# Modeling Heterogeneity in Microbial Population Dynamics

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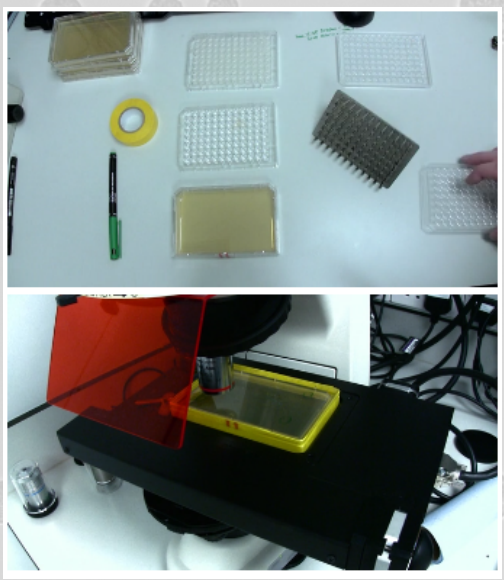
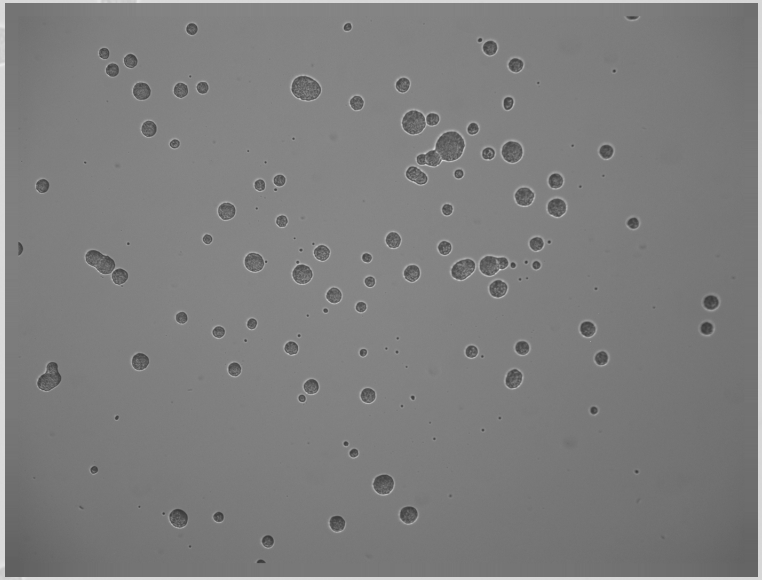
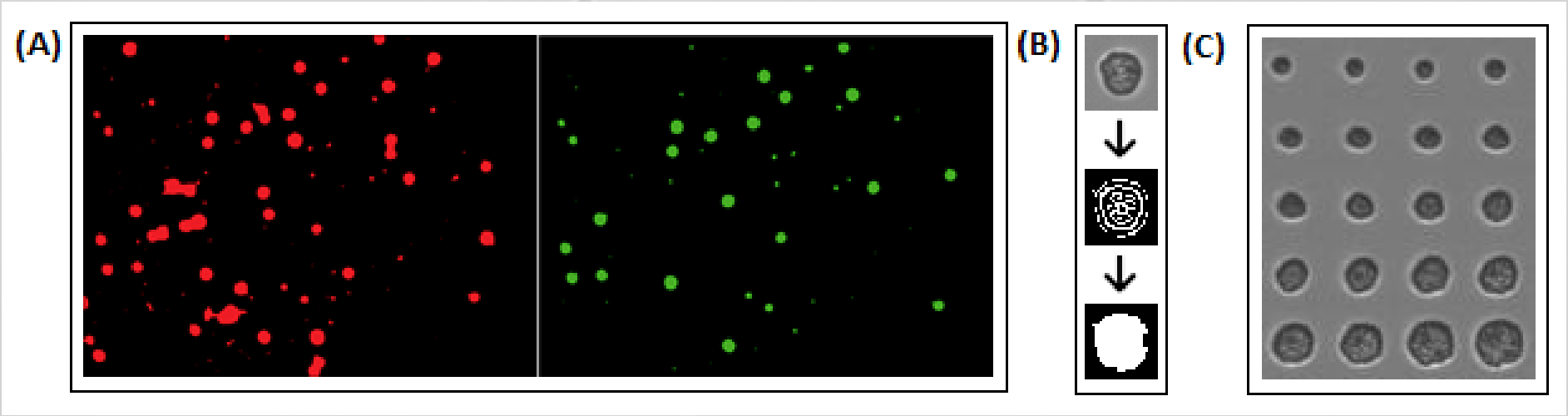
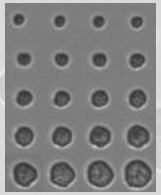
# High-Throughput Microscopy Data - $\mu$QFA



