

# Prolonged Wait Time is Associated with Increased Mortality for Chilean Waiting List Patients with Non-Prioritized Conditions

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## Additional File 3: Data Analysis Procedures

```
####0. SCRIPT PARAMETERS####
#set working directory
setwd("C:/XXX")
getwd()
#specify the location of the cleaned datasets
link1<-"C:/XXX/Atacama Cleaned.csv"
link2<-"C:/XXX/Valparaiso Cleaned.csv"
link3<-"C:/XXX/Osorno Cleaned.csv"
link1<-read.csv(file.choose(), header = TRUE)#"Atacama Cleaned.csv"
link2<-read.csv(file.choose(), header = TRUE)#"Valparaiso Cleaned.csv"
link3<-read.csv(file.choose(), header = TRUE)#"Osorno Cleaned.csv"
#####
#####
```

```
####1. LOAD PACKAGES####
library(openxlsx)
library(survival)
library(dplyr)
library(ggplot2)
library(survminer)
library(rms)
library(coxme)
library(Rmisc)
library(ggfortify)
#####
#####
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####2. LOAD CLEANED DATASETS####
Atadata<-link1
Atadata<-Atadata %>%
  mutate(deathtime = as.numeric(deathtime),
         age_category = as.factor(ifelse(age_category=="<15",ifelse(age_numeric<=3,"0-3",ifelse(age_numeric<=7,"4-7",ifelse(age_numeric<=11,"8-11","12-14"))),as.character(age_category))),
         death2y = ifelse(death==0,0,ifelse(deathtime<=365*2,1,0)),
         time_to_event2y = ifelse(death2y==1,deathtime,2*365),
         death2.5y = ifelse(death==0,0,ifelse(deathtime<=floor(365*2.5),1,0)),
         time_to_event2.5y = ifelse(death2y==1,deathtime,floor(365*2.5)),
         death3y = ifelse(death==0,0,ifelse(deathtime<=365*3,1,0)),
         time_to_event3y = ifelse(death2y==1,deathtime,3*365)
  )
Atadata$age_category<-ordered(Atadata$age_category,levels=c("0-3","4-7","8-11","12-14","15-45","46-55","56-65","66-75","76-85","85+"))
str(Atadata)
Valdata<-link2
Valdata<-Valdata %>%
  mutate(deathtime = as.numeric(deathtime),
         age_category = as.factor(ifelse(age_category=="<15",ifelse(age_numeric<=3,"0-3",ifelse(age_numeric<=7,"4-7",ifelse(age_numeric<=11,"8-11","12-14"))),as.character(age_category))),
         death2y = ifelse(death==0,0,ifelse(deathtime<=365*2,1,0)),
         time_to_event2y = ifelse(death2y==1,deathtime,2*365),
         death2.5y = ifelse(death==0,0,ifelse(deathtime<=floor(365*2.5),1,0)),
         time_to_event2.5y = ifelse(death2y==1,deathtime,floor(365*2.5)),
         death3y = ifelse(death==0,0,ifelse(deathtime<=365*3,1,0)),
         time_to_event3y = ifelse(death2y==1,deathtime,3*365)
  )
Valdata$age_category<-ordered(Valdata$age_category,levels=c("0-3","4-7","8-11","12-14","15-45","46-55","56-65","66-75","76-85","85+"))
str(Valdata)
Osodata<-link3
Osodata<-Osodata %>%
  mutate(deathtime = as.numeric(deathtime),
         age_category = as.factor(ifelse(age_category=="<15",ifelse(age_numeric<=3,"0-3",ifelse(age_numeric<=7,"4-7",ifelse(age_numeric<=11,"8-11","12-14"))),as.character(age_category))),
         death2y = ifelse(death==0,0,ifelse(deathtime<=365*2,1,0)),
         time_to_event2y = ifelse(death2y==1,deathtime,2*365),
         death2.5y = ifelse(death==0,0,ifelse(deathtime<=floor(365*2.5),1,0)),
         time_to_event2.5y = ifelse(death2y==1,deathtime,floor(365*2.5)),
         death3y = ifelse(death==0,0,ifelse(deathtime<=365*3,1,0)),
         time_to_event3y = ifelse(death2y==1,deathtime,3*365)
  )
Osodata$age_category<-ordered(Osodata$age_category,levels=c("0-3","4-7","8-11","12-14","15-45","46-55","56-65","66-75","76-85","85+"))
#####
#####

####3. DATASET PREPARATION####
all<-function(data){return(subset(data,data$age_numeric>=0))}
id<-Valdata[which(Valdata$healthdept=="Atacama"),]$id_orig
Atadata[which(Atadata$id_orig%in$id),]
Valdata[which(Valdata$healthdept=="Atacama"),]
Valdata2<-Valdata[-which(Valdata$healthdept=="Atacama"),]

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```

data<-rbind(Atadata,Valdata2,Osodata)
summary(data$healthdept)
data$healthdept<-as.character(data$healthdept)
data$healthdept<-ifelse(data$healthdept%in%("Vaparaiso-
SanAntonio", "Atacama", "Osorno"),data$healthdept,"Other")
data$healthdept<-as.factor(data$healthdept)
data_all<-data

##SET REFERENCE LEVELS AND GROUP MEDICAL SPECIALTIES WITH LOW N
#AGE
data_all$age_category<-factor(data_all$age_category, ordered=FALSE)
data_all$age_category<-relevel(data_all$age_category, ref="15-45")
#RESIDENCE
data_all$rural_urban<-relevel(data_all$rural_urban, ref="rural")
#INSURANCE
data_all$insurance<-ifelse(data_all$insurance=="public","public","private")
data_all$insurance<-factor(data_all$insurance)
data_all$insurance<-relevel(data_all$insurance, ref="public")
#SPECIALTY
#re-label those with low N and no contribution to mortality status death=yes, and group specialties with
low n
data_all$specialty2<-as.character(data_all$specialty)
data_all$specialty3<-ifelse(data_all$healthdept=="Atacama" & data_all$specialty2=="Anesthesiology",
"Other", # n=1, no death within 2 years
                           ifelse(data_all$healthdept=="Atacama" & data_all$specialty2=="Breast
Surgery","Other", # n=2, no death within 2 years
                                   ifelse(data_all$specialty2=="Occupational Health","Other", # n=28, no
death within 2 years
                                           ifelse(data_all$healthdept=="Atacama" &
data_all$specialty2=="Physical Medicine and Rehabilitation","Other",# n=1, no death within 2 years
                                               ifelse(data_all$healthdept=="Atacama" &
data_all$specialty2=="Rheumatology","Other", # n=6, no death within 2 years
                                                   ifelse(data_all$healthdept=="Osorno" &
data_all$specialty2=="Infectious Disease","Other",# n=20, no death within 2 years
                                                       ifelse(data_all$specialty2=="Cardiac
Surgery","Cardiovascular Surgery", # n=32, registrants from Valparaiso

ifelse(data_all$specialty2=="Vascular Surgery", "Cardiovascular Surgery", # 2512 from Atacama, 7107 from
Osorno, 5849 from Valparaiso

ifelse(data_all$specialty2=="Geriatrics", "Other",#geriatrics N = 1

ifelse(data_all$specialty2=="Thorax Surgery","Adult Surgery",#thorax surgery n=210

ifelse(data_all$specialty2=="Abdominal Surgery","Adult Surgery",#abdominal surgery n=51

ifelse(data_all$specialty2=="Pediatric Surgery","Pediatrics",data_all$specialty2))))))))))#pediatric
surgery n=167 from Valparaiso
#setting ref levels
data_all$specialty4<-as.factor(data_all$specialty3)
data_all$specialty4<-relevel(data_all$specialty4, ref="Internal Medicine")
#REFERRING LOCATION
data_all$referring_location<-relevel(data_all$referring_location, ref="Urban")
#ACCEPTING
data_all$accepting_type<-relevel(data_all$accepting_type, ref="tertiary")
#REFERRING SUBTYPE
data_all$referring_subtype2<-as.character(data_all$referring_subtype)
data_all$referring_subtype2<-ifelse(data_all$referring_subtype2=="mobile unit", "urban primary center",
data_all$referring_subtype2)
data_all$referring_subtype2<-as.factor(data_all$referring_subtype2)
data_all$referring_subtype2<-relevel(data_all$referring_subtype2, ref="tertiary high complexity")
#ACCEPTING SUBTYPE
data_all$accepting_subtype<-relevel(data_all$accepting_subtype, ref="tertiary high complexity")
#YEAR OF WAITLIST ENTRY
data_all$year_entry2<-as.factor(data_all$year_entry)
data_all$year_entry2<-relevel(data_all$year_entry2, ref="2008")
#ACCEPTING LEVEL OF CARE
data_all$accepting_type<-as.factor(data_all$accepting_type)
data_all$accepting_type<-relevel(data_all$accepting_type, ref="primary")

