CURRICULUM VITAE

Allen Gerard Rodrigo

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		Email: a.rodrigo@nescent.org
Citizenship		New Zealand
Residency		US Permanent Resident
Tertiary Education:	1986	B.Sc. (Hons) in Zoology, University of Canterbury
	1990	Ph.D. in Zoology, University of Canterbury
	2009	Doctor of Science, University of Canterbury
Employment:	2010 – 2014	Director, The US National Evolutionary Synthesis Center
	2010 --	Professor, Department of Biology, Duke University
	2010 – 2013	Adjunct Professor, School of Biological Sciences, University of Auckland
	2008 – 2009	Associate Dean, IT, Faculty of Science, University of Auckland
	2003 – 2009	Director, Bioinformatics Institute (New Zealand), University of Auckland
	2002 – 2010	Professor of Computational Biology and Bioinformatics, School of Biological Sciences, University of Auckland
	1999-2002	Lecturer, later Senior Lecturer, School of Biological Sciences, University of Auckland
	1995-1999	Acting Assistant Professor, later Research Assistant Professor, Department of Microbiology, School of Medicine, University of Washington
	1994	Research Associate, Department of Microbiology and Immunology, Stanford University
	1990-1994	NZ University Grants Committee Post Doctoral Research Fellow
Teaching	2002 – 2006	Programme Coordinator, B.Sc. (Hons) Bioinformatics
		Course Coordinator for:
	2000 – 2006	BIOSCI209 Biometry
	2000 – 2004	BIOSCI732 Ecological Theory and Analysis
	2004 – 2006	BIOSCI743 Advanced Bioinformatics 1
	2004 – 2009	BIOSCI745 Dialogues in Biology

	2012 --	BIOLOGY189 Biological Data Analysis
University appointments	**2010 --**	Duke Biology Department IT Committee
	2009	Vice-Chancellor's representative, University Staffing Committee
	2008 – 2009	Associate Dean, IT, Faculty of Science, University of Auckland
	2008 – 2009	Executive Committee, Centre for e-Research
	2002 – 2009	Director, Bioinformatics Institute
	2005	Member, IT Administrative Function Review Panel
	2003 – 2009	Member, Information Technology Strategy and Policy Committee
	2003	Chair, ITSS Enterprise Expenditure Sub-committee
	2002 – 2006	Programme coordinator, BSc(Hons)Bioinformatics
Distinctions/Honours	**2010 -- 2012**	Associate Editor, *BMC Evolutionary Biology*
	2009	Elected Fellow of the Royal Society of New Zealand
	2009	Doctor of Science, University of Canterbury
	2008 – 2012	Editorial Board, *Mathematical Biosciences*
	2007	Visiting Fellow, Australian National University
	2007	Visiting Fellow, Department of Statistics, University of Oxford
	2007	Visiting Fellow, Isaac Newton Institute for the Mathematical Sciences, Cambridge, UK
	2007 – 2009	Scientific Advisory Board, NetValue Ltd
	2006 – 2007	Invited Professor, Laboratoire d'Informatique, de Robotique, et de Microelectronique de Montpellier, CNRS, France
	2006 – pres	Partner Investigator, Australian Research Council Centre of Research Excellence in Bioinformatics
	2005 – 2007	International Examiner, Bioinformatics Undergraduate Programme, University of Malaya
	2005 – pres	Associate Editor, *Evolutionary Bioinformatics*
	2004 – pres	Scientific Advisory Board, Biomatters Ltd.
	2004	Council Member, International Immunomics Society
	2003 – pres	New Zealand A-ranked Researcher (highest rank in the Performance-Based Research Fund national assessment exercise)
	2003	Universitas21 Travel Fellowship
	2001 – pres.	Associate Investigator, Allan Wilson Centre for Molecular Ecology and Evolution
	2001 – 2004	Founding Editor-in-Chief, *Applied Bioinformatics*
	2000 – 2006	Affiliate Faculty, School of Forestry, University of Montana
	1998	Visiting Fellow, Isaac Newton Institute for the Mathematical Sciences, Cambridge, UK.
	1992-1994	President, Systematics Association of New Zealand
	1990-1994	NZ University Grants Committee Postdoctoral Fellow
	1986-1989	NZ University Grants Committee Doctoral Award
	1986	Canterbury University Prize for Science
Other Information:		***Meetings (organisation)***
	2008	Programme Committee, 2nd Conceptual Modelling in the Life Sciences Workshop, Barcelona
	2008	Programme Committee, 8th Workshop on Algorithms in Bioinformatics, Germany
	2008	Programme Committee, 13th International Conference on Genome Informatics, Brisbane
	2007	Organiser, Dumont D'Urville Workshop on Applied Evolutionary Bioinformatics

