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► **To cite this version:**

Maxime Lecomte, David James Sherman, H el ene Falentin, Cl emence Frioux. Characterising competition and cooperation potentials in microbial communities using discrete models of metabolism. An exploratory analysis. JOBIM 2022 - JOURN EES OUVERTES EN BIOLOGIE, INFORMATIQUE ET MATH EMATIQUES, Jul 2022, Rennes, France. hal-03839337

HAL Id: hal-03839337

<https://hal.inrae.fr/hal-03839337>

Submitted on 4 Nov 2022

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Characterising competition and cooperation potentials in microbial communities using discrete models of metabolism

An exploratory analysis

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Introduction

Modeling the metabolism enables characterizing of the potential metabolic

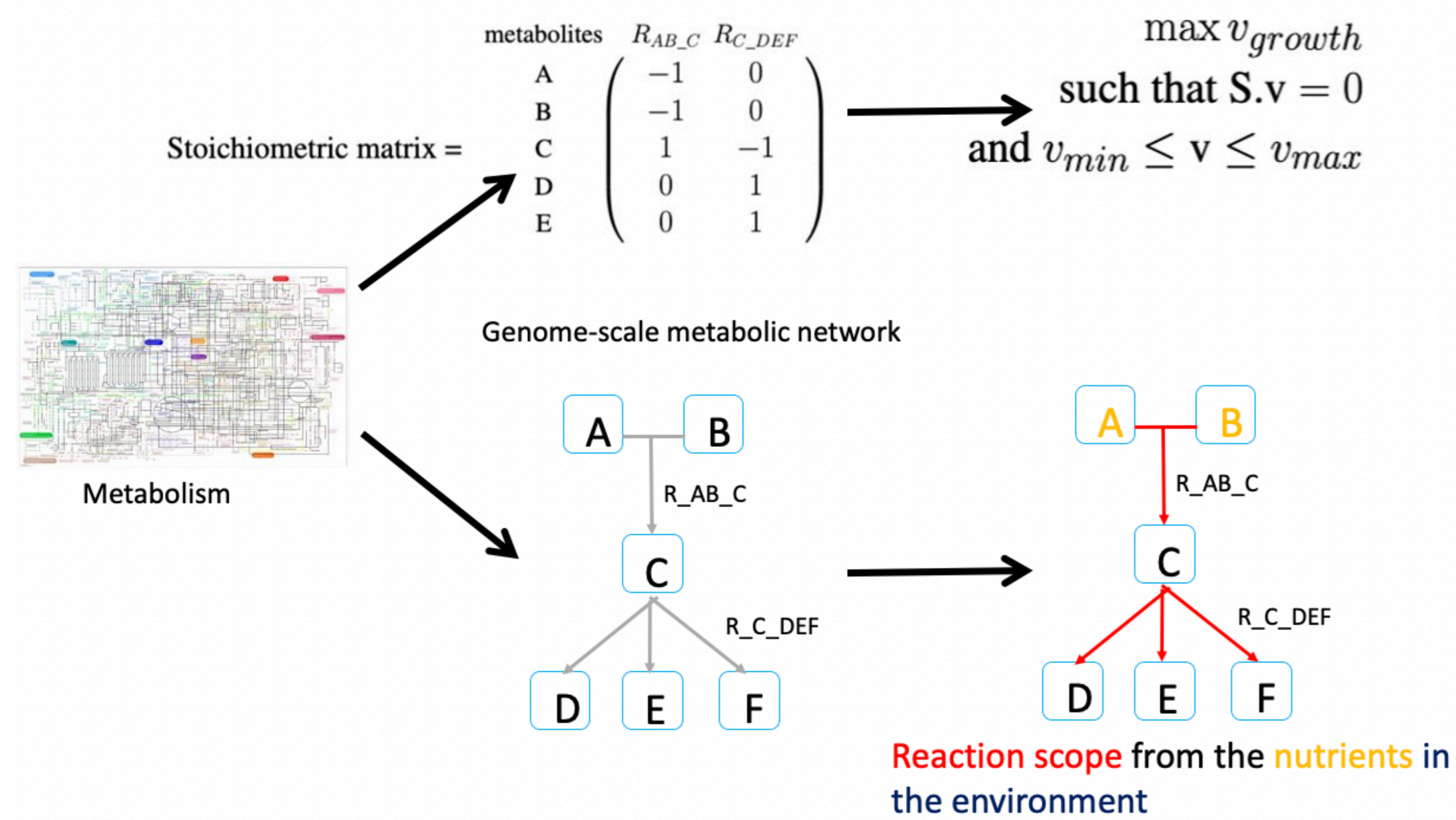


Figure 1: From annotated genomes, genome-scale metabolic networks are reconstructed and constraint-based[4] or topological methods [1] permit the understanding of metabolism.

