IBV Transmission study to determine the transmission of pathogenic IBV (Challenge) among vaccinated Commercial Broilers compared to that of unvaccinated birds

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Source required code-files including loading the data

Document structure

- Estimation of the upperlimit of R in the vaccinated and lowerlimit of R in the unvaccinated birds (Velthuis et al. 2007).
- Considerations for next trials

Based on previous discussions the "M41" strain is excluded.

For the unvaccinated groups in the "GA08" strain challenged group all contact and seeder birds were positive at the first measurement. In the vaccinated groups only a few seeders were positive, but none of the contacts.

Final size

The final size are the number of animals that were infected during the entire duration of an outbreak (or experiment). For small numbers the exact distribution can be determined numerically for a known value of R. This can be used to determine the most likely value of R and its boundaries given an observed final size. In case of no or all contact animals being infected the most likely value is respectively 0 or inf and only the upper- and lower boundary of the confidence interval can be given.

```
## `summarise()` has grouped output by 'Group'. You can override using the `.groups` argument.
```

Table 1: Input values for the final size calculations. fs = susceptibles end of experiment, iS = contact birds beginning of experiment, iI = challenged birds that excreed during experiment, iR = challenged birds that do not excrete

Group	Vaccinated	fs	iS	iI	iR
DMV_1	Yes	10	10	4	6
DMV_2	No	0	10	10	0
GA08_1	Yes	10	10	3	7
GA08_2	No	0	10	10	0

R of vaccinated

Table 2: Estimate of R based on the final size. point.est = best value, ci.ul = upper limit, pval.above1 = probability R is above 1

strain	point.est	ci.ul	pval.above1
DMV	0	2.23	0.20
GA08	0	3.43	0.30
Both	0	1.07	0.06

R of unvaccinated

Table 3: Estimate of R based on the final size. point.est = best value, ci.ul = lower limit, pval.below1 = probability R is below 1

strain	point.est	ci.ll	pval.below1
DMV	Inf	1.349	0.0120
GA08	Inf	1.349	0.0120
Both	Inf	2.055	0.0001

R of vaccinated Non excreting challenged are S

Table 4: Estimate of R based on the final size. point.est = best value, ci.ul = upper limit, pval.above1 = probability R is above 1

strain	point.est	ci.ul	pval.above1
DMV	0	1.39	0.10
GA08	0	2.02	0.16
Both	0	0.65	0.02

