

# Bacterial colonization of phenotypic spaces



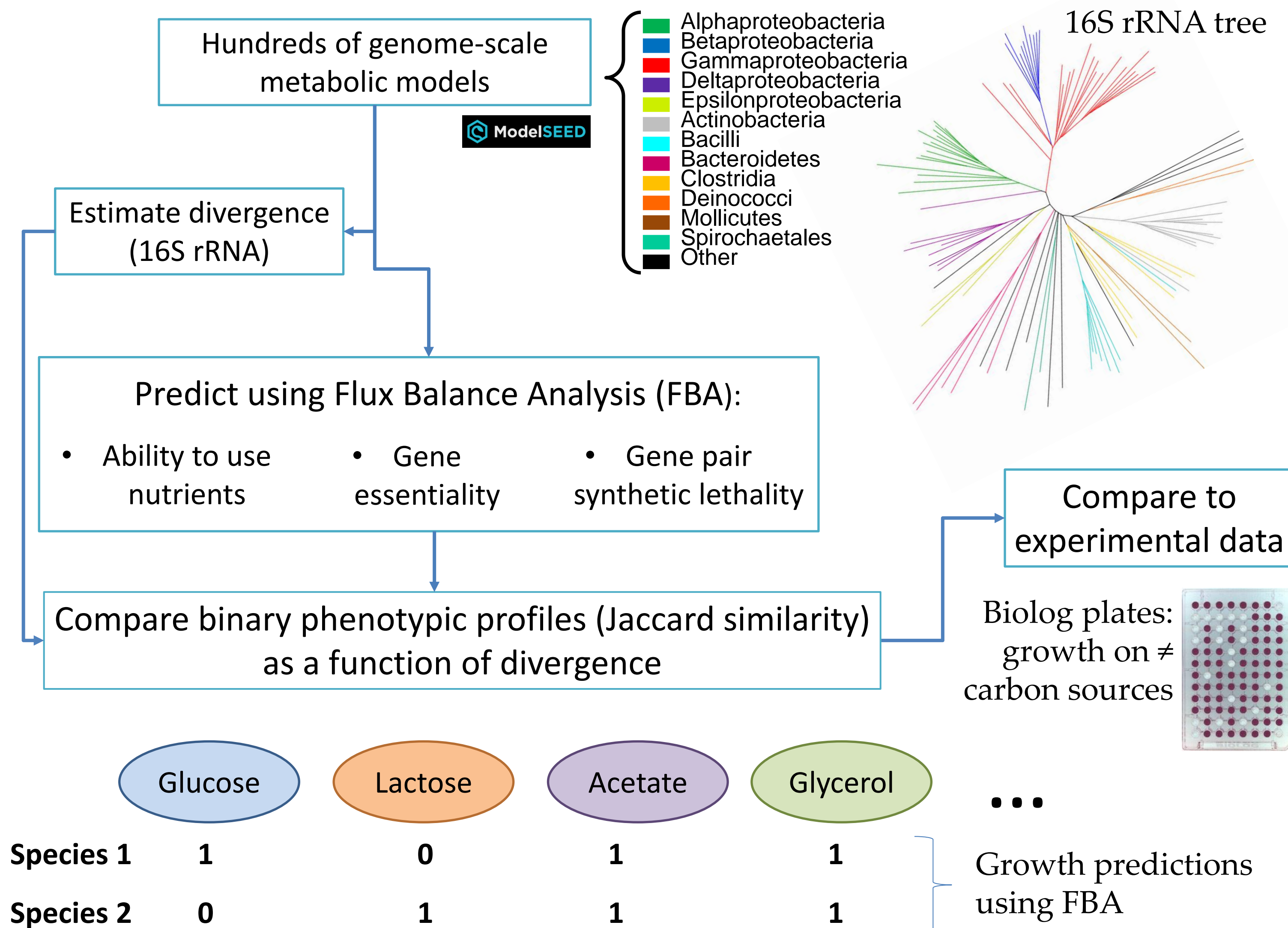
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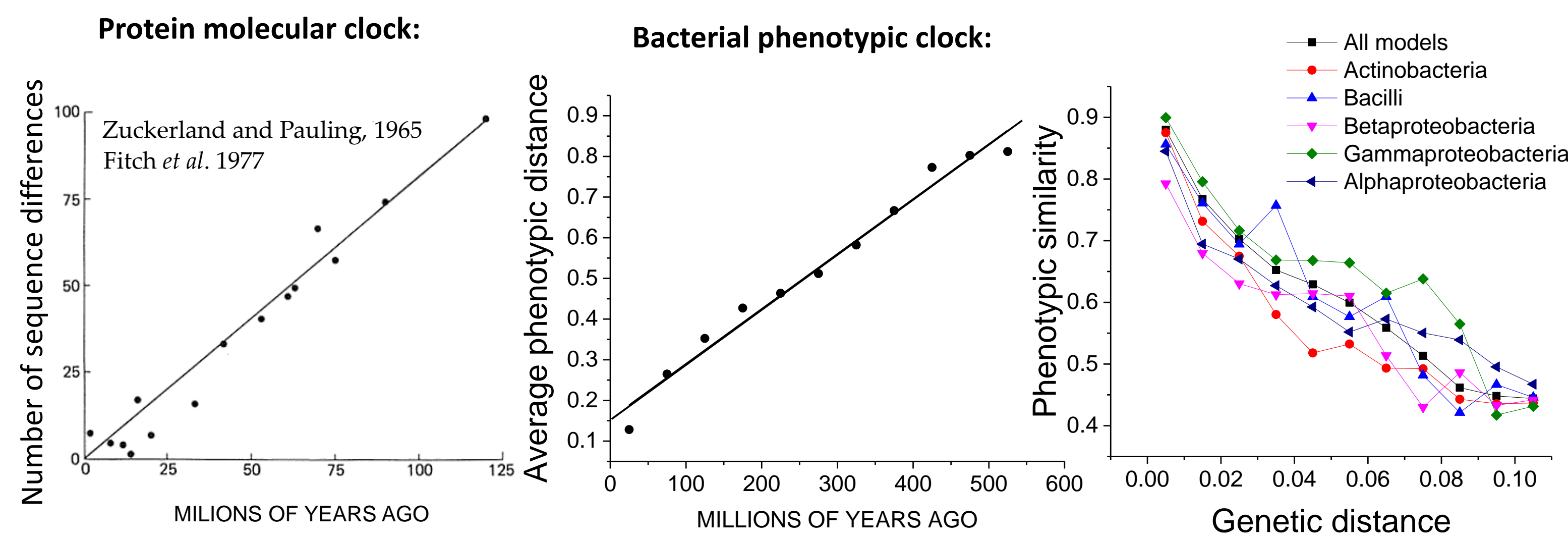


