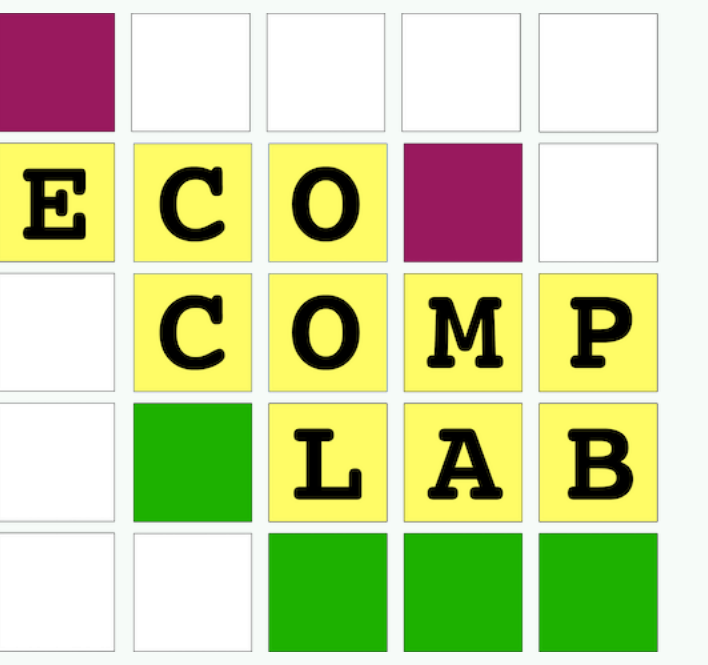




# Predicting Microbial Co-Occurrence Across Farms Using Phylogeny and Network Structure



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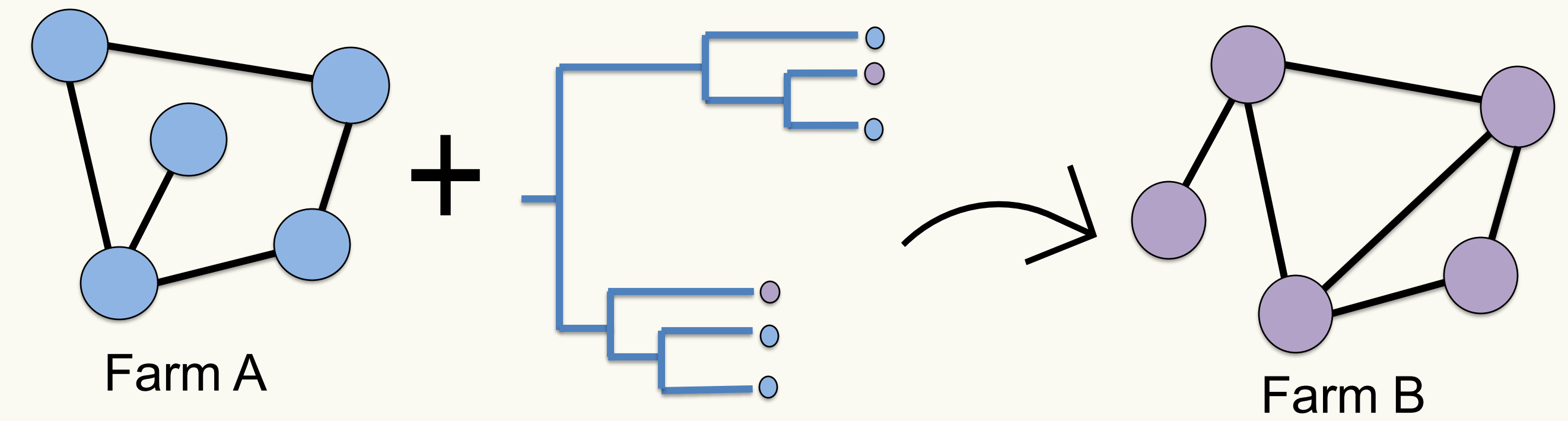
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## 1 Introduction

- **Microbial co-occurrence networks are often incomplete due to technical and biological limitations<sup>1</sup>.**
- Such missing data limits our understanding of microbial interactions and function.
- Predictive approaches such as phylogenetic imputation and Singular Value Decomposition (SVD) can infer missing links in ecological networks<sup>2,3</sup>.
- It is unclear whether these approaches can be used to transfer knowledge between microbial communities in different areas.

