

Sergei L. Kosakovsky Pond, Ph.D.
Curriculum Vitae
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Contact Information.

Antiviral Research Center
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Research Interests.

Computational biology, molecular evolution, phylogenetics and statistical genetics with an emphasis on viral evolution and methodology/algorithm development.

Positions Held.

- 2008-* Assistant Adjunct Professor.
Division of Infectious Diseases
Division of Biomedical Informatics
Department of Medicine, University of California San Diego.
- 2005-2008* Assistant Project Scientist. Antiviral Research Center
Department of Pathology, University of California San Diego.
- 2004-2005* Postgraduate Researcher. Antiviral Research Center
Department of Pathology, University of California San Diego.
- 2003-2004* Postdoctoral Fellow. Antiviral Research Center
Department of Pathology, University of California San Diego.

Education.

- 1998-2003* Ph.D. in the Interdisciplinary Program in Applied Mathematics
at the University of Arizona.
Dissertation: *Modeling Evolutionary Rates in Coding Regions of
DNA Sequences*. Advisor: Dr. Joseph C. Watkins.
- 1996-1998* M.S. in Applied Mathematics, University of Missouri, Columbia.
Project: *Stability Radii of Linear Operators*.
Advisor: Dr. Yuri Latushkin.
- 1990-1995* Undergraduate Degree (with honors) in Cybernetics (Applied Mathematics
and Computer Science) Kiev State University (Kiev, Ukraine).
Project: *Arbitrary precision numerical methods aided by
symbolic computations*. Advisor: Dr. Vladimir Makarov.

Peer-reviewed publications.

h-index :12; 613 total citations

1. Poon, A.F.Y., Lewis, F.I., Frost, S.D.W and **Kosakovsky Pond, S.L.** (2008) “Spidermonkey: rapid detection of co-evolving sites using Bayesian graphical models.” *Bioinformatics* (in press)
2. Duan J, Mu J, Thera MA, Joy D, **Kosakovsky Pond, S.L.**, Diemert D, Long C, Zhou H, Miura K, Ouattara A, Dolo A, Doumbo O, Su XZ, Miller L. (2008) “Population structure of the genes encoding the polymorphic Plasmodium falciparum apical membrane antigen 1: implications for vaccine design.” *Proc Natl Acad Sci U S A.* 105(22):7857-62
3. **Kosakovsky Pond, S.L.**, Poon, A.F.Y., Leigh Brown, A.J. and Frost, S.D.W. (2008) “A Maximum Likelihood Method for Detecting Directional Evolution in Protein Sequences and its Application to Influenza A Virus” *Mol. Biol. Evol.* (in press)
4. Nickle D.C., Jojic N., Heckerman D., Jojic V, Kirovski D., Rolland M., **Kosakovsky Pond, S.L.** and Mullins J.I. (2008) “Comparison of immunogen designs that optimize peptide coverage: reply to Fischer et al.” *PLoS Comput Biol* 4(1):e25.
5. Little S.J., Frost S.D.W., Wong J.K., Smith D.M., **Kosakovsky Pond, S.L.**, Ignacio C.C., Parkin N.T., Petropoulos C.J., Richman D.D. (2008) “Persistence of transmitted drug resistance among subjects with primary human immunodeficiency virus infection.” *J Virol.* 82(11):5510-5518.
6. Gorbach P.M., Drumright L.N., Javanbakht M., **Kosakovsky Pond, S.L.**, Woelk C.H., Daar E.S. and Little SJ. (2008) “Antiretroviral drug resistance and risk behavior among recently HIV-infected men who have sex with men.” *J Acquir Immune Defic Syndr.* 47(5):639+643.
7. **Kosakovsky Pond, S.L.**, Poon, A.F.Y., Zarate D. M. Smith, S. J. Little, S. K. Pillai, R. J. Ellis, J. K. Wong, A. J. Leigh Brown, D. D. Richman, and S. D. W. Frost “Estimating selection pressures on HIV-1 using phylogenetic likelihood models” (2008) *Statist. Med.* (in press)
8. Miller W, Rosenbloom K, Hardison RC, Hou M, Taylor J, Raney B, Burhans R, King DC, Baertsch R, Blankenberg D, **Kosakovsky Pond, S.L.**, Nekrutenko A, Giardine B, Harris RS, Tyekucheva S, Diekhans M, Pringle TH, Murphy WJ, Lesk A, Weinstock GM, Lindblad-Toh K, Gibbs RA, Lander ES, Siepel A, Haussler D, Kent WJ. “28-Way vertebrate alignment and conservation track in the UCSC Genome Browser.” (2007) *Genome Res.* 17(12):1797-1808.
9. Poon A.F.Y., Lewis F.I., **Kosakovsky Pond, S.L.**, Frost S.D.W. (2007) An Evolutionary-Network Model Reveals Stratified Interactions in the V3 Loop of the HIV-1 Envelope. *PLoS Comput Biol* 3(11): e231
10. Poon, A.F.Y., **Kosakovsky Pond, S.L.**, Bennett, P., Richman. D.D., Leigh Brown, A.J., Frost, S.D.W. (2007) “Adaptation to Human Populations Is Revealed by Within-Host Polymorphisms in HIV-1 and Hepatitis C Virus” *PLoS Pathogens* 3(3): e45
11. Poon A.F.Y, **Kosakovsky Pond, S.L.**, Richman D.D., Frost S.D.W. (2007) “Mapping protease inhibitor resistance to HIV-1 sequence polymorphisms within patients” *J. Virol.* 81(24): 13598-13607

