

# Scalable and biologically realistic methods for inferring selective pressures from molecular sequence data



**Dr. Sergei Kosakovsky-Pond**  
**Friday December 11, 2015**  
**10:30 – 11:30AM Seminar**  
**Pelton Auditorium**

*Directions can be found [here](#)*

*Light refreshments will be served*

*Sergei Kosakovsky-Pond is an Associate Professor at the University of San Diego. He has developed many of the leading methodologies and software packages for detecting sites of positive selection in protein-coding genes, including the widely used [HyPhy](#) package and [DataMonkey](#) website. He has applied these methodologies to answer questions in virology, phylogenetics, and evolutionary biology. More information can be found at [Sergei L. Kosakovsky Pond](#)*

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*To arrange a meeting with Dr. Kosakovsky-Pond,  
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