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# factoring and scaling the cov for analysis  
PatientData <- read\_excel("C:/MyData-Late Fall/510-prin 2/Assignment/PatientData.xlsx") #  
PatientData$severe <- factor(PatientData$severe)   
PatientData$cognitivedecline <- factor(PatientData$cognitivedecline)  
PatientData$depression <- factor(PatientData$depression)  
PatientData$cancer <- factor(PatientData$cancer)  
PatientData$autoimmune <- factor(PatientData$autoimmune)  
PatientData$transferedin <- factor(PatientData$transferedin)  
PatientData$sex <- factor(PatientData$sex)  
PatientData$yearseducation <- factor(PatientData$yearseducation)  
PatientData$nolifesupportorder <- factor(PatientData$nolifesupportorder)  
PatientData$insurancetype <- factor(PatientData$insurancetype)  
PatientData$resp <- factor(PatientData$resp)  
PatientData$infection <- factor(PatientData$infection)  
PatientData$trauma <- factor(PatientData$trauma)  
PatientData$race <- factor(PatientData$race)  
PatientData$age <- scale(PatientData$age)  
PatientData$bloodpressure <- scale(PatientData$bloodpressure)  
PatientData$temperature <- scale(PatientData$temperature)  
PatientData$creatinelevels <- scale(PatientData$creatinelevels)  
PatientData$sodiumlevels <- scale(PatientData$sodiumlevels)  
PatientData$urineweight <- scale(PatientData$urineweight)  
PatientData$kg <- scale(PatientData$kg)  
PatientData$income <- scale(PatientData$income)  
PatientData$surgerytype <- PatientData$surgerytype  
  
#build the full model (all potential IVs to see if they predict assignment):  
psmodel <- glm(surgerytype ~ age + bloodpressure + temperature + creatinelevels + sodiumlevels + urineweight + kg + income + severe + cognitivedecline + depression + cancer + autoimmune + transferedin + sex + yearseducation + nolifesupportorder + insurancetype + resp + infection + trauma + race , data = PatientData, family = 'binomial')  
  
summary(psmodel)

##   
## Call:  
## glm(formula = surgerytype ~ age + bloodpressure + temperature +   
## creatinelevels + sodiumlevels + urineweight + kg + income +   
## severe + cognitivedecline + depression + cancer + autoimmune +   
## transferedin + sex + yearseducation + nolifesupportorder +   
## insurancetype + resp + infection + trauma + race, family = "binomial",   
## data = PatientData)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -2.1919 -0.9445 -0.6410 1.1233 2.4776   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -0.83801 0.42185 -1.987 0.046974 \*   
## age 0.01459 0.04074 0.358 0.720205   
## bloodpressure -0.44860 0.03232 -13.879 < 2e-16 \*\*\*  
## temperature 0.00276 0.03017 0.091 0.927102   
## creatinelevels 0.17409 0.03062 5.685 1.31e-08 \*\*\*  
## sodiumlevels -0.06953 0.02948 -2.359 0.018347 \*   
## urineweight -0.07486 0.03038 -2.464 0.013732 \*   
## kg 0.20911 0.03150 6.638 3.17e-11 \*\*\*  
## income 0.01644 0.03389 0.485 0.627603   
## severe1 0.19423 0.07842 2.477 0.013251 \*   
## cognitivedecline1 -0.40728 0.10969 -3.713 0.000205 \*\*\*  
## depression1 -0.48549 0.12814 -3.789 0.000151 \*\*\*  
## cancer1 -0.28414 0.07269 -3.909 9.26e-05 \*\*\*  
## autoimmune1 0.07125 0.06718 1.061 0.288858   
## transferedin1 0.42524 0.08980 4.735 2.19e-06 \*\*\*  
## sexMale 0.02981 0.06123 0.487 0.626347   
## yearseducation1 -0.94417 1.25217 -0.754 0.450834   
## yearseducation2 0.11920 0.77102 0.155 0.877135   
## yearseducation3 0.36165 0.51495 0.702 0.482495   
## yearseducation4 0.15957 0.55815 0.286 0.774964   
## yearseducation5 -0.22551 0.52665 -0.428 0.668518   
## yearseducation6 0.08933 0.46093 0.194 0.846337   
## yearseducation7 0.25431 0.45172 0.563 0.573442   
## yearseducation8 -0.15042 0.41653 -0.361 0.718011   
## yearseducation9 0.34514 0.42902 0.804 0.421121   
## yearseducation10 0.29623 0.41352 0.716 0.473768   
## yearseducation11 0.07519 0.41169 0.183 0.855081   
## yearseducation12 0.14324 0.40799 0.351 0.725522   
## yearseducation13 0.18799 0.42706 0.440 0.659806   
## yearseducation14 0.42810 0.41487 1.032 0.302115   
## yearseducation15 0.34276 0.44590 0.769 0.442069   
## yearseducation16 0.35484 0.42117 0.843 0.399508   
## yearseducation17 0.25061 0.47776 0.525 0.599885   
## yearseducation18 -0.06601 0.45927 -0.144 0.885713   
## yearseducation19 0.03169 0.57052 0.056 0.955705   
## yearseducation20 0.37160 0.51417 0.723 0.469852   
## yearseducation21 -0.21417 0.77006 -0.278 0.780918   
## yearseducation22 1.06324 0.95249 1.116 0.264301   
## yearseducation23 0.92578 1.47486 0.628 0.530197   
## yearseducation24 -0.09427 0.97188 -0.097 0.922729   
## yearseducation25 12.10970 324.74401 0.037 0.970254   
## yearseducation26 -11.24634 324.74396 -0.035 0.972374   
## yearseducation27 12.63451 324.74401 0.039 0.968965   
## yearseducation30 -10.77699 324.74397 -0.033 0.973526   
## nolifesupportorderYes -0.67948 0.10518 -6.460 1.04e-10 \*\*\*  
## insurancetypeMedicare 0.22098 0.12296 1.797 0.072310 .   
## insurancetypeMedicare & Medicaid 0.25466 0.15472 1.646 0.099787 .   
## insurancetypeNo insurance 0.44688 0.15260 2.928 0.003406 \*\*   
## insurancetypePrivate 0.41256 0.11121 3.710 0.000207 \*\*\*  
## insurancetypePrivate & Medicare 0.41124 0.12614 3.260 0.001114 \*\*   
## respYes -0.45482 0.06301 -7.218 5.27e-13 \*\*\*  
## infectionYes 0.34602 0.07698 4.495 6.97e-06 \*\*\*  
## traumaYes 1.17182 0.31070 3.772 0.000162 \*\*\*  
## raceother 0.01381 0.13986 0.099 0.921335   
## racewhite -0.03117 0.08673 -0.359 0.719304   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 7621.4 on 5734 degrees of freedom  
## Residual deviance: 6862.7 on 5680 degrees of freedom  
## AIC: 6972.7  
##   
## Number of Fisher Scoring iterations: 11

