

Marco Salemi, Ph.D.

Citizenship: USA, Italy

Primary Languages: Italian, English

Other Languages: Spanish (Intermediate), Portuguese (Intermediate), French (Beginner), Dutch (Beginner).

CURRENT AFFILIATION

University of Florida College of Medicine (UF-COM), Department of Pathology, Immunology and Laboratory Medicine, Emerging Pathogens Institute, P.O. Box 100009, 2055 Mowry Rd, Gainesville, FL 32610-3633, Phone/fax +1 352 273 9567/8284.

DEGREES

- Ph.D. in Science. 1999. Catholic University, Leuven, Belgium.
- Post-graduate school in Biotechnology Application. 1995. University of Milan, Italy.
- B.Sc./Master with full marks in Chemistry, 1991. University of Pavia, Italy.

SCIENTIFIC APPOINTMENTS

- 2019-current. Holloway and McClamma Endowed Chair in Chronic and Infectious Diseases. Department of Pathology Immunology and Laboratory Medicine. University of Florida, Gainesville, FL, USA
- 2017-current. Full Professor with Tenure. Department of Pathology Immunology and Laboratory Medicine. University of Florida, Gainesville, FL, USA
- 2015-2017. Associate Professor with Tenure. Department of Pathology Immunology and Laboratory Medicine. University of Florida, Gainesville, FL, USA.
- 2013-2014. Associate Professor. Department of Pathology Immunology and Laboratory Medicine. University of Florida, Gainesville, FL, USA.
- 2010-2012. Assistant Professor. Department of Pathology Immunology and Laboratory Medicine. University of Florida, Gainesville, FL, USA.
- 2004-2009. Research Assistant Professor. Department of Pathology, University of Florida (UF), Gainesville, Florida, U.S.A.
- 2002-2004. Postdoctoral Researcher. Laboratory of Prof. Walter Fitch, University of California Irvine (UCI), Irvine, California, U.S.A.
- 1999-2002, Postdoctoral scientist. Laboratory of Prof. Anne-Mieke Vandamme, Rega Institute, Catholic University of Leuven, Belgium.
- 1996-1999. Mary Curie Fellow. Laboratory of Prof. Anne-Mieke Vandamme, Rega Institute, Catholic University of Leuven, Belgium.
- 1991-1996. Postgraduate fellow. Laboratory of Prof. Umberto Bertazzoni, "Istituto di Genetica Biochimica ed Evoluzionistica" (Institute of Genetics, Biochemistry and Evolution) of CNR (National Research Center), Pavia, Italy.

RESEARCH INTERESTS

As a Marie-Curie Fellow at the Rega Institute (Leuven, Belgium), and post-doctoral scientist with Walter M. Fitch at the University of California, Irvine (USA), I have been trained in the field of molecular evolution of viruses and phylogenetic analysis. During the last twenty years, as faculty at the University of Florida, Gainesville, my research interests have included molecular epidemiology, intra-host viral evolution, and the application of phylogenetic and population genetic methods to the study of human and simian pathogenic viruses (in particular HIV/SIV, HCV,

HTLV, arboviruses, and SARS-CoVs). I have also been applying the Bayesian coalescent framework to study molecular evolution and phylogeography of emergent and re-emergent bacterial pathogens, such as *MRSA*, *Shigella*, and *Vibrio cholerae*, using genome-wide SNPs. In addition, my laboratory has developed *ad hoc* protocols for the generation of high-throughput sequence data (including DNA sequencing, transcriptomics, and miRNA expression profiles) and droplet digital PCR quantitative analyses of viral and bacterial pathogens, as well as several automated bioinformatic and machine learning (artificial intelligence) pipelines for large sequence data sets (big data) analysis.

HONORS & AWARDS

- 2020. University of Florida Exemplary Teacher Award.
- 2019. McClamma Endowed Chair in Pediatric Research.
- 2019. Holloway Endowed Chair for Chronic and Infectious Diseases Research.
- 2017. UF Term Professorships award.
- 2012. University of Florida Excellence Awards for Assistant Professors.
- 2008. *Honor Aedificanti* Award for his efforts in AIDS research, Kiwanis International Association, Caltanissetta, Italy, December 5th, 2008.
- 2004. Distinguished International Educator of the Year Award, University of Florida, Gainesville, U.S.A.
- 2002. Award from the Catholic University of Leuven for the best PhD dissertation in science.
- 2001. Award for best scientific paper originated in Ireland: **M. Salemi, et al.** Dating the common ancestor of SIVcpz and HIV-1 group M and the origin of HIV-1 subtypes using a new method to uncover clock-like molecular evolution. *The FASEB J.* **15**:267-268, 2000.
- 1996. Awarded with Marie Curie Fellowship, European Union, for the project "Molecular investigation on the origin and genetic stability of Human T-lymphotropic viruses".

EDITORIAL REVIEWER

Nature, *Nature Medicine*, *Nature Microbiology*, *Nature Communications*, *Science*, *Science Translational Medicine*, *P.N.A.S.*, *PLoS Pathogens*, *PLoS Computational Biology*, *Bioinformatics*, *Molecular Biology and Evolution*, *Journal of Virology*, *Journal of Molecular Evolution*, *Emerging Infectious Diseases*, *Retrovirology*, *Journal of Infectious Diseases*.

