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 in vaccinated and unvaccinated birds using final size estimation
* Estimation of (transmission coefficient in birds per day) in vaccinated and unvaccinated birds using generalized linear model reference: (Velthuis et al. 2007)

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 . This can be used to determine the most likely value of 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 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.

Input values for the final size calculations. fs = susceptibles infected at 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 | n |
| --- | --- | --- | --- | --- | --- | --- |
| DMV 1639\_1\_1 | Yes | 1 | 10 | 10 | 0 | 20 |
| DMV 1639\_1\_2 | Yes | 0 | 10 | 7 | 3 | 20 |
| DMV 1639\_2\_1 | No | 9 | 10 | 10 | 0 | 20 |
| DMV 1639\_2\_2 | No | 10 | 10 | 10 | 0 | 20 |

## with final size estimation

Estimate of based on the final size. Estimate = best value, 95%-LL= lower limit,95%-UL = upper limit, pval.above1 = probability is above 1

| Vaccinated | Estimate | 95%-LL | 95%-UL | pval.above1 |
| --- | --- | --- | --- | --- |
| Yes | 0.12 | 0.01 | 0.61 | 0.01 |
| No | 3.41 | 1.63 | 7.34 | 1.00 |

## with final size estimation: Non excreting challenged are S

Estimate of based on the final size. Estimate = best value, 95%-LL= lower limit,95%-UL = upper limit, pval.above1 = probability is above 1

| Vaccinated | Estimate | 95%-LL | 95%-UL | pval.above1 |
| --- | --- | --- | --- | --- |
| Yes | 0.10 | 0.01 | 0.54 | 0 |
| No | 3.41 | 1.63 | 7.34 | 1 |

# Regression estimation of the transmission coefficient

Using a complementary log-log link function in a generalized linear model, the transmission coefficient (number of infected birds in one day by one infectious bird) is estimated.

kable(cbind(summary(fit)$coefficients, confint(fit)),  
 caption = c("Estimate of log(beta) using glm."),  
 digits = 3)

## Waiting for profiling to be done...

Estimate of log(beta) using glm.

|  | Estimate | Std. Error | z value | Pr(>|z|) | 2.5 % | 97.5 % |
| --- | --- | --- | --- | --- | --- | --- |
| (Intercept) | 0.968 | 0.296 | 3.270 | 0.001 | 0.374 | 1.530 |
| VaccinatedYes | -5.530 | 1.043 | -5.304 | 0.000 | -8.435 | -3.911 |

kable(rbind(c("Estimate","2.5%","97.5%"),signif(cbind(exp(cumsum(summary(fit)$coefficients[,1])), exp(cumsum(confint(fit)[,1])),exp(cumsum(confint(fit)[,2]))),digits =3)),  
 caption = c("Transform to beta"),  
 digits = 3)

## Waiting for profiling to be done...  
## Waiting for profiling to be done...

Transform to beta

|  |  |  |  |
| --- | --- | --- | --- |
|  | Estimate | 2.5% | 97.5% |
| (Intercept) | 2.63 | 1.45 | 4.62 |
| VaccinatedYes | 0.0104 | 0.000316 | 0.0925 |

# 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>