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Impact of yeast cell cycle specificity on demography inference

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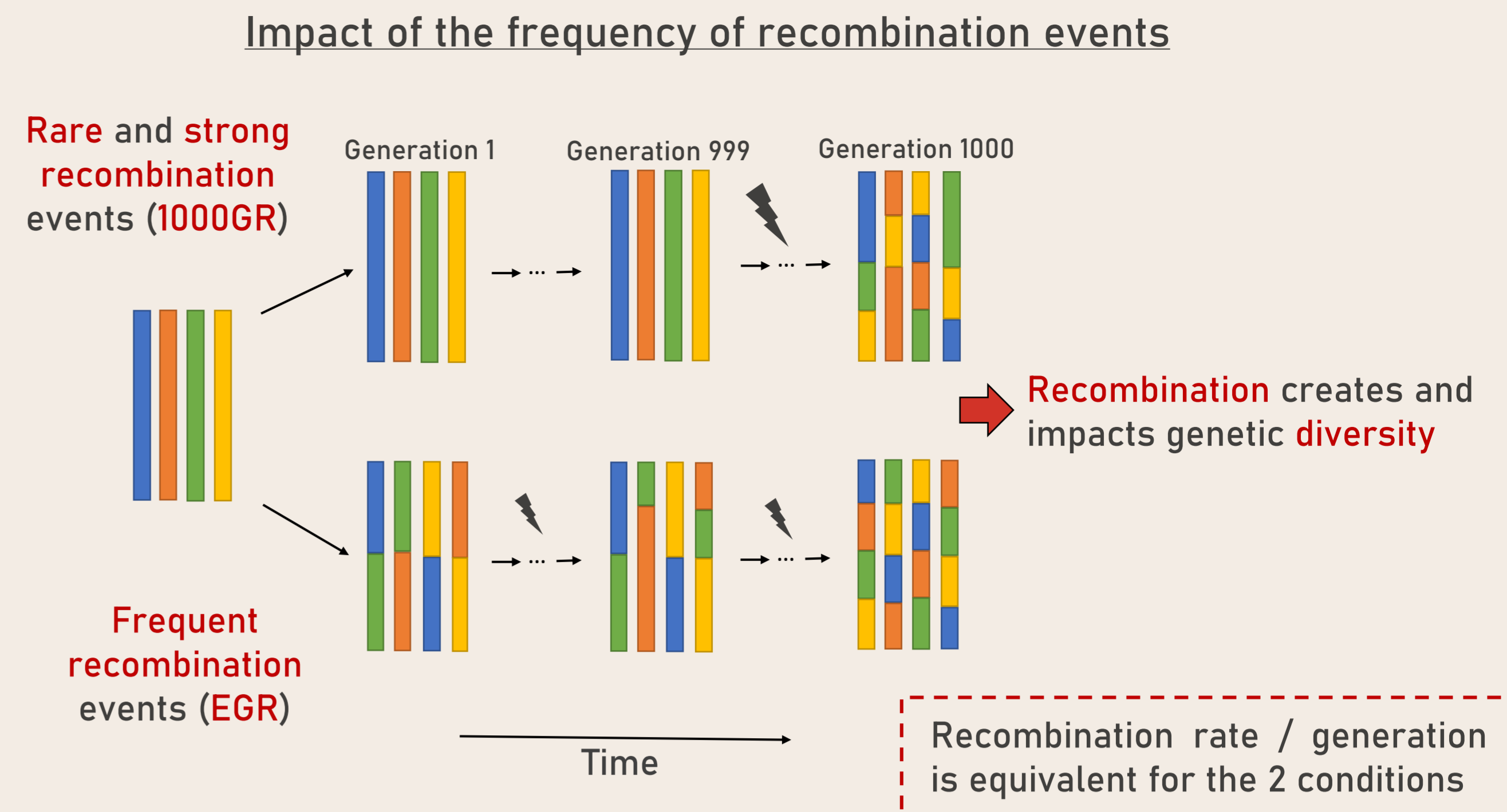
Context

The canonical life cycle of *Saccharomyces cerevisiae* consists of an alternation between **mitosis** (clonal reproduction) and **meiosis** events (outcrossing and intratetrad mating). In this life cycle, meiosis events and then recombination events are known to be rare.

