Cristina Lanzas

Address: 1051 William Moore Drive, Raleigh, NC 27607
Telephone: 919-513-6202
Email: clanzas@ncsu.edu

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Education

Veterinary Medicine 2000
Universitat Autonoma de Barcelona Bellaterra, Spain
Graduation Honors: With highest honors

Master of Science 2003
Cornell University Ithaca, NY
Thesis: Prediction of digestion kinetics using near infrared reflectance spectroscopy
Advisor: Dr. Alice Pell

Doctor of Philosophy 2007
Cornell University Ithaca, NY
Thesis: Models to predict carbohydrate and nitrogen supply and nitrogen excretion in cattle
Advisor: Dr. Danny Fox

Professional Experience

2022- present Assistant Department Head, Department of Population Health and Pathobiology, North Carolina State University, Raleigh, NC

2022- present Professor of Infectious Disease, North Carolina State University, Raleigh, NC

2020- present Associate Director, Emerging and Infectious Disease, Comparative Medicine Institute, North Carolina State University, Raleigh, NC

2017-2022 Associate Professor of Infectious Disease, North Carolina State University, Raleigh, NC

2015-2017 Assistant Professor of Infectious Disease, North Carolina State University, Raleigh, NC

2010-2014 Assistant Professor of Epidemiology, University of Tennessee, Knoxville, TN

2010-2014 Senior Personnel, National Institute for Mathematical and Biological Synthesis, Knoxville, TN

2009-2010 Research Associate, Cornell University, Ithaca, NY

2006-2009 Postdoctoral Associate, Cornell University, Ithaca, NY

2001-2006 Research Assistant, Cornell University, Ithaca, NY

2000 Intern, Research department, Agribrands International-Europe Region, Barcelona, Spain

1998-1999 Veterinary assistant, Inti, Taradell, Spain

1998 Intern, Services of Ecopathology of Wildlife Animals and Hematology, Universitat Autonoma de Barcelona , Bellaterra, Spain

Honors

2020-present University Faculty Scholar, NCSU

2018 Distinguished Associate Professor, Qingdao Agricultural University, China

2000 Best of 2000 Class Award (from 180 graduates). Universitat Autonoma de Barcelona, Spain

1997-8 Best Student Awards. Caixa Manresa Bank Fellowship Recipient, Spain

1998-9 Best Student Awards. Caixa Manresa Bank Fellowship Recipient, Spain

LEADERSHIP DEVELOPMENT

2022-2023 Maven Senior Scientist. MAVEN Institute for Academic Science and Healthcare Leadership, Northwell Health, NY

2016 Penn Executive Veterinary Leadership Program. Wharton Executive Education Program, University of Pennsylvania

FUNDING

Active

- PI: Chen, S. Building Next-generation Mathematical Biology Modeling Workforce for HAI Control. CDC U01CK000677. Total amount: 750,000. Period: 09/22-09/25. *Train predoctoral fellows in infectious disease modeling. Role: Collaborator*
- PI: Nunn, C. Modeling the Pandemic Lifecycle for Disease Control. NSF Predictive Intelligence for Pandemic Prevention (PIPP) Phase I grant. Amount: 1,000,000. Period: 09/22-02/24. *To prepare a Phase II center grant to connect local universities in predictive approaches to mitigate future outbreaks, Role: Collaborator*
- PI: Lanzas. Co-PIs: Papich, M., Jacob, M., Messenger, K., Frey, E., Love, W. Automated data collection on antimicrobial use in dogs and cats in a tertiary hospital and private practices. FDA U01FD007057. Amount: 999,999. Period: 09/20-08/25
  Public -Private partnership to develop a nationwide surveillance system to collect data on antimicrobial use in dogs and cats
- PI: Lanzas. Co-PIs: Dubberke, E., Lenhart, S., Lloyd, A., Rasmussen, D., Odoi, A. Multi-scale modeling and phylodynamics for healthcare associated infections. CDC U01CK000587. Total Amount: 2,470,030. Period: 08/20 - 07/25
  To improve the prevention and control of health-care associated infections by advancing quantitative methods that address pathogen transmission including multiscale models to quantify emergence and transmission pathways for resistant pathogens and phylodynamics methods that use sequence data to quantify the effect of resistant traits on bacteria fitness.
- PI: Lanzas. Multi-scale modeling and phylodynamics for healthcare associated infections. CDC U01CK000587-01M001. Covid-19 Supplement. 1,200,000. Period: 08/20-08/25
  To develop models that estimate COVID-19 impacts on healthcare resources and delivery and project cases and hospitalizations at regional level.
- PI: Wang. Advancing analytical methods for investigating the epidemiology of antimicrobial resistance using *Campylobacter coli* from swine populations as a model system. NIH F30OD30022. Amount: 164,820. Period: 2020-2023
  Role: Sponsor
- PI: Lanzas. Analytical pipelines for data and model integration: finding informed pathways for antimicrobial resistance control. NIH-R35GM134934. Amount: 2,139,970. Period: 01/20-12/24
  To develop quantitative methods to harness information on resistance from surveillance data and to evaluate resistance interactions using computational models to design and evaluate interventions.

Complete

- PI: Lanzas, C, Co-PIs: Sanderson, M., White, B, Nagaraja, T., Renter, D. Exposure heterogeneity and environmental transmission dynamics of *Escherichia coli*: linking mechanisms and patterns. NSF-NIH-USDA Ecology and Evolution of Infectious Diseases Program. Funded by NIGMS, R01GM117618, Amount: 1,693,435 , Period: 08/01/15- 07/31/20
  PI, to characterize the sources of heterogeneity for enteric disease transmission. The project integrates data generated in a natural infection model system (Escherichia coli – cattle) through experimental challenge studies, field transmission studies, and animal movement monitoring systems with mathematical models

- PI: Lanzas. Co-PIs: Rasmussen, D., Dawson, D., Peng, X. Phylodynamics of environmentally-transmitted pathogens. TRiCEM. Amount: 11,507. Period: 05/19-20
  Evaluate phylodynamics methods to quantify environmental transmission of pathogens

- PI: Machado, G. Co-PIs: Lanzas, Correa and Stringer. Use of swine movement information to improve risk-based surveillance. NCSU CVM Global Health. Amount: 19,792. Period: 03/19-20
  Co-PI, mentor student on transmission modeling

- PI: Lanzas, C, Co-PIs: Lenhart, S, Day, J. Modeling and control of environmentally transmitted pathogens. Joint DMS/ NIGMS Initiative to Support Research at the Interface of the Biological and Mathematical Sciences. Funded by NIGMS, R01GM113239, Amount: 766,424, Period: 07/01/14-10/31/19
  PI, to develop and analyze mathematical models that address relevant mechanisms and spatial heterogeneity associated with environmental transmission. As a case study, we use the transmission of Clostridium difficile in hospitals to identify environmental control strategies

