Zombie Outbreak Vis Ideas

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Contents

Overview

This document presents some sketched ideas of how the line list data will be visualized. In the final version of this project, an individual will be able to manipulate the basic timeline and network (see below) to colour points, add or remove data, in order to interactively explore the content in the line list. This document *doesn't showcase that interactivity* it just *sketches* what is possible - so please take it as a work in progress and not the final version. What's different here relative to what the graphic desing folks at science world have done is the interactive component. Maybe they came up with a similar visualization and it's just one very nice picture, but I am allowing people to dynamically change the visualization as they explore the data and ask more questions.

My goal is to allow someone to interact with this data on their phone, through this visualization. I have been exploring mobile visualizations, some work, some don't, I've met some constraints because of the screen realestate. As a back-up,if I can't make a good phone vis application in this time, a projector connected to my computer would work.

Base visualizations

These are the "starting" visualizations, they are simple. They will be "decorated" or changed based upon user interactions (I'll provide examples of how those interacitons could look like shortly). But this will be the first thing people see.
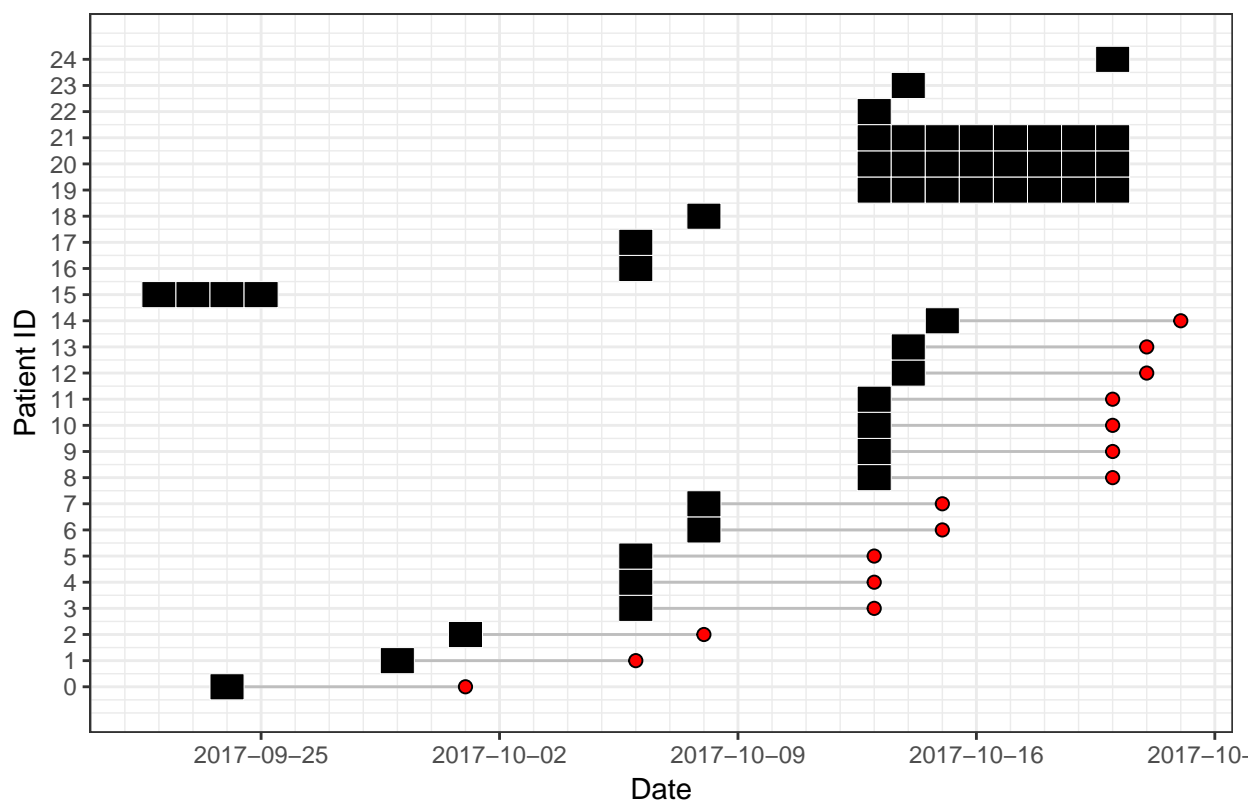
Basic Timeline

The first place to start is just a basic timeline. The interactivity component is that users will be able to select different options to add interesting information to this base. Althought this document is not interactive I will simulate types of interactions that will be supported. The users can slice and colour the data to try to understand what is going on. All of these interactions will be controlled through menus (not shown here).

Ideally I would like to display this visualization on a cell phone, but some different design decisions need to be made (i.e. maybe more aggregation), to work on a phone.

```
## Warning: Removed 47 rows containing missing values (geom_segment).
```

```
## Warning: Removed 47 rows containing missing values (geom_point).
```


Base Timeline of Exposure Times (black tiles) + symptom onset (red circle)

Basic Network Connections

There is a network of patient connections, but it changes over time! Here's the basic network of patient connections. The user will have to *toggle* this option over the existing timeline. This visualization below is interesting, but there is still visual clutter (you can't quite see where the lines go), so either I will provide some base level optimization, or I will allow the user to figure that one out.

