Ariel L. Rivas, DVM, PhD, PhD
Research Associate Professor
Center for Global Health
Department of Internal Medicine MSC10 5550
1 University of New Mexico
Albuquerque, NM 87131
Phone: 505-272- 8207
Email: alrivas@unm.edu

Biography: Dr. Rivas received his DVM from the Veterinary Collage of the University of the Republic, Uruguay. He completed a post-graduate training in Pathology at the Royal Veterinary College of Uppsala University (Sweden), and holds one MS and two PhD degrees (one in Immunology, the other in Education) from Cornell University. He then became a Sr. Research Associate at Cornell University, working in bovine immunology. In 2005-2006, he became a member of the Mexican National Research System (SNI), serving as a professor of Epidemiology at the Autonomous University of Yucatan. In 2006 he became an adjunct Associate Professor at the Department of Public Health and Pathobiology of North Carolina State University. In 2012, he joined the Center for Global Health of the Medical School at UNM.

Academic and Research Interests: Dr Rivas' interests include development of biomedical methods related to infectious diseases and evaluation of educational systems. In education, he has been the external evaluator of foreign graduate programs. He has evaluated the Central University of Maracay (Venezuela) and has been invited to evaluate the National Autonomous University of Mexico (UNAM) in 2012 and in 2014.

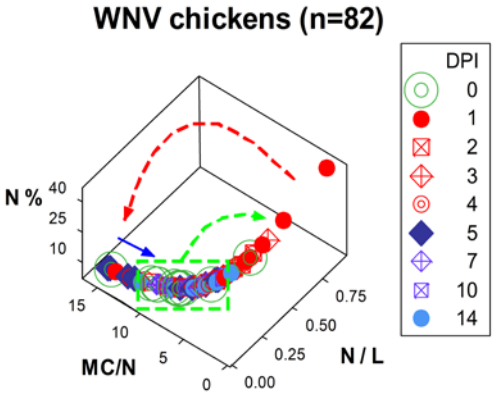
His research record includes publications involving viral (Marek's Disease, Avian Influenza, Foot-and-Mouth Disease), bacterial (*Staphylococcus aureus, Escherichia coli*, *Mycobacterium paratuberculosis*), and parasite-mediated (*Boophilus microplus*, *Plasmodium falciparum*) diseases affecting birds, cows, dogs, and humans. Such studies focus on personalized diagnostics and population medicine. To that end, a variety of technologies have been used (including automated ribotyping, flow cytometry, and geographical information systems) and a double library of datasets has been developed. For instance, Dr. Rivas has created geo-referenced datasets on epidemics that have occurred in England, Kenya, Mexico, Nigeria, Israel, US, and Uruguay. In diagnostics, he has built datasets on immunological-microbial interactions that include: (i) HIV, (ii) methicilin-sensitive *S. aureus*, (iii) methicilin-resistant *S. aureus*, (iv) septic syndromes, (v) malaria, (vi) *E. coli*. Using a data-driven, evolutionary approach, his current work centers on elucidating the properties of infectious disease data, as well as those of epidemic dissemination. The central concept of his approach is that Biology is complex, but not complicated: if complexity is uncovered, it may reveal useful information.

His research program has resulted in the first:

- temporal and multifactorial evaluation of cell surface markers involved in antigen recognition and diapedesis of bovines experimentally challenged with *S. aureus* (2001);
- spatial-temporal analysis of epidemic progression, in which high-resolution geographical data were utilized (2003);

- geo-referenced analysis of resistance against acaricides (2006)
- spatial-temporal report of a pandemic (Avian Influenza H5N1, 2010)
- demonstration of connectivity-related epidemic properties in rapidly disseminating epidemics (2012);
- demonstration of data circularity (feedback) in infectious diseases, as shown by single (one data point-wide) lines of observations (2013);
- application of dimensionless indicators in medicine, with the purpose of uncovering complex host-microbial interactions (2015).

Uncovering the hidden (feedbac related) properties of host-microbial Interactions: One example of a compl data format that results in interpretab patterns is described. It integrates a *simp* (non-structured) metric (the neutrophil [percent), together with at least *three leve of complexity*: (i) the neutrophil/lymphocy [N/L] interaction (complexity level I); (ii) tl interaction that includes both lymphocyt and macrophages (mononuclear cells MC) and N (MC/N or level II; and (iii) tl overall spatial-temporal interaction amo all interactions, which is assessed with a three-dimensional plot (complexity level III).



