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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

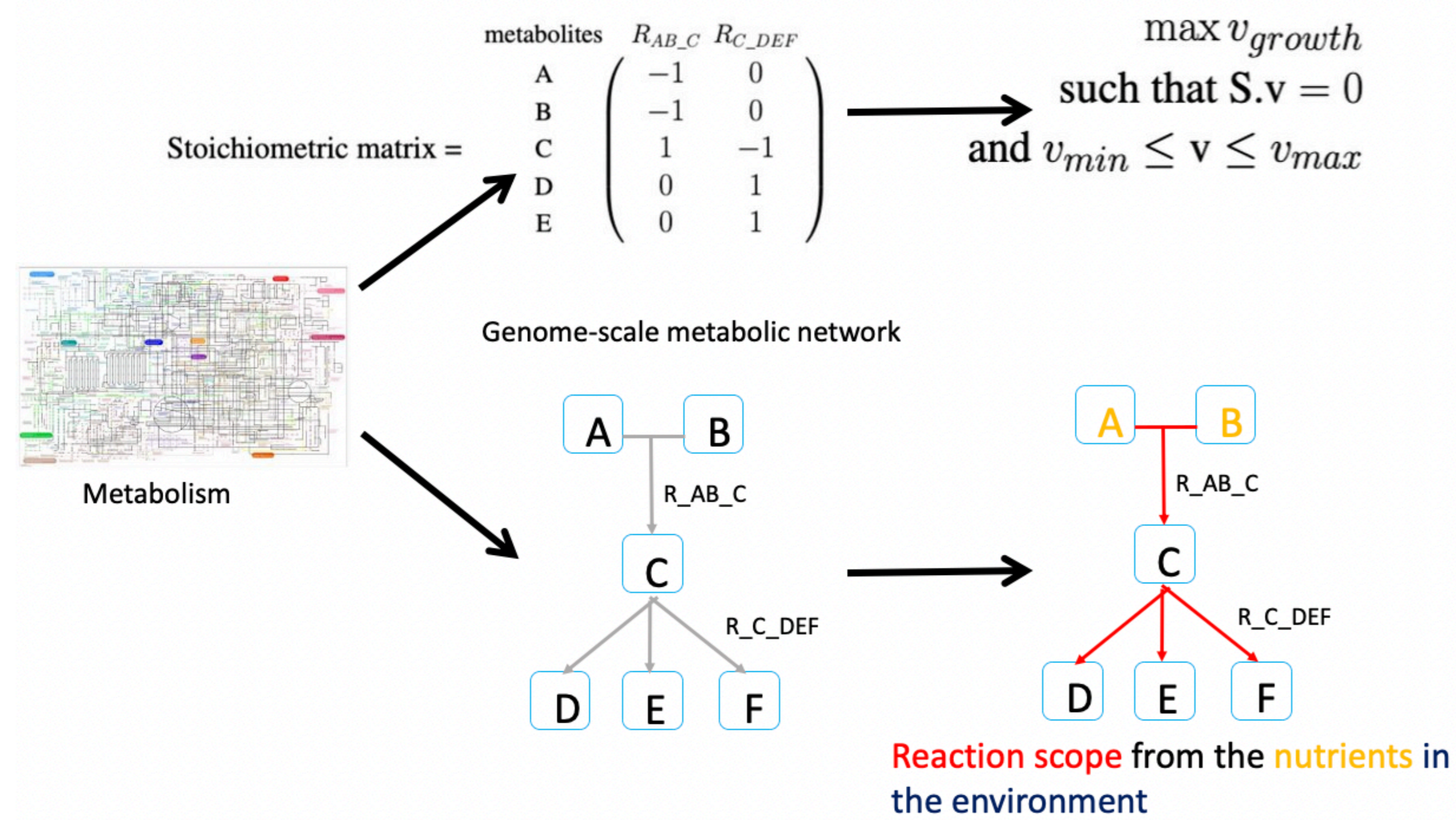


Figure 1: From annotated genomes, genome-scale metabolic networks are reconstructed and constraint-based[4] or topological methods [1] permit the understanding of metabolism.

