

Model Animations

Chris Hoover

July 3, 2019

```
#Base time and starting values for state variables
base_start <- c(S=5000, E=0, I=0, Wt=10, Wu=10)
years <- 20
base_time <- c(0:(365*years))

#Run to equilibrium with base parameter set
base_eqbm <- runsteady(y = base_start, func = DDNTD::schisto_base_mod,
                         parms = DDNTD::base_pars)[["y"]]

#simulate annual MDA
eff = 0.93 #93% efficacy
base_pars["cvrg"] <- 0.8 # 80 percent coverage

mda.events = data.frame(var = rep('Wt', years/2),
                        time = c(1:(years/2))*365,
                        value = rep((1 - eff), years/2),
                        method = rep('mult', years/2))

schisto_base_sim <- sim_schisto_mod(nstart = base_eqbm,
                                      time = base_time,
                                      model = schisto_base_mod,
                                      parameters = base_pars,
                                      events_df = mda.events) %>%
  mutate(W = Wt*base_pars["cvrg"] + Wu*(1-base_pars["cvrg"]),
         kap = map_dbl(W, k_from_log_W),
         Reff = pmap_dbl(list(parameters = list(base_pars),
                               W = W,
                               kap = kap), getReff))

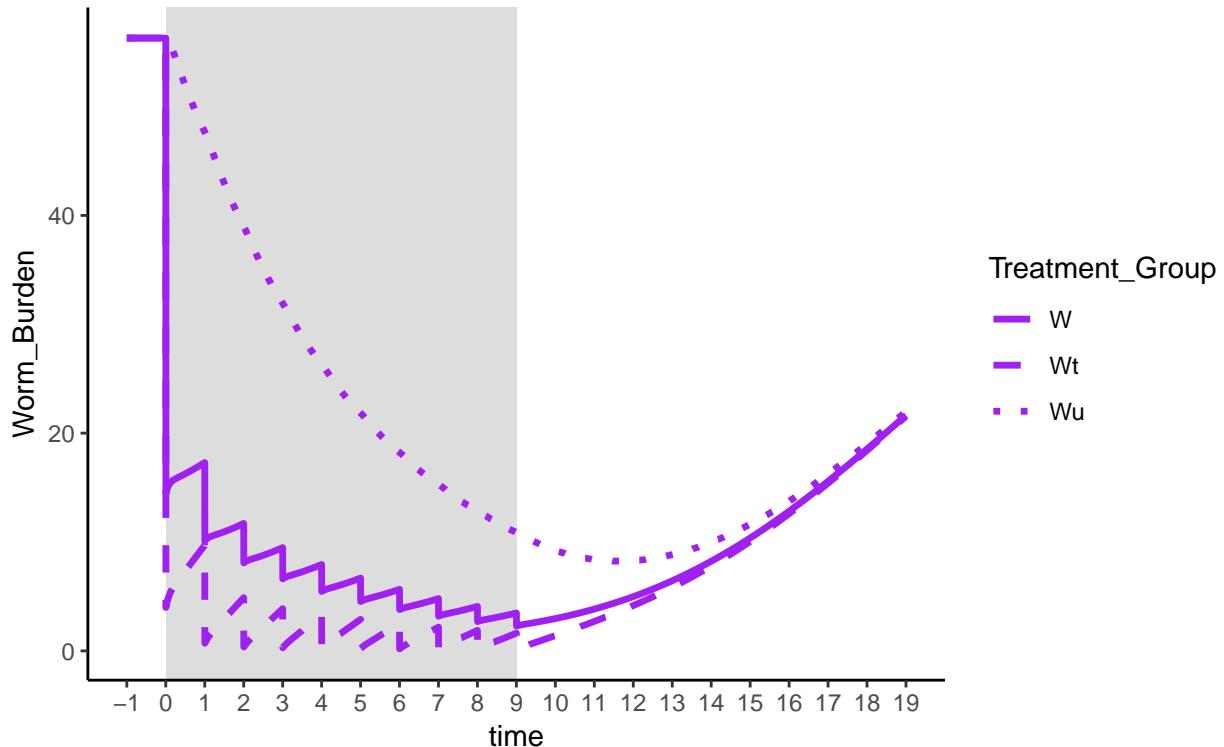
## Warning in if (is.na(events_df)) {: the condition has length > 1 and only
## the first element will be used

schisto_base_plot <- schisto_base_sim %>%
  gather("Treatment_Group", "Worm_Burden", Wt:W) %>%
  ggplot(aes(x = time, y = Worm_Burden, lty = Treatment_Group)) +
  annotate("rect", xmin = 365, xmax = max(mda.events$time), ymin = -Inf, ymax = Inf,
           alpha = .2) +
  geom_line(size = 1.2, col = "purple") +
  scale_linetype_manual(values = c("W" = 1,
                                    "Wt" = 2,
                                    "Wu" = 3)) +
  scale_x_continuous(breaks = c(0:years)*365,
                     labels = c(-1:(years-1))) +
  theme_classic() +
  ggtitle("Human infection dynamics",
          subtitle = paste0("Annual MDA for ", years/2, " years"))
```

```
schisto_base_plot
```

Human infection dynamics

Anual MDA for 10 years



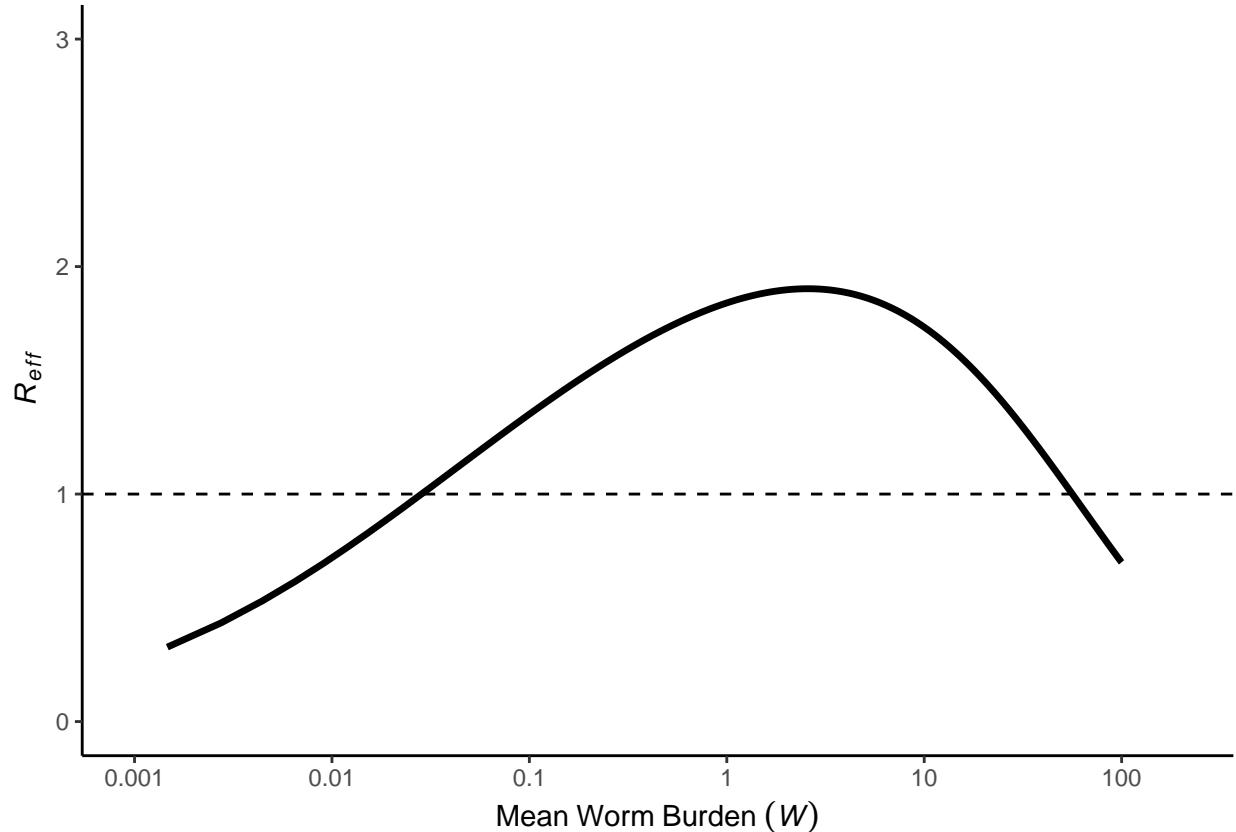
```
test_ws <- seq(1e-2, sqrt(100),
                 by = sqrt(100*2)/1000)^2

#Get values of mean worm burden to plot R effective curve over
Reffs <- data.frame(test_ws = test_ws) %>%
  mutate(w_det_ks = sapply(test_ws, k_from_log_W),
         Reff = pmap_dbl(list(parameters = list(base_pars),
                               W = test_ws,
                               kap = w_det_ks), getReff))

base_reff <- Reffs %>%
  ggplot(aes(x = test_ws, y = Reff)) +
  geom_line(size = 1.2) +
  theme_classic() +
  scale_x_continuous(trans = "log",
                     breaks = c(0.001, 0.01, 0.1, 1, 10, 100),
                     labels = c("0.001", "0.01", "0.1", "1", "10", "100"),
                     limits = c(0.001, 200)) +
  scale_y_continuous(breaks = c(0:3),
                     limits = c(0,3)) +
  geom_hline(yintercept = 1, lty = 2) +
  labs(x = expression(Mean~Worm~Burden~(italic(W))),
       y = expression(italic(R[eff])))
```

```
base_reff
```

```
## Warning: Removed 2 rows containing missing values (geom_path).
```

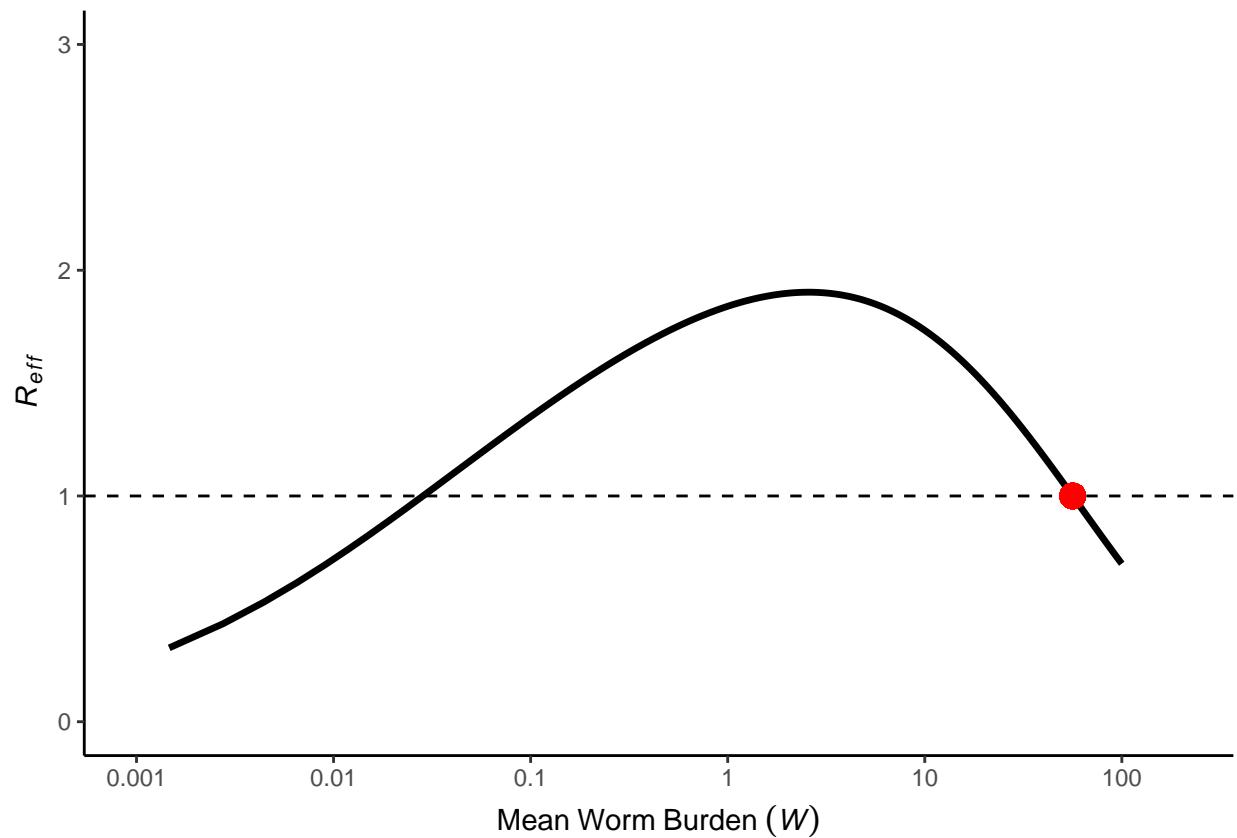


```
base_reff +
  geom_point(data = schisto_base_sim, aes(x = W, y = Reff),
             size = 4, col = "red") +
  transition_time(time)
```