- PI: Dubberke. *Clostridium difficile* Nucleic Acid Amplification Test Cycle Threshold Value Associated Environmental Contamination (CONTAM Study). CDC-BAA-200-2018-02926. Amount subaward: 31,130, Period: 10/01/18-19
  Collaborator, to determine how the amount of C. difficile shedding and environmental contamination impact risk of C. difficile transmission among patients admitted to leukemia units

- PI: Lanzas. Co-PIs: Jacob, M, Papich, M, Vaden, S. Improving methods for antimicrobial stewardship at NCSU Veterinary Teaching Hospital: a prototype based on persistent UTIs, NCSU CVM Research Award. Amount: 22,599, Period: 07/01/18-19
  PI, to develop clinical tools to improve antibiotic prescription practices for bacterial lower urinary tract infections in dogs

- PI: Wang, C. Role: mentor. Evolutionary medicine framework for evaluating methicillin-resistant Staphylococcus aureus at the human-animal interface. Comparative Medical Institute and TriCEM, Amount: 5,000, Period: 03/01/18-19
  Mentor

- PI: Dawson, D. From contact to colonization: characterizing how genomic variability allows microbial enteric pathogens to colonize within-host and environmental niches. Comparative Medical Institute. Amount: 5,000. Period: 04/01/18-19.
  Mentor

- PIs: Foster, D and Kathariou, S. Co-PIs: Papick, M, Jacob, M, Lanzas, C and Theriot, C. Impact of intestinal concentration on the microbiota and antimicrobial susceptibility of foodborne pathogens in cattle. NCSU-CALS/CVM. Amount: 150,000. Period: 07/01/16-06/30/17.
  Co-PI, to develop a risk quantitative framework to evaluate microbiological withdrawn

- PI: Foster, D., Co-PIs: Jacob M, Papich M, Lanzas C. The impact of dosing schedule of enrofloxacin on gastrointestinal tract drug concentration and selection for fluoroquinolone-resistant *Esherichia coli.* NCSU CVM Research Award. Amount: 25,000 07/01/15 - 06/30/16
  Co-PI, to develop within gut models of antimicrobial resistance

- PI: Sobsey, M, Co-PIs: Jacob, M and Lanzas, C. Surveillance of antimicrobial resistant enteric bacteria in human and animal waste and wastewaters and nearby ambient waters and their evolutionary trends over time and space. Comparative Medical Institute and TriCEM, Amount: 10,000, Period: 03/03/15-03/03/16
  Co-PI, to integrate genotypic and phenotypic resistant data and covariate information using probabilistic graphical models.

- PI: Lanzas, C. Transmission dynamics of shiga-toxigenic *Escherichia coli* serotypes in cattle. Funded by the Coordinated Agricultural Project: STEC in the beef chain: assessing and mitigating the risk by translational science, education and outreach, USDA-NIFA- 2012-68003-30155 (University of Nebraska), Amount: 55,032, Period: 01/01/14-12/31/15
  CAP collaborator, to develop models to quantify STEC transmission in cattle
- PI: Lanzas, C. Co-PI: Chen, S, Krawczel, P., Rius, A., Caldwell, M. A real-time location system to enhance dairy research and herd management. USDA 1433 formula funding AHDR program. University of Tennessee. Amount: 26,895. Period: 06/01/14-05/31/15
  PI, to implement a real time location system in the dairy research farm
- PI: Lanzas, C. Environmentally transmitted pathogens in cattle: linking contact network properties, and disease transmission. Funded by the Center of Excellence in Livestock Diseases and Human Health - University of Tennessee. Amount: 14,188. Period: 06/01/13- 05/31/14
  PI, develop networks models for disease transmission in cattle
- PI: Grohn, Y.T., Co-PI: Lanzas, C., Dubberke, E., Samore, M.Dynamics of *Clostridium difficile* transmission and infection control measures in health-care settings. Funded by NIH-NIAID. N01-AI-30054; ZC-0007-09, Amount: 190,177, Period: 06/01/09 to 09/01/10.
  Role: Wrote proposal, develop mathematical models for C. difficile transmission

PUBLICATIONS

∗ indicates mentored student or postdoctoral fellow

1. Liton Chandra Deb*, Manuel Jara*, and Cristina Lanzas. 2023. Early evaluation of the Food and Drug Administration (FDA) guidance on antibiotic use in food animals on antimicrobial resistance trends reported by the National Antimicrobial Resistance Monitoring System (2012-2019). **One Health**. In press.
2. Farthing, Trevor S.*, Ashlan Jolley*, Katelin B. Nickel, Cherie Hill, Dustin Stwalley, Kimberly A. Reske , Jennie H. Kwon, Margaret A. Olsen, Jason P. Burnham, Erik R. Dubberke, and Cristina Lanzas. 2023. Early COVID-19 pandemic effects on individual-level risk for healthcare-associated infections in hospitalized patients. **Infection Control and Hospital Epidemiology**. In press.
3. Ashlan Jolley*, William Love, Erin Frey, Cristina Lanzas. 2023. Impacts of the COVID-19 pandemic on antimicrobial use in companion animals in a tertiary veterinary teaching hospital in North Carolina. **Zoonoses and Public Health**, 70; 393-402
4. Davies, K.*, Lenhart, S., Day, J., Lloyd., A., Lanzas, C. 2023. Extensions of mean-field approximations for environmentally-transmitted pathogen networks. **Mathematical Biosciences and Engineering**, 20: 1637-1673
5. Das, Praachi, Morganne Igoe, Suzanne Lenhart, Alun Lloyd, Lan Luong, Dajun Tian, Cristina Lanzas, Agricola Odoi. 2022. Geographic Disparities and Predictors of COVID-19 Incidence Risk in the St. Louis Area, Missouri (USA). **PloS One**, 17: e0274899
6. Mahmud, Bejan, Meghan A. Wallace, Kimberly A. Reske, Kelly Alvarado, David A. Rasmussen, Carey-Ann D. Burnham, Cristina Lanzas, Erik R. Dubberke, Gautam Dantas. 2022. Epidemiology of Plasmid Lineages Mediating The Clinical Spread of Extended Spectrum Beta-Lactamases. **mSystems**, e00519-22
7. Love, W.*, Wang. C.A.*, Lanzas, C. 2022. Identifying patient-level risk factors associated with non-β-lactam resistance outcomes in invasive methicillin-resistant *Staphylococcus aureus* infections in the United States using chain graphs. **Journal of Antimicrobial Chemotherapy-Antimicrobial Resistance**, 4: dlac068
8. Lanzas, C., Jara, M.*, Tucker, R.*, Curtis, S.* 2022. A review of epidemiological models of *Clostridioides difficile* transmission and control (2009-2021). **Anaerobe**, 74: 102541. Role: *Role: Conceived paper, wrote paper*

