

# appropriate\_abx\_public

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## Define Variables

When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document.

```
## Warning: NAs introduced by coercion
```

```
#Show table to ensure columns & data are loaded and joined correctly  
head(abxculturedata)
```

```
## # A tibble: 6 x 20  
##       CSN      MRN DOB   AdmitDT Service ServiceDesc ICD   ICDdesc MedDT Med  
##       <dbl>   <dbl> <chr> <chr>   <chr>   <chr>      <chr> <chr>   <chr> <chr>  
## 1 6125535304 4691446 9/4/~ 8/10/2~ HEM      Hematology A01.~ Typhoi~ 8/10~ cefT~  
## 2 6125535304 4691446 9/4/~ 8/10/2~ HEM      Hematology A01.~ Typhoi~ 8/10~ azit~  
## 3 6125535304 4691446 9/4/~ 8/10/2~ HEM      Hematology A01.~ Typhoi~ 8/10~ cefT~  
## 4 6125535304 4691446 9/4/~ 8/10/2~ HEM      Hematology A01.~ Typhoi~ 8/10~ azit~  
## 5 6125535304 4691446 9/4/~ 8/10/2~ HEM      Hematology A01.~ Typhoi~ 8/18~ cefT~  
## 6 6125535304 4691446 9/4/~ 8/10/2~ HEM      Hematology A01.~ Typhoi~ 8/18~ cefT~  
## # ... with 10 more variables: MedRoute <chr>, Orderset <dbl>, Allergy <chr>,  
## #   AllergyType <chr>, LabOrder <chr>, CollectionDT <chr>, Organism <chr>,  
## #   Susceptibility <chr>, SusceptibilityAntibiotic <chr>,  
## #   SusceptibilityDT <chr>
```

```
## [1] "Total starting encounters 1515"
```

```
#Define guideline exclusions and guideline choices
```

```
#Select services of interest
```

```
servicesofinterest<-c('PMA','PMB','PMC','PMD','CCS','PUL','EMR','ADL')
```

```
#Ages to exclude (e.g. this guideline excludes children less than 3 months old)
```

```
minagemonths=3
```

```
#Co-morbid conditions to exclude (make all lowercase)
```

```
exclusiondiagnoses=c("cystic fibrosis","sickle-cell","hb-ss","sickle cell","leukemia","lymphoma",'neopl  
"tracheostomy","end stage renal","immunodeficiency",'immunodeficiencies','hypogamma  
"rheumatoid arthritis","lupus","muscular dystrophy","spinal muscular atrophy","hyp  
"pulmonary hypertension","cardiomyopathy","heart failure")
```

```
#filter out some common infections based on ICD prefixes
```

```
#A0: exclude gastroenteritis/colitis, "B0*":exclude many viral infections, "J95.851":exclude ventilator
```

```
exclusioninfections<-c("A0*","B0*","J95.851","M00*","M01*","N39*")
```

```
exclusioninfections2=c("abscess","cellulitis","osteomyelitis",  
"mastoiditis","lymphangitis","sinusitis","streptococcal pharyngitis","impetigo","l
```

```

      "omphalitis","aspiration","arthritis due to other bacteria","myositis","sinusitis"

#filter out certain antimicrobials
exclusionantimicrobials<- c('oseltamivir','bacitracin','nystatin','nystatin','valacyclovir','hydroxychloroquine')

#identify list of pneumonia ICD codes of interest (these are the codes of pneumonia that you are INCLUDING)
pnalist<-c('J13', 'J13', 'J14', 'J14', 'J15.0', 'J15.0', 'J15.1', 'J15.1', 'J15.20', 'J15.20', 'J15.211', 'J15.211')

#define first line choices
#####first line is ampicillin or amox
#####if PCN allergy then, ceftriaxone, clindamycin, cefdinir, levofloxacin
#####if cephalosporin allergy then, levofloxacin, clindamycin
#first line atypical coverage is azithromycin
#####if azithromycin allergy then levofloxacin or doxycycline
firstline=c("amoxicillin","ampicillin")
PCNallergy=c("amoxicillin","ampicillin",'penicillin','augmentin','penicillins','amoxicillin-clavulanate')
ifPCNallergy=c("ceftriaxone","clindamycin","cefdinir","levofloxacin")
cephalosporinallergy=c("cefdinir","cefotaxime","ceftriaxone","cephalexin","cephalosporins") #list of medications
ifcephalosporinallergy=c("levofloxacin","clindamycin")
atypicalfirstline="azithromycin"
azithroallergy="azithromycin"
atypicalwithazithroallergy=c("levofloxacin","doxycycline")

#if over 4 then azithromycin is appropriate
ageforazithro=4

##### Define culture exclusions #####

#pcnresistance list
narrowpcnsusceptibilitylist<-c("ampicillin","oxacillin",'Penicillin (meningitis)','Penicillin (non-meningitis)')
broadpcnsusceptibilitylist<-c("ampicillin","oxacillin",'ampicillin/sulbactam','Penicillin (meningitis)','Penicillin (non-meningitis)')

##          reasonforexclusions CSN
## 1          below min age 10
## 2 excluded other common infection 120
## 3          excluded service 404
## 4          included 976

