

# Recent Explosive Human Population Growth Has Resulted in an Excess of Rare Genetic Variants

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# Introduction

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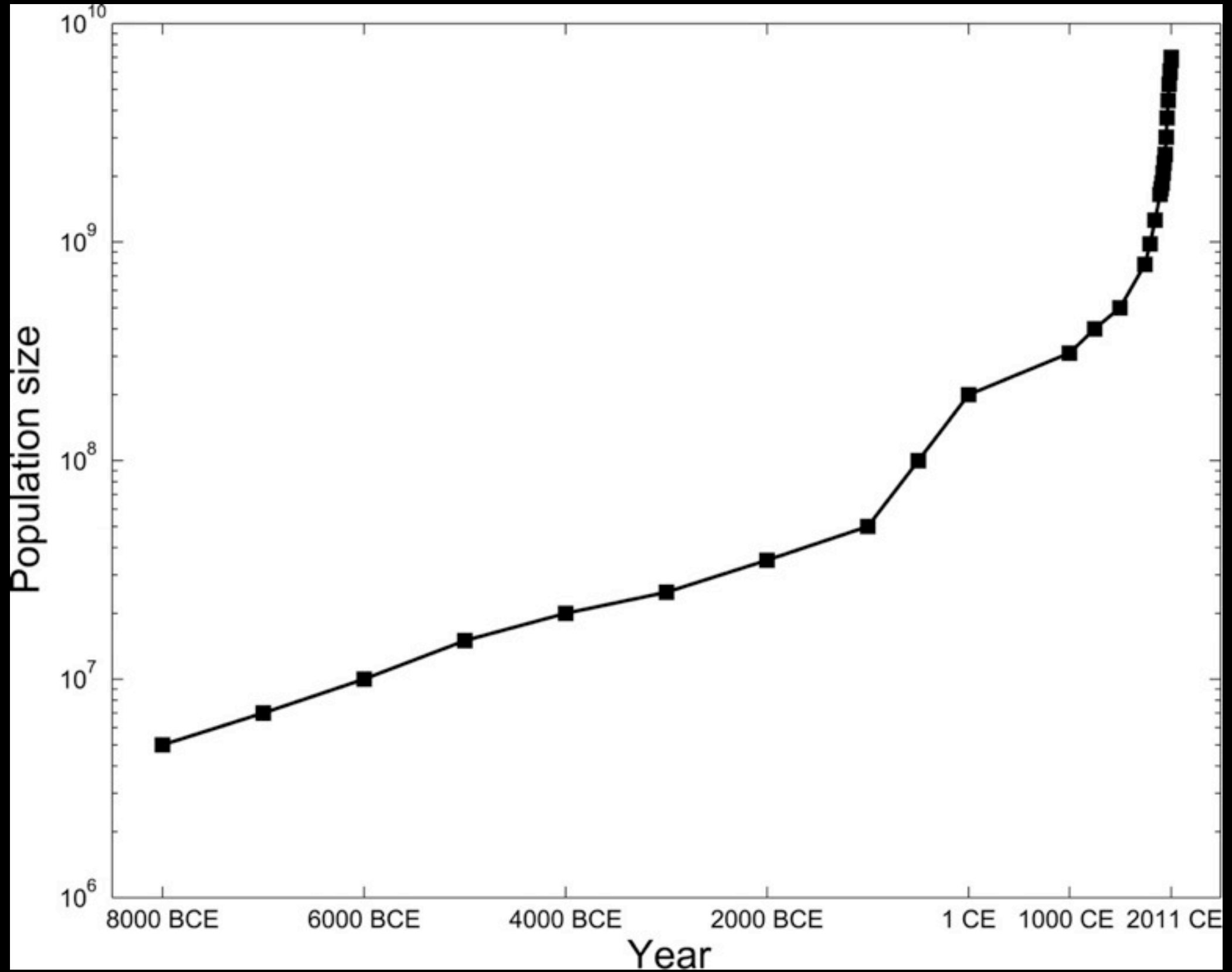


- Human population have experienced recent explosive growth, expanding by at least three orders of magnitude over the past 400 generations.

# Introduction(cont'd)

- We characterized the empirical signatures of explosive growth on the site frequency spectrum.
- The discrepancy in rare variant abundance across demographic modeling studies is mostly due to difference in sample size.

