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Modeling metabolic network dynamics in a cheese bacterial community

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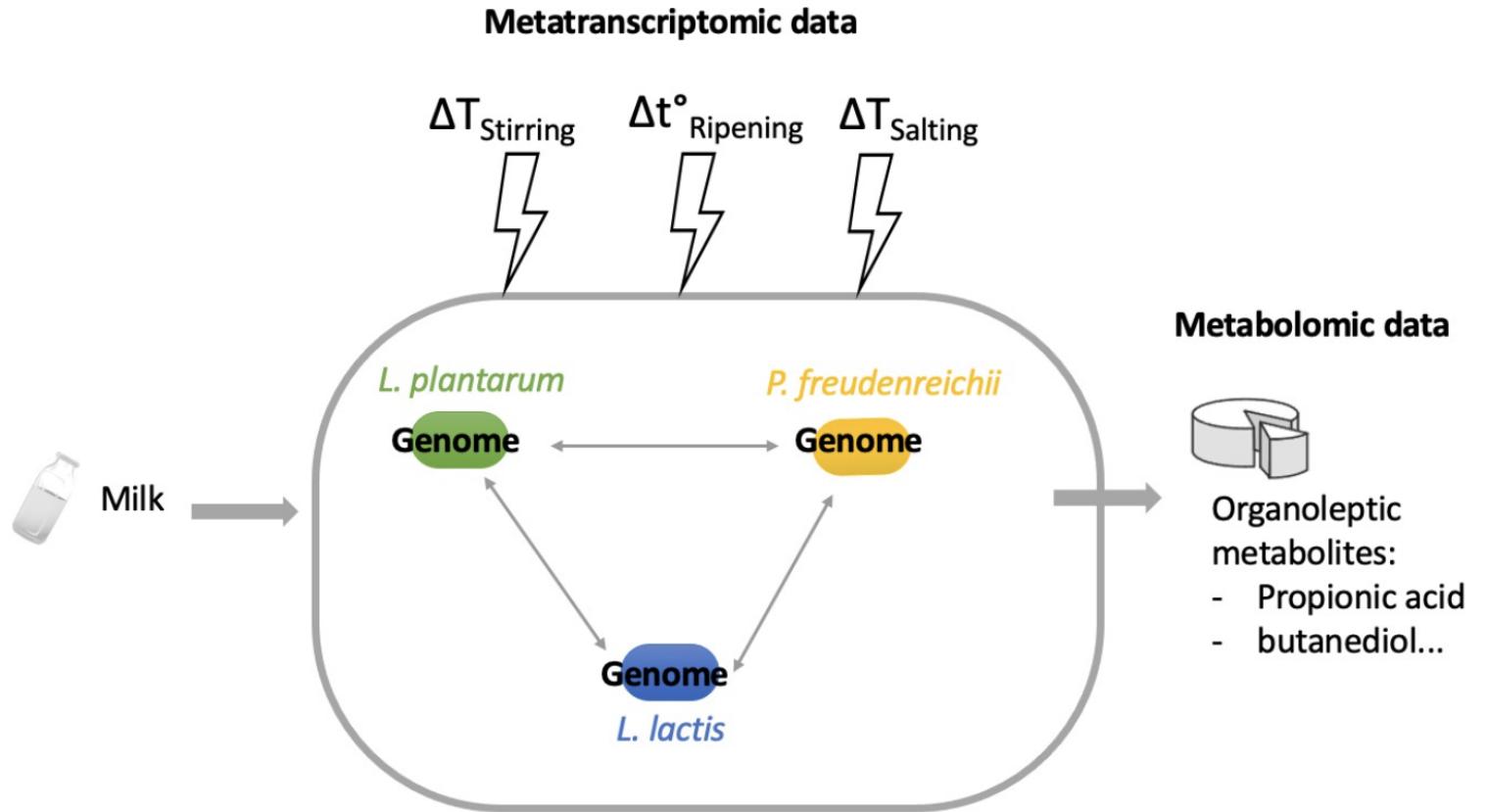
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Modeling metabolic network deciphers interactions in a bacterial community