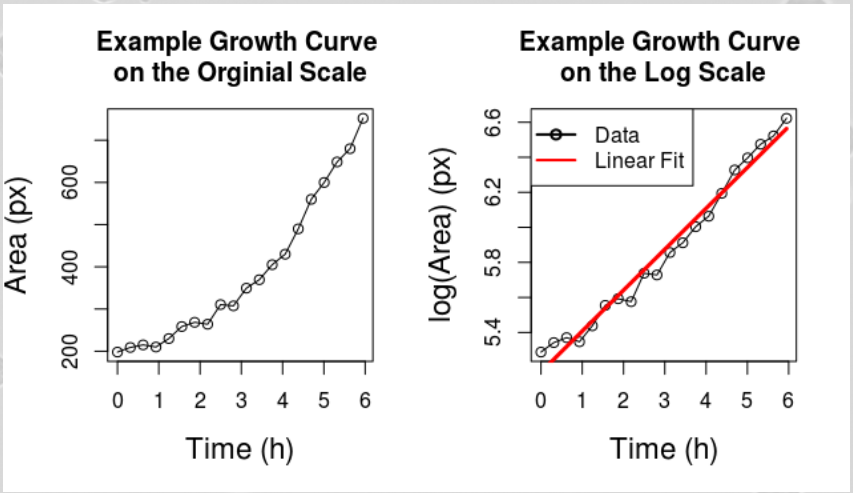




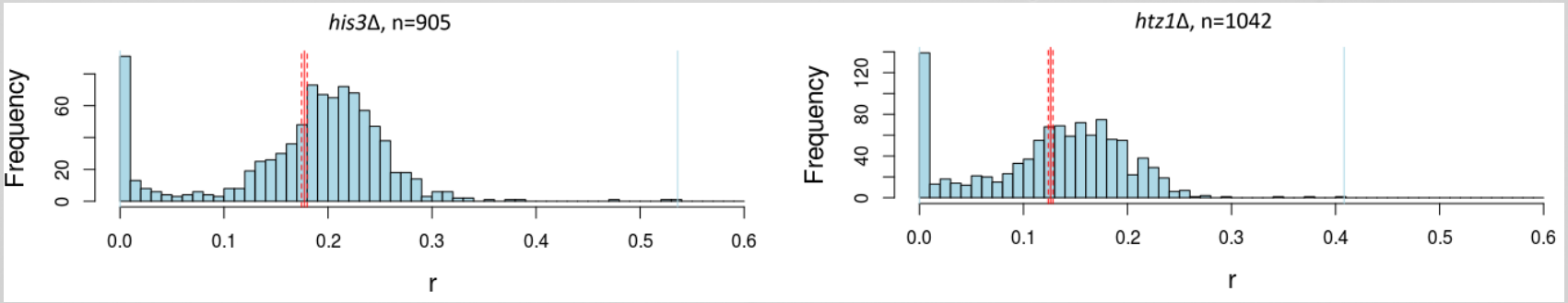
# Estimating Individual Lineage Growth Rates