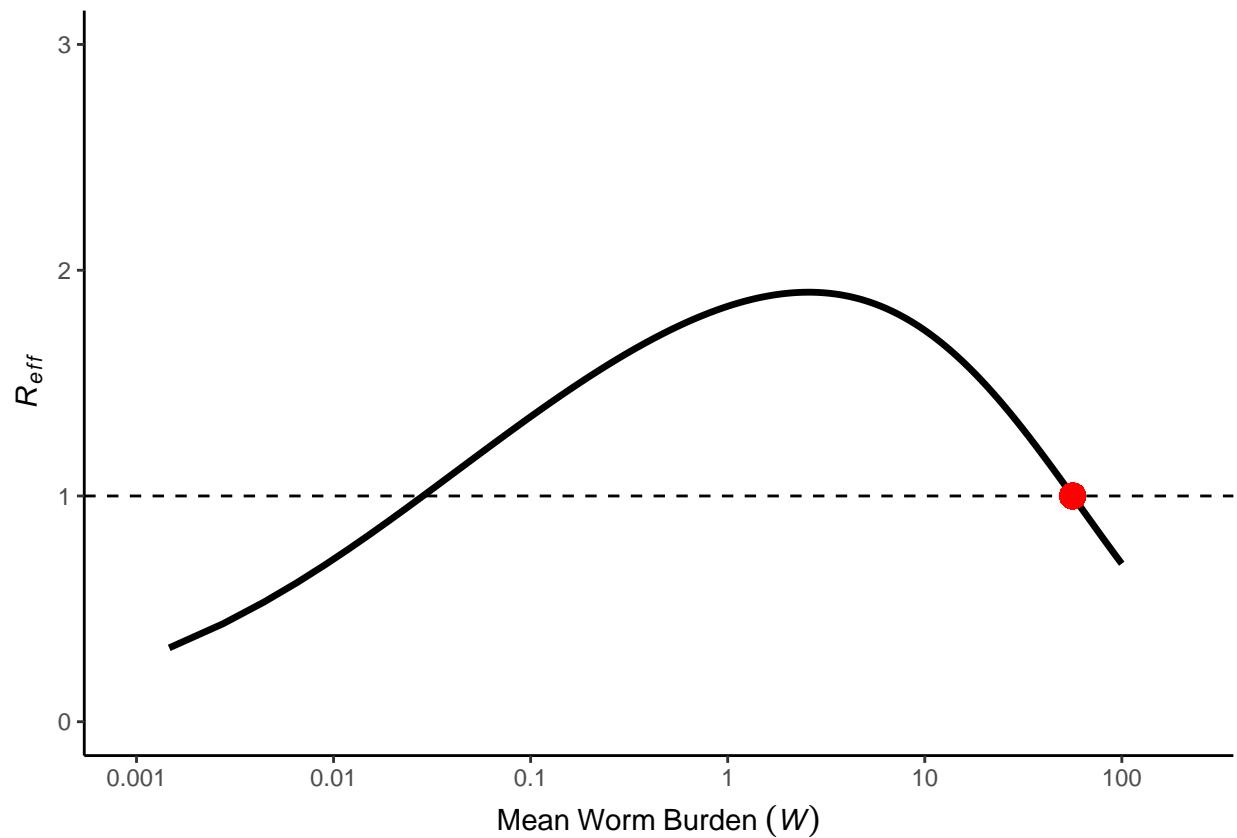
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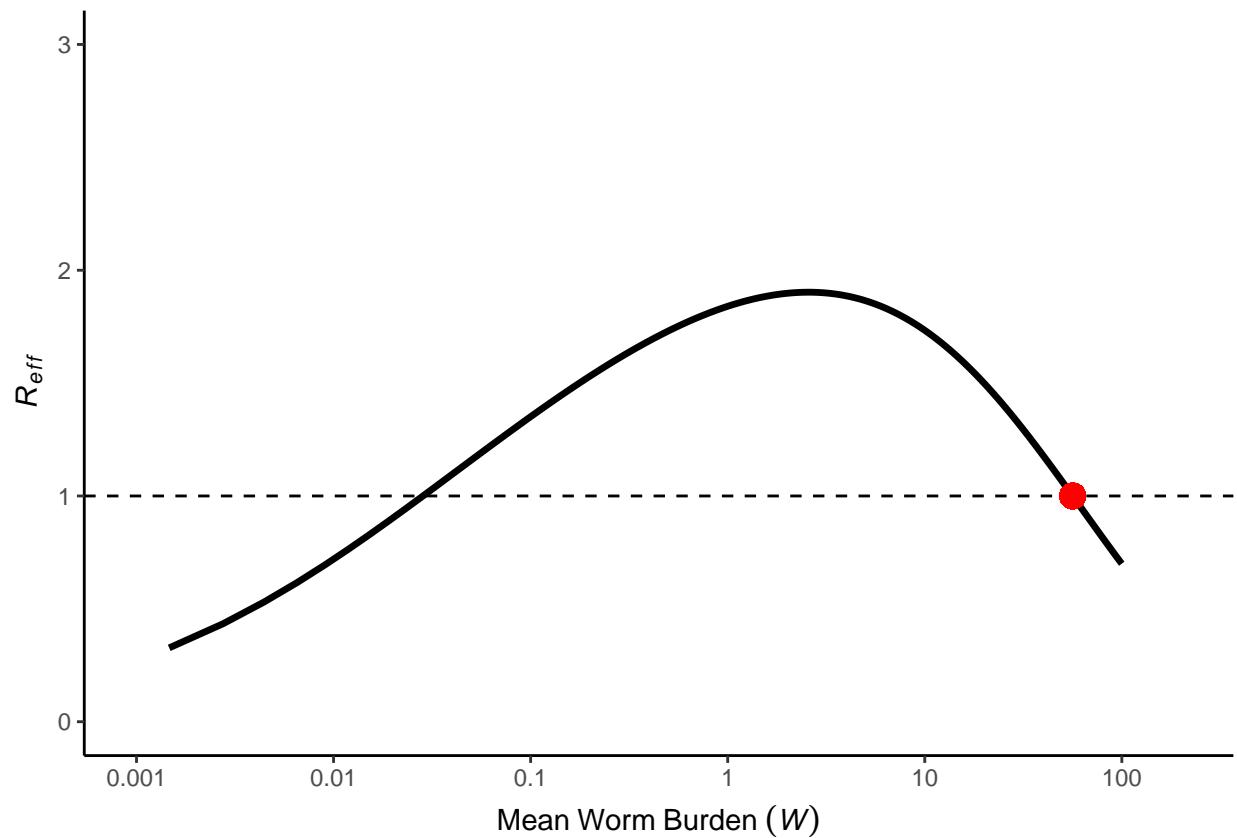
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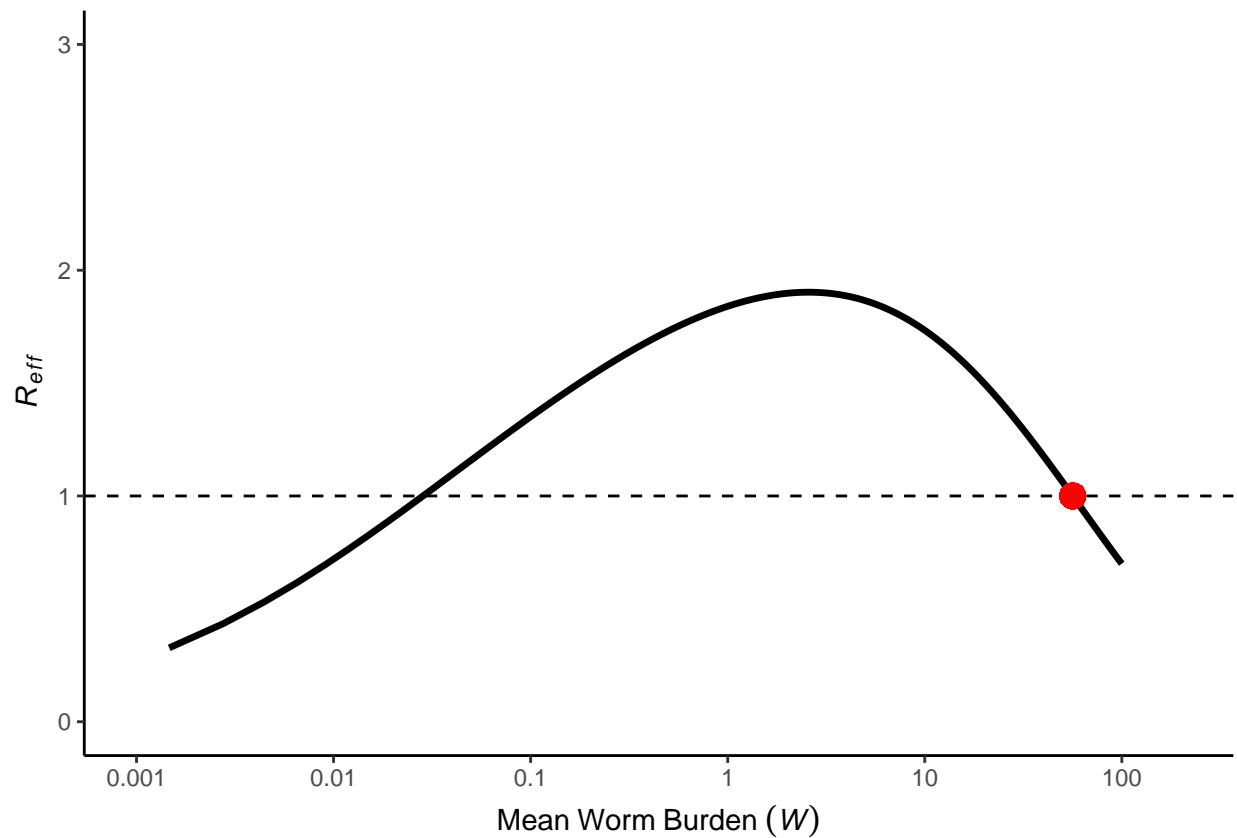
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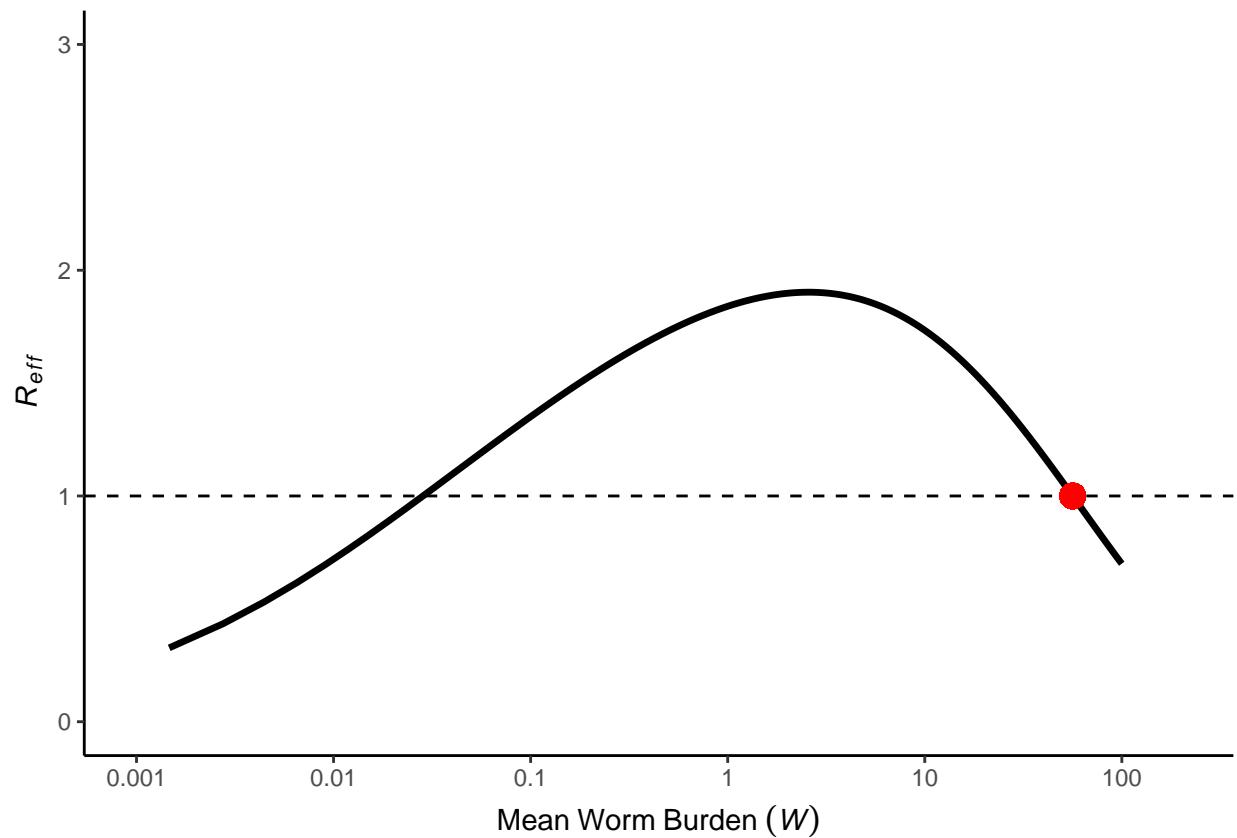
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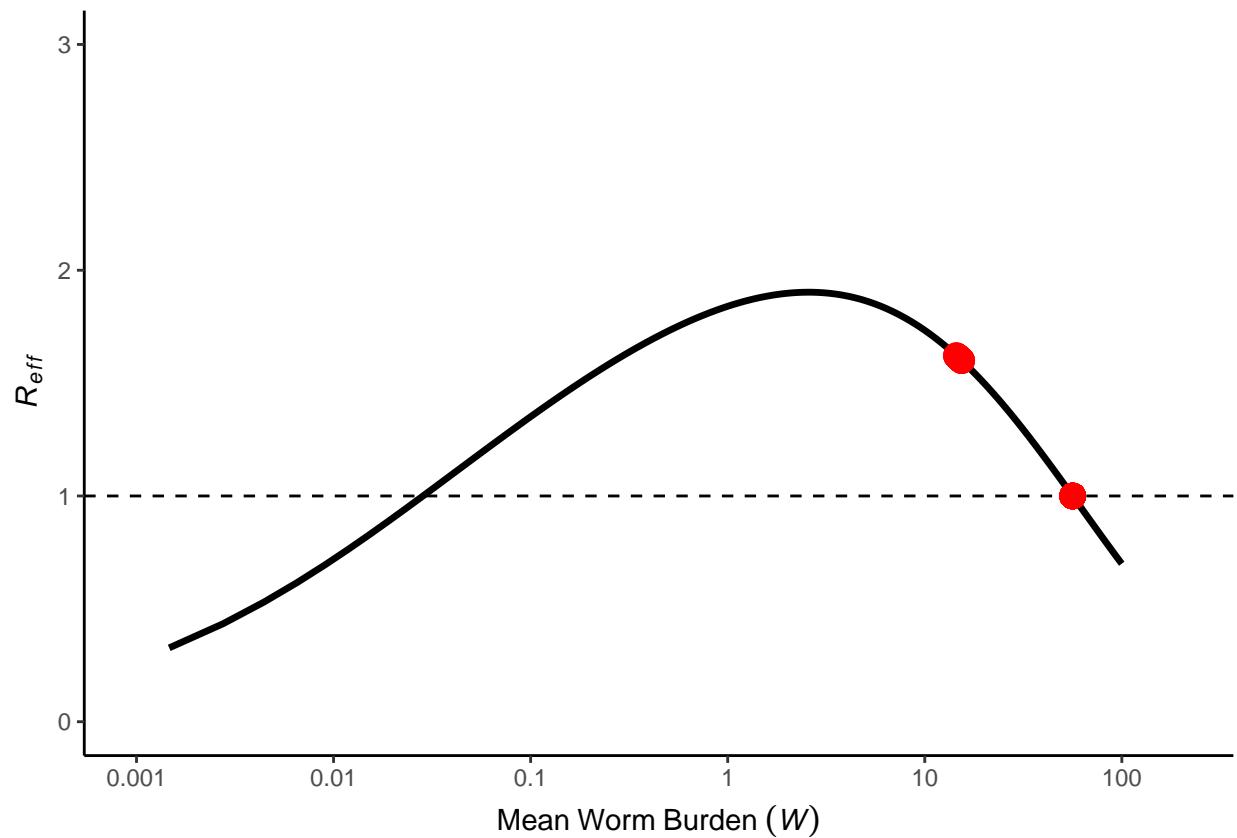
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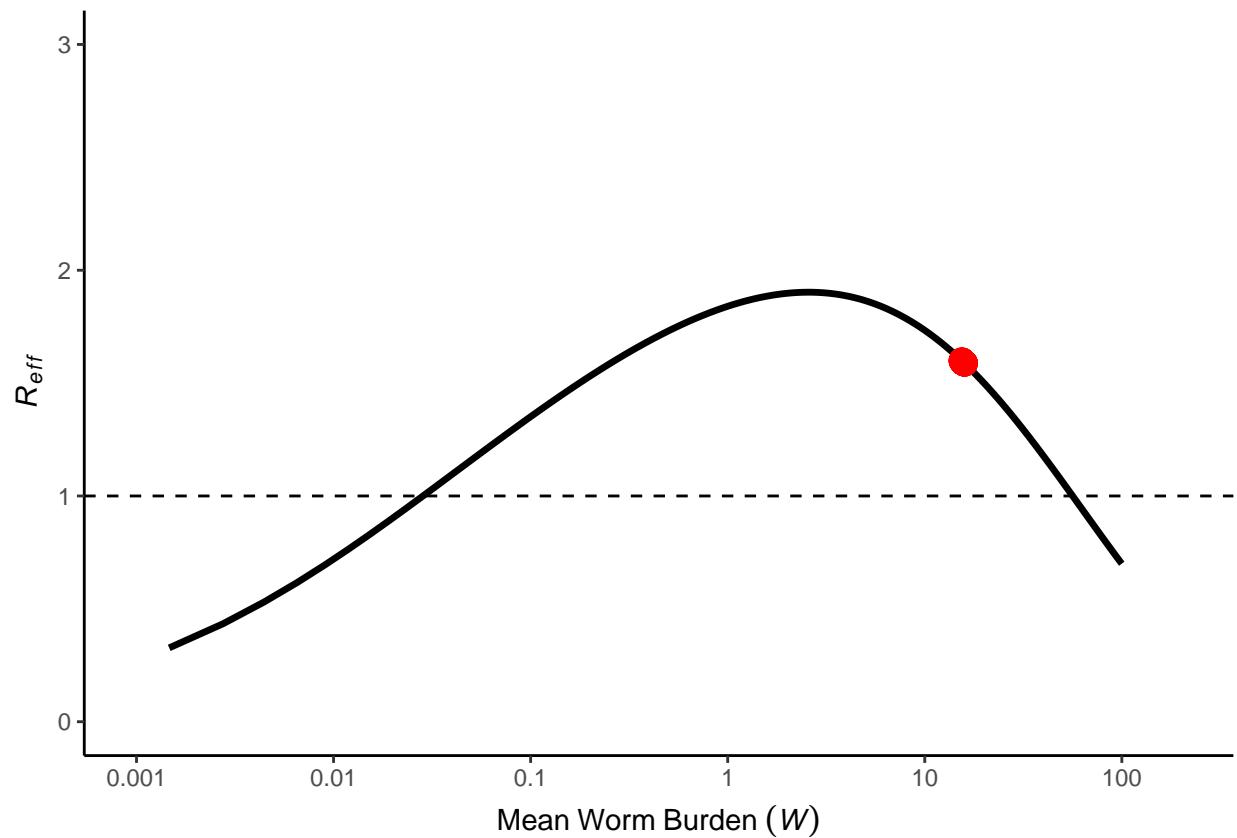
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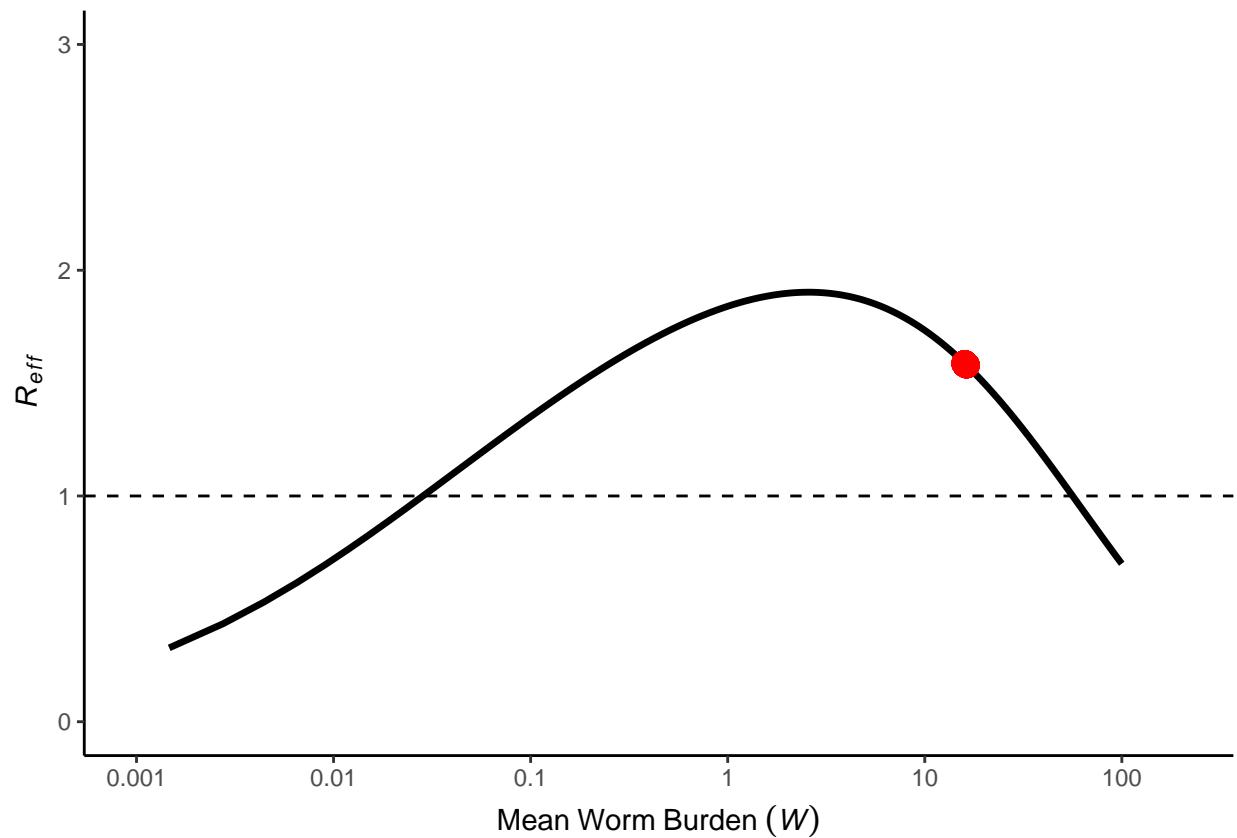
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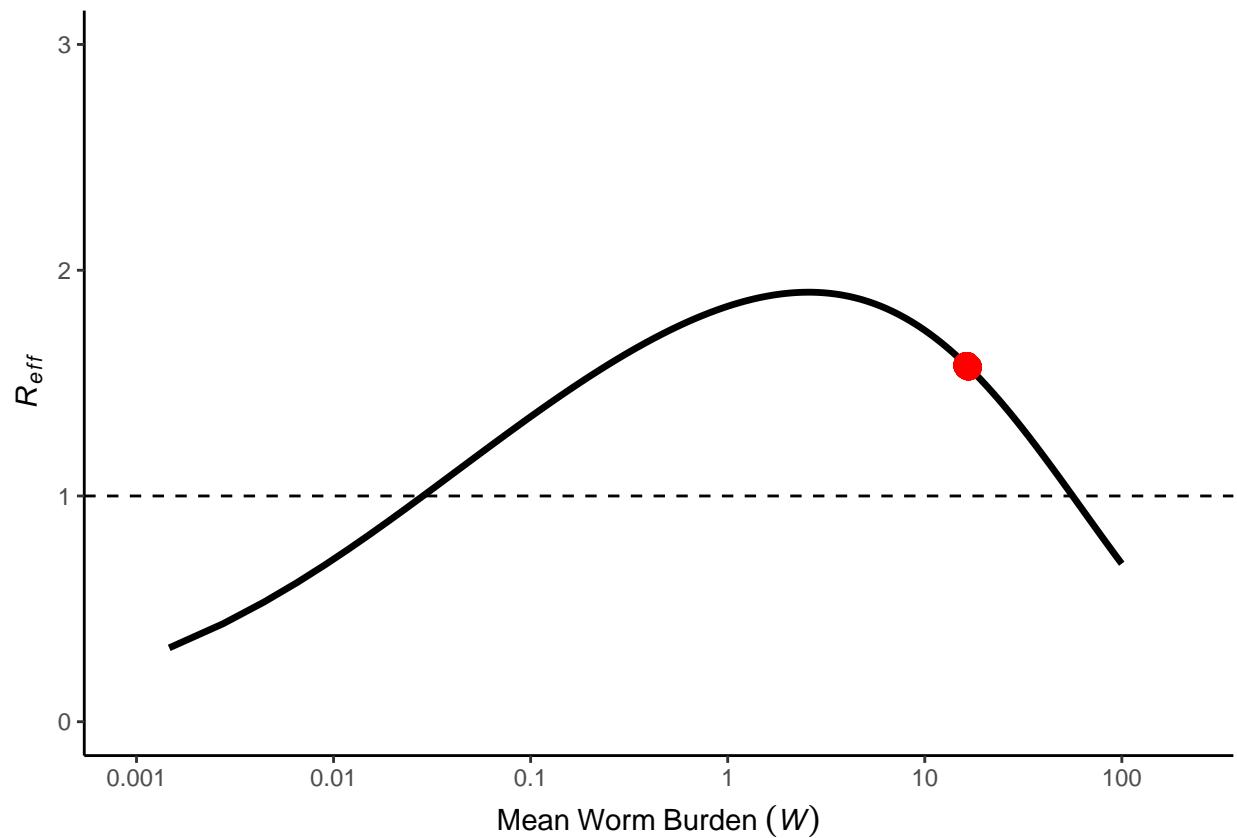
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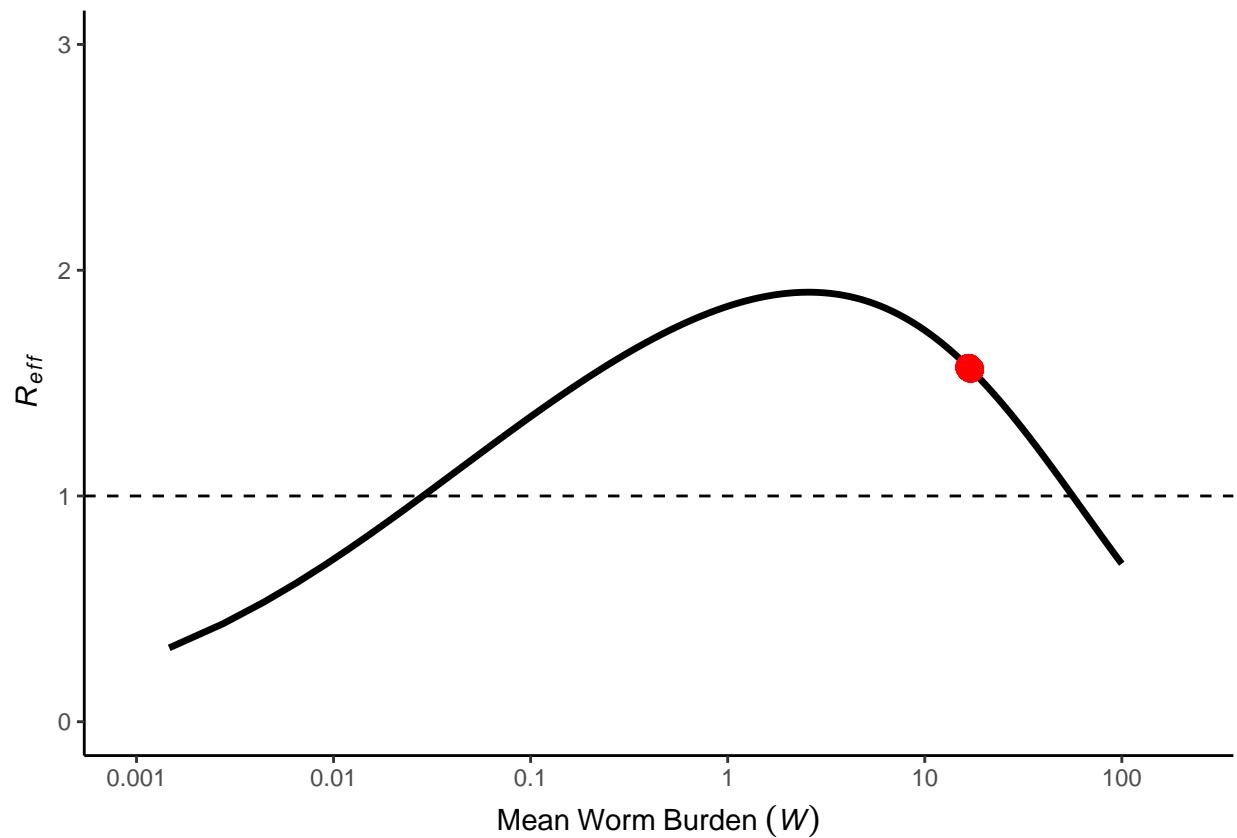
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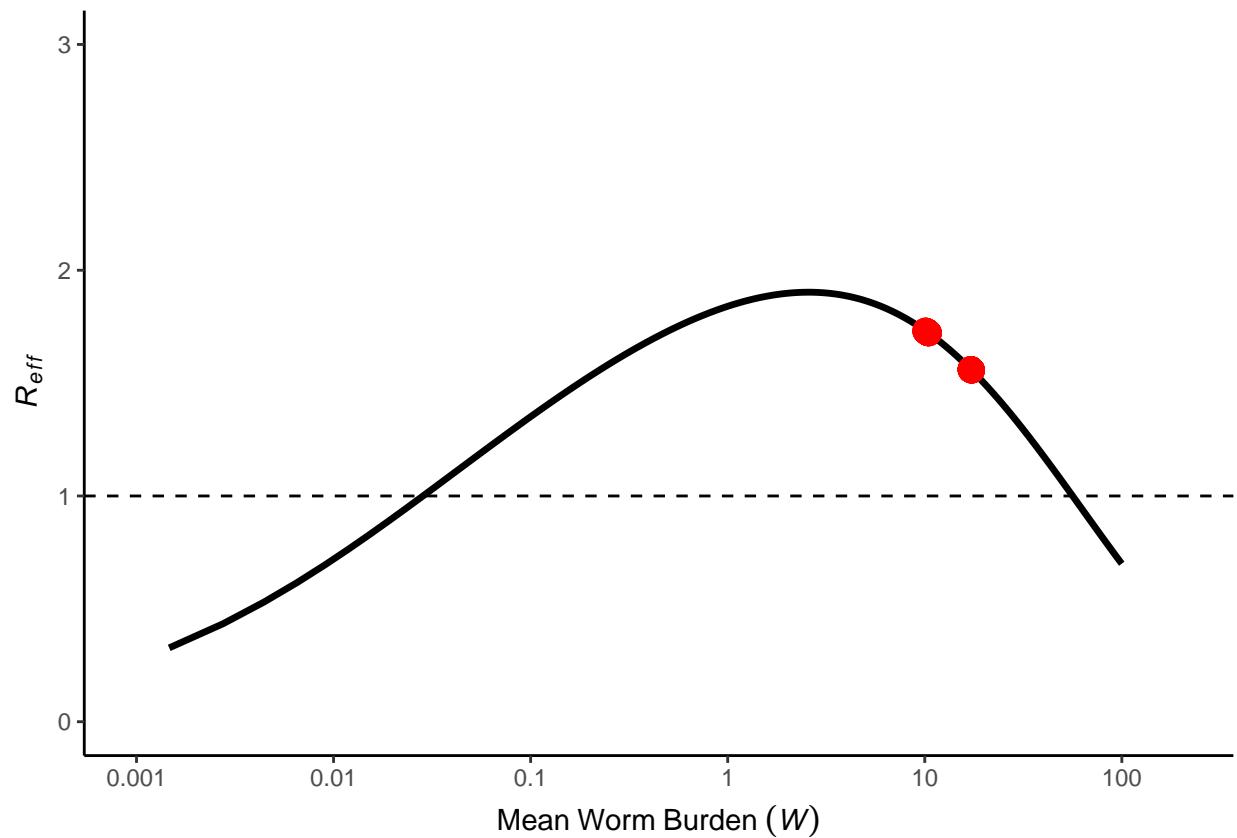
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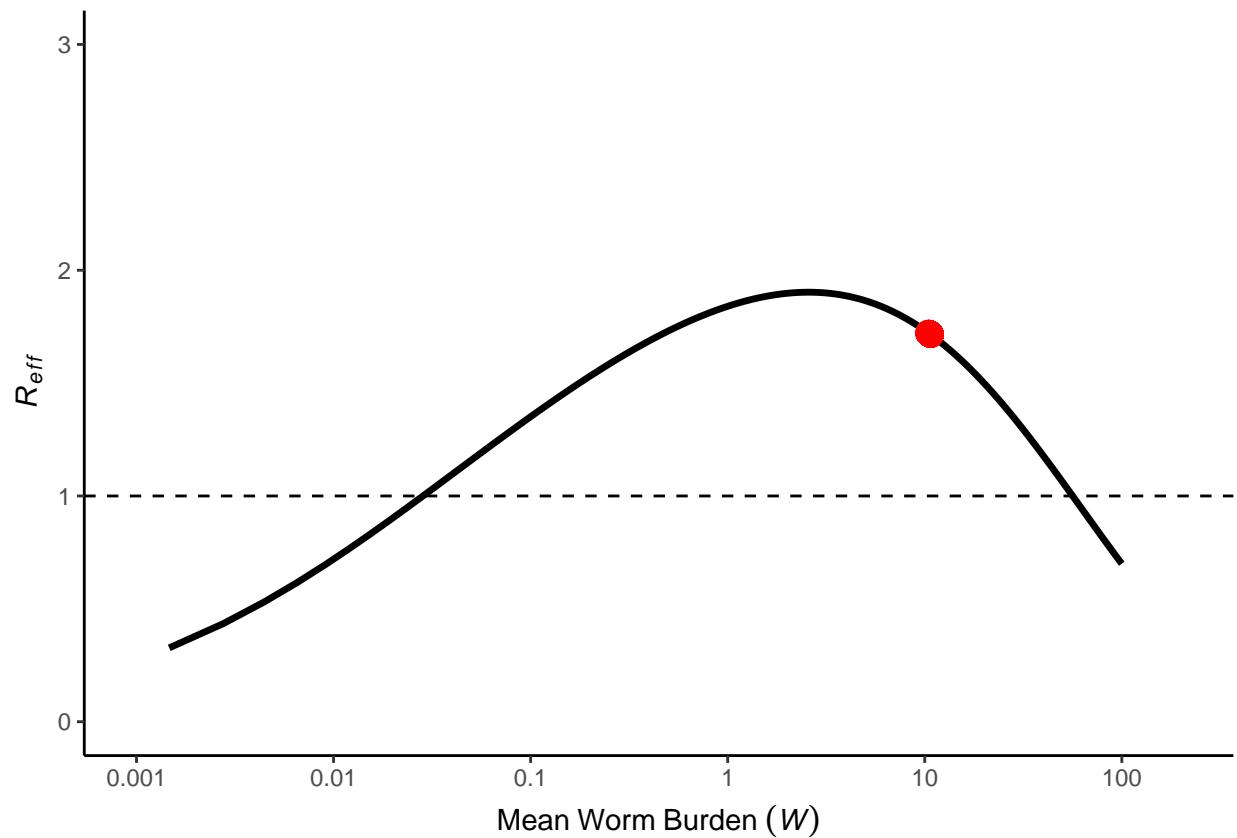
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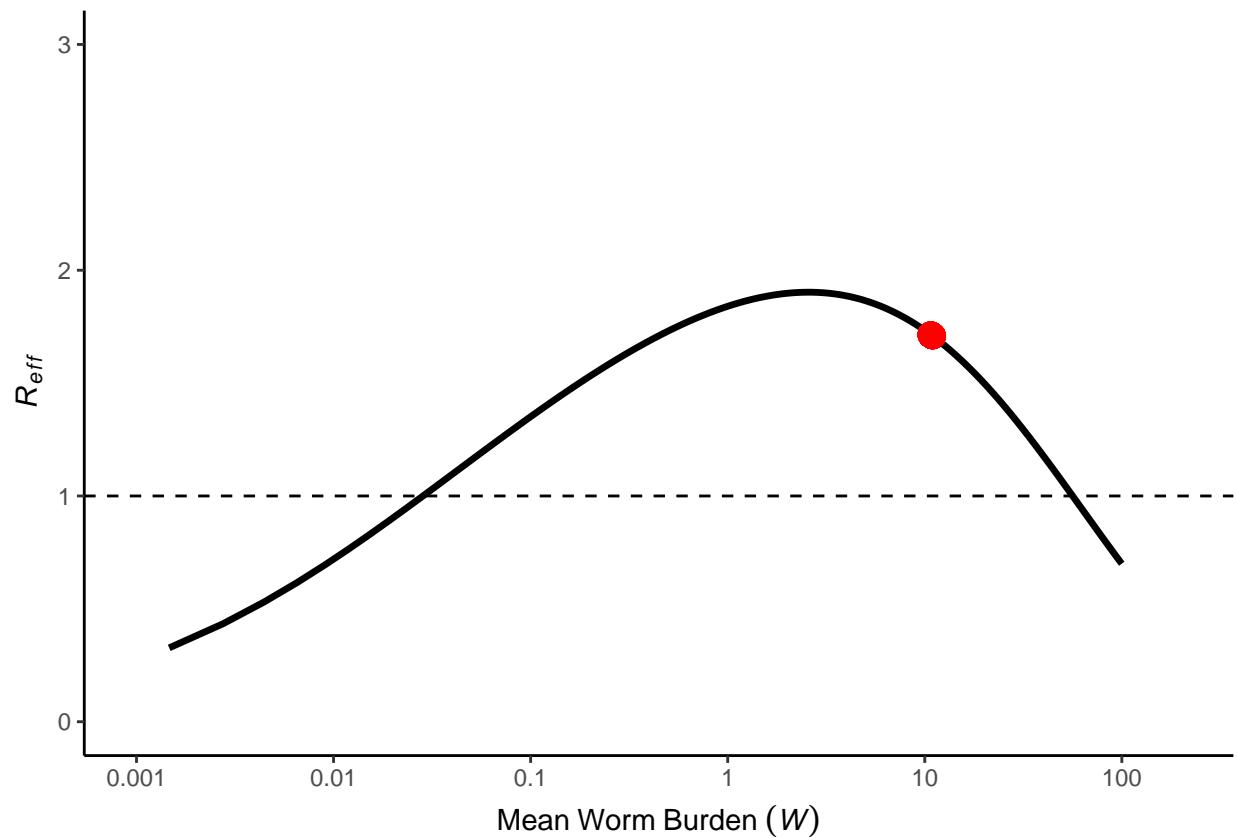
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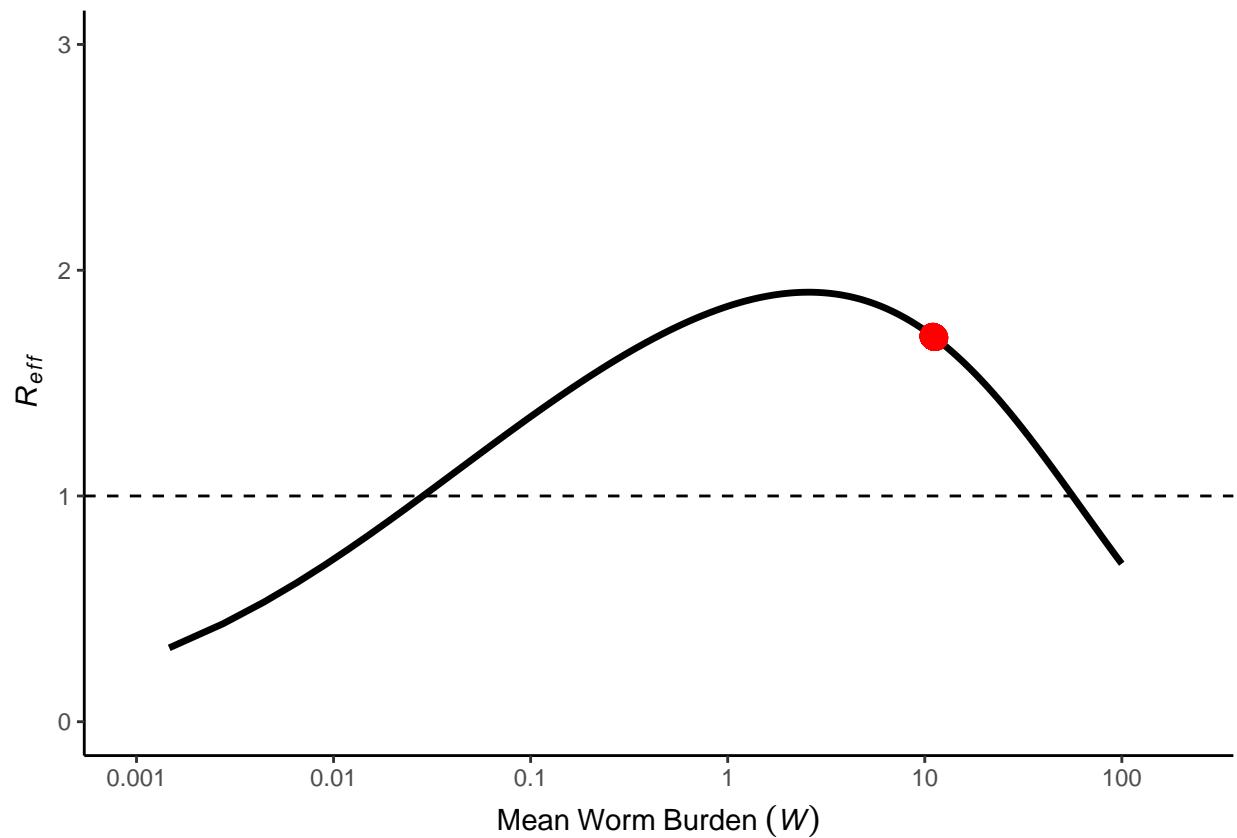
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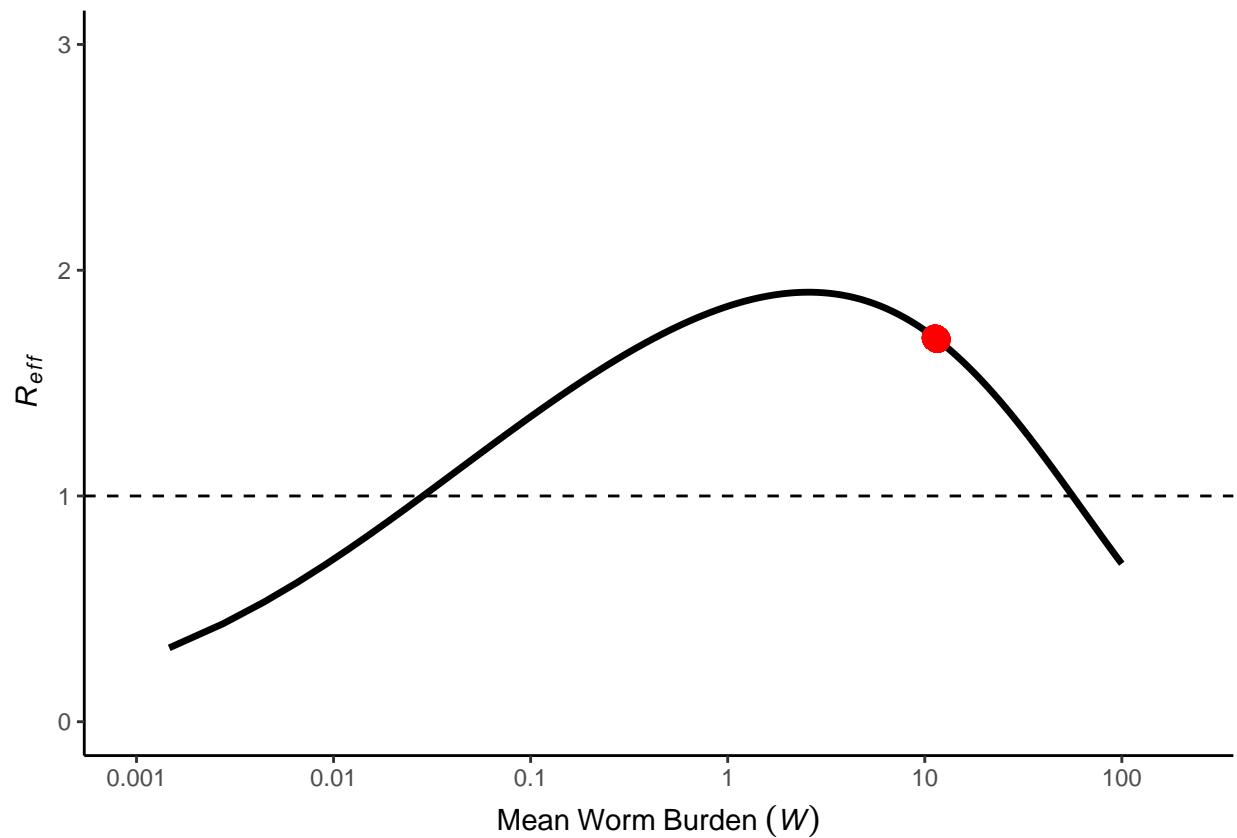
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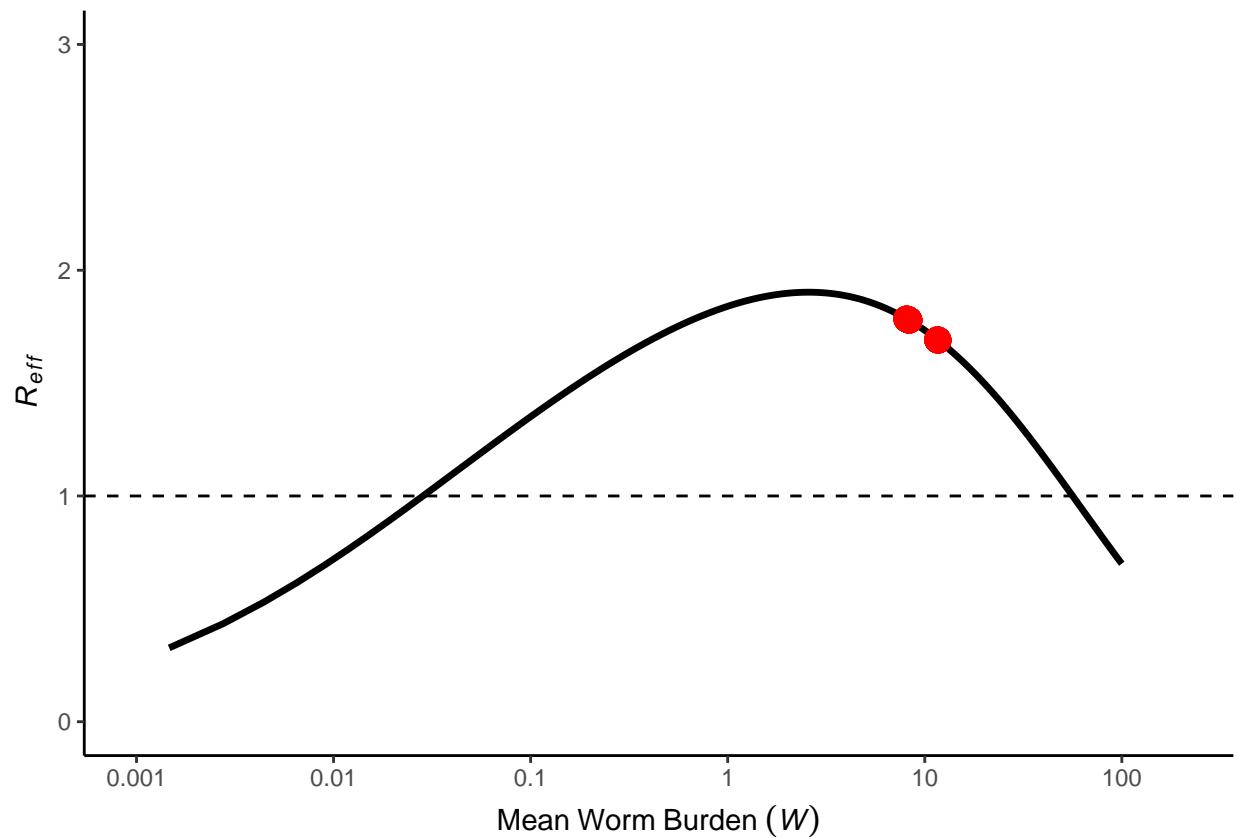
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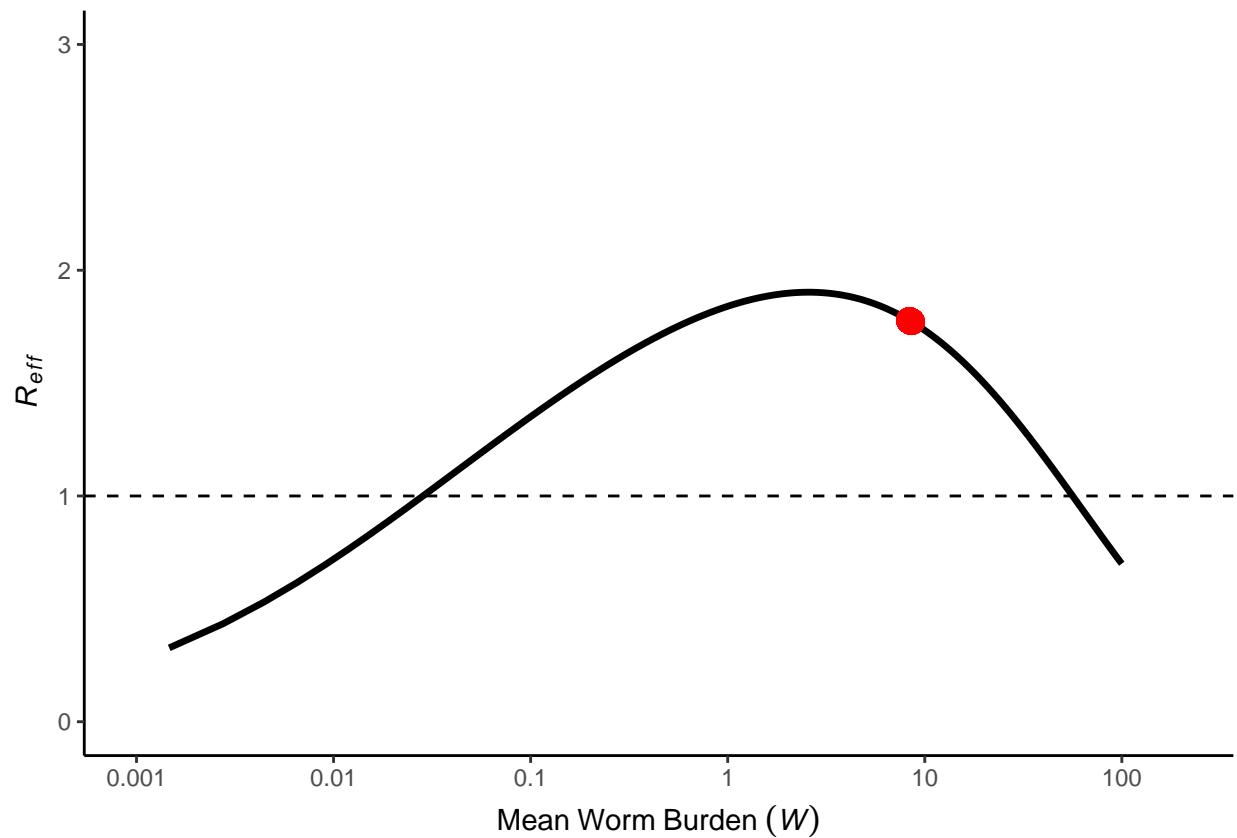
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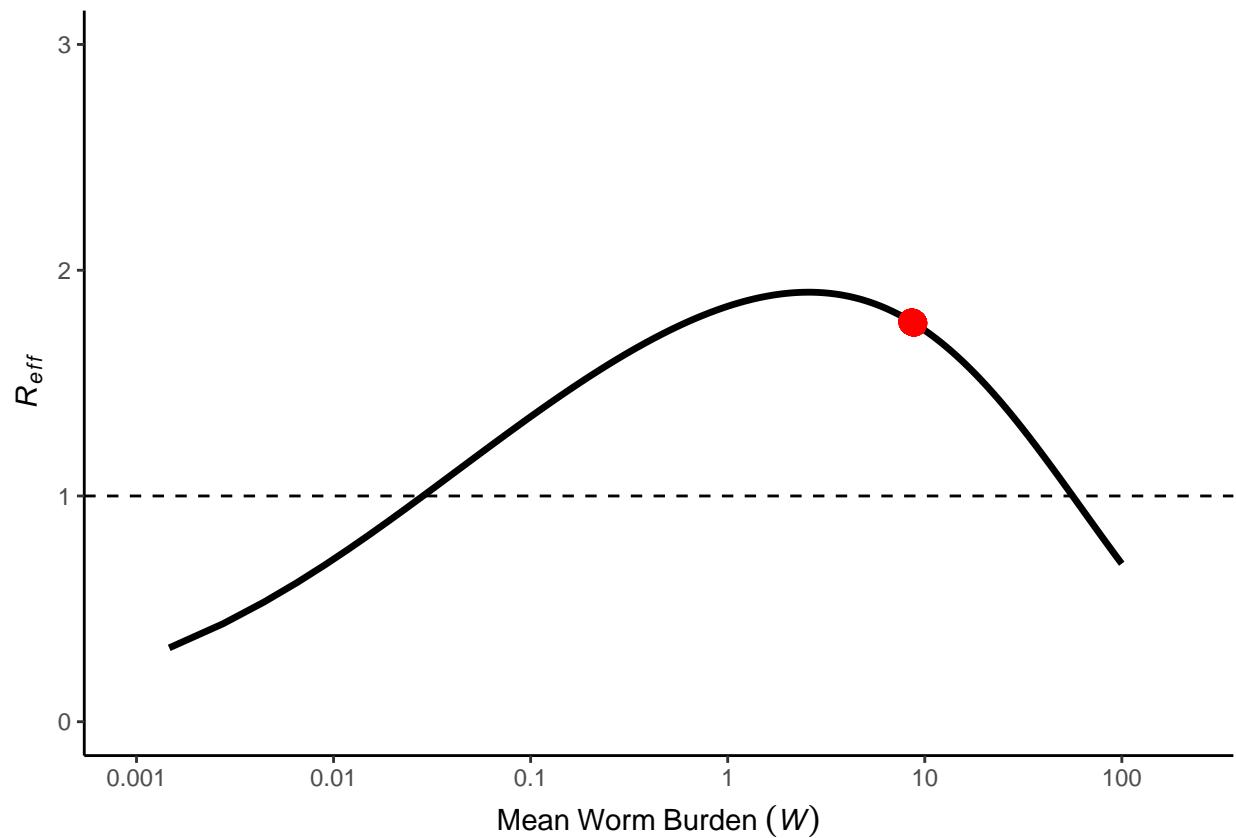
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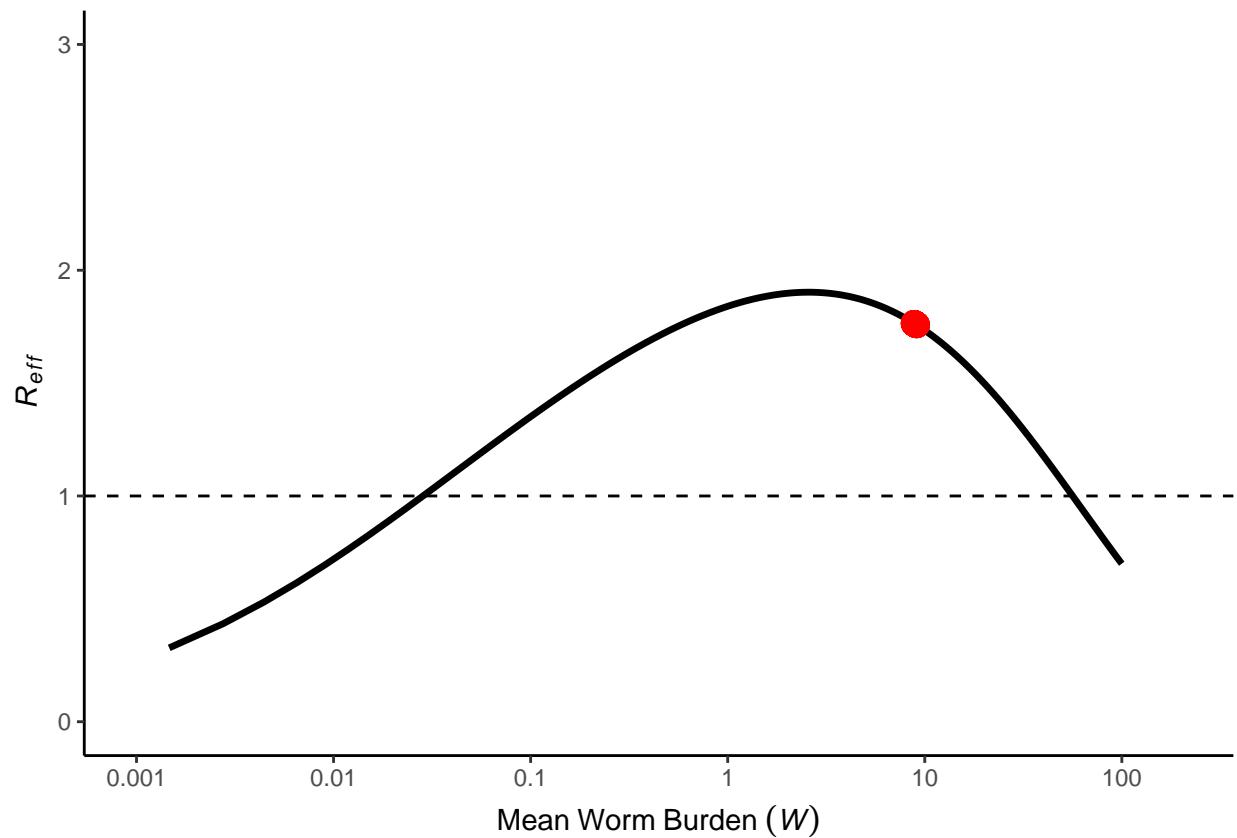
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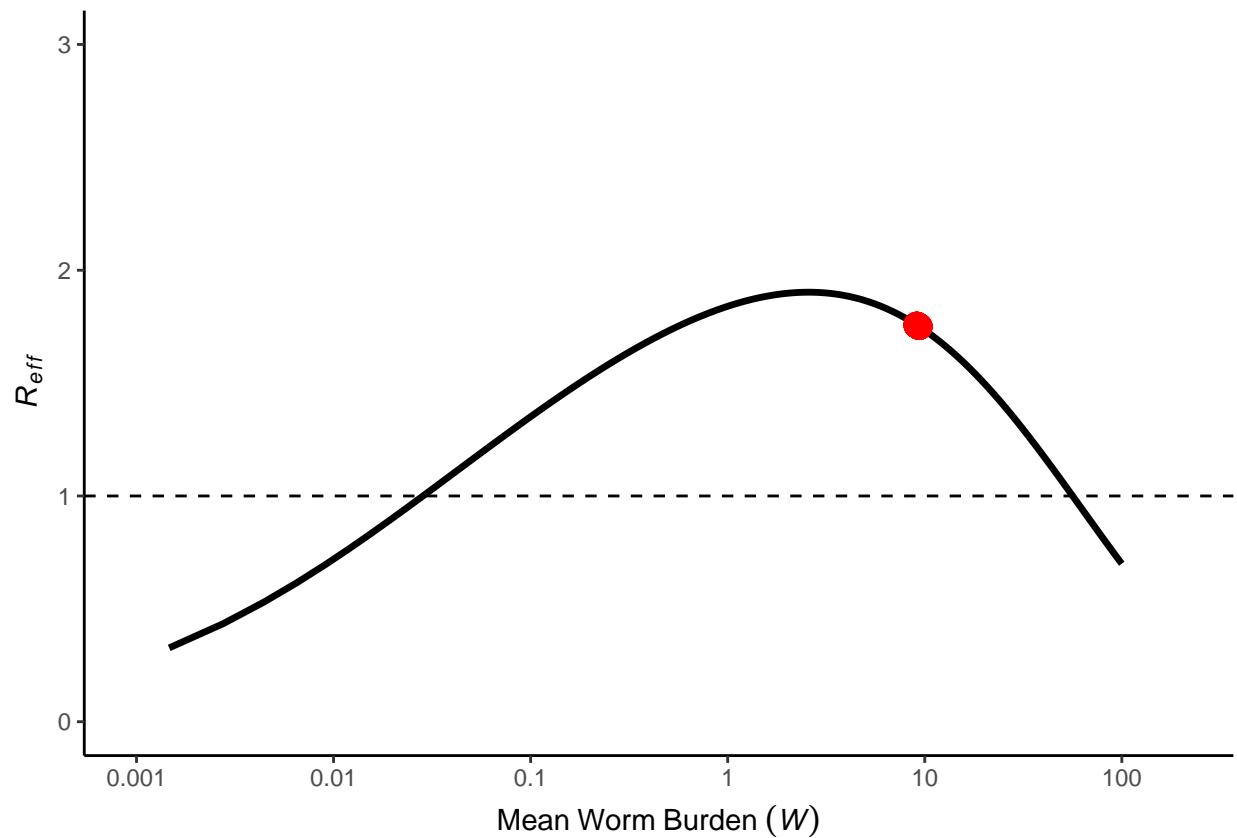
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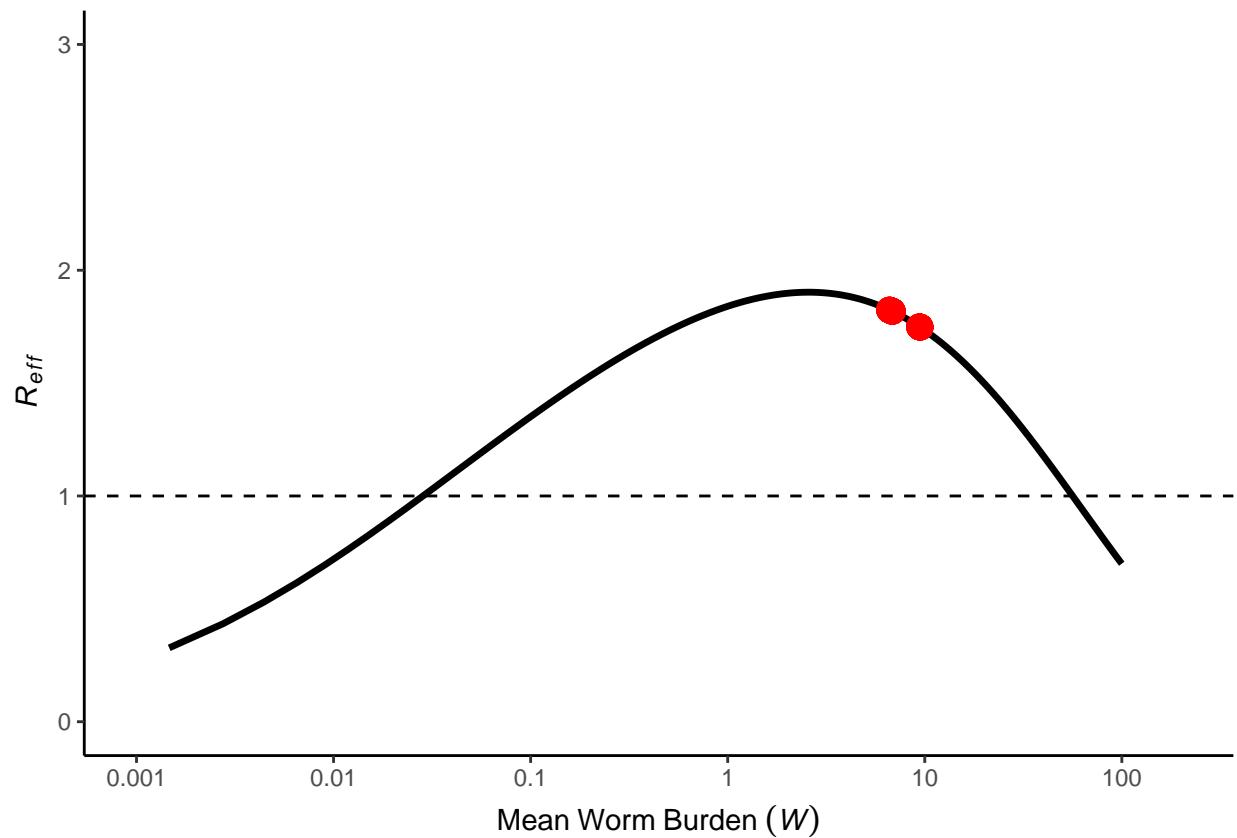
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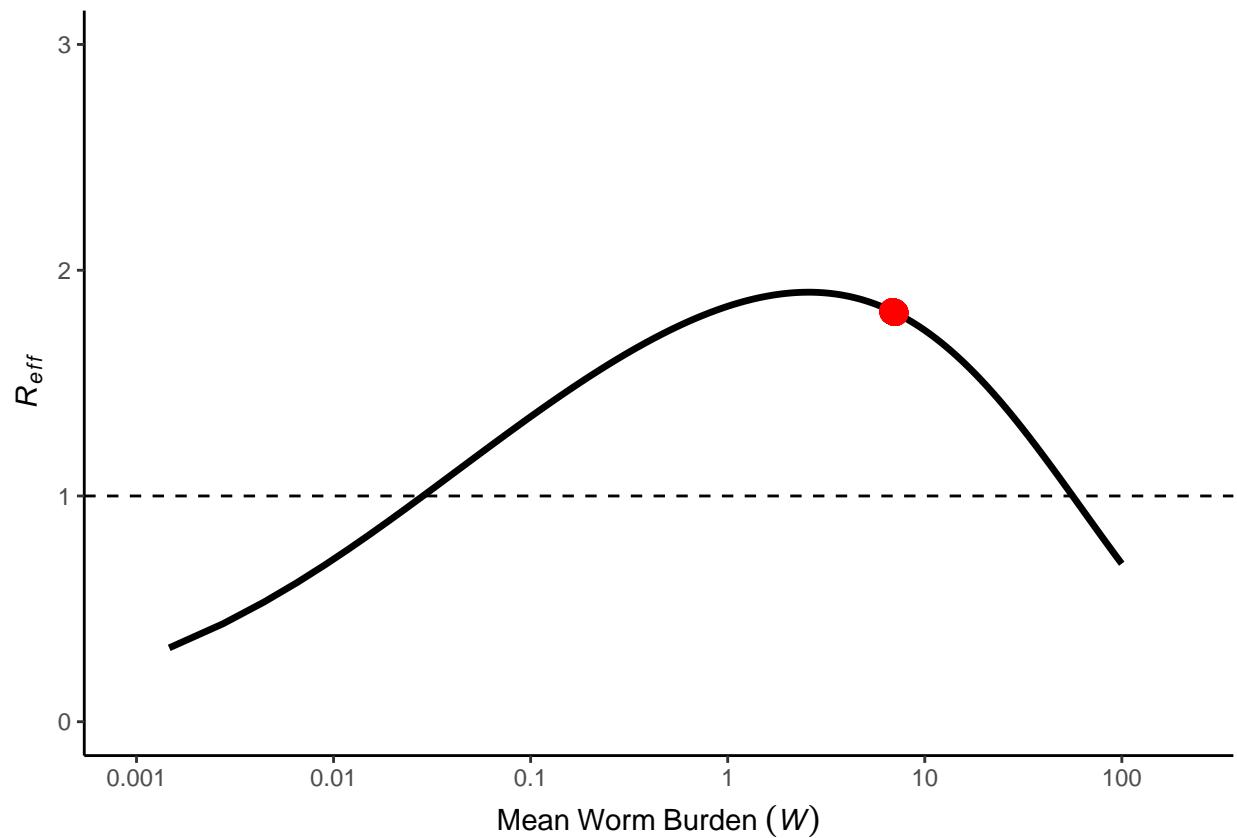
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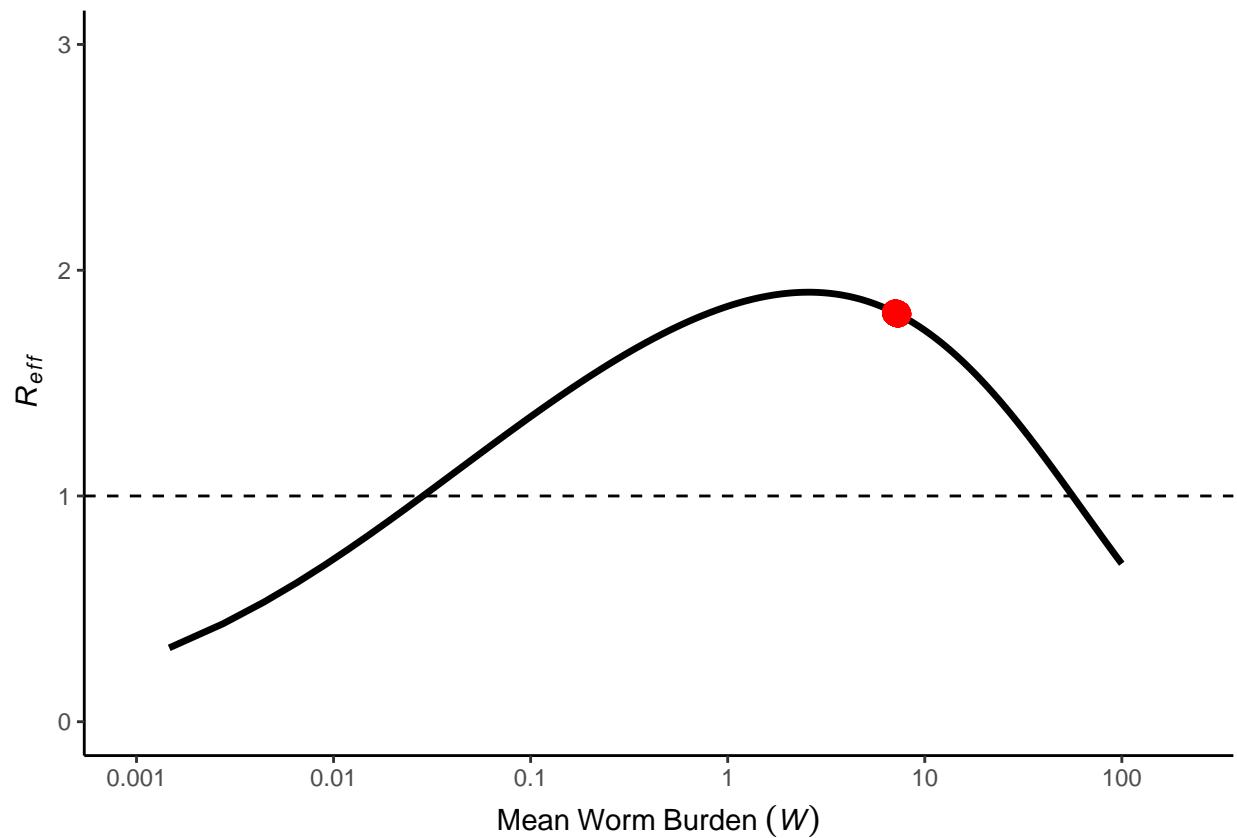
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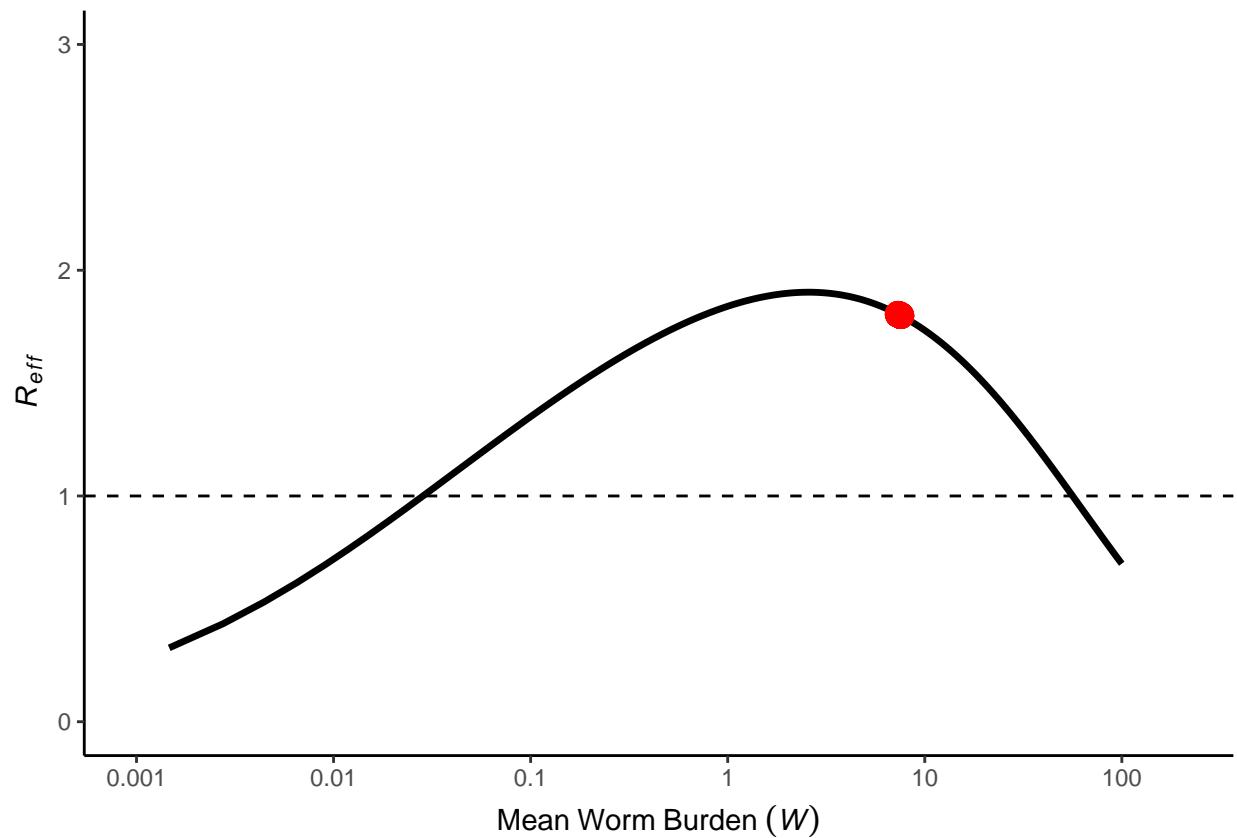
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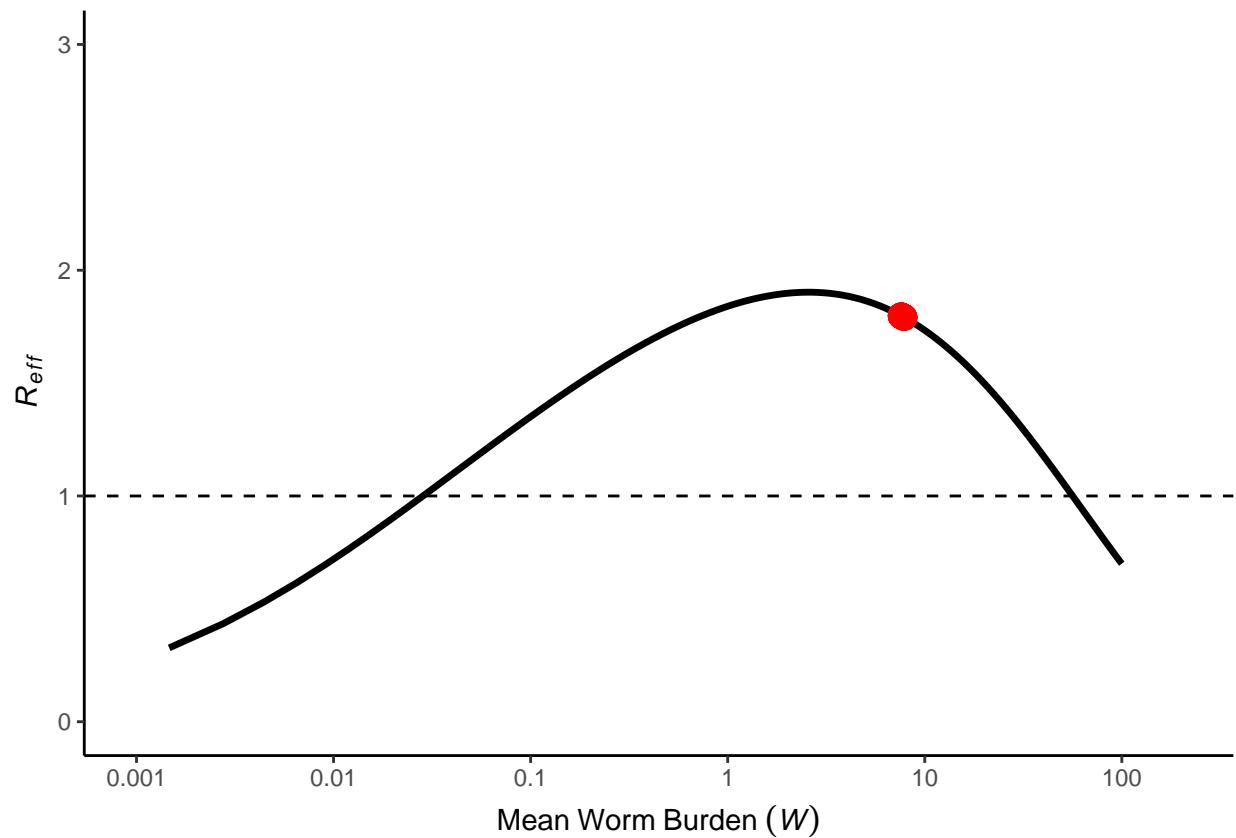
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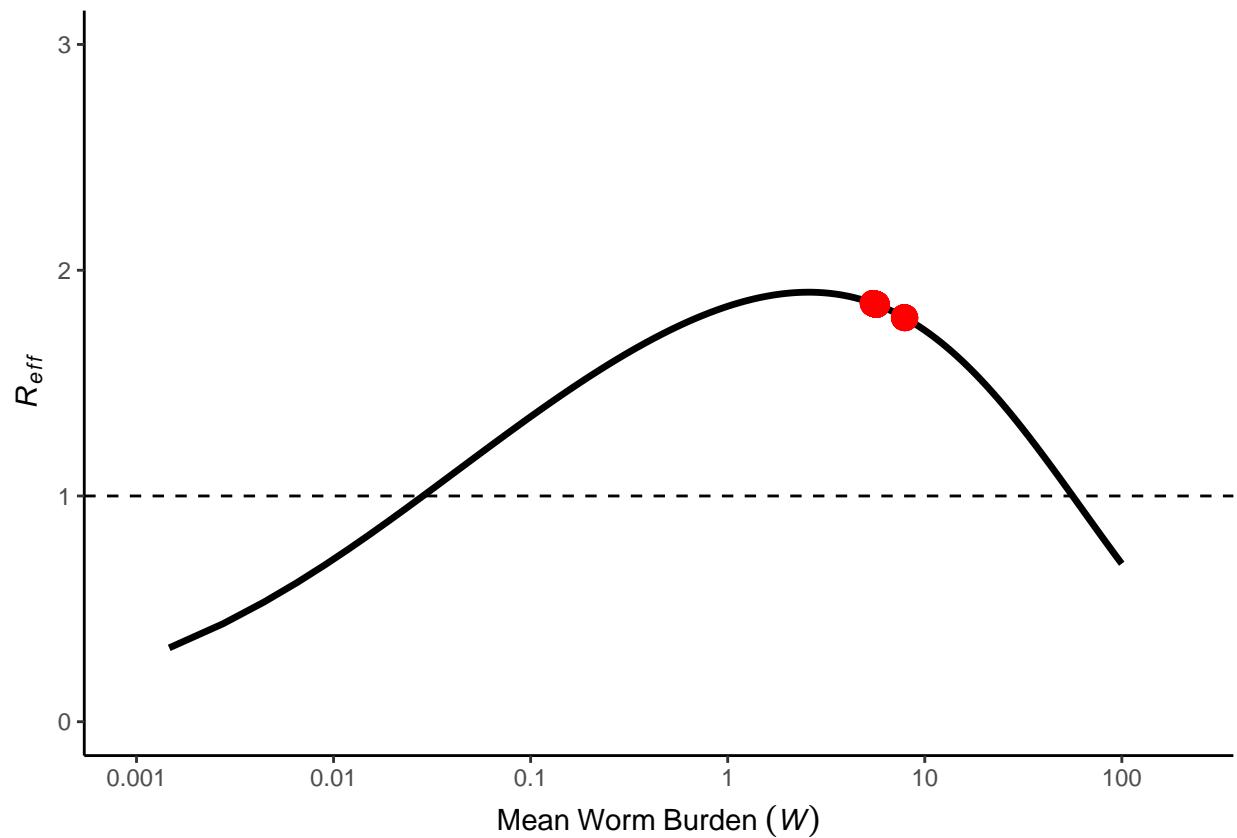
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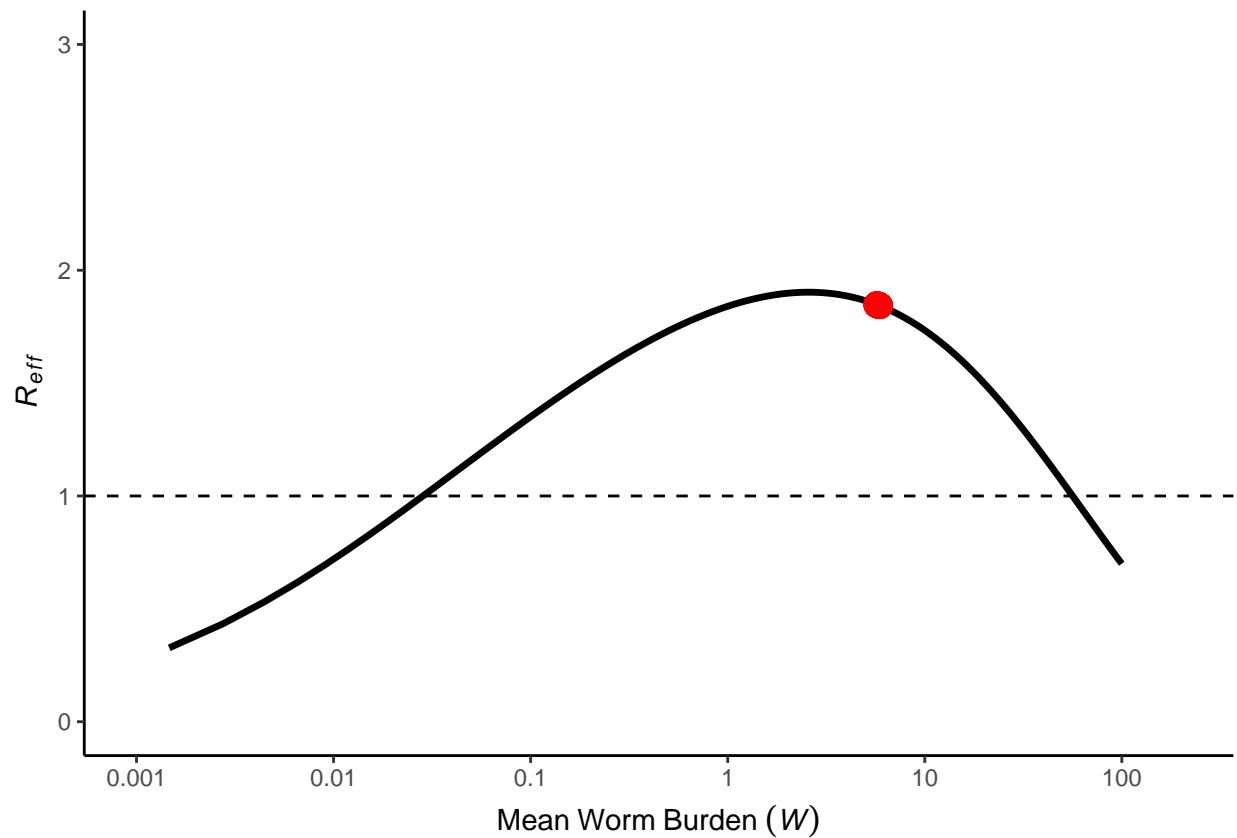
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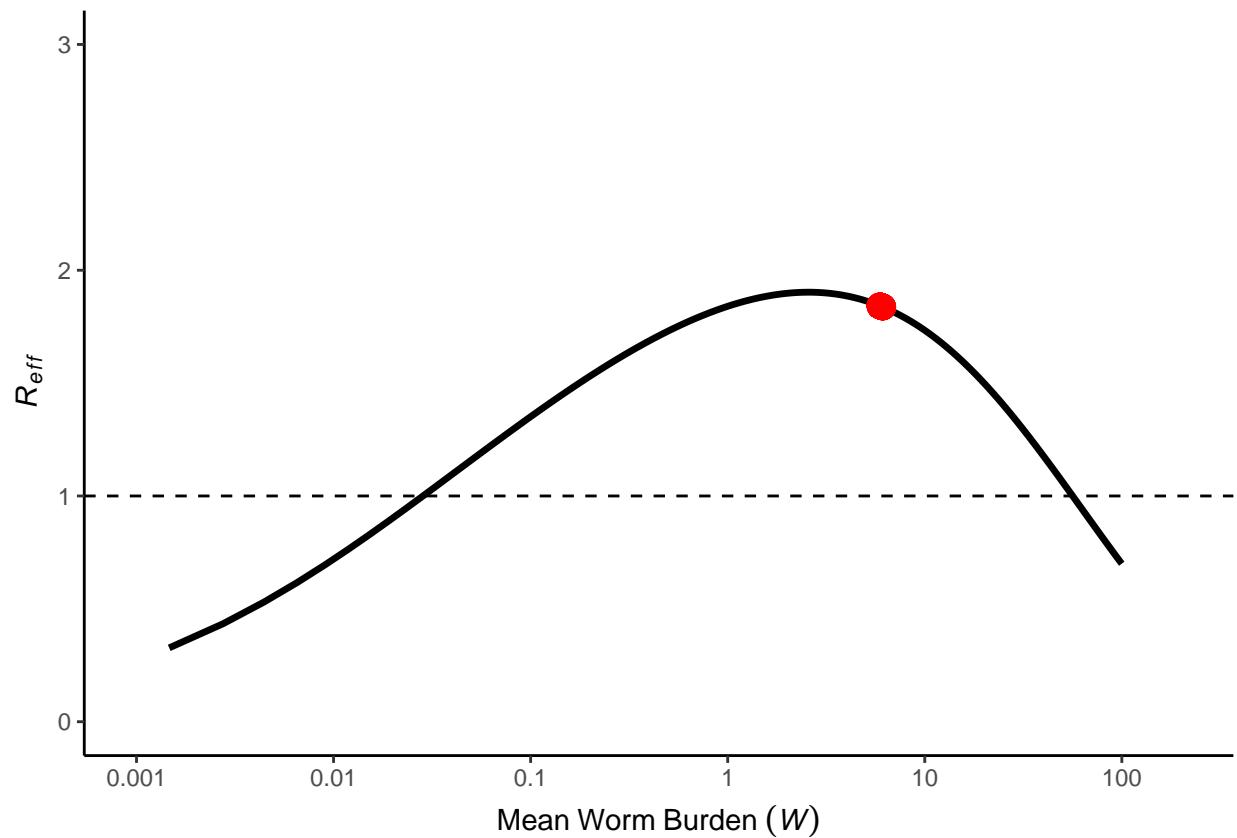
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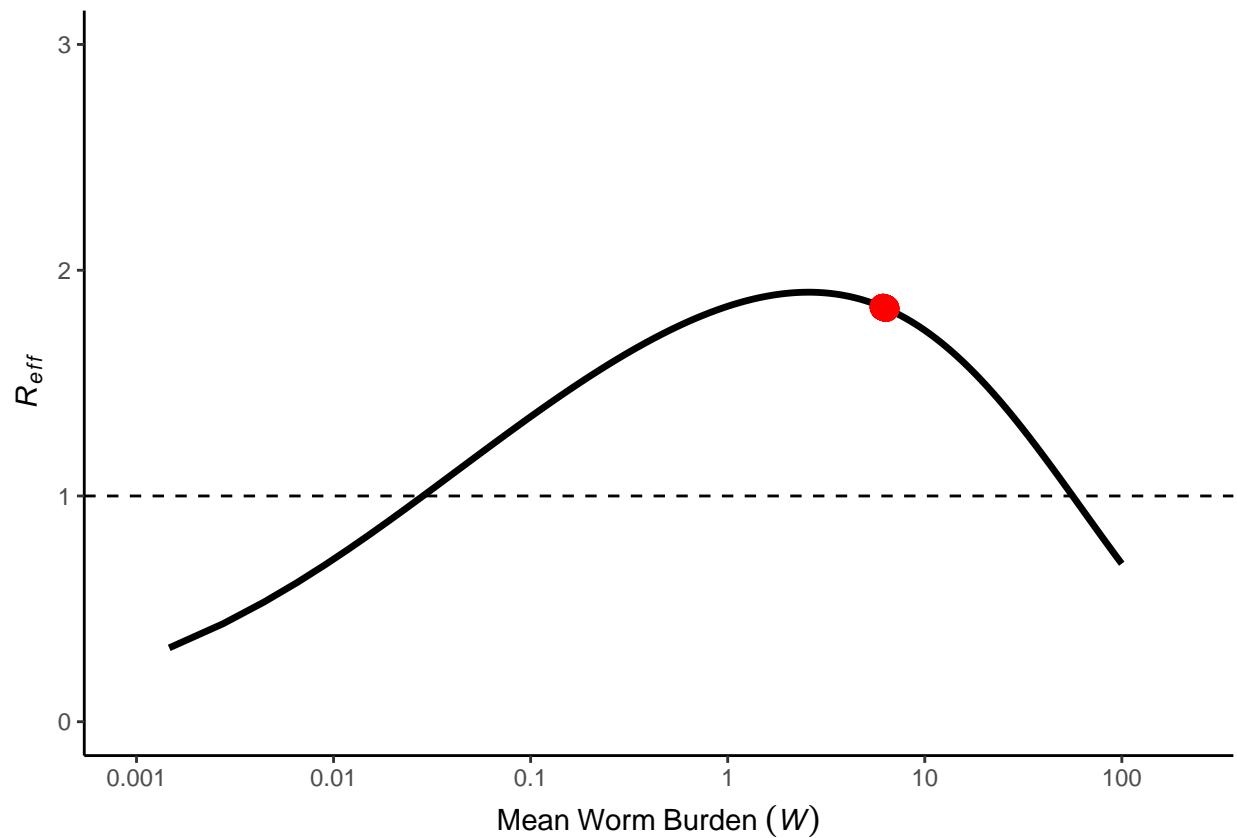
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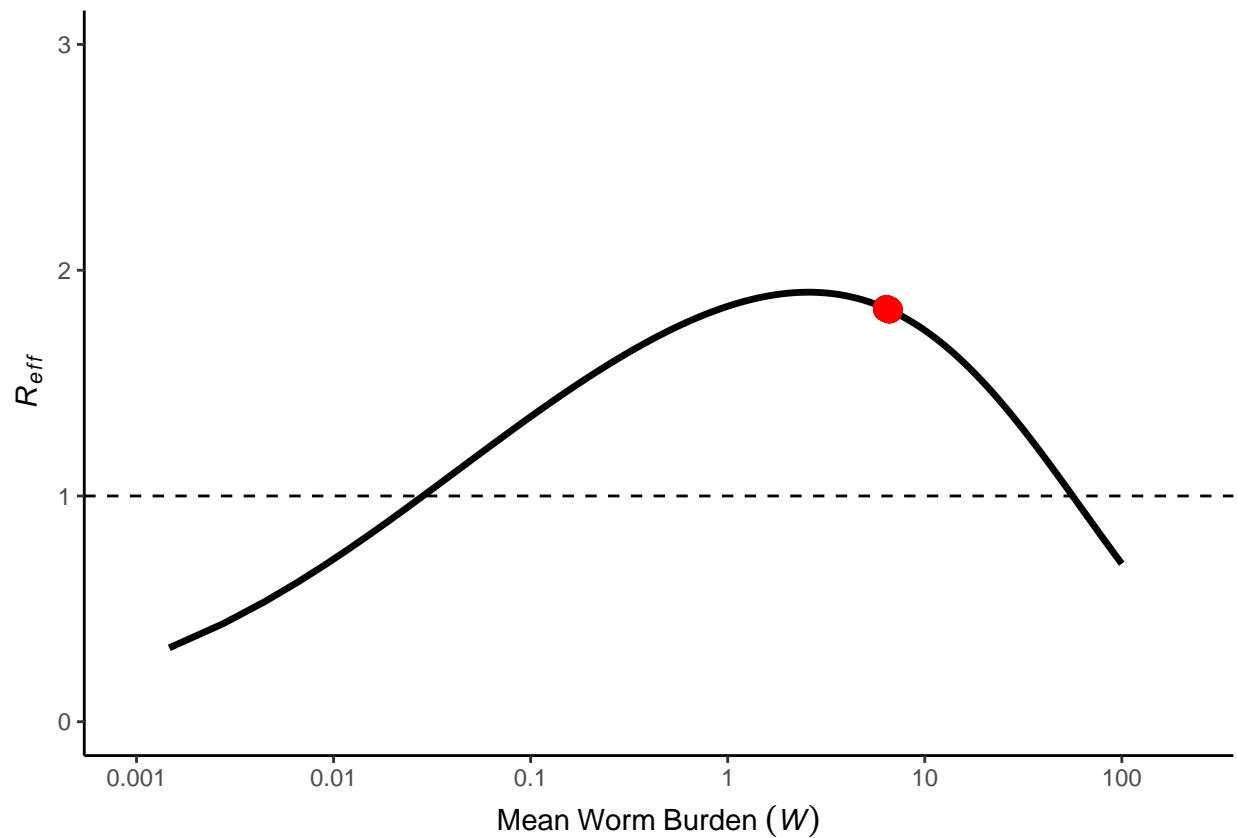
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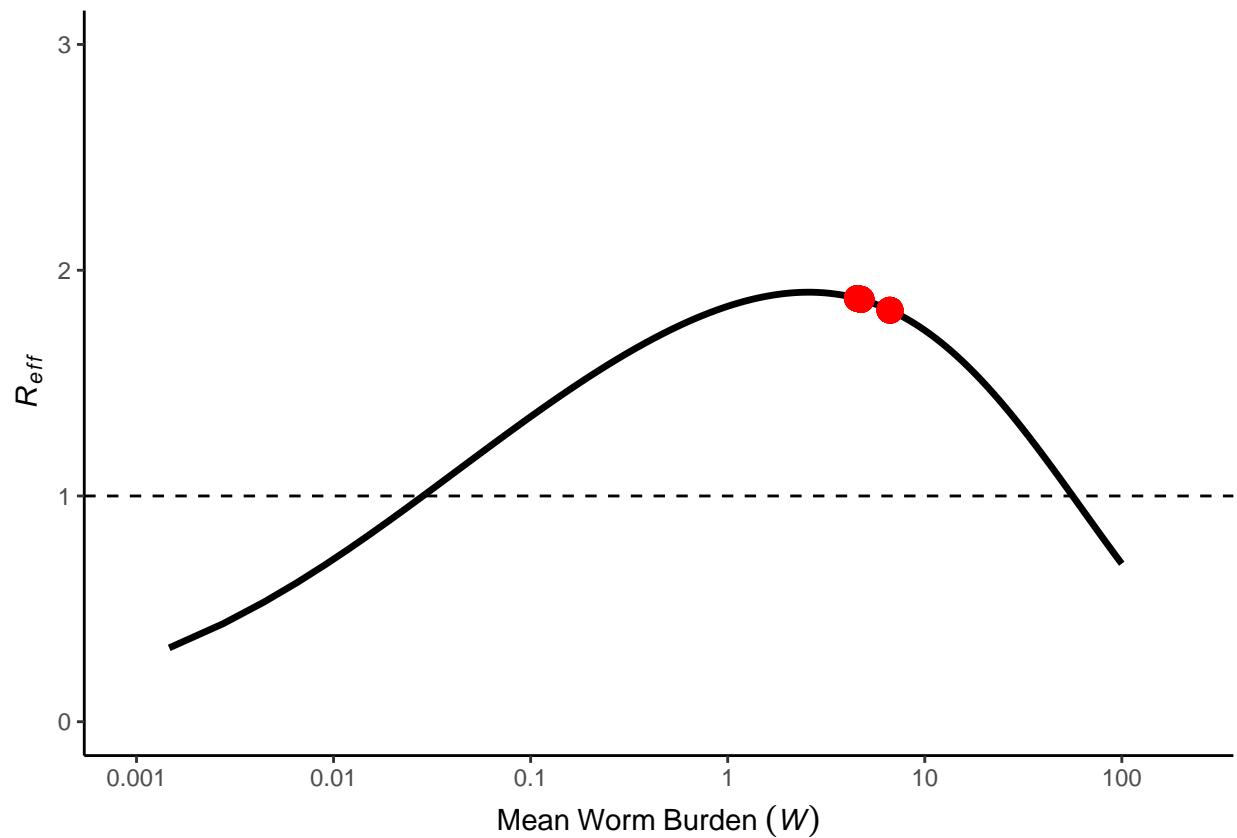
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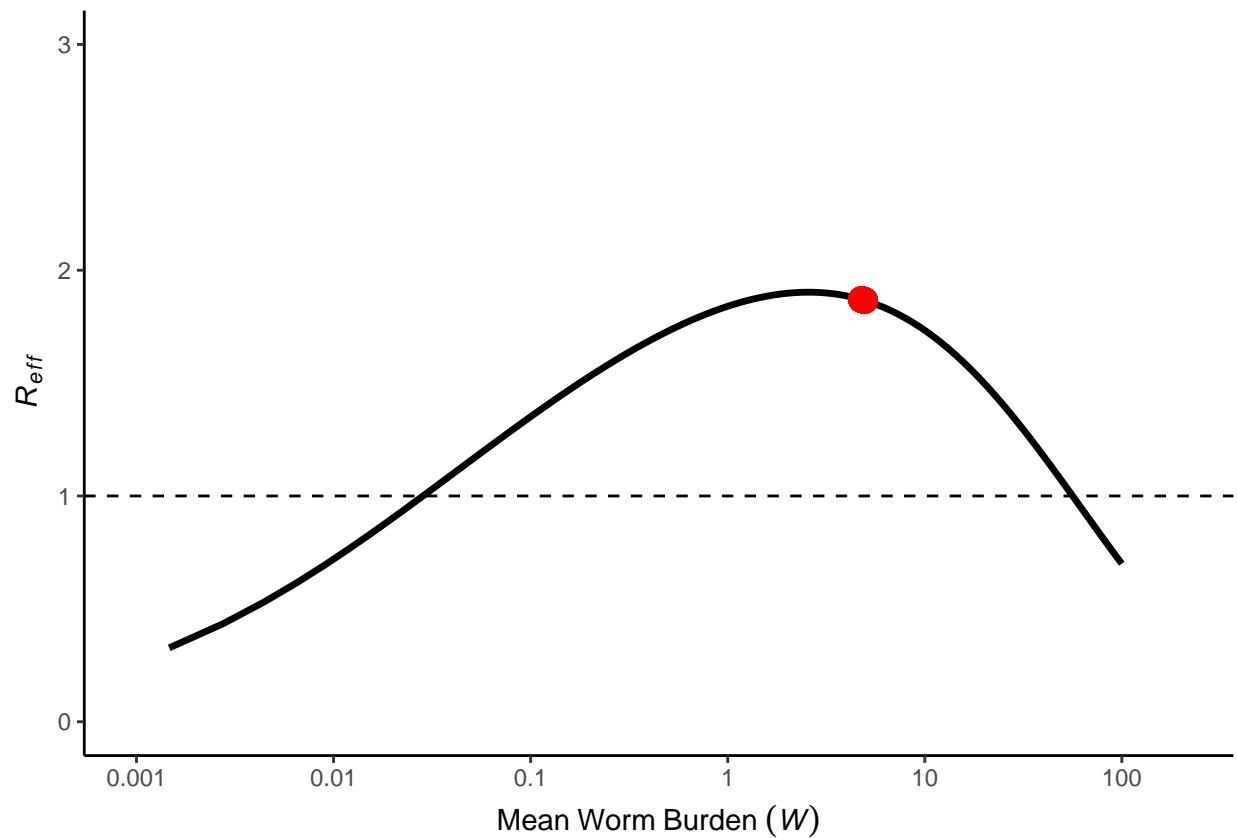
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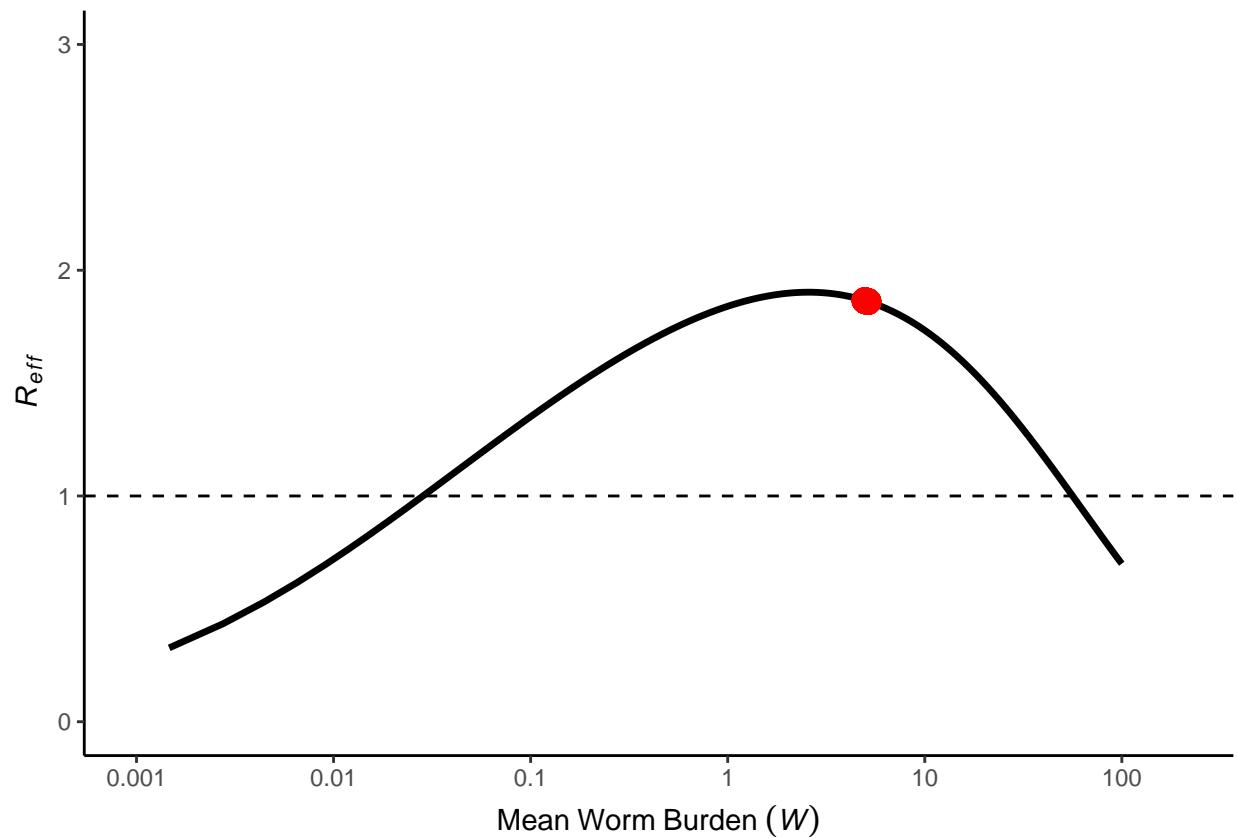
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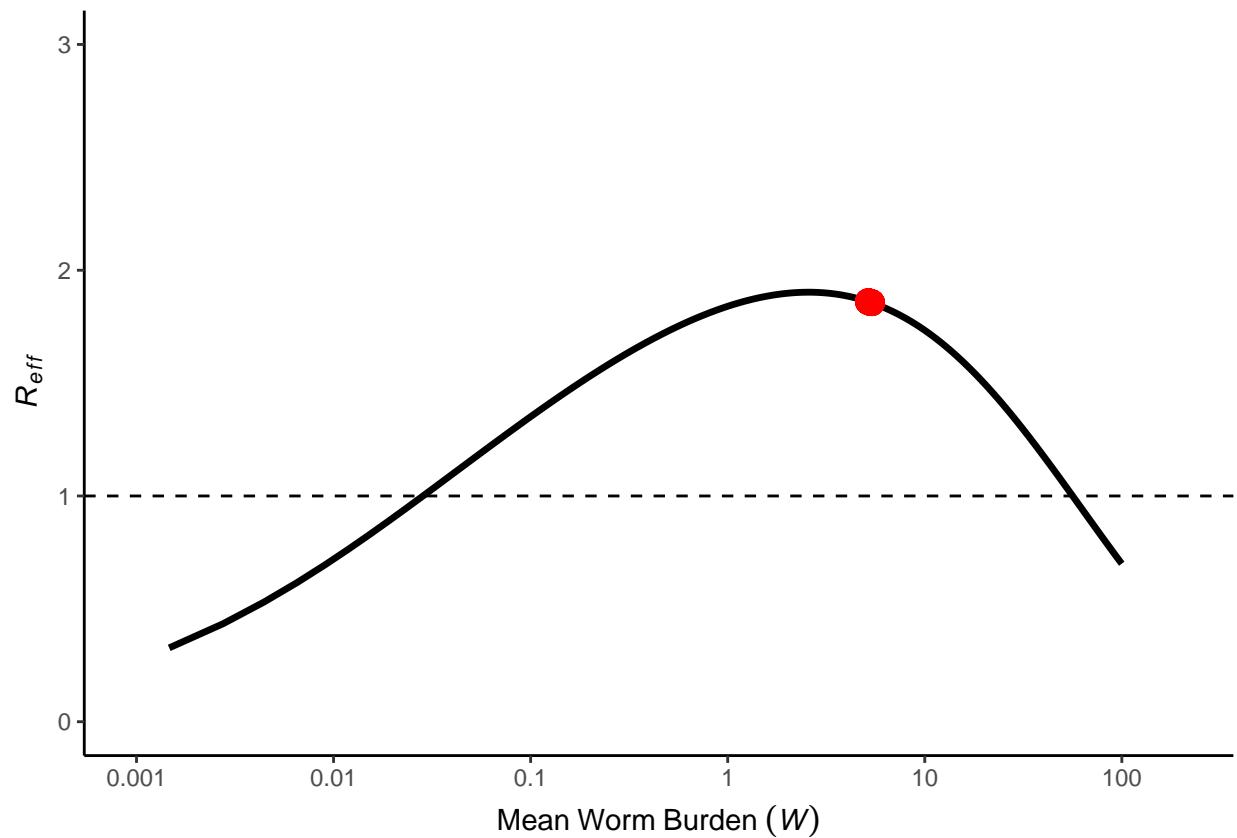
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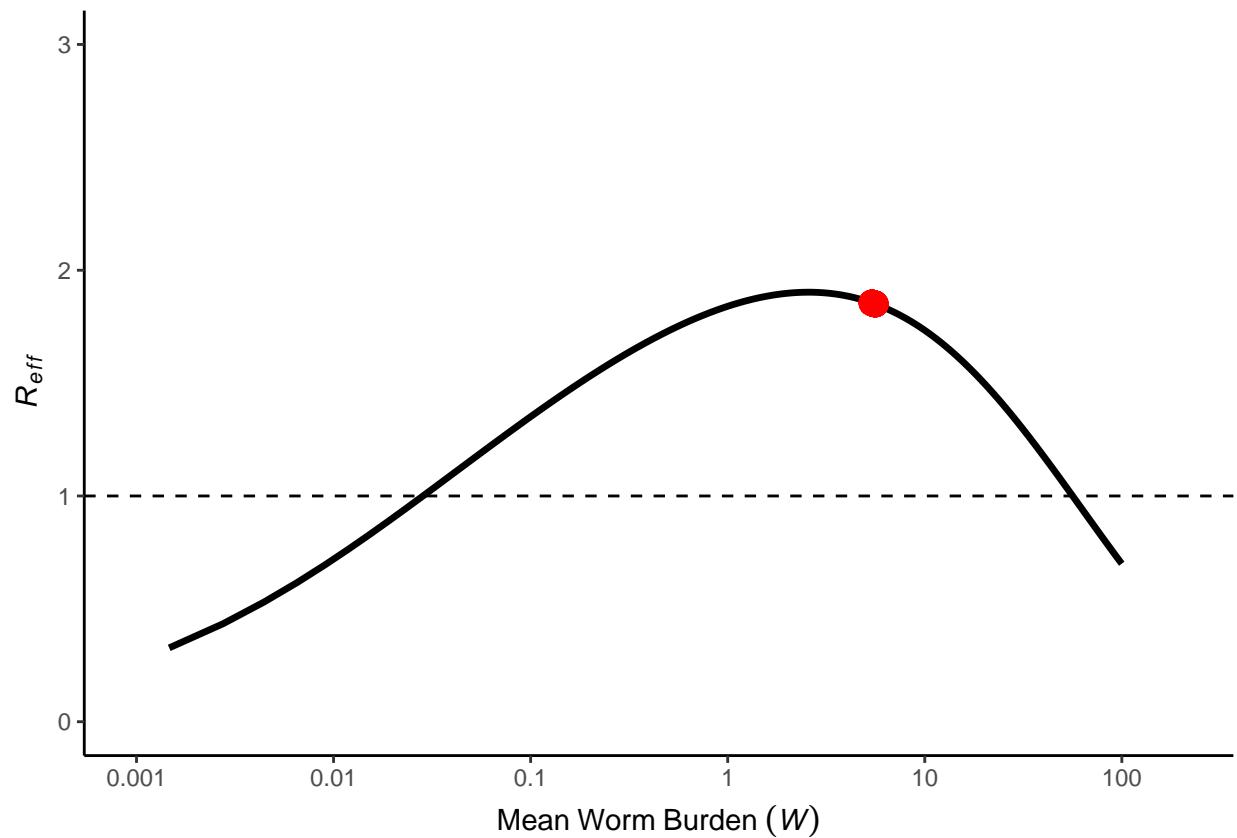
