**Force of Infection (FOI) Analysis**

In order to investigate the endemicity and/or recent emergence of the viruses under study, we analysed and compared two age-structured sero-surveys from Panama. One, conducted in the Darien region, surveyed by our team in 20121 and the 2017 sero-survey described in this paper. The population surveyed in 2012 was previously described1.

The force-of-infection (FOI) was estimated using a catalytic model2 from seroprevalence data that were assumed to follow binomial distributions. We tested whether or not the MADV, VEEV or UNAV incidence per susceptible person per time unit has remained constant over time or has varied, for example due to the

recent introduction of these viruses into the human populations included in both 2012 and 2017 sero-surveys. Other assumptions include no sero-reversion, and no age dependence in susceptibility or exposure 3

For a **constant FOI** (λ), we can express the sero-prevalence for age in the year of the sero-survey as:

For a **time-varying FOI**, we can express the sero-prevalence for age in the year of the sero-survey as:

Time  is 2012 or 2017 according to the sero-survey analysed.

For convenience and due to sample size restrictions, we estimated the time-varying FOI as five parameters over the total exposure time (. One parameter per decade from to for a total of four decades, and then one value for the period between the minimum year of birth in the sampled population () until , meaning this last period is usually slightly longer than 10 years, but the exact number could differ between surveys.

Models were fitted to sero-prevalence data for the three viruses (UNAV, MADV and VEEV) using a Bayesian Markov Chain Monte Carlo (MCMC) method with Metropolis-Hasting algorithm with 5,000 iterations and 50% of burn-in period. Convergence was assessed visually and using R^ statistic. Best model was chosen according to lowest Deviance Information Criterion (DIC). The analyses were conducted using R and RStan 4.

References

1 Vittor AY, Armien B, Gonzalez P, *et al.* Epidemiology of Emergent Madariaga Encephalitis in a Region with Endemic Venezuelan Equine Encephalitis: Initial Host Studies and Human Cross-Sectional Study in Darien, Panama. *PLoS Negl Trop Dis* 2016; **10**. DOI:10.1371/journal.pntd.0004554.

2 Muench H. Catalytic Models in Epidemiology, Harvard Un. 1959 http://www.sciencemag.org/cgi/doi/10.1126/science.131.3407.1091.

3 Salje H, Cauchemez S, Alera MT, *et al.* Reconstruction of 60 years of chikungunya epidemiology in the philippines demonstrates episodic and focal transmission. *J Infect Dis* 2016; **213**: 604–10.

4 Carpenter B, Gelman A, Hoffman MD, *et al.* Stan : A Probabilistic Programming Language. *J Stat Softw* 2017; **76**. DOI:10.18637/jss.v076.i01.