12. Szklarczyk, R., Heringa, J., **Kosakovsky Pond, S.L.**, and Nekrutenko, A. (2007) "Rapid asymmetric evolution of a dual-coding tumor suppressor INK4a/ARF locus contradicts its function" *PNAS* 104(31): 12807-12812
13. Nickle, D.C., Heath, L., Jensen, M.A., Gilbert, P.B., Mullins, J.I., **Kosakovsky Pond, S.L.**(2007) "HIV-specific probabilistic models of protein evolution" *PLoS One* 2(6):e503
14. Mazumder R., Hu Z.Z., Vinayaka C.R., Sagripanti J.L., Frost S.D., **Kosakovsky Pond, S.L.**, Wu C.H. (2007) "Computational analysis and identification of amino acid sites in dengue E proteins relevant to development of diagnostics and vaccines." *Virus genes* 35(2):175-186
15. Zarate, S., **Kosakovsky Pond, S.L.**, Shapsak, P. and Frost, S.D.W. (2007) "Comparative Study of Methods for Detecting Sequence Compartmentalization in Human Immunodeficiency Virus Type 1" *J. Virol.* 81(12): 6643-6651
16. Chung, W., Wadhawan, S., Szklarczyk, R., **Kosakovsky Pond, S.L.**, and Nekrutenko, A. (2007) "A first look at ARFome: dual-coding genes in mammalian genomes" *PLoS Comp. Biol.* 3(5): e91
17. Nickle, D.C., Rolland, M., Jensen, M.A., **Kosakovsky Pond, S.L.**, Deng, W., Seligman, M., Heckerman, D., Mullins, J.I., and Jojic, N. (2007) "Coping with viral diversity in HIV vaccine design" *PLoS Comp. Biol.* 3(4): e75
18. Woelk, C.H, Frost, S.D.W., Richman, D.D., Higley, P.E. and **Kosakovsky Pond, S.L.**(2007) "Evolution of the interferon alpha gene family in eutherian mammals" *Gene* 397(1-2): 38-50
19. Noviello, C. M., **Kosakovsky Pond, S.L.**, Lewis, M. J., Richman, D. D., Pillai, S. K., Yang, O. O., Little, S. J., Smith, D. M., Guatelli, J. C. (2007) "Maintenance of Nef-mediated modulation of MHC-I and CD4 after sexual transmission of HIV-" *J. Virol.* 81(9): 4776-4786
20. Lemey P, **Kosakovsky Pond, S.L.**, Drummond AJ, Pybus OG, Shapiro B, et al. (2007) "Synonymous Substitution Rates Predict HIV Disease Progression as a Result of Underlying Replication Dynamics" *PLoS Comp. Biol.* 3(2): e29
21. Poon, A.F.Y., Lewis, F., **Kosakovsky Pond, S.L.**, Frost, S.D.W. (2006) "Evolutionary interactions between N-linked glycosylation sites in the HIV-1 envelope" *PLoS Comp. Biol.* 3(1): e11
22. **Kosakovsky Pond, S.L.**, Mannino, F., Gravenor, M.B., Muse, S.V. and Frost, S.D.W. (2007) "Evolutionary model selection with a genetic algorithm: a case study using stem RNA" *Mol. Biol. Evol.* 24(1):159-170
23. **Kosakovsky Pond, S.L.**, Posada, D., Gravenor, M.B., Woelk, C.H. and Frost, S.D.W. (2006) "GARD: A Genetic Algorithm for Recombination Detection" (2006) *Bioinformatics* 22(24):3096-3098
24. **Kosakovsky Pond, S.L.**, Posada, D., Gravenor, M.B., Woelk, C.H. and Frost, S.D.W. "Automated Phylogenetic Detection of Recombination Using a Genetic Algorithm" (2006) *Mol.Biol.Evol.* 23(10):1891-1901
25. Pillai, S.K., **Kosakovsky Pond, S.L.**, Liu, Y., Good, B.M., Strain, M.C., Ellis, R.J., Letendre, S., Smith, D.M., Gunthard, H.F., Grant, I., Marcotte, T.D., McCutchan, A.J., Richman, D.D. and Wong, J.K. "Genetic attributes of cerebrospinal fluid-derived HIV-1 env" (2006) *Brain* 129(7):1872-1883

