Modelling metabolic network dynamics in a cheese bacterial community

Maxime Lecomte, David Sherman, Hélène Falentin, Clémence Frioux, Simon Labarthe

HAL Id: hal-03533804
https://hal.inria.fr/hal-03533804

Modeling metabolic network dynamics in a cheese bacterial community

Maxime Lecomte*, David Sherman, Hélène Falentin, Clémence Frioux, Simon Labarthe

19th International Conference on Computational methods in Systems Biology - 2021

*maxime.lecomte@inrae.fr

Modeling metabolic network deciphers interactions in a bacterial community

- Bacterial communities occur in every environment and are also important in industrial processes.

- Reveal interactions in a microbiota --> model the metabolism

- Study small cheese bacterial community --> small-scale controlled model
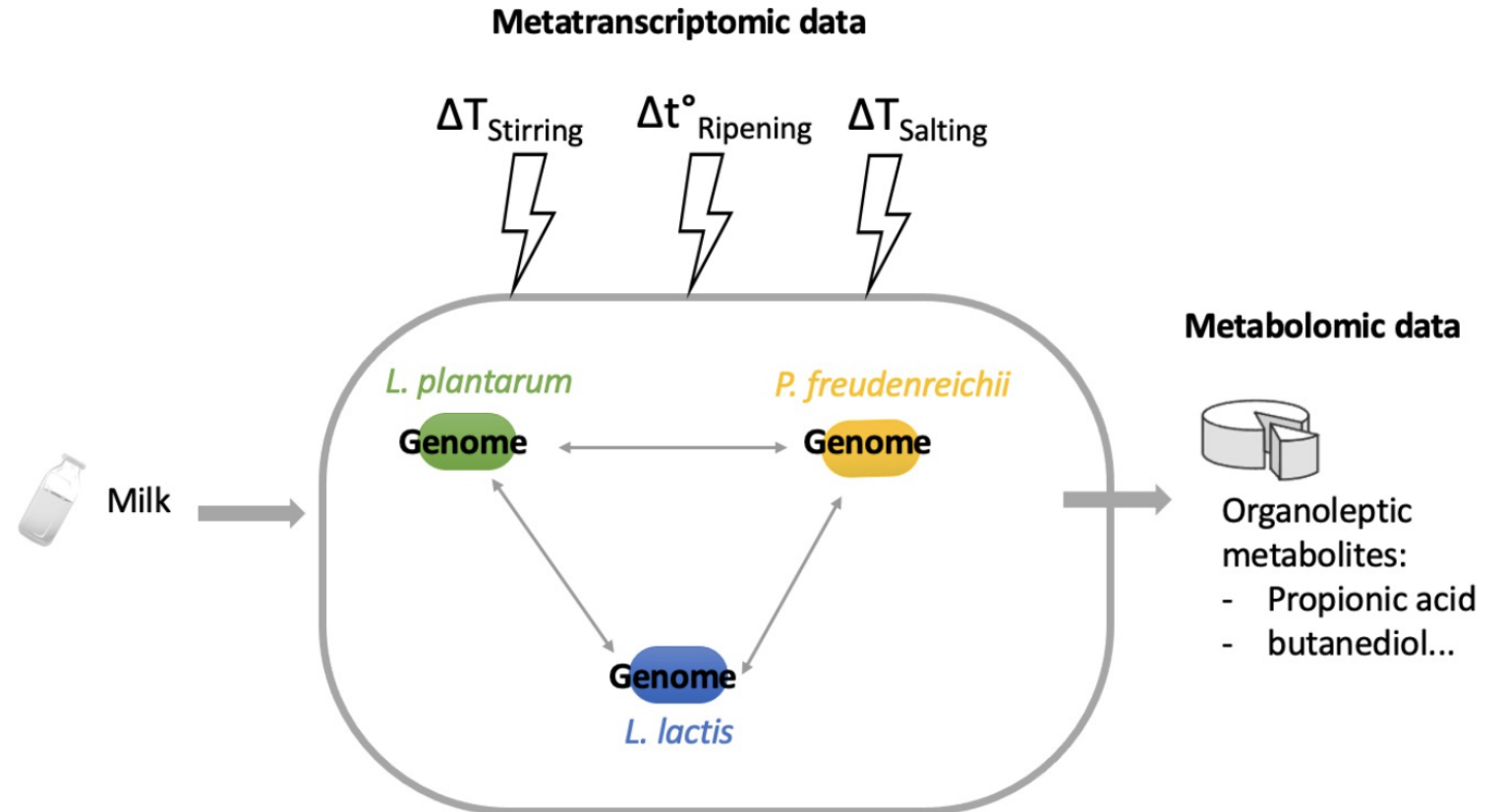
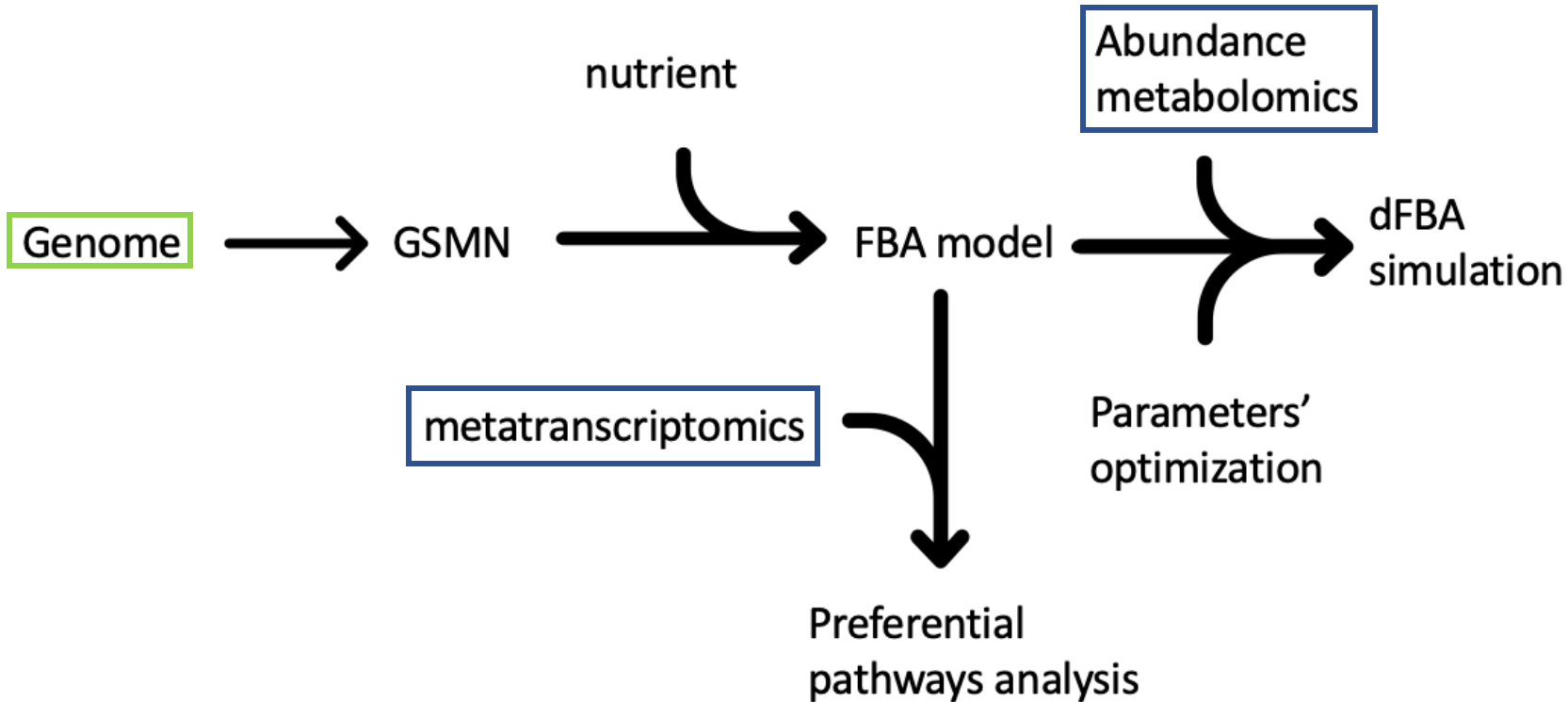# Integration of multi-omics data in the pipeline

Figure 1: Pipeline used to run simulations on the small bacterial community (is being automated).

