



# Advancing biorefinery design through the integration of metabolic models in superstructure optimization

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**33<sup>RD</sup>** EUROPEAN SYMPOSIUM  
ON COMPUTER-AIDED  
PROCESS ENGINEERING  
GREEN AND SUSTAINABLE PROCESS SYSTEMS  
ENGINEERING IN THE DIGITAL AGE

#escape2023

# The biorefinery concept



# Challenges of biorefinery design

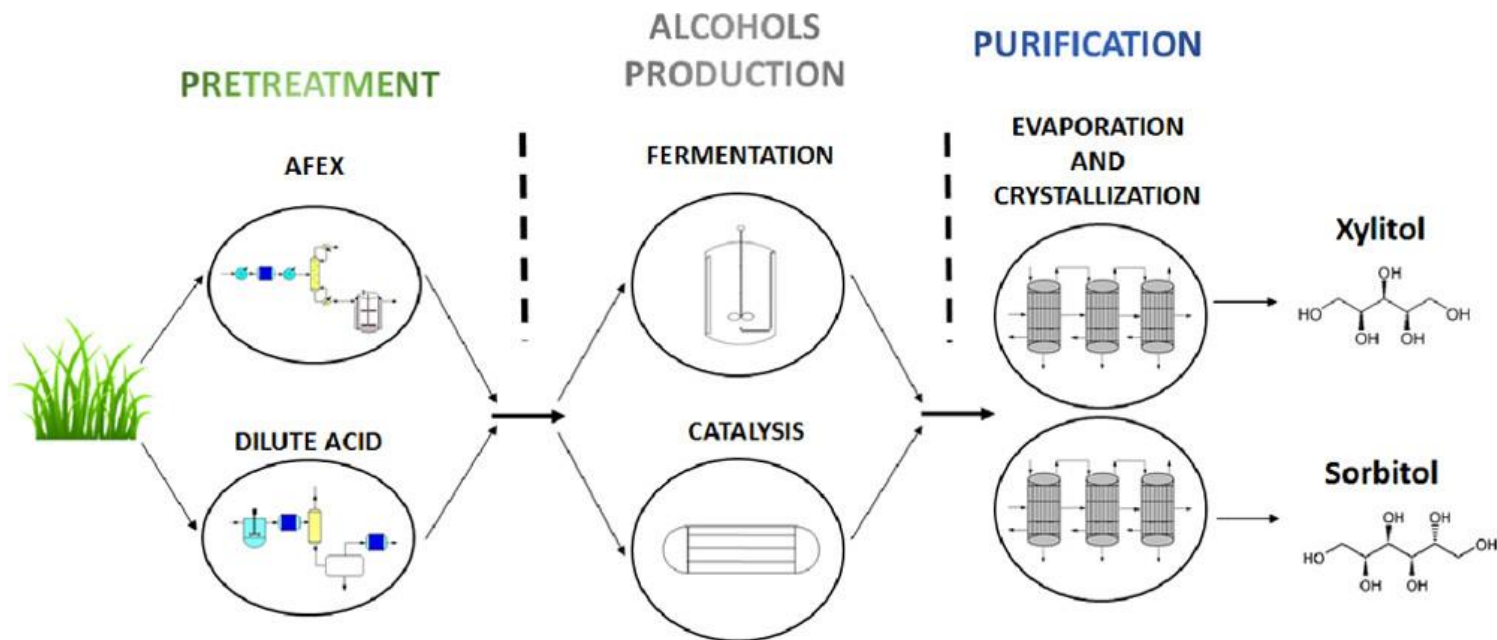


- Techno-economic viability & Scale up  
Product Diversification
- Feedstock Availability and Variability  
Linking substrates to potential products



How do we assure investors to develop biorefineries?