9. Igoe, Morganne Elizabeth, Praachi Das, Suzanne Lenhart, Alun Lloyd, Lan Luong, Dajun Tian, Cristina Lanzas, Agricola Odoi. 2022. Geographic Disparities and Predictors of COVID-19 Hospitalization Risk in the St. Louis Area, Missouri (USA). **BMC Public Health**, 22: 1-10. *Role: Study concept, analysis and edit manuscript*

10. Farthing, T.*, Lanzas, C. 2021. Assessing the efficacy of interventions to control indoor SARS-Cov-2 transmission: an agent-based modeling approach. **Epidemics**, 34: 100524. *Role: mentor, study concept and design, data interpretation, manuscript writing and review*

11. Machado, G., Farthing, T*, Andraud, M., Nunes Lopes, F., Lanzas, C. 2021. Modeling the role of mortality-based response triggers on the effectiveness of African swine fever control strategies. **Transboundary and Emerging Diseases**:1-15. *Role: Mentor student performing the transmission modeling, data interpretation, manuscript review*

12. Farthing, T.*, Dawson, D*, Sanderson, M., Senger, H., Lanzas, C. 2021. Combining epidemiological and ecological methods to quantify social effects on *Escherichia coli* transmission. **Royal Society Open Science**, 8: 210328, *Role: mentor, study concept and design, data interpretation, manuscript writing and review*

13. Sulyok, C, Fox, L., Ritchie, H., Lanzas, C, Lenhart, S., Day, J. 2021. Mathematically Modeling the Effect of Touch Frequency on the Environmental Transmission of Clostridioides difficile in Health-care Settings. **Mathematical Biosciences**. 340, 108666 *Role: study concept and design, data interpretation, manuscript writing and review*

14. Dawson, D.*, Rasmussen, D., Peng, X., Lanzas, C. 2021. Inferring environmental transmission using phylodynamics: A case-study using simulated evolution of an enteric pathogen. **Journal of the Royal Society Interface**, 18: 20210041 *Role: mentor, study concept, data interpretation and manuscript writing*

15. Stephenson, B., Lanzas, C., Lenhart, Ponce, E., Bintz, J., Dubberke, E., Day, J. 2020. Comparing intervention strategies for reducing *Clostridiodes difficile* transmission: An agent-based modeling study. **BMC Infectious Diseases**, 20: 1-17 *Role: Model formulation, edited manuscript*

16. Farthing, T.*. Dawson, D*, Sanderson, M., Lanzas, C. 2020. Accounting for space and uncertainty in real-time-location-system derived contact networks. **Ecology and Evolution**, 10: 4702-4715 *Role: mentor, study design, edited manuscript*

17. Erwin, S*, Foster, D., Jacob, M., Papich, M., Lanzas, C. 2020. The effect of enrofloxacin on enteric Escherichia coli: fitting a mathematical model to in vivo data. **PLoS ONE**, 15: e0228138 *Role: mentor, study design, edited manuscript*

18. Garabed, R., Jolles, A., Garira, W., Lanzas, C., Gutierrez, J., Rempala, G. 2020. Multiscale dynamics of infectious diseases. **Interface Focus**. 10: 20190118 *Role: Wrote one section, discussed and review paper*

19. Lanzas, C., Davis, K.*, Erwin, S.*, Dawson, D.* 2019. On modelling environmentally-transmitted pathogens. **Interface Focus**. 10: 20190056 *Role: Conceived paper, wrote paper*

20. Lashnits, E.*, Dawson, D*., Breitschwerdt, E.B., Lanzas., C. 2019. Ecological and socioeconomic drivers of *Bartonella henselae* exposure in dogs in North Carolina. **Vector-Borne and Zoonotic Diseases**., 19:582-595 *Role: Modeling mentor, study design, edited manuscript*

21. Cazer, C., Al-Mamun, M., Kaniyamattam, K., Love, W.*, Booth, J.G., Lanzas, C., Grohn, Y.T. 2019. Shared multidrug resistance patterns in chicken-associated *Escherichia coli* identified by association rule mining. **Frontiers in Microbiology**, 10: 687 *Role: contributed in study design and discussion, commented and edited paper*

22. Zawack, K., Love, W.*, Lanzas, C., Booth, J.G., Grohn, Y.T. 2019. Estimation of Multidrug Resistance Variability in the National Antimicrobial Monitoring System. **Preventive Veterinary Medicine**, 167: 137-145 *Role: partook on model development and analysis, contributed in discussion, commented and edited paper*

23. Chen, C., Lanzas, C., Lee, C., Zenarosa, G., Arif, A., Dulin, M. 2019. Metapopulation Model from Pathogen's Perspective: A Versatile Framework to Quantify Pathogen Transfer and Circulation between Environment and Hosts. **Nature Scientific Reports**. 9: 1694 *Role: partook on model development and analysis, contributed in discussion, commented and edited paper*

24. Dawson, D.*, Farthing, T.*, Sanderson, M. Lanzas, C. 2019. Transmission on empirical dynamic contact networks is influenced by data processing decisions. **Epidemics**. 26: 32-42 *Role: mentor, study design, edited manuscript*

25. Dawson, D.*, Keung, J.H.*, Napoles, M.G.*, Vella, M.R.*, Chen, S.*, Sanderson, M., Lanzas, C. 2018. Investigating behavioral drivers of seasonal Shiga-toxigenic *Escherichia coli* (STEC) patterns in grazing cattle using an agent-based model. **PLoS ONE**, 13: e0205418 *Role: mentor, partook on model development and analysis, contributed in discussion, commented and edited paper*

26. Love, W.,* Zawack, K., Booth, J.G., Grohn, Y.T., Lanzas, C. 2018. Resistance correlation networks for 10 nontyphoidal *Salmonella* subpopulations in an active antimicrobial surveillance program. **Epidemiology and Infection**, 146: 991-1002 *Role: mentor, conceived model, partook on model development, edited manuscript*

27. Fletcher, J., Erwin, S.*, Lanzas, C. Theriot, C. 2018. Shifts in the gut metabolome and *Clostridium difficile* transcriptome throughout colonization and infection in a mouse model. **mSphere**, 3: e00089-18 *Role: data integration analysis, commented and edited paper*

28. Zawack, K., Love, W.* Lanzas, C., Booth, J.G., Grohn, Y.T. 2018. Inferring the interaction structure of resistance to antimicrobials. **Preventive Veterinary Medicine**. 152: 81-88. *Role: partook on model development and analysis, contributed in discussion, commented and edited paper*