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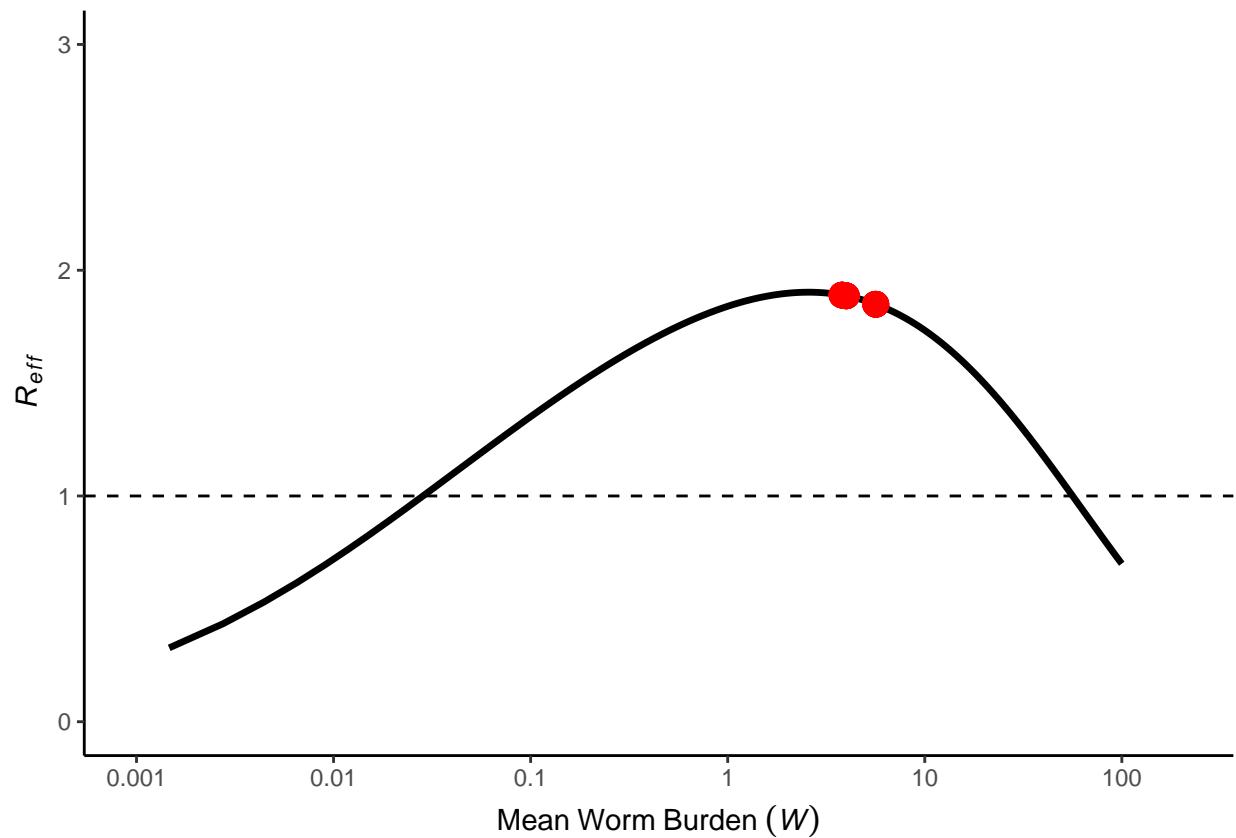
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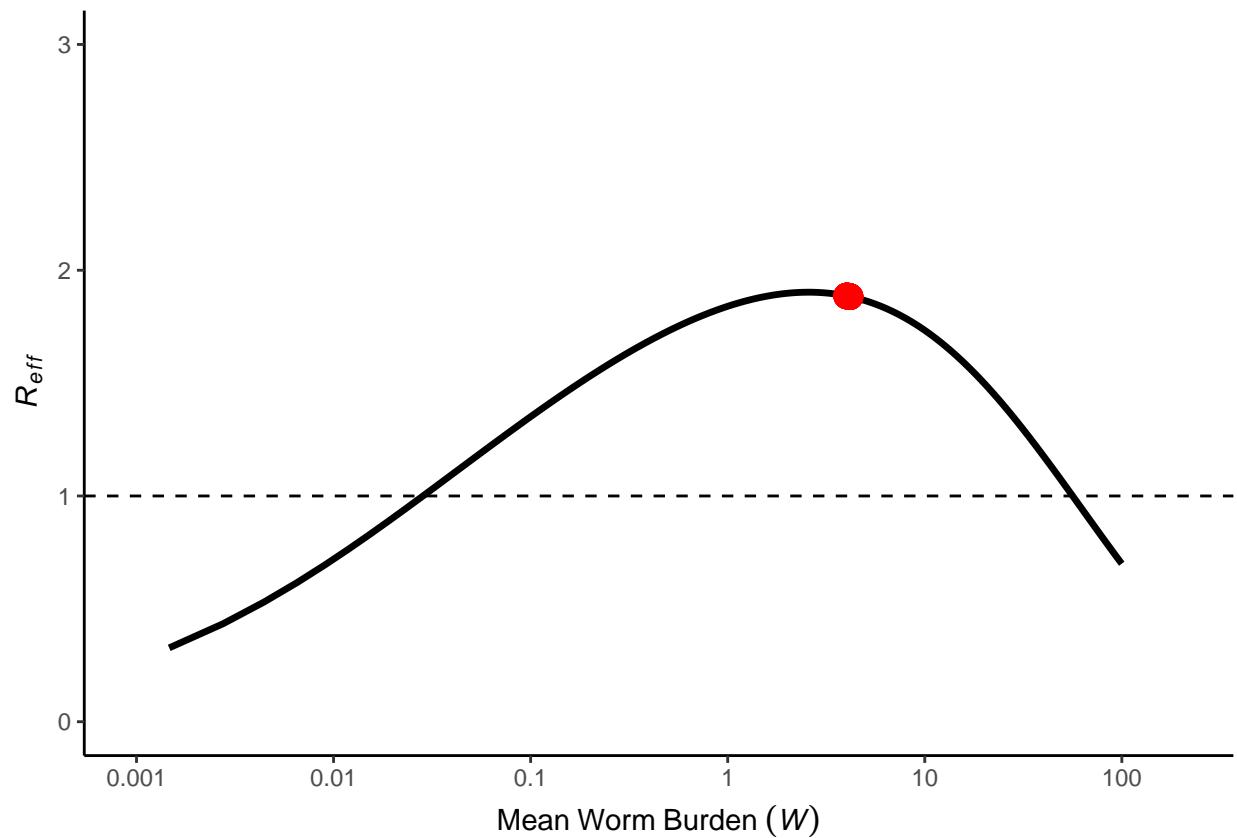
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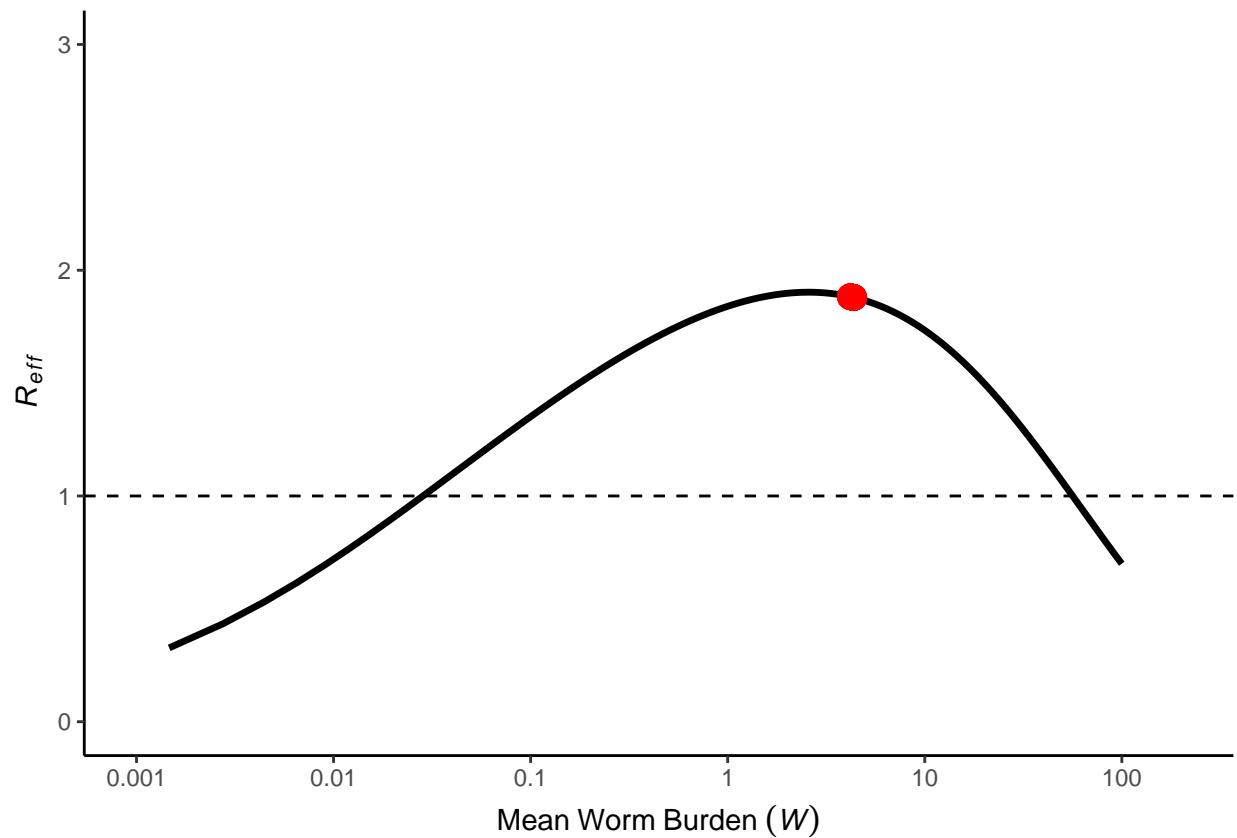
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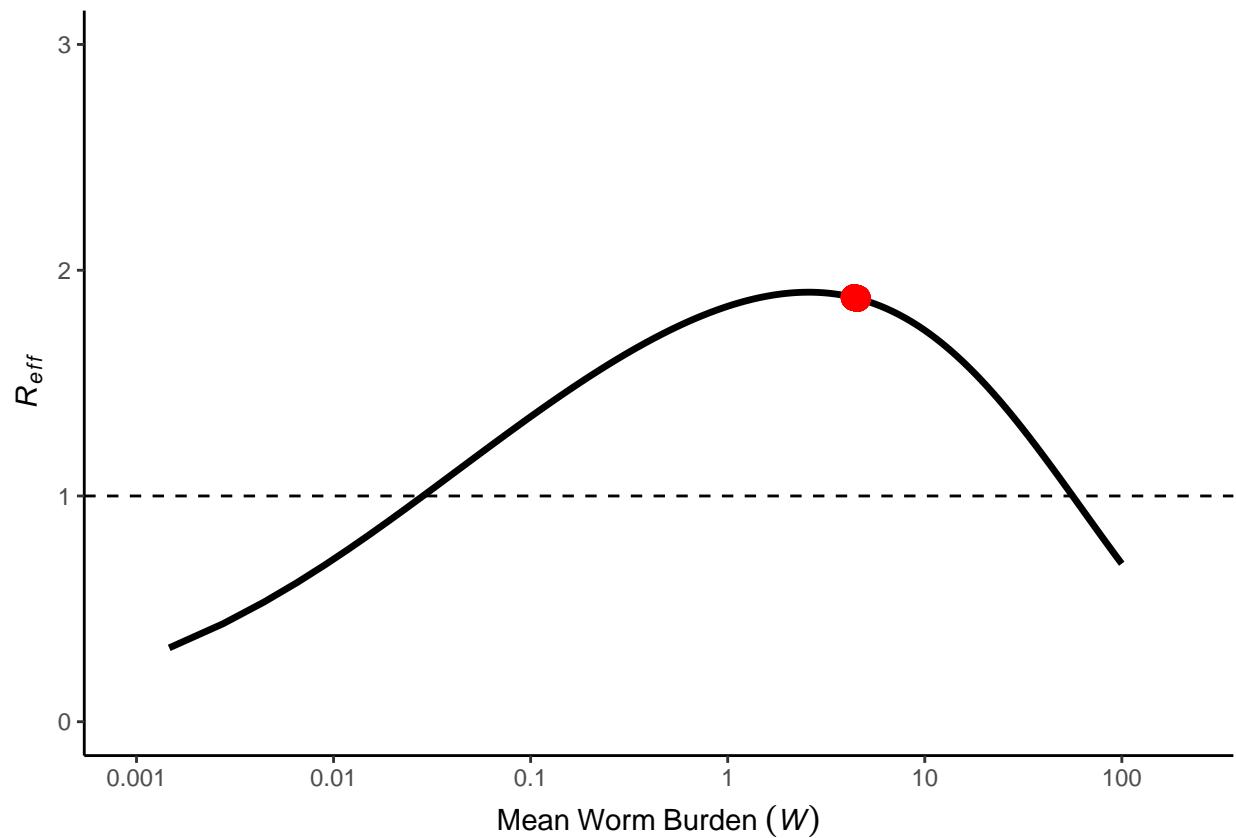
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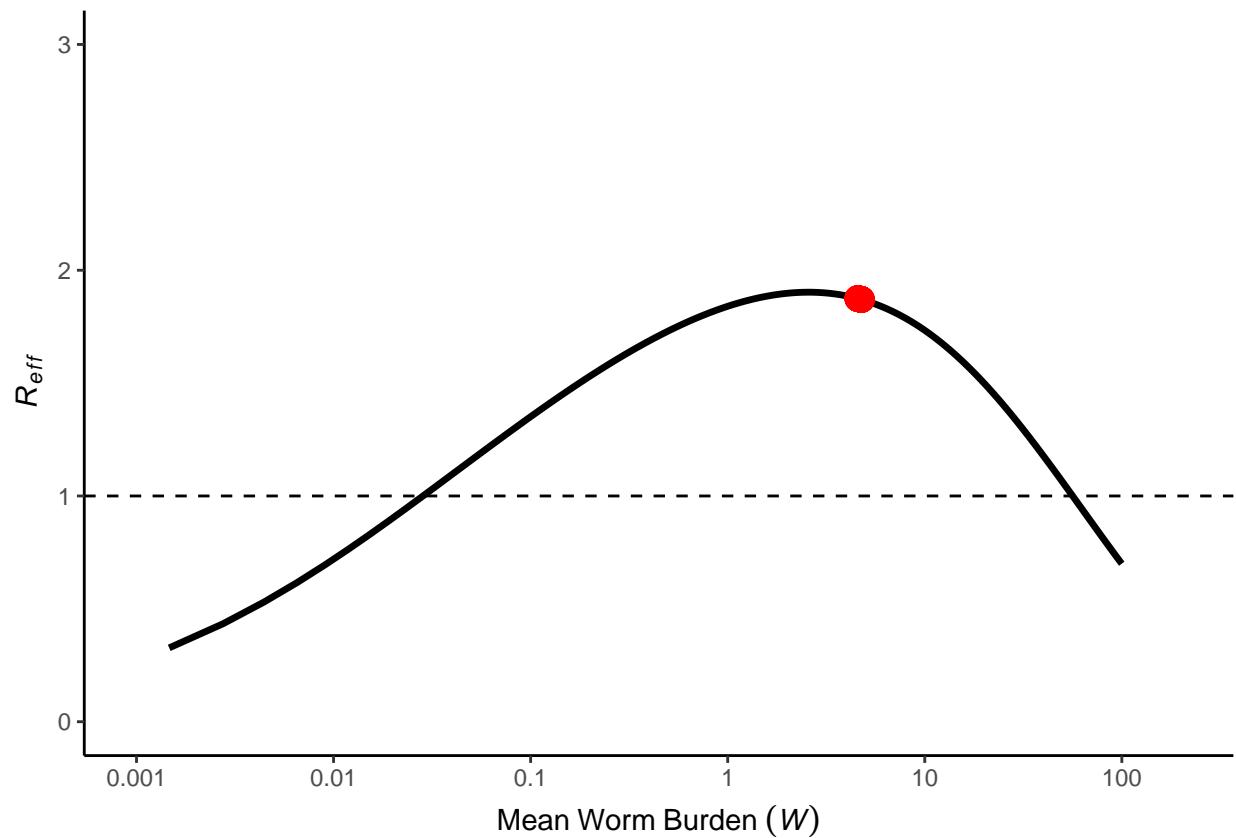
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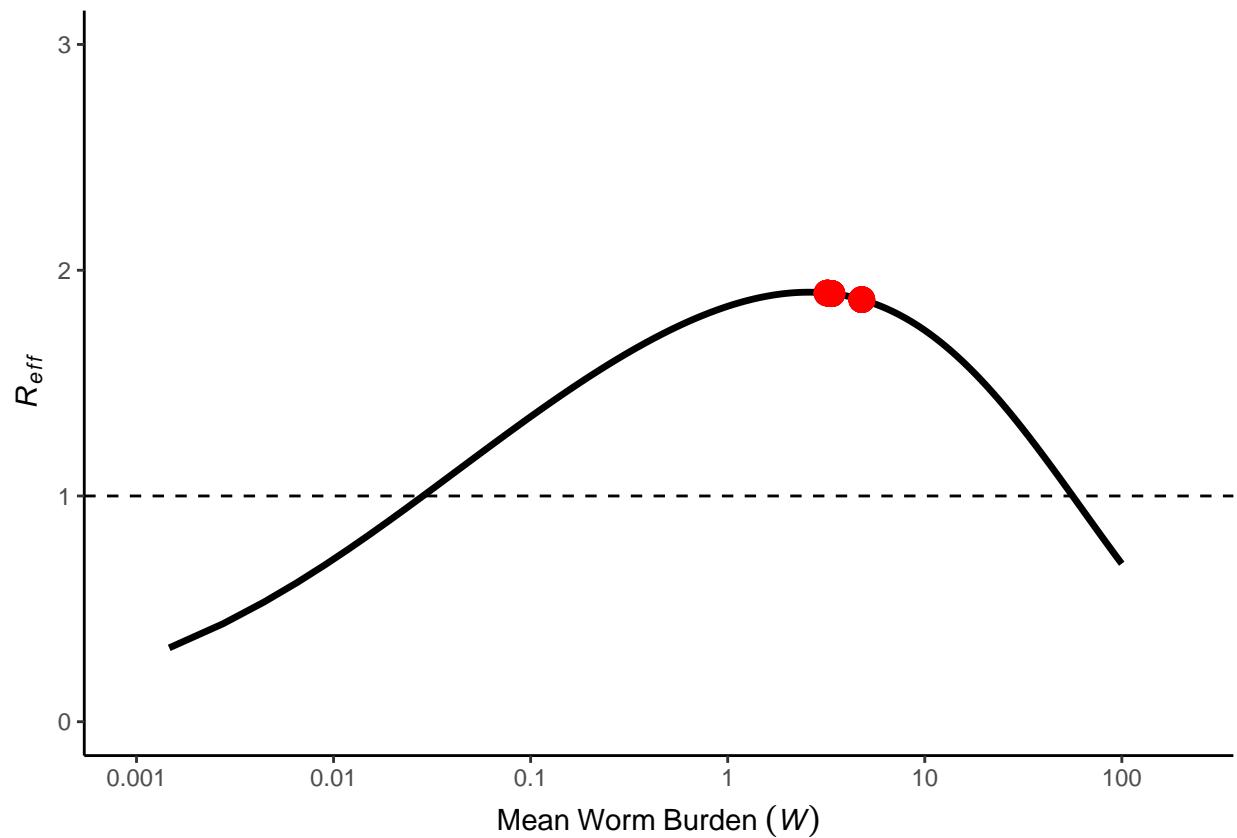
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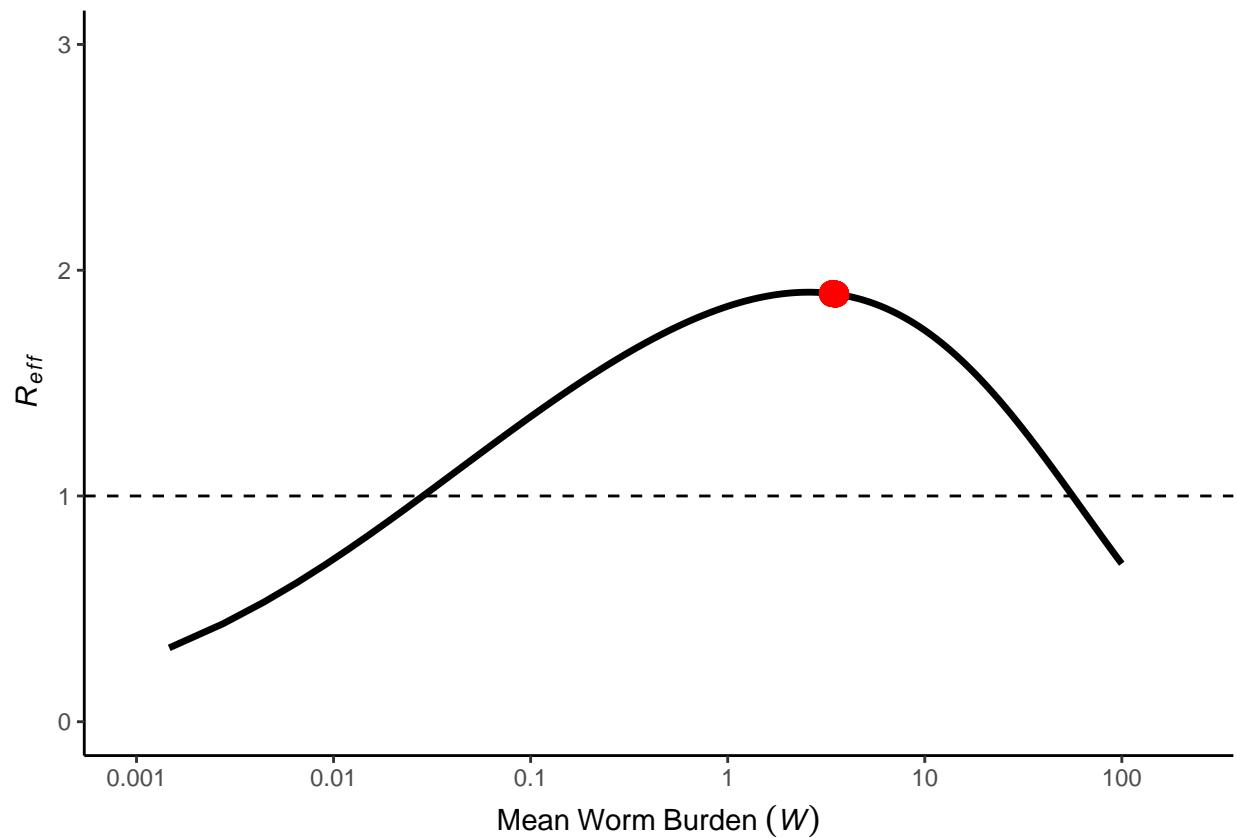
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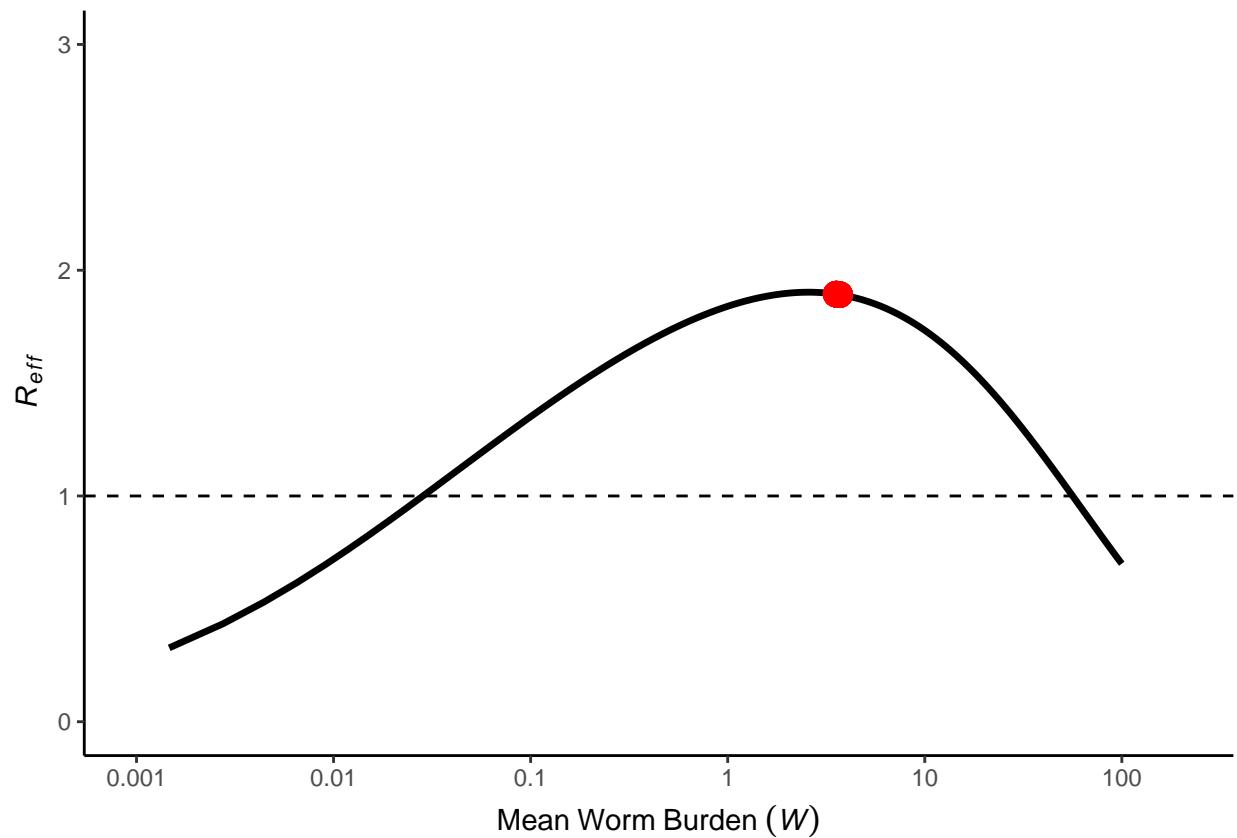
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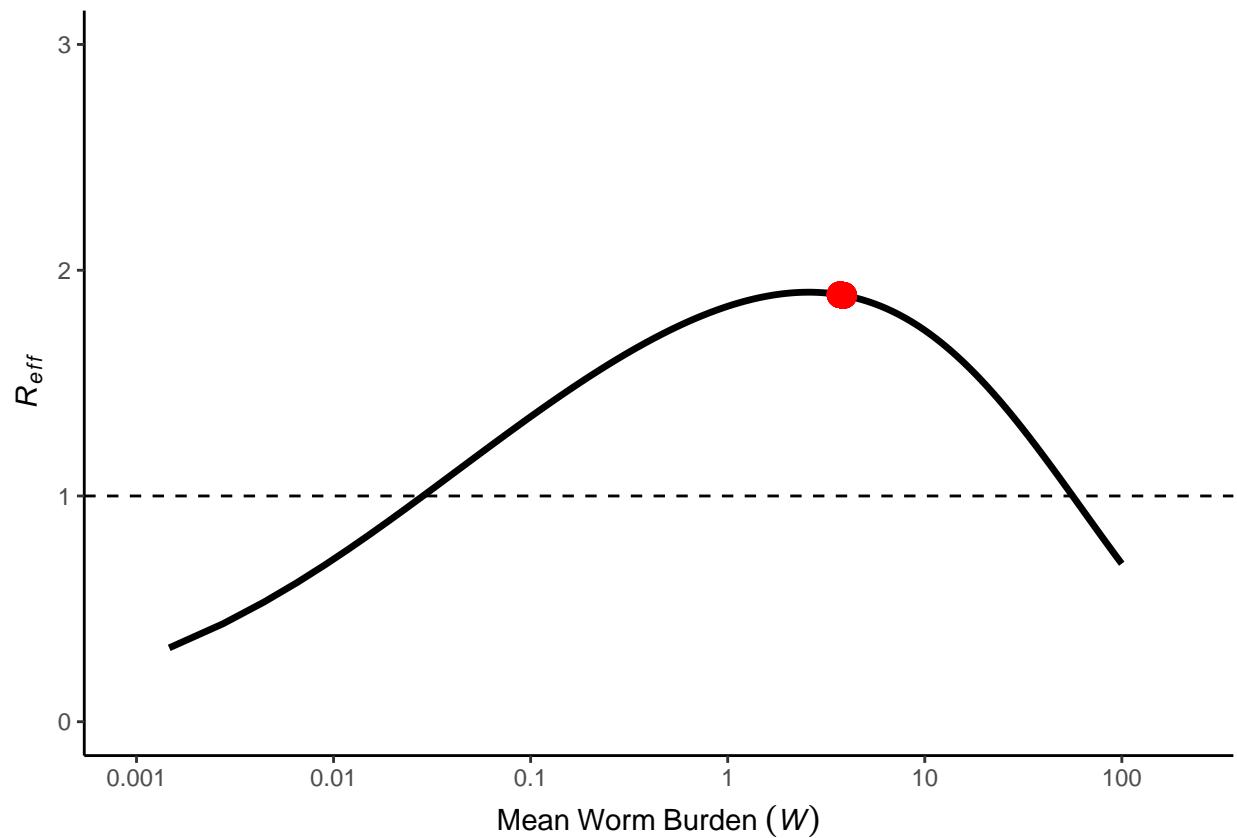
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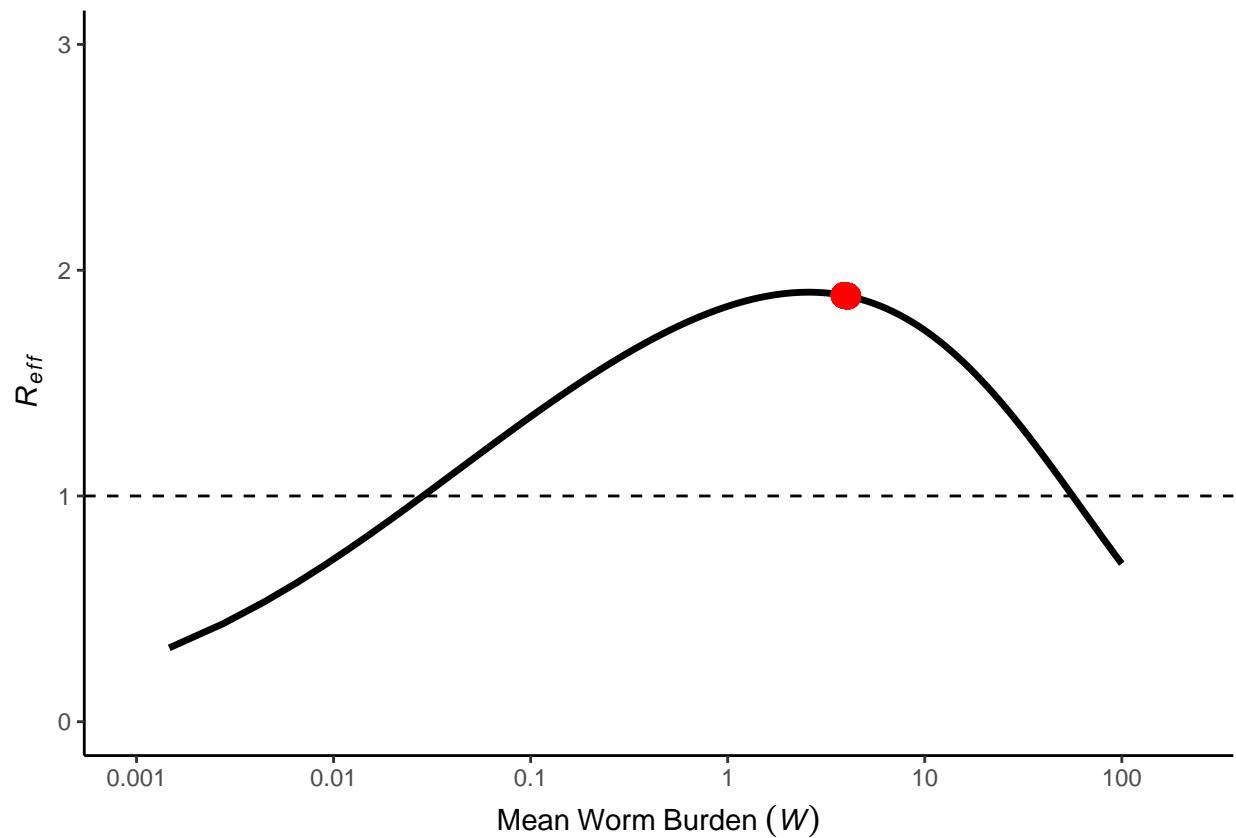
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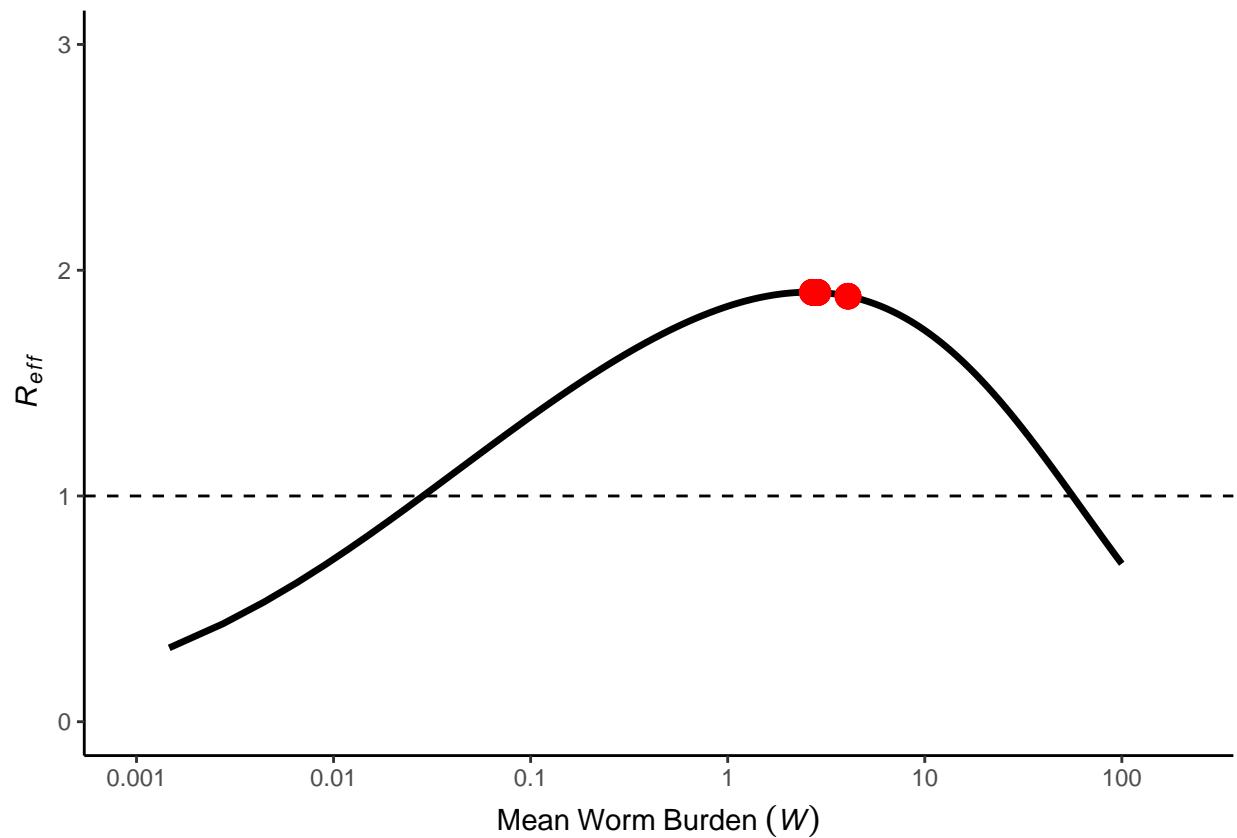
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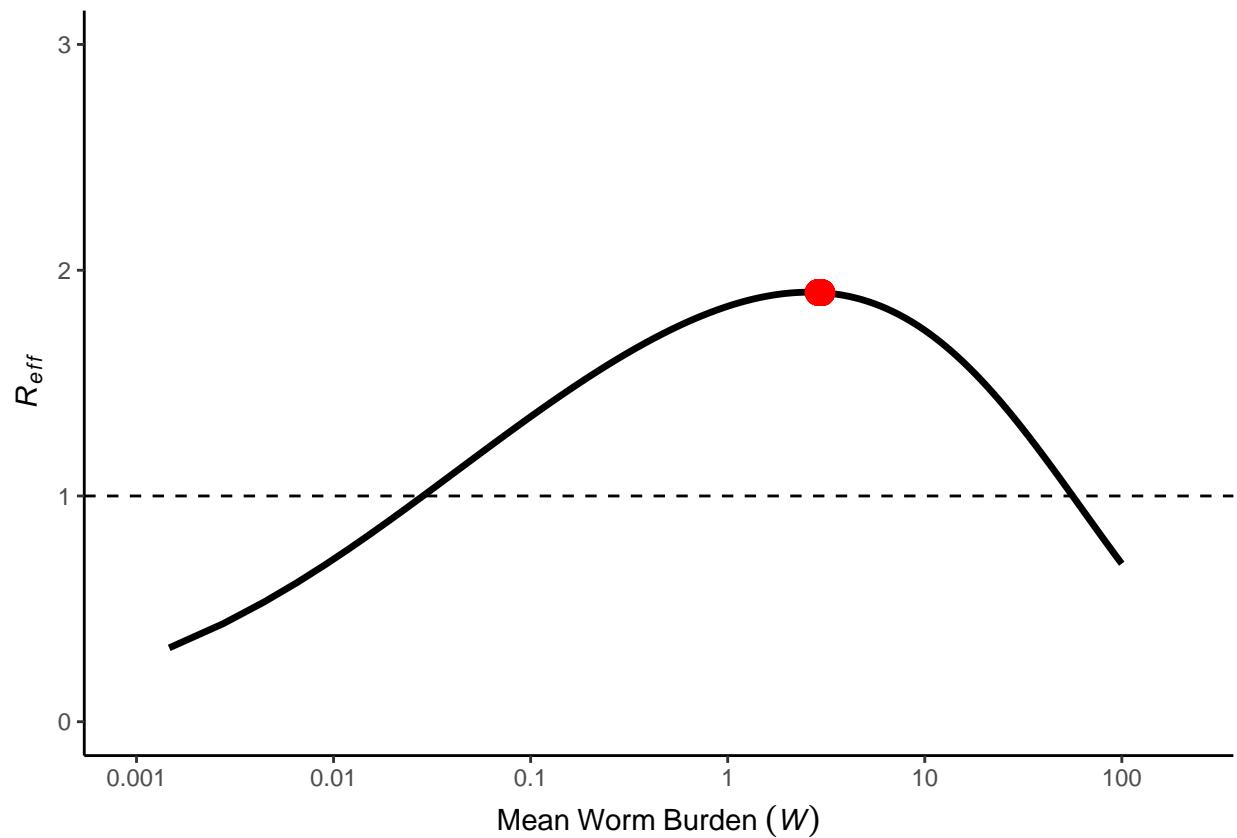
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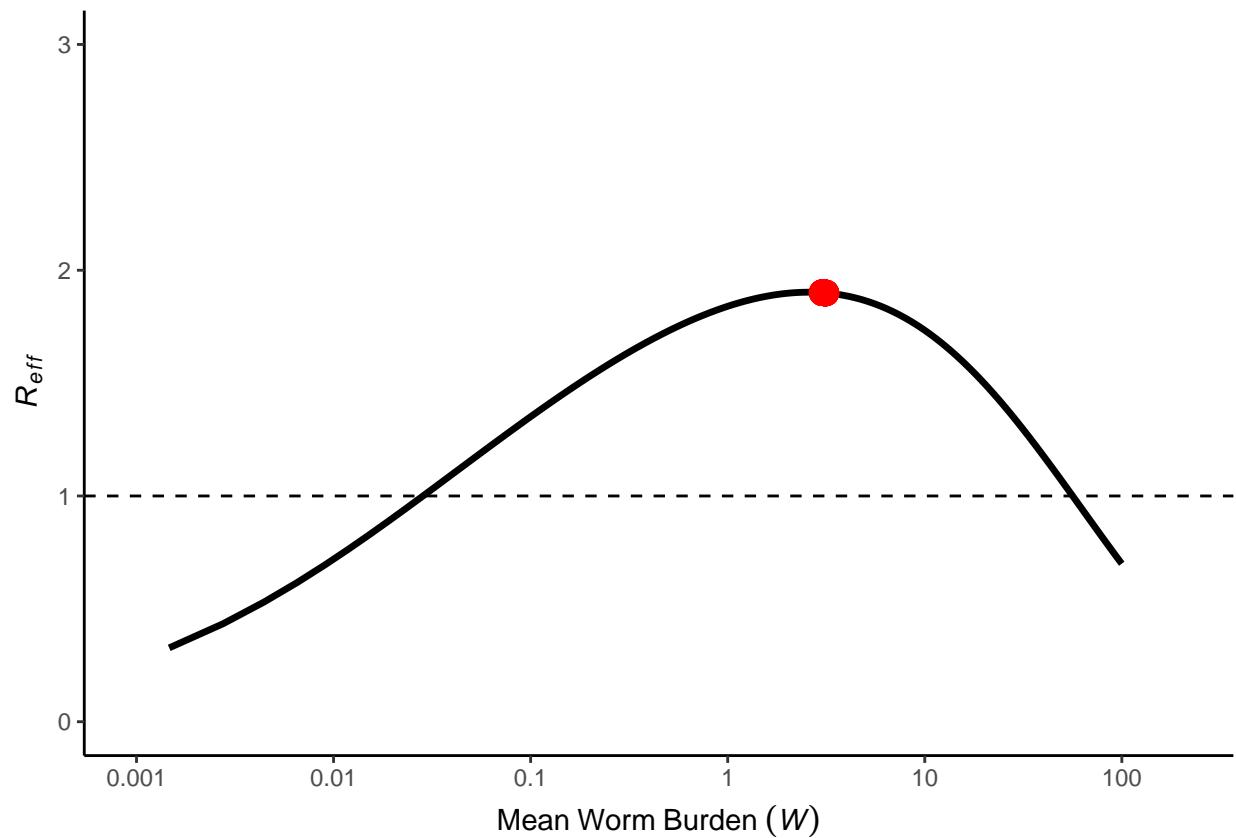
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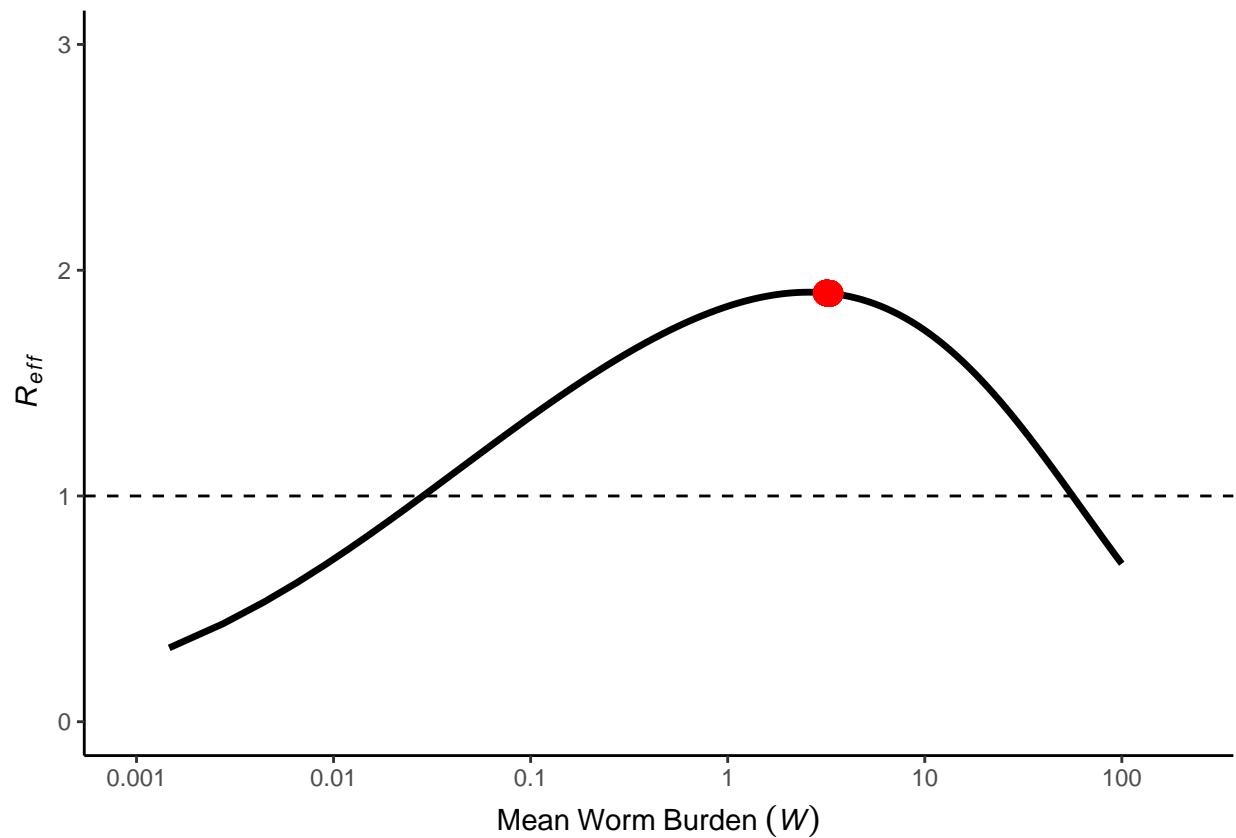
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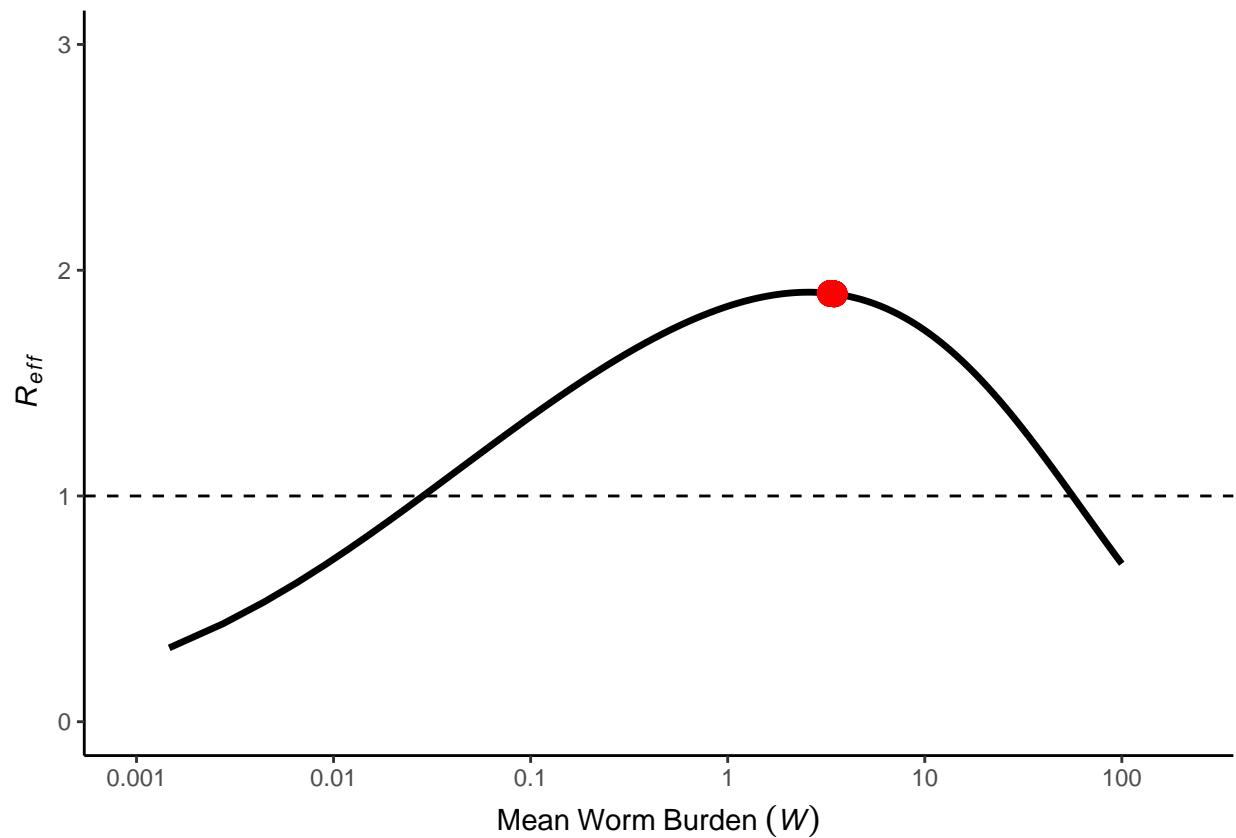
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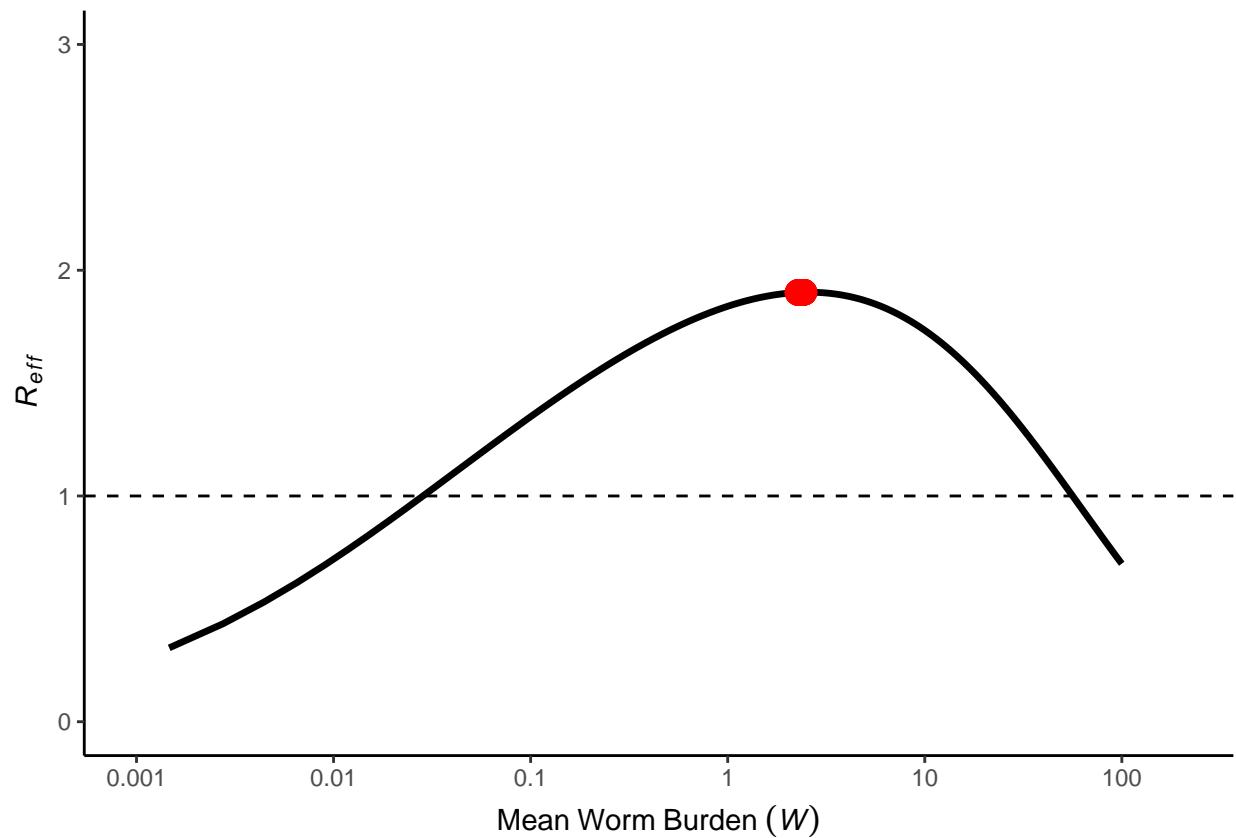
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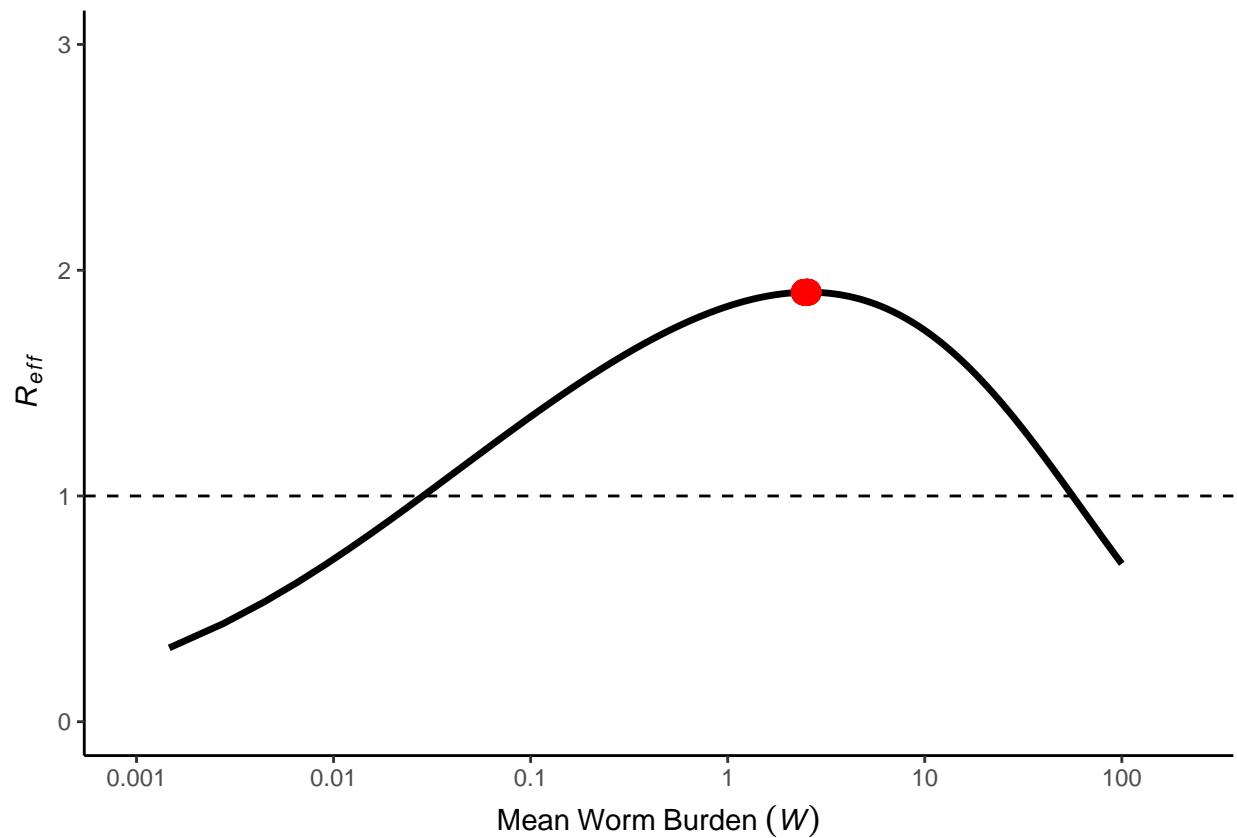
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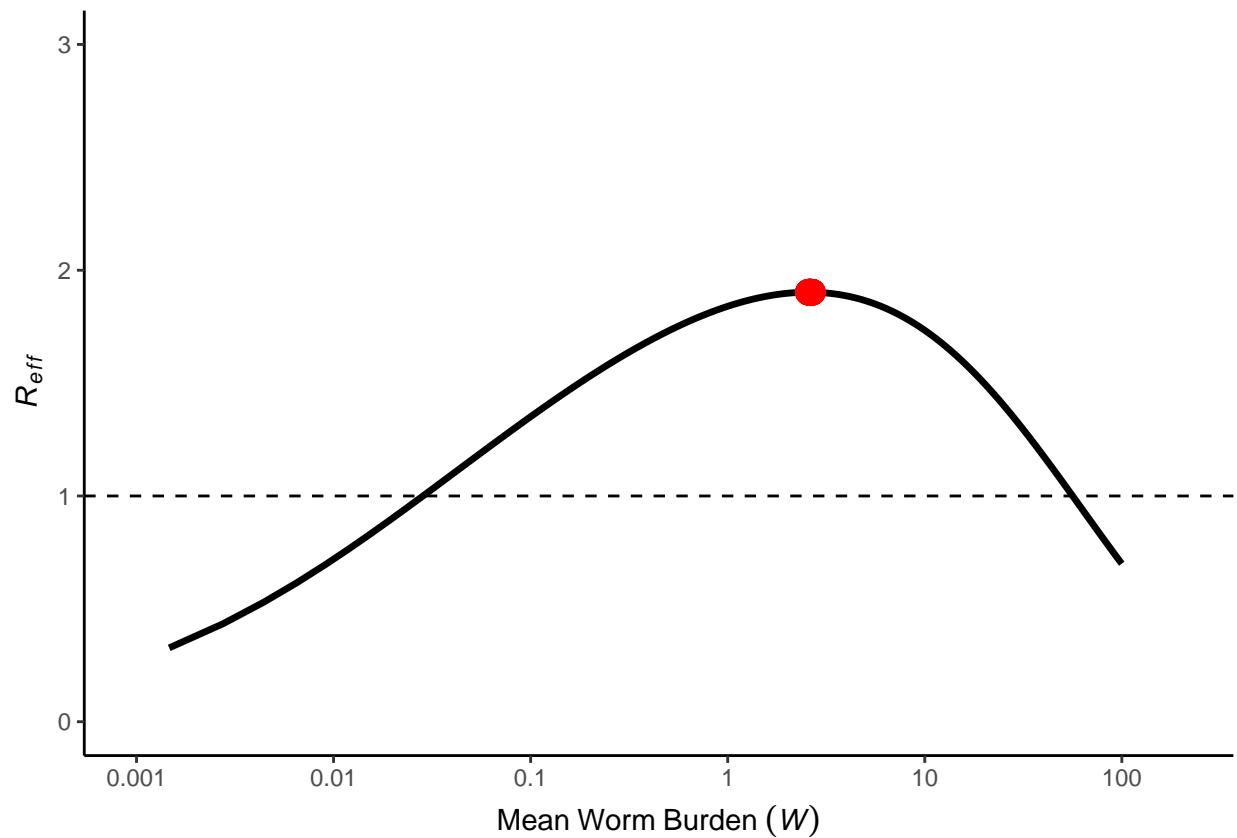
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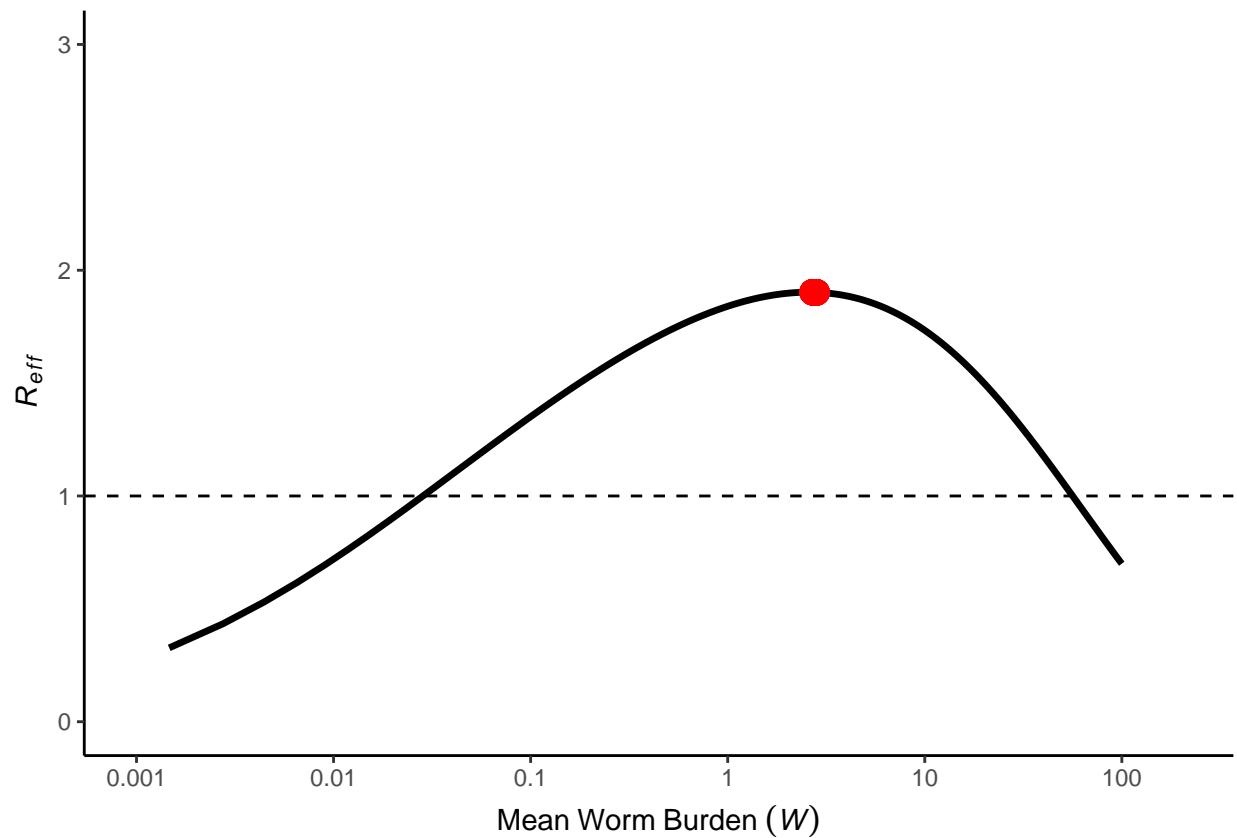
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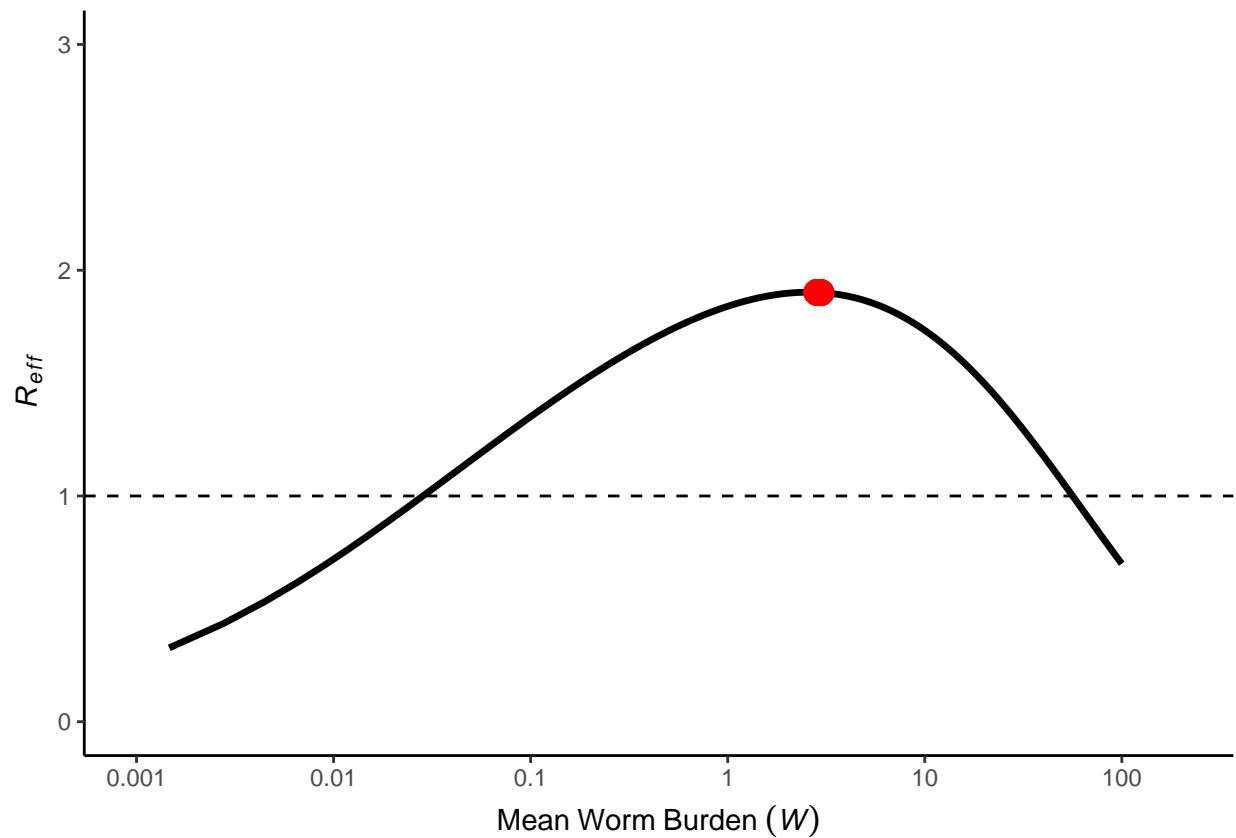
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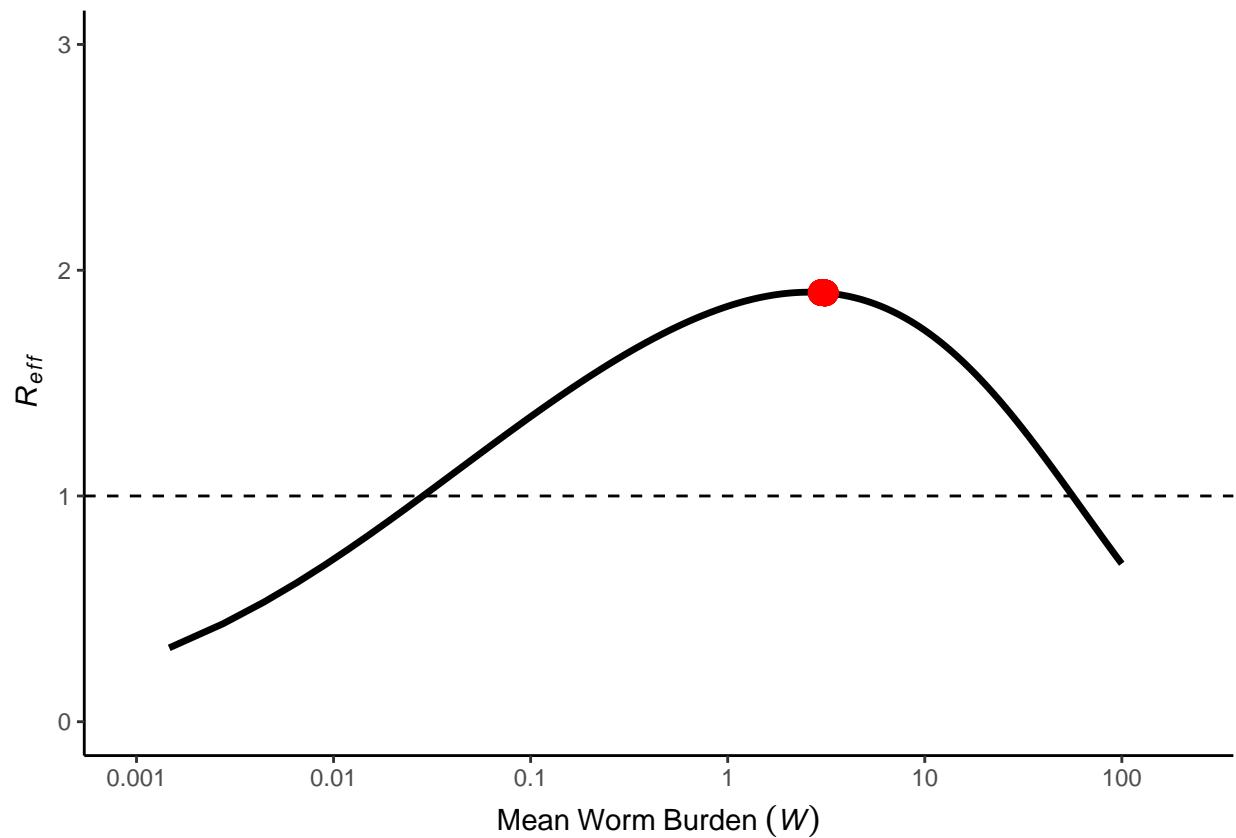
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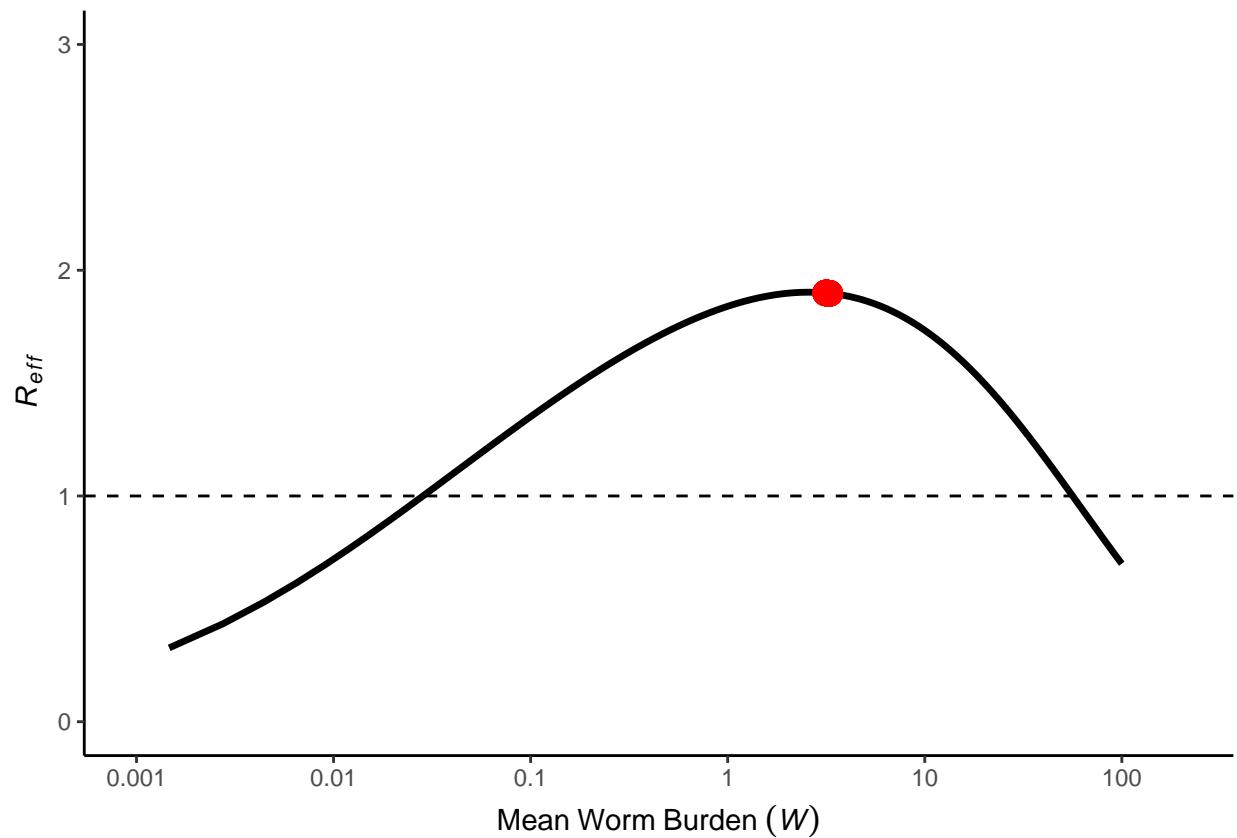
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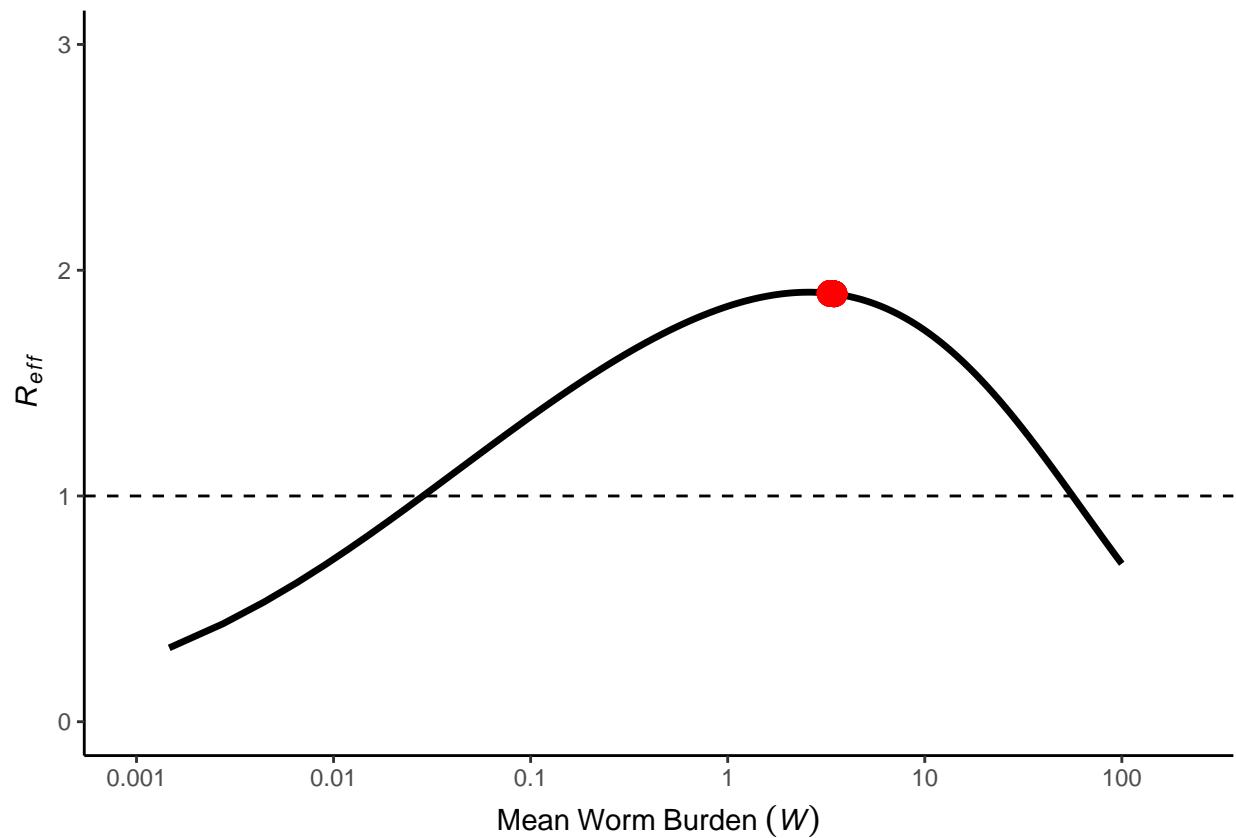
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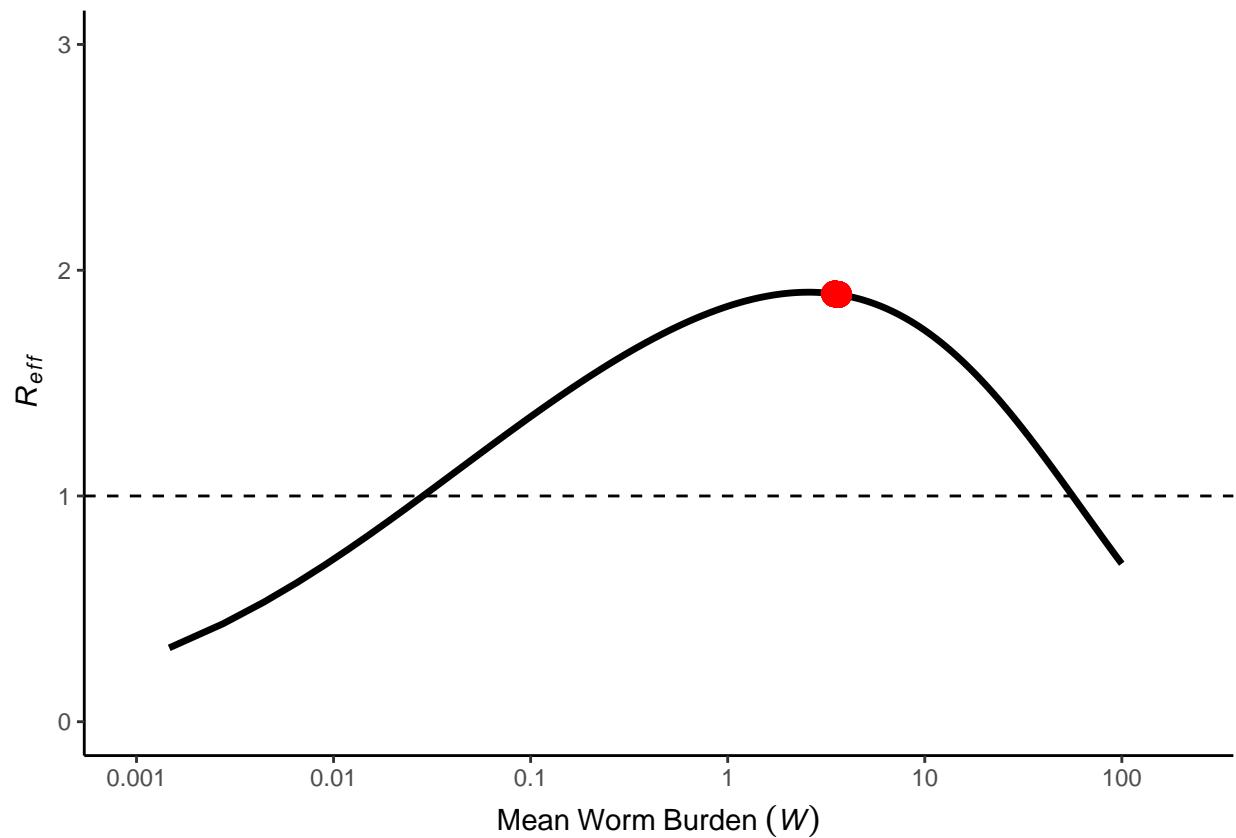
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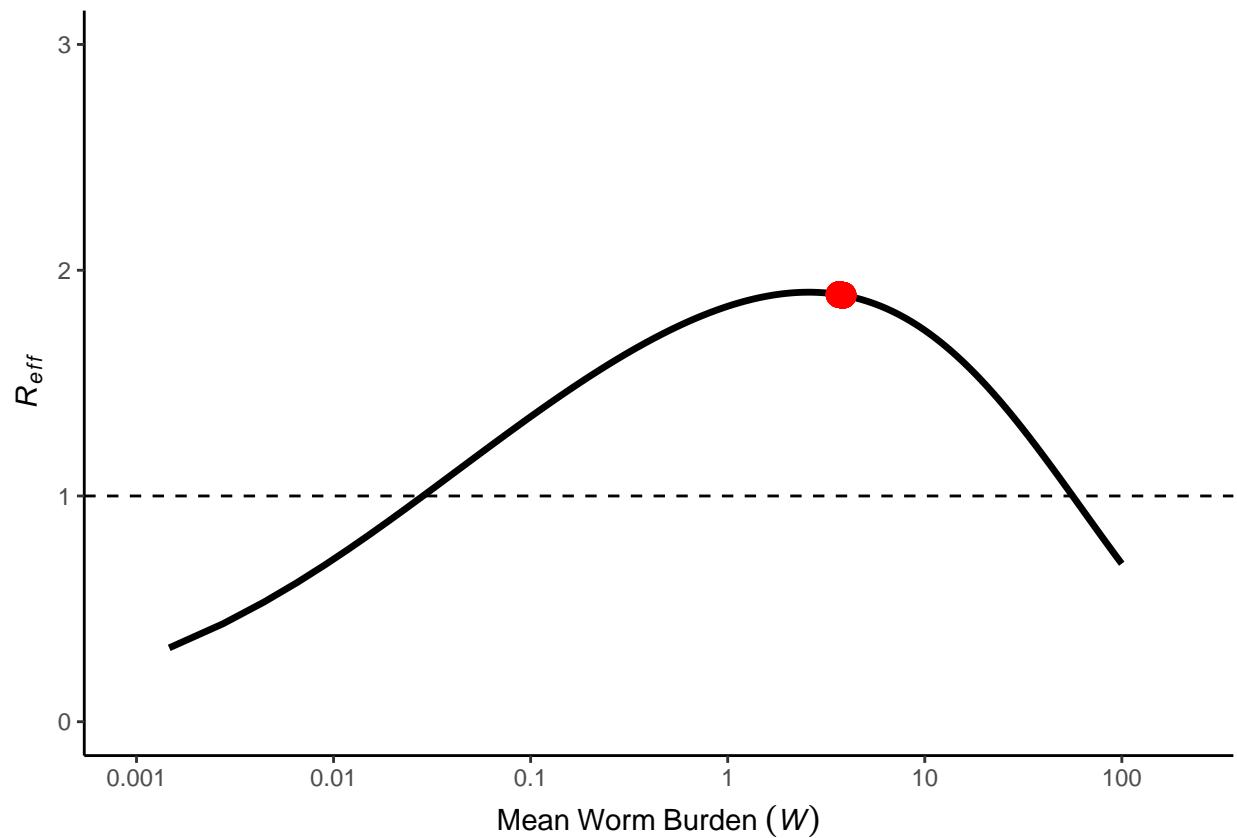
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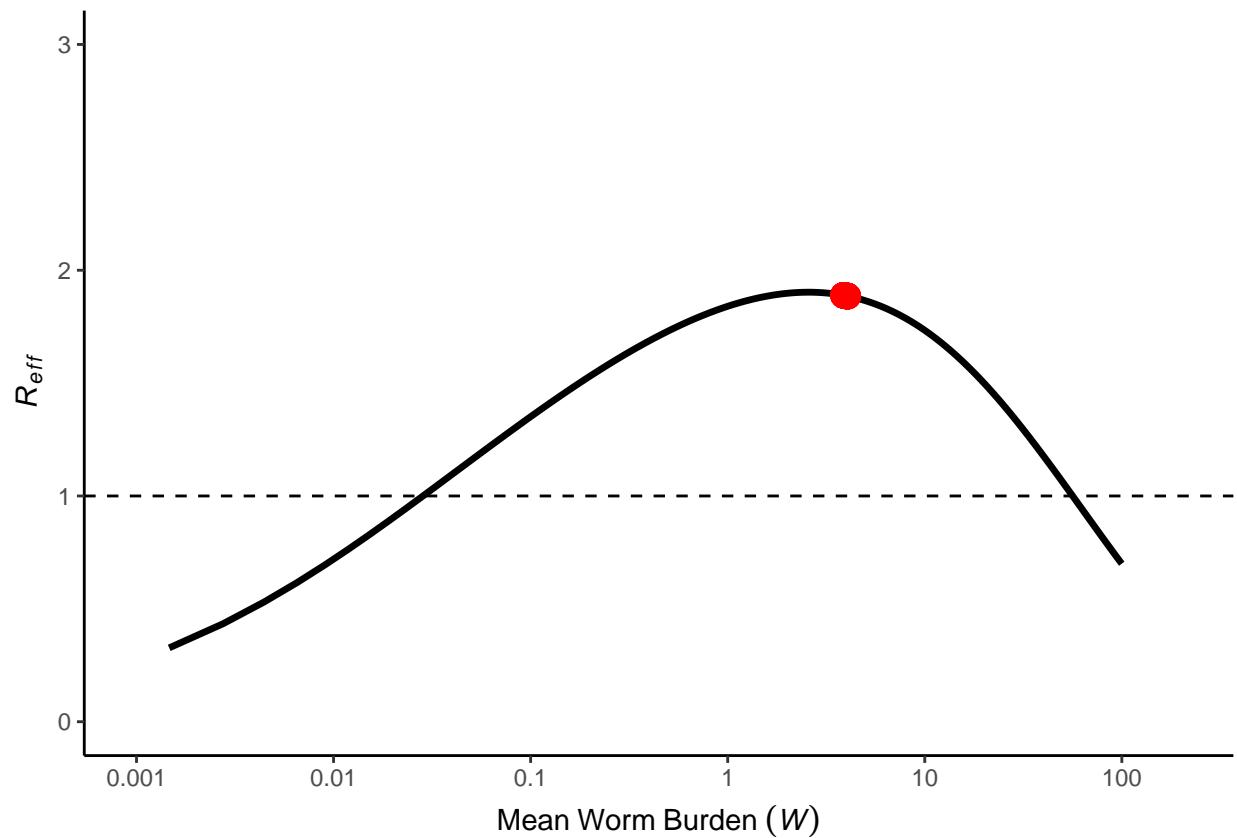
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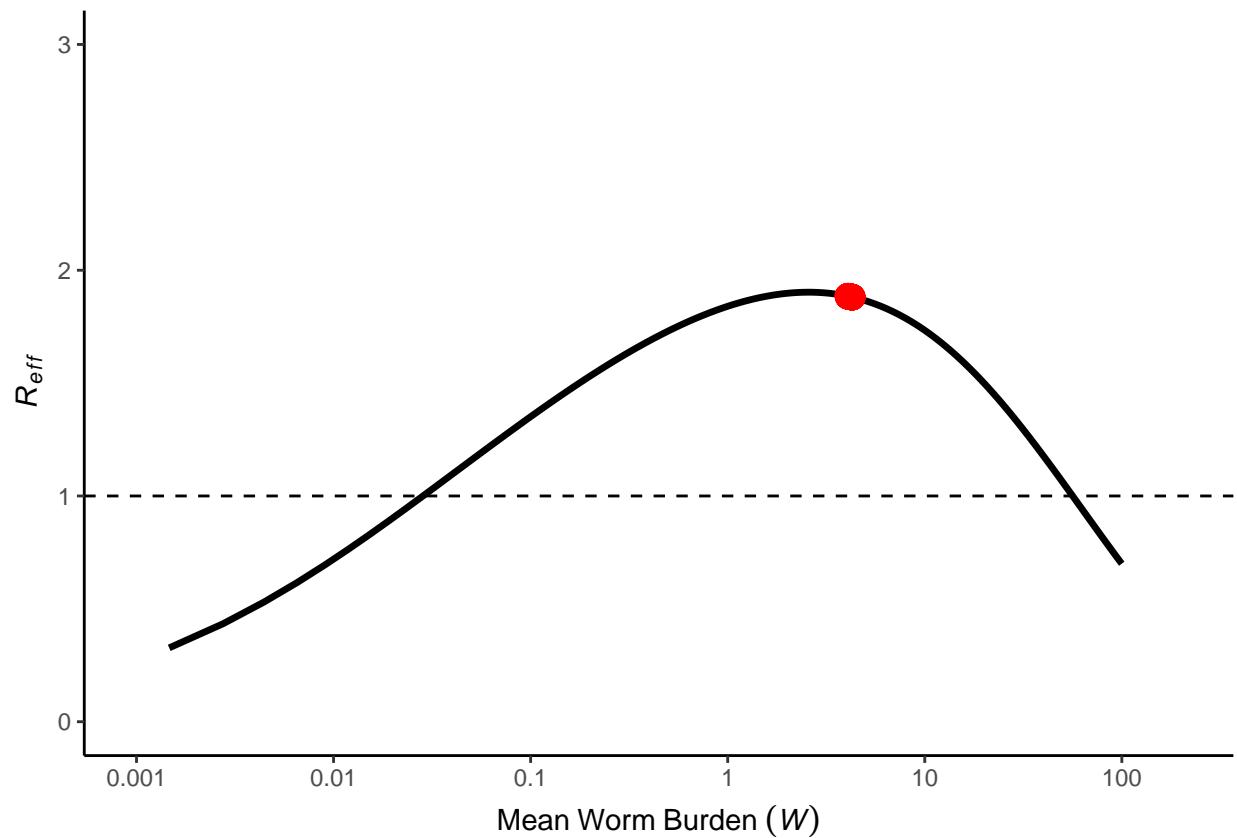
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## Warning: Removed 2 rows containing missing values (geom_path).
```



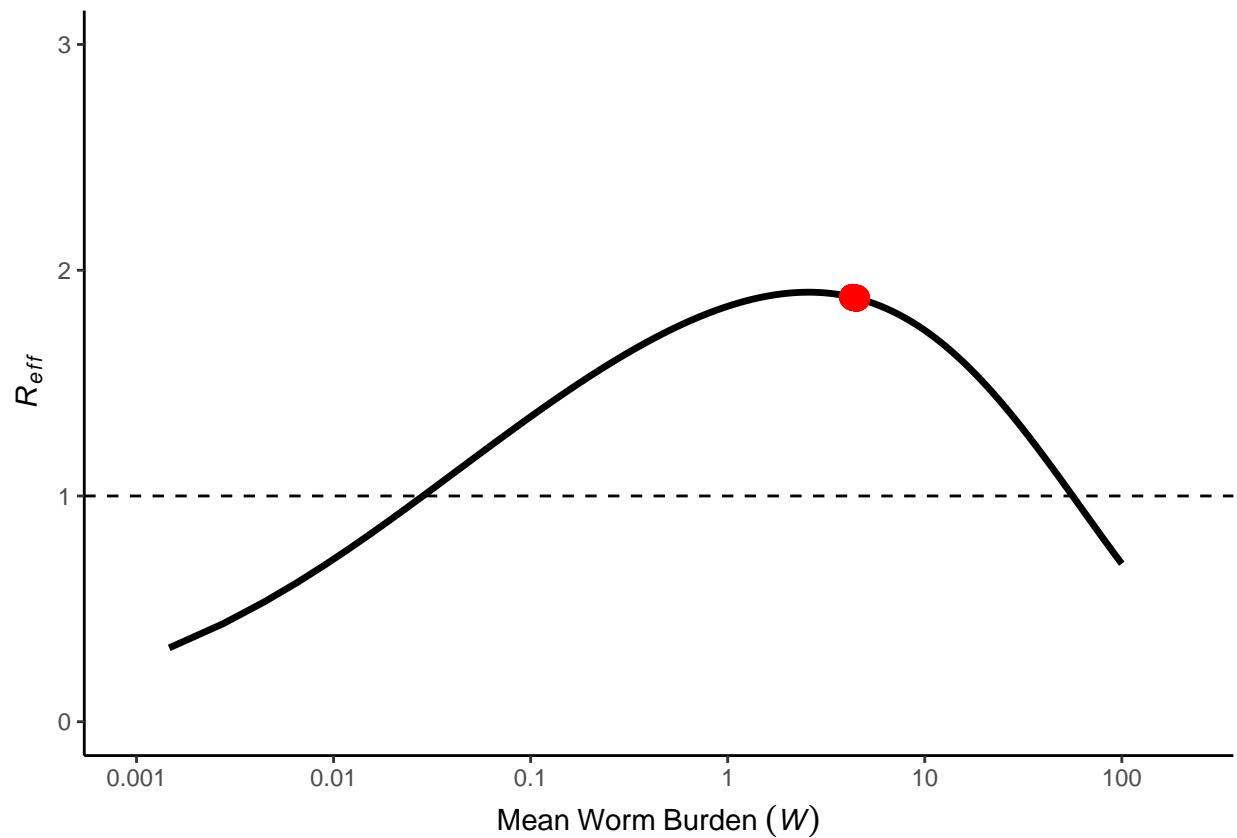
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



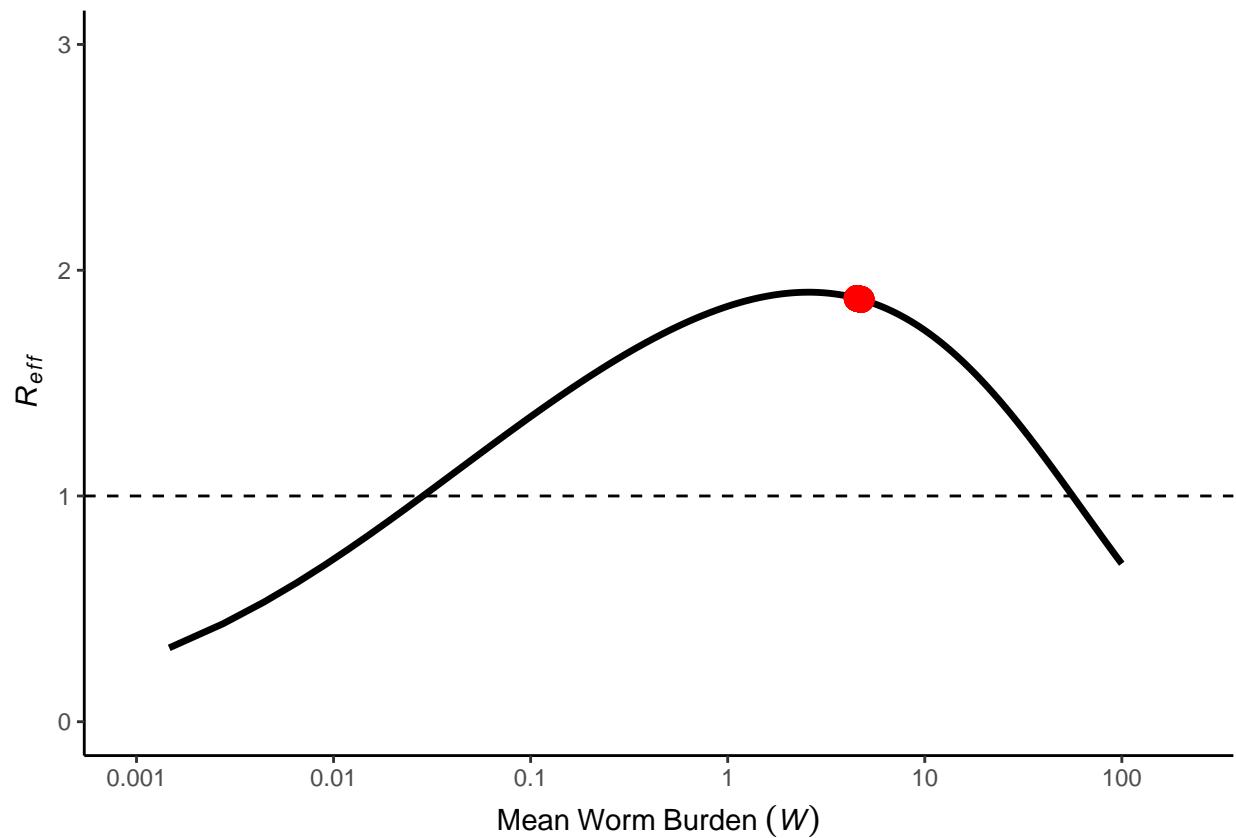
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



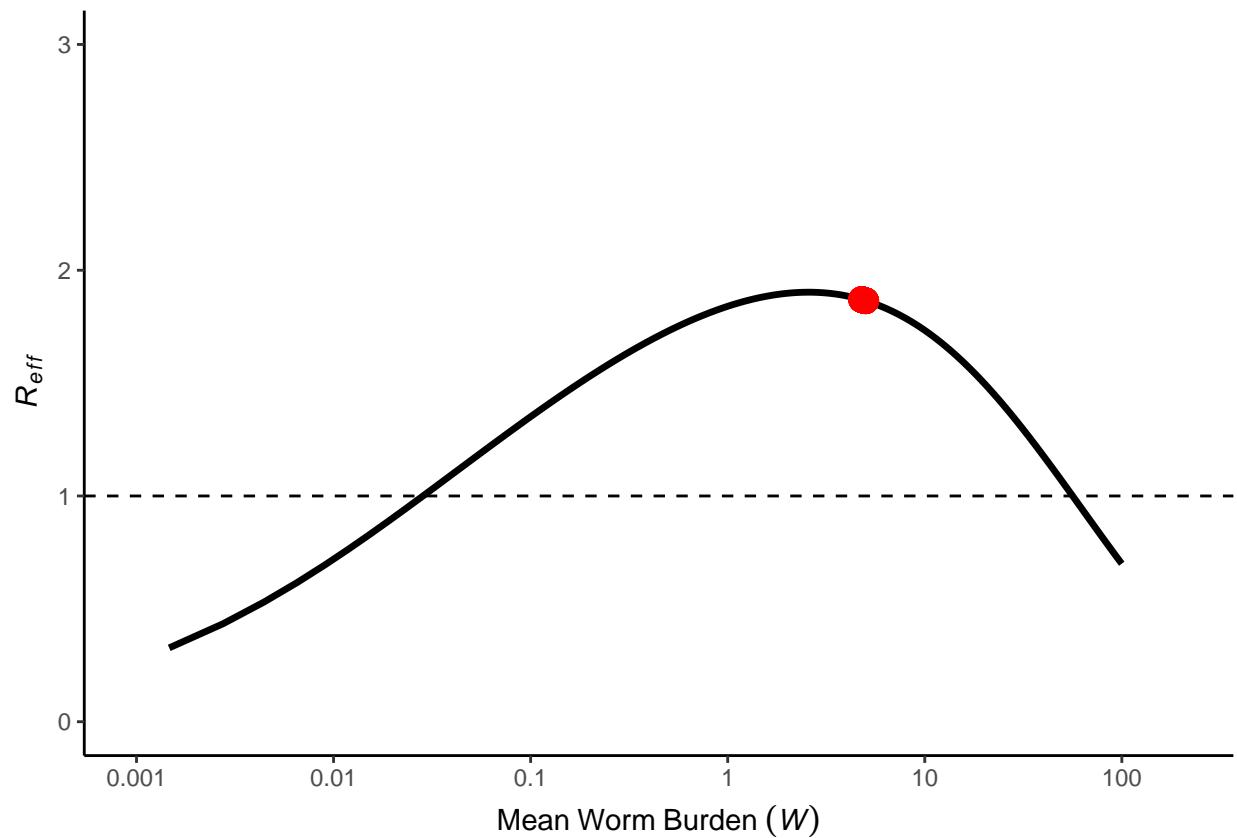
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



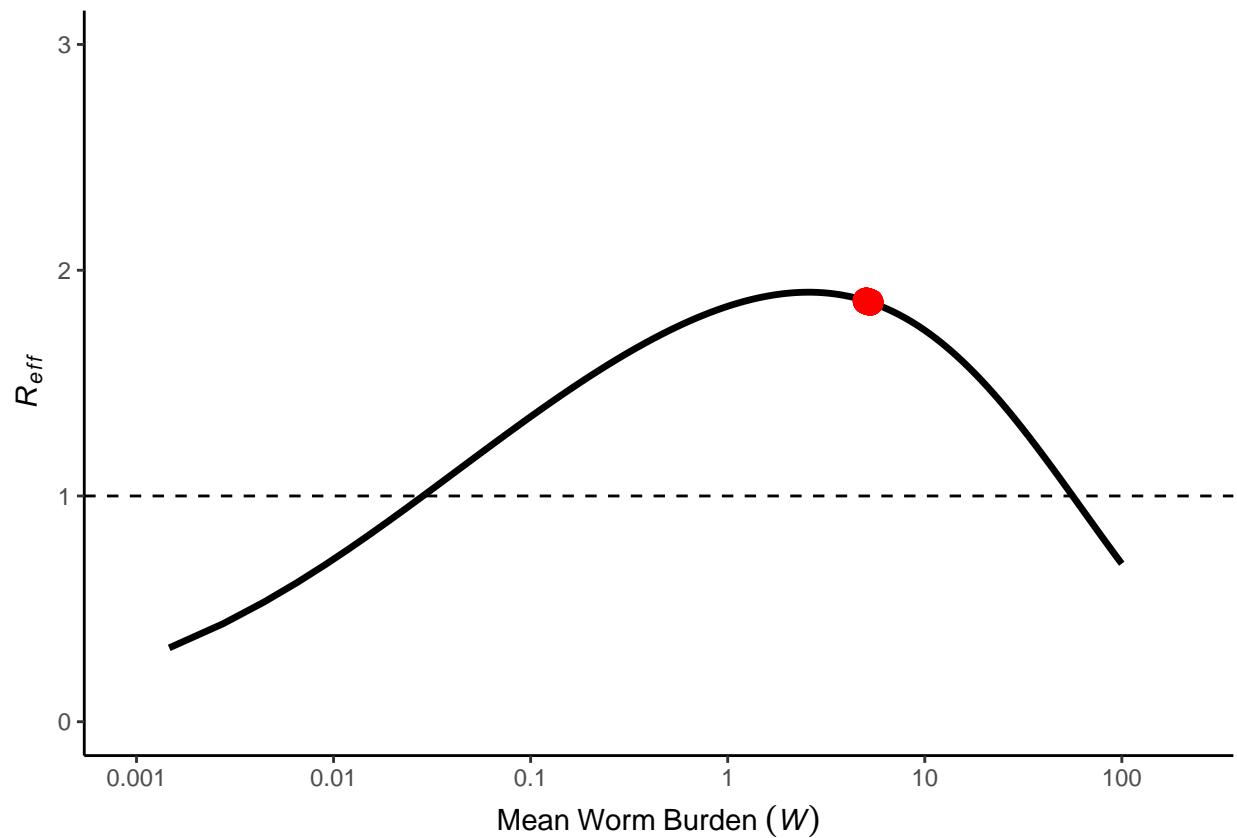
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



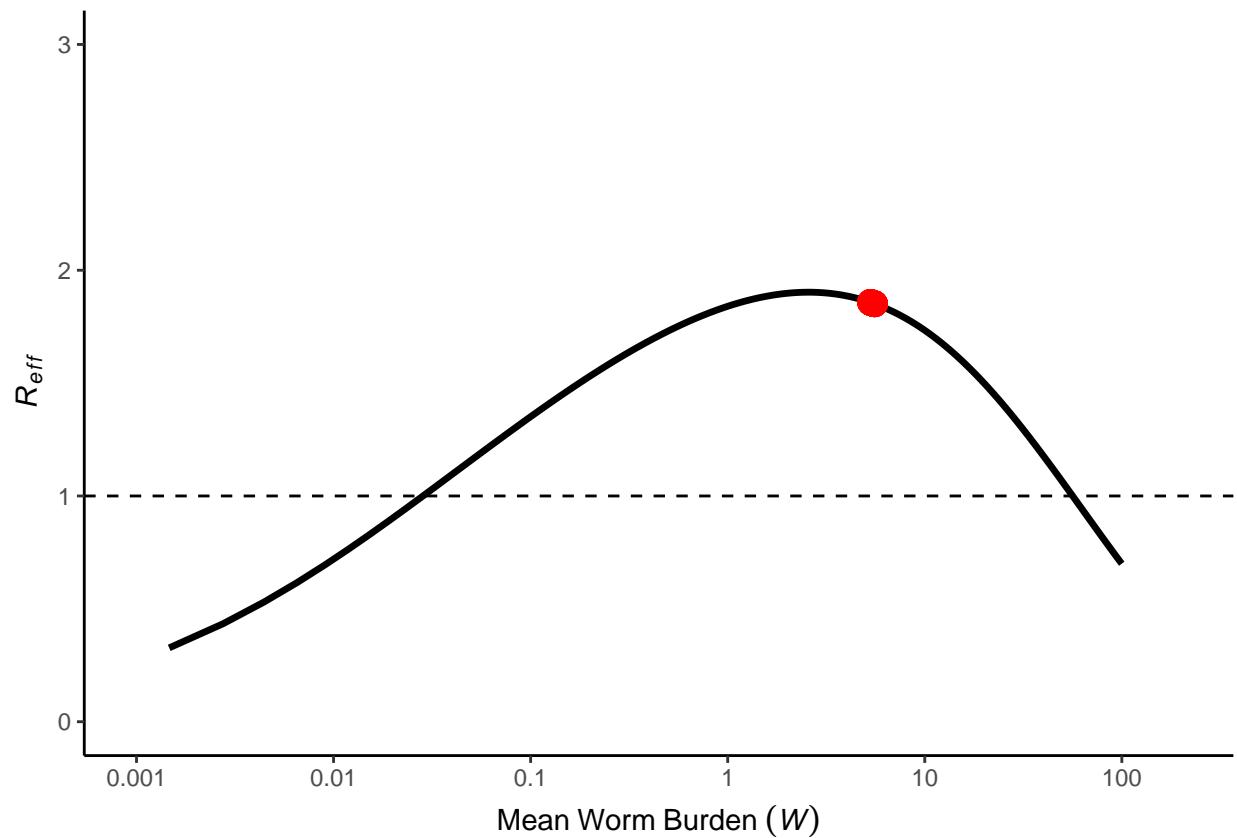
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



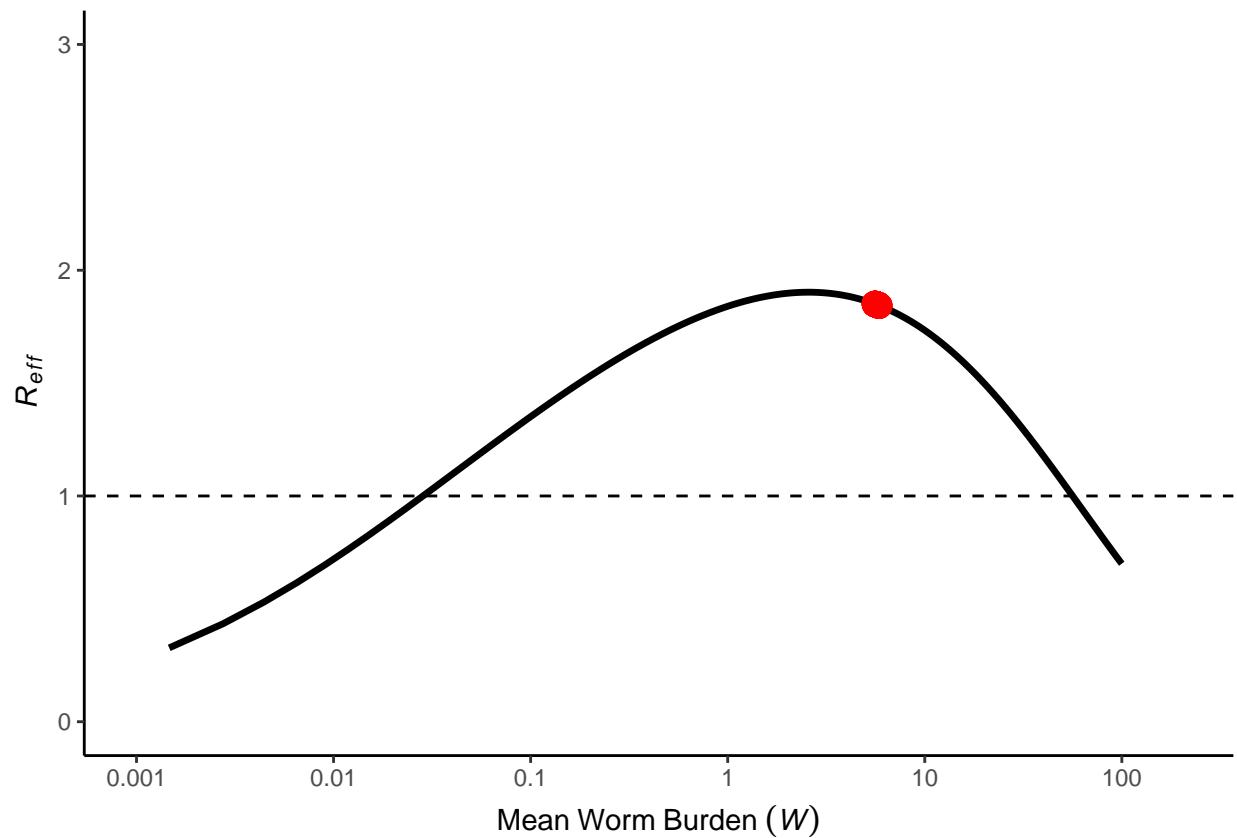
