



19th European Conference on Computational Biology

Planetary Health and Biodiversity

31st August 8th September 2020

T05 Part 2: Introduction to COBRA

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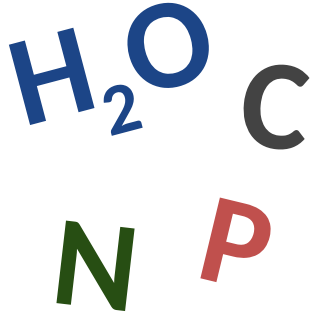
Marta Cascante - UB (martacascante@ub.edu)



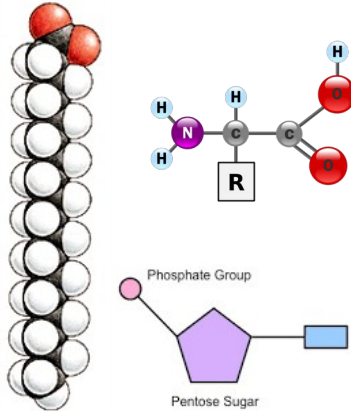
What is a cell made of?

Level (scale) of description

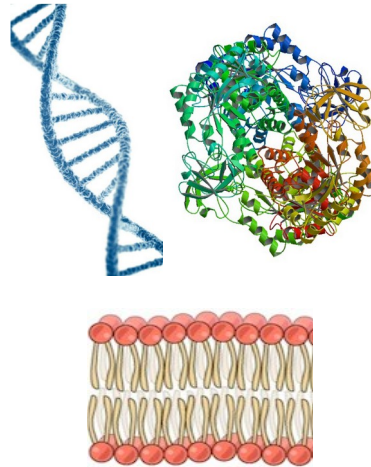
Chemistry



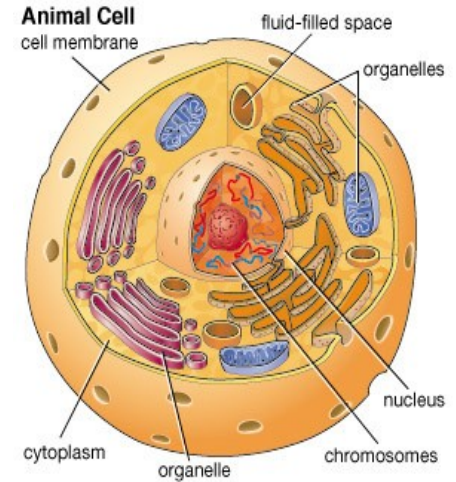
Building blocks



Macromolecules



Cell



Cell's molecular factory: metabolism → What is metabolism?

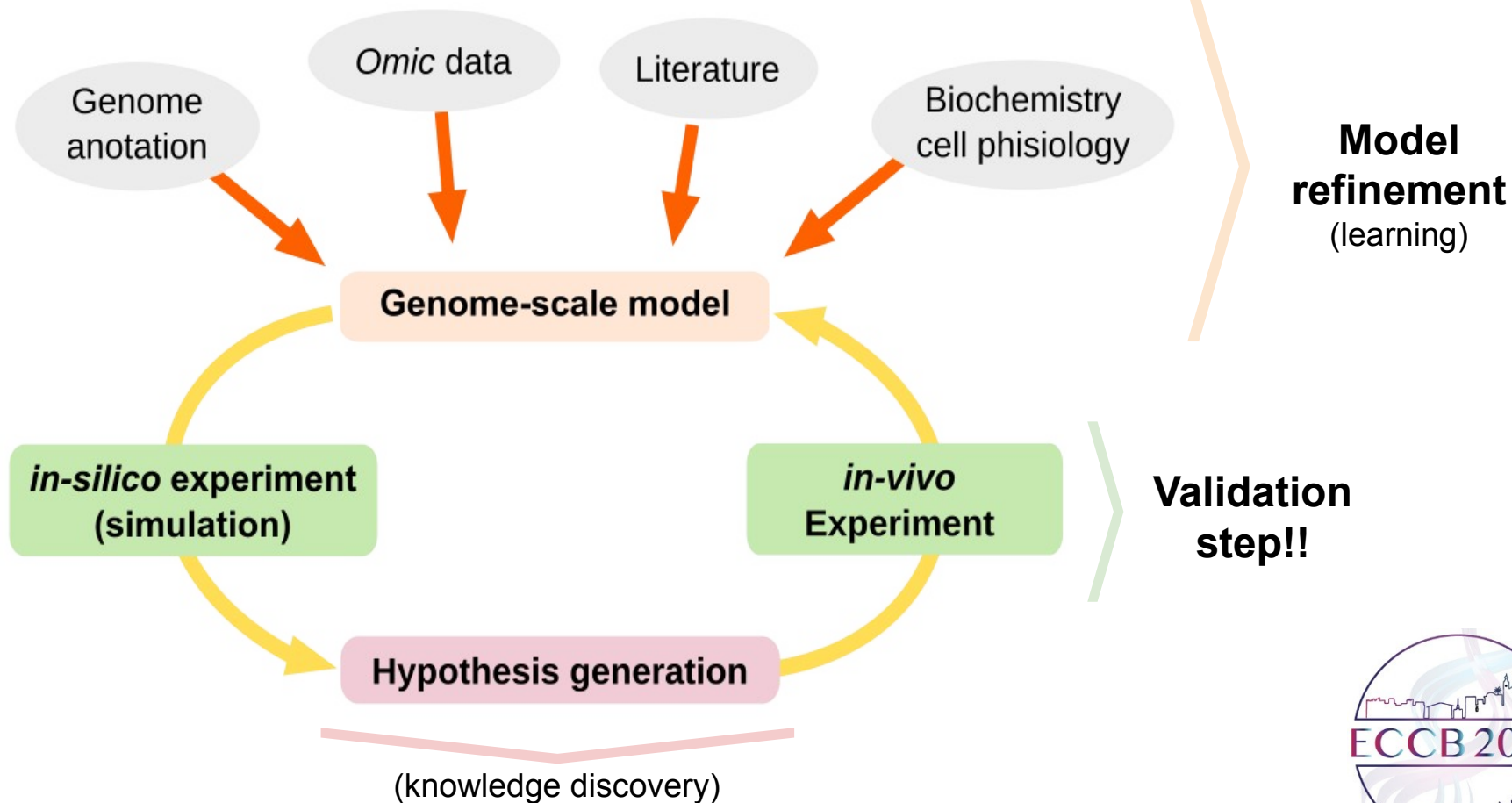
What is a Genome-scale metabolic model?

Is a computational representation the metabolism of a cell

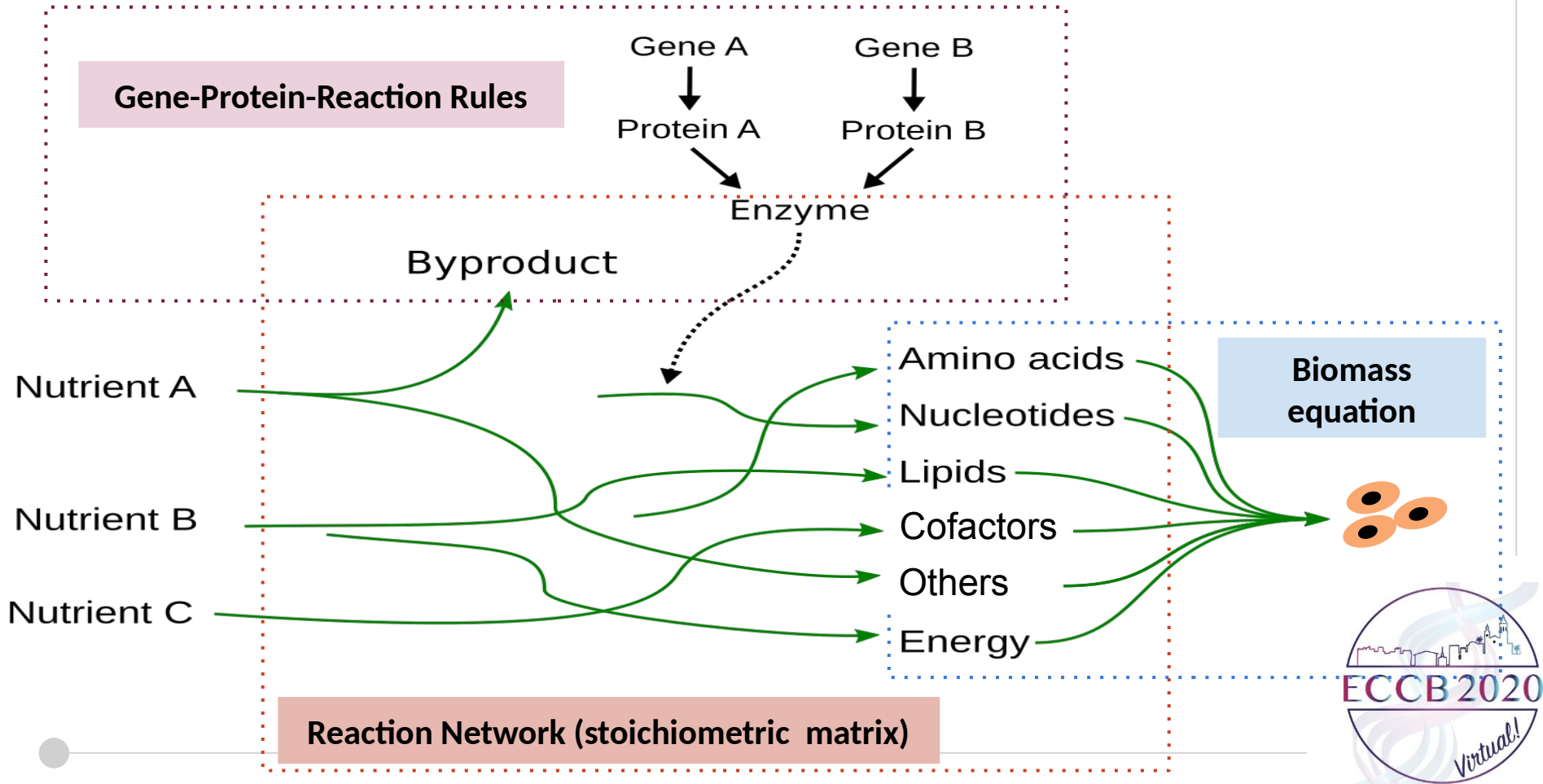
- **Includes:** genes and complexes, biochemical reactions, metabolites, transporters, cell compartments.
- **Uses:** Omic data integration, simulations, *in-silico* predictions.