# Superstructure optimisation: Sorbitol and Xylitol

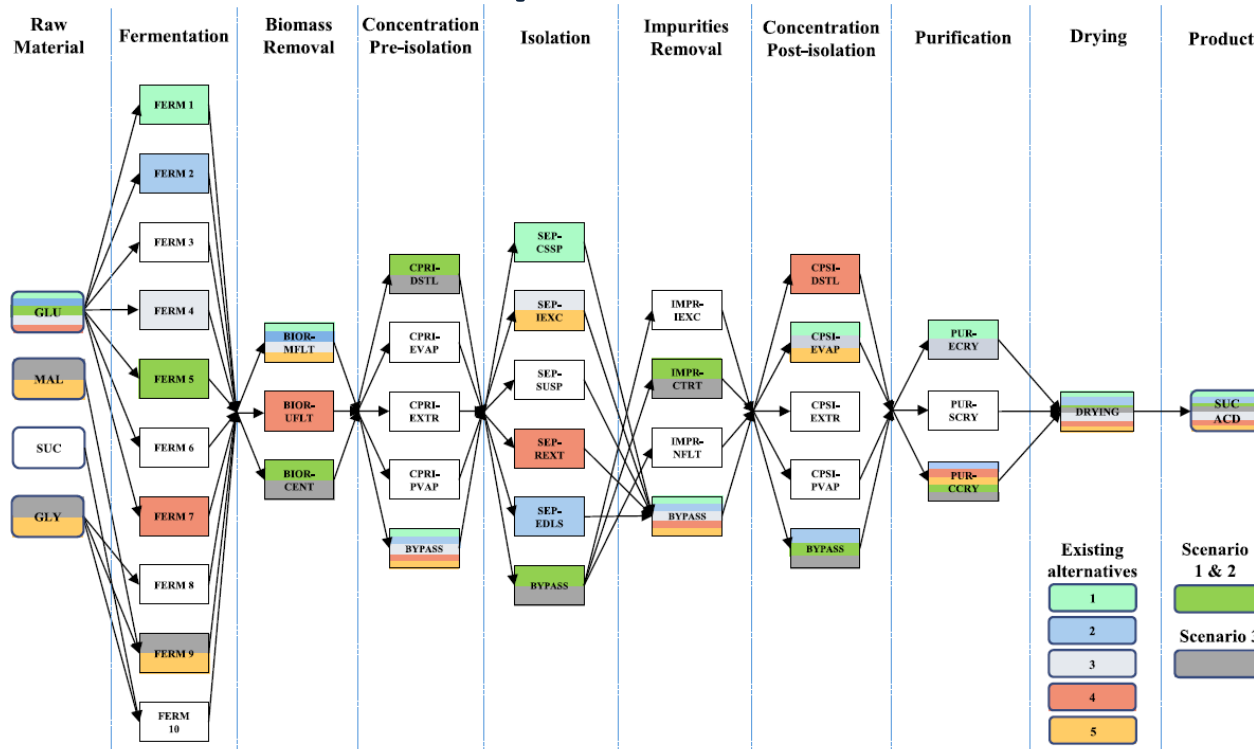


Objective



Galan et al. (2021)

# Superstructure optimisation: succinate acid

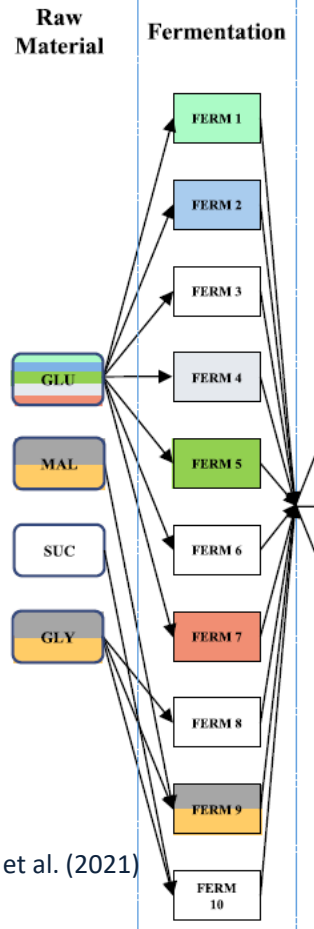


Objective



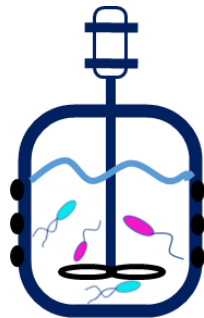
Galan et al. (2021)

# Representation bio-reactor stage



Bio chemical conversion of substrates to products

4 distinct microorganisms with well established fermentation outcomes

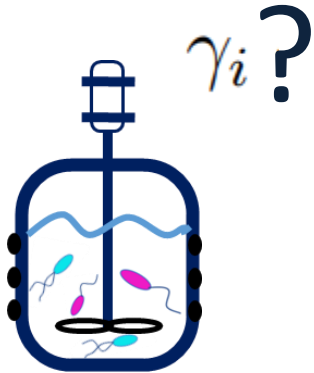


**BUT** Enormous Diversity of microorganisms for bioreactors and the potential substrates they can consume

# Getting the bioreactions in superstructures

## Research question:

How to integrate bioreactions of microorganisms in the most effective and efficient way in the superstructure?



