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# Impact of yeast cell cycle specificity on demography inference

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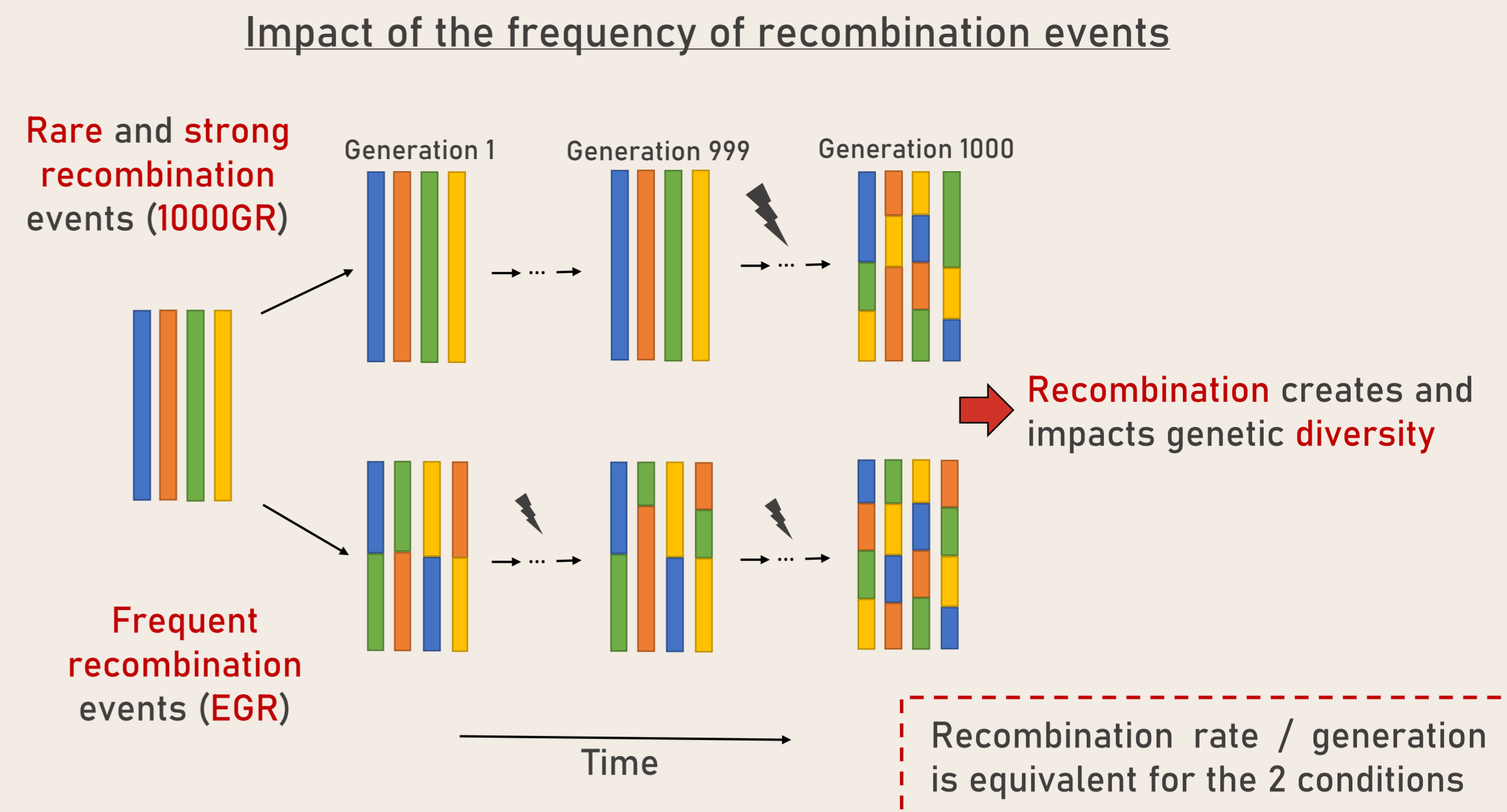
## Context

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.