Genome-Scale Modeling in Systems Biology



Genome-scale metabolic model

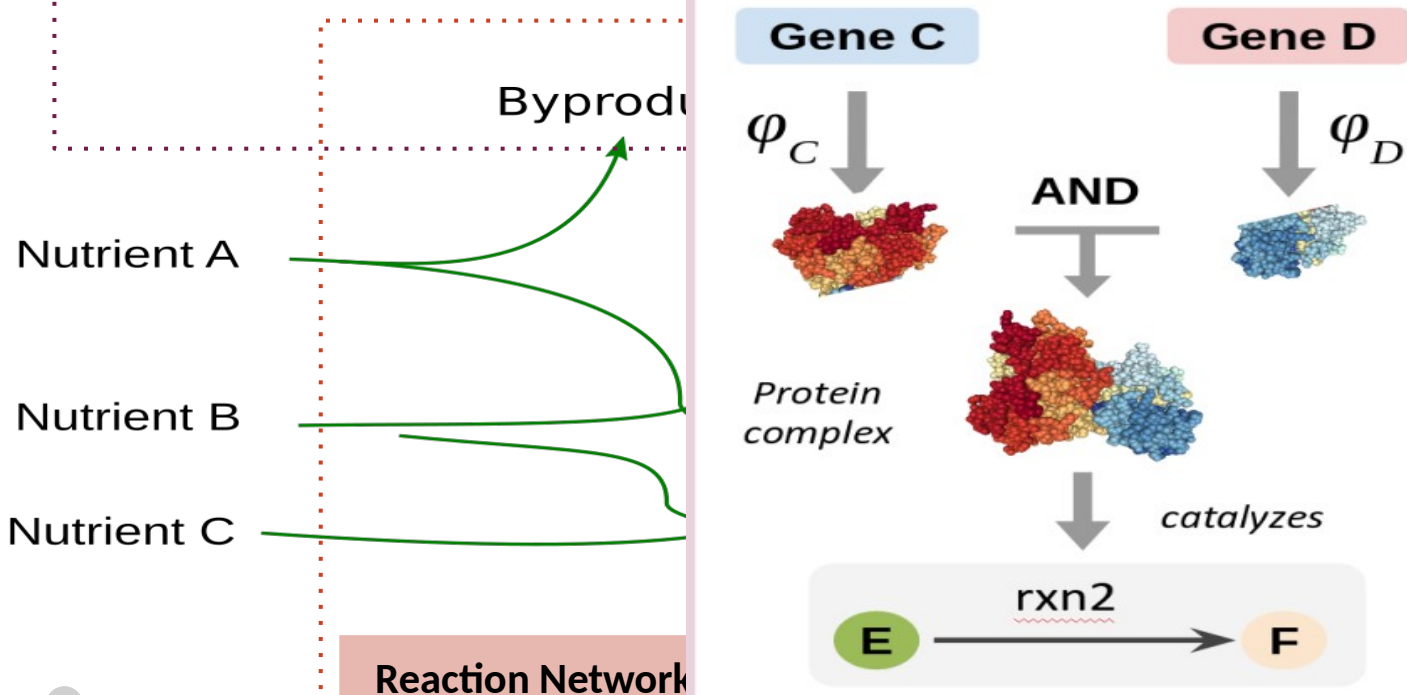


Genome-scale metabolic model

Gene-Protein-Reaction Rules

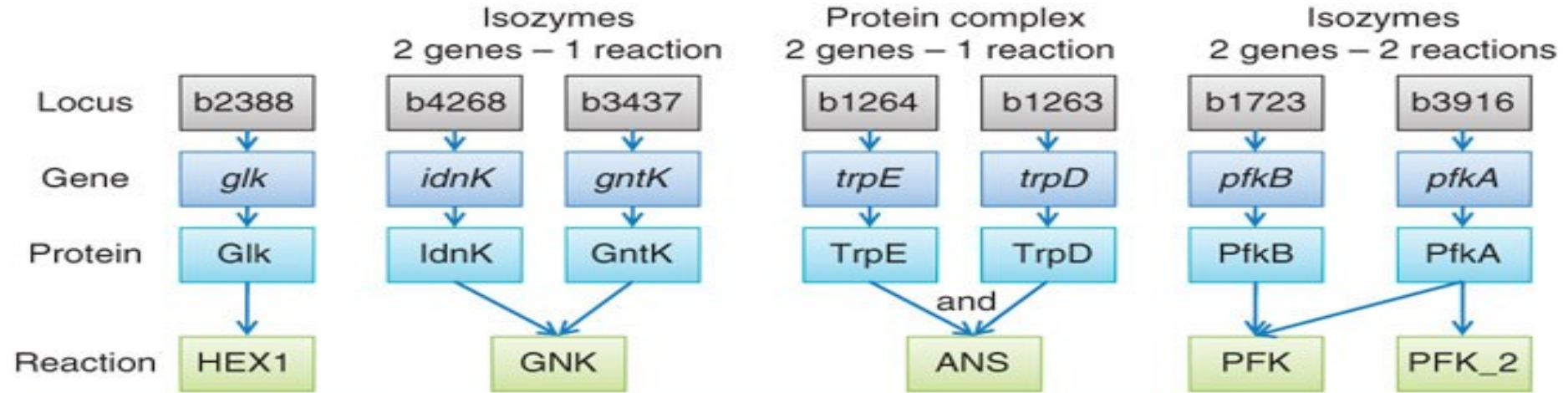
Gene-Protein Reaction Rules

Logical relation between gene complexes and biochemical reactions



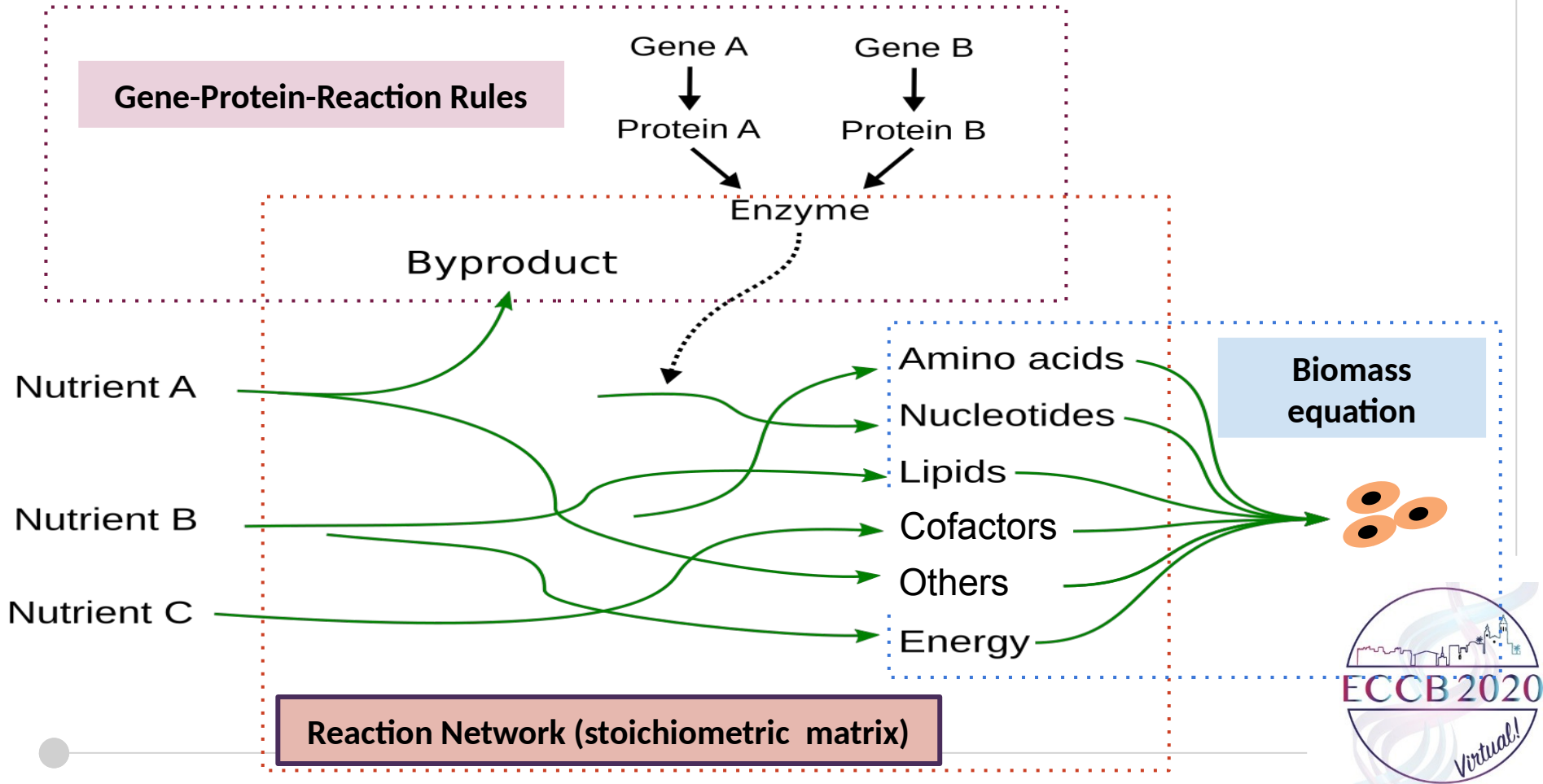
Biomass equation

Gene Protein Reaction rules: examples



Reaction abbreviation	Reaction name	E. C.number	GPR
HEX1	Hexokinase (D-glucose:ATP)	2.7.1.1	(b2388)
GNK	Gluconokinase	2.7.1.12	(b3437) or (b4268)
ANS	Anthranilate synthase	4.1.3.27	(b1264) and (b1263)
PFK	Phosphofructokinase	2.7.1.11	(b1723) or (b3916)
PFK_2	Phosphofructokinase (2)	2.7.1.11	(b3916)

