

TD METABOLIC MODEL

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- Internal reaction :
 - Metabolic reaction
 - Transport reaction
 - Biomass reaction
- External reaction
 - Exchange Reaction
 - Demand Reaction
 - Sink Reaction

METABOLIC MODELS

	Rx1	Rx2	Rx3	Rx4
a	1	0	-2	1
b	1	-1	0	-1
c	0	0	1	0
d	0	-2	0	-2
e	0	2	0	0
f	-1	0	1	1

Stoichiometric Matrix

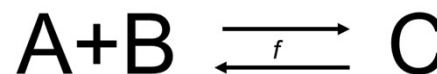
Rx2 : $b + 2d \rightarrow 2e$

Mathematic structure containing:

- Reactions (id, names, bounds)
- Metabolites (ids, name, formula, charge)
- Genes
- Stoichiometric matrix

unit = mmol/gDW/h

$lb < f < ub$



$lb < 0 < ub$	=	\rightleftharpoons
$lb \& ub < 0$	=	\leftarrow
$lb \& ub > 0$	=	\rightarrow

FLUX BALANCE ANALYSIS

(linear problem with steady state approximation)

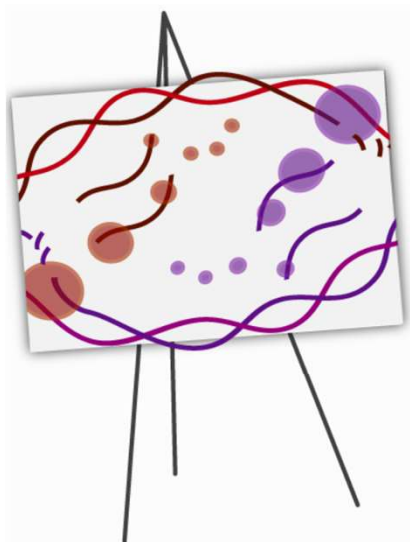
- Define phenotypes & environmental constraints
 - Set of reactions to constrain to represent **environmental and phenotype conditions**
 - Change bounds of targeted reactions
 - Open or close the model
- Define an objective function :
 - The observed and **observable parameter** (readout) to validate the expected cell behavior
 - Change objective function
 - Minimization or maximization of the objective function

