



Jeff Thorne



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### Evolutionary Statistical Genetics

**Research emphasis:**

My colleagues and I study evolution. We do this by developing statistical techniques for analyzing DNA and protein sequence data. Our main efforts concern:

- (1) Improving probabilistic models of DNA sequence evolution by incorporating phenotype and reconciling these models with population genetics. The phenotypic information that we have considered includes protein tertiary structure, RNA secondary structure, and data regarding which mutations cause disease or have other functional impacts.
- (2) Evolution of the rate of evolution and disentangling evolutionary rates from divergence times.
- (3) Understanding how interlocus gene conversion affects evolution of multigene families.

**Selected publications:**

Lee, H.-J., Rodrigue, N., and Thorne, J.L. (2015) Relaxing the Molecular Clock to Different Degrees for Different Substitution Types. *Molecular Biology and Evolution* 32(8) 1948-1961.

Wang, K., Yu, S., Ji, X., Lakner, C., Griffing, A., and Thorne, J.L. (2015) Roles of solvent accessibility and gene expression in modeling protein sequence evolution. *Evolutionary Bioinformatics* 11:85-96.

Robinson DM, Jones DT, Kishino H, Goldman N, Thorne JL (2003) Protein evolution with dependence among codons due to tertiary structure. *Mol. Biol. Evol.* 20(10):1692-1704.

Thorne JL, Kishino H, Felsenstein J (1991) An evolutionary model for the maximum likelihood alignment of DNA sequences. *J Mol Evol* 33:114-124.

**Application:**

- Divergence Time Estimation
- Phylogeny Inference

**Collaboration potential:**

- Multigene family evolution and gene conversion
- Incorporation of functional and structural information into studies of molecular evolution