Dear E²M² organizers,

Please find:

- A current *Curriculum Vitae*
- An abstract describing a current research project that incorporates modeling
- A Statement of Interest and Intent indicating how the experience of attending this workshop will enhance my short-term and long-term research goals

I hope you will consider my application although I'm not a student anymore; I have been looking for a course on modelling applied to epidemiology and ecology for a while and am very interested by the entire program of the course as it will considerably strengthen my modelling capacities.

Best regards,

Helene Guis

Hélène GUIS

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Current position:

Researcher in epidemiology
Animals, health, Territories, Risks and Ecosystems (Astre) Unit
French agricultural research and international cooperation organization (CIRAD)

Expertise: Spatial epidemiology of vector-borne diseases ; Surveillance and control of animal diseases ; Risk mapping, modelling, statistics, data analysis; Geographic Information Systems and geomatics

Research fields: One Health, Zoonoses, Vector-borne diseases, Spatial epidemiology, Surveillance

Education and qualifications:

PhD in spatial epidemiology of vector-borne diseases (2007) (University of Franche-Comté, France)
Specialised Masters in Localised Information Systems for Spatial Planning (2004) (AgroParisTech, Engref, Montpellier Sup Agro, France)
Doctor in Veterinary Medicine (2003) (University of Toulouse, Veterinary School of Toulouse, France)
Masters in Science on Environnement, Health, Society (2003) (University of Franche-Comté, France)
Certificate of specialised studies in animal epidemiology (2002) (Veterinary School of Paris, France)
Certificate of veterinary specialised studies in tropical animal health (2002) (Veterinary School of Toulouse, France)
“Maîtrise” in biological and medical sciences (2001)(University of Toulouse, France)

Level 1 (basic) to 5 (excellent)	Reading	Oral	Written
French	5	5	5
English	5	5	5

Professional experience:

Since 08/2015 : Located in Institut Pasteur Madagascar, Epidemiology and clinical research Unit.

Since 03/2009 : Researcher at Astre, Cirad.

10/2007 - 02/2009 : Post-doc at Liverpool University, United Kingdom on Modeling the effets of climate change on bluetongue in Europe

Training courses given:

2007 - 2015 : Involved in training in GIS applied to epidemiological surveillance, Cirad, Master SAEPS and EPSED – France (2 weeks/year)

PhD thesis co-supervised:

2017 – Soledad Castano - Heterogeneity in hidden developmental processes: inference and analysis for stage-structured populations in fluctuating environments, West Indies University.
2014 - Maryam Diarra – Modeling the temporal dynamics and spatial distribution of *Culicoides* (Diptera : Ceratopogonidae) in Senegal, University G Berger, Senegal.
2013 - Georgette Kluiters - Modelling *Culicoides* distribution in the UK, Liverpool University, UK
2012 - Nicolas Moiroux – Spatial heterogeniety of malaria in Benin, University of Montpellier, France

Veterinary thesis co-supervised:

2018 – Nirina Raveloarijaona - Prevalence, incidence and risk factors on infection of horses by West Nile virus around Antananarivo, Madagascar, University of Anatanarivo, Madagascar
2017 – Felana Rasolonjatovo – Evaluation of filter paper for molecular diagnosis of rabic virus infection, University of Anatanarivo, Madagascar

Publications:

Diarra M., Fall M., Fall A.G., Diop A., Lancelot R, Seck M. T., Rakotoarivony I., Allene X., Bouyer J., Guis H. 2018. Spatial distribution modelling of *Culicoides* (Diptera: Ceratopogonidae) biting midges, potential vectors of African horse sickness and bluetongue viruses in Senegal Parasite and Vectors; **11**(1):341. doi: 10.1186/s13071-018-2920-7.