```

```

#REFERRING LEVEL OF CARE
data_all$referring_type<-as.factor(data_all$referring_type)
data_all$referring_type<-relevel(data_all$referring_type, ref="primary")

##inclusion/exclusion criteria based on "health department"
#we excluded 4740 out of 1044528 (0.45%) registrants listed in health departments other than atacama,
valparaiso, and osorno
data_all<-data_all[which(data_all$healthdept!="Other"),]

##inclusion/exclusion criteria based on "reason of exit from the waitlist"
#include: Death, Completed Case by Resolutivity, Completed Case by Telemedicine, Completed Cases,
Completed Cases Externally??. Health Coverage Change, Informed Procedure??. Medical Reevaluation, Patient
Missed, Patient Reject, Patient Spontaneous Recovery, Surgery Not Necessary, Clinical Case Change
#exclude: Contact Doesn't Match??. Digitation Error, Duplicated Request??. Ges, No pertinencia??
#we excluded 26222 out of 987497 (2.66%) registrants because follow up was not possible, i.e., "Contact
Doesn't Match" (N=25,572), "Digitation Error" (N=650)
#and we also excluded 15643 out of 987497 (1.58%) registrants because they were GES, i.e., "GES"
(N=13782), "No Pertinencia" (N=1861)
data_all<-data_all[which(data_all$exit_reason!="Contact Doesn't Match??" &
                        data_all$exit_reason!="Digitation Error" &
                        data_all$exit_reason!="Duplicated Request??" &
                        data_all$exit_reason!="Ges" &
                        data_all$exit_reason!="No pertinencia??"),]

##subsetting based on three outcomes of interest: 2-, 2.5- and 3-year mortality
myvars2 <-
c("age_category", "sex", "rural_urban", "specialty4", "healthdept", "insurance", "referring_type", "accepting_type",
  "time_to_event2y", "death2y", "waitingtime_numeric", "accepting")
myvars2.5 <-
c("age_category", "sex", "rural_urban", "specialty4", "healthdept", "insurance", "referring_type", "accepting_type",
  "time_to_event2.5y", "death2.5y", "waitingtime_numeric", "accepting")
myvars3 <-
c("age_category", "sex", "rural_urban", "specialty4", "healthdept", "insurance", "referring_type", "accepting_type",
  "time_to_event3y", "death3y", "waitingtime_numeric", "accepting")
data_all2y<-data_all[myvars2]
data_all2.5y<-data_all[myvars2.5]
data_all3y<-data_all[myvars3]
#####
#####

```

####3. STATISTICAL ANALYSIS: INDIVIDUAL-LEVEL SURVIVAL MODELING####

##SURVIVAL OVERALL####

```

all_RandomEffects2<-coxme(Surv(time_to_event2y, death2y)~
                           age_category+
                           sex+
                           rural_urban+
                           specialty4+
                           insurance+
                           referring_type+
                           (1|healthdept/accepting_type),
                           data=data_all2y)

```

```

##SURVIVAL OVERALL 2-, 2.5-, AND 3-YEAR MORTLITY####
all_RandomEffects2<-coxme(Surv(time_to_event2y, death2y)~
    age_category+
    sex+
    rural_urban+
    specialty4+
    insurance+
    referring_type+
    (1|healthdept/accepting_type),
    data=data_all2y)
all_RandomEffects2.5<-coxme(Surv(time_to_event2.5y, death2.5y)~
    age_category+
    sex+
    rural_urban+
    specialty4+
    insurance+
    referring_type+
    (1|healthdept/accepting_type),
    data=data_all2.5y)
all_RandomEffects3<-coxme(Surv(time_to_event3y, death3y)~
    age_category+
    sex+
    rural_urban+
    specialty4+
    insurance+
    referring_type+
    (1|healthdept/accepting_type),
    data=data_all3y)

##SURVIVAL ATACAMA####
all_RandomEffects2_atacama<-coxph(Surv(time_to_event2y, death2y)~
    age_category+
    sex+
    rural_urban+
    specialty4+
    insurance+
    referring_type+
    accepting_type,
    data=data_all2y[which(data_all2y$healthdept=="Atacama"),])

##SURVIVAL VALPARAISO####
all_RandomEffects2_valparaiso<-coxph(Surv(time_to_event2y, death2y)~
    age_category+
    sex+
    rural_urban+
    specialty4+
    insurance+
    referring_type+
    accepting_type,
    data=data_all2y[which(data_all2y$healthdept=="Vaparaiso-SanAntonio"),])

##SURVIVAL OSORNO####
all_RandomEffects2_osorno<-coxph(Surv(time_to_event2y, death2y)~
    age_category+
    sex+
    rural_urban+
    specialty4+
    insurance+
    referring_type+
    accepting_type,
    data=data_all2y[which(data_all2y$healthdept=="Osorno"),])

##SURVIVAL ONCOLOGY####
#ggsvplot(survfit(Surv(time_to_event2y, death2y)~specialty4, data=data_all2y))
summary(as.factor(data_all2y$age_category))
oncology<-data_all2y[data_all2y$specialty4 == "Oncology",]
table(data_all2y$age_category,data_all2y$death2y)
oncology<-oncology[oncology$age_category == "85+"|
    oncology$age_category == "76-85"|
    oncology$age_category == "66-75"|
    oncology$age_category == "56-65"|
    oncology$age_category == "46-55"|
    oncology$age_category == "15-45",]

