

Stat 400 Presentation

12/7/2021

```
## -- Attaching packages -----
```

```
## v ggplot2 3.3.5      v purrr 0.3.4
```

```
## v tibble 3.1.6      v dplyr 1.0.7
```

```
## v tidyr 1.1.4      v stringr 1.4.0
```

```
## v readr 2.1.1      v forcats 0.5.1
```

```
## -- Conflicts -----
```

```
## x dplyr::filter() masks stats::filter()
```

```
## x dplyr::lag() masks stats::lag()
```

Plot of infected people with bootstrap

Simulating Step Distance and Direction

```
get_step_length <- function(df, x_dim, y_dim){  
  step_lengths <- rnorm(n=nrow(df), mean=min(x_dim, y_dim)/4, sd=min(x_dim, y_dim)/12)  
  return(step_lengths)  
}  
  
get_step_direction <- function(length_vec){  
  direction <- runif(n=length(length_vec), min=0, max=2*pi)  
}  
  
get_delts <- function(length_vec, direc_vec){  
  delta_x <- length_vec * cos(direc_vec)  
  delta_y <- length_vec * sin(direc_vec)  
  return(cbind(delta_x, delta_y))  
}
```

Updating Coordinates and In-Bounds Check

```
update_coords <- function(og_df, delta_df){
  new_mx <- matrix(data=NA, nrow=nrow(og_df), ncol=5)
  new_df <- data.frame(new_mx)
  new_df[,1] <- as.numeric(og_df[, 'x']) + delta_df[, 'delta_x']
  new_df[,2] <- as.numeric(og_df[, 'y']) + delta_df[, 'delta_y']
  new_df[,3] <- og_df[,3]
  new_df[,4] <- og_df[,4]
  new_df[,5] <- og_df[,5]
  colnames(new_df) <- c('x', 'y', 'subjects', 'incubation', 'recovery')
  new_df
}

coord_checker <- function(og_df, new_df, x_dim, y_dim){
  baddies <- NULL
  for(i in 1:nrow(new_df)){
    if(as.numeric(new_df[i, 'x']) > x_dim | as.numeric(new_df[i, 'x']) < 0 | as.numeric(new_df[i, 'y']) >
      baddies <- append(baddies, i)
    }
  }

  if(is.null(baddies)){
    return(new_df)
  }else{
    new_step <- get_step_length(new_df[i,], x_dim, y_dim)
    new_direction <- get_step_direction(new_step)
    new_change <- get_deltas(new_step, new_direction)
    new_df <- update_coords(og_df[baddies,], new_change)
    full_df <- rbind(new_df, og_df[-baddies,])
    return(coord_checker(og_df, full_df, x_dim, y_dim))
  }
}
```