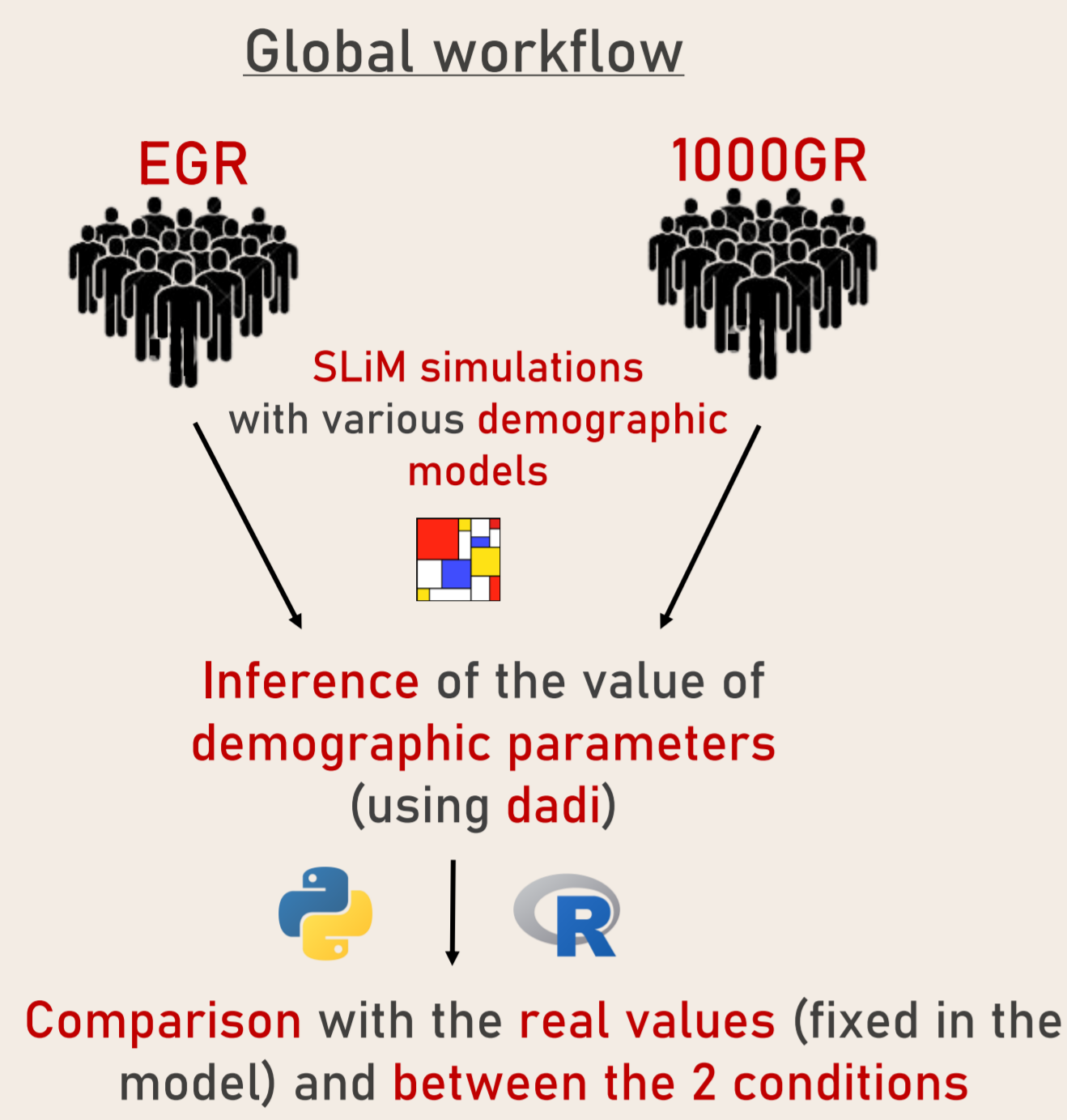
However, recent studies¹ start to show that **heterozygosity in yeast would be greater** than previously thought, which implies that maybe **recombination events are more frequent**. Indeed, these events are estimated at frequencies ranging from 1 per 50000 generations to 1 per 1000 generations.

Using SLiM² and dadi³ (which is based on the SFS), we wanted to see if we can **correctly infer demographic parameters** given this **specific feature** (frequency of recombination events). For this, we **tested 2 conditions**: a population with **recombination events every generation (EGR)** and a population with **recombination events every 1000 generations (1000GR)**, the recombination rate (ρ) is scaled so that the number of individual events remains the same on average. We simulated 4 simple demographic models to evaluate if the **frequency of recombination events** has an **effect on demography inference**.