## How do bacterial phenotypes change over billions of years?

### Materials and methods



## Rates of phenotypic change



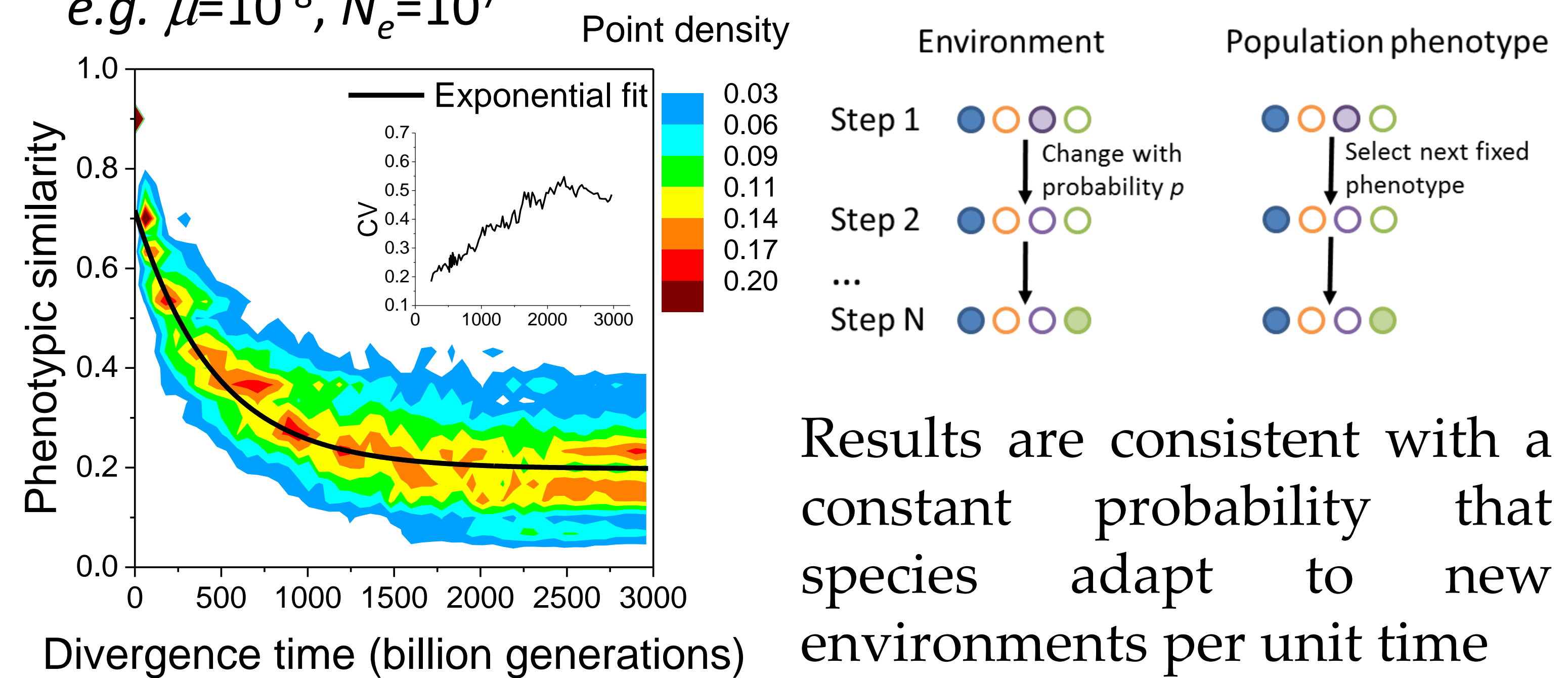
- Metabolic phenotypes change at a rate of **~1% per carbon source per 10 million years**
- Rates deviate less than 30% across bacterial classes