Some considerations for setting up follow-up experiments

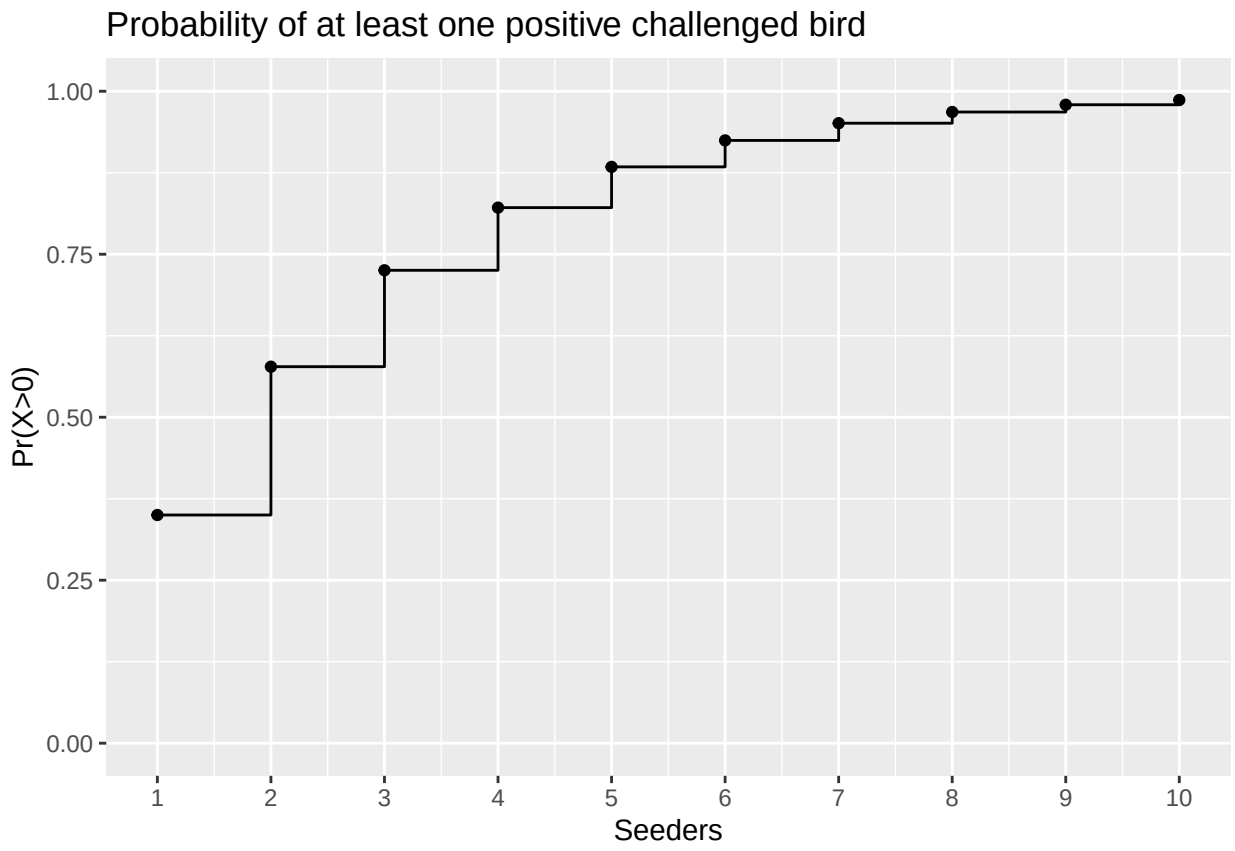
From Table 3 in Velthuis et al 2007, we can already see that with two repetitions of 9 S0 and 9 I0 birds we can easily determine a difference in R.

Table 5: Table 3. in Velthuis et al. Power calculations for different experimental designs to find a difference in transmission between two treatment groups. Velthuis et al 2007

S0I0	repetitions	R1.5R0.5	R3.5R0.5	R10.0R0.5	R10.0R1.5	R10.0R3.5
(1, 1)	18	0.306	0.814	0.991	0.755	0.224
(2,2)	9	0.372	0.886	0.995	0.678	0.080
(3,3)	6	0.461	0.932	0.997	0.619	0.040
(6,6)	3	0.461	0.938	0.990	0.343	0.004
(9,9)	2	0.505	0.950	0.987	0.288	0.002
(18,18)	1	0.552	0.957	0.983	0.229	0.001

The number of successful challenges in the vaccine groups was limited. Smaller groups could increase the risk of complete failure.

```r
# The probability of an successful challenge in the vaccine seeders is:
p = 7/20
#probability of more than zero successful challenges
ggplot(data = data.frame(x = c(1:10),
        y = 1-sapply(c(1:10), dbinom, x =0, prob =p )), aes(x,y))+
  geom_step()+
  geom_point()+
  scale_x_continuous(breaks = c(0:11))+
  scale_y_continuous(limits = c(0,1))+
  labs(x = "Seeders",y = "Pr(X>0)")+ggtitle("Probability of at least one positive challenged bird")
```



Reference

Velthuis, A. G. J., Bouma, A., Katsma, W. E. A., Nodelijk, G., & De Jong, M. C. M. (2007). Design and analysis of small-scale transmission experiments with animals. Epidemiology and Infection, 135(2), 202–217. https://doi.org/10.1017/S095026880600673X