```

```

summary(as.factor(data_all2y$age_category))
summary(as.factor(oncology$insurance))
ggsurvplot(survfit(Surv(time_to_event2y, death2y)~age_category, data=oncology))
fit_onc<-survfit(Surv(time_to_event2y, death2y)~1, data=oncology)
autoplot(fit_onc, censor.shape = '*', censor.size = 5)
summary(as.factor(oncology$rural_urban))
list(names(oncology))
str(oncology)
oncology$age_category<-as.factor(oncology$age_category)
oncology$sex<-as.factor(oncology$sex)
oncology$rural_urban<-as.factor(oncology$rural_urban)
oncology$healthdept<-as.factor(oncology$healthdept)
oncology$insurance<-as.factor(oncology$insurance)
oncology$referring_type<-as.factor(oncology$referring_type)
oncology$accepting_type<-as.factor(oncology$accepting_type)
summary(oncology)

oncology$referring_type[oncology$referring_type == "secondary"]<-"primary"
oncology$referring_type<-as.character(oncology$referring_type)
oncology$referring_type<-as.factor(oncology$referring_type)
table(oncology$sex, oncology$death2y)

#insurance, referring_type. accepting_type
oncology_ph<-coxph(Surv(time_to_event2y, death2y)~
  age_category+
  sex+
  age_category:age_category+
  rural_urban+
  #insurance+
  referring_type+
  healthdept+
  #accepting_type+
  age_category:sex+
  age_category:rural_urban+
  age_category:healthdept+
  age_category:referring_type+
  #age_category:insurance+
  age_category:rural_urban,
  data=oncology)
summary(oncology_ph)
anova(oncology_ph)
fit<-survfit(oncology_ph, data=oncology)
obs<-survfit(Surv(time_to_event2y, death2y)~1, data=oncology)
KmPh <- list(Model = fit, KM = obs)
ggsurvplot(KmPh, data = oncology, combine = TRUE, # Combine curves
  risk.table = TRUE, # Add risk table
  conf.int = FALSE, # Add confidence interval
  conf.int.style = "step", # CI style, use "step" or "ribbon"
  censor = FALSE, # Remove censor points
  tables.theme = theme_cleantable(), # Clean risk table
  palette = "jco", ylim=c(0,1), xlim=c(0,1000))

resd<-resid(oncology_ph, "mart")
dev.off()
plot(resd)
hist(resd)
oncology2<-oncology
oncology2$resd<-resd
oncology2$ID <- seq.int(nrow(oncology2))
names(oncology2)
ggplot(oncology2, aes(x=ID, y=resd))+ geom_point(aes(colour = factor(age_category)))

#residual plots
par(mfrow=c(2,4))
plot(resd~as.factor(oncology$age_category))
plot(resd~as.factor(oncology$sex))
plot(resd~as.factor(oncology$rural_urban))
plot(resd~as.factor(oncology$specialty4))
plot(resd~as.factor(oncology$insurance))

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plot(resd~as.factor(oncology$referring_type))
plot(resd~as.factor(oncology$healthdept))
plot(resd~as.factor(oncology$accepting_type))

par(mfrow=c(3,2))
interaction.plot(as.factor(oncology$age_category), as.factor(oncology$sex), resd)
interaction.plot(as.factor(oncology$age_category), as.factor(oncology$rural_urban), resd)
interaction.plot(as.factor(oncology$age_category), as.factor(oncology$specialty4), resd)
interaction.plot(as.factor(oncology$age_category), as.factor(oncology$insurance), resd)
interaction.plot(as.factor(oncology$age_category), as.factor(oncology$referring_type), resd)
interaction.plot(as.factor(oncology$age_category), as.factor(oncology$healthdept), resd)

summary(as.factor(oncology_2$death2y))
oncology2<-oncology[oncology$death2y=="0",]
oncology_2<-oncology[oncology$death2y=="1",]
oncology3<-sample_n(oncology2, 2236*1.5)
oncology4<-rbind(oncology3, oncology_2)
names(oncology4)
oncology4$age_category<-as.character(oncology4$age_category)
oncology4$age_category<-as.factor(oncology4$age_category)
oncology4$sex<-as.character(oncology4$sex)
oncology4$sex<-as.factor(oncology4$sex)
oncology4$rural_urban<-as.character(oncology4$rural_urban)
oncology4$rural_urban<-as.factor(oncology4$rural_urban)
oncology4$healthdept<-as.character(oncology4$healthdept)
oncology4$healthdept<-as.factor(oncology4$healthdept)
oncology4$referring_type<-as.character(oncology4$referring_type)
oncology4$referring_type<-as.factor(oncology4$referring_type)

oncology_ph<-coxph(Surv(time_to_event2y, death2y)~
  age_category+
  sex+
  age_category:age_category+
  rural_urban+
  #insurance+
  referring_type+
  healthdept+
  #accepting_type+
  age_category:sex+
  age_category:rural_urban+
  age_category:healthdept+
  age_category:referring_type+
  #age_category:insurance+
  age_category:rural_urban+
  #sex:rural_urban+
  sex:healthdept,
  #sex:referring_type,
  #healthdept:rural_urban,
  #referring_type:rural_urban,
  data=oncology4)

summary(oncology_ph)
anova(oncology_ph)
summary(oncology4$rural_urban)

fit<-survfit(oncology_ph,data=oncology4)
obs<-survfit(Surv(time_to_event2y, death2y)~1, data=oncology4)
KmPh <- list(Model = fit, KM = obs)
ggsurvplot(KmPh, data = oncology4, combine = TRUE, # Combine curves
  risk.table = TRUE, # Add risk table
  conf.int = FALSE, # Add confidence interval
  conf.int.style = "step", # CI style, use "step" or "ribbon"
  censor = FALSE, # Remove censor points
  tables.theme = theme_cleantable(), # Clean risk table
  palette = "jco",ylim=c(0,1),xlim=c(0,1000))

resd<-resid(oncology_ph, "mart")
oncology4$resd<-resd
par(mfrow=c(2,4))
plot(resd~as.factor(oncology4$age_category))

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```

plot(resd~as.factor(oncology4$sex))
plot(resd~as.factor(oncology4$rural_urban))
plot(resd~as.factor(oncology4$specialty4))
plot(resd~as.factor(oncology4$insurance))
plot(resd~as.factor(oncology4$referring_type))
plot(resd~as.factor(oncology4$healthdept))
plot(resd~as.factor(oncology4$accepting_type))

par(mfrow=c(3,2))
interaction.plot(as.factor(oncology4$age_category), as.factor(oncology4$sex), resd)
interaction.plot(as.factor(oncology4$age_category), as.factor(oncology4$rural_urban), resd)
interaction.plot(as.factor(oncology4$age_category), as.factor(oncology4$specialty4), resd)
interaction.plot(as.factor(oncology4$age_category), as.factor(oncology4$insurance), resd)
interaction.plot(as.factor(oncology4$age_category), as.factor(oncology4$referring_type), resd)
interaction.plot(as.factor(oncology4$age_category), as.factor(oncology4$healthdept), resd)

par(mfrow=c(3,2))
interaction.plot(as.factor(oncology4$sex), as.factor(oncology4$rural_urban), resd)
interaction.plot(as.factor(oncology4$sex), as.factor(oncology4$specialty4), resd)
interaction.plot(as.factor(oncology4$sex), as.factor(oncology4$insurance), resd)
interaction.plot(as.factor(oncology4$sex), as.factor(oncology4$referring_type), resd)
interaction.plot(as.factor(oncology4$sex), as.factor(oncology4$healthdept), resd)

##figures oncology
tiff("Residuals versus age category for Oncology area.tiff", width = 6, height = 6, pointsize = 1/300,
units = 'in', res = 300)
ggplot(oncology4, aes(x=age_category, y=resd, fill=age_category)) +
  geom_boxplot(alpha=.7)+
  theme_bw()+
  ylim(-3,3) +
  xlab("Age group") +
  ylab("Residuals")+
  theme(legend.title=element_blank()) + scale_color_grey()
dev.off()

tiff("Survival curve (Kaplan Meier) for Oncology.tiff", width = 6, height = 6, pointsize = 1/300, units =
'in', res = 300)
obs<-survfit(Surv(time_to_event2y, death2y)~1, data=oncology4)
ggsurvplot(obs, data = oncology4, combine = TRUE, # Combine curves
  risk.table = FALSE, # Add risk table
  conf.int = TRUE, # Add confidence interval
  conf.int.style = "step", # CI style, use "step" or "ribbon"
  censor = FALSE, # Remove censor points
  #tables.theme = theme_cleantable(), # Clean risk table
  palette = "jco",ylim=c(0,1),xlim=c(0,800))
dev.off()

tiff("Survival curve (Kaplan Meier) and fitted Proportional Hazard model (Oncology).tiff", width = 6,
height = 4, pointsize = 1/300, units = 'in', res = 300)
fit<-survfit(oncology_ph,data=oncology4)
obs<-survfit(Surv(time_to_event2y, death2y)~1, data=oncology4)
KmPh <- list(Model = fit, KM = obs)
ggsurvplot(KmPh, data = oncology4, combine = TRUE, # Combine curves
  risk.table = FALSE, # Add risk table
  conf.int = FALSE, # Add confidence interval
  conf.int.style = "step", # CI style, use "step" or "ribbon"
  censor = FALSE, # Remove censor points
  tables.theme = theme_cleantable(), # Clean risk table
  palette = "jco",ylim=c(0,1),xlim=c(0,800))
dev.off()

#KM CURVES FOR ONCOLOGY
tiff("Survival curve (Kaplan Meier) for sex group (Oncology).tiff", width = 6, height = 6, pointsize =
1/300, units = 'in', res = 300)
obs<-survfit(Surv(time_to_event2y, death2y)~sex, data=oncology4)
sex_plot<-ggsurvplot(obs, data = oncology4, combine = TRUE, # Combine curves
  risk.table = FALSE, # Add risk table
  conf.int = TRUE, # Add confidence interval
  conf.int.style = "step", # CI style, use "step" or "ribbon"