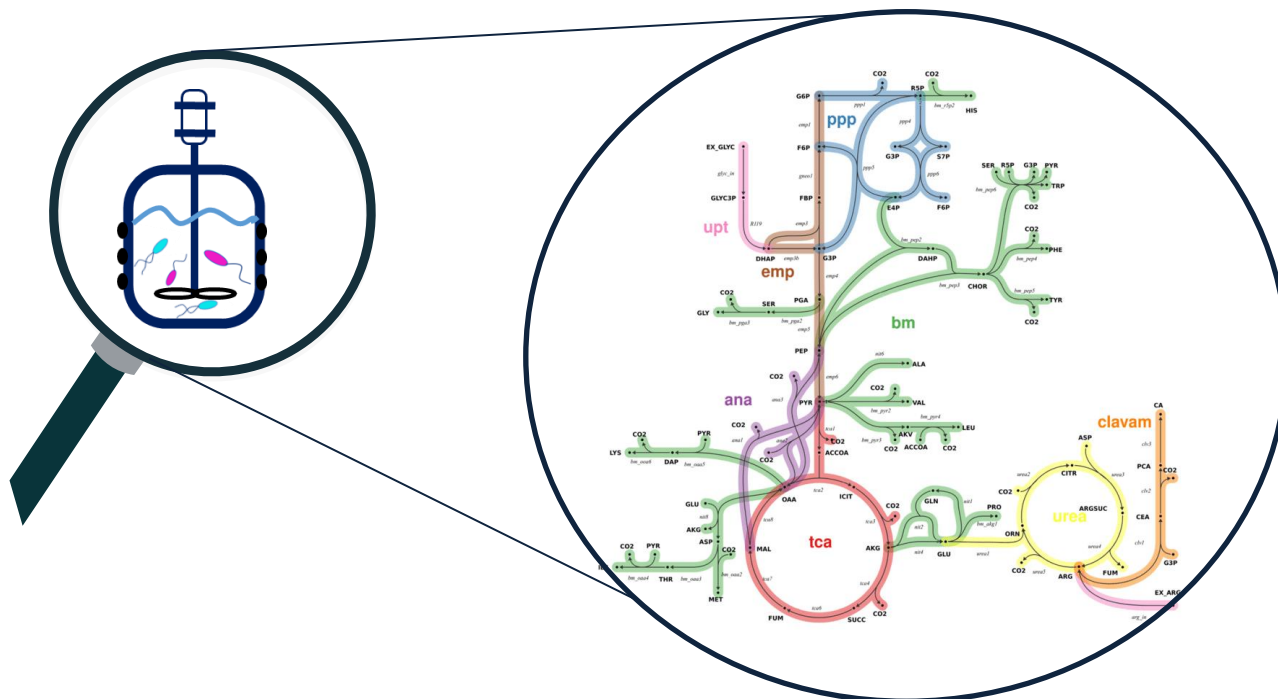
Or

How to unlock the full potential of microorganism in a superstructure framework?

**Goal:** Can we explore completely new designs linking new microorganisms to substrates and products?

# Representing Bioreactors in Superstructures

## *Metabolic models*



### Advantages

- Predictive from omics data
- Able to handle multiple substrates

# Considered biotransformations in bioreactors

## Pure cultures

### Genome Metabolic Models (GEMS)

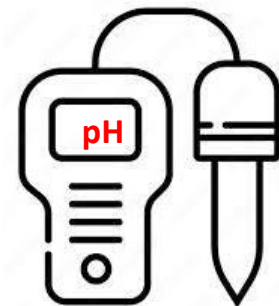
Recreation of the metabolic network,  
starting from the **genome**



## Open mixed cultures

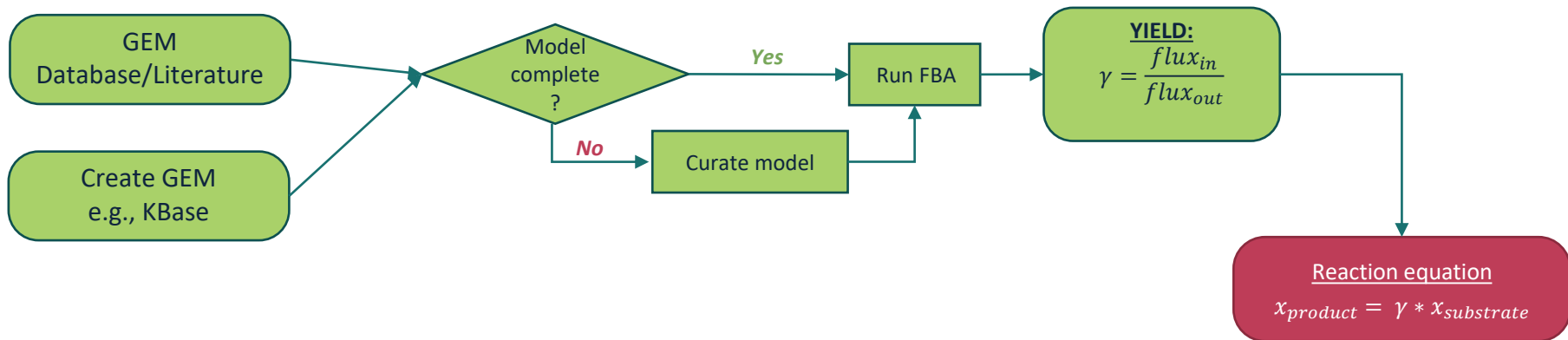
### Bioenergetic model

Recreation of metabolic  
networks, But dependent on  
**environmental influences**

