

# Modeling Blood Donation Workflows

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## Modeling Assumptions

This set of simulations aims to compare different workflows for arranging healthcare workers at a blood donation site to minimize risk of viral transmission. We are using it to suggest workflow improvements for blood donation sites in the context of COVID-19. This model **DOES NOT** aim to accurately estimate the risk of healthcare workers or blood donors contracting COVID-19. It is just a tool used to compare workflow designs.

We are going to work with a very simplified model of virus transmission where the risk of virus spread from any given interaction is a combination of 3 factors:

1. The likelihood that a person involved in the interactions is COVID+
2. The likelihood that the virus is transmitted during the interaction with no protective equipment in place
3. The likelihood that the protective equipment fails to stop the transmission from occurring.

```
proportion_positive <- 0.1
transmission_rate <- 0.2
ppe_failure_rate <- 0.1
interaction_risk <- proportion_positive * transmission_rate * ppe_failure_rate
cat(interaction_risk,"or",interaction_risk*100,"%")
```

```
## 0.002 or 0.2 %
```

Therefore, all three factors can be combined into the single relevant parameter `interaction_risk`. We will run simulations across a range of the parameter `interaction_risk` so that we can encompass the uncertainty in all three of the factors which define it.

## Modeling the Risk of Transmission to Healthcare Workers

The basic model will be this: a donor enters and must complete a 1) health screening and 2) blood collection. Each of those actions involves an interaction with a healthcare worker.

In each case, there is a set number of healthcare workers who can either act as screeners (S) who do the healthcare screening or phlebotomists (P) who draw the blood. The donor sees one screener and one phlebotomist.

The simulation will start with all healthcare workers being COVID-negative and simulate their random interactions with donors for the specified number of days. The output will be how many of the healthcare workers have contracted COVID-19 after X amount of days under various conditions for `interaction_risk`.

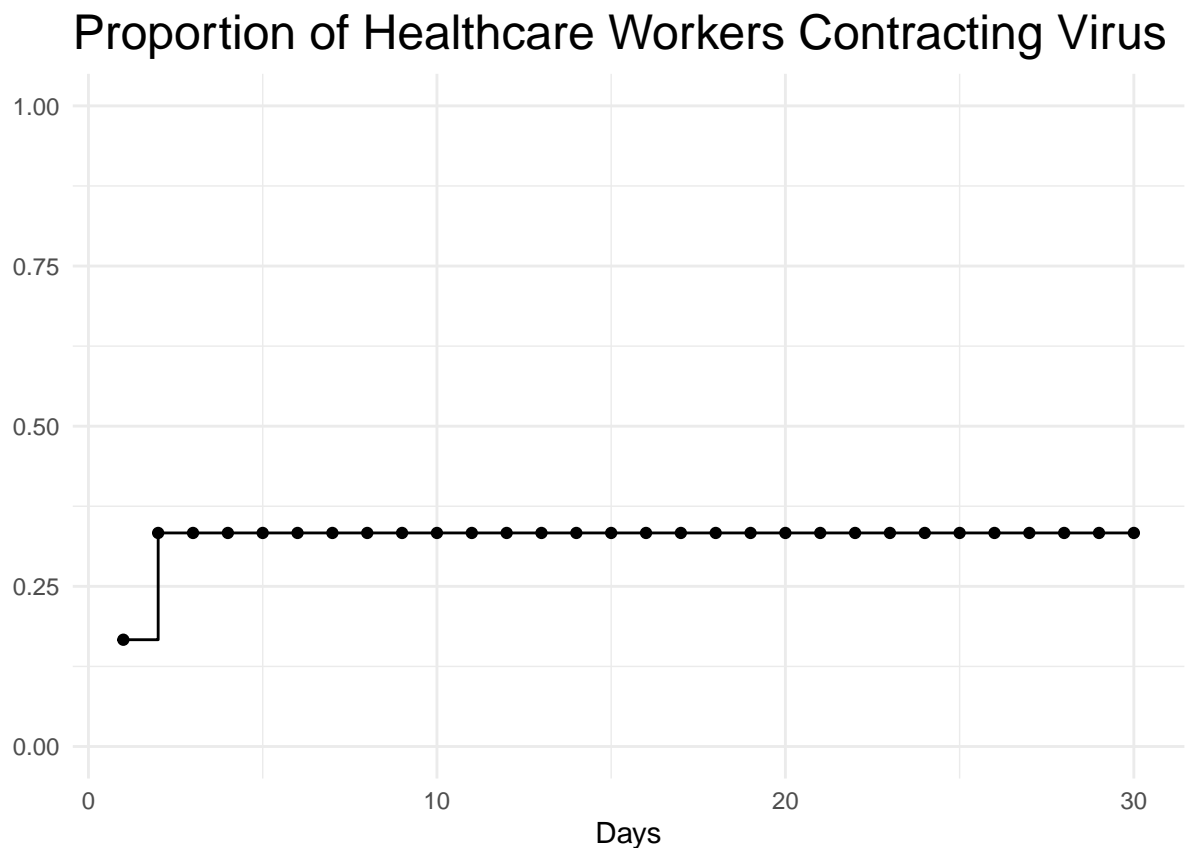
We will start with the following two necessary parameters:

- Number of healthcare workers (`n_hcw`) = 6
- Number of donors per day (`n_donors`) = 20
- Number of days (`n_days`) = 30

We are going to start with our simplest workflow design: the blood donation center has 10 healthcare workers, all of whom can be S or P. They interact with donors randomly. The simulation is carried out by the function `simulate_hcw_risk`.

```
hcw_risk_vec <- simulate_hcw_risk(n_hcw = 6,
                                n_donors = 20,
                                n_days = 30,
                                interaction_risk = 0.002)
```

We can plot the proportion of healthcare workers contracting the virus over time.



Since we are doing a random simulation for each interaction, we should simulate 100 times and take the average.

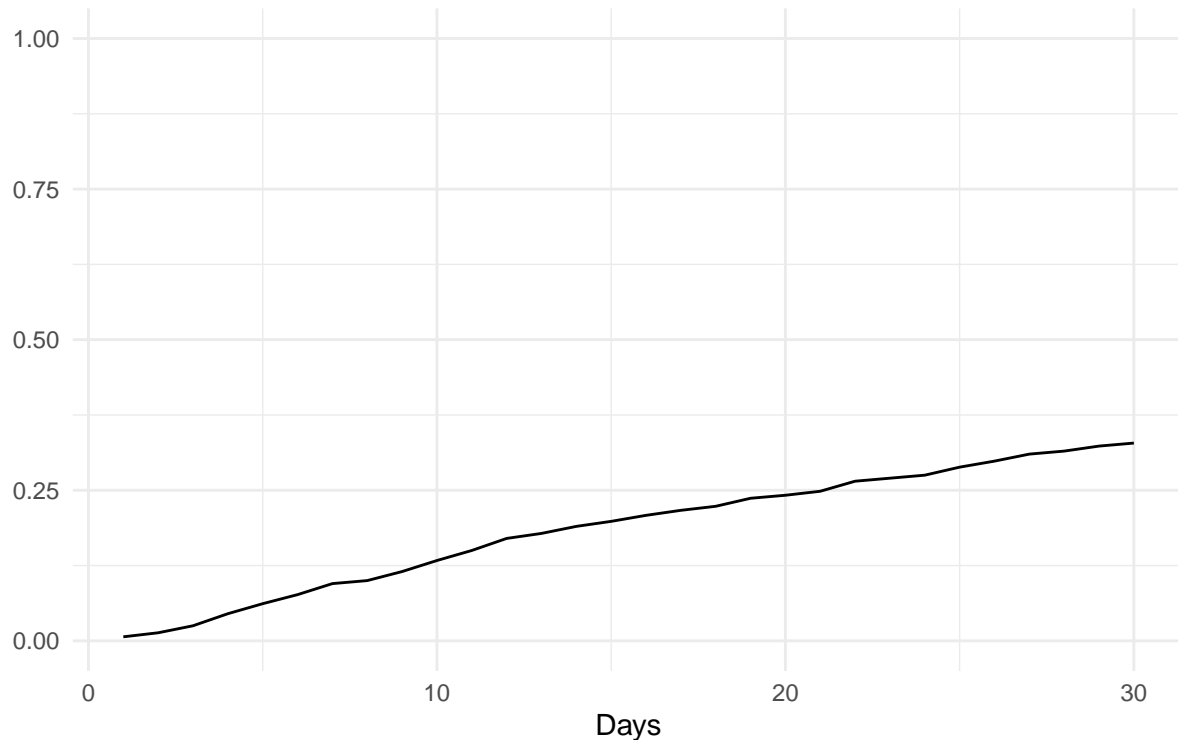
```
n_sim <- 100
hcw_risk_mat <- matrix(nrow = n_sim, ncol = 30)
for (i in 1:n_sim){
  hcw_risk_mat[i,] <- simulate_hcw_risk(n_hcw = 6,
                                        n_donors = 20,
                                        n_days = 30,
                                        interaction_risk = 0.002)
}
```

```
hcw_risk_mean <- apply(hcw_risk_mat, MARGIN = 2, FUN = mean)
```

And we can plot the mean value over the 30 days.

## Proportion of Healthcare Workers Contracting Virus

Average across 100 simulations



We are also interested in how the transmission is affected by the interaction risk, which is a lumped parameter which describes how likely a healthcare worker is to contract COVID from interacting with a blood donor. Below, we will vary the interaction risk, simulate for a given number of days 100 times, and take the average at the final timepoint as the final proportion of healthcare workers contracting the disease.

```
# Set which values of interaction_risk to explore
interaction_risk_vec <- seq(from = 0.0001, to = 0.02, by = 0.001)

# Set the number of simulations
n_sim <- 100

# Initialize a vector
interaction_risk_results <- rep(0, times = length(interaction_risk_vec))

# Simulate for each value of interaction_risk
for (i in 1:length(interaction_risk_vec)){

  # Initialize matrix for results
  hcw_risk_mat <- matrix(nrow = n_sim, ncol = 30)

  # Simulate the model across chosen number of simulations
```

```

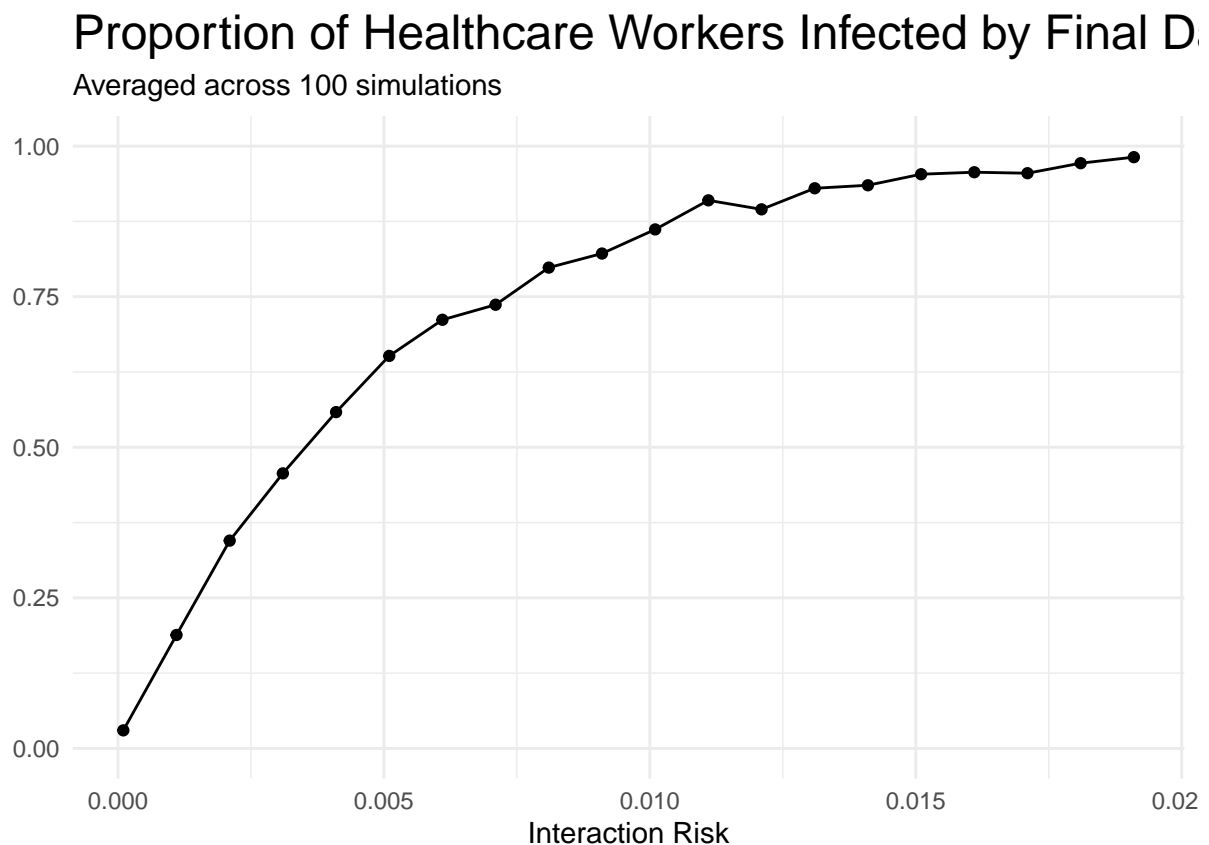
for (j in 1:n_sim){
  hcw_risk_mat[j,] <- simulate_hcw_risk(n_hcw = 6,
                                       n_donors = 20,
                                       n_days = 30,
                                       interaction_risk = interaction_risk_vec[i])
}

# Take the average across all simulations
hcw_risk_mean <- apply(hcw_risk_mat, MARGIN = 2, FUN = mean)

# Store into result vector
interaction_risk_results[i] <- hcw_risk_mean[length(hcw_risk_mean)]
}

```

And we can plot the result:



## Modeling the risk of transmission to donors

Within the same basic model, we want to include the possibility that once infected, a healthcare worker can become an asymptomatic carrier and spread the disease to donors they interact with in the future.

This can be achieved by using the same simulation but incorporating a risk of interaction from healthcare worker to donor. The risk of this happening (`donor_interaction_risk`) can be calculated similarly to the `interaction_risk` above. There is no `proportion_positive` term since the chance of this spread only happens if the healthcare worker is positive for the virus.

```

transmission_rate <- 0.2
ppe_failure_rate <- 0.1
donor_interaction_risk <- transmission_rate * ppe_failure_rate
cat(donor_interaction_risk, "or", donor_interaction_risk*100, "%")

```

## 0.02 or 2 %

The simulation takes place within the function `simulate_donor_risk`:

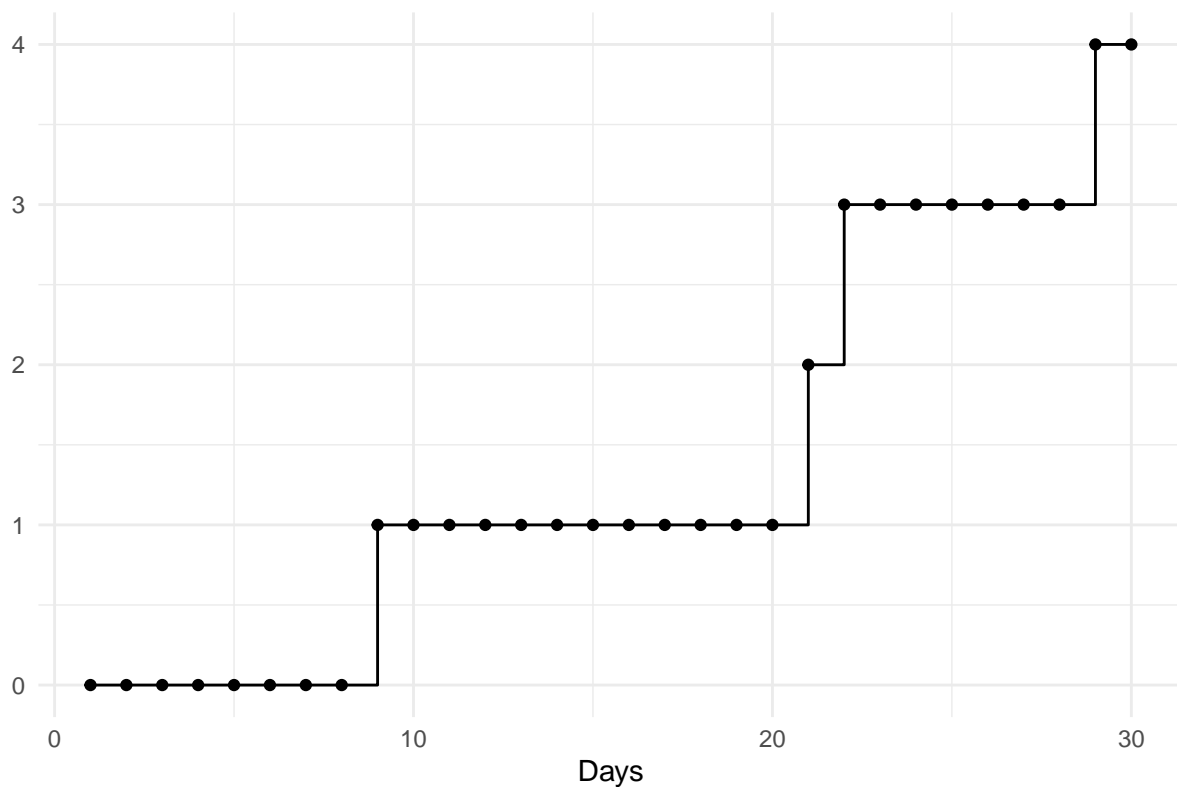
```

donor_new_cases <- simulate_donor_risk(n_hcw = 6,
                                       n_donors = 20,
                                       n_days = 30,
                                       interaction_risk = 0.002,
                                       proportion_positive = 0.1)