Just a network graph

The graph is interesting because it gives us some very clear hubs of the transmission and dead ends.

**Graph connections overlain on timeline**

```
#overlay connection on top of base
pBase +geom_curve(data=connections,aes(x=sourceEnd,y=source,xend=targetStart,yend=ID),colour="black",cu
```

```
## Warning: Removed 47 rows containing missing values (geom_segment).
```

```
## Warning: Removed 47 rows containing missing values (geom_point).
```


Base Timeline of Exposure Times (black tiles) + symptom onset (red circle)
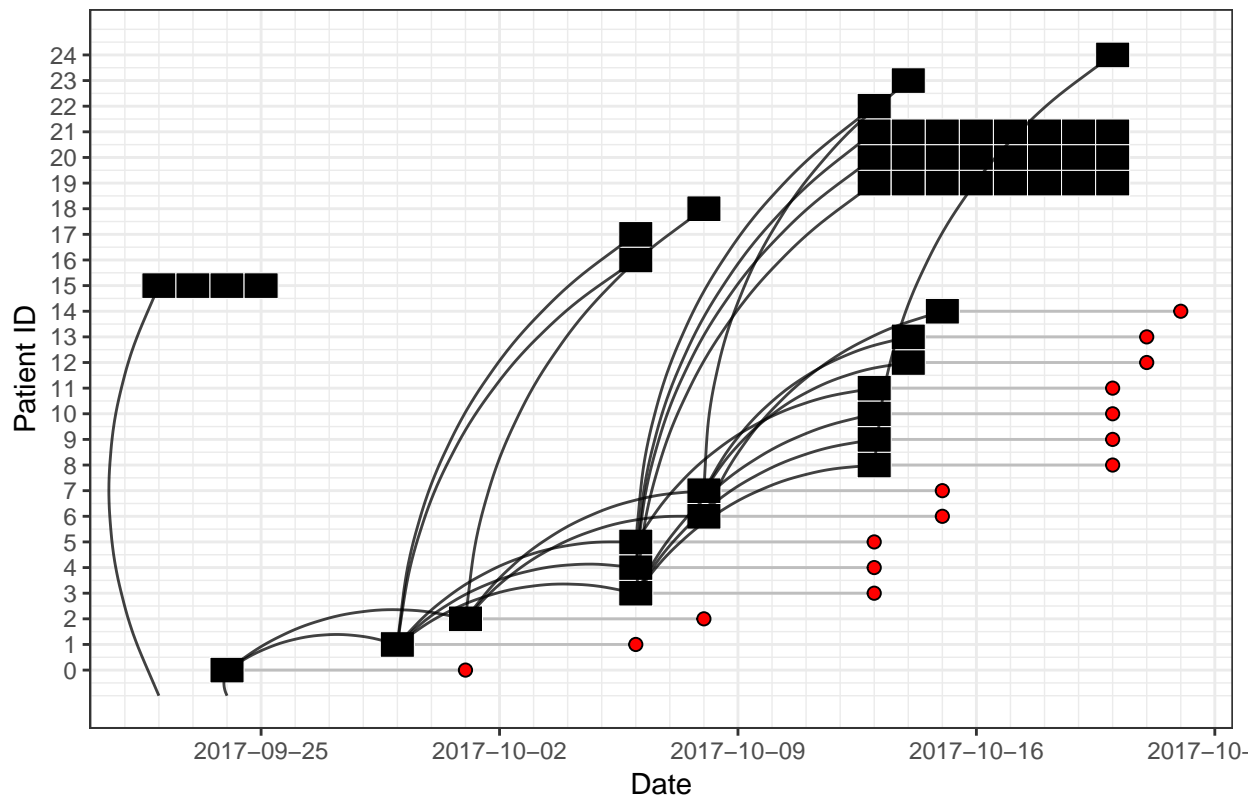
Interactions

From above base graph, people will have the options to interact with an interface that allows them to do a certain range of things to explore the data. Note, the document here is *not* interactive, and it's not optimized for aesthetics. So please consider this to be a *rough* sketch of what interactions look like so you get a sense of how these interactions will look like. So far I think these will be done by drop down menus where someone can select a variable to colour by, or to add more data, or to highlight something.. etc.. that part is not 100% down yet.