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



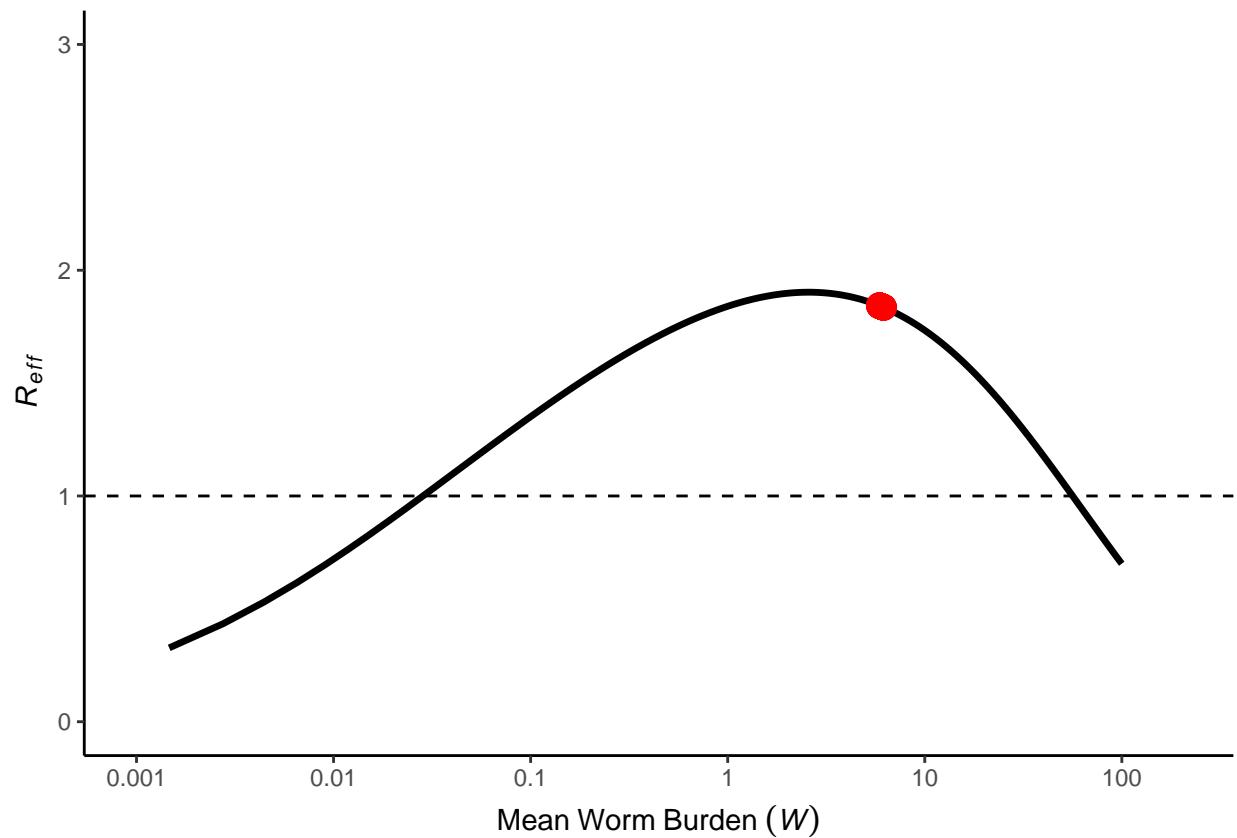
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



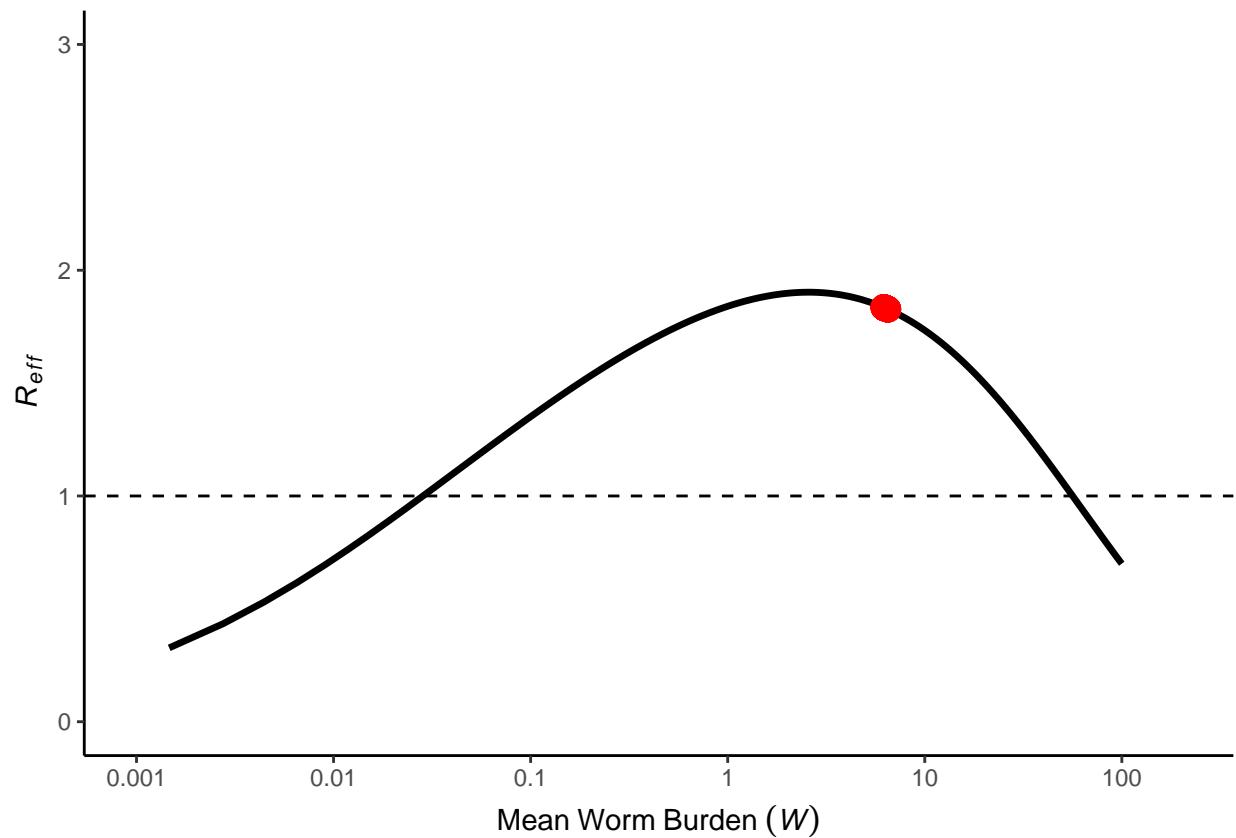
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



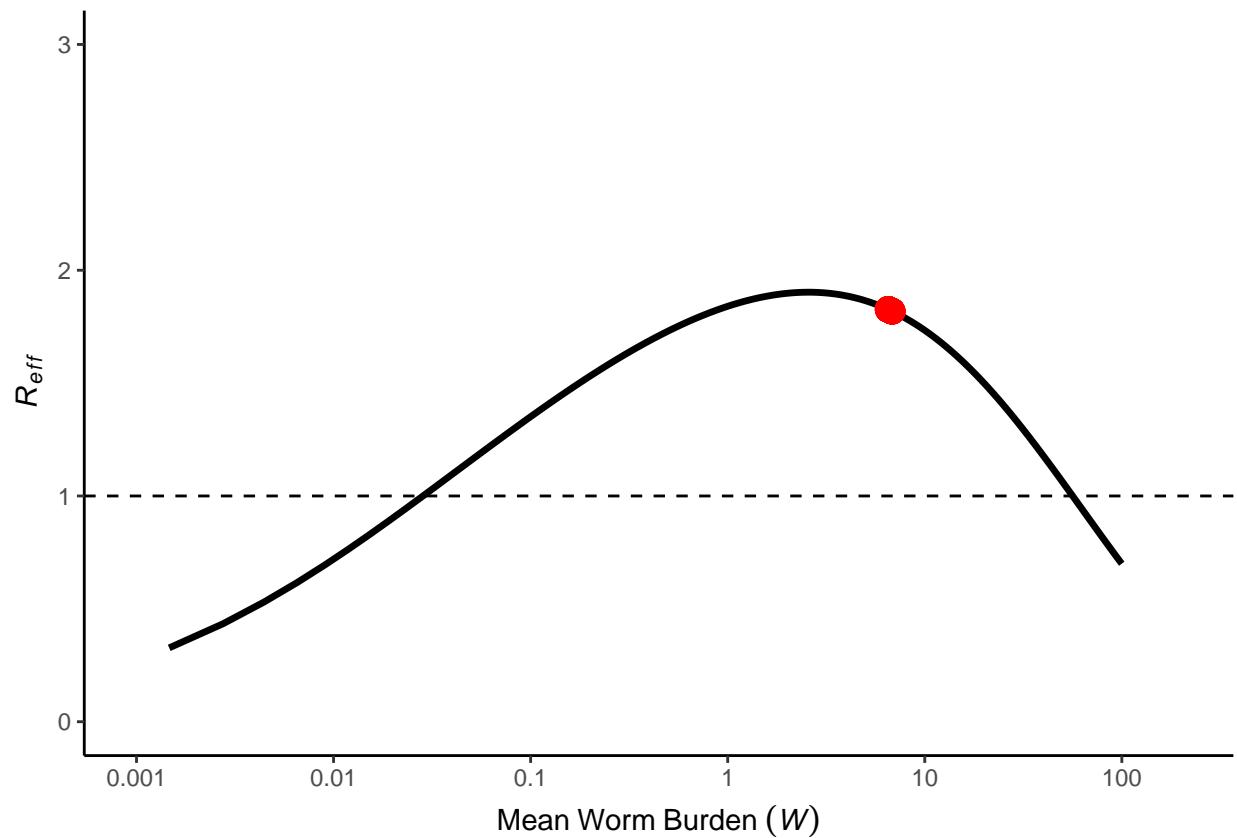
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



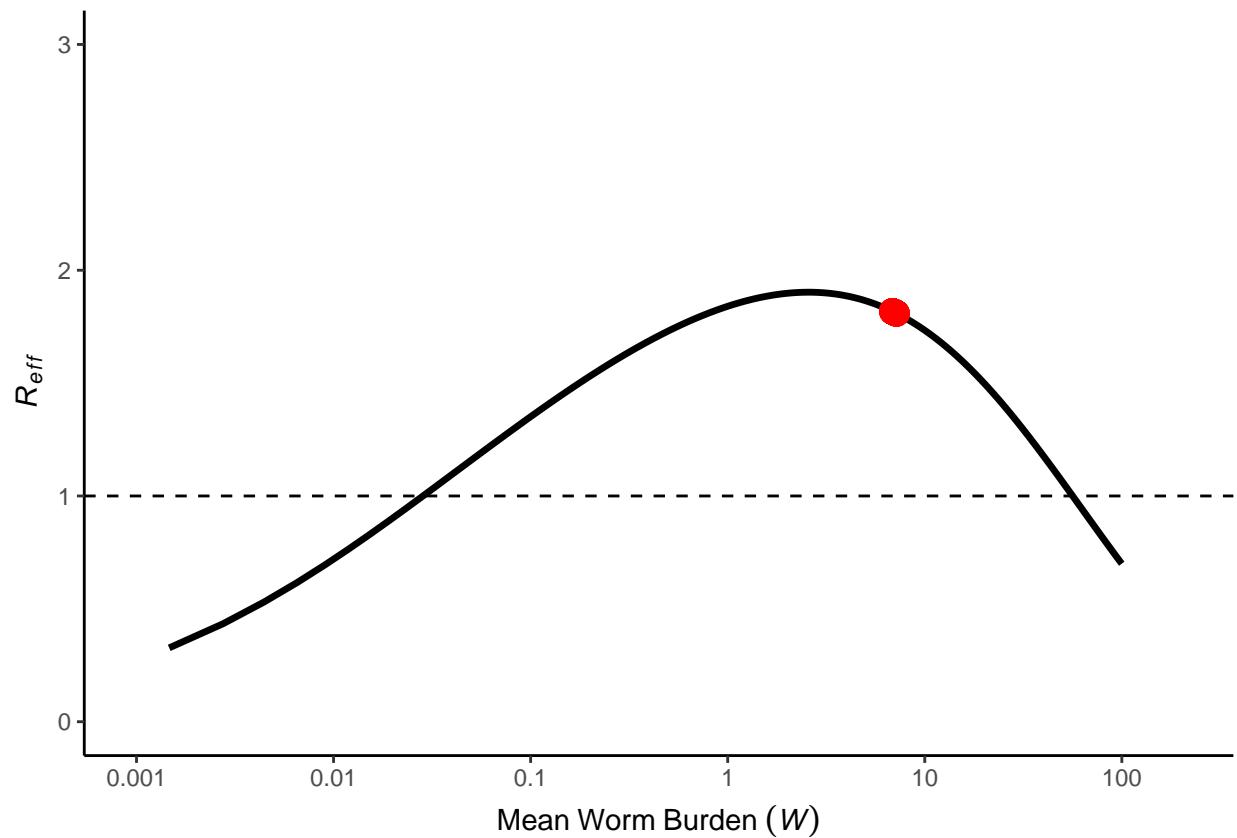
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



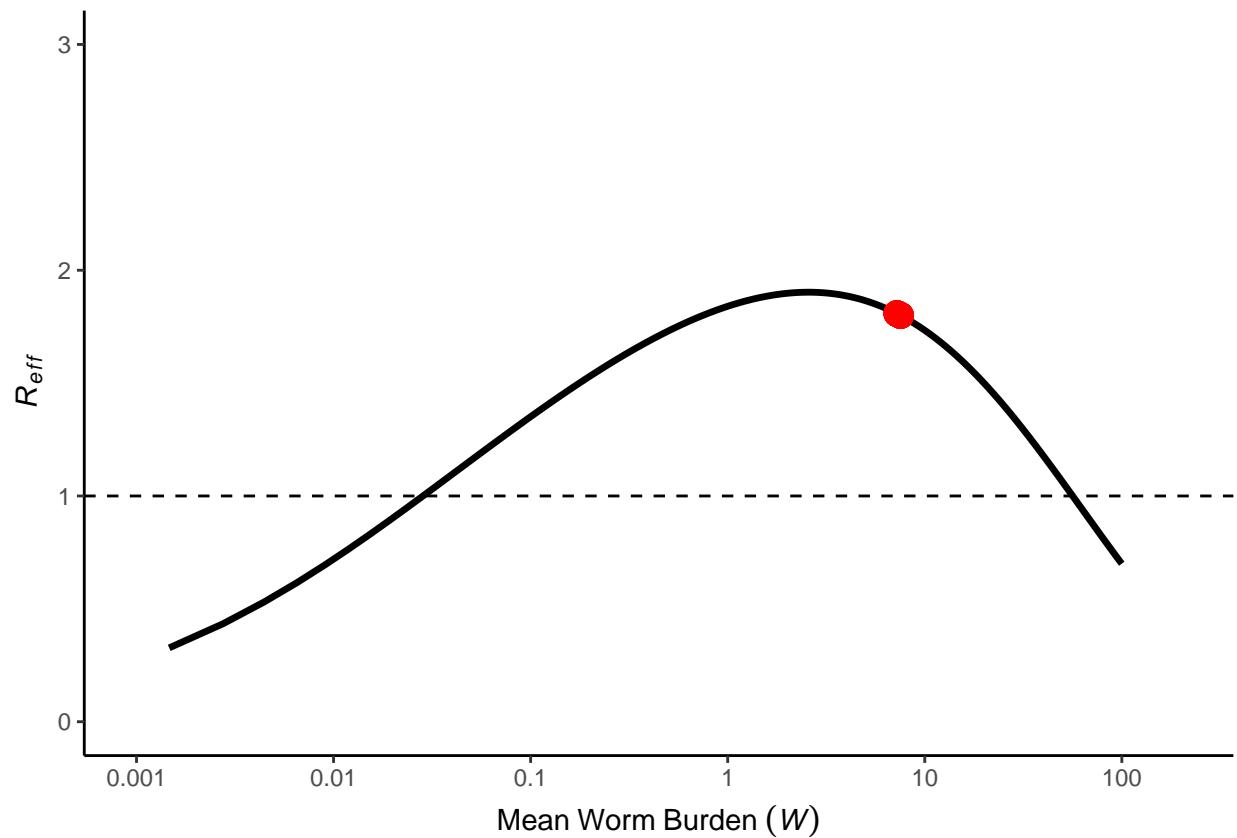
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



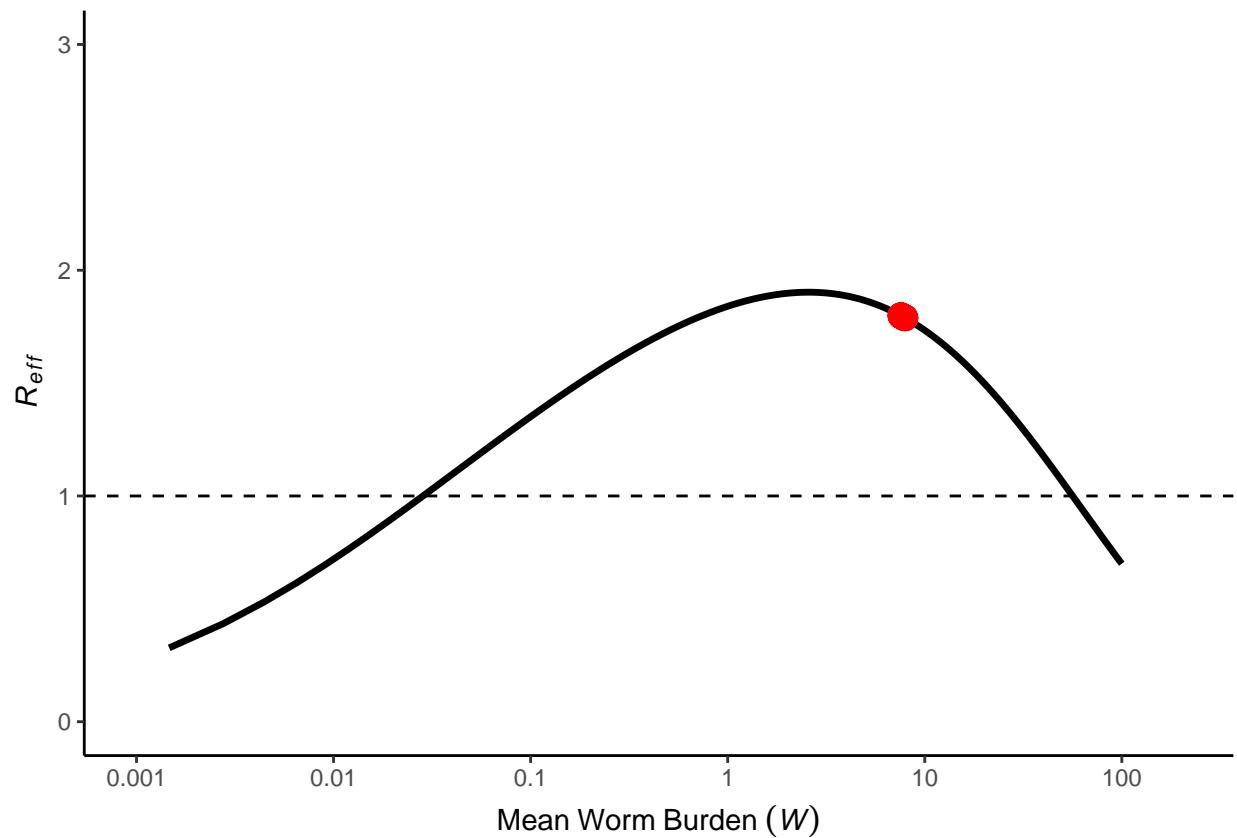
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



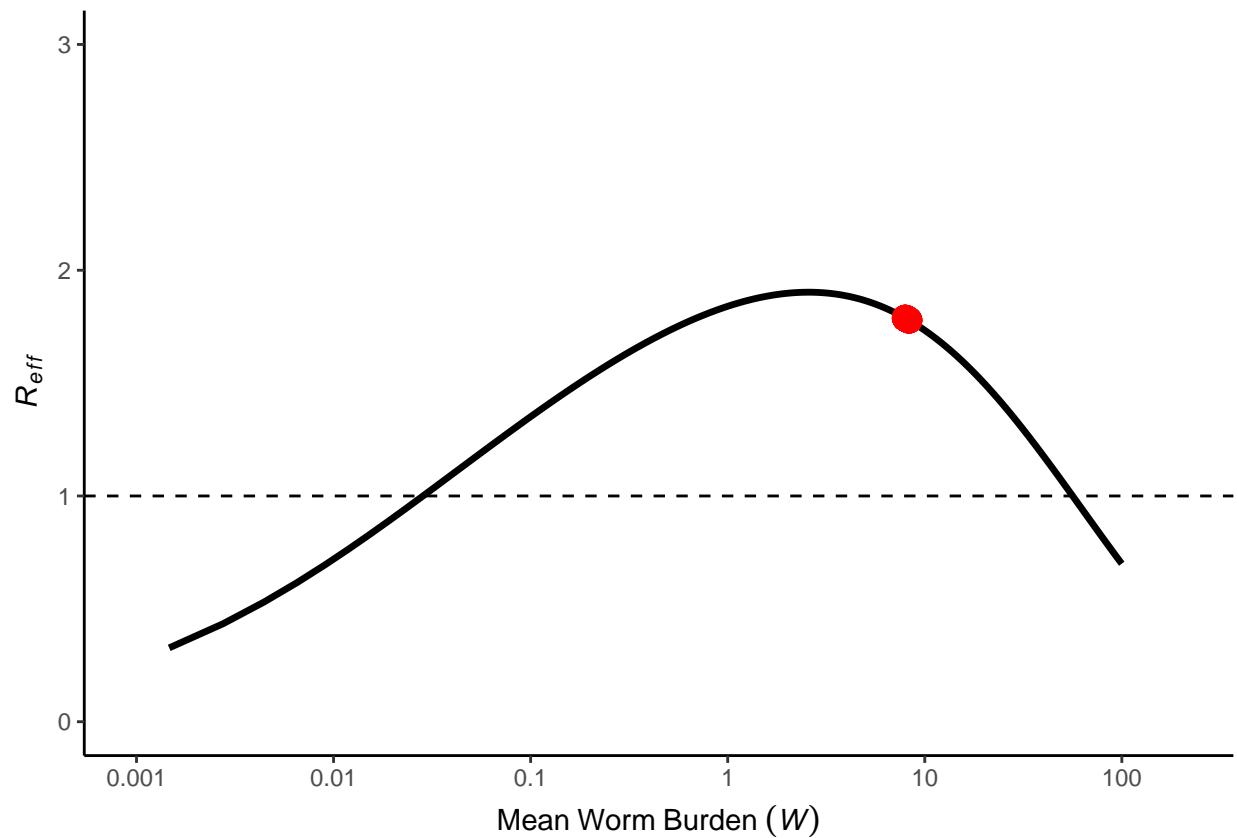
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



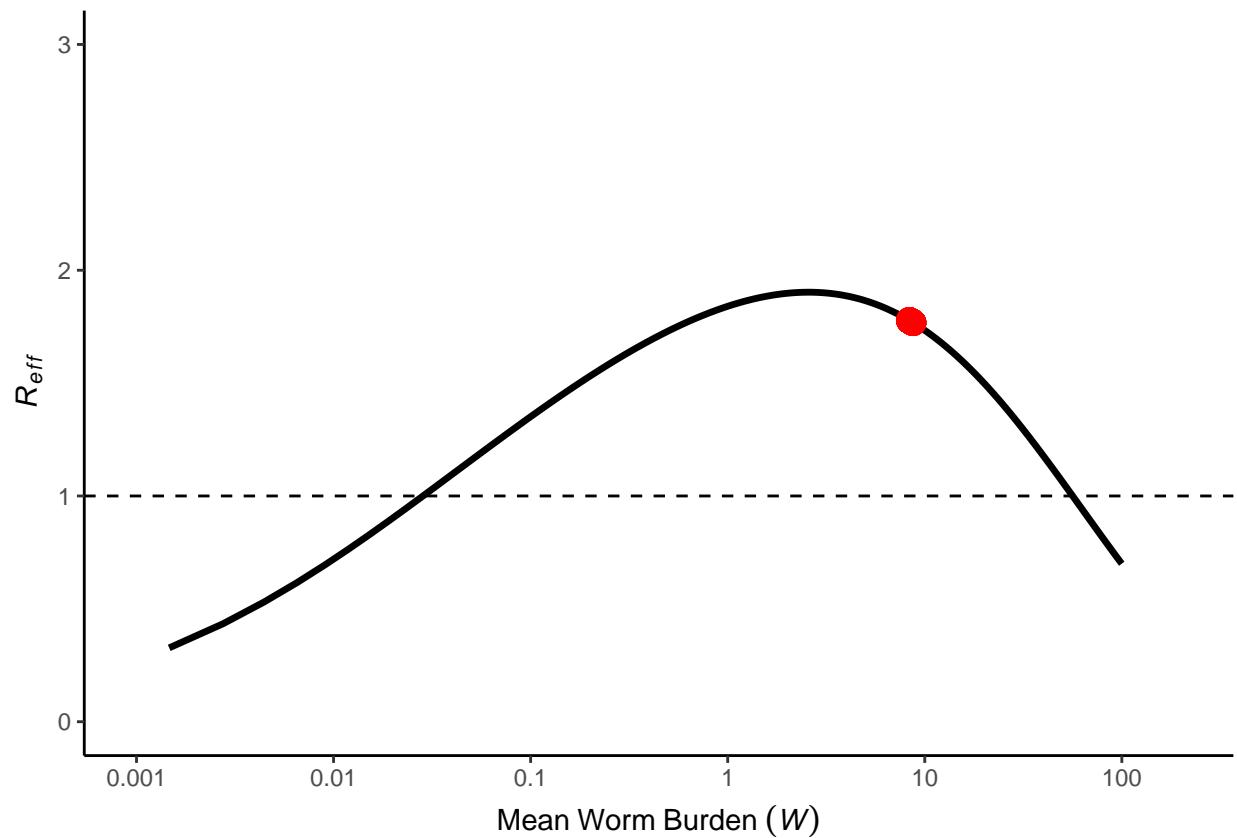
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



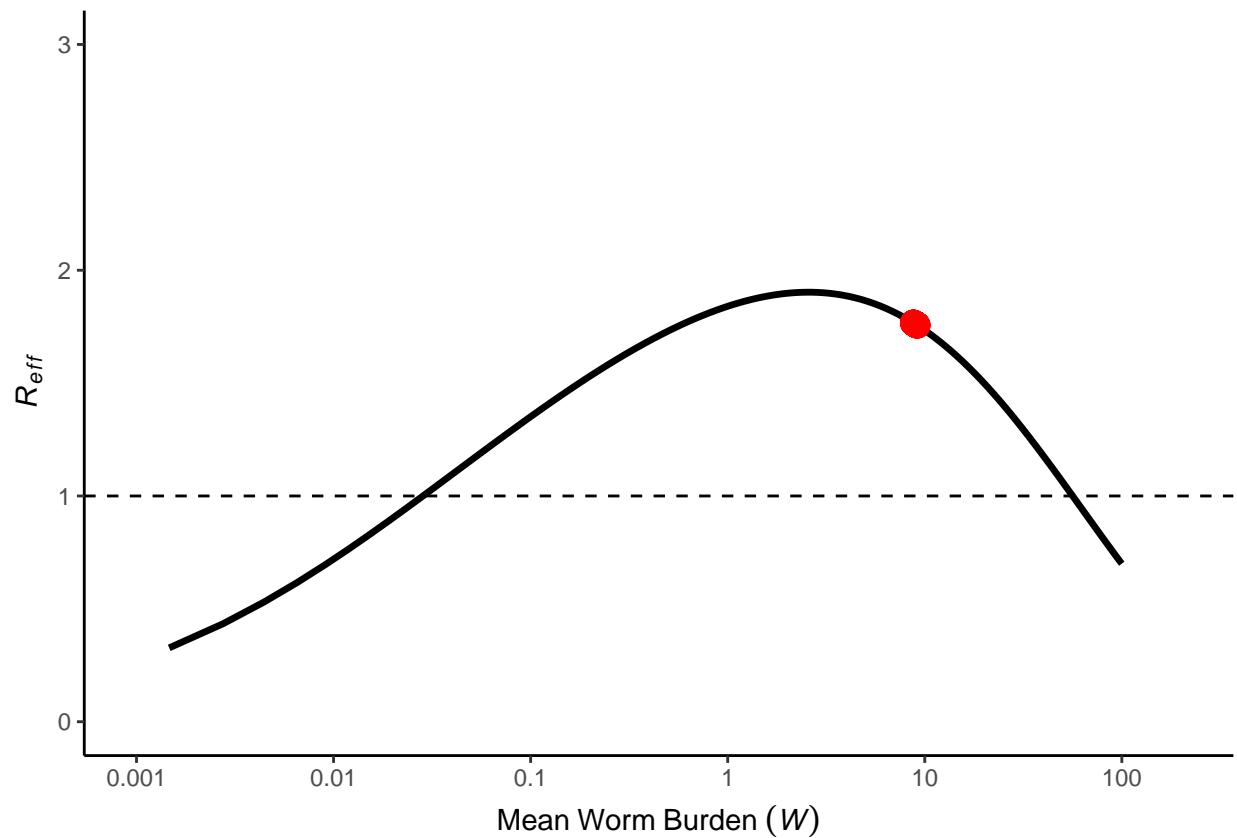
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



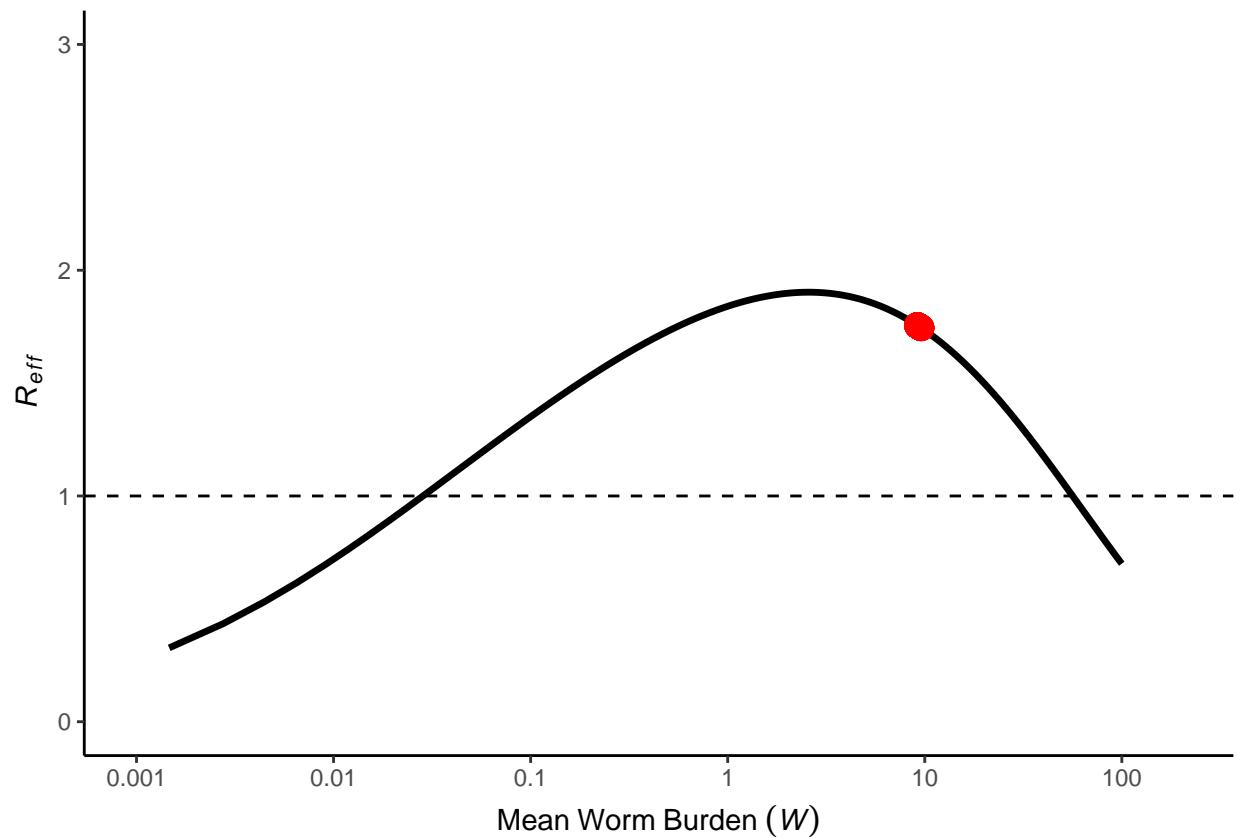
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



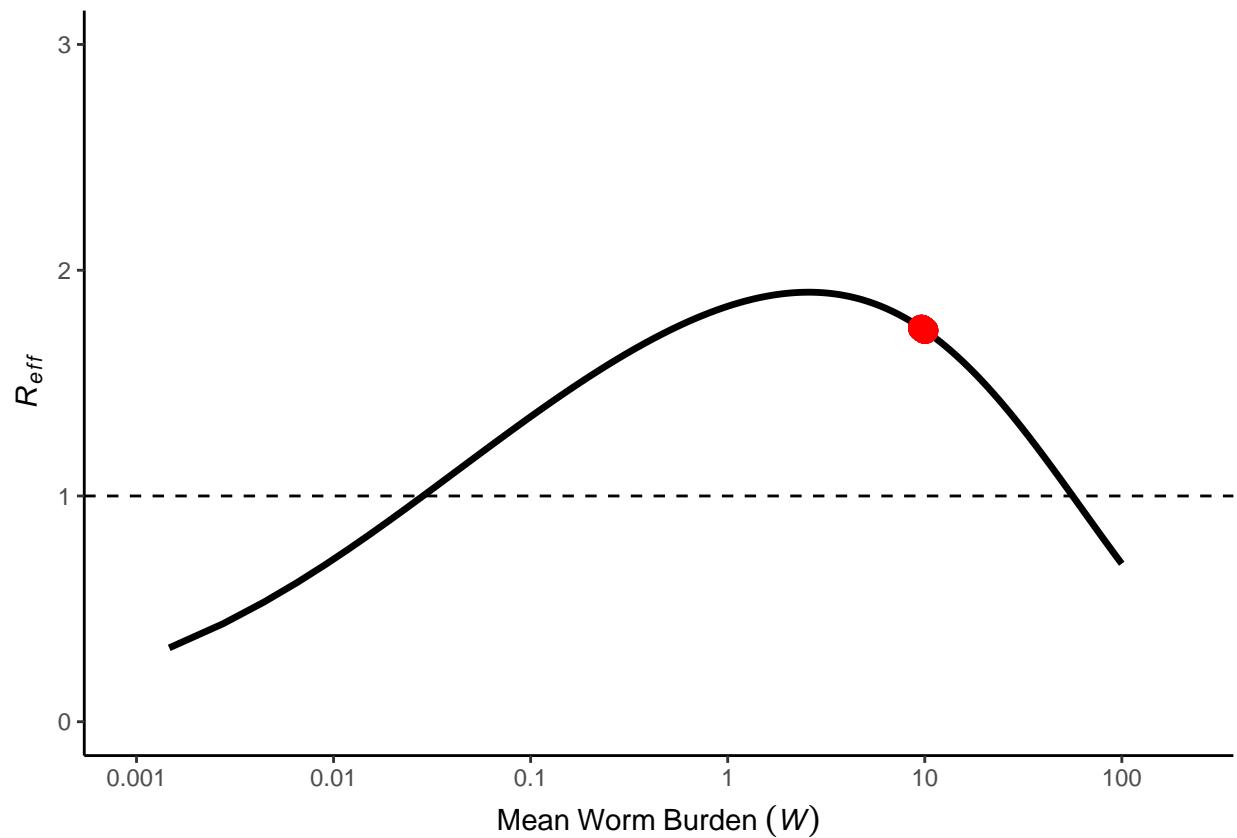
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



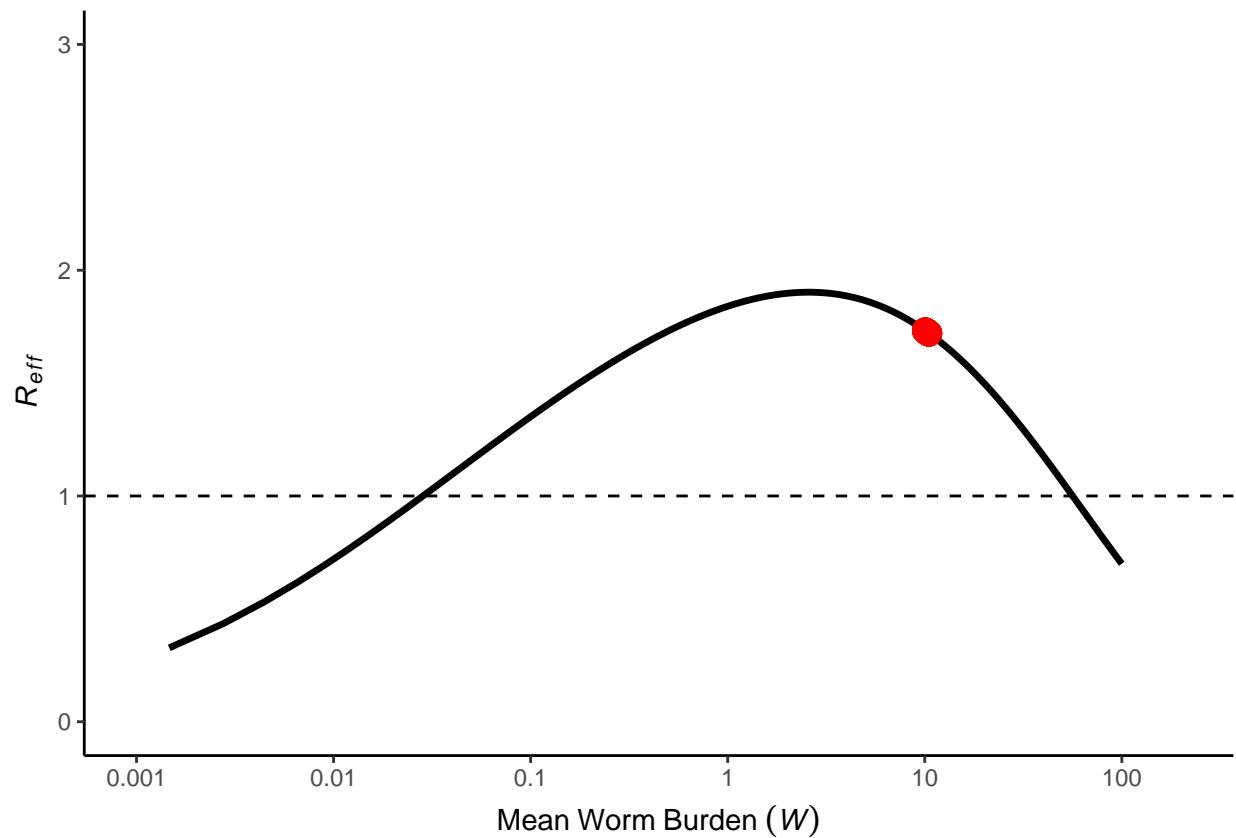
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



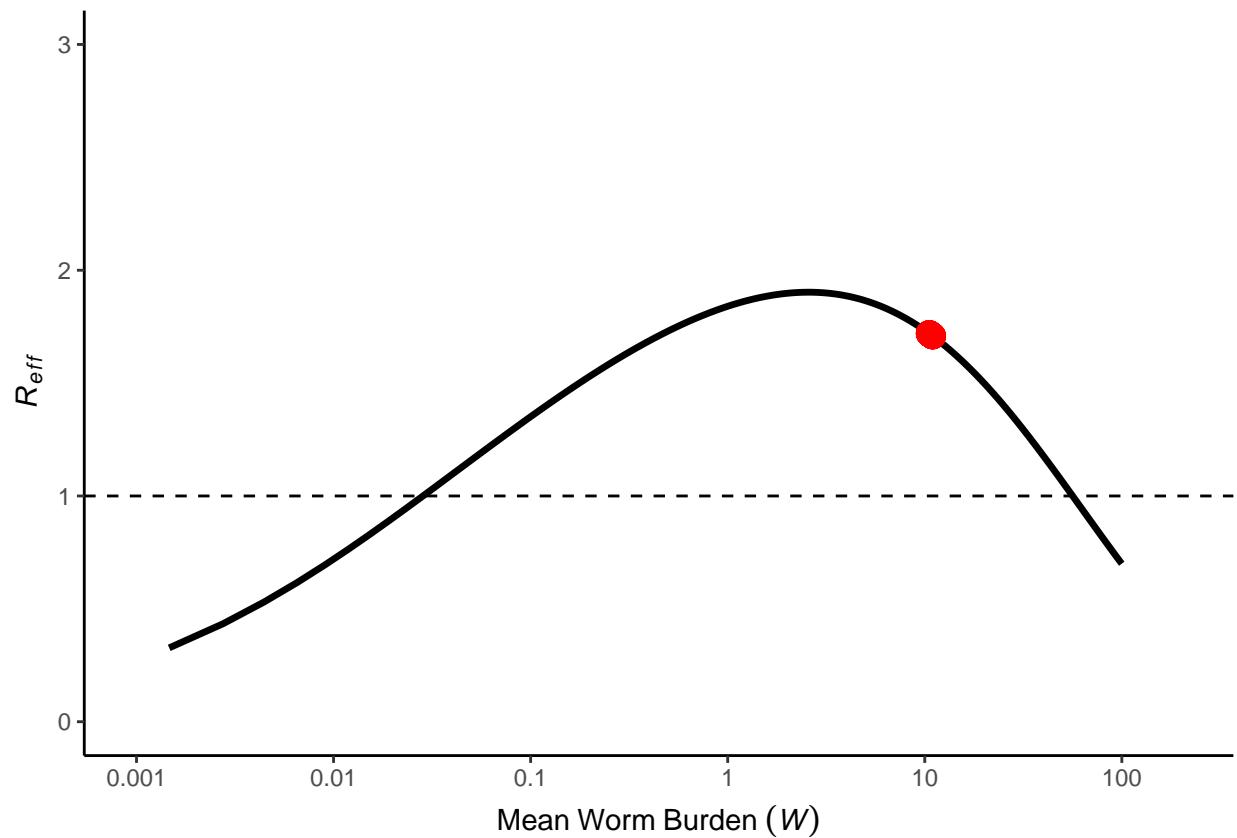
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



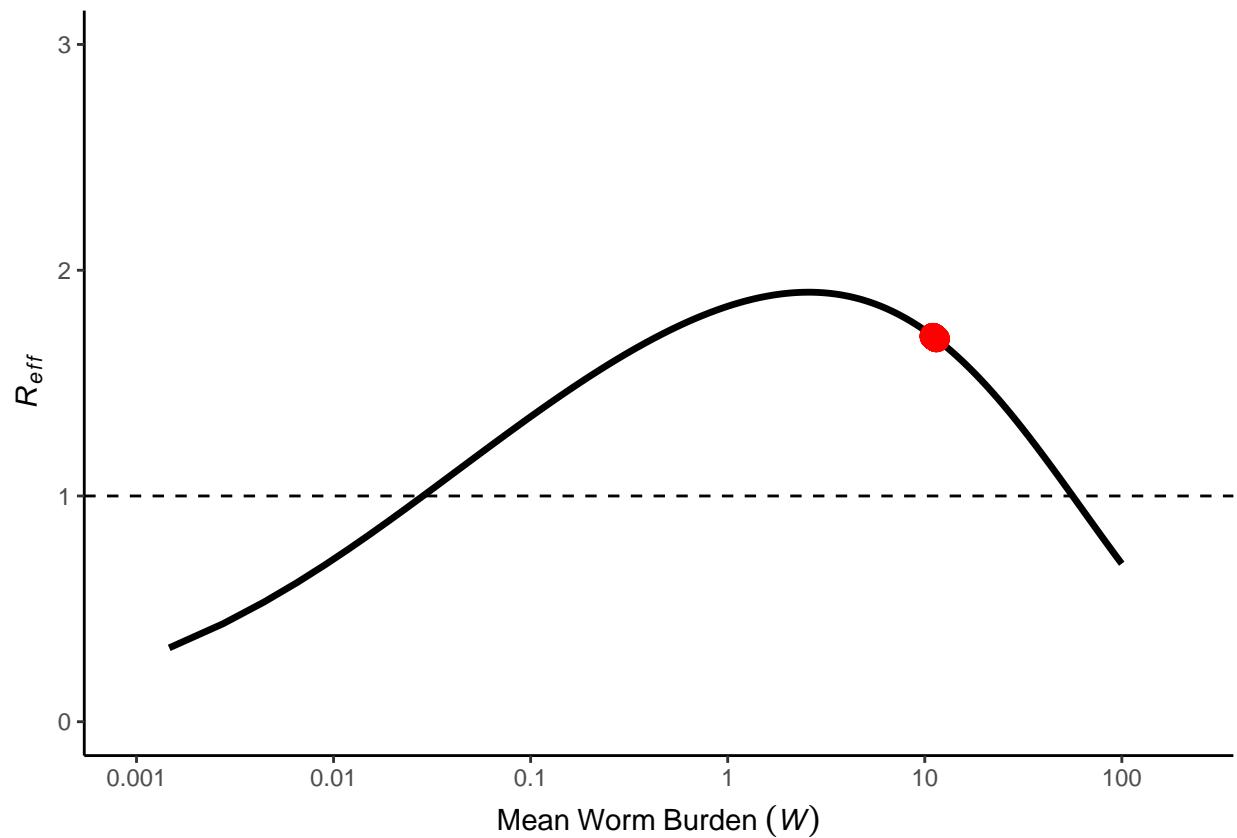
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



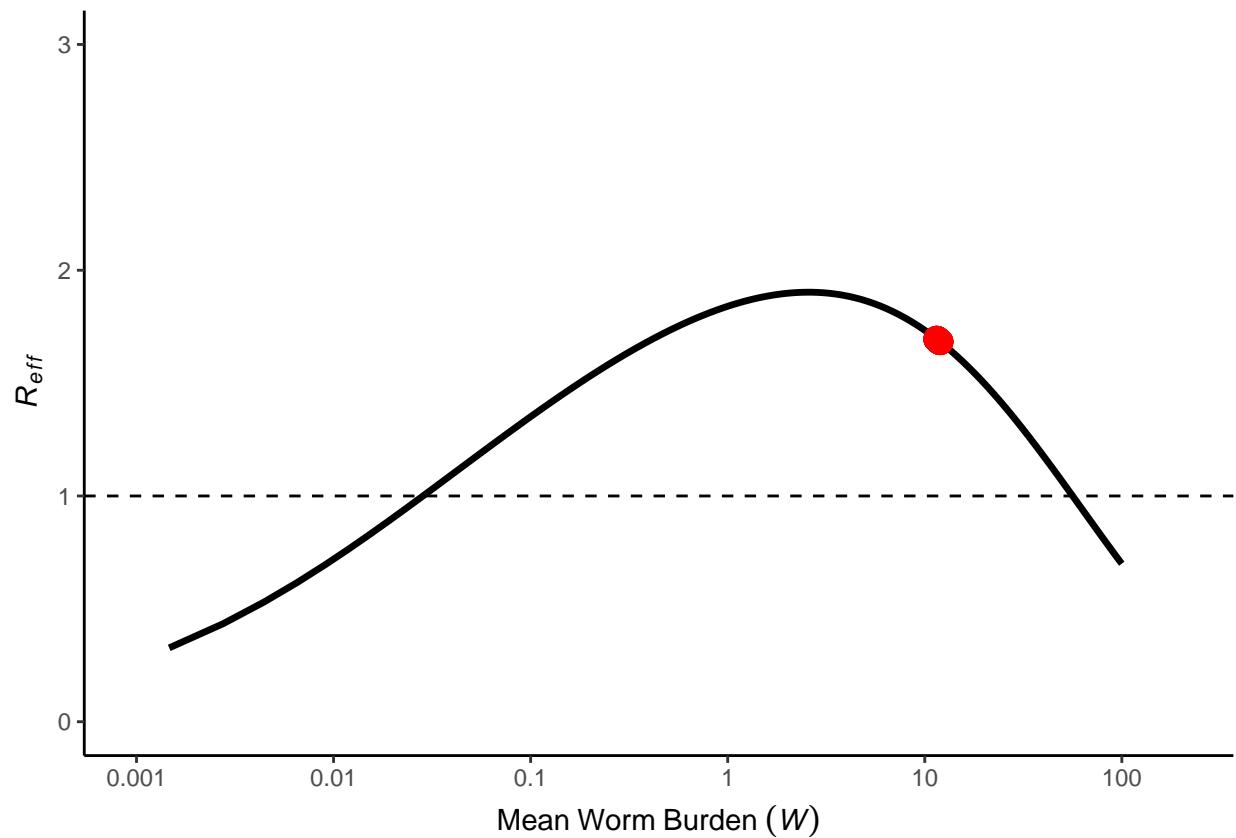
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



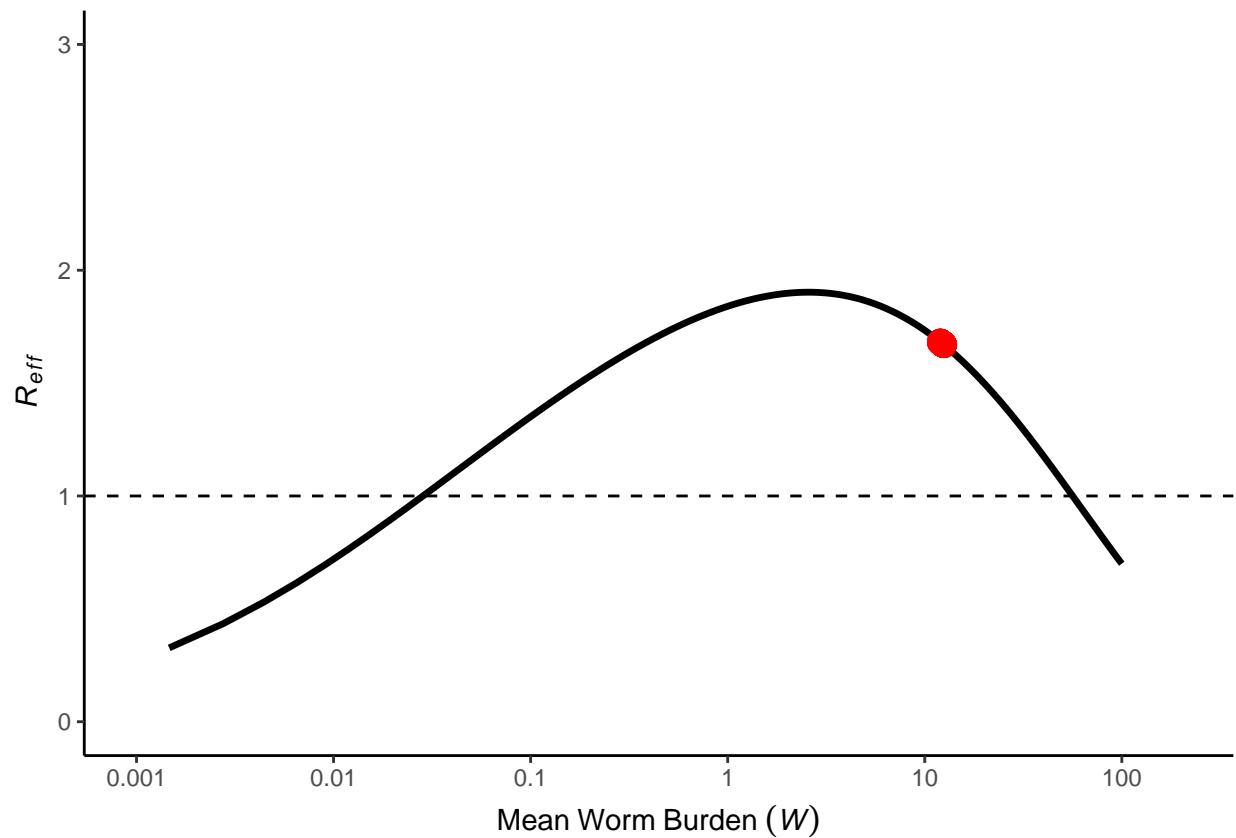
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



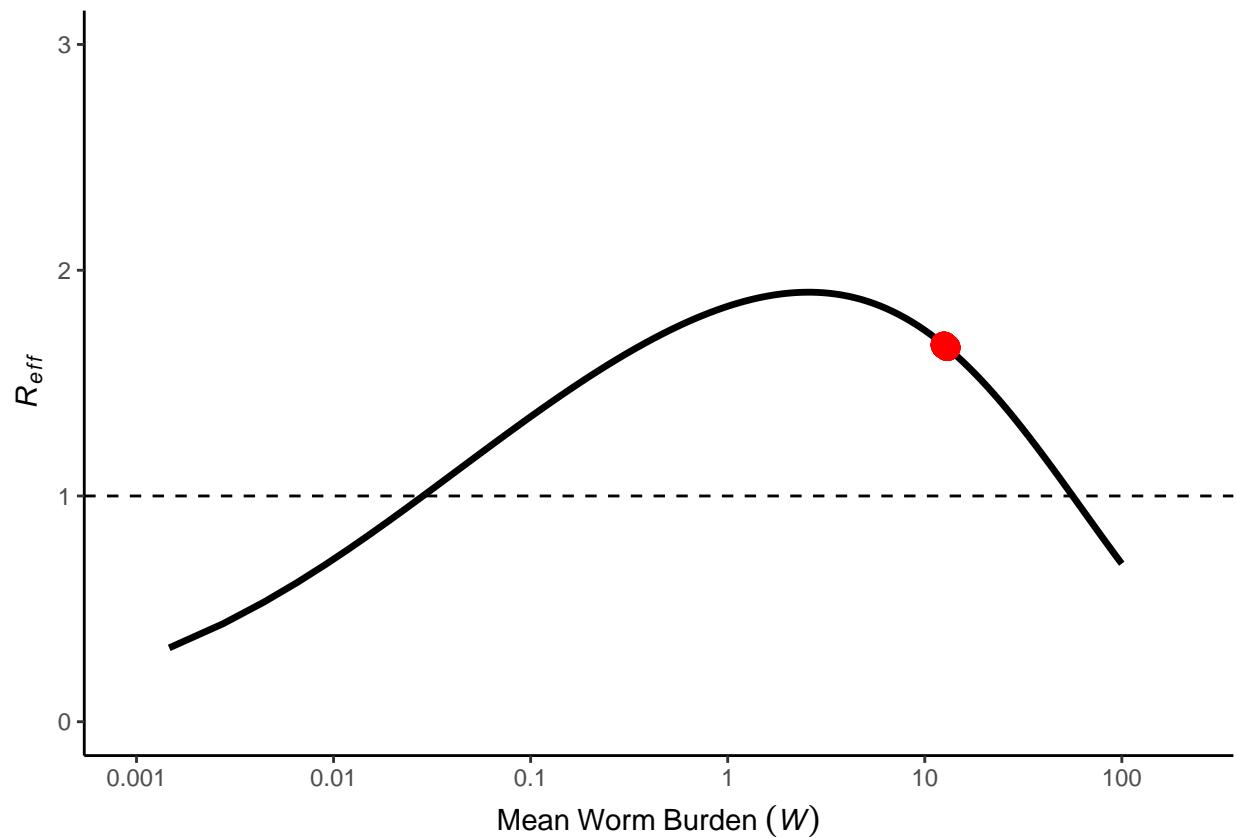
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



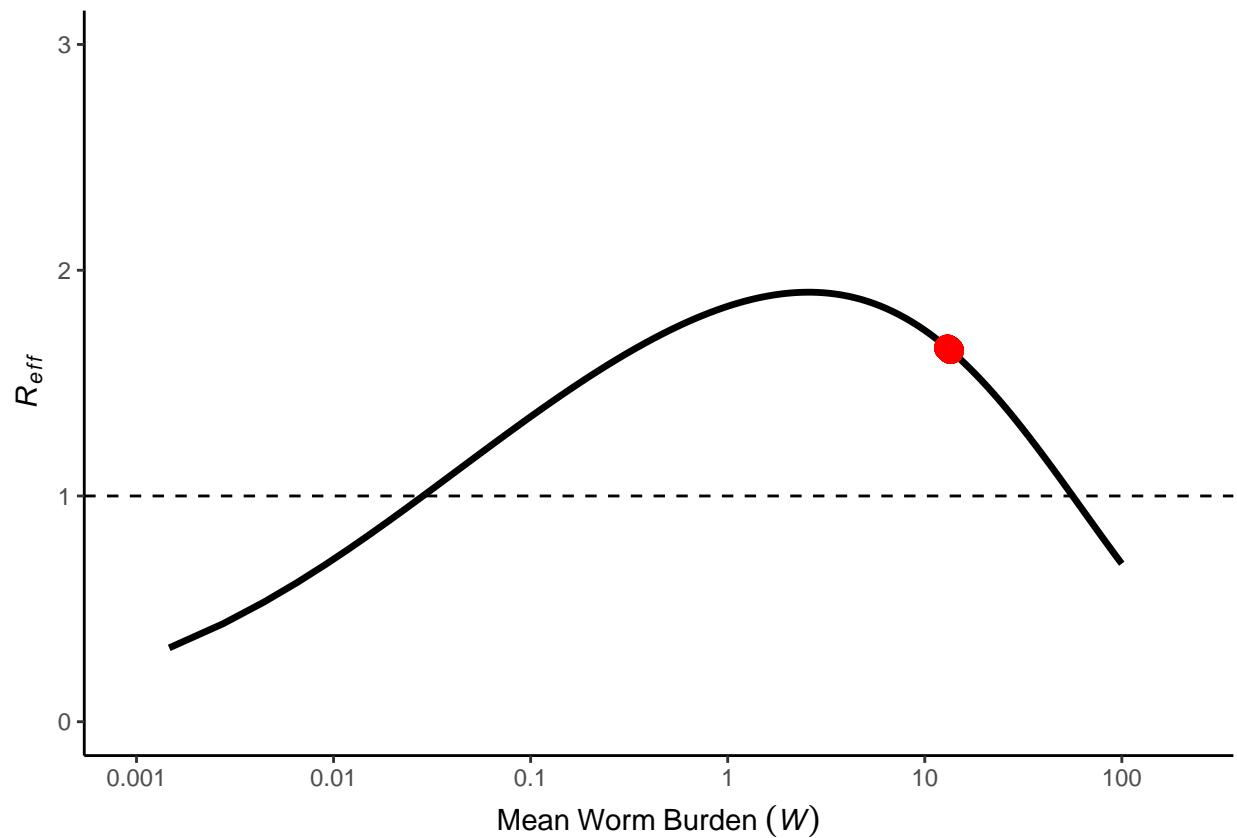
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



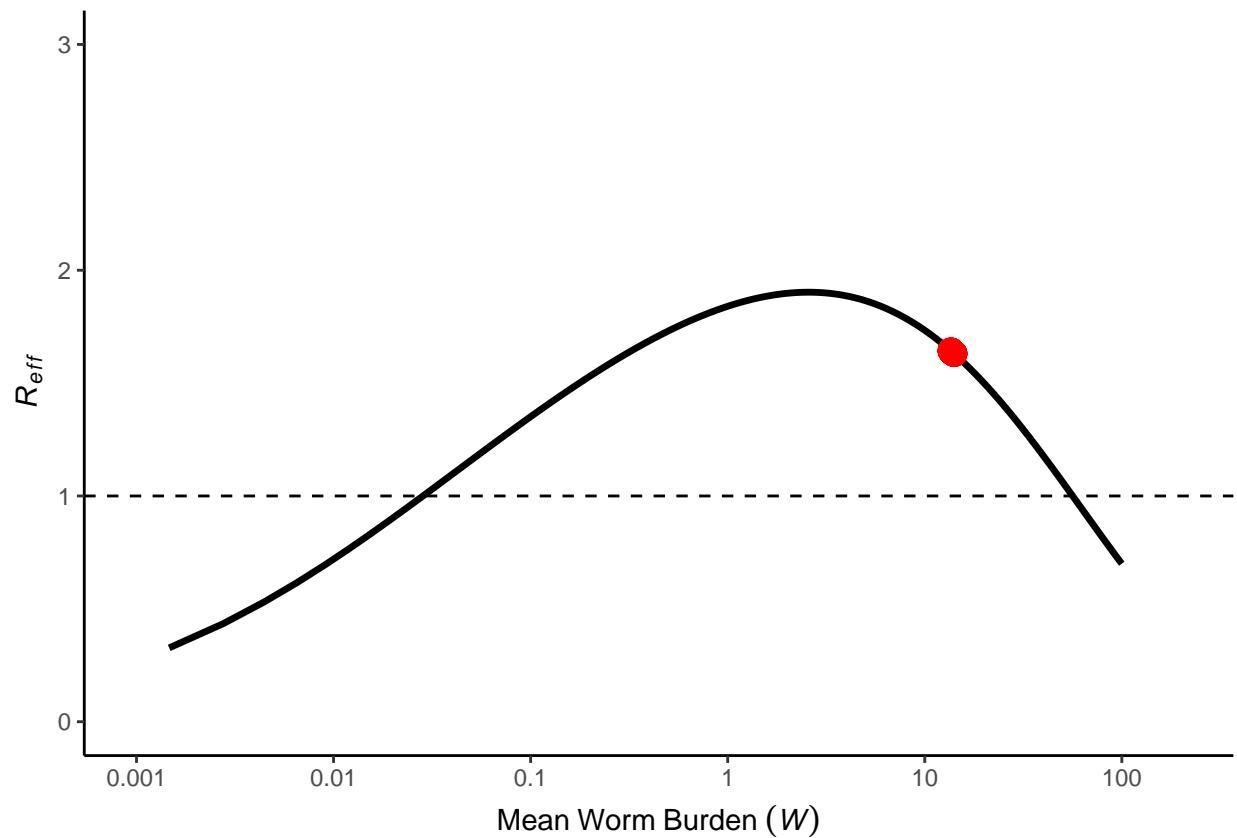
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



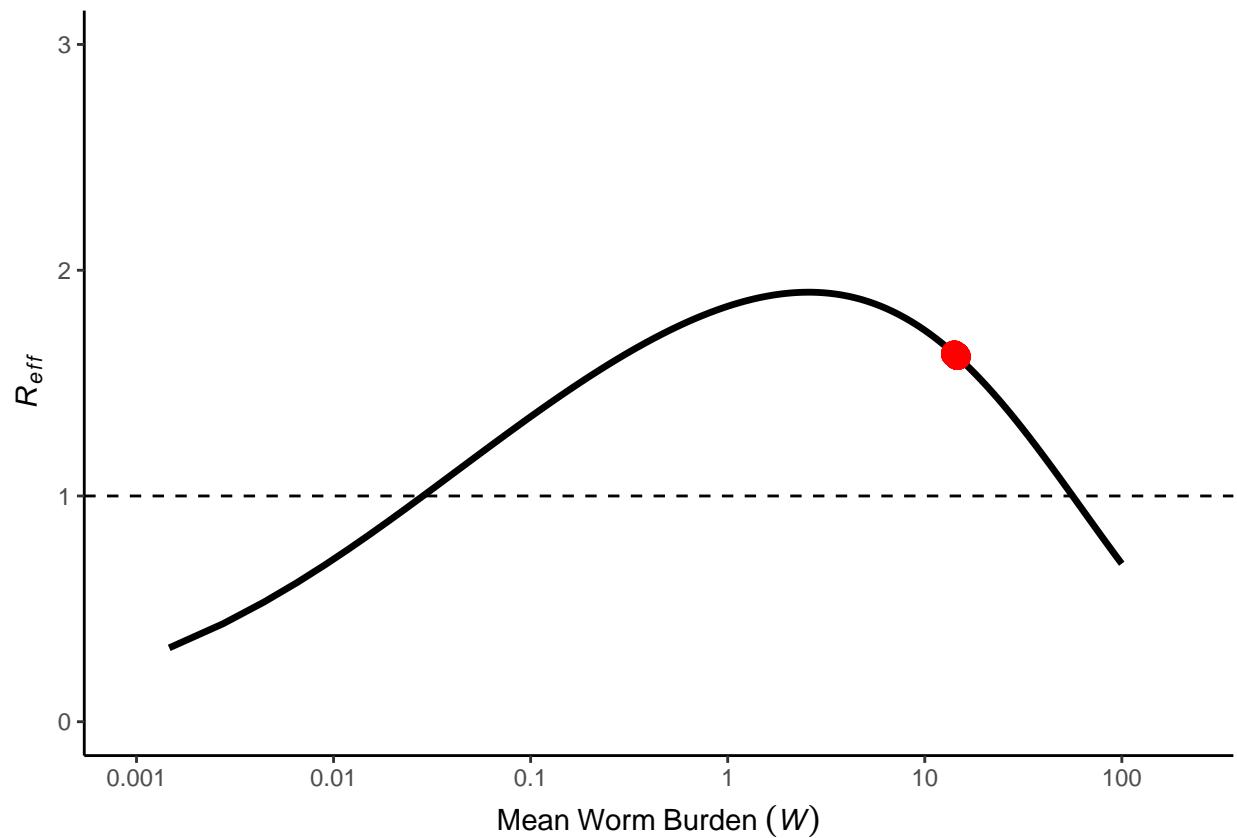
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



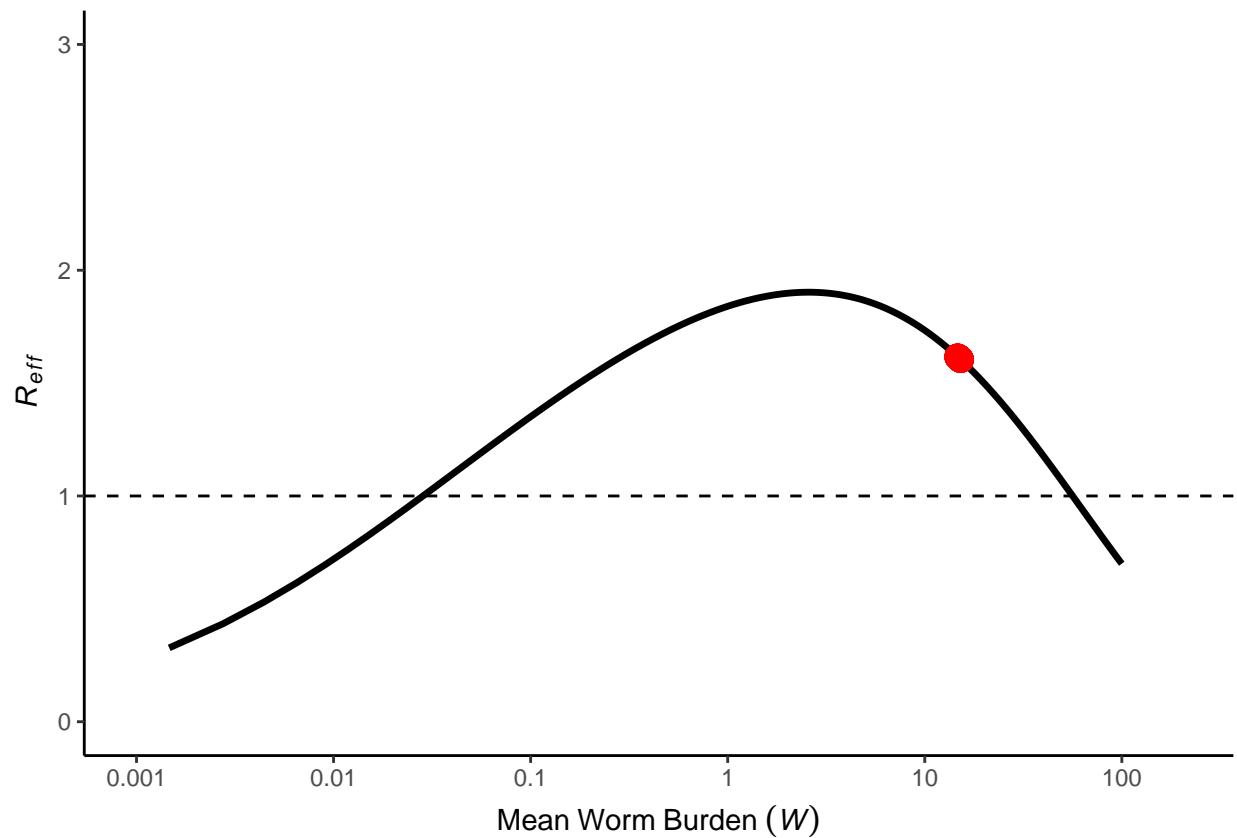
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



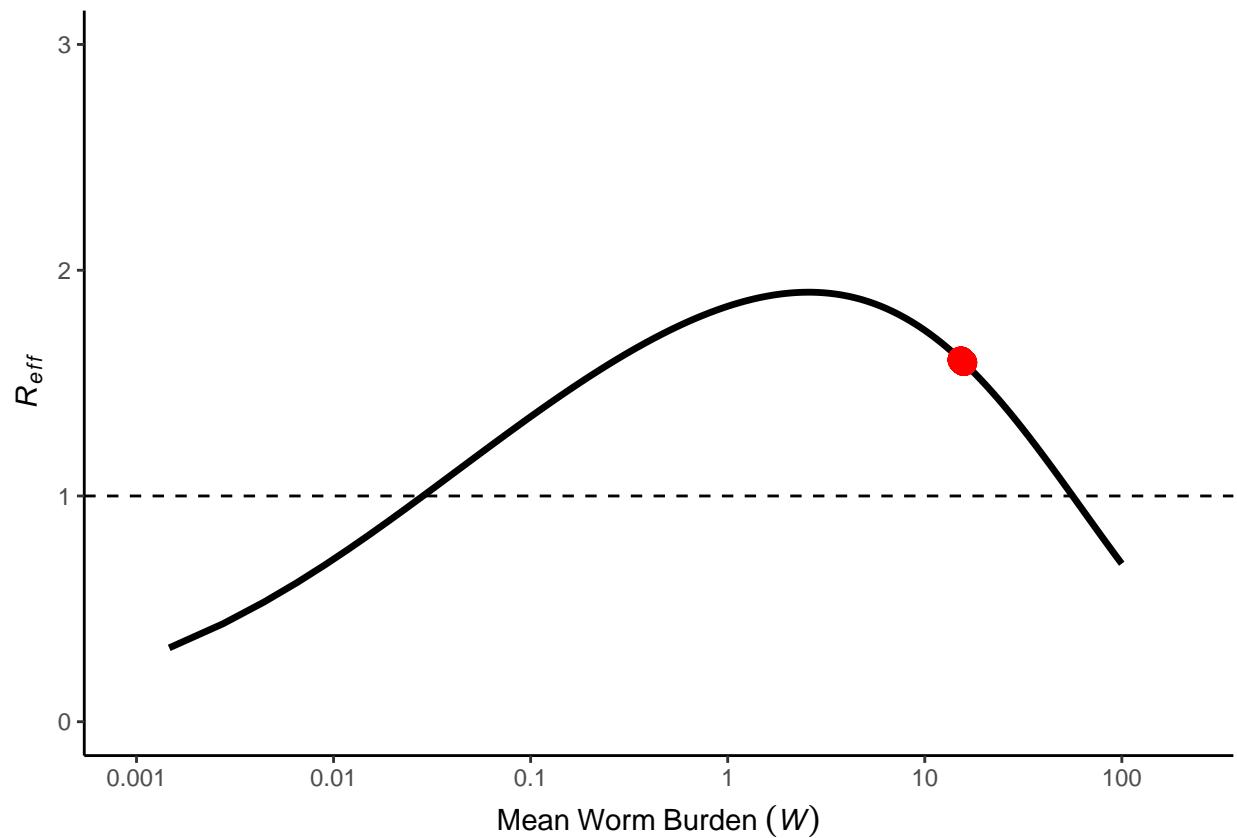
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



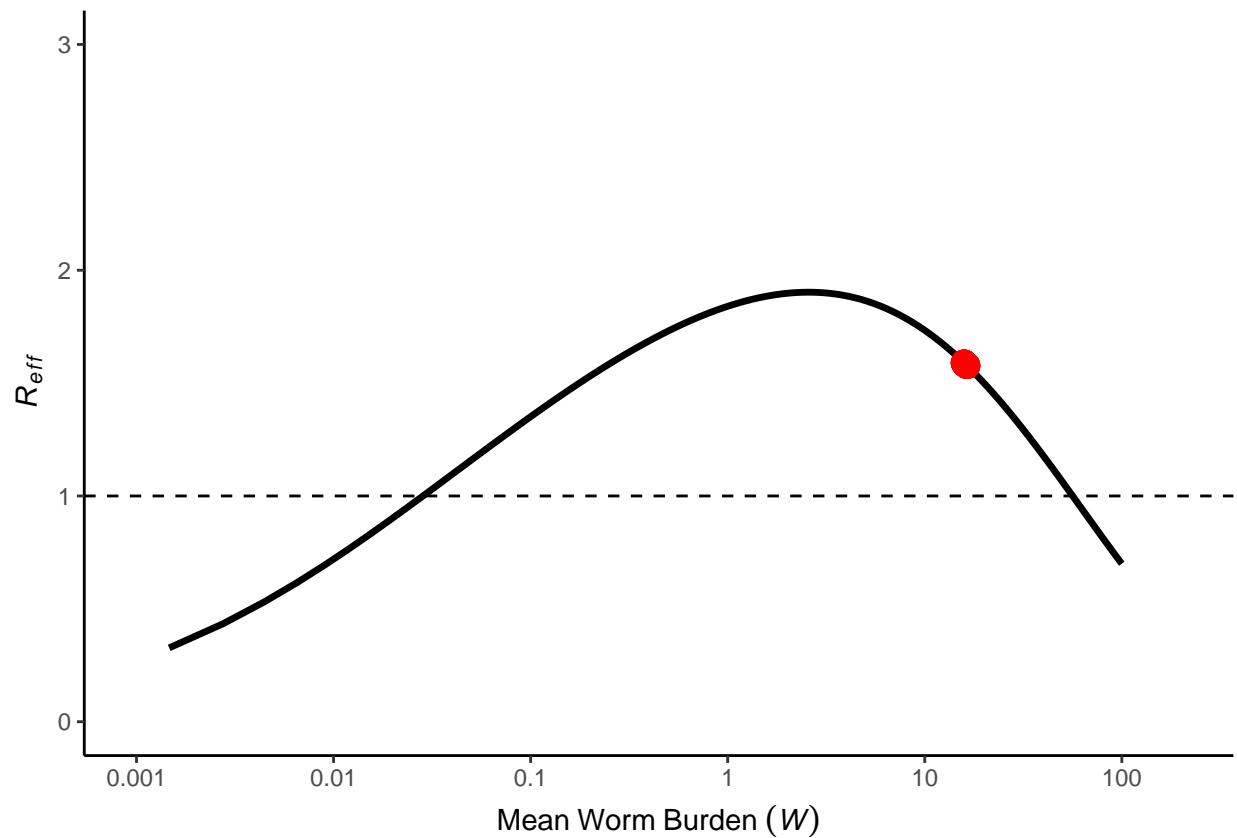
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



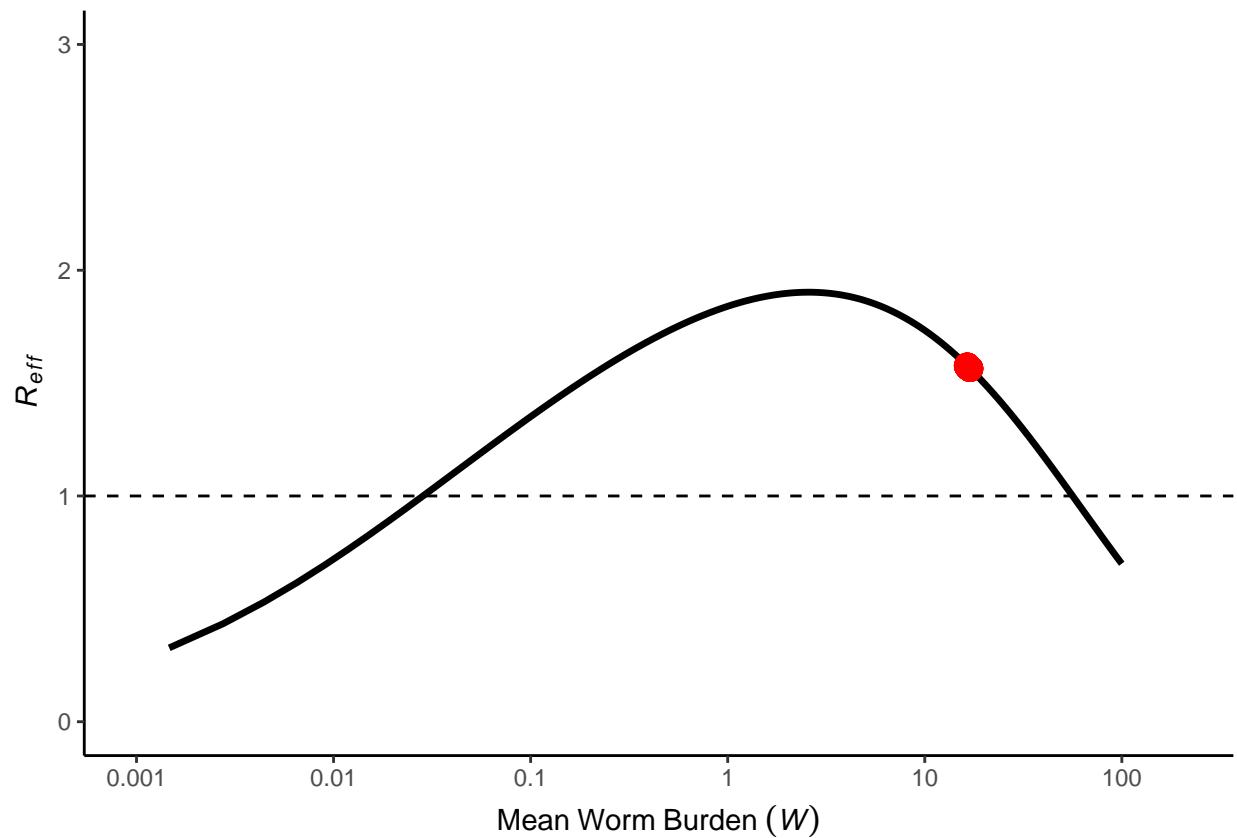
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



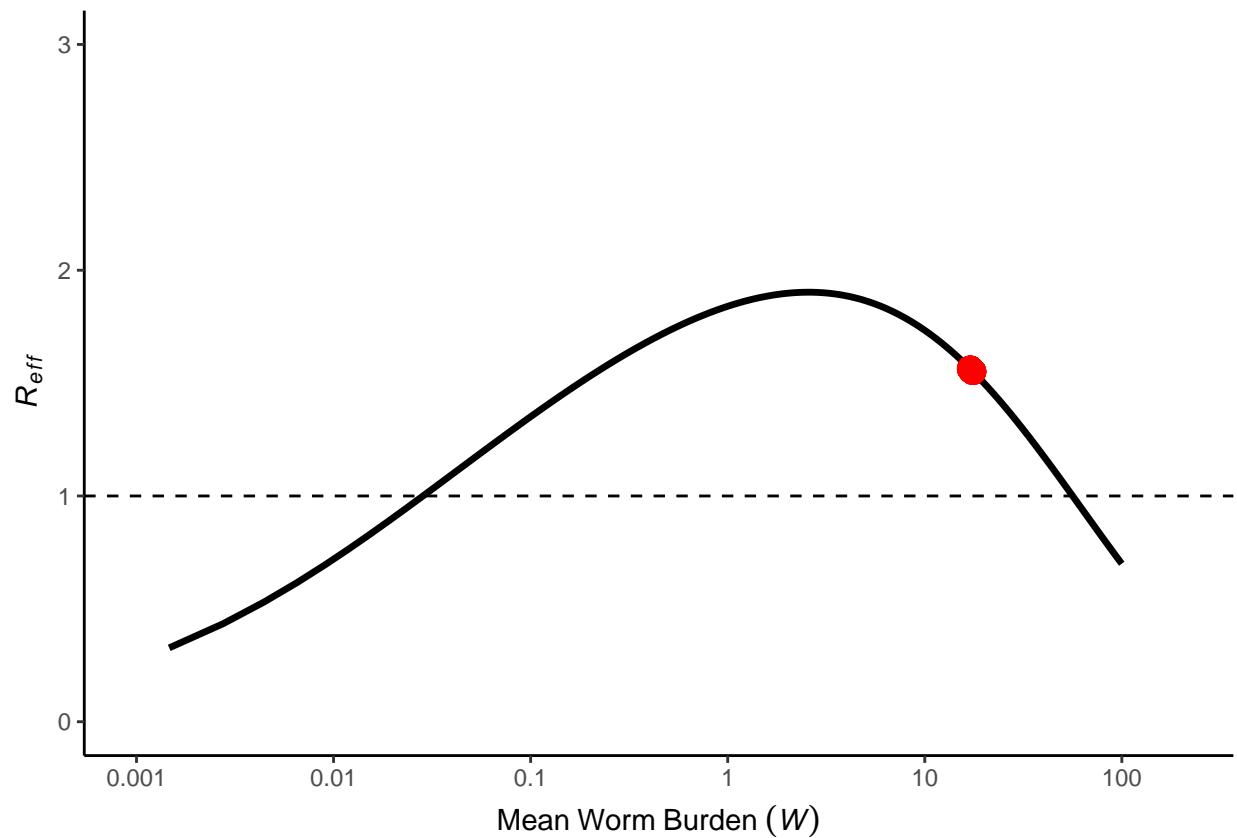
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



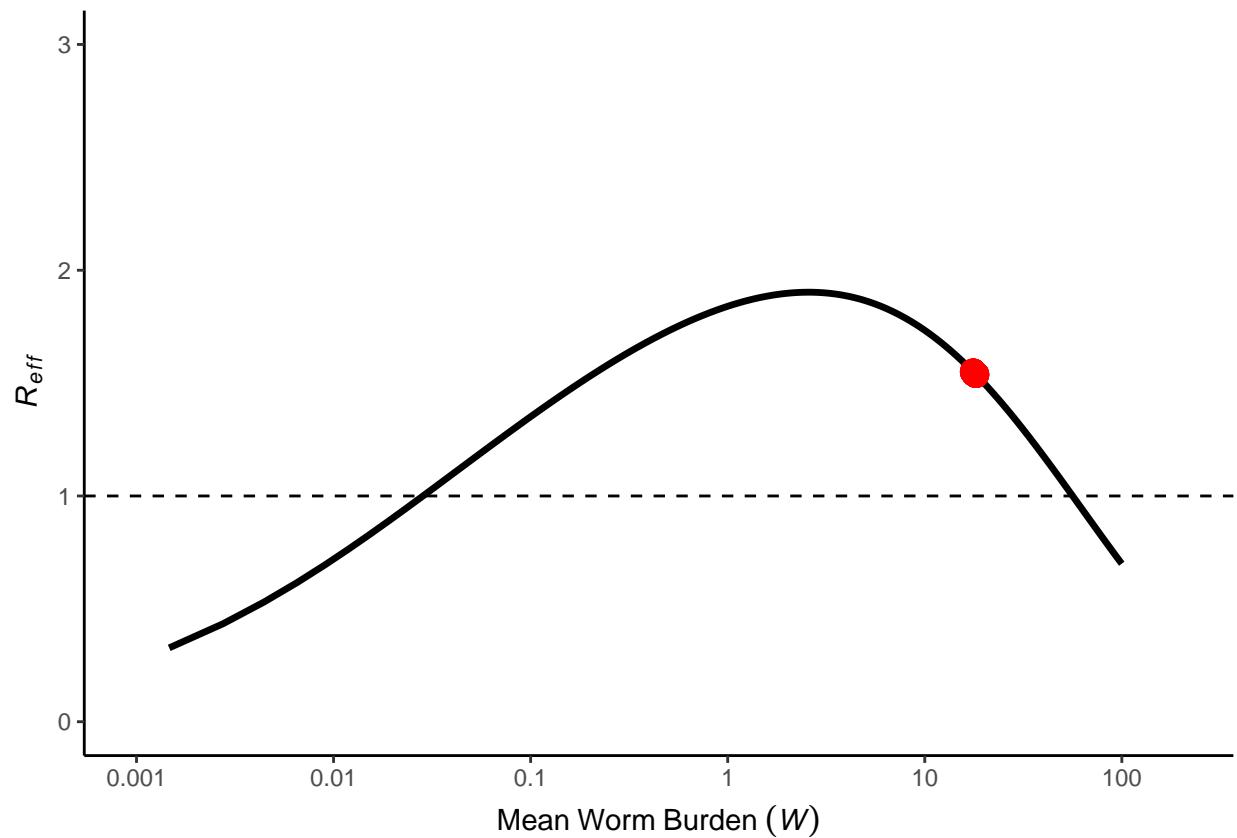
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



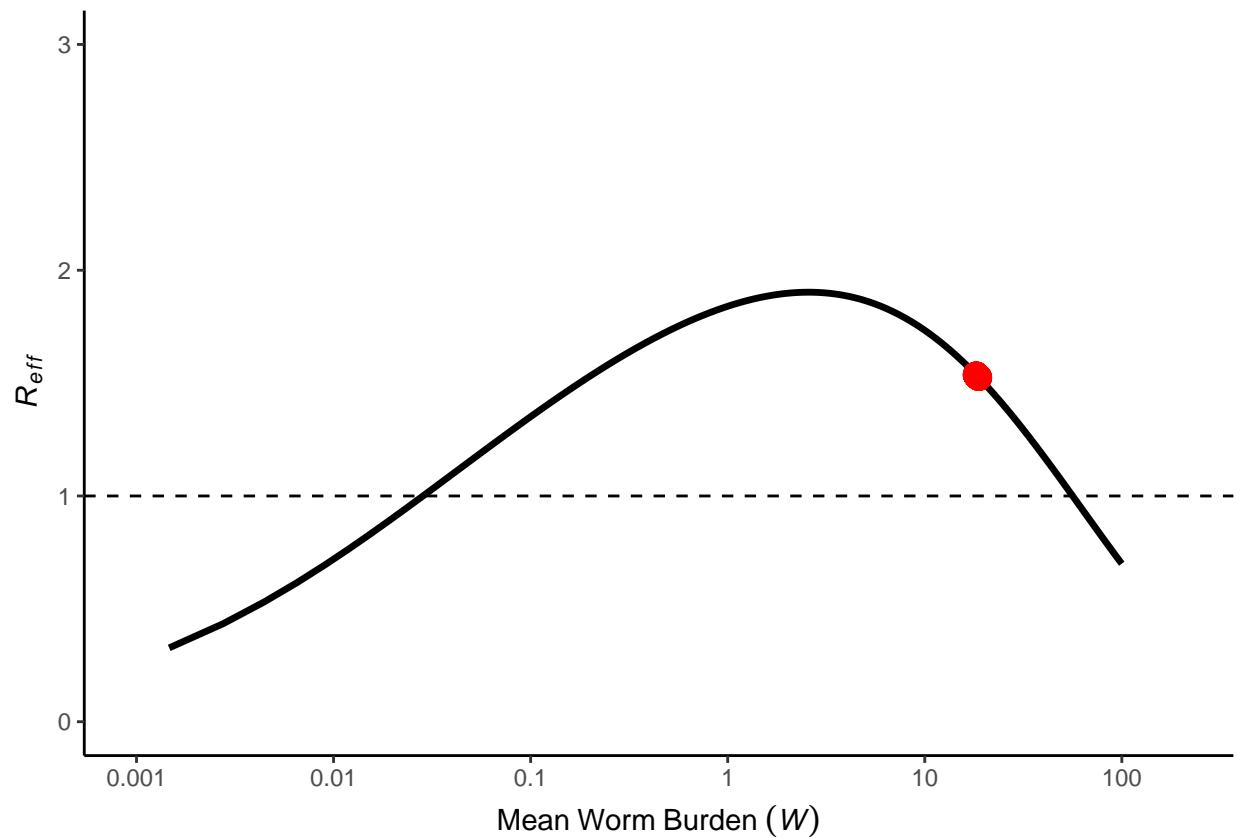
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



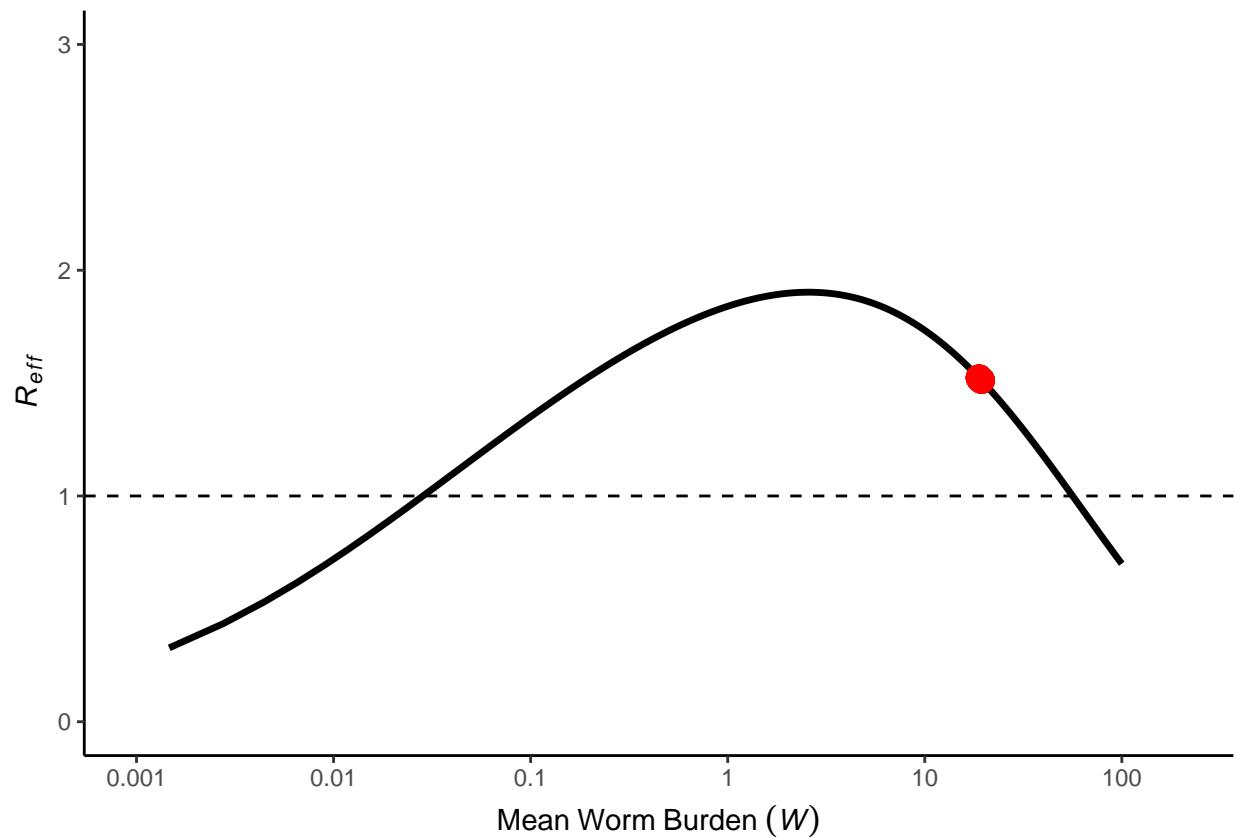
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



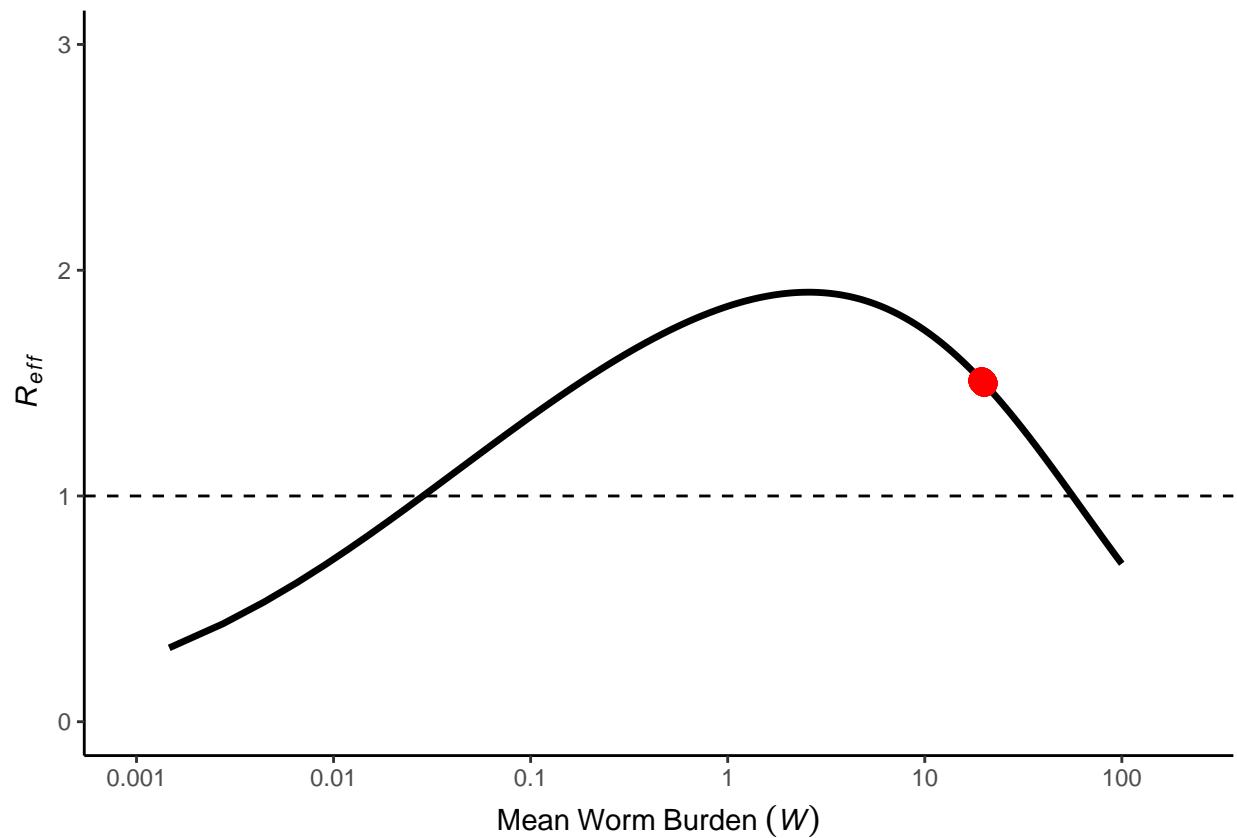
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



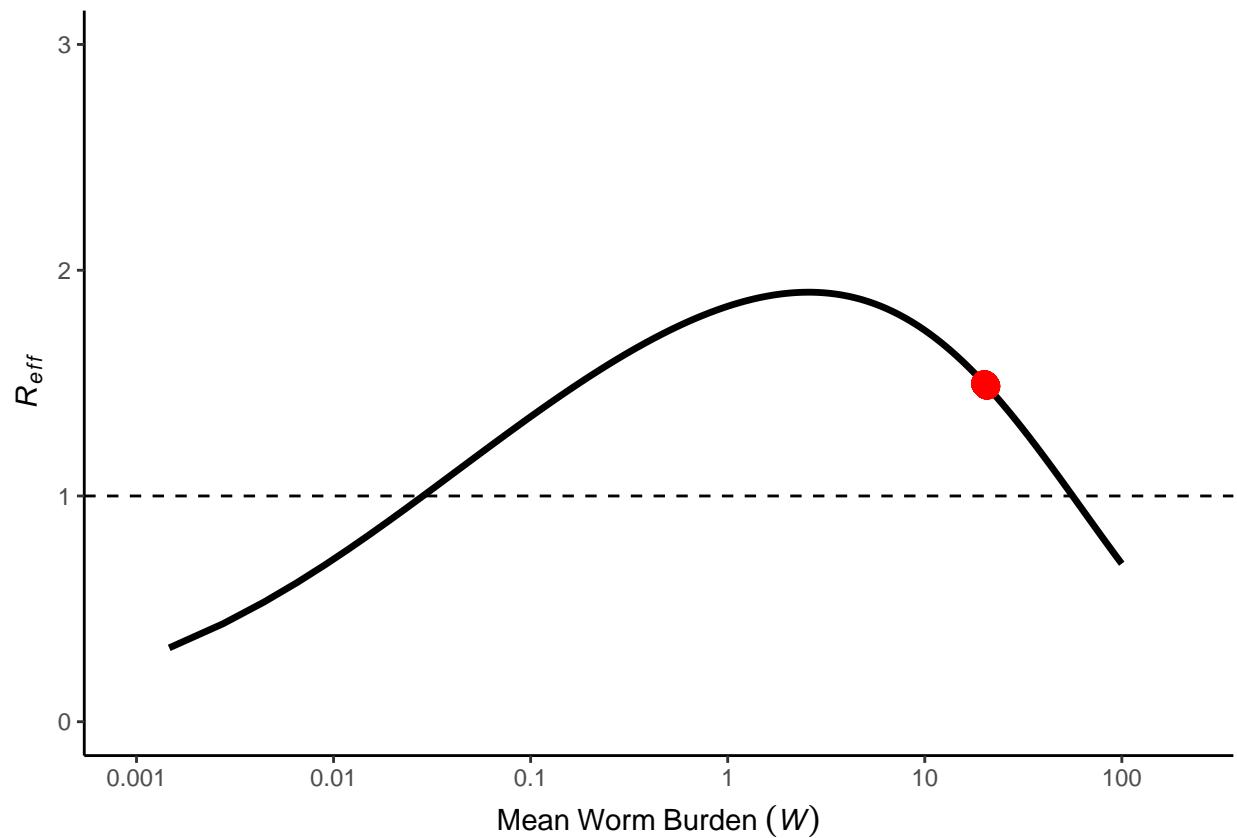
```
## Warning: Removed 2 rows containing missing values (geom_path).
```



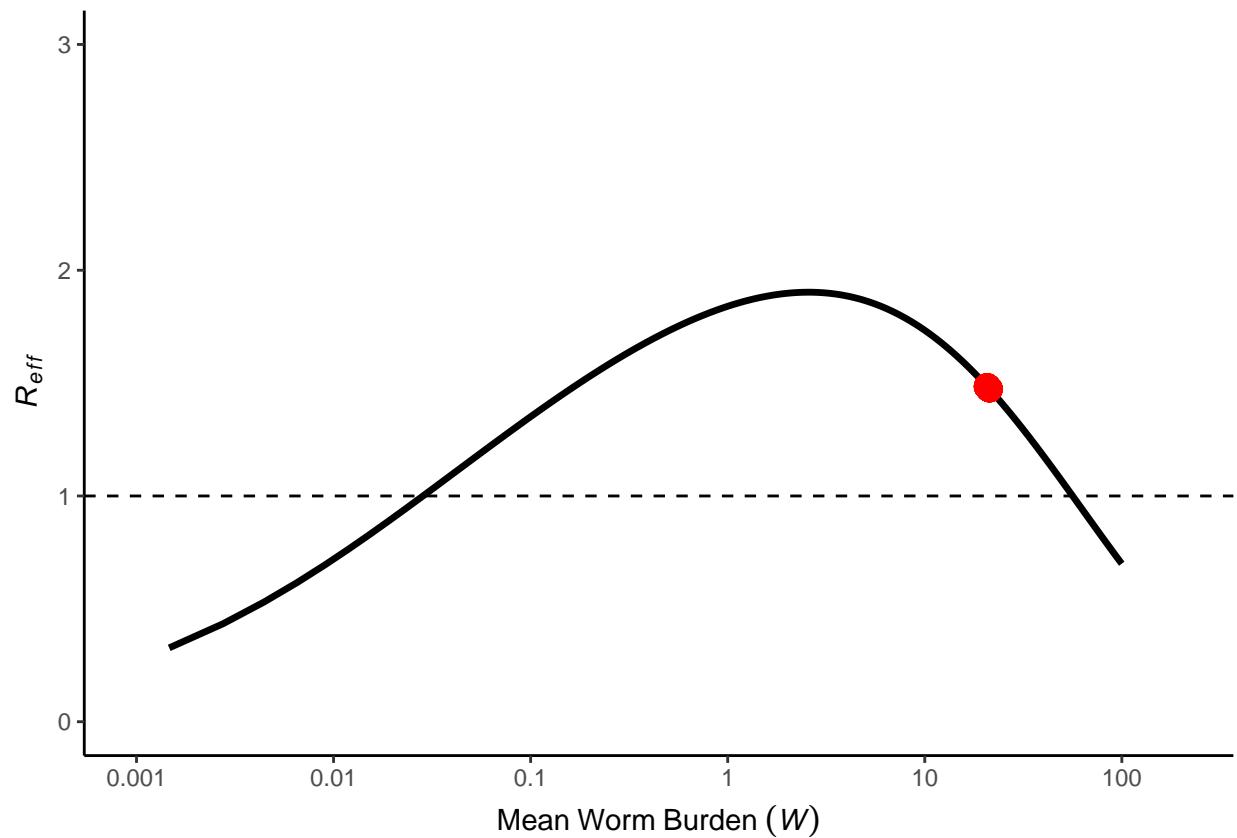
```
## Warning: Removed 2 rows containing missing values (geom_path).
```

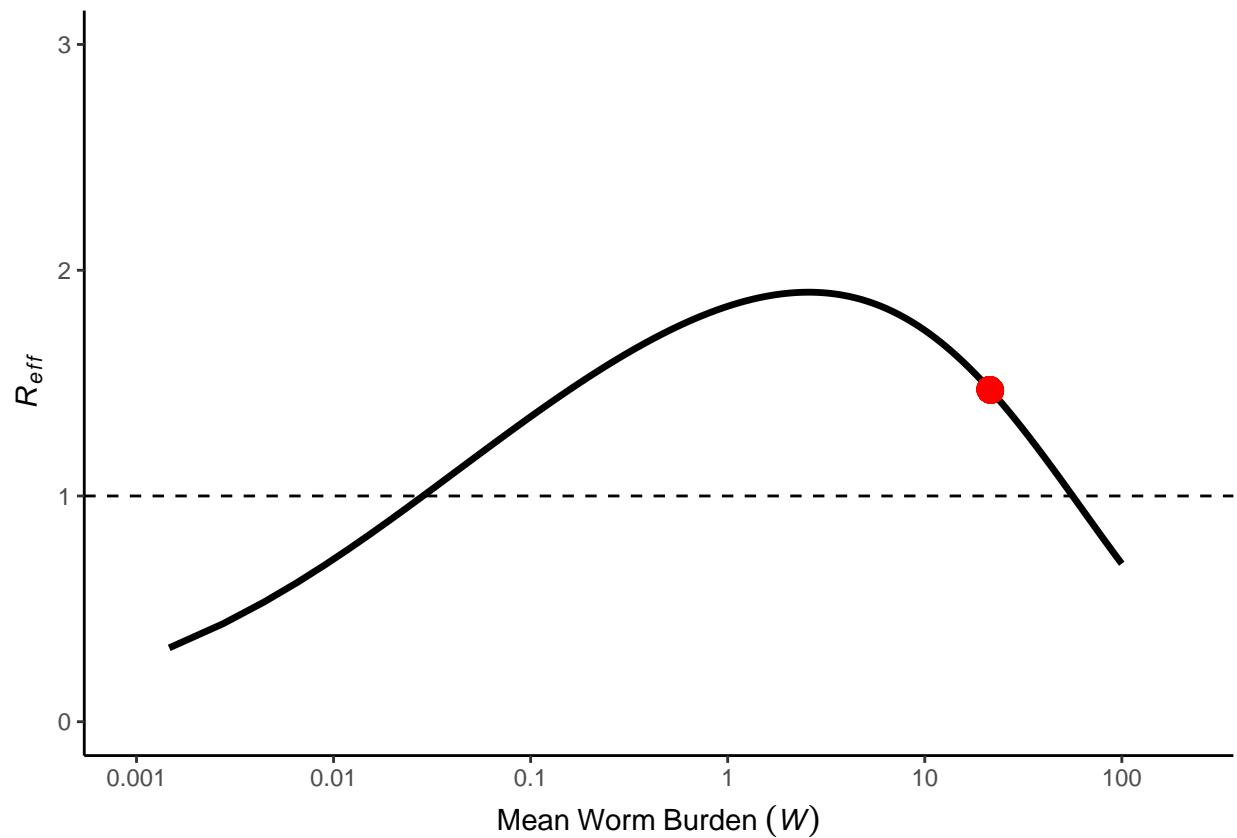