## Evolutionary simulation

Lineages simulated using the Gillespie algorithm: Next fixed phenotype and time to fixation proportional to fixation rates:

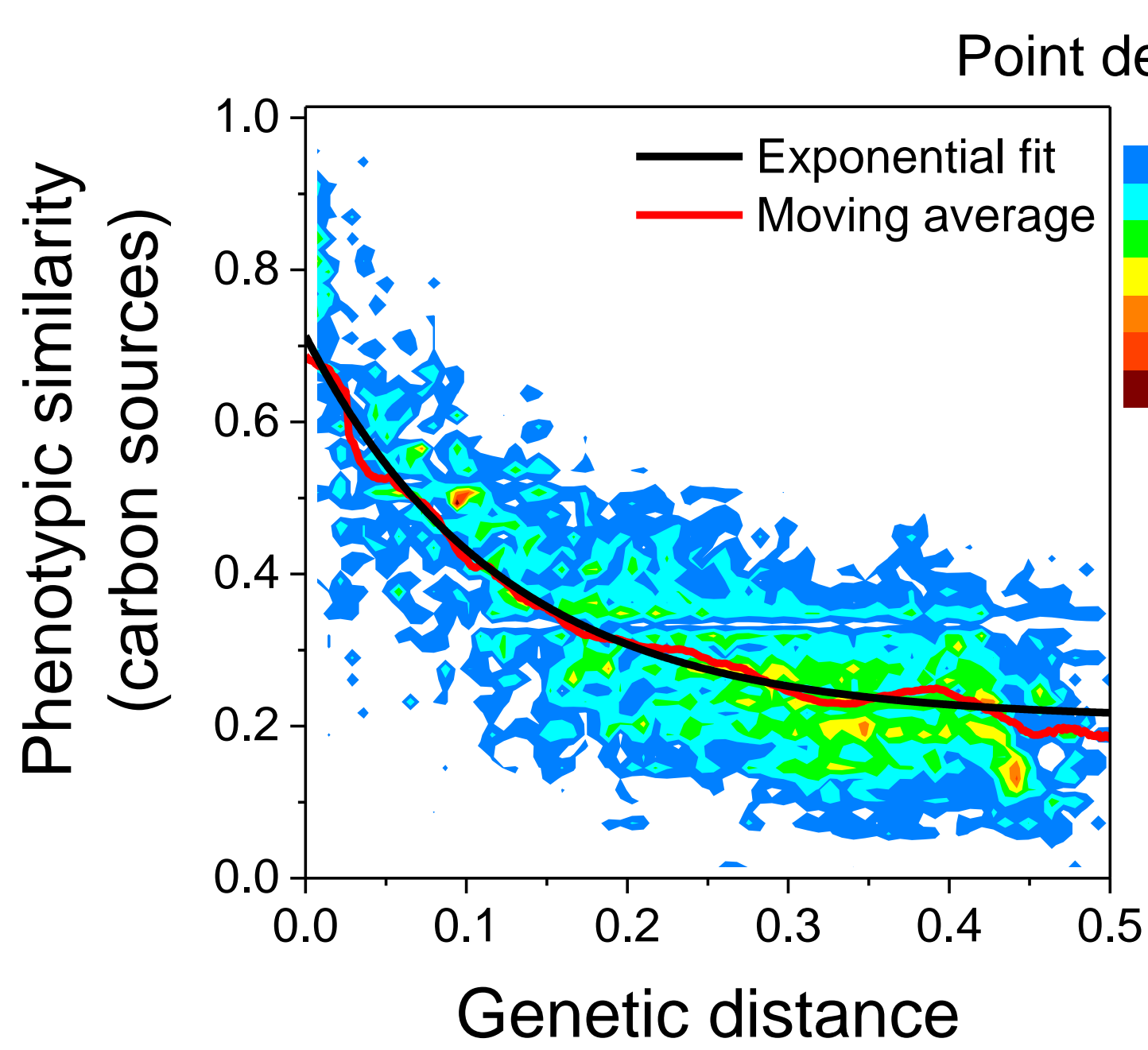
$$r = \mu N_e \frac{(1-s^{-2})}{(1-s^{-2}N_e)}$$