Changing SIR Status

```
infection_status <- function(state, mean_crit_dist){

  current_infected <- state[state[,3]=='I' & state[,4] <= 0,]
  current_suceptable <- state[state[,3]=='S',]
  current_removed <- state[state[,3]=='R',]
  current_non_contagious <- state[state[,3]=='I' & state[,4] > 0,]

  newly_infected <- NULL

  if(nrow(current_suceptable) != 0 & nrow(current_infected) != 0){
    for(i in 1:nrow(current_infected)){
      for(j in 1:nrow(current_suceptable)){
        x_i <- as.numeric(current_infected[i, 'x'])
        y_i <- as.numeric(current_infected[i, 'y'])
        x_s <- as.numeric(current_suceptable[j, 'x'])
        y_s <- as.numeric(current_suceptable[j, 'y'])

        crucial_distance <- rexp(1, 1/mean_crit_dist)

        d <- sqrt((x_i - x_s)^2 + (y_i - y_s)^2)
        if(d <= crucial_distance){
          newly_infected <- c(newly_infected, j)
        }
      }
    }
    current_suceptable[newly_infected, 3] <- 'I'
    current_suceptable[newly_infected, 4] <- rpois(n=length(newly_infected), lambda = 5)
    current_suceptable[newly_infected, 5] <- rpois(n=length(newly_infected), lambda = 14)

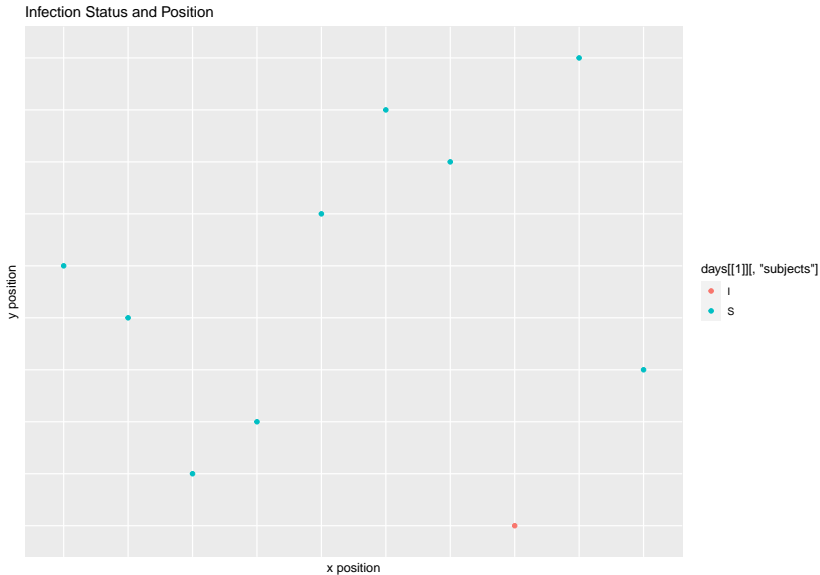
    new_state <- rbind(current_infected, current_suceptable, current_removed, current_non_contagious)
    return(new_state)
  }else{return(state)}
}
```

Simulation

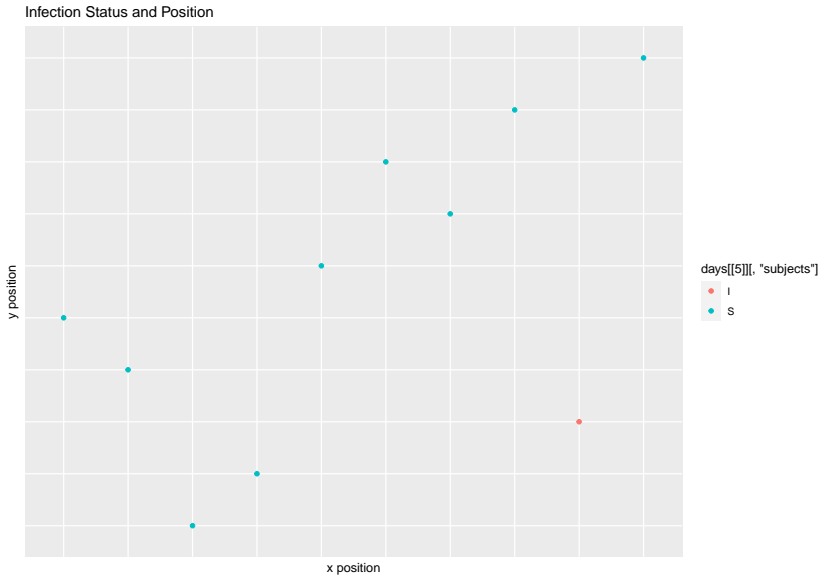
```
dummy_simulator <- function(days, num_subjects, x_dim, y_dim, I_0, inf_dist){
  initial_data <- starting_vals(num_subjects = num_subjects, x_dim=x_dim, y_dim=y_dim, I_0=I_0)
  end_day <- list()
  num_cases <- rep(NA, days)
  num_cases <- c(I_0, num_cases)
  num_new_cases <- rep(NA, days)
  for(i in 1:days){
    if(i == 1){
      step_size <- get_step_length(initial_data, x_dim, y_dim)
      direction <- get_step_direction(step_size)
      change <- get_delts(step_size, direction)
      updated_positions <- update_coords(initial_data, change)
      checked_positions <- coord_checker(og_df=initial_data, new_df=updated_positions, x_dim=x_dim, y_dim=y_dim, inf_dist=inf_dist)
      new_status <- infection_status(checked_positions, inf_dist)

      not_recovered <- new_status[as.numeric(new_status[, 5]) > 0, ]
      new_time <- as.numeric(not_recovered[, 5]) - 1
      not_recovered[, 5] <- new_time
      infected_0 <- new_status[as.numeric(new_status[, 5]) == 0, ]
      infected_0[, 3] <- rep('R', nrow(infected_0))
      not_infected = new_status[as.numeric(new_status[, 5]) < 0, ]
      new_status = rbind(not_recovered, infected_0, not_infected)
      infected_people <- new_status[new_status[,3] == 'I',]
      new_inc_time <- as.numeric(infected_people[,4]) - 1
      infected_people[,4] <- new_inc_time
      other_people <- new_status[new_status[,3] != 'I',]
      new_status <- rbind(infected_people, other_people)
      end_day[[i]] <- new_status
      num_cases[i+1] <- sum(new_status[,3]=='I')
      num_new_cases[i] <- sum(new_status[,3]=='I') - I_0
    }
  }
  return(num_cases)
}
```

