

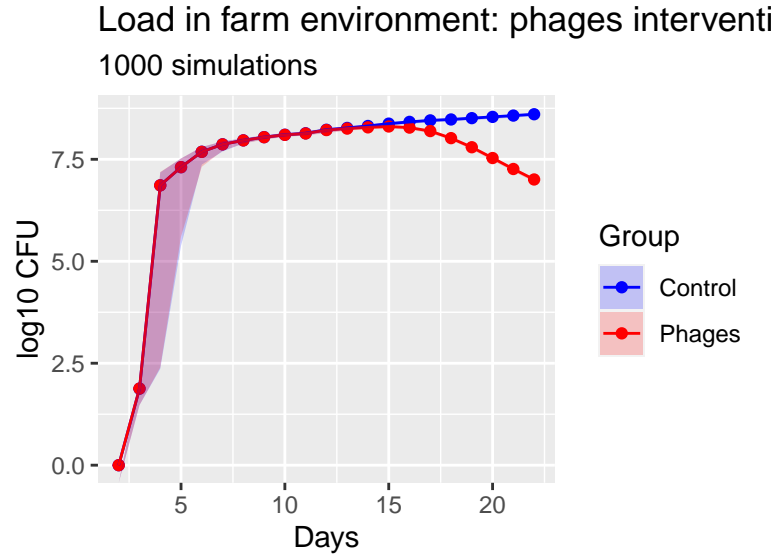
Becker et al.(2022) experiment reproduction

Reference experiment figure 2. page 9 (Becker et al. (2022))

Plots

```
## Plot for load in farm environment
data1 = get_data(1, parallel_output)
data2 = get_data(1, parallel_output_phages)

plot_qois(
  data1 = data1,
  data2 = data2,
  title = "Load in farm environment: phages intervention",
  subtitle = paste(dim(parallel_output)[3], "simulations"),
  xlab = "Days",
  ylab = "log10 CFU"
)
```



```
## Plot for average Within flock prevalence
data1 = get_data(2, parallel_output)
data2 = get_data(2, parallel_output_phages)

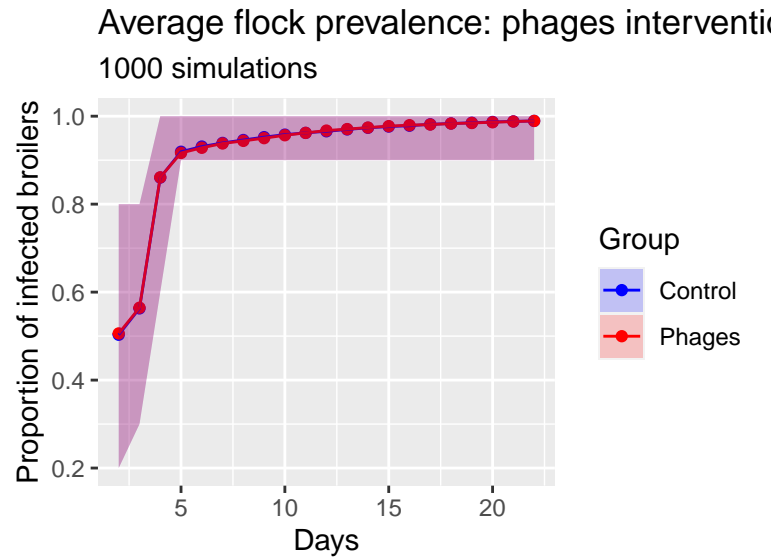
plot_qois(
  data1 = data1,
  data2 = data2,
  title = "Average flock prevalence: phages intervention",

```

```

    subtitle = paste(dim(parallel_output)[3], "simulations"),
    xlab      = "Days",
    ylab      = "Proportion of infected broilers"
  )

