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RITHMS : An advanced stochastic framework for the simulation of transgenerational hologenomic data

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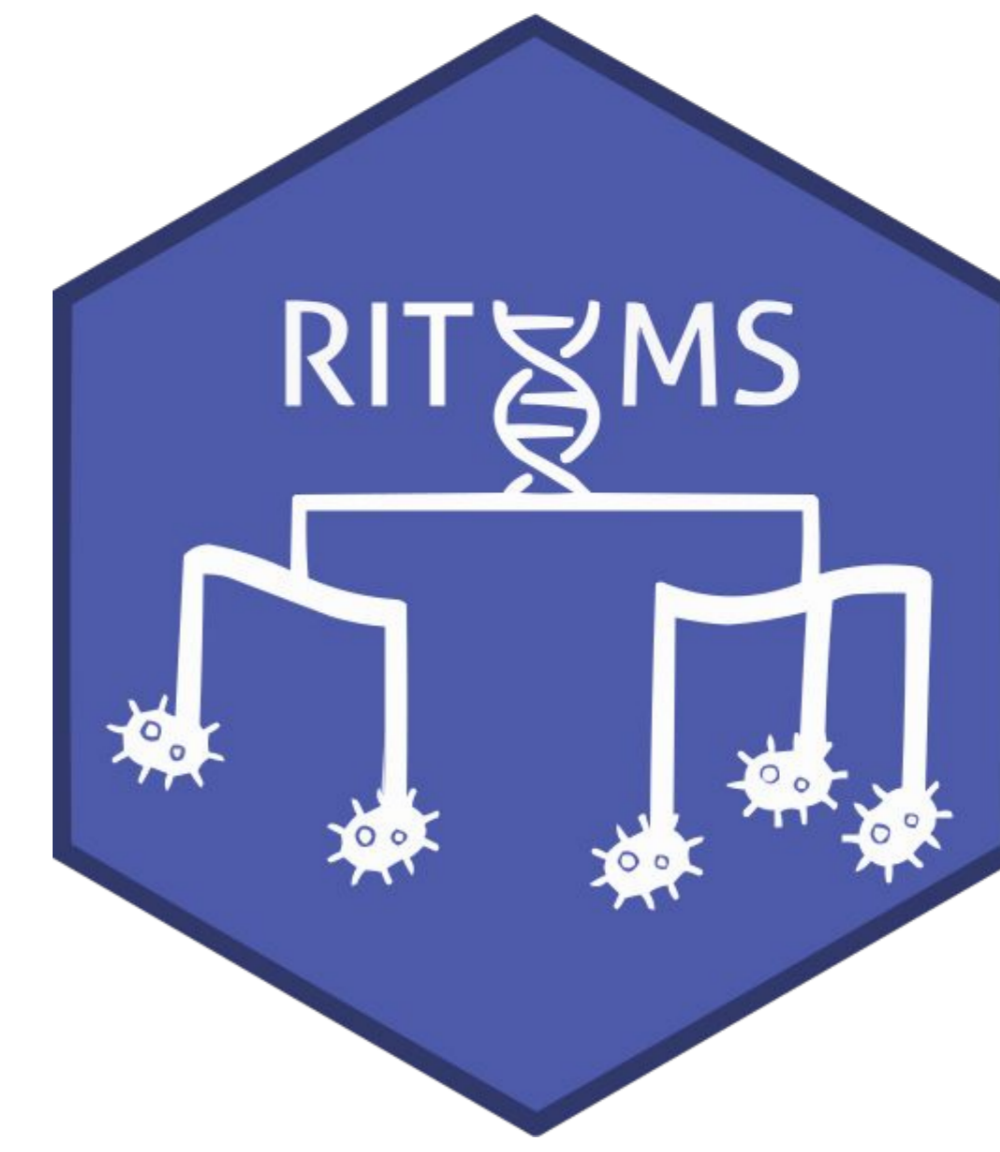
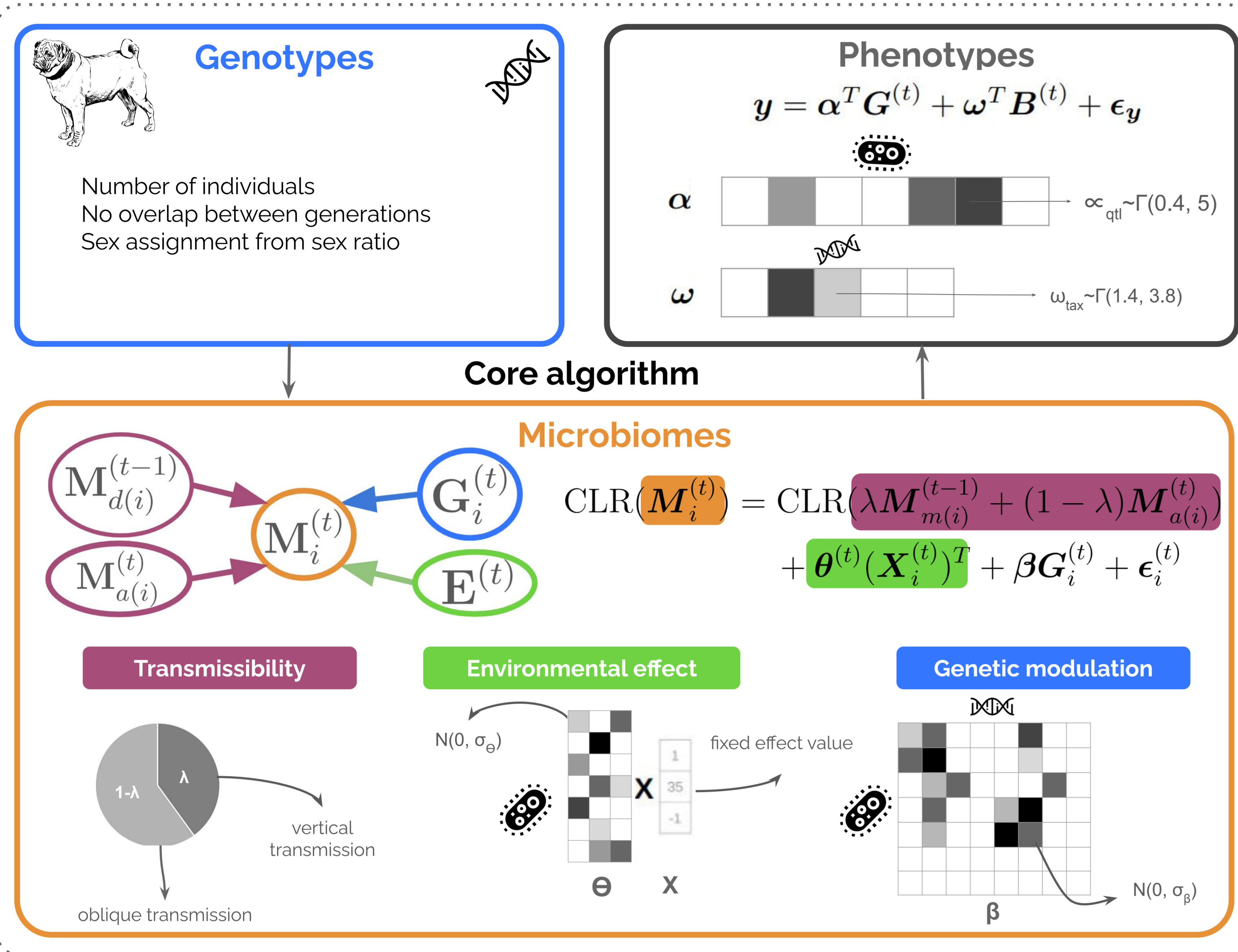
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