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Jean-Claude Thill holds a M.Sc. in Spatial Planning from the Catholic University of Louvain, Belgium, and a Doctorate in Geography from the same institution. In 2006 he joined the University of North Carolina at Charlotte as the Knight Foundation Distinguished Professor of Public Policy in the Department of Geography and Earth Sciences. Thill’s research focuses on the spatio-temporal dimensions of socio-economic organizations, particularly the interfacing between transportation and mobility systems, and urban land use, urban regional forms and functions. He is the Editor-in-Chief of Computers, Environment and Urban Systems. He served as Executive Director of the North American Regional Science Council, a branch of the Regional Science Association International (RSAI), from 2005 to 2012. He just stepped down from a two-year term as President of the Regional Science Association International and has been elected Fellow of the RSAI. Since 2013, Thill has served as Director of Project Mosaic, a major Social Science research initiative of the University of North Carolina at Charlotte. He is the recipient of multiple awards, including the 2012 Hirotada Kohno Prize, the 2012 Edward L. Ullman Award, the 2009 Michael Breheny Prize, the 2008 David Boyce Award, the 1996 J.G.D. Hewings, and the 1988 Philippe Aydalot Prize.

Daniel Janies joined the faculty of the University of North Carolina at Charlotte as The Carol Grotnes Belk Distinguished Professor of Bioinformatics and Genomics. Janies received a Bachelor of Sciences degree in Biology from the University of Michigan in 1988 and a Ph.D. in Zoology from the University of Florida in 1995. Janies worked as a postdoctoral fellow (1996–1999) and a principal investigator (2000–2002) at the American Museum of Natural History in New York City where he lead a team that, using off-the-shelf PC components, built one of the world’s largest computing clusters in 2001. Most recently Janies was a tenured faculty member in the College of Medicine at the Ohio State University. He is a national principal investigator in the Tree of Life program (http://echinotol.org/) of the National Science foundation and is funded by the Defense Applied Research Projects Agency. His work involves empirical studies of organismal diversity and development of software, such as Supramap (https://supramap.herokuapp.com/). Supramap is used by public health scientists to put pathogen genomic data into context with geography and hosts. The results are akin to weather maps for disease.

Analyzing and Forecasting the Range of Chikungunya Virus

Chikungunya is a viral disease spread by infected mosquitoes to humans and various animals, including rodents and monkeys. The animals are not obligate intermediate hosts—the infection cycle is considered a mosquito-human disease. Thousands of travelers have
brought the disease to the Americas from trips around the world, and local transmission has been reported in at least eleven cases in Florida just last year. There have been several cases in Mexico as well. Health organizations all over the world are conducting surveillance for and response to Chikungunya outbreaks as places like Fiji and the Brazilian State of Amazonas are experiencing their first imported cases.

Symptoms of the disease in humans are similar to those of dengue and include abrupt-onset fever and severe joint pain, and sometimes headache, nausea, fatigue, and rashes. Treatment is targeted towards relieving symptoms, as there are currently no treatments for the disease itself.

Chikungunya is caused by the Chikungunya virus, an RNA alphavirus of the family Togaviridae. The primary vector of the virus, the yellow fever mosquito \textit{(Aedes aegypti)}. A strain of Chikungunya is also spread by the Asian tiger mosquito \textit{(Aedes albopictus)}. The role of other vectors (e.g., mosquitoes in the genus \textit{Culex}) is understudied. Though \textit{A. aegypti} originated in Africa, it has expanded to tropical and subtropical regions around the world including parts of the Americas (e.g., Southeastern US, Caribbean, South America and Mexico) and Europe (e.g., Italy and Spain). Recent outbreaks in Myanmar, China, and Northern India, however, have been linked to \textit{A. albopictus}, which is native to Asia and now found in much more temperate regions than \textit{A. aegypti}. \textit{A. albopictus} has recently expanded its range to include parts of Africa, Europe, and the Americas.

This research is aimed at studying the current and future expansion of Chikungunya virus’ geographic spread in light of a mutation that confers host range. In the lab, it has been shown that the transmission of a variant of Chikungunya virus that carry valine at position 226 (E1-226V) in the envelope protein (E1) is increased in \textit{A. albopictus}, while both the variant (E1-226V) and wild type (E1-A226) Chikungunya viruses are transmitted by \textit{A. aegypti}. \textit{A. albopictus} has been found to out-compete \textit{A. aegypti} and other mosquitoes. These facts, combined with a broader geographic distribution of \textit{A. albopictus} towards temperate latitudes and the dynamics of climate change, render the epidemiology of Chikungunya virus a particularly wicked problem to analyze and forecast across space and through time. Implications for the public health response to the spread of Chikungunya virus are important, and lessons for the epidemiology of other viruses (such as dengue) that may also develop new strains through mutation in the future are considerable.

In a pilot study, we have used geographic and phylogenetic visualization of viral variants along with the current geographic distribution of \textit{A. aegypti} and \textit{A. albopictus} to create a risk map for the disease, to help understand the spread of the virus, and inform control measures. We found that the E1-A226V mutation has occurred at least six times in the history of the virus. The largest clade in terms of sequenced isolates carrying E1-226V is found in Southern Asia. We conclude that high-risk areas for the disease, based on the co-occurrence of viral variants and the distribution of mosquitoes, include Northern Africa, Puerto Rico, Southeast Asia, and Madagascar.

Based on this knowledge, we will model the spread of Chikungunya virus by decomposing the process into three steps: (1) the modeling of the potential range of the hosts of the two
strains of the virus, (2) the modeling of the effective geographic range of the hosts, and (3) the modeling of the transmission and infection of the hosts, animal reservoirs, and humans. Step 1 will be implemented with a MaxEnt Species Distribution Model (SDM) calibrated on the basis of presence and absence data of *A. aegypti* and *A. albopictus* and climatic and physiographic predictors. MaxEnt has been proven to be an effective SDM approach for binary data. The calibration accounts for multicollinearity about predictors and for spatial dependence effects. In Step 2, we use an Agent-based Model (ABM) to evaluate the effective geographic extent of *A. aegypti* and *A. albopictus* according to known and potential facilitators and barriers to the diffusion of the mosquitoes. Mosquito hosts cannot effectively spread across space, and large ocean basins in particular, on their own. Human-aided transport of mosquitoes such as via freight flows are important. Records of shipping across the world will be used to calibrate the spatial-temporal spread of mosquitoes. In step 3, we will implement an ABM of the infection of two strains of Chikungunya virus that is conditional upon the effective spatial distribution of all hosts (mosquitoes, humans, other animals) and of the two strains of Chikungunya virus as agents responding to spatio-temporal drivers. Markov chain stochastic models will be used to operationalize the transmission and infection process. Sensitivity analysis is conducted to establish the stability of resulting patterns. The three-step model will be then used under various scenarios to simulate the continued spread of Chikungunya around the world, according to anticipated patterns of climate change and the effectiveness of control measures. The proposed modulator framework enables to disentangle the space-time complexity of Chikungunya and construct various scenarios for use in public health analysis and policy making.