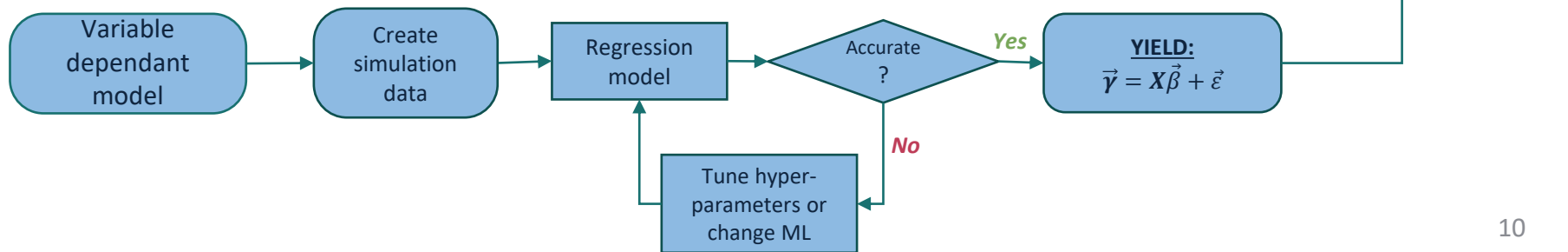


# Making Surrogate models

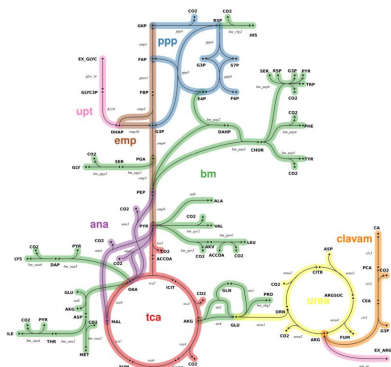
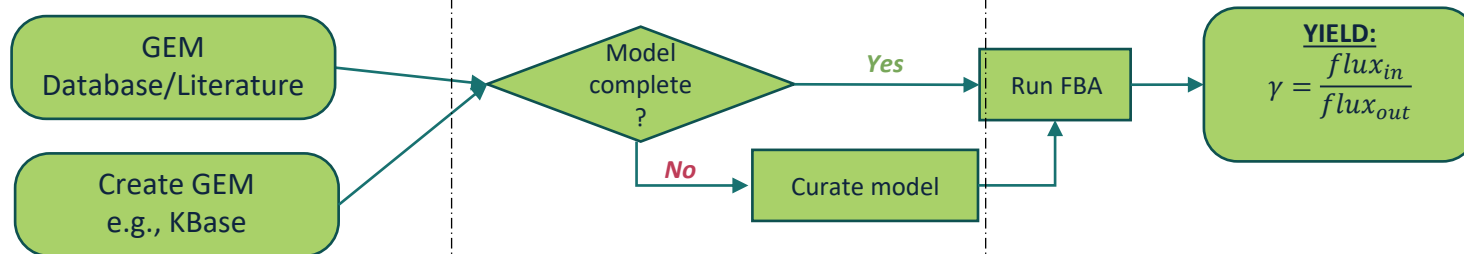
## Path 1



## Path 2



# Integration pure culture models



**MEMOTE**

- Check mass and electron balances
- Check “dead end” metabolites
- Perform leak tests



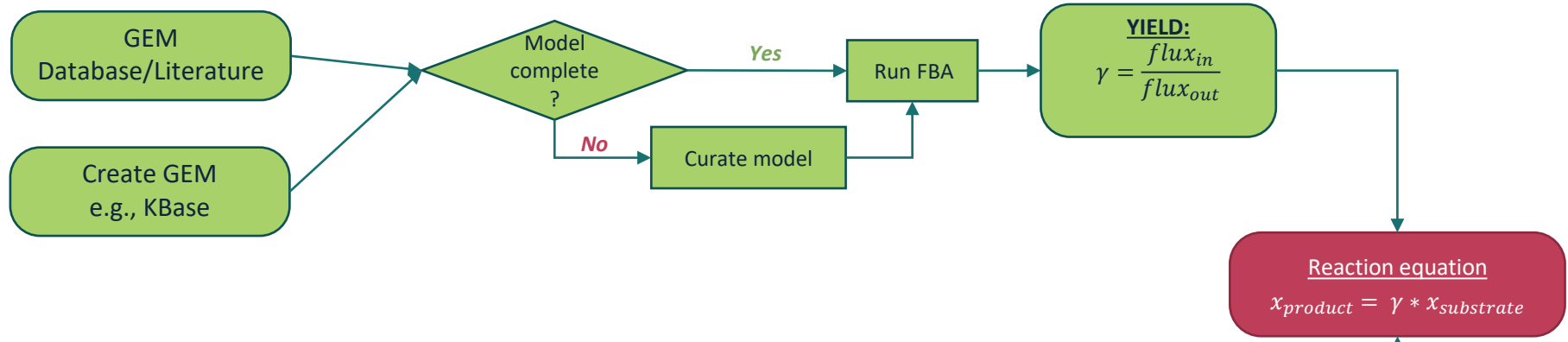
**FBA**

$$\frac{d}{dt} \begin{pmatrix} A \\ B \\ C \\ D \\ E \end{pmatrix} = Sv = S \begin{pmatrix} v_1 \\ v_2 \\ b_1 \\ b_2 \\ b_3 \\ b_4 \\ b_5 \end{pmatrix} = 0$$

