NDVtrailPresent

Egil Fischer

Introduction

Material and
methods

Results

Conclusion
and discussion

NDVtrailPresentation

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Trial set-up

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NDV trial:

- Transmission in vaccinated and unvaccinated groups

- Four separate groups (i.e. 2 replicates per treatment)

- Challenge in 10 out of 20 birds

- ON- and CLO-swab at each day post challenge (DPI) for 14 days

- ELISA at the end of the trial

$R = \beta \cdot T_{inf}$

- Infectious period T_{inf} = number of days a bird is infectious

- Transmission coefficient β = number of new infections by one infectious bird per day

- Reproduction ratio R = number of new infectious birds per infectious bird during its entire infectious period

If $R < 1$ an infection will go extinct.

Research questions

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- What are the values of the transmission parameters?
- Do the transmission parameters differ between vaccinated and unvaccinated groups?
- Is the R in vaccinated groups below 1?

Material and methods

Visualization of descriptive data

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- Survival plot

- Epidemic curves (number of infectious animals divided by the total) were produced.

- Histogram of infectious period

Statistical analyses

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The infectious period T_{inf}: Parametric survival analyses assuming Normal distribution

The transmission parameter β: Generalized linear model with a complementary loglog-link function:

```
glm(cbind(C, S-C) ~ 1,offset = log(I/N), family =
binomial(link = "cloglog"), data = data.set,
na.action = na.omit)
```

The basic reproduction number $R_0 = \beta \cdot T_{inf}$ The confidence interval is calculated by
$$\log(R) = \log(\beta) + \log(T_{inf}) \pm Z_{0.05} \cdot (\log(SE(\beta)) + \log(SE(T_{inf})))$$

Assumes independence between the transmission parameter and the infectious period.

Transmission model

- SIR: Susceptible $\rightarrow$ Infectious $\rightarrow$ Recovered and immune

The determination of a single sample to be positive depends on
two assumptions

- Detection threshold (default set to Ct < 36)

- Sample is positive if at least one consecutive sample is
  positive: Pos , Neg , Pos, Pos $=$ first positive is assumed to
  be negative, 3rd and 4th positive (same for negative but
  the opposite)
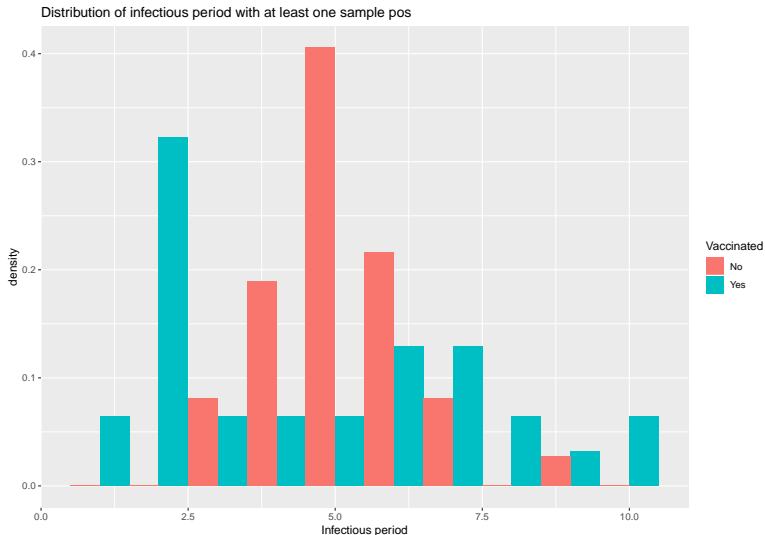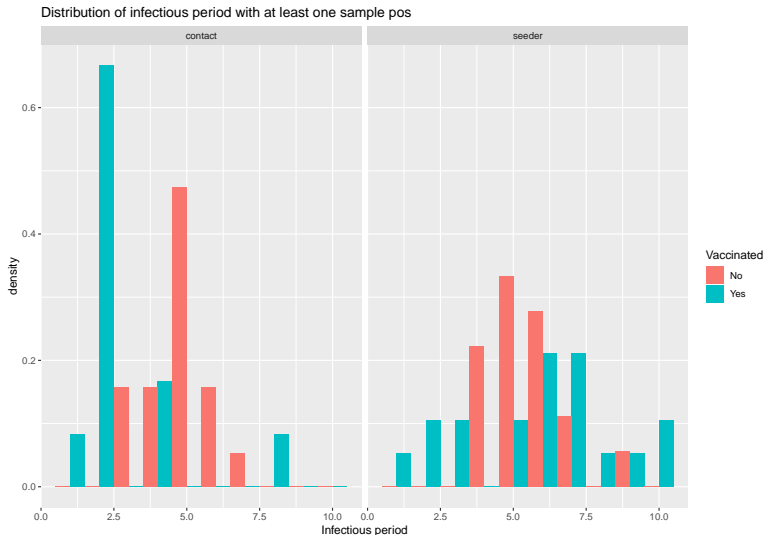
Results