```

We can plot the result of new cases over the timecourse:

## Number of Donors Contracting Virus from Donation Site



Again, we can simulate 100 times and take the mean, then plot over 30 days.

```

n_sim <- 100
donor_risk_mat <- matrix(nrow = n_sim, ncol = 30)
for (i in 1:n_sim){
  donor_risk_mat[i,] <- simulate_donor_risk(n_hcw = 6,
                                             n_donors = 20,
                                             n_days = 30,

```

```

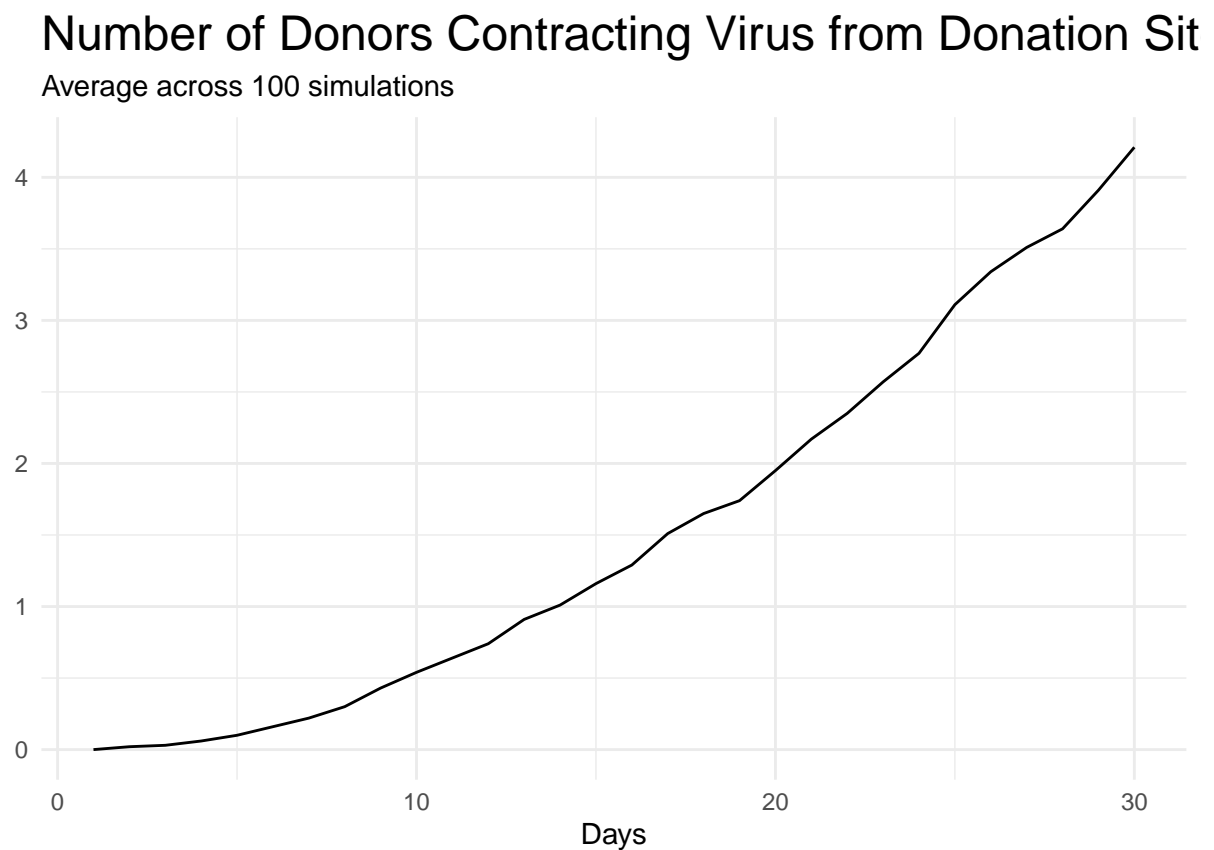
    interaction_risk = 0.002,
    proportion_positive = 0.1)
}

donor_risk_mean <- apply(donor_risk_mat, MARGIN = 2, FUN = mean)

donor_risk_mean_df <- data.frame(donor_risk_mean)

ggplot(data = donor_risk_mean_df, aes(y = donor_risk_mean, x = 1:length(donor_risk_mean))) +
  labs(x = "Days", y = "", title = "Number of Donors Contracting Virus from Donation Site",
       subtitle = paste("Average across",n_sim,"simulations")) +
  geom_line() + theme_minimal() +
  theme(plot.title = element_text(size = 18), axis.title.y = element_text(size = 16))

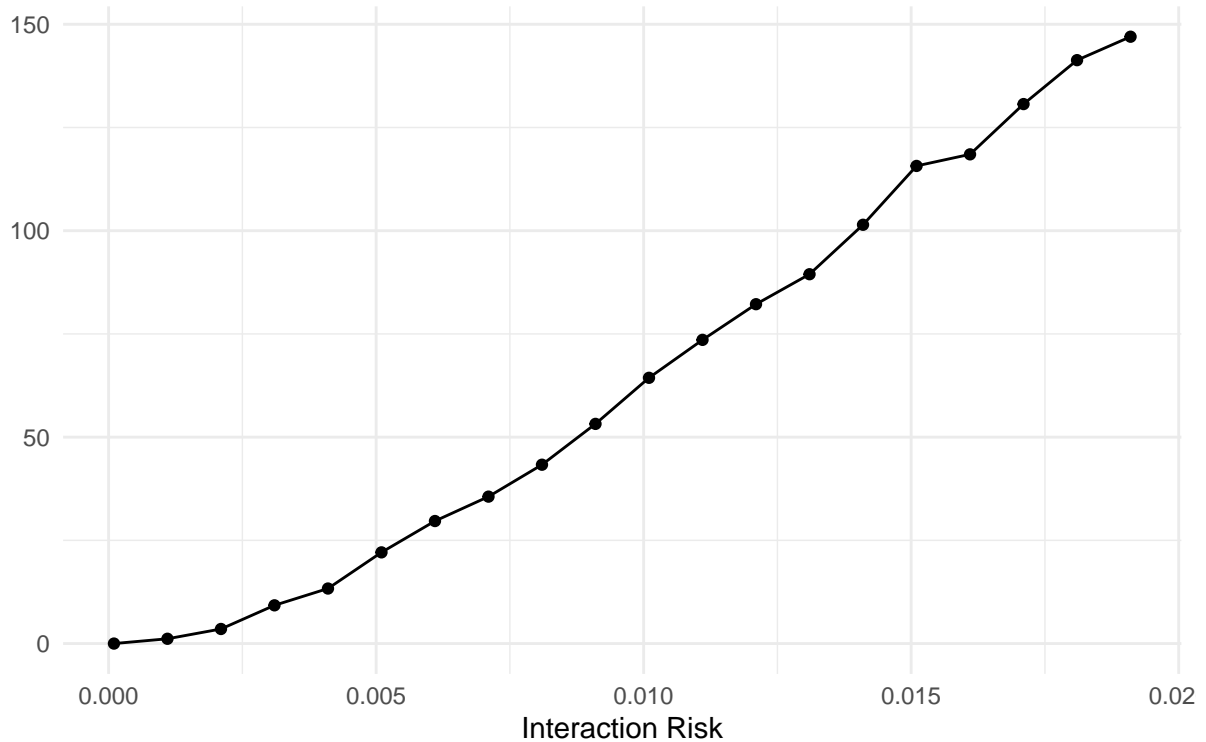
```



And we can also explore the impact of the `interaction_risk` parameter on the number of new cases acquired from the blood donation site at the end of the time period.

## Number of New Cases Acquired from Donation Site at Final

Averaged across 100 simulations



### Now to simulate and compare different workflow arrangements

We will compare the following 5 ways of arranging health screeners (S) and phlebotomists (P).

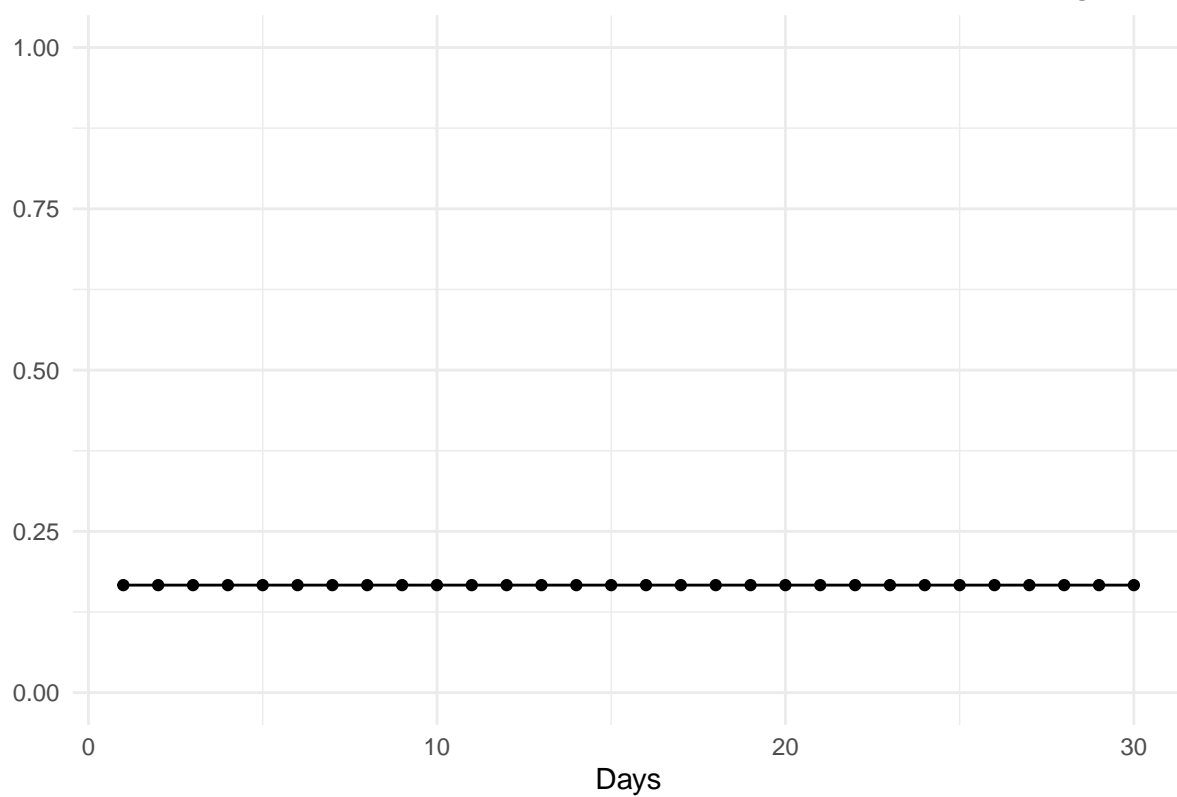
1. S and P are separate groups, assigned at random to each donor.
2. S and P are separate groups, paired for each donor
3. Healthcare workers can act as S or P, assigned at random.
4. Healthcare workers can act as S or P, stay with same donor for both steps
5. Same as case 4, but some fraction of the time, help is required from another worker.

The simulations above represent case 3. Below we will repeat the same analysis steps for cases 1, 2, 4 and 5.

### Case 1: Separate, Unpaired S and P

The proportion of healthcare workers infected over 30 days.

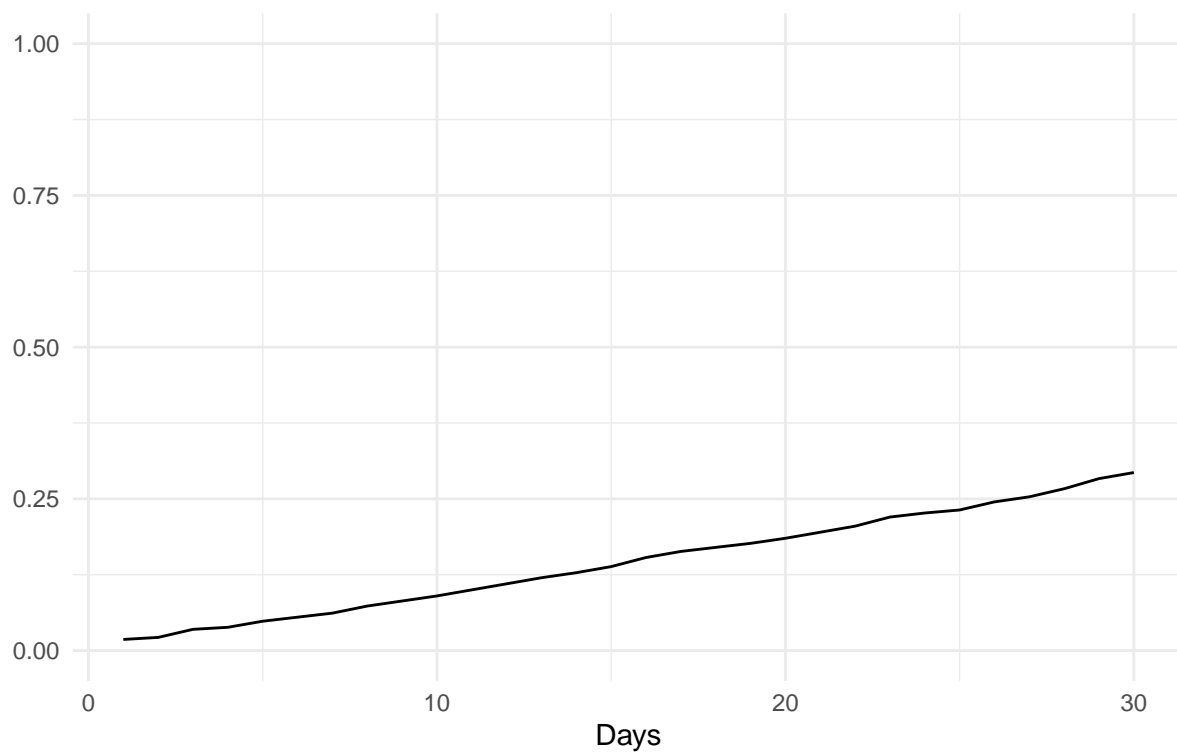
## Case 1: Proportion of Healthcare Workers Contracting Virus