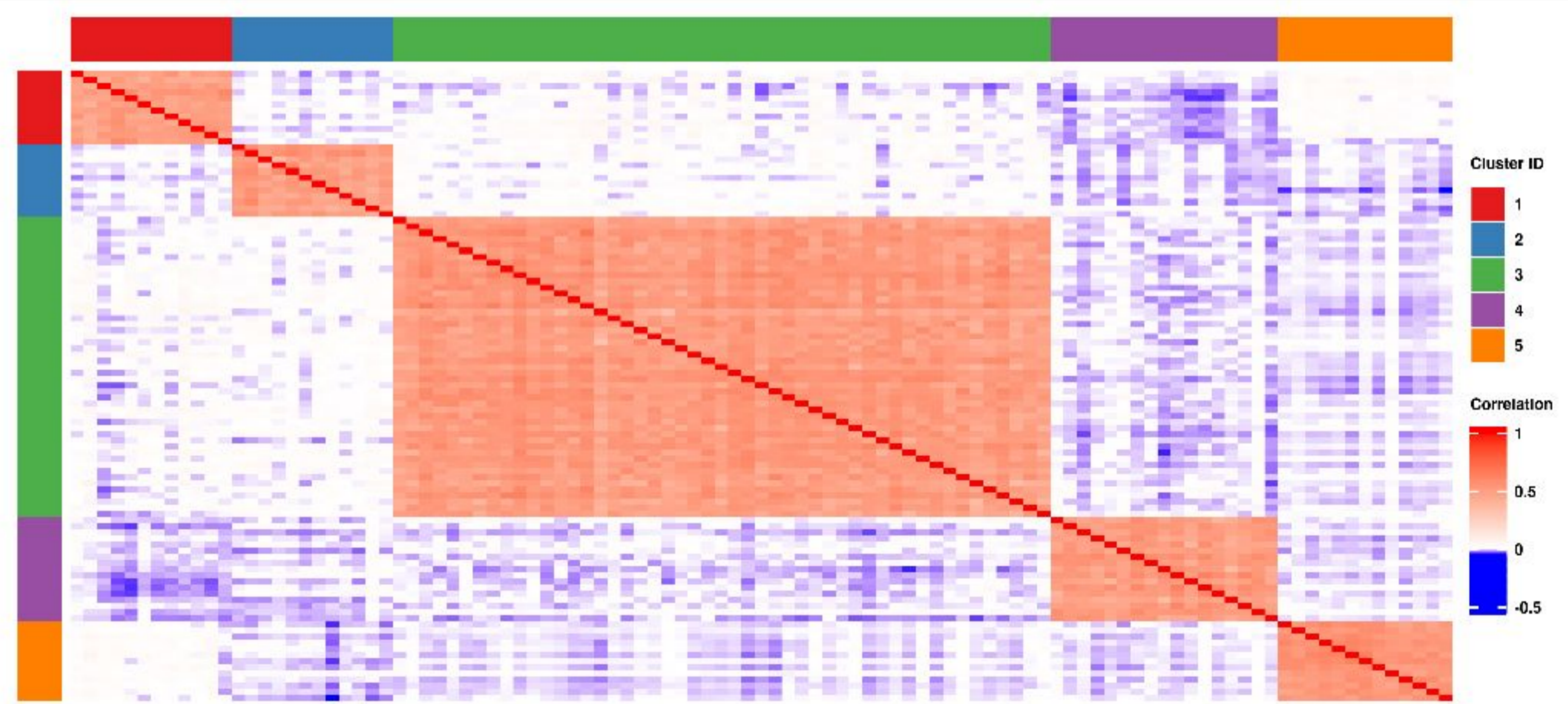
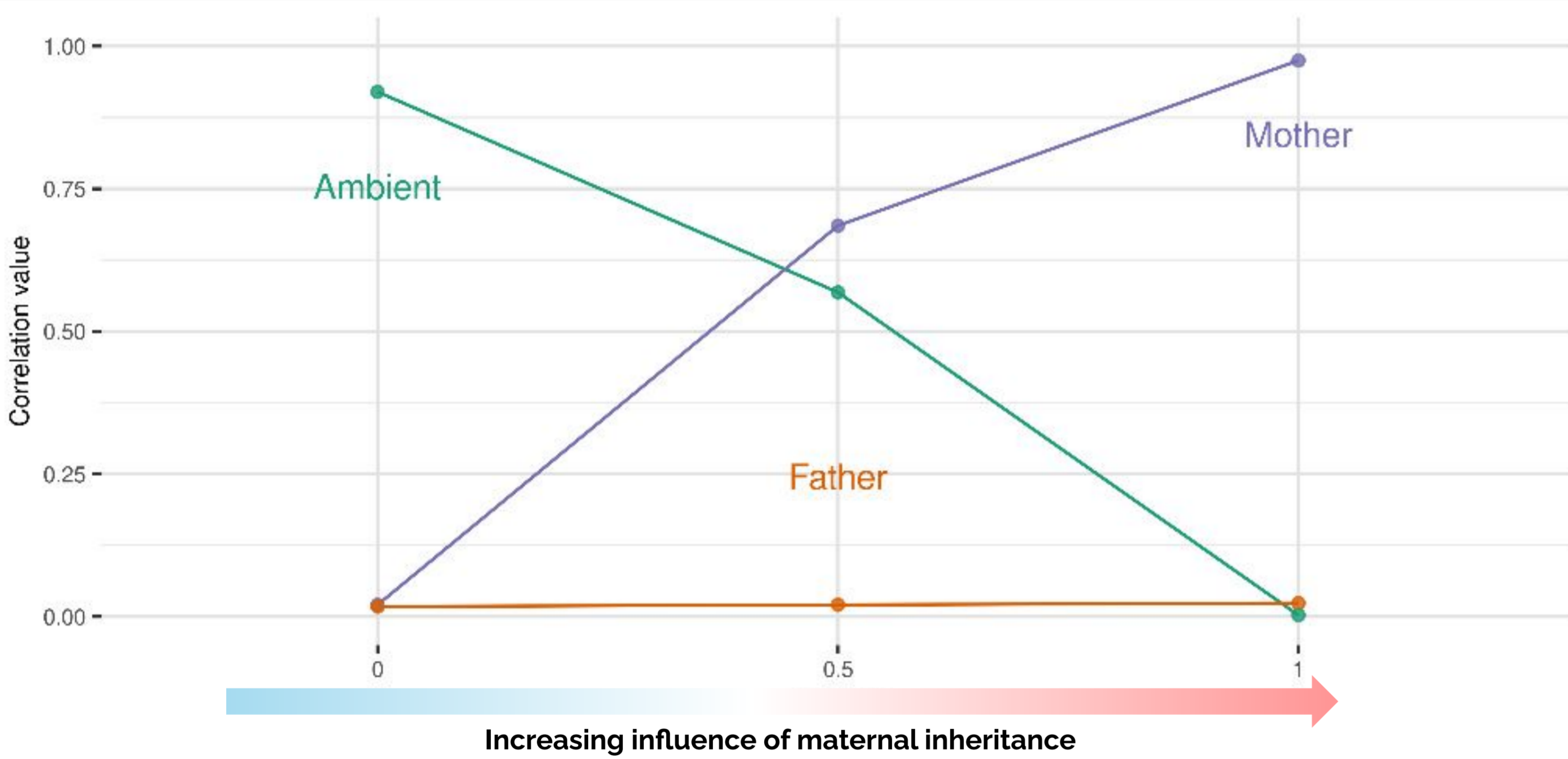
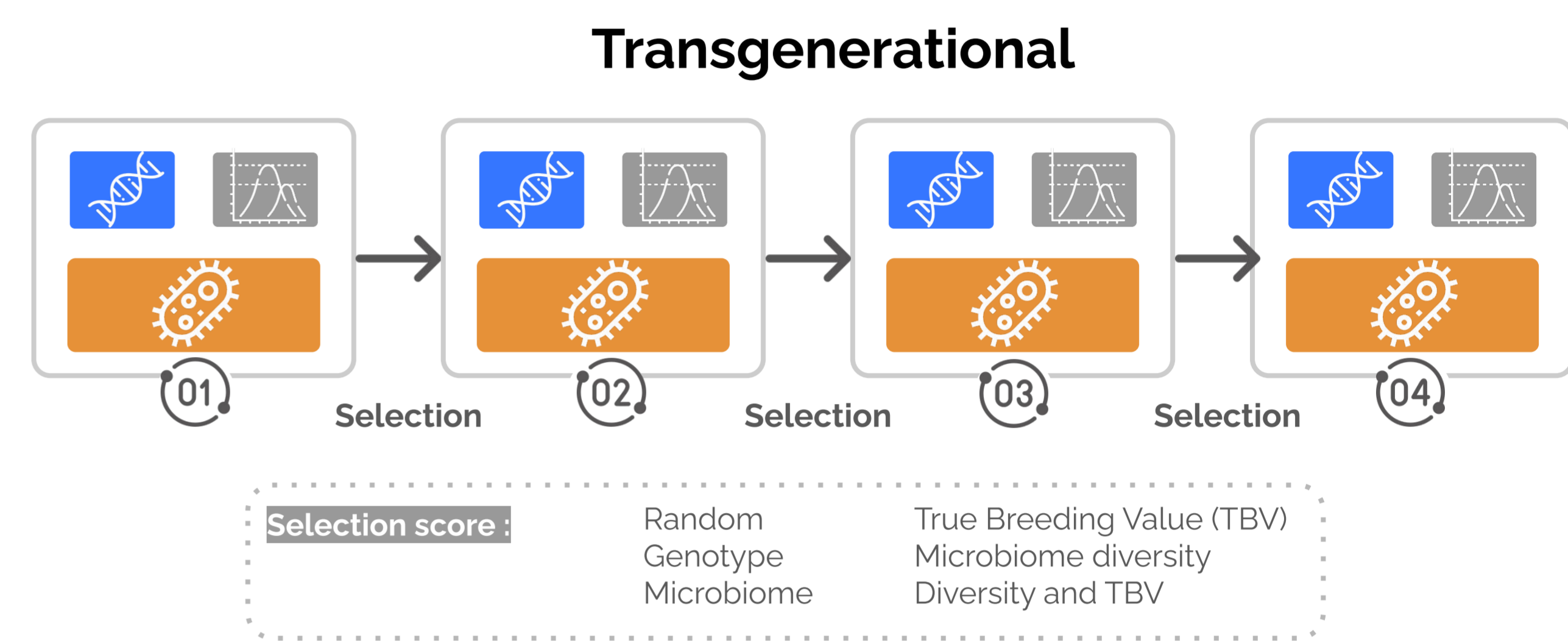
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