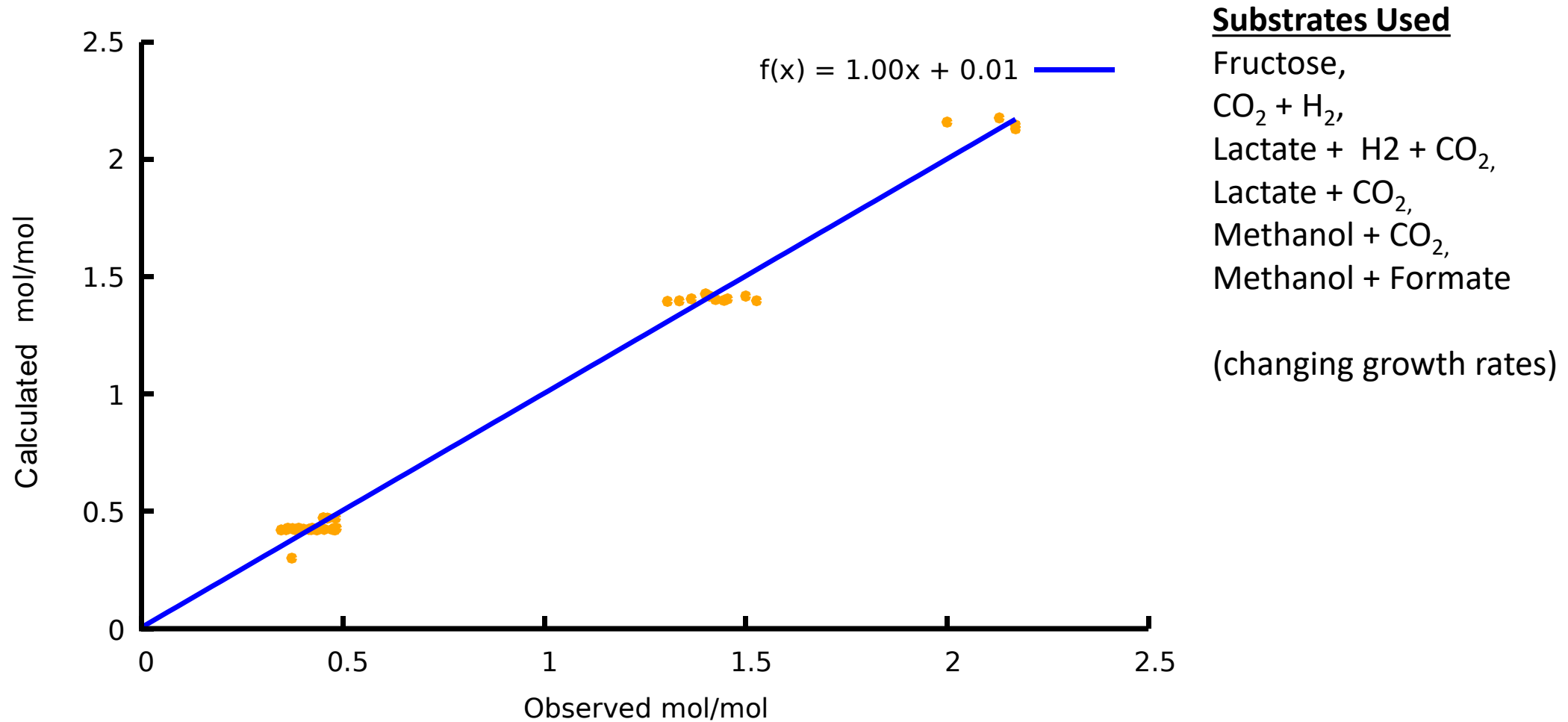
Modelling Approaches

- Structural modelling. Metabolism at **steady state**; where the **change in concentration** of internal metabolites and the **change in reaction** fluxes is zero.
- **Construction** of a genome-scale metabolic model of *A.woodii* using a recently sequenced genome of strain DSMZ1030.
- Model **validation**
- **Extraction of a sub-model** from the genome-scale model for elementary mode analysis