#Reduced model based on the covariates which are significant  
psmodelfinal <- glm(surgerytype ~ bloodpressure + creatinelevels + sodiumlevels + urineweight + kg + severe +   
 cognitivedecline + depression + cancer + transferedin + nolifesupportorder + insurancetype + resp   
 + infection + trauma, data = PatientData, family = "binomial")  
  
summary(psmodelfinal)

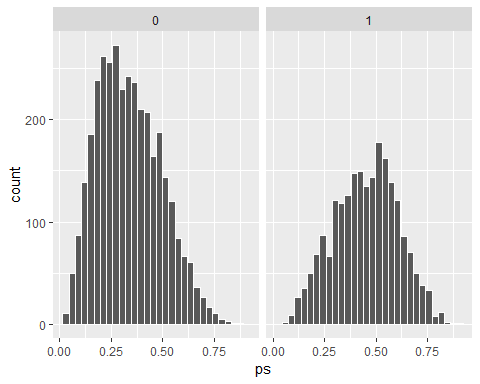
##   
## Call:  
## glm(formula = surgerytype ~ bloodpressure + creatinelevels +   
## sodiumlevels + urineweight + kg + severe + cognitivedecline +   
## depression + cancer + transferedin + nolifesupportorder +   
## insurancetype + resp + infection + trauma, family = "binomial",   
## data = PatientData)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -2.1364 -0.9457 -0.6473 1.1321 2.4668   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -0.67763 0.09754 -6.947 3.73e-12 \*\*\*  
## bloodpressure -0.45077 0.03203 -14.071 < 2e-16 \*\*\*  
## creatinelevels 0.17589 0.02987 5.888 3.92e-09 \*\*\*  
## sodiumlevels -0.06890 0.02916 -2.363 0.018115 \*   
## urineweight -0.06932 0.02992 -2.317 0.020504 \*   
## kg 0.20661 0.03063 6.746 1.52e-11 \*\*\*  
## severe1 0.19948 0.07673 2.600 0.009327 \*\*   
## cognitivedecline1 -0.40950 0.10812 -3.788 0.000152 \*\*\*  
## depression1 -0.50278 0.12675 -3.967 7.29e-05 \*\*\*  
## cancer1 -0.27534 0.07206 -3.821 0.000133 \*\*\*  
## transferedin1 0.42271 0.08909 4.745 2.09e-06 \*\*\*  
## nolifesupportorderYes -0.68479 0.10373 -6.602 4.06e-11 \*\*\*  
## insurancetypeMedicare 0.23505 0.10909 2.155 0.031198 \*   
## insurancetypeMedicare & Medicaid 0.25610 0.14900 1.719 0.085649 .   
## insurancetypeNo insurance 0.46278 0.15146 3.055 0.002247 \*\*   
## insurancetypePrivate 0.47459 0.10552 4.498 6.87e-06 \*\*\*  
## insurancetypePrivate & Medicare 0.44259 0.11149 3.970 7.19e-05 \*\*\*  
## respYes -0.44858 0.06233 -7.196 6.19e-13 \*\*\*  
## infectionYes 0.36002 0.07598 4.738 2.15e-06 \*\*\*  
## traumaYes 1.16260 0.30981 3.753 0.000175 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 7621.4 on 5734 degrees of freedom  
## Residual deviance: 6900.9 on 5715 degrees of freedom  
## AIC: 6940.9  
##   
## Number of Fisher Scoring iterations: 4

vif(psmodelfinal)

## GVIF Df GVIF^(1/(2\*Df))  
## bloodpressure 1.062348 1 1.030703  
## creatinelevels 1.064190 1 1.031596  
## sodiumlevels 1.013823 1 1.006888  
## urineweight 1.065545 1 1.032252  
## kg 1.024902 1 1.012374  
## severe 1.075410 1 1.037020  
## cognitivedecline 1.052195 1 1.025765  
## depression 1.014781 1 1.007363  
## cancer 1.063992 1 1.031500  
## transferedin 1.021458 1 1.010672  
## nolifesupportorder 1.044883 1 1.022195  
## insurancetype 1.128336 5 1.012148  
## resp 1.037704 1 1.018678  
## infection 1.076618 1 1.037602  
## trauma 1.018416 1 1.009166

#no mulitcollinearity is found.  
  