- 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

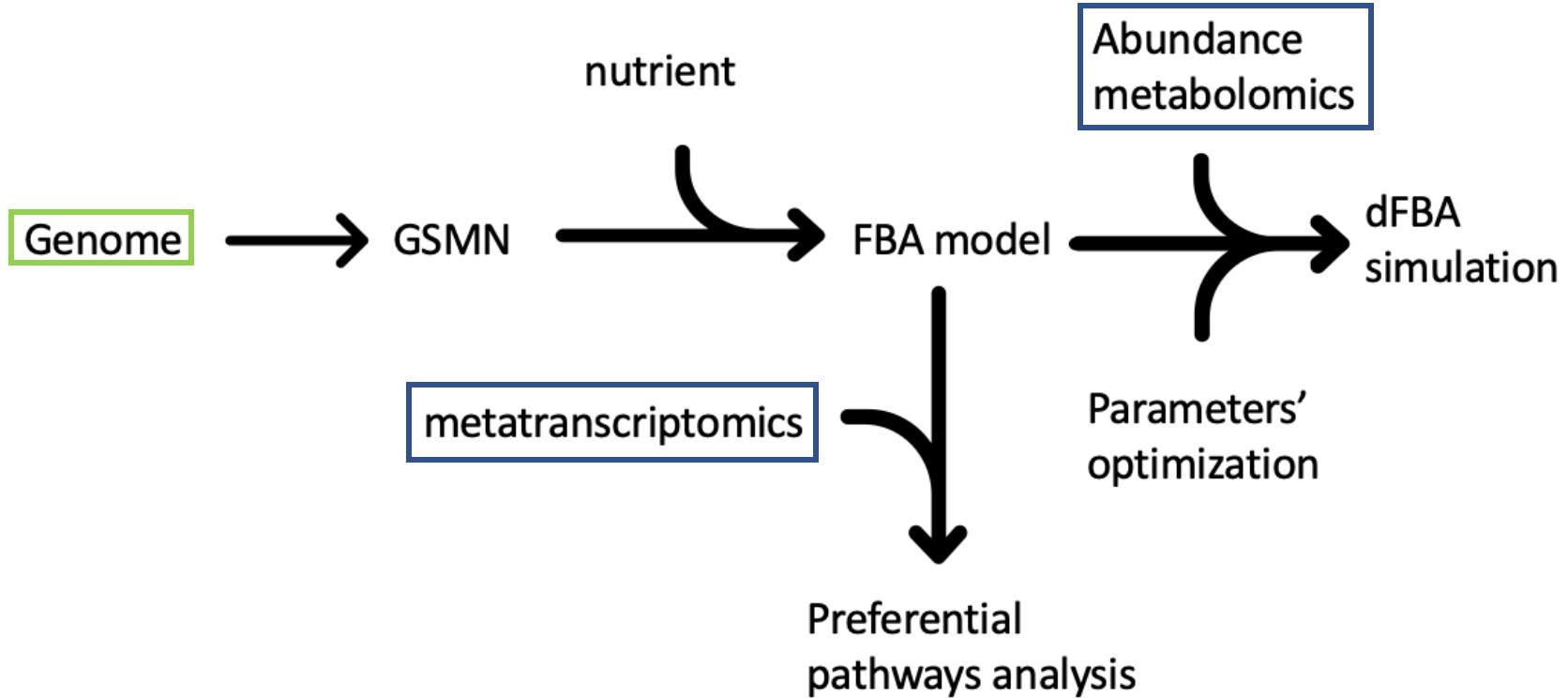


Figure 1: Pipeline used to run simulations on the small bacterial community (is being automated).