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

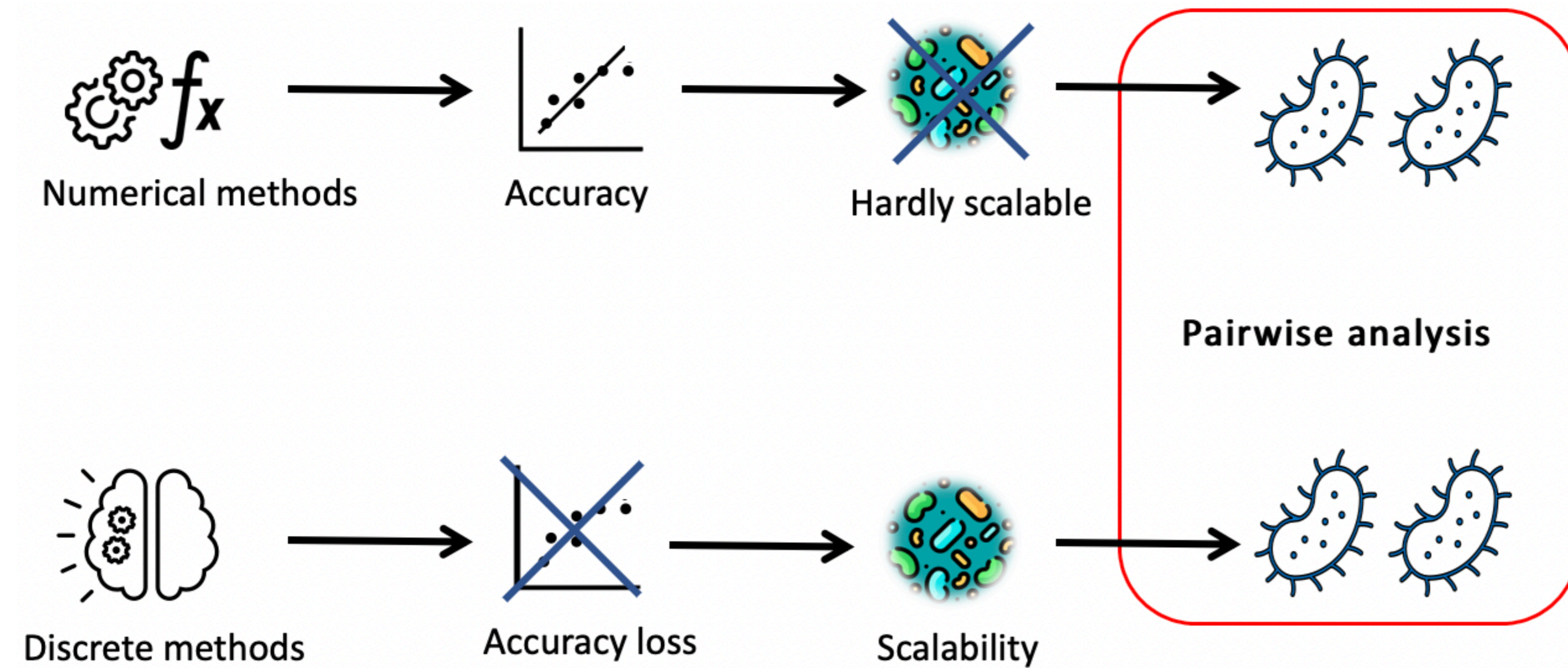


Figure 2: Numerical methods quantify exchanged metabolites within small bacterial communities. Unlike of them, discrete modeling can be scaled to natural communities. Both methods use pairwise analysis [2]