I Escher model and visualisation

Lets use a metabolic model via a web platform

Open Escher and answer questions

- <https://escher.github.io/#/>
- practical-metabolic-model.pdf



ESCHER

*Build, share, and embed visualizations of
metabolic pathways*

II- Model Structure

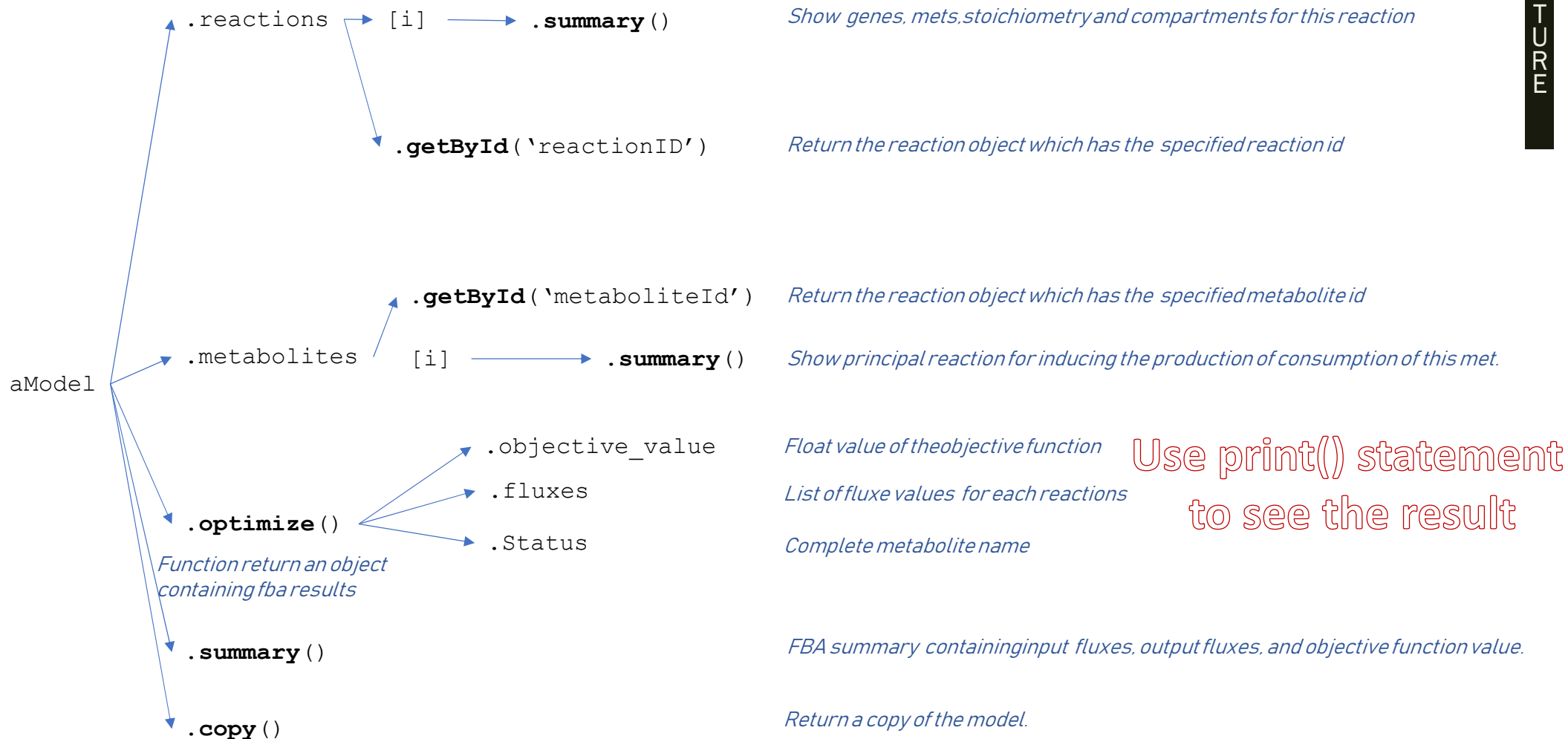
Let's understand how is build a model and how we can look on it!

How to access data? (object language)



Use `print()` statement
to see the result

How to access data? (object language)