Interactions highlighted at the community scale

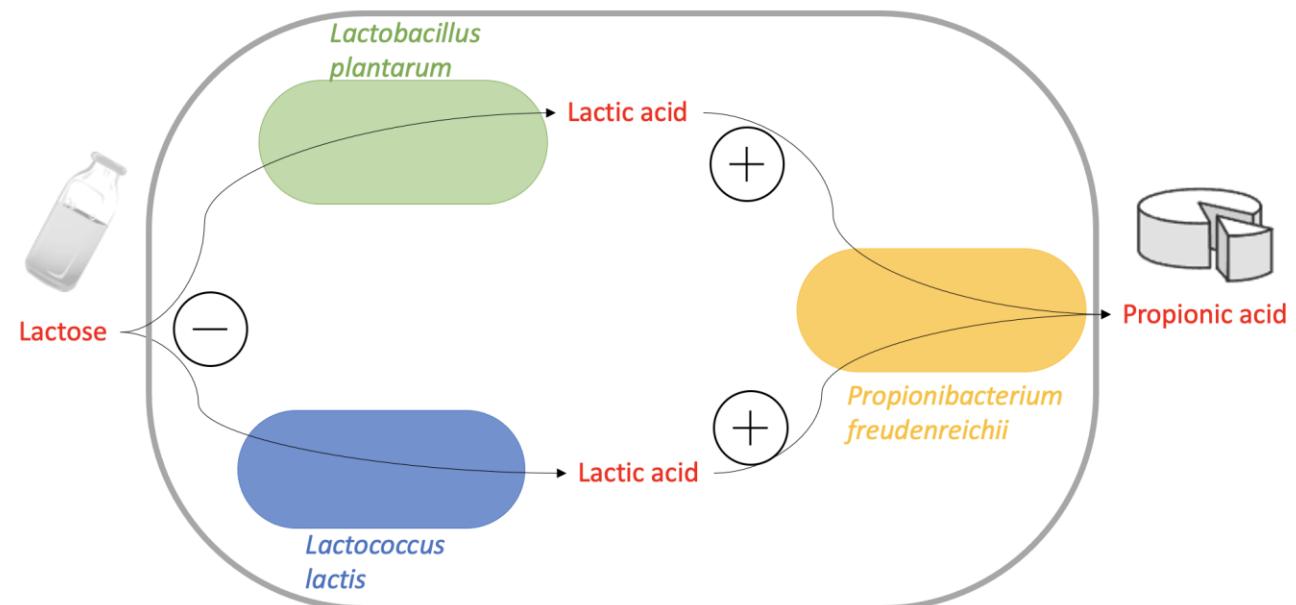
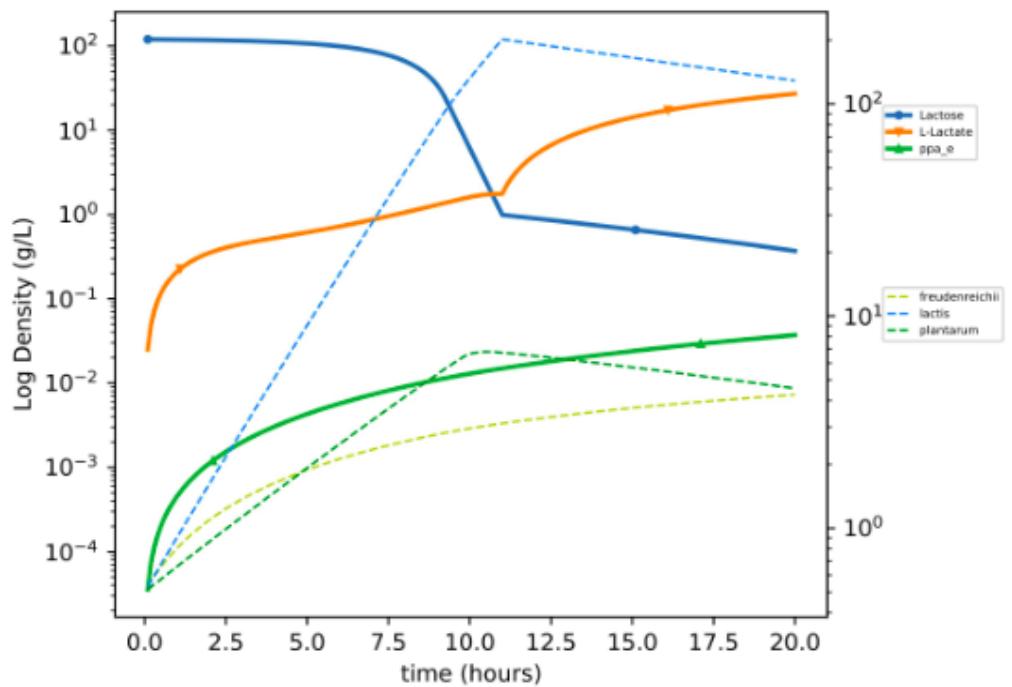


Figure 2: Preliminary results of dFBA on the whole community.

