BASE_MODEL

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```r
# Plot using ggplot2
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 4.4.2
```

```r
# Define parameters

beta_S = 0.27       # Transmission rate between susceptible and infected
beta_F = 0.79       # Transmission rate between susceptible and funerals
gamma = 0.1782      # Recovery rate
sigma = 0.5         # Funeral clearance rate
mu = 0.0111 / 365   # Birth and natural death rate (per day)


# Initial conditions
N = 1                    # Total population
initial_state <- list(
  S = 1 - 1 / 11472914,  # Initial susceptible population
  I = 1 / 11472914,      # Initial infected individuals
  F = 0,                 # Initial funeral population
  R = 0                  # Initial recovered individuals
)

# Time frame for simulation
time_steps <- 150        # Simulate for 1 year (365 days)

# Initialize vectors to store results
S <- numeric(time_steps + 1)
I <- numeric(time_steps + 1)
F <- numeric(time_steps + 1)
R <- numeric(time_steps + 1)

# Set initial values
S[1] <- initial_state$S
I[1] <- initial_state$I
F[1] <- initial_state$F
R[1] <- initial_state$R

# Simulation loop
for (t in 1:time_steps) {
  # Update each compartment using the discrete equations with birth and death
```

```r
    S[t + 1] <- S[t] + mu - mu * S[t] - beta_S * S[t] * I[t] - beta_F * S[t] * F[t]
    I[t + 1] <- I[t] - mu * I[t] + beta_S * S[t] * I[t] + beta_F * S[t] * F[t] - gamma * I[t]
    F[t + 1] <- F[t] + gamma * I[t] - sigma * F[t]
    R[t + 1] <- R[t] + sigma * F[t]
}
# Time vector
time <- 0:time_steps

# Combine results into a data frame
soln <- data.frame(
  time = time,
  Susceptible = S,
  Infected = I,
  Funeral = F,
  Recovered = R
)


# Define custom colors
colours <- c(
  "Susceptible" = "blue",
  "Infected" = "red",
  "Funeral" = "green",
  "Recovered" = "purple"
)

# Plot using ggplot2
library(ggplot2)
ggplot(soln) +
  geom_line(mapping = aes(x = time, y = Susceptible, colour = "Susceptible"), lwd = 2) +
  geom_line(mapping = aes(x = time, y = Infected, colour = "Infected"), lwd = 2) +
  geom_line(mapping = aes(x = time, y = Funeral, colour = "Funeral"), lwd = 2) +
  geom_line(mapping = aes(x = time, y = Recovered, colour = "Recovered"), lwd = 2) +
  labs(
    x = "Time (days)",
    y = "Propothion of population",
    title = "SIFR Model Dynamics with Birth and Death Rates",
  ) +
  scale_colour_manual(values = colours)
```

SIFR Model Dynamics with Birth and Death Rates