

## AMONG-SITE-RATE VARIATION READINGS:

Read prepare summary:

Sullivan, J. and D. L. Swofford. 2001. Should we use model-based methods for phylogenetic inference when we know that assumptions about among-site rate variation and nucleotide substitution pattern are violated? *Systematic Biology* 50:723-729.

Also of particular interest:

Kjer and Honeycutt. 2007. Site specific rates of mitochondrial genomes and the phylogeny of eutheria. *BMC Evolutionary Biology* 2007: 7:8 (9 pages)  
doi:10.1186/1471-2148-7-8

J. Soubrier, M. Steel, M. S. Y. Lee, C. Der Sarkissian, S. Guindon, S. Y. W. Ho, and A. Cooper. 2012. The Influence of Rate Heterogeneity among Sites on the Time Dependence of Molecular Rates. *Molecular Biology and Evolution*, <http://dx.doi.org/10.1093/molbev/mss140>

At least read the Introduction and Discussion of Soubrier et al. to help understand the concerns with ASRV or RHAS.

Other relevant references:

Page and Holmes: pp: 159-171

- \*Buckley, T.R. and C. Cunningham. 2002. The effects of nucleotide substitution model assumptions on estimates of nonparametric bootstrap support. *Molec. Biol. Evol.* 19: 394-402.
- Buckley, T.R., C. Simon, and G.K. Chambers. 2001. Exploring among-site rate variation models in a maximum likelihood framework using empirical data: the effects of model assumptions on estimates of topology, edge lengths, and bootstrap support. *Systematic Biology* 50:67-86.
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- Huelsenbeck, J.P. and M.A. Suchard. 2007. A nonparametric method for accommodating and testing across-site rate variation. *Systematic Biology* 56:975-987.

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- Sullivan, J., K. E. Holsinger, and C. Simon. 1996. The effect of topology on estimates of among-site rate variation. *J. Molecular Evolution* 42: 308-312.
- Sullivan, J., and D. L. Swofford. 1997. Are guinea pigs rodents? The importance of adequate models in molecular phylogenetics. *J. Mammalian. Evol.* 4:77-86.
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- Waddell, P. J., and M. A. Steel. 1997. General time-reversible distances with unequal rates across sites: mixing  $\Gamma$  and inverse Gaussian distributions with invariant sites. *Mol. Phylogenet. Evol.* 8:398-414.
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- Yang, Z., N. Goldman, and A. Friday. 1994. Comparison of models for nucleotide substitution used in maximum likelihood phylogenetic estimation. *Mol Biol Evol* 11:316-324.

See also the Model Choice Readings on your first Readings handout, "How molecules evolve."