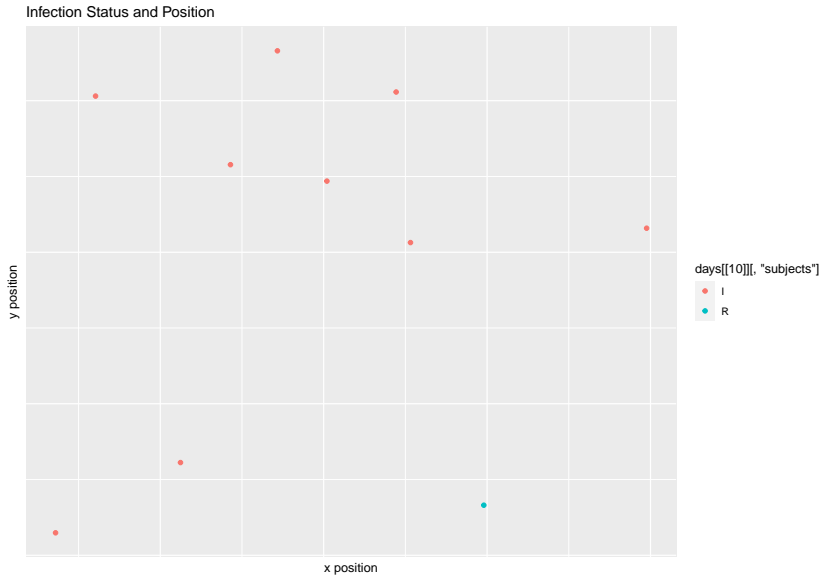
Demonstration Day 1



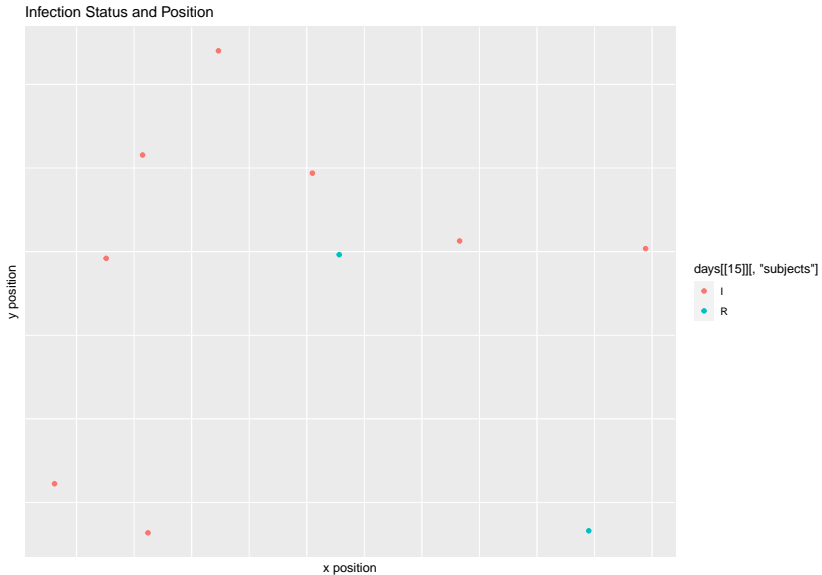
Demonstration Day 5



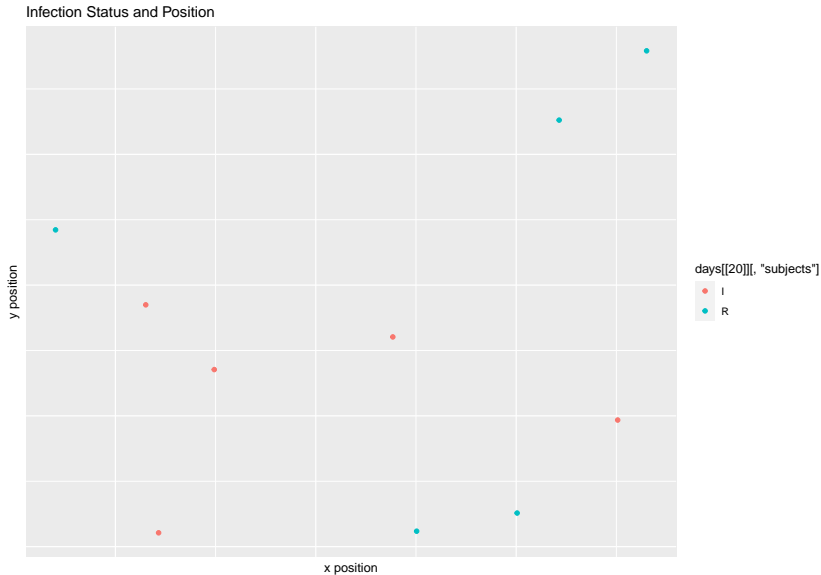
Demonstration Day 10



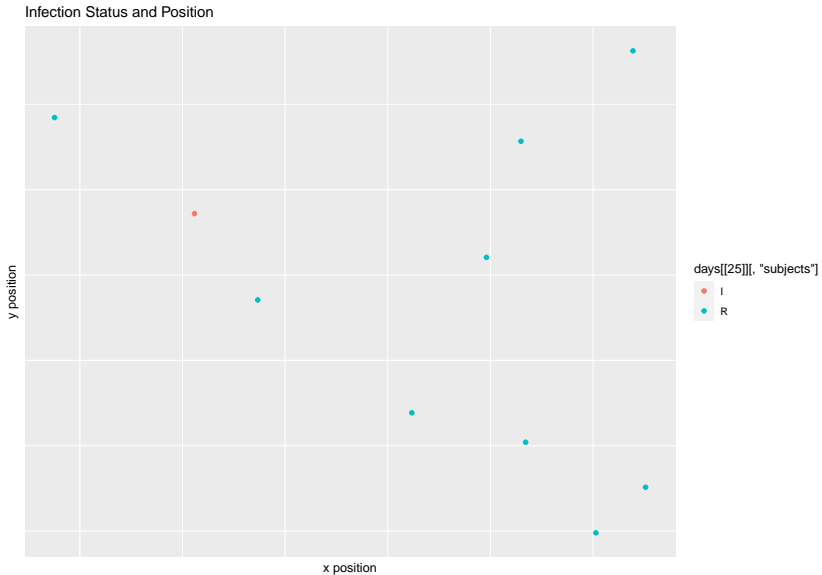
Demonstration Day 15



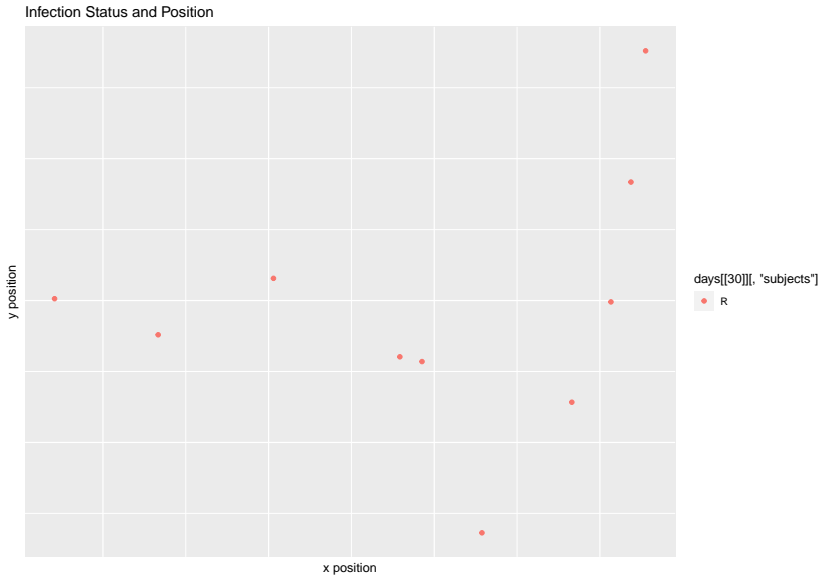
Demonstration Day 20



Demonstration Day 25



Demonstration Day 30



Bootstrap Confidence Intervals

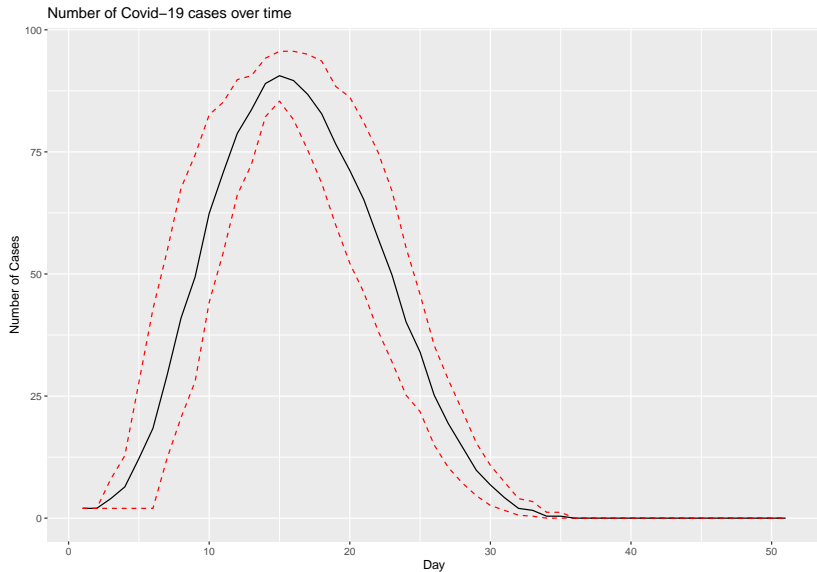
```
