01_proc_HPP

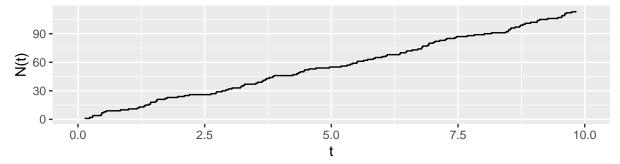
Frances Lin 4/15/2021

```
library(tidyverse)
library(ggplot2)
library(patchwork)
set.seed(1) # for reproducibility
t_max <- 10
t <- 0
lmbda <- 10
X <- numeric(0) # vector of t</pre>
while(t <= t_max){</pre>
          <- runif(1)
 u
         \leftarrow t - log(u)/lmbda
                                               # t \sim exp(1/lambda)
 if(t < t_max) {
   X \leftarrow c(X,t)
                                                 # update index
  }
}
# Check to see if the total #s matches
length(X)
## [1] 114
# Create dataframe
df_HPP = tibble(
x = X
 y = 1:(length(X)) #0:(length(X) - 1)
# Plot HPP
p_HPP <- ggplot(data=df_HPP, mapping=aes(x=x, y=y)) +</pre>
  geom_step() +
 labs(title = "Homogeneous Poisson Process (lambda = 10)",
       x = "t",
       y = "N(t)") +
 xlim(0, 10) # so that scale lines up
#p_HPP
# # Can probably delete
\# df\_HPP \leftarrow df\_HPP \%\% add\_column(
\# t_fix = rep(2, length(df_HPP$x))
# )
```

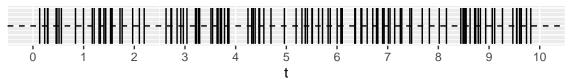
```
# Combine plots
# require(gridExtra)
# grid.arrange(p_HPP, p_HPP_time)
p_HPP / p_HPP_time / p_HPP_hist + plot_layout(heights = c(0.6, 0.2, 0.2))
```

Warning: Removed 2 rows containing missing values (geom_bar).

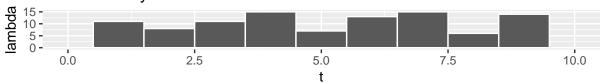
Homogeneous Poisson Process (lambda = 10)



Corresponding Inter-Arrivial Times



Rate/Intensity



```
# Save output and adjust size
png(file = '/Users/franceslinyc/Hawkes-Process-2021/results/plot_1D_HPP.png', width = 450*2, height = 4
p_HPP / p_HPP_time / p_HPP_hist + plot_layout(heights = c(0.7, 0.1, 0.2))
```

Warning: Removed 2 rows containing missing values (geom_bar).