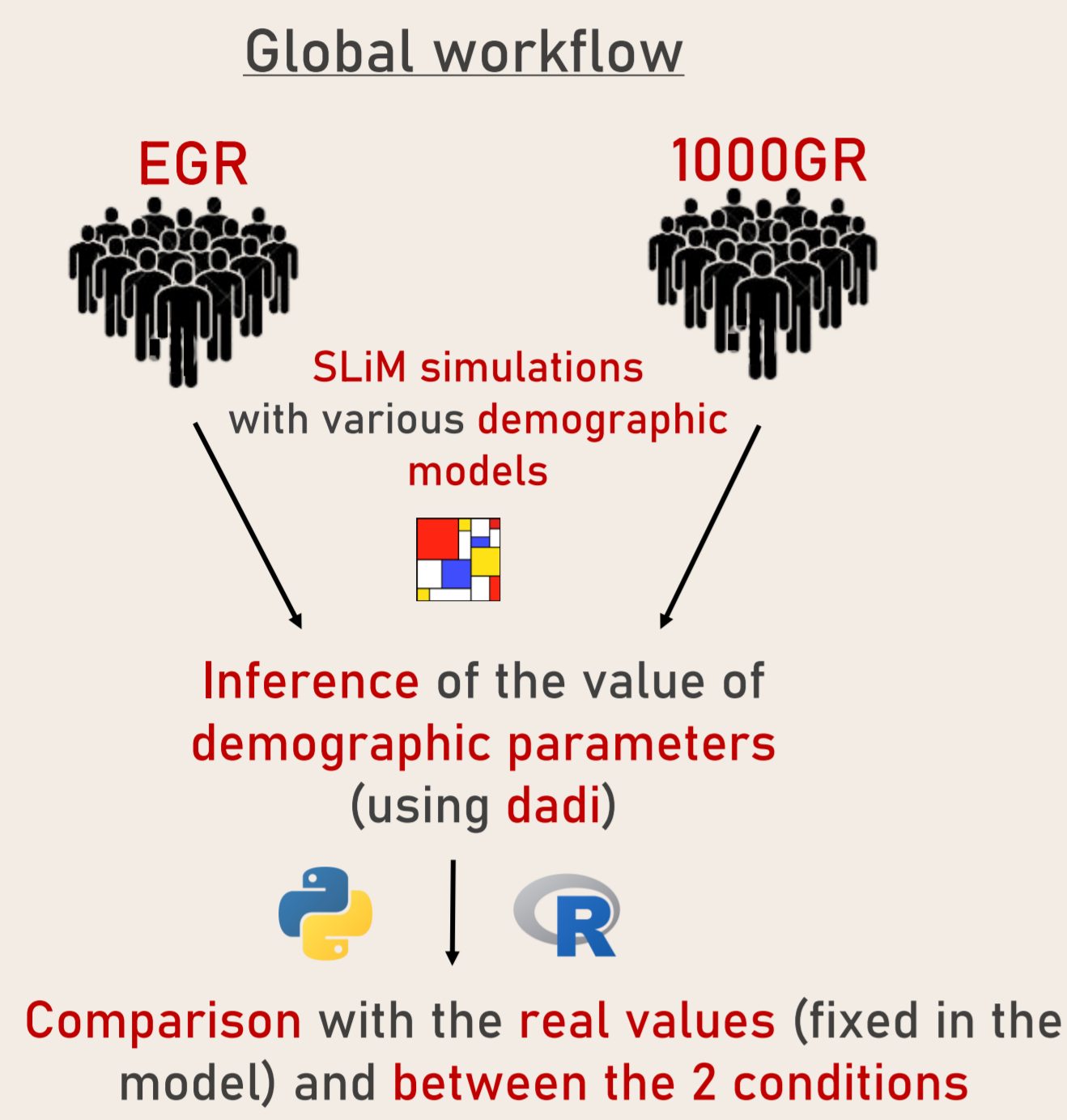
However, recent studies<sup>1</sup> start to show that **heterozygosity in yeast would be greater** than previously thought, which implies that maybe **recombination events are more frequent**. Indeed, these events are estimated at frequencies ranging from 1 per 50000 generations to 1 per 1000 generations.

Using SLiM<sup>2</sup> and dadi<sup>3</sup> (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 ( $\rho$ ) 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**.