### Main Objective

Characterize communities as cooperative or competitive from scores

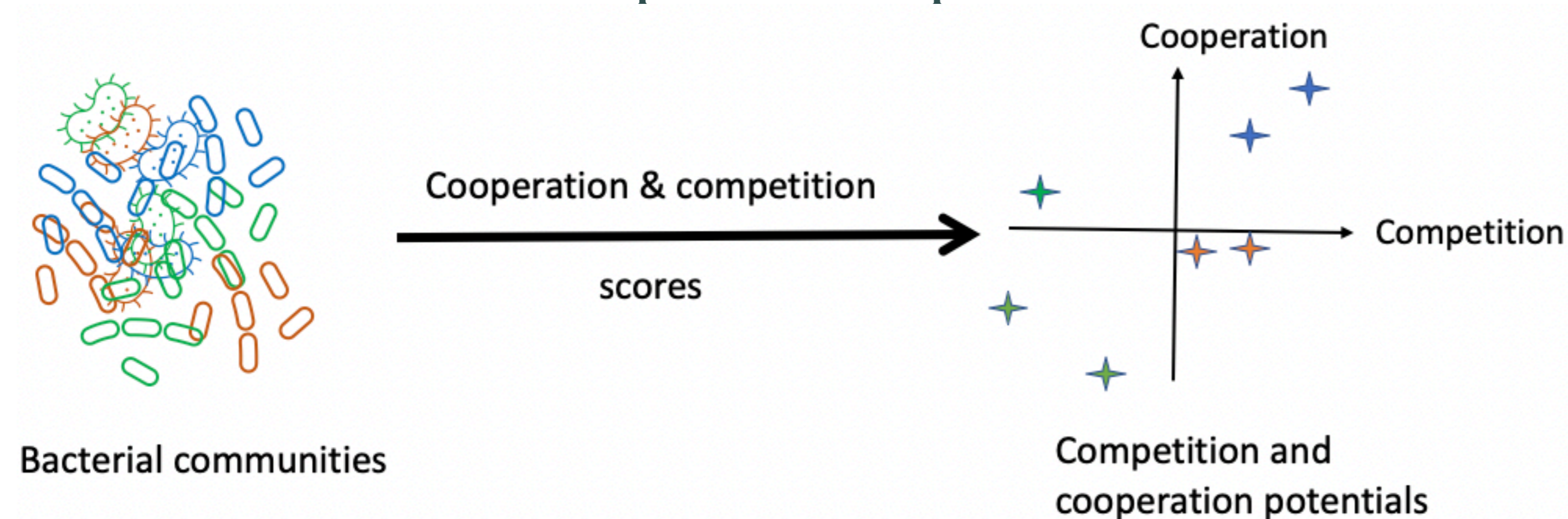


Figure 3: From bacterial communities, we build cooperation and competition scores in order to characterize communities as cooperative or competitive.

