

## Biographical Sketch

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### **A. Professional preparation**

<b>Institution</b>	<b>Degree</b>	<b>Year</b>	<b>Field of study</b>
Universidade Federal de Santa Maria (Brazil)	DVM	03/2010	Veterinary Medicine
Universidade Federal do Rio Grande do Sul (Brazil)	MVSc	02/2013	Veterinary Epidemiology and Public Health
Universidade Federal do Rio Grande do Sul (Brazil)	PhD	03/2016	Veterinary Population Sciences
University of Minnesota (Saint Paul, MN)	Postdoctoral	12/2017	Veterinary Epidemiology and Public Health

### **B. Appointments**

2015-2015	Pan American Health Organization / World Health Organization. Contract Epidemiologist.
2015-2016	Assistant Professor (Department of Preventive Medicine-College of Veterinary Medicine) Universidade Federal do Rio Grande do Sul (Brazil).
2018-2023	Assistant Professor, North Carolina State University, College of Veterinary Medicine.
2023- Present	<b>Associate Professor, North Carolina State University, College of Veterinary Medicine.</b>

### **C. Personal Statement**

My main research develops and applies epidemiological tools and models to investigate the dynamics of animal infectious diseases' spread. I have dedicated my efforts to developing machine-learning, mathematical modeling methods, and tools directly applying to emerging and transboundary animal diseases. Ultimately, we are interested in understanding infectious disease transmission processes among livestock populations, providing science-based support for decision-making about prevention and control. In the past few years, my research focused on mathematical modeling and traditional statistics for practical mapping of the spread of infectious diseases among pig populations. I authored or co-authored more than 150 peer-reviewed publications in animal and human health. My research provides training opportunities in interdisciplinary research at the interface of disease spread and control strategies nationally and internationally. As a faculty member, I have been a research mentor for 15 undergraduate students, twelve veterinary students, four graduate students, and four postdoctoral fellows. My laboratory

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in the College of Veterinary Medicine at North Carolina State University is currently funded by USDA-NIFA, USDA-APHIS, Foundation for Food & Agriculture Research (FFAR), Swine Health Information Center (SHIC), and internationally by FUNDESA-Fundo de Desenvolvimento e Defesa Sanitaria Animal (Brazil).

### **D. Professional Memberships**

2016- International Society for Infectious Diseases  
2017- American Association of Swine Veterinarians.  
2018- NC Veterinary Medical Association.  
2021- USAHA, United States Animal Health Association

### **E. Professional Service (last 4 years)**

2018- Panelist, FFAR, Foundation for Food and Agriculture Research Scientific Committee.  
2019- Panelist, OMAFRA, Ontario Ministry of Agriculture, Food and Rural Affairs.  
2020- Panelist, CARE, Critical Agricultural Research and Extension.  
2021- Co-Chair of the AAVLD/USAHA/Subcommittee on Information Technology Standards Permit Data Standards Workgroup.

### **F. Contribution to Science**

*1. Multiscale model combining spatially explicit network model of animal movements with compartmental models in the dynamics of swine pathogens and its implications on disease transmission.*

My lab and collaborators have reconstructed swine population dynamics, including direct and indirect contact among farms, to estimate the relative contribution of each route in disease propagation, later using calibrated models to forecast and visualize the spatial distribution of at-risk farm locations. The publications below document our investigations on modes of transmission and implications in disease control strategies. We have demonstrated that a, b, c) the animal contact network represented ~ 70% of transmission events, while distance spread accounted for ~ 15%. d) We also demonstrated that along with farm density, distance to the main public road facilitated the spread of disease to proximal sites, while elevation farms surrounded by denser vegetation were less likely to be infected, indicating their role as dissemination barriers.

*2. Develop interpretable machine learning for on-farm biosecurity and swine disease risk.*

With the recent advancements in interpretable machine learning that allow for an improved understanding of model reasoning, research has emerged into Explainable AI (XAI). Together has led to increased development of machine learning methodologies with more explainability. In this study, we developed and applied an interpretable machine learning methodology to assess the impact of on-farm biosecurity practices on the predicted risk of PRRSV outbreaks. We developed a novel interpretable machine learning framework and R package, *MrIML* (<https://nfj1380.github.io/mrIML/>), capable of predicting and benchmarking outbreak risk based on biosecurity practices and farm demographics. We have shown that local interpretable machine learning can generate accurate and individualized biosecurity assessments and provide the opportunity to better guide biosecurity implementation on a case-by-case basis and individualized farms.