Jacquet S., Huber K., Guis H., Setier-Rio M.L., Goffredo M., Allene X., Rakotoarivony I., Chevillon C., Bouyer J., Baldet T., Balenghien T., Garros C. 2016. Spatio-temporal genetic variation of the biting midge vector species *Culicoides imicola* (Ceratopogonidae) Kieffer in France. *Parasites and Vectors*, **9** (*141*) : 12 p., http://dx.doi.org/10.1186/s13071-016-1426-4

Jacquet S., Huber K., Pagès N., Talavera S., Burgin L.E., Carpenter S., Sanders C., Dicko A.H., Djerbal M., Goffredo M., Lhor Y., Lucientes J., Miranda-Chueca M.A., Pereira da Fonseca I.,

Ramilo D., Setier-Rio M.L., Bouyer J., Chevillon C., Balenghien T., Guis H., Garros C. 2016. Range expansion of the Bluetongue vector, *Culicoides imicola*, in continental France likely due to rare wind-transport events. *Scientific Reports*, **6** (*27247*) : 14 p., http://dx.doi.org/10.1038/srep27247

Diarra M., Fall M., Lancelot R., Diop A., Fall A.G., Dicko A., Seck M.T., Garros C., Allene X., Rakotoarivony I., Bakhoum M.T., Bouyer J., Guis H. 2015. Modelling the abundances of two major *Culicoides* (Diptera: Ceratopogonidae) species in the Niayes Area of Senegal. *PloS One*, **10** (*6*) : 16 p. http://dx.doi.org/10.1371/journal.pone.0131021

Desvars A., Grimaud Y., Guis H., Esnault O., Allene X., Gardes L., Balenghien T., Baldet T., Delecolle J.C., Garros C. 2015. First overview of the *Culicoides* Latreille (Diptera: Ceratopogonidae) livestock associated species of Reunion Island, Indian Ocean. *Acta Tropica*, **142** : p. 5-19.

Guichard S., Guis H., Tran A., Garros C., Balenghien T., Kriticos D.J. 2014. Worldwide niche and future potential distribution of *Culicoides imicola*, a major vector of bluetongue and african horse sickness viruses. *PloS One*, **9** (*11*) : 8 p., http://dx.doi.org/10.1371/journal.pone.0112491

Pioz M., Guis H., Pleydell D., Gay E., Calavas D., Durand B., Ducrot C., Lancelot R., Sutton R. 2014. Did vaccination slow the spread of bluetongue in France?. *PloS One*, **9** (*1*) : 12 p., http://dx.doi.org/10.1371/journal.pone.0085444

Diarra M., Fall M., Fall A.G., Diop A., Seck M.T., Garros C., Balenghien T., Allene X., Rakotoarivony I., Lancelot R., Mall I., Bakhoum M.T., Dosum A.M., Ndao M., Bouyer J., Guis H. 2014. Seasonal dynamics of *Culicoides* (Diptera: Ceratopogonidae) biting midges, potential vectors of African horse sickness and bluetongue viruses in the Niayes area of Senegal. *Parasites and Vectors*, **7** (*147*) : 11 p., http://dx.doi.org/10.1186/1756-3305-7-147

Moiroux N., Djènontin A., Bio-Bangana S., Chandre F., Corbel V., Guis H. 2014. Spatio-temporal analysis of abundances of three malaria vector species in southern Benin using zero-truncated models. *Parasites and Vectors*, **7** (*103*) : 11 p., http://dx.doi.org/10.1186/1756-3305-7-103

Garni R., Tran A., Guis H., Baldet T., Benallal K., Boubidi S., Harrat Z. 2014. Remote sensing, land cover changes, and vector-borne diseases: Use of high spatial resolution satellite imagery to map the risk of occurrence of cutaneous leishmaniasis in Ghardaïa, Algeria. *Infection, Genetics and Evolution*. 28:725-34. doi: 10.1016/j.meegid.2014.09.036. Epub 2014 Oct 7

Moiroux N., Bio-Bangana S., Djènontin A., Chandre F., Corbel V., Guis H. 2013. Modelling the risk of being bitten by malaria vectors in a vector control area in southern Benin, west Africa. *Parasites and Vectors*, **6** (*71*) : 13 p., http://dx.doi.org/10.1186/1756-3305-6-71

Kluiters G., Sugden D., Guis H., McIntyre K.M., Labuschagne K., Vilar M.J., Baylis M. 2013. Modelling the spatial distribution of Culicoides biting midges at the local scale. *Journal of Applied Ecology*, **50** (*1*) : p. 232-242., http://dx.doi.org/10.1111/1365-2664.12030