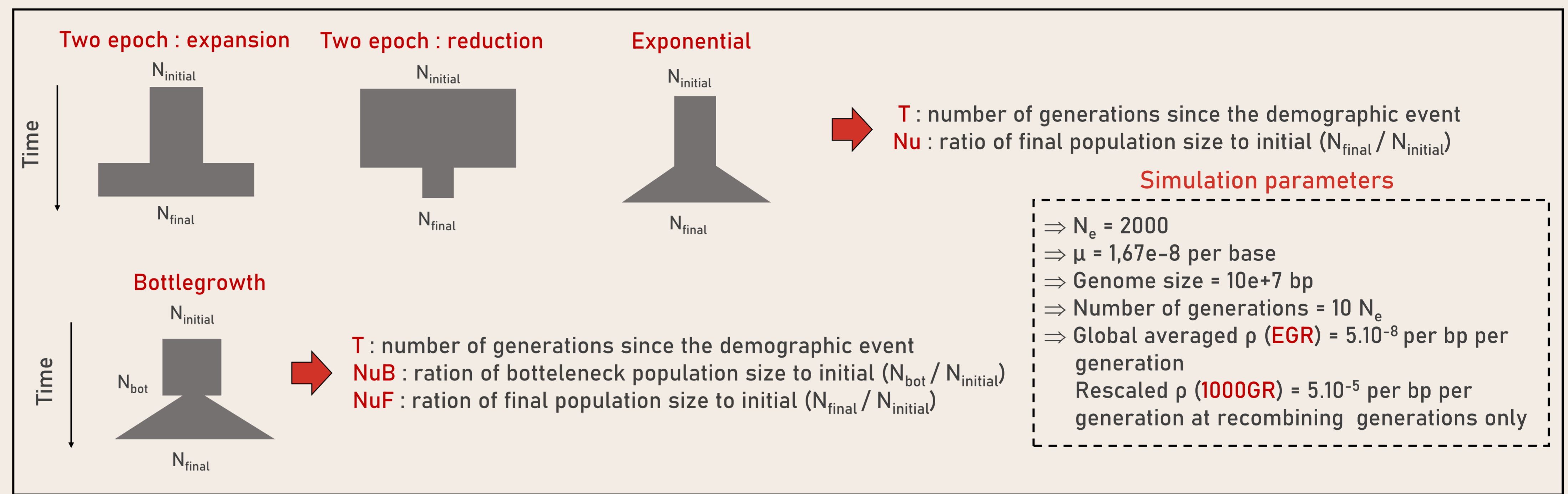
➔ Does **recombination frequency** (= sexual reproduction events) impact **demography inference** ?