e.g.  $\mu=10^{-8}$ ,  $N_e=10^7$



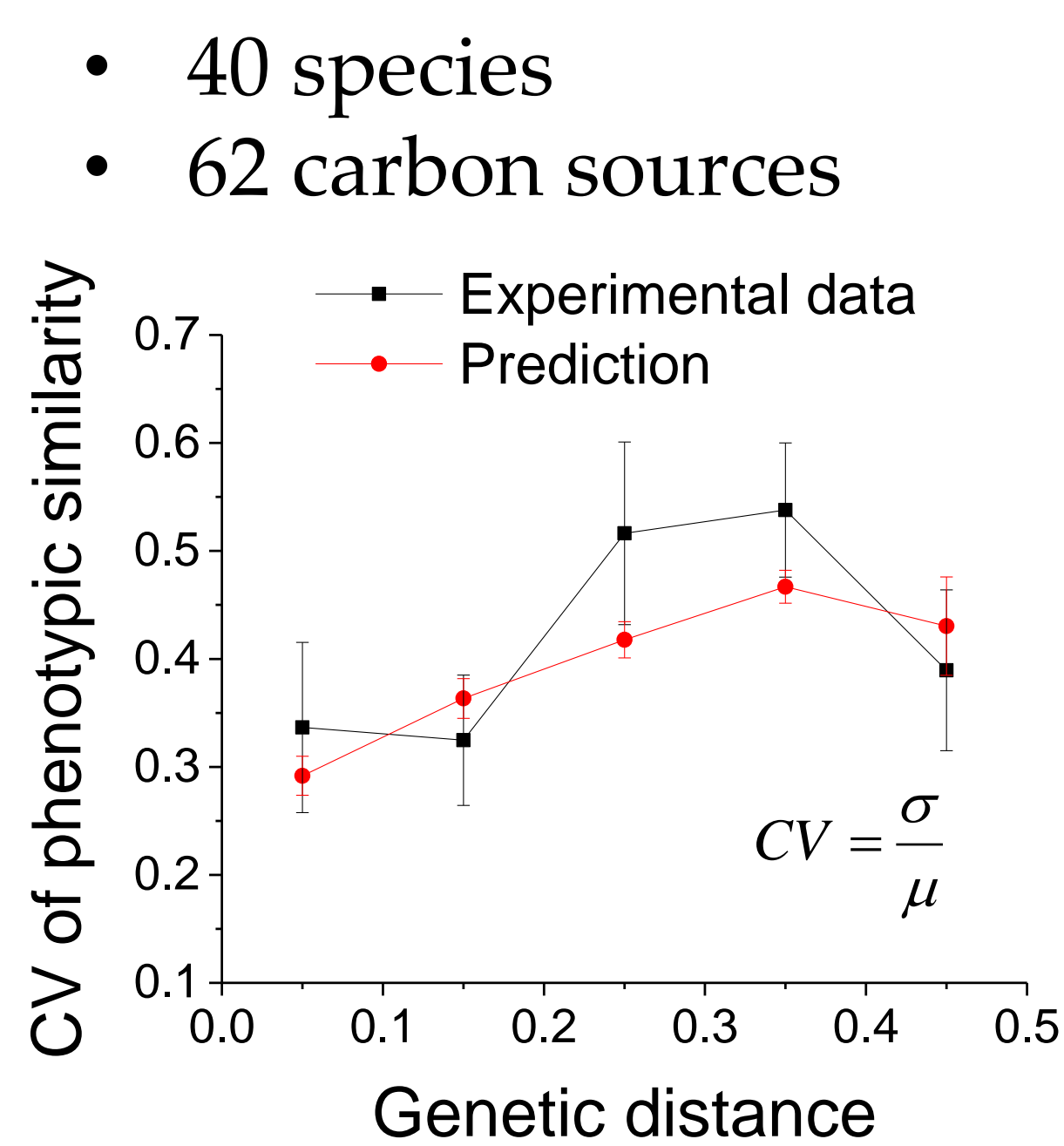
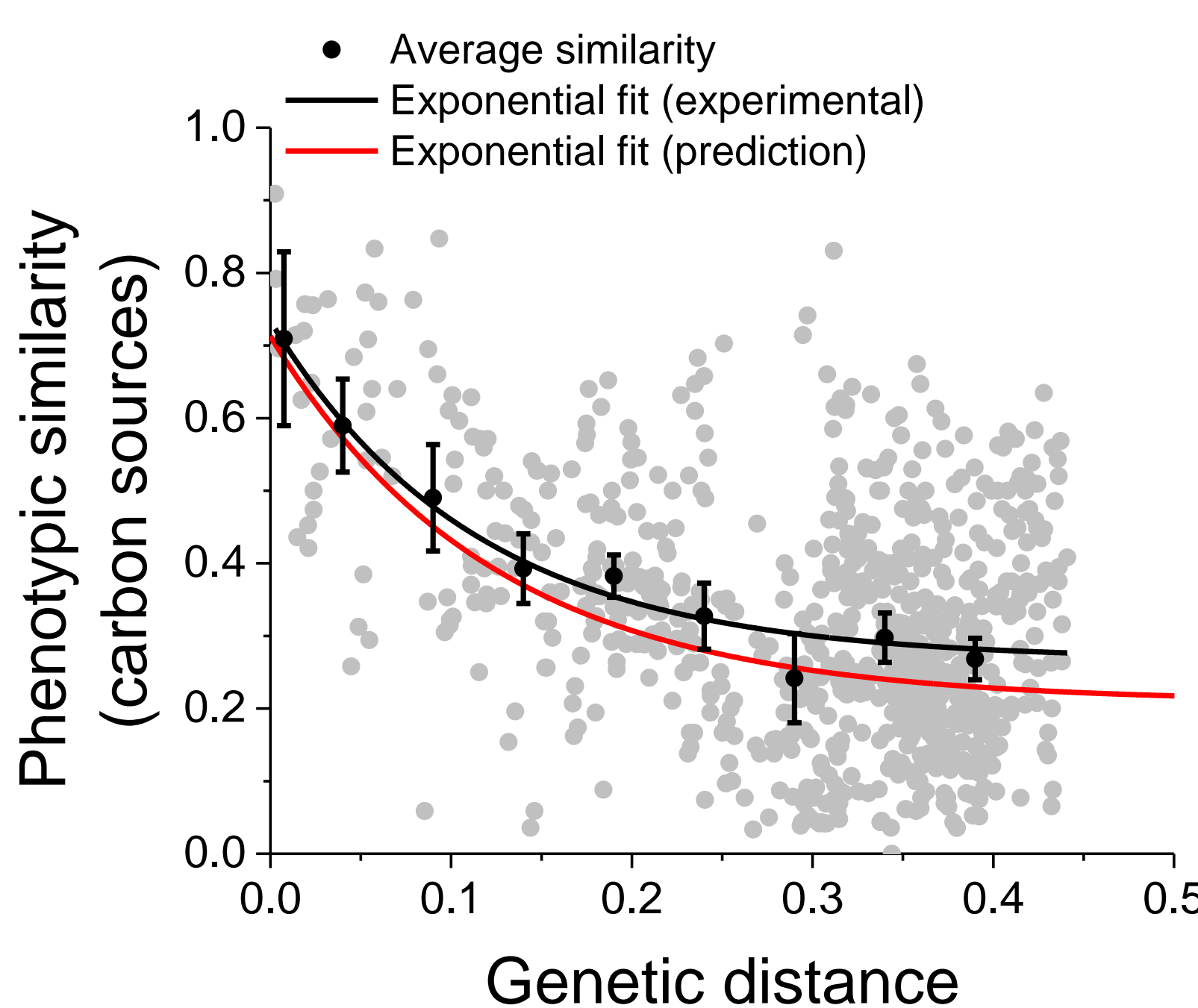
Results are consistent with a constant probability that species adapt to new environments per unit time