$$A = A_0 \cdot e^{r \cdot t} \rightarrow log(A) = log(A_0) + (r \cdot t)$$

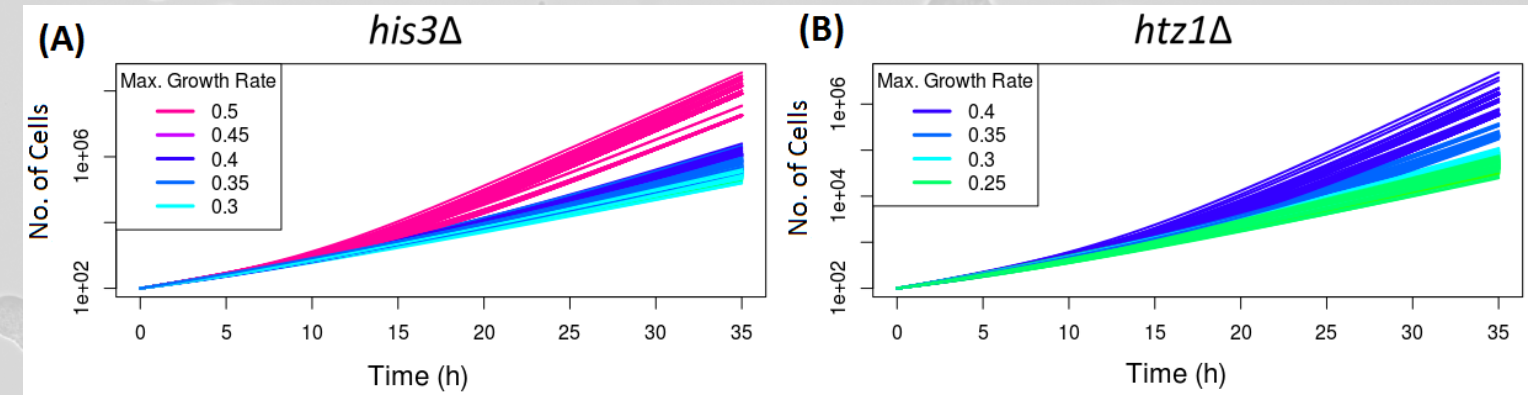



Edge peak distributions with a long right-hand tail

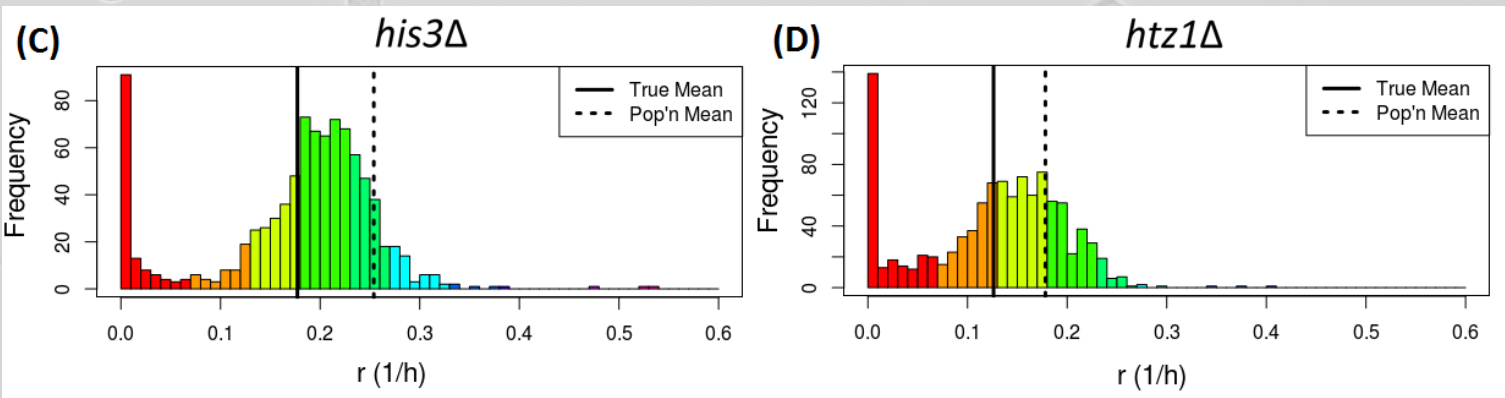


# Heterogeneity gives rise to an apparent lag phase.

Population Simulations[1]: $N(t) = \sum_{i=1}^{n}(N_{0_i} \cdot e^{r_i \cdot t})$