```

## Apply Guidelines to label antibiotics

```

## # A tibble: 2 x 2
##   finalcorrectinitialabx count
##   <dbl> <int>
## 1         0   373
## 2         1   603

##### Culture Results Analysis #####

#find history of positive culture preceding abx order date
abxchoice <- abxchoice %>%
  mutate(hxposculture=NA)

abxchoice<-abxchoice %>%
  mutate(hxposculture= if_else(CollectionDT<AdmitDT,1,0,missing=NULL)) #1 if culture collected prior to admission

```

```

#if hx pos culture resistant to penicillin and prescribed cephalosporin, clinda then correct
abxchoice<-abxchoice %>%
  mutate(correctinitialabx= if_else(
    ((hxposculture==1 & Susceptibility=='Resistant'&
      (SusceptibilityAntibiotic %in% broadpcnsuscetibilitylist)
      &(Med=='cefTRIAxone'|Med=='clindamycin'|Med=='cefdinir'))|
    (hxposculture==1 & Susceptibility=='Resistant'&(SusceptibilityAntibiotic %in%narrowpcnsusceptibi

abxchoice<-abxchoice %>%
  mutate(label= if_else(
    ((hxposculture==1 & Susceptibility=='Resistant'&
      (SusceptibilityAntibiotic %in% broadpcnsuscetibilitylist)
      &(Med=='cefTRIAxone'|Med=='clindamycin'|Med=='cefdinir'))|
    (hxposculture==1 & Susceptibility=='Resistant'&(SusceptibilityAntibiotic %in%narrowpcnsusceptibi

#take max of choice per patient
abxchoice<-abxchoice %>% group_by(CSN) %>%
  mutate(finalcorrectinitialabx= max(correctinitialabx)) %>%
  ungroup()

#summary of correct vs incorrect choices
abxchoice %>%
  group_by(finalcorrectinitialabx)%>%
  summarise(count=n_distinct(CSN))

## # A tibble: 2 x 2
##   finalcorrectinitialabx count
##           <dbl> <int>
## 1             0     373
## 2             1     603

#summary of incorrect and correct choices
abxchoicesummarized <-abxchoice%>%
  group_by(finalcorrectinitialabx,Med)%>%
  summarise(count=n_distinct(CSN))%>%
  arrange(finalcorrectinitialabx,-count)

## `summarise()` has grouped output by 'finalcorrectinitialabx'. You can override using the `.groups` a
##### get list of all remaining patients who are incorrect for NLP below #####

#get CSN list of remaining "incorrect" patients
csnlist<-abxchoice%>%
  select(CSN)%>%
  filter(abxchoice$finalcorrectinitialabx==0)
csnlist<-unique(csnlist$CSN)

#save CSN list as CSV

write.csv(csnlist,"/Volumes/dmcommon/_DM.Private/CI Program Faculty/+Fellow Franchise/Yarahuan/Protected

##### Start NLP #####

#File path variable: Input your file path to note contents file here

```

```

notefile="/Volumes/dmcommon/_DM.Private/CI Program Faculty/+Fellow Franchise/Yarahuan/Protected/NoteCon

#Load Datasets
notedata <- read_csv(notefile)

## Rows: 847 Columns: 4

## -- Column specification -----
## Delimiter: ","
## chr (3): Note Sign Dt Tm, Note Type, Note Contents
## dbl (1): Contact Serial Number

##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.

#NoteData Columns
#1=CSN, 2=NoteDT, 3=NoteType, 4=NoteText

#rename columns
notedata<-notedata %>%
  rename(CSN=1) %>%
  rename(NoteDT=2) %>%
  rename(NoteType=3) %>%
  rename(NoteText=4)

#make text columns lowercase
notedata$NoteType=tolower(notedata$NoteType)

## Warning: One or more parsing issues, see `problems()` for details
notedata$NoteText=str_replace_all(notedata$NoteText, "[^[:alnum:]]", " ")
notedata$NoteText=tolower(notedata$NoteText)

##### Create your NLP phrases #####

treatmentfailurephrases=c("treatment failure","failed outpatient treatment","failed outpatient therapy"
  "failure of outpatient treatment", "failure of outpatient therapy", "failure o
  ,"failure of outpatient HD amoxicillin","failure of outpatient high dose amox
  ,"despite amoxicillin","despite outpatient antibiotics", "despite outpatient t
  "in spite of outpatient treatment","s p outpatient therapy","s p outpatient t
  "s p outpatient amoxicillin", "started on amoxicillin as outpatient", "starte
  "started on high dose amoxicillin as outpatient","started on amoxicillin as an
  "started on high dose amoxicillin as an outpatient")

aspirationphrases=c("aspiration pneumonia","likely aspiration")

unimmunizedphrases=c("unimmunized","unvaccinated","partially vaccinated","partially immunized")

##### Apply NLP phrases #####

#apply treatment failure phrases
treatmentfailure<-notedata %>%
  select(CSN) %>%
  filter(str_detect(notedata$NoteText, paste(treatmentfailurephrases,collapse='|'))))

#apply aspiration phrases