State-of-the-art for deciphering cooperation and competition potentials of a community

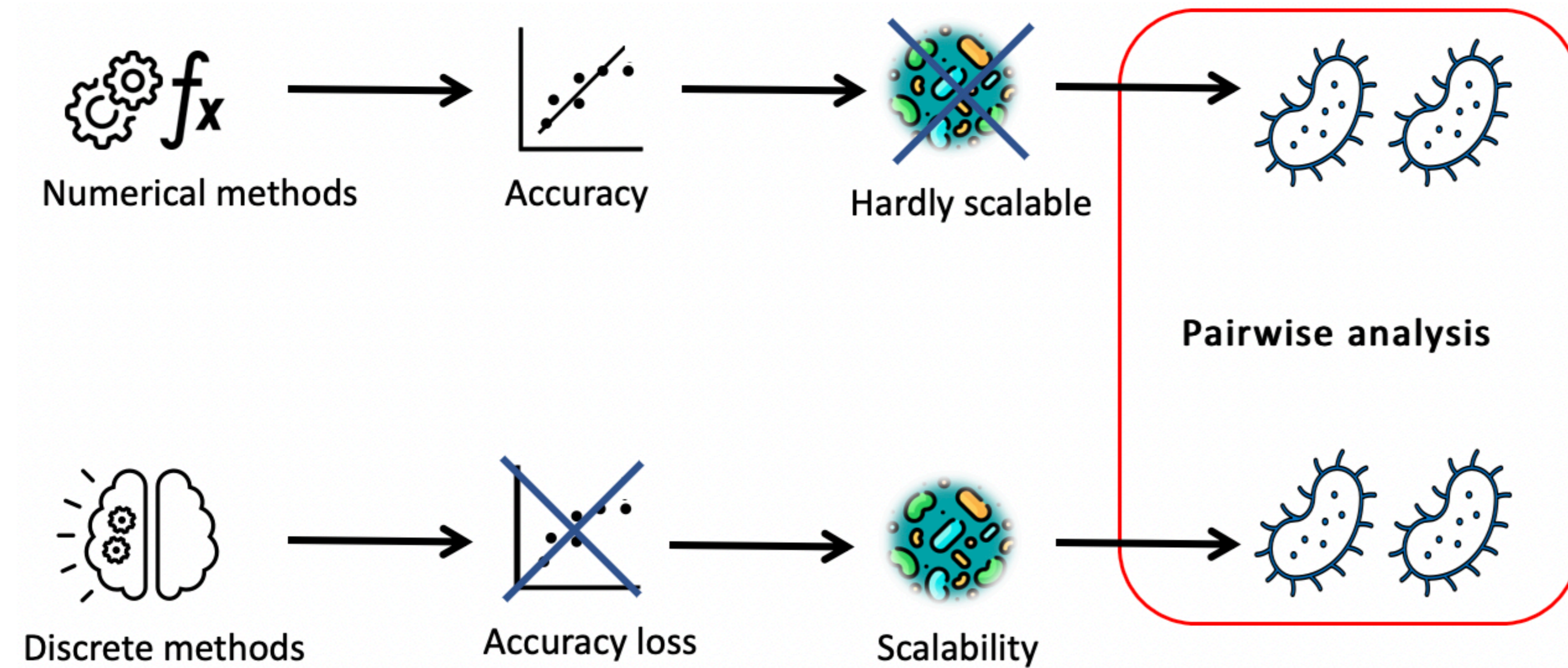


Figure 2: Numerical methods quantify exchanged metabolites within small bacterial communities. Unlike of them, discrete modeling can be scaled to natural communities. Both methods use pairwise analysis [2]

