

Phylogenetic scale

Protein coding DNA alignment (sites 121-127)



Mutation-selection model



S_0 : change in amino-acid fitness for a mutation

Scaled selection coefficient (S_ρ) at the phylogenetic scale

- Deleterious mutations ($\mathcal{D}_0 := S_0 < -1$)
- Nearly-neutral mutations ($\mathcal{N}_0 := -1 < S_0 < 1$)
- Non-adaptive beneficial mutations ($\mathcal{B}_0 := S_0 > 1$)
- Synonymous mutations

Population scale

Population scale $\longrightarrow \mathcal{B} := S > 1$

Phylogenetic scale $\rightarrow \mathcal{B}_0 := S_0 > 1$

Precision

Among mutations predicted as non-adaptive beneficial at the phylogenetic scale, which ones are effectively beneficial in extant populations.

$$\frac{\mathbb{P}[\mathcal{B} \cap \mathcal{B}_0]}{\mathbb{P}[\mathcal{B}_0]} = \mathbb{P}[\mathcal{B} \mid \mathcal{B}_0]$$

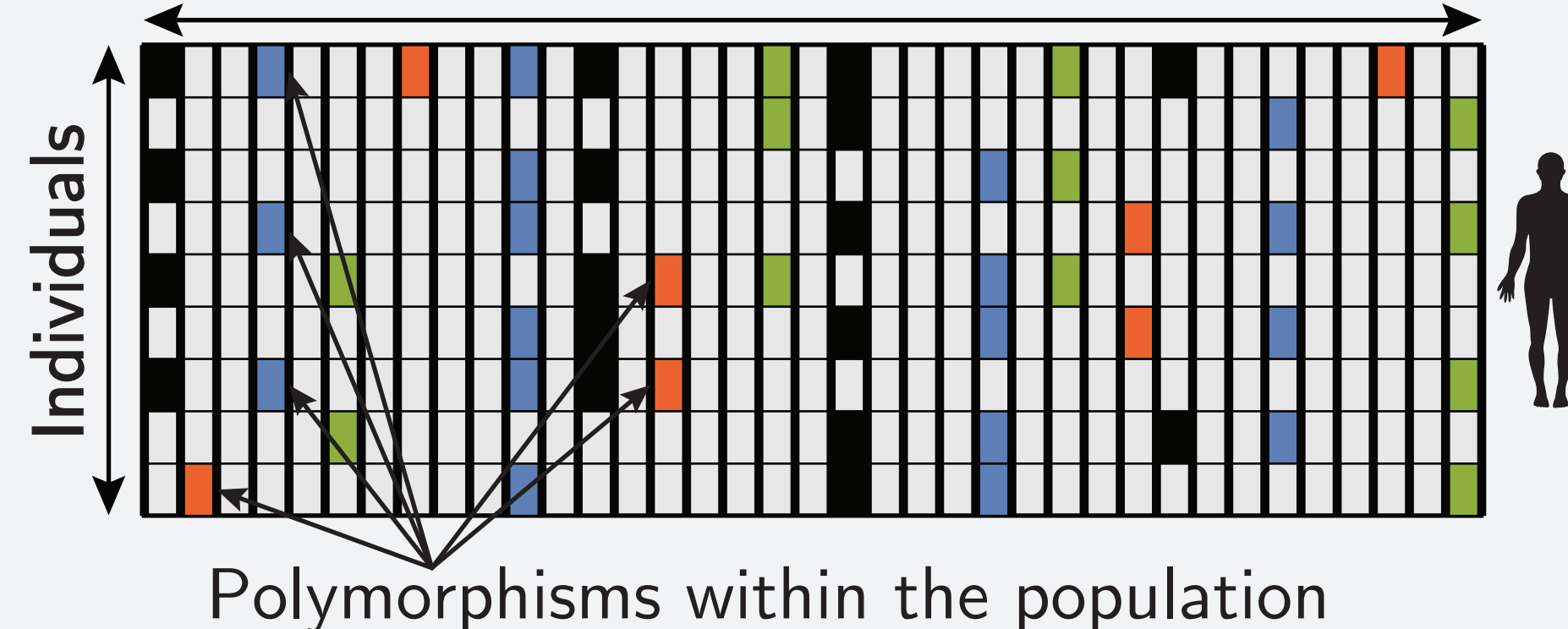
Recall

Among mutations predicted as beneficial at the population scale, which ones are non-adaptive.