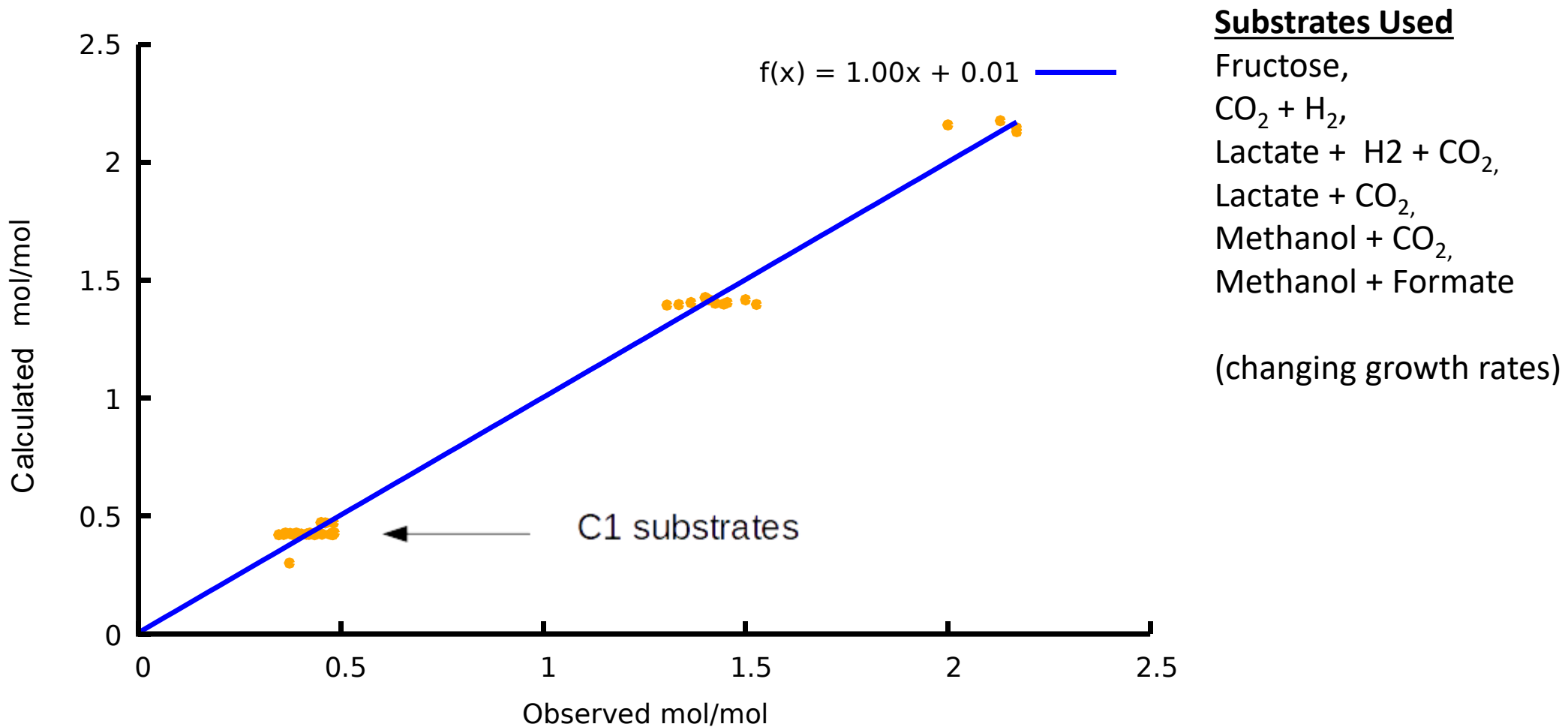
Model Validations

- Conservation of mass. Carbon, nitrogen, phosphorus, sulphur atoms cannot be produced unless appropriate substrate is supplied
- Conservation of energy. ATP cannot be produced without substrate, and redox reactions cannot occur unless appropriate substrates are supplied
- Substrates reported to support growth in the literature where tested against what is supported in the model
- Compared published acetate yields in several conditions to model produced acetate yields in same conditions.