Genome-scale metabolic model



Genome-scale metabolic model

Gene-Protein-Reaction Rules

Gene A

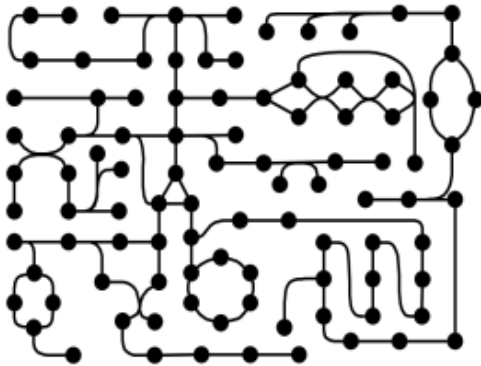


Gene B



Metabolic Network: Human Metabolic model Recon 2.2.1

Reactions, Transports, Metabolites & Cell compartments (-> stoichiometric matrix)



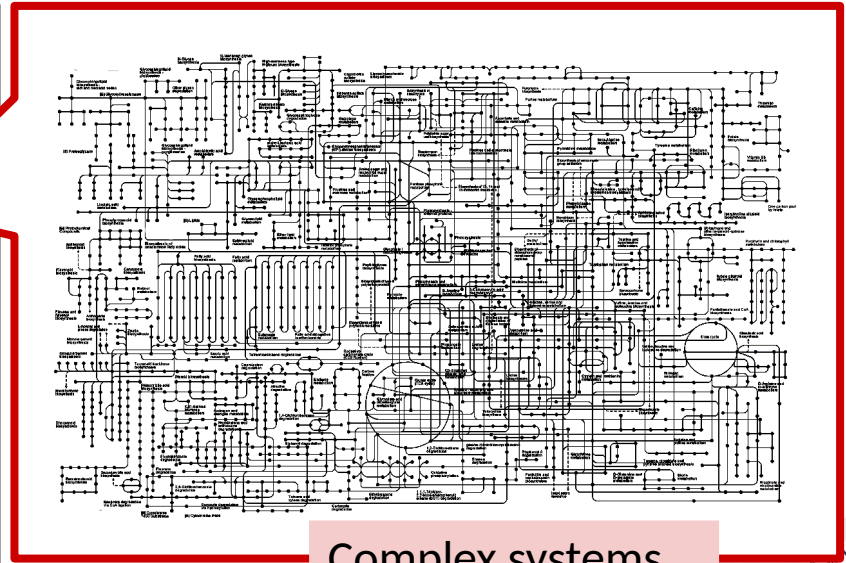
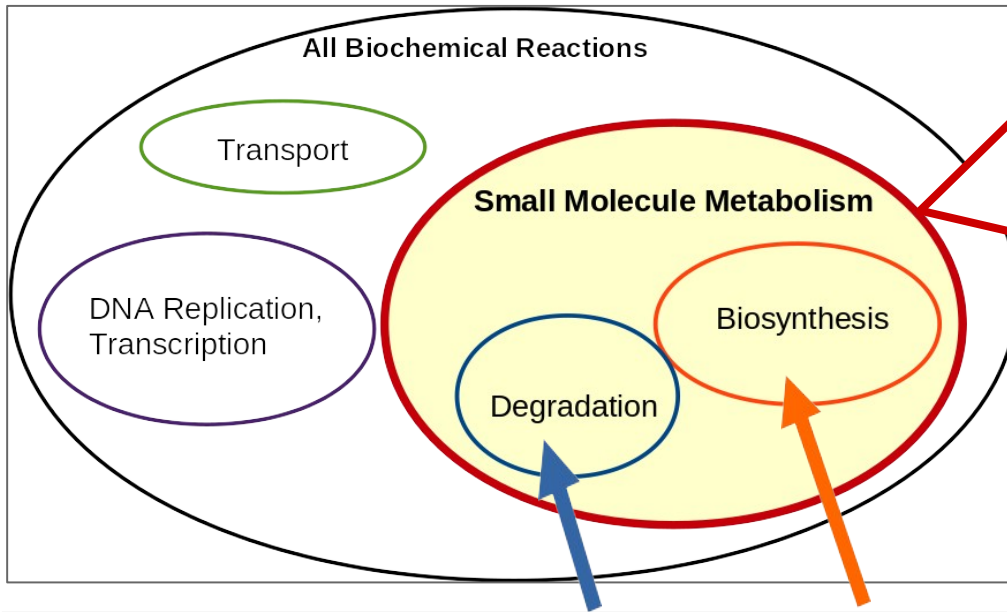
	...	rxn2
A		0
B		0
⋮		
E		-1
F		+1

	Total
Genes	1675
Metabolites	5324
Reactions	7785

Reaction Network (stoichiometric matrix)

Metabolism: the molecular factory of the cell

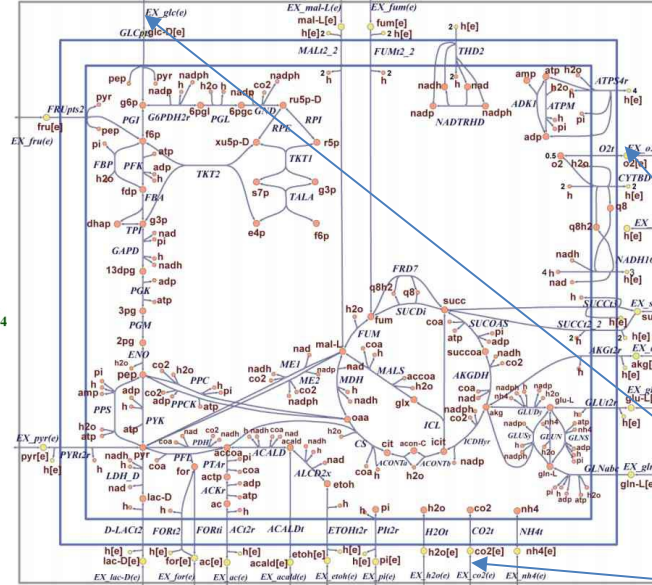
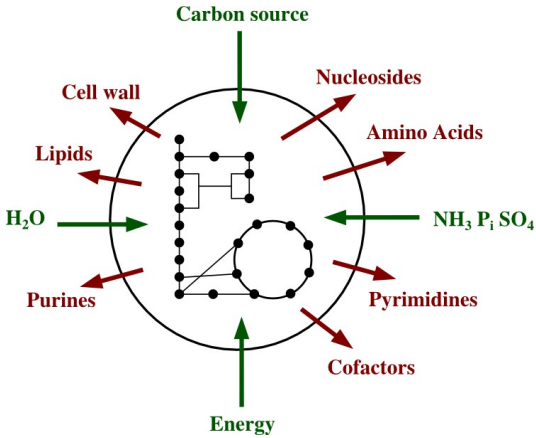
Is the **network** of biochemical reactions and transport processes that occur within a cell and allow **cell maintenance and growth**



Complex systems

- Generation of **energy (catabolism)** and **building block (anabolism)**
- Include the enzymatic reaction that act over small molecules

Stoichiometric Matrix → Mass Balance Equations & Exchange fluxes (E.coli core)



Mass Balance:

$$d[13\text{pg}(c)] / dt = \text{GAPD} - \text{PGK}$$

$$d[2\text{pg}(c)] / dt = \text{PGM} - \text{ENO}$$

$$d[6\text{pgc}(c)] / dt = \text{PGL} - \text{GND}$$

$$d[6\text{pgl}(c)] / dt = \text{G6PDH2r} - \text{PGL}$$

$$d[\text{cit}(c)] / dt = \text{CS} - \text{ACONTa}$$

$$d[\text{dhap}(c)] / dt = \text{FBA} - \text{TPI}$$

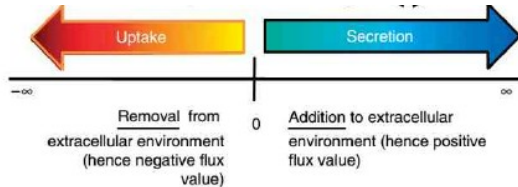
...(continues)

(c): cytosol

Exchange fluxes: variables that represent the exchanges of nutrients/by-products between the organism and its environment (uptake/secretion)