26. Huelsenbeck, J.P., Jain, S., Frost, S.D.W., and **Kosakovsky Pond, S.L.** (2006) "A Dirichlet process model for detecting positive selection in protein-coding DNA sequences" *PNAS* 103(16): 6263-6268
27. Sorhannus, U. and **Kosakovsky Pond, S.L.** (2006) "Evidence For Positive Selection On A Sexual Reproduction Gene In The Diatom Genus *Thalassiosira* (Bacillariophyta)" *J. Mol. Evol.* 63(2): 231-239
28. **Kosakovsky Pond, S.L.**, Frost, S.D.W., Grossman, Z., Gravenor, M.B., Richman, D.D. and Leigh Brown, A.J. "Adaptation to different human populations by HIV-1 revealed by codon-based analyses" (2006) *PLoS Comp. Biol.* 2(6): e62
29. Frost, S.D.W., Wrin, T., Smith, D.M., **Kosakovsky Pond, S.L.**, Liu, Y., Paxinos, E., Chappay, C., Galovich, J., Beauchaine, J., Petropoulos, C.J., Little, S.J. and Richman, D.D. (2005) "Neutralizing antibody responses drive the evolution of human immunodeficiency virus type 1 envelope during recent HIV infection" *PNAS* 102(51): 18514-1851
30. Pillai, S.K., **Kosakovsky Pond, S.L.**, Woelk, C.H., Richman, D.D. and Smith, D.M. (2005) "Codon volatility does not reflect selective pressure on the HIV-1 genome." *Virology* 336(2): 137-143.
31. **Kosakovsky Pond, S.L.** and Muse, S.V. (2005) "Site-to-site Variation of Synonymous Substitution Rates" *Mol. Biol. Evol.* 22(12):2375-2385
32. **Kosakovsky Pond, S.L.** and Frost, S.D.W. (2005) "Datamonkey: Rapid Detection of Selective Pressure on Individual Sites of Codon Alignments." *Bioinformatics.* 21(10): 2531-2533
33. Frost, S.D.W., Little, S.J., **Kosakovsky Pond, S.L.**, Chappay, C., Liu, Y., Wrin, T., Petropoulos, C.J. and Richman, D.D. (2005) "Characterization of HIV-1 envelope variation and neutralizing antibody responses during transmission of HIV-1 subtype B." *J. Virol.* 79(10): 6523-6527.
34. S. Pillai, B. Good, **Kosakovsky Pond, S.L.**, J. Wong, M. Strain, D. Richman, D. Smith. (2005) "Semen-specific genetic characteristics of HIV-1 env" *J. Virol.* 79(3), 1734-1742
35. **Kosakovsky Pond, S.L.** and Frost, S.D.W. (2005) "Not so different after all: comparison of various methods for detecting amino-acid sites under selection." *Mol. Biol. Evol.* 22(5):1208-1222
36. **Kosakovsky Pond, S.L.**, Frost, S.D.W. (2005) "A Genetic Algorithm Approach to Detecting Lineage-specific Variation in Selection Pressure." *Mol. Biol. Evol.* 22(3):478-485
37. **Kosakovsky Pond, S.L.**, Frost, S.D.W. and Muse, S.V. (2005) "HyPhy: hypothesis testing using phylogenies." *Bioinformatics.* Bioinformatics 21(5):676-679
38. **Kosakovsky Pond, S.L.** and Frost, S.D.W. (2005) "A simple hierarchical approach to modeling distributions of substitution rates." *Mol. Biol. Evol.* 22 (2):223-234
39. **Kosakovsky Pond, S.L.** and Muse, S.V. (2004) "Column Sorting: Rapid Calculation of the Phylogenetic Likelihood Function" *Systematic Biology* 53(5):1-8, 2004
40. Israel, R.L., **Kosakovsky Pond, S.L.**, Muse, S.V., Katz, L.A. (2002) "Evolution of ciliate alpha-tubulin genes." *Evolution* 56(6) 2002: 1110-1122

41. Zhang, L., **Kosakovsky Pond, S.L.** Gaut, B.S. (2001) "A survey of the molecular evolutionary dynamics of twenty-five multigene families from four grass taxa." *J.Mol.Evol* (2001) 52:144-156.

Contributed book chapters.