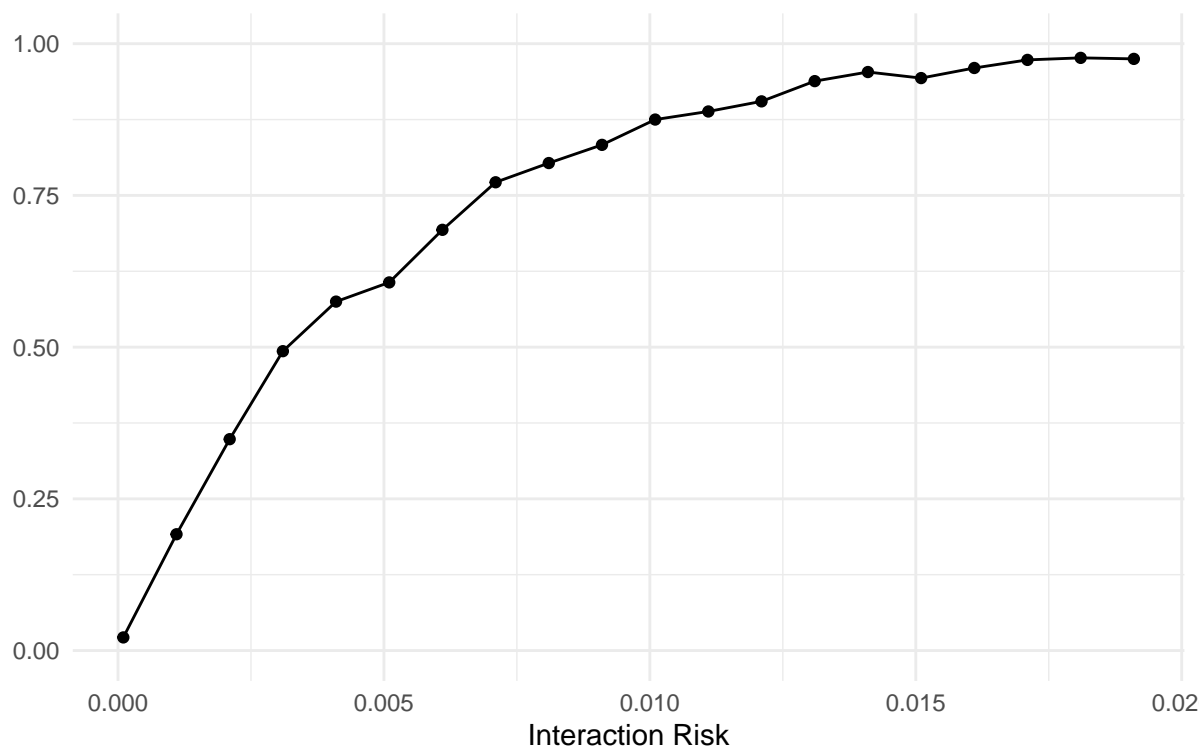


## Case 1: Proportion of Healthcare Workers Contracting Virus

Average across 100 simulations

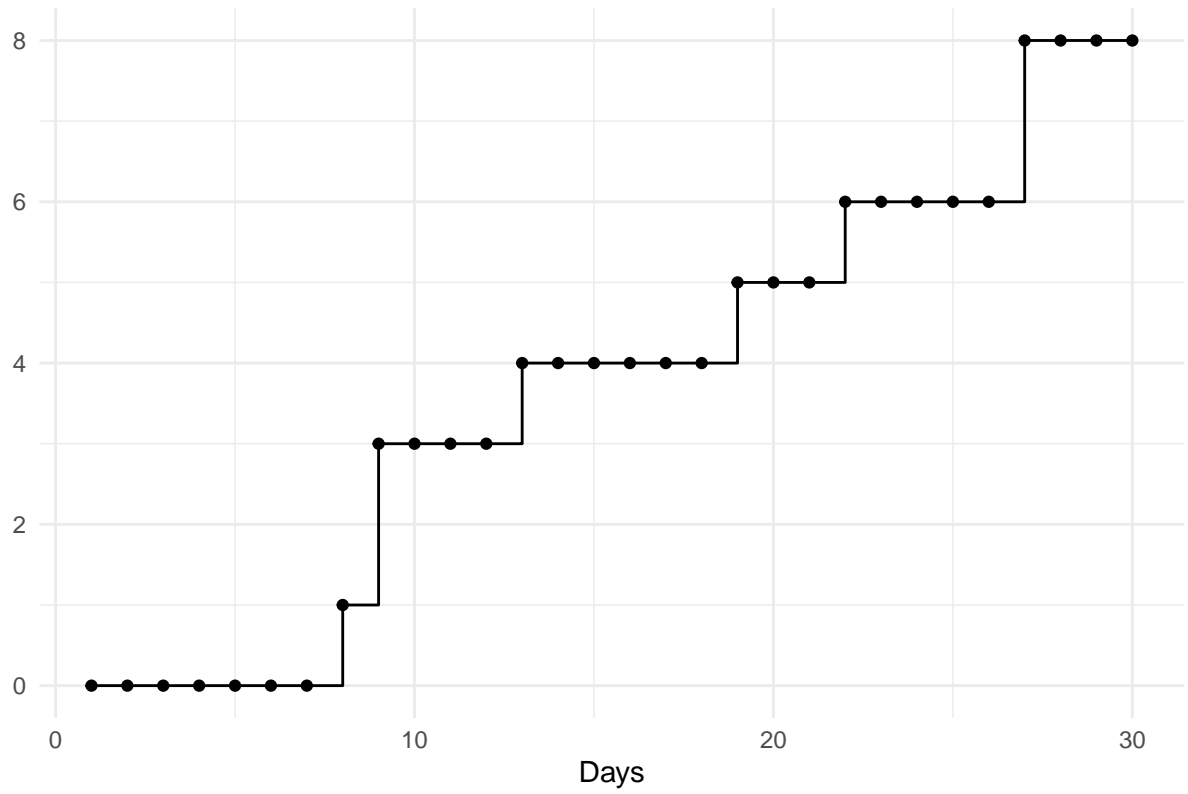


Case 1: Proportion of Healthcare Workers Infected by Final  
Averaged across 100 simulations



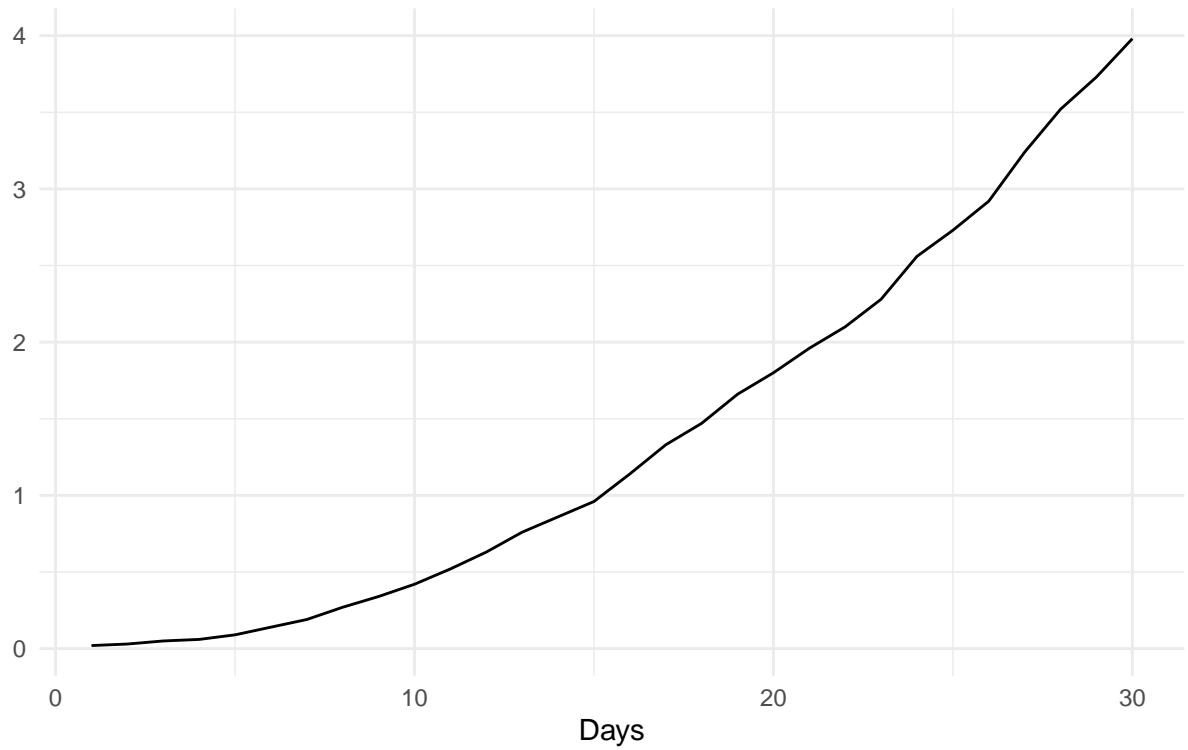
The number of new donor cases acquired at the donation center.

## Case 1: Number of Donors Contracting Virus from Donation S



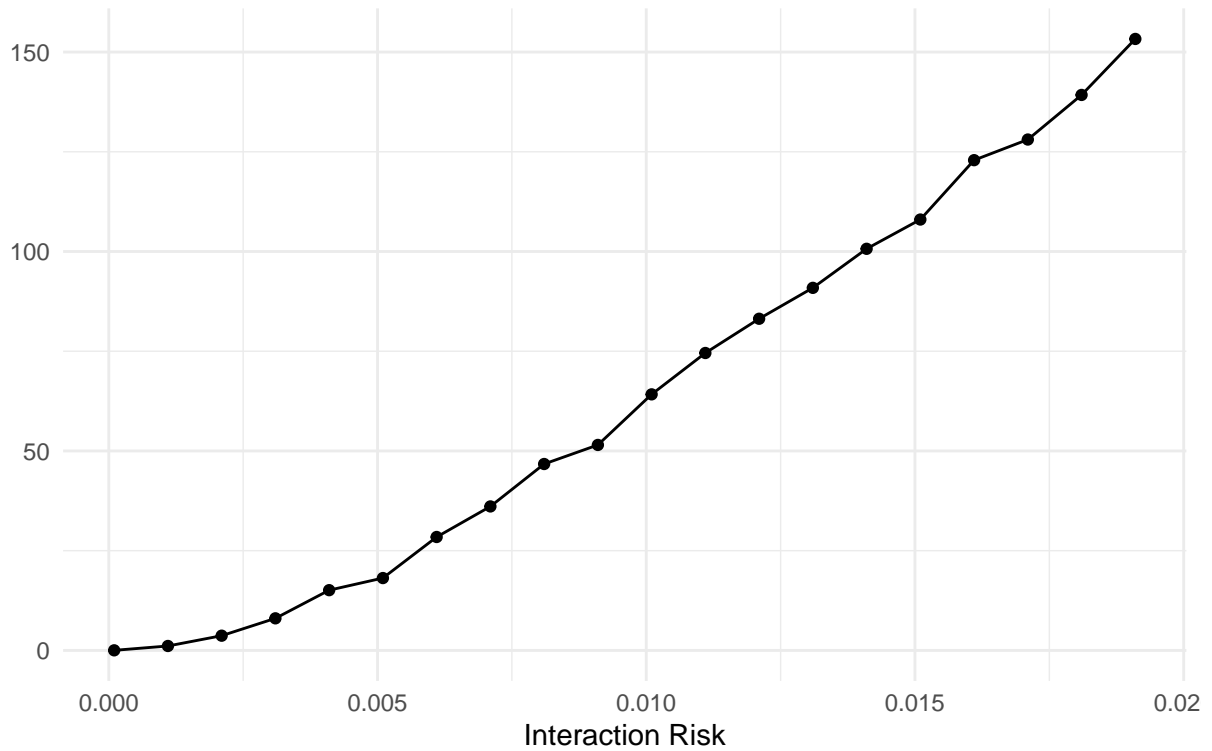
## Case 1: Number of Donors Contracting Virus from Donation S

Average across 100 simulations



### Case 1: Number of New Cases Acquired from Donation Site at Final I

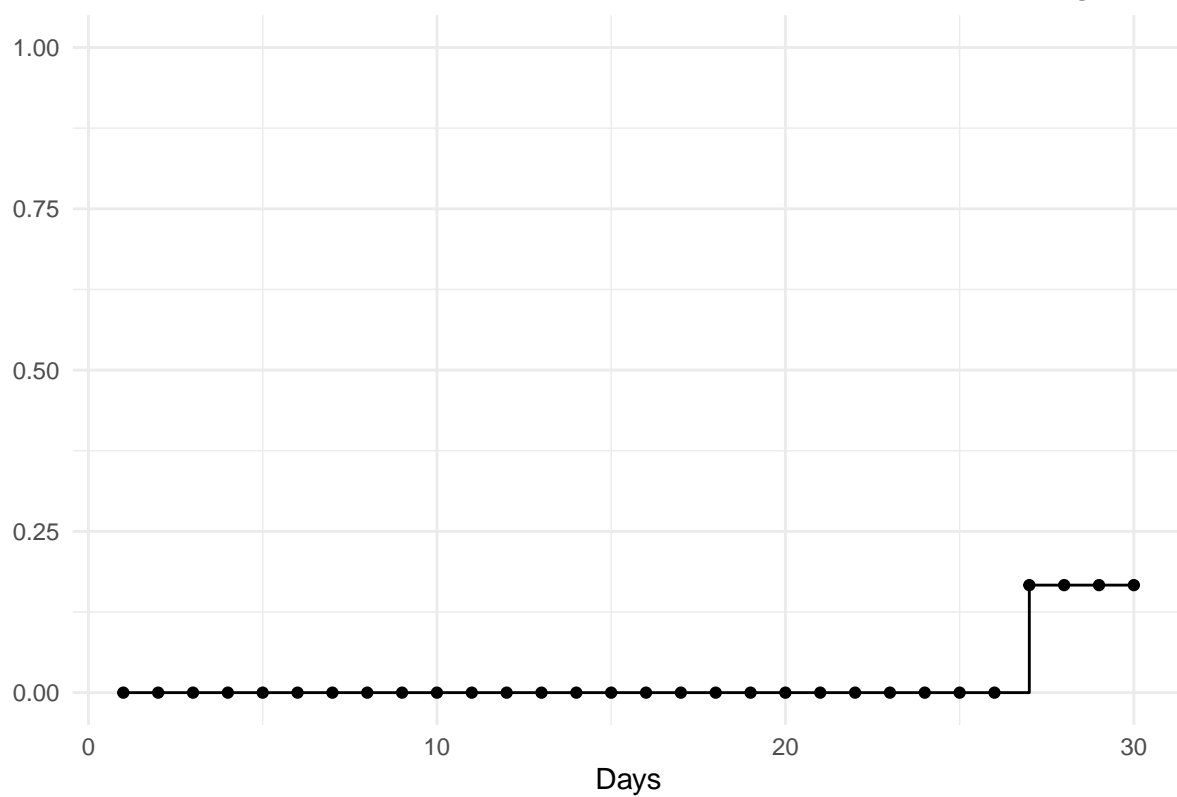
Averaged across 100 simulations



### Case 2: Separate, Paired S and P

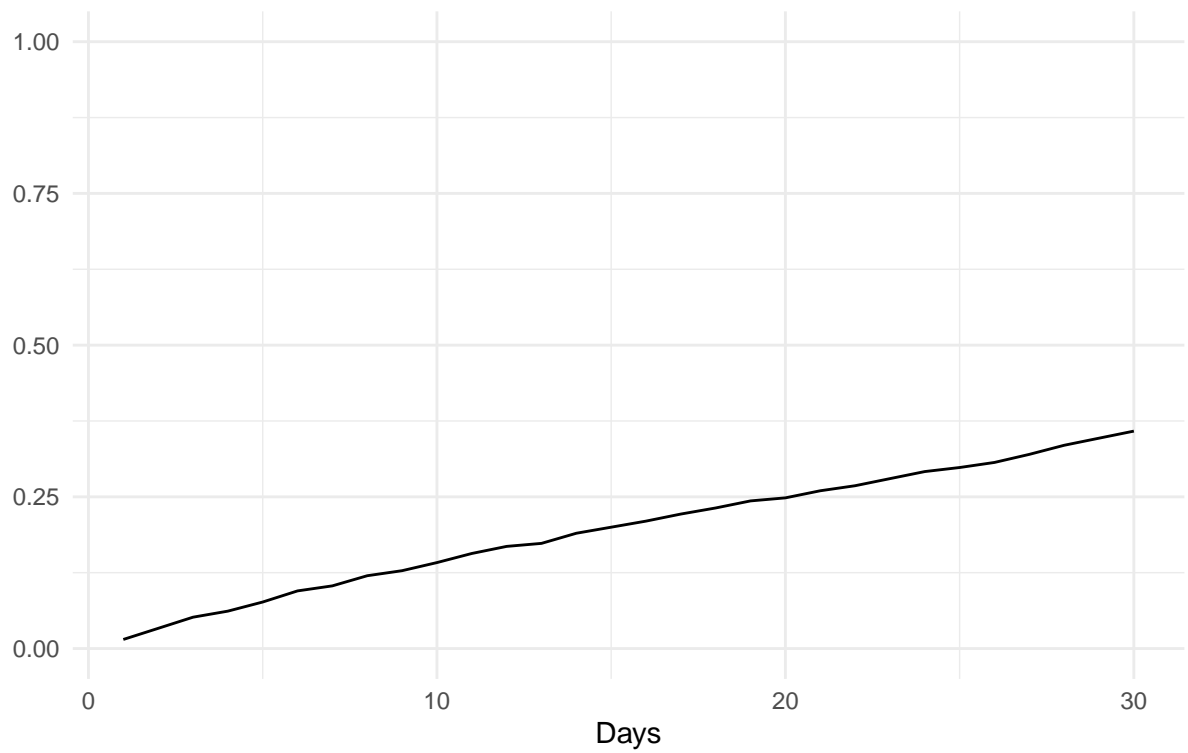
The proportion of healthcare workers infected over 30 days.