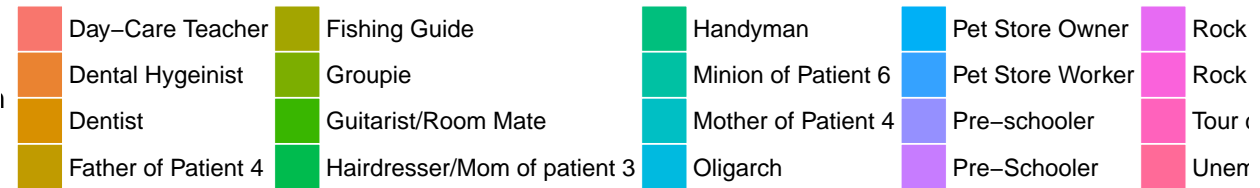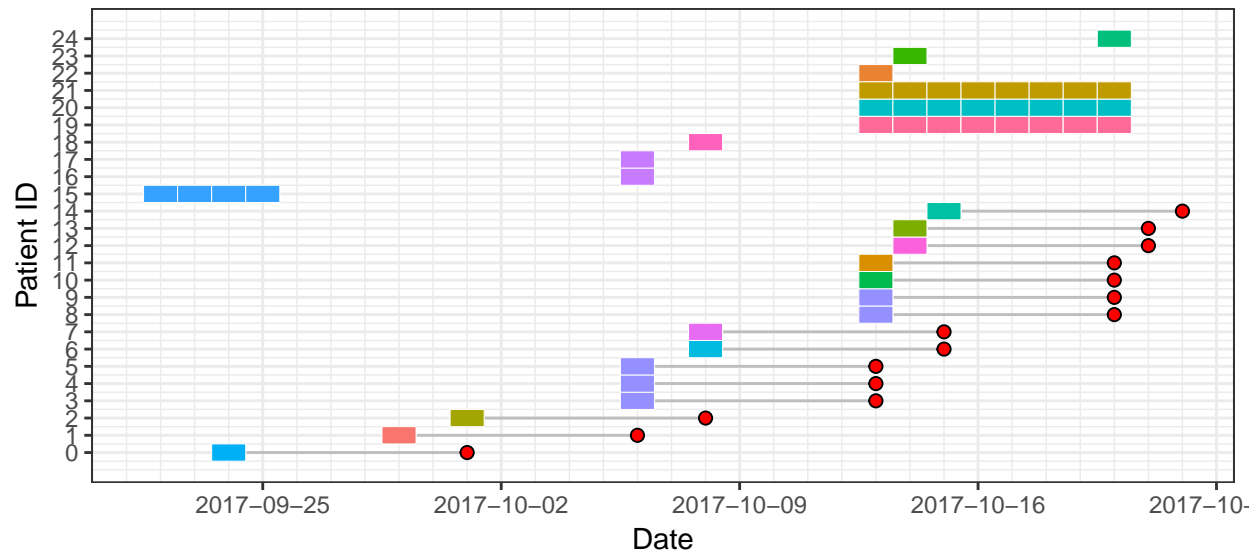## Example interaction 1 (Univariable): Colouring by different categorical variables

Colouring by occupation

People can choose to colour by patient occupationg for example. Again, the colour and the fact that the legend is currently cut off will be fixed later. But from below, they should be able to see that many occupations eventually had a symptom onset. They should also maybe realise that colour is not super useful because we quickly run out of colours.

```
## Warning: Removed 47 rows containing missing values (geom_segment).
```

```
## Warning: Removed 47 rows containing missing values (geom_point).
```

Base Timeline of Exposure Times (black tiles) + symptom onset (red circle)

Legend:

Day–Care Teacher	Fishing Guide	Handyman	Pet Store Owner	Rock
Dental Hygeinist	Groupie	Minion of Patient 6	Pet Store Worker	Rock
Dentist	Guitarist/Room Mate	Mother of Patient 4	Pre–schooler	Tour
Father of Patient 4	Hairdresser/Mom of patient 3	Oligarch	Pre–Schooler	Unem

An example now of that this looks like if we "toggle" connection to be on

```
## Warning: Removed 47 rows containing missing values (geom_segment).
```

```
## Warning: Removed 47 rows containing missing values (geom_point).
```