EDITORIAL APPOINTMENTS

Associate Editor of *PLoS ONE*; Editorial Board of *Retrovirology*; Editorial Board of *Scientific Reports*.

SELECTED INVITED TALKS

- Oct 2022 Modeling and forecasting virus evolution and pathogenesis in the XXI century: from genomic epidemiology to single cell sequencing. The Paul J. Galkin Memorial Lectureship Series. Invited Lecture. Brown Medicine, Providence, RI, USA.
- Feb 2022 Phylogenomic tracking of SARS-CoV-2 variants and emerging coronavirus zoonoses. Emerging Pathogens Institute Research Day. Keynote Lecture. Virtual.
- Nov 2020 SARS-CoV-2 transmission dynamics and challenges of vaccine development and scale up. Italian Biologists Association Annual Meeting. Keynote Speaker. Virtual.
- Jun 2020 SARS-CoV-2 origin and molecular epidemiology: what we know so far. SHARC seminar. Invited Lecture. University of Florida, Gainesville, FL, USA.
- Mar 2019 Multiscale phylodynamics of viral and bacterial pathogens: from pandemic spread to intra-host evolution. Invited Lecture. University of Tulane, New Orleans, LA, USA.
- Oct 2018 The SIV macaque model of neuroAIDS: phylodynamics and pathogenesis. Invited Lecture. Tulane National Research Primate Center, Covington, LA, USA.

- May 2017 Viral phylodynamics of emerging epidemics in the Caribbean area. Invited Seminar. Centers for Disease Control and Prevention (CDC), Atlanta, GA, USA.
- July 2016 SIV phylodynamic and pathogenesis in the macaque model of neuroAIDS. Invited Seminar. University of Hawaii, Honolulu, HI, USA.
- Apr 2016 SIV phyloanatomy in the macaque model of neuroAIDS: a new framework to study the interplay between viral evolution and pathogenesis. Invited Lecture. CFAR Seminar Series, University of Miami, FL, USA.
- Mar 2016 Phylodynamics and phylogeography of infectious diseases. Invited Speaker. Academician Nicolae Cajal Symposium of the Romanian Academy of Medical Sciences, Bucharest, Romania.
- Sep 2015 Phylodynamic analysis of viral and bacterial pathogens in the genomics era. Invited Speaker. 10th International Conference on Information Processing in Cells and Tissues. San Diego, CA, USA.
- Aug 2015 SIV intra-host population dynamics in peripheral blood and tissues. Invited Seminar. University of Miami CFAR Web-seminars, Miami, FL, USA.
- Jul 2015 Towards a genomic epidemiology of microbial pathogens. Invited Seminar. University Hospitals – Campus Bio-Medico, Rome, Italy.
- Mar 2015 Genomic epidemiology of bacterial pathogens: from cutting-edge research to clinical practice. Invited Seminar. University Hospitals – Campus Bio-Medico, Rome, Italy.
- Feb 2015 The phylodynamics and phylogeography of infectious diseases. Invited Seminar. Boston College, Boston, MA, USA.
- Nov 2014 Phylodynamics of Clinical and Environmental Toxigenic *Vibrio cholerae* O1 in Haiti. Invited Seminar. Sanger Institute, Cambridge, UK.
- Oct 2014 Intra-host evolution and pathogenesis of human and simian immunodeficiency viruses. Invited Seminar. University of Missouri Kansas City (UMKC), Oct 23, 2014.
- May 2014 HIV-1 Evolutionary Dynamics in HLA-B*5701 Subjects with Different Risk of Disease Progression. Invited Speaker. 21st Annual HIV Dynamics & Evolution Conference, Tucson, AZ, USA.
- April 2014 Intra-host phylodynamics and phylogeography in the SIV macaque model of neuroAIDS. Invited Speaker. Center for Disease Control and Prevention, Atlanta, GA, USA.
- Nov 2013 Intra-host Bayesian Phylogeography Infers Tempo and Mode of Neuropathogenesis in SIVmac251 Infected CD8-lymphocyte Depleted Rhesus Macaques. Invited Speaker. 31st Annual Symposium on Nonhuman Primate Models for AIDS. Atlanta, GA, USA.
- Oct 2013 Intra-host phylogeography of SIV brain invasion in the rhesus macaque model of NeuroAIDS. Invited Speaker. HIV/SIV phylodynamics and neuroAIDS Discussion. Italian Institute of Health, Rome, Italy.
- April 2013 Phylodynamic analysis of brain infection in the SIV infected macaque model of NeuroAIDS. Invited Speaker. 19th Society for NeuroImmunopharmacology (SNIP) Conference. San Juan, Puerto Rico.
- Mar 2012 Themed discussion on “Molecular epidemiology: primate viruses and how they affect humans”. Discussant and Chairman. 19th Conference on Retroviruses and Opportunistic Infections (CROI). Seattle, WA, USA.
- Nov 2011 Phylogeography of human infectious diseases. Keynote Speaker. 12th Annual Symposium on Antiviral Drug Resistance: Targets & Mechanisms. Hershey, PA, USA.
- June 2011 HIV/SIV intra-host phylodynamics and neuropathogenesis. Invited Lecturer. Henry M. Jackson Foundation, Rockville, MD, USA.
- June 2011 Retrovirus evolution and molecular anthropology HTLV and Related Viruses. Invited Speaker. Tenth International Conference on Human Retrovirology. Trinity College, Dublin, Ireland.
- May 2010 HIV-1 Molecular Epidemiology and Pathogenesis: A Phylodynamic Approach. Invited Speaker. Aaron Diamond AIDS Research Center. New York, NY, USA.
- April 2010 Phylogenetic challenges in the retroviridae branch of the tree of life. Keynote Speaker. 1st Symposium on Reconstructing the Tree of Life: Computational Challenges and Solutions. Gainesville, FL, USA.
- Oct 2009 Investigating HIV-1 epidemic emergence in Africa by Landscape Phylodynamics: a framework integrating geospatial, anthropological and phylogenetic data. Invited Speaker. International USA-Russia Symposium on HIV prevention science. Moscow, Russia.