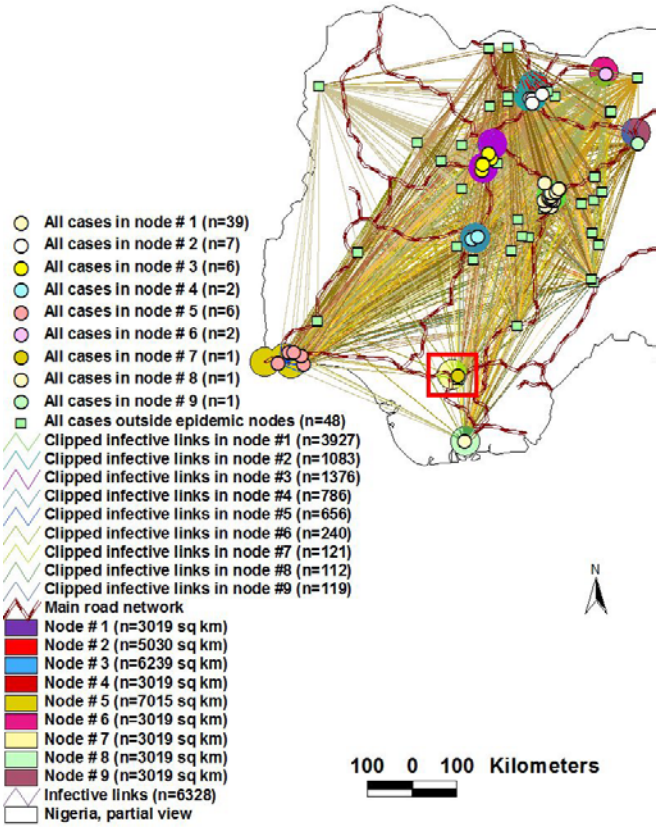
Such structure reveals several properties, including (i) *circularity* (feedback loops) and (ii) a *single* (one data-point wide) *line of observations*, as depicted in the figure shown above (data collected from 10 chickens regarded to be healthy at day 0 [day{s} post-inoculation or DPI], which revealed a perpendicular data inflection one day [1 DPI] after being challenged with West Nile Virus [WNV], then displayed a second data inflection by DPI 5, and, later [~DPI 14], moved back toward the center of the plot).

The 3D patterns so revealed help detect a recent inflammatory process (when data points are located on the right half of this plot), or support a 'recovery' hypothesis (when data points are located on the left half of this plot). Because similar patterns are observed in all vertebrates, when a simple source of data is available (e.g., a blood sample), this method can support diagnostic/prognostic inferences, even before microbiological tests are conducted.

Properties of disease dissemination (epidemics).

Integrating geography with mathematics and biology, the properties of rapidly disseminating epidemics (as as those of highly pathogenic Avian Influenza [AI] H5N1 virus) can be uncovered. Using geo-temporal data of an AI epidemic that took place in Nigeria, in 2006-2007, and focusing on connecting epidemic properties, this method predicted twice as many cases as classic alternatives. This approach assumes that emergent pathogens can only generate an epidemic if they take advantage of pre-existing, geographically explicit networks –such as those of the highway network, as shown here. Measuring actual (not simulated) data on roads, critical 'nodes' can be determined.

Control of the (usually, very few) critical nodes could result in earlier, less costly, and more effective control measures.



Key Publications:

1. Rivas AL, Quimby FW, Blue J and Coksaygan O. Longitudinal evaluation of bovine mammary gland health status by somatic cell counts, flow cytometry and cytology. *J Vet Diagn Invest* 13:399-407, 2001. PMID: 11580061
2. Rivas AL, Smith S, Sullivan PJ, Gardner B, Hoogesteyn AL, Castillo-Chávez C. Identification of geographical factors associated with early epidemic spread of Foot-and-Mouth Disease. *Amer J Vet Res* 64: 1519-1527, 2003. DOI: 10.2460/ajvr.2003.64.1519 PMID: 14672431
3. Rodríguez-Vivas RI, Rivas AL*****, Chowell G, Fragoso SH, Rosario CR, García Z, Smith SD, Williams JJ and Schwager SJ. Spatial distribution of acaricide profiles (*Boophilus microplus* strains susceptible or resistant to acaricides) in southeastern Mexico. *Vet Parasitol* 146: 158-169, 2007. DOI: 10.1016/j.vetpar.2007.01.016 PMID:17349747 *****:*corresponding author*
4. Rivas AL, Chowell G, Schwager SJ, Fasina FO, Hoogesteijn AL, Smith SD, Bisschop SPR and Anderson KL. Lessons from Nigeria: the role of roads in the geo-temporal progression of the avian influenza (H5N1). *Epid & Inf* 138: 192-198, 2010. DOI: 10.1017/S0950268809990495 PMID: 19653927
5. Rivas AL, Fasina FO, Hoogesteyn AL, Konah SN, Febles JL, Perkins DJ, Hyman JM, Fair JM, Hittner JB and Smith SD. Connecting network properties of rapidly disseminating epizoonotics. *PLoS ONE* 7(6): e39778, 2012. DOI:10.1371/journal.pone.0039778 PMID: 22761900

6. Rivas AL, Jankowski MD, Piccinini R, Leitner L, Schwarz D, Anderson KL, Fair JM, Hoogesteijn AL, Wolter W, Chaffer M, Blum S, Were T, Konah SN, Kempaiah P, Ong'echa JM, Diesterbeck US, Pilla R, Czerny CP, Hittner JB, Hyman JM and Perkins DJ. Feedback-based, system-level properties of vertebrate-microbial interactions. *PLoS ONE* 8(2): e53984, 2013. DOI:10.1371/journal.pone.0053984 PMID: 23437039
7. Leitner G, Blum S and Rivas AL. Visualizing the indefinable: three-dimensional complexity of 'infectious diseases. *PLoS ONE* 10(4):e0123674, 2015. DOI: 10.1371/journal.pone.0123674 PMID: 25875169