Base Timeline of Exposure Times (black tiles) + symptom onset (red circle)
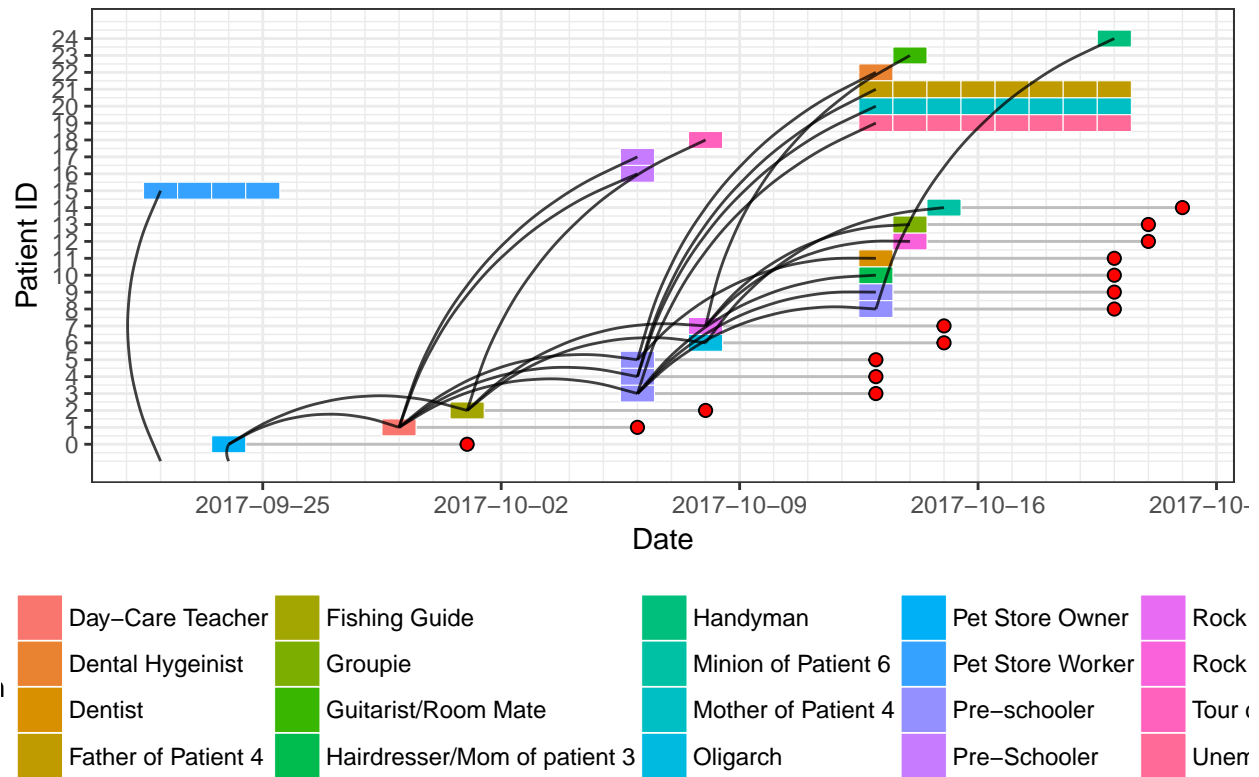
Legend:

- Day–Care Teacher
- Dental Hygeinist
- Dentist
- Father of Patient 4
- Fishing Guide
- Groupie
- Guitarist/Room Mate
- Hairdresser/Mom of patient 3
- Handyman
- Minion of Patient 6
- Mother of Patient 4
- Oligarch
- Pet Store Owner
- Pet Store Worker
- Pre–schooler
- Pre–Schooler
- Rock
- Rock
- Tour
- Unem

