

what are iRep values?

- quantitative (not relative) measurements
- ideal for tracking responses to conditions
- in low-complexity environments iRep predicts increases in population size
- because population size is determined by many factors (cell death, predation, etc.) it is not expected that they will always match
- abundance, population size, and iRep all described different aspects of a microbe and its community

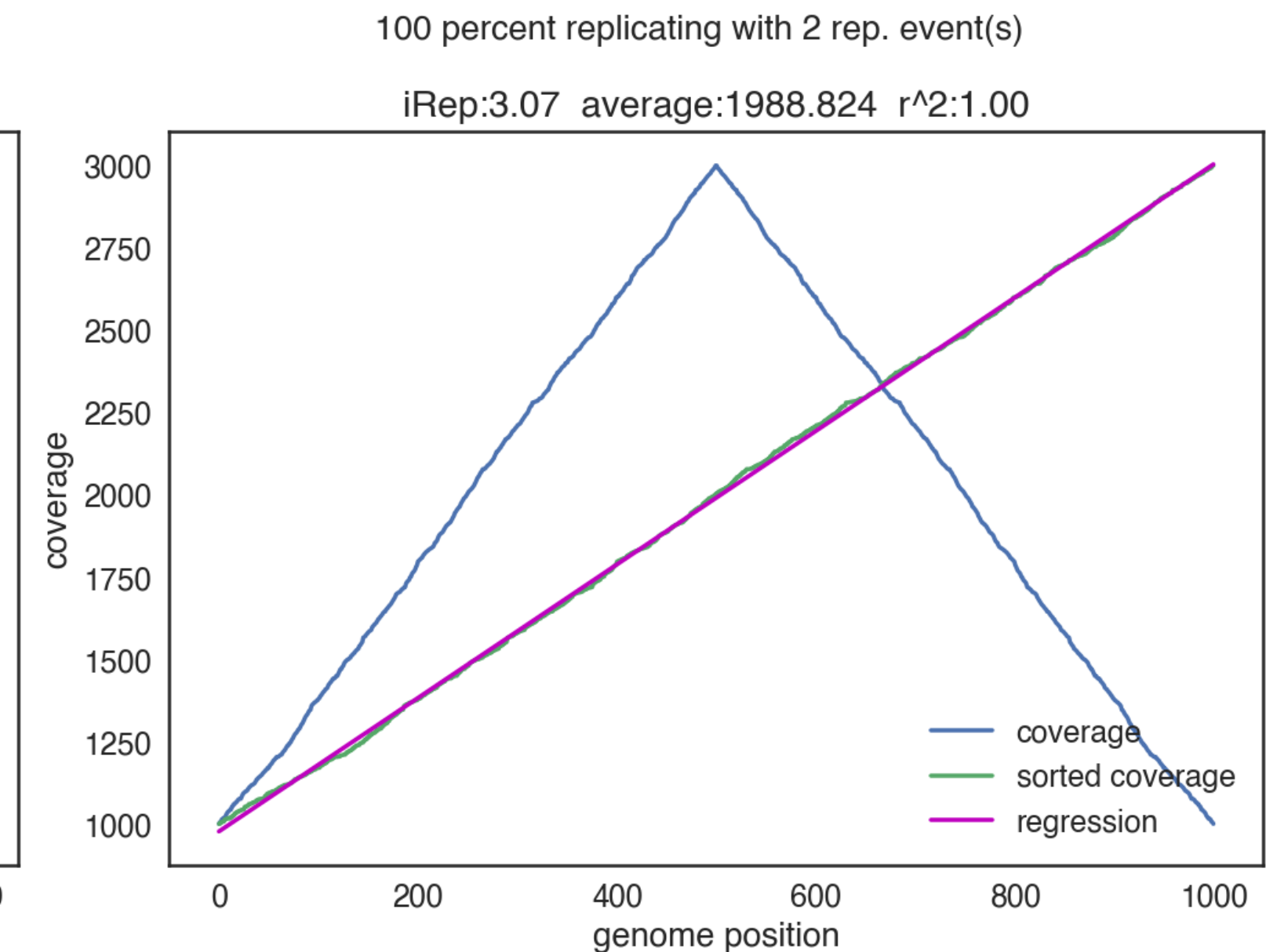
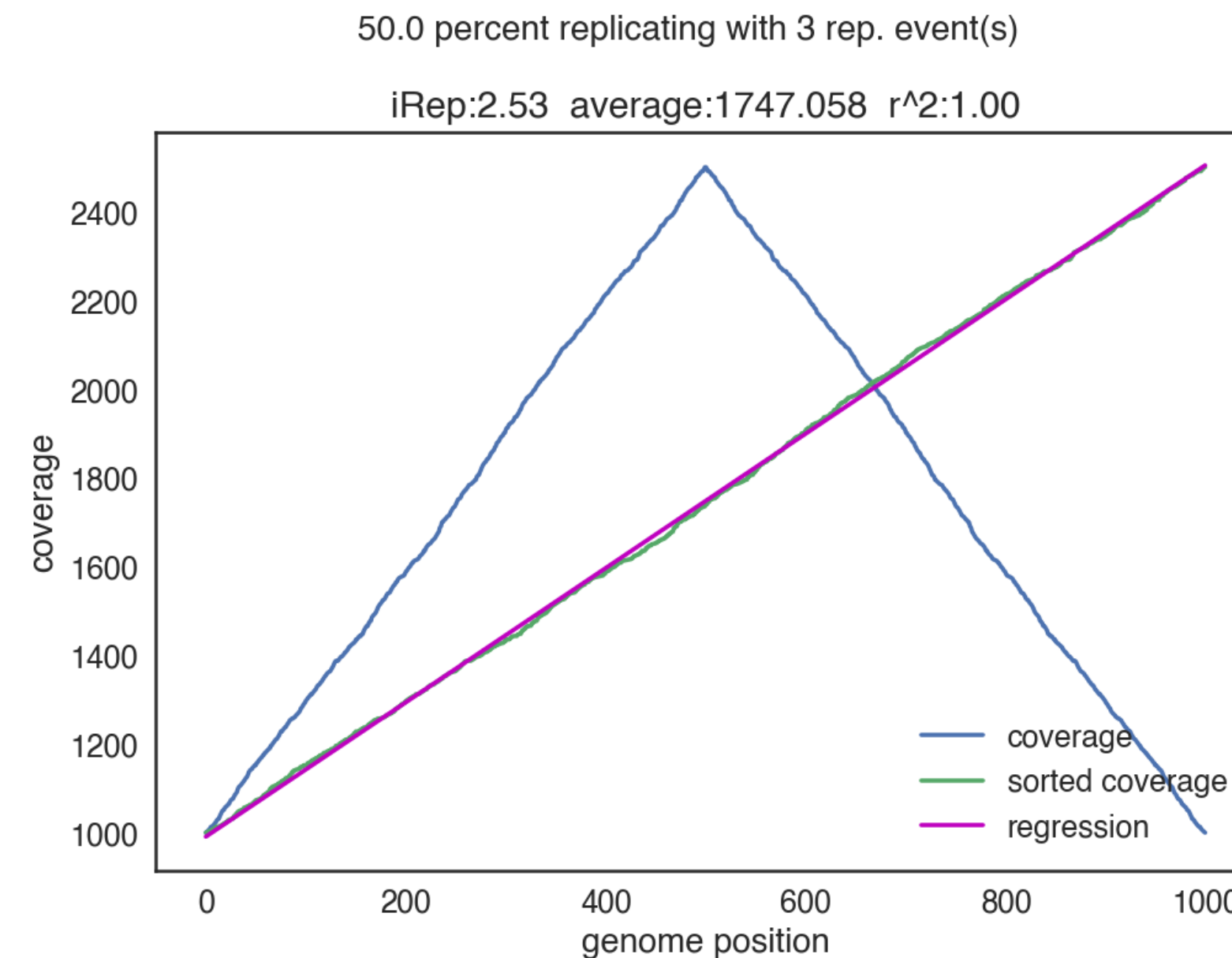
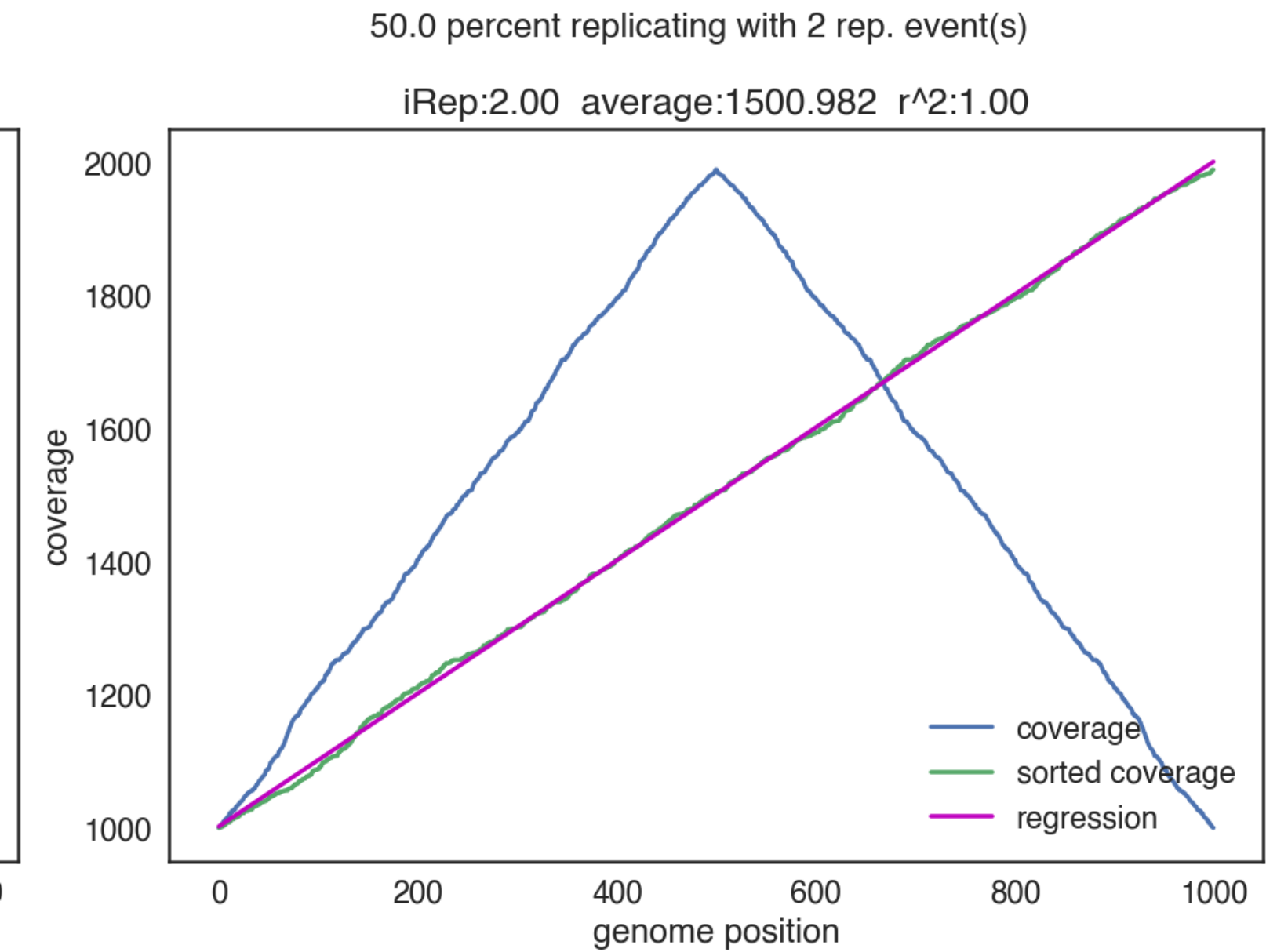
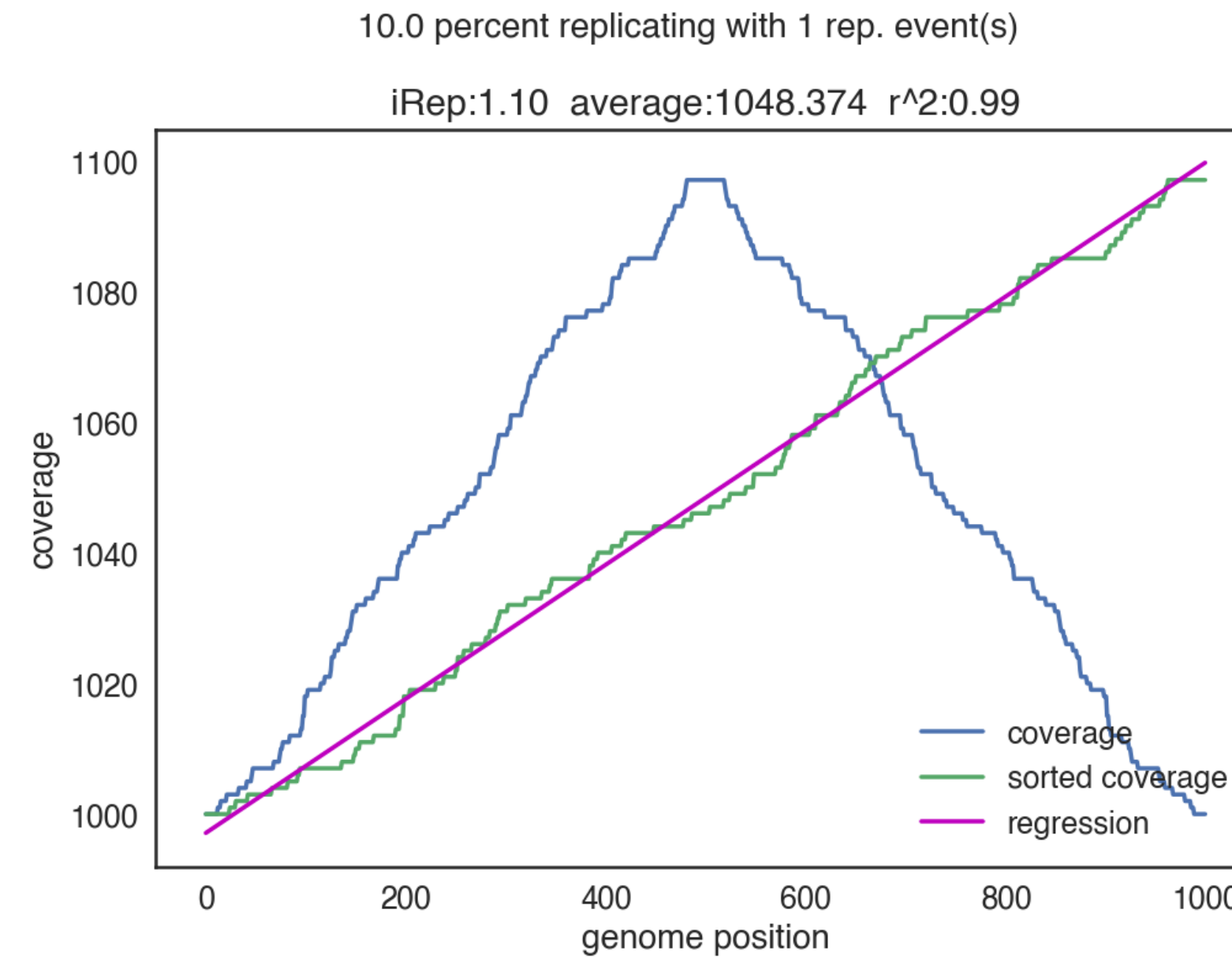
what if **all** cells in the population are making a copy of their genome?

- example:
coverage at origin = 2
coverage at terminus = 1
iRep = PTR = 2/1 = 2
- likewise, if **half** of cells are making one copy of their genome then
iRep = 1.5
- iRep values >2 are possible due to multi-forked genome replication
- but, populations are heterogeneous
 - across a single population, some cells may not be replicating, while others may be replicating using one or more replication forks
 - because of this, there are multiple ways in which a given iRep value can be achieved

iRep values

- iRep values are a function of both the percent of the population that is replicating, and the number of simultaneous replication events
- conducted a series of simulations to test the range of possible iRep values based on these factors

example simulations:



iRep values based on population
and number of replication events