29. Chen, S,* Lenhart, S., Day, J., Lee, C., Dulin, M., Lanzas, C. 2017. Pathogen transfer through environment-host contact: An agent-based queueing theoretic framework. **Mathematical Medicine and Biology**. 35: 409-425. *Role: mentor, partook on model development and analysis, contributed in discussion, commented and edited paper*

30. Grohn, Y.T., Carson, C., Lanzas, C., Pullum, L., Stanhope, M.J., and Volkova, V. 2017. A proposed analytic framework for determining the impact of an antimicrobial resistance intervention. **Animal Health Reviews**, 18: 1-25. *Role: wrote one of the sections, commented and edited paper*

31. Stephenson, B., Lanzas, C., Lenhart, S., Day, J. 2017. Optimal control of vaccination rate in an epidemiological model of *Clostridium difficile* transmission. **Journal of Mathematical Biology**, 75: 1693-1713. *Role: partook on model development and analysis, contributed in discussion, commented and edited paper*

32. Bintz, J., Lenhart, S., Lanzas, C. 2017. Antimicrobial stewardship and environmental decontamination for the control of *Clostridium difficile* transmission in healthcare settings. **Bulletin of Mathematical Biology**, 79: 36-62 *Role: conceived model, partook on model development and analysis, edited manuscript*

33. Love, W.,* Zawack, K., Booth, J.G., Grohn, Y.T., Lanzas, C. 2016. Markov networks of collateral antibiotic resistance: National antimicrobial resistance monitoring system surveillance results from *Escherichia coli* isolates, 2004-2013. **PLoS Computational Biology**,12: e1005160 *Role: mentor, conceived and designed experiments, edited manuscript*

34. Kwon, J., Lanzas, C., Reske, K., Hink, T., Seiler, S., Bommarito, K., Burnham, C., Dubberke, E. 2016. The role of food as a potential source of *Clostridium difficile* acquisition in hospitalized patients. **Infection Control and Hospital Epidemiology**, 37:1401-1407 *Role: developed model for risk assessment, wrote modeling section*

35. Chen, S* and Lanzas, C. 2016. Distinction and connection between contact network, social network, and disease transmission network. **Preventive Veterinary Medicine**, 131:8-11 *Role: mentor, commented and edited paper*

36. Chen, S.*, Sanderson, M., Lee, C., Cernicchiaro, N., Renter, D., Lanzas., C. 2016. Basic reproduction number and transmission dynamics of common serogroups of enterohemorrhagic *Escherichia coli.* **Applied and Environmental Microbiology**, 82: 5612-5620 *Role: mentor, support analysis, commented and edited paper*

37. Zawack, K., Li, M. Booth, J.G., Love, W.*, Lanzas, C., Grohn, Y.T. 2016. Monitoring antimicrobial resistance in the food supply chain and its implications for FDA policy initiatives. **Antimicrobial Agents and Chemotherapy**, 602:5302-5311 *Role: contribute in modeling, commented and edited paper*

38. Lanzas, C., and Chen, S.* 2015. Mathematical modeling tools to study pre-harvest food safety. **Microbiology spectrum**, 4: doi:10.1128/microbiolspec.PFS-0001-2013 *Role: conceived and wrote paper*

39. Chen, S.*, Ilany, A, White, B.J., Sanderson, M.W., Lanzas, C. 2015. Spatial-temporal dynamics of high-resolution animal networks: What can we learn from domestic animals? **PLoS ONE**, 10: e0129253. *Role: mentor, contribute to write paper*

40. Lanzas, C., and Chen, S.* 2015. Complex system modeling for veterinary epidemiology. **Preventive Veterinary Medicine**, 118: 207-214 *Role: concieved and wrote paper*

41. Aguilar-Bonavides, C.*, Sanchez-Arias, R., Lanzas, C. 2014. Major Histocompatibility Complex Class II Epitope Accurate Prediction by Sparse Representation. **BioData Minding**, 7:23 *Role: mentor, supported algorithm evaluation, commented and edited paper*

42. Lanzas, C and Dubberke, E. 2014. Effectiveness of screening hospital admissions for colonization in reducing *Clostridium difficile* transmission: a modeling evaluation. **Infection Control and Hospital Epidemiology**, 35: 1043-1050 *Role: developed model, wrote paper*

43. Chen, S.*, White, B., Sanderson, M., Amrine, D., Ilany, A., Lanzas, C. 2014. A highly dynamic animal contact network and implications on disease transmission. **Nature Scientific Reports**, 4: 4472 *Role: mentor, contribute to write paper*

44. Chen, S.*, Sanderson, M., White, B., Amrine, D., Lanzas, C. 2013. Temporal-spatial heterogeneity in animal-environment contact: implications for the exposure and transmission of pathogens. **Nature Scientific Reports**, 3:3112 *Role: mentor, contribute to write paper*

45. Magombedze, G.*, Ngonghala, C.*, Lanzas, C. 2013. Evaluation of the Iceberg phenomenon in Johne's disease through mathematical modelling. **PLoS ONE**. 8: e76636 *Role: mentor, commented and edited paper*

46. Volkova, V. V., Lu. Z., Lanzas, C., Scott, H.M., Grohn, Y.T. 2013. Modelling dynamics of plasmid-gene mediated antimicrobial resistance in enteric bacteria using stochastic differential equations.**Nature Scientific Reports**, 3: 2463 *Role: partook in the design and parameterization of the models, and engaged in the discussion of the results*

47. Volkova, V. V., Lu., Z., Lanzas, C., Grohn, Y.T. 2013. Evaluating targets for control of plasmid-mediated antimicrobial resistance in enteric commensals of beef cattle: modeling approach. **Epidemiology and Infection**, 141: 2294-2312 *Role: partook in the design and parameterization of the models, edited manuscript*

48. Chen, S.*, Sanderson, M., Lanzas, C. 2013. Investigating effects of between- and within- host variability on *Escherichia coli* O157 shedding pattern and transmission. **Preventive Veterinary Medicine**. 109: 47-57 *Role: mentor, designed study, contributed on manuscript writing*

49. Volkova, V. V., Lanzas, C., Lu, Z., Grohn, Y.T. 2012. Mathematical model of plasmid-mediated resistance to ceftiofur in commensal enteric *Escherichia coli* of cattle. **PLoS ONE**. 7: e367 *Role: conceived and designed the model, partook on model development, edit manuscript*

50. Lanzas, C., Dubberke, E.R,, Lu, Z., Reske, K.A., Grohn, Y.T. 2011. Epidemiological model for *Clostridium difficile* transmission in health care settings. **Infection Control and Hospital Epidemiology**. 32: 553-561 *Role: conceived and developed model, wrote manuscript*

51. Lanzas, C., Lu, Z., Grohn, Y.T. 2011. Mathematical modeling of the transmission and control of foodborne pathogens and antimicrobial resistance at preharvest. **Foodborne Pathogens and Disease**, 8: 1-10 *Role: Wrote manuscript*