## Case 2: Proportion of Healthcare Workers Contracting Virus



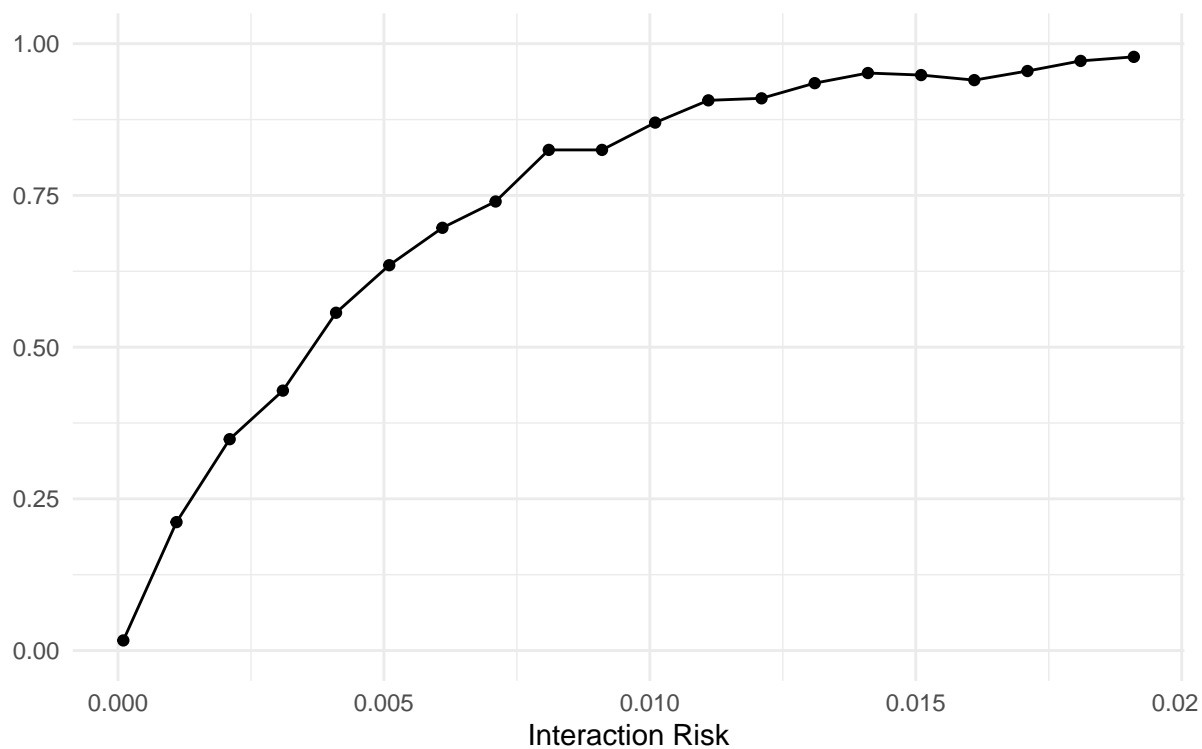
## Case 2: Proportion of Healthcare Workers Contracting Virus

Average across 100 simulations



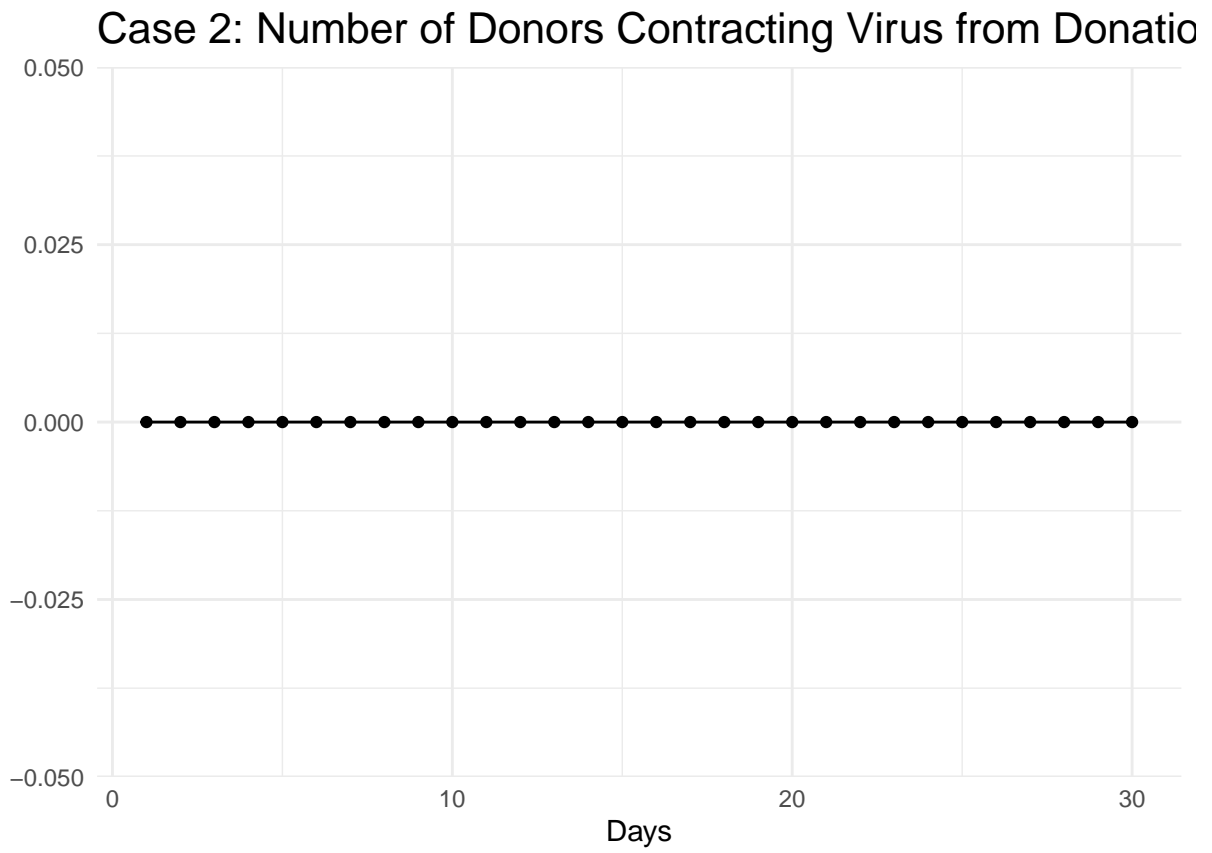
## Case 2: Proportion of Healthcare Workers Infected by Final

Averaged across 100 simulations



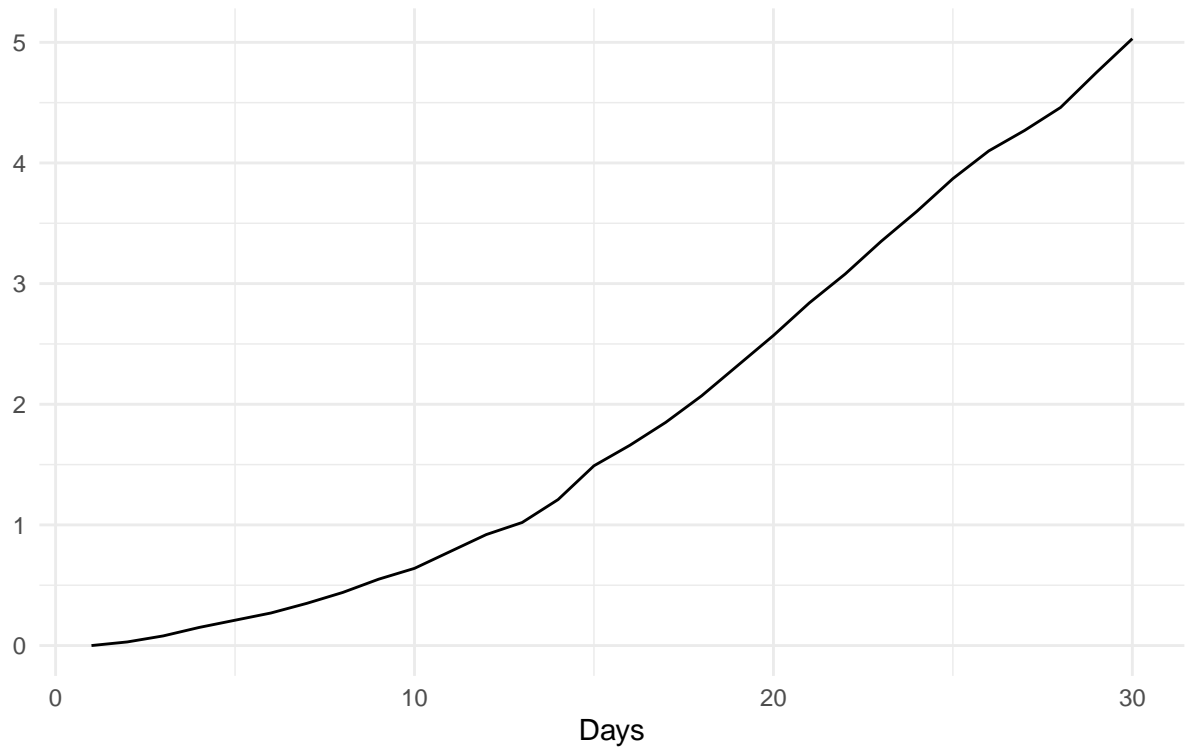
The number of new donor cases acquired at the donation center.





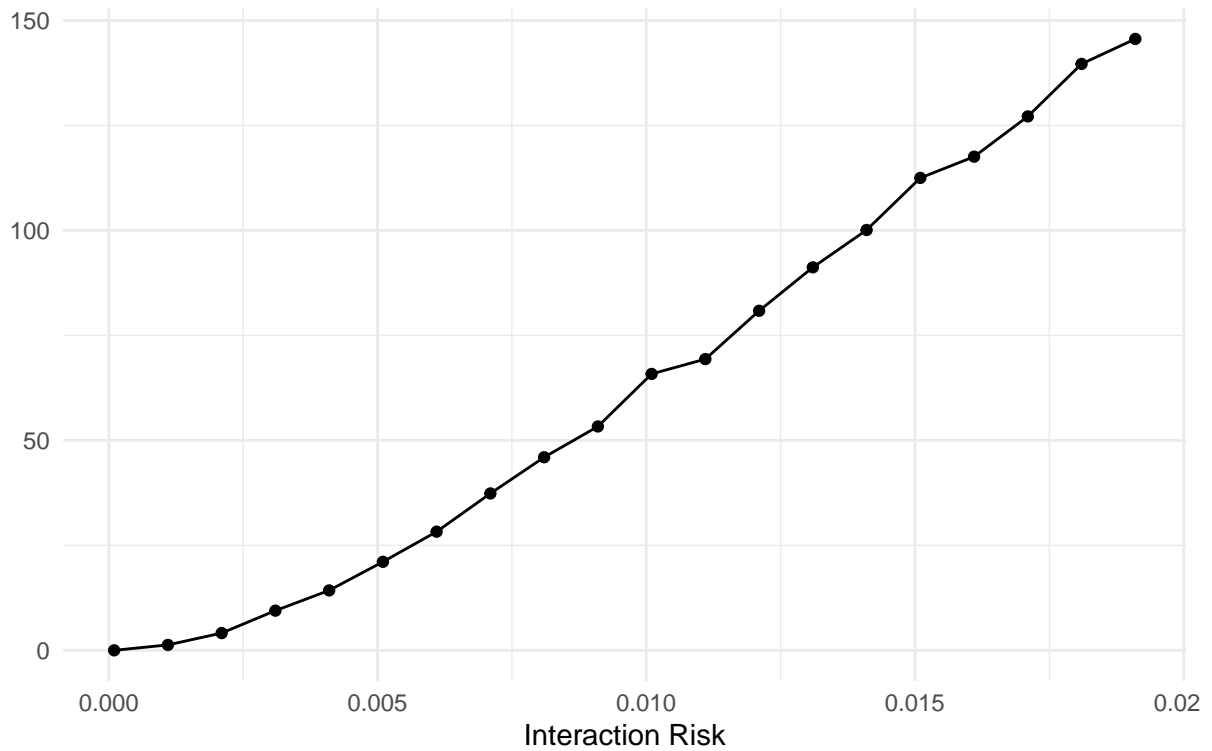
## Case 2: Number of Donors Contracting Virus from Donation S

Average across 100 simulations



### Case 2: Number of New Cases Acquired from Donation Site at Final I

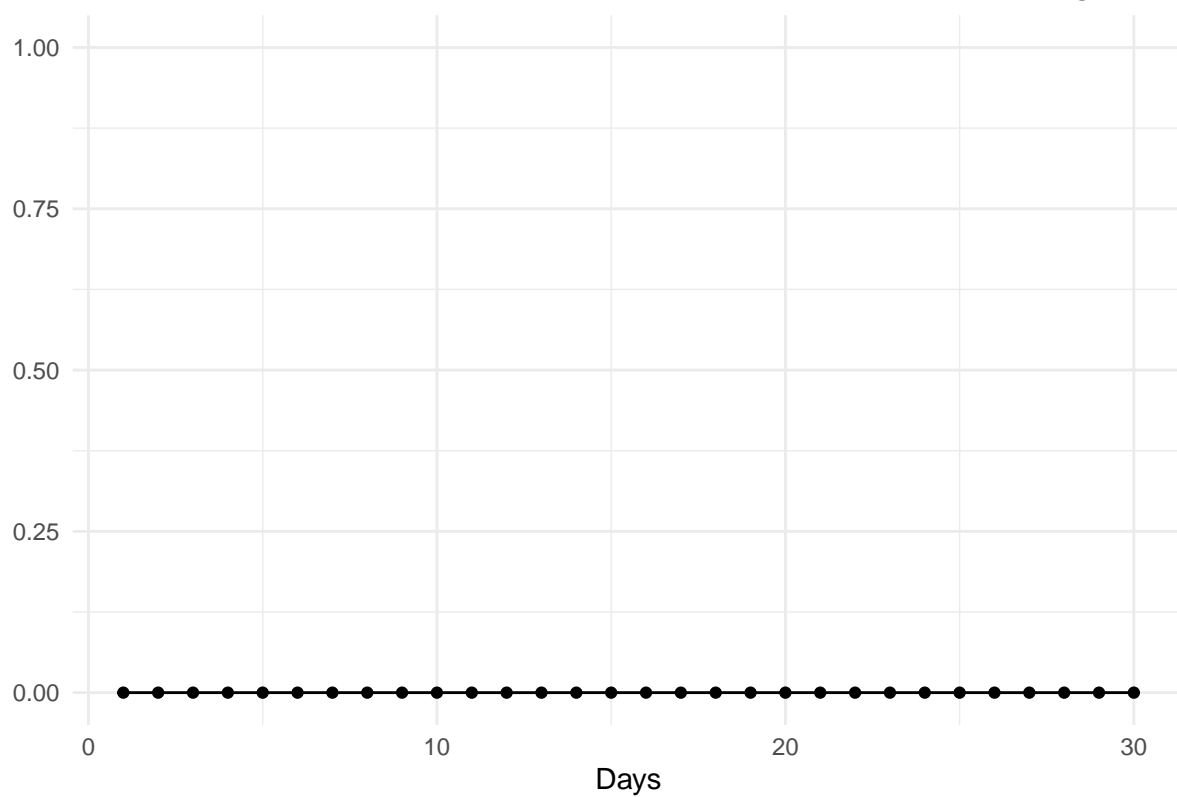
Averaged across 100 simulations



### Case 3: Dual Function S and P, Mixed Donors

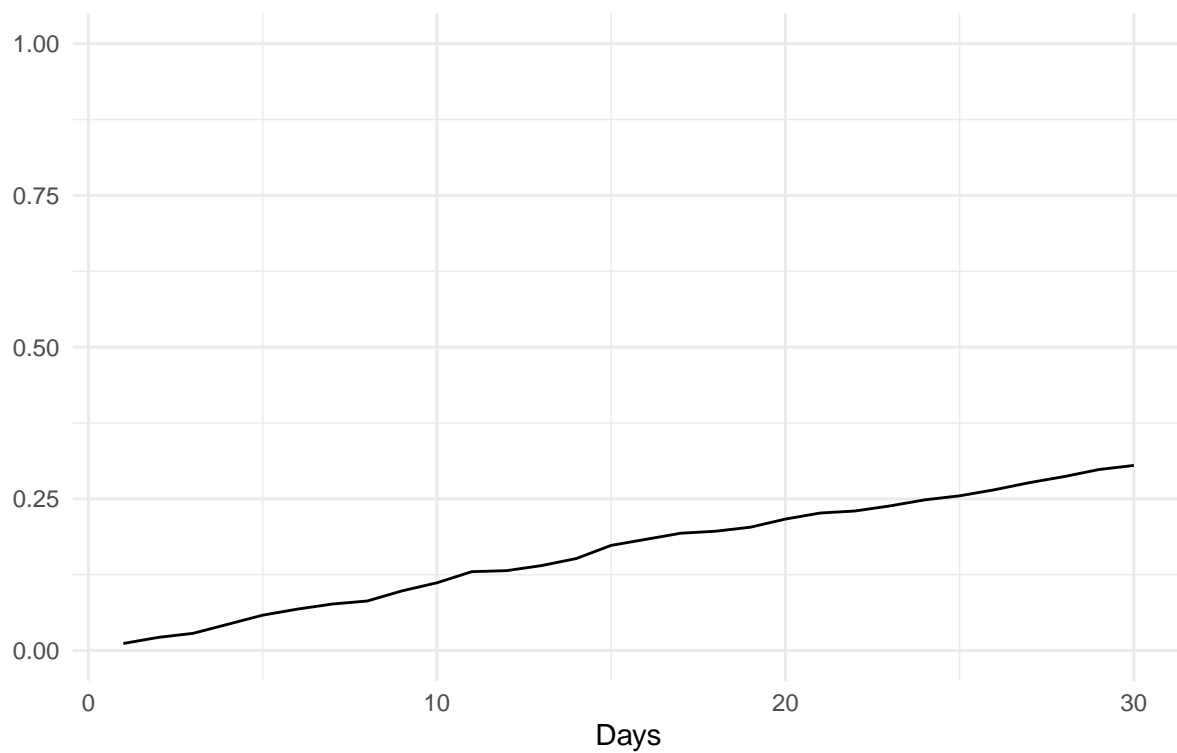
The proportion of healthcare workers infected over 30 days.