```
## Warning: Removed 2 rows containing missing values (geom_path).
```



```
## Warning: Removed 2 rows containing missing values (geom_path).
```

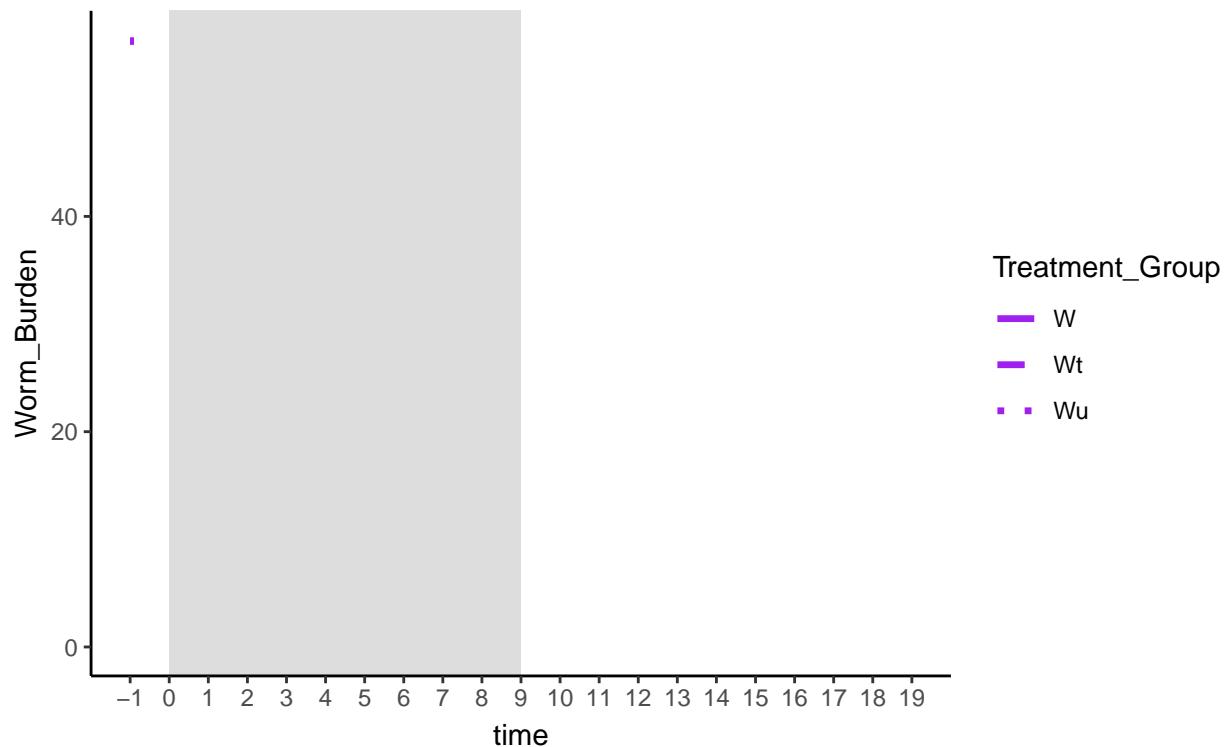