get_bootstrap_cis <- function(days, num_subjects, x_dim, y_dim, I_0, inf_dist, sample_size, ci_type='perc
  #Create data frame to store samples
  samps <- matrix(data=NA, nrow=sample_size, ncol=days + 1)
  samps <- data.frame(samps)

  #Create data frame to store confidence intervals
  ci_df <- matrix(data=NA, nrow=days + 1, ncol=3)
  ci_df <- data.frame(ci_df)

  for(i in 1:sample_size){
    samps[i, ] <- simulator(days, num_subjects, x_dim, y_dim, I_0, inf_dist)
  }

  for(i in 1:ncol(samps)){
    #Make sure column has more than one unique value
    check <- (length(unique(samps[,i])) != 1)
    if(check){
      boot_obj <- boot(samps[,i], mean_func, 2000)
      ci_obj <- boot.ci(boot_obj, conf = .95, type = ci_type)
      ci_df[i, 1] <- ci_obj$percent[4]
      ci_df[i, 2] <- ci_obj$t0
      ci_df[i, 3] <- ci_obj$percent[5]
    }else{ci_df[i, ] <- c(samps[1, i], samps[1, i], samps[1, i])}
  }
  return(ci_df)
}
```

Bootstrap plot of infected people



Bootstrap

Histogram of t

