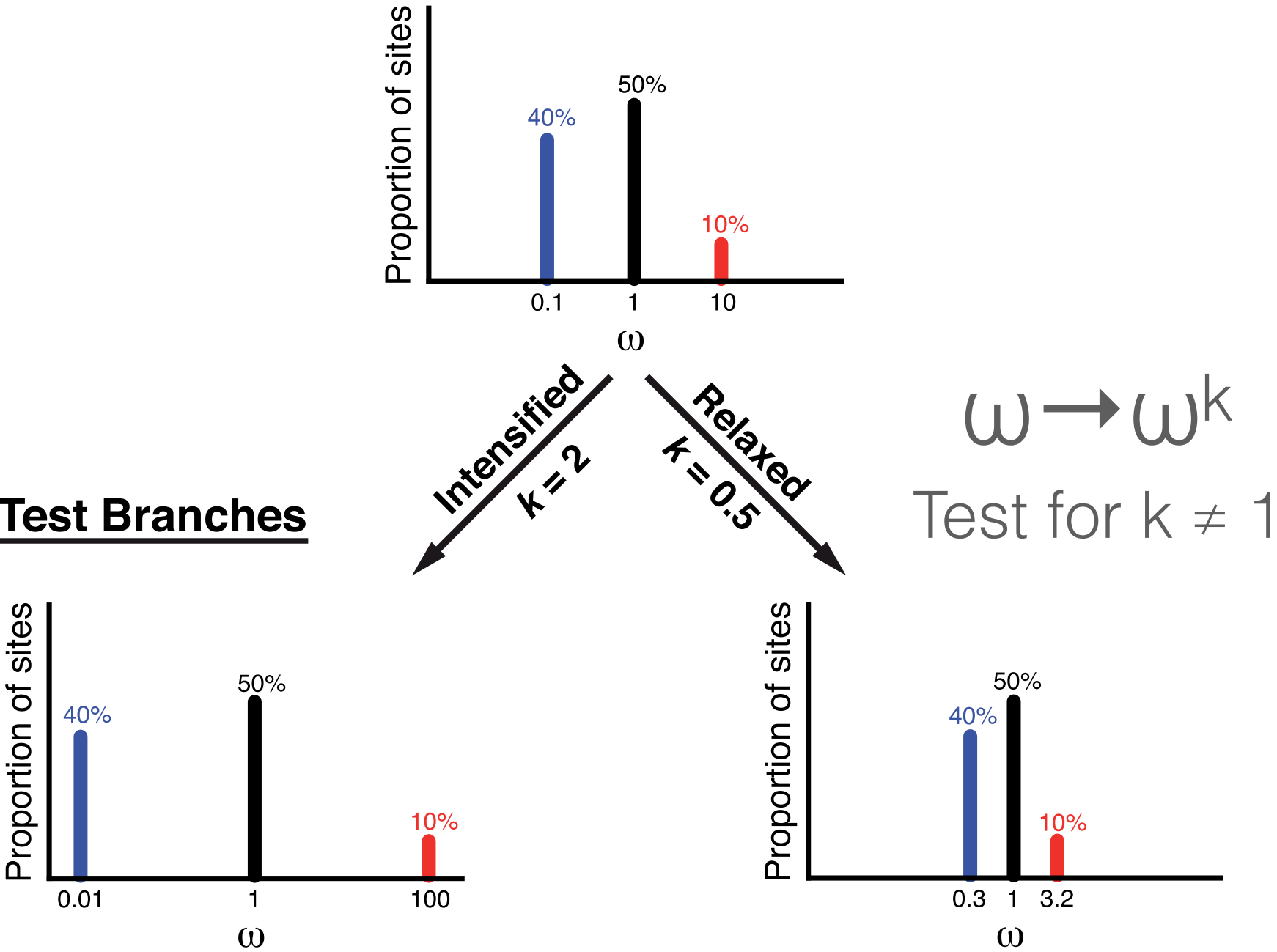


# Purpose-built models

- It is tempting to “hack” existing tools to answer questions that they are not designed to answer
- A recent example we tackled is a rigorous test for relaxation of selection (or more generally a difference in selective regimes) in a part of the tree, relative to the rest of the tree
- Typical approaches have been to estimate dN/dS ratios from two sets of branches, and interpret an *elevation* in dN/dS as evidence of selective constraint relaxation
- Two problems with this approach
- An increase in mean dN/dS could also be caused by an **intensification** of selective forces.
- *Post-hoc* analyses (e.g., estimate branch-level dN/dS and then compare [t-test, etc] them as if they were observed quantities) discard a lot of information (e.g., variance of individual estimates), and make obviously wrong assumptions (e.g., estimates are uncorrelated).

Reference Branches



**Table 1.** Test for Relaxed Selection Using RELAX in Various Taxonomic Groups.

Taxa	Gene/Genes	Test Branches	Reference Branches	$k^a$	P-Value
$\gamma$ -proteobacteria	Single-copy orthologs	Primary/secondary endosymbionts	Free-living $\gamma$ -proteobacteria	0.30	< 0.0001
		Primary endosymbionts	Free-living $\gamma$ -proteobacteria	0.28	< 0.0001
		Secondary endosymbionts	Free-living $\gamma$ -proteobacteria	0.61	< 0.0001
Bats	SWS1	Primary endosymbionts	Secondary endosymbionts	0.56	< 0.0001
		HDC echolocating and cave roosting (pseudogenes)	LDC echolocating and tree roosting (functional genes)	0.16	< 0.0001
		LDC echolocating	Tree roosting	1.07	0.577
	M/LWS1	HDC echolocating and cave roosting	LDC echolocating and tree roosting	0.70	0.495
		Echolocating species	Tree- and cave-roosting species	0.21	0.0005
		HDC echolocating	LDC echolocating	0.84	0.427
Bornavirus	Nucleoprotein	Endogenous viral elements	Exogenous virus	0.02	< 0.0001
<i>Daphnia pulex</i>	Mitochondrial protein-coding genes	Asexual	Sexual	0.63	< 0.0001

<sup>a</sup>Estimated selection intensity.