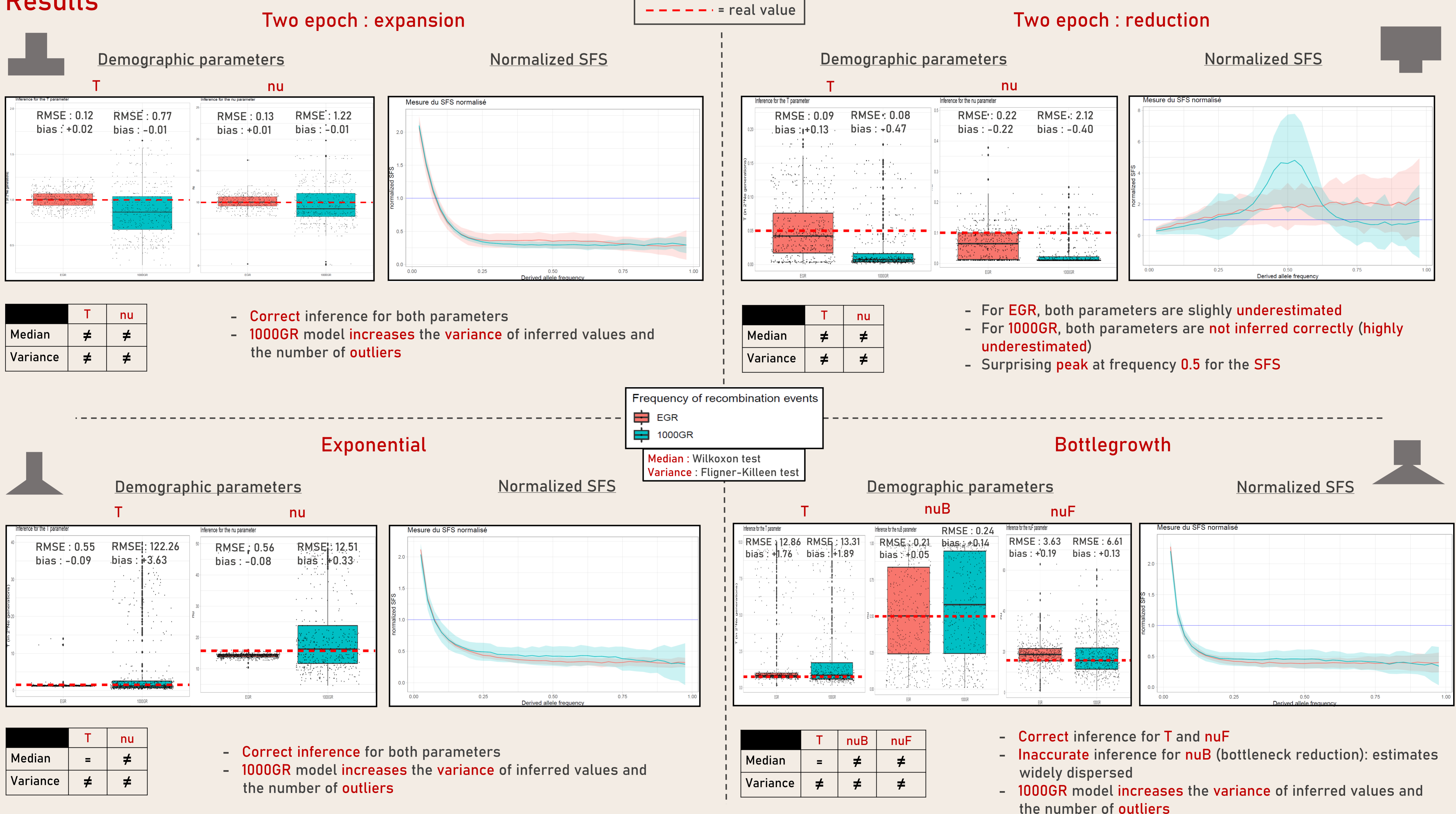
Workflow and methods



Tested demographic models and associated parameters



Results



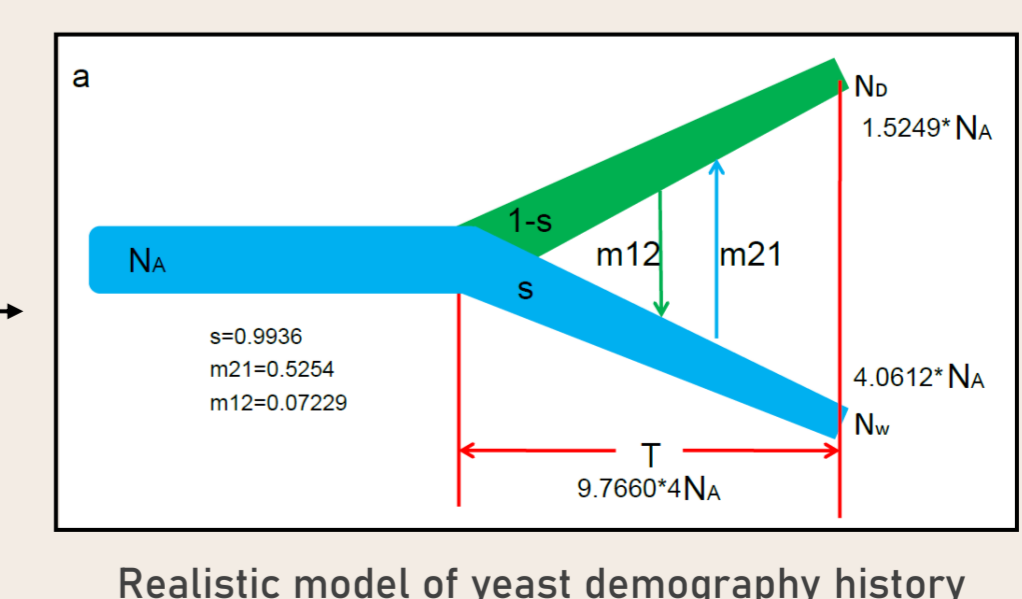
Conclusions

- ➔ We built a **pipeline** to **simulate yeast genetic data** which includes its specific **cell cycle**
- ➔ We evaluated if **intermittent recombination** has an **impact** on **demography inference**
- ➔ **EGR** and **1000GR** estimations are **accurate** for parameters related to **expansion** but **1000GR** estimations are **inaccurate** for parameters related to **bottlenecks**
 - ➔ This is an important path to explore and understand because there are **bottleneck** in **real yeast demography** (domestication, ...)
- ➔ **Difference** between **EGR** and **1000GR** is **not clear** yet : it seems to have an **effect** on the **variance** of estimated demographic parameters
 - ➔ Need to understand how variance and estimations are linked to **EGR** and **1000GR** **coalescent trees**

Perspectives

- ➔ Evaluate **other** demography inference **softwares** (SMC++, fastsimcoal, ...) – WIP
- ➔ Evaluate **other** simple demographic **models** (instantaneous growth, ...) – WIP
 - ➔ Aim for more **complex** and **realistic** models (intratetrad mating, Duan et al.⁴ model)

ARTICLE
[https://doi.org/10.1093/mbe/mz005](#) OPEN
 The origin and adaptive evolution of domesticated populations of yeast from Far East Asia
 Shou-Fu Duan^{1,2}, Pei-Jie Han¹, Qi-Ming Wang¹, Wan-Qu Liu¹, Xun-Yan Shi^{1,2}, Kuan Li¹, Xiao-Ling Zhang¹ & Feng-Yan Bai^{1,2}



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