### Case 3: Proportion of Healthcare Workers Contracting Virus



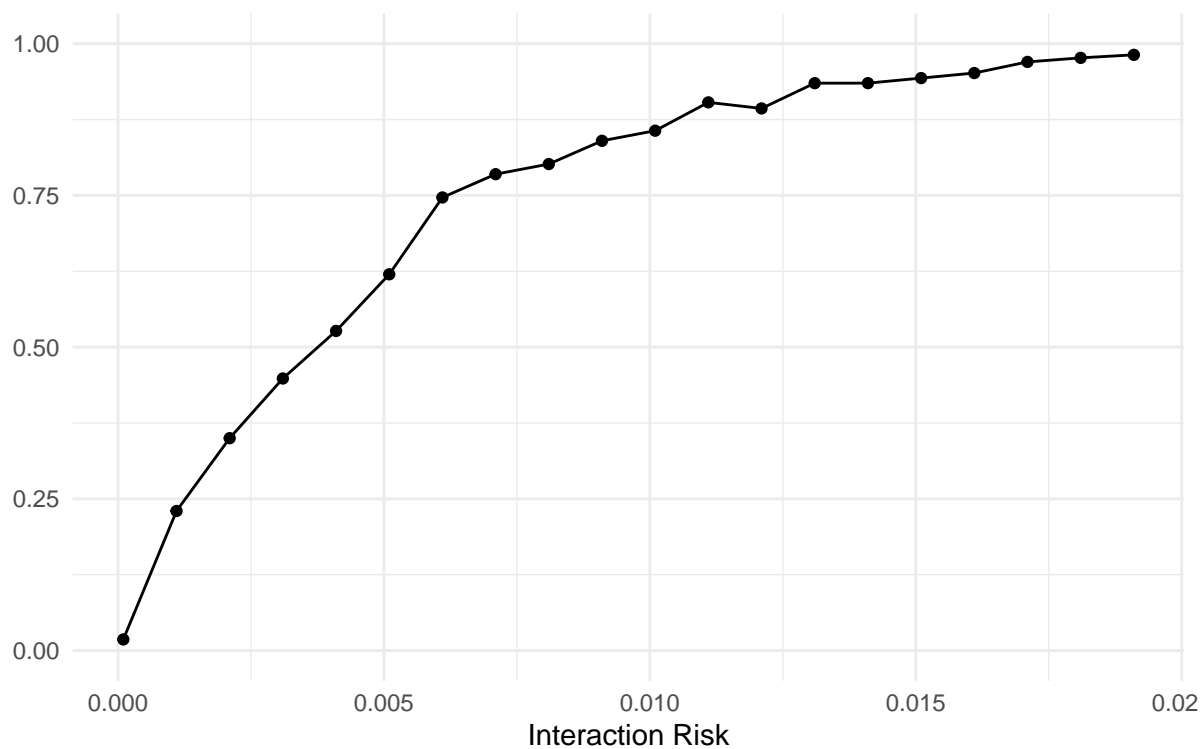
### Case 3: Proportion of Healthcare Workers Contracting Virus

Average across 100 simulations



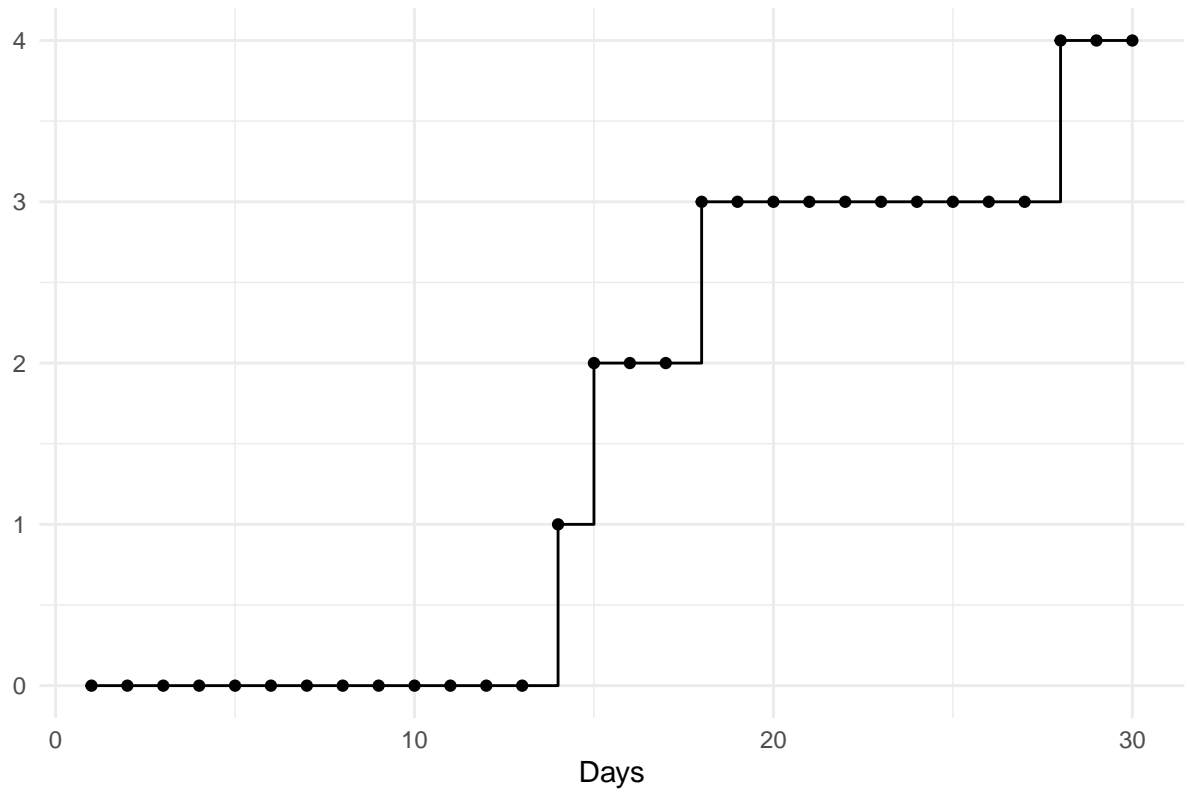
### Case 3: Proportion of Healthcare Workers Infected by Final

Averaged across 100 simulations



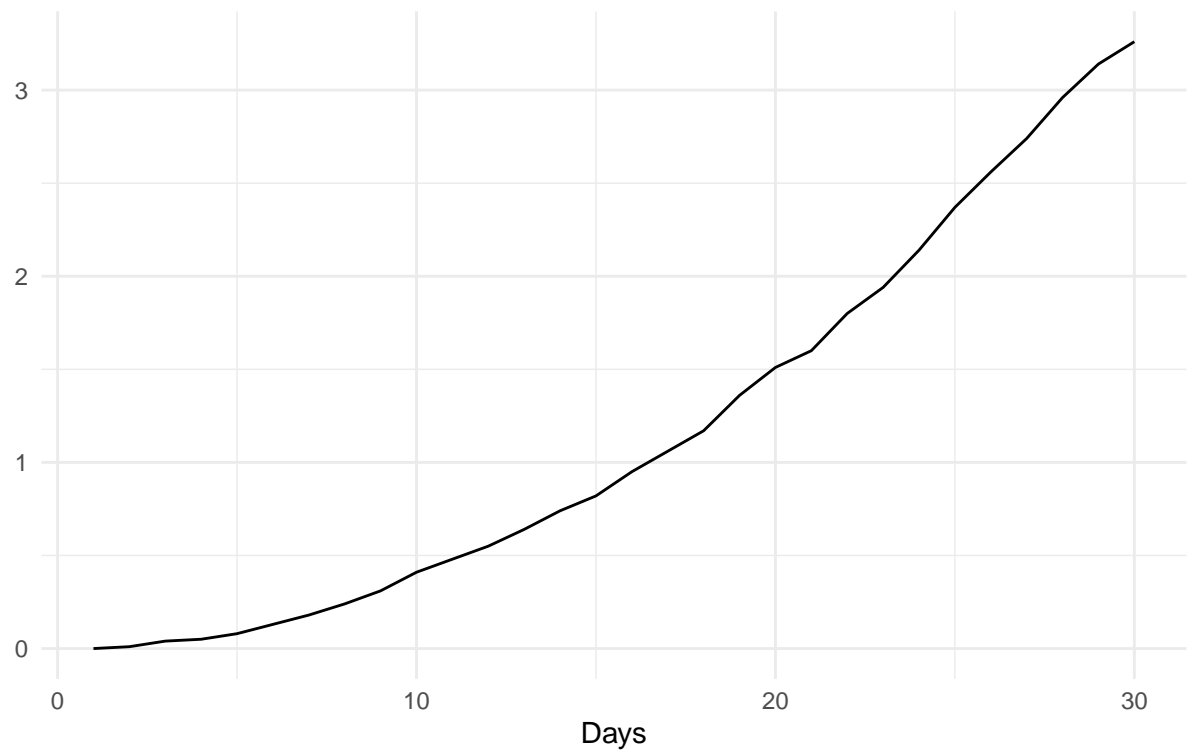
The number of new donor cases acquired at the donation center.

### Case 3: Number of Donors Contracting Virus from Donation S



### Case 3: Number of Donors Contracting Virus from Donation S

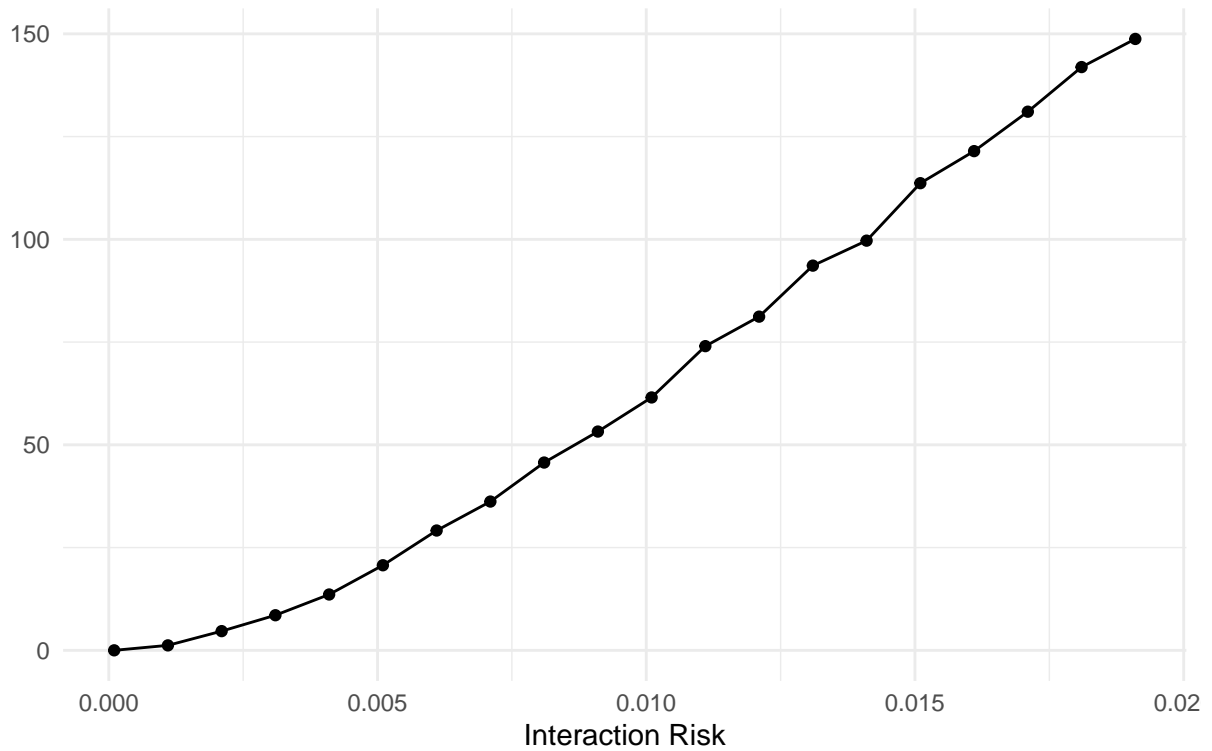
Average across 100 simulations





### Case 3: Number of New Cases Acquired from Donation Site at Final I

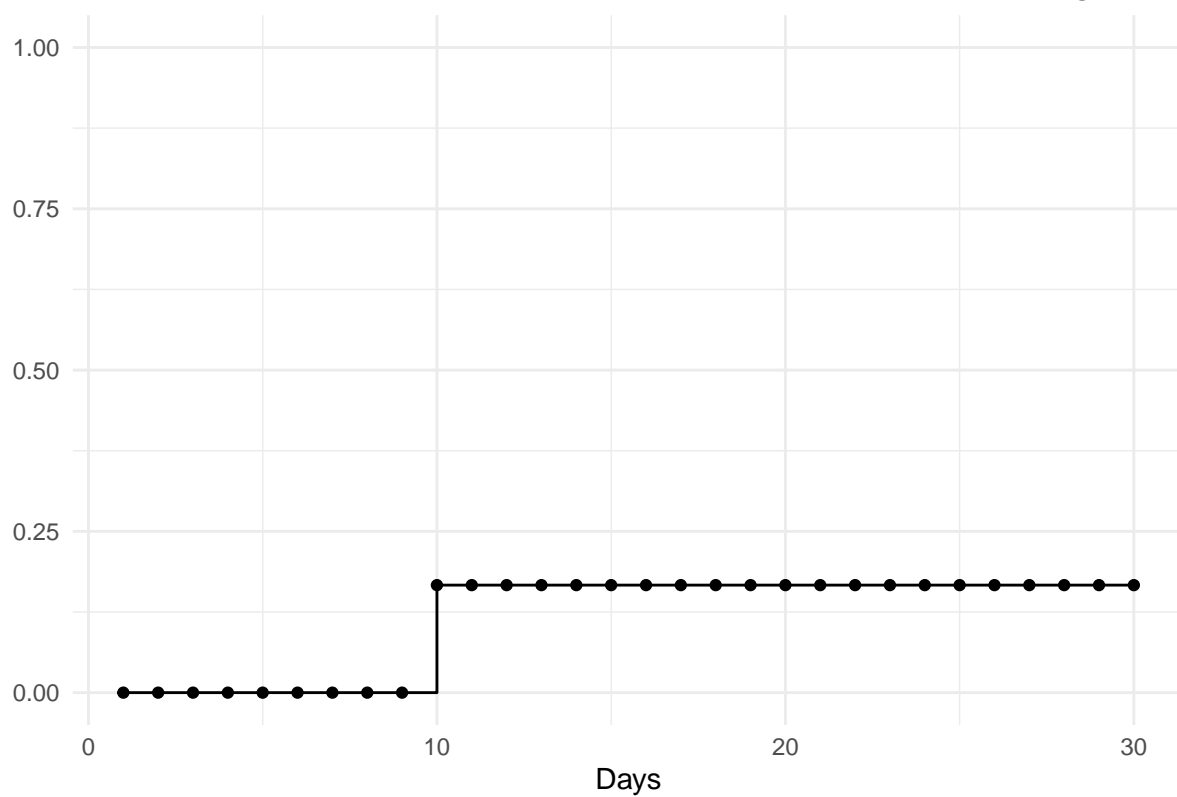
Averaged across 100 simulations



### Case 4: Dual Function S and P, Fixed Donor

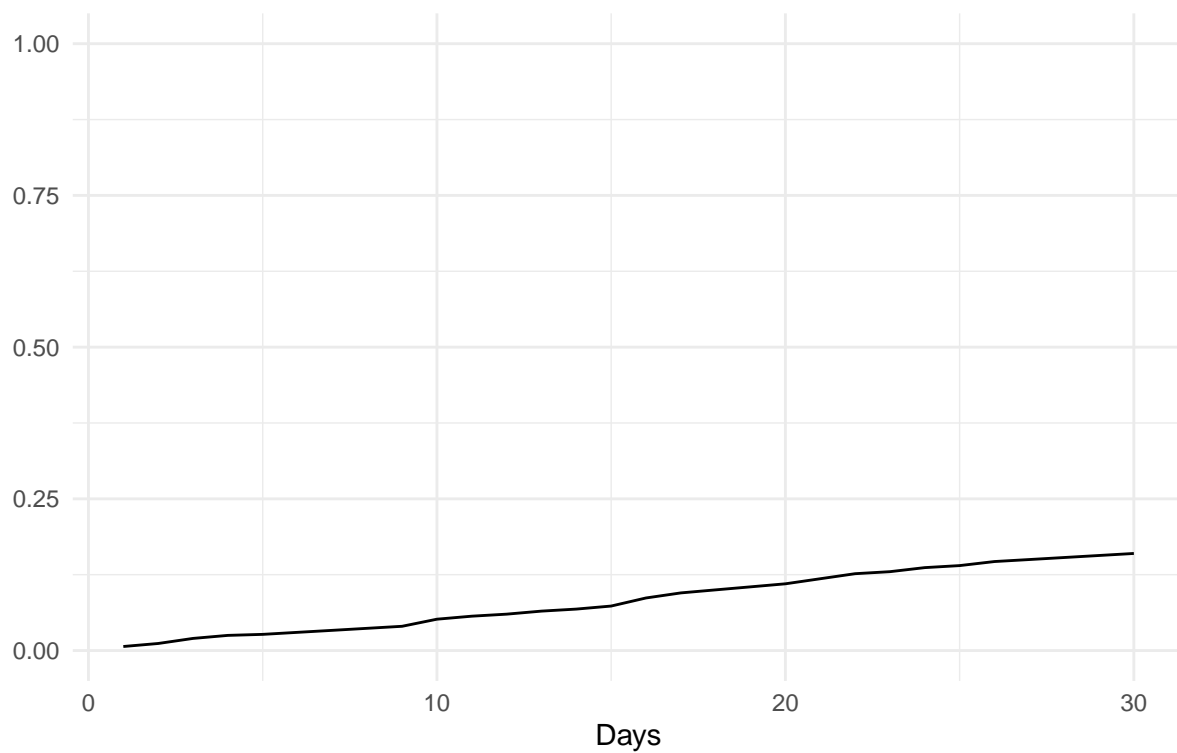
The proportion of healthcare workers infected over 30 days.