```

```

        censor = FALSE, # Remove censor points
        #tables.theme = theme_cleantable(), # Clean risk table
        palette = "jco",ylim=c(0,1),xlim=c(0,800),legend.title = "Covariate: Sex
Levels:",
        legend.labs = c("Female", "Male"), font.legend = c(14, "plain", "black"))
dev.off()

tiff("Survival curve (Kaplan Meier) for age group (Oncology).tiff", width = 6, height = 6, pointsize =
1/300, units = 'in', res = 300)
summary(oncology4$age_category)
obs<-survfit(Surv(time_to_event2y, death2y)~age_category, data=oncology4)
age_plot<-ggsurvplot(obs, data = oncology4, combine = TRUE, # Combine curves
        risk.table = FALSE, # Add risk table
        conf.int = FALSE, # Add confidence interval
        conf.int.style = "step", # CI style, use "step" or "ribbon"
        censor = FALSE, # Remove censor points
        #tables.theme = theme_cleantable(), # Clean risk table
        palette = "jco",ylim=c(0,1),xlim=c(0,800),legend.title = "Covariate: Age
Levels:",
        legend.labs = c("14-45", "46-55","56-65","66-75","76-85", "85+"), font.legend = c(14,
"plain", "black"))
dev.off()

summary(oncology4$rural_urban)
tiff("Survival curve (Kaplan Meier) for area of residence (Oncology).tiff", width = 6, height = 6,
pointsize = 1/300, units = 'in', res = 300)
obs<-survfit(Surv(time_to_event2y, death2y)~rural_urban, data=oncology4)
Residence_plot<-ggsurvplot(obs, data = oncology4, combine = TRUE, # Combine curves
        risk.table = FALSE, # Add risk table
        conf.int = FALSE, # Add confidence interval
        conf.int.style = "step", # CI style, use "step" or "ribbon"
        censor = FALSE, # Remove censor points
        #tables.theme = theme_cleantable(), # Clean risk table
        palette = "jco",ylim=c(0,1),xlim=c(0,800),legend.title = "Covariate: Residence
Levels:",
        legend.labs = c("Other", "Rural","Urban"), font.legend = c(14, "plain",
"black"))
dev.off()

summary(oncology4$healthdept)
tiff("Survival curve (Kaplan Meier) for Health service (Oncology).tiff", width = 8, height = 6, pointsize
= 1/300, units = 'in', res = 300)
obs<-survfit(Surv(time_to_event2y, death2y)~healthdept, data=oncology4)
healthdept_Plot<-ggsurvplot(obs, data = oncology4, combine = TRUE, # Combine curves
        risk.table = FALSE, # Add risk table
        conf.int = FALSE, # Add confidence interval
        conf.int.style = "step", # CI style, use "step" or "ribbon"
        censor = FALSE, # Remove censor points
        #tables.theme = theme_cleantable(), # Clean risk table
        palette = "jco",ylim=c(0,1),xlim=c(0,800),legend.title = "Covariate: Health
Service Levels:",
        legend.labs = c("Atacama", "Osorno","Valparaiso-San Antonio"), font.legend =
c(14, "plain", "black"))+ guides(colour = guide_legend(nrow = 2))
dev.off()

require(gridExtra)
require("survminer")
splots <- list()
splots[[1]] <- sex_plot
splots[[2]] <- healthdept_Plot
splots[[3]] <- age_plot
splots[[4]] <- Residence_plot

tiff("Survival curves (Kaplan Meier) for covariates in Oncology specialty Cox proportional model.tiff",
width = 14, height = 14, pointsize = 1/300, units = 'in', res = 300)
arrange_ggsurvplots(splots, print = TRUE,