### Materials and Methods

Descriptive rules of the community interactions based on discrete method

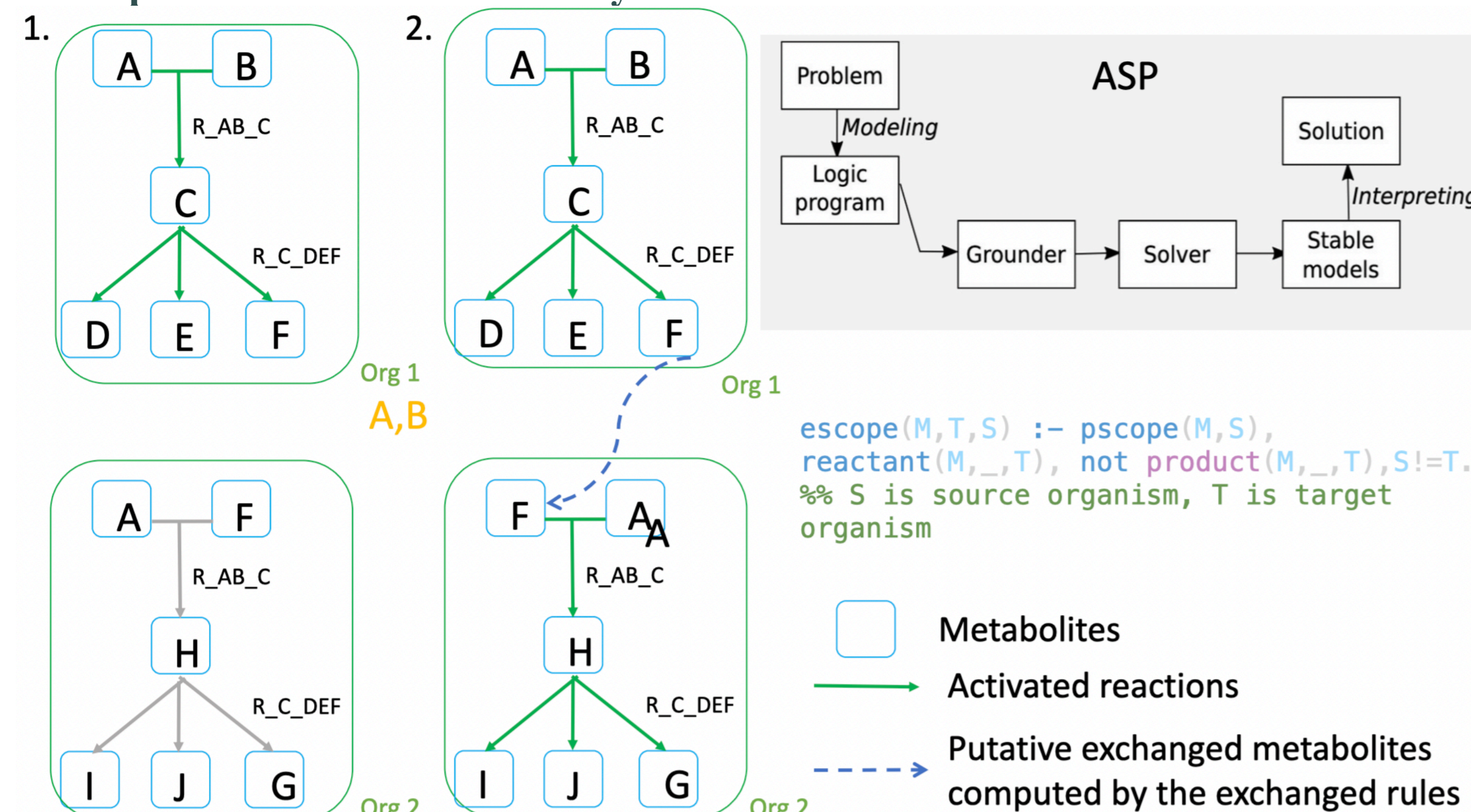


Figure 4: We show in this figure how exchanged metabolites are computed. To characterize cooperative and competition communities, we use ASP [3] that describes the metabolism under list of facts and rules.

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** ( $\Delta_{score}$ ):

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

number of **activable reactions** ( $\rho_{score}$ ):