## Case 4: Proportion of Healthcare Workers Contracting Virus



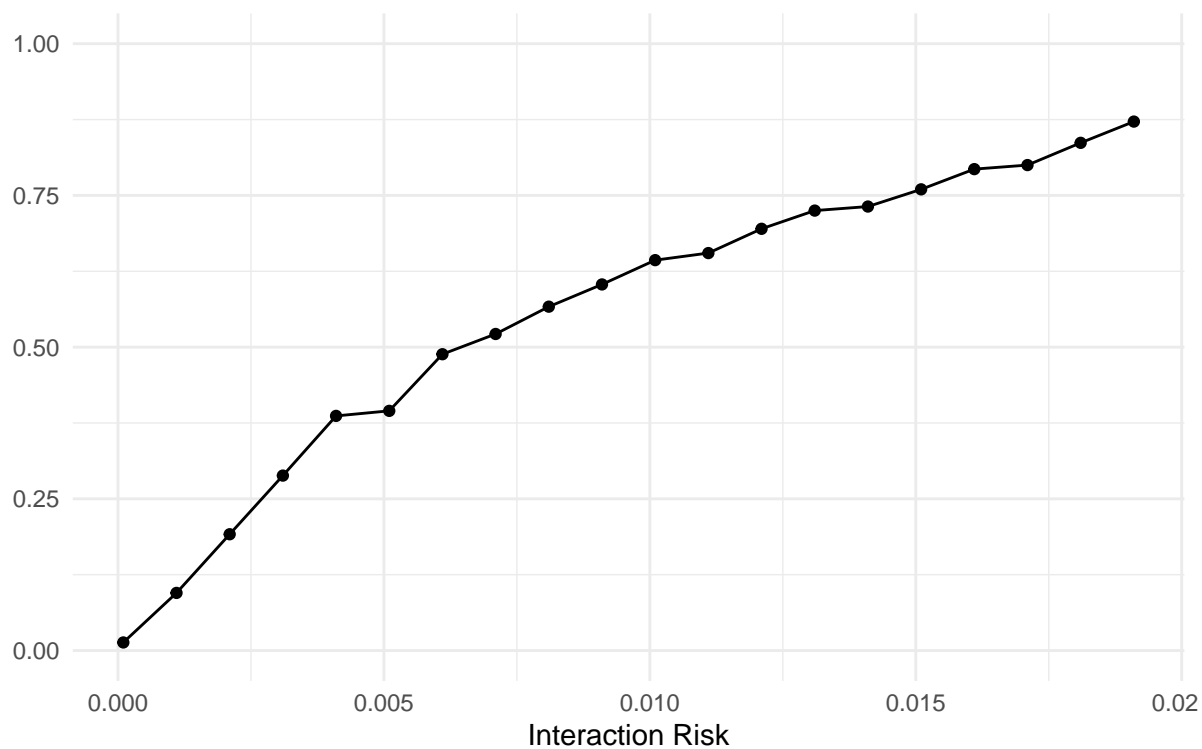
## Case 4: Proportion of Healthcare Workers Contracting Virus

Average across 100 simulations

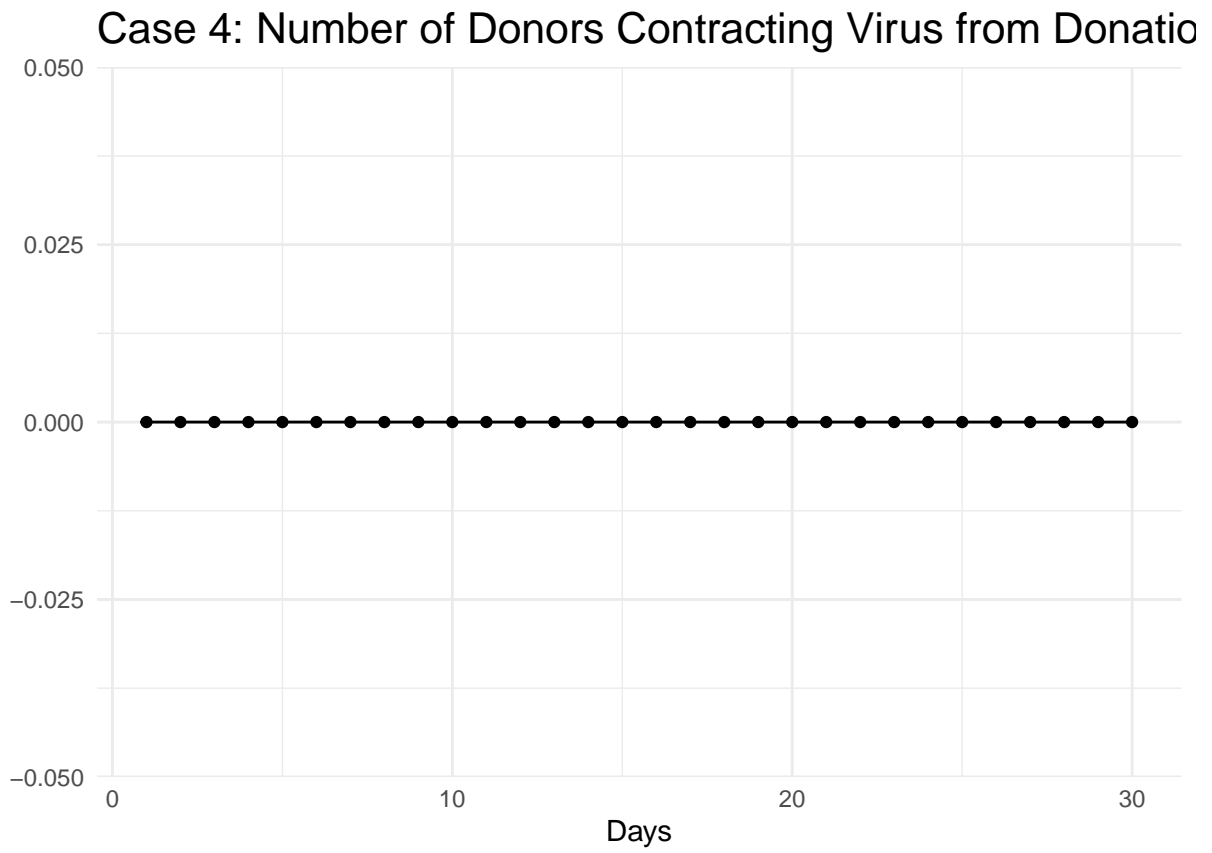


## Case 4: Proportion of Healthcare Workers Infected by Final

Averaged across 100 simulations

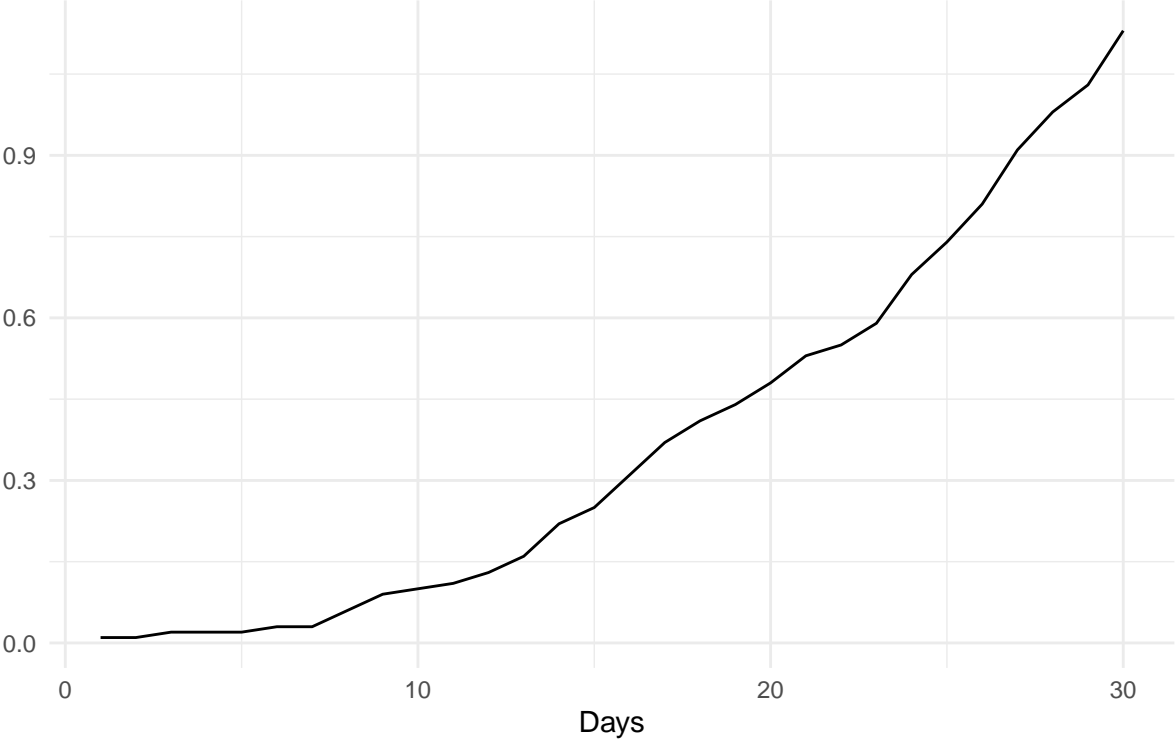


The number of new donor cases acquired at the donation center.

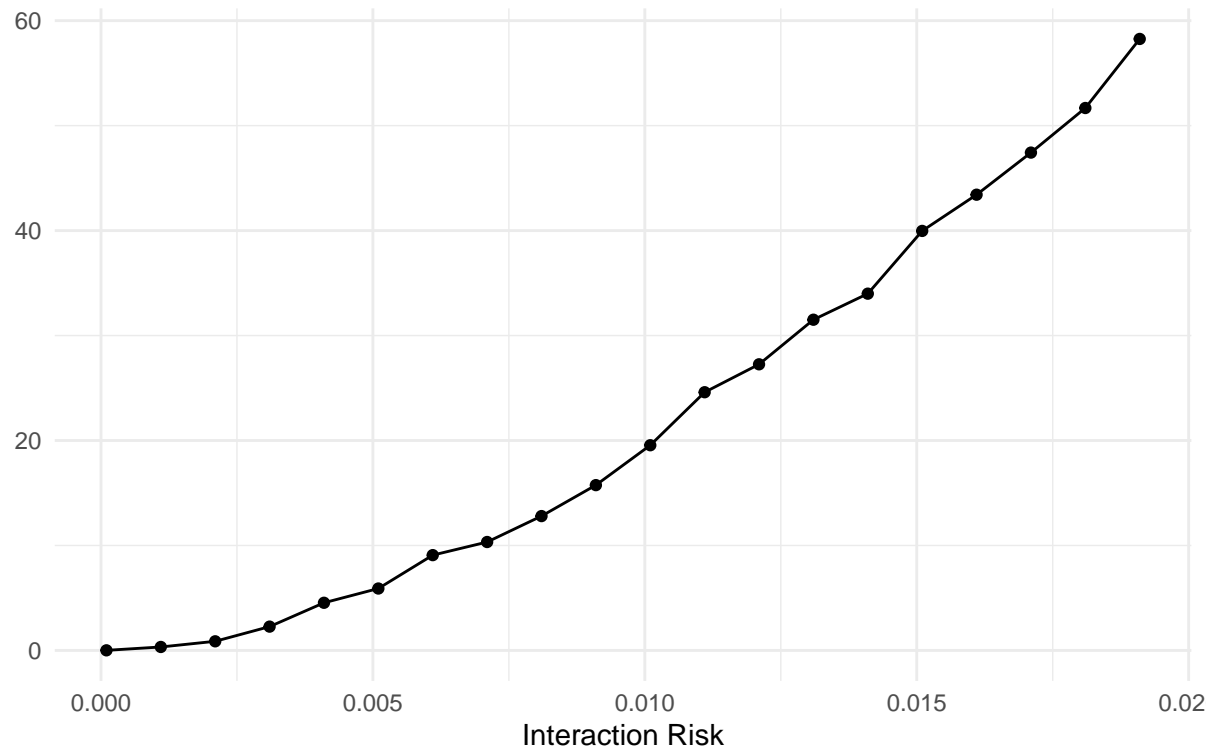


# Case 4: Number of Donors Contracting Virus from Donation

Average across 100 simulations



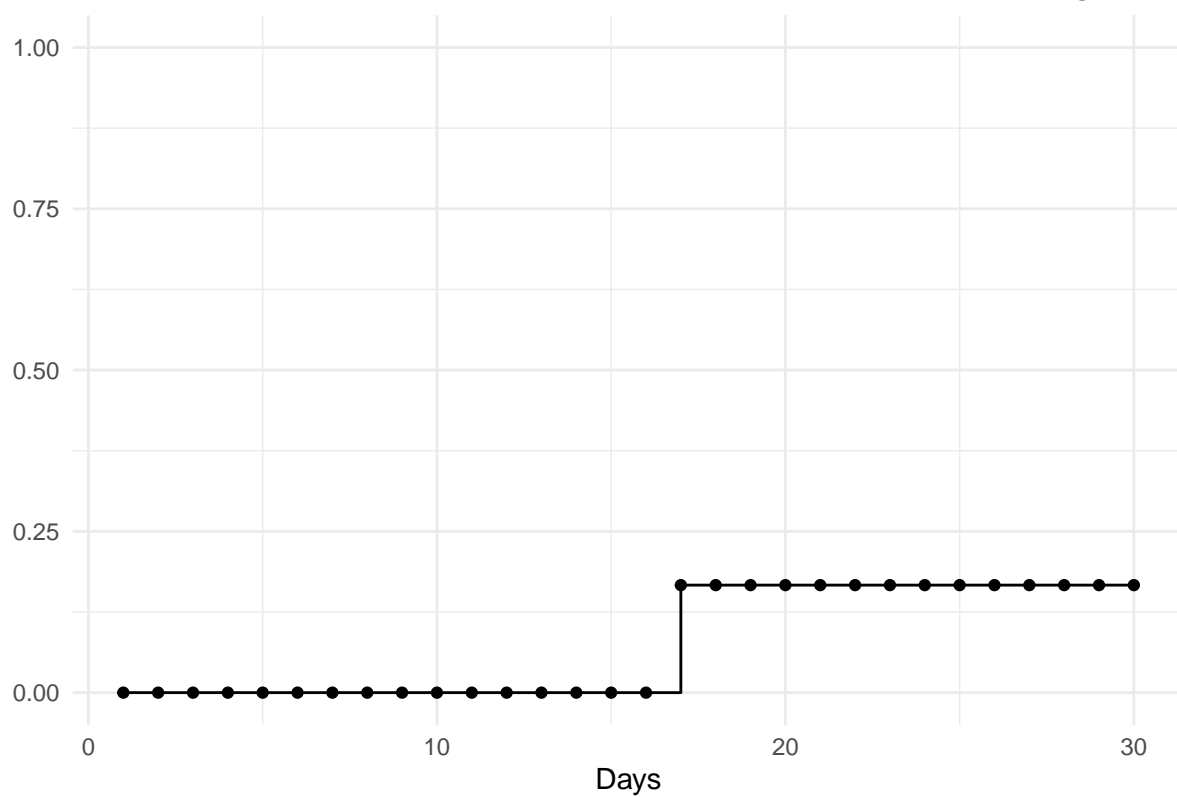
#### Case 4: Number of New Cases Acquired from Donation Site at Final C Averaged across 100 simulations



#### Case 5: Dual Function S and P, Fixed Donor, with Assist Rate

The proportion of healthcare workers infected over 30 days.