2004 - 05	Programme Committee, International Meeting, Life Sciences GRID
2004	Co-convenor, Working Group on Phylogenetics and Rapidly Evolving Pathogens, DIMACS (Centre for Discrete Mathematics and Theoretical Computer Science, Rutgers University) NSF-funded programme on Computational and Mathematical Epidemiology, New Jersey, USA
2004	Co-convenor, International Conference on Bioinformatics
2004	Organising Committee, Asia Pacific Bioinformatics Conference
2003	Convenor, NZ Bioinformatics Roundtable
2002-pres	Executive Committee, International Conference on Bioinformatics
2002, 2005	Organiser, New Zealand Annual Phylogenetics Meeting, Whitianga, NZ
2001	Organising committee, Queenstown Molecular Biology Meeting, Queenstown, NZ.
2001	Organiser, Symposium on HIV Evolutionary Genetics at the HIV Dynamics and Evolution Meeting, Seattle, Washington, USA.
2001	Organiser, University of Auckland Vice Chancellor's Symposium on Bioinformatics and Computational Biology, Auckland, NZ.
1998	Organising committee, Virus Evolution Meeting, Isaac Newton Institute for the Mathematical Sciences, Cambridge, UK.

Reviews
Manuscript reviewer for more than 15 journals including
Philosophical Transactions of the Royal Society
Proceedings of the National Academy of Sciences, USA
Nature Genetics
Bioinformatics
PLoS Computational Biology
BMC Bioinformatics
Genetics
Journal of Virology
Molecular Biology and Evolution
Systematic Biology

Grant reviewer for
National Institutes of Health, USA
National Science Foundation, USA
Wellcome Trust, UK
BBSRC, UK
Health Research Council, NZ

Grants (external)	
2009	Principal Investigator, ISAT Travel Grant
	Statistical metagenomics
2008 – 2011	Principal Investigator, Allan Wilson Centre for Molecular Ecology and Evolution
2007 – 2009	Principal Investigator, REANNZ Grant
	NZ BioGrid
2005 – 2011	Investigator, NZ HRC Grant
	Structure and Function in Failing Hearts
2004 – 2010	Investigator, NZ NERF Grant
	International SCOPE (Screening of Pregnancy Endpoints) Study
2003 – 2006	Co-Principal Investigator, NZ Marsden Grant
	Call me Ishmael, Mr Bayes

2003 – 2006	Associate Investigator, NZ Marsden Grant
	Singing in the trees: genealogies of bird song
2003 – 2008	Objective Leader, Bioinformatics, NZ NERF Grant
	Sequencing the Acidovorax *genome*
2002 – 2008	Associate Investigator, Centre of Research Excellence Grant
	Allan Wilson Centre for Molecular Ecology and Evolution
2002 – 2006	Collaborator, NIH R01 Grant (via subcontract with University of Montana)
	Pathogenesis of Feline Immunodeficiency Virus
2002- 2005	Associate Investigator, NZ Marsden Grant
	Rebuilding ancient genes to study the Last Universal Common Ancestor
2000–2002	Associate Investigator, NZ Marsden Grant
	Are bacteria the same the world over? Establishing the importance of endemic bacteria.
1999-2002	Principal Investigator, NIH RO1 Grant (via subcontract with University of Washington)
	Coalescent methods for measurably evolving populations
1999–2001	Associate Investigator, NSF IGERT Grant
	Development of an astrobiology training program
1996–1998	Principal Investigator, University of Washington's Center for AIDS Research New Investigators' Award
	Intrapatient recombination in HIV-1
1994–1997	Principal Investigator, NZ Public Good Science Fund
	A rapid assay for microbial diversity