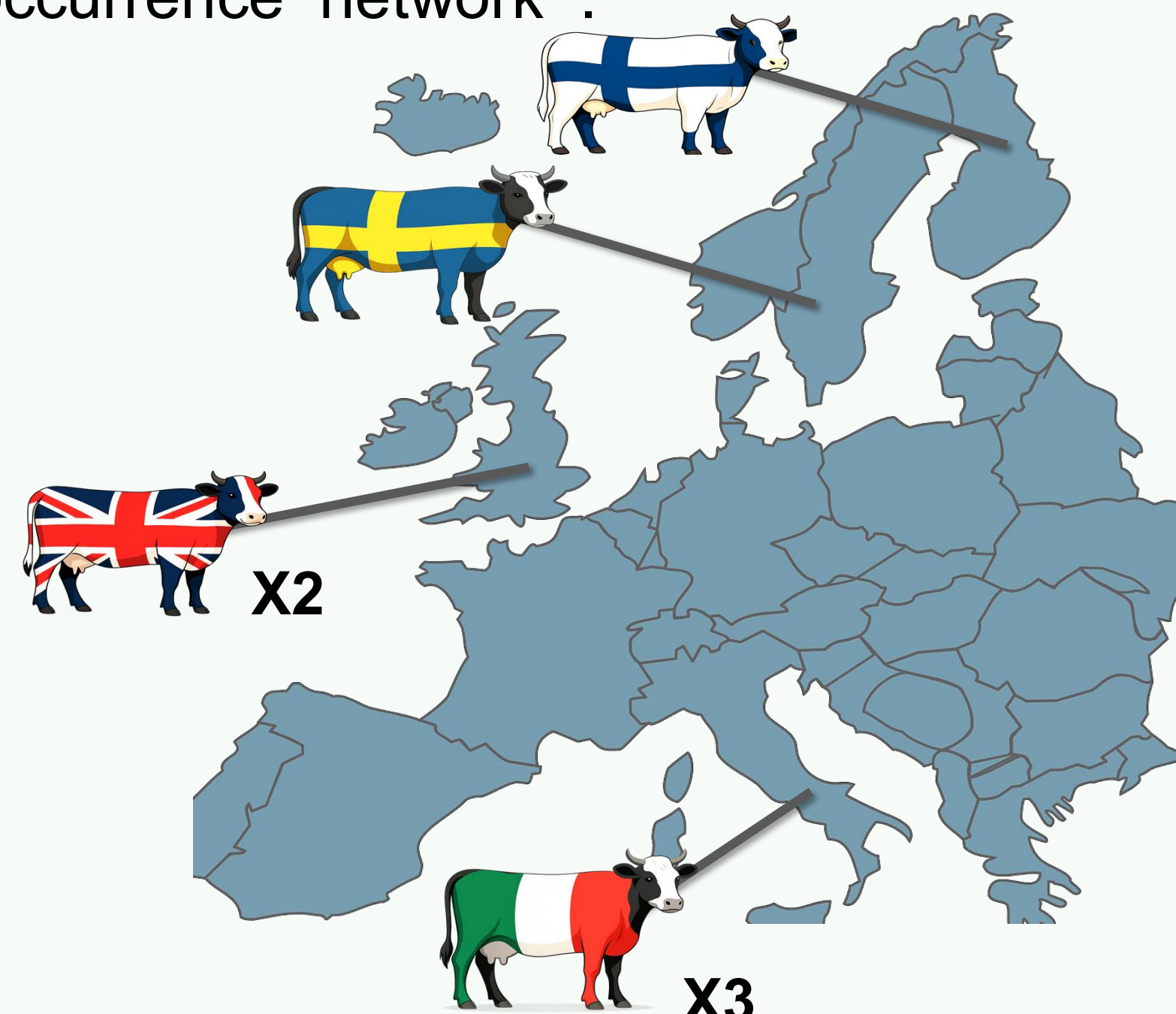
## 2 Research goals

To predict microbial co-occurrence patterns across farms using phylogeny and network structure derived from a known farm.