```



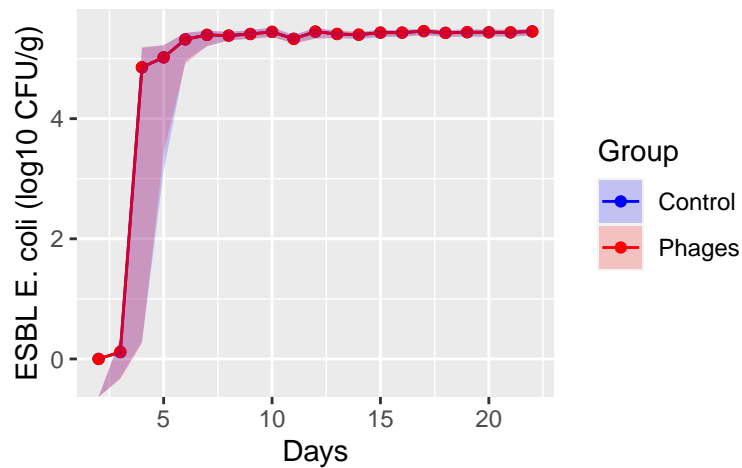
```

## Plot for average (over broilers + iterations) excreted bacteria
data1 = get_data(3, parallel_output)
data2 = get_data(3, parallel_output_phages)

plot_qois(
  data1 = data1,
  data2 = data2,
  title = "Average Bacterial concentration in excreted feces",
  subtitle = paste(dim(parallel_output)[3], "simulations"),
  xlab    = "Days",
  ylab    = "ESBL E. coli (log10 CFU/g)"
)

```

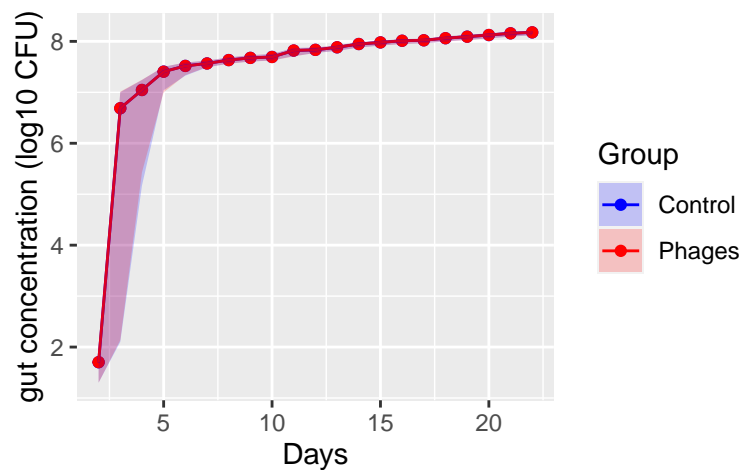
Average Bacterial concentration in excreted feces
1000 simulations



```
## Plot for average number of bacteria in the broiler's gut
data1 = get_data(5, parallel_output)
data2 = get_data(5, parallel_output_phages)

plot_qois(
  data1 = data1,
  data2 = data2,
  title = "Concentration in bacteria in broilers gut",
  subtitle = paste(dim(parallel_output)[3], "simulations"),
  xlab = "Days",
  ylab = "gut concentration (log10 CFU)"
)
```