```
schisto_base_plot +  
  transition_reveal(time)
```

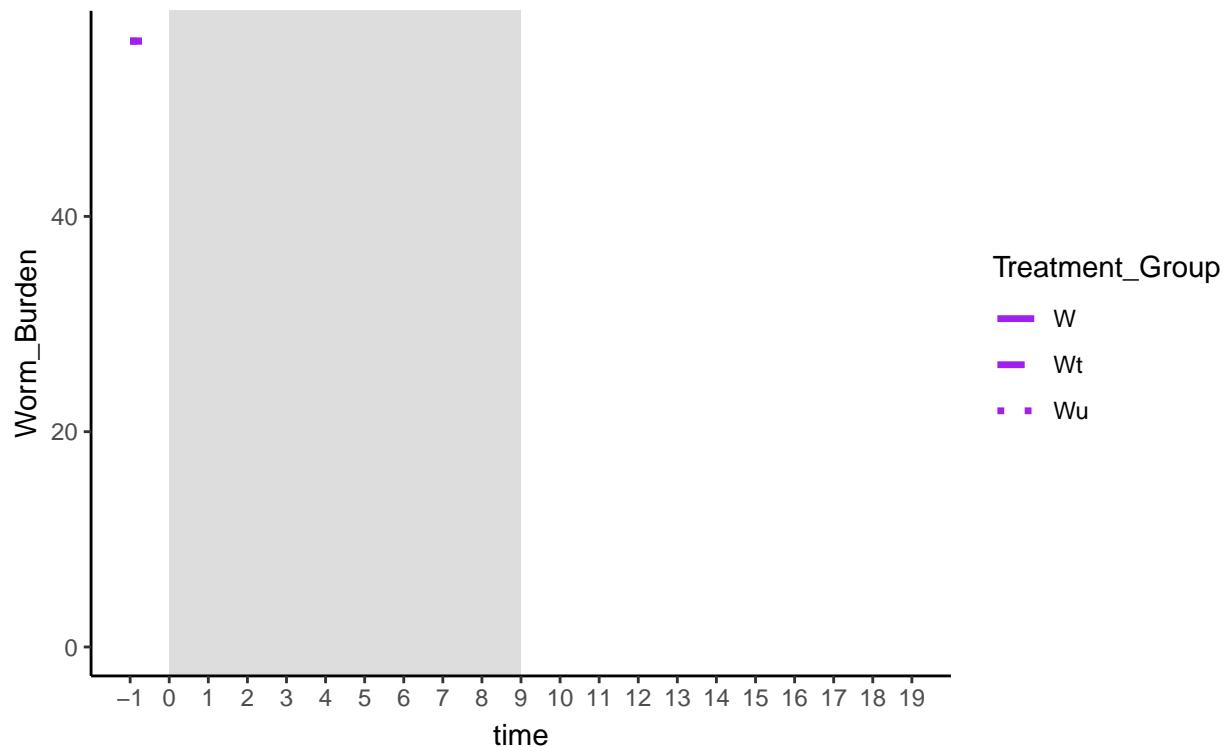
Human infection dynamics

Anual MDA for 10 years



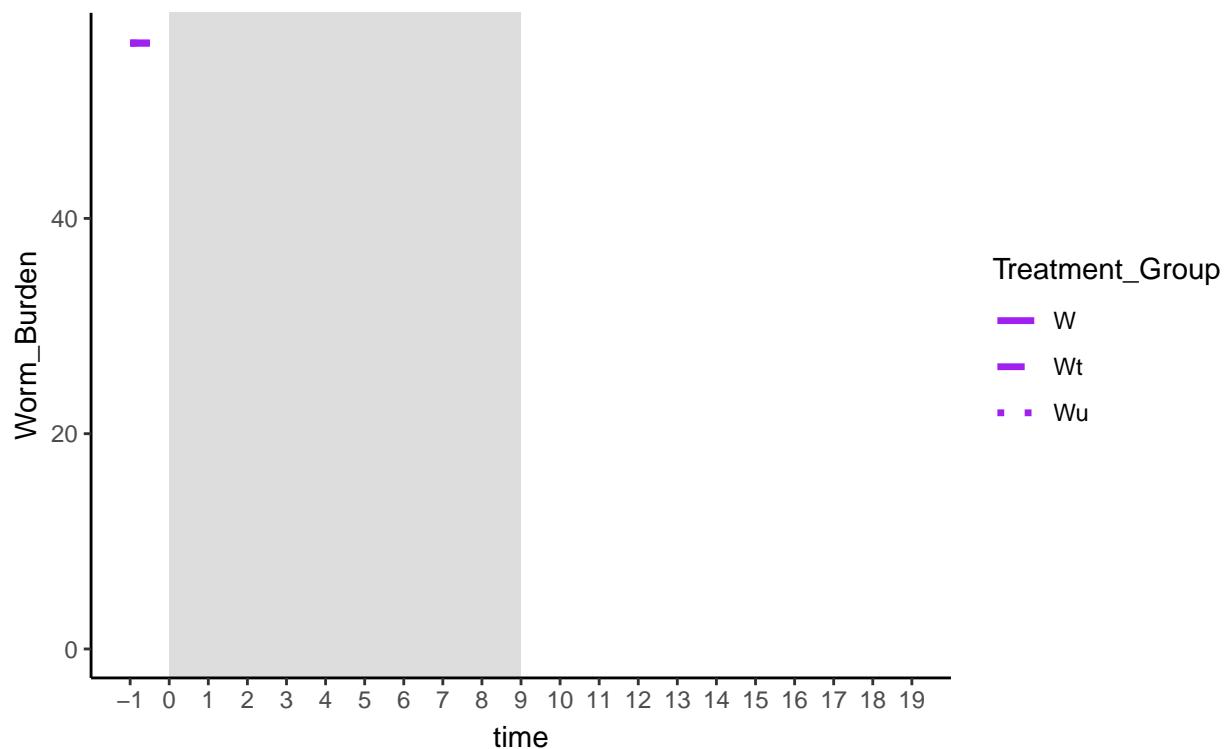
Human infection dynamics

Anual MDA for 10 years



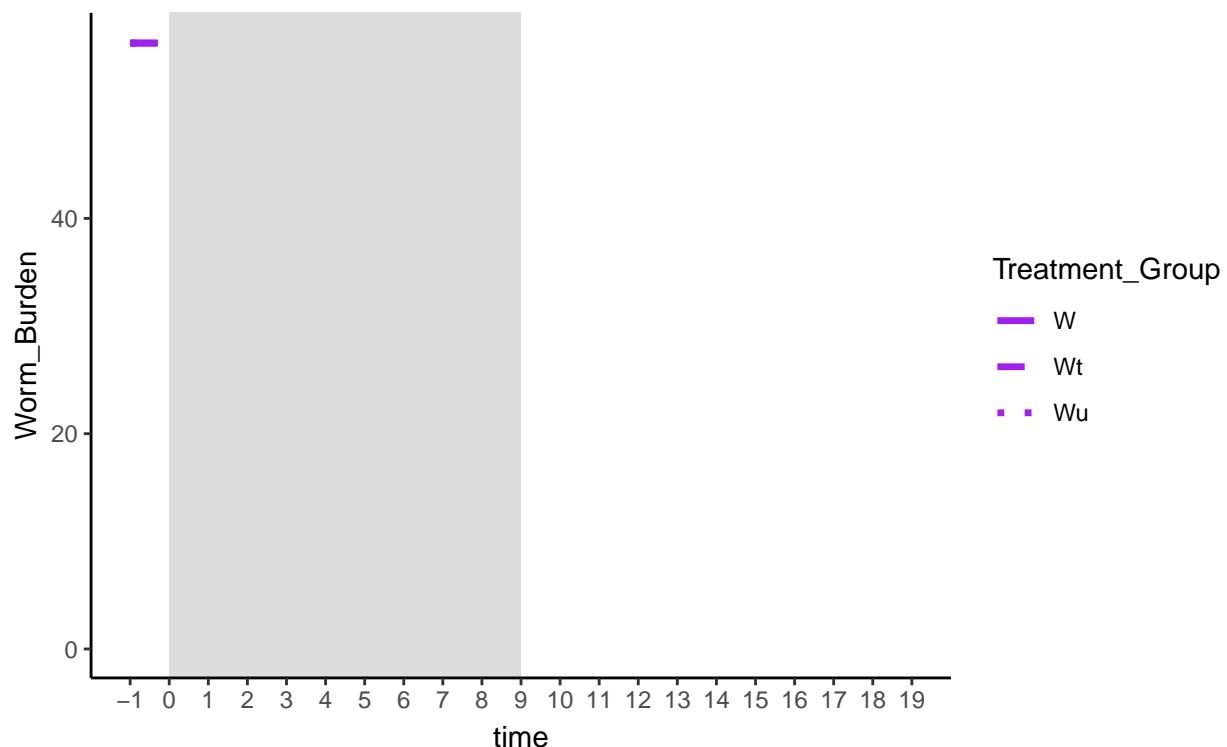
Human infection dynamics

Annual MDA for 10 years



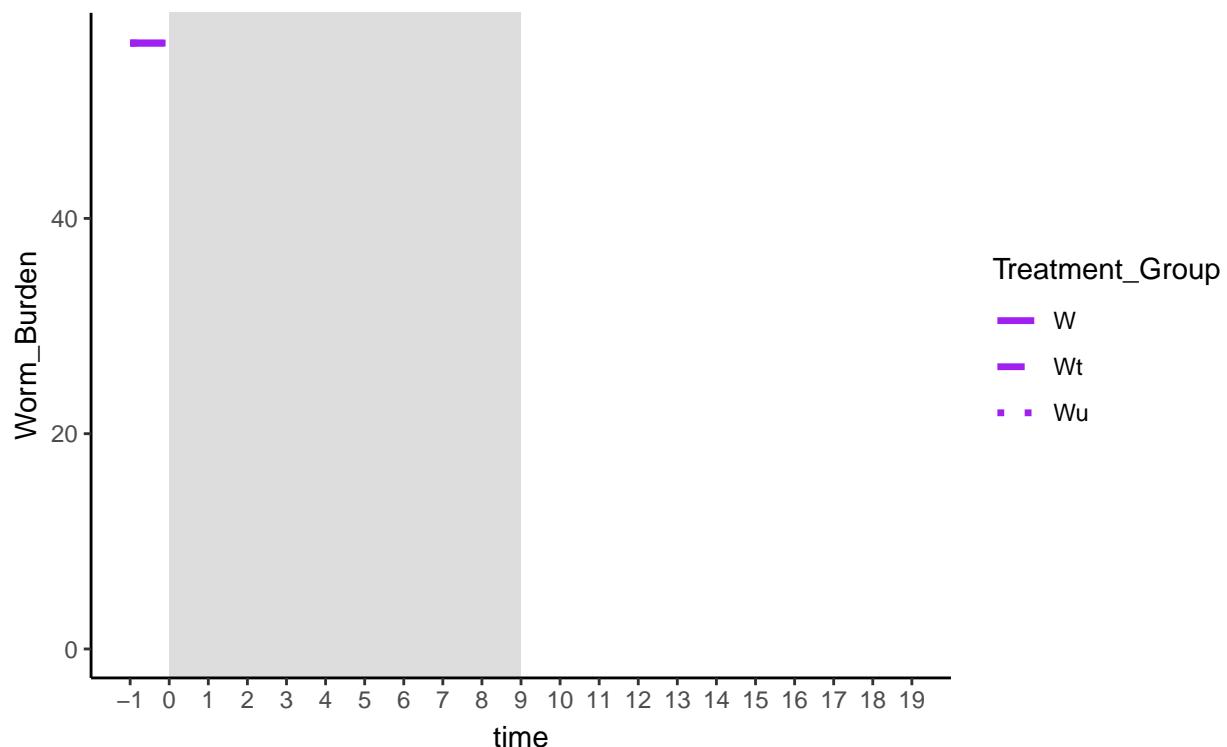
Human infection dynamics

Annual MDA for 10 years



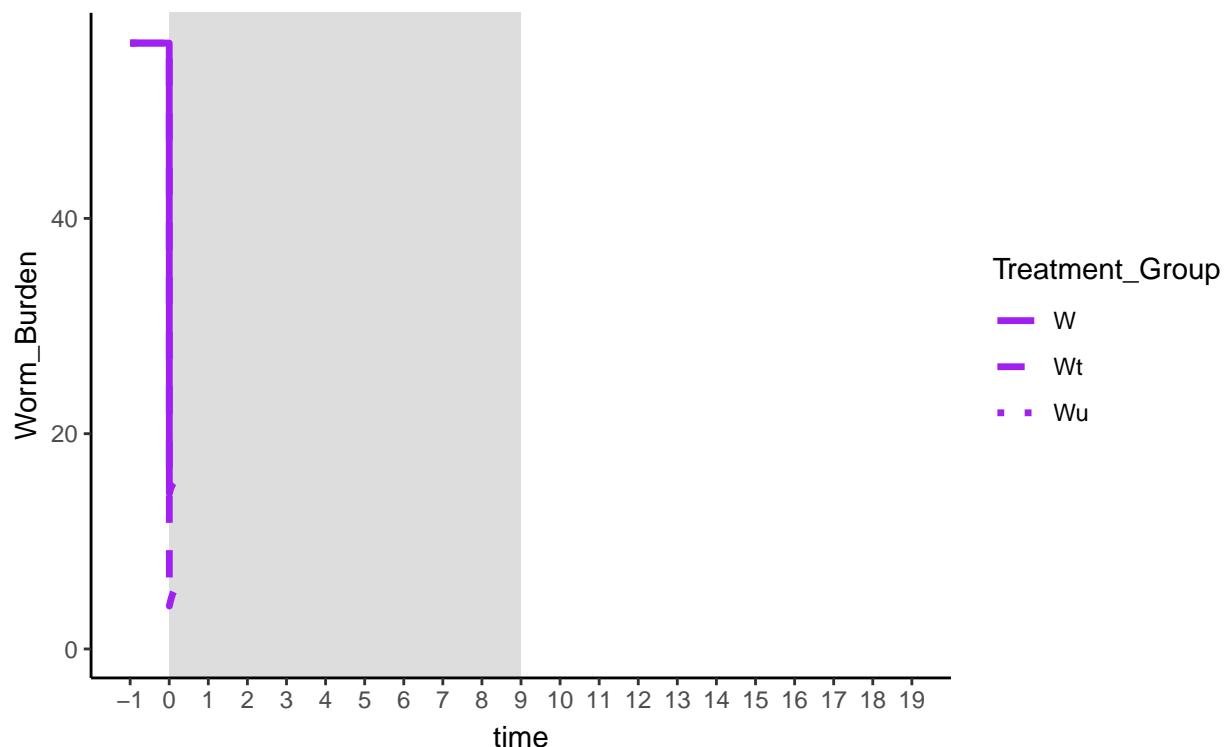
Human infection dynamics

Annual MDA for 10 years



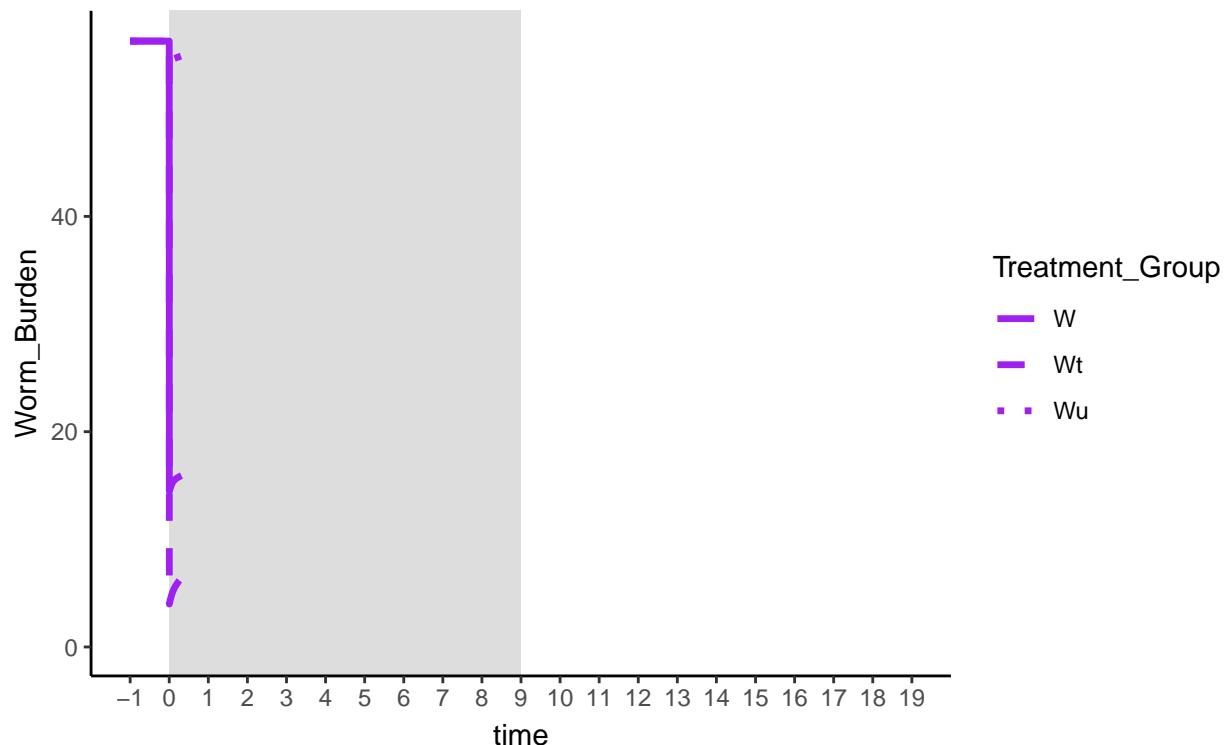
Human infection dynamics

Annual MDA for 10 years



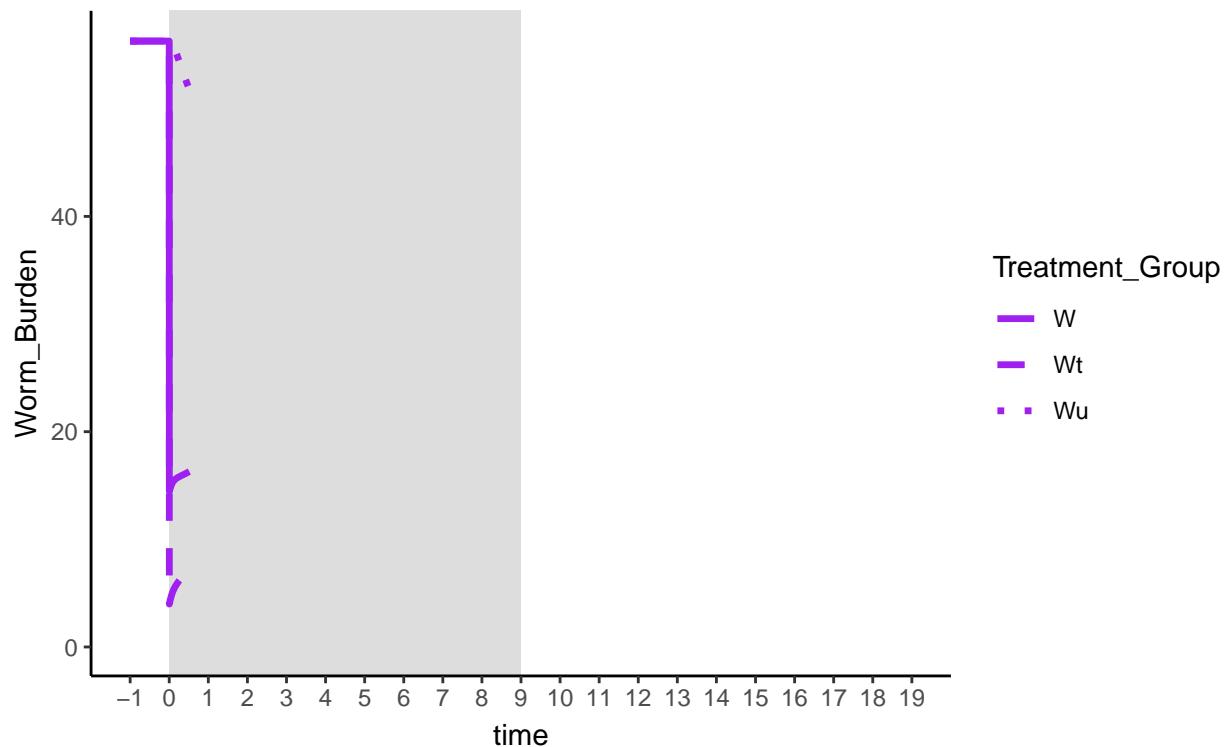
Human infection dynamics

Annual MDA for 10 years



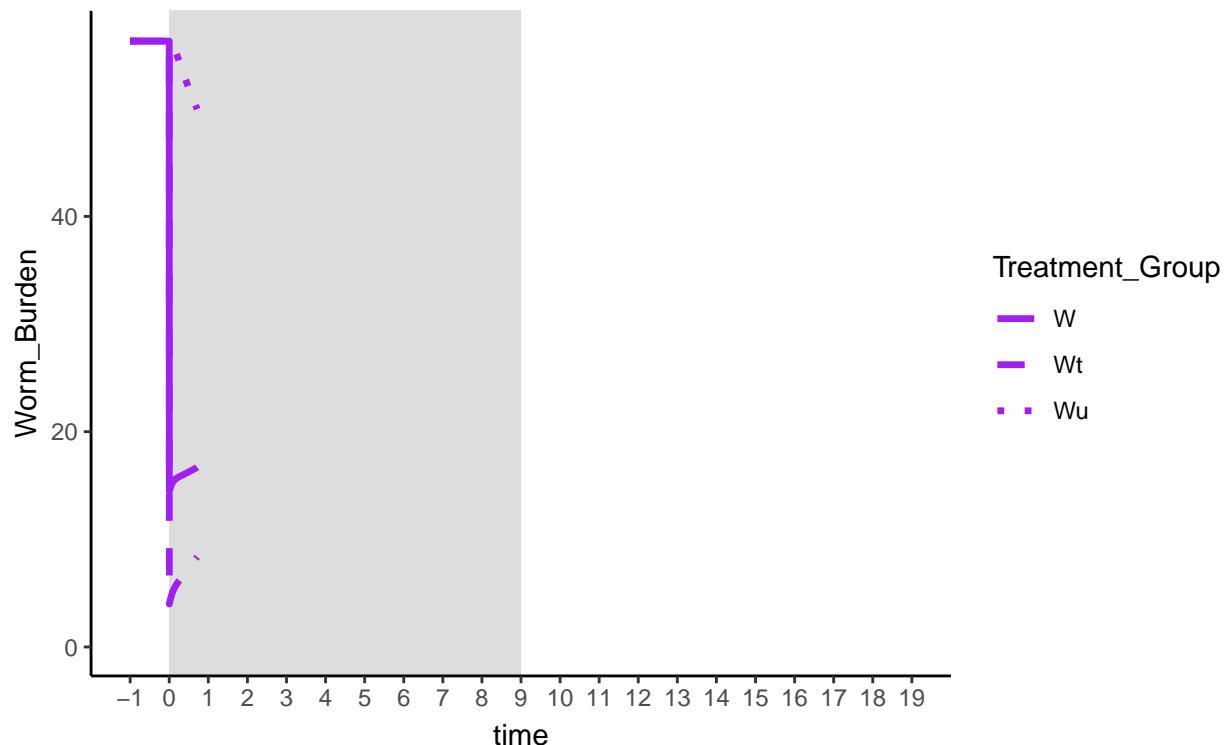
Human infection dynamics

Annual MDA for 10 years



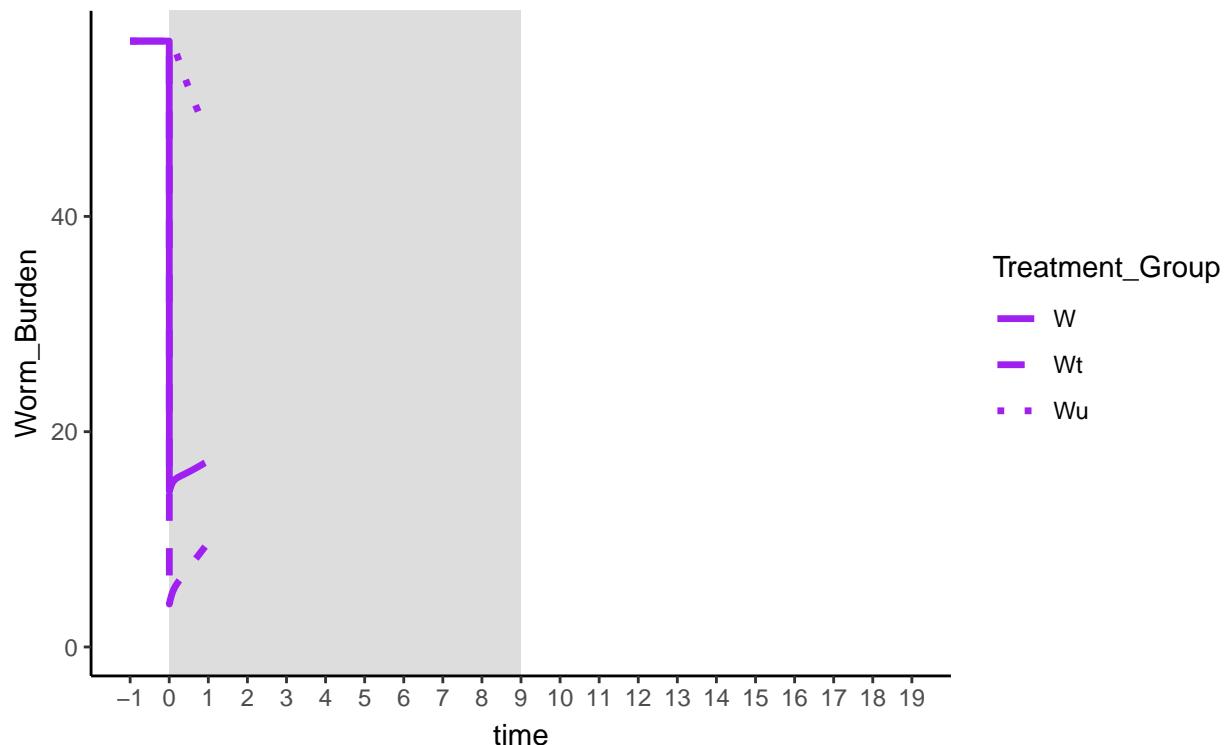
Human infection dynamics

Annual MDA for 10 years



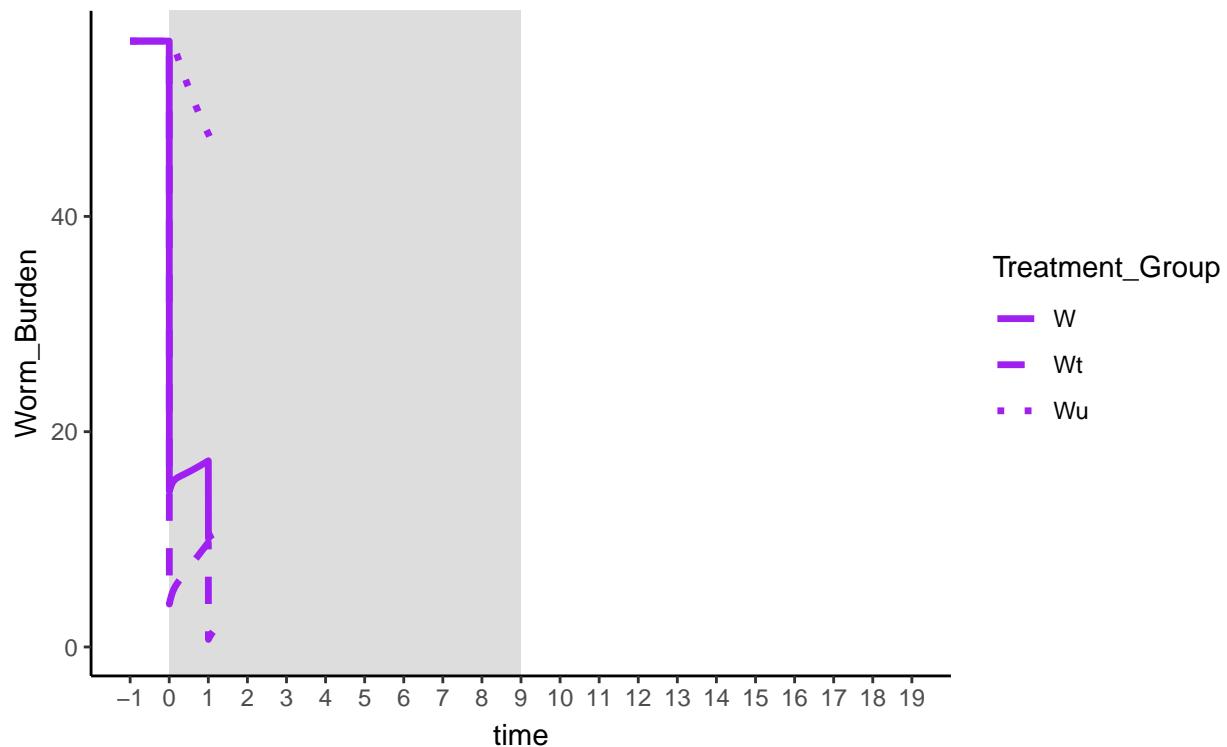
Human infection dynamics

Annual MDA for 10 years



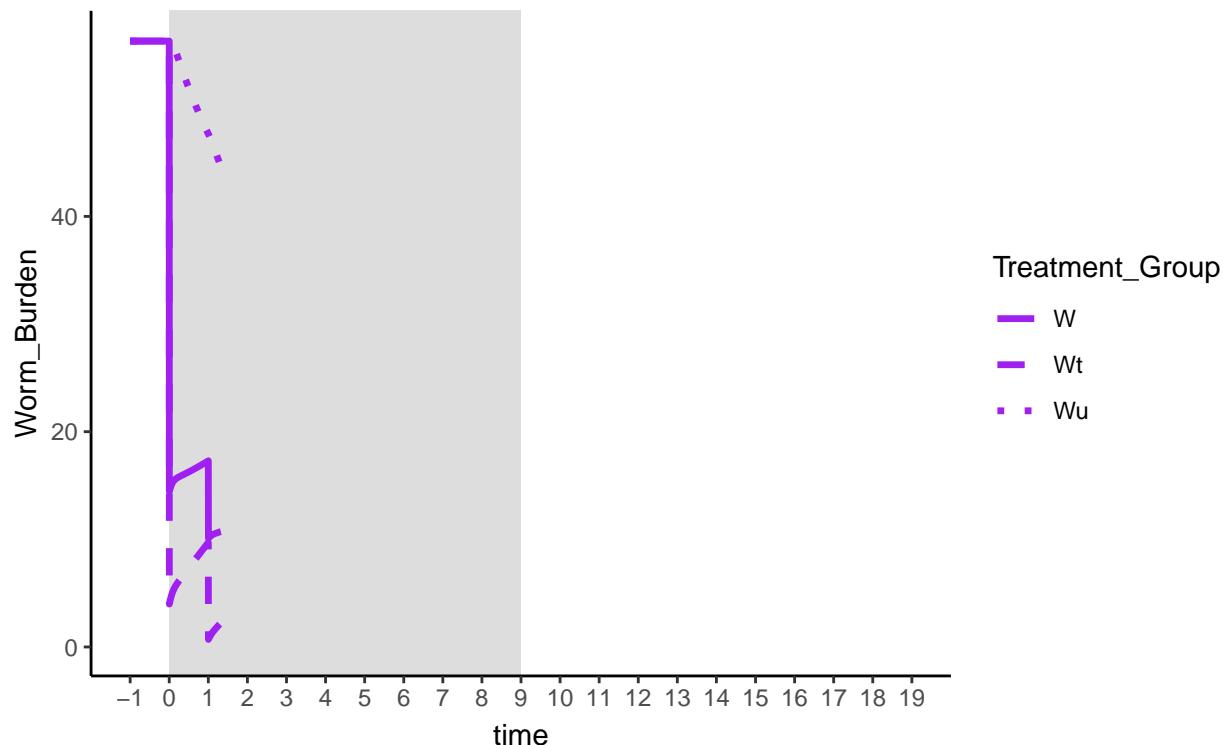
Human infection dynamics

Annual MDA for 10 years



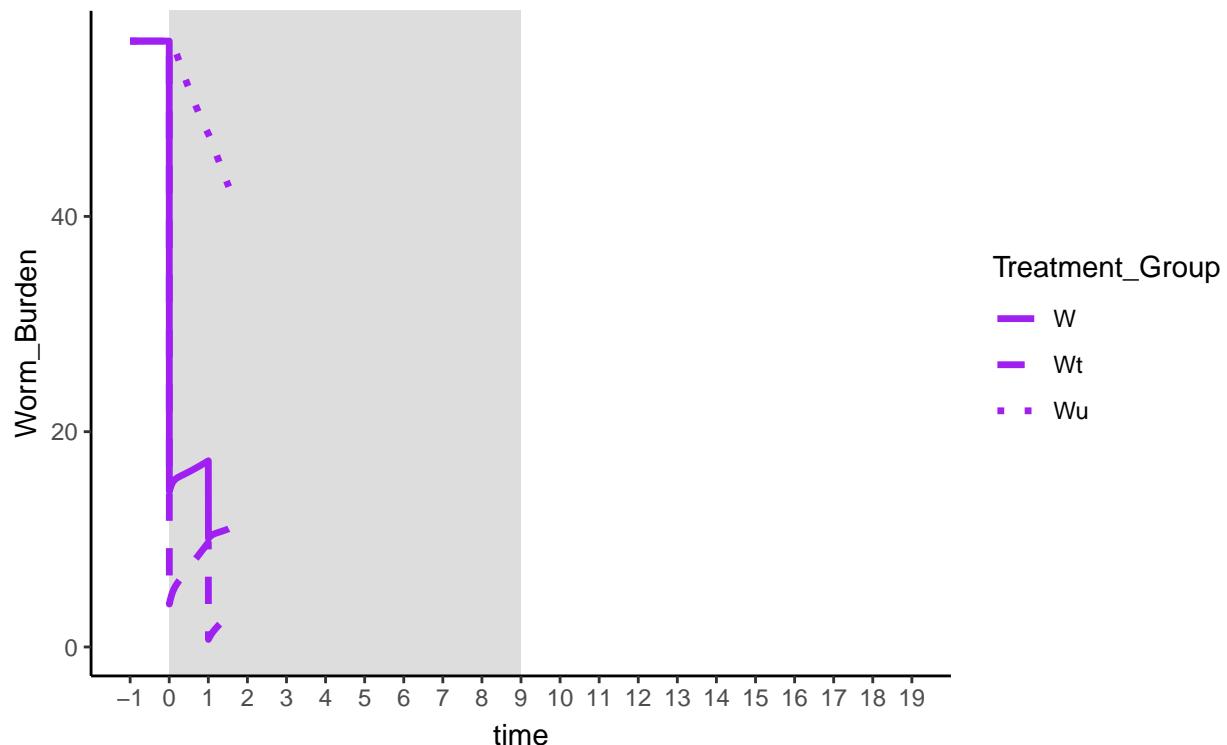
Human infection dynamics

Annual MDA for 10 years



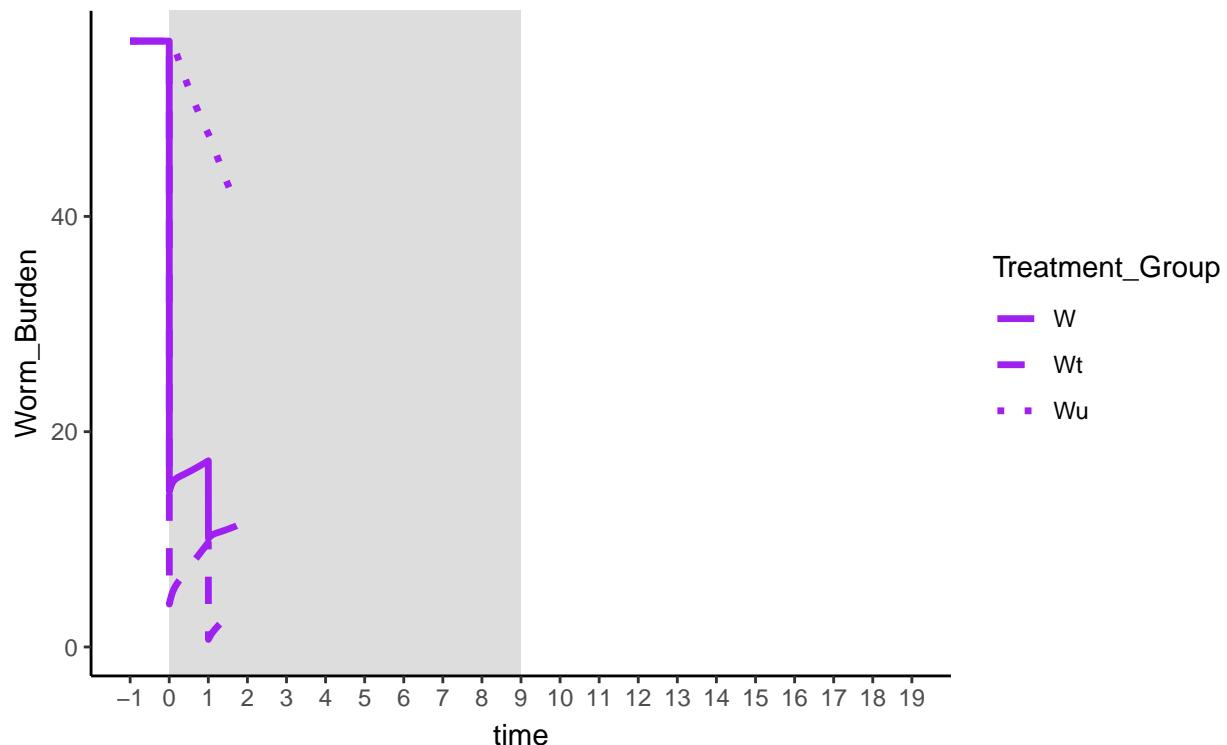
Human infection dynamics

Annual MDA for 10 years



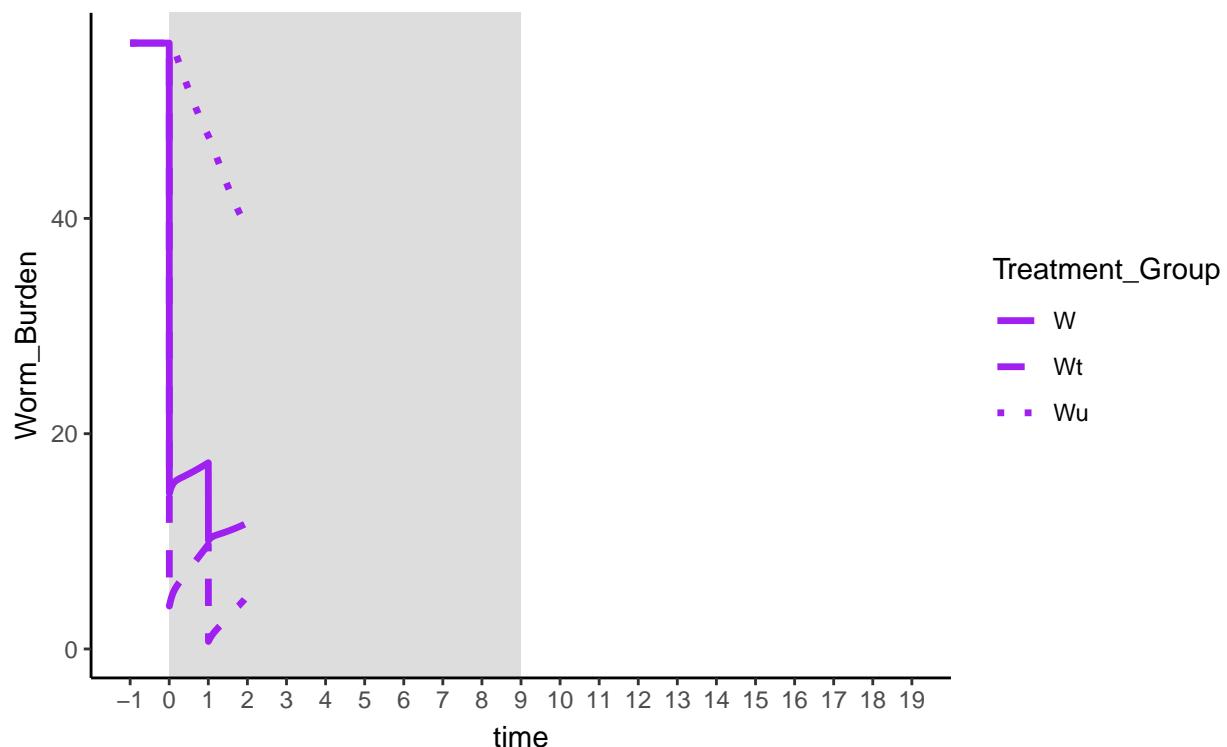
Human infection dynamics

Annual MDA for 10 years



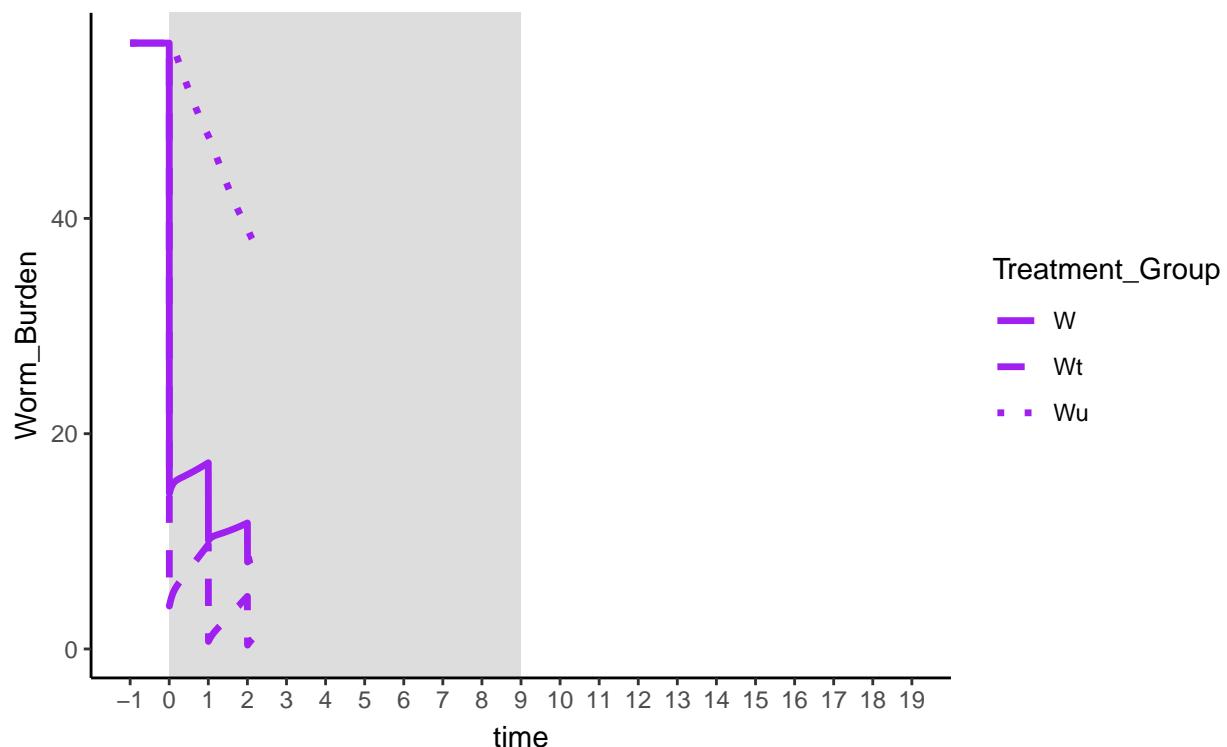
Human infection dynamics

Annual MDA for 10 years



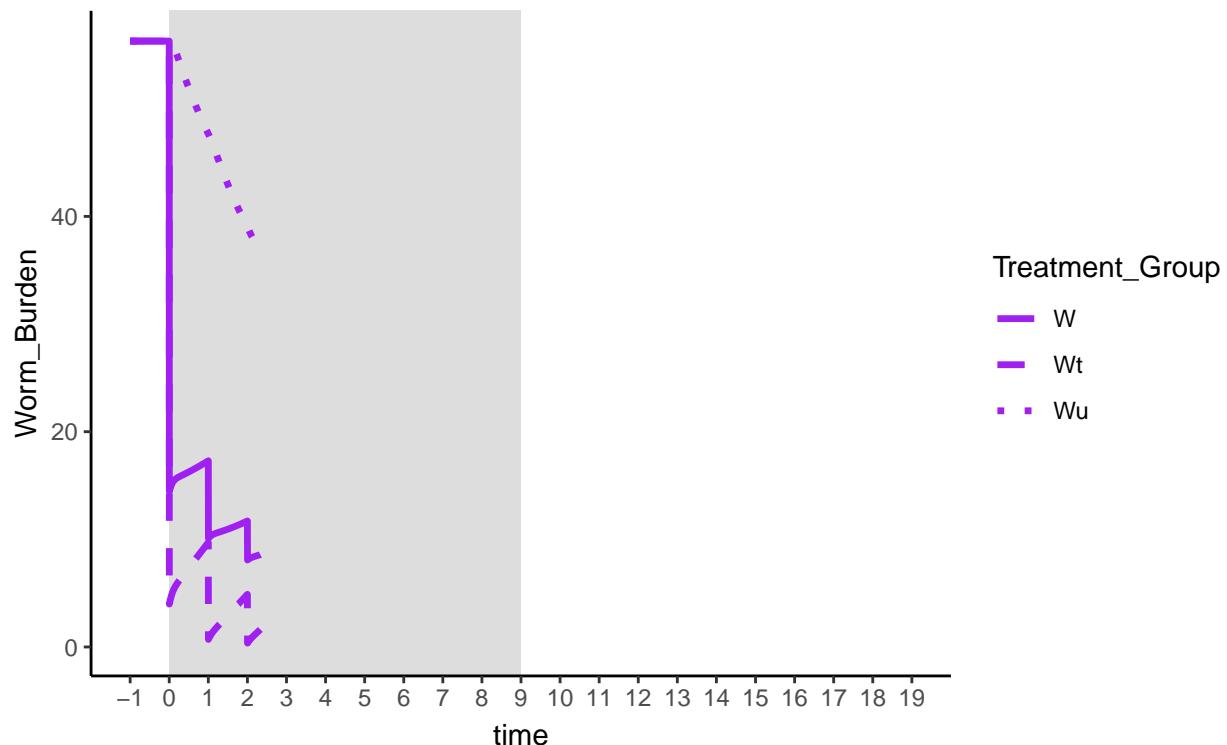
Human infection dynamics

Anual MDA for 10 years



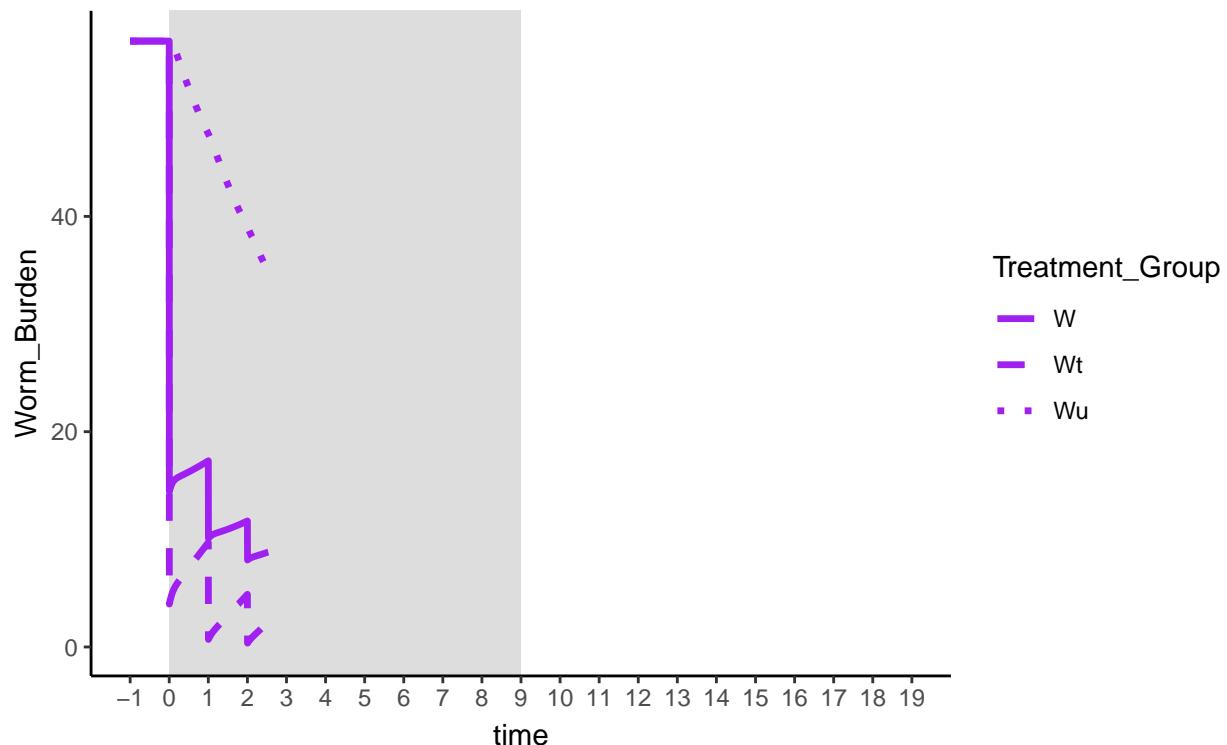
Human infection dynamics

Anual MDA for 10 years



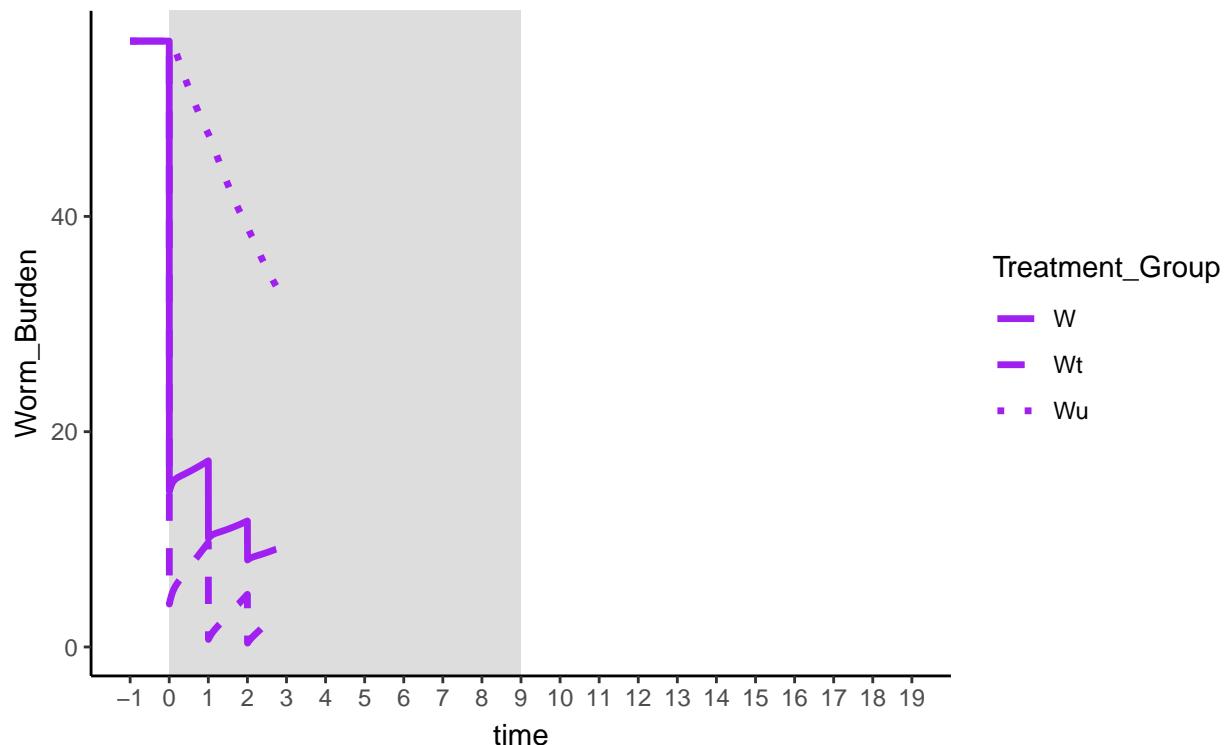
Human infection dynamics

Annual MDA for 10 years



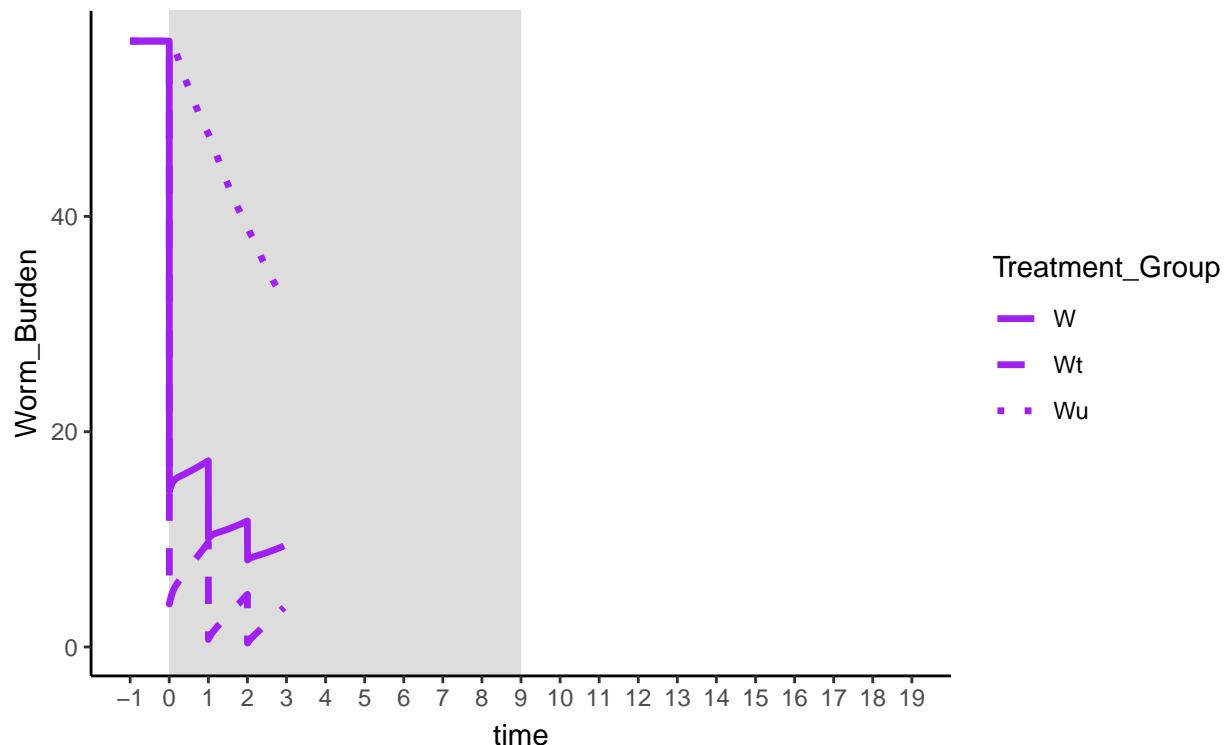
Human infection dynamics

Annual MDA for 10 years



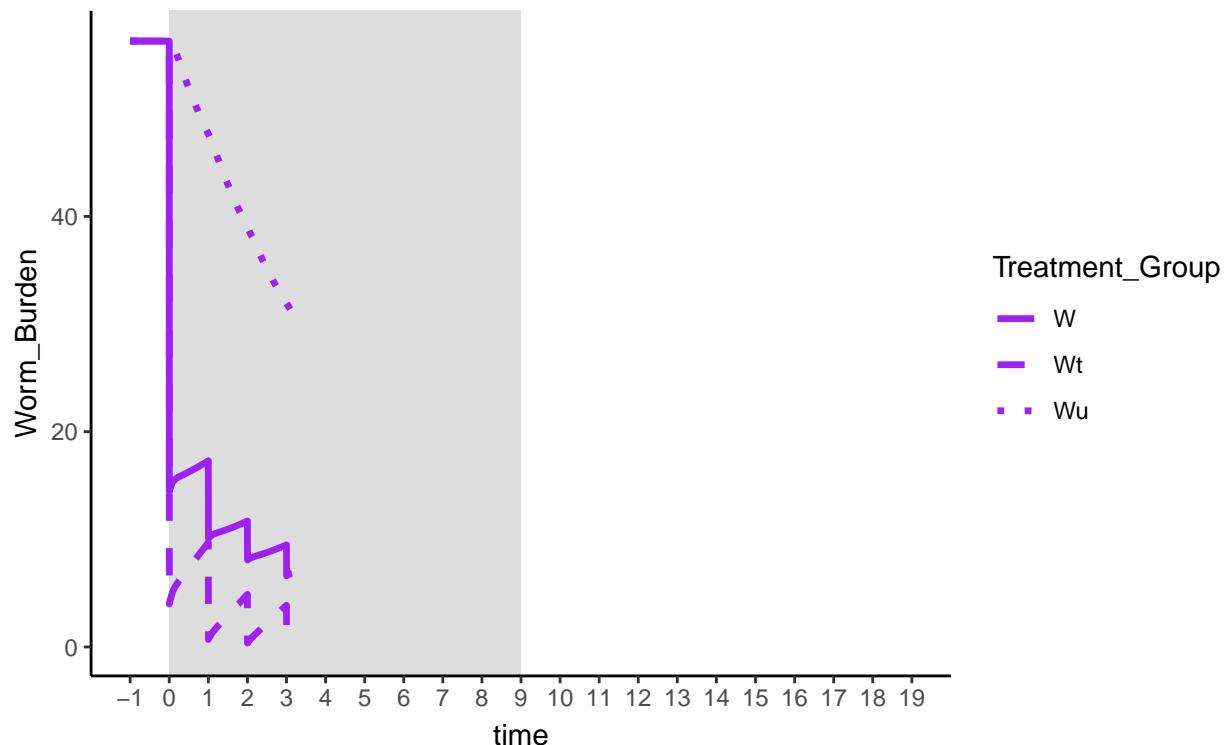
Human infection dynamics

Annual MDA for 10 years



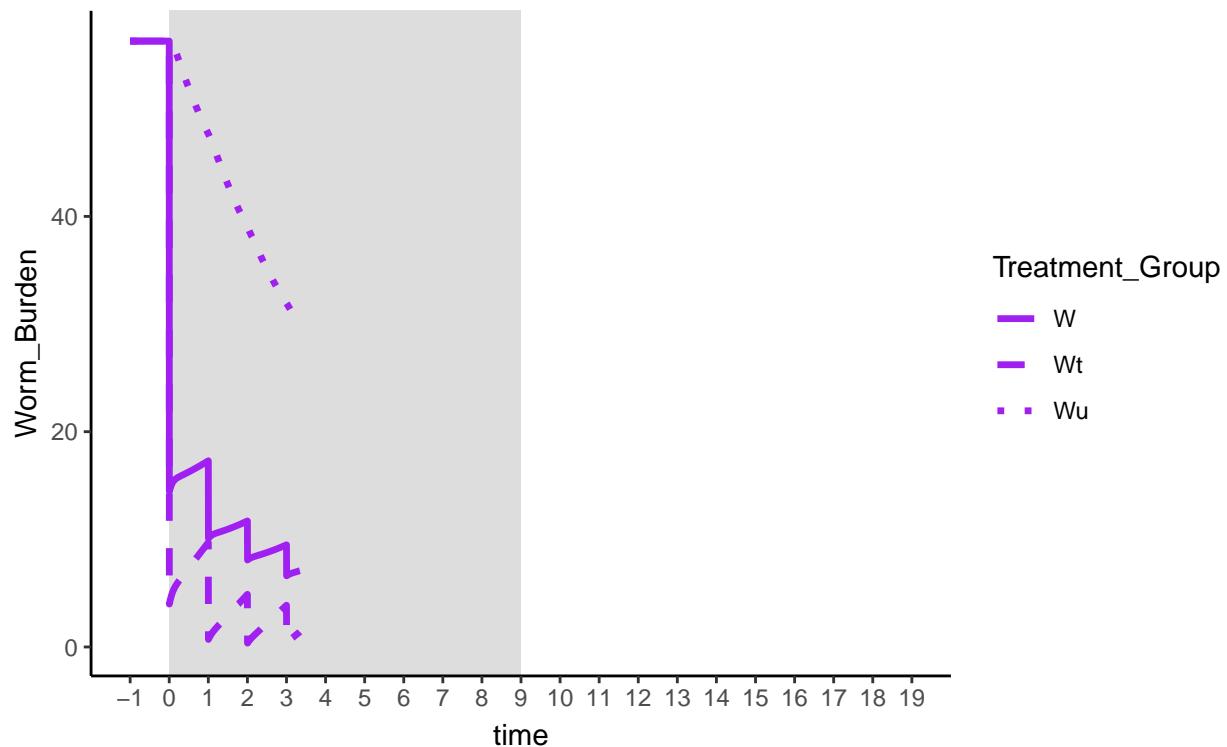
Human infection dynamics

Annual MDA for 10 years



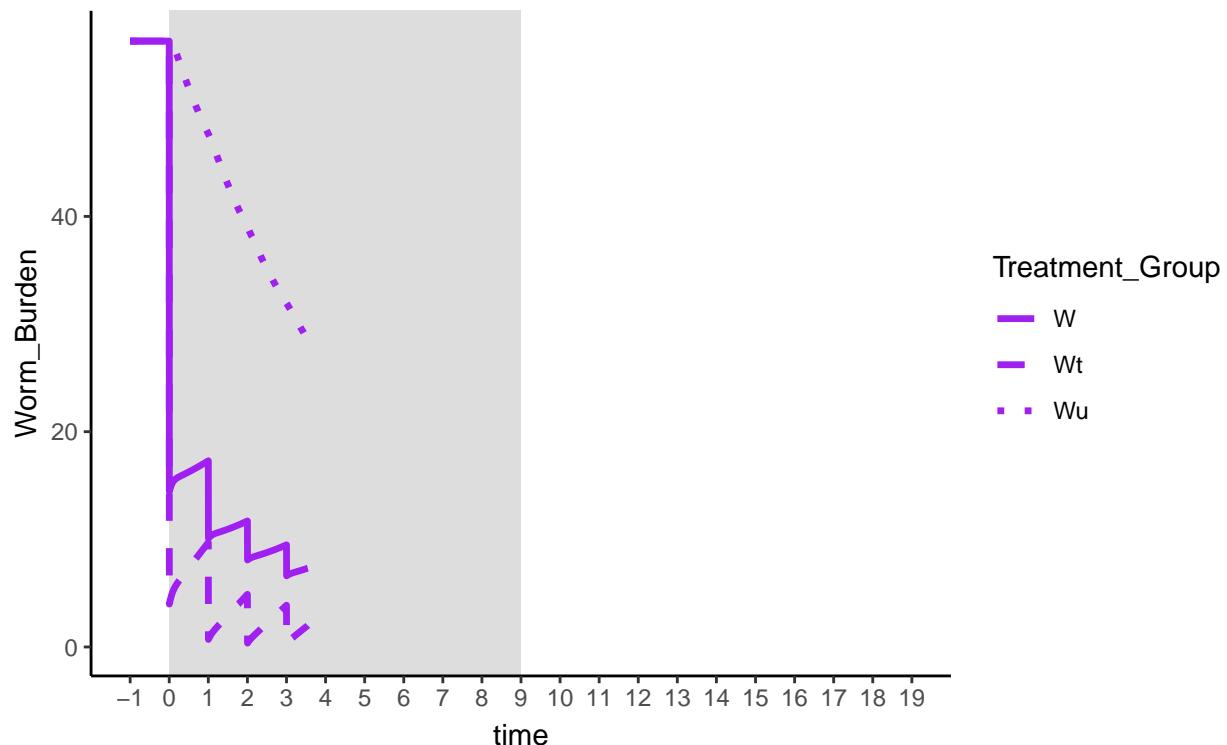
Human infection dynamics

Annual MDA for 10 years



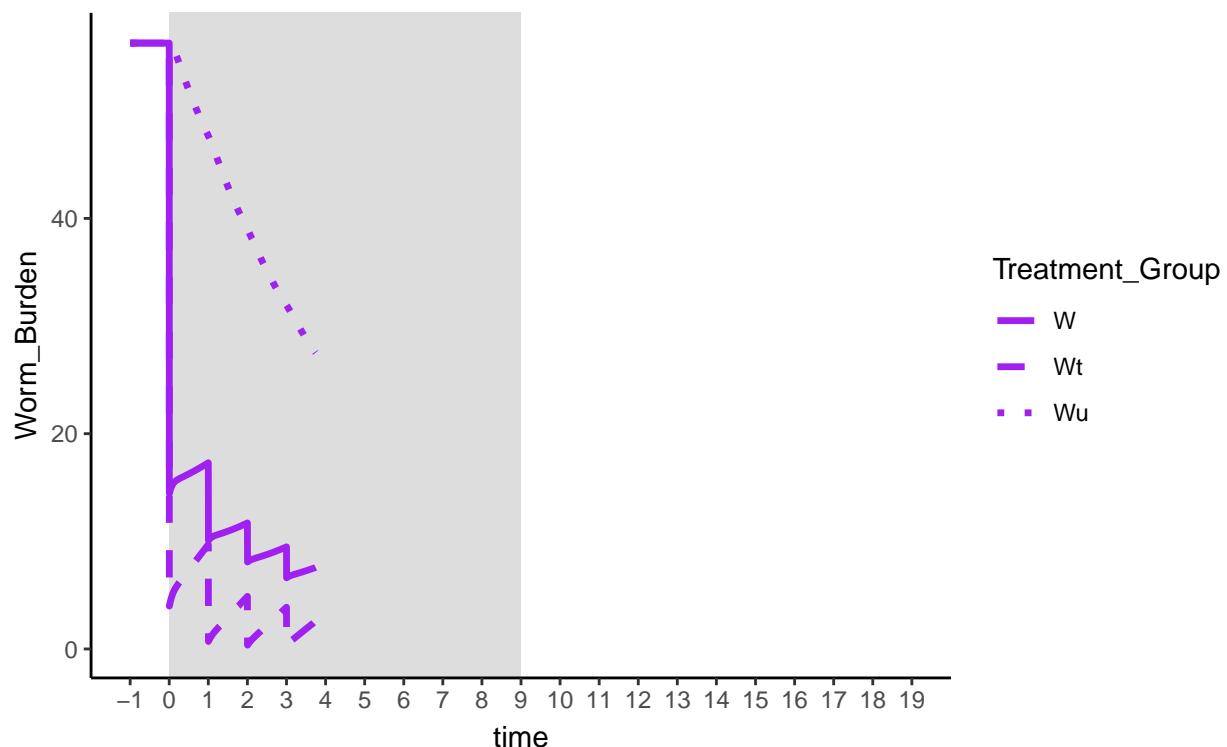
Human infection dynamics

Annual MDA for 10 years



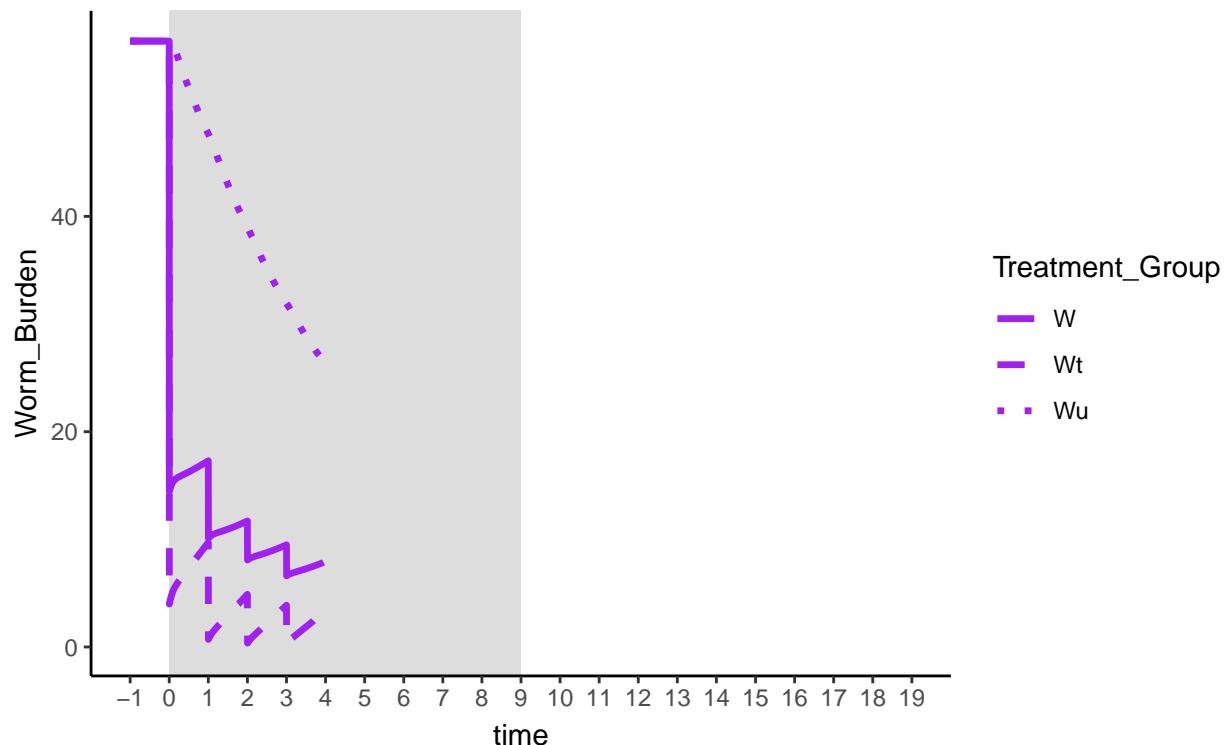
Human infection dynamics

Anual MDA for 10 years



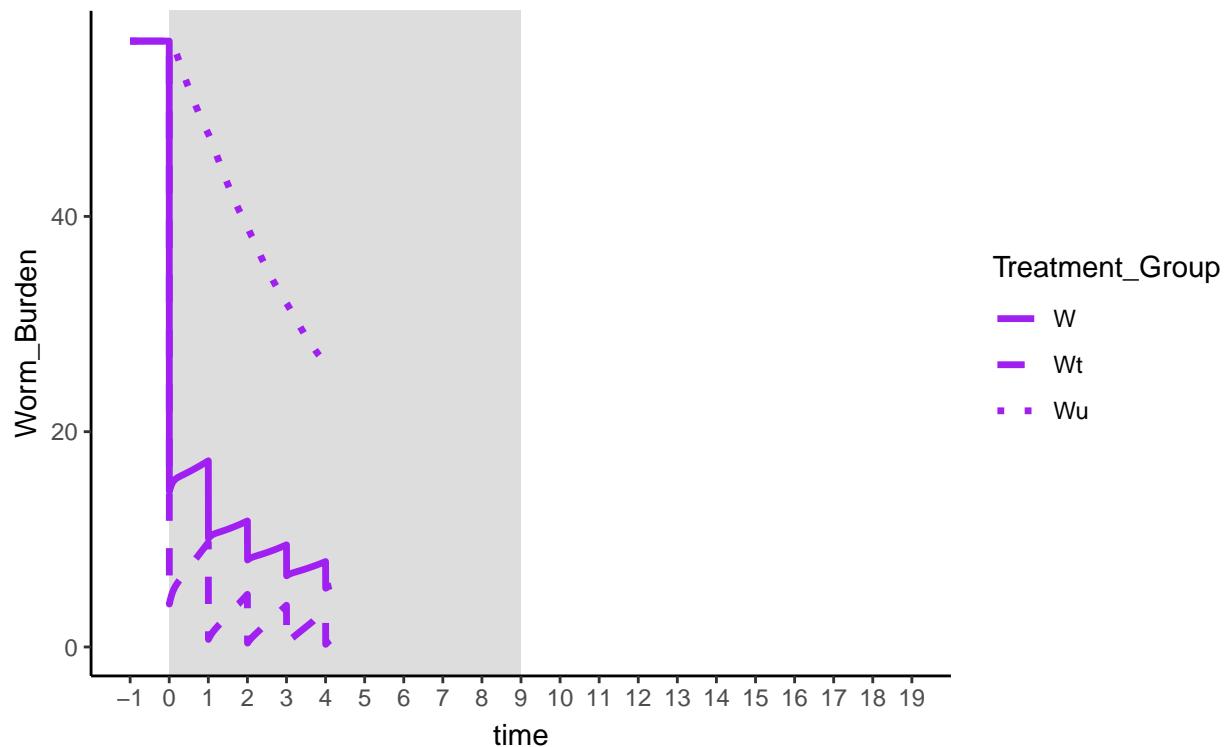
Human infection dynamics

Annual MDA for 10 years



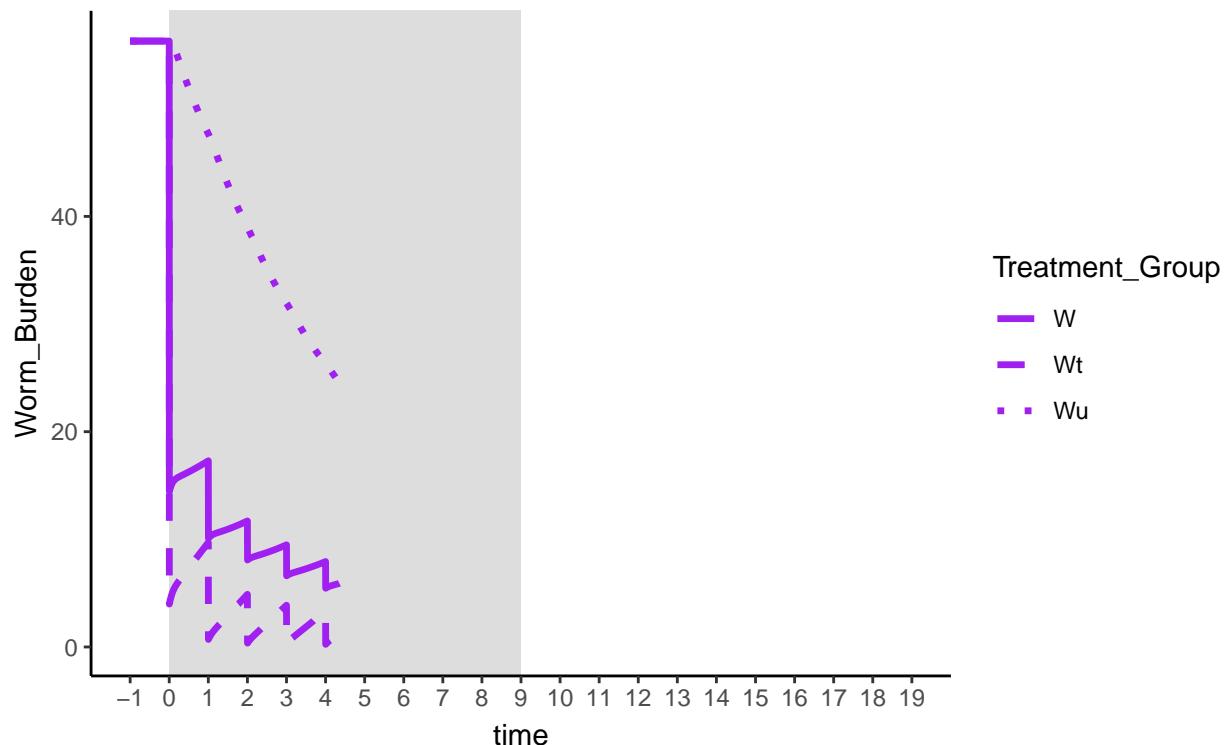
Human infection dynamics

Annual MDA for 10 years



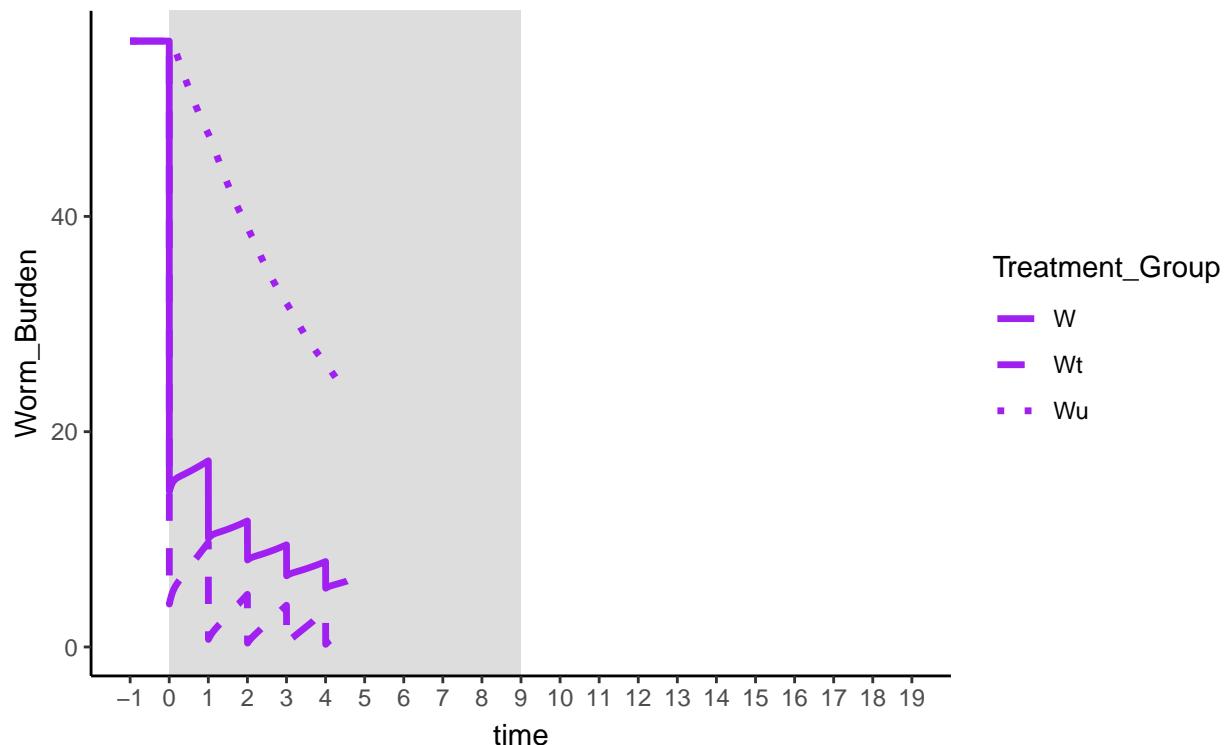
Human infection dynamics

Annual MDA for 10 years



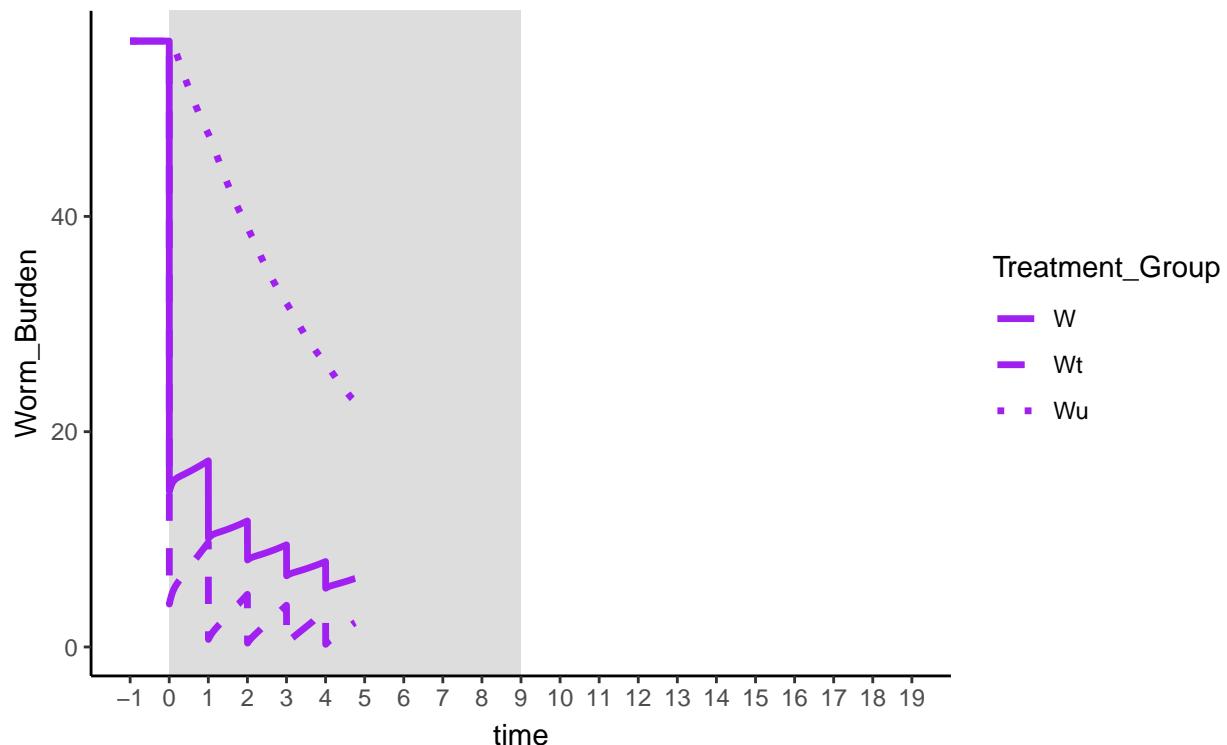
Human infection dynamics

Annual MDA for 10 years



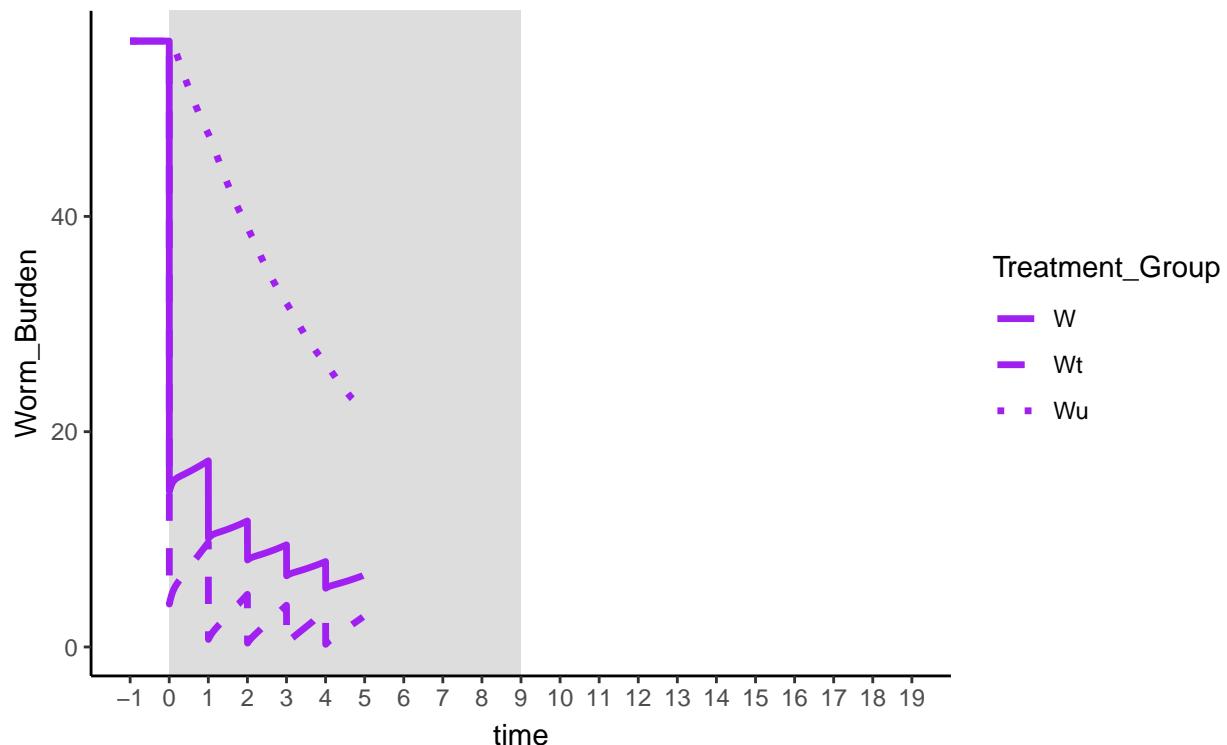
Human infection dynamics

Annual MDA for 10 years



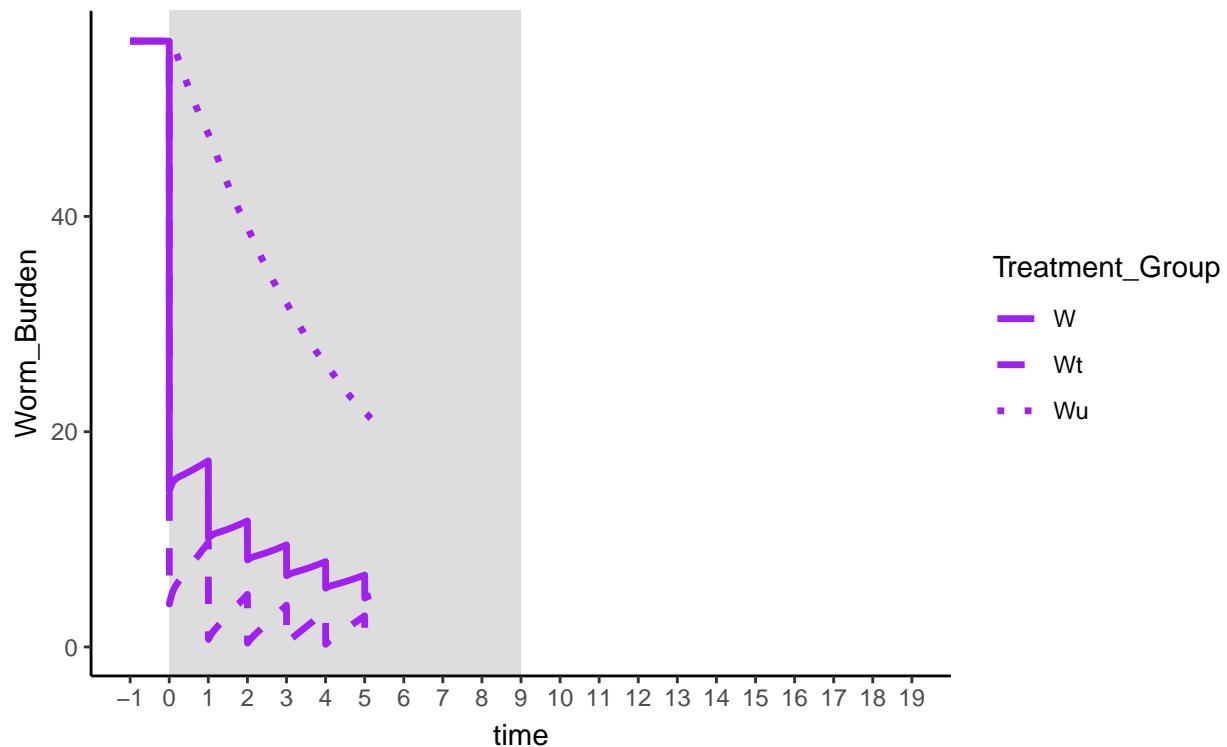
Human infection dynamics

Annual MDA for 10 years



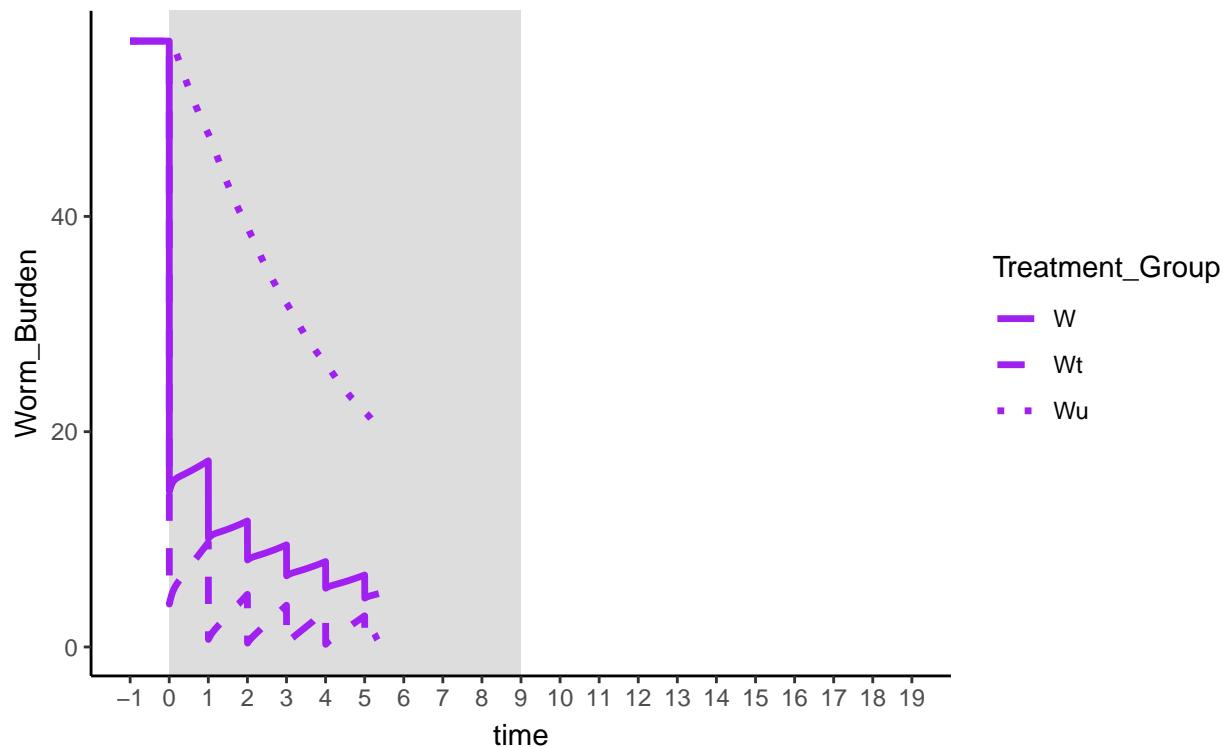
Human infection dynamics

Annual MDA for 10 years



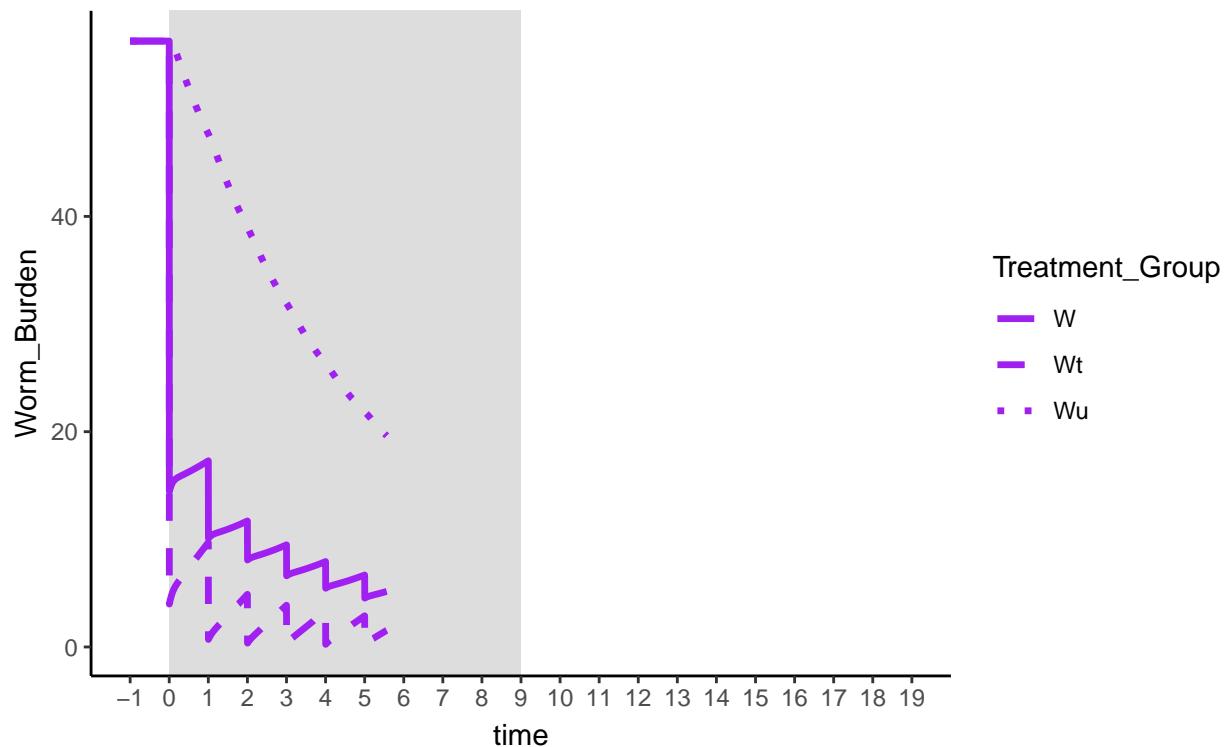
Human infection dynamics

Annual MDA for 10 years



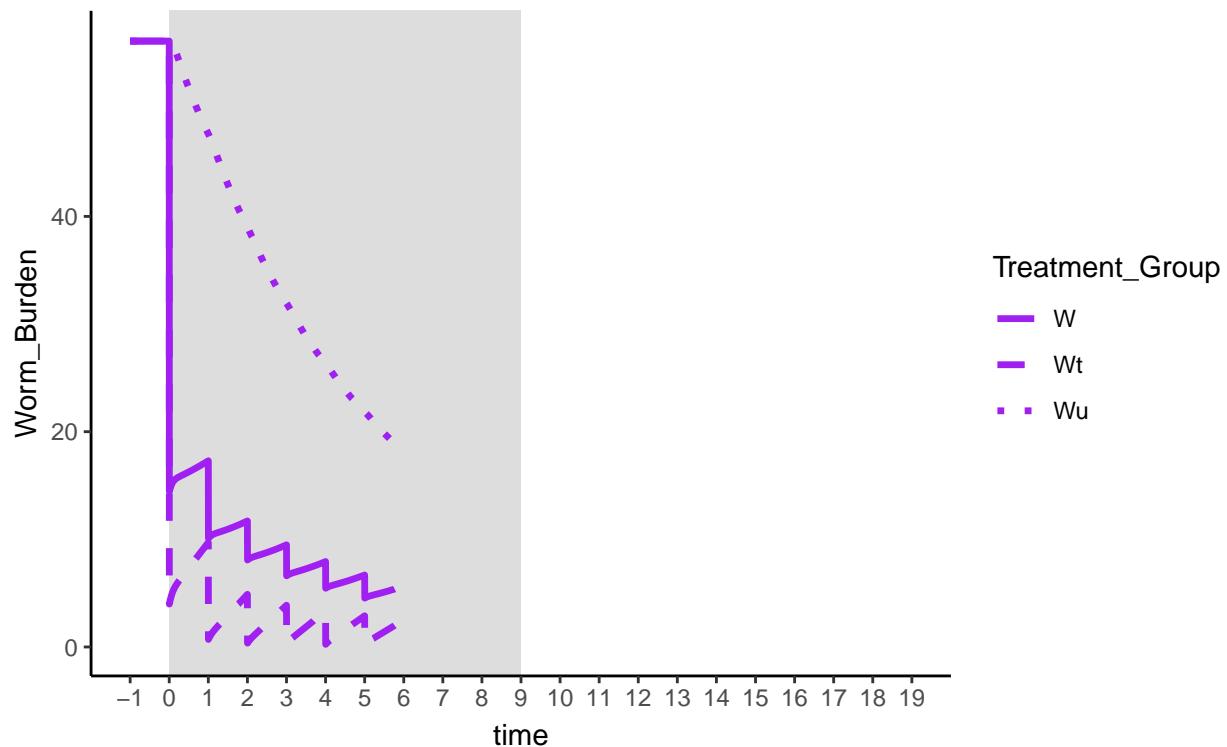
Human infection dynamics

Annual MDA for 10 years



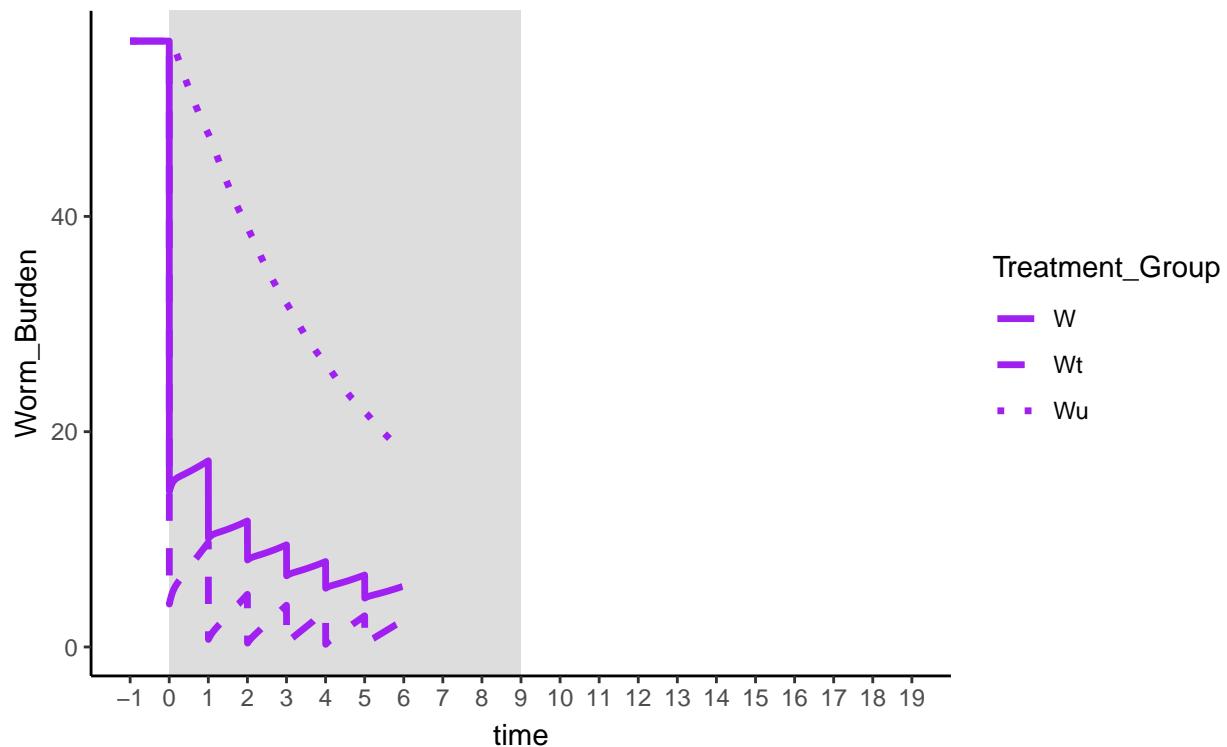
Human infection dynamics

Anual MDA for 10 years



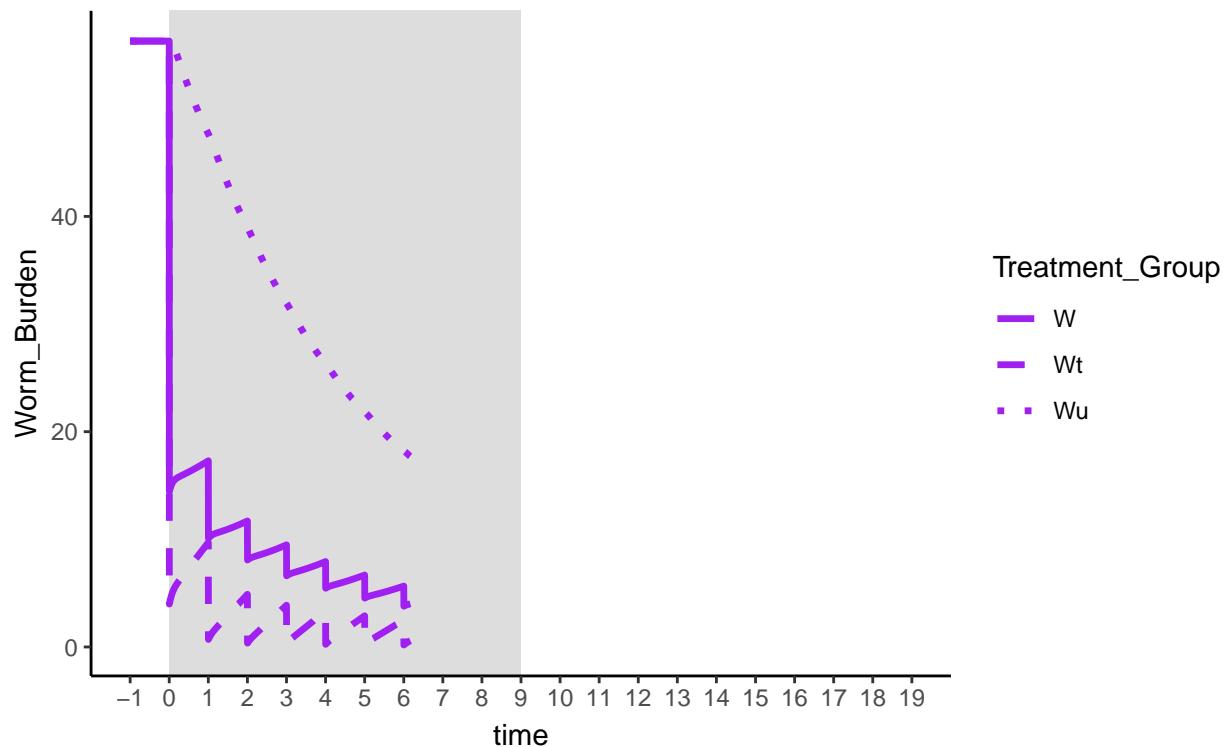
Human infection dynamics

Anual MDA for 10 years



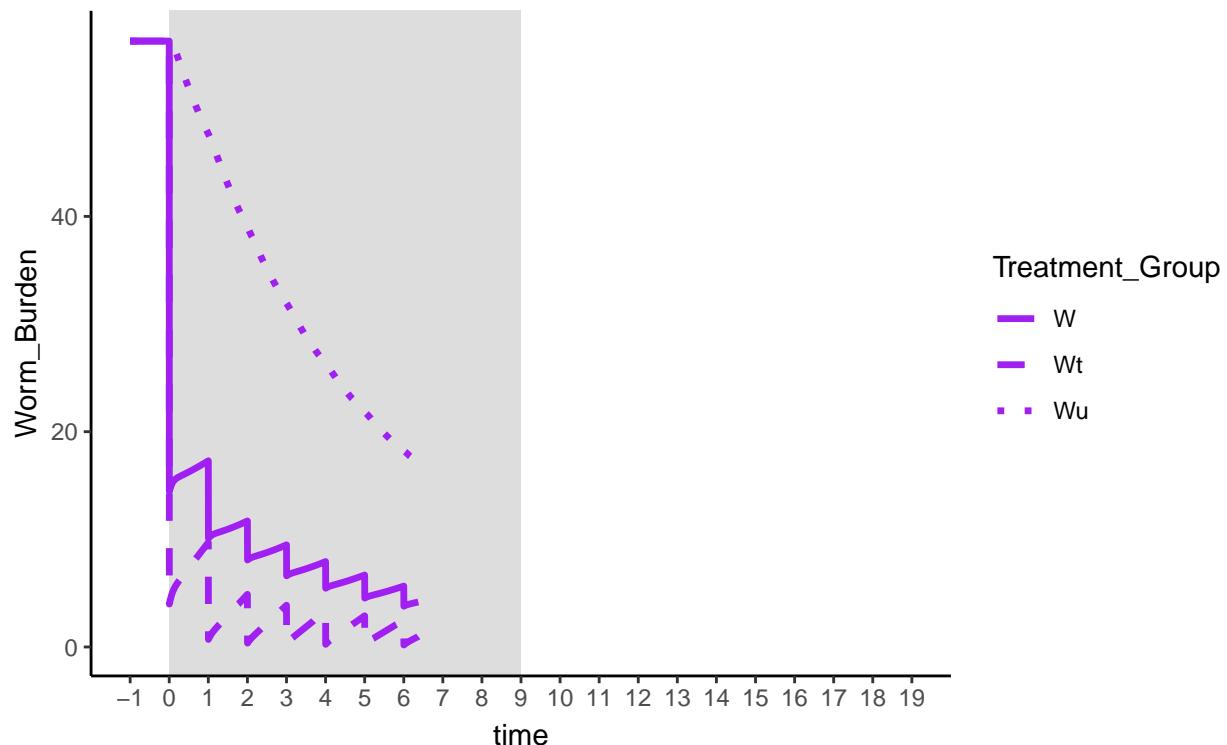
Human infection dynamics

Annual MDA for 10 years



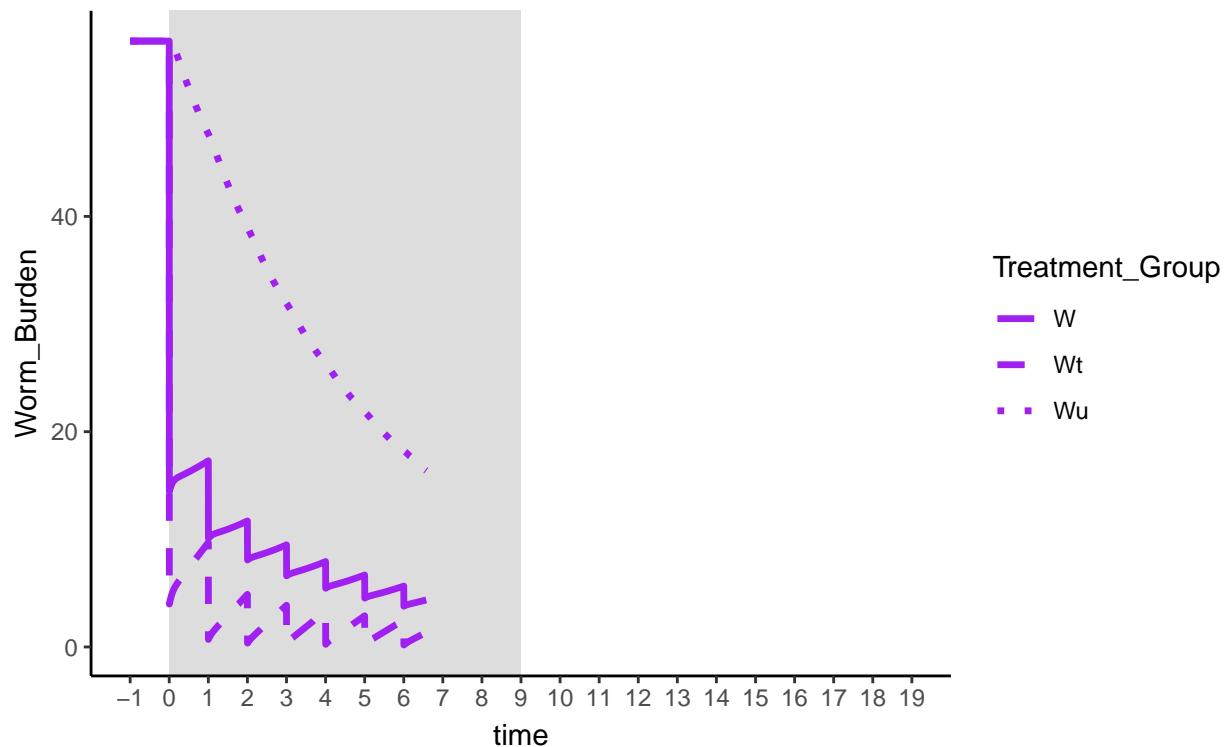
Human infection dynamics

Annual MDA for 10 years



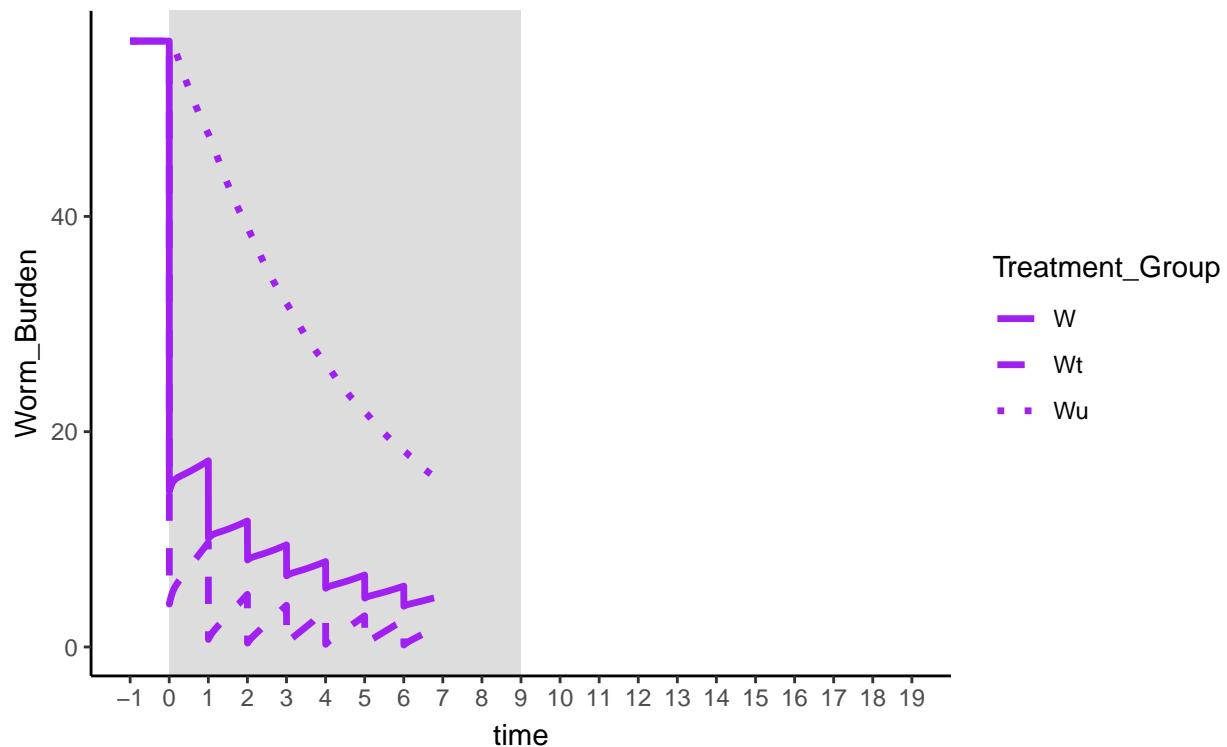
Human infection dynamics

Anual MDA for 10 years



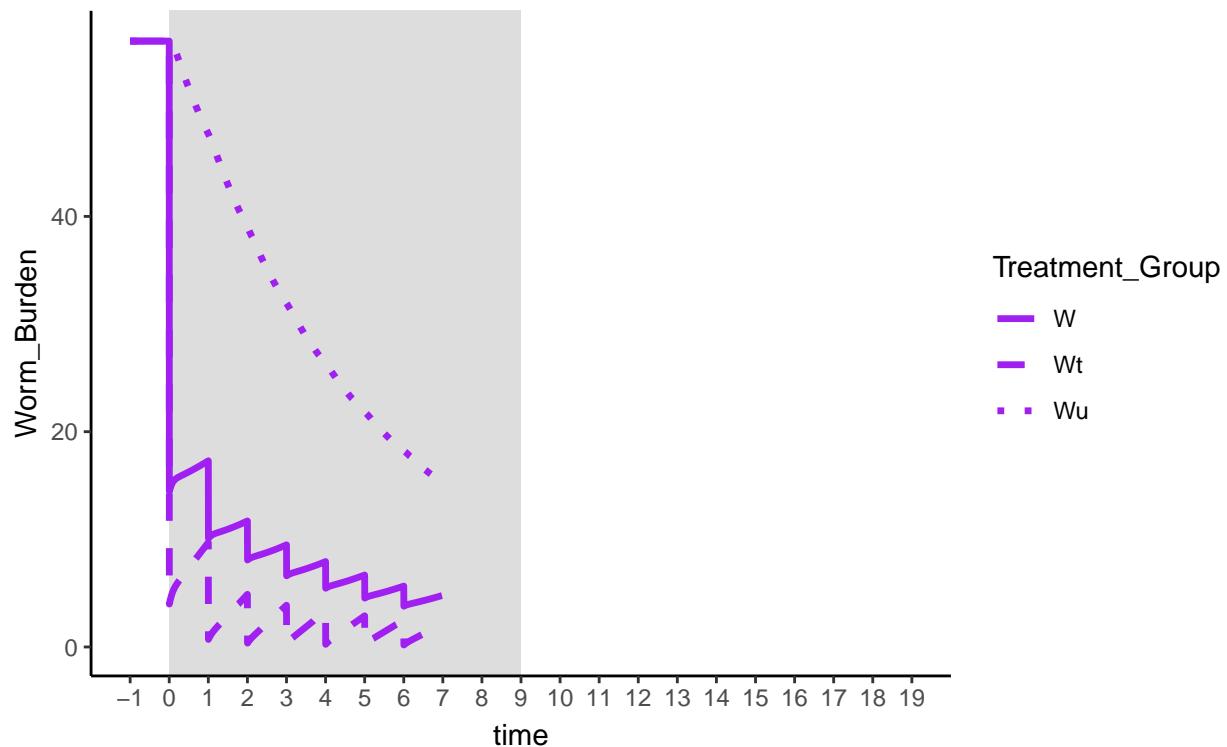
Human infection dynamics

Anual MDA for 10 years



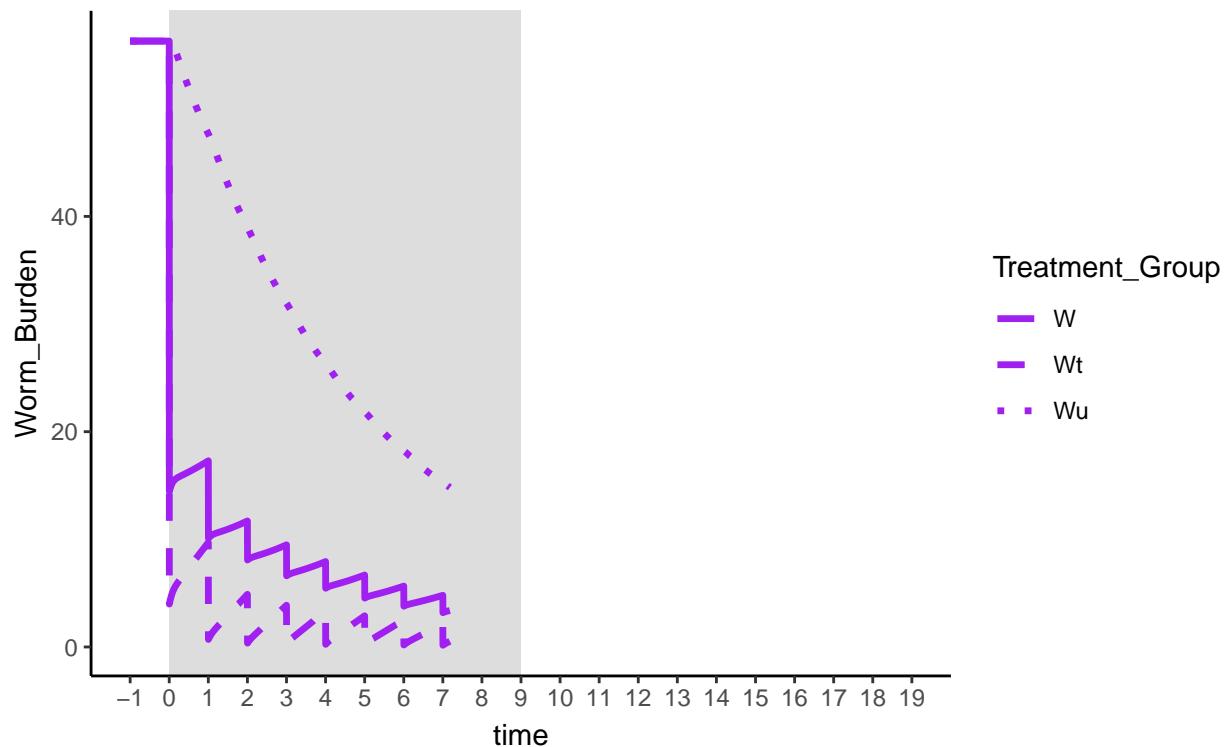
Human infection dynamics

Annual MDA for 10 years



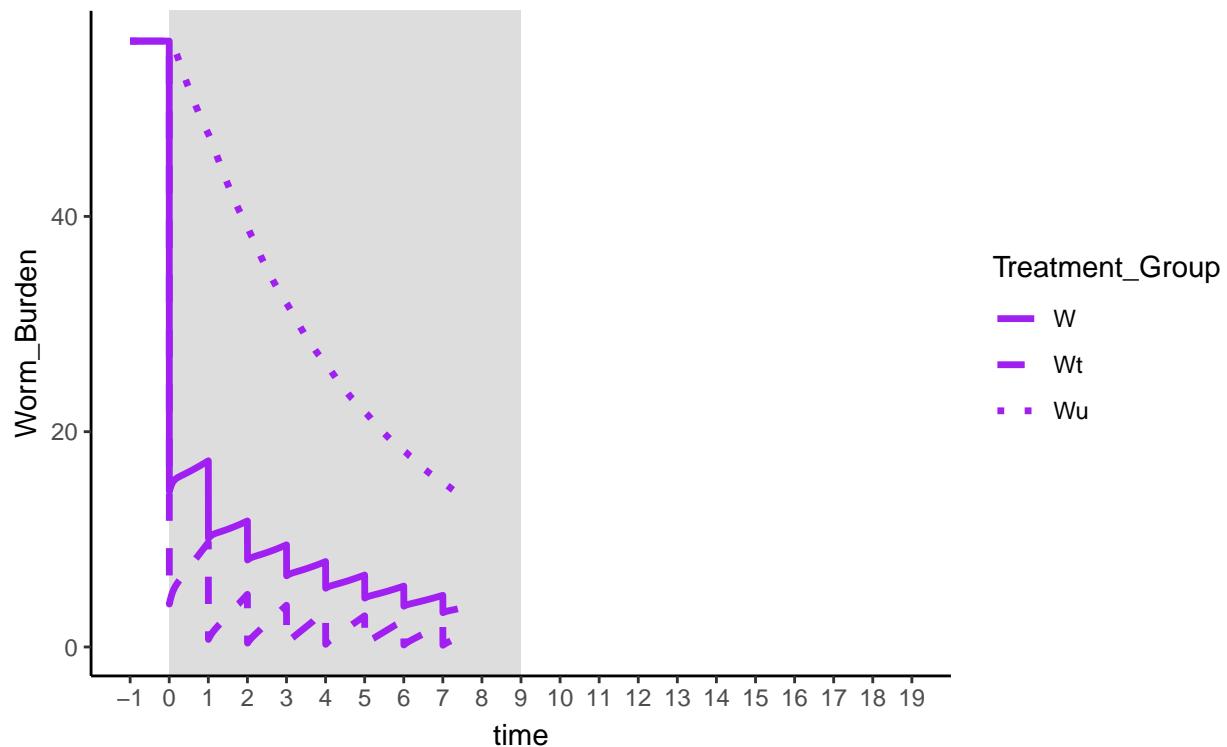
Human infection dynamics

Annual MDA for 10 years



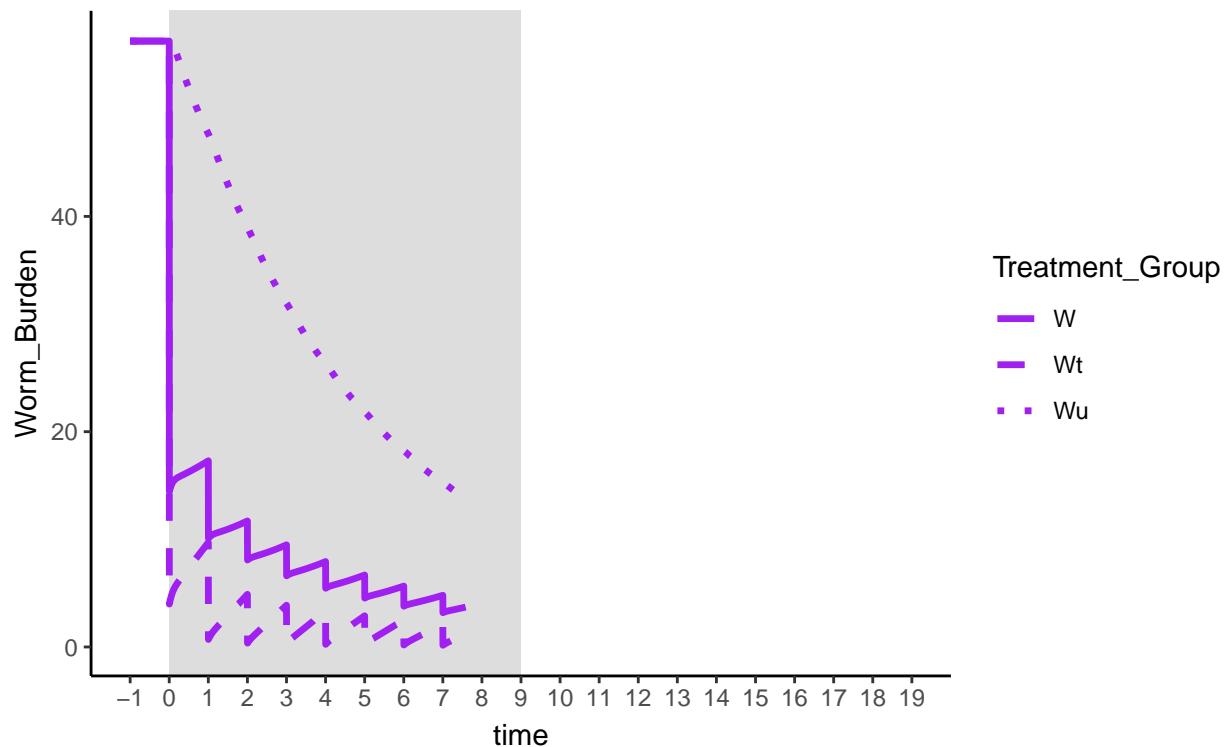
Human infection dynamics

Annual MDA for 10 years



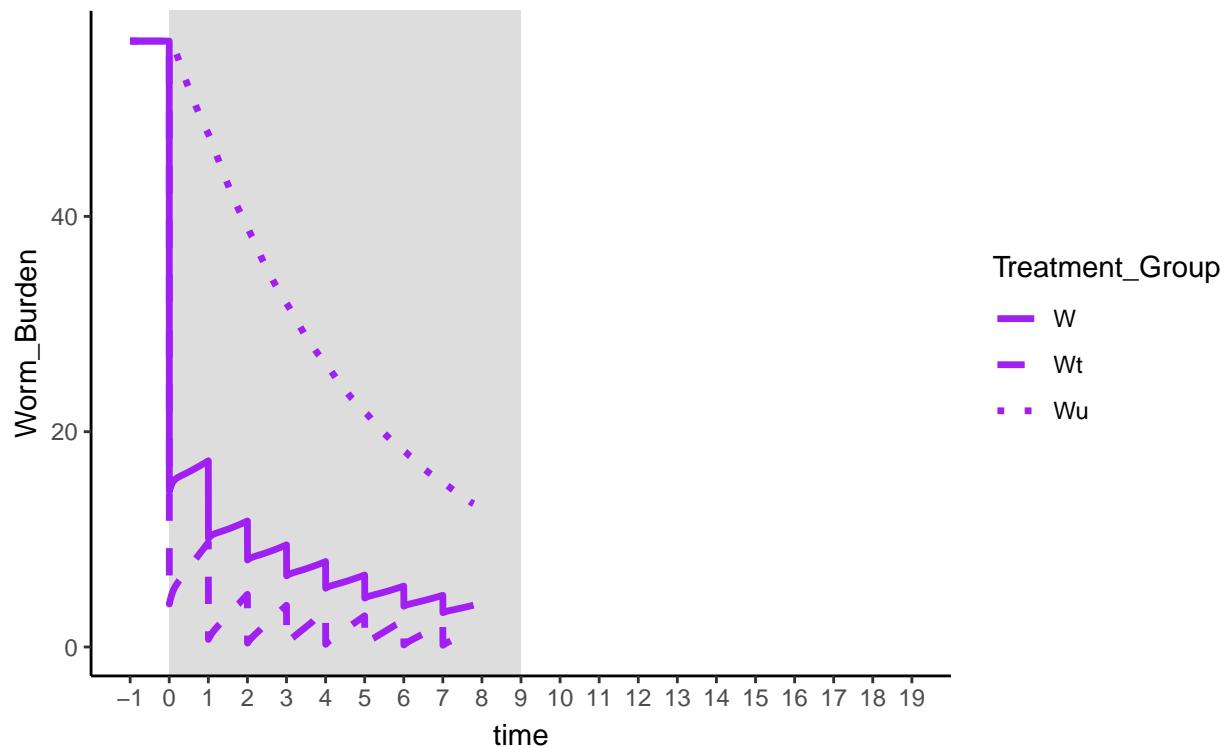
Human infection dynamics

Annual MDA for 10 years



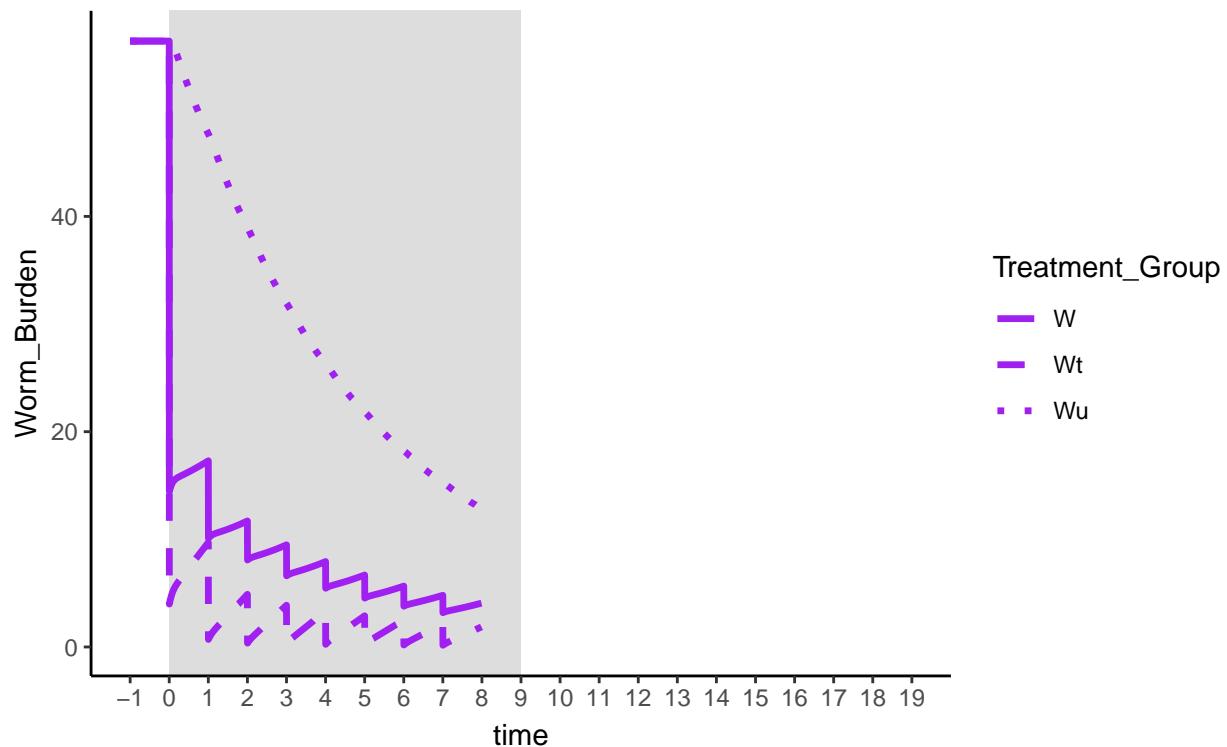
Human infection dynamics

Anual MDA for 10 years



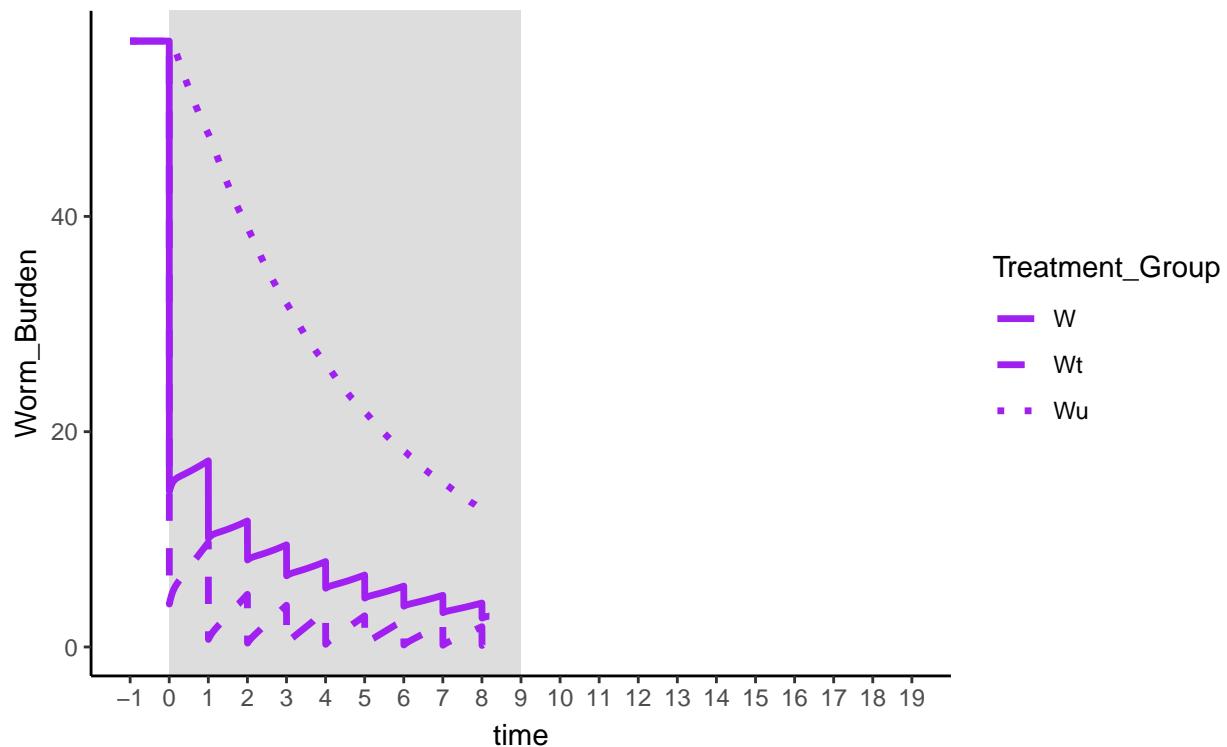
Human infection dynamics

Anual MDA for 10 years



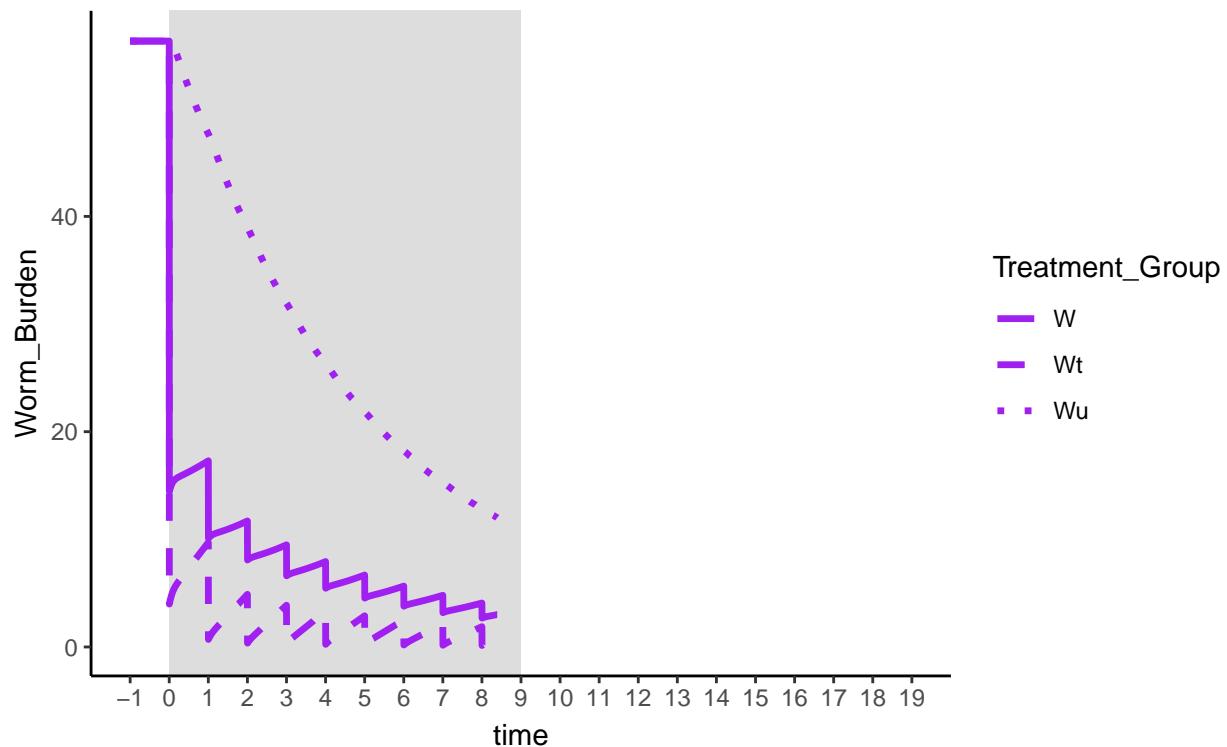
Human infection dynamics

Annual MDA for 10 years



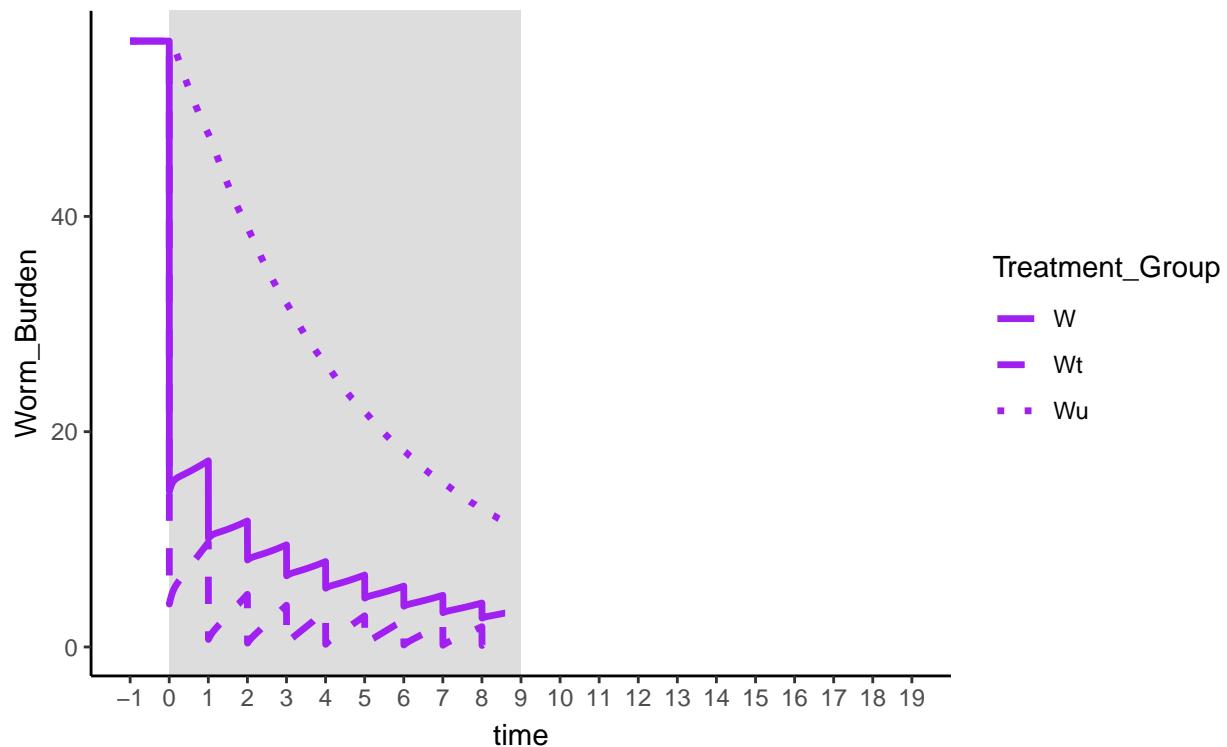
Human infection dynamics

Anual MDA for 10 years



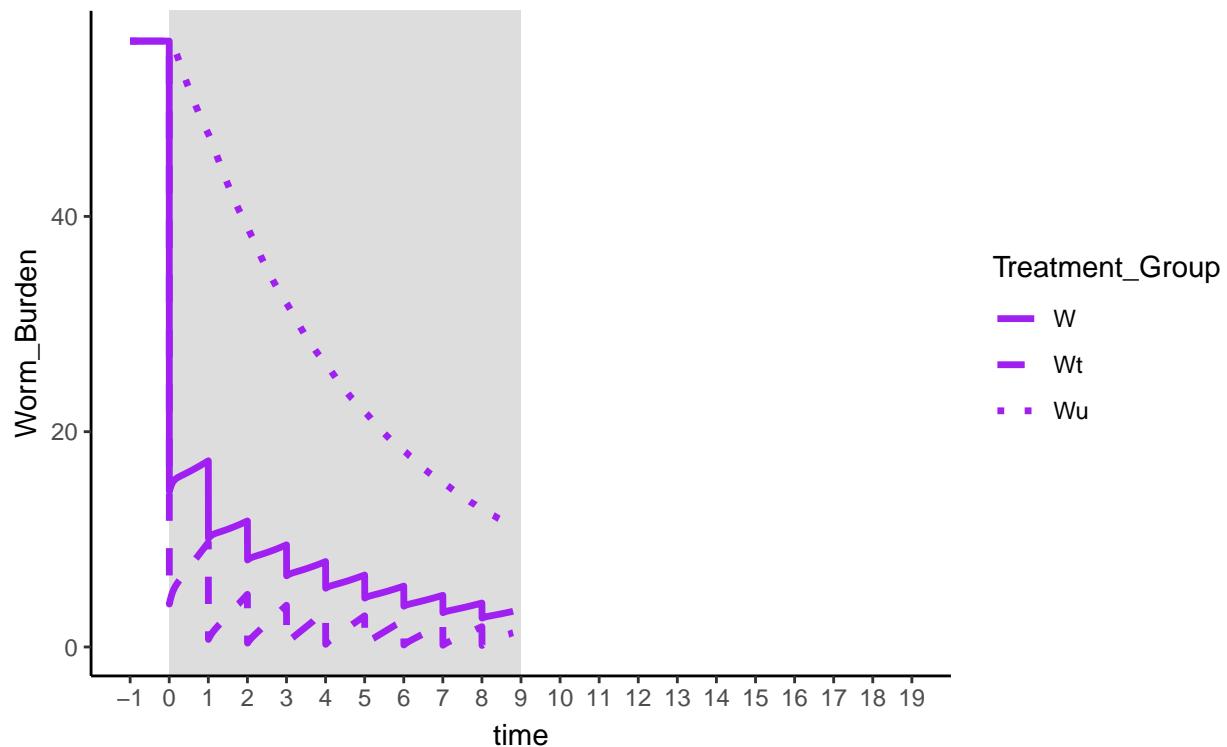
Human infection dynamics

Annual MDA for 10 years



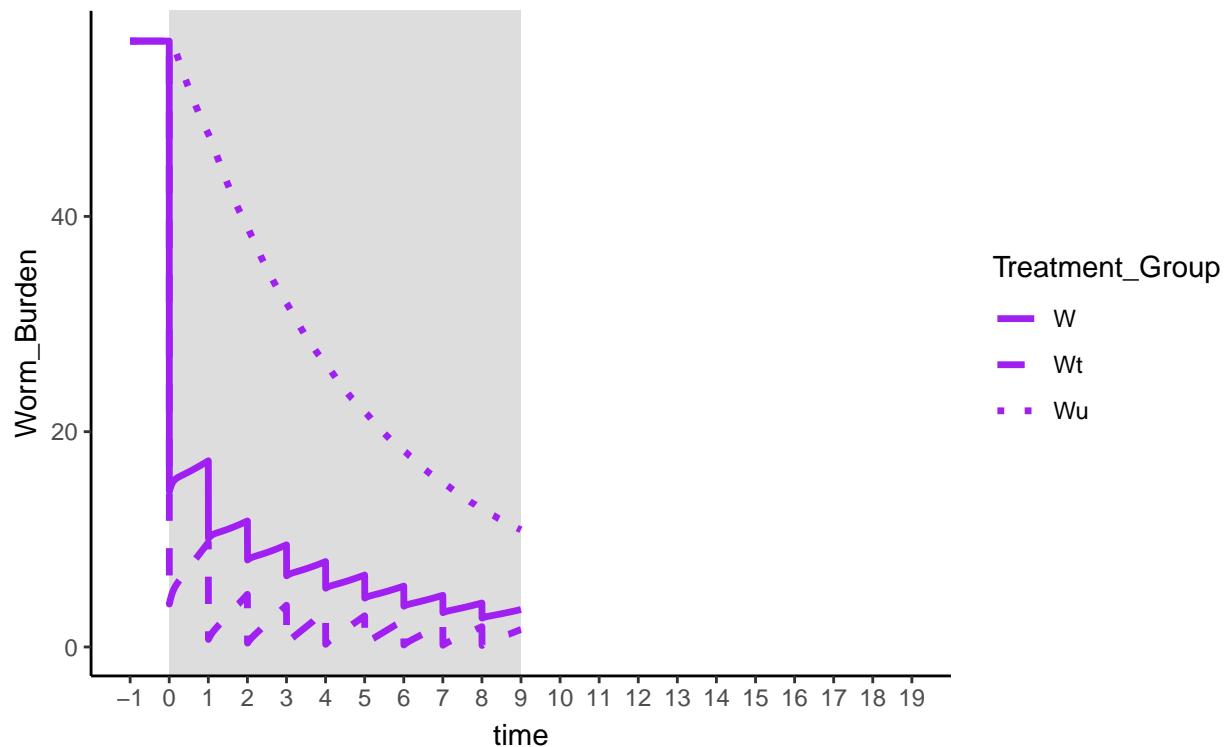
Human infection dynamics

Anual MDA for 10 years



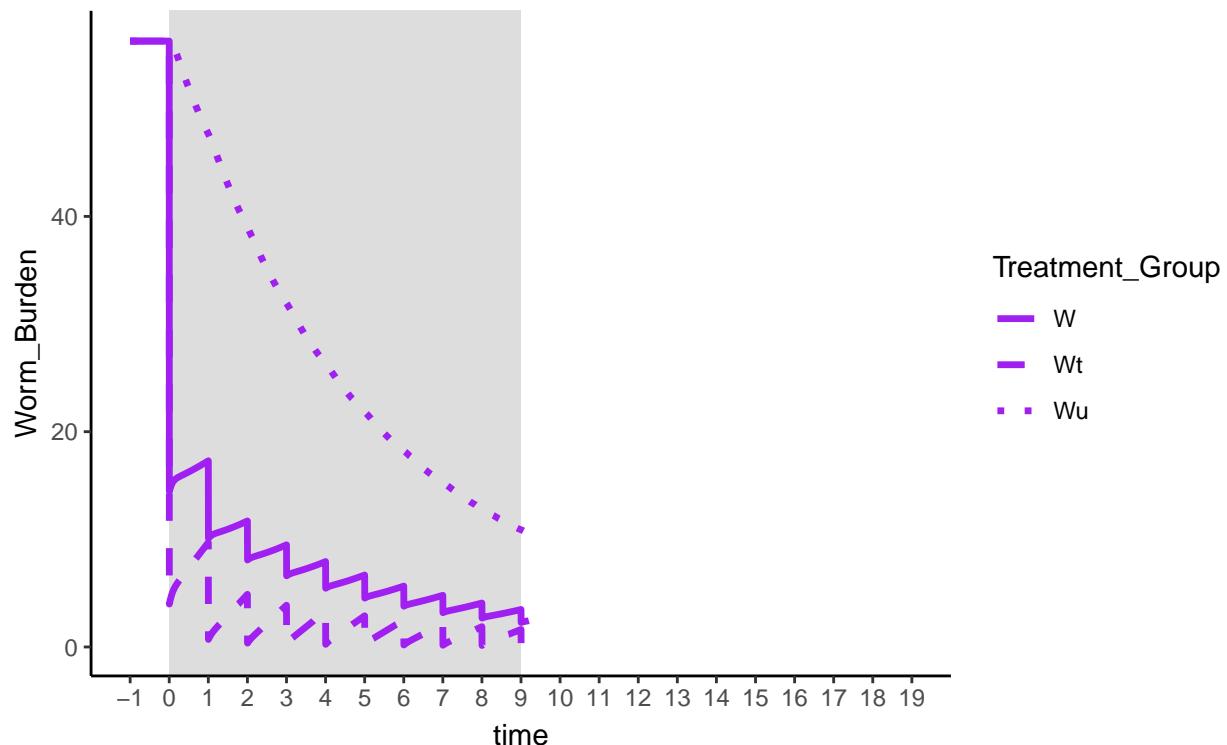