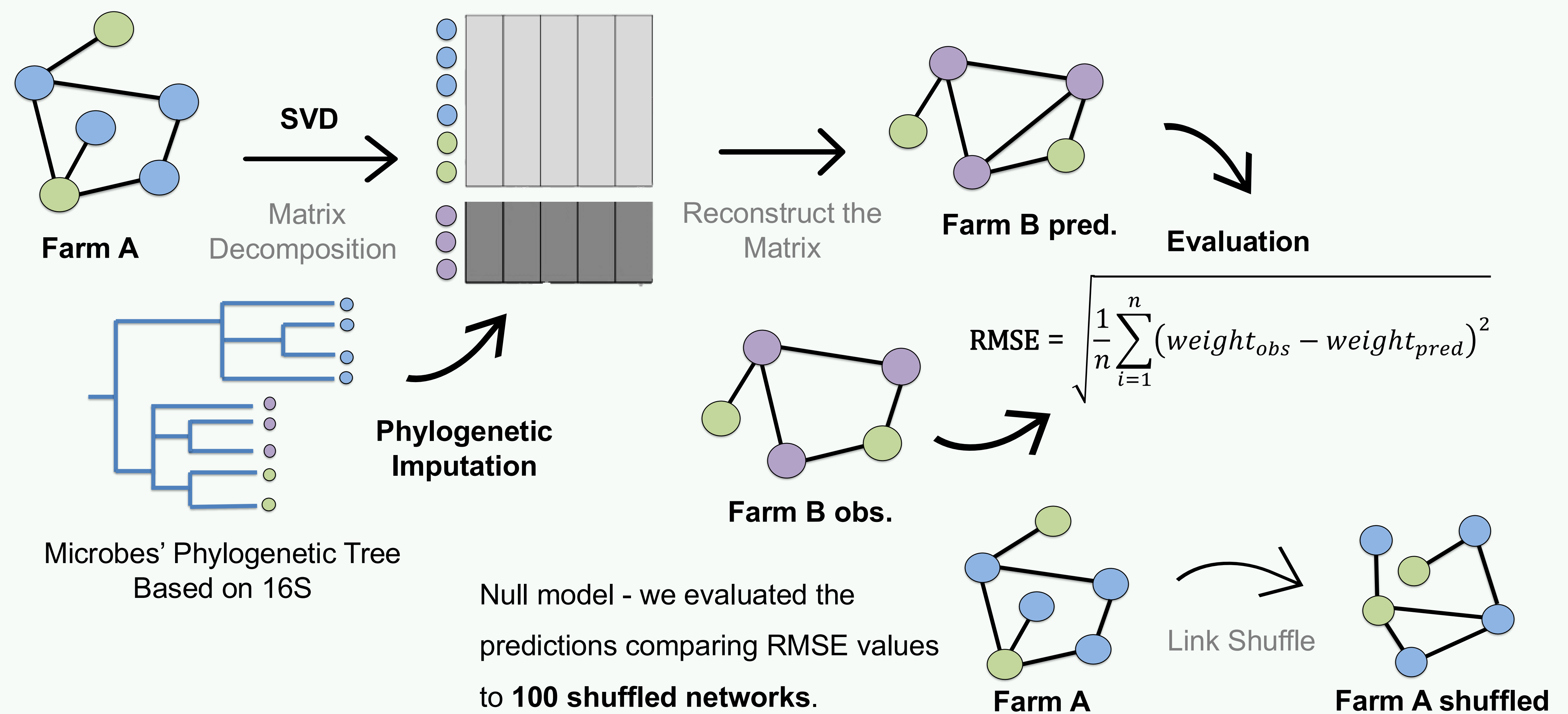


## 3 Experimental Strategy

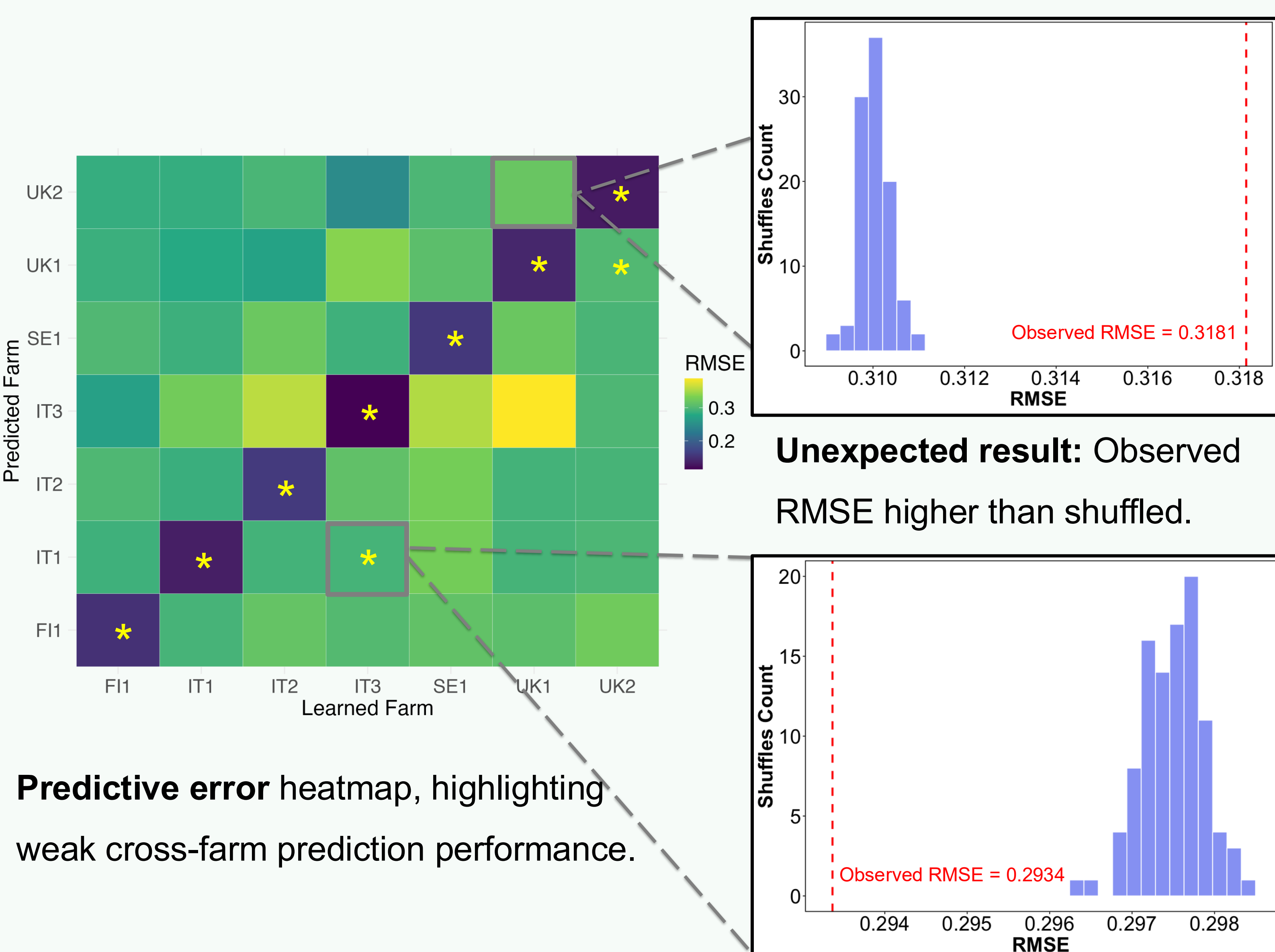
- We used co-occurrence data from 7 farms, each representing a microbial co-occurrence network<sup>1</sup>.



- We extracted network components capturing **20% of the variance** to predict co-occurrence.



