

Using ABC to Infer Parameters of a Simulated Zombie Epidemic

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The REVISIT package

Need to create a package with appropriate folders and documentation - am happy to start on this

Documentation

Integration of R and C++

Simulations

```
# ----- Working Examples -----

# Replace source call with install.github() and library calls when package is finished!
# install.github("https://github.com/RaspberryEmma/Intractable-Models-Sim-Study")
# library(intractmodelinf)

source("intractmodelinf/R/generate_data.R")
suppressPackageStartupMessages({
  library(dplyr)
  library(ggplot2)
  library(knitr)
  library(tidyverse)
})

bristol.uni.N <- 29434
bristol.N     <- 467099
UK.N         <- 67081234

bristol.uni.example <- generate.SIR.data(total.N      = bristol.uni.N,
                                         initial.inf = 10,
                                         total.T      = 150)

bristol.example <- generate.SIR.data(total.N      = bristol.N,
                                     initial.inf = 10,
                                     total.T      = 150)

UK.example <- generate.SIR.data(total.N      = UK.N,
```

```

initial.inf = 10,
total.T      = 150)

bristol.uni.example %>% head() %>% knitr::kable()

```

t	S.t	I.t	R.t	N	b	k
1	29434	10	0	29434	0.6378667	0.3453372
2	29427	12	3	29434	0.6378667	0.3453372
3	29419	15	7	29434	0.6378667	0.3453372
4	29409	19	12	29434	0.6378667	0.3453372
5	29396	24	18	29434	0.6378667	0.3453372
6	29380	31	26	29434	0.6378667	0.3453372

```

# ----- Save Data -----

write.csv( bristol.uni.example, file = "data/bristol_uni_example.csv", row.names = FALSE )
write.csv( bristol.example,    file = "data/bristol_example.csv",   row.names = FALSE )
write.csv( UK.example,         file = "data/UK_example.csv",       row.names = FALSE )

```

Parallelisation

Simulating an Epidemic

Implementing ABC

Checking Results

```

# ----- Read Results Data from CSV -----

bristol.uni.example <- read.csv("data/bristol_uni_example.csv", header = TRUE)
bristol.example     <- read.csv("data/bristol_example.csv",   header = TRUE)
UK.example          <- read.csv("data/UK_example.csv",       header = TRUE)

# ----- Plot Results -----

legend.colors <- c("Susceptible" = "red", "Infected" = "blue", "Recovered" = "green")

bristol.uni.plot <- ggplot(bristol.uni.example, aes(x = t)) +
  geom_line(aes(y = S.t, color = "Susceptible")) +
  geom_line(aes(y = I.t, color = "Infected")) +
  geom_line(aes(y = R.t, color = "Recovered")) +
  labs(color = "Legend") +
  scale_color_manual(values = legend.colors) +
  ggtitle("SIR Model - Bristol Uni Example") +
  xlab("Time") +

```

```

ylab("SIR Populations")

bristol.plot <- ggplot(bristol.example, aes(x = t)) +
  geom_line(aes(y = S.t, color = "Susceptible")) +
  geom_line(aes(y = I.t, color = "Infected")) +
  geom_line(aes(y = R.t, color = "Recovered")) +
  labs(color = "Legend") +
  scale_color_manual(values = legend.colors) +
  ggtitle("SIR Model - Bristol City Example") +
  xlab("Time") +
  ylab("SIR Populations")

UK.plot <- ggplot(UK.example, aes(x = t)) +
  geom_line(aes(y = S.t, color = "Susceptible")) +
  geom_line(aes(y = I.t, color = "Infected")) +
  geom_line(aes(y = R.t, color = "Recovered")) +
  labs(color = "Legend") +
  scale_color_manual(values = legend.colors) +
  ggtitle("SIR Model - UK Example") +
  xlab("Time") +
  ylab("SIR Populations")

```

```
# ----- Save Plots -----
```

```

png("plots/bristol_uni_plot.png")
bristol.uni.plot
dev.off()

```

```
## pdf
## 2
```

```

png("plots/bristol_plot.png")
bristol.plot
dev.off()

```

```
## pdf
## 2
```

```

png("plots/UK_plot.png")
UK.plot
dev.off()

```

```
## pdf
## 2
```