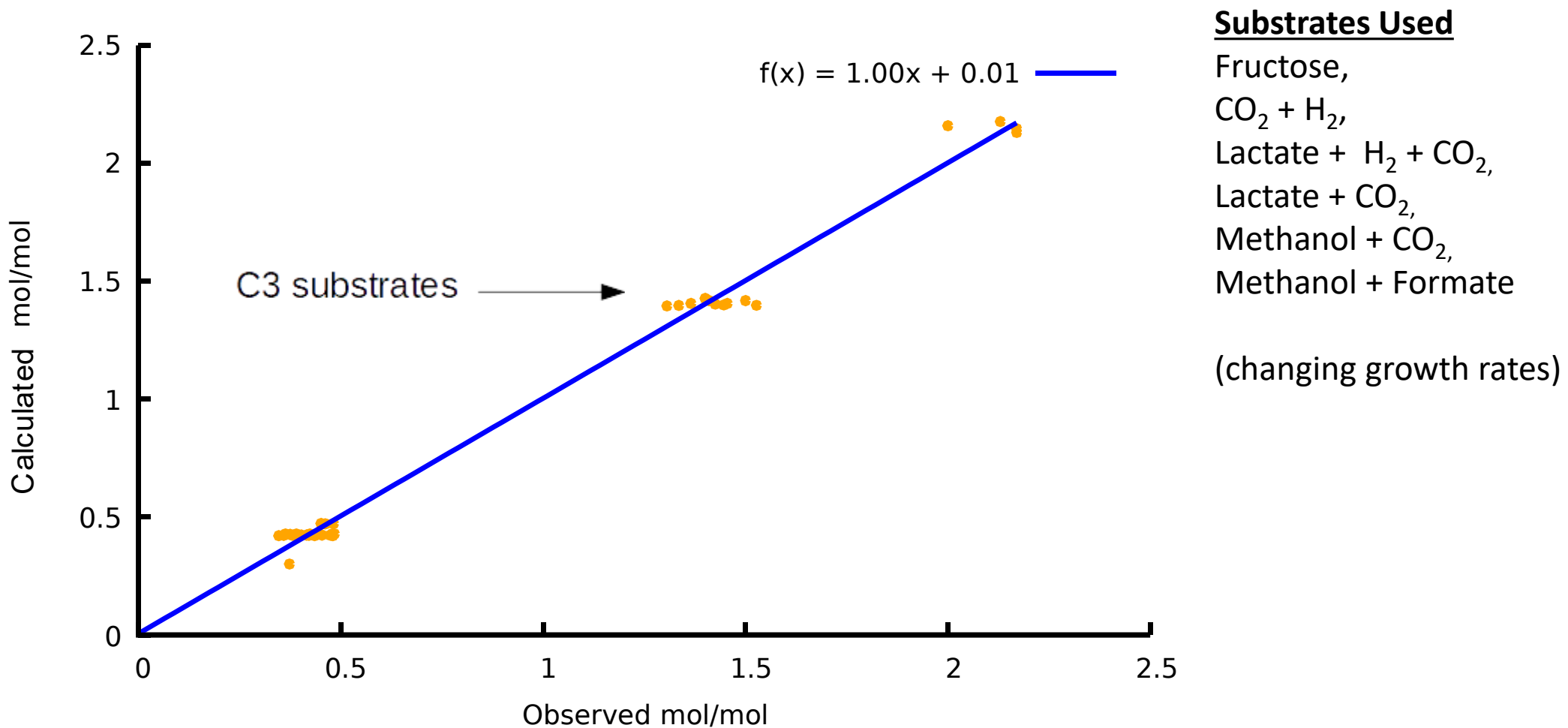
Model Predicted Acetate Yields vs Observed Acetate Yields