```

```

ncol = 2, nrow = 2, risk.table.height = 0.4)
dev.off()

oncology_ph$xllevels

#KM CURVES ALL DATA
tiff("Survival curve (Kaplan Meier) for sex group (Oncology).tiff", width = 6, height = 6, pointsize =
1/300, units = 'in', res = 300)
obs<-survfit(Surv(time_to_event2y, death2y)~sex, data=data_all2y)
sex_plot<-ggsurvplot(obs, data = oncology4, combine = TRUE, # Combine curves
risk.table = FALSE, # Add risk table
conf.int = TRUE, # Add confidence interval
conf.int.style = "step", # CI style, use "step" or "ribbon"
censor = FALSE, # Remove censor points
#tables.theme = theme_cleantable(), # Clean risk table
palette = "jco",ylim=c(0.75,1),xlim=c(0,800),legend.title = "Covariate: Sex
Levels:",
legend.labs = c("Female", "Male"), font.legend = c(14, "plain", "black"))
dev.off()

tiff("Survival curve (Kaplan Meier) for age group (Oncology).tiff", width = 6, height = 6, pointsize =
1/300, units = 'in', res = 300)
summary(data_all2y$age_category)
obs<-survfit(Surv(time_to_event2y, death2y)~age_category, data=data_all2y)
age_plot<-ggsurvplot(obs, data = oncology4, combine = TRUE, # Combine curves
risk.table = FALSE, # Add risk table
conf.int = FALSE, # Add confidence interval
conf.int.style = "step", # CI style, use "step" or "ribbon"
censor = FALSE, # Remove censor points
#tables.theme = theme_cleantable(), # Clean risk table
palette = "jco",ylim=c(0.5,1),xlim=c(0,800),legend.title = "Covariate: Age
Levels:",
legend.labs = c("14-45","0-3","4-7","8-11","12-14","46-55","56-65","66-75","76-85",
"85+"), font.legend = c(14, "plain", "black"))
dev.off()

summary(data_all2y$rural_urban)
tiff("Survival curve (Kaplan Meier) for area of residence (Oncology).tiff", width = 6, height = 6,
pointsize = 1/300, units = 'in', res = 300)
obs<-survfit(Surv(time_to_event2y, death2y)~rural_urban, data=data_all2y)
Residence_plot<-ggsurvplot(obs, data = oncology4, combine = TRUE, # Combine curves
risk.table = FALSE, # Add risk table
conf.int = FALSE, # Add confidence interval
conf.int.style = "step", # CI style, use "step" or "ribbon"
censor = FALSE, # Remove censor points
#tables.theme = theme_cleantable(), # Clean risk table
palette = "jco",ylim=c(0.75,1),xlim=c(0,800),legend.title = "Covariate:
Residence Levels:",
legend.labs = c("Rural", "Other","Urban"), font.legend = c(14, "plain",
"black"))
dev.off()

summary(data_all2y$healthdept)
tiff("Survival curve (Kaplan Meier) for Health service (Oncology).tiff", width = 8, height = 6, pointsize
= 1/300, units = 'in', res = 300)
obs<-survfit(Surv(time_to_event2y, death2y)~healthdept, data=data_all2y)
healthdept_Plot<-ggsurvplot(obs, data = oncology4, combine = TRUE, # Combine curves
risk.table = FALSE, # Add risk table
conf.int = FALSE, # Add confidence interval
conf.int.style = "step", # CI style, use "step" or "ribbon"
censor = FALSE, # Remove censor points
#tables.theme = theme_cleantable(), # Clean risk table
palette = "jco",ylim=c(0.75,1),xlim=c(0,800),legend.title = "Covariate: Health
Service Levels:",
legend.labs = c("Atacama", "Osorno","Valparaiso-San Antonio"), font.legend =
c(14, "plain", "black"))+ guides(colour = guide_legend(nrow = 2))
dev.off()

require(gridExtra)