NATIONAL AND INTERNATIONAL TEACHING EXPERIENCE

- 1997-2022. Co-organizer and Instructor at the Annual Workshop on *Virus Evolution and Molecular Epidemiology* (<http://regaweb.med.kuleuven.be/workshop>), Katholieke Universiteit Leuven, Belgium, 1997-2002; Stanford University, CA, USA, 2003; The Finnish National Public Health Institute, Helsinki, Finland, 2004; Institute of Health, Lisbon, Portugal, 2007; South African National Bioinformatics Institute, Cape Town, South Africa, 2008; Erasmus Medical Center, Rotterdam, The Netherlands, 2009; Johns Hopkins University, Baltimore, MD, USA, 2010; University of Belgrade, Serbia, 2012; University of Florida Gainesville, FL, USA, 2013; National Institute for Infectious Diseases "L. Spallanzani", Rome, Italy, 2014; University of the West Indies, Trinidad and Tobago, 2015; Pan American Health Organization, Panama City, Panama, 2022).
- 2015-2017. Co-organizer and Instructor at the *3rd (2015) and 4th (2017) International Workshops "Bioinformatics for NextGen sequence analysis and phylodynamics of infectious diseases"*, Hospital Nacional de Pediatría "Juan P. Garrahan", Buenos Aires, Argentina.
- 2013-2017. Spring semester – 3 credits course – *Introduction to phylodynamics: a practical approach to molecular phylogenetics of pathogens*. University of Florida, Gainesville.
- 2012. Spring semester – 2 credits course – *Introduction to phylodynamics: a practical approach to molecular phylogenetics of pathogens*. University of Florida, Gainesville.
- 2010. Fall semester – 1 credit course – *Molecular evolution and phylogenetics journal club*. University of Florida, Gainesville.
- 2011. Instructor at the *Bioinformatics for Phylogenetic Reconstruction in Virology training course*, Hospital Nacional de Pediatría "Juan P. Garrahan", Buenos Aires, Argentina.
- 2002-2010. Instructor and co-Organizer of the *Yearly Italian Workshop on Virus Evolution and Molecular Epidemiology*, Istituto Superiore di Sanità (Italian Institute of Health), Roma, Italy.
- 2007. Instructor and Lecturer at the *Brazilian Workshop on Virus evolution and Data mining*, University of Fiocruz, Salvador de Bahia, Brazil.
- 2005. Instructor at the *Taiwan Workshop of Molecular Evolution*, Taipei, Taiwan.
- 2004. Instructor at the *Second Brazilian Workshop on Virus Evolution and Molecular Epidemiology*, Salvador de Bahia, Brazil.
- 2003. Instructor at the *South African Workshop on Viral Molecular evolution* at the Nelson Mandela School Medicine, Durban, South Africa.
- 2002. Instructor at the *First Brazilian Workshop on Virus Evolution and Molecular Epidemiology*, Salvador de Bahia, Brazil.

TEACHING/MENTORING

Junior faculty mentorship

- Dr. **Mattia Prosperi** [Tenure track advisor], currently Tenured Professor at UF Department of Epidemiology
- Dr. **Philip Chan** [Co-mentor, K-award, 2011-2015], currently Associate Professor at Brown University Department of Medicine
- Dr. **Taj Azarian** [PhD mentor and junior faculty advisor], currently Assistant Professor at University of Central Florida Burnett School of Biomedical Sciences
- Dr. **Marie Nancy Seraphin** [Mentor, K-award], Assistant Professor at UF Department of Medicine
- Dr. **Simone Marini**, Assistant Professor in Dr. Salemi's and Dr. Prosperi's labs at UF Emerging Pathogens Institute
- Dr. **Carla Mavian**, Assistant Scientist in Dr. Salemi's lab at UF Emerging Pathogens Institute
- Dr. **Britany Rife Magalis**, Assistant Scientist in Dr. Salemi's lab at UF Emerging Pathogens Institute
- Dr. **Massimo Tagliamonte**, Assistant Scientist in Dr. Salemi's lab at UF Emerging Pathogens Institute

