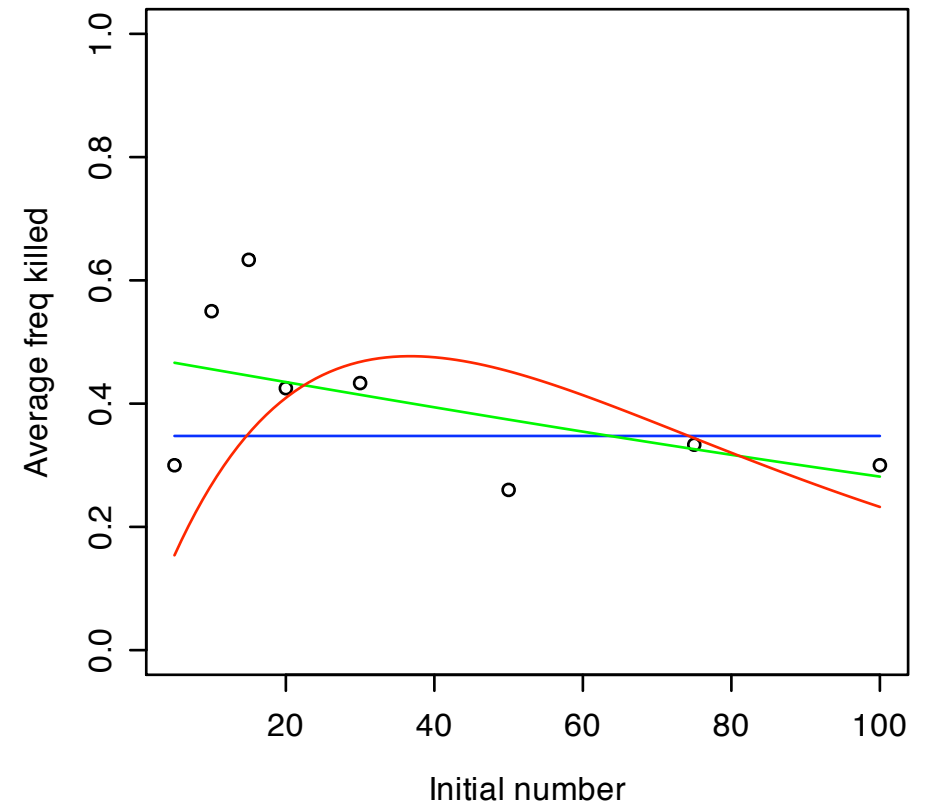


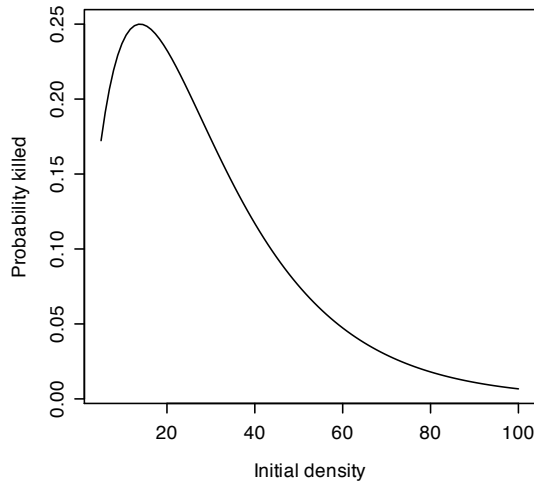
IN ALL STEPS, THINK

- are any of these models satisfactory?