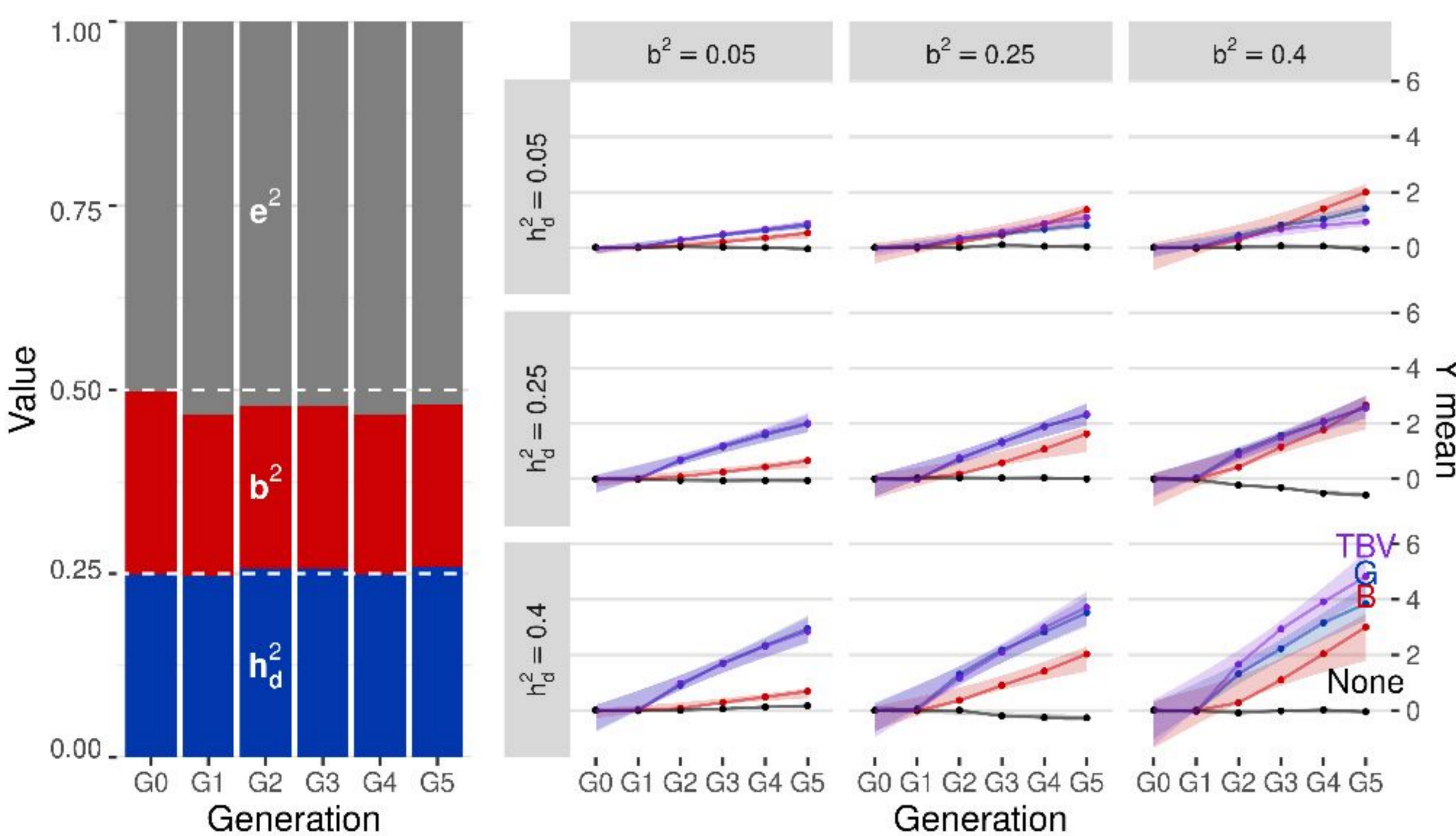
R Implementation of a Transgenerational Hologenomic Model-based Simulator (RITHMS) is a framework for simulating **transgenerational hologenomic data** that relies on **MoBPS** features for genomic data, accounts for the particularities of microbiota transmission, uses **real genomic and microbiota data** to construct a base population, and is flexible enough to cover a variety of scenarios defined by heritability, microbiability, and microbiota heritability.