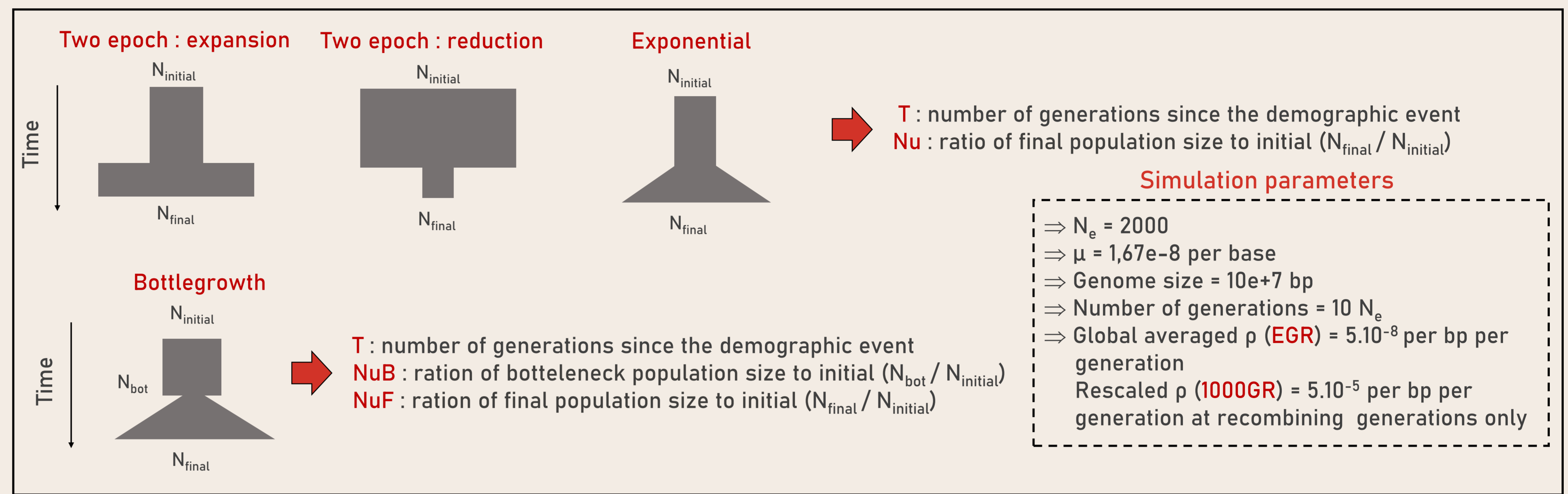
➔ Does **recombination frequency** (= sexual reproduction events) impact **demography inference** ?