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

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

number of **exchanged compounds** ( $\Pi_{score}$ ) =

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

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

Experimental design for creating a benchmark and testing scores

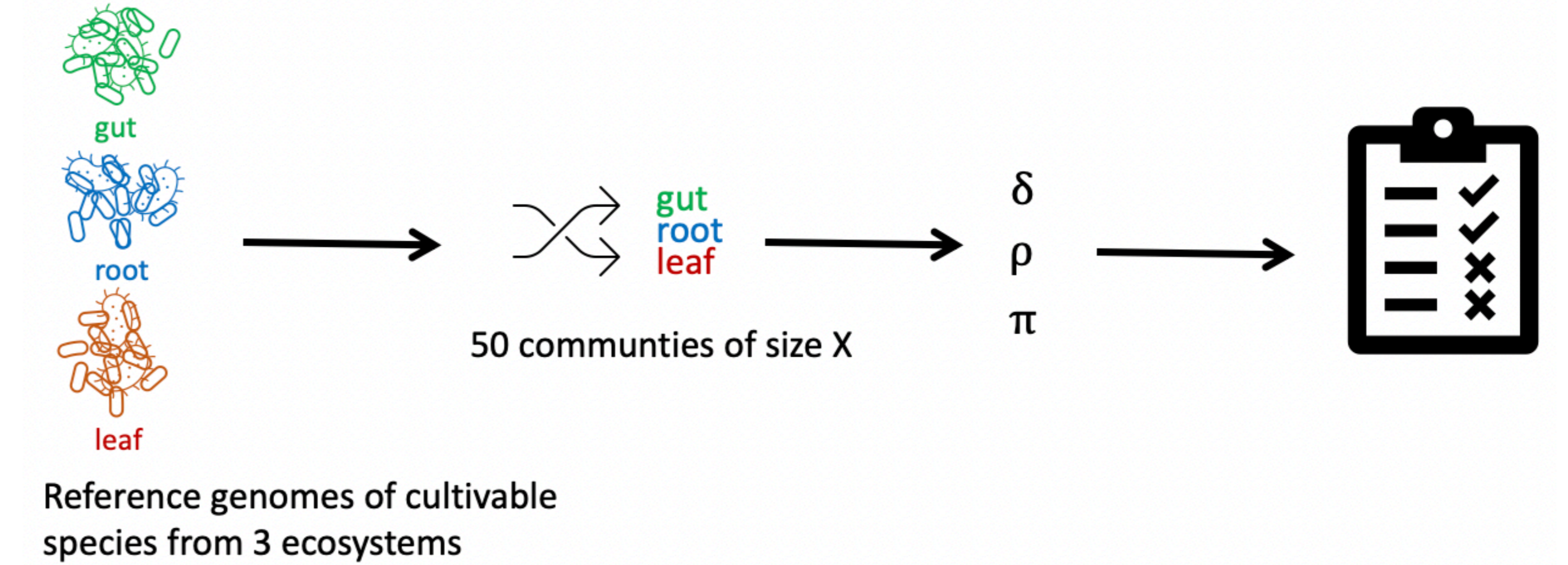


Figure 5: From reference genomes of different ecosystems, we randomly create 50 communities of size ranging from 3 to 150. Cooperative scores are computed and compared.

### Results

Distribution brings by cooperation scores

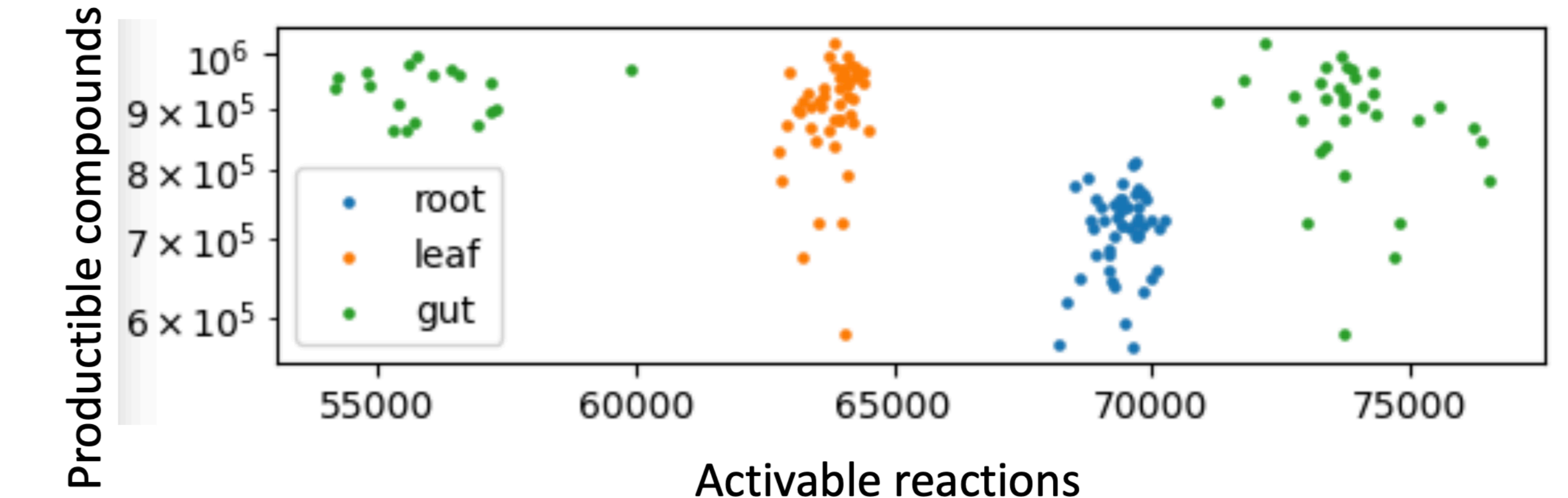


Figure 6: For each community size and ecosystems, we plot in pairwise cooperation scores to evaluate the added-value and the distribution brought by each score. Here, we plot 50 communities of size = 150 bacteria.