Pioz M., Guis H., Crespin L., Gay E., Calavas D., Durand B., Abrial D., Ducrot C. 2012. Why did Bluetongue spread the way it did? Environmental factors influencing the velocity of Bluetongue Virus serotype 8 epizootic wave in France. *PloS One*, **7** (*8*) : 14 p., http://dx.doi.org/10.1371/journal.pone.0043360

Cetre-Sossah C., Pedarrieu A., Guis H., Defernez C., Bouloy M., Favre J., Girard S., Cardinale E., Albina E. 2012. Prevalence of Rift Valley Fever among ruminants, Mayotte. *Emerging Infectious Diseases*, **18** (*6*) : p. 972-975., http://dx.doi.org/10.3201/eid1806.111165

Moiroux N., Boussari O., Djènontin A., Damien G., Cottrell G., Henry M.C., Guis H., Corbel V. 2012. Dry season determinants of malaria disease and net use in Benin, West Africa. *PloS One*, **7** (*1*) : 7 p., http://dx.doi.org/10.1371/journal.pone.0030558

Guis H., Caminade C., Calvete C., Morse A.P., Tran A., Baylis M. 2012. Modelling the effects of past and future climate on the risk of bluetongue emergence in Europe. *Journal of the Royal Society Interface*, **9** (*67*) : p. 339-350., http://dx.doi.org/10.1098/rsif.2011.0255

Moiroux N., Gomez M., Pennetier C., Elanga E., Djènontin A., Chandre F., Djegbe I., Guis H., Corbel V. 2012. Changes in *Anopheles funestus* biting behavior following universal coverage of long-lasting insecticidal nets in Benin. *Journal of Infectious Diseases*, **206** (*10*) : p. 1622-1629. http://dx.doi.org/10.1093/infdis/jis565

Pioz M., Guis H., Calavas D., Durand B., Abrial D., Ducrot C. 2011. Estimating front-wave velocity of infectious diseases: A simple, efficient method applied to bluetongue. *Veterinary Research*, **42** : 13 p. http://dx.doi.org/10.1186/1297-9716-42-60

Guis H., Caminade C., Calvete C., Morse A. P., Tran A., Baylis M. 2011. Modelling the effects of past and future climate on the risk of bluetongue emergence in Europe. *Journal of the Royal Society Interface*.

Durand B., Zanella G., Biteau-Coroller F., Locatelli C., Baurier F., Simon C., Le Dréan E., Delaval J., Prengère E., Beauté V., Guis H. 2010. Anatomy of bluetongue virus serotype 8 epizootic wave, France, 2007-2008. *Emerging Infectious Diseases*, **16** (*12*) : p. 1861-1868., http://dx.doi.org/10.3201/eid1612.100412

Abstract

Background: Rift Valley Fever virus (RVFV) and West Nile virus (WNV) are two endemic zoonotic arboviruses in Madagascar. RVFV mainly affects humans and ruminants and WNV circulates among birds and can spill-over in humans and horses. Both are frequent and largely distributed in Madagascar. *Culex antennatus* and *Culex quinquefasciatus* are major vectors of these viruses in Madagascar. Little is known on the dynamics of these species, especially in the Central Highlands where seasonal temperature variations are the strongest. Identifying drivers of vector dynamics can help understand and predict periods of high transmission risk.

Aims and methods: In order to describe the dynamics of these two vector species in the Central Highlands, a 16 month longitudinal study consisting of bi-monthly catches in one farm located near Antananarivo was set up in 2017-8. Each fortnight, 6 CDC light traps were set: near cattle, horses, chicken, pigs, in an occupied house, and near a water point. A temperature and humidity data logger was set in the centroid of the traps. Data on rainfall and vegetation indices were extracted from MODIS satellite images and lunar phase was recorded. In parallel to adult catches, larvae were collected from the closest rice fields.

Results: During the 32 night catches, 46,737 mosquitoes belonging to 23 species were collected. *Culex antennatus* and *Cx. quinquefasciatus* represented the most abundant species (68.9% and 19.8% of catches respectively). *Culex antennatus* was more abundant near animal hosts whereas *Cx. quinquefasciatus* was dominant inside the house.

