

Supplement S4 R code for the maximum likelihood estimation of the force of infection (λ) from an age-specific seroprevalence curve

```
library(bbmle)

### Model fitting requires the use of the bbmle library

sero<-function(lambda,sd){
-sum(dnorm(seroprevalence,mean=(1-exp(lambda*age)),sd=sd,log=T))
}

### sero is the maximum likelihood function to be optimized. We assumed that
### seroprevalence was normally distributed Its parameters are lambda which
### corresponds to  $\lambda$  in equation (2) and sd, which is the standard deviation
### of the error.
### For the maximum likelihood estimation we need a vector with age specific
### seroprevalence and age to define the relations presented in equation 2.
### the sum corresponds the log-likelihood expression for the model, i.e.,
###  $L(S(a)|\lambda, \text{var}) = \sum_{a=0}^{\omega} \kappa - \frac{(\omega+1)\ln(sd)}{2} - \frac{1}{2sd^2} \sum_{a=0}^{\omega} \left( S(a) - (1 - e^{-\lambda a}) \right)^2$ , where  $\kappa$  is a constant
### from the normal distribution,  $\omega$  is the maximum age in the dog population
### and  $sd^2$  is the variance of the error.

modelfit=mle2(sero,start=list(lambda=-.16,sd=0.14))

### mle2 is a command to fit the maximum likelihood model, with initial
### guesses for the parameters defined in "start=list(...)"

summary(modelfit)

### summary is a command that summarizes the output from the maximum
### likelihood estimation

confint(modelfit)

### confint is a command that estimates the 95% confidence intervals for the
### parameters in the maximum likelihood function via maximum likelihood
### profiling.
```