	Invited presentations (external; 1998 – present)
2009	*The curse of the possible: why biological educators are failing the public.* BioEd2009, Christchurch.
2009	*The challenge of diversity presents a diversity of challenges: new research directions in computational biology.* Harvard University
2009	*An age of abundance: computational biology in a data-rich environment.* Universiti Kebangsaan Malaysia, Kuala Lumpur.
2008	*Penny's Probably Powerful Phylometer^{TM} and the rise of statistical phylogenetics.* Lecture in honour of David Penny's 70th Birthday. Ruapehu.
2008	*Computational challenges in a metagenomic age.* University of Ballarat, Ballarat.
2008	*The artifactual causes of variation in rate estimation.* Genetics Society of Australia Conference, Adelaide.
2008	*What are we going to do with all these genes?* Royal Society Workshop on Statistical and Computational Challenges in Molecular Phylogenetics and Evolution, London.
2008	*Trees, trees, trees: Big, super, and diverse.* Adelaide Conference on Mathematical Biology.
2007	*Computational Challenges in the Metagenomic Age.* Keynote, Conceptual Modelling in the Life Sciences Workshop, Auckland.
2007	*Statistical phylogenetics.* Lectures at the Bioinformatics Summer School, Australian National University
2007	*Big Trees.* Isaac Newton Institute for the Mathematical Sciences, Cambridge, UK.
2007	*Measurably Evolving Populations.* University of Oxford
2007	*Big Trees.* Univesity of Vienna, Austria.

2007	*Quantifying changes in evolutionary parameters.* University of Grenoble, France.
2007	*Quantifying changes in evolutionary parameters.* Algorithms in Phylogeny Meeting, CNRS, Montpellier, France.
2007	*Measurably Evolving Populations.* University of Aarhus, Denmark.
2007	*Measurably Evolving Populations.* University of Copenhagen, Denmark.
2007	*Measurably Evolving Populations.* Imperial College, London.
2007	*Measurably Evolving Populations.* University of Paris II
2006	*Measurably Evolving Populations.* University of Lyon
2006	*Workshop on Phylogenetic Reconstruction.* Biotechnology Institute, National University of Mexico.
2006	*Statistical Inference and Evolutionary Trees.* Joint Australian and New Zealand Statistics Conference, Auckland.
2006	*The Next Big Thing in Bioinformatics.* NZBio Conference, Auckland
2006	*The Evolutionary Analysis of HIV.* University of Malaya
2006	*Measurably Evolving Populations.* DIMACS meeting, Rutgers University, New Jersey
2005	Allan Wilson Centre Lectures *Tending Darwin's Garden: growing evolutionary trees with genes on*
2005	*Bioinformatics: Innovation in a Data-Rich Environment.* Invited Lecture, NZBio Conference, Auckland.
2005	*Statistical Evolutionary Inference and Rapidly Evolving Pathogens.* Invited Lecture. Institut Henri Poincare Phylogenetics Conference, Paris.
2004	*Measurably Evolving Populations.* Invited Lecture, Australian National University
2004	*The Evolutionary Genetics of HIV.* Annual Invited Lecture. Association for Medical and Bio-Informatics, Singapore
2003	*Microbial genomes: where to next?* Invited participant. Workshop organised by the American Academy of Microbiology, Florida, USA.
2003	*Phylogenies are a Nuisance.* Keynote address. International Conference on Bioinformatics, Penang, Malaysia
2003	*Phylogenetic Inference.* Invited Lecture, Macquarie University, Sydney, Australia.
2002	*Positive selection acts on the HIV-1 population* in vivo *and correlates with disease progression.* HIV Dynamics and Evolution Meeting, Lake Arrowhead, California.
2000	*The analysis of serially sampled populations*. Queenstown Molecular Biology Meeting, Queenstown, NZ.
2000	*Serial sampling of HIV and tests of continued evolution*. HIV Dynamics and Evolution Meeting, Seattle, Washington.
1999	*Classification philosophies.* HIV Nomenclature Working Group, Los Alamos National Laboratories and the Santa Fe Institute.
1999	*Phylogenetic inference.* Society for the Advancement of Native Americans and Chicanos in Science, Portland, Oregon.
1998	*The evolutionary genetics of HIV.* Viral Evolution Meeting, Isaac Newton Institute for the Mathematical Sciences, Cambridge, UK.
1998	*HIV and the coalescent.* HIV Dynamics and Evolution Meeting, Santa Fe, New Mexico.