Modeling perspectives: Three main modelling perspectives are foreseen. A statistical model of the dynamics of each of the two species will be carried out in order to identify climatic, environmental and host variables impacting the dynamics of adults. A similar model could be built to explain larvae dynamics according to climatic variables. Models will need to take into account the repeated and over-dispersed nature of the data. If these two models correctly fit the data, a mathematical model of population dynamics could also be developed taking into account the larvae and adult counts and explanatory variables impacting both stages. A third modelling perspective could consist in developing a mathematical transmission model: the basic reproduction ratio R_0 (the number of secondary cases arising from the introduction of one infected host in a susceptible population) by combining vector dynamics and the best published estimates of vector competence, biting rate, and survival, and lengths of incubation period and viremia.

Statement of interest and intent

I'm very interested in following this course as it will i) strengthen my modelling capacities, ii) be directly applicable to analyze data sets I have already collected or that I plan to collect in 2019 and after, iii) help me supervise students.

1. Overview of the training program and how it will strengthen my modelling capacities.

This course would be extremely beneficial for me as it would considerably strengthen my modeling capacities. As a researcher in veterinary epidemiology, I often work at the interface of disciplines (ecology, climatology, statistics, physics, sociology, virology…) and professions (farmers, decision makers, researchers from other disciplines, practitioners…). As research questions are multifactorial and involve handling complex data, I'm hoping this course will enable me to take in charge a greater part of the modelling work, build more robust models and models which are more in adequacy with the design and the structure of the data.

I am particularly interested in attending the workshop as in my every day work I'm confronted to various statistical and mathematical modelling approaches. I can develop simple statistical multivariate models (*e.g.* logistic regression models to identify risk factors of exposure to pathogens), but I often have to seek help of statisticians and modelers for more complex designs. In particular, as I mainly work on vector-borne diseases, I often have to deal with repeated/clustered count data and over-dispersed data. I'm therefore very keen on following the course on mixed modeling. I also work on species distribution models (mainly statistical models), and am very interested in having an overview of the diversity of approaches to model distribution or niches and elements that should drive the choice between them.

Although I have worked on R_0 models, I used the simple R_0 equation which applies for vector-borne diseases or equations developed by others. I have no experience in developing compartmental models and differential equations, so the course would be very interesting so as to be able to conceive models adapted to any particular epidemiological situation, both for assessing transmission risk and working on population dynamic models.

Finally, whatever the models developed, one is always confronted to model fitting, comparison and validation steps. Training on these topics would therefore also be very beneficial for me as I only master basic procedures such as Akaike selection criteria to compare several models or ROC curves to validate logistic regression models. This course would give me a broader overview of tools and indicators and globally strengthen my modelling capacities.

2. Modelling projects foreseen

Among the past and ongoing projects I'm working on, I have data on horse and bird West Nile Virus (WNV) serological status and different explanatory variables at the individual (horse or bird) level and at higher levels (stable, species, region levels). We're developing models to identify WNV exposure risk factors. We are also currently carrying out a project on leptospirosis and West Nile in hospitalized patients. In that project we are collecting a long list of possible risk factors (individual, house design, activities, mosquito exposure, water exposure, animal exposure). Here also we aim to identify exposure factors in humans.

Alongside to the longitudinal data we have collected on mosquito dynamics near Antananarivo (presented in the abstract), we will be starting a project on the distribution and dynamics of arboviral vectors throughout Madagascar. An intense trapping campaign will be carried out next year, in 25 sites covering the 5 eco-climatic regions of Madagascar. In each site, traps will be set near a village, near a water point and near a forest. Five types of traps will be set in each site. Sites will be sampled every two months for a year, and two extra trappings will be carried out (one in the dry and one in the rainy season) the following year for model validation.

Data already collected and data which will be collected next year guarantee that I will be using what I will have learnt during the course straight away. I will not be an expert modeler after a one week course, but it will significantly contribute to strengthen my capacities, it will enable me to take in charge a greater part of the modelling work and facilitate interactions and discussions with other modelers. Similarly, it will increase my capacities in supervising veterinary students.