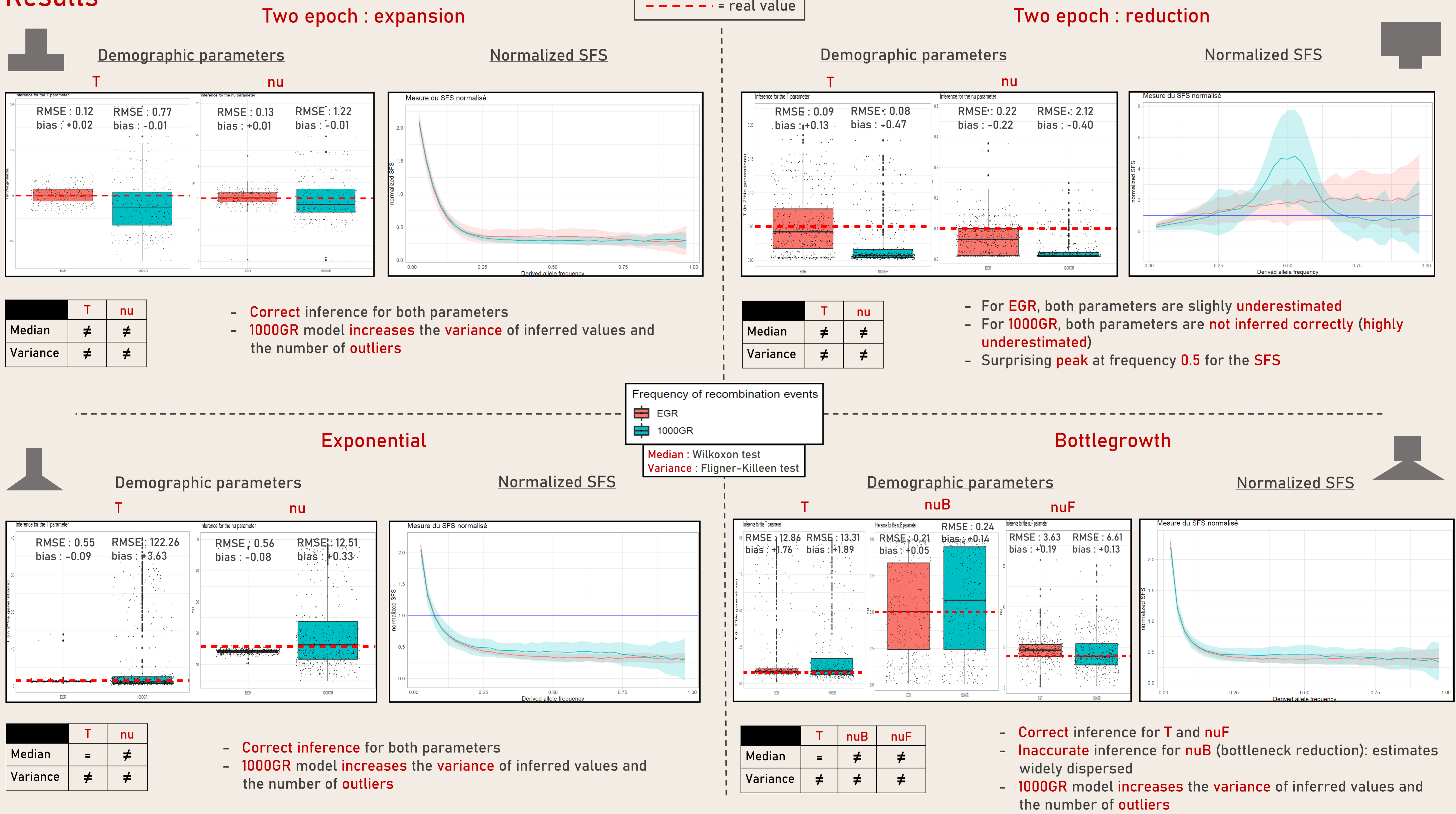
## Workflow and methods



## Tested demographic models and associated parameters



## Results



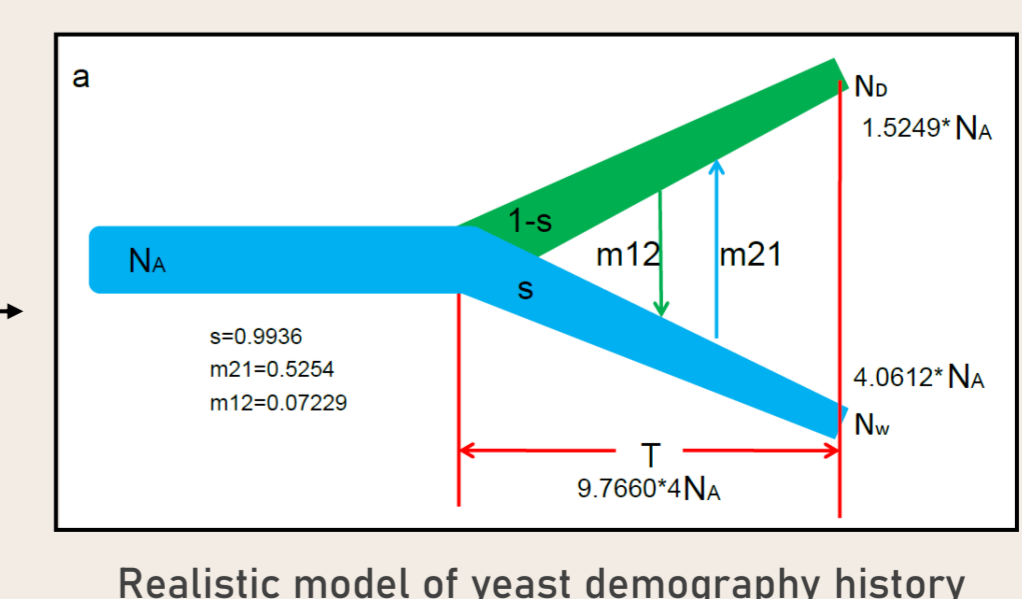
## Conclusions

- ➔ 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.<sup>4</sup> model)

ARTICLE  
The origin and adaptive evolution of domesticated populations of yeast from Far East Asia  
Shou-Fu Duan<sup>1,2</sup>, Pei-Jie Han<sup>1</sup>, Qi-Ming Wang<sup>1</sup>, Wan-Qu Liu<sup>1</sup>, Xun-Yan Shi<sup>1,2</sup>, Kuan Li<sup>1</sup>, Xiao-Ling Zhang<sup>1</sup> & Feng-Yan Bai<sup>1,2</sup>



[1] Fischer, G., Liti, G., Lorente, B. The budding yeast life cycle: More complex than anticipated? *Yeast*, 2021; 38: 5–11.  
[2] Haller, B.C., & Messer, P.W. (2019). SLiM 3: Forward genetic simulations beyond the Wright-Fisher model. *Molecular Biology and Evolution* 36(3), 632–637.  
[3] RN Gutenkunst, RD Hernandez, SH Williamson, CD Bustamante. "Inferring the joint demographic history of multiple populations from multidimensional SNP data" *PLoS Genetics* 5:e1000695 (2009)  
[4] Duan, S.F., Han, P.J., Wang, Q.M. et al. The origin and adaptive evolution of domesticated populations of yeast from Far East Asia. *Nat Commun* 9, 2690 (2018).