colouring by only ONE exposure

So maybe you want to look at more than one exposure, we'll get to that. Right now, we'll consider just colouring by one exposure.
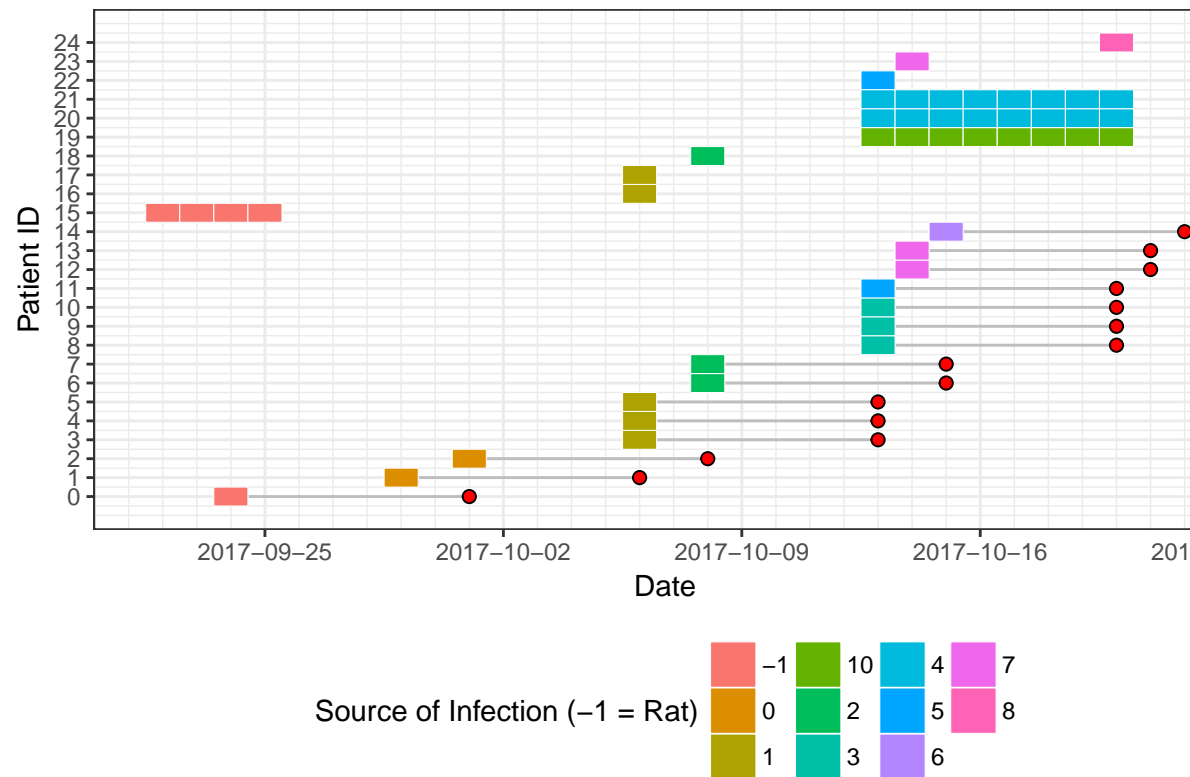
Exposed to bite + symptom onset (red circle)
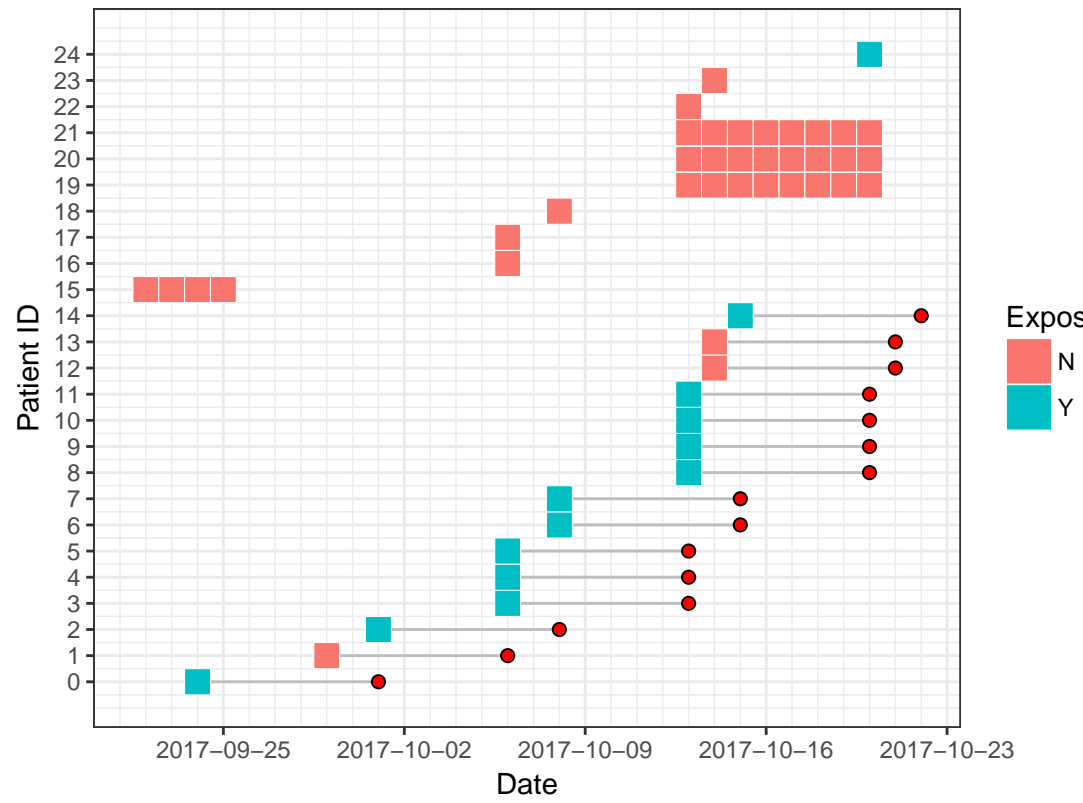
example:exposure to being bitten

colour by people the patient knows

Here, I've made -1 be the Rat (this can be better done, but the rest are patient IDS). Also it's sorted by teh first

Base Timeline of Exposure Times (black tiles) + symptom onset (red cir

number, instead of the

other things to colour by not mentioned here it's also possible to colour by their sex, or even age. It's pretty open, i've only given a few examples.

## Example interaction 2 (Bivariable): Using Colour and Facets

It will also be possible to look at bivariable relationships. Here I will explore facet interactions. Again, these are example of things a user could do. They technically have to discovery this ability and play around with the features of the graph.

Example: Patient and Exposure to Bites

Shown here, are individuals that were exposed to bites as well as the *people* they were exposed to.