	• Computational biology and bioinformatics
Research Interests	• Statistical evolutionary genetics
	• Metagenomics
	• Molecular evolution of viruses

PUBLICATIONS (100 total)

(i) **Peer-reviewed papers**

[89]   Wu, S. H., Koelle, K., Rodrigo, A. G. (2012). *Coalescent* entanglement and the conditional dependence of the times-to-common-ancestry of mutually exclusive pairs of individuals*. Journal of Heredity (in press)*

[88]   Wu, S. H., Black, M. A., North, R. A., Rodrigo, A. G. (2012). A Bayesian model for classifying all differentially expressed proteins simultaneously in 2D PAGE gels. *BMC Bioinformatics* **13**:137

[87]   Delaney, N. F., Balenger, S., Bonneaud, C., Marx, C. J., Hill, G. E., Ferguson-Noel, N., Tsai, P., Rodrigo, A., & Edwards, S. V. (2012). Ultrafast evolution and loss of CRISPRs following a host shift in a novel wildlife pathogen, *Mycoplasma gallisepticum. PLoS Genetics* **8**: e1002511

[86]   Schmitt S, Tsai P, Bell J, Fromont J, Ilan M, Lindquist N, Perez T, Rodrigo A, Schupp PJ, Vacelet J, Webster N, Hentschel U, Taylor MW. (2012). Assessing the complex sponge microbiota: core, variable and species-specific bacterial communities in marine sponges. *ISME Journal* **6**:564-76

[85]   Ho SY, Lanfear R, Bromham L, Phillips MJ, Soubrier J, Rodrigo AG, Cooper A. (2011) Time-dependent rates of molecular evolution. *Molecular Ecology* **20**:3087-101.

[84]   Warner BG, Tsai P, Rodrigo AG, 'ofanoa M, Gane EJ, Munn SR, Abbott WG. (2011). Evidence for reduced selection pressure on the hepatitis B virus core gene in hepatitis B e antigen-negative chronic hepatitis B. *Journal of General Virology* **92**:1800-1808.

[83]   Marks, E. J., Rodrigo, A. G., and Brunton, D. H. (2010). Using logistic regression models to predict breeding success in male Adelie penguins (*Pygoscelis adeliae)*. *Polar Biology* **33:**1083–1094.

[82]   Abbott, W. G. H., Tsai, P., Leung, E., Trevarton, A., 'Ofanoa, M., Hornell, J., Gane, E. J., Munn, S.R., and Rodrigo, A. G. (2010) Associations between HLA Class I Alleles and Escape Mutations in the Hepatitis B Virus Core Gene in New Zealand-Resident Tongans. *Journal of Virology* **84**:621-629

[81]   Marks E. J., Rodrigo A. G. and Brunton D. H (2010) Ecstatic Display Calls of the Adelie penguin honestly predict male condition and breeding success. *Behaviour* **147:**165-184.

