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

Parallelisation

Generating SZR data

We simulate the zombie epidemic using the generate.SIR.data() function, which is given by the code below. For ease, this function has also been included in our intractmodelinf package.

We use this to simulate an outbreak for 3 different populations of different sizes:

- Students (**REVISIT** and staff?) at the University of Bristol
- Residents in the city of Bristol
- Residents in the UK

The data on these simulated outbreaks is included in our package

```
N <-5000
initial <- generateStartCond(N, initial.inf = 10)
new.example <- generateSZRdata(initial ,total.T = 50)</pre>
```

Implementing ABC

Checking Results

```
plot.SZR(new.example$results) + theme_linedraw() +theme_bw()
```

```
Susceptible — Zombies

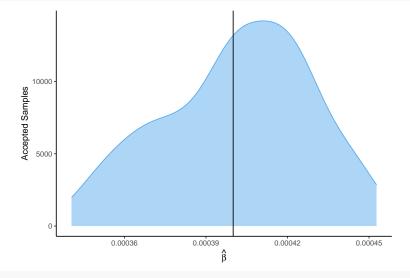
Legend — Removed — Susceptible — Zombies
```

```
simulated.mat <- new.example$results</pre>
simulated.mat <- as.matrix(simulated.mat[,2:4])</pre>
head(simulated.mat )
##
         S.t Z.t R.t
## [1,] 4990 10
## [2,] 4966 24
                   10
## [3,] 4906 60
## [4,] 4796 110
                   94
## [5,] 4592 204 204
## [6,] 4234 358 408
priorMin \leftarrow c(0.000004, 0.000004, 0.000004)
priorMax \leftarrow c(0.0015, 0.001, 0.001)
res <- abcRej(simulated.mat , 10000, 400, priorMin, priorMax)
head(res)
##
                 [,1]
                               [,2]
## [1,] 0.0004250723 0.0008617067 0.0006589291
## [2,] 0.0004237616 0.0009770686 0.0007613837
## [3,] 0.0003875616 0.0004843493 0.0006826764
## [4,] 0.0003708313 0.0006252518 0.0007569413
## [5,] 0.0004010205 0.0007269969 0.0005887166
## [6,] 0.0004492728 0.0009563075 0.0002842800
library(latex2exp)
require(ggplot2)
require(gridExtra)
plot.posterior.samples <- function(sample, mean){</pre>
  beta_plot <- ggplot(\frac{data}{data} = sample, aes(x = beta)) +
    geom_density(colour = "steelblue2", fill = "steelblue2", alpha = 0.5) +
    geom_vline(aes(xintercept = mean[1]))+
    labs(x = TeX("\$\hat{\beta}$"), y = "Accepted Samples") +
    theme classic()
  kappa_plot \leftarrow ggplot(data = sample, aes(x = kappa)) +
```

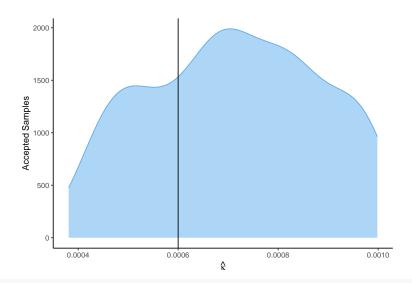
```
geom_density(fill = "steelblue2", alpha = 0.5,colour = "steelblue2") +
    geom_vline(aes(xintercept = mean[2])) +
    labs(x = TeX("$\\hat{\\kappa}$"), y = "Accepted Samples") +
    theme_classic()
    rho_plot <- ggplot(data = sample, aes(x = rho)) +
        geom_density(colour = "steelblue2", fill = "steelblue2", alpha = 0.5) +
        geom_vline(aes(xintercept = mean[3]))+
        labs(x = TeX("$\\hat{\\rho}$"), y = "Accepted Samples") +
        theme_classic()
    return(list(beta_plot, kappa_plot, rho_plot))
}</pre>
```

```
library(ggplot2)
library(dplyr)
library(ggthemes)
means <- c(new.example$beta, new.example$kappa, new.example$rho)
samples <- res %>%
    as_tibble()
colnames(samples) <- c("beta", "kappa", "rho")

plots <- plot.posterior.samples(samples, means)
plots[[1]]</pre>
```



plots[[2]]



plots[[3]]