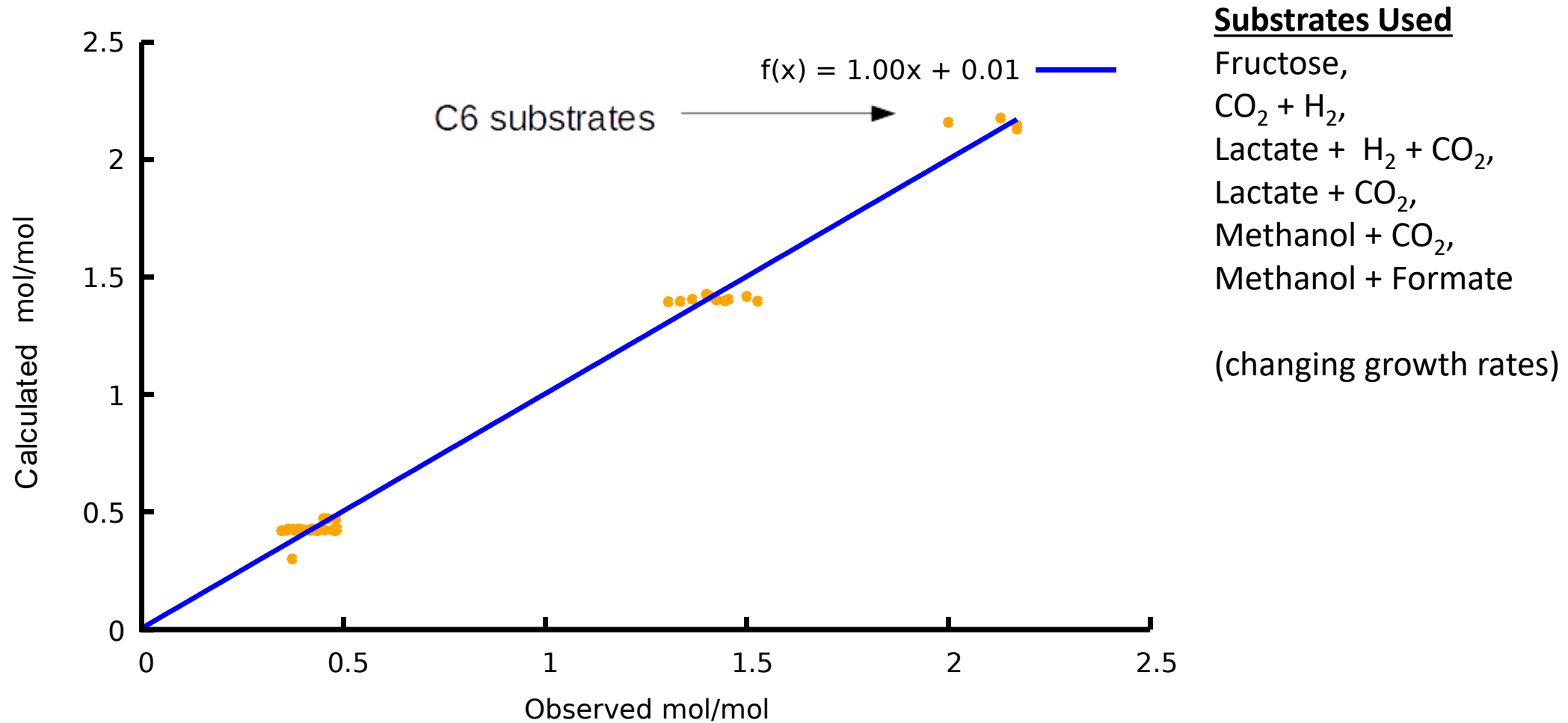
Model Predicted Acetate Yields vs Observed Acetate Yields



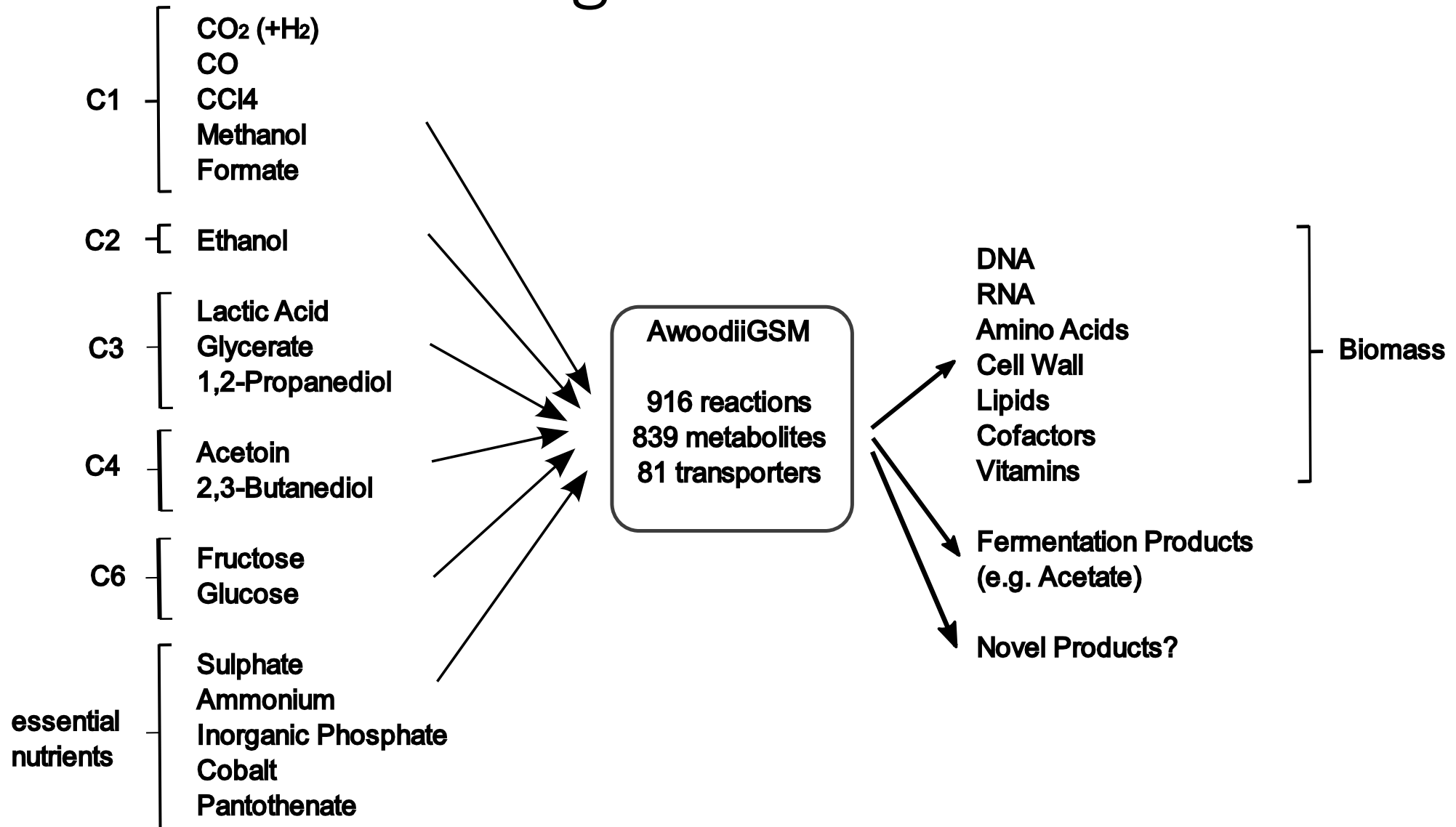
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Model Predicted Acetate Yields vs Observed Acetate Yields