Main Objective

Characterize communities as cooperative or competitive from scores

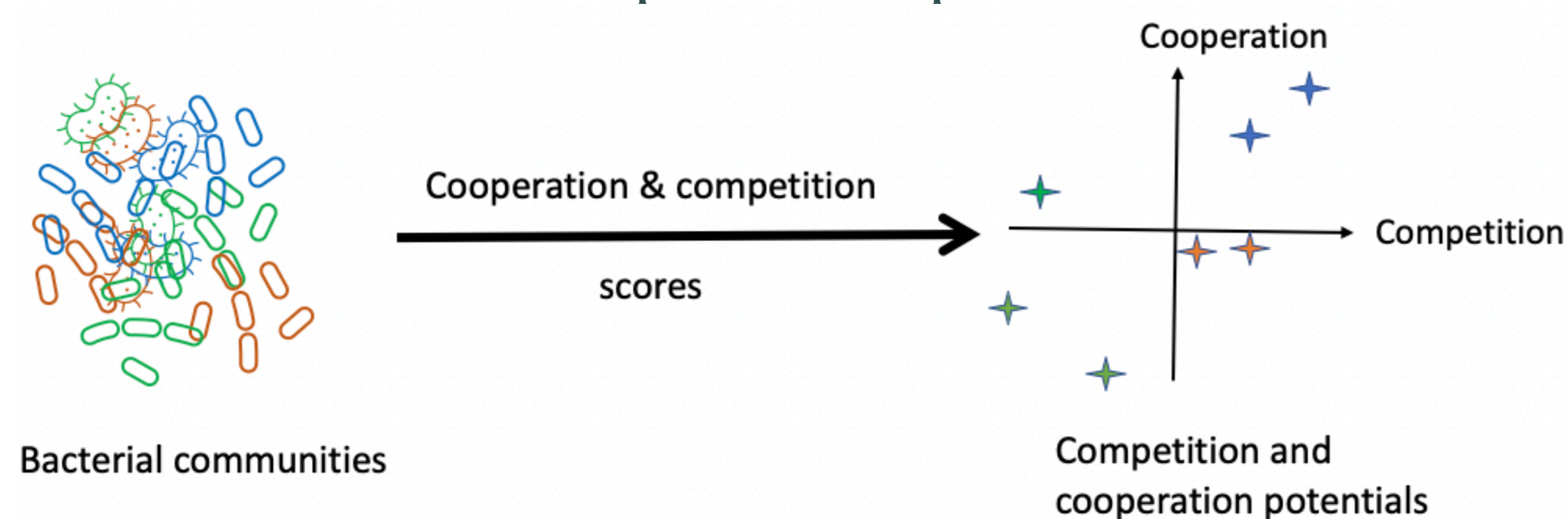


Figure 3: From bacterial communities, we build cooperation and competition scores in order to characterize communities as cooperative or competitive.