Lower bound:
rate of nutrient uptake

Upper bound:
rate of nutrient release



units: mmol/gDw/hr

	Min	Max
Glucose	- 6	0
Oxygen	- 20	0
CO ₂	0	Inf

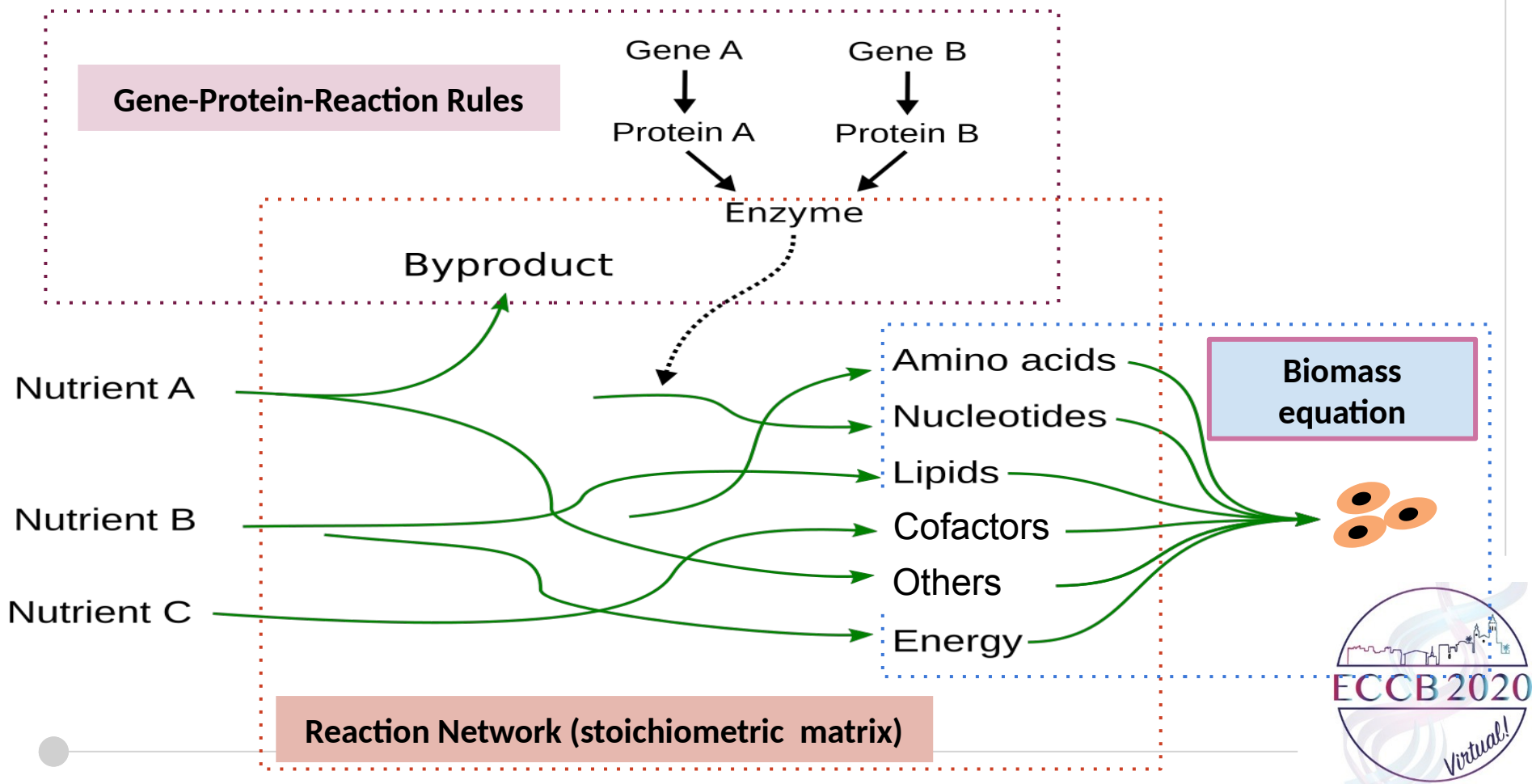
GLC_{Ex} O_{Ex} CO_2_{Ex}

-1

-1



Genome-scale metabolic model



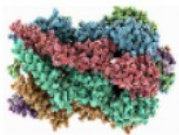
Genome-scale metabolic model

Biomass Equation

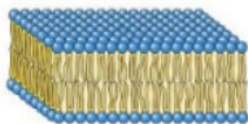
Quantitative molecular composition of a cell



DNA + RNA



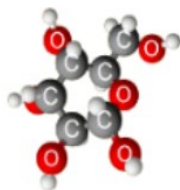
Proteins



Lipids



Vitamins/coenzymes



Carbohydrate

Biomass	Total
RNA components:	4
DNA components:	4
Protein components:	20
Carbohydrates:	1
Lipid components:	16
Cofactors and vitamins:	10

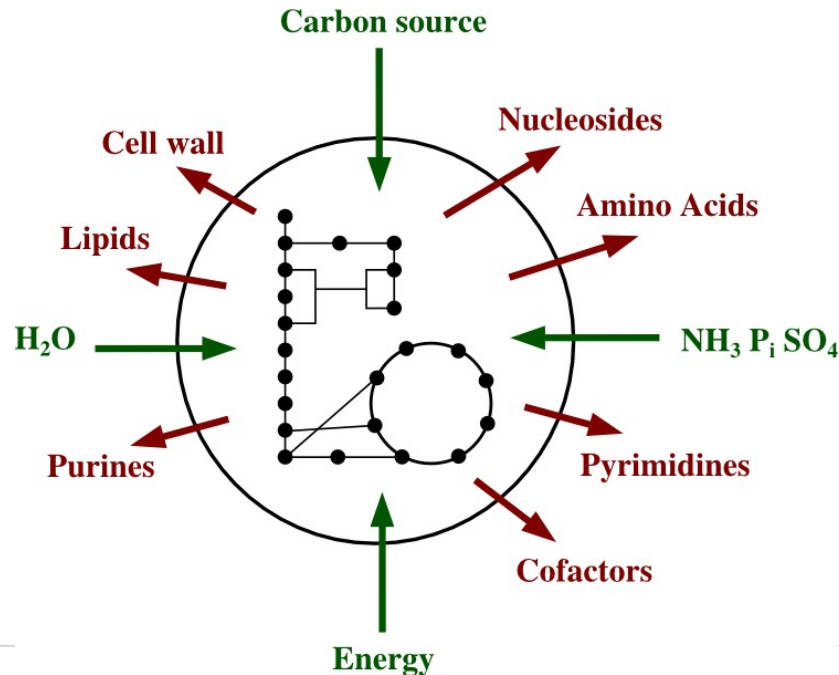
**Biomass
equation**



Reaction Network (stoichiometric matrix)

Biomass Equation of a cell

Description in stoichiometric terms of all components present in a gram (dry weight) of a cell.



Metabolite	Demand (mmol)
ATP	41.2570
NADH	-3.5470
NADPH	18.2250
G6P	0.2050
F6P	0.0709
R5P	0.8977
E4P	0.3610
T3P	0.1290
3PG	1.4960
PEP	0.5191
PYR	2.8328
AcCoA	3.7478
OAA	1.7867
AKG	1.0789

Neidhardt, et al. *Physiology of the Bacterial Cell* (1990)

Modeling metabolic systems

Kinetic Modelling (Differential equations)

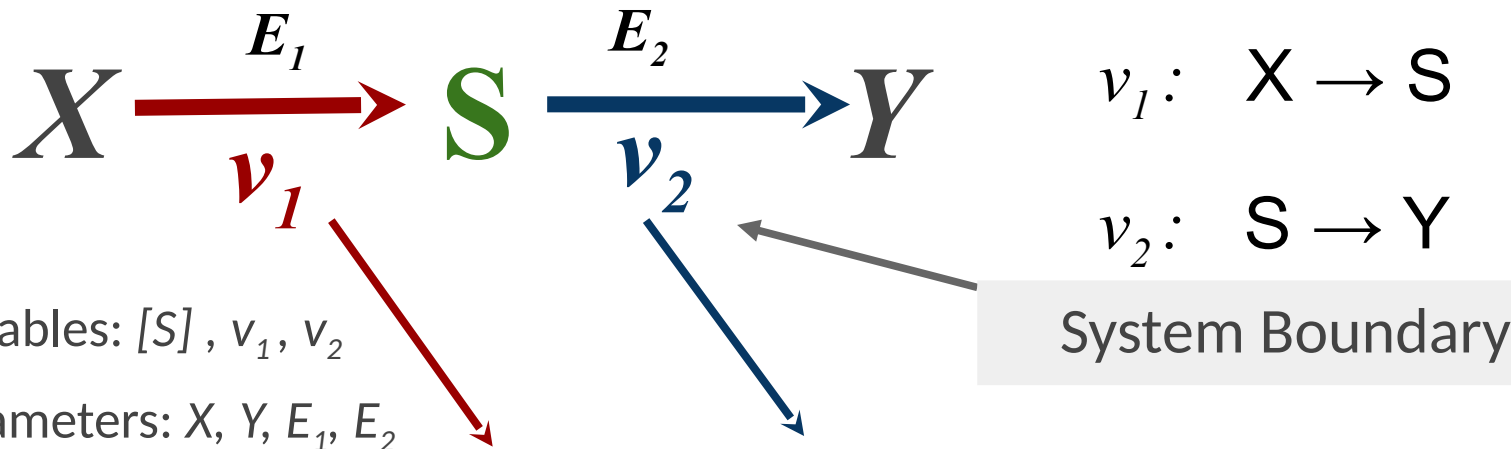
- Time evolution of system variables (+)
- Sensitivity Analysis (+)
- Unknown Kinetic Parameter (-)
- Unknown Enzymatic Mechanisms (-)

Constraint-Based Modeling (CBM)

- Only need stoichiometry (+)
- Structure is an invariant property (+)
- Computationally tractable using **genome-scale models** (+)
- No information of metabolite concentrations (-)
- Only valid under steady-state (-)



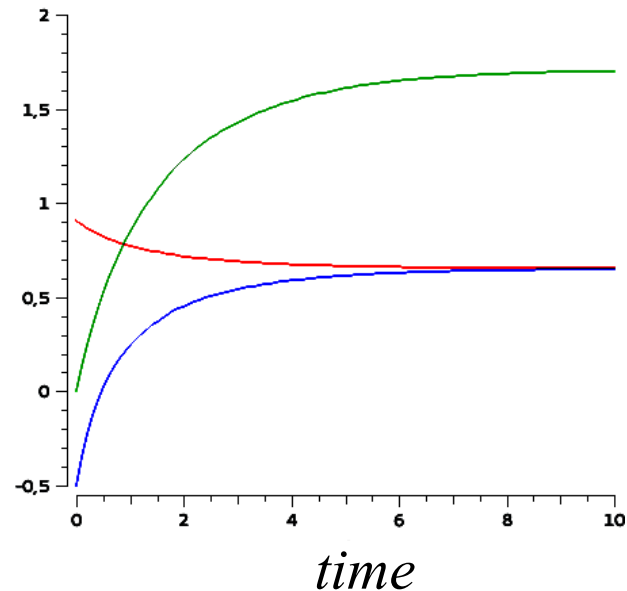
Modeling metabolic systems



Kinetic Mechanisms:

- Mass action
- Michaelis-Menten
- Others

Kinetic description



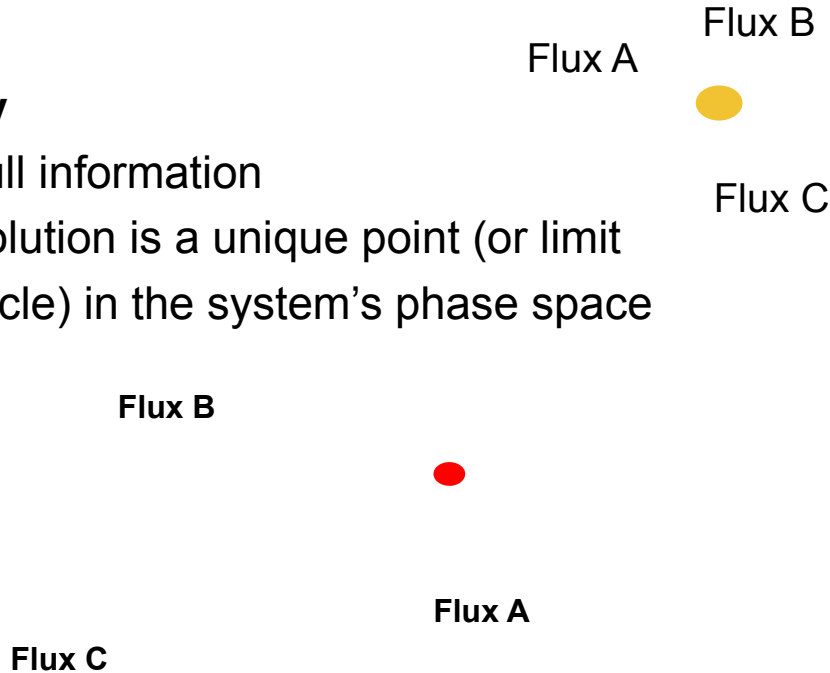
Many parameters!

