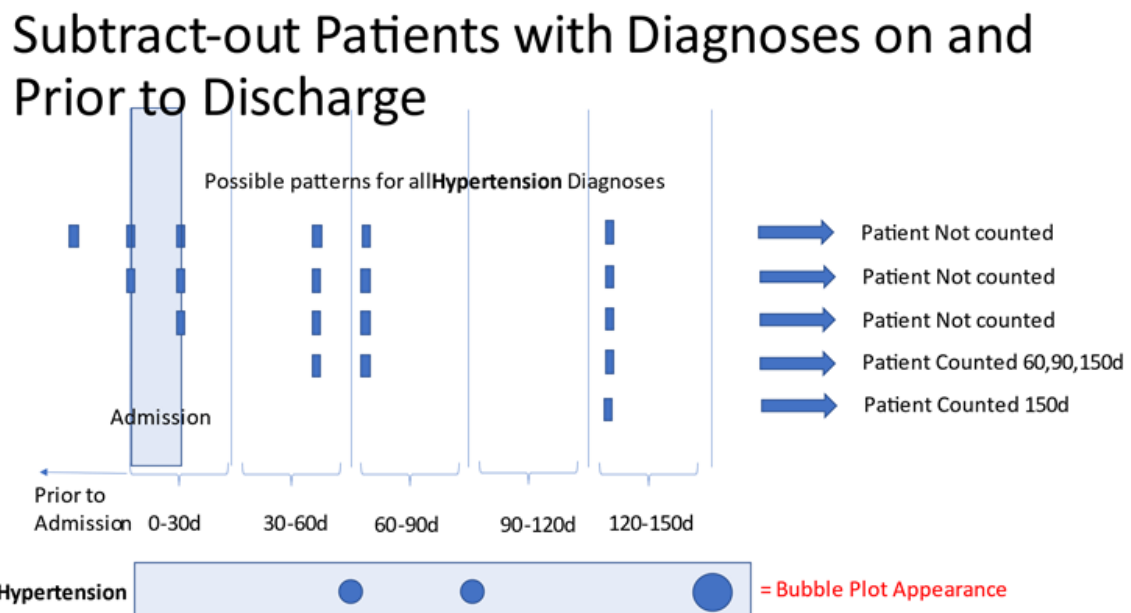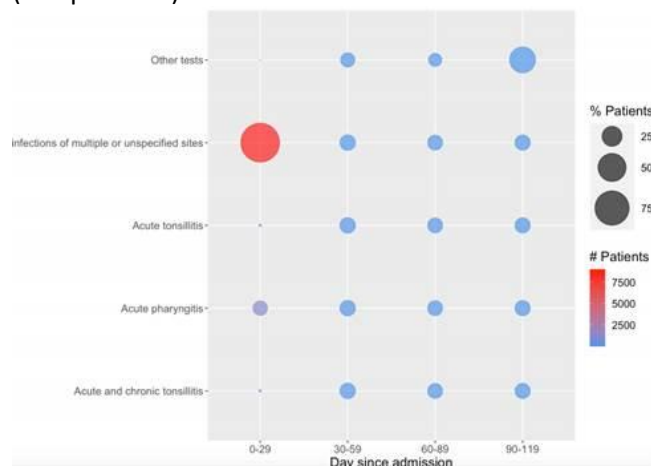Here is our next calculation, one that will take a first stab at a subtraction of the pre-existing diseases.

In the disease counts, the patients are eliminated who have that same disease prior or during the covid admission. This will only leave the disease annotations that appear after the covid admission. For example, if a patient was diagnosed with hypertension prior to the covid admission, and a resulting code for hypertension appears in the chart with a date prior to or during the admission for covid, that will eliminate the patient from being included in the row of bubbles in the chart that represent the hypertension phecode.

Several examples are included below:

The plot will follow the following format, but with an expanded color range for the number of patients (sample code):


```
colfunc<-colorRampPalette(c("royalblue","springgreen","yellow","red"))
plot(rep(1,50),col=(colfunc(50)), pch=19,cex=2)
```