Human infection dynamics

Annual MDA for 10 years



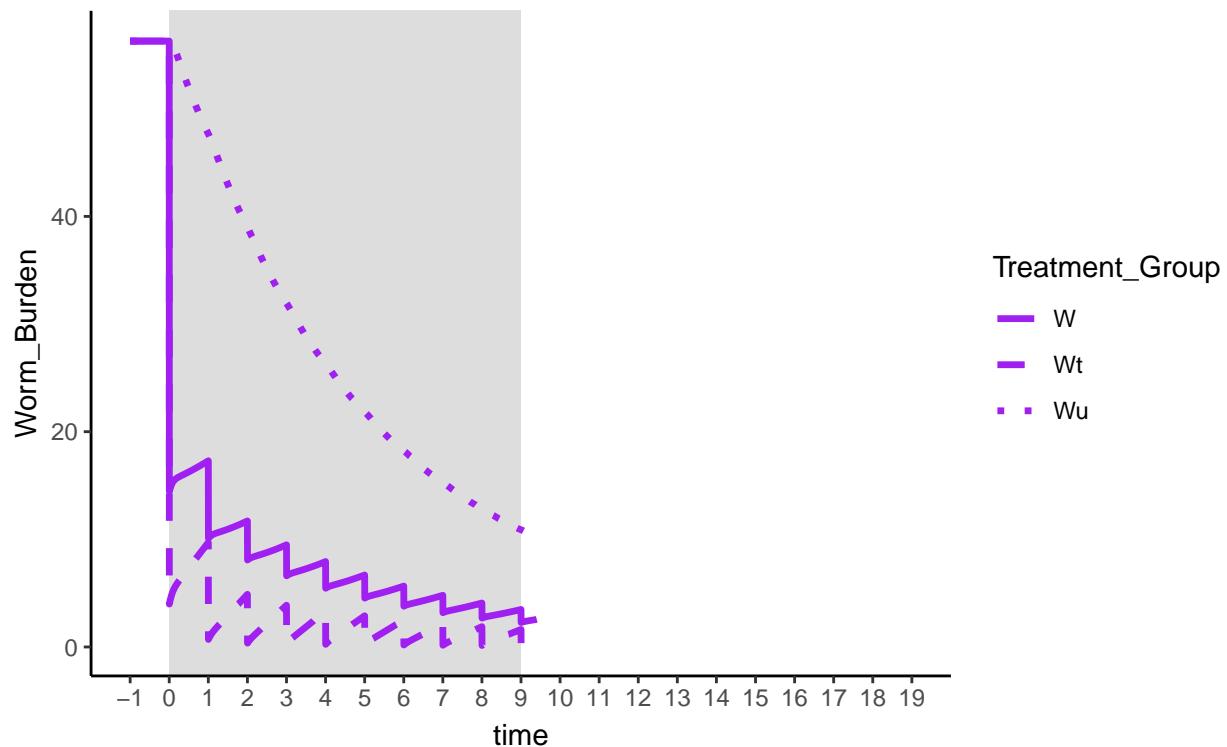
Human infection dynamics

Annual MDA for 10 years



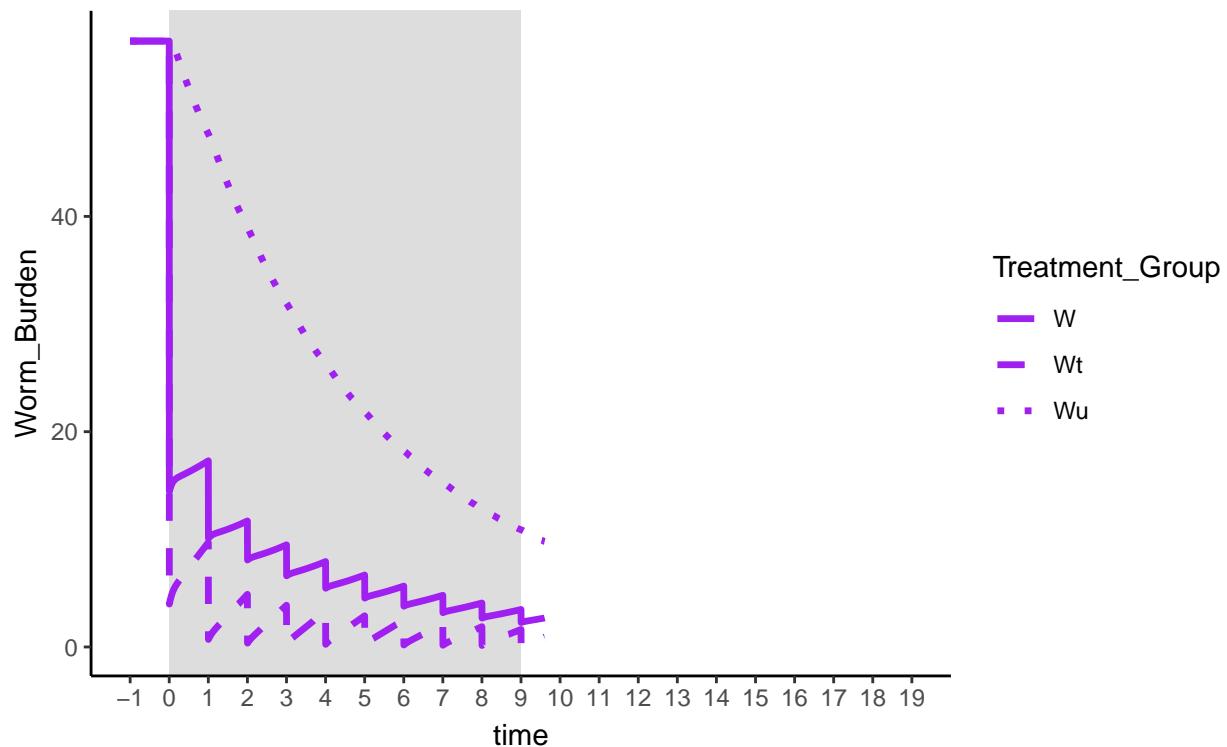
Human infection dynamics

Annual MDA for 10 years



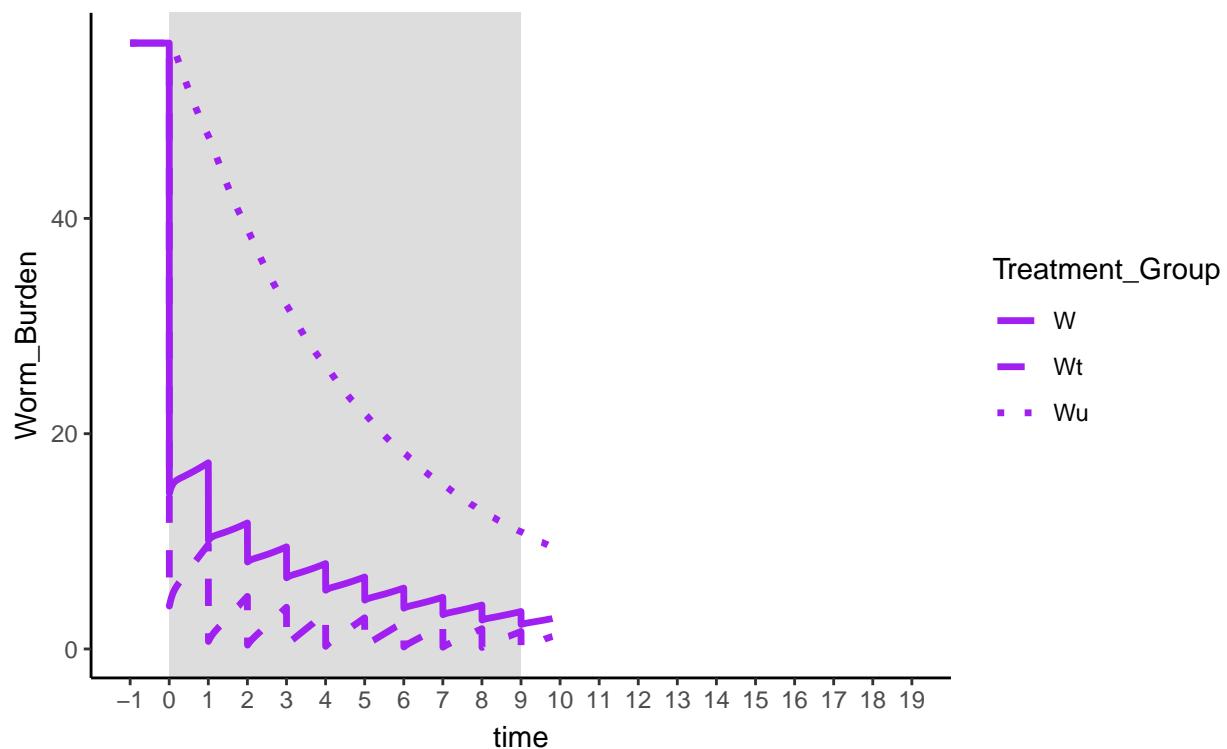
Human infection dynamics

Anual MDA for 10 years



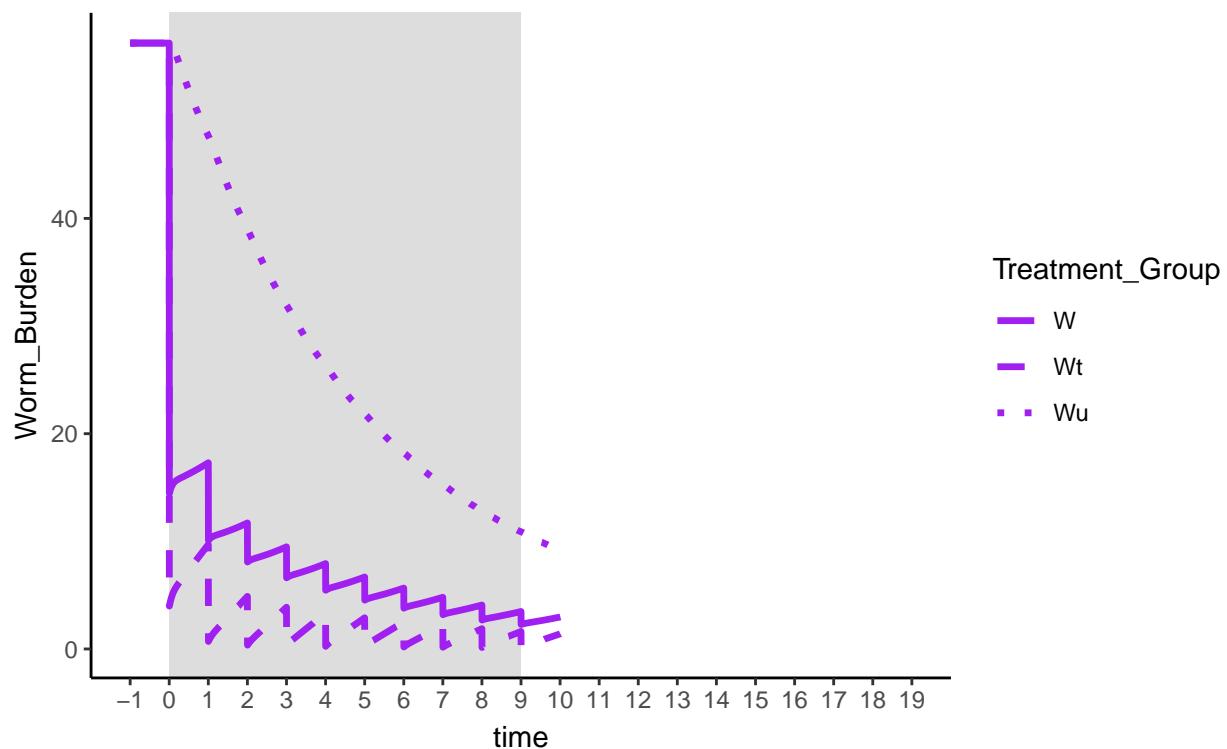
Human infection dynamics

Anual MDA for 10 years



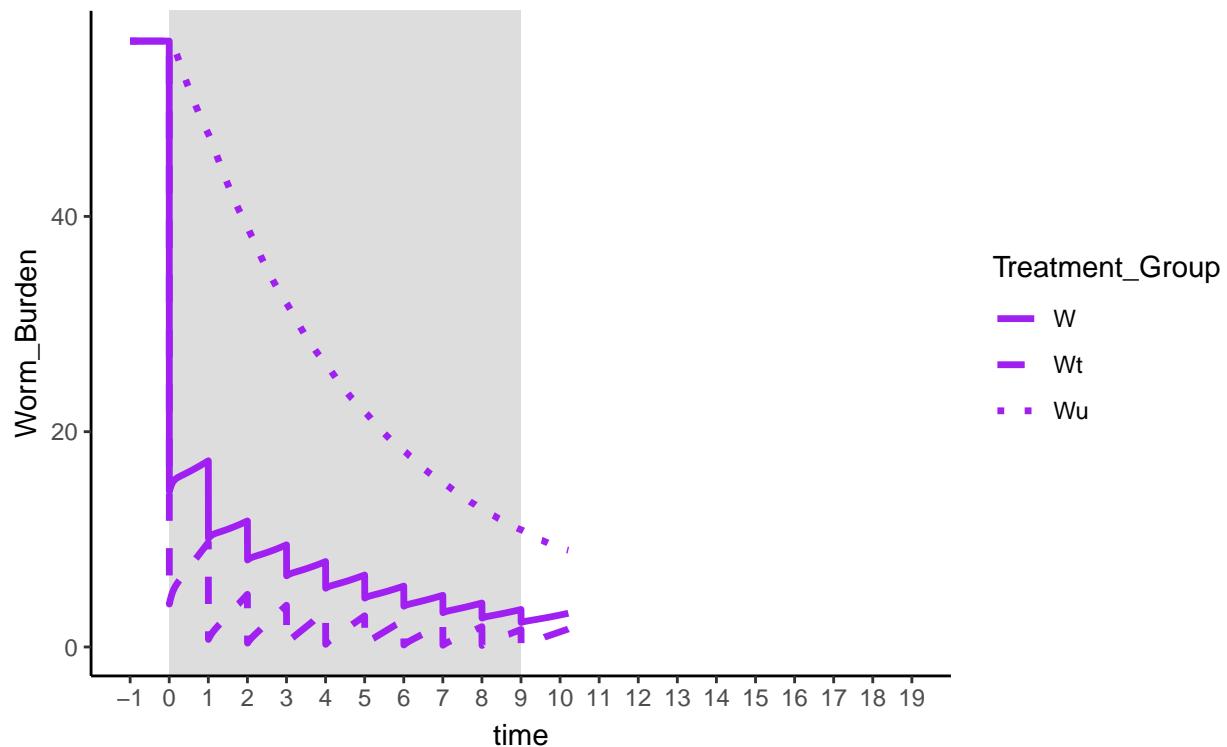
Human infection dynamics

Anual MDA for 10 years



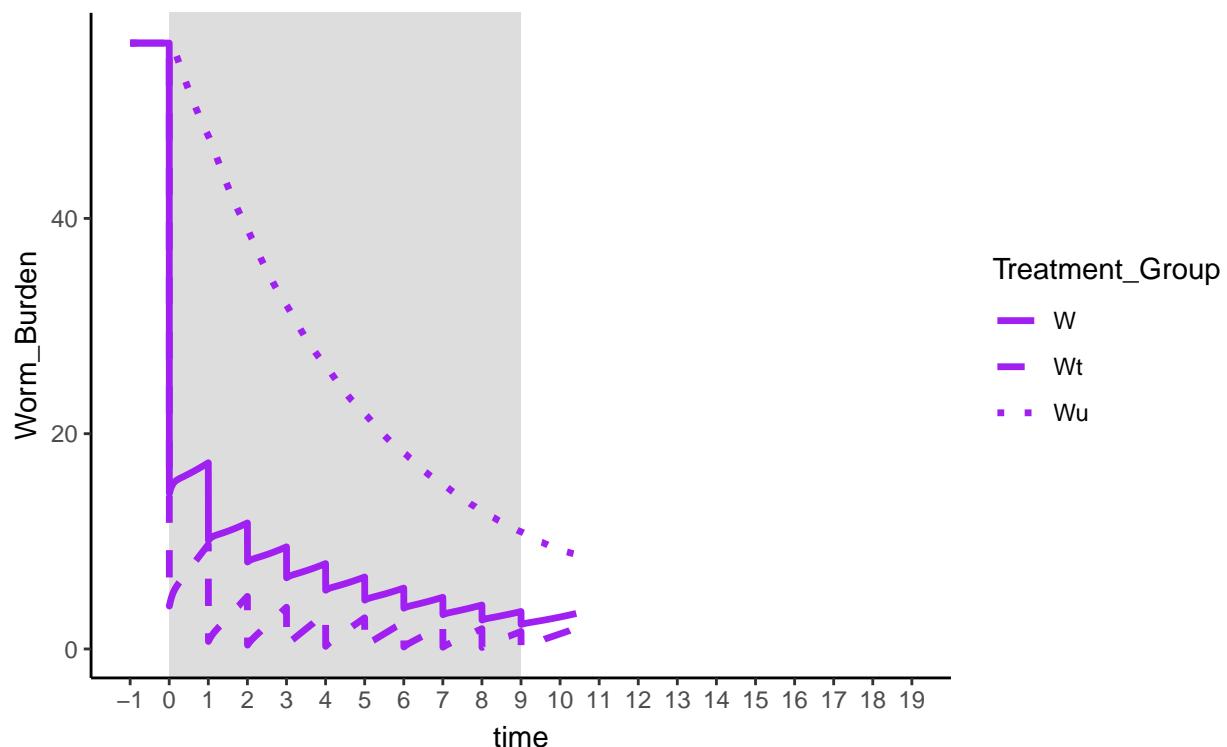
Human infection dynamics

Annual MDA for 10 years



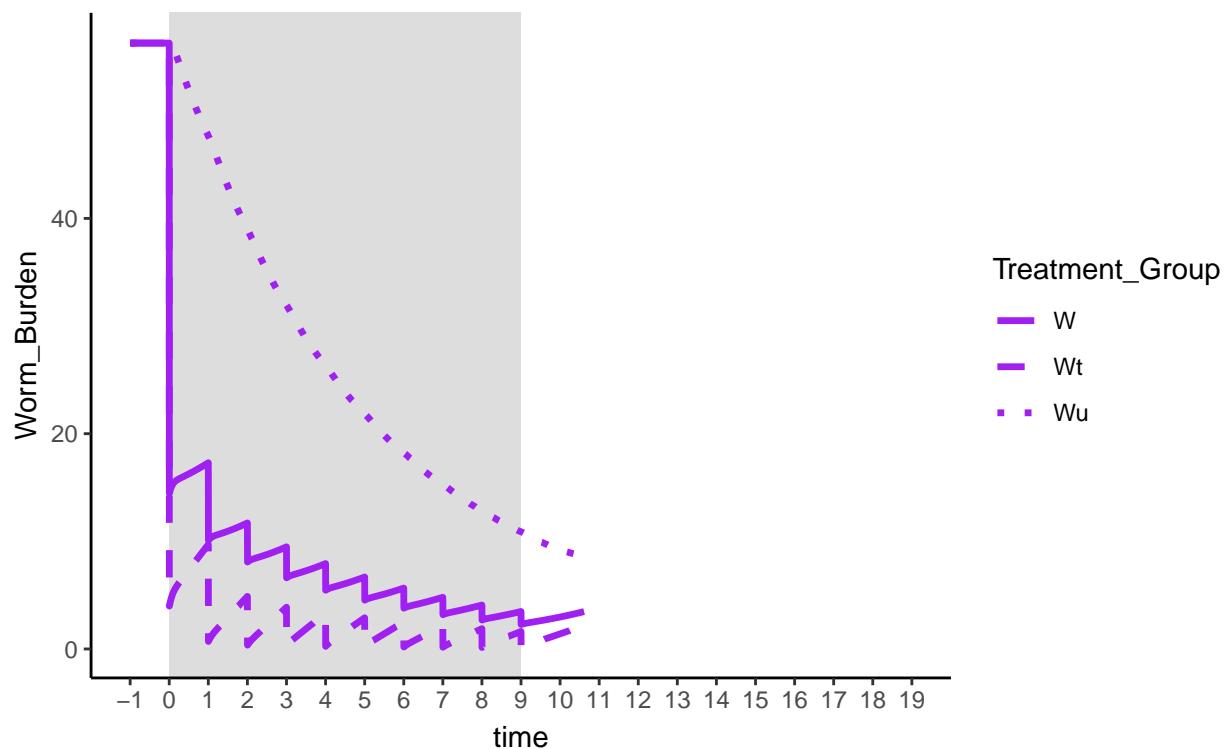
Human infection dynamics

Anual MDA for 10 years



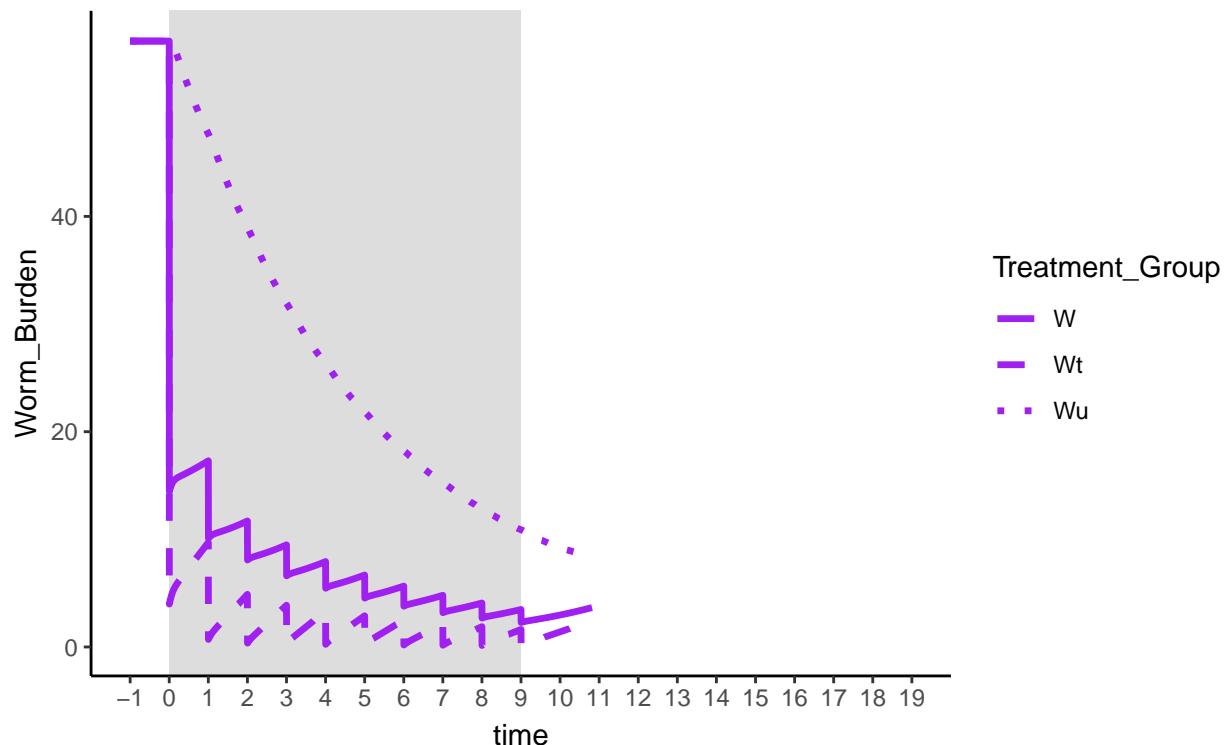
Human infection dynamics

Anual MDA for 10 years



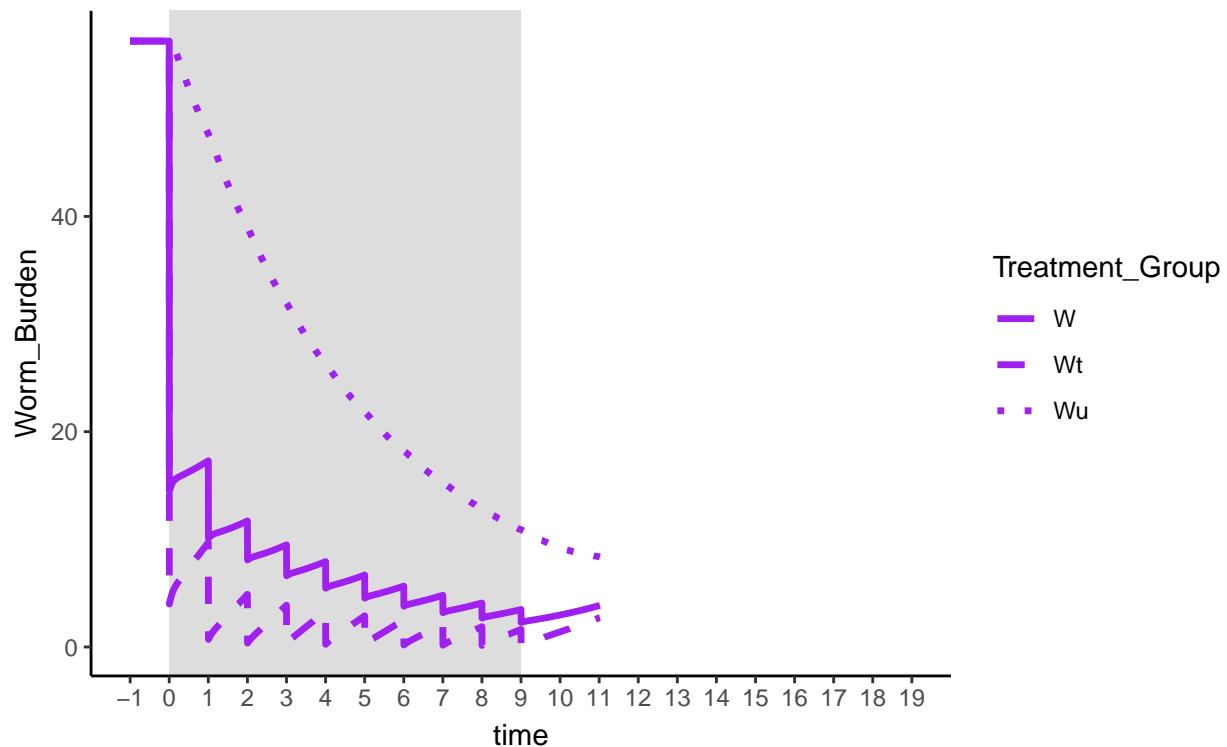
Human infection dynamics

Anual MDA for 10 years



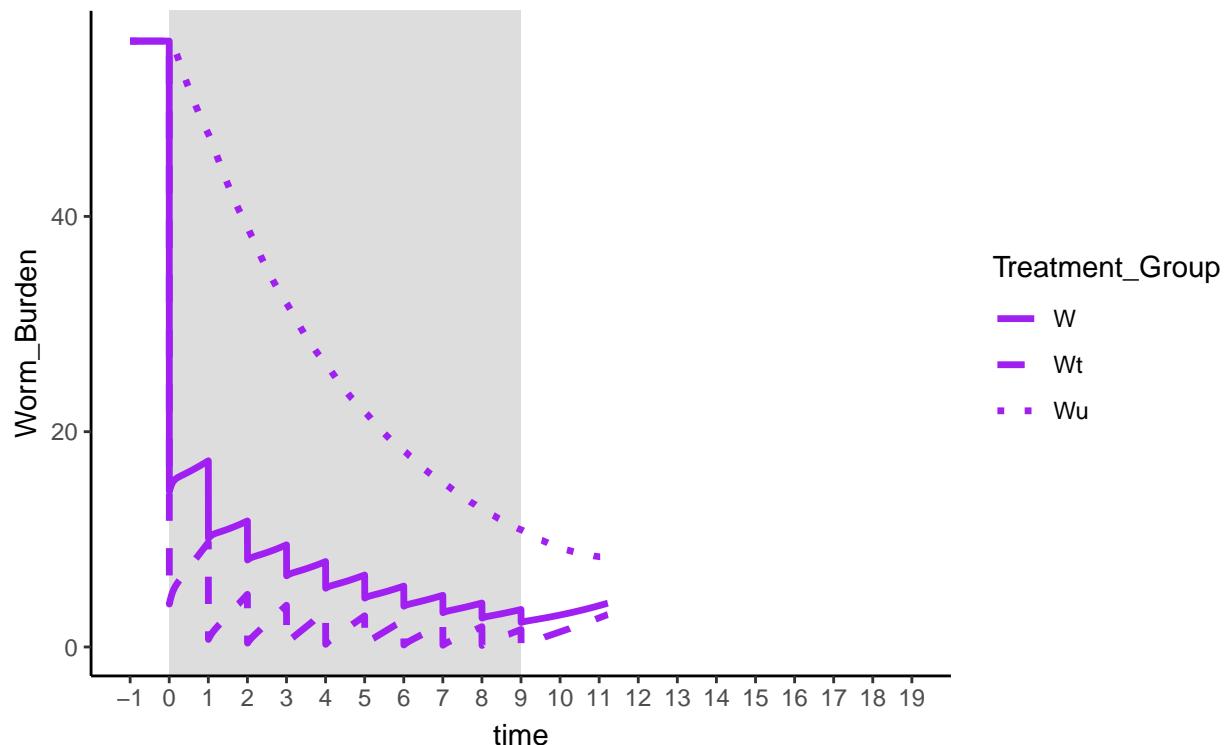
Human infection dynamics

Annual MDA for 10 years



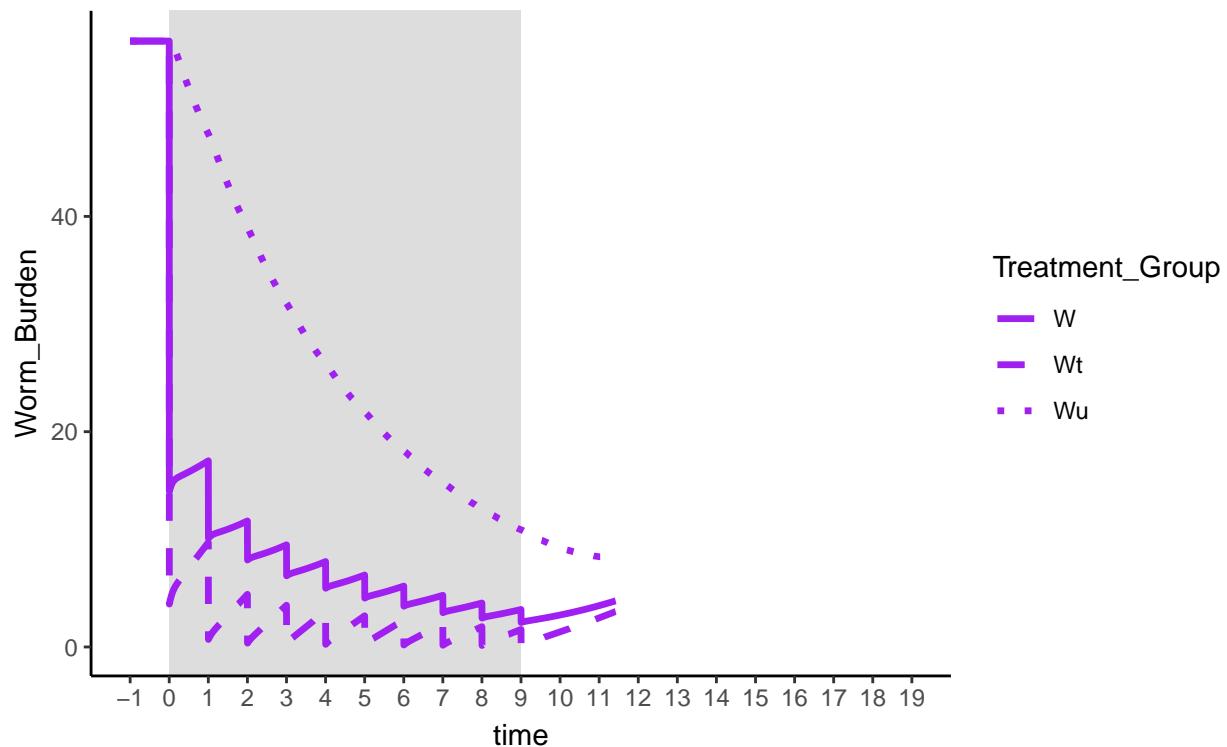
Human infection dynamics

Annual MDA for 10 years



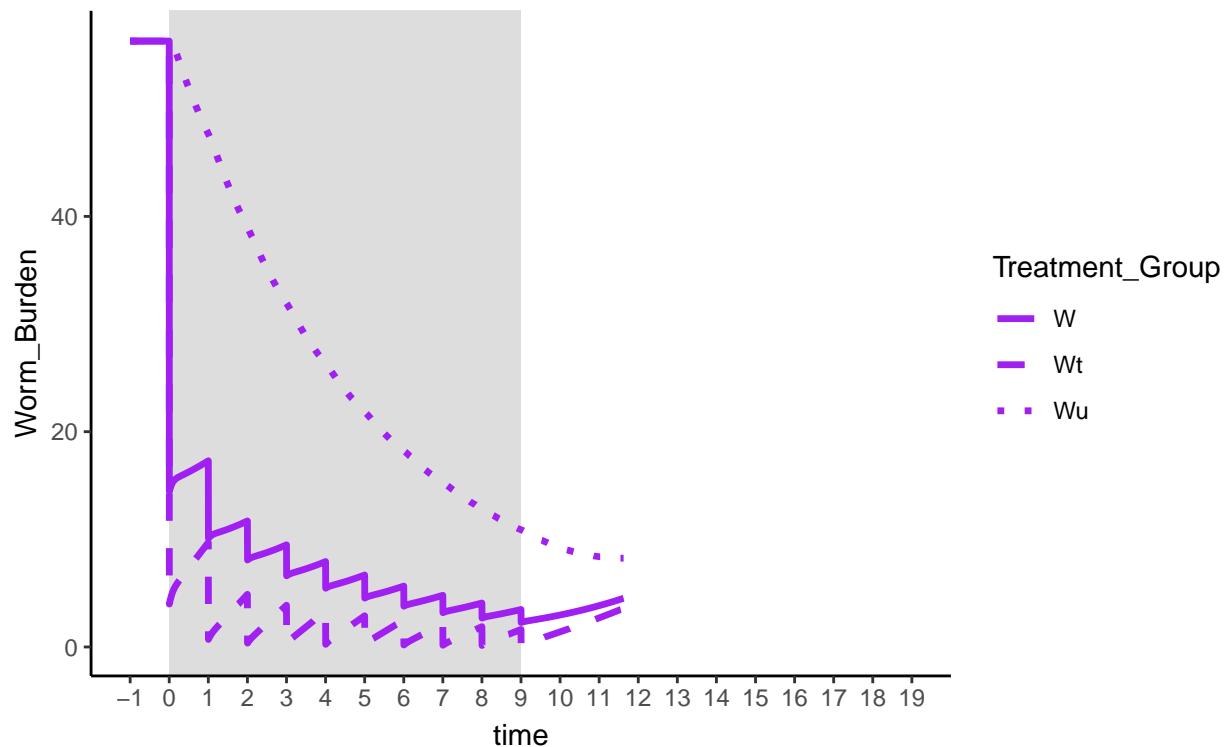
Human infection dynamics

Annual MDA for 10 years



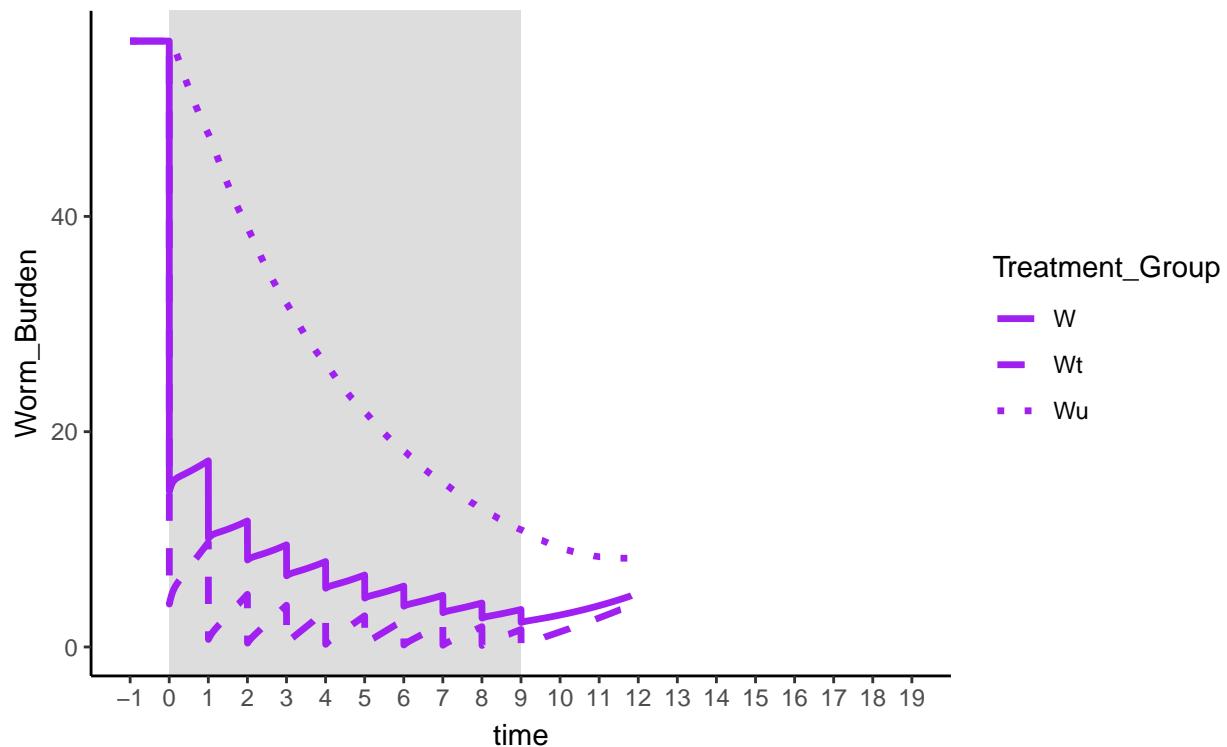
Human infection dynamics

Annual MDA for 10 years



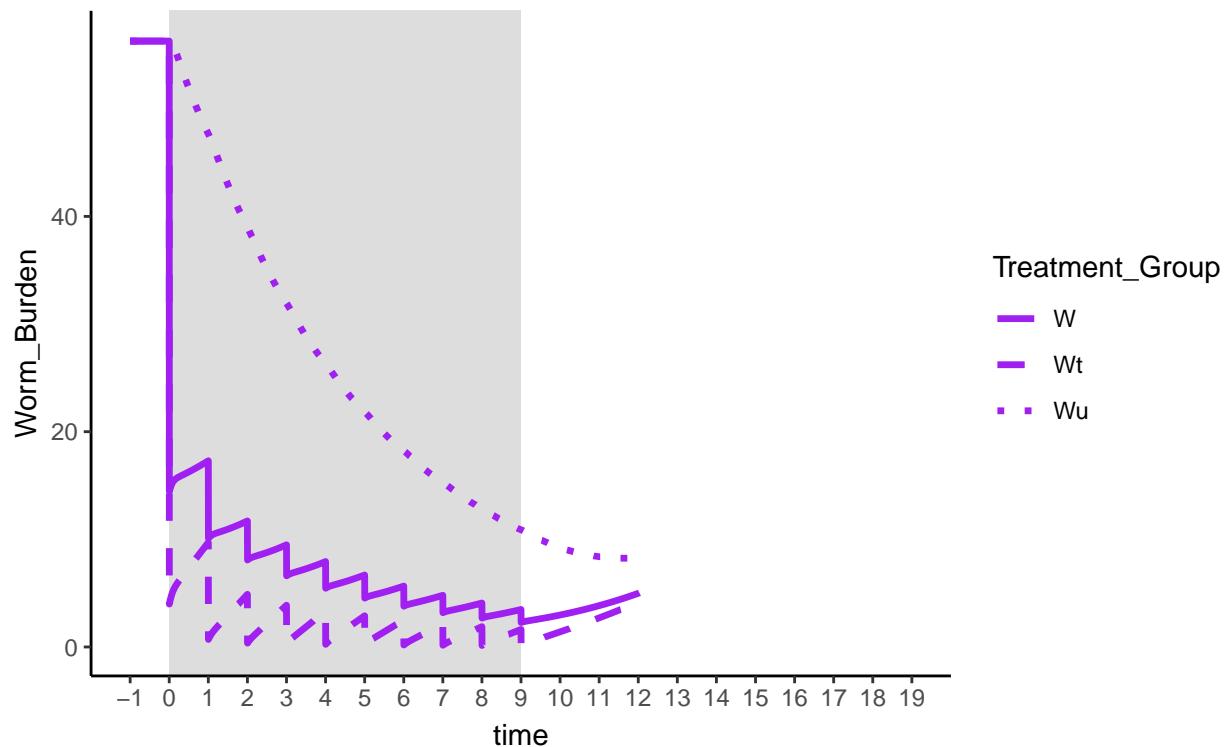
Human infection dynamics

Anual MDA for 10 years



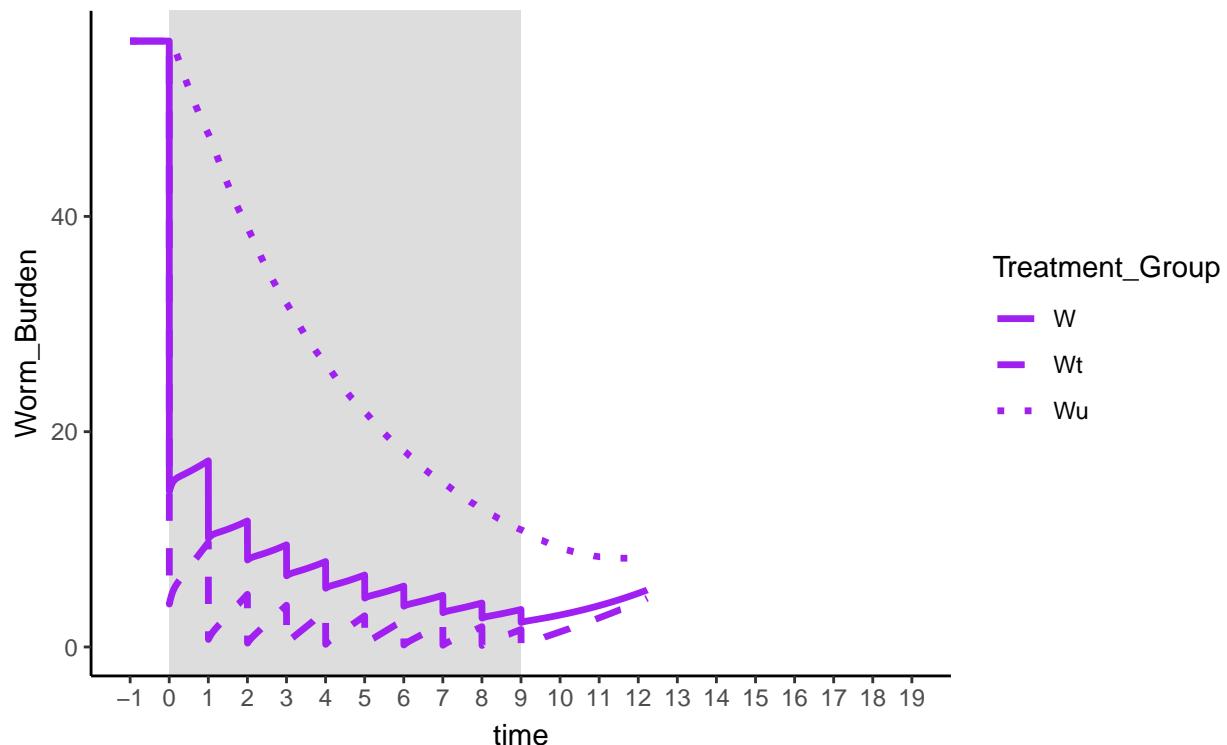
Human infection dynamics

Anual MDA for 10 years



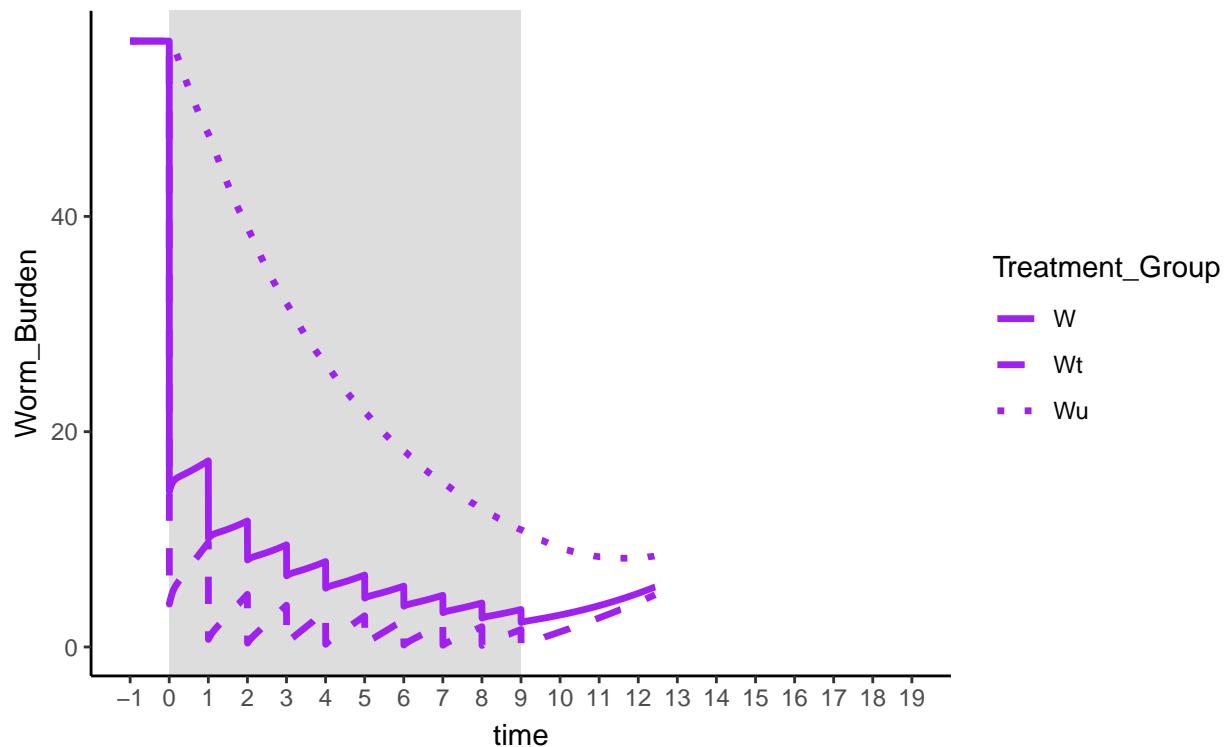
Human infection dynamics

Annual MDA for 10 years



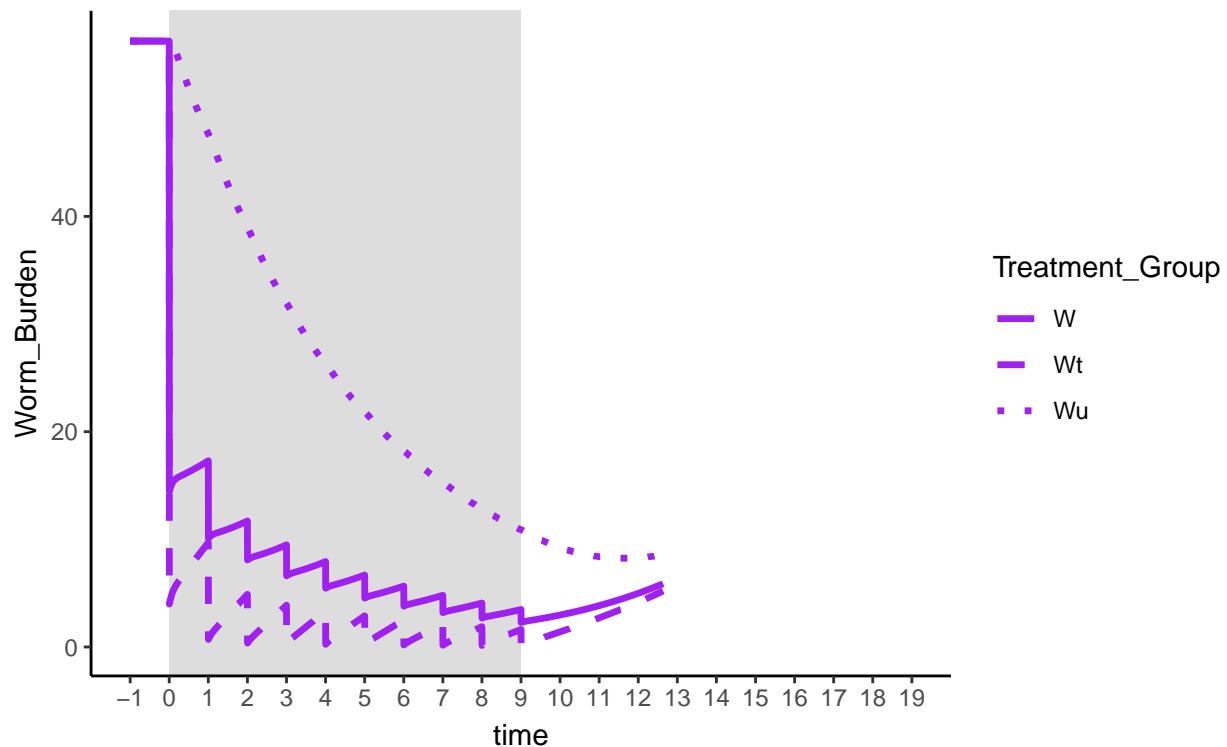
Human infection dynamics

Annual MDA for 10 years



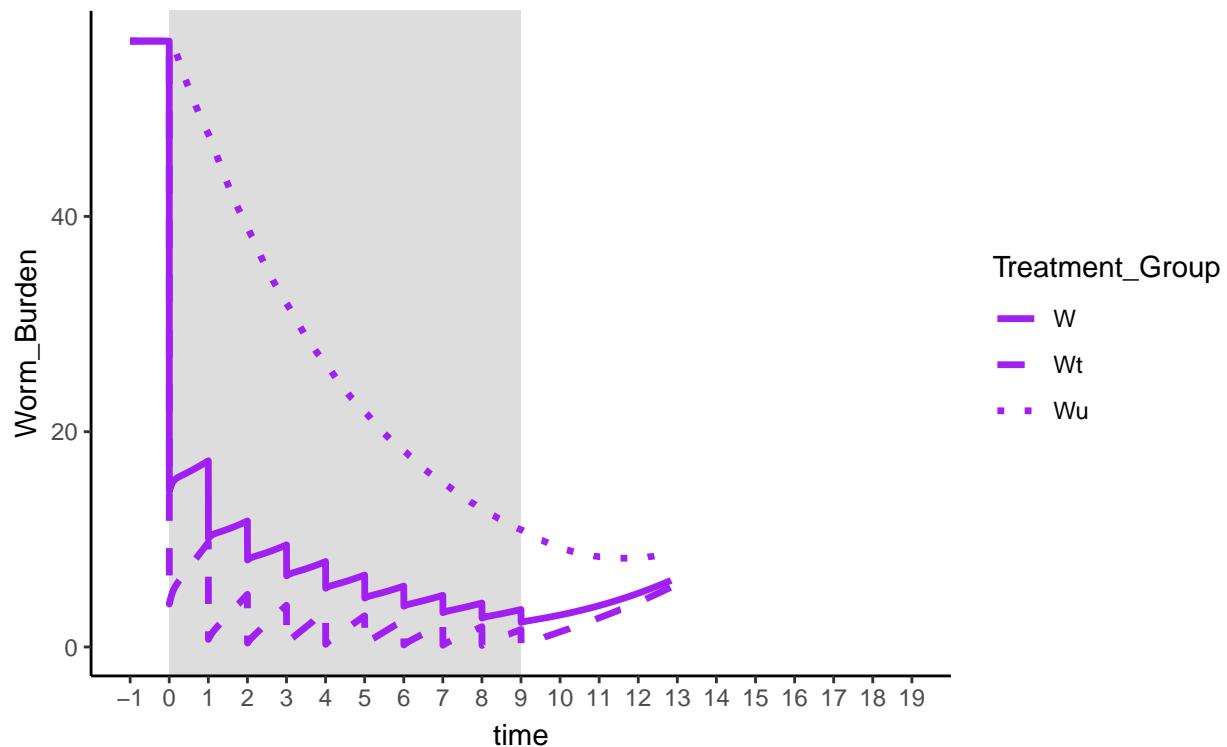
Human infection dynamics

Annual MDA for 10 years



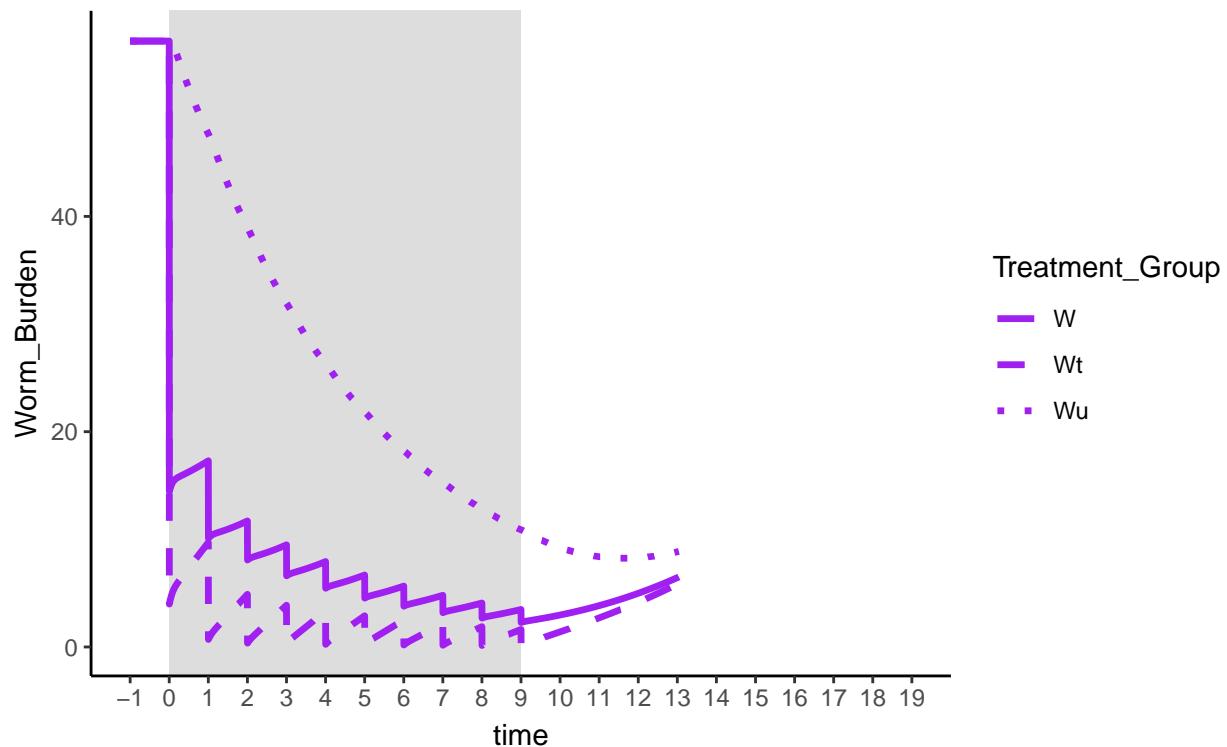
Human infection dynamics

Annual MDA for 10 years



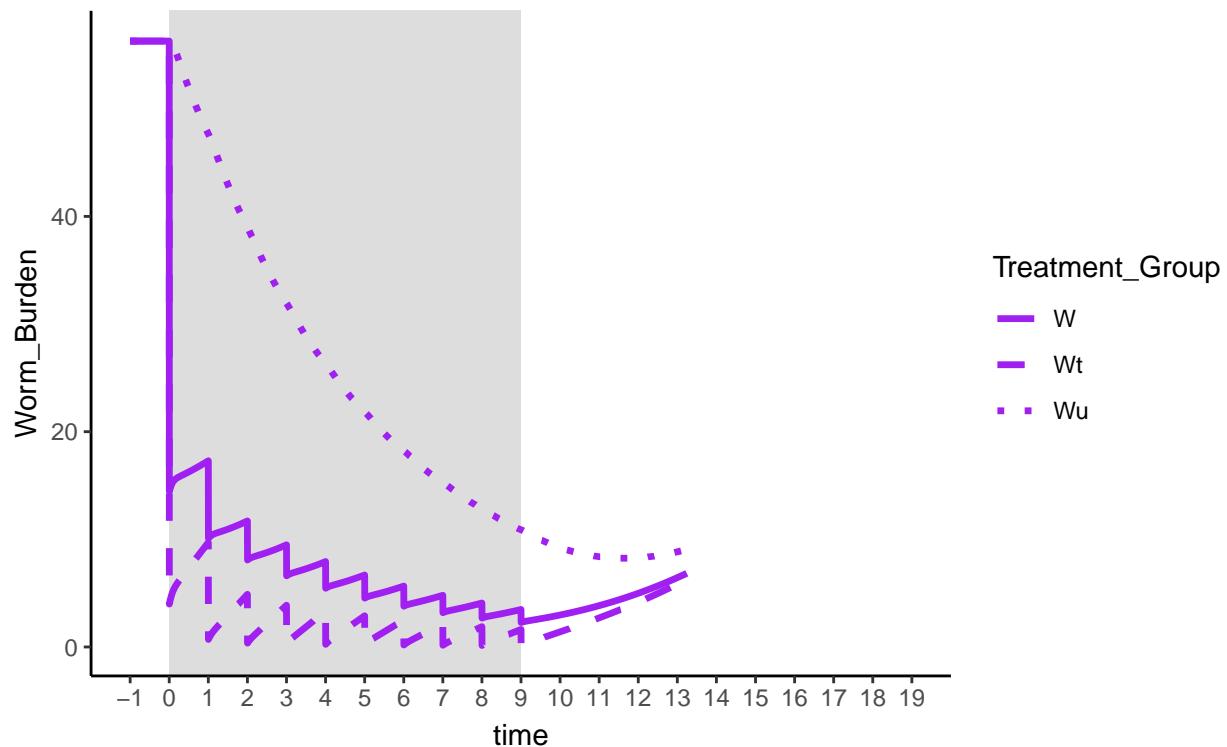
Human infection dynamics

Anual MDA for 10 years



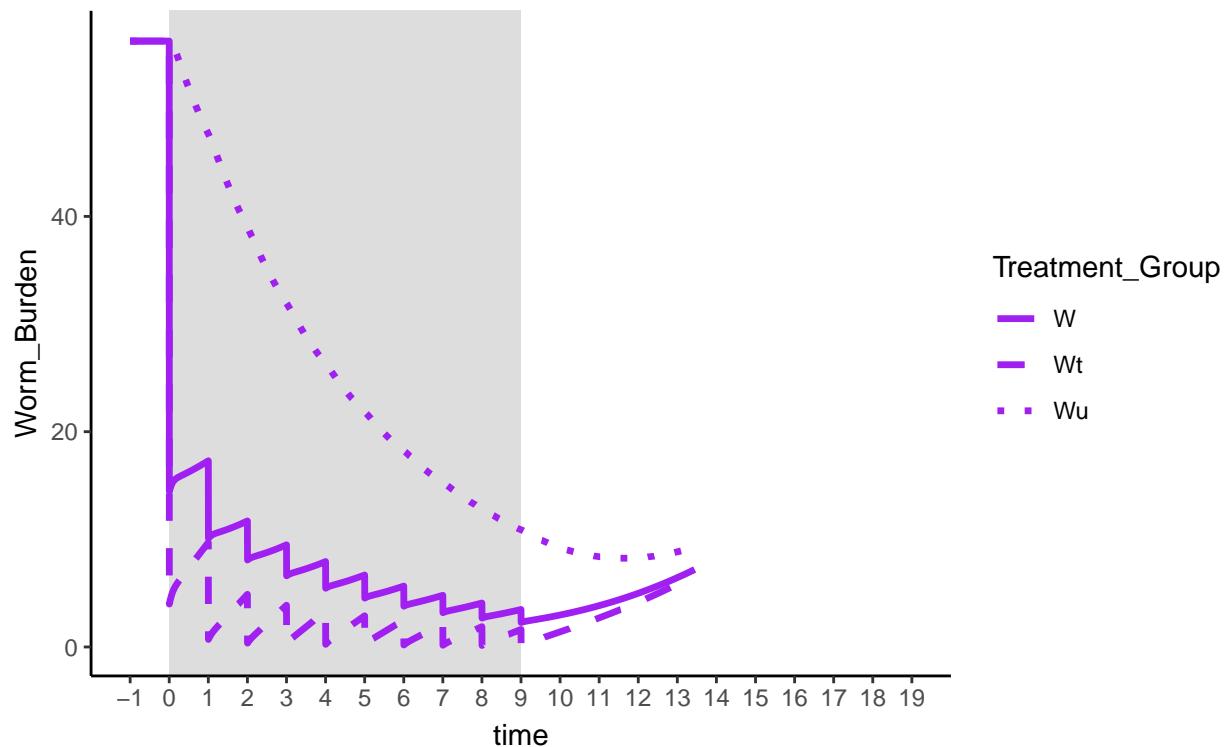
Human infection dynamics

Annual MDA for 10 years



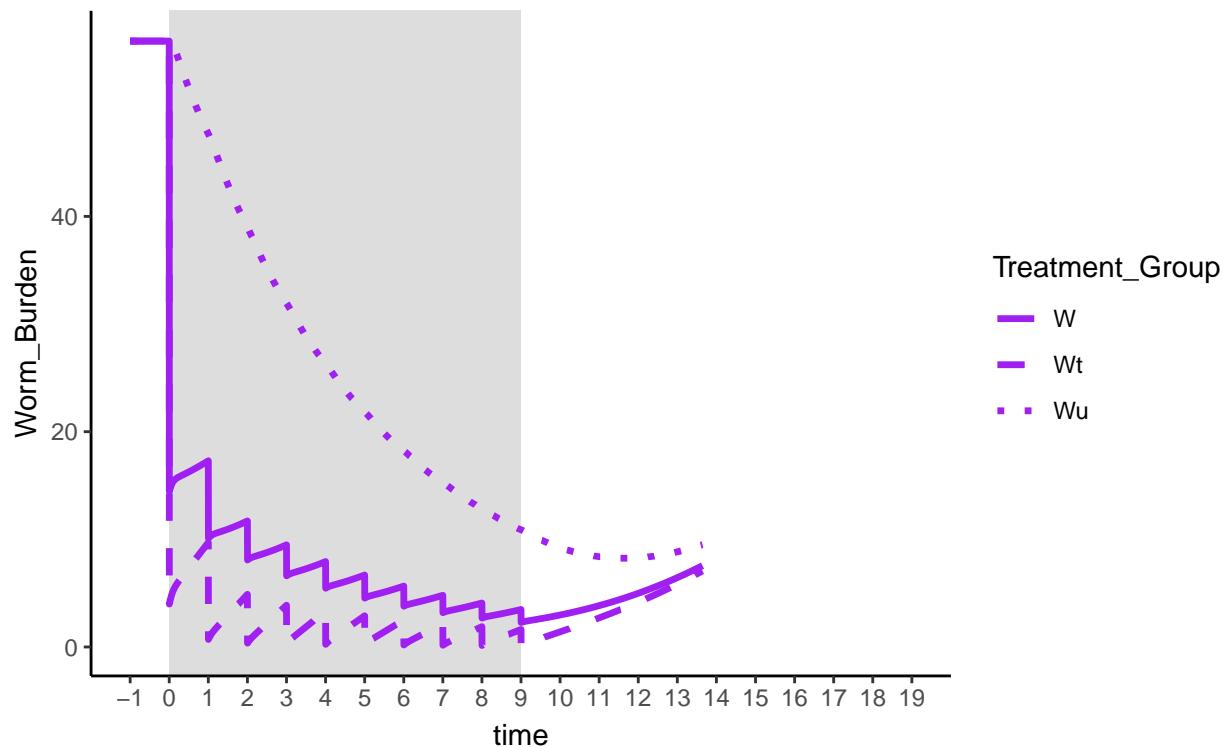
Human infection dynamics

Annual MDA for 10 years



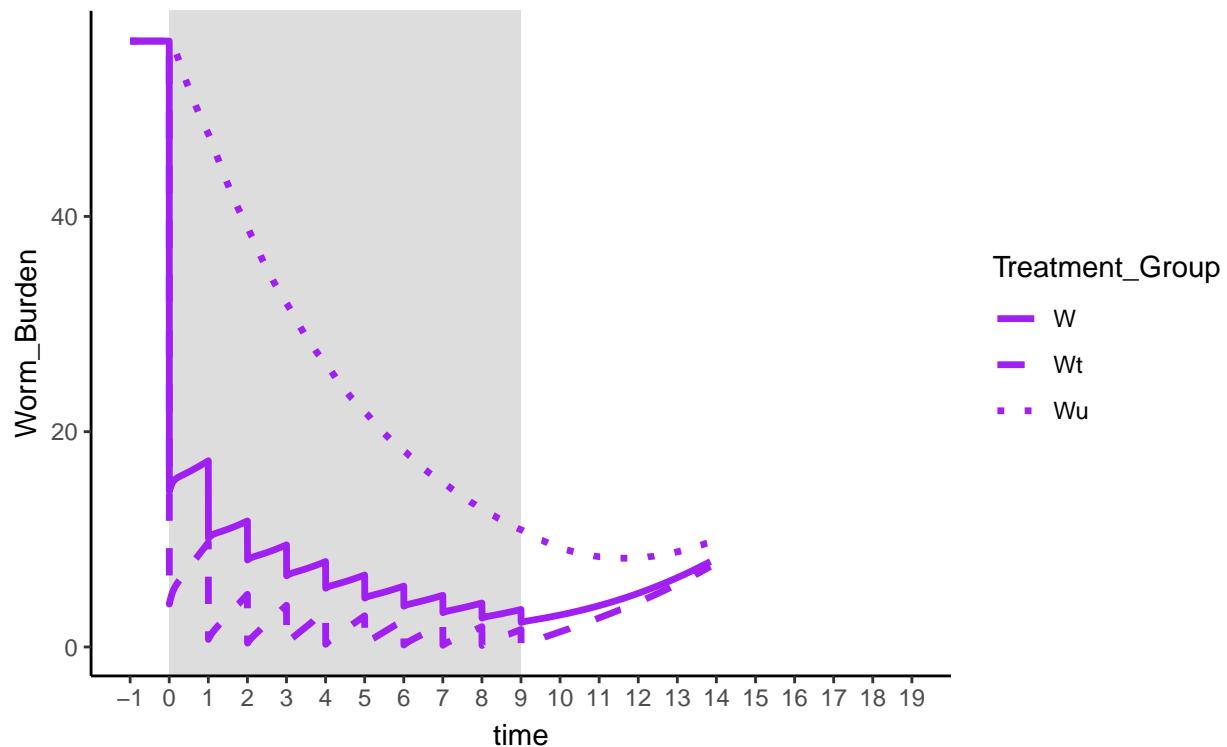
Human infection dynamics

Annual MDA for 10 years



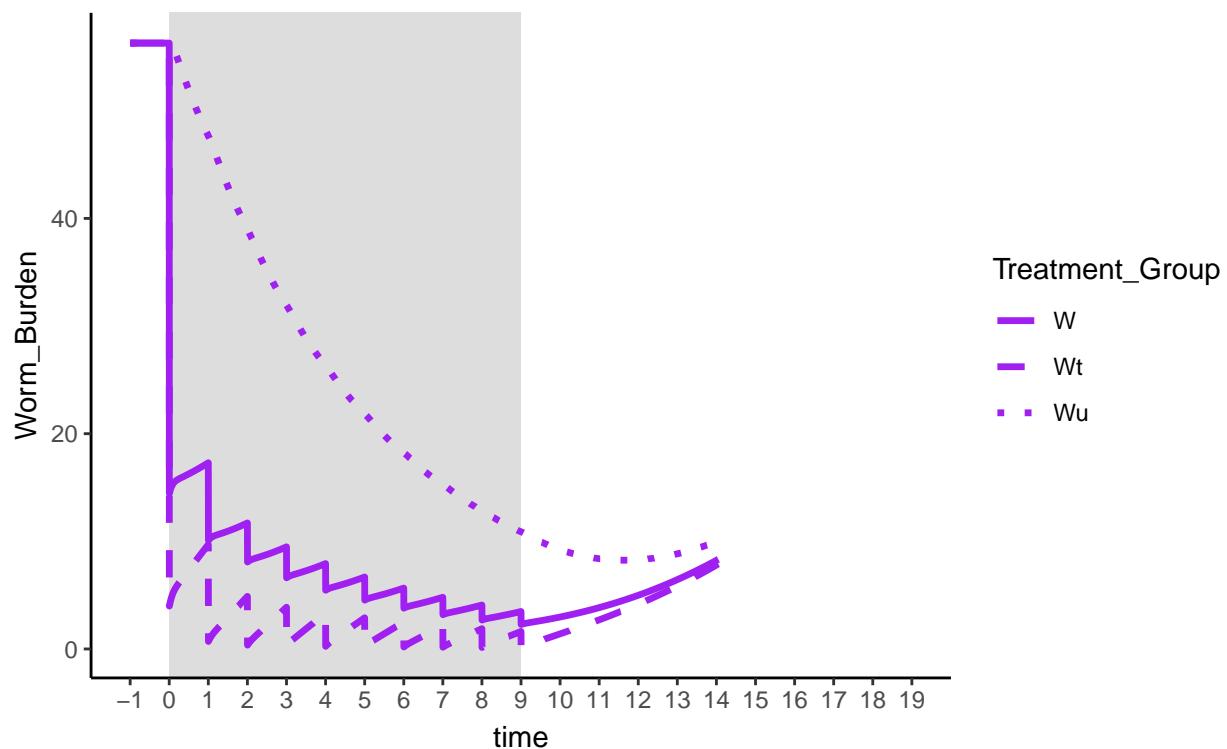
Human infection dynamics

Annual MDA for 10 years



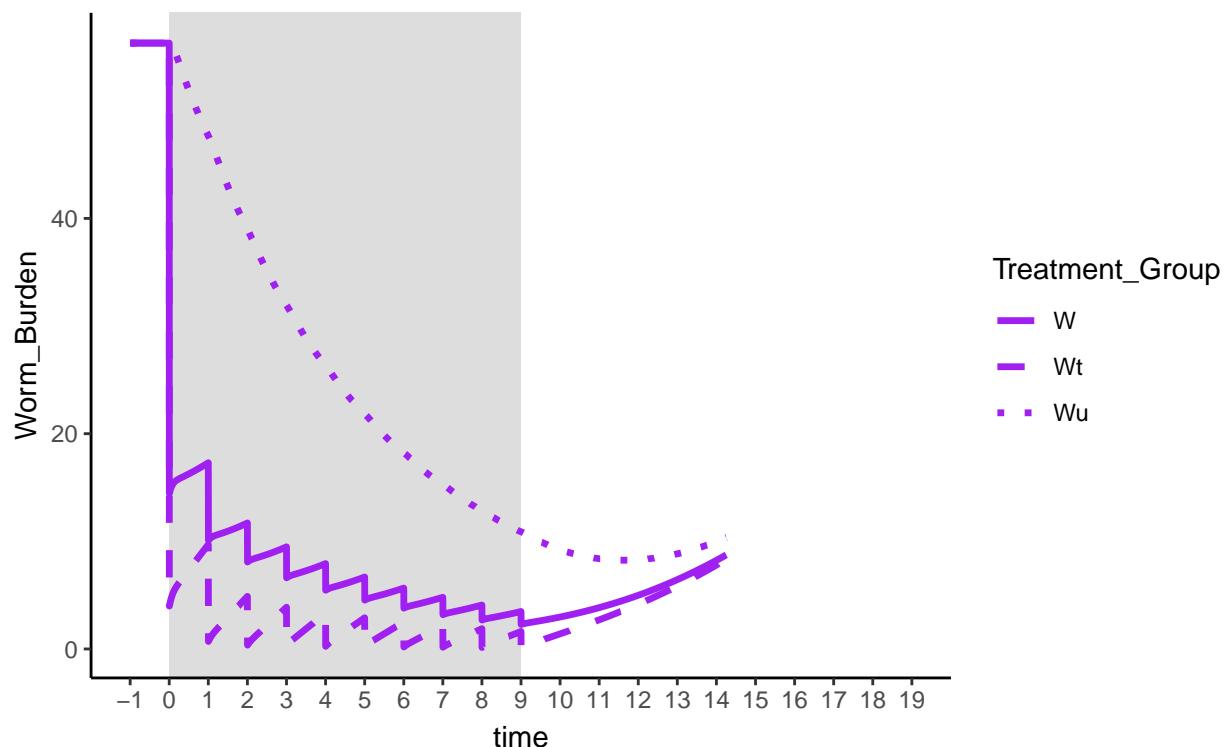
Human infection dynamics

Annual MDA for 10 years



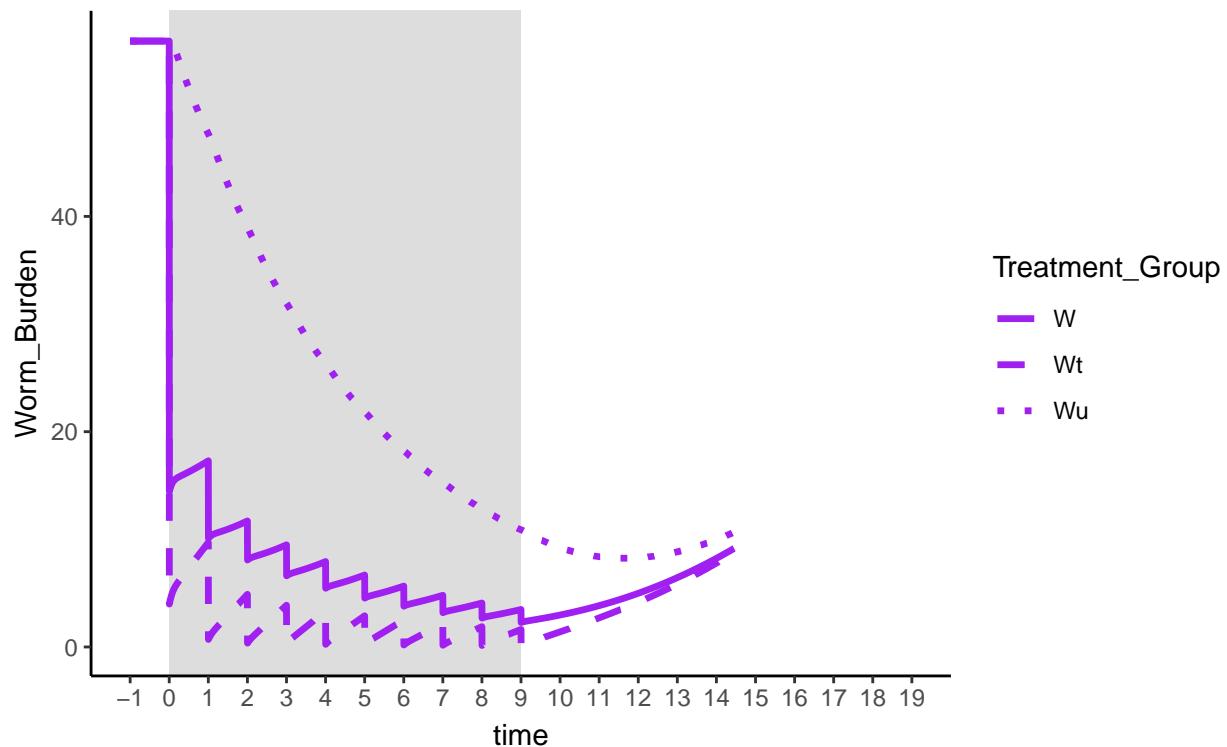
Human infection dynamics

Annual MDA for 10 years



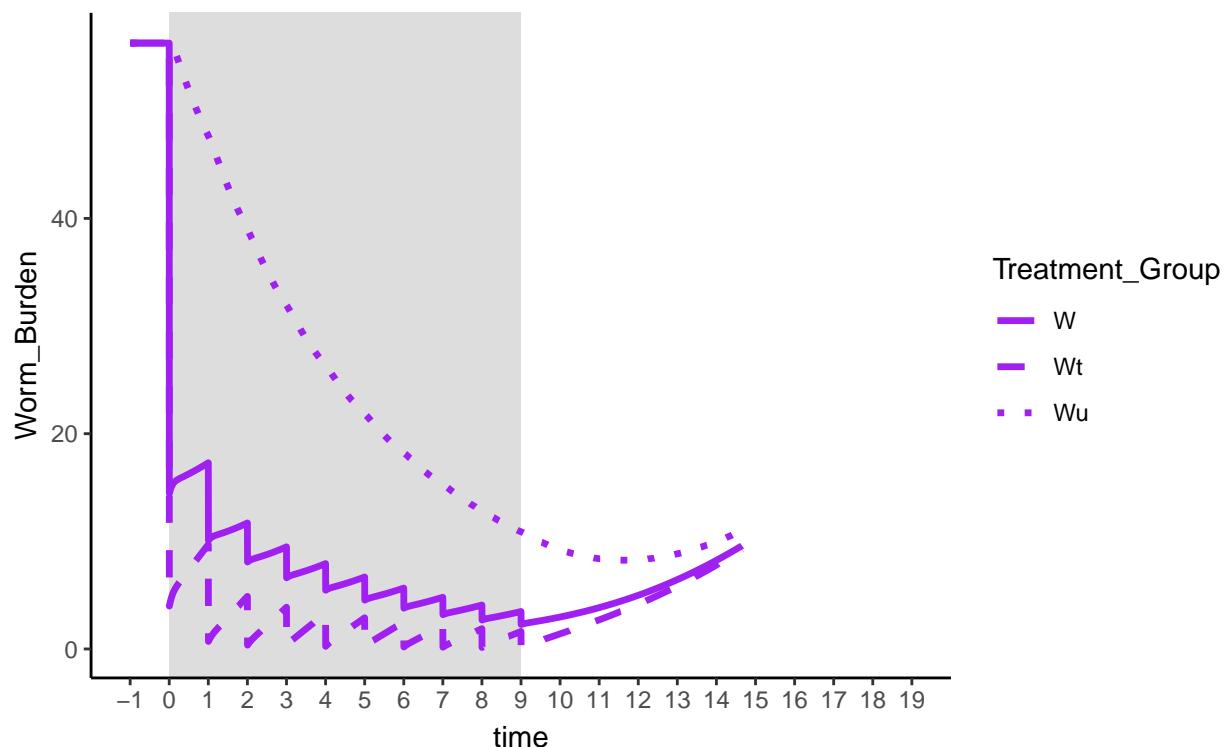
Human infection dynamics

Annual MDA for 10 years



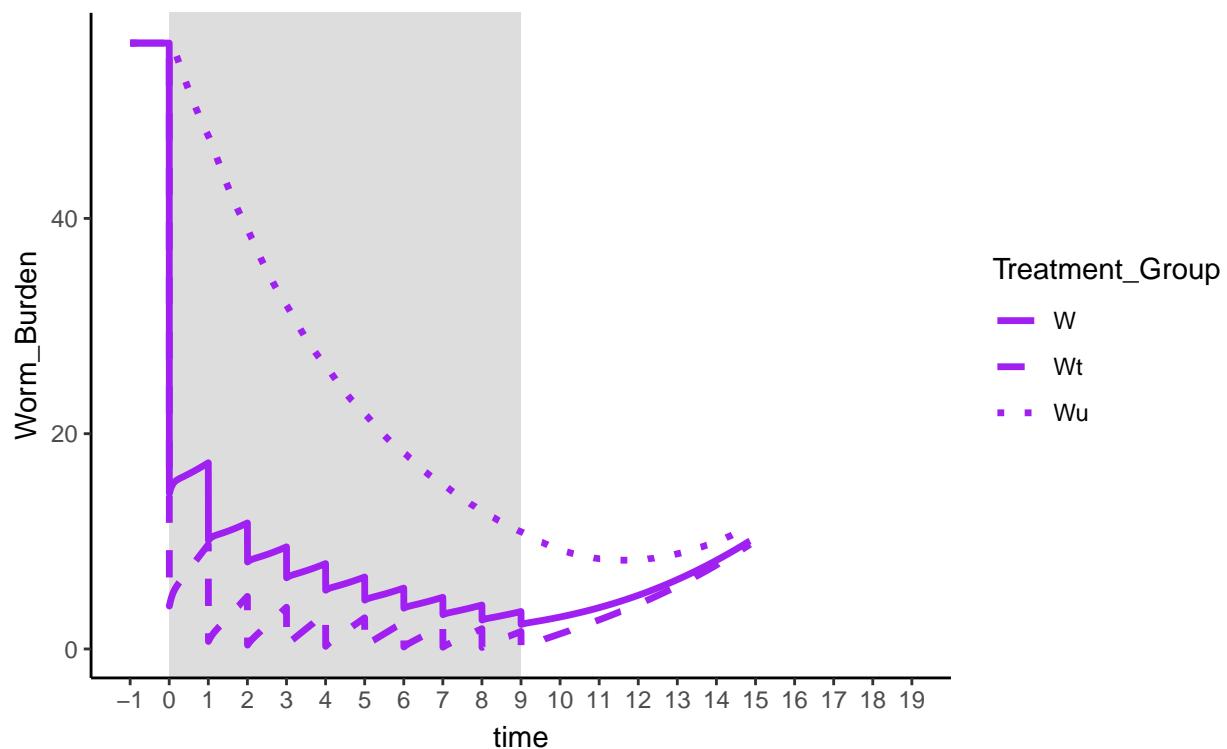
Human infection dynamics

Annual MDA for 10 years



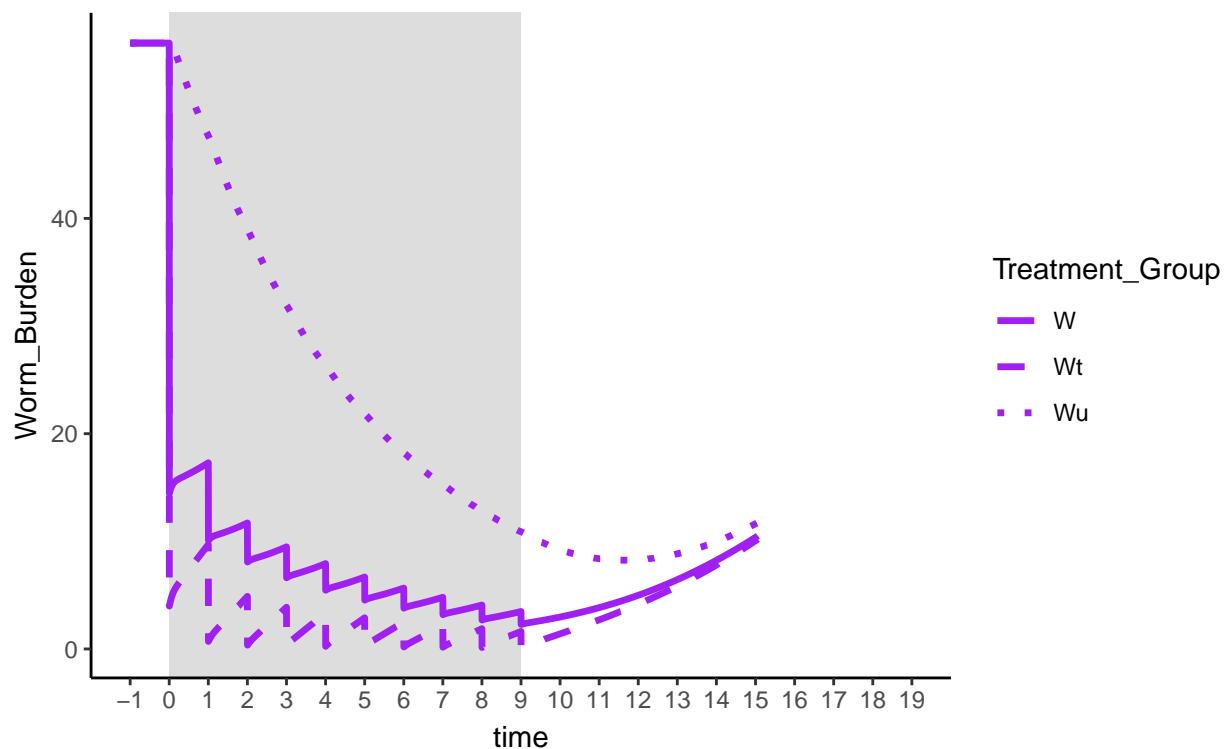
Human infection dynamics

Annual MDA for 10 years



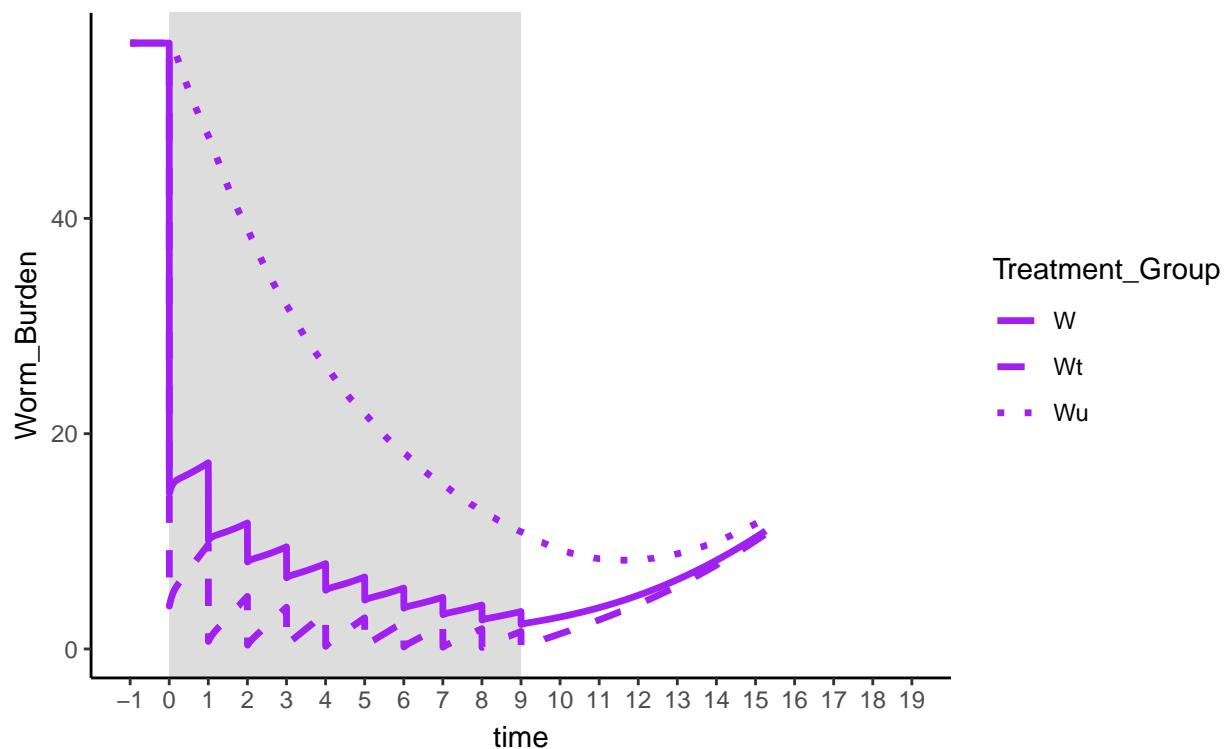
Human infection dynamics

Annual MDA for 10 years



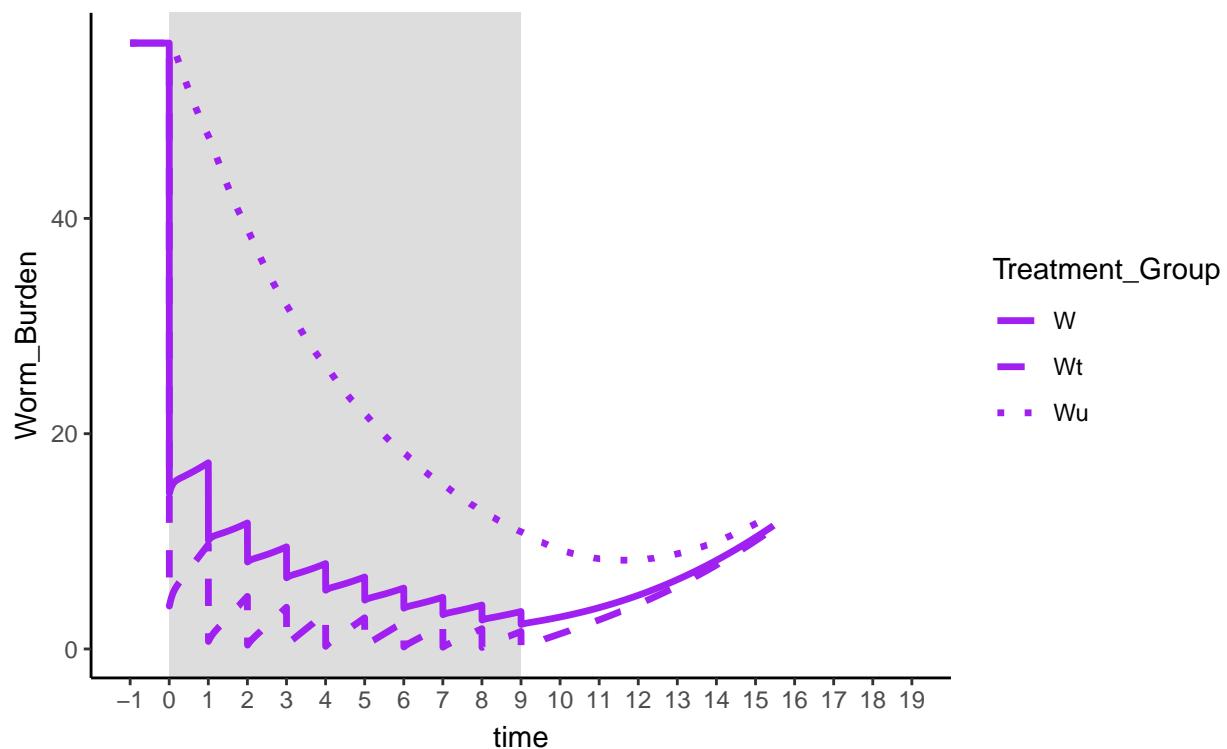
Human infection dynamics

Annual MDA for 10 years



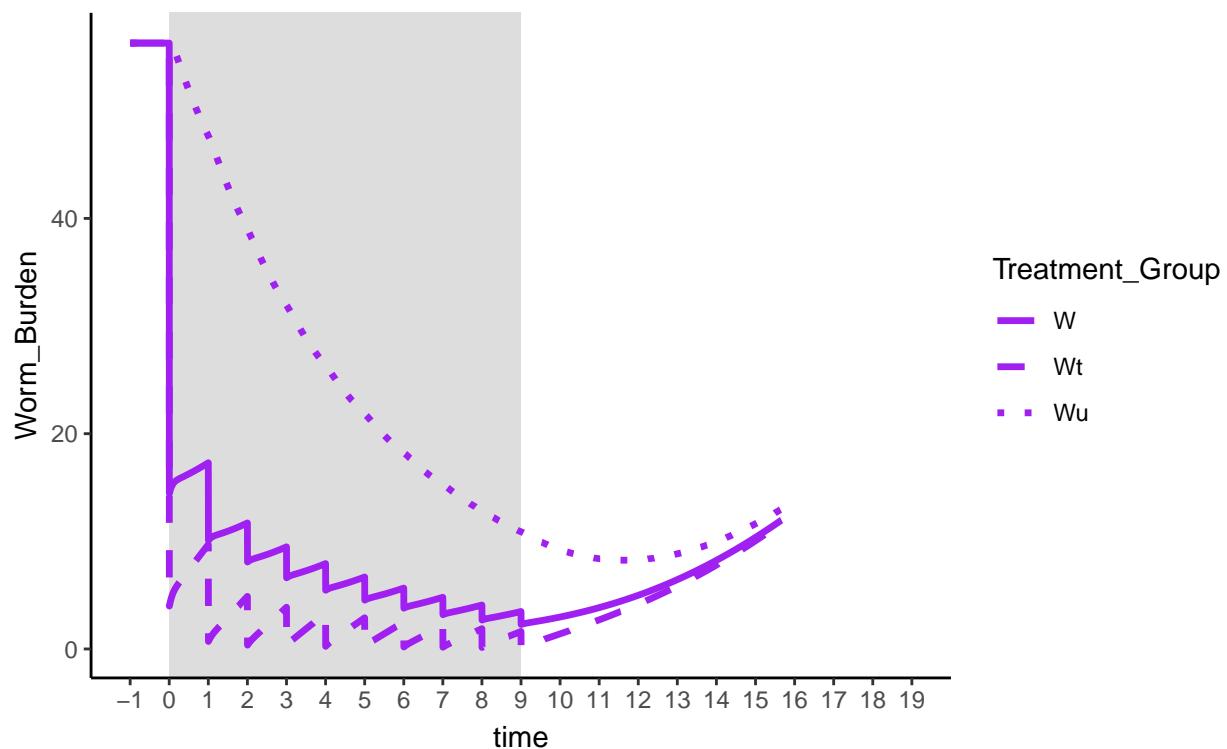
Human infection dynamics

Annual MDA for 10 years



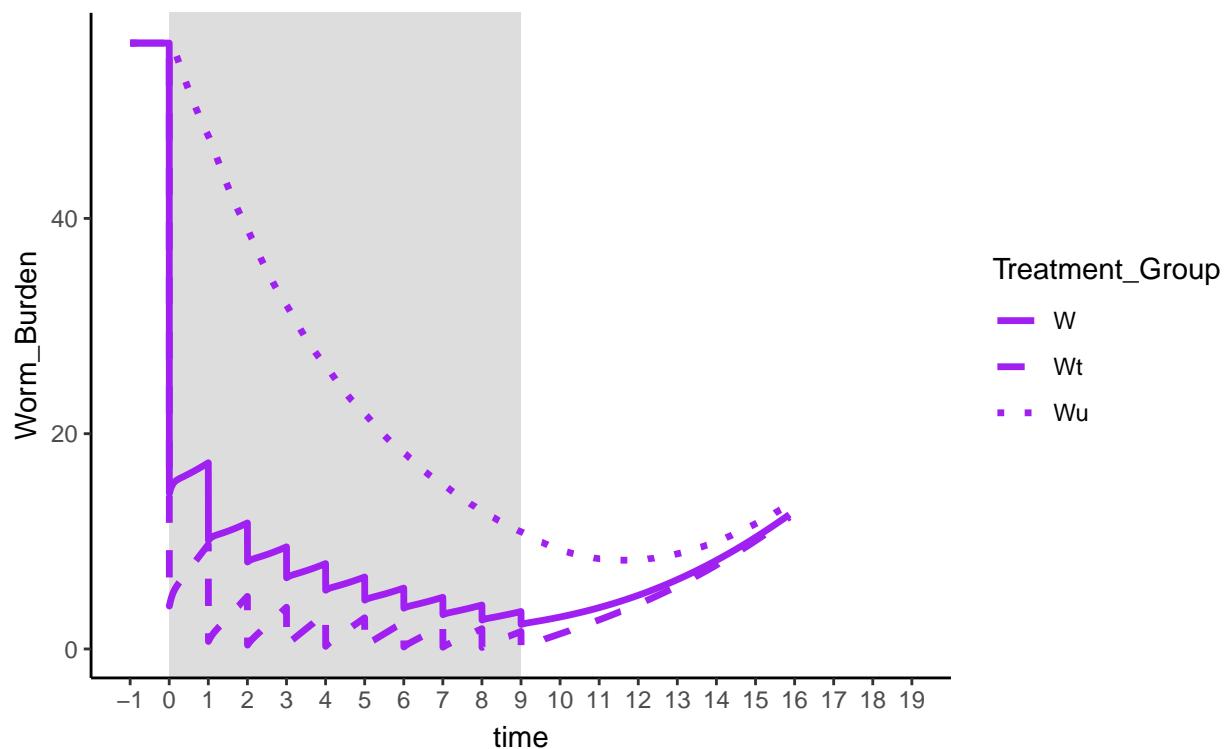
Human infection dynamics

Annual MDA for 10 years



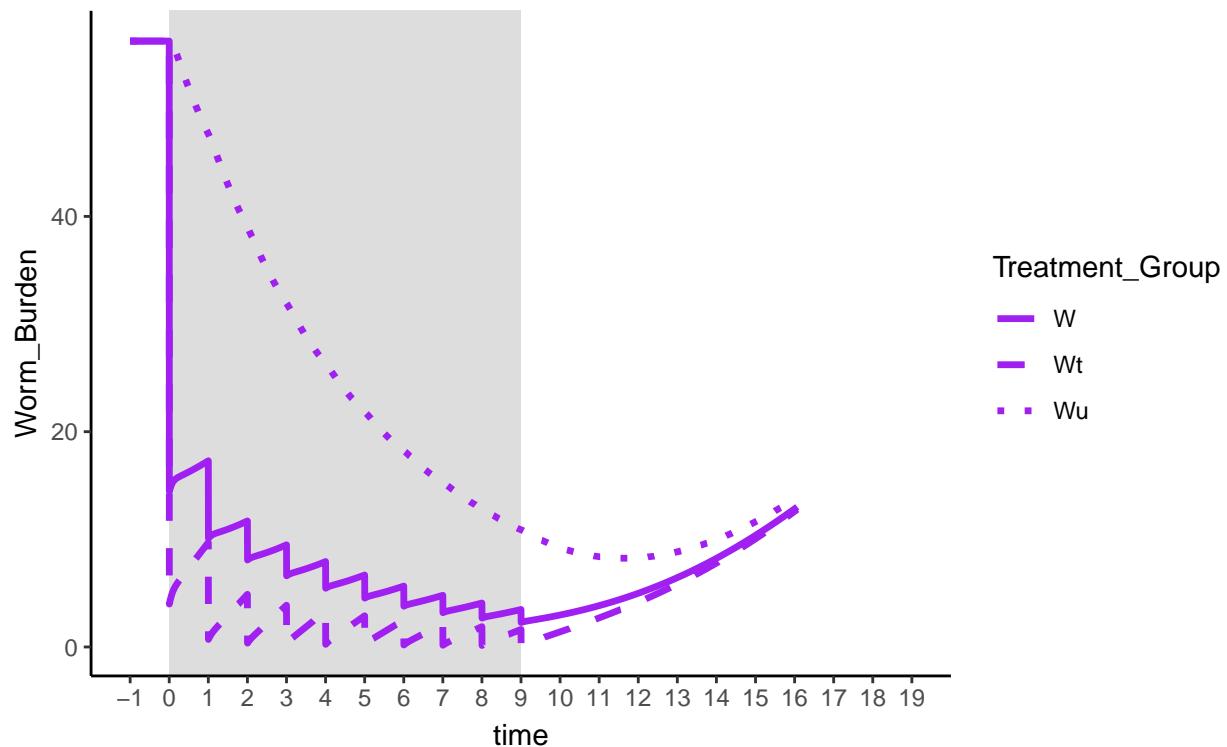
Human infection dynamics

Annual MDA for 10 years



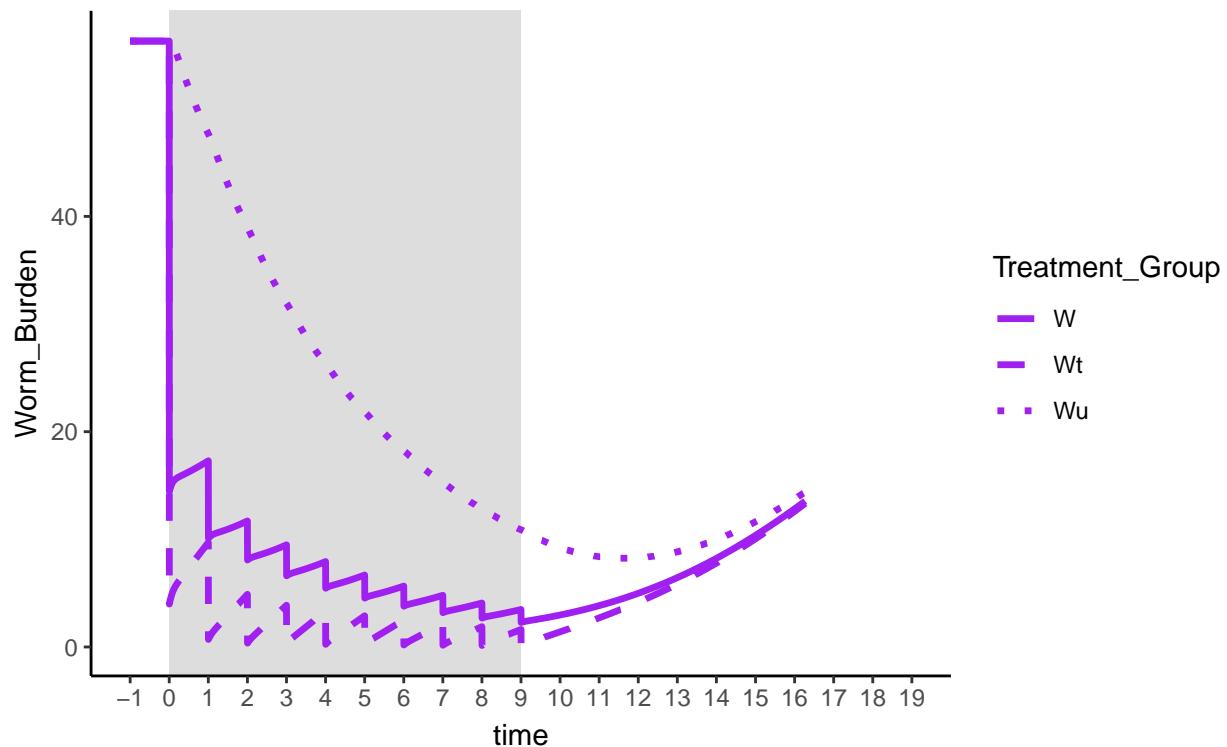
Human infection dynamics

Annual MDA for 10 years



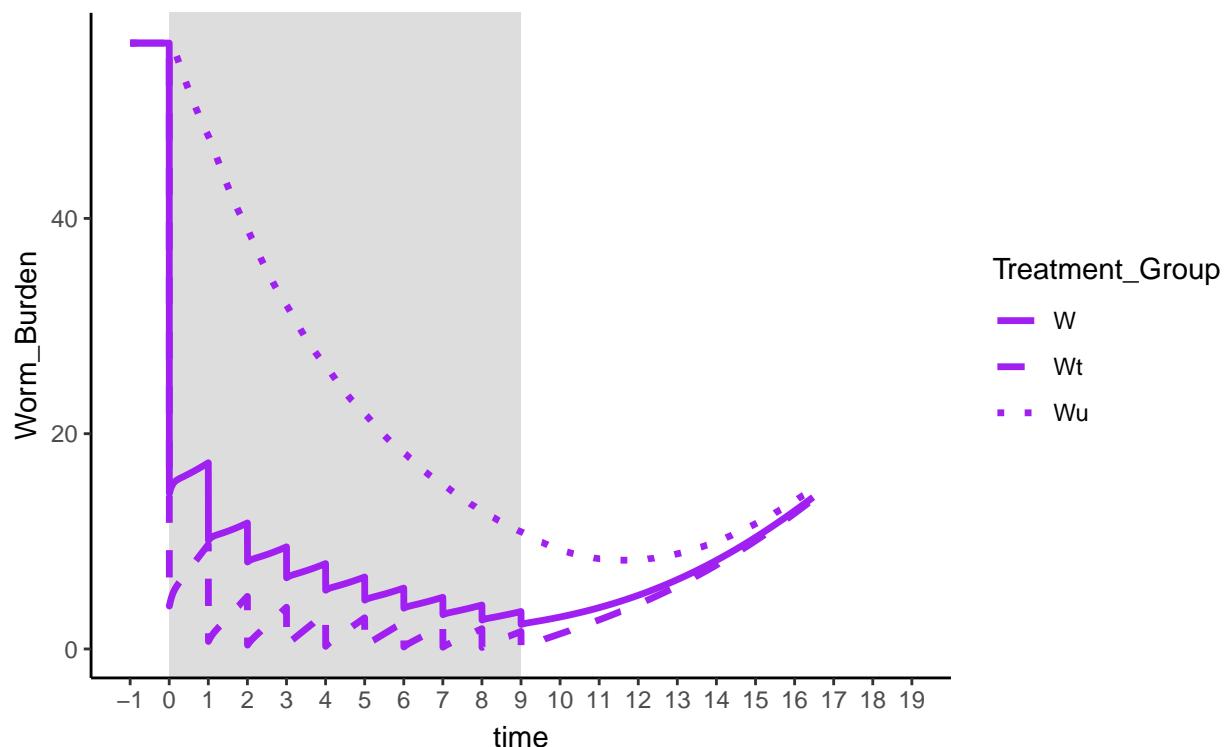
Human infection dynamics

Anual MDA for 10 years



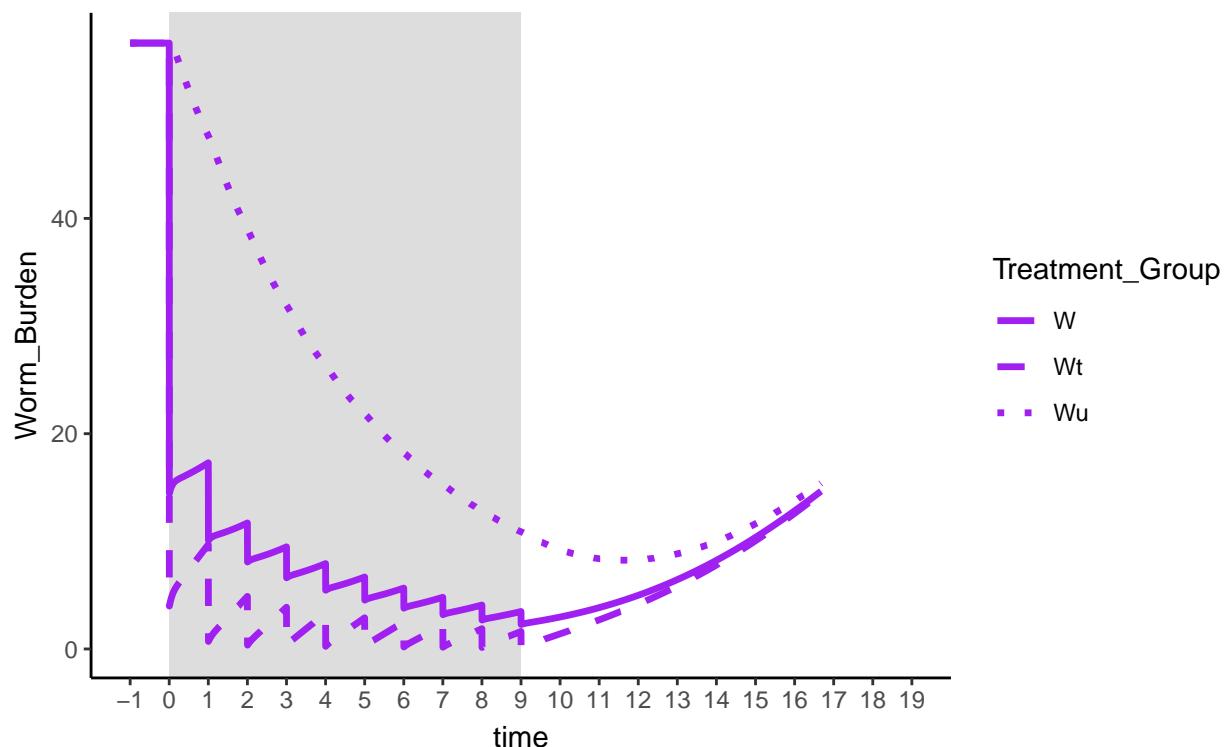
Human infection dynamics

Anual MDA for 10 years



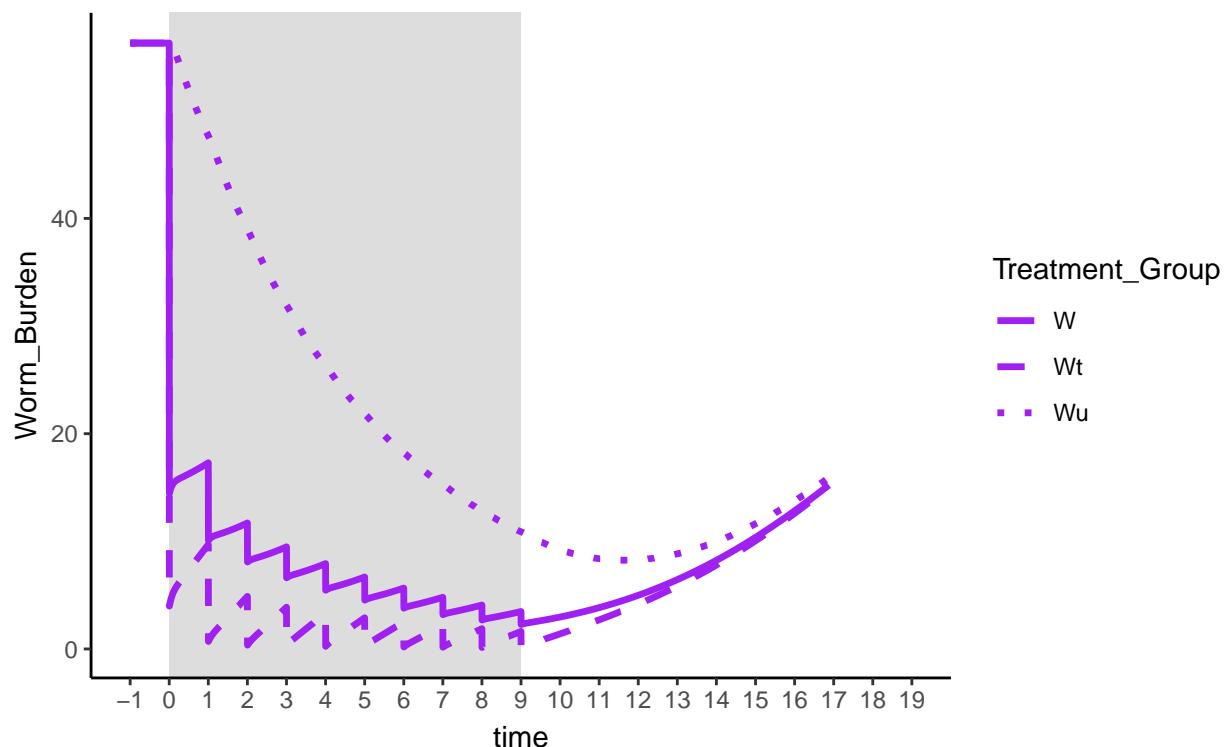
Human infection dynamics

Anual MDA for 10 years



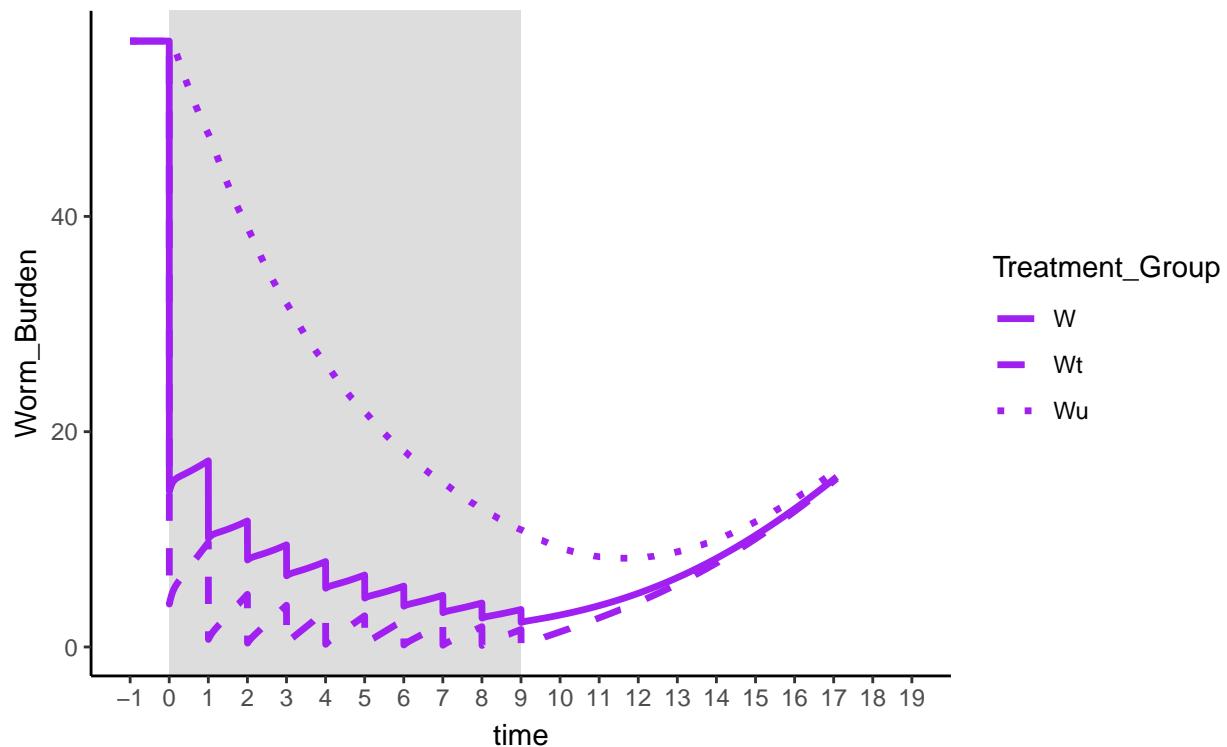
Human infection dynamics

Anual MDA for 10 years



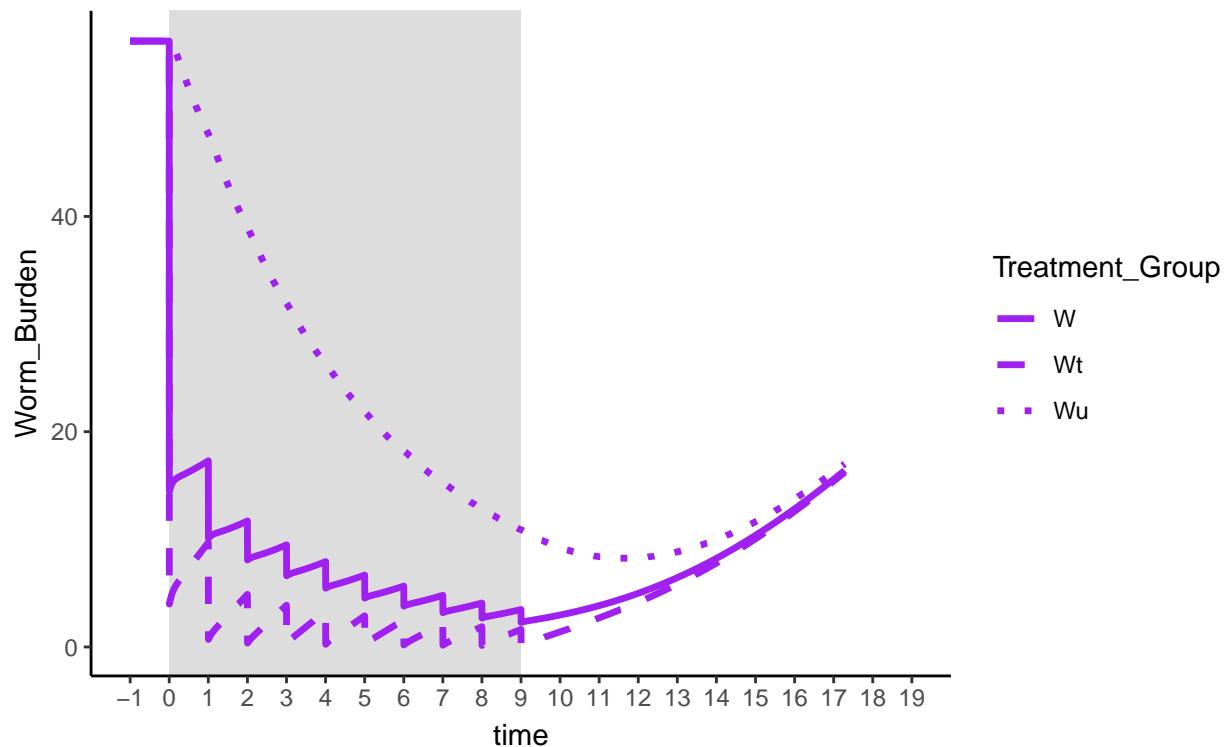
Human infection dynamics

Annual MDA for 10 years



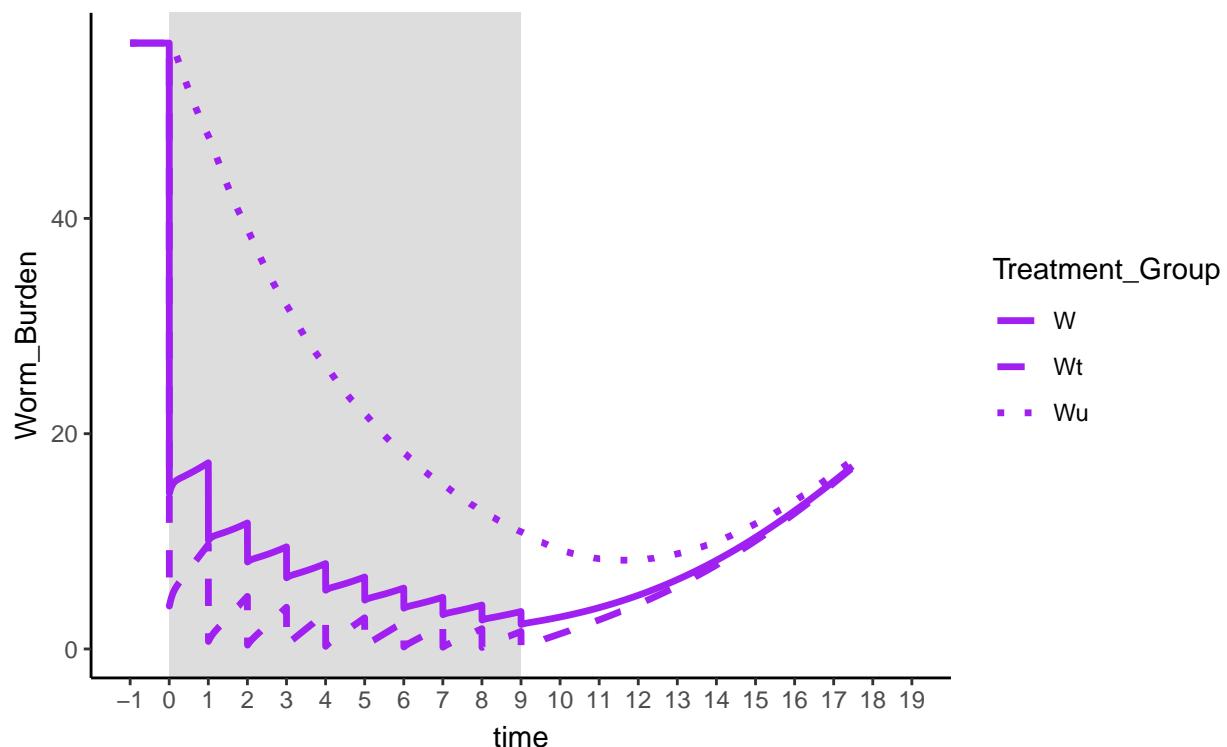
Human infection dynamics

Annual MDA for 10 years



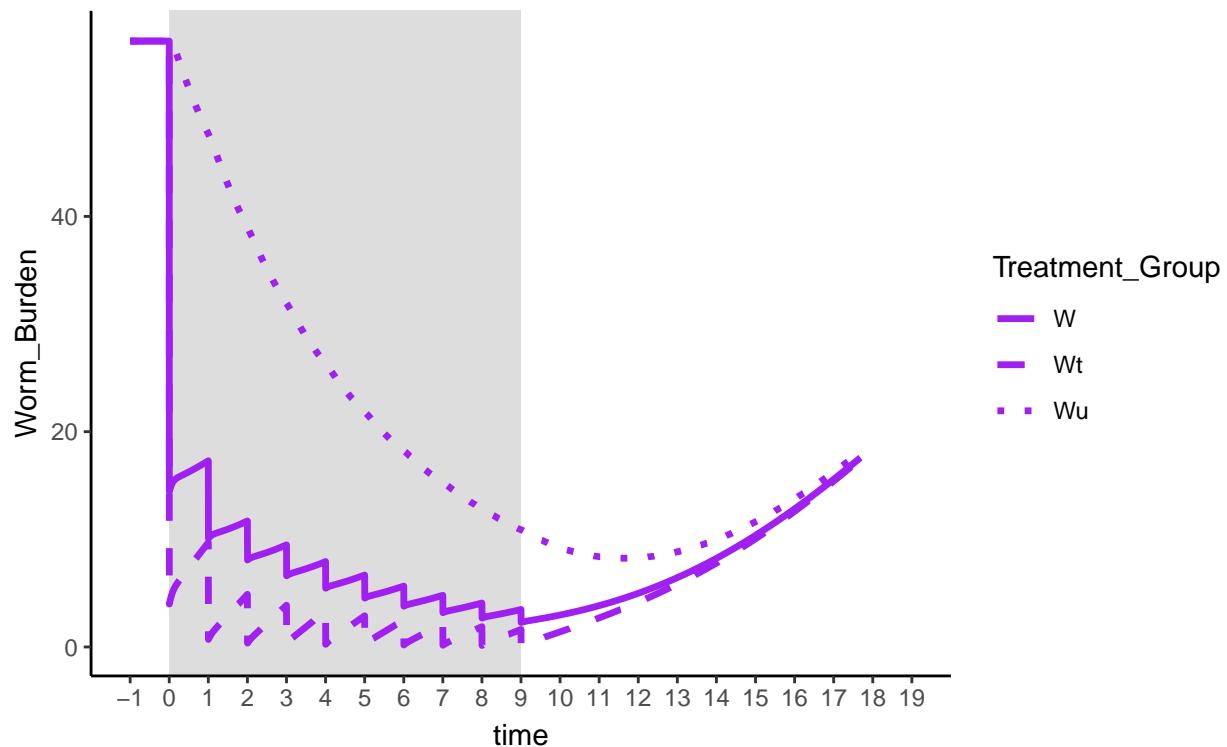
Human infection dynamics

Annual MDA for 10 years



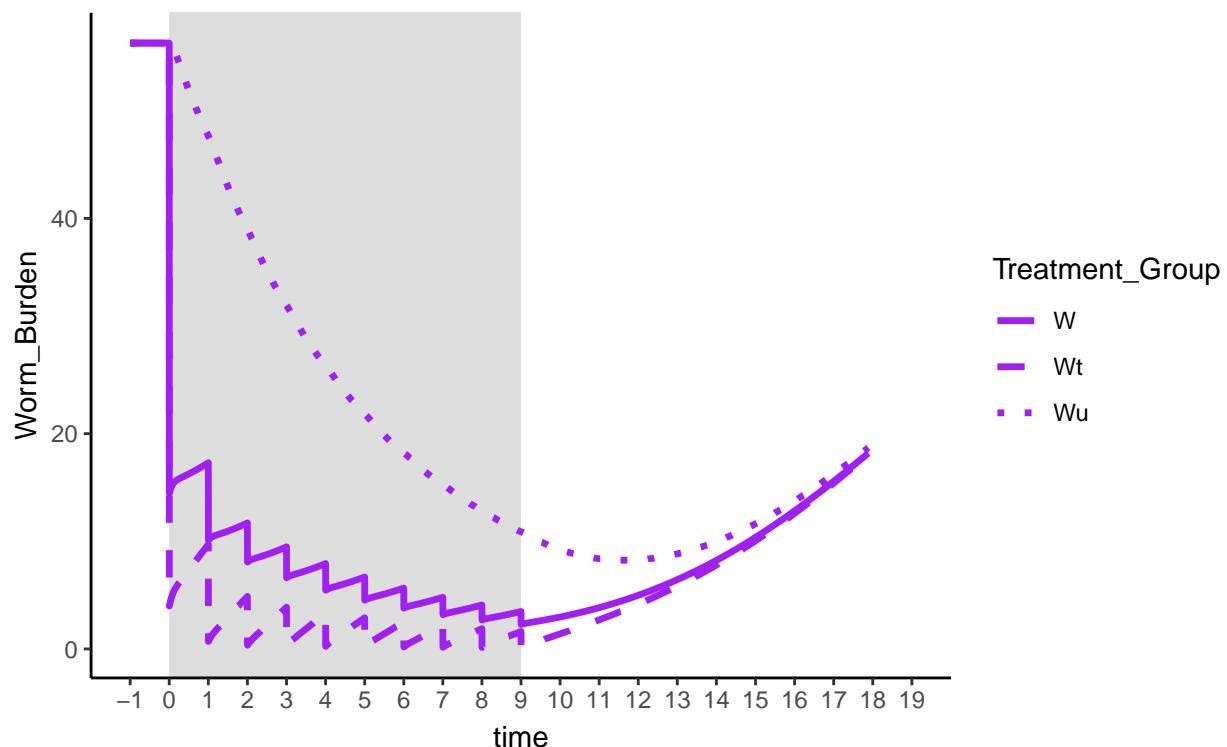
Human infection dynamics

Annual MDA for 10 years



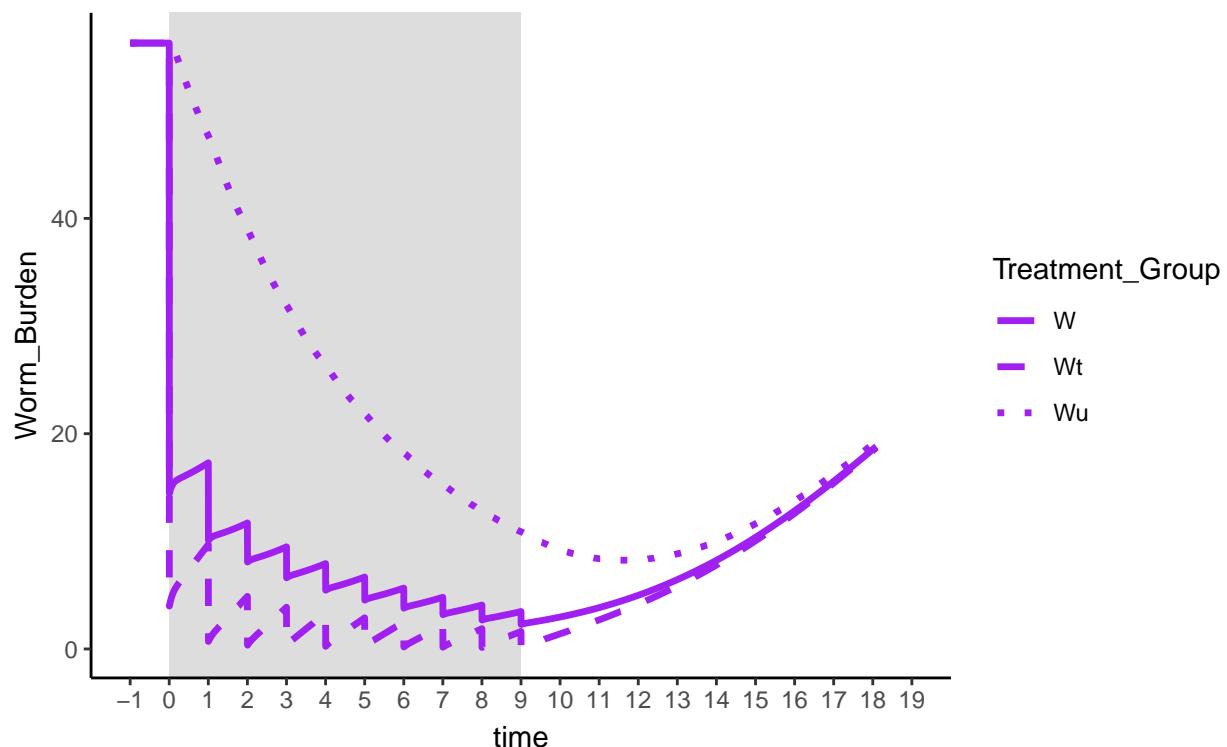
Human infection dynamics

Anual MDA for 10 years



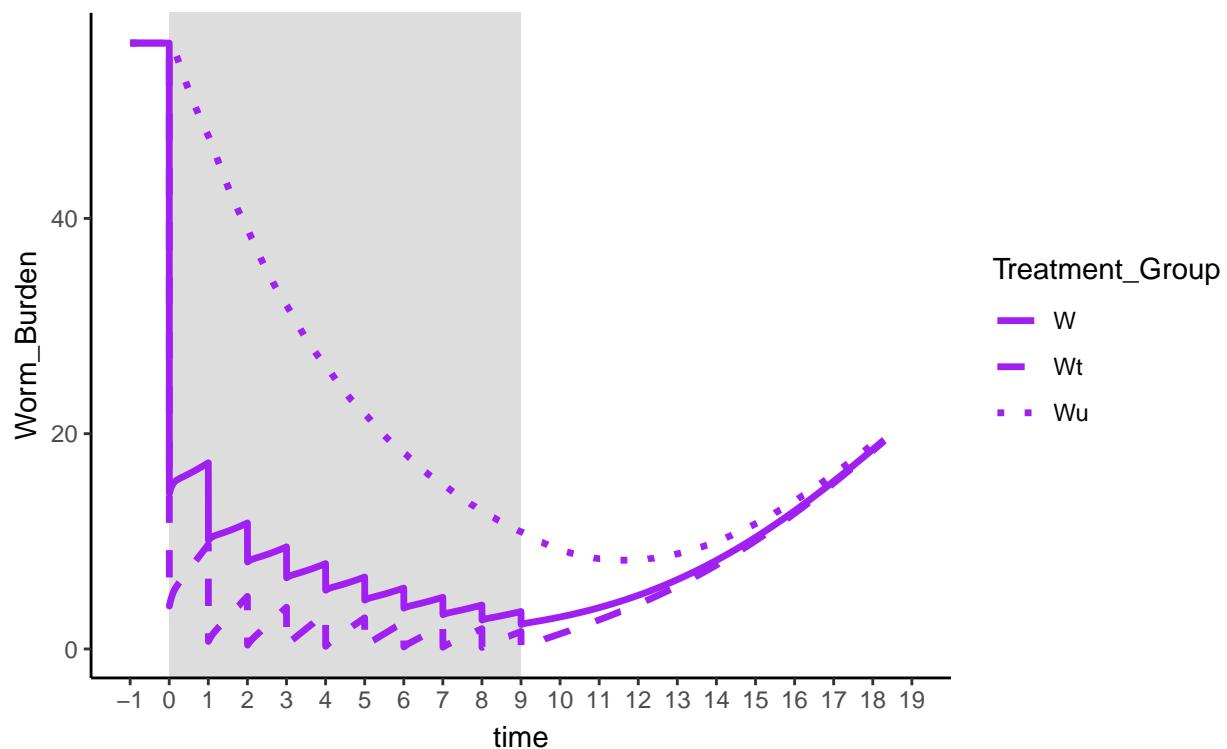
Human infection dynamics

Anual MDA for 10 years



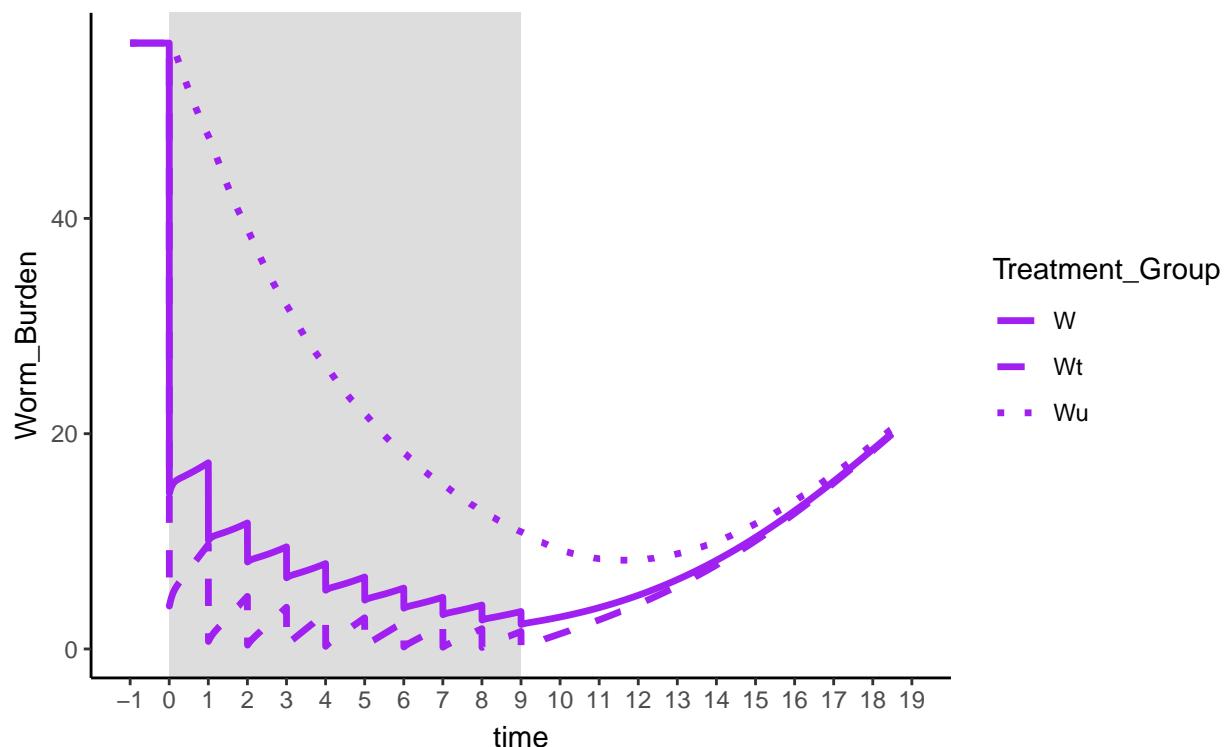
Human infection dynamics

Annual MDA for 10 years



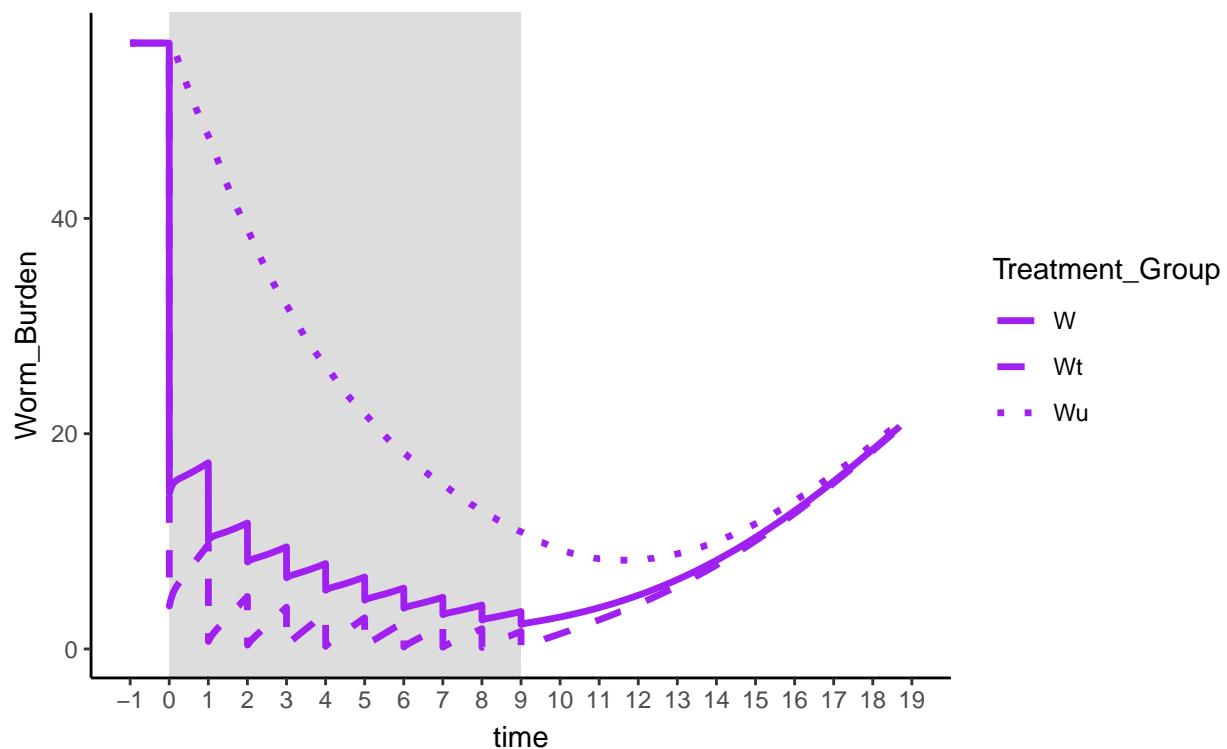
Human infection dynamics

Annual MDA for 10 years



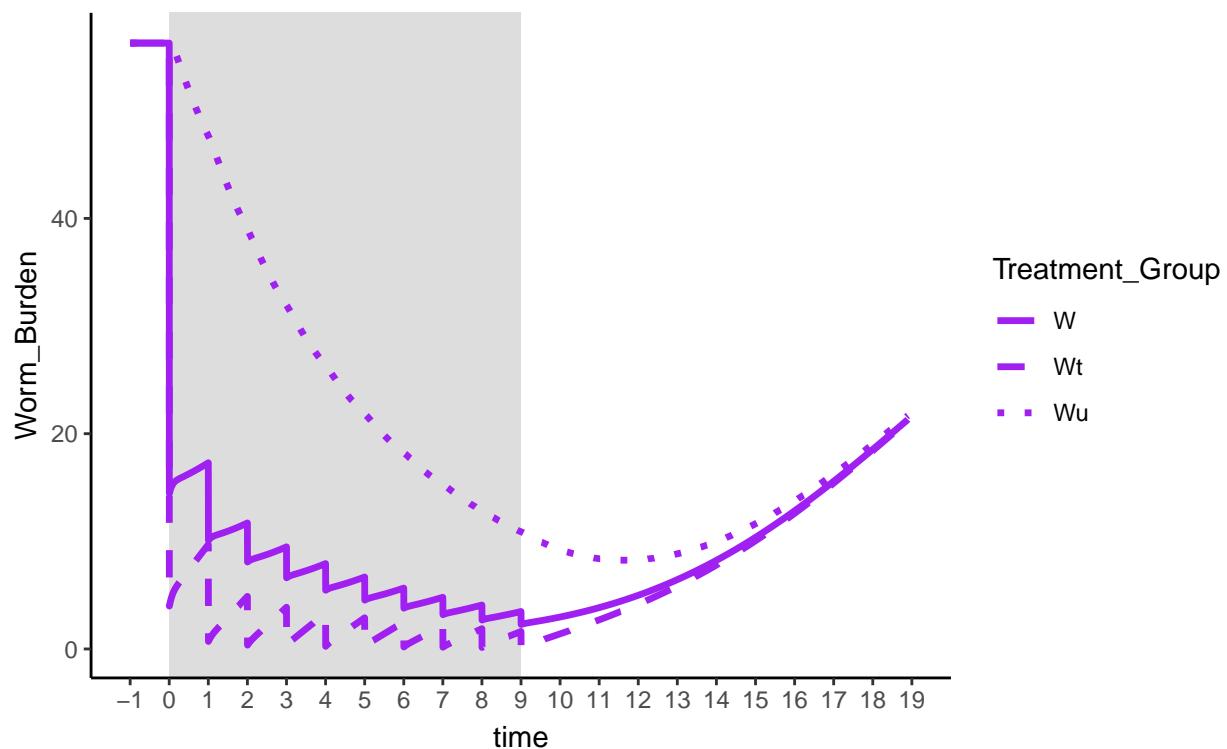
Human infection dynamics

Anual MDA for 10 years



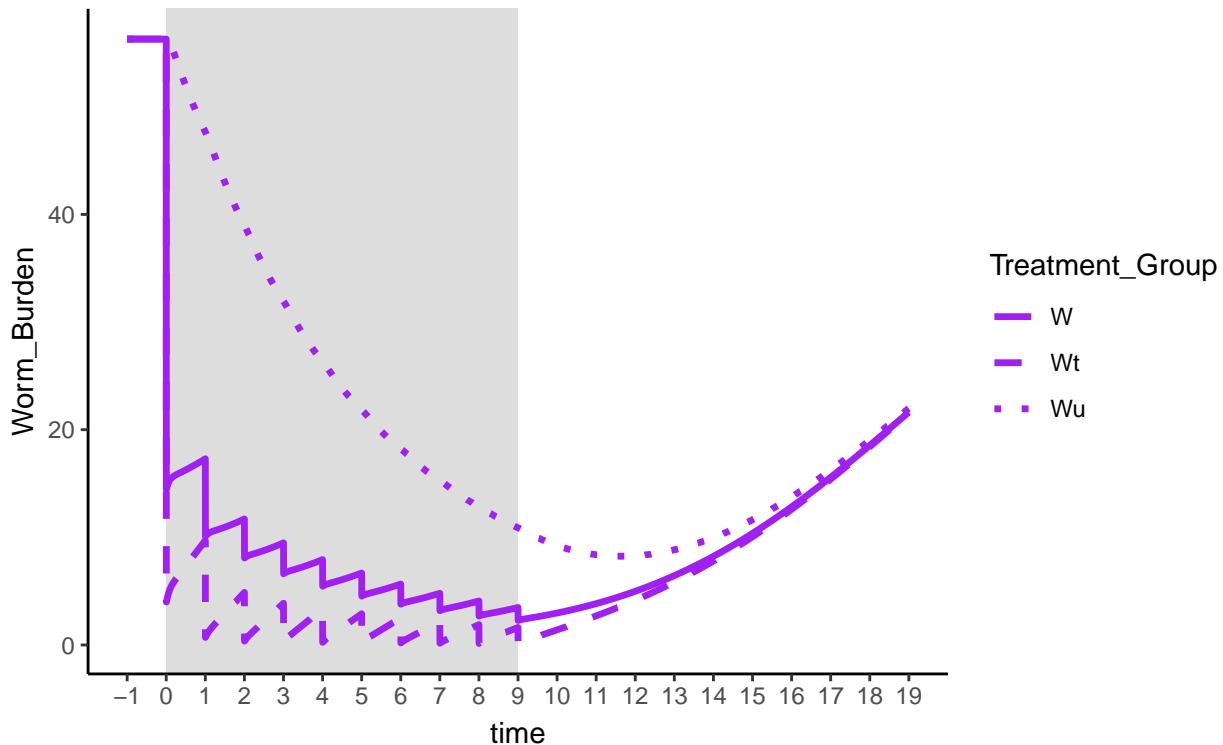
Human infection dynamics

Annual MDA for 10 years



Human infection dynamics

Annual MDA for 10 years