$$\frac{d[S]}{dt} = \left(\frac{v_{f(v1)}[X] - v_{r(v1)}[S]}{K_{ms(v1)} + \frac{[X]}{K_{ms(v1)}} + \frac{[S]}{K_{mp(v1)}}} \right) + \left(\frac{v_{f(v2)}[S] - v_{r(v2)}[Y]}{K_{ms(v2)} + \frac{[S]}{K_{ms(v2)}} + \frac{[Y]}{K_{mp(v2)}}} \right)$$

Constraint-based approach

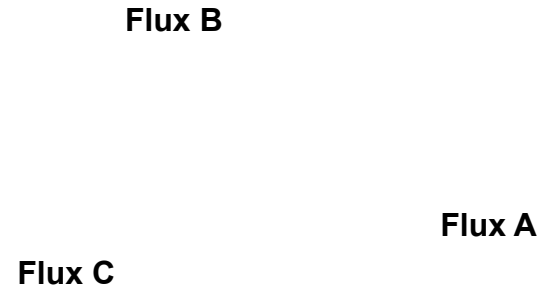
Theory

- Full information
- Solution is a unique point (or limit cycle) in the system's phase space



Genome-scale

- Incomplete information
- Solution (flux) space

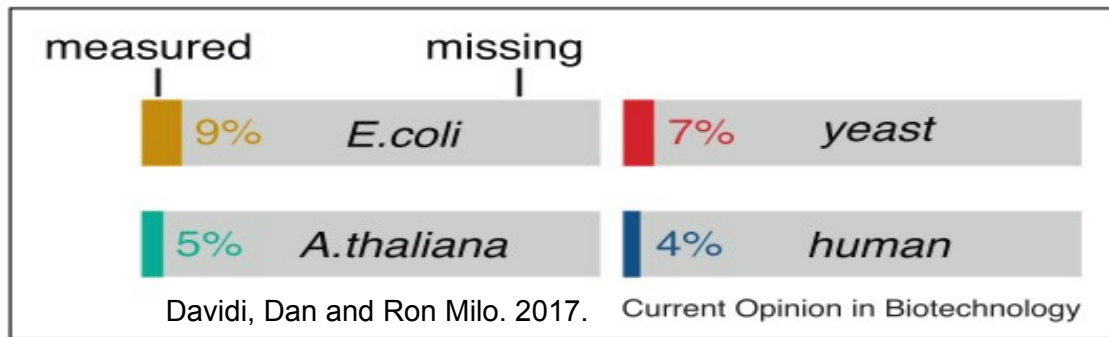


For genome-scale reconstructed metabolic network there are still not enough information to create the full kinetic description → too many unknown parameters!

Kinetic constants: the state of the art

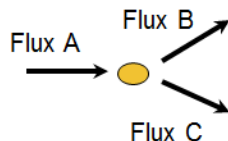
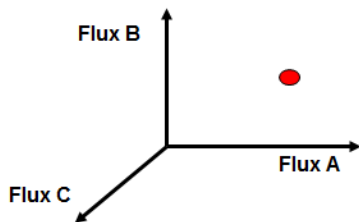
N° of reactions from GEMs:

- *E. coli* (iJO1266): 2251
- Budding yeast (iND750): 1149
- Arabidopsis (--): 1363
- Human (Recon1): 7785



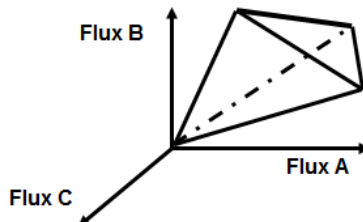
Theory

- Full information
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Genome-scale

- Incomplete information
- Solution (flux) space



For **genome-scale** reconstructed metabolic network there are still not enough information to create the full **kinetic description** → **too many unknown parameters!**

Constraint-based modeling

Glucose + ATP



Glucose-6-P + ADP

Glucokinase (single reaction)

Glucokinase

Glucose

-1

ATP

-1

G-6-P

+1

ADP

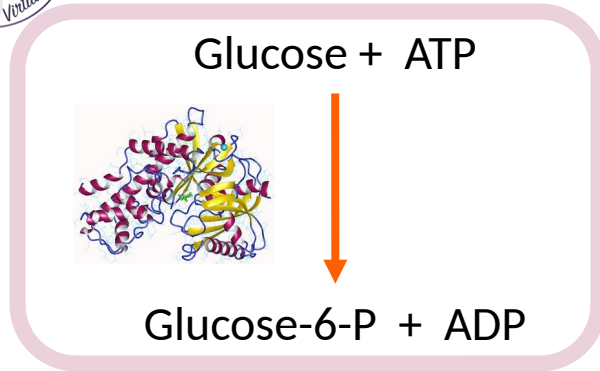
+1

→ N

Stoichiometric matrix N (metabolic network)

The Constraints

Constraint-based modeling



Glucokinase (single reaction)

Glucokinase		
Glucose	-1	$\rightarrow N$
ATP	-1	
G-6-P	+1	
ADP	+1	

Stoichiometric matrix N (metabolic network)

The Constraints

Mass Balance

$$N \cdot v = 0$$

Thermodynamics

$$v_i > 0$$

Capacities (bounds)

$$v_i < v_{max}$$

Flux Space

Cell Objective
Flux Balance Analysis

$$\text{Max } c^T \cdot v$$



How does it look (under the hood)?