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3. Active developer of web-based application used to communicate with stakeholder and to deploy analytical tools named RABapp <https://machado-lab.github.io/rabapp/>

### G. Publications (Past 4 years)

**Selected publications +160 complete list at [google scholar](#)**

1. Sykes, A.L., Galvis, J.A., O'Hara, K.C., Corzo, C., **Machado, G.** 2023. Estimating the effectiveness of control actions on African swine fever transmission in commercial swine populations in the United States. **Prev Vet Medicine.** <https://doi.org/10.1016/j.prevetmed.2023.105962>
2. Sanchez, F. Galvis, J.A., Cardenas, N.C., Corzo, C., **Machado, G.** 2023. Spatiotemporal relative risk distribution of porcine reproductive and respiratory syndrome virus in the United States. **Front. Vet. Sci.** <https://doi.org/10.3389/fvets.2023.1158306>
3. Janoušková, E., Rokhsar, J., Jara, M., Entezami, M., Horton, D.L., Dias, R.D., **Machado, G.**, Prada, J.M. 2023. Quantifying Spillover Risk with an Integrated Bat-Rabies Dynamic Modeling Framework. **Transbound. Emerg. Dis.** <https://doi.org/10.1155/2023/2611577>
4. Galvis, J.A., Corzo, C., Prada, J.M., **Machado, G.** 2022. Modeling between-farm transmission dynamics of porcine epidemic diarrhea virus: characterizing the dominant transmission routes. **Prev Vet Medicine.** <https://doi.org/10.1016/j.prevetmed.2022.105759>
5. Trostle, P., Corzo, C., Reich, B.J., **Machado, G.** 2022. A discrete-time survival model for porcine epidemic diarrhea virus. **Transbound. Emerg. Dis.** <https://doi.org/10.1111/tbed.14739>
6. Galvis, J.A., Prada, J.M., Corzo, C.A., **Machado, G.** 2022. Modeling and assessing additional porcine reproductive and respiratory syndrome virus transmission routes: Vehicle movements and feed ingredients. **Transbound. Emerg. Dis.** <https://doi.org/10.1111/tbed.14488>.
7. Cardenas, N.C., Sykes, A.L., Lopes F.P.N., **Machado, G.** 2022. Multiple species animal movements: network properties, disease dynamic and the impact of targeted control actions. **Veterinary Research.** <https://doi.org/10.1186/s13567-022-01031-2>.
8. Cardenas, N.C., Sanchez, AF, Lopes F.P.N., **Machado, G.** 2022. Coupling spatial statistics with social network analysis to estimate distinct risk areas of disease circulation to improve risk-based surveillance. **Transbound. Emerg. Dis.** <https://doi.org/10.1111/tbed.14627>.
9. Galvis, J.A., C.M. Jones, J.M. Prada, C.A. Corzo, and **G. Machado**, 2021: The between-farm transmission dynamics of Porcine Epidemic Diarrhea Virus: A short-term forecast modeling comparison and the effectiveness of control strategies. **Transbound. Emerg. Dis.** 13997, <https://doi.org/10.1111/tbed.13997>.
10. Gunasekera, U., Biswal, J.K., **Machado, G.**, Ranjan, R., Subramaniam, S., Rout, M., Mohapatra, J.K., Pattnaik, B., Singh, R.P., Arzt, J., Perez, A., VanderWaal, K. 2022. **Transbound. Emerg. Dis.** <https://doi.org/10.1111/tbed.14528>.
11. Espíndola, J., **Machado, G.**, Diehl, G., Dos Santos, L., Vargas, A., Gressler, L. 2022. Culturable microbial population from the upper respiratory tract of 1,010 clinically healthy horses in Southern Brazil. **Journal of Equine Veterinary Science.** <https://doi.org/10.1016/j.jevs.2022.103946>