- Earlier studies used small amounts of data and did not observe population growth.
- However, these studies did not capture the full scope of human expansion, which may be due to the models not allowing for a recent acceleration in growth rate.









- There are several differences between the models of population history assumed by the different studies that considered recent population growth— as well as between the inference methods used— that can potentially explain the differences in results (Table 1).

**Table 1**

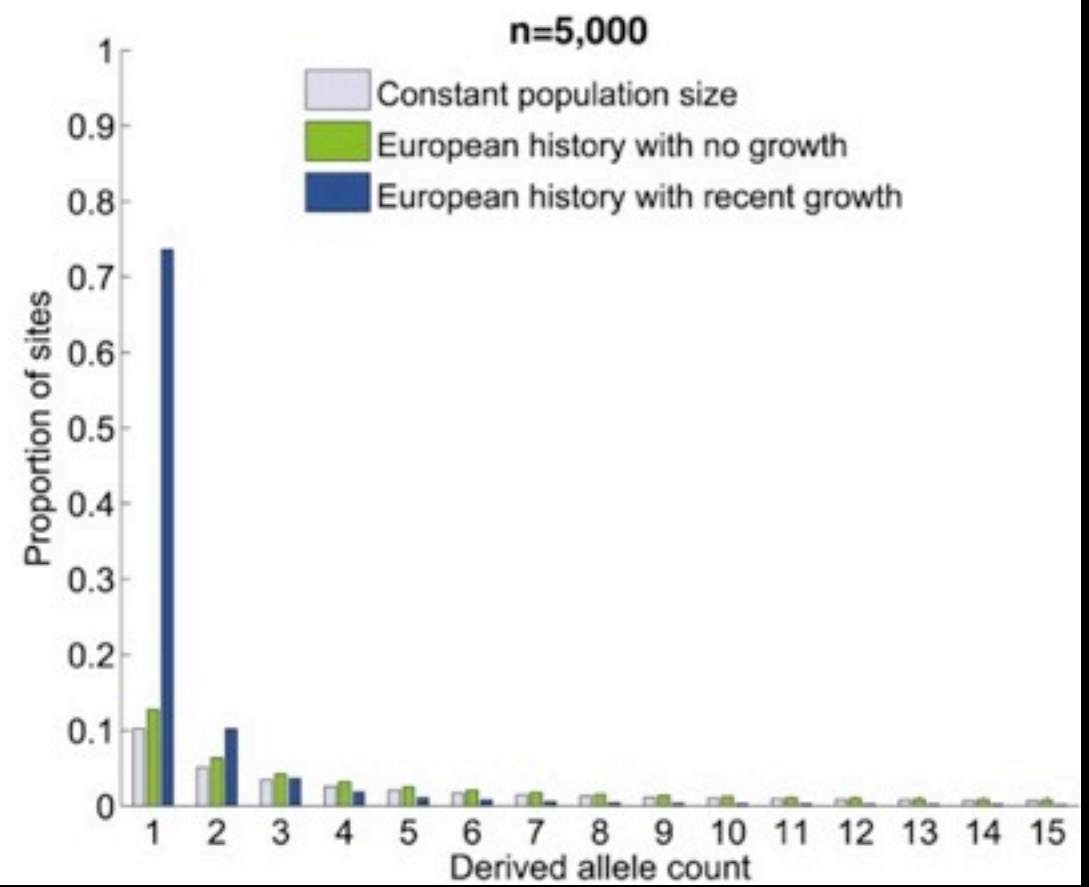
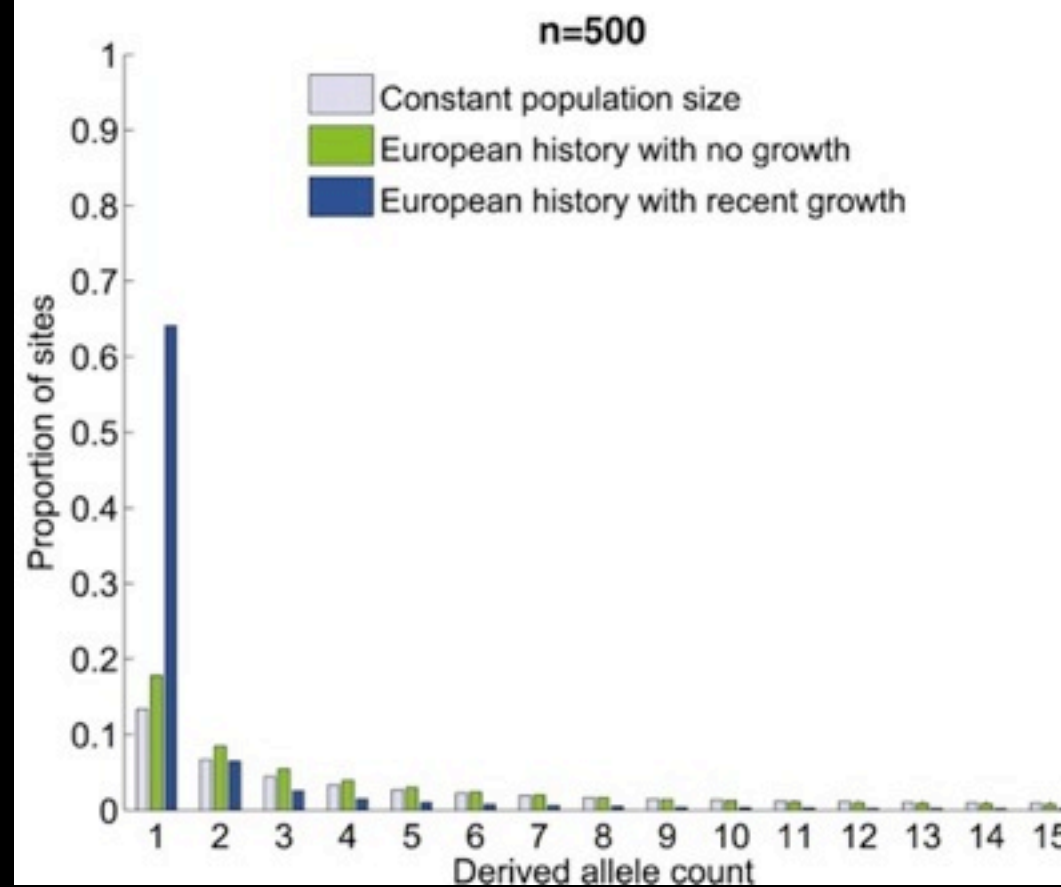
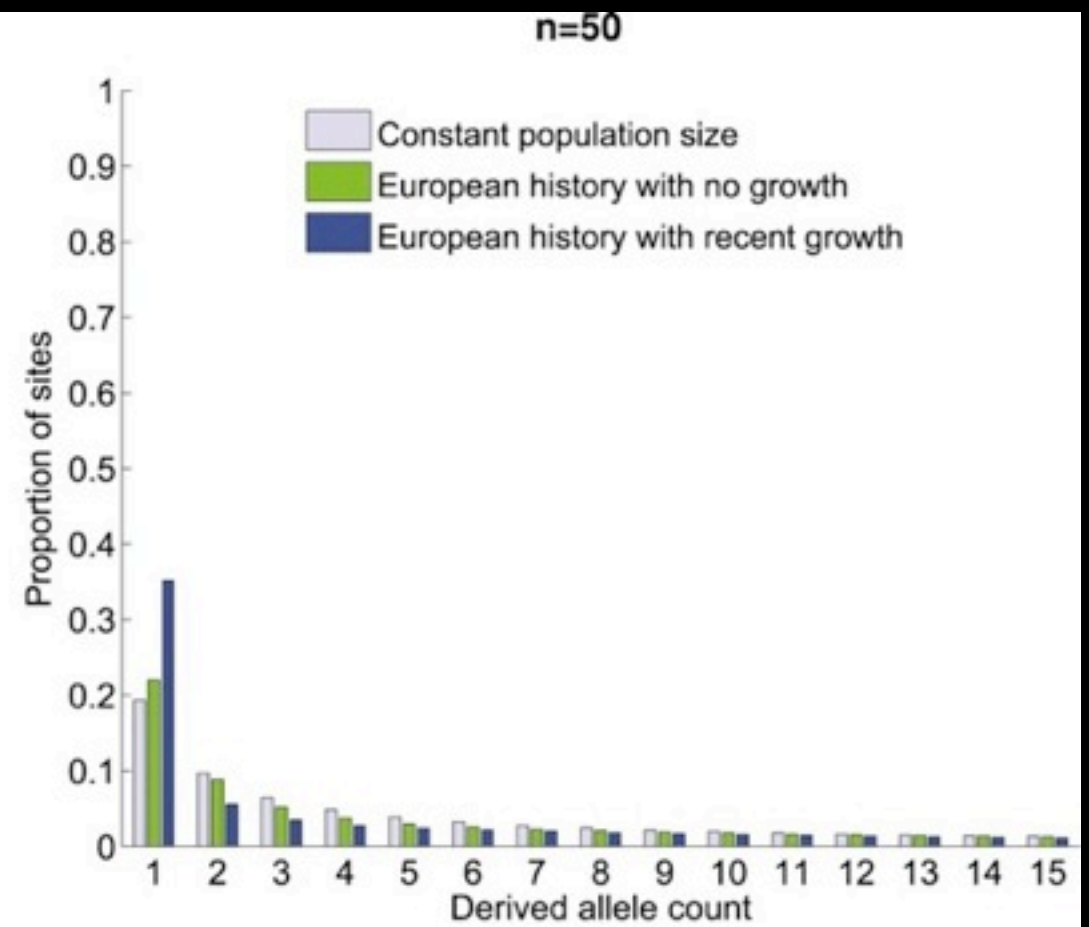
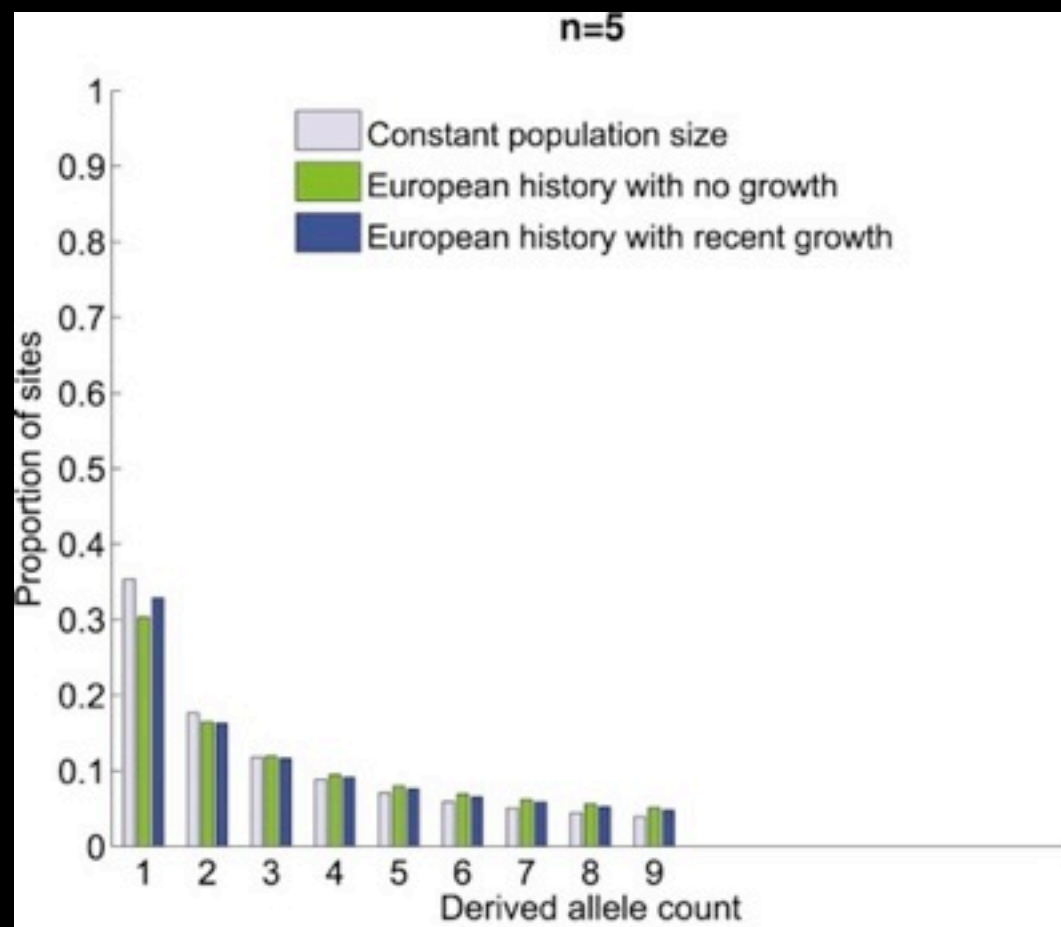
Genetic estimates of recent exponential growth in Europe.