$$\frac{\mathbb{P}[\mathcal{B} \cap \mathcal{B}_0]}{\mathbb{P}[\mathcal{B}]} = \mathbb{P}[\mathcal{B}_0 \mid \mathcal{B}]$$

©

Sites



Polymorphisms within the population

- Pan troglodytes 

- Homo sapiens 

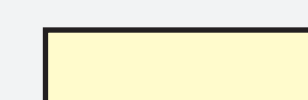
Substitutions in the terminal branch

D

Deleterious

Nearly-neutral

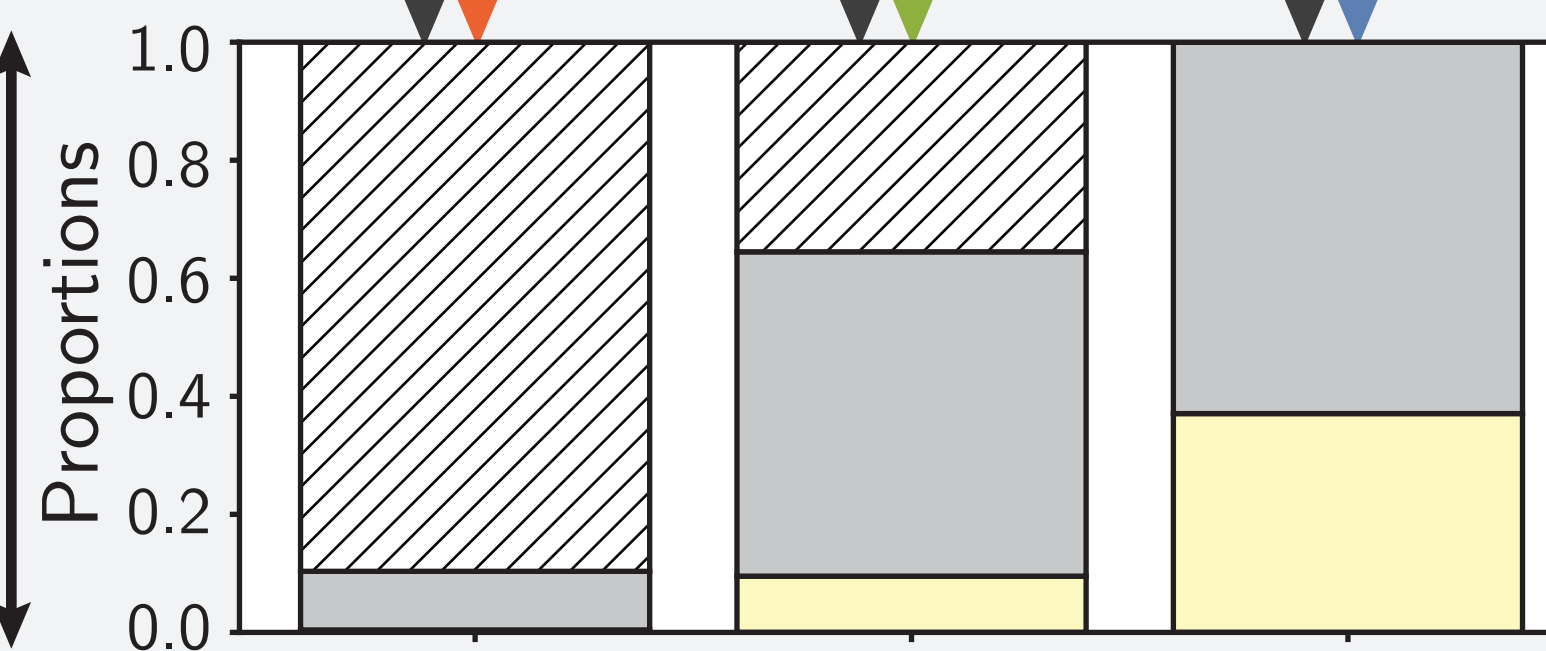
Beneficial


$$\mathbb{P}[S < -1]$$
$$\mathbb{P} \left[\overline{-1 < S < 1} \right]$$
$$\mathbb{P} [S > 1]$$

Population-genetic estimation of selection (S)

E

Population scale



Phylogenetic scale