PhD students

- Juan Perez [Supervisor]
- Andrea Ramirez [Supervisor]
- MacLean Basset [Supervisor]
- Yaser Alasahafi [co-Supervisor], graduated in Dec 2018
- Brittany Rife, IDP Medical Sciences [Supervisor], graduated in Fall 2017
- Taj Hassan Azarian, Epidemiology [Co-Supervisor], graduated in spring 2015
- Samantha Strickland, IDP Medical Sciences [Supervisor], graduated in fall 2013
- Cameron Browne, Applied Mathematics [Co-supervisor], graduated in spring 2013

Master students

- Lauren Droske [Supervisor], graduated Summer 2022
- Maria Menes [co-Supervisor], graduated Spring 2022
- Taylor Paisie [Supervisor], graduated Fall 2021

REVIEWING PANEL AND COMMITTEE APPOINTMENTS

- Standing Member of N.I.H. Public Health Approaches to HIV/AIDS (PPAH) study section. Bethesda, 2020 – current.
- Member of the N.I.H SARS-CoV-2 Serological Sciences Research Projects (U01) study section. August 17-18, 2020.
- Member of the N.I.H Emergency Awards: Rapid Investigation of Severe Acute Respiratory Syndrome Coronavirus 2 study section. January 21-22, 2021.
- Member of the N.I.H. Special Emphasis Panel — Centers for AIDS Research (CFAR). Bethesda, MD, USA, December 16 – 17, 2019.
- Member of the N.I.H Population and Public Health Approaches to HIV/AIDS Study Section, November 14-15, 2019.
- Member of the N.I.H. AIDS Research Review Charter Committee Study Section, August 14-15, 2019.
- Member of the N.I.H. ZRG1 AARR-Q (50) Study Section, June 12, 2019.
- Member of the N.I.H. ACE Study Section, December 5, 2018.
- Member of the N.I.H. ACE Study Section, July 31, 2018.
- Member of the N.I.H. ACE Study Section, March 22, 2019.
- Member of the N.I.H. ACE Study Section, March 13 – 14, 2018.
- Member of the N.I.H. HIV/AIDS Vaccine study section (VACC), November 7, 2017.
- Member of the N.I.H. Study Section for PAR-17-048 – Phylogenetic tracking of HIV transmission, June 22, 2017.
- Member of the N.I.H. Study Section for PAR-14-041 – Centers for AIDS Research and Developmental Centers for AIDS Research (P30), December 12 – 13, 2016.
- Member of the N.I.H. study section for AARRH52 Planning Grant for Global Infectious Disease Research Training Program. Bethesda, MD, USA, December 11, 2015.
- Member of the N.I.H. Special Emphasis Panel for ZAI1-UKS-A-J1 — Centers for AIDS Research (CFAR). Bethesda, MD, USA, October 26 – 27, 2015.
- Member of the N.I.H. Special Emphasis Panel for AARR M 50, RFA-AI-14-057 — U.S.-China Program for Research Toward a Cure for HIV/AIDS. Bethesda, MD, USA, March 24, 2015.
- Member of the N.I.H. Special Emphasis Panel — Centers for AIDS Research (CFAR). Bethesda, MD, USA, November 17 – 19, 2014.
- Member of the N.I.H. Special Emphasis Panel/Scientific Review Group 2014/01 ZRG1 AARR-E02 —HIV/AIDS. Bethesda, MD, USA, April 9 – 10, 2014.
- Member of the N.I.H. Special Emphasis Panel/Scientific Review Group 2014/01 ZRG1 AARR-E (03) M) —HIV/AIDS. Bethesda, MD, USA, December 18 – 19, 2013.

- Member of the N.I.H. *Study Section for ZRG1 AARR-D(50) — Eradication of HIV-1 from CNS reservoirs: implication for therapeutics (RFA)*. Bethesda, MD, USA, November 15, 2013.
- Member of the N.I.H. *Special Emphasis for PAR 11-108 — Centers for AIDS Research (CFAR)*. Bethesda, MD, USA, September 21 – 23, 2011.
- Member of the N.I.H. *Study Section for RFA-AI-10-009 — Martin Delaney Collaboratory: Towards an HIV-1 Cure (U19)*. Bethesda, MD, USA, April 4 – 6, 2011.
- Member of the *Natural History and Epidemiology Planning Group*, U.S. Department of Health and Human Services, NIH, Office of AIDS Research, 2011 – 2016.
- Member of the *UFII Seed Grants Committee*, University of Florida Gainesville, 2015.
- Member of the *Computational Biology Seed Grants Committee*, University of Florida Gainesville, 2009.

ADMINISTRATION AND SERVICE

- Fund Administrator of the Stephany W. Holloway University Chair (\$4M endowed research “super chair”) in Infectious and Chronic Disease Research since 2019.
- Member of UFII Steering Committee since 2015.
- Member of UF ICBR-Genomic Cores Advisory Board since 2015.
- Member of the *Computational Biology Advisory Committee*, University of Florida Gainesville, 2010 – 2013.