```

```

require("survminer")
splots <- list()
splots[[1]] <- sex_plot
splots[[2]] <- healthdept_Plot
splots[[3]] <- age_plot
splots[[4]] <- Residence_plot

tiff("Survival curves (Kaplan Meier) for covariates Cox proportional model.tiff", width = 14, height = 14,
pointsize = 1/300, units = 'in', res = 300)
arrange_ggsurvplots(splots, print = TRUE,
                    ncol = 2, nrow = 2, risk.table.height = 0.4)
dev.off()

fit<-survfit(all_RandomEffects2,data=data_all2y)
obs<-survfit(Surv(time_to_event2y, death2y)~1, data=data_all2y)
KmPh <- list(Model = fit, KM = obs)
ggsurvplot(KmPh, data = data_all2y, combine = TRUE, # Combine curves
            risk.table = TRUE, # Add risk table
            conf.int = TRUE, # Add confidence interval
            conf.int.style = "step", # CI style, use "step" or "ribbon"
            censor = FALSE, # Remove censor points
            tables.theme = theme_cleantable(), # Clean risk table
            palette = "jco",ylim=c(0.9,1))
resd<-resid(all_RandomEffects2,"mart")
plot(resd)
hist(resd)
#residual plots
dev.off()
plot(resd~as.factor(data_all2y$age_category))
plot(resd~as.factor(data_all2y$sex))
plot(resd~as.factor(data_all2y$rural_urban))
plot(resd~as.factor(data_all2y$specialty4))
plot(resd~as.factor(data_all2y$insurance))
plot(resd~as.factor(data_all2y$referring_type))
plot(resd~as.factor(data_all2y$healthdept))
plot(resd~as.factor(data_all2y$accepting_type))
#interaction plots
par(mfrow=c(2,3))
interaction.plot(as.factor(data_all2y$age_category), as.factor(data_all2y$sex), resd)
interaction.plot(as.factor(data_all2y$age_category), as.factor(data_all2y$rural_urban), resd)
interaction.plot(as.factor(data_all2y$age_category), as.factor(data_all2y$specialty4), resd)
interaction.plot(as.factor(data_all2y$age_category), as.factor(data_all2y$insurance), resd)
interaction.plot(as.factor(data_all2y$age_category), as.factor(data_all2y$referring_type), resd)
interaction.plot(as.factor(data_all2y$age_category), as.factor(data_all2y$healthdept), resd)
#Update model with the interaction
all_fixedEffect_Interactions<-coxph(Surv(time_to_event2y, death2y)~
                                     age_category+
                                     sex+
                                     rural_urban+
                                     specialty4+
                                     insurance+
                                     referring_type+
                                     healthdept+
                                     accepting_type+
                                     age_category:sex,
                                     #age_category:healthdept,
                                     data=data_all2y)

#Checking model results
summary(all_RandomEffects2)
fit_interactions<-survfit(all_fixedEffect_Interactions,data=data_all2y)
obs<-survfit(Surv(time_to_event2y, death2y)~1, data=data_all2y)
KmPh <- list(Model = fit, KM = obs, Interactions=fit_interactions)
ggsurvplot(KmPh, data = data_all2y, combine = TRUE, # Combine curves
            risk.table = TRUE, # Add risk table
            conf.int = TRUE, # Add confidence interval
            conf.int.style = "step", # CI style, use "step" or "ribbon"
            censor = FALSE, # Remove censor points
            tables.theme = theme_cleantable(), # Clean risk table
            palette = "jco",ylim=c(0.9,1))

```

```
summary(as.factor(data_all2y$death2y))
sum(data_all2y$death2y)/length(data_all2y$death2y)*100
#####
```

#4. STATISTICAL ANALYSIS: MEDICAL CENTER-LEVEL CORRELATION ANALYSIS####  
 ##CORRELATION ALL MEDICAL CENTERS####

```
all_RandomEffects2_Center<-coxph(Surv(time_to_event2y, death2y)~
  age_category+
  sex+
  rural_urban+
  specialty4+
  insurance+
  referring_type+
  accepting,
  data=data_all2y)
```

```
#median waiting
waiting<-c(0,
  120,
  139.5,
  77,
  145,
  100,
  36,
  86,
  104,
  8,
  0,
  92.5,
  92,
  98.5,
  101,
  97,
  48,
  56,
  1,
  7,
  139,
  43,
  104,
  174.5,
  143,
  59,
  91,
  89,
  0,
  0,
  0,
  51,
  60,
```

```

70,
71,
71,
71,
71,
71,
122,
36)
RR<-c(0.00003084,
0.00003134,
0.0000317,
0.00003211,
0.00003498,
0.00003525,
0.00003541,
0.00003552,
0.00003642,
0.00004914,
0.00005047,
0.00005419,
0.00005788,
0.0000635,
0.00006628,
0.1808,
0.2187,
0.271,
0.3797,
0.425,
0.4325,
0.4612,
0.4637,
0.5638,
0.6166,
0.6514,
0.6578,
0.7457,
0.7579,
0.7788,
0.8503,
0.9584,
0.9629,
1.047,
1.426,
1.656,
1.656,
1.656,
1.656,
1.962,
2.008)
cor.test(waiting, RR, method = "kendall", alternative = "two.sided")
#average waiting
waiting<-c(125.186667,
150.470588,
195.630435,
131.619835,
254.258065,
152.516129,
50.492918,
158.858025,
194.753894,
24.819905,
91.61194,
112.005155,
97.548387,
113.948276,
96.165062,
91.72833,
85.210247,
81.541219,

```

```

95.55538,
14.457803,
189.232812,
89.450768,
125.263687,
227.617849,
215.618705,
70.026905,
117.051944,
150.290498,
1.178868,
140.631579,
172.370968,
122.705908,
87.800578,
125.612245,
174.643837,
174.643837,
174.643837,
174.643837,
174.643837,
148.955882,
167.762992)
cor.test(waiting, RR, method = "kendall", alternative = "two.sided")
#SD of waiting
waiting<-c(187.7244,
150.3531,
202.88161,
141.50396,
225.29077,
126.67935,
45.49408,
179.6641,
270.54994,
42.72976,
193.46811,
123.0942,
36.42603,
33.71054,
55.27824,
43.06713,
103.88298,
81.7793,
202.4768,
19.10705,
169.99146,
121.14803,
100.82476,
205.20558,
243.34717,
79.85872,
104.0488,
171.04455,
22.96973,
226.86953,
252.37172,
170.69587,
140.98386,
170.56448,
258.49471,
258.49471,
258.49471,
258.49471,
258.49471,
104.54485,
330.03614)
cor.test(waiting, RR, method = "kendall", alternative = "two.sided")
##CORRELATION STRATIFIED BY LEVEL OF CARE####

```

```

##TERTIARY AND SECONDARY CARE####
#median
waiting<-c(36,
           71,
           71,
           71,
           71,
           89,
           51)
RR<-c(2.008,
      1.426,
      1.656,
      1.656,
      1.656,
      0.7457,
      0.9584)
cor.test(waiting, RR, method = "kendall", alternative = "two.sided", exact=FALSE)
#average waiting
waiting<-c(167.762992,
          174.643837,
          174.643837,
          174.643837,
          174.643837,
          150.290498,
          122.705908)
cor.test(waiting, RR, method = "kendall", alternative = "two.sided", exact=FALSE)
#SD of waiting
waiting<-c(330.03614,
          258.49471,
          258.49471,
          258.49471,
          258.49471,
          171.04455,
          170.69587)
cor.test(waiting, RR, method = "kendall", alternative = "two.sided", exact=FALSE)
##PRIMARY CARE####
#median waiting
waiting<-c(104,
          71,
          0,
          143,
          0,
          145,
          174.5,
          139.5,
          1,
          0,
          0,
          86,
          70,
          139,
          120,
          77,
          60,
          100,
          92.5,
          43,
          122,
          91,
          48,
          104,
          56,
          59,
          101,
          36,
          97,
          8,
          92,
          98.5,