Exposed to bite + symptom onset (red circle)

Example: Patient and Exposure to Sex

Shown here, are individuals that were exposed to bites as well as the *people* they were exposed to.
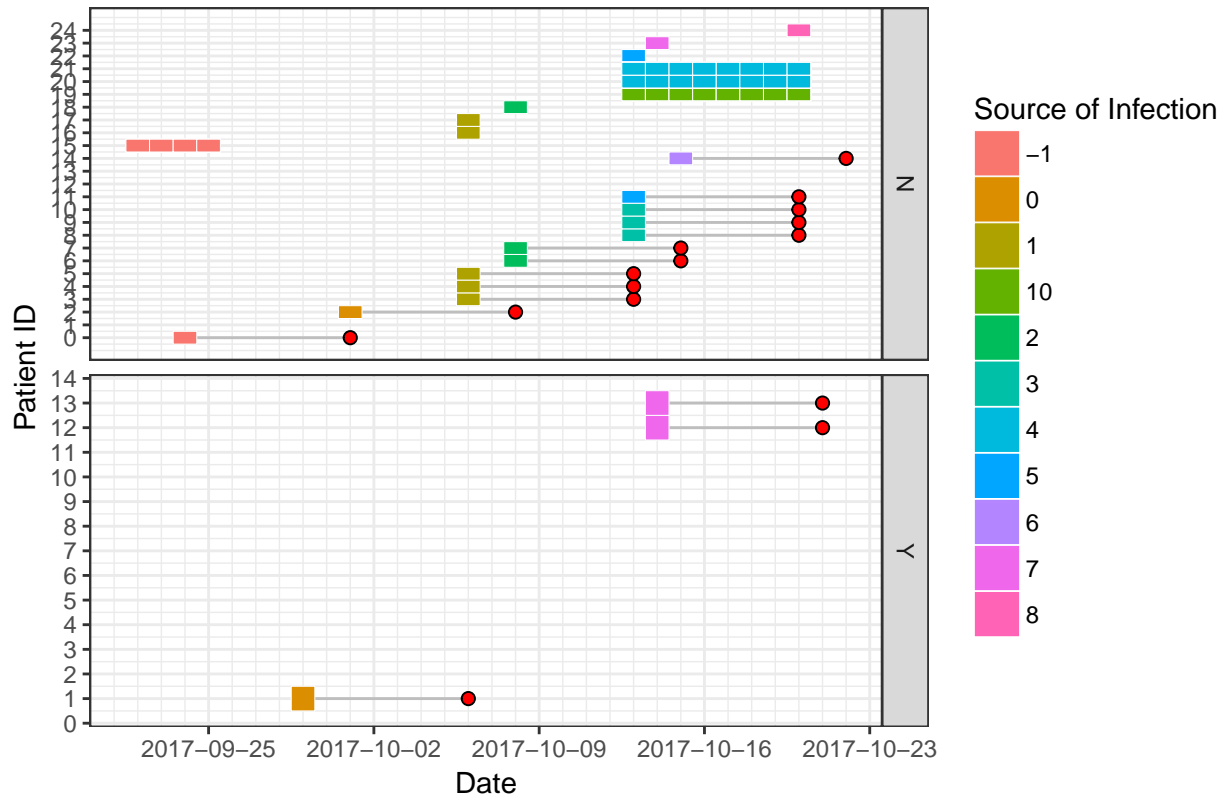
One thing that should be clear is that colour coding by exposed or not can be useful, but it is not super clear what transmission looks like. So, in addition to the timeline, participiants need another visualization.

Example interaction 3: Hiding and showing data

All connections originating from one patient

This will change the base graph to emphasize chains of transmissions from some patient to later on. Please note, there may be some bugs I haven't fully cleaned up in the path tracing code. Again, thus *USER* has to make this kind of visualization appear.

```
paths<-all_simple_paths(g,from="3")

showNodes<-unique(names(unlist(paths)))

connections<-connections %>%
  mutate(showConnect = ifelse(source %in% showNodes,"Y","N"))

connectFilt<-connections %>%
  filter(showConnect == "Y")

pBase +geom_curve(data=connectFilt,aes(x=sourceEnd,y=source,xend=targetStart,yend=ID,colour=showConnect
  ggtitle("All of the connections for patient # 3 and who they infected")
```
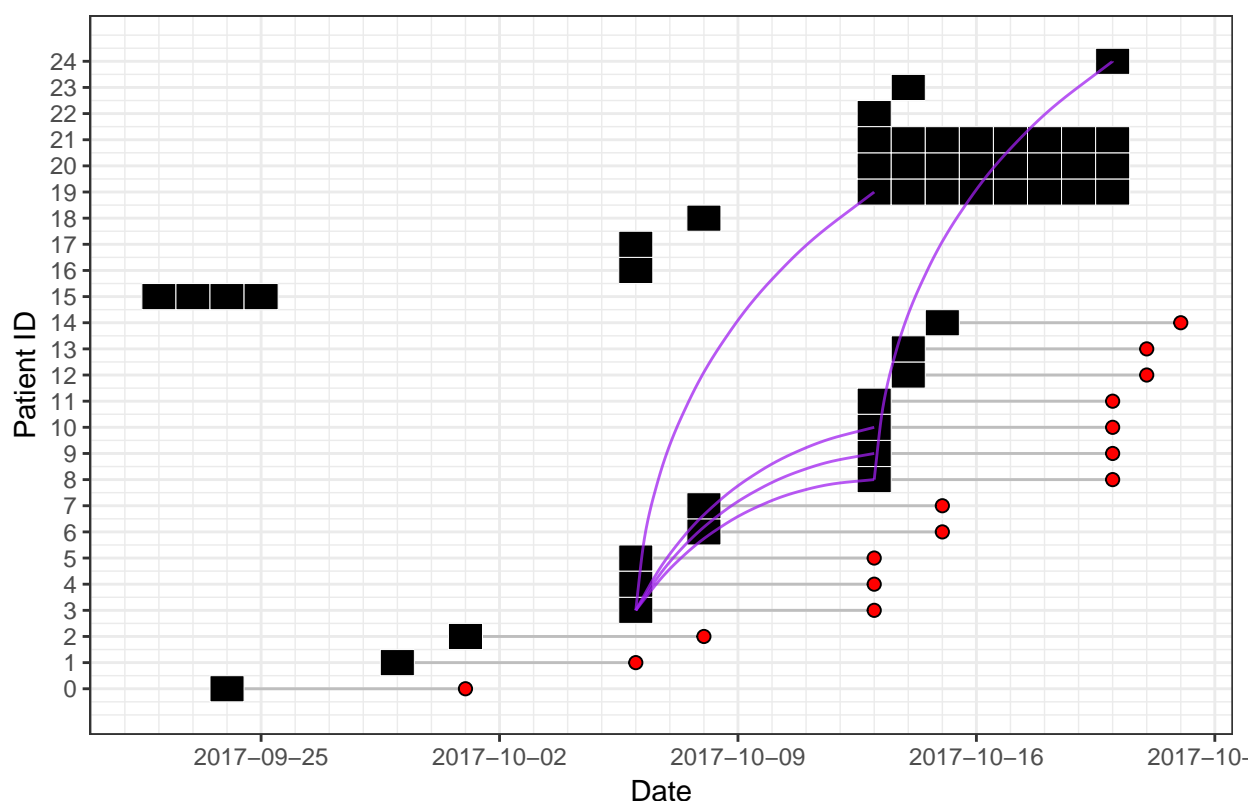
All of the connections for patient # 3 and who they infected