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12. Andraud, M., Brandon, P.H., Hayes, H., Galvis, J.A., Vergne, T., **Machado, G.**, Rose, N. 2022. Modelling African swine fever virus spread in pigs using time-respective network data: Scientific support for decision-makers. **Transbound. Emerg. Dis.** <https://doi.org/10.1111/tbed.14550>.
13. Galvis, J.A., J.M. Prada, C.A. Corzo, and **G. Machado**, 2021: Modeling the transmission and vaccination strategy for porcine reproductive and respiratory syndrome virus. **Transbound. Emerg. Dis.** 14007, <https://doi.org/10.1111/tbed.14007>.
14. **Machado, G.**, T. Farthing, M. Andraud, F.P.N. Lopes, and C. Lanzas, 2021: Modeling the role of mortality-based response triggers on the effectiveness of African swine fever control strategies. bioRxiv2021.04.05.438400, <https://doi.org/10.1101/2021.04.05.438400>.
15. Sykes, A.L., Silva, G.S., Holtkamp, D.J., Mauch, B.W., Osemeke, O., Linhares, D.C.L., **Machado, G.**, 2021. Interpretable machine learning applied to on-farm biosecurity and porcine reproductive and respiratory syndrome virus. <https://arxiv.org/abs/2106.06506>.
16. **Machado, G.**, Corbellini, L.G., Frias-De-Diego, A., Dieh, G.N., Dos Santos, D.V., Jara, M., De Freitas Costa, E., 2021a. Impact of changes of horse movement regulations on the risks of equine infectious anemia: a risk assessment approach. **Prev. Vet. Med.** 105319. <https://doi.org/10.1016/j.prevetmed.2021.105319>.
17. Jara, M., Crespo, R., Roberts, D., Chapman, A., Banda, A., **Machado, G.**, 2021a. Development of a dissemination platform for spatiotemporal and phylogenetic analysis of avian infectious bronchitis virus. **Front. Vet. Sci.** 8. <https://doi.org/10.3389/fvets.2021.624233>
18. Jara, M., Holcomb, K., Wang, X., Goss, E.M., **Machado, G.**, 2021b. The Potential Distribution of *Pythium insidiosum* in the Chincoteague National Wildlife Refuge, Virginia. **Front. Vet. Sci.** 8, 640339. <https://doi.org/10.3389/fvets.2021.640339>.
19. Escobar, L.E., Pritzkow, S., Winter, S.N., Grear, D.A., Kirchgessner, M.S., Dominguez-Villegas, E., **Machado, G.**, Townsend Peterson, A., Soto, C., 2020. The ecology of chronic wasting disease in wildlife. **Biol. Rev.** <https://doi.org/10.1111/brv.12568>
20. Fountain-Jones, N., Kozakiewicz, C., Forester, B., Landguth, E., Carver, S., Charleston, M., Gagne, R., Greenwell, B., Kraberger, S., Trumbo, D., Mayer, M., Clark, N., **Machado, G.**, 2020. MrIML: Multi-response interpretable machine learning to map genomic landscapes (preprint). Preprints. <https://doi.org/10.22541/au.160855820.09604024/v1>
21. Jara, M., D.A. Rasmussen, C.A. Corzo, and **G. Machado**, 2020: Porcine reproductive and respiratory syndrome virus dissemination across pig production systems in the United States. **Transbound. Emerg. Dis.** 13728, <https://doi.org/10.1111/tbed.13728>.
22. Krasteva, S., Jara, M., Frias-De-Diego, A., **Machado, G.**, 2020. Nairobi sheep disease virus: A historical and epidemiological perspective. **Front. Vet. Sci.** 7, 419. <https://doi.org/10.3389/fvets.2020.00419>.
23. **Machado, G.**, Galvis, J.A., Lopes, F.P.N., Voges, J., Medeiros, A.A.R., Cárdenas, N.C., 2020. Quantifying the dynamics of pig movements improves targeted disease surveillance and control plans. **Transbound. Emerg. Dis.** tbed.13841. <https://doi.org/10.1111/tbed.13841>.
24. Servadio, J.L., **Machado, G.**, Alvarez, J., de Ferreira Lima Júnior, F.E., Vieira Alves, R., Convertino, M., 2020. Information differences across spatial resolutions and scales for disease surveillance and analysis: The case of Visceral Leishmaniasis in Brazil. **PLOS ONE** 15, e0235920. <https://doi.org/10.1371/journal.pone.0235920>.
25. Biezus, G., **Machado, G.**, Ferian, P.E., da Costa, U.M., Pereira, L.H.H. da S., Withoeft, J.A., Nunes, I.A.C., Muller, T.R., de Cristo, T.G., Casagrande, R.A., 2019. Prevalence of and factors associated with feline leukemia virus (FeLV) and feline immunodeficiency virus (FIV) in cats