Genome-scale metabolic model naked

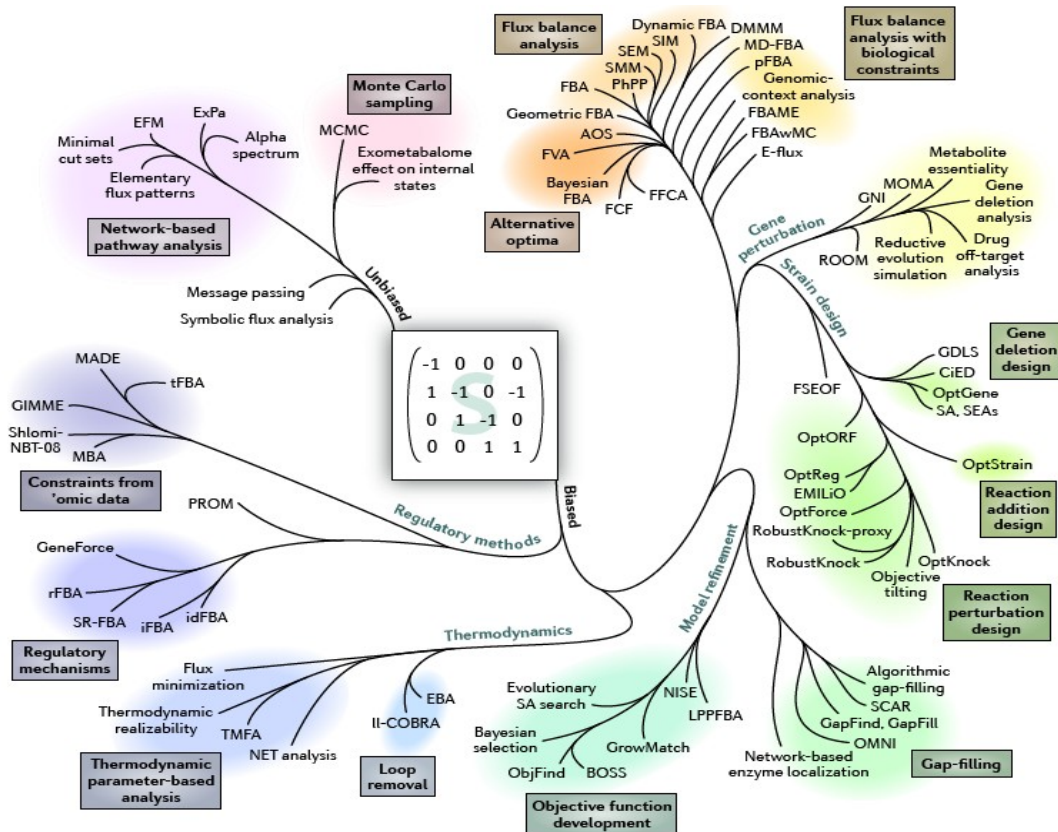


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    <unitDefinition id="mmol_per_gDW_per_hr"> ... </listOfUnitDefinitions>
  <listOfCompartments>
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    <compartment id="c" name="cytoplasm" size="1"/>
    ...
  </listOfCompartments>
  <listOfSpecies>
    <species id="M_10fthf5glu_c" name="10-formyltetrahydrofolate-[Glu](5)" compartment="c" charge="-6">
      <notes>FORMULA: C40H45N11O19</notes>
    </species>
    ...
  <reaction id="R_ENO" name="enolase" reversible="true">
    <notes>
      <p>GENE ASSOCIATION: HGNC:3350 or HGNC:3354 or HGNC:3353</p>
      <p>CONFIDENCE LEVEL: 5</p>
      <p>SUBSYSTEM: Glycolysis/gluconeogenesis</p>
    </notes>
    <listOfReactants>
      <speciesReference species="M_2pg_c" stoichiometry="1"/>
    </listOfReactants>
    <listOfProducts>
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      <speciesReference species="M_pep_c" stoichiometry="1"/>
    </listOfProducts>
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      <listOfParameters>
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        <parameter id="FLUX_VALUE" value="0" units="mmol_per_gDW_per_hr"/>
        <parameter id="OBJECTIVE_COEFFICIENT" value="0" units="dimensionless"/>
        <parameter id="LOWER_BOUND" value="-1000" units="mmol_per_gDW_per_hr"/>
      </listOfParameters>
    </kineticLaw>
  </reaction>
```

A phylogeny of **CO**nstraint-Based **Re**construction and **A**nalysis (**COBRA**) methods for GSMMs

Because of the versatility and scalability, more than 100 COBRA methods have been developed for constraint-based modeling and analysis. Many of them implemented in software packages: <http://opencobra.github.io/>

All are based on the analysis of the underlying metabolic network structure (i.e., the stoichiometric matrix).



The phylogenetic tree depict similarities between applications of the COBRA methods, and the underlying algorithms (Lewis et al. 2012)

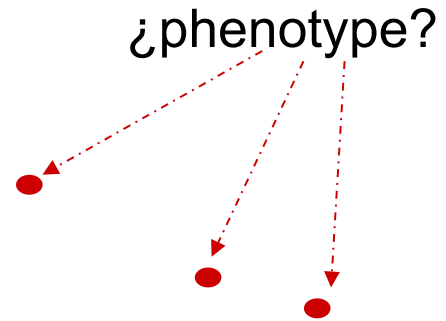


Predicting plausible physiological states (phenotypes)

¿How to identify a particular flux distribution?

Using optimization principles

- Adjusting with experimental data
- Maximize de Biomass production (growth rate)
- Maximize ATP production