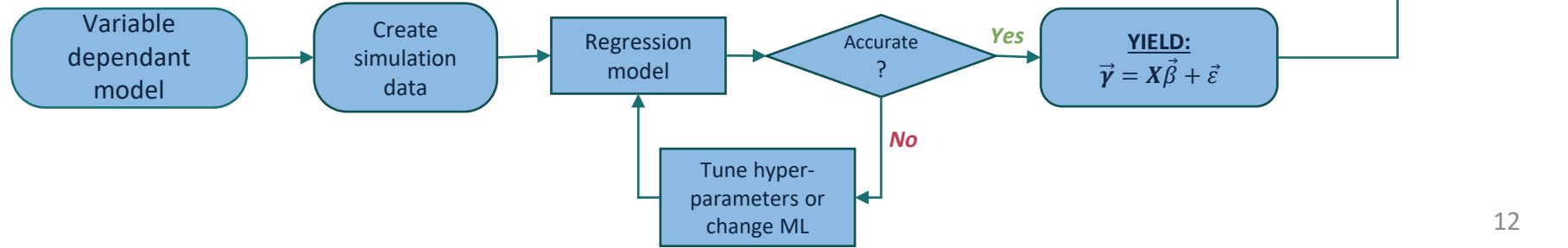
Steady State Mass balance

# Making Surrogate models

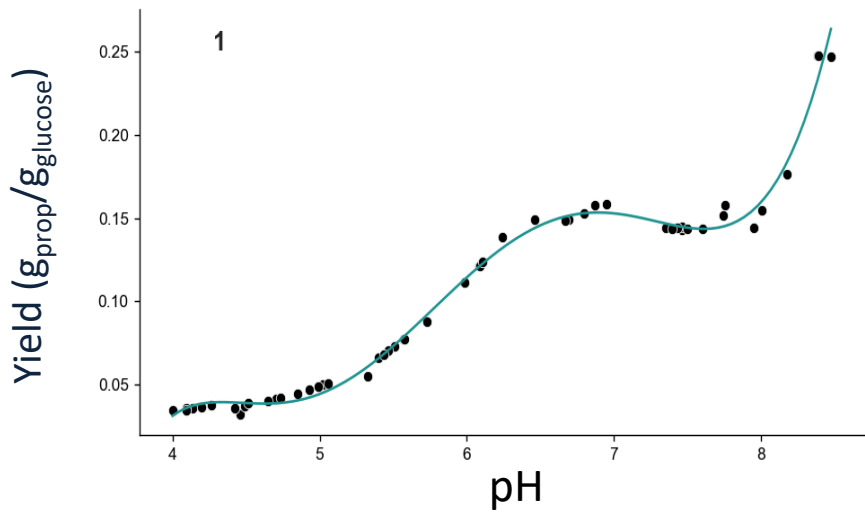
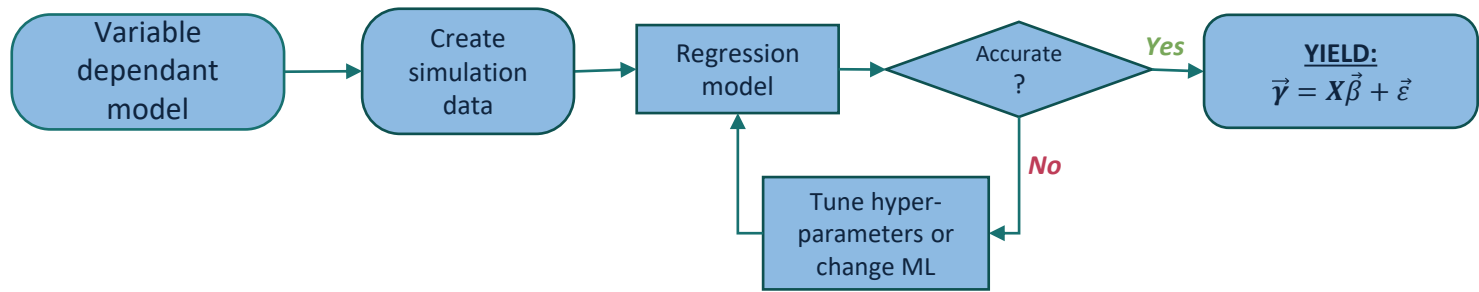
## Path 1