PUBLICATIONS

Google Scholar (10/18/2022)

Citations: 11,347

h-index: 52

i10-index: 162

Chief Editor and contributor of two major textbooks in the field of molecular evolution and phylogenetic analysis:

1. **M. Salemi** and A-M. Vandamme (eds.) *The Phylogenetic Handbook: A Practical Approach to DNA and protein phylogeny*. Cambridge University Press, New York, NY, USA, 2003.
2. P. Lemey, **M. Salemi**, A-M Vandamme (eds.) *The Phylogenetic Handbook: A Practical Approach to phylogenetic analysis and hypothesis testing*. Cambridge University Press, New York, NY, USA, 2009.

Additional contribution to book chapters:

3. B. Rife Magalis, **M. Salemi**. Chapter 4: *Molecular epidemiology of foodborne diseases*, pp 47-62. Foodborne Infections and Intoxications. Elsevier, USA, 2021.
4. **M. Salemi**. Bioinformatics. *Telemedicine Glossary 3rd edition*, pp. 33-34. European Commission Directorate General, Brussels, 2001.

Peer-reviewed papers:

High profile papers

1. S. N. Rich, M. C. F. Prosperi, S. Dellicour, B. Vrancken, R. L. Cook, E. C. Spencer, **M. Salemi***, C. Mavian. Molecular Epidemiology of HIV-1 Subtype B Infection across Florida Reveals Few Large Superclusters with Metropolitan Origin. *Microbiology Spectrum*: in press. * Corresponding author.
2. C. Hendricks, M. Cash, M. Tagliamonte, A. Riva, C. Brander, A. Llano, **M. Salemi**, M. Stevenson, C. Mavian. Discordance between HIV-1 population in plasma at rebound after structured treatment interruption and archived provirus population in peripheral blood mononuclear cells. *Microbiology Spectrum* **10**(4), e0135322, 2022. doi: 10.1128
3. M. Bassett, **M. Salemi**, B. Rife Magalis. Lessons learned and yet-to-be learned on the importance of RNA structure in SARS-CoV-2 replication. *Microbiology and Molecular Biology Reviews* **86**(3), e0005721, 2022. doi: 10.1128/mmbr.00057-21

4. B. Rife Magalis, S. Rich, M. S. Tagliamonte, C. Mavian, M. N. Cash, A. Riva, S. Marini, D. Moraga Amador, Y. Zhang, J. Shapiro A. Horine, P. Starostik, M. Pieretti, S. Vega, A. P. Lacombe, J. Salinas, M. Stevenson, P. Myers, J. G. Morris, Jr., M. Lauzardo, M. Prosperi, **M. Salemi**. SARS-CoV-2 Delta vaccine breakthrough transmissibility in Alachua County, Florida. *Clinical Infectious Diseases* ciac197, 2022. doi: 10.1093/cid/ciac197
5. L. T. Nguyena, N. C. Macaluso, B. L. M. Pizzano, M. N. Cash, J. Space, J. Karasek, M. R. Millerd, J. A. Lednicky, R. R. Dinglasan, **M. Salemi**, P. K. Jain. A thermostable Cas12b from *Brevibacillus* leverages one-pot discrimination of SARS-CoV-2 variants of concern. *EBioMedicine* 77, 103926, 2022.
6. J. A. Lednicky, M. S. Tagliamonte, S. K. White, M. A. Elbadry, M. M. Alam, C. J. Stephenson, T. S. Bonny, J. C. Loeb, T. Telisma, S. Chavannes, D. A. Ostrov, C. Mavian, V. Madsen Beau De Rochars, **M. Salemi***, J. G. Morris Jr. Independent infections of porcine delta-coronavirus among Haitian children. *Nature* 600 (7887), 133–137, 2021. * Corresponding author
7. B. Rife Magalis, P. Autissier, K. C. Williams, X. Chen, C. Browne, **M. Salemi**. Predator-Prey Dynamics of Intra-Host Simian Immunodeficiency Virus evolution within the untreated host. *Frontiers Immunology* 12, 709962, 2021. doi: 10.3390/v13112193
8. M. S. Tagliamonte, C. Mavian, K. Zainabadi, M. N. Cash, J. A. Lednicky, B. Rife Magalis, A. Riva, M. M. Deschamps, B. Liautaud, V. Rouzier, D. W Fitzgerald, J. W. Pape, J. G. Morris Jr, **M. Salemi**. Rapid emergence and spread of SARS-CoV-2 gamma (P.1) variant in Haiti. *Clinical Infectious Disease* ciab736, 2021. doi: 10.1093/cid/ciab736
9. J. A. Lednicky, M. A. Tagliamonte, S. K. White, G. M. Blohm, M. M. Alam, N. M. Iovine, **M. Salemi**, C. Mavian, J. G. Morris Jr. Isolation of a Novel Recombinant Canine Coronavirus from a Visitor to Haiti: Further Evidence of Transmission of Coronaviruses of Zoonotic Origin to Humans. *Clinical Infectious Diseases* ciab924, 2021. doi: 10.1093/cid/ciab924
10. C. Mavian, S. Kosakovsky Pond, S. Marini, B. Rife Magalis, A-M. Vandamme, S. Dellicour, S. V. Scarpino, C. Houldcroft, J. Villabona-Arenas, T. K. Paisie, N. S. Trovão, C. Boucher, Y. Zhang, R. H. Scheuermann, O. Gascuel, T. T-Y. Lam, M. A. Suchard, A. Abecasis, E. Wilkinson, T. de Oliveira, A. I. Bento, H. A. Schmidt, D. Martin, J. Hadfield, N. Faria, N. D. Grubaugh, R. A. Neher, G. Baele, P. Lemey, T. Stadler, J. Albert, K. A. Crandall, T. Leitner, A. Stamatakis, M. Prosperi, **M. Salemi**. Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. *Proceedings of the National Academy of Sciences USA* 117(23), 12522–12523, 2020.
11. V. M. Andrade, C. Mavian, D. Babic, T. Cordeiro, M. Sharkey, L. Barrios, C. Brander, J. MartinezPicado, J. Dalmau, A. Llano, J. Li, J. Jacobson, M. S. Seaman, C. L. Lavine, **M. Salemi**, M. Stevenson. A minor population of macrophage-tropic HIV-1 variants is identified in recrudescing viremia following analytic treatment interruption. *Proceedings of the National Academy of Sciences USA* 117(18), 9981-9990, 2020.
12. C. Mavian, T. K. Paisie, M. T. Alam, C. Browne, V. Madsen Beau De Rochars, S. Nembrini, M. N. Cash, E. J. Nelson, T. Azarian, A. Ali, J. G. Morris Jr, **M. Salemi**. Toxigenic *Vibrio cholerae* evolution and establishment of reservoirs in aquatic ecosystems. *Proceedings of the National Academy of Sciences USA* 117(14), 7897-7904, 2020.
13. S. C. Keane, X. Heng, K. Lu, S. Kharytonchyk, V. Ramakrishnan, G. Carter, S. Barton, A. Hosic, A. Florwick, J. Santos, N. Bolden, S. McCowin, D. A. Case, B. Johnson, **M. Salemi**, A. Telesnitsky, M. F. Summers. Structure of the HIV-1 RNA packaging signal. *Science* 348(6237), 917-21, 2015.
14. M. C. F. Prosperi, M. Cic

