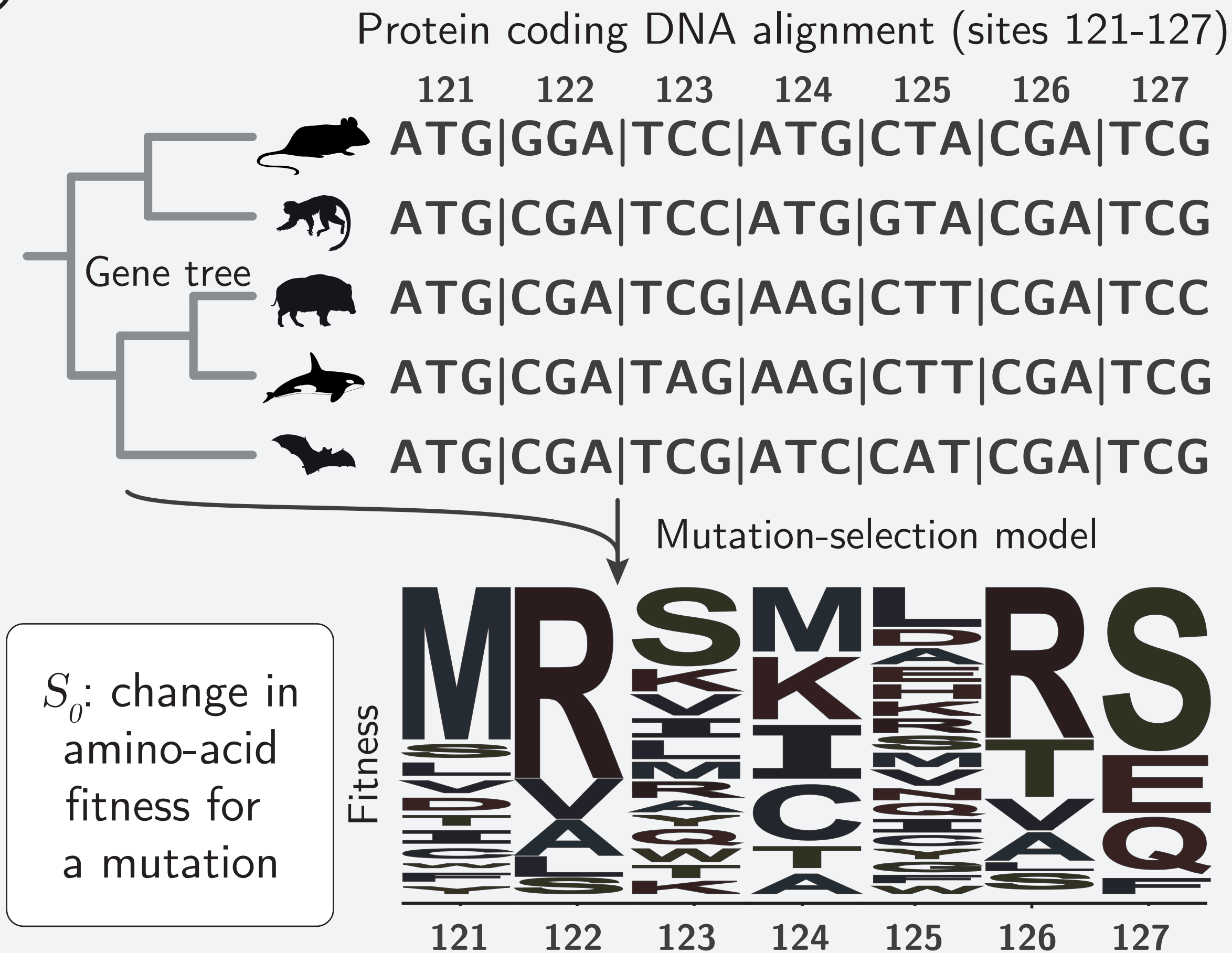






Phylogenetic scale

(A



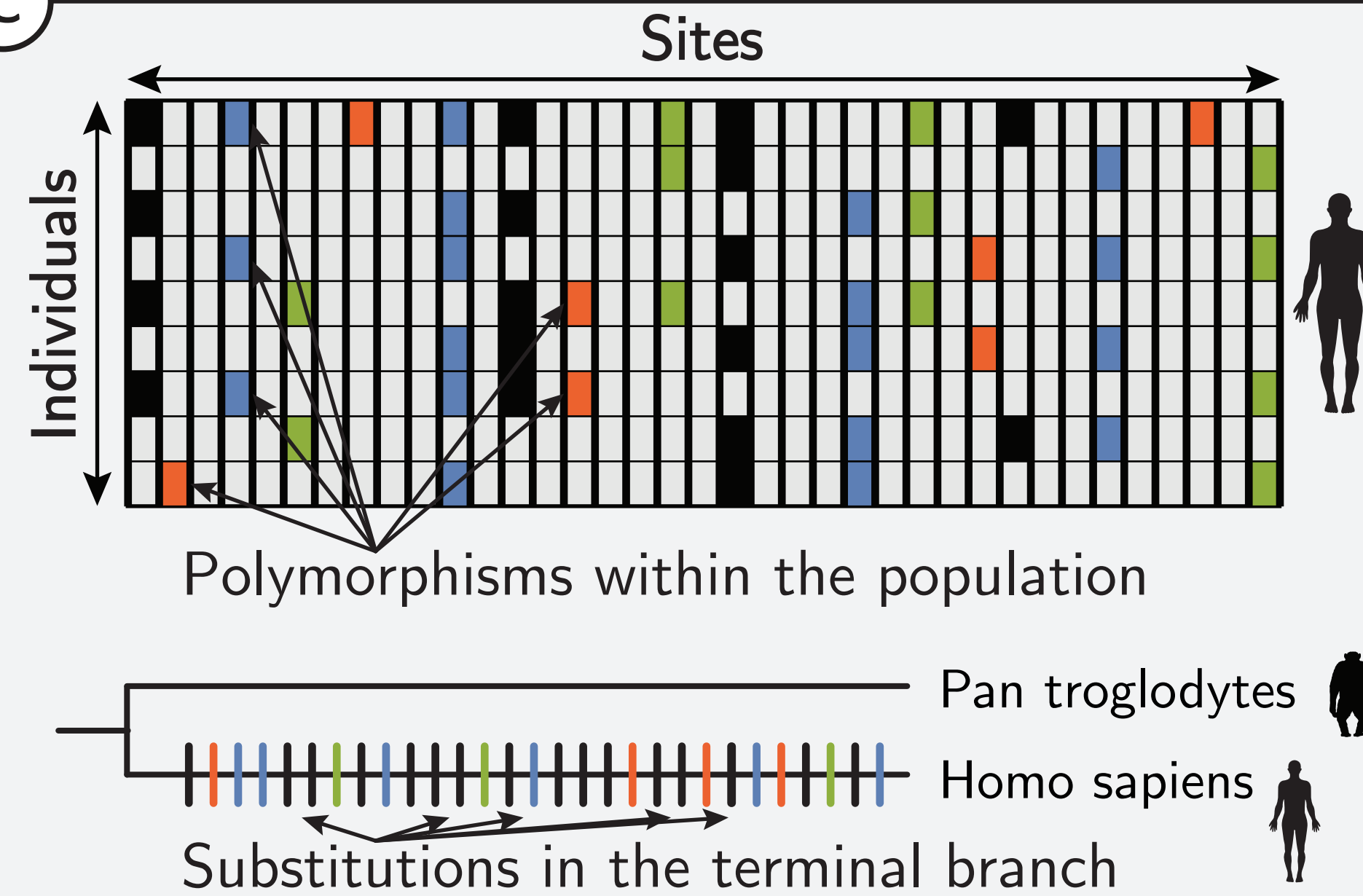
B

-  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

Scaled selection coefficient (S_ρ) at the phylogenetic scale

Terminal lineage

(c)