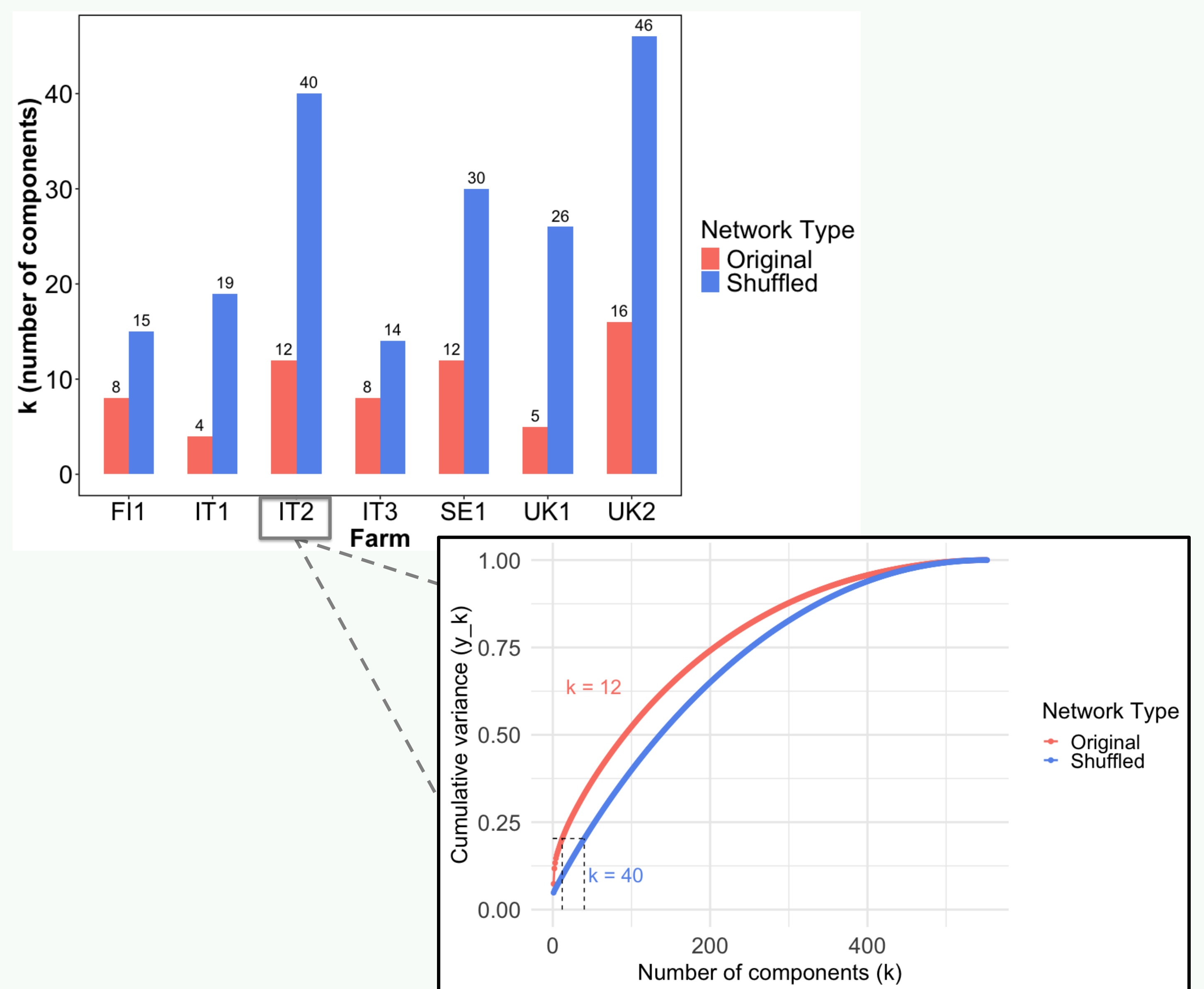
## 3 Results



**Predictive error heatmap**, highlighting weak cross-farm prediction performance.

**Expected result:** Lower RMSE in the observed data.

**More components needed in shuffled networks to explain 20% variance.**



## 5 Conclusions

- Our current results indicate that phylogeny is not a good predictor of co-occurrence across microbial systems.
- Shuffled networks required more components to explain variation in structure, indicating a loss of structure.
- However, most cross-farm predictions did not outperform random expectations.
- Future work: test alternative phylogenetic models and imputation methods.

## 6 References

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2. Nunes Martinez, A. & Mistretta Pires, M. Estimated missing interactions change the structure and alter species roles in one of the world's largest seed-dispersal networks. *Oikos* e10521 (2024).
3. Strydom, T. *et al.* Food web reconstruction through phylogenetic transfer of low-rank network representation. *Methods Ecol. Evol.* **13**, 2838–2849 (2022).