Materials and Methods

Descriptive rules of the community interactions based on discrete method

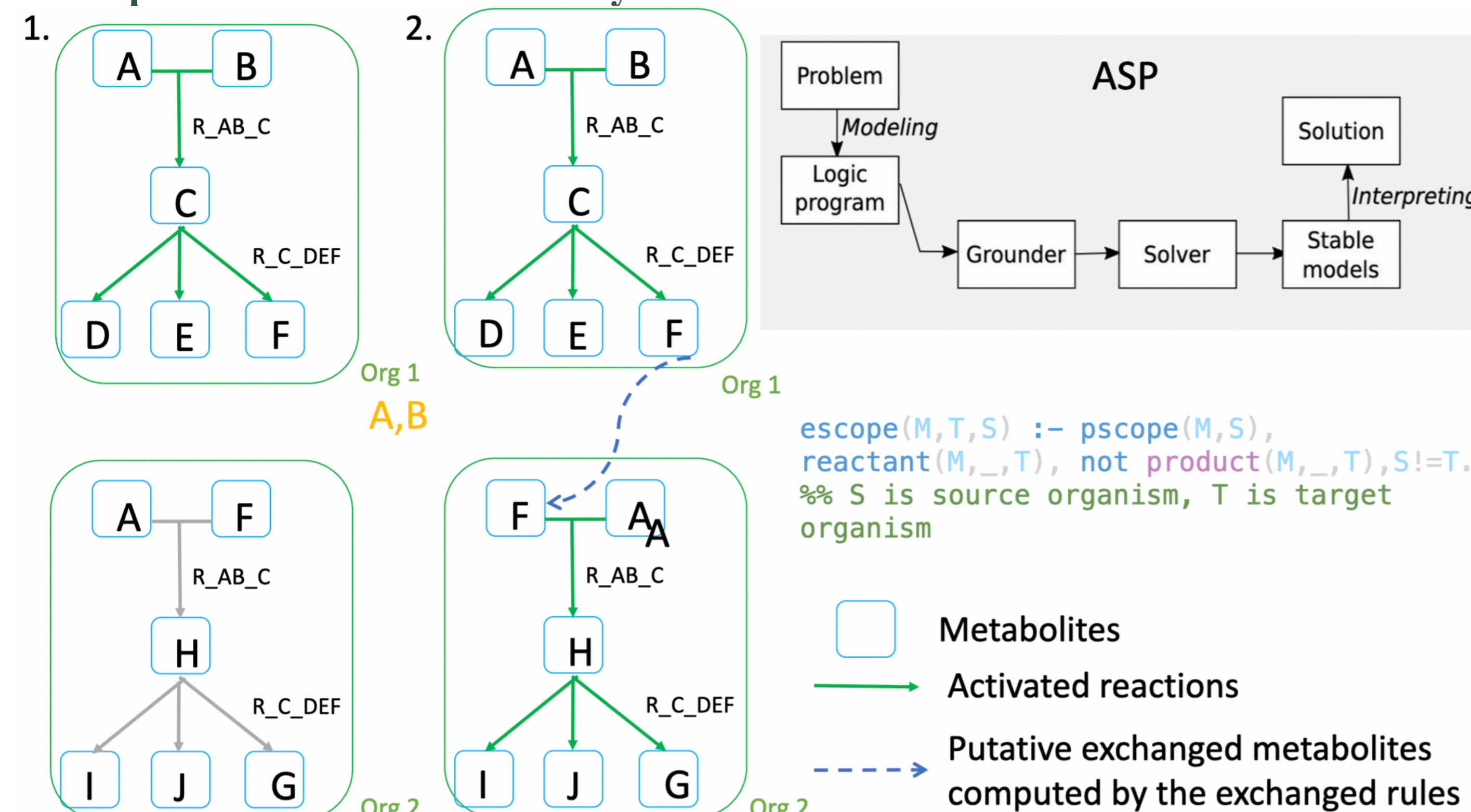


Figure 4: We show in this figure how exchanged metabolites are computed. To characterize cooperative and competition communities, we use ASP [3] that describes the metabolism under list of facts and rules.

Mathematical expressions of cooperation scores

$$\text{Scope}(G,S) = \bigcup_i M_i$$

where $M_0 = S$ and $M_{i+1} = M_i \cup \text{products}(r) \in R \mid \text{reactants}(r) \subseteq M_i$

where S the seed compounds according to the metabolic network G.

number of **producible compounds** (Δ_{score}):

$$\text{scope}(G_{com}, S) - \bigcup_{i \in G} \text{scope}(G_i, S)$$

number of **activable reactions** (ρ_{score}):

$$\text{scope}(G_{com}, R) - \bigcup_{i \in G} \text{scope}(G_i, R)$$

where $R \in \text{Reactions}$ of a metabolic network G.

number of **exchanged compounds** (Π_{score}) =

$$\text{scope}(G_s, S), \text{not reactant}(S, G_t), \text{products}(S, G_t)$$

where s and t $\in G$ and s \neq t.

