11/16/21

Next steps of analysis plan:

1. Different sites of cultures:
   1. I’ll run two parallel analyses to the bloodstream infection analysis I’ve done so far: one for respiratory, one for urine
   2. Consider covid patients only
   3. Consider all pathogens together
   4. Initially, use the same definition for infection that I used for bloodstream infection (we can update this with input from AC, Jason later)
   5. First, I’ll ignore cultures at other sites (I won’t consider whether the patient has had an infection detected at another sites when choosing controls), and will consider later-infected people as eligible controls
   6. Second, I’ll still ignore cultures at other sites (I won’t consider whether the patient has had an infection detected at another sites when choosing controls), and will *not* consider later-infected people as eligible controls
   7. (I figure we can discuss alternatives to e and f next time)
2. Individual pathogens:
   1. For each of blood, urine, and respiratory infections, I’ll consider the top few (I’m thinking five) pathogens.
   2. I’ll run a parallel analysis to the analyses above, considering only individuals who had an infection with the pathogen of interest as their first infection at the given site.
   3. I’ll select controls from among individuals who didn’t have an infection of a different pathogen at the same site. For the moment, as in e and f above, I’ll ignore cultures at other sites all together.
3. Incorporating additional covariates: Once I’ve gotten 1 and 2 underway, my next step will be incorporating an ICU covariate, and considering what other variable to match on for the urine and respiratory infections.