Phylogenetic scale

A Protein coding DNA alignment (sites 121-127)

| 121 | 122 | 123 | 124 | 125 | 126 | 127 |

Gene tree

ATG|GGA|TCC|ATG|CTA|CGA|TCG

ATG|CGA|TCC|ATG|GTA|CGA|TCG

ATG|CGA|TCG|AAG|CTT|CGA|TCC

ATG|CGA|TAG|AAG|CTT|CGA|TCG

ATG|CGA|TCG|ATC|CAT|CGA|TCG

Mutation-selection model

S_0: change in amino-acid fitness for a mutation

Fitness

| 121 | 122 | 123 | 124 | 125 | 126 | 127 |

B

Deleterious mutations ($\mathcal{D}_0 := S_0 < -1$)

Nearly-neutral mutations ($\mathcal{N}_0 := -1 < S_0 < 1$)

Beneficial back-mutations ($\mathcal{B}_0 := S_0 > 1$)

Synonymous mutations

Scaled selection coefficient (S_0) at the phylogenetic scale

Population scale

C Sites

Individuals

Polymorphisms within the population

D

Deleterious	Nearly-neutral	Beneficial
$\mathbb{P}[S < -1]$	$\mathbb{P}[-1 < S < 1]$	$\mathbb{P}[S > 1]$

Population-genetic estimation of selection (S)