[80]   Hayward, J. and Rodrigo, A. G. (2010). The distribution of feline immunodeficiency virus in tissue compartments of feral domestic cats. *Archives of Virology* **155**:411-416.

[79]   Hayward, J. H. and Rodrigo, A. G. (2010). Molecular epidemiology of feline immunodeficiency virus in the domestic cat (*Felis catus*). *Veterinary Immunology and Immunopathology* **134**:68-74

[78]   Li, Wai-Lok and Rodrigo, A. G. (2009). Covariation of branch lengths in phylogenies of functionally related genes. PLoS ONE. **4**:e8487

[77]   Wu, S.H., Black, M.A., North, R. A., Atkinson, K.,R. and Rodrigo, A. G. (2009). A statistical model to identify differentially expressed proteins in 2D PAGE gels. *PLoS Computational Biology* **5(9)**: e1000509.

[76]   Rodrigo, A. G., Tsai, P., and Shearman, H. (2009). On the use of bootstrapped topologies in coalescent-based Bayesian MCMC inference: a comparison of estimation and computational efficiencies. *Evolutionary Bioinformatics* **5**:97-105.

[75]   Langhoff, P., Authier, A., Buckley, T. R., Dugdale, J. S., Rodrigo, A., and Newcomb, R.D. (2009). DNA barcoding of the endemic New Zealand leafroller moth genera, *Ctenopseustis* and *Planotortrix. Molecular Ecology Notes* **9**:691-698

[74]   Goode, M., Guindon, S. and Rodrigo, A. G. (2008). Modelling the evolution of protein coding sequences sampled from Measurably Evolving Populations. *Genome Informatics* **21**:150-164

[73]   Bordewich, M., Rodrigo, A. G., Semple, C. (2008). Selecting taxa to save or sequence: desirable criteria and a greedy solution. *Systematic Biology* **57**: 825-834

[72]   Rodrigo, A. G., Bertels, F., Heled, J., Noder, R., Shearman, H., and Tsai, P. (2008). The perils of plenty: what are we going to do with all these genes? *Phil. Trans. Roy. Soc. B* **363**:3893-902

[71]   Hayward, J. J. and Rodrigo, A. G. (2008) Recombination in feline immunodeficiency virus from feral and companion domestic cats. *Virology Journal* **5**:76.

[70]   Steel, M. A. and Rodrigo, A. G. (2008). Maximum likelihood supertrees. *Systematic Biology.* **57**:243-250

[69]   Poss, M., H. A. Ross, A. G. Rodrigo, J. A. Terwee and S. VandeWoude. (2008). The molecular biology and evolution of feline immunodeficiency viruses of cougars. *Veterinary Immunology and Immunopathology* **123**:154-158

[68]   Lim SG, Cheng Y, Guindon S, Seet BL, Lee LY, Hu P, Wasser S, Tan T, Goode M, Rodrigo A. (2007) Viral quasispecies evolution in chronic hepatitis B: new light on an old story. *Gastroenterology* **33**:951-8

[67]   Goode, M. and Rodrigo, A. G. (2007) SQUINT: A multiple alignment program and editor. *Bioinformatics* **23**:1553-1555

[66]   Jess Hayward, John Taylor, Allen Rodrigo (2007) Phylogenetic Analysis of Feline Immunodeficiency Virus in Domestic Cats of New Zealand. *Journal of Virology* **81**:2999-3004

[65]   Mary Poss, Adam Idoine, Howard A Ross, Julie A Terwee, Sue VandeWoude, Allen Rodrigo. (2007). Recombination in feline lentiviral genomes during experimental cross-species infection. *Virology* **359**:146-151

[64]   Gregory Ewing and Allen G. Rodrigo. (2006) Estimating Population Parameters using the Structured Serial Coalescent with Bayesian MCMC Inference when some Demes are Hidden. *Evolutionary Bioinformatics Online* **2**:239-247

[63]   Gregory Ewing and Allen G. Rodrigo. (2006). Coalescent-based estimation of population parameters when the number of demes changes over time. *Molecular Biology and Evolution* **23**:988-996*.*