19. **M. Salemi**, K. Strimmer, W. W. Hall, M. Duffy, E. Delaporte, S. Mboup, M. Peeters, A-M. Vandamme. Dating the common ancestor of SIVcpz and HIV-1 group M and the origin of HIV-1 subtypes using a new method to uncover clock-like molecular evolution. *FASEB Journal* **15**, 267-268, 2001. Highly cited paper: 186 citations
20. A-M. Vandamme, W. W. Hall, M. J. Lewis, P. Goubau, **M. Salemi**. Origin of HTLV-I in South America. *Nature Medicine* **3**, 232-233, 2000.
21. **M. Salemi**, M. J. Lewis, J. F. Egan, W. W. Hall, J. Desmyter, A-M. Vandamme. Different population dynamics and evolutionary rates of human T-cell lymphotropic virus type II (HTLV-II) in injecting drug users compared to in endemically infected Amerindian and Pygmy tribes. *Proceedings of the National Academy of Sciences USA* **96**, 13253-13259, 1999.

Bioinformatic – machine learning

22. S. Marini, C. Mavian, A. Riva, **M. Salemi***, B. Rife Magalis. Optimizing viral genome subsampling by genetic diversity and temporal distribution (TARDiS) for Phylogenetics. *Bioinformatics* **38**(3), 856-60, 2021. doi: 10.1093/bioinformatics/btab725, * Corresponding author.
23. M. Prosperi, S. Ghosh, Z. Chen, **M. Salemi**, T. Lyu, J. Zhao, J. Bian. Causal AI with Real World Data: Do statins protect from Alzheimer's Disease onset? *International Conference on Medical and Health Informatics Proceedings* 296-303, 2021. doi.org/10.1145/3472813.3473206
24. C. Mavian, A. S. Ramirez-Mata, J. J. Dollar, D. J. Nolan, M. Cash, K. White, S. N. Rich, B. Rife Magalis, S. Marini, M. C. F. Prosperi, D. Moraga Amador, A. Riva, K. C. Williams, **M. Salemi**. Brain tissue transcriptomic analysis of SIV-infected macaques identifies several altered metabolic pathways linked to neuropathogenesis and poly (ADP-ribose) polymerases (PARPs) as potential therapeutic targets. *Journal of Neurovirology* **6**:1-15, 2021.
25. S. N. Rich, V. L. Richards, C. N. Mavian, W. M. Switzer, B. Rife Magalis, K. Poschman, S. Geary, S. E. Broadway, S. B. Bennett, J. Blanton, T. Leitner, J. L. Boatwright, N. E. Stetten, R. L. Cook, E. C. Spencer, **M. Salemi**, Mattia Prosperi. Employing Molecular Phylodynamic Methods to Identify and Forecast HIV Transmission Clusters in Public Health Settings: A Qualitative Study. *Viruses* **12**(9), 921, 2020.
26. M. Prosperi, **M. Salemi**, T. Azarian, F. Milicchio, J. A. Johnson, M. Oliva. Unexpected predictors of antibiotic resistance in housekeeping genes of staphylococcus aureus. *ACM Conference in Bioinformatics, Computational Biology and Biomedicine* pp. 259-268. doi: 10.1145/3307339.334213, 2019.
27. G. B. Fogel, S. L. Lamers, E. S. Liu, **M. Salemi**, M. S. McGrath. Identification of dual-tropic HIV-1 using evolved neural networks. *Biosystems* **137**, 12-9, doi: 10.1016/j.biosystems.2015.09.007, 2015.
28. G. Fogel, E. Liu, **M. Salemi**, S. L. Lamers, M. S. McGrath. Evolved Neural Networks for HIV-1 Co-receptor Identification. *IEEE Congress on Evolutionary Computation* 2778-84, doi: 10.1109/CEC.2014.6900628, 2014.
29. S. L. Lamers, G. B. Fogel, D. J. Nolan, M. S. McGrath, **M. Salemi**. HIV-Associated neuropathogenesis: a systems biology perspective for modeling and therapy. *BioSystems* **119C**, 53-61, 2014.
30. M. C. F. Prosperi, L. Yin, D. J. Nolan, A. D. Lowe, M. M. Goodenow **M. Salemi**. Empirical validation of viral quasispecies assembly algorithms: state-of-the-art and challenges. *Scientific Reports* **3**, 2837, doi: 10.1038/srep02837, 2013.
31. M. C. F. Prosperi, S. Meloni, I. Fanti, S. Panzeri, G. Ulivi, **M. Salemi**. Characterization of *de novo* assemblies of quasispecies from next-generation sequencing via complex network modeling. *Scientific Research and Essays* **7**(33), 2997-3009, 2012.
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Molecular epidemiology, evolution, and pathogenesis