Survival curve

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survivalplot

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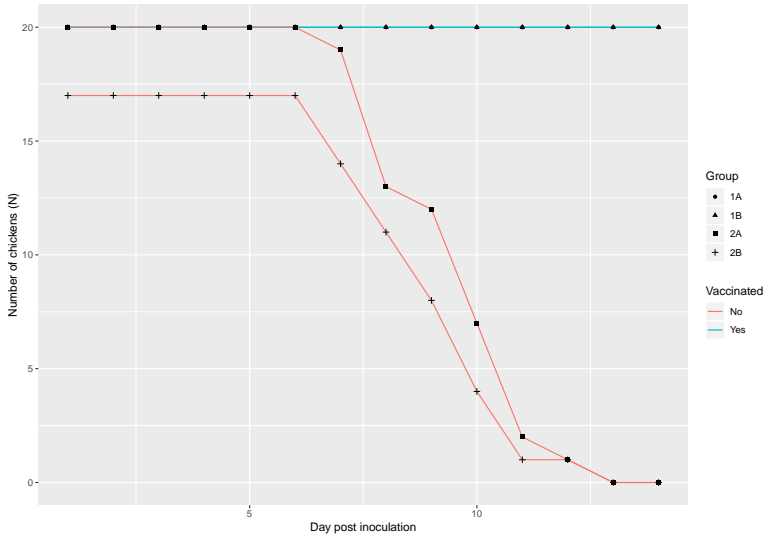
T_{inf} at least one (CLO or ON) positive sample

hist.one

Distribution of infectious period with at least one sample pos

`hist.one.chal`

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Statistical analyses $\sim$ using parametric survival analyses

Survival analyses assuming a Gaussian distributed T_{Inf} and only using the contact birds.

```
summary(surv.fit.one.SIR.gaussian)
```

```
##
## Call:
## survival::survreg(formula = survival::Surv(infper,
##      data = out.indiv.one.SIR[out.indiv.one.SIR$Cha
##          ], na.action = na.omit, dist = "gaussian")
##                  Value Std. Error     z      p
## (Intercept)     4.789      0.323 14.81 <2e-16
## VaccinatedYes  -1.622      0.547 -2.96 0.0030
## Log(scale)      0.343      0.132  2.60 0.0093
##
## Scale= 1.41
##
```

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```
summary(fit.one.SIR.fixed)
```

```
##
## Call:
## glm(formula = cbind(C, S - C) ~ Vaccinated, family
##     data = out.nona.one.SIR, na.action = na.omit,
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -2.66807  -1.18662   0.06918   1.31868   2.82900
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)     0.1069     0.1730   0.618    0.537
## VaccinatedYes  -0.3525     0.2231  -1.580    0.114
##
## (Dispersion parameter for binomial family taken to
```

β estimates

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```
beta.table
```

```
##   Treatment  beta  2.5%  97.5
## 1     Unvac 1.113 0.777 1.537
## 2       Vac 0.782 0.507 1.221
```

Vaccination does not lower the infection parameter β.

Summarize ~ infectious period

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```
mean.beta.inf.R[, c(1,5,6,7)]
```

```
##   Vaccinated   infper llinfper ulinfper
## 1         No 4.789474 4.155548 5.423399
## 2        Yes 3.167164 1.460171 4.874158
```

Vaccine reduces length of infectious period ($p = 0.004$)

Summarize $\sim \beta$

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```
mean.beta.inf.R[, c(1,2,3,4)]
```

```
##   Vaccinated      beta    llbeta   ulbeta
## 1         No 1.1128227 0.7766340 1.536829
## 2        Yes 0.7822649 0.3540352 1.686715
```

No difference is transmission rate

Summarize ~ *R*

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```
mean.beta.inf.R[, c(1,11,12,13)]
```

```
##   Vaccinated        R       llR      ulR
## 1         No 5.329835 3.5914571 9.275196
## 2        Yes 2.477561 0.4043934 6.431245
```

No difference in reproduction number

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Conclusion

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Based on the assumption of one of both samples required to be positive, we find that the transmission parameter β is not lower, but the mean infectious period T_{inf} in the contact birds is lower, which results in a reproduction number R which is smaller (although not statistically significant), but is not lower than the threshold $R \leq 1$.

Preliminary results (models not checked)

- Different Ct as cut-off: e.g if Ct $=$ 30, β lower values for vaccinated, T_{inf} cannot be estimated

- One positive sample means that animal is positive and first negative is negative: β lower values for vaccinated, and T_{inf} lower for vaccinated

Following no preliminary results

- Only base results on ON swabs

- SI model

- Use ELISA to determine infection yes/no.