The code I’m submitting to you is code from my work with Dr. Stephanie Fritz. Her project looked at families of patients that came the St. Louis Children’s Hospital for an infection due to Methicillin resistant Staphylococcus aureus (MRSA). They followed up with these families for 5 visits over a 9 month period. The data downloaded from REDCap was in long format, which made the subsequent analysis challenging as we wanted to find the prevalence and incidence of MRSA colonization (and other staph strains collected in the study). One of the questions we wanted to know was simply how many of the participants were colonized with MRSA during the study. To do this we needed the data in wide format in order to make this easy to assess. In the script file I’m sending you, the first code chunk is how I went from long to wide format. The subsequent code demonstrates how I determined if an individual was colonized with MRSA at 3 different anatomical sites (Nares, Axilla, and Inguinal fold). I exclude the rest of the code that essentially for all the other variables that we were interested in because it is essentially the same thing.