```

```

aspiration<-notedata %>%
  select(CSN) %>%
  filter(str_detect(notedata$NoteText, paste(aspirationphrases,collapse='|'))))

#apply unimmunized phrases
unimmunized<-notedata %>%
  select(CSN) %>%
  filter(str_detect(notedata$NoteText, paste(unimmunizedphrases,collapse='|'))))

#####Summarize NLP findings #####
#count number of treatment failures/aspirations/unimmunized
n_distinct(treatmentfailure$CSN)

## [1] 47
n_distinct(aspiration$CSN)

## [1] 53
n_distinct(unimmunized$CSN)

## [1] 3

#get all CSNs from treatment failure list
treatmentfailurecsnlist<-unique(treatmentfailure$CSN)
aspirationcsnlist<-unique(aspiration$CSN)
unimmunizedcsnlist<-unique(unimmunized$CSN)

#if CSN in treatmet failure list, assign to value of 2
abxchoice<-abxchoice %>%
  mutate(correctinitialabx= if_else(abxchoice$CSN %in% treatmentfailurecsnlist
                                   ,2,correctinitialabx,correctinitialabx))

abxchoice<-abxchoice %>%
  mutate(label= if_else(abxchoice$CSN %in% treatmentfailurecsnlist
                        ,"outpatient treatment failure",label,label))

#if CSN in aspiration list, assign to value of 3
abxchoice<-abxchoice %>%
  mutate(correctinitialabx= if_else(abxchoice$CSN %in% aspirationcsnlist
                                   ,3,correctinitialabx,correctinitialabx))

abxchoice<-abxchoice %>%
  mutate(label= if_else(abxchoice$CSN %in% aspirationcsnlist
                        ,"aspiration pneumonia",label,label))

#if CSN in unimmunized list, assign to value of 4
abxchoice<-abxchoice %>%
  mutate(correctinitialabx= if_else(abxchoice$CSN %in% unimmunizedcsnlist
                                   ,4,correctinitialabx,correctinitialabx))

abxchoice<-abxchoice %>%
  mutate(label= if_else(abxchoice$CSN %in% unimmunizedcsnlist
                        ,"unimmunized",label,label))

#take max of choice per patietn

```

```

abxchoice<-abxchoice %>% group_by(CSN) %>%
  mutate(finalcorrectinitialabx= max(correctinitialabx)) %>%
  ungroup()

#summary of correct vs incorrectn vs treatment failure choices (0=incorrect, 1=correct, 2=outpatient tr
abxchoice %>%
  group_by(label)%>%
  summarise(count=n_distinct(CSN))

## # A tibble: 6 x 2
##   label                                count
##   <chr>                                <int>
## 1 aspiration pneumonia                  53
## 2 correct                             603
## 3 incorrect abx without justification  311
## 4 outpatient treatment failure         43
## 5 unimmunized                         3
## 6 <NA>                                2

##### Apply additional guidelines based on above NLP #####

#define guidelinechoices (if hospitalized & unimmunized or failed outpatient treatment then--> Ceftriax
optreatmentorunimmunized=c("ceftriaxone","cefotaxime")

#apply guidelines
abxchoice<-abxchoice %>%
  mutate(correctinitialabx= if_else(servicelocation=="Inpatient"&(finalcorrectinitialabx==2 |finalcorrec

#max per patient
abxchoice<-abxchoice %>% group_by(CSN) %>%
  mutate(finalcorrectinitialabx= max(correctinitialabx)) %>%
  ungroup()

#summary of correct vs incorrectn vs treatment failure choices (0=incorrect, 1=correct, 2=outpatient tr
abxchoice %>%
  group_by(finalcorrectinitialabx)%>%
  summarise(count=n_distinct(CSN))

## # A tibble: 4 x 2
##   finalcorrectinitialabx count
##   <dbl> <int>
## 1         0    274
## 2         1   632
## 3         2    17
## 4         3    53

```