Concentration in bacteria in broilers gut
1000 simulations



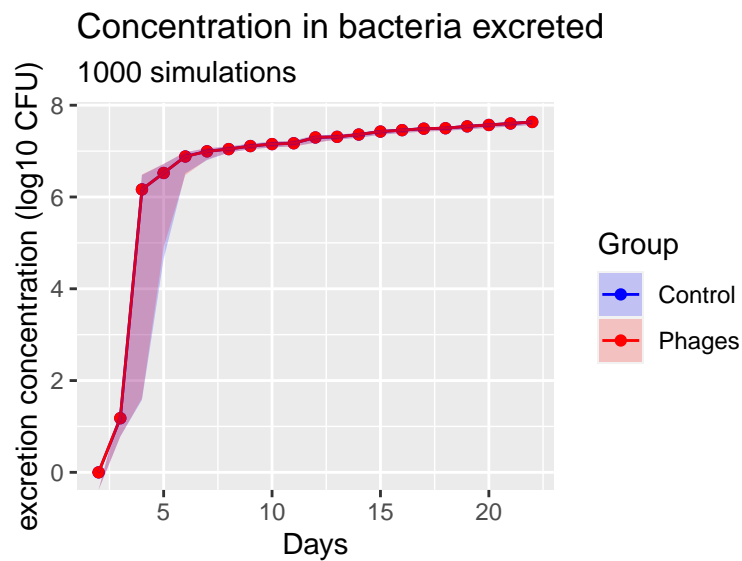
```
## Plot for average number of bacteria excreted
data1 = get_data(6, parallel_output)
```

```

data2 = get_data(6, parallel_output_phages)

plot_qois(
  data1 = data1,
  data2 = data2,
  title = "Concentration in bacteria excreted",
  subtitle = paste(dim(parallel_output)[3], "simulations"),
  xlab = "Days",
  ylab = "excretion concentration (log10 CFU)"
)

```

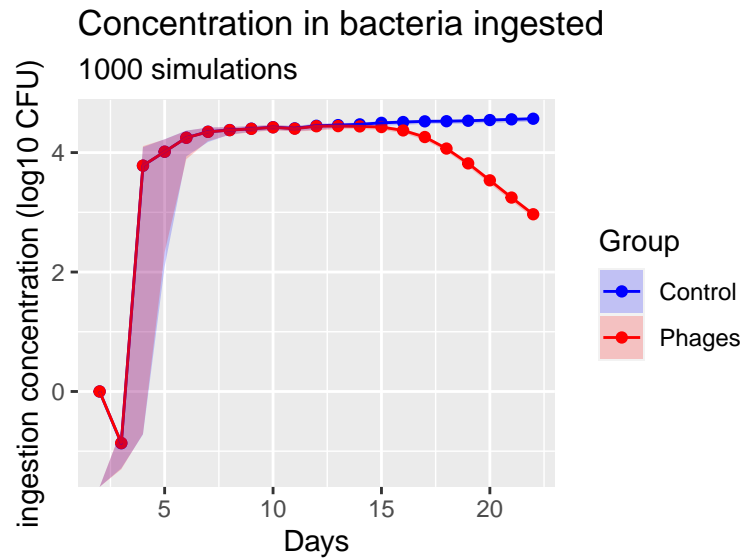


```

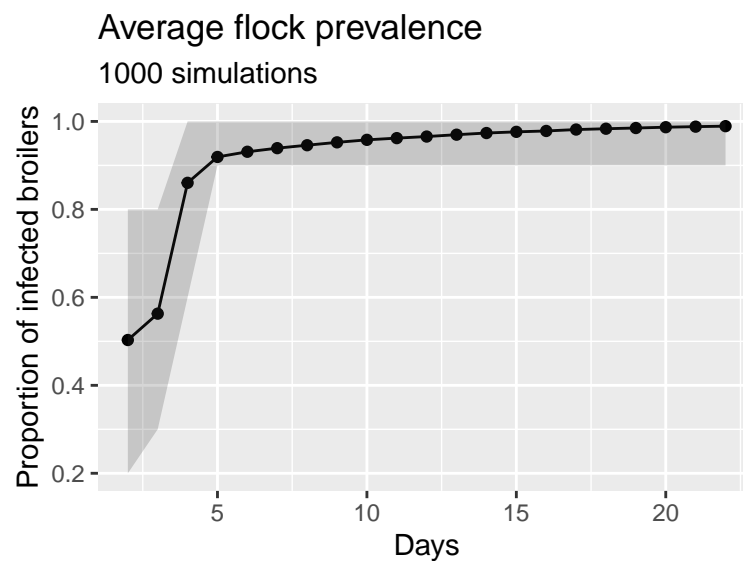
## Plot for average number of bacteria ingested
data1 = get_data(7, parallel_output)
data2 = get_data(7, parallel_output_phages)

plot_qois(
  data1 = data1,
  data2 = data2,
  title = "Concentration in bacteria ingested",
  subtitle = paste(dim(parallel_output)[3], "simulations"),
  xlab = "Days",
  ylab = "ingestion concentration (log10 CFU)"
)