Rho score distribution within different ecosystems

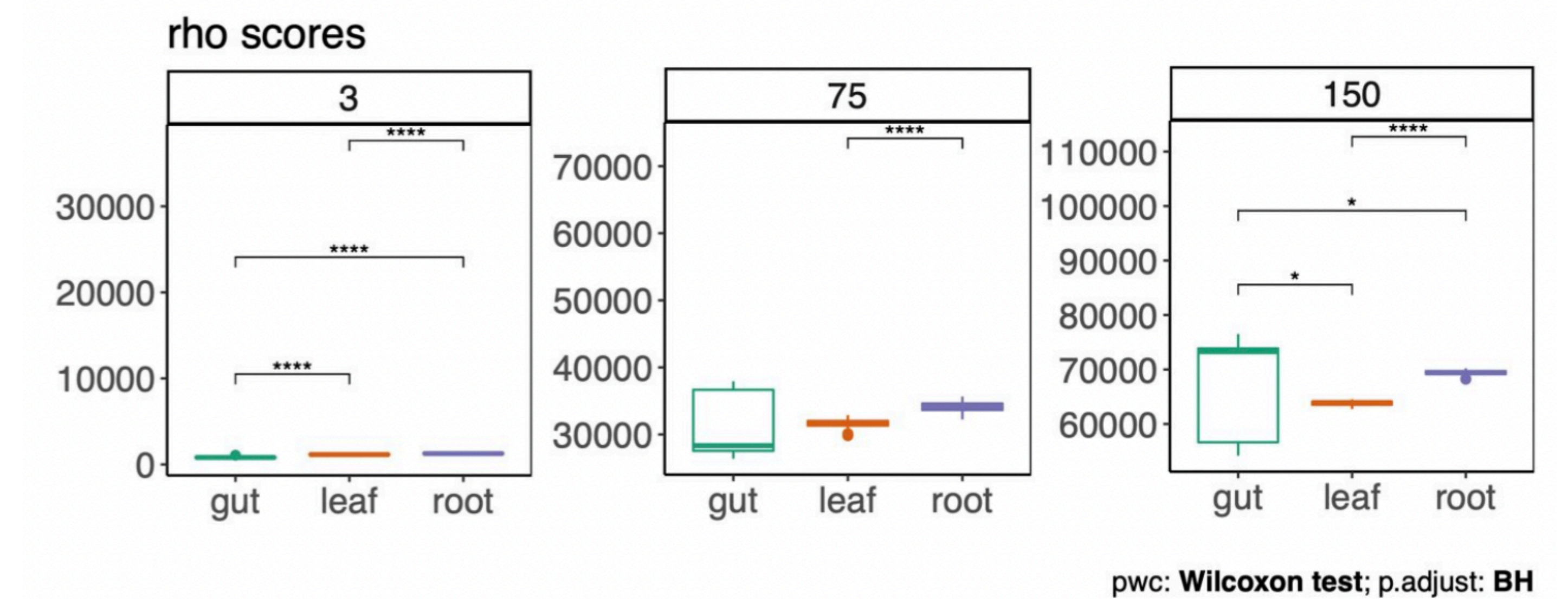


Figure 7: Distribution of  $\rho$  score in all ecosystems and for a community size = 3, 75 and 150. We observe that metrics distributions are different for each ecosystems except for a community size = 75 bacteria.

### 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

[1] Arnaud Belcour, Clémence Frioux, Méziane Aite, Anthony Bretaudeau, Falk Hildebrand, and Anne Siegel. Metage2metabo, microbiota-scale metabolic complementarity for the identification of key species. *eLife*, 2020.

[2] Shiri Freilich, Raphy Zarecki, Omer Eilam, Ella Shtifman Segal, Christopher S. Henry, Martin Kupiec, Uri Gophna, Roded Sharan, and Eytan Rupp. Competitive and cooperative metabolic interactions in bacterial communities. *Nature Communications*, 2(1), 2011.

[3] Vladimir Lifschitz. What is answer set programming? *Proceedings of the National Conference on Artificial Intelligence*, 3:1594–1597, 2008.

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