Here's an example with the index case

```
paths<-all_simple_paths(g,from="0")

showNodes<-unique(names(unlist(paths)))

connections<-connections %>%
  mutate(showConnect = ifelse(source %in% showNodes,"Y","N"))

connectFilt<-connections %>%
  filter(showConnect == "Y")

pBase +geom_curve(data=connectFilt,aes(x=sourceEnd,y=source,xend=targetStart,yend=ID,colour=showConnect)
  ggtitle("All of the connections for patient # 0 and who they infected")
```
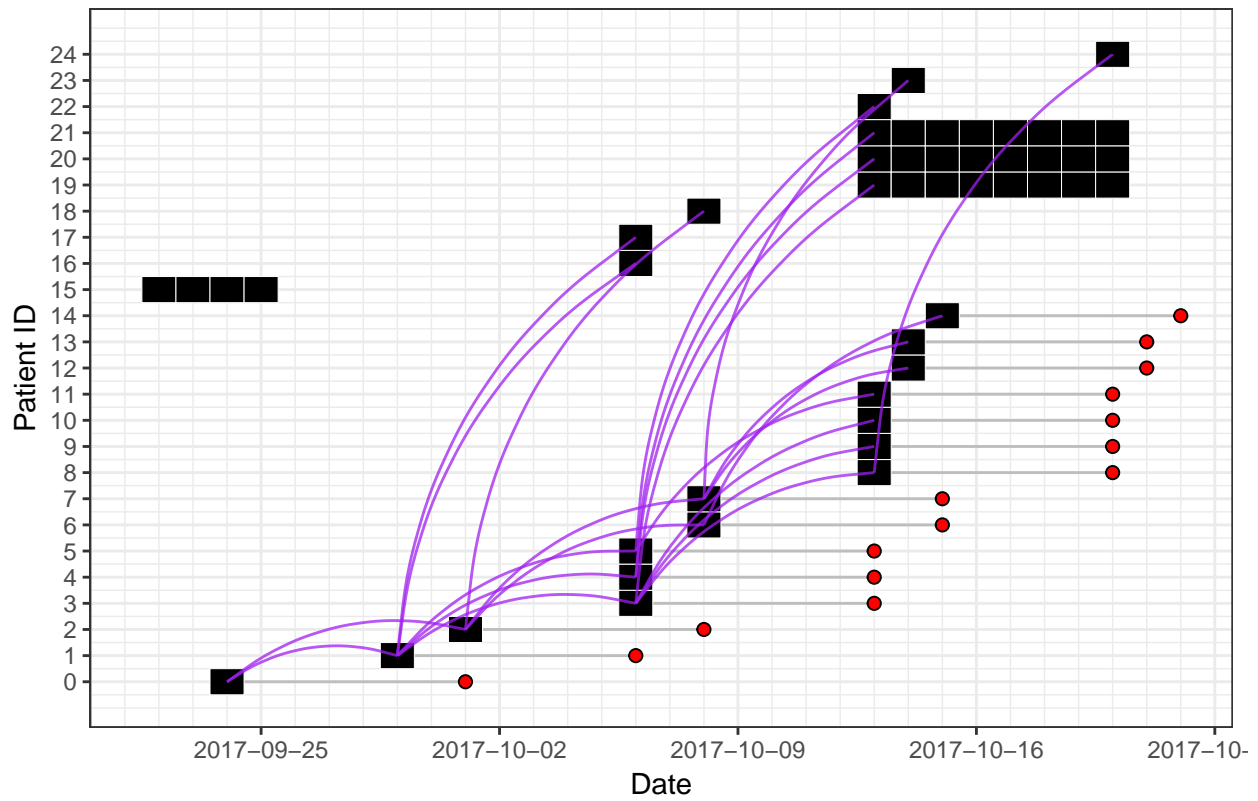
```
## Warning: Removed 47 rows containing missing values (geom_segment).
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```
## Warning: Removed 47 rows containing missing values (geom_point).
```