Experimental design for creating a benchmark and testing scores

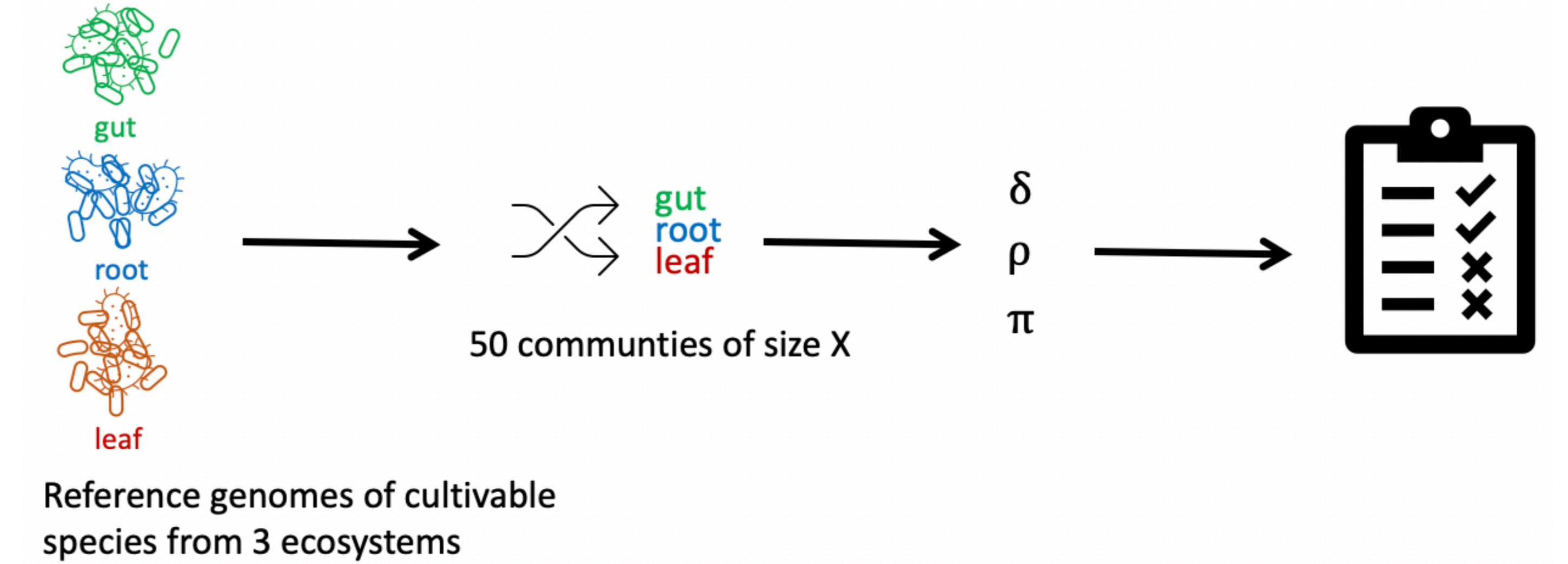


Figure 5: From reference genomes of different ecosystems, we randomly create 50 communities of size ranging from 3 to 150. Cooperative scores are computed and compared.