```

```

0,
7)
RR<-c(0.00003642,
1.656,
0.8503,
0.6166,
0.7788,
0.00003498,
0.5638,
0.0000317,
0.3797,
0.00005047,
0.00003084,
0.00003552,
1.047,
0.4325,
0.00003134,
0.00003211,
0.9629,
0.00003525,
0.00005419,
0.4612,
1.962,
0.6578,
0.2187,
0.4637,
0.271,
0.6514,
0.00006628,
0.00003541,
0.1808,
0.00004914,
0.00005788,
0.00006635,
0.7579,
0.425)
cor.test(waiting, RR, method = "kendall", alternative = "two.sided", exact=FALSE)
#average waiting
waiting<-c(194.753894,
174.643837,
172.370968,
215.618705,
140.631579,
254.258065,
227.617849,
195.630435,
95.55538,
91.61194,
125.186667,
158.858025,
125.612245,
189.232812,
150.470588,
131.619835,
87.800578,
152.516129,
112.005155,
89.450768,
148.955882,
117.051944,
85.210247,
125.263687,
81.541219,
70.026905,
96.165062,
50.492918,
91.72833,
24.819905,
97.548387,

```

```

113.948276,
1.178868,
14.457803)
cor.test(waiting, RR, method = "kendall", alternative = "two.sided", exact=FALSE)
#SD of waiting
waiting<-c(270.54994,
258.49471,
252.37172,
243.34717,
226.86953,
225.29077,
205.20558,
202.88161,
202.4768,
193.46811,
187.7244,
179.6641,
170.56448,
169.99146,
150.3531,
141.50396,
140.98386,
126.67935,
123.0942,
121.14803,
104.54485,
104.0488,
103.88298,
100.82476,
81.7793,
79.85872,
55.27824,
45.49408,
43.06713,
42.72976,
36.42603,
33.71054,
22.96973,
19.10705)
cor.test(waiting, RR, method = "kendall", alternative = "two.sided", exact=FALSE)
##CORRELATION FOR RISKY MEDICAL CENTERS:WAITING AND HAZARD RATIO >50th PERCENTILE####
myfun1 <- function(x){c(m=mean(x), s=sd(x), N=length(x))}
Mortality<-as.data.frame(summaryBy(death2y ~ specialty4,data=data_all2y, FUN=myfun1))
Waiting<-as.data.frame(summaryBy(waitingtime_numeric ~ specialty4,data=data_all2y, FUN=myfun1))
MortalityAndWaiting<-merge(Mortality,Waiting,by="specialty4")
Mortality<-NULL
Waiting<-NULL
HighMortality_HighWaitingVariability<-
as.data.frame(MortalityAndWaiting[which(MortalityAndWaiting$death2y.m>summary(MortalityAndWaiting$death2y.
m)[3] &
MortalityAndWaiting$waitingtime_numeric.s>summary(MortalityAndWaiting$waitingtime_numeric.s)[3]),])
#Overall - mixed-effects Cox model (these are the ones used in main manuscript Fig 3 [sensitivity analysis
including high mortality and high waiting time variability])
all_RandomEffects2_Center_RiskyAndVariable<-coxph(Surv(time_to_event2y, death2y)~
age_category+
sex+
rural_urban+
specialty4+
insurance+
referring_type+
accepting,
data=data_all2y[which(data_all2y$specialty4 %in%
HighMortality_HighWaitingVariability$specialty4),])
summary(all_RandomEffects2_Center_RiskyAndVariable)
#median waiting
waiting<-c(36,
104,
71,
71,

```

```

71,
71,
0,
143,
0,
1,
0,
0,
86,
89,
51,
70,
60,
59,
97)
RR<-c(1.945,
0.000007315,
1.71,
1.71,
1.71,
1.71,
0.00001038,
1.157,
0.000004933,
0.3098,
0.000004252,
0.000007654,
0.00001181,
0.6848,
0.7975,
0.00001039,
0.000004422,
0.000006312,
0.00002732)
cor.test(waiting, RR, method = "kendall", alternative = "two.sided", exact=FALSE)
#average waiting
waiting<-c(167.762992,
194.753894,
174.643837,
174.643837,
174.643837,
174.643837,
172.370968,
215.618705,
140.631579,
95.55538,
91.61194,
125.186667,
158.858025,
150.290498,
122.705908,
125.612245,
87.800578,
70.026905,
91.72833)
cor.test(waiting, RR, method = "kendall", alternative = "two.sided", exact=FALSE)
#SD of waiting
waiting<-c(330.03614,
270.54994,
258.49471,
258.49471,
258.49471,
258.49471,
252.37172,
243.34717,
226.86953,
202.4768,
193.46811,
187.7244,

```

179.6641,  
171.04455,  
170.69587,  
170.56448,  
140.98386,  
79.85872,  
43.06713)

cor.test(waiting, RR, method = "kendall", alternative = "two.sided", exact=FALSE)