Open Python and answer questions

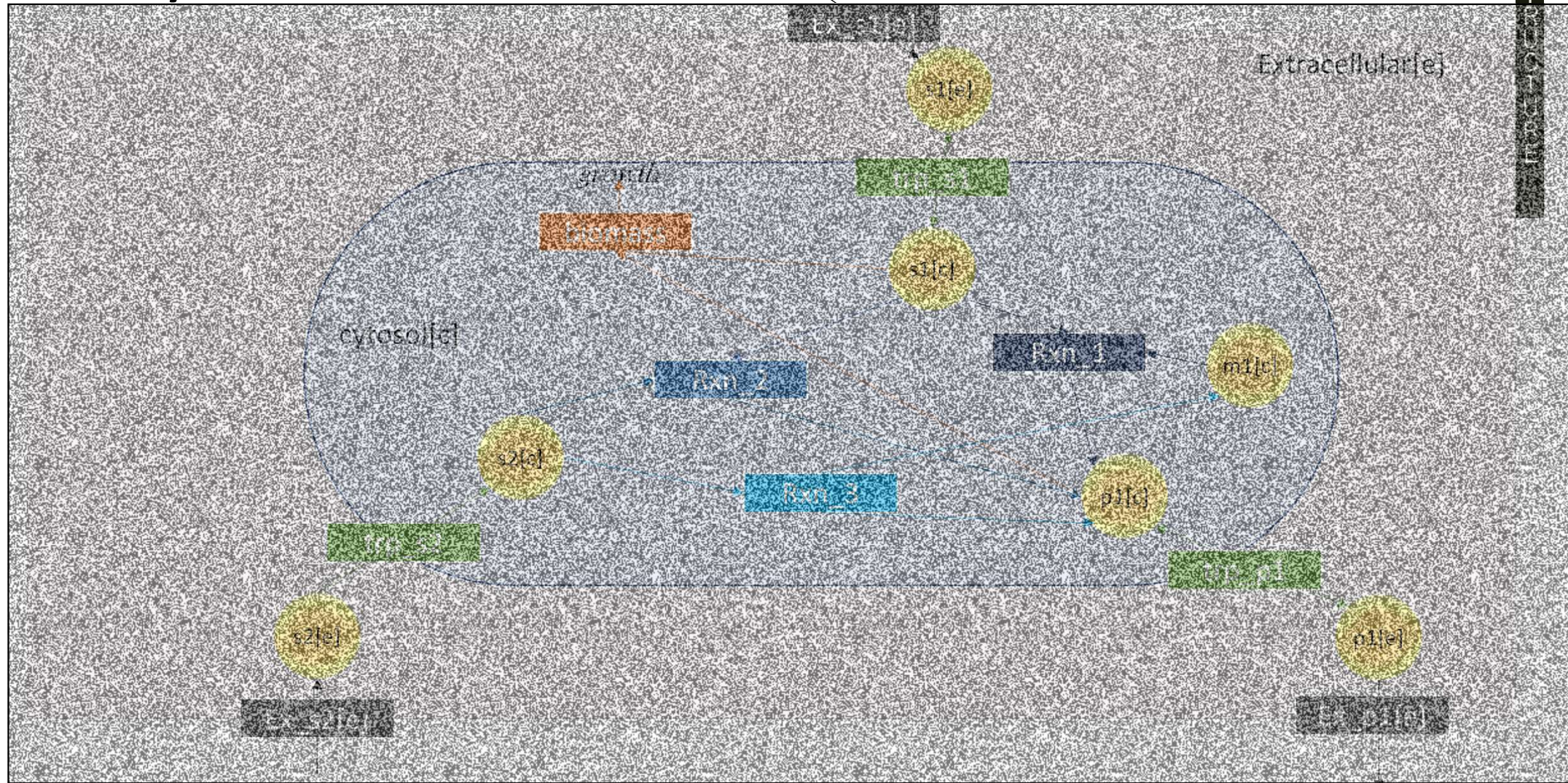


- `ll-Structure.py`

Stoichiometric matrix

Mets/Pxns	Trp_x1	Sp_x1	Trp_p1	Ex_x1_e	Ex_x2_e	Ex_p1_e	Rxn_1	Rxn_2	Rxn_3	Normal
Met_e	0	0	0	0	0	0	1	0	1	0
Sp_e	1	0	0	0	0	0	-1	-1	0	1
Trp_e	-1	0	0	1	0	0	0	0	0	0
Ex_x1_e	0	1	0	0	0	0	0	-1	-1	0
Ex_x2_e	0	1	0	0	-1	0	0	0	0	0
Trp_p1	0	0	1	0	0	0	0	0	0	0
Ex_p1_e	0	0	-1	0	0	-1	1	2	1	-0.5

Study model



Discover an unknown model

Chose a model on BiGG Models database :

<http://bigg.ucsd.edu>

The logo for BiGG Models, featuring the text "BiGG Models" in white, bold, sans-serif font on a blue rectangular background. A thin white horizontal line is positioned below the text.

BiGG Models

III- Model Analysis

Let's answer biological questions thanks to metabolic models

From e_coli_core model (==Escher)

- Answer questions : Ill-Analysis.py
- Compare the results to those obtained in part 1.

From entire models (download from BiGG)

I- Define the best media to grow *Saccharomyces cerevisiae*

Model :

➤ *Saccharomyces cerevisiae* = 'iND750.xml'

II- Define which microorganism is the best RR 2 3 Butanediol producer.

Models:

➤ *Saccharomyces cerevisiae* : 'iMM904'

➤ *Lactococcus lactis* : 'iNF517'

➤ *Klebsiella pneumoniae* : 'iYL1228'

From entire models (download from VMH)

III- Define the more likely species to cooperate with *Faecalibacterium prausnitzii*:

- *Blautia hydrogenotrophica*
- *Roseburia intestinalis*

<https://www.vmh.life/#microbes/search>

II- Model Reconstruction

Lets understand how its build a model and how we can look on it

METABOLIC MODELS

