

The mechanistic Analysis of Founder Virus Data in Challenge Models



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Repeated low-dose (RLD) challenge studies provide valuable information when evaluating candidate vaccines since they resemble the typical exposure of natural transmission and inform on the number of exposures prior to infection. This work uses the number of infecting viruses at the time of infection (rather than occurrence of infection) to characterize candidate vaccine's protective effect, by determining the vaccine's mechanism of action. We consider a null mechanism (no protection), a Leaky mechanism in which the number of infecting viruses is reduced by some factor in vaccinated subjects, the All-or-none mechanism in which the vaccine either offers complete protection or no protection in vaccinated subjects, and a Combination model with both Leaky and All-or-none mechanisms. We consider two discrete marked survival models where the number of founder viruses follow a Poisson distribution with either a fixed mean parameter (Poisson model), or a random mean parameter that follows a Gamma distribution (Negative Binomial Model). We illustrate the performance of these methodologies with a data example of SIV on non-human primates and a simulation study.

Thursday, March 30, 2023, 3:30-4:30 PM Eastern

133 Rosenau Hall

Virtual using link and info below.

<https://unc.zoom.us/j/91249030964?pwd=UXloTWlHajdQbkRqd1d5TnRaMitYdz09>

Meeting ID: 912 4903 0964

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