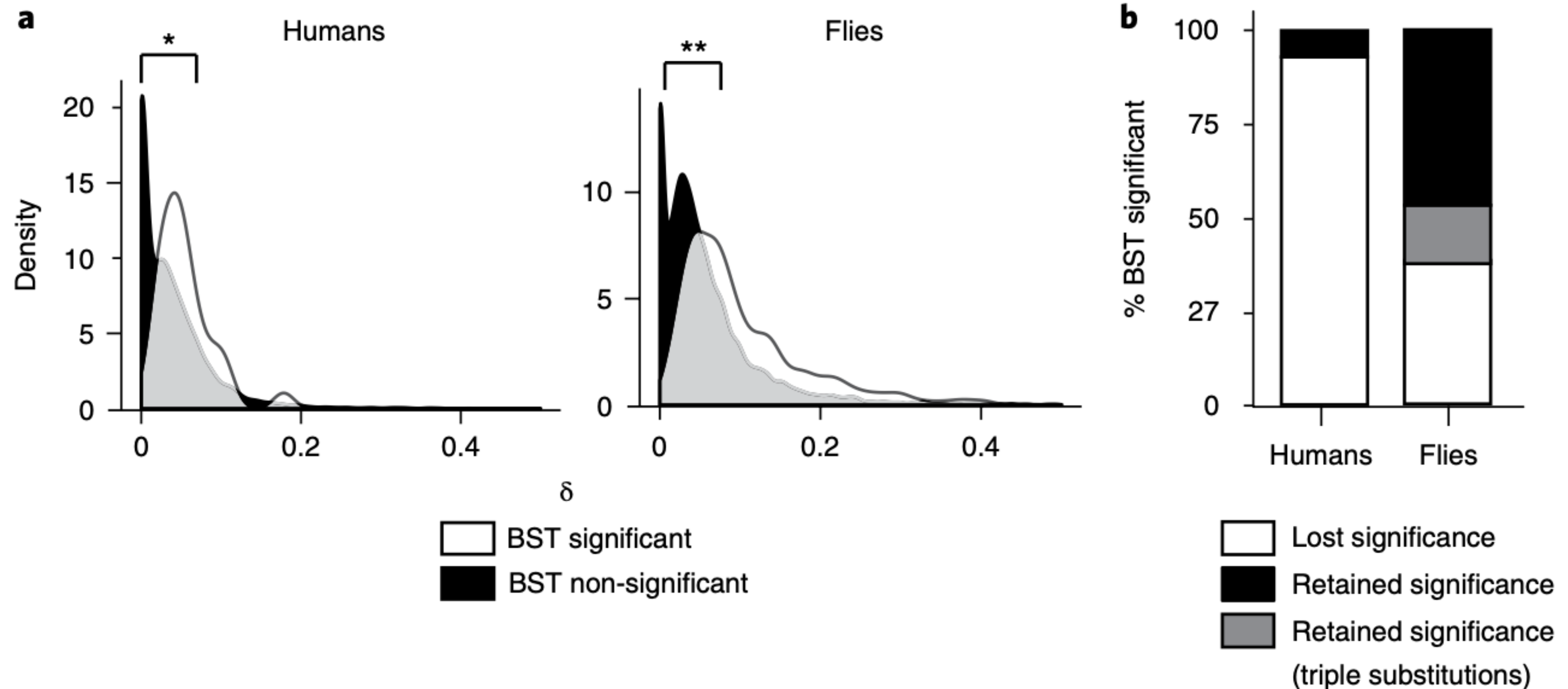


Incorporating MNMs into the branch-site model eliminates the signature of positive selection in many genes.



Outline

- Brief background and examples of natural selection
- **dN/dS** as a tool to measure the action of natural selection, explained using the first counting method for estimating dN/dS (Nei-Gojobori, 1986) and its extensions.
- Codon substitution models — the basis of modern (1998-) dN/dS estimation approaches
- Confounding processes (synonymous rate variation, recombination, multiple nucleotide substitutions)
- On the suitability of dN/dS for within-species inference
- Different types of selection analyses enabled by **dN/dS**, told by examples from West Nile virus and HIV and analogies from image analysis
 - Gene-wide selection (BUSTED)
 - Lineage-specific selection (aBSREL)
 - Site-level **episodic** selection (MEME)
 - Site-level **pervasive** selection (SLAC, FEL, FUBAR)
 - Relaxed or intensified selection (RELAX)
 - Detecting **differences** in selective pressure (Contrast-FEL)