All of the connections for patient # 0 and who they infected

This can also be manipulate by time to constrain the number of connections being shown. Here's the results for between two time periods : the start of the infection to October 16

All of the connections for patient # 0 and
who were infected before Oct 6
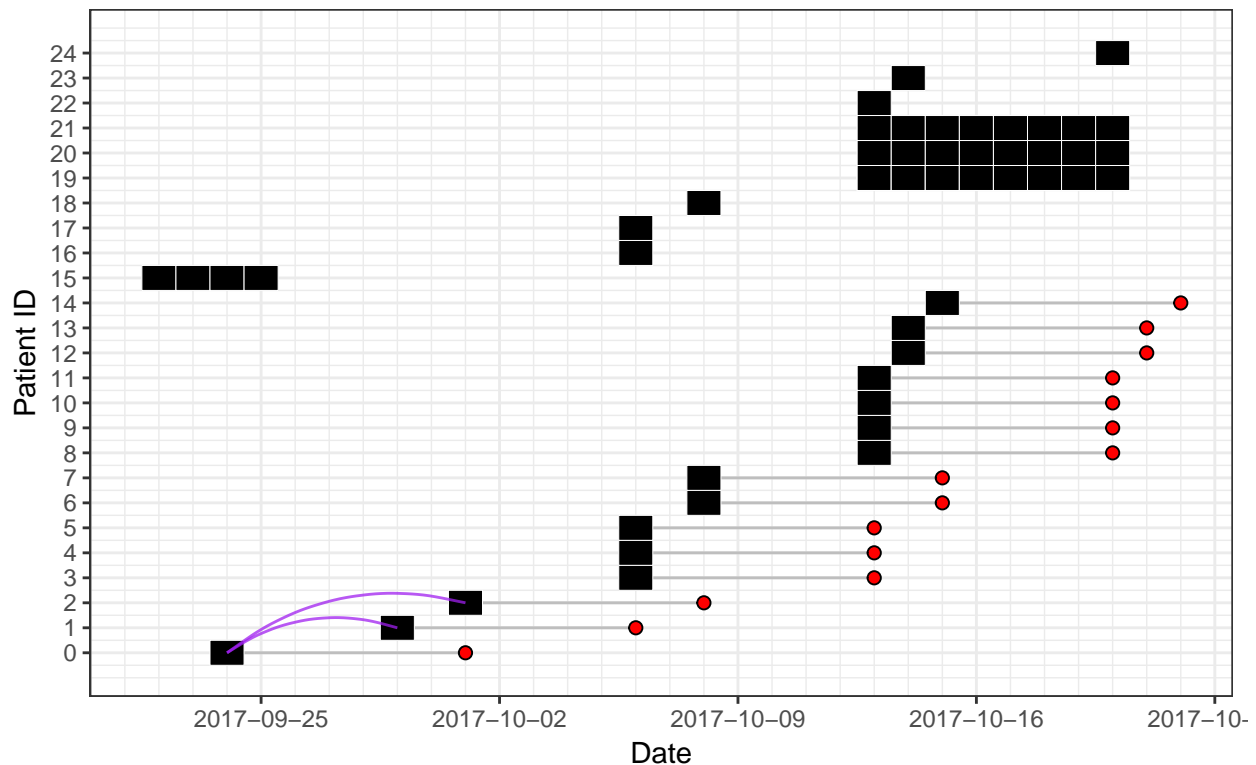
So you can imagine a patient changing a date slider and showing the connections. We can also show on a graph below they types of exposures so we can see what the dominant type of exposure is for the transmission. I have hestitated from putting graphs side by side or ontop of each other because screen realeaste on a phone is small.

End thoughts

These are scratch example of a base timeline visualization and how in can be manipulated (presented here using static examples of interactions). It is NOT the final product, but this is the direciton I am going in.

Still to be done :

Make things pretty Implement the interactive version

IMPORANTLY : A SLIDE PROJECTOR HOOKED UP TO A LAPTIO MAYBE BE A VERY GOOD BACK IN CASE THE PHONE STUFF DOESN'T WORK

Thanks!