52. Dubberke, E. R., Haslam, D. B., Lanzas, C., Bobo, L. D., Burnham, C. D., Grohn, Y. T., Tarr. P. I. 2011. The ecology and pathobiology of *Clostridium difficile infections*: an interdisciplinary challenge. **Zoonoses and Public Health**, 58: 4-20

53. Lanzas, C., Warnick, L. D., James, K. L., Wright, E. M., Wiedmann, M. and Grohn, Y. T., 2010. Transmission dynamics of a multi-drug resistant *Salmonella* typhimurium outbreak in a dairy farm. **Foodborne Pathogens and Disease**, 7: 467-474

54. Lanzas, C., Ayscue, P., Ivanek, R., Grohn, Y.T. 2010. Model or meal? Farm animal populations as models for infectious diseases of humans. **Nature Reviews Microbiology**, 8:139-148

55. Seo, S., Lanzas, C., Tedeschi, L.O., Pell, A., Fox, D.G., 2009. Development of a mechanistic model to represent the dynamics of particle flow out of the rumen and to predict rate of passage of forage particles in dairy cattle. **Journal of Dairy Science**, 92: 3981-4000

56. Ayscue, P., Lanzas, C., Ivanek, R., Grohn, Y.T., 2009. Modeling on-farm *Escherichia coli* O157:H7 population dynamics. **Foodborne Pathogens and Disease**, 6: 461-470

57. Lanzas, C., Broderick, G.A., Fox, D.G., 2008. Improved feed protein fractionation schemes for formulating rations with the Cornell Net Carbohydrate and Protein System. **Journal of Dairy Science**, 91:4881-4891

58. Lanzas, C., Warnick, L.D., Ivanek, R., Ayscue, P., Nydam, D.V., Grohn, Y.T., 2008. The risk and control of *Salmonella* outbreaks in calf-raising operations: a mathematical modeling approach. **Veterinary Research**, 39:61

59. Lanzas, C., Brien, S., Ivanek, R., Lo, Y., Chapagain, P.P., Ray, K.A., Ayscue, P., Warnick, L.D., Grohn, Y.T., 2008. The effect of heterogeneous infectious period and contagiousness on the dynamics of *Salmonella* transmission in dairy cows.**Epidemiology and Infection**, 136:1496-1510

60. Lanzas, C., Sniffen, C.J., Seo, S., Tedeschi, L.O., Fox, D.G. 2007. A revised CNCPS feed carbohydrate fractionation scheme for formulating rations for ruminants. **Animal Feed Science Technology**, 136: 167-190

61. Lanzas, C., Pell, A.N., Fox, D.G., 2007. Digestion kinetics of dried cereal grains. **Animal Feed Science Technology**, 136: 265-280

62. Seo, S., Lanzas, C., Tedeschi, L.O., Fox, D.G., 2007. Development of a mechanistic model to represent the dynamics of liquid flow out of the rumen and to predict rate of passage of liquid in dairy cattle. **Journal Dairy Science**, 90: 840-855

63. Lanzas, C., Seo, S., Tedeschi, L.O., Fox, D.G., 2007. Evaluation of protein fractionation systems used in formulating rations for dairy cattle. **Journal Dairy Science**, 90: 507-521

64. Seo, S., Tedeschi, L.O., Lanzas, C., Schwab, C.G., Fox, D.G., 2006. Development and evaluation of empirical equations to predict feed passage rate in cattle. **Animal Feed Science Technology**, 128: 67-83

Book Chapters and Books

1. Fleming-Davies, A. Jabbari, S., Robertson, S., Sri Noor Asih, T., Lanzas, C., Lenhart, S., Theriot. C., 2017. Mathematical modeling of the effects of nutrient competition and bile acid metabolism by the gut microbiota on colonization resistance against *Clostridium difficile*. Association for Women in Mathematics Series (Springer). pp: 137-161

2. Lanzas, C., and Chen, S*. 2018. Mathematical modeling tools to study pre-harvest food safety. In Preharvest Food Safety, S. Thakur and K. Kniel, eds. (American Society for Microbiology).

Proceedings

1. Population Modeling Working Group (contributor C. Lanzas). Population Modeling by Examples. 2015 Proceedings for the Spring Simulation Multi-Conference. Alexandria, VA, 12-15th April, 2015

2. Aguilar-Bonavides, C.*, Cruz-Cano, R., Lanzas, C. Prediction and rule extraction of major histocompatibility complex class II epitopes by logic minimization. Proceedings of 2014 International Conference on Bioinformatics and Computational Biology, Las Vegas, NE, 21-24th July, 2014.

3. Aguilar-Bonavides, C.*, Sanchez-Arias, R., Lanzas, C. Major Histocompatibility Complex Class II Epitope Accurate Prediction by Sparse Representation. BioMath Communication 2014, Sofia, Bulgaria, 22-27th June 2014

4. Lanzas, C. Modeling antimicrobial resistance in farm animal populations. Proceedings of the Dutch Society for Veterinary Epidemiology and Economics 2011 Meetings. November 22, 2011

5. Aquino, D. L., Tedeschi, L.O., Lanzas, C., Lee, S.S., Russell, J.B., 2003. Evaluation of CNCPS predictions of milk production of dairy cows fed alfalfa silage. In: Cornell Nutritional Conference for Feed Manufacturers, Syracuse, NY