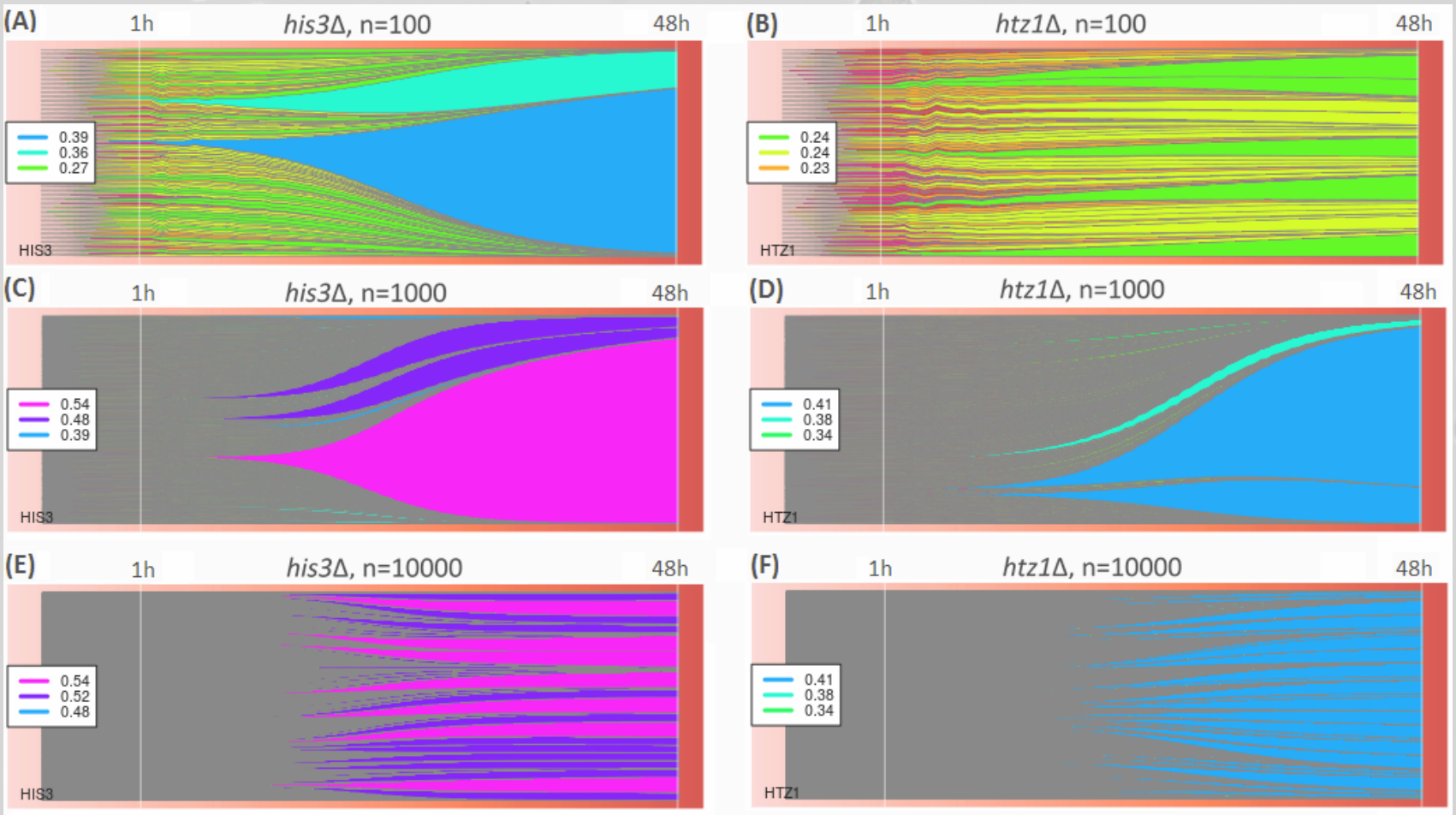

Observed Single Lineage Growth Rates




[1] $N_0 = (1, \ldots, 1)$ and $n = 100$

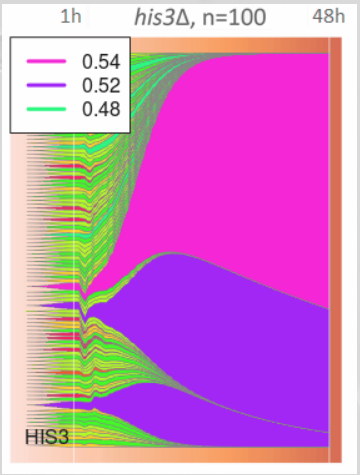
# Population growth masks single lineage heterogeneity.

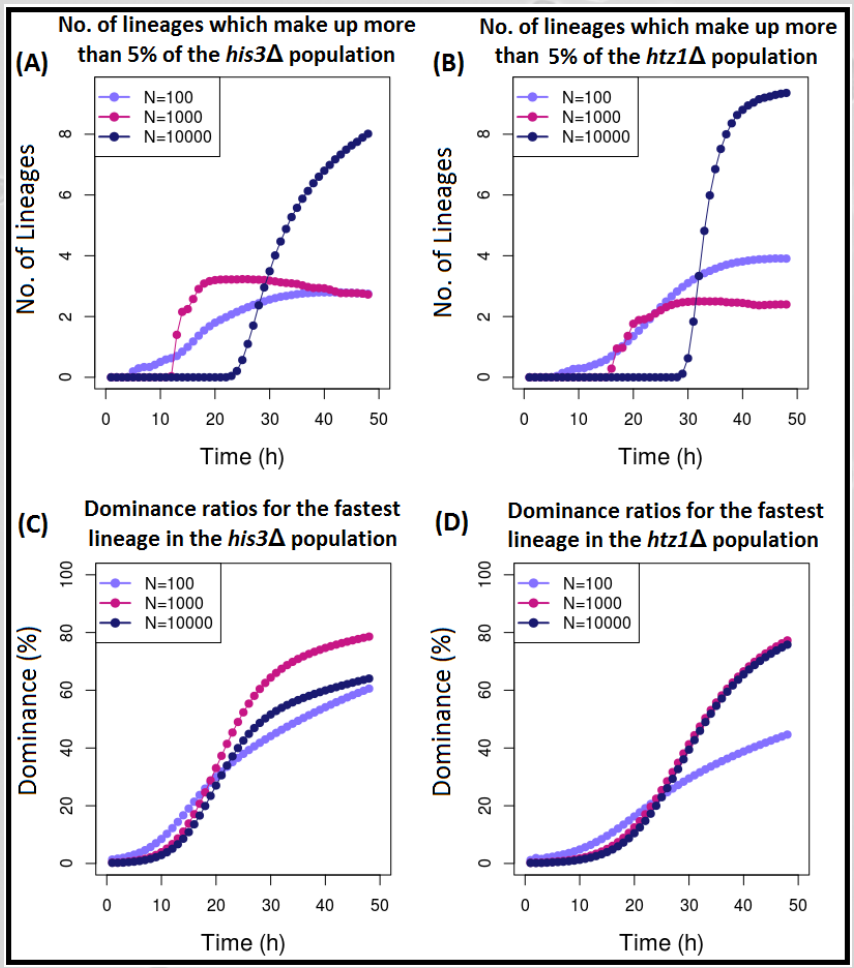
## Mixed → Clonal

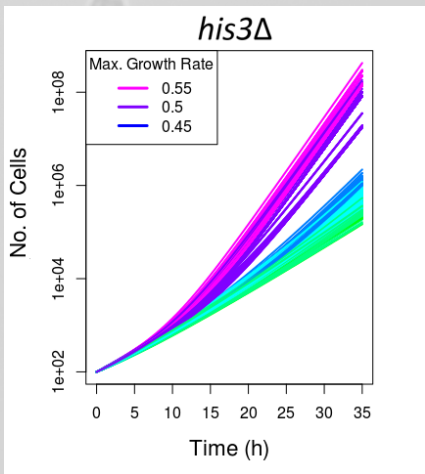


# Fast growing lineages dominate population growth.

- The apparent lag phase corresponds to the time required for fast-growing lineages to dominate population growth.