```
base_pars -> base_pars_C.90 ; base_pars_C.90["C"] = base_pars["C"]*.90
base_pars -> base_pars_C.80 ; base_pars_C.80["C"] = base_pars["C"]*.80
base_pars -> base_pars_C.70 ; base_pars_C.70["C"] = base_pars["C"]*.70
base_pars -> base_pars_C.60 ; base_pars_C.60["C"] = base_pars["C"]*.60
```

```
Reffs_C_red <- Reffs %>%
  mutate(Reff_C.90 = pmap_dbl(list(parameters = list(base_pars_C.90),
                                    W = test_ws,
                                    kap = w_det_ks), getReff),
        Reff_C.80 = pmap_dbl(list(parameters = list(base_pars_C.80),
                                    W = test_ws,
                                    kap = w_det_ks), getReff),
        Reff_C.70 = pmap_dbl(list(parameters = list(base_pars_C.70),
                                    W = test_ws,
                                    kap = w_det_ks), getReff),
        Reff_C.60 = pmap_dbl(list(parameters = list(base_pars_C.60),
                                    W = test_ws,
                                    kap = w_det_ks), getReff))
```

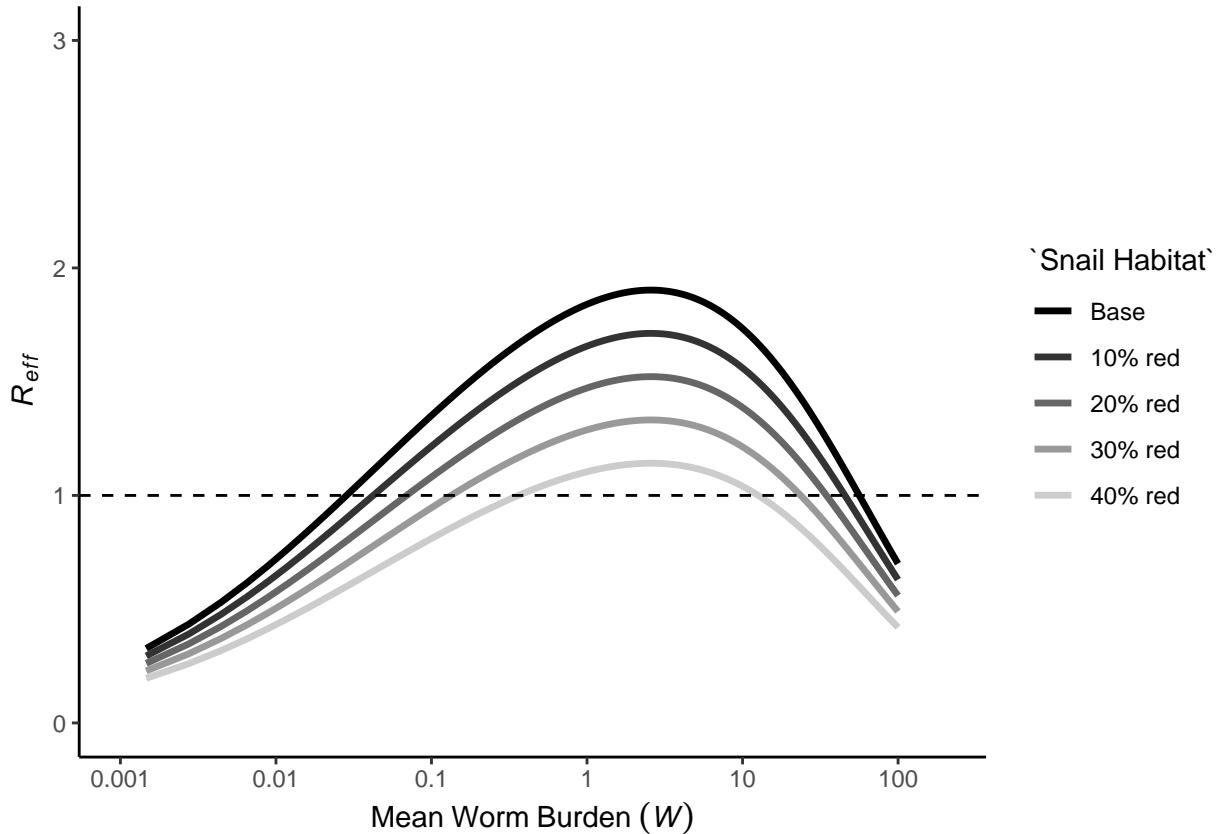
```
Reffs_C_red %>%
  gather("Snail Habitat", "Reff", Reff:Reff_C.60) %>%
  ggplot(aes(x = test_ws, y = Reff, col = `Snail Habitat`)) +
  geom_line(size = 1.2) +
  theme_classic() +
  scale_x_continuous(trans = "log",
```

```

    breaks = c(0.001, 0.01, 0.1, 1, 10, 100),
    labels = c("0.001", "0.01", "0.1", "1", "10", "100"),
    limits = c(0.001, 200)) +
  scale_y_continuous(breaks = c(0:3),
                     limits = c(0,3)) +
  geom_hline(yintercept = 1, lty = 2) +
  scale_color_manual(breaks = c("Reff", "Reff_C.90", "Reff_C.80", "Reff_C.70", "Reff_C.60"),
                     labels = c("Base",
                               "10% red",
                               "20% red",
                               "30% red",
                               "40% red"),
                     values = c("black", "grey80", "grey60", "grey40", "grey20")) +
  labs(x = expression(Mean~Worm~Burden~(italic(W))),
       y = expression(italic(R[eff])))

```

Warning: Removed 10 rows containing missing values (geom_path).



```

snail.events = data.frame(var = c(rep('S', years/2),
                                   rep('E', years/2),
                                   rep('I', years/2)),
                           time = rep(c(1:(years/2))*365, 3),
                           value = rep(0.5, (years/2)*3),
                           method = rep('mult', (years/2)*3))

```

```
schisto_base_sim <- sim_schisto_mod(nstart = base_eqbm,
                                      time = base_time,
                                      model = schisto_base_mod,
                                      parameters = base_pars,
                                      events_df = mda.events) %>%
  mutate(W = Wt*base_pars["cvrg"] + Wu*(1-base_pars["cvrg"]),
         kap = map_dbl(W, k_from_log_W),
         Reff = pmap_dbl(list(parameters = list(base_pars),
                               W = W,
                               kap = kap), getReff))
```