#Lets make our data frame excluding any NA and missing data.  
dataready <- na.omit(PatientData)  
psf <- formula('surgerytype ~ bloodpressure + creatinelevels + sodiumlevels + urineweight + kg + severe +   
 cognitivedecline + depression + cancer + transferedin + nolifesupportorder + insurancetype + resp   
 + infection + trauma')  
  
#Let's get our PS generated by Logit:  
logit <- glm(psf, family = "binomial", data = dataready)  
dataready$ps <- fitted(logit)  
  
#Plotting the data we get the overlap which looks good . It does look like we have quite a bit of common support:  
dataready %>%  
ggplot(aes(x = ps)) +  
geom\_histogram(color = "white") +  
facet\_wrap(~surgerytype)

## `stat\_bin()` using `bins = 30`. Pick better value with `binwidth`.

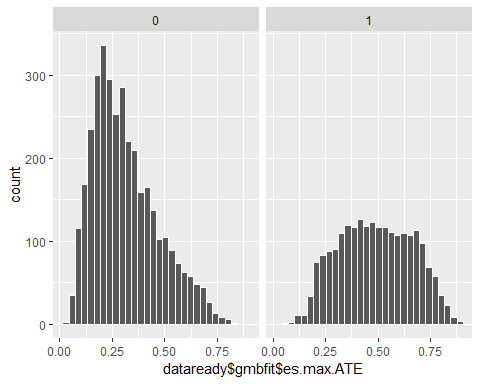


#Lets try at least one other method (recursive partitioning with 5000 trees):  
#controls <- cforest\_unbiased(ntree = 1000, mtry = 2)  
#forest <- cforest(psf, data = as.data.frame(dataready), controls = controls)  
#forestfit <- predict(forest, type="prob")  
#dataready$fps <- matrix(unlist(forestfit),,2,byrow=T)[,2]  
  
##error in cforest data so trying gbm - Generalized Boosting Model  
  
gbm <- ps(psf, data = as.data.frame(dataready), n.trees = 3000, stop.method=c("es.max"), verbose = TRUE)

## Fitting gbm model  
## Iter TrainDeviance ValidDeviance StepSize Improve  
## 1 1.3274 nan 0.0100 nan  
## 2 1.3259 nan 0.0100 nan  
## 3 1.3244 nan 0.0100 nan  
## 4 1.3230 nan 0.0100 nan  
## 5 1.3216 nan 0.0100 nan  
## 220 1.2096 nan 0.0100 nan  
## 240 1.2052 nan 0.0100 nan  
## 260 1.2013 nan 0.0100 nan  
## 280 1.1978 nan 0.0100 nan  
## 300 1.1945 nan 0.0100 nan  
## 320 1.1915 nan 0.0100 nan  
## 2980 1.0775 nan 0.0100 nan  
## 3000 1.0770 nan 0.0100 nan  
##   
## Diagnosis of unweighted analysis  
## Optimizing with es.max.ATE stopping rule  
## Optimized at 1979   
## Diagnosis of es.max.ATE weights

dataready$gmbfit <- gbm$ps  
  
dataready %>%  
ggplot(aes(x = dataready$gmbfit$es.max.ATE)) +  
geom\_histogram(color = "white") +  
facet\_wrap(~surgerytype)

## `stat\_bin()` using `bins = 30`. Pick better value with `binwidth`.



#due to error cforest is aborted , so tried gbm where overlap looks worse than logit so we will use logit score so Lets stick with the first model using standard regression estimation of PS (dataready$ps).   
  
dataready$logps <- log(dataready$ps/(1- dataready$ps))  
  
#\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**Stratified**\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_  
  
#Will go with the method provided in the matchit ,lets go with 5 stratum.  
stratified <- matchit(psf, data = dataready, distance = dataready$logps, method = "subclass", sub.by = "treat", subclass = 5)  
stratified

##   
## Call:   
## matchit(formula = psf, data = dataready, method = "subclass",   
## distance = dataready$logps, sub.by = "treat", subclass = 5)  
##   
## Sample sizes by subclasses:  
##   
## Control Treated  
## All 3551 2184  
## Subclass 1 1686 437  
## Subclass 2 759 437  
## Subclass 3 561 436  
## Subclass 4 305 437  
## Subclass 5 240 437

stratumworking <- match.data(stratified)  
  
  
#Lets look at the standard mean difference to see how well we balanced this data:  
check <- summary(stratified, standardize = TRUE)  
stdmeandifferences <- data.frame(check$q.table[,3,])  
summary(stdmeandifferences)

## Subclass.1 Subclass.2 Subclass.3   
## Min. :-0.215250 Min. :-0.101959 Min. :-0.093547   
## 1st Qu.:-0.088896 1st Qu.:-0.017951 1st Qu.:-0.054316   
## Median : 0.032330 Median : 0.012330 Median : 0.001901   
## Mean :-0.005531 Mean : 0.004332 Mean : 0.002322   
## 3rd Qu.: 0.068127 3rd Qu.: 0.028398 3rd Qu.: 0.044327   
## Max. : 0.236529 Max. : 0.091663 Max. : 0.144868   
## Subclass.4 Subclass.5   
## Min. :-0.095793 Min. :-0.244291   
## 1st Qu.:-0.028724 1st Qu.:-0.041217   
## Median :-0.004763 Median : 0.008241   
## Mean :-0.003869 Mean :-0.005827   
## 3rd Qu.: 0.026228 3rd Qu.: 0.038908   
## Max. : 0.068381 Max. : 0.163197

#We are above our .1 strict cut off for some but all below our .25 cutoff. So balance does look good.  
  
design <- svydesign(id = ~0, data = stratumworking)