A. woodii Genome-scale Metabolic Model – high level view



Complete Growth Stoichiometry

Growth on $\text{CO}_2 + \text{H}_2$ ($\mu = 0.2 \text{ h}^{-1}$):

171mM CO_2 + 343mM H_2 + 0.04mM SO_4 + 2.4mM NH_3 + 0.4mM Pi + trace components

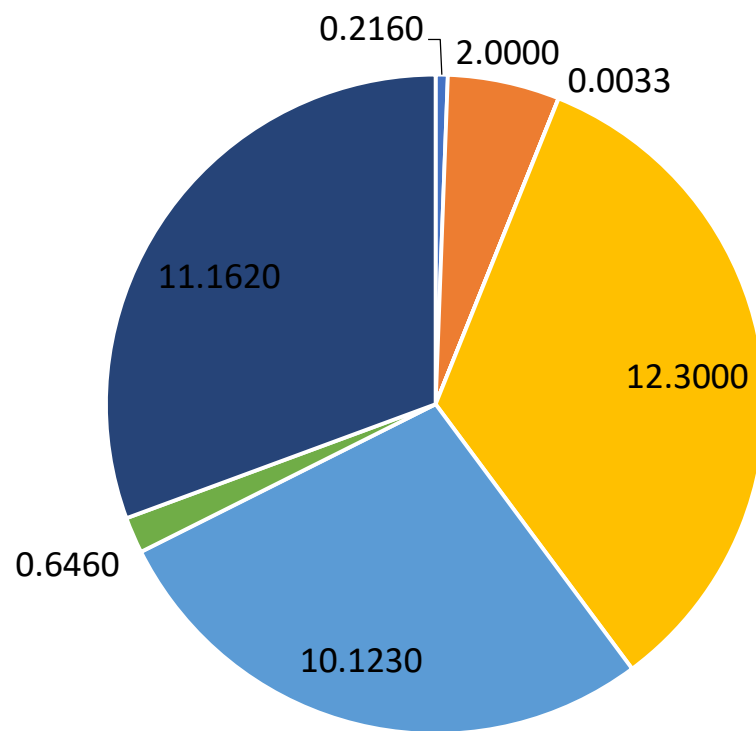


1g Biomass + 80.3mM Acetate + trace components

93.8% Carbon in acetate

6.1% Carbon in biomass

ATP producing reactions during growth – Fructose



- Pyruvate-phosphate dikinase
- ATP synthase
- Nucleoside-diphosphate kinase
- Acetate Kinase
- Pyruvate kinase
- PEP-carboxy kinase
- Phosphoglycerate kinase

Extracting a Bioenergetic Core

Rationale:

- Useful for analysis not possible on large model
- Would represent all catabolic reactions involved with energy metabolism