- Minimize metabolic cost
- Multiple criteria



Flux space (~genotype)



Do we have Strategies to found a unique flux distribution?

Flux Balance Analysis (FBA)

Definition: computational strategy that uses a set of constraints (e.g. mass balance, thermodynamics, etc)) and linear optimization to determine the steady-state reaction flux distribution in a metabolic network by maximizing an objective function (e.g. growth rate)

Constraints:

$$N \cdot \vec{v} = 0$$

Mass balance

$$v_j \geq 0 \quad \forall j \in R_{irrev}$$

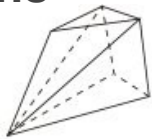
Thermodynamics

$$\alpha_j \leq v_j \leq \beta_j, \quad \forall j \in R$$

Enzyme and transport capacities

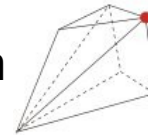
Feasible space
(flux space)

Optimizations



Feasible space (Genotype)

Maximize an objective function



Feasible space (Genotype)

Flux distribution (phenotype)

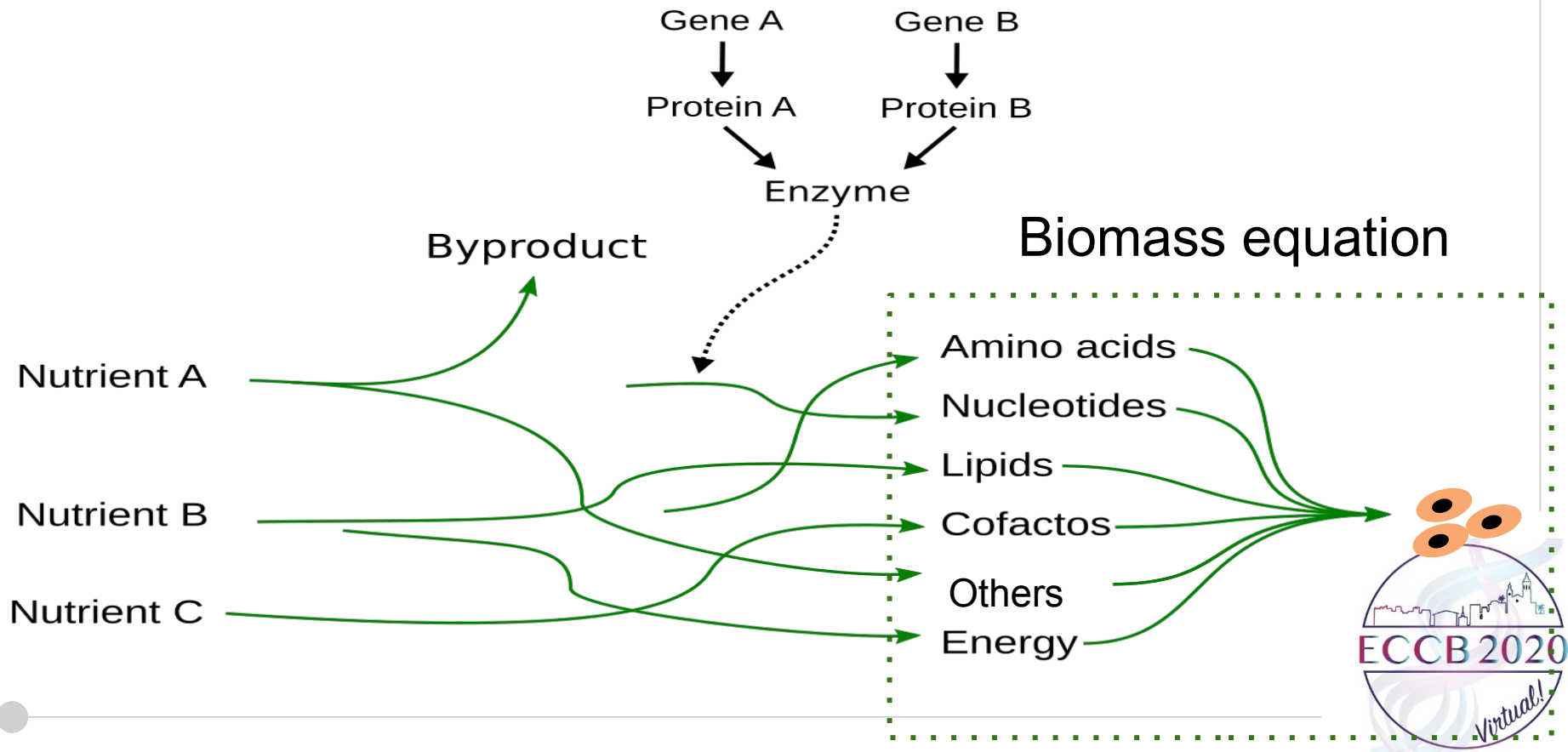
Applications

Gene *knockouts* predictions



<https://opencobra.github.io/> Open-source, community-developed code base for COnstraint-Based Reconstruction and Analysis.

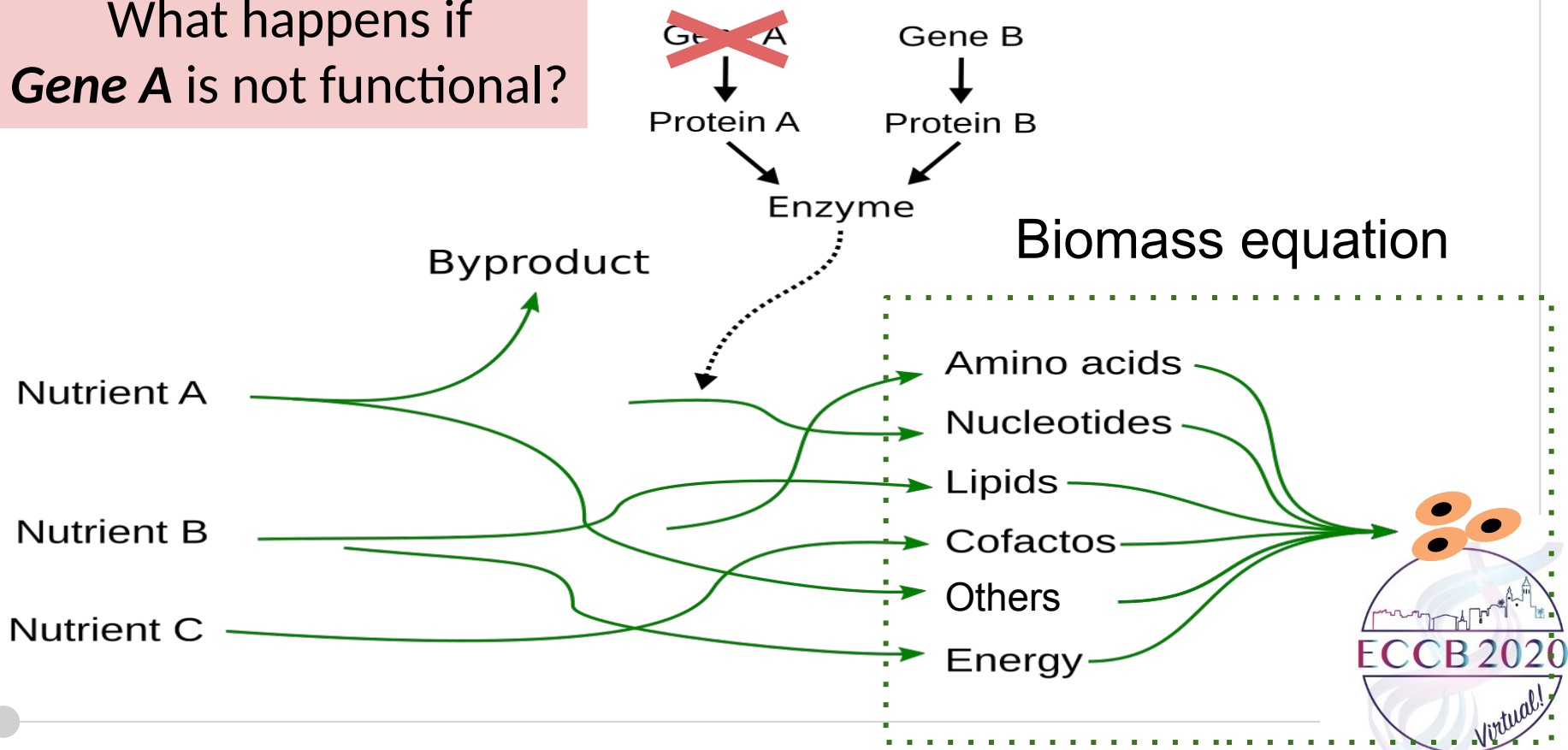
Simulations → *in-silico* predictions of gene KO effect





Simulations → *in-silico* predictions of gene KO effect

What happens if
Gene A is not functional?



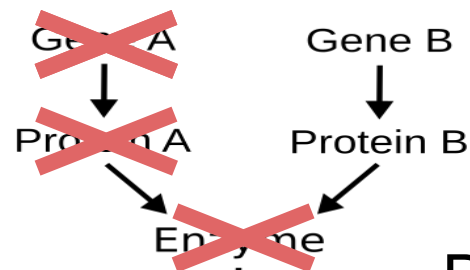


Simulations → *in-silico* predictions of gene KO effect

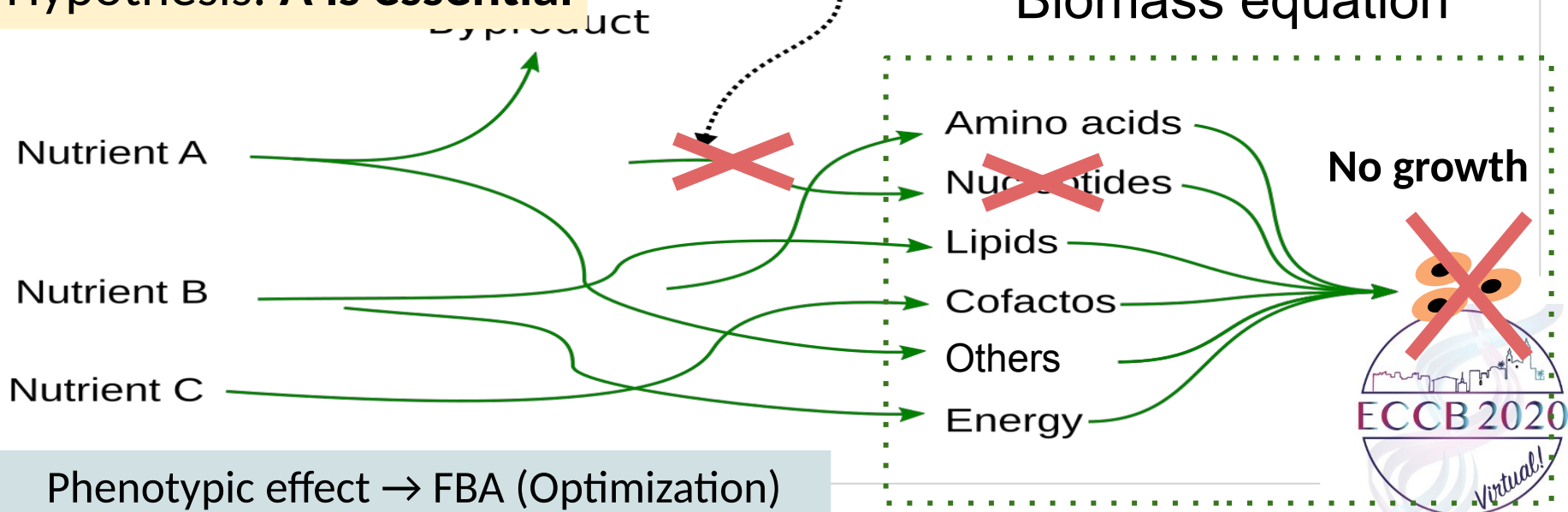
What happens if
Gene A is not functional?

Simulation → no growth

Hypothesis: **A is essential**



Biomass equation



Applications

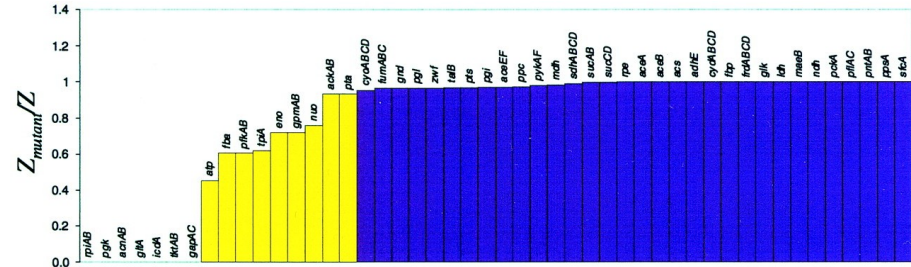
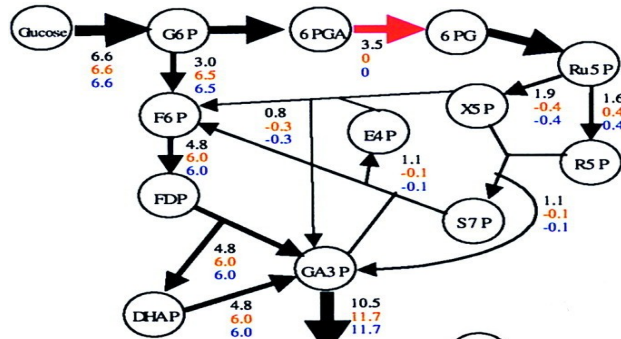
Gene *knockouts* predictions

Does it really work?

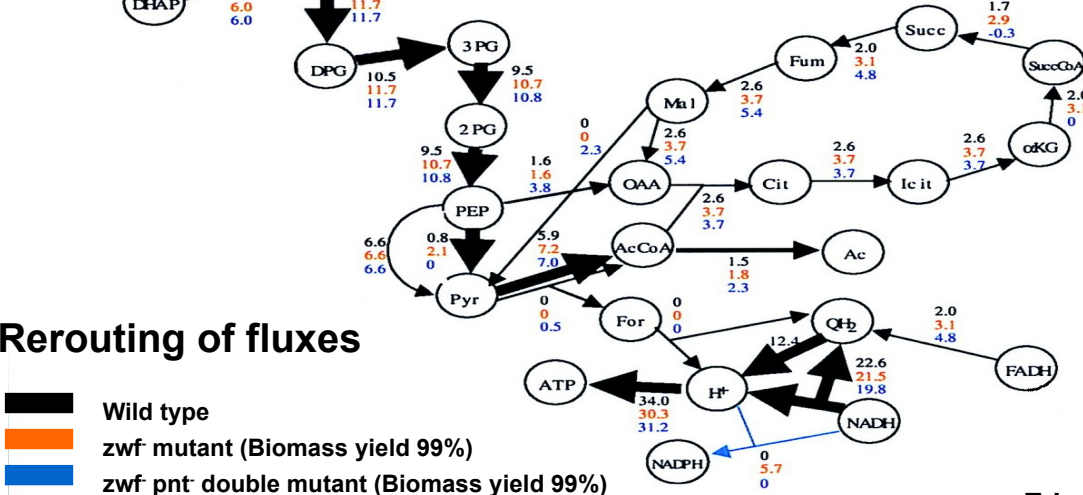


Knockout predictions: original study

In-silico knockout predictions; maximal biomass



86% (68 of 79 cases) of the *in-silico* predictions were consistent with the experimental data.



Rerouting of fluxes

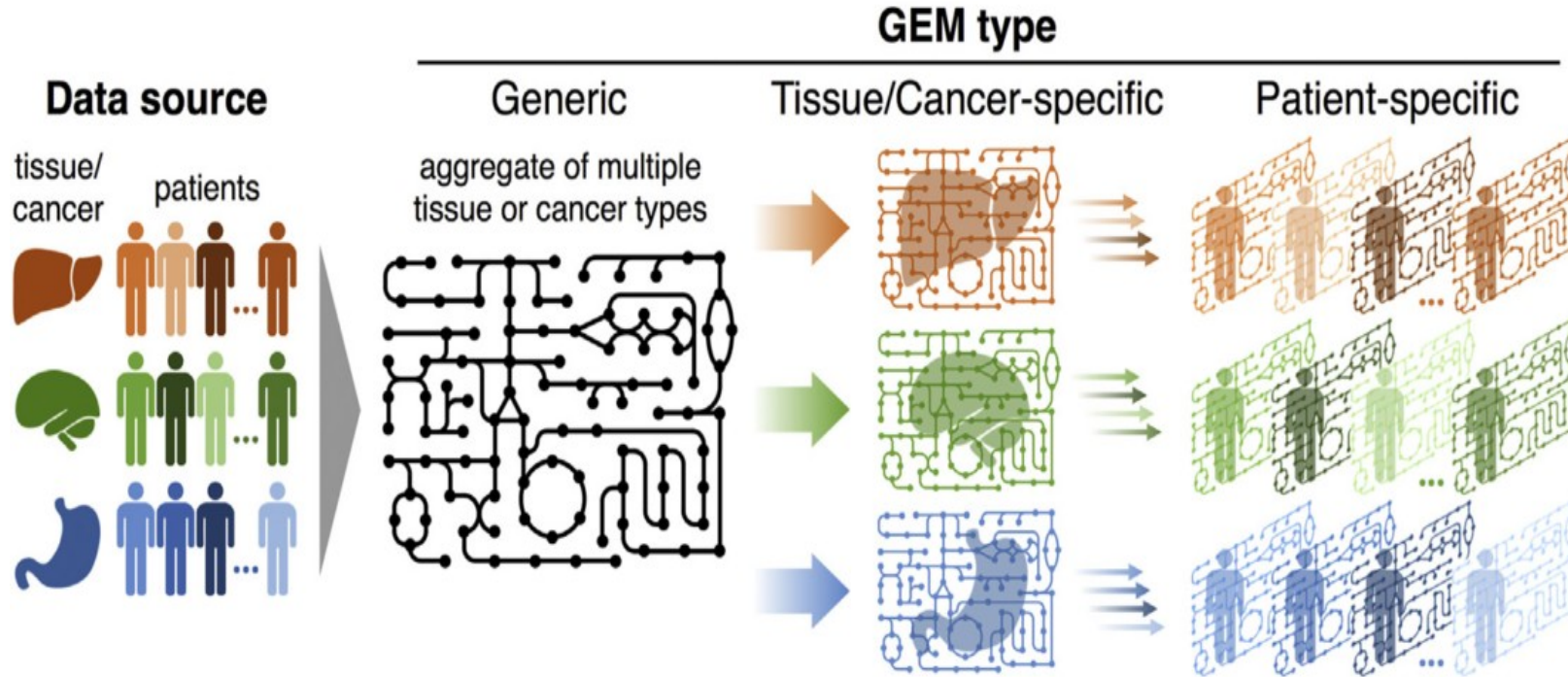
- Wild type
- zwf* mutant (Biomass yield 99%)
- zwf pnt* double mutant (Biomass yield 99%)

Edwards JS, Palsson BO. PNAS (2000)

Metabolic modeling in humans

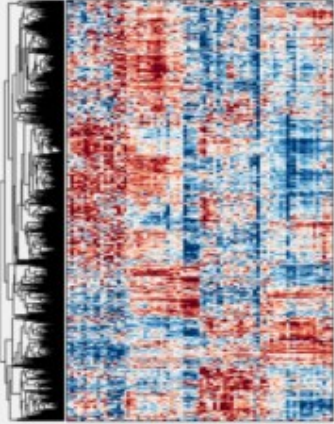


Metabolic modeling in humans



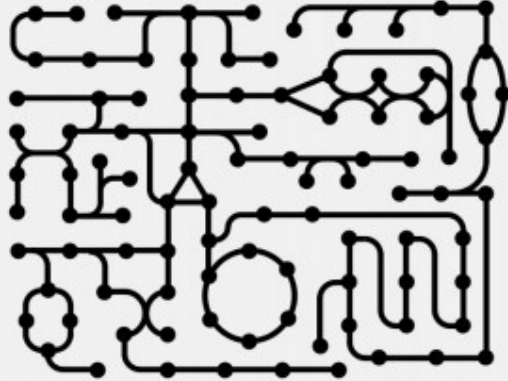
Context-Specific Metabolic Modeling (CSM)

