

# Mean gene-wide dN/dS estimates

- Are not the way to go, **except** when you have very small (2-3 sequence) datasets
- For example:
  - The humoral arm of the immune system mounts a potent defense against viral infections
  - Existing successful vaccines are based on raising a neutralizing antibody (nAb) response to the pathogen
  - No simple host genetic basis (epitopes) of the specificity of neutralizing antibody responses is known
  - Need to measure these responses

# Neutralizing antibody responses drive the evolution of human immunodeficiency virus type 1 envelope during recent HIV infection

Simon D. W. Frost<sup>†</sup>, Terri Wrin<sup>‡</sup>, Davey M. Smith<sup>§</sup>, Sergei L. Kosakovsky Pond<sup>\*</sup>, Yang Liu<sup>‡</sup>, Ellen Paxinos<sup>‡</sup>, Colombe Chappey<sup>‡</sup>, Justin Galovich<sup>‡</sup>, Jeff Beauchaine<sup>‡</sup>, Christos J. Petropoulos<sup>‡</sup>, Susan J. Little<sup>\*</sup>, and Douglas D. Richman<sup>§</sup>

An example of mean dN/dS utility

The extent of immune selection pressure drives intra-host evolution in HIV-1