Results

Distribution brings by cooperation scores

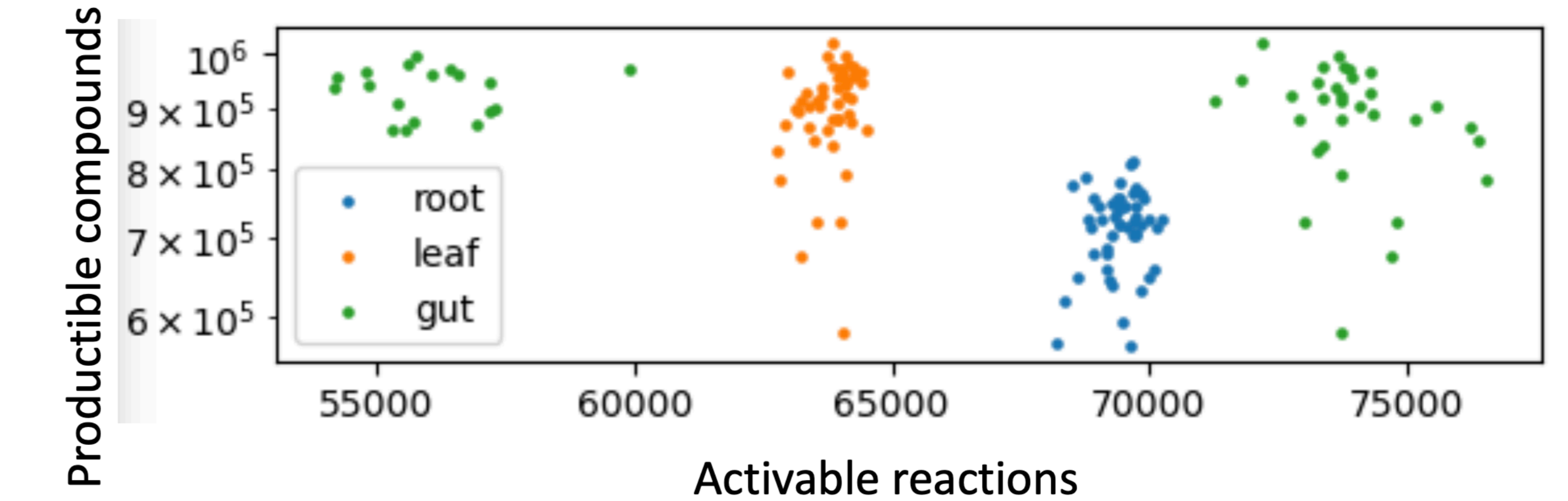


Figure 6: For each community size and ecosystems, we plot in pairwise cooperation scores to evaluate the added-value and the distribution brought by each score. Here, we plot 50 communities of size = 150 bacteria.

Rho score distribution within different ecosystems

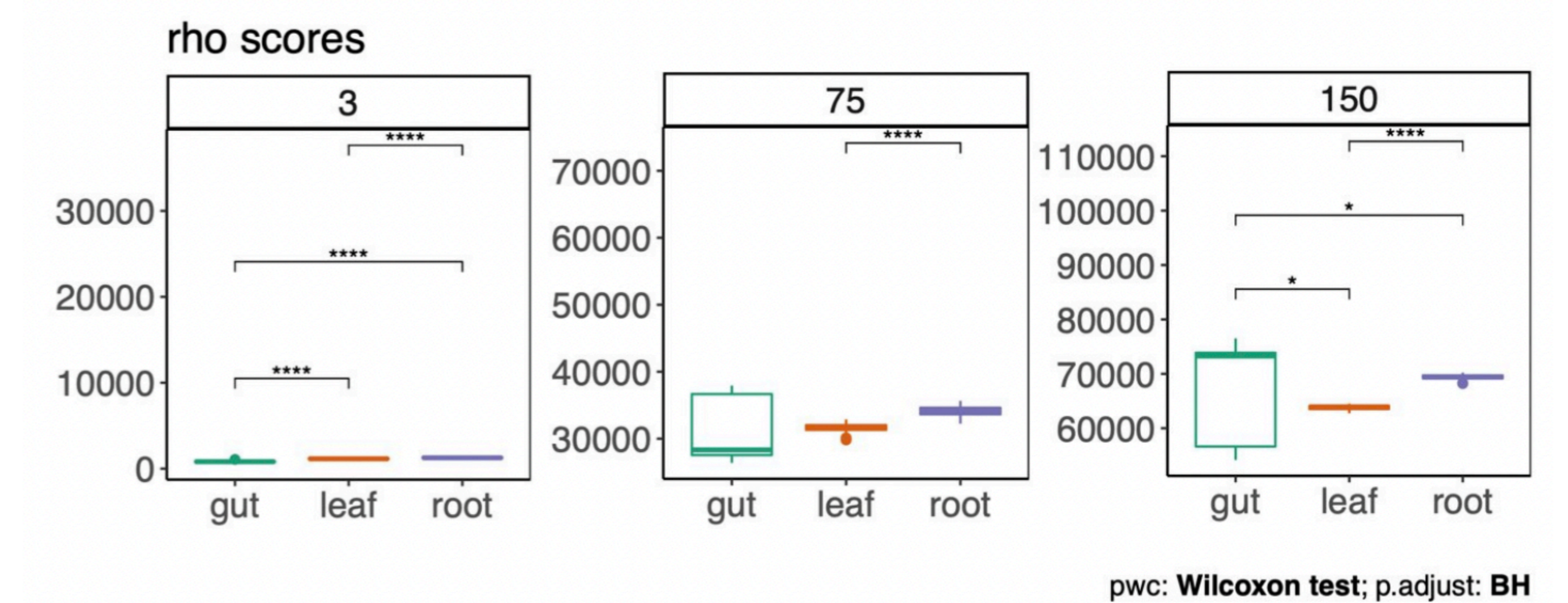


Figure 7: Distribution of ρ score in all ecosystems and for a community size = 3, 75 and 150. We observe that metrics distributions are different for each ecosystems except for a community size = 75 bacteria.

Conclusions and forthcoming research

- Our metrics highlight differences between ecosystems regarding the cooperation potentials
- Cross validation methods could be implemented to validate the differences observed.

References

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[4] Jeffrey D. Orth, Ines Thiele, and Bernhard O. Palsson. What is flux balance analysis?, 2010.