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RESEARCH SUPPORT

CURRENT:

- **NIH R01 – R01AI170187 – A Phylodynamic Artificial Intelligence framework to predict evolution of SARS-CoV-2 variants of concern in Immunocompromised persons with HIV (PhAI-CoV)**
 Dates: 07/01/22-06/30/27
 Role: Principal investigator (Prosperi, MPI)
 Effort: 10%
 Budget: \$3,735,351
- **NIH R01 – AI145552 – Forecasting trajectories of HIV transmission clusters with a novel phylodynamic and deep learning framework.**
 Role: Principal Investigator (Salemi, Prosperi, MPIs)
 Dates: 05/01/20 – 04/30/24
 Effort: 10%
 Budget: \$2,809,658
- **NIH R01 NS063897 – Viral evolution in peripheral macrophages and brain during progression to AIDS.**
 Role: Principal Investigator
 Dates 09/22/17 – 06/30/22 (NCE 06/30/23)
 Effort: 40%
 Budget: \$3,794,832
- **NIH R01 – Cholera persistence, transmission, and evolution in Goma, DRC.**
 Role: Co-Investigator (Morris, UF, PI)
 Effort: 10%
 Dates 04/01/19 – 31/03/24
 Budget: \$215,586
- **NIH R01 – Effects of CSFR1 blockade on repopulation of SIV reservoirs from the CNS to the periphery after antiretroviral therapy interruption**

Role: Co-investigator (Williams, Boston College, PI)

Effort: 10%

Dates: 07/15/21-06/30/24

Budget: \$388,688

- **AIDS Healthcare Foundation – Identification of SARS-CoV-2 Genomic Epidemiology.**

Dates: 03/01/21-02/28/23

Role: Principal investigator

Effort: 5%

Budget: \$240,000

PREVIOUS:

- **NIH R01 AI128750 – Cholera persistence, transmission and clinical illness in Haiti**

Role: Co-Investigator (Morris, PI)

Dates: 1/1/17 – 12/31/21 – currently NCE

Budget: \$490,000

- **NIH R01 AI126357 – Cholera transmission and evolution in Port-au-Prince, Haiti**

Role: Co-Investigator (Morris, PI)

Dates: 7/1/16 – 6/30/21– currently NCE

Budget: \$494,290

- **The Rockefeller Foundation – Florida coronavirus genomics regional accelerator**

Dates: 06/01/21-05/31/22

Role: Principal investigator

Budget: \$340,000

- **UF Office of Research and Health Science Center – Florida Coronavirus Genomic and AI Network (CGNet)**

Dates: 03/01/21-02/28/22

Role: Principal investigator

Budget: \$250,000

- **NSF RAPID – Dynamic Identification of SARS-COV-2 Transmission Epicenters in Presence of Spatial Heterogeneity**

Dates: 04/15/20-12/31/21

Role: co-Principal investigator Budget:
\$166,000

- **NSF RAPID – Epidemiological and Phylogenetic Models for Contact-Based Control of COVID-19** Dates:
04/17/20-12/31/21

Role: co-Principal investigator Budget:
\$200,000

- **NIH R01 sub award – Monocyte Traffic and Neuropathogenesis of AIDS**

Budget: \$141,868

Role: co-Investigator (Williams, PI)

Dates: 04/01/18 – 03/31/21

- **NIH R01AI123657-01S1 – Transmission of Zika and other arboviruses in Haiti**

Role: Co-investigator (Morris, PI)

Dates 7/01/16 – 6/30/20

Budget: \$1,758,905

- **NIH R01 AI116770 – Regression, Phylogenetics, and Study Design in Infectious Disease Epidemiology** Role:

- **NIH R21 AI138815 – HIV Dynamic Modelling for Identification of Transmission Epicenters (HIV-DYNAMITE)**
Role: Principal Investigator (Salemi, Prosperi, MPIs)
Dates 04/01/18 – 03/31/20 [NCE until 3/31/21] Budget: \$419,375.
- **2019 UF Research Opportunity Fund – Single-cell sequencing of the citrus Huanglongbing pathogen, *Candidatus Liberibacter asiaticus*, to advance understanding of pathogen biology.**
Role: co-Principal Investigator (Goss, PI)
Dates 07/01/19 – 06/31/21 Budget: \$ 85,000
- **UF Moonshot Award – Confronting the Threat of Emerging Pathogens and Eliminating Hospital-Acquired Drug Resistant Infections.**
Role: co-Investigator (Morris, Lauzardo, MPIs)
Dates 01/01/19 – 12/31/19
Budget: \$ 265,332
- **UF Moonshot Award – Advanced Data Capabilities: Integrating Precision Public Health and Precision Medicine.**
Role: co-Investigator (Hogan, Shenkman, MPIs)
Dates 01/01/19 – 12/31/19 Budget: \$ 501,150.
- **UF Opportunity Funds – DeepPhylo: integrating Deep Learning and Bayesian Phylogenetic Inference to optimize and improve phylodynamic analyses using Zika Virus Epidemic data.** Role: Principal Investigator
Dates: 08/15/17-08/15/18
Budget: \$44,000
- **NIH P50 GM103297 – The Center for HIV RNA Studies (CRNA)**
Role: Principal Investigator of Bioinformatics Core
Dates 9/17/12 - 08/31/17 Budget: \$823,808
- **NIH F31 AI126357 – Intra-host phylogeography and population dynamics of SIV in the rhesus macaque model of neuroAIDS**
Role: Mentor/Principal Investigator
Dates: 7/1/16 – 6/30/17 Budget: \$75,530
- **NIH RO1MH100984 Molecular Features and Approach to the HIV CNS Reservoir Post cART** Role: Co-Principal Investigator
Dates: 04/01/13-08/31/17 Budget: \$555,957
- **US Department of Homeland Security. Mapping and modeling Bacillus anthracis and Clostridium botulinum across North Africa and the Middle East with high-resolution genetic sequencing and spatial analysis.** Role: Co-Investigator
Dates: 6/1/16 – 5/31/17
Budget: \$44,272
- **Florida Department of Health (FL DOH) – Whole Genome Sequencing of Neisseria meningitidis serogroup W135 Isolates Belonging to a Clone Emerging in Florida.**
Role: Principal Investigator
Dates 09/01/2014 - 08/31/16
Budget: \$102,000
- **NIH R01 sub award – Monocyte Traffic and Neuropathogenesis of AIDS**
Role: Investigator
Dates 10/01/15 to 6/30/2016
- **NIH R01 AI097405 – Cholera transmission in Gressier region, Haiti.**
Role: Co- Principal Investigator

Dates 12/1/11-11/30/15

- **NIH R01AI097405 – Cholera transmission in Gressier Region, Haiti - Supplement** Role: Principal Investigator of supplement
Dates: 08/01/14 - 11/30/15
- **NIH R01 NS063897 – Viral evolution in peripheral macrophages and brain during progression to AIDS.** Role: Principal Investigator Dates 02/15/09 – 01/31/15
- **NIH R01 NS053359 – HIV-1 specific immune responses in Thai individuals with HIV dementia.** Role: Principal Investigator of UF subcontract Dates 08/11/10- 07/31/13
- **2011 UF Clinical and Translational Science Institute (CTSI) Pilot Award—Solving the puzzle of quasispecies reconstruction using next-generation sequencing technologies.**
Role: Principal Investigator (no salary for faculty) Dates: 05/01/11-09/30/12
- **2010 UF Research Opportunity Fund - Development of a phylogeographic framework to investigate the origin and spread of cholera pandemics.**
Role: Co-Principal Investigator (no salary for faculty) Dates: 05/10-04/12.
- **EPI seed funding—Preliminary study on the phylogeography of hospital acquired methicillin-resistant staphylococcus aureus (HA-MRSA) in different North Florida hospitals using genome-wide data.** Role: Principal Investigator (no salary for faculty) Dates: 12/01/10-05/31/11
- **NIH R01 AI065265 - Role of HIV-1 *env* diversity in cellular tropism.**
Role: Co-Investigator
Dates: 02/15/06- 01/31/11
- **NIH Contract Award # 00075848 - Analysis of HIV sequence data.**
Role: Principal Investigator Dates: 06/29/07- 04/30/10
- **FLORIDA CFAR seed grant - Molecular epidemiology and anthropological determinants of HIV-1 emerging epidemic in Southern Morocco.** Role: Principal Investigator Dates: 12/08-05/10.
- **UF Experimental Pathology Innovative Grant (EPIG) Award - Landscape Phylodynamics: A New Framework to Study Epidemics of Emerging Pathogens.** Role: Principal Investigator Dates: 09/08-05/09.