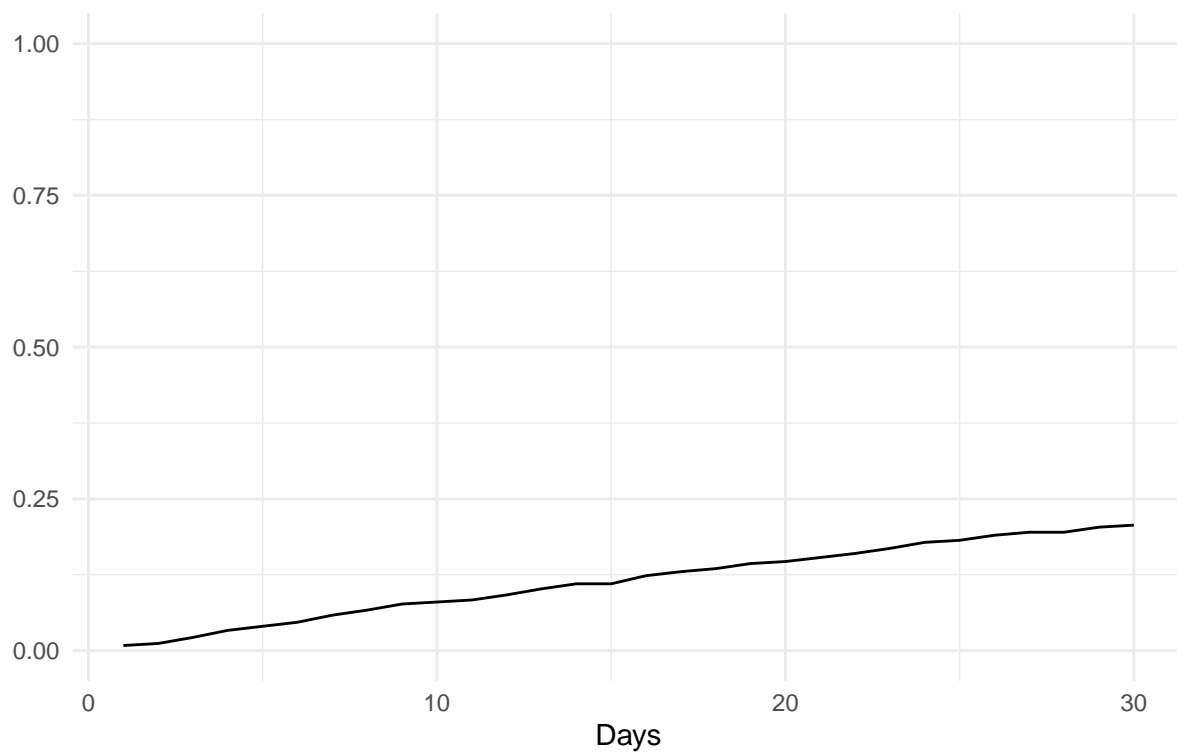
## Case 5: Proportion of Healthcare Workers Contracting Virus





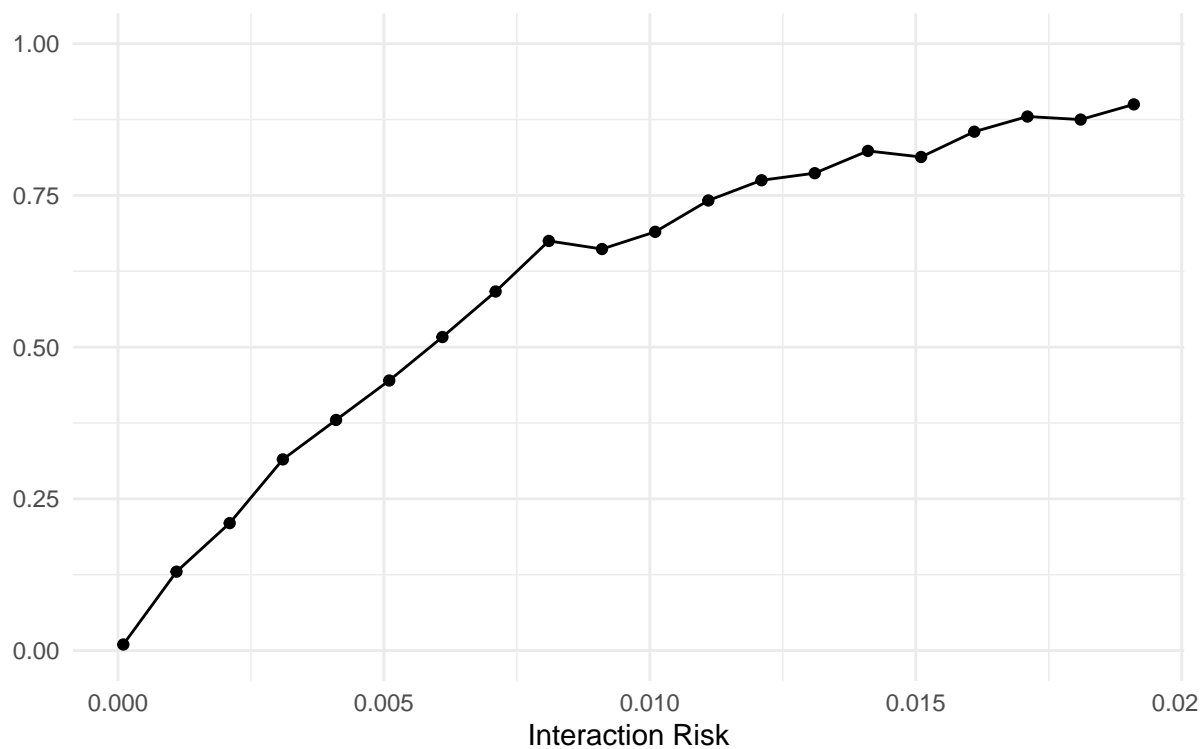
## Case 5: Proportion of Healthcare Workers Contracting Virus

Average across 100 simulations



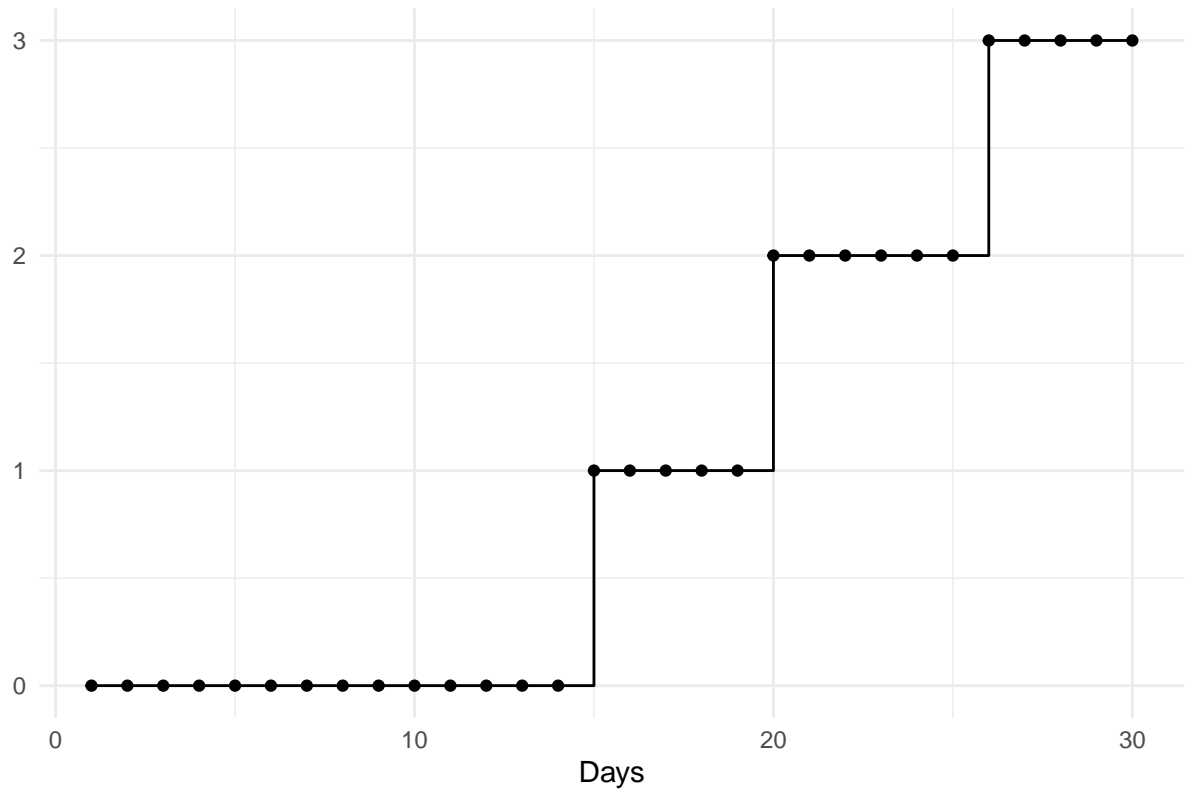
## Case 5: Proportion of Healthcare Workers Infected by Final

Averaged across 100 simulations



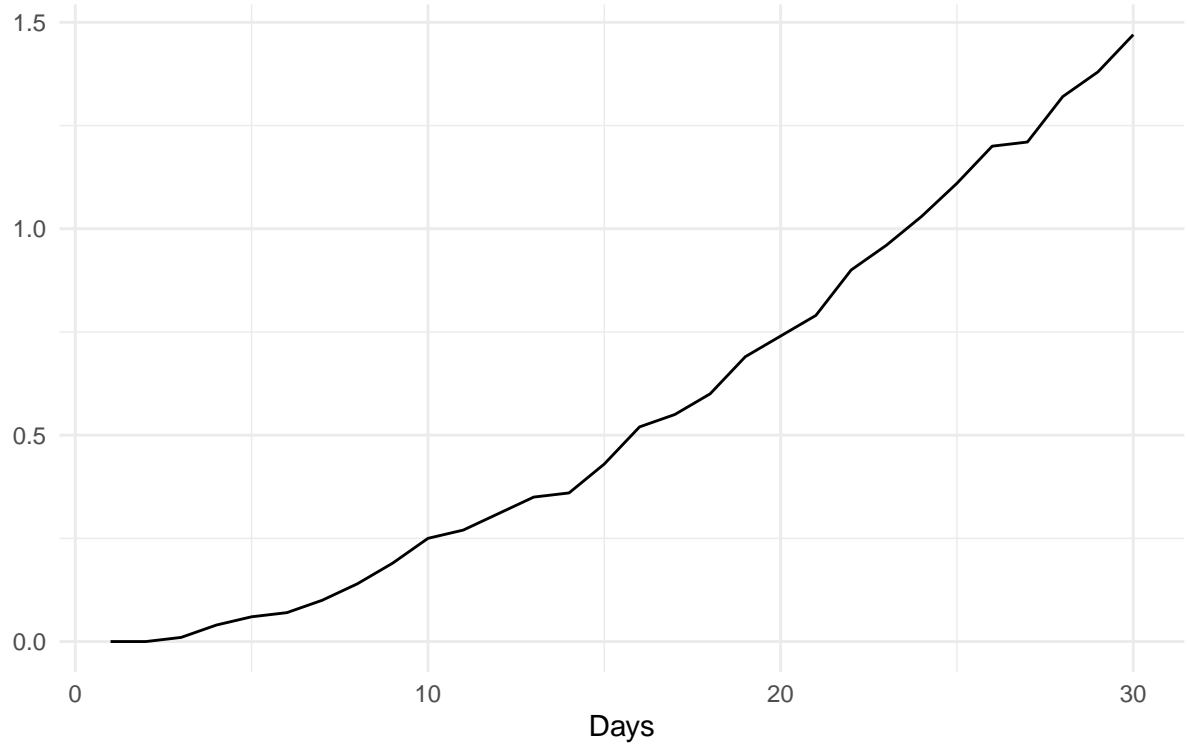
The number of new donor cases acquired at the donation center.

### Case 5: Number of Donors Contracting Virus from Donation S

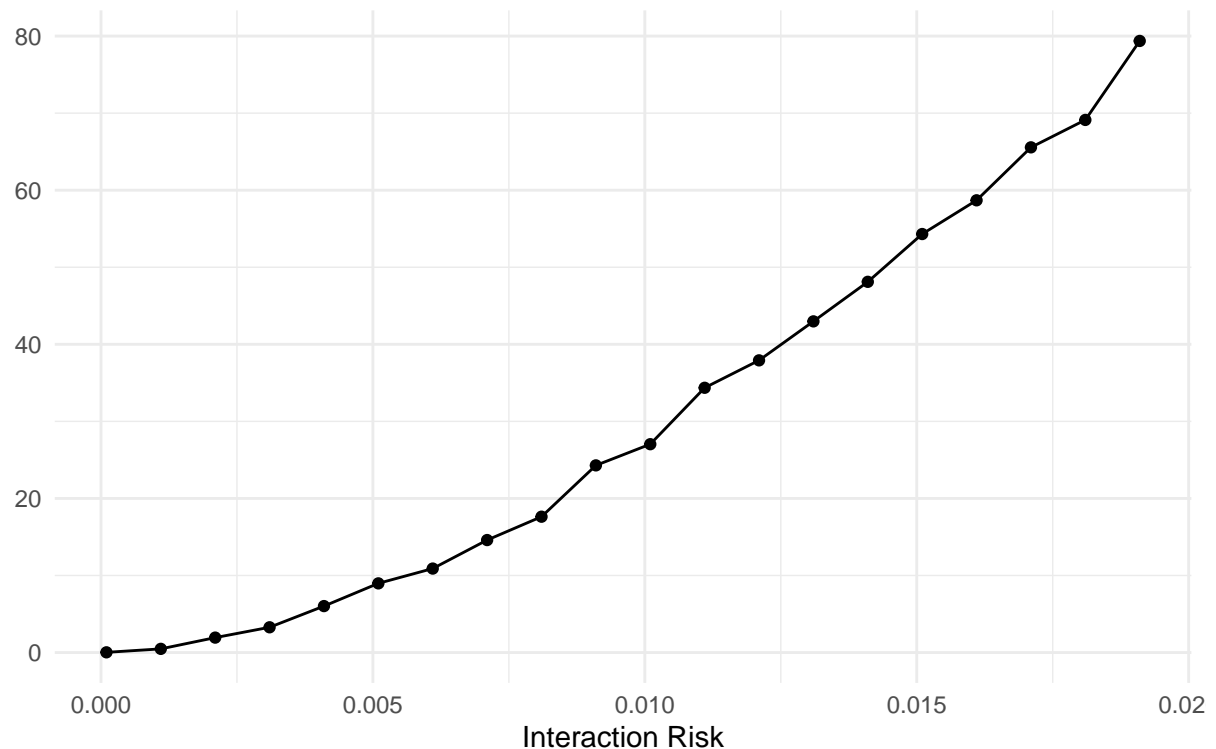


## Case 5: Number of Donors Contracting Virus from Donation

Average across 100 simulations



## Case 5: Number of New Cases Acquired from Donation Site at Final Day Averaged across 100 simulations



### Compare the results

Comparing the 5 workflow strategy in the transmission to healthcare workers and to donors.

## Modeling the Risk of Transmission to Healthcare Workers

We can compare the proportion of healthcare workers who contract the virus over time. And how the final number of infected healthcare workers varies with interaction risk.

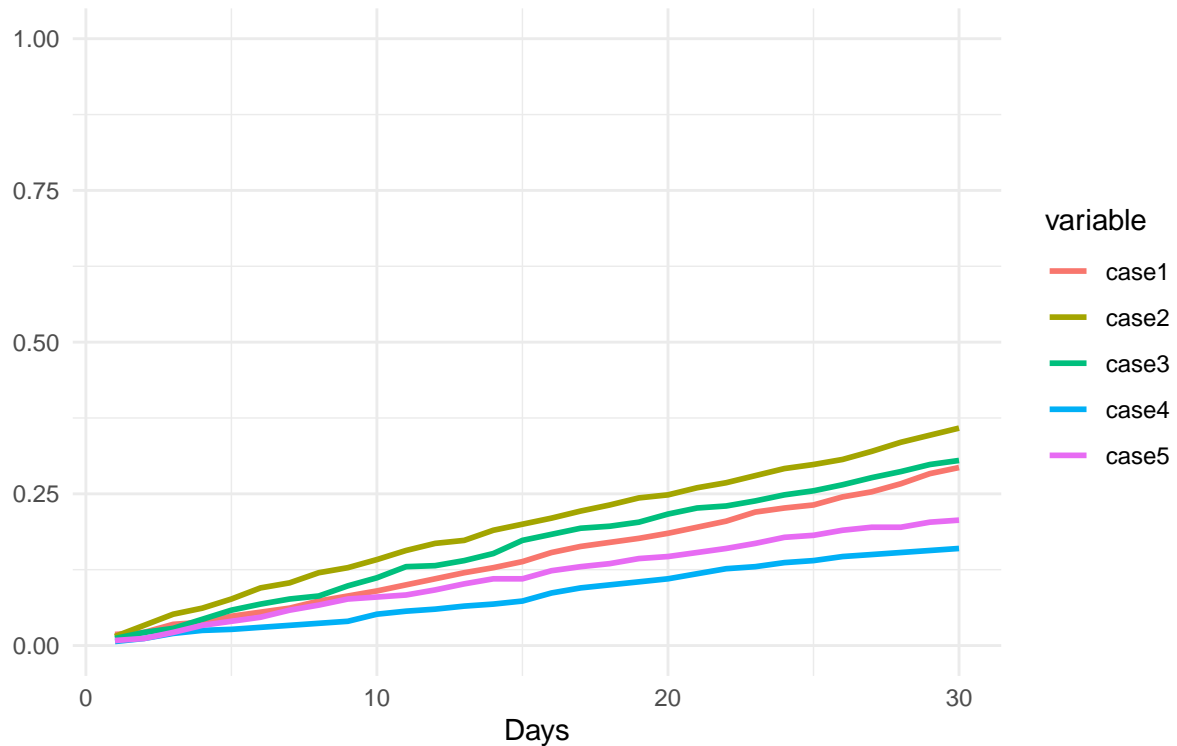
```
hcw_risk_mean_combined <- data.frame(case1 = hcw_risk_mean_case1,
                                     case2 = hcw_risk_mean_case2,
                                     case3 = hcw_risk_mean_case3,
                                     case4 = hcw_risk_mean_case4,
                                     case5 = hcw_risk_mean_case5,
                                     time = 1:n_days)

hcw_risk_mean_combined_melted <- melt(hcw_risk_mean_combined, id = 'time')

ggplot(data = hcw_risk_mean_combined_melted, aes(y = value, x = time, color = variable)) +
  labs(x = "Days", y = "", title = "Proportion of Healthcare Workers Contracting Virus",
       subtitle = paste("Average across", n_sim, "simulations")) + ylim(0,1) +
  geom_line(size = 1) + theme_minimal() +
  theme(plot.title = element_text(size = 16), axis.title.y = element_text(size = 16))
```