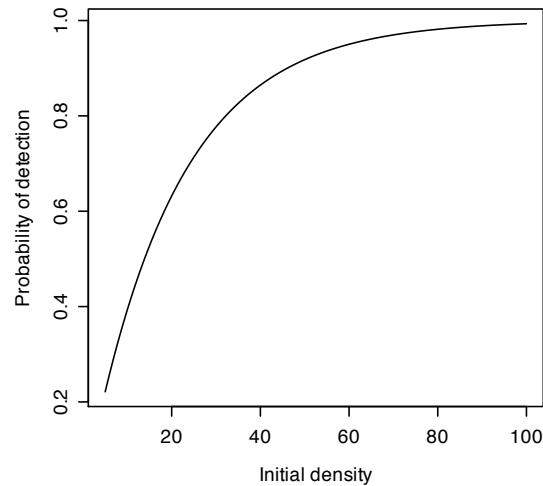


A BIOLOGICAL MODEL

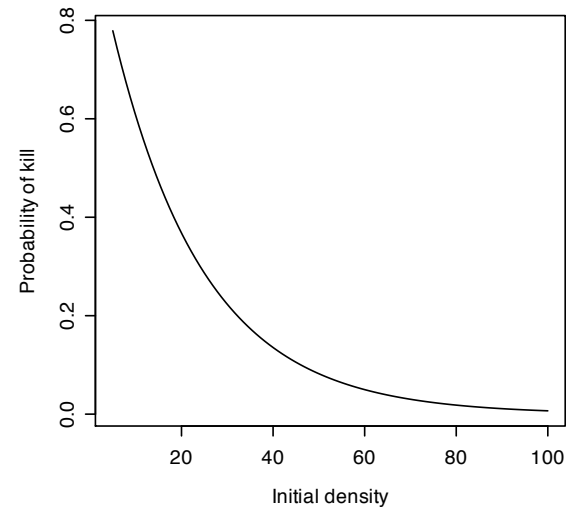
$$\Pr(\text{killed}) = \Pr(\text{detect}) \times \Pr(\text{kill})$$



=



×



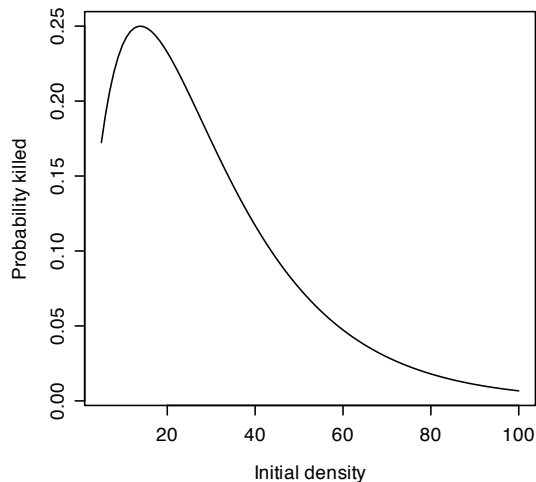
$$1 - \exp(-a_1 - b_1 x)$$

$$a_2 + \exp(-b_2 x)$$

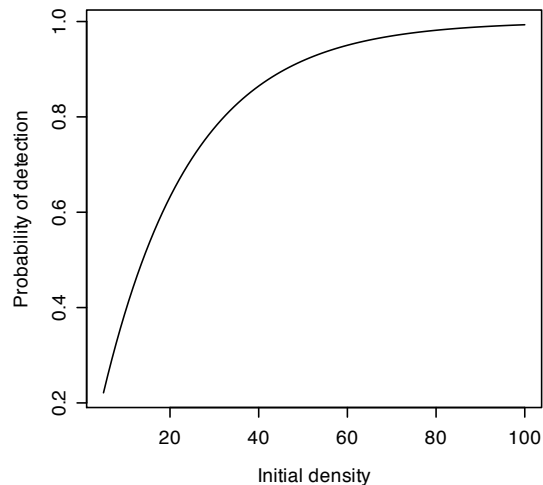
A BIOLOGICAL MODEL

```
prob.detect <- function( a , b , x ) {  
  (1 - exp(-(a+b*x)))  
}
```

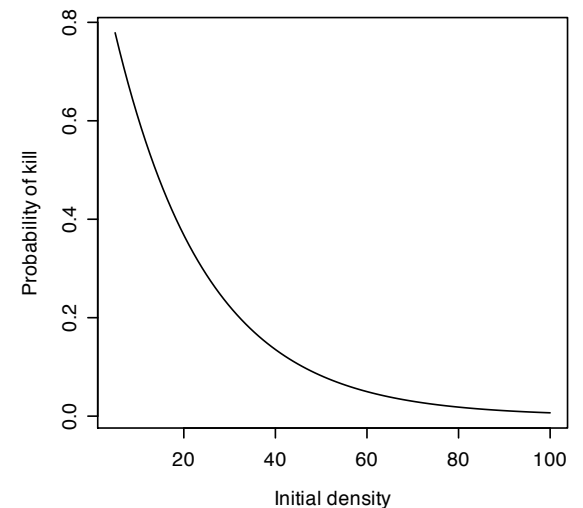
```
prob.kill <- function( a , b , x ) {  
  a + exp(-b*x)  
}
```



==



×



FIT!

```
m5 <- mle2( d$Killed ~ dbinom( prob=prob.detect(a1,b1,d  
$Initial)*prob.kill(a2,b2,d$Initial) , size=d$Initial ) ,  
start=list( a1=0 , b1=0.05 , a2=0.3 , b2=0.1 ) )
```

Coefficients:

	a1	b1	a2	b2
	-0.81734127	0.23596031	0.30170248	0.08144609

Log-likelihood: -43.2