collect omics data



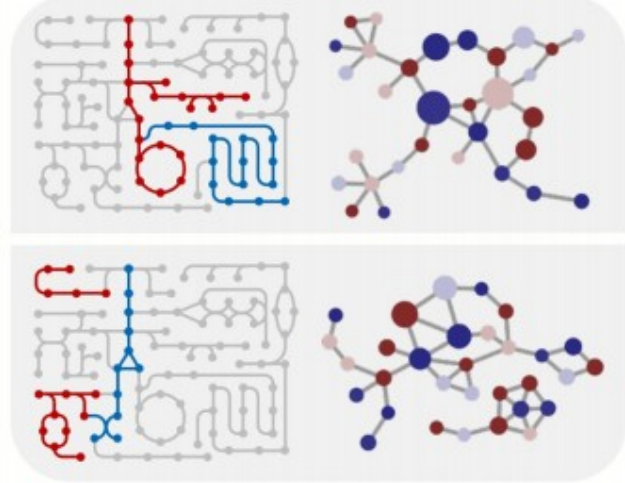
Cell Context (omics)

map to GEM



Universal Human metabolism

identify subnetworks, reporters



Cell-type specific metabolic models

Genome-Scale Model of Human Metabolism

Table 1

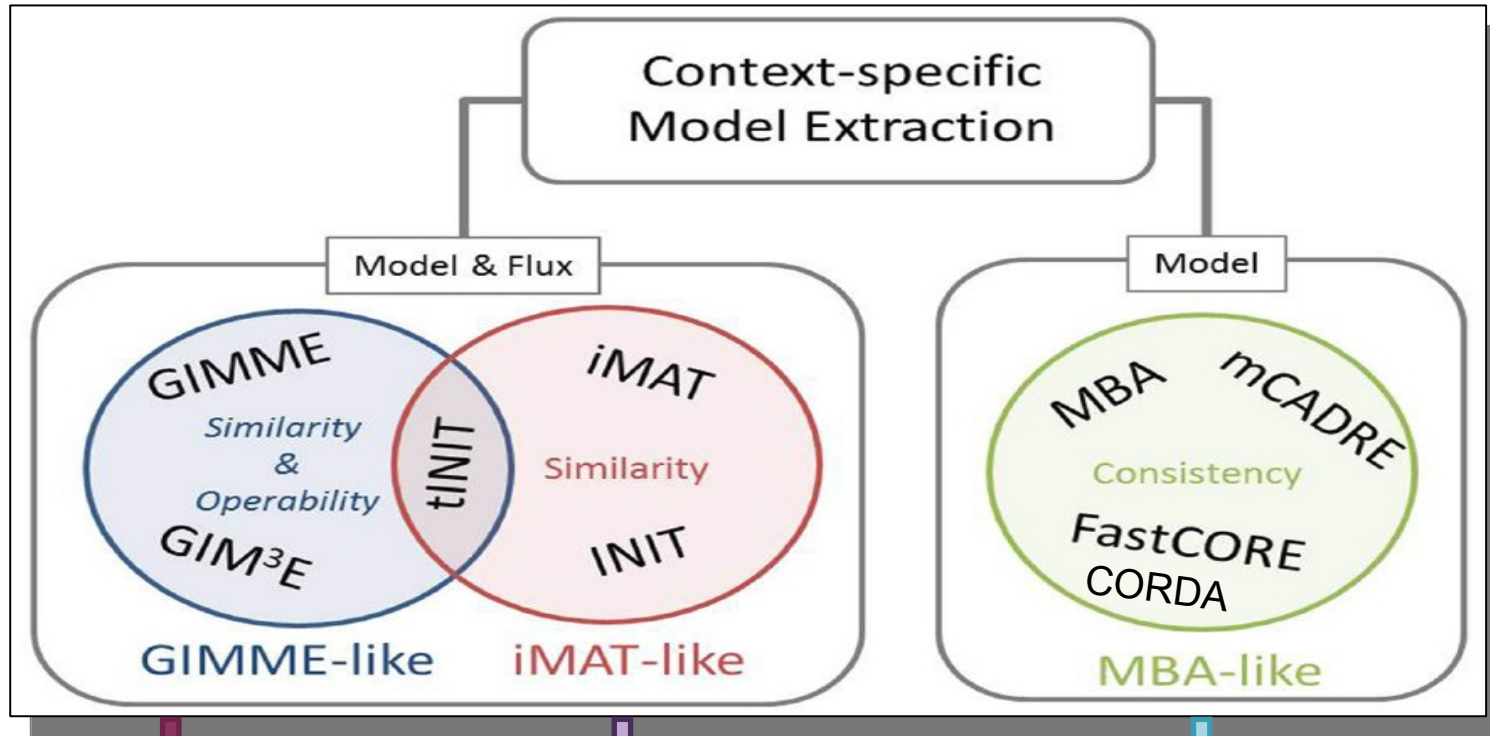
Statistics of currently published generic human GEMs.

Generic GEMs	Genes	Metabolites ^a	Reactions ^a	Features
RECON1	1496	1509	3744	Manually reconstructed from bibliomics data
EHMN	2322	2671	2823	Manually reconstructed from bibliomics data
RECON2	1789	2626	7440	Merging EHMN and HepatoNet1 with RECON1
RECON 2.2	1675	5324	7785	Reconstructed by integrating previous versions, with emphasis on mass and charge balance
HMR1.0	1512	3397	4144	Reconstructed based on RECON1, EHMN, HumanCyc and KEGG
HMR2.0	3765	3160	8181	Reconstructed based on HMR1, with additional emphasis on lipid metabolism by integrating iAdipocytes1809, KEGG, Lipidomics Gateway
Recon3D	2248	5835	10600	Reconstructed based on RECON2 and includes mapping to 3D structure of proteins through PDB ids

Swainston, N., et al (2016). Metabolomics, 12(7), 109.

- Several options available (all derived from RECON1)
- Recon3D is most recent version

Classes of Model Extraction Methods (MEMs)

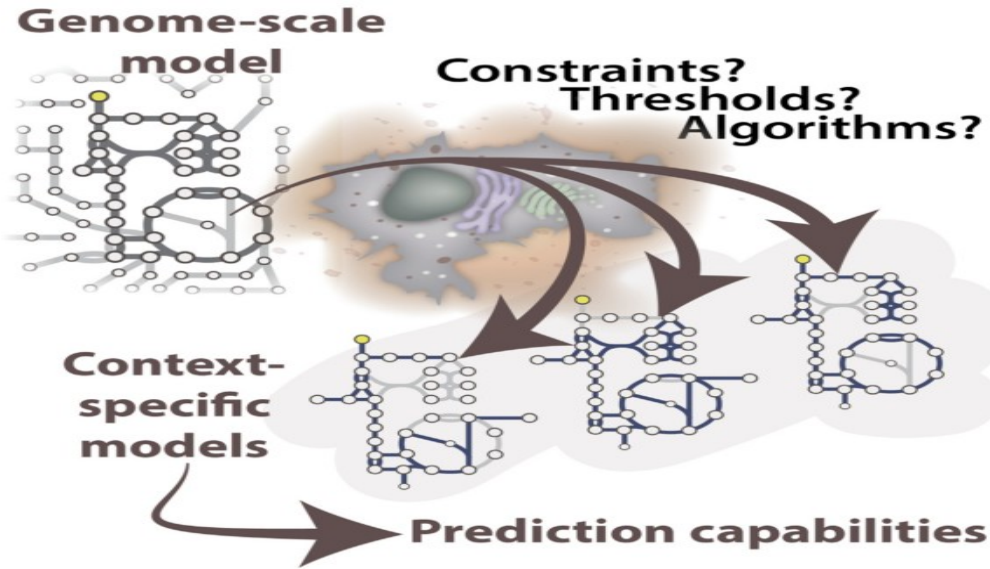


Minimizes flux through reactions associated with low gene expression

Finds an optimal trade-off between removing reactions associated with low gene expression and keeping reactions with high gene expression

The algorithms use sets of core reactions that should be retained and active while removing other reactions if possible

Context-Specific Metabolic Modeling (CSM) depend on key decisions on methodology and data processing



Updam, Sjoera et al. 2017

- No strong evidence that a Model extraction Method gives the most accurate models
- Each method has different underlying assumptions that affect the resulting model
- **Gene expression discretization** seems to be the most determinant decision

Hands on!

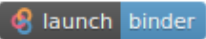
<https://github.com/migp11/ECCB2020-T05>

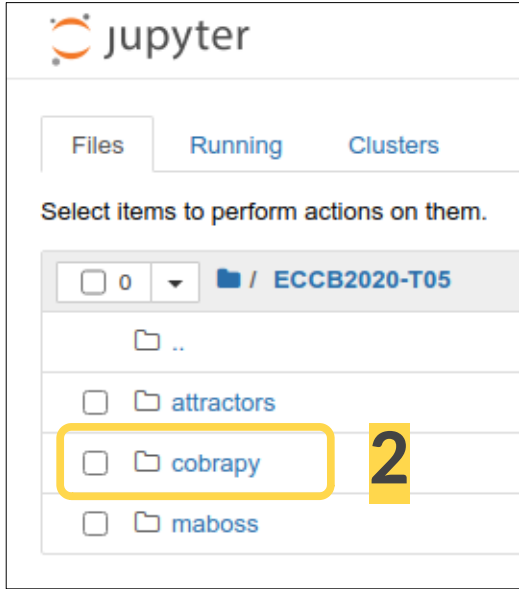
ECCB2020-T05

Computational modelling systems

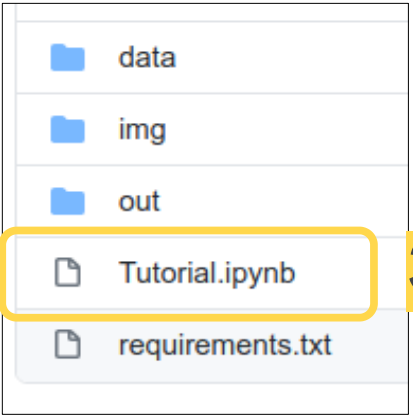
This repo contains all the material for the

Use with binder


 **1**



2



3



ECCB 2020
Virtual!