1. Poon, A.F.Y., Frost, S.D.W and **Kosakovsky Pond, S.L.**(2007) "Detecting signatures of selection from DNA sequences using Datamonkey" A contributed book chapter in "Bioinformatics for DNA Sequence Analysis" (D. Posada Ed. Humana Press, USA) in press.
2. **Kosakovsky Pond, S.L.** Poon, A.F.Y. and Frost, S.D.W (2007) "HyPhy: Hypothesis Testing Using Phylogenies" A contributed book chapter in "The Phylogenetic Handbook" 2nd edition (P. Lemey, M. Salemi, and A-M Vandamme, Ed. Cambridge University Press) in press (January 2009).
3. **Kosakovsky Pond, S.L.** and Muse, S.V. (2005) "HyPhy: Hypothesis Testing Using Phylogenies" A contributed book chapter in "Statistical Methods in Molecular Evolution" (Rasmus Nielsen, Ed. Springer, ISBN: 0-387-22333-9).

Software Projects.

HyPhy - Hypothesis Testing Using Phylogenies. Publicly distributed (<http://www.hyphy.org>) molecular evolution and statistical inference package (> 4500 registered users and > 200 citations)

Datamonkey - Adaptive Evolution Server. Public web interface (www.datamonkey.org) to a comprehensive and efficient suite of methods aimed at finding adaptive and purifying selection acting on coding sequences as well as uncovering evidence of recombination in the evolutionary past of the sample (\approx 50000 processed analyses and > 50 citations)

Awards and Fellowships

- 2006** Center for AIDS Research (CFAR) Developmental Grant (PI, \$40,000)
2001-2003 NSF Integrative Graduate Education and Research Traineeship Program (IGERT) Fellowship.
2000-2001 Research Assistant at the Arizona Center of Mathematical Sciences.
1999-2001 Summer Internships, Bioinformatics Research Center, North Carolina State University.
1995-1996 Monstanto Eastern European Scholar Award.

Teaching and Advising.

2004-current, Taught five invited molecular evolution workshops at UT Austin, NESCent, CINES-TAV Mexico City and the University of Pretoria. *2005-current*, Advised and mentored biomedical sciences graduate students

1998-2000, Teaching Assistant (University of Arizona). Courses taught: College Algebra, Business Calculus and Mathematics in Modern Society.

1998, Supervised an undergraduate in an independent summer research project (Bioinformatics Research Center at NCSU).

1996-1998, Teaching Assistant (University of Missouri, Columbia). Courses taught: College Algebra.

Professional Activities.

Reviewer for Nature Genetics, Proc. Royal Society B, Mol Biol Evol, J Mol Evol, PLoS Comp Biol, J Virol, Genetics, Theor Bio, Bioinformatics and BMC Evol Biol
Member of NESCent sponsored Evolutionary Informatics workgroup

Current Grant Support.

- 1 R01 AI57167-02 (Frost, Simon D.W.) 07/01/2004-06/30/2009 2.4 Calendar Mos.
NIH \$1,184,090
Modeling HIV Escape from Neutralizing Antibodies. Major goals: to characterize the escape of HIV from neutralizing antibody responses at the phenotypic and genotypic level using advanced statistical models.
- 1U01AI074521-01 (Schooley, Robert T.) 07/01/2007-06/30/2012 .9 Calendar Mos.
NIH \$3,998,473
Multiplex Nucleic Acid Detection Devices for the Diagnosis of Respiratory Viruses. Major goals: to develop and validate accurate, inexpensive and high-throughput molecular devices for diagnosing respiratory viruses, especially influenza.
- 2 R01 AI47745-05A1 (Richman, Douglas D) 7/01/2000-12/3/2011 6.6. Calendar Mos.
NIH \$1,545,000
Biomathematical Analysis of Viral Dynamics and Evolution. Major goals: To collect increasingly detailed and complex data on viral and host genetic variation, this will necessitate the development of more biologically realistic mathematical and statistical models of HIV dynamics and evolution.
- NSF 0714991 (Frost, Simon D.W.) 07/01/2008-06/30/2011 1.5 Calendar Mos.
NSF \$565,000
Identifying Selection Pressures on Viral Genomes. Major goals: To develop sophisticated likelihood-based models of molecular evolution and to contrast and compare patterns of evolution in viral genes.
- R21 AI077304 (Smith, Davey M.) 04/01/2008-03/31/2010 .6 Calendar Mos.
NIH \$380,850
Detection and Characterization of HIV-1 Interclade Dual Infection. Major goals: In this proposal, we aim to determine: (1) the prevalence, nature, and course of HAND during and after acute and early HIV (AEH) infection, (2) how the clinical signs and symptoms of acute retroviral syndrome (ARS) correlate with the development of HAND, and (3) how HAND responds to antiretroviral therapy (ART) started during AEH infection.