## Decay of phenotypic similarity



- Wide diversity within closely related strains
  - Exponential decay of phenotypic similarity
- $$y = a + b \times e^{-ct}$$
- Maximum divergence within ~ 2 billion years

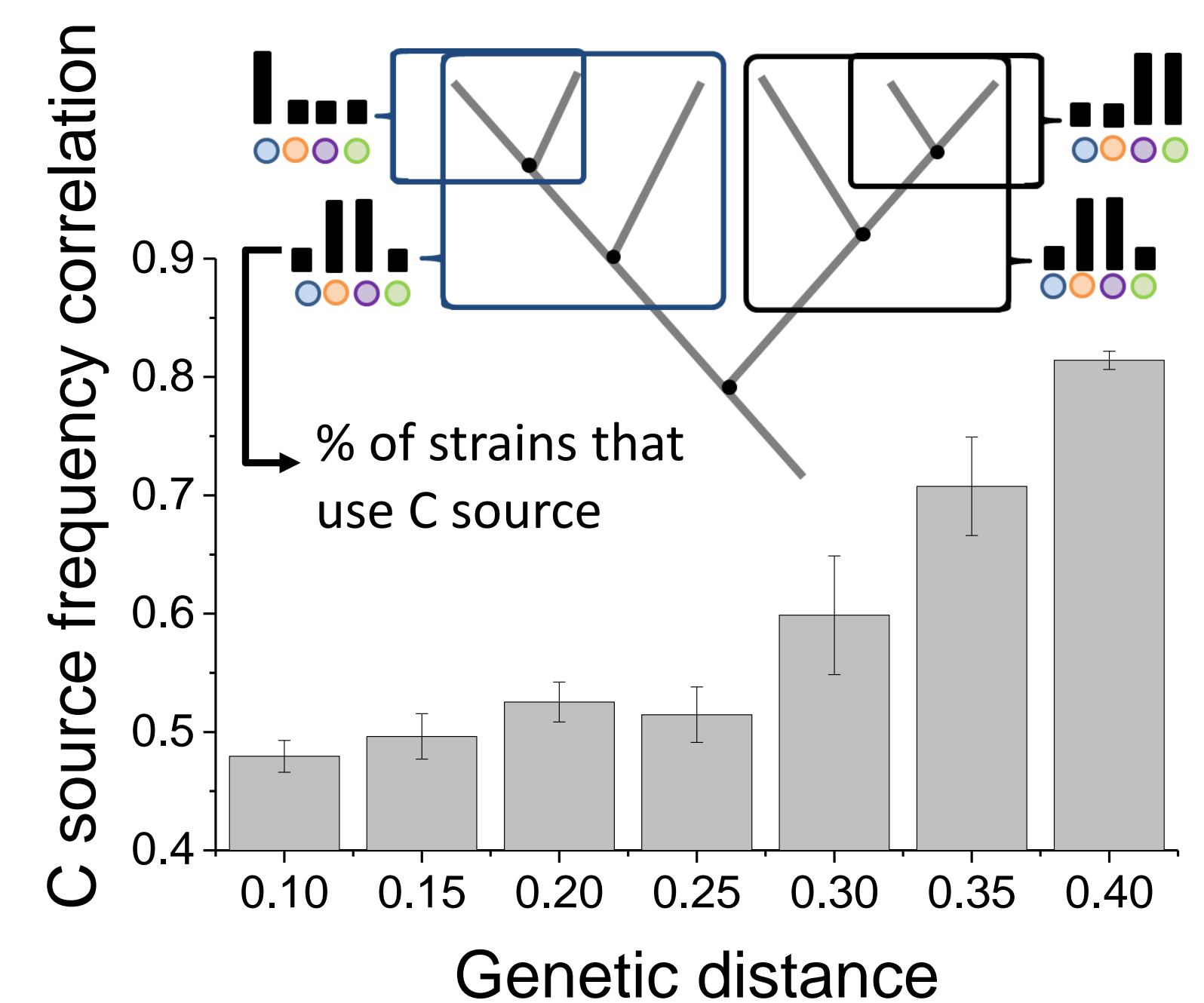