## Path 2



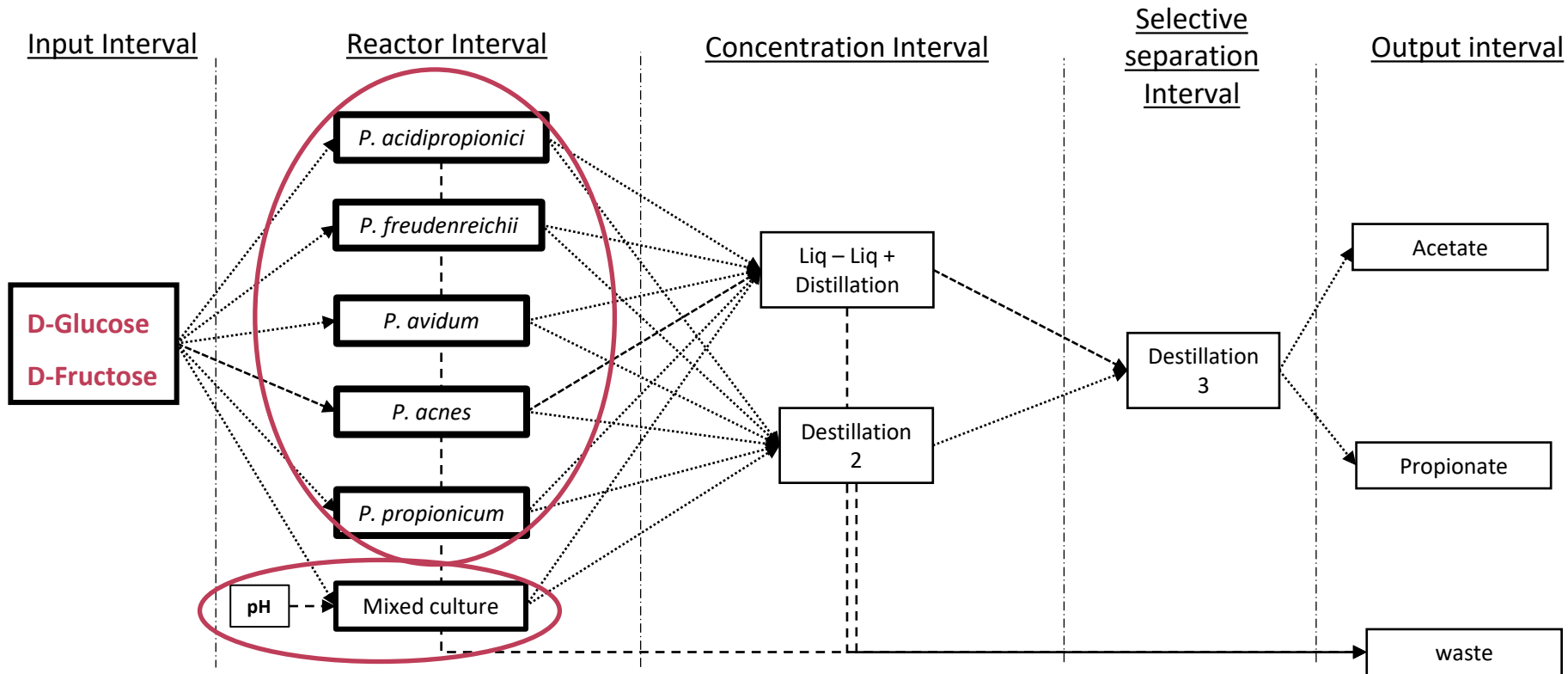
# Mixed culture models



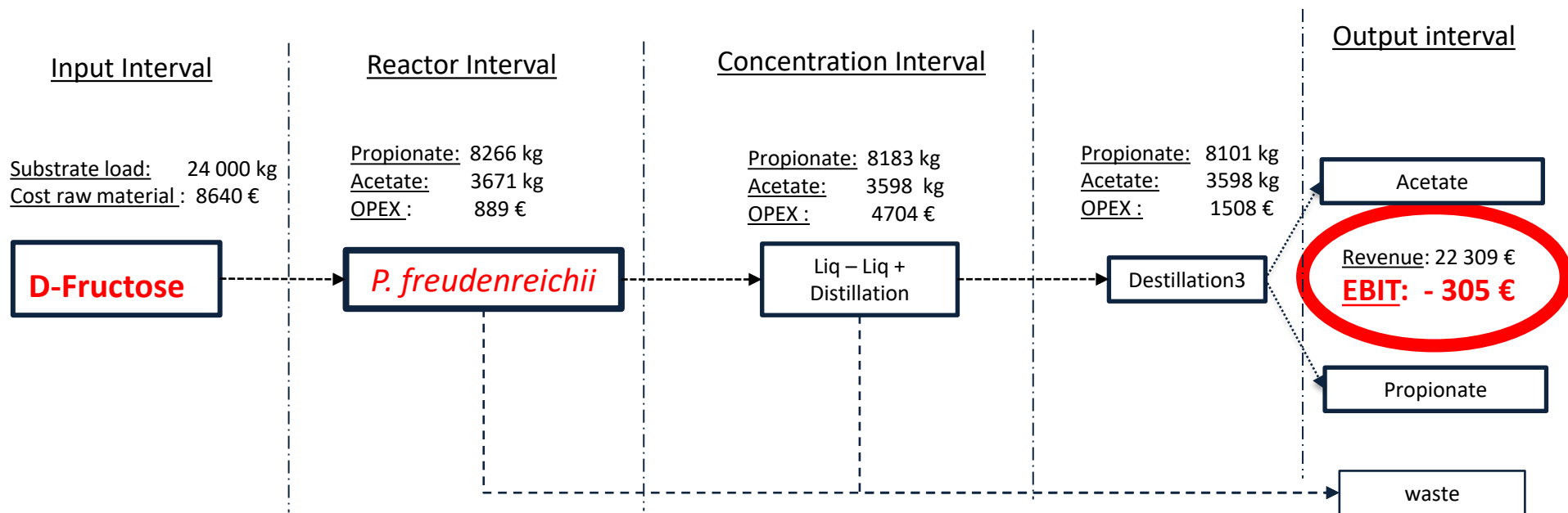
$$\vec{y} = pH \cdot \vec{\beta} + \vec{\epsilon}$$