RECENT PRESENTATIONS 2018-PRESENT

- Science-Policy Interface: Epidemiological modeling in livestock. University of Edinburgh, UK, May 24, 2023
- Characterizing contacts at the human-animal interface. NSF Predictive Intelligence for Pandemic Prevention Catalysis Meeting. RTP, NC, November 4, 2022
- Quantifying antimicrobial resistance drivers across the one health spectrum. Genetics and Environmental Mutagenesis Society of North Carolina. RTP, NC, November 1, 2022
- Epidemiological models of Clostridioides difficile transmission and control: current status and gaps. Centers of Disease Control. Atlanta, GA, September 12, 2022.
- Infectious disease modeling and its applications to healthcare. STEM Talks. Meredith College, March, 29, 2022.
- Modelling environmentally-transmitted pathogens. Biomath Seminar. University of Florida, March 17, 2022.
- SARS-Cov-2 transmission and healthcare use. Infectious Disease Seminar. NCSU, April 14, 2021
- Pathogen transmission and antimicrobial resistance dynamics in livestock in the digital era. Cornell Seminar Series in Antimicrobial Resistance. Originally in Ithaca, NY (moved online), November 11, 2020
- Dynamics and control of *C. difficile*: lessons learned from a decade of modeling. 7th International C. difficile symposium. Originally, in Bled, Slovenia (moved online due to COVID-19), September, 30, 2020
- High-resolution data in veterinary medicine: modeling and applications. GEOVET19. Davis, CA, October 8, 2019
- Antibiotic stewardship: data mining and modeling. SPHINx19-Modelling the spread of pathogens in healthcare institutions and networks conference. Paris, France, June 24, 2019
- Antimicrobial drug use and multi-drug resistance dynamics: surveillance data mining and model integration. MIDAS Network Meeting, Washington DC, May 20, 2019
- Within host *Clostridium difficile* dynamics. University of Tennessee, Knoxville, TN, March 15, 2019
- Modeling *Clostridium difficile* vaccine effectiveness. Workshop: Vaccines against CDI: a roadmap for the future. NIAID, Rockville, MD, September 5, 2018
- Mathematical modeling of *Clostridium difficile* infection and antimicrobial resistance. Anaerobe. Las Vegas, July 10, 2018
- Dynamic high resolution networks for disease transmission. Symposium: Integration of empirical data with network epidemiology. NetSci 2018. Paris, France, June 12, 2018
- Computational approaches to *Clostridium difficile* transmission and infection. UNC Medical School, Chapel Hill, NC, May 3, 2018
- Transmission and infection dynamics of *Clostridium difficile*. Mathematical Biology Institute, Ohio State University, Columbus, OH, April 25, 2018
- How should we model environmental transmission? A comparison of equation- and individual-based models. Presented at the MIDAS Network Meeting, Washington DC, April 3, 2018
- Antimicrobial Resistance Surveillance- Data Mining and Knowledge Discovery. Presented at the Data Science Initative UNCC and Duke, Charlotte, March 21, 2018

SERVICE

Professional Service and Memberships

2021-present Advisory Board. Triangle Center for Evolutionary Medicine.

2021 Panel Member for NIAID Investigator Initiated P01 Program Project Applications

2021 Panel Member for CDC Center for Global Health

2021-present Working group in mathematical modeling. Transatlantic Taskforce on Antimicrobial Resistance.

2020-present Steering committee. CDC MinD Network (Modeling Infectious Diseases in Healthcare Network)

2020-2024 Standing member for the NIH Modeling and Analysis of Biological Systems (MABS) Study Section

2020 NIAID Emergency Awards Panel: Rapid Investigation of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) and Coronavirus Disease 2019 (COVID-19)

2020 Panel Member for CDC Center for Global Health

2020 Panel Member for NIH Topics in Bacterial Pathogenesis and Virulence, April

2019 Reviewer for Wellcome Trust, UK

2019 Panel Member for Office of Research Infrastructure Programs Special Emphasis Panel, October, NIH

2019 Ad-hoc member for the NIH Modeling and Analysis of Biological Systems (MABS) Study Section, October

2019 Proposal reviewer for the Natural Sciences and Engineering Research Council of Canada

2019 Panel Member for Office of Research Infrastructure Programs Special Emphasis Panel, June, NIH

2019 Panel Member for CDC Center for Global Health

2019 Co-Editor for special issue on Multi-scale dynamics of infectious diseases in Journal of the Royal Society Interface Focus

2019 Ad-hoc member for the NIH Modeling and Analysis of Biological Systems (MABS) Study Section, February

2018-19 Participant for the Program Evaluation of NIH Peer Review Processes Study

2018 Program Reviewer for the Research Council KU Leuven, Belgium

2017-present Full Member of the Center for Gastrointestinal Biology and Disease, UNC-Chapell Hill/NCSU

2017-present Member of the Models of Infectious Disease Agent Study (MIDAS) network, a NIH collaborative network of research scientists to assist with infectious disease threats

2017 Grant reviewer for the NSF Focused Research Group in Mathematical Sciences

2017 Member of the Evaluation Committee for the Life Science programs of the French National Institute for Research in Computer Science and Automation, France

2017 Member for the special review panel: Center for Agriculture Safety and Health. Centers for Disease Control and Prevention

2017 Grant reviewer for the U.S. – Israel Binational Science Foundation

2017-present Member, Emerging Infectious Disease - Comparative Medicine Institute, NCSU

2016 White paper reviewer for the Society of Healthcare Epidemiology of America

2016 Member for the special review panel: Center for Agriculture Safety and Health. Centers for Disease Control and Prevention

2016 Ad-hoc member for the NIH Infectious Disease, Reproductive Health, and Asthma/Pulmonary Conditions (IRAP) study section

2015-present Editorial Board Member for Preventive Veterinary Medicine

2015-2016 Mentor for Research Collaborations organized by Association of Women in Mathematics

2015 Grant reviewer for the Sir Henry Wellcome Postdoctoral Fellowships-Wellcome Trust, UK

2015 Grant reviewer for the Swiss National Science Foundation, Switzerland

2015 Grant reviewer for the Exploratory NIFA program, USDA

2014 Member for Special Review Panel: Division of Microbiology and Infectious Diseases: Regulatory Affairs Support. National Institute of Allergy and Infectious Diseases (2014)

2014-2016 Member of NIMBioS Working group organized by FDA, USDA, and CDC as part of the White House released National Action Plan for Combating Antibiotic-Resistant Bacteria. The aim of the working group is to develop analytical frameworks and metrics to evaluate the association between shifts in antimicrobial use practices and antimicrobial resistance resulting from the FDA Risk Mitigation Strategy (FDA guidelines 209 and 213)

2014 Grant reviewer for the French National Research Agency, France

2014 Modeling contamination of fresh produce investigative workshop-NIMBioS

2012 Grant reviewer for the Romanian National Council for Scientific Research, Romania

2011-present Professional Memberships: Society for Mathematical Biology, Association for Veterinary Epidemiology and Preventive Medicine, International Society for Infectious Diseases, American Society for Microbiology

2010-present Ad-hoc reviewer of manuscripts for BioScience, BMC Genomics, BMC Infectious Diseases, BMC Public Health, BMC Veterinary Medicine, Bulletin of Mathematical Biology, Clinical Infectious Diseases, Current Science, Ecology Letters, Epidemics, Epidemiology and Infection, Foodborne Pathogens and Disease, Frontiers in Public Health, Frontiers in Veterinary Medicine, Health Security, Journal of the Science of Food and Agriculture, Journal of Biological Dynamics, Journal of Dairy Science, Journal of Hospital Infection, Journal of Theoretical Biology, Mathematical Medicine and Biology, Nature Scientific Reports, PloS Negleted Diseases, PloS One, Preventive Veterinary Medicine, Proceedings of the National Academy of Sciences, Proceedings of the Royal Society B, Risk Analysis, Scientia Agricola, Transboundary diseases, Theoretical Population Biology, Veterinary Research, Veterinary Microbiology, Water, Zoonoses and Public Health