# Proportion of Healthcare Workers Contracting Virus

Average across 100 simulations



```
# Varying interaction risk
```

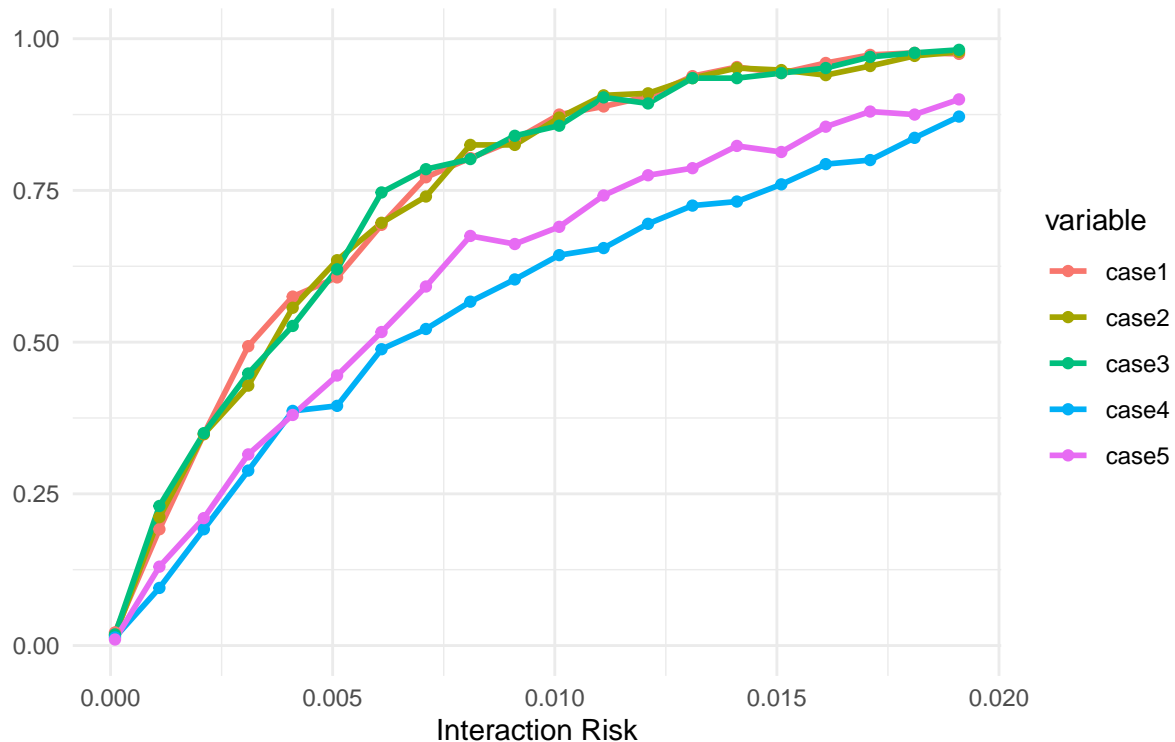
```
interaction_risk_combined <- data.frame(case1 = interaction_risk_results_case1,  
                                         case2 = interaction_risk_results_case2,  
                                         case3 = interaction_risk_results_case3,  
                                         case4 = interaction_risk_results_case4,  
                                         case5 = interaction_risk_results_case5,  
                                         interaction = interaction_risk_vec)
```

```
interaction_risk_combined_melted <- melt(interaction_risk_combined, id = 'interaction')
```

```
ggplot(data = interaction_risk_combined_melted, aes(y = value, x = interaction, color = variable)) +  
  labs(x = "Interaction Risk", y = "", title = "Proportion of Healthcare Workers Infected by Final Day",  
        subtitle = paste("Averaged across", n_sim, "simulations")) + ylim(0,1) +  
  geom_line(size = 1) + geom_point() + theme_minimal() +  
  theme(plot.title = element_text(size = 16), axis.title.y = element_text(size = 16))
```

## Proportion of Healthcare Workers Infected by Final Day

Averaged across 100 simulations



## Modeling the risk of transmission to donors

We can compare the average number of donors acquiring virus from the donation center over time. And then look at the total number of donation center acquired cases at the end of the timecourse, under different interaction risks.

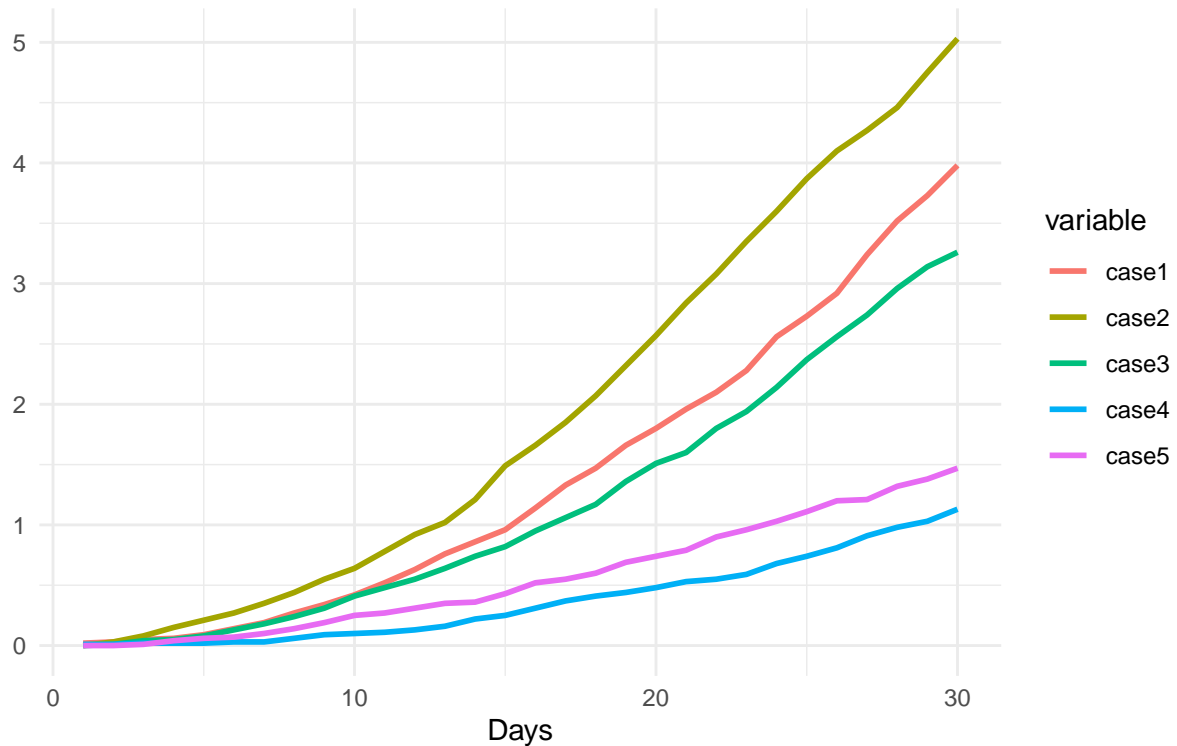
```
donor_risk_mean_combined <- data.frame(case1 = donor_risk_mean_case1,
                                         case2 = donor_risk_mean_case2,
                                         case3 = donor_risk_mean_case3,
                                         case4 = donor_risk_mean_case4,
                                         case5 = donor_risk_mean_case5,
                                         time = 1:n_days)

donor_risk_mean_combined_melted <- melt(donor_risk_mean_combined, id = 'time')

ggplot(data = donor_risk_mean_combined_melted, aes(y = value, x = time, color = variable)) +
  labs(x = "Days", y = "", title = "Number of Donors Contracting Virus from Donation Site",
       subtitle = paste("Average across", n_sim, "simulations")) +
  geom_line(size = 1) + theme_minimal() +
  theme(plot.title = element_text(size = 16), axis.title.y = element_text(size = 16))
```

## Number of Donors Contracting Virus from Donation Site

Average across 100 simulations



```
# Varying interaction risk
```

```
interaction_risk_donor_combined <- data.frame(case1 = interaction_risk_results_donor_case1,  
                                              case2 = interaction_risk_results_donor_case2,  
                                              case3 = interaction_risk_results_donor_case3,  
                                              case4 = interaction_risk_results_donor_case4,  
                                              case5 = interaction_risk_results_donor_case5,  
                                              interaction = interaction_risk_vec)
```

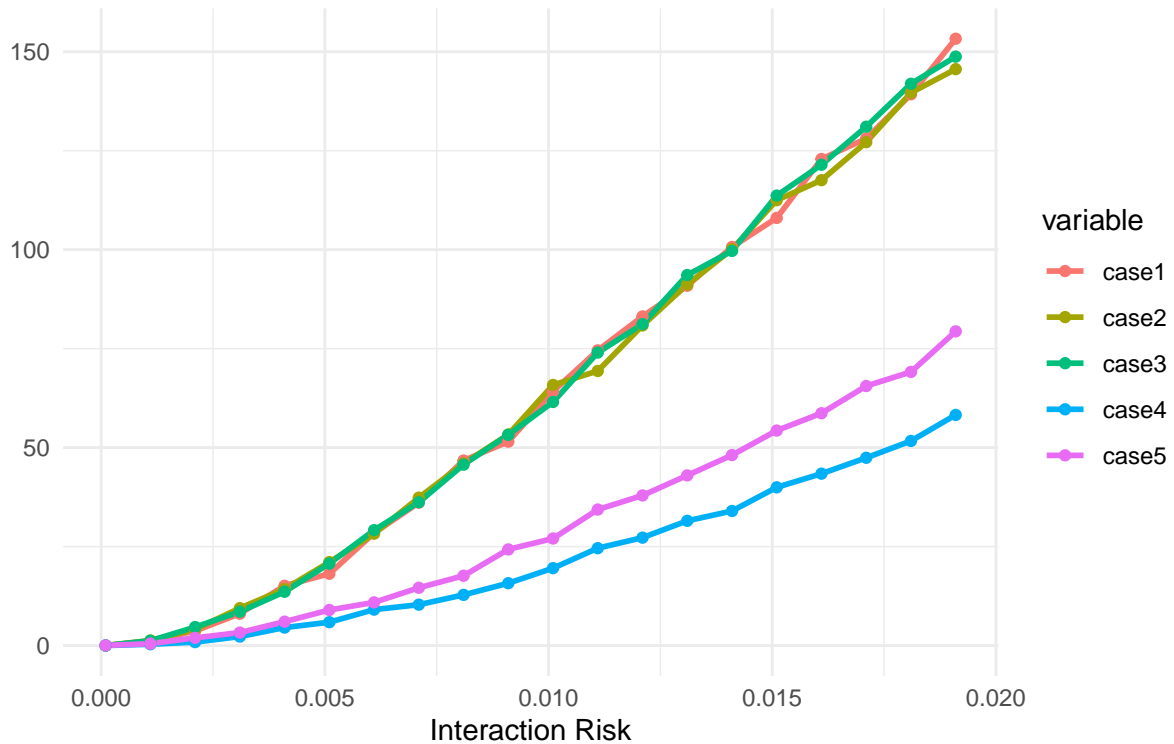
```
interaction_risk_donor_combined_melted <- melt(interaction_risk_donor_combined, id = 'interaction')
```

```
ggplot(data = interaction_risk_donor_combined_melted, aes(y = value, x = interaction, color = variable))  
  labs(x = "Interaction Risk", y = "", title = "Number of New Cases Acquired from Donation Site at Final",  
        subtitle = paste("Averaged across", n_sim, "simulations")) +  
  geom_line(size = 1) + geom_point() + theme_minimal() +  
  theme(plot.title = element_text(size = 16), axis.title.y = element_text(size = 16))
```



## Number of New Cases Acquired from Donation Site at Final

Averaged across 100 simulations



Same two plots but in terms of proportion.

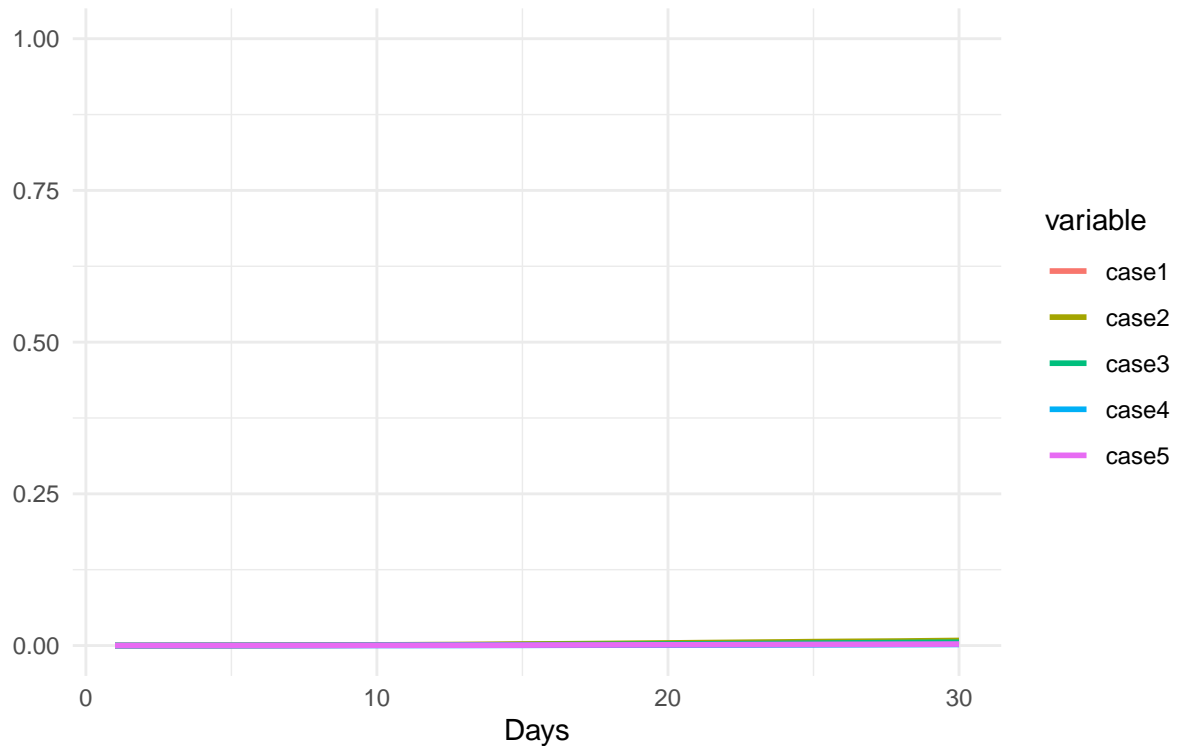
```
donor_risk_mean_combined <- data.frame(case1 = donor_risk_mean_case1/(n_days*n_donors),
                                       case2 = donor_risk_mean_case2/(n_days*n_donors),
                                       case3 = donor_risk_mean_case3/(n_days*n_donors),
                                       case4 = donor_risk_mean_case4/(n_days*n_donors),
                                       case5 = donor_risk_mean_case5/(n_days*n_donors),
                                       time = 1:n_days)

donor_risk_mean_combined_melted <- melt(donor_risk_mean_combined, id = 'time')

ggplot(data = donor_risk_mean_combined_melted, aes(y = value, x = time, color = variable)) +
  labs(x = "Days", y = "", title = "Proportion of Donors Contracting Virus from Donation Site",
       subtitle = paste("Average across", n_sim, "simulations")) +
  geom_line(size = 1) + theme_minimal() + ylim(0,1) +
  theme(plot.title = element_text(size = 16), axis.title.y = element_text(size = 16))
```

# Proportion of Donors Contracting Virus from Donation Site

Average across 100 simulations



```
# Varying interaction risk
```

```
interaction_risk_donor_combined <- data.frame(case1 = interaction_risk_results_donor_case1/(n_days*n_donor),
                                              case2 = interaction_risk_results_donor_case2/(n_days*n_donor),
                                              case3 = interaction_risk_results_donor_case3/(n_days*n_donor),
                                              case4 = interaction_risk_results_donor_case4/(n_days*n_donor),
                                              case5 = interaction_risk_results_donor_case5/(n_days*n_donor),
                                              interaction = interaction_risk_vec)
```

```
interaction_risk_donor_combined_melted <- melt(interaction_risk_donor_combined, id = 'interaction')
```

```
ggplot(data = interaction_risk_donor_combined_melted, aes(y = value, x = interaction, color = variable)) +
  labs(x = "Interaction Risk", y = "", title = "Total Proportion of Donors Contracting Virus from Donation Site",
       subtitle = paste("Averaged across", n_sim, "simulations")) +
  geom_line(size = 1) + geom_point() + theme_minimal() + ylim(0,1) +
  theme(plot.title = element_text(size = 16), axis.title.y = element_text(size = 16))
```

# Total Proportion of Donors Contracting Virus from Donation

Averaged across 100 simulations