# Case study

Objective:  $EBIT = GREV - OPEX$

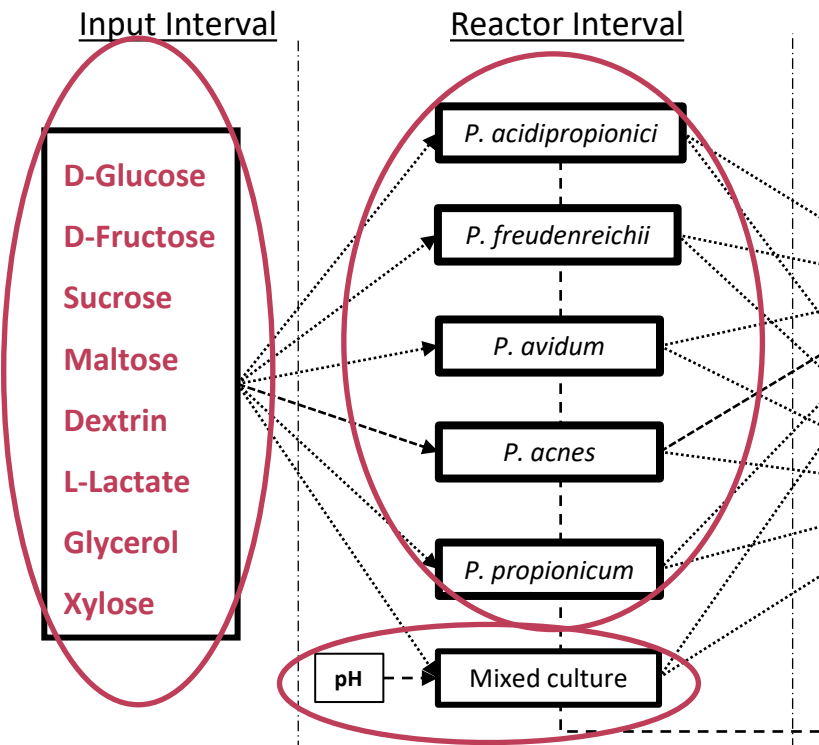


# Results



# Case study

**Objective: EBIT = GREV - OPEX**



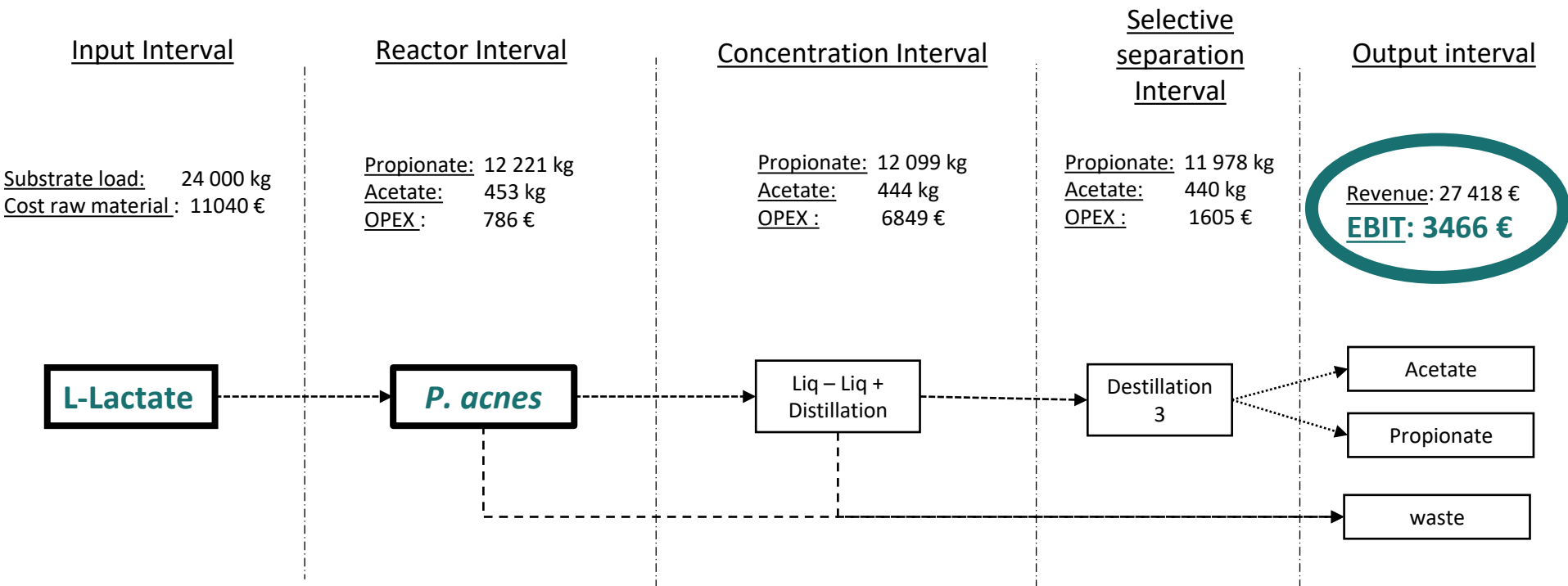
How to identify substrates:

1. Identify Exchange reactions in the GEM
2. Filter out proteins
3. A minimum production of the target products required
4. Final manual selection



substrate – microorganism

# Results



# Conclusion



An efficient **workflow** was created to **integrate metabolic models** for representing bioreactor processes in **superstructure optimization problems**



The surrogate models are capable of

- 1) **Predicting operation conditions** for optimal yields
- 2) **Predictive from genome data**
- 3) Predicting yields from **various substrates**



Case studies demonstrate how superstructure optimization using metabolic models **can identify economically viable combinations of substrates and microorganisms.**

HAVE A NICE DAY

# THANK YOU

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## Acknowledgments











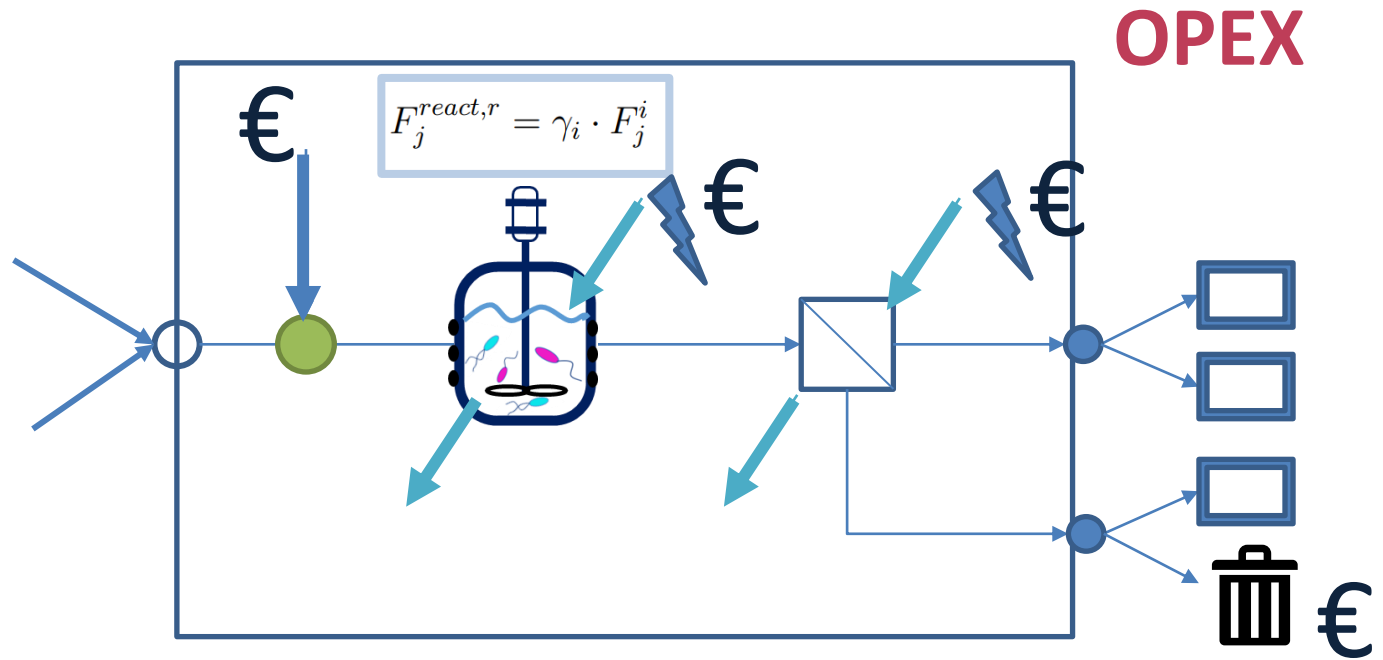
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# EXTRA

# Representation of unit processes

-  Flow divider
-  Mixer
-  Mixer utilities (chemicals)
-  (Bio)Reactor
-  Separator
-  Flow of mass
-  Flow energy
-  Next process unit or waste



Quaglia et al (2015), Bertran et al. (2017)