2009 Modeling bovine tuberculosis investigative workshop- NIMBioS

University Service

2023-present College Reappointment, Promotion, and Tenure Committee

2023 Data Storage Strategic Taskforce, NCSU

2022-2023 Infectious Disease Cluster Search Committee

2022-2023 Department Head Search Committee

2020-2021 Covid-19 Risk Management Advisory Group, CVM, NCSU

2019 Member, Search Committee, Veterinary Clinical Epidemiology Position, NCSU

2018-2019 Department Head Review Committee PHP, NCSU

2018-2019 Member, CVM Global Health Committee, NCSU

2018-present Concentration Leader, Population and Global Health, Comparative Biomedical Graduate Program, NCSU

2018 Chair, Department Tenure Guidelines Committee, NCSU

2018 Member, Food Animal Initiative Faculty Leadership, NCSU

2018 Member, Search Committee, Veterinary Global and Public Health Position, NCSU

2018 Faculty advisor for the College Postdoctoral Association, NCSU

2017-present Member, Research College Committee, NCSU

2017 Member, Faculty Mentoring Guidelines Committee, Population Health and Pathobiology, NCSU

2016 Member, ad hoc committee, CFEF Microbiome Cluster Candidate Interview, NCSU

2016 Chair, search committee, Clinical Assistant Position in Biostatistics, NCSU

2016 Faculty mentor for the Building Future Faculty program, NCSU

2015-2018 Faculty library representative for the College and University Library Committee, NCSU

2012-2014 Member, Faculty and Staff Awards Committee. University of Tennessee

2014 Review member for the Veterinary Medicine Admissions Committee, University of Tennessee

Mentoring

Postdoctoral Research Associates:

1. Alba Frias (December 2022-present). Project: Horizontal gene transfer in health-care settings
2. Sankalp Arya (October 2022-present). Project: Plasmid modeling
3. Archana Timsina (July 2022-present). Project: Pathogen transmission in health-care settings
4. Shamim Ul Hasan (September 2021-present). Project: Multiscale modeling of antimicrobial resistance
5. Trevor Farthing (July 2021-April 2022). Project: COVID-19 modeling (Current Position: Public Health AmeriCorps Data Analyst)
6. Manuel Jara (January 2021- present). Project: Phylodynamics of health-care associated pathogens
7. William Love (April 2015- September 2020). Project: Network approaches for antimicrobial resistance surveillance (Current Position: Research Associate, NCSU)
8. Daniel Dawson (August 2016-September 2019). Project: Exposure heterogeneity and environmental transmission dynamics of *Escherichia coli* (Current Position: EPA Fellow)
9. Samantha Erwin (July 2017-July 2019). Project: Modeling *Clostridium difficile* infection and antimicrobial resistance in enteric bacteria (Current Position: Staff Scientist at Oak Ridge National Lab)
10. Kale Davies (December 2016-August 2018). Project: Spatial models of disease transmission and their appoximations (Current Position: Assistant Instructor Professor, University of Chicago)
11. Shi Chen (July 2011-July 2016): Project: Transmission dynamics of enteric pathogens (Current position: Associate Professor, University of North Carolina-Charlotte)
12. Clemente Aguilar (July 2013-November 2014). Project: Prediction and rule inference of MHC Class II epitope binder through logic minimization method (Current position: Senior Scientist in Computational Biology, Janssen Pharmaceutical Company)
13. Calistus Ngonghala (August 2011-October 2013). Project: Mathematical modeling of malaria transmission (Current position: Assistant Professor, University of Florida)

Graduate Students:

1. Sarah Burnash, MS student, Biomedical Engineering, 2022-2023
2. Sarah Harden, DVM-PhD student, Comparative Biomedical Science, 2022-present (Co-chair with Sarah Rhea)
3. Taylor Gin, PhD student, Comparative Biomedical Science, 2022-present (Committee Member)

4. Ashlan Jolley, DVM-PhD student, Comparative Biomedical Science, 2021-present (Chair)
5. Praachi Daas, PhD student, Biomathematics, 2019-2022 (Committee Member)
6. Abagael Skyes, PhD student, Comparative Biomedical Sciences, 2021-present (Co-chair with Gustavo Machado)
7. Liton Chandra Deb, PhD student, Comparative Biomedical Sciences, 2020-present (Chair)
8. Leonor Kleper, PhD student, Bioinformatics, 2019-present (Committee Member)
9. Savannah Bates, PhD student, Biomathematics, 2019-present (Chair)
10. Hannah Seger, Phd-DVM student, Kansas State University 2017-2023 (Committe member)
11. Trevor Farthing, PhD student, Comparative Biomedical Science, 2017-2021 (Co-chair with Ron Baynes)
12. Marco Hamins-Puerto, PhD student, Biomathematics, 2018-2021 (Committee member)
13. Annie Wang, PhD-DVM student, Comparative Biomedical Science, 2016-present (Co-chair with Sid Thakur)
14. Erin Lashnits, PhD student, Comparative Biomedical Science, 2018-2020 (Committee member)
15. Hanna Berman, PhD student, Comparative Biomedical Science, 2017-present (Committee member)
16. Ysenia Victoria Silva Guillen, PhD Student, Animal Science, 2017-2019 (Graduate representative)
17. Meredith Spence, PhD student, Entomology, 2014-2019 (Committee member)
18. Ricardo Videla (MS, Department of Biomedical and Diagnostic Sciences), 2012 (Committee member)

Undergraduate and veterinary medicine students:

1. Avi Sawhney, major: Mechanical engineering, NCSU, project: network modeling of healthcare associated pathogens, 2021-
2. Elizabeth Ward, DVM student, NCSU, project: Multidrug resistance of *Staphylococcus pseudintermedius*, 2021
3. Sara Bird, major: Statistics and Mathematics, NCSU, project: Covid-19 modeling, 2021
4. Loc Nguyen, major: Genetics, NCSU, project: Population genetics of MRSA, 2020-present
5. Katyayani Saripalli, major: Biological Science, NCSU, project: Antibiotic use data in companion animals. 2020
6. Ashlan Jolley, DVM student, NCSU, project: Transmission and control interventions for Shiga toxin-producing Escherichia coli in cattle, 2020
7. Roberta Richarson, DVM student, Agent-based modeling of antimicrobial resistance dissemination in beef cattle, 2020
8. Rachel Tucker, major: Applied Math, NCSU, project: Modeling multidrug resistance, 2020-present
9. Daniel Popkin, major: Animal Science, project: Multidrug resistance trends in surveillance data, 2019-2020
10. Brittany Lee, major: Animal Science, project: Antimicrobial resistance in *Campylobacter*, Honors project, 2019
11. Bayli Wellman, major: Animal Science, project: High-resolution data collection in human subjects, 2019
12. Nichol Henderson, major: Animal Science, project: Cattle behavior and disease transmission, 2018
13. Hillary Dimig, major: Chemical Engineering, capstone project: Modeling the impact of intestinal antibiotic concentrations on gut microbiota, Honors project 2017-2018
14. Lydia Ashburn, major: Biomedical Engineering, project: Creating health care synthetic populations, 2017
15. Kyra Vancil, major: Animal Science, project: Multidrug resistance of *Staphylococcus pseudintermedius*, 2017-2018