```



```
## Plot for average Within flock prevalence
data <- get_data(2, parallel_output)
plot_qoi(
  qoi      = data$qoi,
  ci_lower = data$ci_lower,
  ci_upper = data$ci_upper,
  title    = "Average flock prevalence",
  subtitle = paste(dim(parallel_output)[3], "simulations"),
  xlab     = "Days",
  ylab     = "Proportion of infected broilers"
)
```

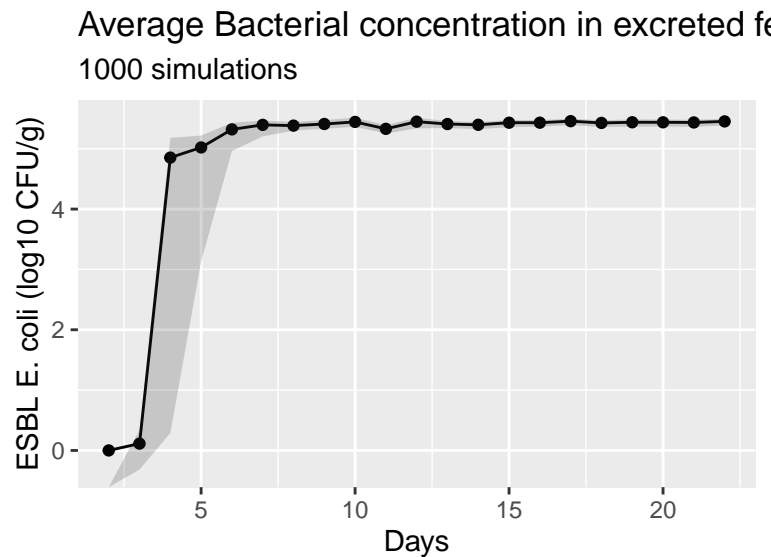


```
## Plot for average (over broilers + iterations) excreted bacteria
data <- get_data(3, parallel_output)
plot_qoi(
```

```

qoi      = data$qoi,
ci_lower = data$ci_lower,
ci_upper = data$ci_upper,
title    = "Average Bacterial concentration in excreted feces",
subtitle = paste(dim(parallel_output)[3], "simulations"),
xlab     = "Days",
ylab     = "ESBL E. coli (log10 CFU/g)"
)

```



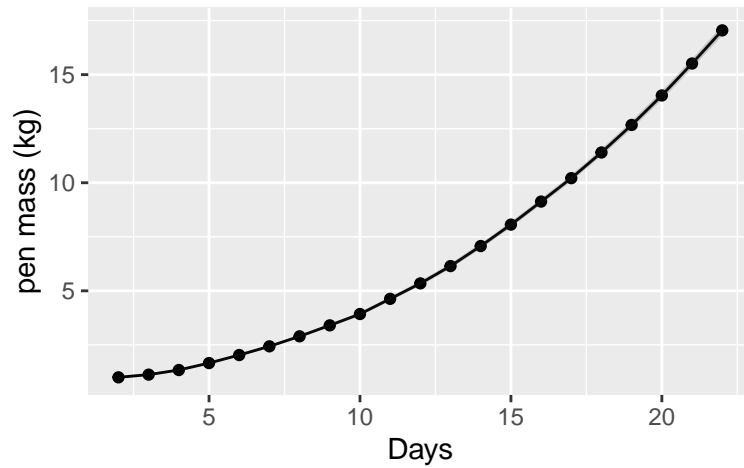
```

## Plot for amount of litter + feces
data <- get_data(4, parallel_output)
plot_qoi(
  qoi      = (data$qoi+inputs$litter_mass)/1000,
  ci_lower = (data$ci_lower+inputs$litter_mass)/1000,
  ci_upper = (data$ci_upper+inputs$litter_mass)/1000,
  title    = "Mass of litter + feces",
  subtitle = paste(dim(parallel_output)[3], "simulations"),
  xlab     = "Days",
  ylab     = "pen mass (kg)"
)