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- of the state of Santa Catarina, Brazil. **Comp. Immunol. Microbiol. Infect. Dis.** <https://doi.org/10.1016/j.cimid.2018.12.004>
26. Boaz, R., Corberán-Vallet, A., Lawson, A., Ferreira Lima, F.E. de, Donato, L.E., Alves, R.V., **Machado, G.**, Carvalho M., F. de, Pompei, J., Vilas, V.J.D.R., 2019. Integration of animal health and public health surveillance sources to exhaustively inform the risk of zoonosis: An application to visceral leishmaniasis data in Brazil. **Spat. Spatio-Temporal Epidemiol.** 29, 177–185. <https://doi.org/10.1016/j.sste.2018.09.001>
27. Cárdenas, N.C., Galvis, J.O.A., Farinati, A.A., Grisi-Filho, J.H.H., Diehl, G.N., **Machado, G.**, 2019. Burkholderia mallei: The dynamics of networks and disease transmission. **Transbound. Emerg. Dis.** 66, 715–728. <https://doi.org/10.1111/tbed.13071>
28. Fountain-Jones, N.M., **Machado, G.**, Carver, S., Packer, C., Recamonde-Mendoza, M., Craft, M.E., 2019. How to make more from exposure data? An integrated machine learning pipeline to predict pathogen exposure. **J. Anim. Ecol.** 88. <https://doi.org/10.1111/1365-2656.13076>
29. Kanankege, K.S.T., **Machado, G.**, Zhang, L., Dokkebakken, B., Schumann, V., Wells, S.J., Perez, A.M., Alvarez, J., 2019. Use of a voluntary testing program to study the spatial epidemiology of Johne's disease affecting dairy herds in Minnesota: a cross sectional study. **BMC Vet. Res.** 15, 429. <https://doi.org/10.1186/s12917-019-2155-7>
30. **Machado, G.**, Alvarez, J., Bakka, H.C., Perez, A., Donato, L.E., De Ferreira Lima Júnior, F.E., Alves, R.V., Del Rio Vilas, V.J., 2019a. Revisiting area risk classification of visceral leishmaniasis in Brazil. **BMC Infect. Dis.** <https://doi.org/10.1186/s12879-018-3564-0>.
31. **Machado, G.**, Korennoy, F., Alvarez, J., Picasso-Risso, C., Perez, A., VanderWaal, K., 2019b. Mapping changes in the spatiotemporal distribution of lumpy skin disease virus. **Transbound. Emerg. Dis.** <https://doi.org/10.1111/tbed.13253>
32. **Machado, G.**, Vilalta, C., Recamonde-Mendoza, M., Corzo, C., Torremorell, M., Perez, A., VanderWaal, K., 2019c. Identifying outbreaks of Porcine Epidemic Diarrhea virus through animal movements and spatial neighborhoods. **Sci. Rep.** 9, 457. <https://doi.org/10.1038/s41598-018-36934-8>.
33. Perez, A.M., Linhares, D.C.L., Arruda, A.G., VanderWaal, K., **Machado, G.**, Vilalta, C., Sanhueza, J.M., Torrison, J., Torremorell, M., Corzo, C.A., 2019. Individual or Common Good? Voluntary Data Sharing to Inform Disease Surveillance Systems in Food Animals. **Front. Vet. Sci.** 6, 194. <https://doi.org/10.3389/fvets.2019.00194>
34. Pires Espíndola, J., Balbinott, N., Trevisan Gressler, L., **Machado, G.**, Silene Klein, C., Rebelatto, R., Gutiérrez Martín, C.B., Kreutz, L.C., Schryvers, A.B., Frandoloso, R., 2019. Molecular serotyping of clinical strains of *Haemophilus (Glaesserella) parasuis* brings new insights regarding Glässer's disease outbreaks in Brazil. **PeerJ** 7, e6817. <https://doi.org/10.7717/peerj.6817>
35. Polo, N., **Machado, G.**, Rodrigues, R., Hamrick, P.N., Munoz-Zanzi, C., Pereira, M.M., Bercini, M., Timm, L.N., Schneider, M.C., 2019. A one health approach to investigating Leptospira serogroups and their spatial distributions among humans and animals in Rio Grande do Sul, Brazil, 2013-2015. **Trop. Med. Infect. Dis.** 4. <https://doi.org/10.3390/tropicalmed4010042>