[62]   Mary Poss, Howard A. Ross, Sally L. Painter, David C. Holley, Julie A. Terwee, Sue Vandewoude, and Allen G. Rodrigo. (2006). Feline lentivirus evolution in cross-species infection reveals high error burdens and selection on key residues in the viral polymerase. *Journal of Virology* **80**:2728-2737

[61]   Stéphane Guindon, Mik Black, and Allen Rodrigo (2006). Control of the false discover rate applied to the detection of positively detected sites. *Molecular Biology and Evolution* **23**:919-926.

[60]   Howard A. Ross, David C. Nickle, Yi Liu, Laura Heath, Mark A. Jensen, Allen G. Rodrigo and James I. Mullins. (2006) Sources of variation in ancestral sequence reconstruction for HIV-1 envelope genes. *Evolutionary Bioinformatics Online* **2**:18-41

[59]   Doria-Rose NA, Learn GH, Rodrigo AG, Nickle DC, Li F, Mahalanabis M, Hensel MT, McLaughlin S, Edmonson PF, Montefiori D, Barnett SW, Haigwood NL, Mullins JI. (2005). Human immunodeficiency virus type 1 subtype B ancestral envelope protein is functional and elicits neutralizing antibodies in rabbits similar to those elicited by a circulating subtype B envelope. *Journal of Virology.* **79**:11214-24.

[58]   Welch, D., Nicholls, G., Rodrigo, A. G., Solomon, W. (2005). Integrating Genealogy and Epidemiology: The Ancestral Infection and Selection Graph as a Model for Reconstructing Host Virus Histories. *Theoretical Population Biology* **68**:65-75*.*

[57]   Meintjes, P. and Rodrigo, A. G. (2005). Evolution of Relative Synonymous Codon Usage in Human Immunodeficiency Virus Type-1. *Journal of Bioinformatics and Computational Biology*.**3**:157-168.

[56]   Olshen, A. B., Cosman, P. C., Rodrigo, A. G., Bickel, P. J., and Olshen, R. A. (2005). Vector quantization of amino acids: analysis of the HIV V3 loop region. *Journal of Statistical Planning and Inference*.**130**:277-298

[55]   James I Mullins, David C Nickle, Laura Heath, Allen G Rodrigo, and Gerald H Learn. (2004) Immunogen sequence: the fourth tier of AIDS vaccine design. *Expert Review of Vaccines.Suppl* **1**:159-162

[54]   Ewing, G., Nicholls, G. and Rodrigo, A. (2004). Using temporally spaced sequences to simultaneously estimate migration rates, mutation rate and population sizes in measurably evolving populations (MEPs). *Genetics.***168**:2407-2420

[53]   Shriner, D., Rodrigo, A. G, Nickle, D. C., and Mullins, J. I. (2004). Pervasive Genomic Recombination of HIV-1 *In Vivo. Genetics* **167**:1573-1587

[52]   Guindon, S., Rodrigo, A. G., Dyer, K., Huelsenbeck, J. P. (2004) Modeling the site-specific variation of selection patterns along lineages. *Proceedings of the National Academy of Sciences, USA.***101:**12957-12962

[51]   Rodrigo, A. G., M. Goode, R. Forsberg, H. Ross, & A. Drummond. (2003) Inferring Evolutionary Rates Using Serially Sampled Sequences from Several Populations. *Molecular Biology and Evolution* **20**:2010-2018*.*

[50]   Drummond, A.J., O.G. Pybus, A. Rambaut, R. Forsberg & A.G. Rodrigo. 2003. Measurably evolving populations. *Trends in Ecology and Evolution* **18**:481-488.