```

Mass of litter + feces

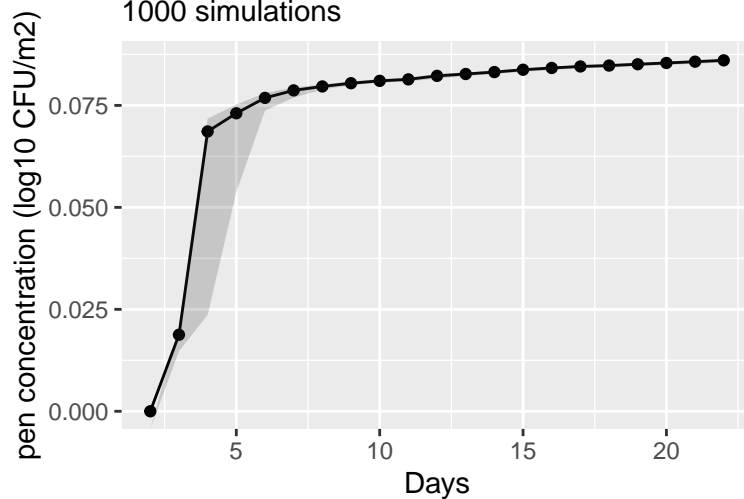
1000 simulations



```
## Plot for number of bacteria per sq. meter
data <- get_data(1, parallel_output)
plot_qoi(
  qoi      = data$qoi/inputs$farm_size,
  ci_lower = data$ci_lower/inputs$farm_size,
  ci_upper = data$ci_upper/inputs$farm_size,
  title    = "Concentration in bacteria in farm",
  subtitle = paste(dim(parallel_output)[3], "simulations"),
  xlab     = "Days",
  ylab     = "pen concentration (log10 CFU/m2)"
)
```

Concentration in bacteria in farm

1000 simulations

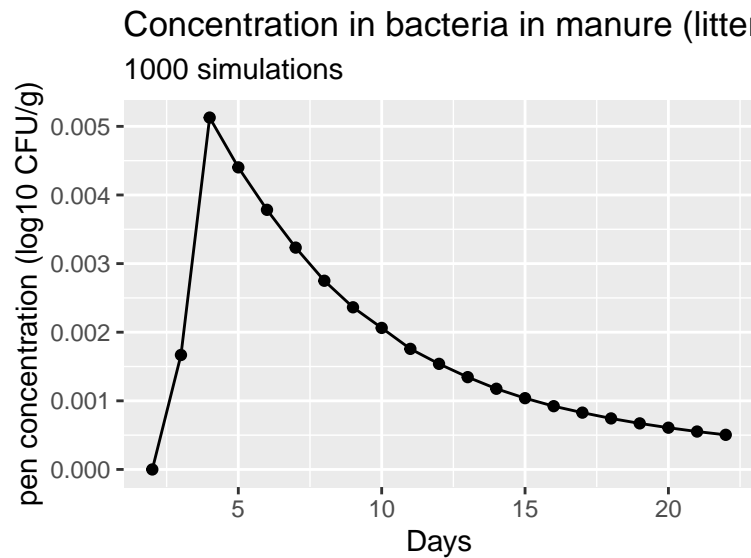


```
## Plot for number of bacteria per g of pen mass
data1 <- get_data(1, parallel_output)
data2 <- get_data(4, parallel_output)
```

```

plot_qoi(
  qoi      = data1$qoi/(data2$qoi+inputs$litter_mass),
  ci_lower = NA,
  ci_upper = NA,
  title    = "Concentration in bacteria in manure (litter + feces)",
  subtitle = paste(dim(parallel_output)[3], "simulations"),
  xlab     = "Days",
  ylab     = "pen concentration (log10 CFU/g)"
)