## Warning in svydesign.default(id = ~0, data = stratumworking): No weights or  
## probabilities supplied, assuming equal probability

ntreat <- data.frame(table(stratumworking$subclass[stratumworking$surgerytype == 1]))  
names(ntreat) <- c("subclass", "N.1s")  
ncontrol <- data.frame(table(stratumworking$subclass[stratumworking$surgerytype == 0]))  
names(ncontrol) <- c("subclass", "N.0s")  
scounts <- merge(ntreat, ncontrol)  
stratumworking <- merge(stratumworking, scounts)  
propt <- svymean(~factor(surgerytype), design)  
  
stratumworking$weights <- with(stratumworking, ifelse(surgerytype == 1, 1, stratumworking$N.1s\*propt[1]/ stratumworking$N.0s\*propt[2]))  
xtabs(~weights +subclass, stratumworking)

## subclass  
## weights 1 2 3 4 5  
## 0.0611167608076526 1686 0 0 0 0  
## 0.135761342189331 0 759 0 0 0  
## 0.183256796267952 0 0 561 0 0  
## 0.337845438431811 0 0 0 305 0  
## 0.429345244673759 0 0 0 0 240  
## 1 437 437 436 437 437

stratumworking$ATTwFinal <- stratumworking$weights /mean(stratumworking$weights)  
  
  
bal.stat(stratumworking, estimand = "ATT", w.all = stratumworking$ATTwFinal, vars = cbind('bloodpressure' , 'creatinelevels' , 'sodiumlevels' , 'urineweight' , 'kg', 'severe' , 'cognitivedecline' , 'depression' , 'cancer' , 'transferedin' , 'nolifesupportorder' , 'insurancetype' , 'resp' , 'infection' , 'trauma'), sampw = 1, get.ks = FALSE, treat.var = "surgerytype", multinom = FALSE)$results

## tx.mn tx.sd ct.mn  
## bloodpressure -0.27130558 0.9000075 -0.22689280  
## creatinelevels 0.16581144 0.9999377 0.16291518  
## sodiumlevels -0.05696642 0.9928137 -0.04632826  
## urineweight -0.07461033 1.0365402 -0.06252928  
## kg 0.15598968 0.9543641 0.12279285  
## severe:0 0.79578755 0.4031250 0.79797695  
## severe:1 0.20421245 0.4031250 0.20202305  
## cognitivedecline:0 0.93086081 0.2536907 0.92690708  
## cognitivedecline:1 0.06913919 0.2536907 0.07309292  
## depression:0 0.95421245 0.2090240 0.95260973  
## depression:1 0.04578755 0.2090240 0.04739027  
## cancer:0 0.79670330 0.4024514 0.79069983  
## cancer:1 0.20329670 0.4024514 0.20930017  
## transferedin:0 0.85027473 0.3568019 0.85731656  
## transferedin:1 0.14972527 0.3568019 0.14268344  
## nolifesupportorder:No 0.92902930 0.2567759 0.91792989  
## nolifesupportorder:Yes 0.07097070 0.2567759 0.08207011  
## insurancetype:Medicaid 0.08836996 0.2838322 0.09016829  
## insurancetype:Medicare 0.23397436 0.4233561 0.23261999  
## insurancetype:Medicare & Medicaid 0.05631868 0.2305361 0.05523831  
## insurancetype:No insurance 0.06227106 0.2416472 0.06274937  
## insurancetype:Private 0.33470696 0.4718879 0.33041349  
## insurancetype:Private & Medicare 0.22435897 0.4171595 0.22881055  
## resp:No 0.71062271 0.4534733 0.70655018  
## resp:Yes 0.28937729 0.4534733 0.29344982  
## infection:No 0.76373626 0.4247860 0.81150440  
## infection:Yes 0.23626374 0.4247860 0.18849560  
## trauma:No 0.98443223 0.1237958 0.99335616  
## trauma:Yes 0.01556777 0.1237958 0.00664384  
## ct.sd **std.eff.sz** stat  
## bloodpressure 0.89881836 -0.049347124 -1.76211062  
## creatinelevels 1.33736641 0.002896440 0.07119327  
## sodiumlevels 1.01008368 -0.010715156 -0.35234533  
## urineweight 1.03125669 -0.011655171 -0.37742085  
## kg 0.93779555 0.034784247 1.20407976  
## severe:0 0.40150933 -0.005431074 0.03075533  
## severe:1 0.40150933 0.005431074 NA  
## cognitivedecline:0 0.26028896 0.015584810 0.31338336  
## cognitivedecline:1 0.26028896 -0.015584810 NA  
## depression:0 0.21247219 0.007667658 0.08293555  
## depression:1 0.21247219 -0.007667658 NA  
## cancer:0 0.40680906 0.014917243 0.26049035  
## cancer:1 0.40680906 -0.014917243 NA  
## transferedin:0 0.34974974 -0.019735965 0.38635639  
## transferedin:1 0.34974974 0.019735965 NA  
## nolifesupportorder:No 0.27447150 0.043226066 2.38413789  
## nolifesupportorder:Yes 0.27447150 -0.043226066 NA  
## insurancetype:Medicaid 0.28642272 -0.006335892 0.04829596  
## insurancetype:Medicare 0.42250199 0.003199130 NA  
## insurancetype:Medicare & Medicaid 0.22844482 0.004686359 NA  
## insurancetype:No insurance 0.24251163 -0.001979382 NA  
## insurancetype:Private 0.47036200 0.009098503 NA  
## insurancetype:Private & Medicare 0.42006700 -0.010671165 NA  
## resp:No 0.45534275 0.008980756 0.09890412  
## resp:Yes 0.45534275 -0.008980756 NA  
## infection:No 0.39110742 -0.112452216 13.91530014  
## infection:Yes 0.39110742 0.112452216 NA  
## trauma:No 0.08123853 -0.072085830 7.41251723  
## trauma:Yes 0.08123853 0.072085830 NA  
## p  
## bloodpressure 0.0781038939  
## creatinelevels 0.9432464242  
## sodiumlevels 0.7245922496  
## urineweight 0.7058748439  
## kg 0.2286084604  
## severe:0 0.8607935558  
## severe:1 NA  
## cognitivedecline:0 0.5756332720  
## cognitivedecline:1 NA  
## depression:0 0.7733683709  
## depression:1 NA  
## cancer:0 0.6098031267  
## cancer:1 NA  
## transferedin:0 0.5342455910  
## transferedin:1 NA  
## nolifesupportorder:No 0.1226276796  
## nolifesupportorder:Yes NA  
## insurancetype:Medicaid 0.9985400099  
## insurancetype:Medicare NA  
## insurancetype:Medicare & Medicaid NA  
## insurancetype:No insurance NA  
## insurancetype:Private NA  
## insurancetype:Private & Medicare NA  
## resp:No 0.7531601619  
## resp:Yes NA  
## infection:No 0.0001930827  
## infection:Yes NA  
## trauma:No 0.0064967529  
## trauma:Yes NA