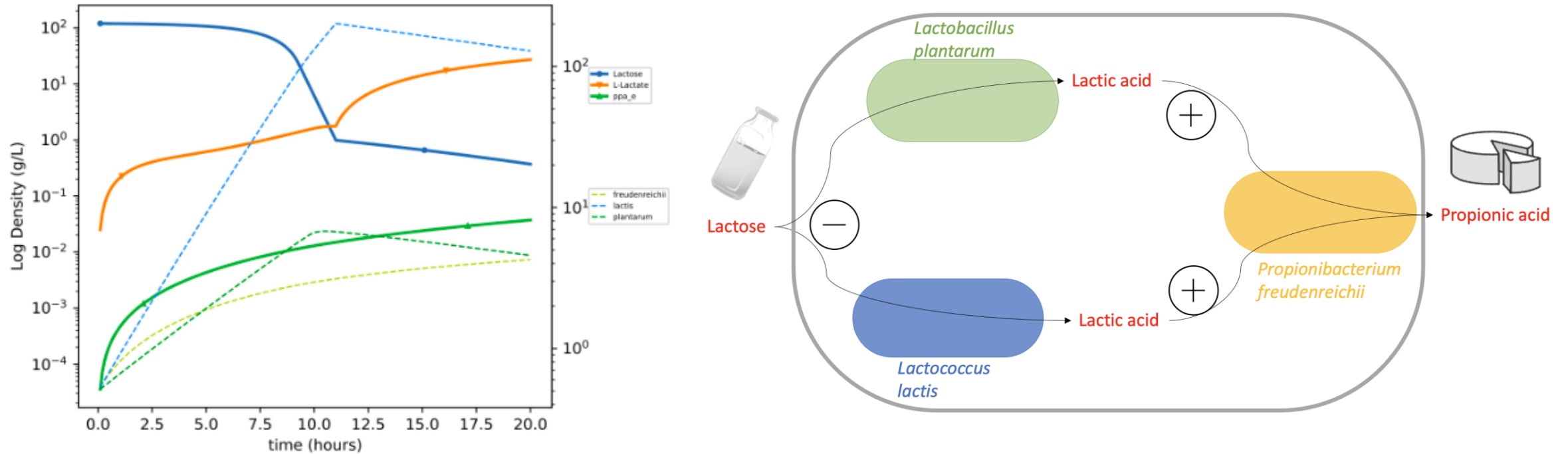# Interactions highlighted at the community scale

Figure 2: Preliminary results of dFBA on the whole community.

- Same interaction bacterium-bacterium are highlighted with metabolic modeling, tools [6] and literature

- Production of lactate by Lactic acid bacteria creates a mutualistic interaction with *P. freudenreichii* responsible of the production of organoleptic compounds