```

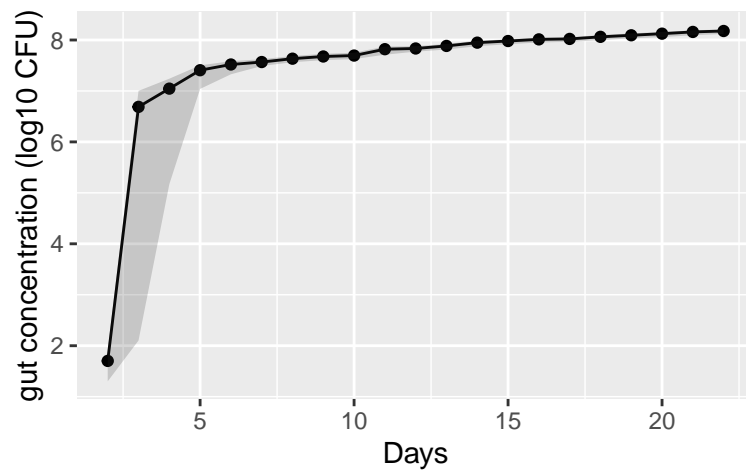


```

## Plot for average number of bacteria in the broiler's gut
data <- get_data(5, parallel_output)
plot_qoi(
  qoi      = data$qoi,
  ci_lower = data$ci_lower,
  ci_upper = data$ci_upper,
  title    = "Concentration in bacteria in broilers gut",
  subtitle = paste(dim(parallel_output)[3], "simulations"),
  xlab     = "Days",
  ylab     = "gut concentration (log10 CFU)"
)

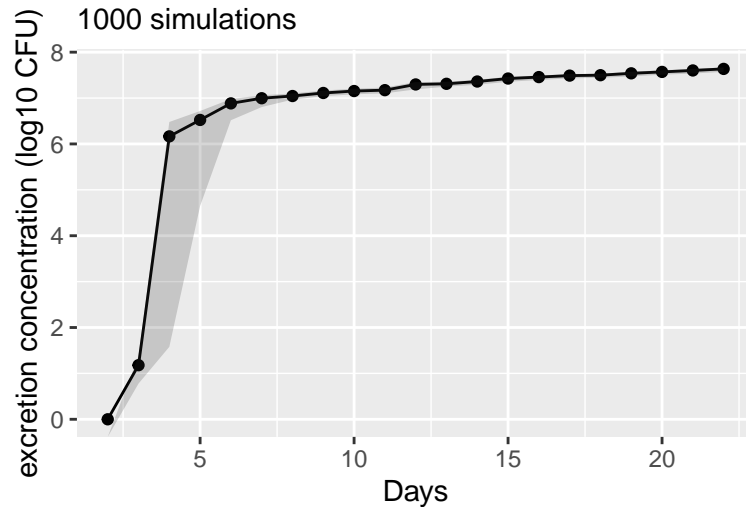
```


Concentration in bacteria in broilers gut
1000 simulations



```
## Plot for average number of bacteria excreted
data <- get_data(6, parallel_output)
plot_qoi(
  qoi      = data$qoi,
  ci_lower = data$ci_lower,
  ci_upper = data$ci_upper,
  title    = "Concentration in bacteria excreted",
  subtitle = paste(dim(parallel_output)[3], "simulations"),
  xlab     = "Days",
  ylab     = "excretion concentration (log10 CFU)"
)
```

Concentration in bacteria excreted
1000 simulations



```
## Plot for average number of bacteria ingested
data <- get_data(7, parallel_output)
plot_qoi(
```

```

qoi      = data$qoi,
ci_lower = data$ci_lower,
ci_upper = data$ci_upper,
title    = "Concentration in bacteria ingested",
subtitle = paste(dim(parallel_output)[3], "simulations"),
xlab     = "Days",
ylab     = "ingestion concentration (log10 CFU)"
)

```