16. Amy Trey, DVM student, project: Multidrug resistance of *Staphylococcus pseudintermedius*, 2016
17. Diya Sashidhar, major: Mathematics, NCSU, project: ODEs models for nosocomial pathogens, 2015-2017
18. Brinkley Raynor, major: Animal Science, NCSU, project: Systematic review of models with environmental transmission, 2015-2017
19. Leland Raynor, DVM student, project summer 2015: Modeling antibiotic selective pressure in the gut
20. Research experiences for undergraduate students Summer 2014 NIMBioS: Vivian Anyaeche (Biology), Project: Modeling transmission and control of bovine respiratory disease.
21. Research experiences for undergraduate students Summer 2014 NIMBioS: Taylor Nelsen (Environmental Science). Project: Modeling transmission and control of bovine respiratory disease.
22. Research experiences for undergraduate students Summer 2014 NIMBioS: Taylor Kuramoto (Mathematics). Project: Modeling transmission and control of bovine respiratory disease.
23. Research experiences for undergraduate students Summer 2014 NIMBioS: James Tashika (Biology). Project: Modeling transmission and control of bovine respiratory disease.
24. Research experiences for undergraduate students Summer 2013 NIMBioS: Michael Vella (Computational Mathematics and Statistics). Project: Modeling the enviromental transmission of infectious diseases.
25. Research experiences for undergraduate students Summer 2013 NIMBioS: Jocelyn Keung (Mathematical Decision Science and Environmental Sciences). Project: Modeling the enviromental transmission of infectious diseases.
26. Research experiences for undergraduate students Summer 2013 NIMBioS: Monica Napoles (Environmental Resources Engineering). Project: Modeling the enviromental transmission of infectious diseases.
27. Research experiences for undergraduate students Summer 2012 NIMBioS: Ilian Rubin (Computational biology). Project: Transmission of multidrug resistant *Salmonella* in swine.
28. Research experiences for undergraduate students Summer 2012 NIMBioS: Elena Crosley (Mathematics). Project: Transmission of multidrug resistant *Salmonella* in swine.
29. Research experiences for undergraduate students Summer 2012 NIMBioS: Arielle Nivens (Mathematics). Project: Transmission of multidrug resistant *Salmonella* in swine.
30. Research experiences for undergraduate and veterinary students Summer 2011 NIMBioS: Brooke Daniel (DVM student), Project: Enterohemorrhagic Escherichia coli dynamics in cattle
31. Research experiences for undergraduate and veterinary students Summer 2011 NIMBioS: Rachel Johnson (DVM student),. Project: Enterohemorrhagic Escherichia coli dynamics in cattle
32. Research experiences for undergraduate and veterinary students Summer 2011 NIMBioS: Daniel Haycraft (Majors: Mathematics, Biology and Chemistry). Project: Enterohemorrhagic Escherichia coli dynamics in cattle
33. Lahari Subraveti, major: Biochemistry, Cellular, and Molecular Biology, project: Antibiotic disturbance of the gut microbiota: a systematic review, 2011

Teaching

Courses

- VPM VMP991-170. Guess Lecture on antimicrobial resistance evolution. Fall 2022 (2 hours)
- CBS595 Special topics in disease epidemiology. Fall 2022 (10 hours)
- CBS 800. Lecturer. Epidemiological models of infectious disease. Spring 2021 (2 hours)
- CBS 775. Designing Population-based Research. Coordinator and Lecturer. Spring 2021 (20 hours), Spring 2022 (12 hours)

- CBS 595-004 and CBS 650-001. Population Medicine Forum. Coordinator. Spring 2020, Fall 2020, Spring 2021 (12 hours)
- CBS 565. Fundamentals of Biomedical Sciences. Lecturer. Fall 2019 (1 hour). Fall 2020, Fall 2021, Fall 2022 (2 hours)
- CBS 595-007 Epidemiology I. Lecturer. Spring 2018 (6 hours)
- VMP991-160 Infectious disease dynamics. 1-Week Selective, Fall 2016, 2018, 2019, 2020
- CBS 810/CBS 595-003 Modeling in infectious disease dynamics. Course coordinator and main lecturer. Fall 2015, 2016, Spring 2018 (24 hours)
- CEM 503 Infectious Disease Modeling. Graduate Course. Course coordinator and main lecturer. Spring 2014 (24 hours)
- CMVM 501 Special topics: Infectious Disease Modeling. Course coordinator and main lecturer. Spring 2012 (24 hours)
- CEM 504 Descriptive and Applied Epidemiology. Lecturer (8 hours). Fall 2011, Fall 2012, Fall 2013
- VM 833 Epidemiology and Evidence-based medicine. Course coordinator and main lecturer. 16 one-hour lectures and 6 two-hour lab sections. Spring 2011, Spring 2012, Spring 2013. (28 hours)

Workshops and guess lectures

- Tricem (Duke University). Evolutionary Medicine Summer Institute. Introduction to infectious disease epidemiology and modeling (4 hours). May, 2021, 2022
- Guest lecturer: CBS 650. NCSU (Spring 2018)
- Guest lecturer: VMP 991 239 Vet Med Terminology in Spanish. NCSU (Spring 2015 and 2016)
- Mathematical and epidemiological modeling of infectious diseases: a hands-on workshop. Instructor. International Society for Veterinary Epidemiology and Economics. Merida, Mexico 1-2 November 2015
- Guest lecturer: Infectious disease dynamics: linking patterns and mechanisms. Comparative Biomedical Sciences graduate program seminar. NCSU. September 9 2015
- Guest lecturer: Spatial models in epidemiology. Epidemiological modeling graduate course. Kansas State University. April 26 2012
- Workshop: Tools for infectious disease epidemiology: diagnosis, modeling and risk. Instructor. Cornell University. August 2-4 2010
- Workshop: Tools for infectious disease epidemiology: diagnosis, modeling and risk. Instructor. Cornell University. August 11-13 2008
- Guest lecturer: Introduction to infectious disease modeling. Veterinary medicine course. Purdue University. December 2008 and 2009
- Guest lecturer: Evaluating cattle nutrition in tropical conditions. Livestock in tropical systems. Cornell University. March 2006 and 2007.

Teaching assistant and laboratory instructor

- Laboratory instructor for Animal Nutrition (2003), laboratory instructor for Domestic Animal Biology (2003), teaching assistant for Livestock and Environment (2002) and Applied Cattle Nutrition (2005). Cornell University.