4

Modeling metabolic network dynamics in a cheese bacterial community

- Thanks for your attention

Poster 49
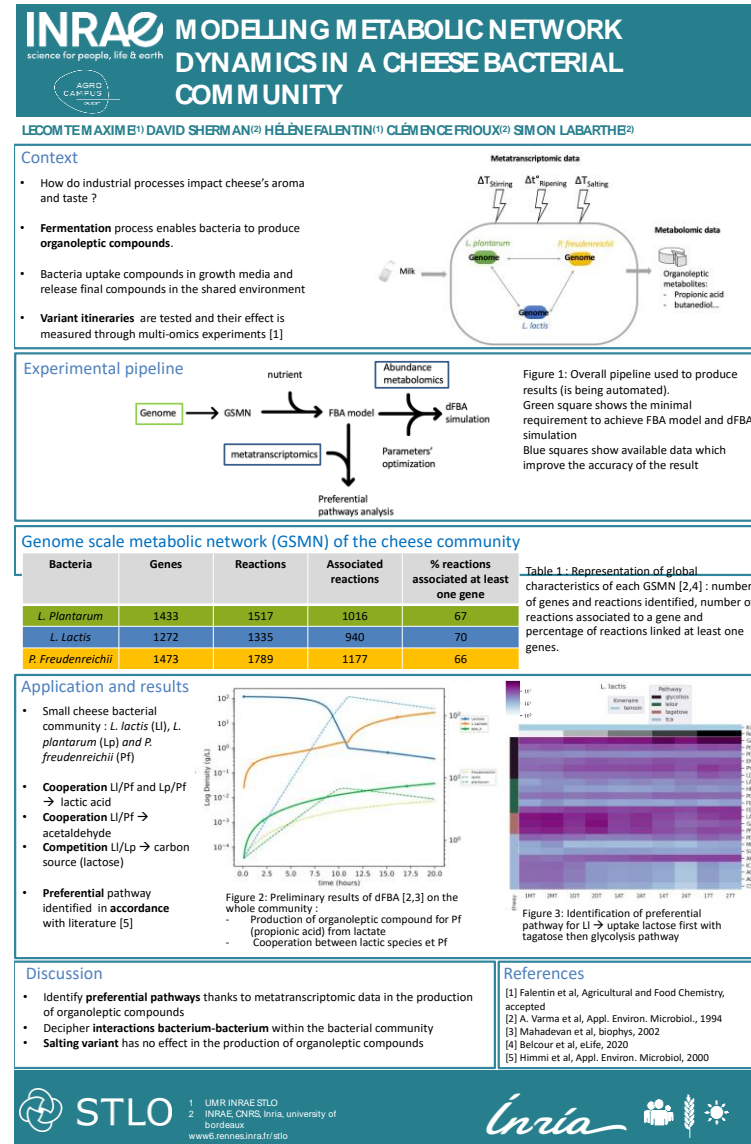
[1] Falentin et al, Agricultural and Food Chemistry, 2021
[2] A. Varma et al, Appl. Environ. Microbiol., 1994
[3] Mahadevan et al, biophys, 2002
[4] Belcour et al, eLife, 2020
[5] Himmi et al, Appl. Environ. Microbiol, 2000
[6] Zelezniak et al, PNAS, 2015
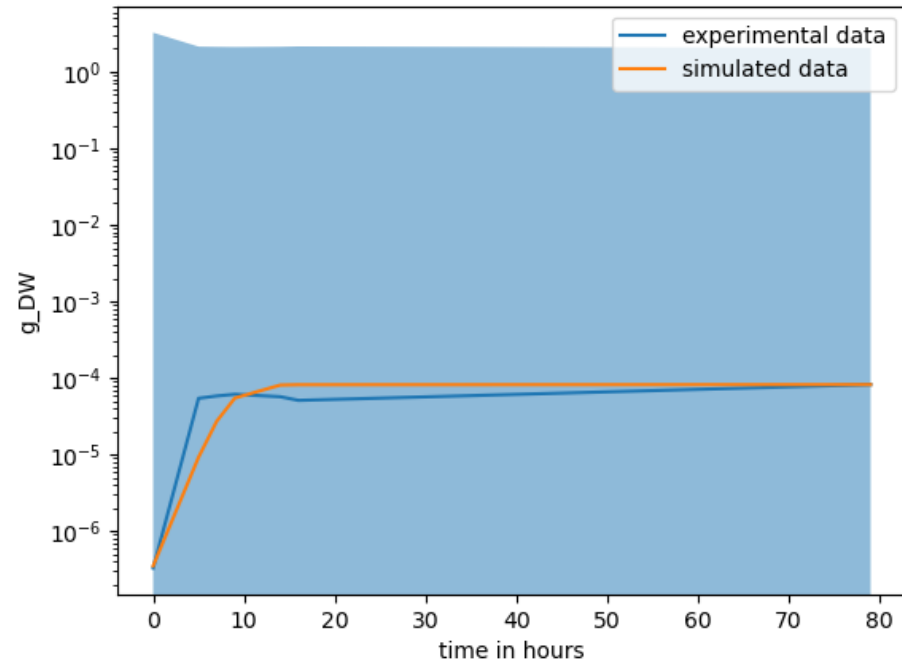[7] D. Machado et al, Nucleic Acids Research, 2018

Figure 3: Comparison of growth rate of freudenreichii