- 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

Modeling metabolic network dynamics in a cheese bacterial community

Poster 49

- Thanks for your attention

INRAE MODELLING METABOLIC NETWORK DYNAMICS IN A CHEESE BACTERIAL COMMUNITY

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Context

- How do industrial processes impact cheese's aroma and taste ?
- Fermentation process enables bacteria to produce organoleptic compounds.
- Bacteria uptake compounds in growth media and release final compounds in the shared environment
- Variant itineraries are tested and their effect is measured through multi-omics experiments [1]

Metatranscriptomic data

Metabolomic data

Experimental pipeline

nutrient → GSMN → FBA model → dFBA simulation

metatranscriptomics → Parameters' optimization → Preferential pathways analysis

Figure 1: Overall pipeline used to produce results (is being automated). Green square shows the minimal requirement to achieve FBA model and dFBA simulation. Blue squares show available data which improve the accuracy of the result

Genome scale metabolic network (GSMN) of the cheese community

Bacteria	Genes	Reactions	Associated reactions	% reactions associated at least one gene
<i>L. Plantarum</i>	1433	1517	1016	67
<i>L. Lactis</i>	1272	1335	940	70
<i>P. Freudenreichii</i>	1473	1789	1177	66

Table 1 : Representation of global characteristics of each GSMN [2,4] : number of genes and reactions identified, number of reactions associated to a gene and percentage of reactions linked at least one genes.

Application and results

- Small cheese bacterial community : *L. lactis* (L), *L. plantarum* (Lp) and *P. freudenreichii* (Pf)
- Cooperation L/Pf and Lp/Pf → lactic acid
- Cooperation L/Pf → acetaldehyde
- Competition L/Lp → carbon source (lactose)
- Preferential pathway identified in accordance with literature [5]

Figure 2: Preliminary results of dFBA [2,3] on the whole community

- Production of organoleptic compound for Pf (propionic acid) from lactate
- Cooperation between lactic species Pf

Figure 3: Identification of preferential pathway for L → uptake lactose first with galactose then glycolysis pathway

Discussion

- Identify preferential pathways thanks to metatranscriptomic data in the production of organoleptic compounds
- Decipher interactions bacterium-bacterium within the bacterial community
- Salting variant has no effect in the production of organoleptic compounds

References

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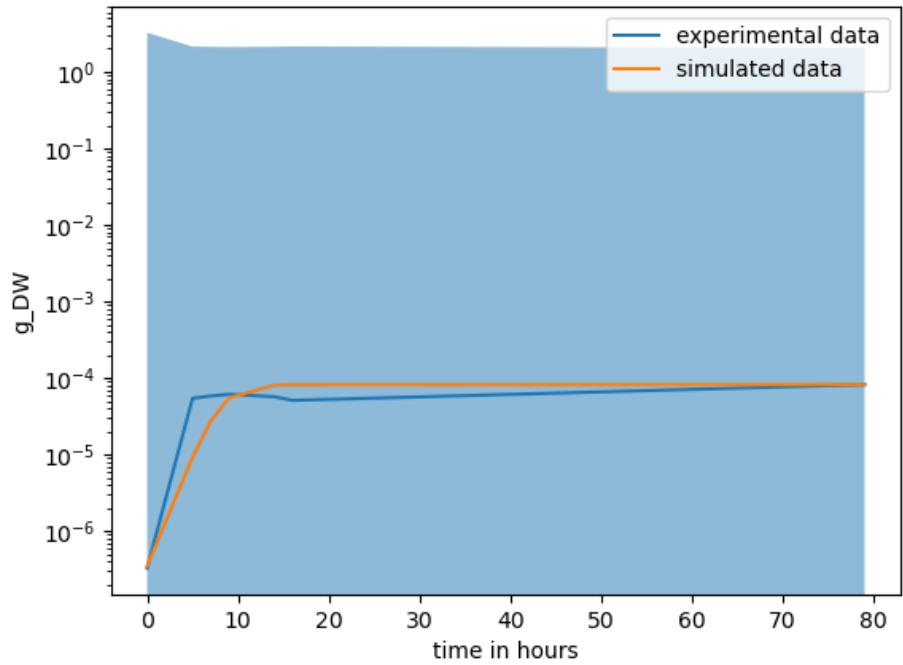


Figure 3: Comparison of growth rate of freudenreichii