[49]   Roman Biek, Allen G. Rodrigo, David Holley, Alexei Drummond, Charles R. Anderson, Jr. Howard A. Ross, and Mary Poss (2003). Epidemiology, Genetic Diversity, and Evolution of Endemic Feline Immunodeficiency Virus in a Population of Wild Cougars. *Journal of Virology* 77:9578-9589

[48]   Jon P. Anderson, Gerald H. Learn , Allen G. Rodrigo, Xi He, Yang Wang, Hillard Weinstock, Marcia L. Kalish, Kenneth E. Robbins, Leroy Hood, and James I. Mullins. (2003). Predicting demographic group structures based on DNA sequence data. *Molecular Biology and Evolution* **20***:1168-1180*.

[47]   H. A. Ross, G. M. Lento, M. L. Dalebout, M. Goode, P. McLaren, G. Ewing, A. G. Rodrigo, S. Lavery, and C. S. Baker (2003).DNA Surveillance: Web-based molecular identification of whales, dolphins and porpoises*. Journal of Heredity* **94***:111-114*

[46]   David C. Nickle, Mark A. Jensen, Geoffrey S. Gottlieb, Daniel Shriner, Gerald H. Learn, Allen G. Rodrigo, James I. Mullins. (2003). Consensus and ancestral state HIV vaccines. *Science*.**299**:1515-1517

[45]   Ross, H. A., and Rodrigo, A. G. (2002). Immune-mediated positive selection drives Human Immunodeficiency Virus Type 1 molecular variation and predicts disease duration. *Journal of Virology* **76**: 11715-11720.

[44]   Liu, S.-L., Mittler, J. E., Nickle, D. C., Mulvania, T. M., Shriner, D., Rodrigo, A G., Kosloff, B., He, X., Corey, L.and Mullins, J. I. (2002). Selection for Human Immunodeficiency Virus Type 1 recombinants in a patient with rapid progression to AIDS. *Journal of Virology* **76**: 10674-10684

[43]   Drummond, A., Nicholls, G.K., Rodrigo A.G. and Solomon.W. (2002) Estimating mutation parameters, population history and genealogy simultaneously from temporally spaced sequence data. *Genetics* **161**:1307-1320

[42]   Turner, S. J., Saul, D. J., Rodrigo, A. G., and Lewis, G. D. (2002). A heteroduplex method for detection of targeted sub-populations of bacterial communities. *FEMS Microbiology Letters* **208**:9-13

[41]   Drummond, A., Forsberg, R., and Rodrigo, A.G. (2001). Estimating stepwise changes in substitution rates using serial samples*. Molecular Biology and Evolution* **18**:1365-1371.

[40]   Anderson, J.P., Rodrigo, A.G,, Learn, G.H., Wang, Y., Weinstock, H., Kalish, M., Robbins, K.E., Hood, L., and Mullins, J.I. (2001). Substitution Model of Sequence Evolution for the Human Immunodeficiency Virus Type I Subtype B gp120 Gene over the C2-V5 Region*. Journal of Molecular Evolution* **53**:55-62

[39]   Rouzine, I.M., Rodrigo, A., and Coffin, J.M. (2001). Transition between Stochastic Evolution and Deterministic Evolution in the Presence of Selection: General Theory and Application to Virology. *Microbiol. Mol. Biol. Rev*. **65**(1):151-185.

[38]   Goldman, N., Anderson, J.P., and Rodrigo, A.G. (2000) Likelihood-Based Tests of Topologies in Phylogenetics. *Systematic Biology* **49**:652-670.

[37]   Anderson, J.P., Rodrigo, A.G., Learn G.H., Madan, A., Delahunty, C., Coon, M., Girard, M., Osmanov, S., Hood, L., and Mullins, J.I. (2000). Testing the Hypothesis of a Recombinant Origin of Human Immunodeficiency Virus Type I Subtype E. *Journal of Virology* **74**:10752-10765.

[36]   Kliks, S., Contag, C.H., Corliss, H., Learn, G., Rodrigo, A., Wara, D., Mullins, J.I., and Levy J.A. (2000). Genetic analysis of viral variants selected in transmission of human immunodeficiency viruses to newborns. *AIDS Research and Human Retroviruses* **16**:1223-1233.