Study	Sample size ( <i>n</i> )*	Time growth started (years ago)†	Initial $N_e$ ‡	Growth per generation (%)
Gravel <i>et al.</i> (5)	60	23,000§ (21,000–27,000)	1032 (677–1290)	0.48 (0.30–0.75)
Gutenkunst <i>et al.</i> (6) (including New World modeling)	22	26,400§ (21,700–30,700)	1500 (900–2200)	0.23 (0.16–0.34)
Gutenkunst <i>et al.</i> (6) (excluding New World modeling)	22	21,200§ (17,600–23,900)	1000 (500–1500)	0.4 (0.26–0.57)
Schaffner <i>et al.</i> (29)	62	8750	7700	0.73
Coventry <i>et al.</i> (18)	10,422	1400 (900–2800)	7700#	9.4 (4.5–14.5)

- However, we hypothesize that the very different results are mostly due to differences in sample size.
- A larger sample size allows identification of rare polymorphisms that are, on average, due to more recent mutations.

- The excess of rare variants found with a large sample size predicts a growth of 5 to 14% per generation over the past 900 to 2800 years, compared to models of smaller sample size that predicted growth of between 0.2 and 0.7% over a longer period of 20,000 to 30,000 years.

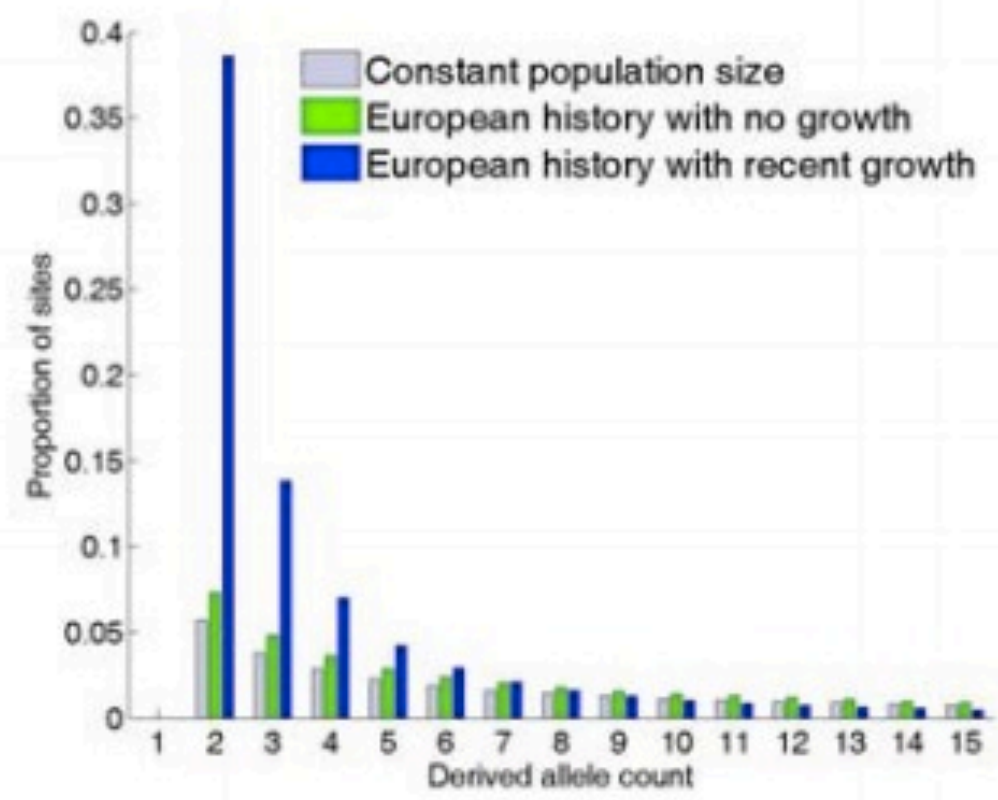
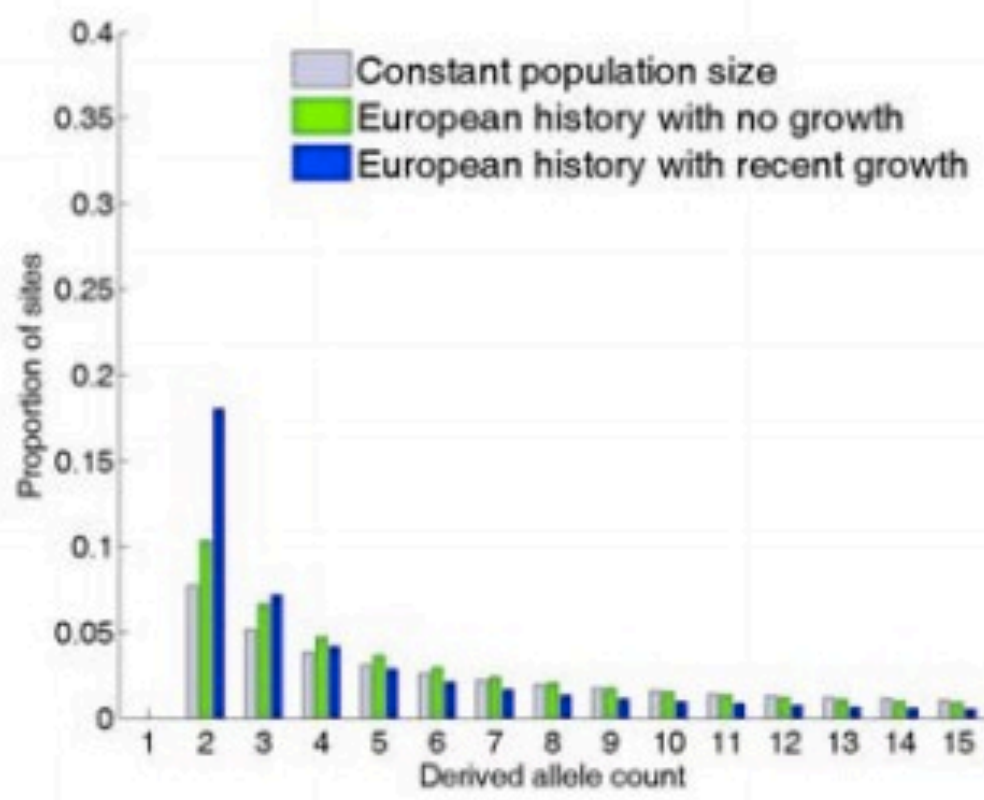
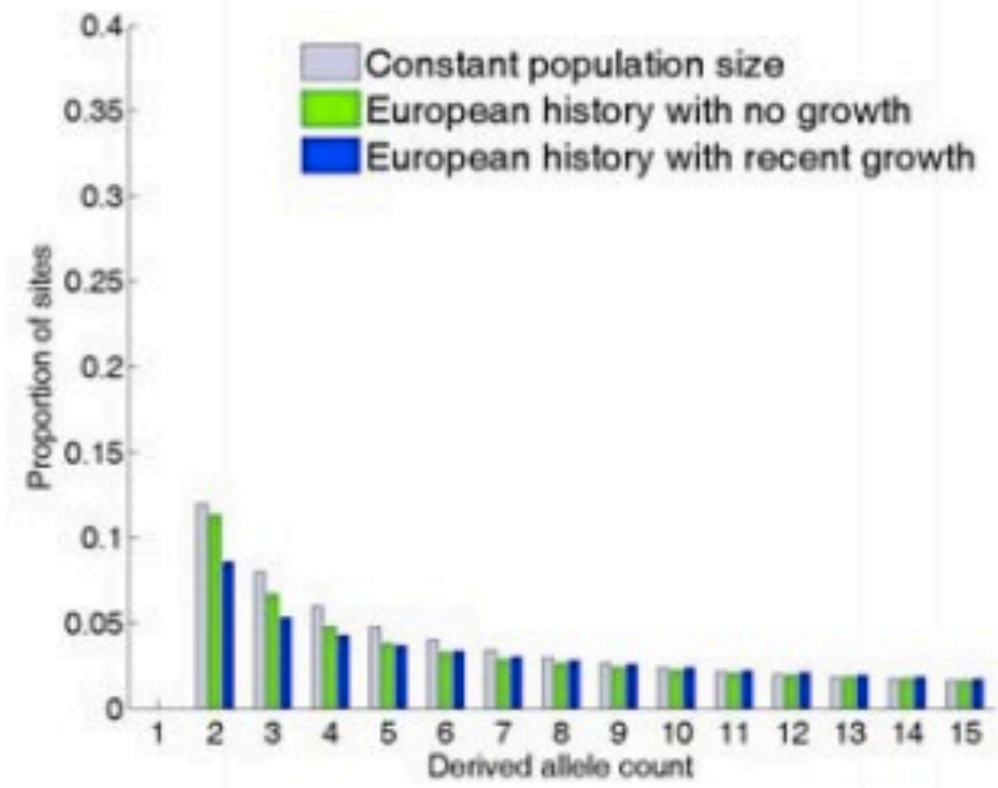
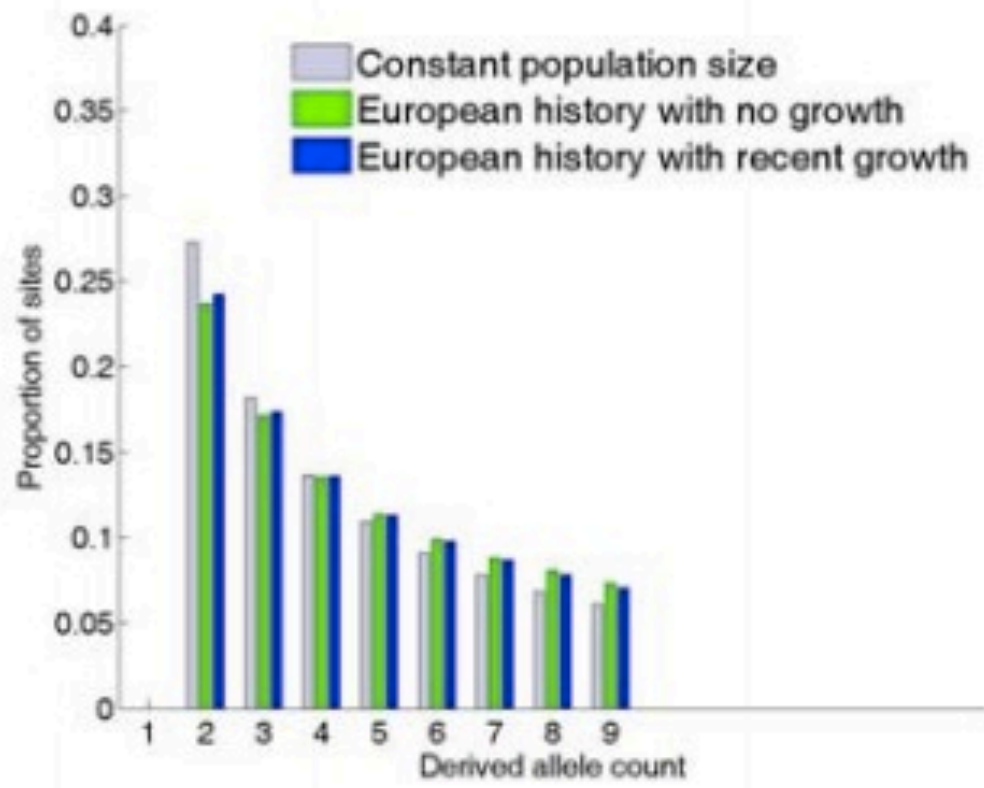
- The expected site frequency spectrum(SFS) of the derived allele (the new mutation arisen in the population) for three different demographic models.