#balance for all looks good , and it is below lazer cut off .25  
  
stratumworking$died <- scale(stratumworking$died)  
#balance looks perfect let’s do an additional analysis with bootstrapping, not required thouhh:  
design <- svydesign(ids = ~0, weights = stratumworking$ATTwFinal, data = stratumworking)  
design <- as.svrepdesign(design, type = c("bootstrap"), replicates = 5000)  
  
model <- svyglm(died ~ factor(surgerytype) + age + bloodpressure + temperature + creatinelevels + sodiumlevels + urineweight + kg + severe + cognitivedecline + depression + cancer + transferedin + nolifesupportorder + insurancetype + resp + infection + trauma , design = design, family = gaussian())  
  
summary(model)

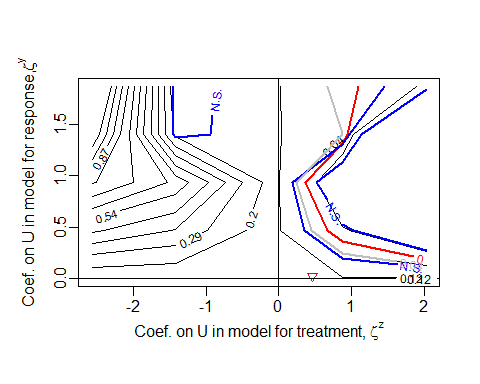
##   
## Call:  
## svyglm(formula = died ~ factor(surgerytype) + bloodpressure +   
## temperature + creatinelevels + sodiumlevels + urineweight +   
## kg + severe + cognitivedecline + depression + cancer + transferedin +   
## nolifesupportorder + insurancetype + resp + infection + trauma,   
## design = design, family = gaussian())  
##   
## Survey design:  
## as.svrepdesign(design, type = c("bootstrap"), replicates = 5000)  
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -0.187805 0.066917 -2.807 0.005027 \*\*   
## factor(surgerytype)1 0.132037 0.028756 4.592 4.51e-06 \*\*\*  
## bloodpressure -0.055680 0.018850 -2.954 0.003153 \*\*   
## temperature -0.056010 0.016484 -3.398 0.000684 \*\*\*  
## creatinelevels 0.064245 0.016043 4.004 6.31e-05 \*\*\*  
## sodiumlevels -0.005832 0.016491 -0.354 0.723604   
## urineweight -0.016624 0.016403 -1.013 0.310911   
## kg -0.041967 0.018670 -2.248 0.024631 \*   
## severe1 0.061128 0.042822 1.428 0.153498   
## cognitivedecline1 0.140672 0.060573 2.322 0.020255 \*   
## depression1 -0.067268 0.082407 -0.816 0.414368   
## cancer1 0.339747 0.039870 8.521 < 2e-16 \*\*\*  
## transferedin1 -0.148168 0.050780 -2.918 0.003541 \*\*   
## nolifesupportorderYes 0.366788 0.045027 8.146 4.71e-16 \*\*\*  
## insurancetypeMedicare 0.085714 0.073282 1.170 0.242197   
## insurancetypeMedicare & Medicaid 0.060191 0.095062 0.633 0.526650   
## insurancetypeNo insurance 0.023929 0.091089 0.263 0.792792   
## insurancetypePrivate -0.010848 0.066683 -0.163 0.870773   
## insurancetypePrivate & Medicare 0.004388 0.075221 0.058 0.953480   
## respYes -0.028795 0.037487 -0.768 0.442432   
## infectionYes 0.021427 0.040481 0.529 0.596608   
## traumaYes -0.348187 0.171123 -2.035 0.041932 \*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 4995.514)  
##   
## Number of Fisher Scoring iterations: 2

#**surgerytype 1** appears to have a significant impact with surgerytype 1 leading to a .0132 SD decrease in death. Lets see how susceptible we are to bias:  
#many covariates also seem to impact  
  
sensitivity <- treatSens(died ~ factor(surgerytype) + ps + I((ps)^2) + I((ps)^3), trt.family = binomial(link = "probit"), grid.dim = c(5,5), nsim = 20, weights = stratumworking$AttwFinal, data = stratumworking)  
#Coefficients on U where tau = 0:  
summary(sensitivity)