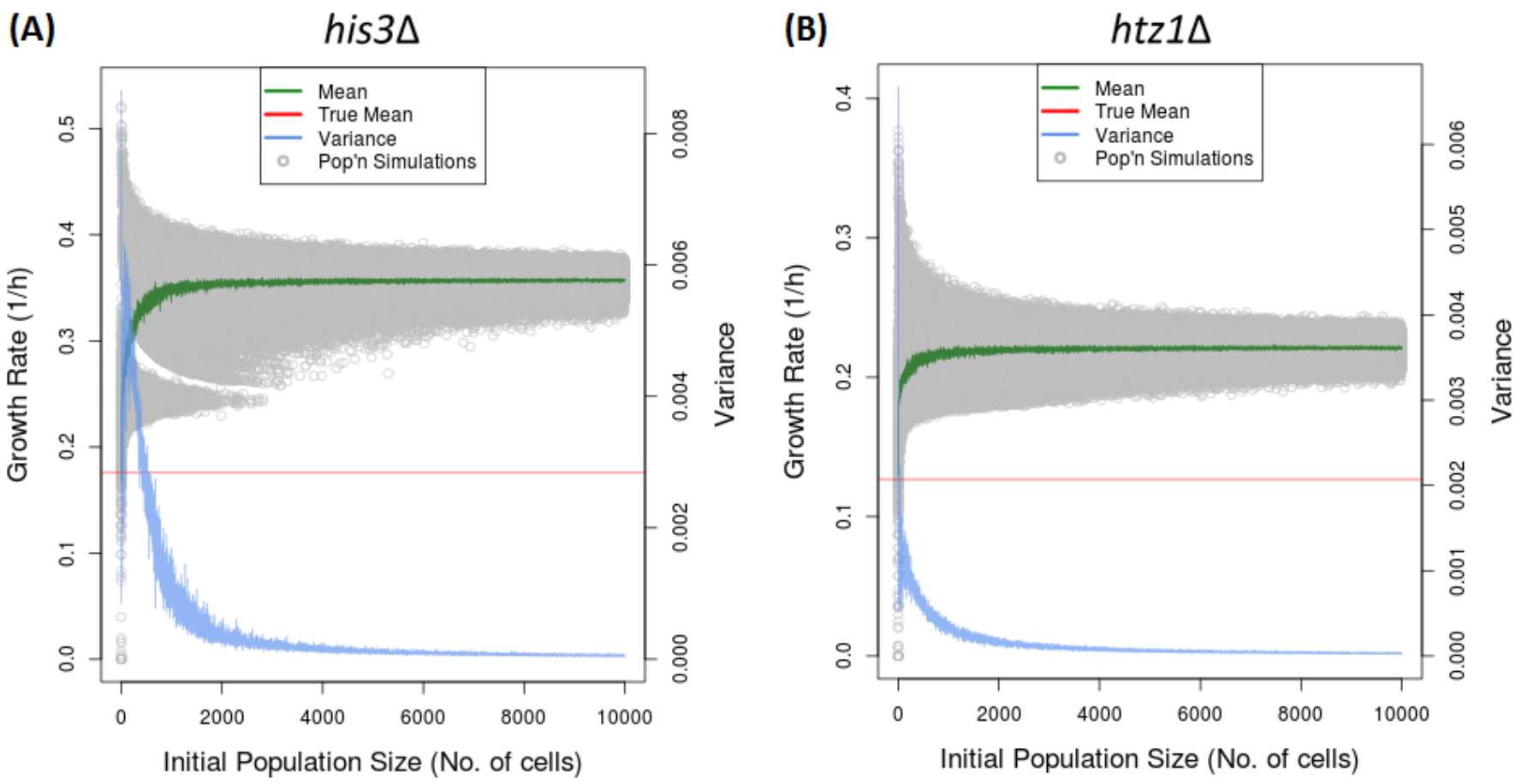


# Experimental Design Implications

- Initial population size affects apparent growth rate.



# Thank you