<https://solenepeety.github.io/RITHMS/>

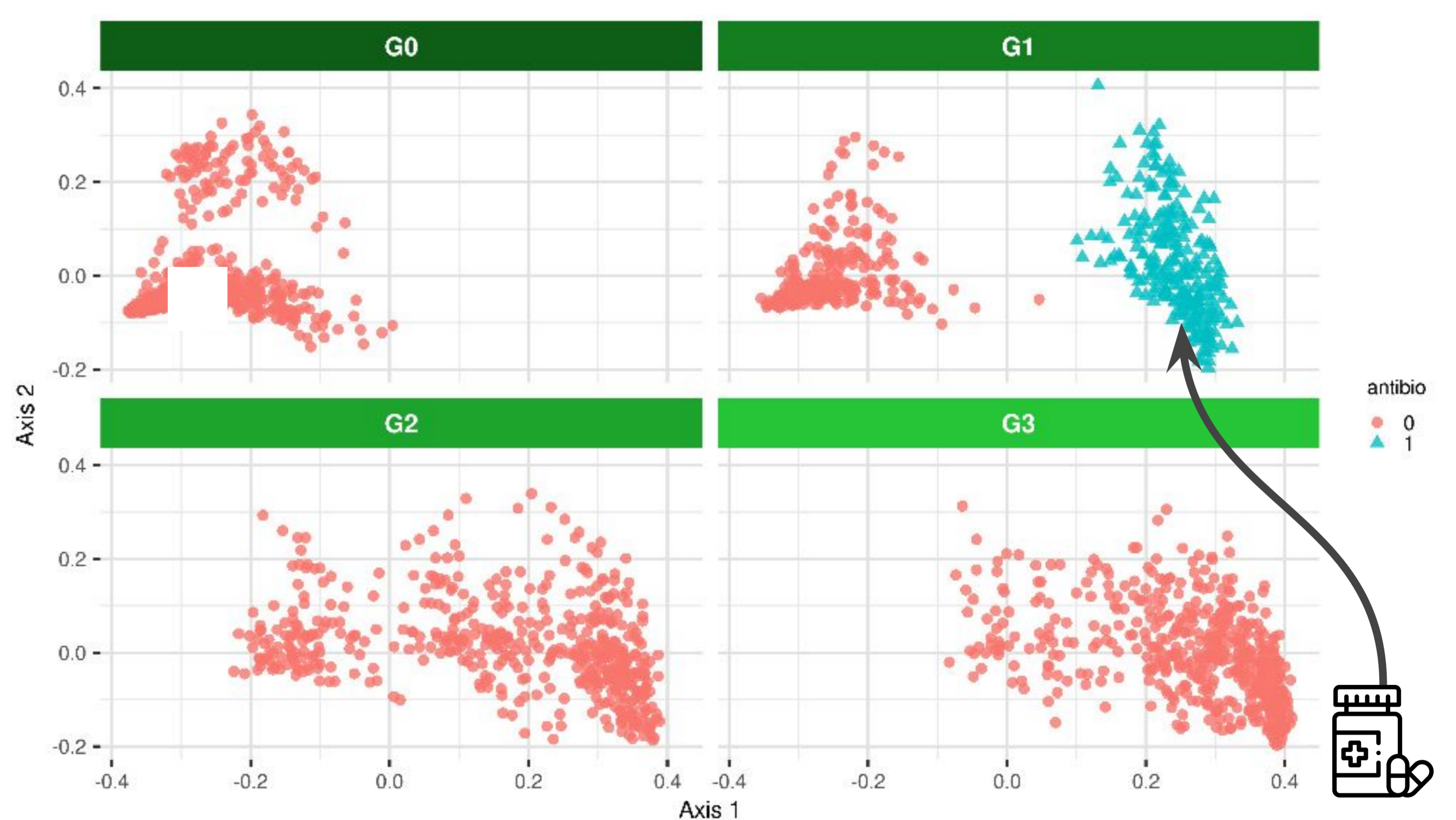


Adjust maternal and environmental contributions



Control direct heritability and microbiability across generations and select individuals according to various criteria

Define complex microbe abundance dependency structures



Model transient perturbations of the microbiota

Summary

In this work, we introduced a novel algorithm for simulating **transgenerational hologenomic data**, implemented in the R package RITHMS. Our tool **expands the scope** of existing simulation methods for multigenerational genotypes (**MoBPS** [1], **AlphaSimR** [2]) or for a single generation of microbiota under genetic influence (**Simubiome** [3]). RITHMS directly accounts for the **structure and characteristics of the microbiota** as well as its complex link with **host genotype transmission via the maternal or ambient environment**, and the impact of **isolated or sustained environmental effects**. We illustrated the use of RITHMS to simulate **complex selection and breeding programs**, both for the performance of various selection strategies incorporating the genome, microbiota, or hologenome as well as for the **construction of a customized integrated selection index**.

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