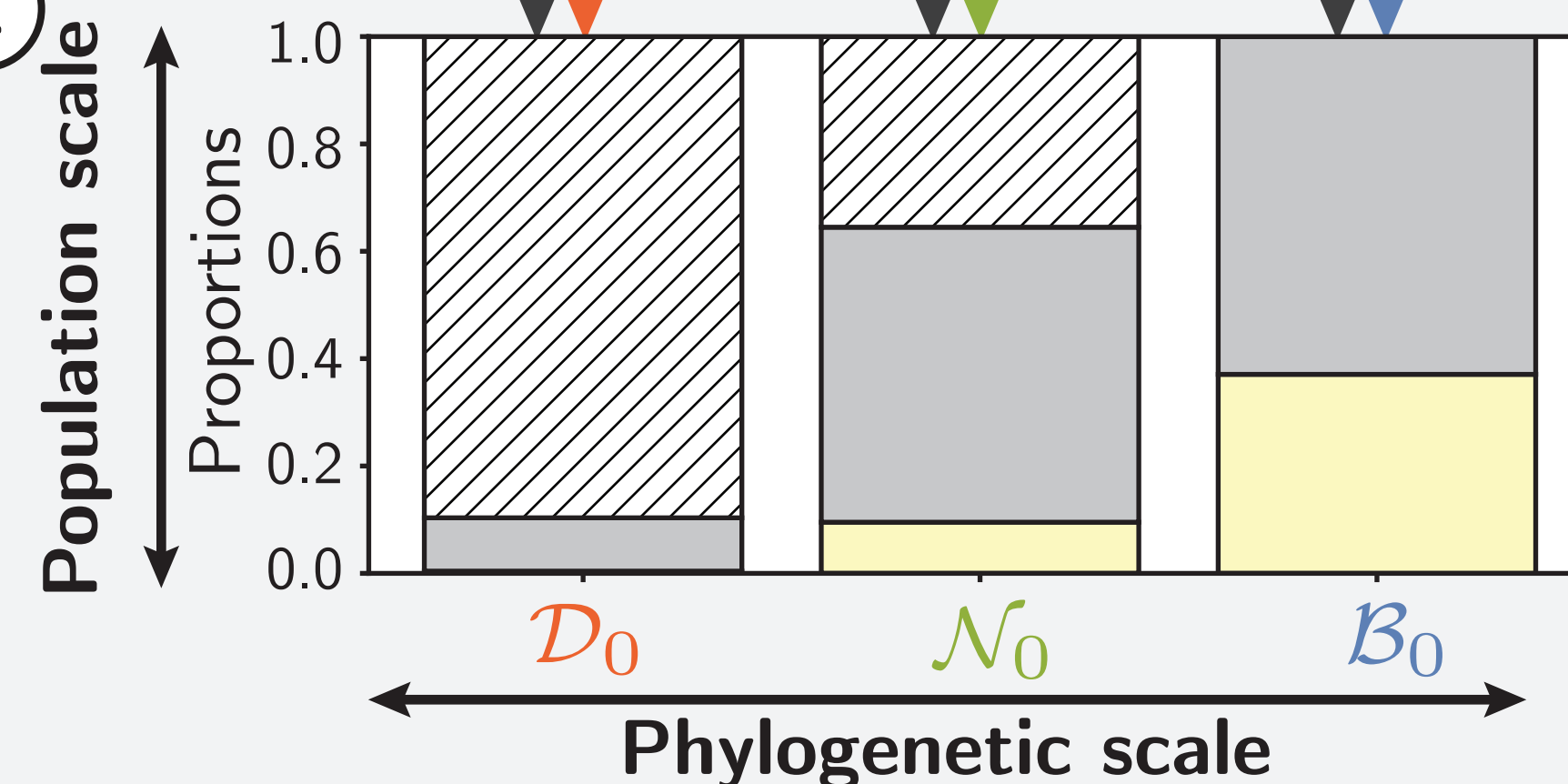
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The diagram illustrates the population-genetic estimation of selection (S) based on the probability of fixation (\mathbb{P}). It is divided into three categories:

- Deleterious:** Represented by a hatched rectangle, corresponding to $\mathbb{P}[S < -1]$.
- Nearly-neutral:** Represented by a gray rectangle, corresponding to $\mathbb{P}[-1 < S < 1]$.
- Beneficial:** Represented by a yellow rectangle, corresponding to $\mathbb{P}[S > 1]$.

Below these categories, the text reads: "Population-genetic estimation of selection (S)".

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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 terminal lineages.

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

Recall

Among mutations predicted as beneficial in terminal lineages, which ones are non-adaptive.

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