## Experimental validation



- 40 species
- 62 carbon sources

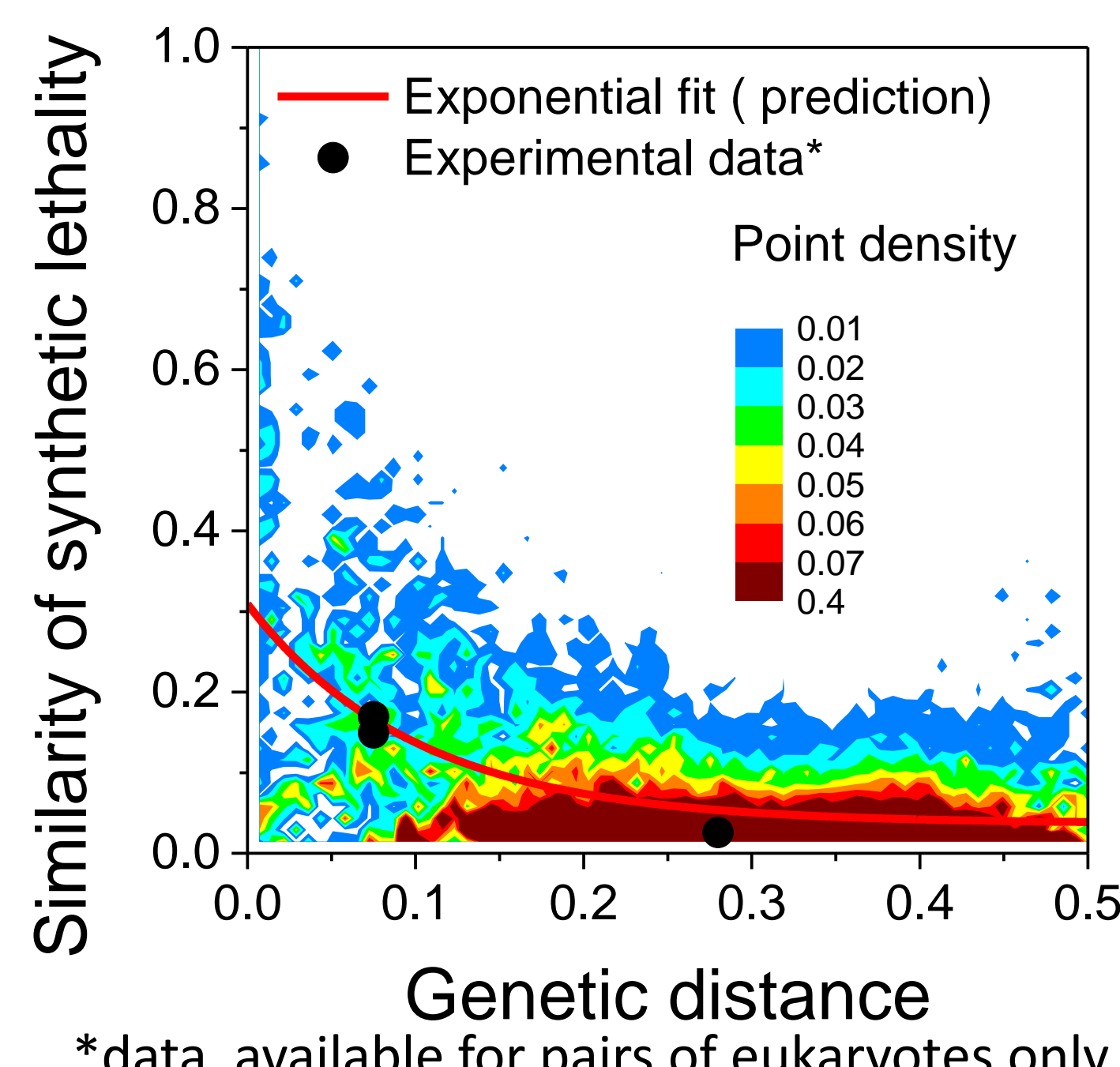
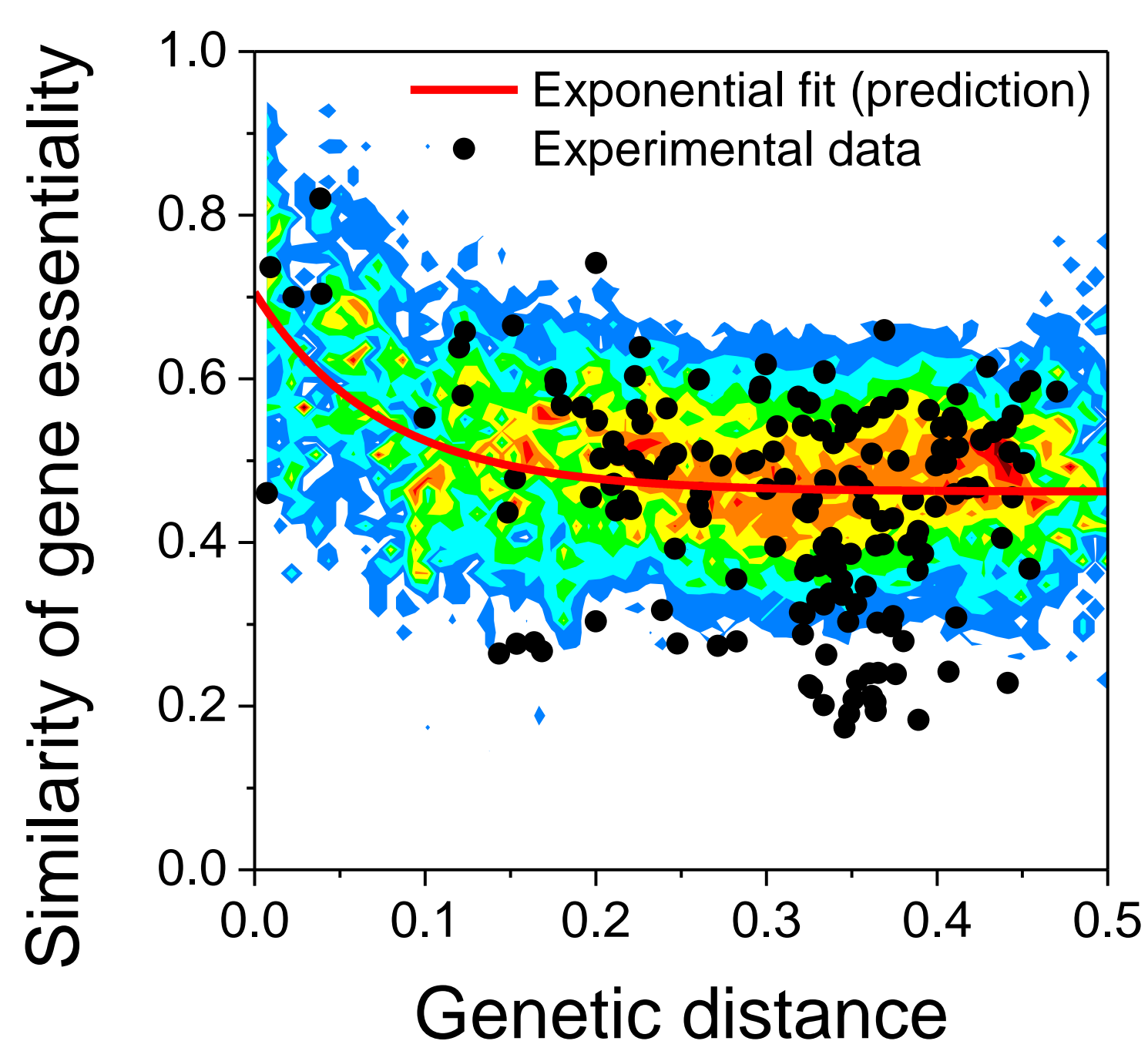
## Long-term sampling of environments

- Compared most common C-sources within clades
- Older clades converge to **similar nutrient usage frequencies**
- Suggests environments are equally accessible in the long-term



## Gene deletion phenotypes

- About **half of essential genes remain essential**
- Synthetic lethality is not conserved



\*data available for pairs of eukaryotes only

## Conclusion