E

Population scale

Proportions

1.0
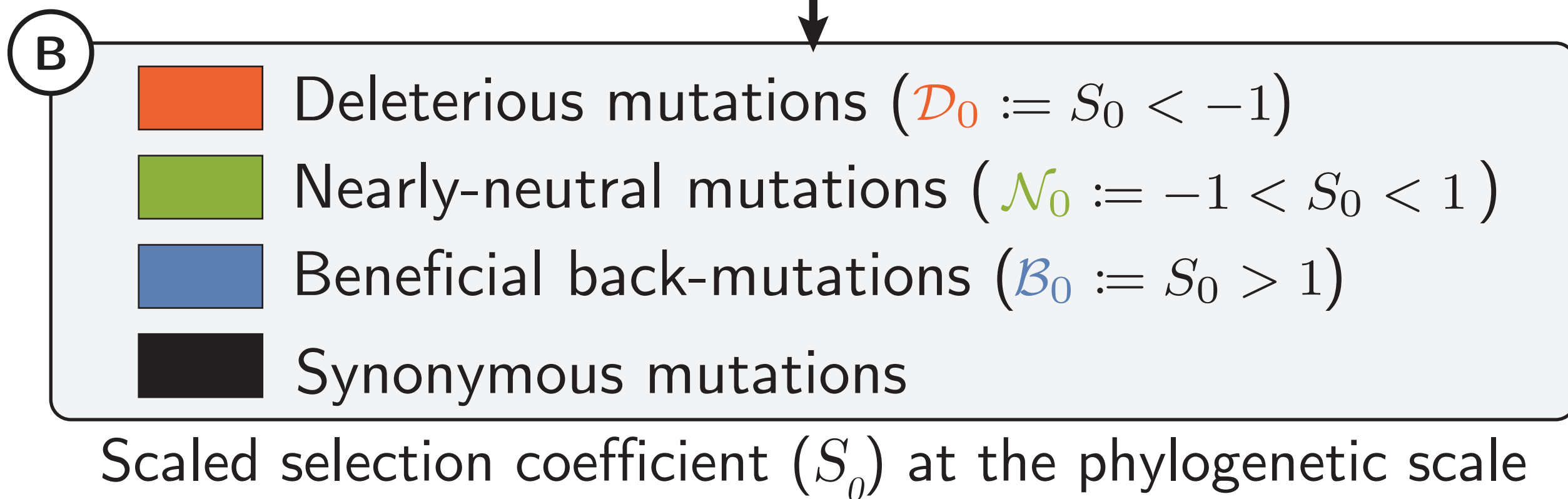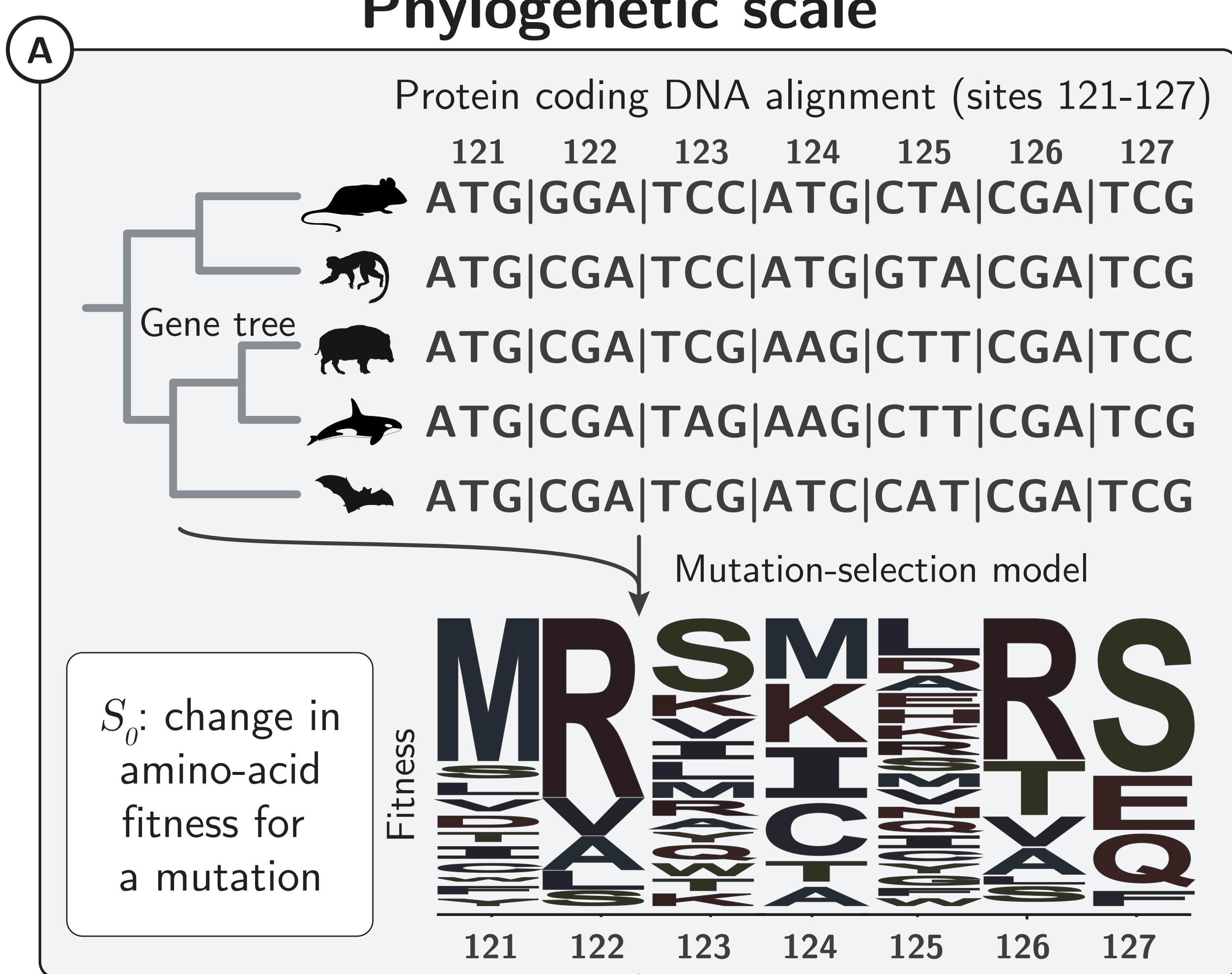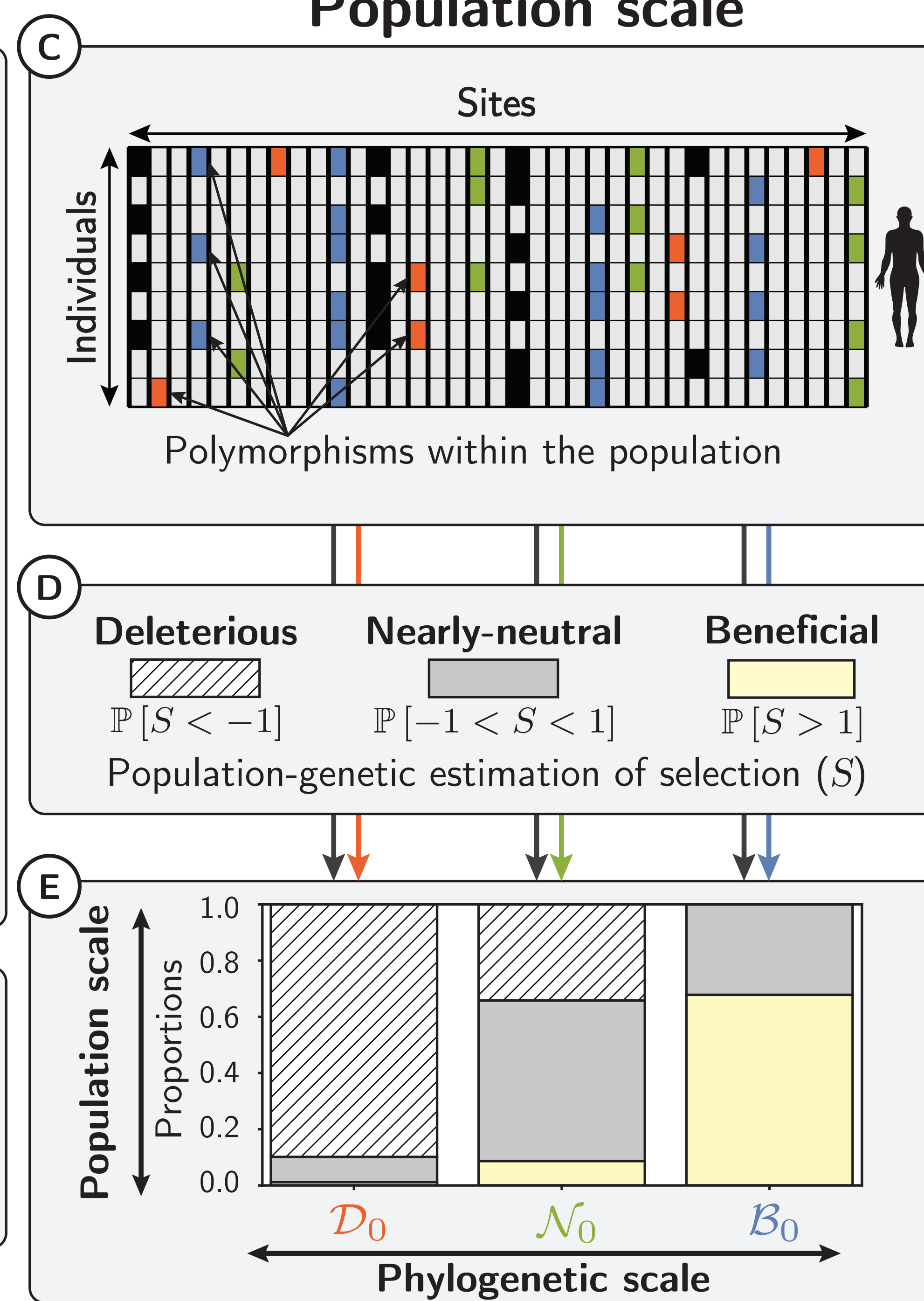0.8
0.6
0.4
0.2
0.0

$\mathcal{D}_0$ $\mathcal{N}_0$ $\mathcal{B}_0$

Phylogenetic scale

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

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

Precision

F Among mutations predicted as beneficial back-mutations at the phylogenetic scale, which one are correctly predicted as beneficial.

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

Recall

G Among mutations predicted as beneficial at the population scale, which one are correctly predicted as beneficial back-mutations.

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