[35]   Drummond, A. and Rodrigo, A.G. (2000). Reconstructing genealogies of serial samples under the assumption of a molecular clock using serial-sample UPGMA (sUPGMA). *Molecular Biology and Evolution* **17**:1807-1815.

[34]   Shankarappa, R., Margolick, R. B., Gange, S. J., Rodrigo, A. G., Upchurch, D., Farzadegan, H., Gupta, P., Rinaldo, C. R., Learn, G. H., He, X., Huang, X.-L., and Mullins, J. I. (1999) Consistent viral evolutionary changes associated with progression of HIV-1 infection. *Journal of Virology* **73**:10489-10502.

[33]   Rodrigo, A. G. (1999) HIV evolutionary genetics [Commentary]. *Proceedings of the National Academy of Sciences, USA* **96:** 10559-10561

[32]   Melvin, A. J., A. G. Rodrigo, K. M. Mohan, P. A. Lewis, L. Manns-Arcuino, R. W. Coombs, J. I. Mullins, and L. M. Frenkel. (1999). HIV-1 dynamics in children. *J. Acquir. Immune Defic. Syndr. Hum. Retrovirol*. **20**: 468-473

[31]   Dodd-Wilson, S. L., Crowhurst, R. N., Rodrigo, A. G., Samuels, G. J., Hill, R. A. and Stewart, A. (1999). Examination of *Trichoderma* phylogenies derived from ribosomal DNA sequence data. *Mycological Research.*

[30]   Rodrigo, A. G., Shpaer, E. G., Delwart, E. L., Iversen, A. K. N., Gallo, M. V., Jxrgen Brojatsch, J., Hirsch, M. S., Walker, B. D., and Mullins, J. I. (1999). Coalescent estimates of HIV-1 generation time in vivo. *Proceedings of the National Academy of Science, USA.* **96**:2187-2191

[29]   Rodrigo, A.G. (1998). Combinability of phylogenies and bootstrap confidence envelopes. *Systematic Biology* **47:**727-733.

[28]   Poss, M., Rodrigo, A. G., Gosink, J. J., Learn, G. H., Panteleeff, D. D., Martin, Jr., H. L., Bwayo, J., Kreiss, J. K., and Overbaugh, J. (1998). Evolution of Envelope Sequences from the Genital Tract and Peripheral Blood of Women Infected with Clade A Human Immunodeficiency Virus Type 1. *Journal of Virology* **72:**8240-8251.

[27]   B. Shankarappa, P. Gupta, G. H. Learn Jr., A. G. Rodrigo, C. R. Rinaldo Jr., M. C. Gorry, J. I. Mullins, P. L. Nara, and G. D. Ehrlich. (1998). Evolution of Human Immunodeficiency Virus Type 1 envelope sequences in infected individuals with differing disease progression profiles. *Virology* **241:**251-259.

[26]   Rodrigo, A. G. (1997). Dynamics of non-syncytium-inducing and syncytium-inducing Type 1 Human Immunodeficiency Viruses during primary infection. *AIDS Research and Human Retroviruses* **17**:1447-1451

[25]   Bachmann, M. H., C. Matthieson-Dubard, G. H. Learn, A. G. Rodrigo, D. L. Sodora, E. A. Hoover, and J. I. Mullins. (1997). Genetic diversity of Feline Immunodeficiency Virus: Dual infection, recombination and distinct evolutionary rates between envelope gene subtypes. *Journal of Virology* **71**:4241-4253.

[24]   Rodrigo, A. G., Goracke, P. C., Rowhanian, K., and Mullins, J. I. (1997). Quantitation of target molecules from PCR-based limiting dilution assays. *AIDS Research and Human Retroviruses* **13:**737-742.

[23]   Ardern, S. L., Lambert, D. M., Rodrigo, A. G., and McLean, I. G. (1997). The effects of bottleneck events on minisatellite DNA variation in robins. *Journal of Heredity* **88:**179-186

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