## Coefficients on U where tau = 0:  
## Y Z  
## 1.491 2.025  
## 1.431 0.878  
## 1.405 0.713  
## 1.121 0.000  
## 1.294 -1.418  
## 1.405 -1.688  
## 1.873 -2.101  
##   
##   
## Coefficients on U where significance level 0.05 is lost:  
## Y Z  
## 1.641 2.025  
## 1.444 0.878  
## 1.405 0.689  
## 1.040 0.000  
## 1.127 -1.418  
## 1.405 -2.091  
## 1.873 -2.316  
##   
##   
## Estimated treatment effects  
## -2.565 -1.418 0 0.878 2.025  
## 0 0.123 0.123 0.123 0.123 0.123  
## 0.468 0.464 0.365 0.122 -0.038 -0.182  
## 0.937 0.801 0.600 0.114 -0.175 -0.471  
## 1.405 1.111 0.182 0.041 0.041 -0.679  
## 1.873 1.294 0.134 0.013 0.013 -0.058

sensPlot(sensitivity)

## Note: Predictors with negative coefficients for the response surface have been transformed through multiplication by -1 and are displayed as inverted triangles.



# the first part of the result of the sensitivity shows coefficients on U where the treatment effect is zero.

these standard coefficients are large , which means that an unmeasured confounder with a strong relationship with

Z or Y would have to exist for the current effect to become zero if the confounder is included in analysis.

the second part coefficients on U where alpha = 0.05 is lost:

these coefficients are also large which means that there would have to be a strong omitted confounder for the effect to be non-significant.

so the result conclude that the estimated treatment effect of surgery type is robust to omitted confounders.

#It looks that the size of the effect is truly 0, and it does appear that it’s a very strong effect.

#\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**Weighting**\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_  
#Lets now turn to weighting and see if it returns more robust or even different results. Note we use the raw ps here as log corrected will result in negative weights which aren’t possible.  
  
dataready$ATTw <- with(dataready, ifelse(surgerytype == 1, 1, ps/(1-ps)))  
with(dataready, by(ATTw, surgerytype, summary))

## surgerytype: 0  
## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 0.0215 0.2776 0.4805 0.6185 0.8070 7.5821   
## --------------------------------------------------------   
## surgerytype: 1  
## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 1 1 1 1 1 1

dataready$correctedweights <- with(dataready, ifelse(surgerytype == 1, mean(ps)/ps, mean(1-ps)/(1-ps)))  
with(dataready, by(correctedweights, surgerytype, summary))

## surgerytype: 0  
## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 0.6325 0.7910 0.9167 1.0021 1.1189 5.3139   
## --------------------------------------------------------   
## surgerytype: 1  
## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 0.4239 0.6778 0.8338 0.9997 1.1255 7.9499

#It looks like the corrected weights are bringing about better balance:  
model1 <- glm (age ~ surgerytype, weights = ATTw, data = dataready)  
summary(model1)

##   
## Call:  
## glm(formula = age ~ surgerytype, data = dataready, weights = ATTw)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -5.4253 -0.5181 0.1563 0.6050 2.3526   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -0.043482 0.018070 -2.406 0.0161 \*  
## surgerytype 0.005756 0.025590 0.225 0.8220   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.7170818)  
##   
## Null deviance: 4111.1 on 5734 degrees of freedom  
## Residual deviance: 4111.0 on 5733 degrees of freedom  
## AIC: 17088  
##   
## Number of Fisher Scoring iterations: 2

model2 <- glm (cancer ~ surgerytype, weights = ATTw, data = dataready, family = "quasibinomial")  
summary(model2)

##   
## Call:  
## glm(formula = cancer ~ surgerytype, family = "quasibinomial",   
## data = dataready, weights = ATTw)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -1.8659 -0.6742 -0.5172 -0.2443 3.1773   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -1.35445 0.04619 -29.323 <2e-16 \*\*\*  
## surgerytype -0.01137 0.06552 -0.173 0.862   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for quasibinomial family taken to be 0.7640205)  
##   
## Null deviance: 4434.5 on 5734 degrees of freedom  
## Residual deviance: 4434.4 on 5733 degrees of freedom  
## AIC: NA  
##   
## Number of Fisher Scoring iterations: 4

model3 <- glm (age ~ surgerytype, weights = correctedweights, data = dataready)  
summary(model3)

##   
## Call:  
## glm(formula = age ~ surgerytype, data = dataready, weights = correctedweights)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -4.7955 -0.6427 0.1702 0.7388 3.5400   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)  
## (Intercept) -0.002279 0.016785 -0.136 0.892  
## surgerytype -0.022638 0.027219 -0.832 0.406  
##   
## (Dispersion parameter for gaussian family taken to be 1.002525)  
##   
## Null deviance: 5748.2 on 5734 degrees of freedom  
## Residual deviance: 5747.5 on 5733 degrees of freedom  
## AIC: 16636  
##   
## Number of Fisher Scoring iterations: 2

model4 <- glm (cancer ~ surgerytype, weights = correctedweights, data = dataready, family = "quasibinomial")  
summary(model4)

##   
## Call:  
## glm(formula = cancer ~ surgerytype, family = "quasibinomial",   
## data = dataready, weights = correctedweights)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -2.0603 -0.7347 -0.6482 -0.5433 4.0968   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -1.20764 0.03986 -30.299 <2e-16 \*\*\*  
## surgerytype 0.02352 0.06439 0.365 0.715   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for quasibinomial family taken to be 1.001557)  
##   
## Null deviance: 6216.6 on 5734 degrees of freedom  
## Residual deviance: 6216.5 on 5733 degrees of freedom  
## AIC: NA  
##   
## Number of Fisher Scoring iterations: 4