Method:

- Available substrates are combined in all possible pairs
- *precondition* - substrate pair must support growth (e.g. a pair like H₂ + caffeine would be excluded)
- ATP extraction is computed with 4 LP formulations per substrate (1,084 total)
- All reactions which show up at least once are saved
- Yield of ATP is calculated as ATP/C-mol

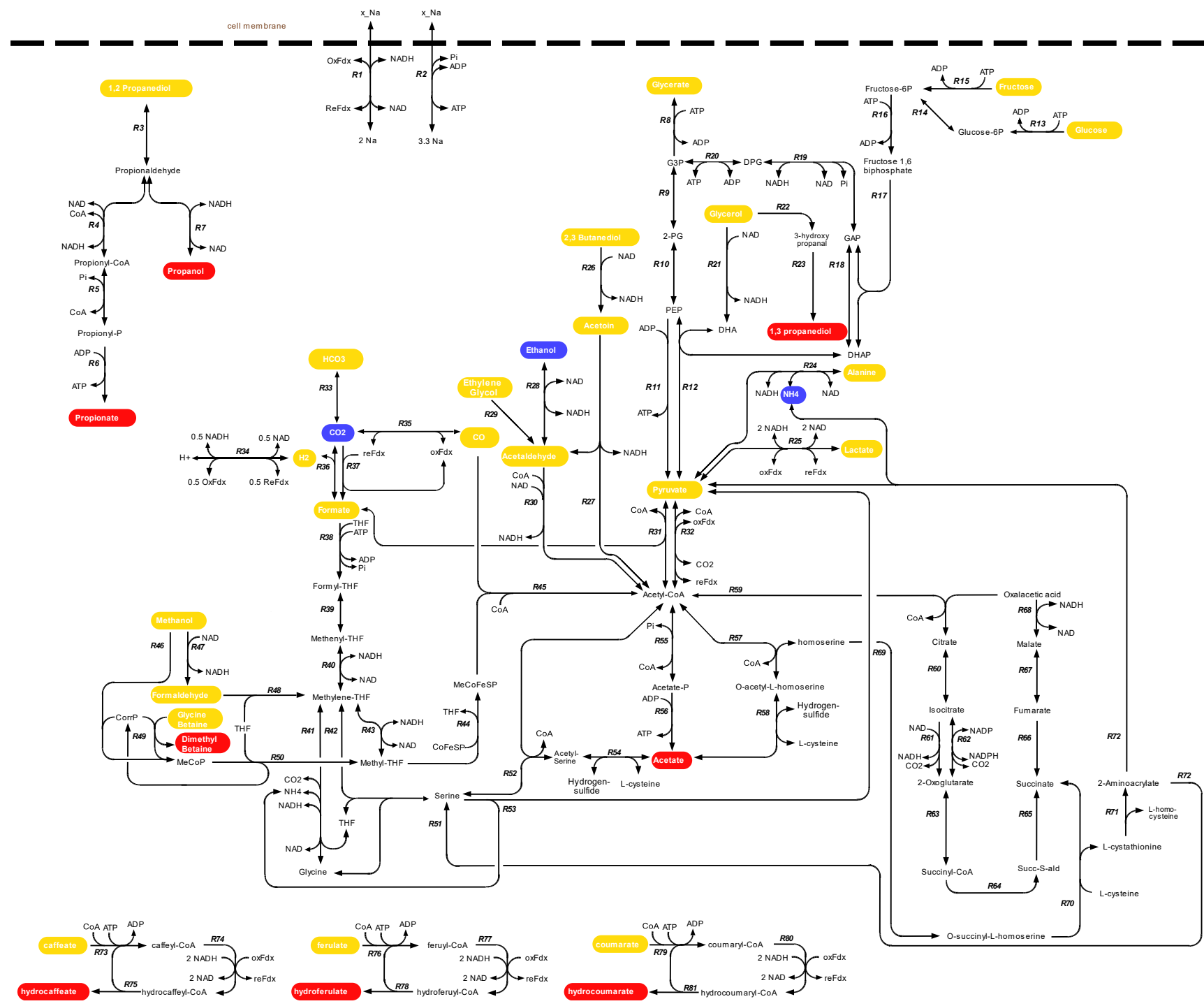
Bioenergetic Core -draft

Reactions: 837 -> 83

Metabolites: 848 -> 95

Comprises all of the reactions needed to extract ATP from 271 growth substrates.

Amenable to elementary modes analysis



demo