##COMPARING WAIT TIMES BY SPECIALTY AND MORTALITY STATUS

```
wilcox.test(data_all2y[which(data_all2y$specialty4=="Internal  
Medicine")],]$waitingtime_numeric~data_all2y[which(data_all2y$specialty4=="Internal Medicine")],]$death2y)  
wilcox.test(data_all2y[which(data_all2y$specialty4=="Adult  
Surgery")],]$waitingtime_numeric~data_all2y[which(data_all2y$specialty4=="Adult Surgery")],]$death2y)  
wilcox.test(data_all2y[which(data_all2y$specialty4=="Anesthesiology")],]$waitingtime_numeric~data_all2y[whi  
ch(data_all2y$specialty4=="Anesthesiology")],]$death2y)  
wilcox.test(data_all2y[which(data_all2y$specialty4=="Breast  
Surgery")],]$waitingtime_numeric~data_all2y[which(data_all2y$specialty4=="Breast Surgery")],]$death2y)  
wilcox.test(data_all2y[which(data_all2y$specialty4=="Broncopulmonary")],]$waitingtime_numeric~data_all2y[wh  
ich(data_all2y$specialty4=="Broncopulmonary")],]$death2y)  
wilcox.test(data_all2y[which(data_all2y$specialty4=="Cardiology")],]$waitingtime_numeric~data_all2y[which(d  
ata_all2y$specialty4=="Cardiology")],]$death2y)  
wilcox.test(data_all2y[which(data_all2y$specialty4=="Cardiovascular  
Surgery")],]$waitingtime_numeric~data_all2y[which(data_all2y$specialty4=="Cardiovascular  
Surgery")],]$death2y)  
wilcox.test(data_all2y[which(data_all2y$specialty4=="Dentistry")],]$waitingtime_numeric~data_all2y[which(da  
ta_all2y$specialty4=="Dentistry")],]$death2y)  
wilcox.test(data_all2y[which(data_all2y$specialty4=="Dermatology")],]$waitingtime_numeric~data_all2y[whic  
h(data_all2y$specialty4=="Dermatology")],]$death2y)  
wilcox.test(data_all2y[which(data_all2y$specialty4=="Endocrinology")],]$waitingtime_numeric~data_all2y[whic  
h(data_all2y$specialty4=="Endocrinology")],]$death2y)  
wilcox.test(data_all2y[which(data_all2y$specialty4=="Family  
Medicine")],]$waitingtime_numeric~data_all2y[which(data_all2y$specialty4=="Family Medicine")],]$death2y)  
wilcox.test(data_all2y[which(data_all2y$specialty4=="Gastroenterology")],]$waitingtime_numeric~data_all2y[w  
hich(data_all2y$specialty4=="Gastroenterology")],]$death2y)  
wilcox.test(data_all2y[which(data_all2y$specialty4=="Genetics")],]$waitingtime_numeric~data_all2y[which(dat  
a_all2y$specialty4=="Genetics")],]$death2y)  
wilcox.test(data_all2y[which(data_all2y$specialty4=="Hematology")],]$waitingtime_numeric~data_all2y[which(d  
ata_all2y$specialty4=="Hematology")],]$death2y)  
wilcox.test(data_all2y[which(data_all2y$specialty4=="Infectious  
Disease")],]$waitingtime_numeric~data_all2y[which(data_all2y$specialty4=="Infectious Disease")],]$death2y)  
wilcox.test(data_all2y[which(data_all2y$specialty4=="Maxillofacial  
Surgery")],]$waitingtime_numeric~data_all2y[which(data_all2y$specialty4=="Maxillofacial  
Surgery")],]$death2y)  
wilcox.test(data_all2y[which(data_all2y$specialty4=="Neonatology")],]$waitingtime_numeric~data_all2y[which(  
data_all2y$specialty4=="Neonatology")],]$death2y)  
wilcox.test(data_all2y[which(data_all2y$specialty4=="Nephrology")],]$waitingtime_numeric~data_all2y[which(d  
ata_all2y$specialty4=="Nephrology")],]$death2y)  
wilcox.test(data_all2y[which(data_all2y$specialty4=="Neurology")],]$waitingtime_numeric~data_all2y[which(da  
ta_all2y$specialty4=="Neurology")],]$death2y)  
wilcox.test(data_all2y[which(data_all2y$specialty4=="Neurosurgery")],]$waitingtime_numeric~data_all2y[which  
(data_all2y$specialty4=="Neurosurgery")],]$death2y)  
wilcox.test(data_all2y[which(data_all2y$specialty4=="Nutrition")],]$waitingtime_numeric~data_all2y[which(da  
ta_all2y$specialty4=="Nutrition")],]$death2y)  
wilcox.test(data_all2y[which(data_all2y$specialty4=="Obstetrics and  
Gynecology")],]$waitingtime_numeric~data_all2y[which(data_all2y$specialty4=="Obstetrics and  
Gynecology")],]$death2y)  
wilcox.test(data_all2y[which(data_all2y$specialty4=="Oncology")],]$waitingtime_numeric~data_all2y[which(dat  
a_all2y$specialty4=="Oncology")],]$death2y)  
wilcox.test(data_all2y[which(data_all2y$specialty4=="Ophtalmology")],]$waitingtime_numeric~data_all2y[which  
(data_all2y$specialty4=="Ophtalmology")],]$death2y)  
wilcox.test(data_all2y[which(data_all2y$specialty4=="Other")],]$waitingtime_numeric~data_all2y[which(data_a  
ll2y$specialty4=="Other")],]$death2y)  
wilcox.test(data_all2y[which(data_all2y$specialty4=="Otorhinolaryngology")],]$waitingtime_numeric~data_all2  
y[which(data_all2y$specialty4=="Otorhinolaryngology")],]$death2y)  
wilcox.test(data_all2y[which(data_all2y$specialty4=="Pediatrics")],]$waitingtime_numeric~data_all2y[which(d  
ata_all2y$specialty4=="Pediatrics")],]$death2y)
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wilcox.test(data_all2y[which(data_all2y$specialty4=="Physical Medicine and
Rehabilitation"),]$waitingtime_numeric~data_all2y[which(data_all2y$specialty4=="Physical Medicine and
Rehabilitation"),]$death2y)
wilcox.test(data_all2y[which(data_all2y$specialty4=="Plastic
Surgery"),]$waitingtime_numeric~data_all2y[which(data_all2y$specialty4=="Plastic Surgery"),]$death2y)
wilcox.test(data_all2y[which(data_all2y$specialty4=="Proctological
Surgery"),]$waitingtime_numeric~data_all2y[which(data_all2y$specialty4=="Proctological
Surgery"),]$death2y)
wilcox.test(data_all2y[which(data_all2y$specialty4=="Psychiatry"),]$waitingtime_numeric~data_all2y[which(d
ata_all2y$specialty4=="Psychiatry"),]$death2y)
wilcox.test(data_all2y[which(data_all2y$specialty4=="Rheumatology"),]$waitingtime_numeric~data_all2y[which
(data_all2y$specialty4=="Rheumatology"),]$death2y)
wilcox.test(data_all2y[which(data_all2y$specialty4=="Sexual Transmitted
Disease"),]$waitingtime_numeric~data_all2y[which(data_all2y$specialty4=="Sexual Transmitted
Disease"),]$death2y)
wilcox.test(data_all2y[which(data_all2y$specialty4=="Traumatology"),]$waitingtime_numeric~data_all2y[which
(data_all2y$specialty4=="Traumatology"),]$death2y)
wilcox.test(data_all2y[which(data_all2y$specialty4=="Urology"),]$waitingtime_numeric~data_all2y[which(data
_all2y$specialty4=="Urology"),]$death2y)
```