#Now we can see what the effect is:  
dataready$died <- scale(dataready$died)  
  
design <- svydesign(ids = ~0, weights = dataready$correctedweights, data = dataready)  
design <- as.svrepdesign(design, type = c("bootstrap"), replicates = 5000)  
  
  
model <- svyglm(died ~ factor(surgerytype) + bloodpressure + temperature + creatinelevels + sodiumlevels + urineweight + kg + severe + cognitivedecline + depression + cancer + transferedin + nolifesupportorder + insurancetype + resp + infection + trauma, design = design, family = gaussian())  
summary(model)

##   
## Call:  
## svyglm(formula = died ~ factor(surgerytype) + bloodpressure +   
## temperature + creatinelevels + sodiumlevels + urineweight +   
## kg + severe + cognitivedecline + depression + cancer + transferedin +   
## nolifesupportorder + insurancetype + resp + infection + trauma,   
## design = design, family = gaussian())  
##   
## Survey design:  
## as.svrepdesign(design, type = c("bootstrap"), replicates = 5000)  
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)  
## (Intercept) -0.1956510 0.0499766 -3.915 9.17e-05  
## factor(surgerytype)1 0.1409714 0.0275134 5.124 3.11e-07  
## bloodpressure -0.0454413 0.0142962 -3.179 0.001489  
## temperature -0.0585985 0.0144243 -4.062 4.93e-05  
## creatinelevels 0.0477368 0.0162184 2.943 0.003262  
## sodiumlevels -0.0041180 0.0136685 -0.301 0.763218  
## urineweight 0.0001903 0.0133859 0.014 0.988661  
## kg -0.0296518 0.0141379 -2.097 0.036015  
## severe1 0.0281150 0.0372316 0.755 0.450202  
## cognitivedecline1 0.1424895 0.0432056 3.298 0.000981  
## depression1 -0.0770762 0.0552929 -1.394 0.163391  
## cancer1 0.3855881 0.0304814 12.650 < 2e-16  
## transferedin1 -0.1190852 0.0445842 -2.671 0.007587  
## nolifesupportorderYes 0.3584150 0.0339162 10.568 < 2e-16  
## insurancetypeMedicare 0.0344393 0.0569519 0.605 0.545401  
## insurancetypeMedicare & Medicaid 0.0725932 0.0700079 1.037 0.299819  
## insurancetypeNo insurance 0.0787213 0.0715226 1.101 0.271103  
## insurancetypePrivate 0.0106526 0.0504651 0.211 0.832827  
## insurancetypePrivate & Medicare -0.0109809 0.0575633 -0.191 0.848720  
## respYes -0.0192409 0.0280381 -0.686 0.492593  
## infectionYes 0.0368476 0.0346779 1.063 0.288030  
## traumaYes -0.4500657 0.1388106 -3.242 0.001194  
##   
## (Intercept) \*\*\*  
## factor(surgerytype)1 \*\*\*  
## bloodpressure \*\*   
## temperature \*\*\*  
## creatinelevels \*\*   
## sodiumlevels   
## urineweight   
## kg \*   
## severe1   
## cognitivedecline1 \*\*\*  
## depression1   
## cancer1 \*\*\*  
## transferedin1 \*\*   
## nolifesupportorderYes \*\*\*  
## insurancetypeMedicare   
## insurancetypeMedicare & Medicaid   
## insurancetypeNo insurance   
## insurancetypePrivate   
## insurancetypePrivate & Medicare   
## respYes   
## infectionYes   
## traumaYes \*\*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 5059.746)  
##   
## Number of Fisher Scoring iterations: 2

# More or less same as Stratified but some of the covariates seems to be non-significant such as sodiumlevels , urineweight , severe1 , depression1 , insurancetypeMedicare , insurancetyp , resp , infection

# so we changed the model and used only significant cov

finalmodelWt <- svyglm(died ~ factor(surgerytype) + bloodpressure + temperature + creatinelevels + kg + cognitivedecline + cancer + transferedin + nolifesupportorder + trauma, design = design, family = gaussian())

summary(finalmodelWt)

Estimate Std. Error t value Pr(>|t|)

(Intercept) -0.19951 0.02164 -9.221 < 2e-16 \*\*\*

factor(surgerytype)1 0.14179 0.02783 5.094 3.63e-07 \*\*\*

bloodpressure -0.05575 0.01422 -3.921 8.95e-05 \*\*\*

temperature -0.07955 0.01398 -5.690 1.35e-08 \*\*\*

creatinelevels 0.04553 0.01606 2.836 0.00459 \*\*

kg -0.03087 0.01444 -2.138 0.03260 \*

cognitivedecline1 0.23898 0.04264 5.605 2.20e-08 \*\*\*

cancer1 0.39961 0.02983 13.395 < 2e-16 \*\*\*

transferedin1 -0.12606 0.04632 -2.722 0.00652 \*\*

nolifesupportorderYes 0.44069 0.03391 12.995 < 2e-16 \*\*\*

traumaYes -0.56678 0.13854 -4.091 4.36e-05 \*\*\*

---

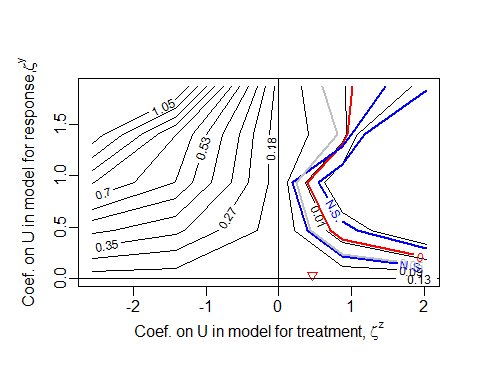
#**surgerytype 1** appears to have a significant impact with surgerytype 1 leading to a .0142 SD decrease in death. Let’s see how susceptible we are to bias: we will use weighing as it improves a little b coefficient.  
#many covariates also seem to impact

sensitivity <- treatSens(died ~ factor(surgerytype) + ps + I((ps)^2) + I((ps)^3), trt.family = binomial(link = "probit"), grid.dim = c(5,5), nsim = 20, weights = dataready$correctedweights, data = dataready)  
summary(sensitivity)