- Sample size exceeds the effective size of the population
- $\Lambda$ -coalescent theory(neutral variation): a retrospective(look back) model of population genetics
- $\theta=4N_e\mu \gg 1$ , the vast majority of allele pairs have at least one difference in nucleotide sequence

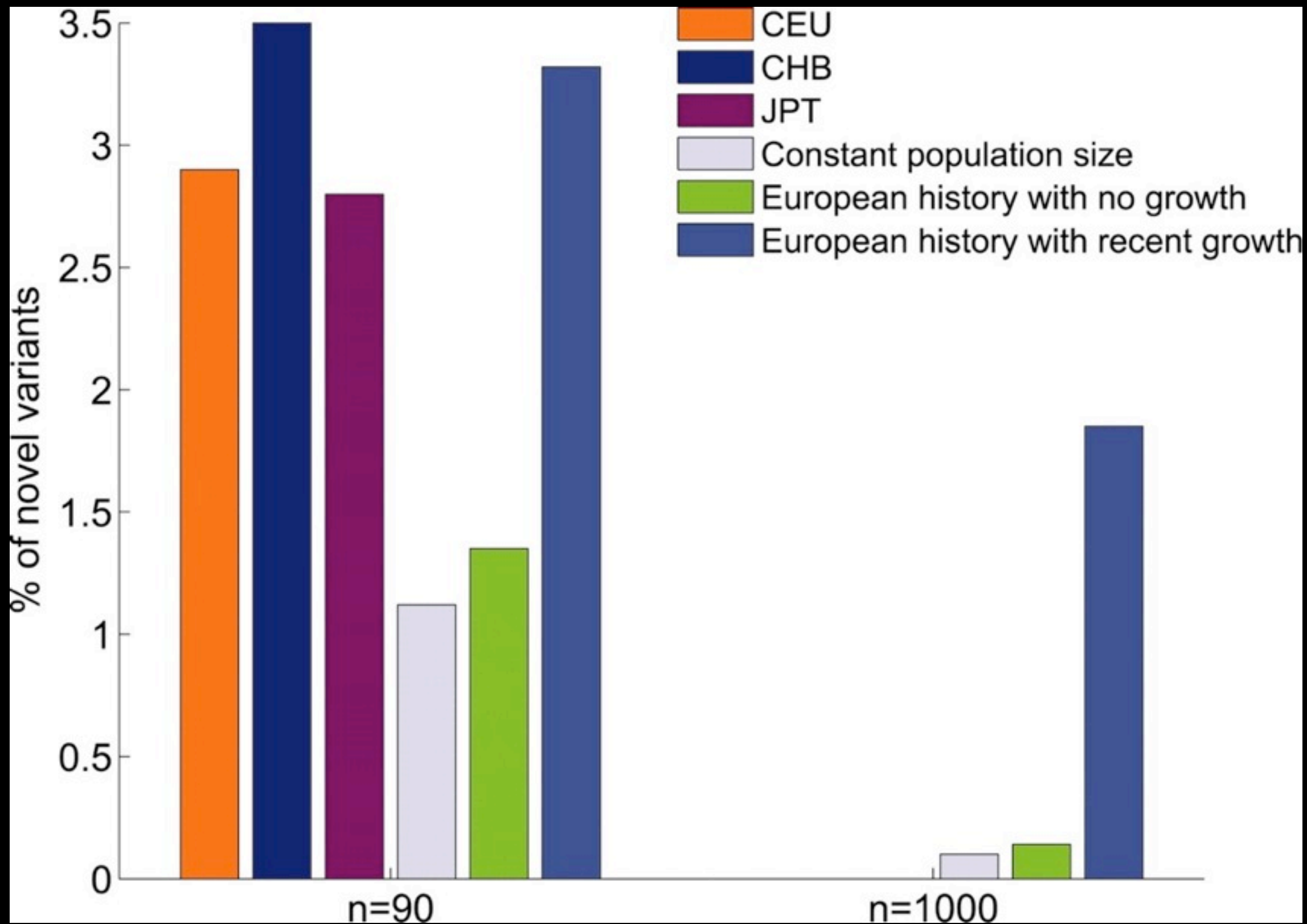
$N_e$ : effective population

$\mu$ : per-site mutation rate





- The fraction of novel variants discovered in each sequenced genome decreases in all models as more individuals are sequenced.



- Recombination will not have broken down linkage disequilibrium between rare mutation and neighboring common variants.
- It is imperative to understand the impact of nature selection during the phase of explosive growth.

Thanks for your attention!