## Coefficients on U where tau = 0:  
## Y Z  
## 1.462 2.025  
## 1.434 0.878  
## 1.405 0.694  
## 1.136 0.000  
## 1.313 -1.418  
## 1.405 -1.643  
## 1.873 -2.067  
##   
##   
## Coefficients on U where significance level 0.05 is lost:  
## Y Z  
## 1.645 2.025  
## 1.453 0.878  
## 1.405 0.663  
## 1.038 0.000  
## 1.147 -1.418  
## 1.405 -2.049  
## 1.873 -2.285  
##   
##   
## Estimated treatment effects  
## -2.565 -1.418 0 0.878 2.025  
## 0 0.130 0.130 0.130 0.130 0.130  
## 0.468 0.464 0.370 0.129 -0.032 -0.170  
## 0.937 0.796 0.608 0.120 -0.162 -0.458  
## 1.405 1.107 0.702 0.043 0.043 -0.647  
## 1.873 1.307 1.185 0.014 0.014 -0.099

sensPlot(sensitivity)

## Note: Predictors with negative coefficients for the response surface have been transformed through multiplication by -1 and are displayed as inverted triangles.



# the first part of the result of the sensitivity shows coefficients on U where the treatment effect is zero.

these standard coefficients are large , which means that an unmeasured confounder with a strong relationship with

Z or Y would have to exist for the current effect to become zero if the confounder is included in analysis.

the second part coefficients on U where alpha = 0.05 is lost:

these coefficients are also large which means that there would have to be a strong omitted confounder for the effect to be non-significant.

so the result conclude that the estimated treatment effect of surgery type is robust to omitted confounders.

#It looks that the size of the effect is truly 0, and it does appear that it’s a very strong effect.

##\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**Matching**\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_  
#Greedy Matching  
greedy <- matchit(psf, distance = dataready$logps, m.order = "largest", data = dataready, method = "nearest", replace = TRUE, caliper = .25)  
summary(greedy)

##   
## Call:  
## matchit(formula = psf, data = dataready, method = "nearest",   
## distance = dataready$logps, m.order = "largest", replace = TRUE,   
## caliper = 0.25)  
##   
## Summary of balance for all data:  
## Means Treated Means Control SD Control  
## distance -0.2235 -0.7650 0.7709  
## bloodpressure -0.2713 0.1669 1.0218  
## creatinelevels 0.1658 -0.1020 0.9864  
## sodiumlevels -0.0570 0.0350 1.0029  
## urineweight -0.0746 0.0459 0.9742  
## kg 0.1560 -0.0959 1.0154  
## severe0 0.7958 0.8403 0.3664  
## severe1 0.2042 0.1597 0.3664  
## cognitivedecline1 0.0691 0.1163 0.3206  
## depression1 0.0458 0.0805 0.2722  
## cancer1 0.2033 0.2456 0.4305  
## transferedin1 0.1497 0.0943 0.2923  
## nolifesupportorderYes 0.0710 0.1405 0.3476  
## insurancetypeMedicare 0.2340 0.2667 0.4423  
## insurancetypeMedicare & Medicaid 0.0563 0.0707 0.2563  
## insurancetypeNo insurance 0.0623 0.0524 0.2228  
## insurancetypePrivate 0.3347 0.2723 0.4452  
## insurancetypePrivate & Medicare 0.2244 0.2101 0.4074  
## respYes 0.2894 0.4171 0.4931  
## Sample sizes:  
*## Control Treated  
## All 3551 2184  
## Matched 1444 2184  
## Unmatched 2107 0  
## Discarded 0 0*

#Genetic Matching was taking very long time so leaving it for now- using pop.size as 100 due to time constraint , ideally it should be 1000 or more for larger sample  
#genetic <- matchit(psf, distance = dataready$logps, data = dataready, method = 'genetic', pop.size = 100, fit.func='pvals', estimand = 'ATT', replace = TRUE, ties = TRUE)  
#summary(genetic)  
  
#Optimal Matching  
optimal <- matchit(psf, distance = dataready$logps, data = as.data.frame(dataready), method = 'optimal', ratio = 1)

## Warning in optmatch::fullmatch(d, min.controls = ratio, max.controls = ratio, : Without 'data' argument the order of the match is not guaranteed  
## to be the same as your original data.

summary(optimal)

##   
## Call:  
## matchit(formula = psf, data = as.data.frame(dataready), method = "optimal",   
## distance = dataready$logps, ratio = 1)  
##   
## Summary of balance for all data:  
## Means Treated Means Control SD Control  
## distance -0.2235 -0.7650 0.7709  
## bloodpressure -0.2713 0.1669 1.0218  
## creatinelevels 0.1658 -0.1020 0.9864  
## sodiumlevels -0.0570 0.0350 1.0029  
## urineweight -0.0746 0.0459 0.9742  
## kg 0.1560 -0.0959 1.0154  
## severe0 0.7958 0.8403 0.3664  
## severe1 0.2042 0.1597 0.3664  
## cognitivedecline1 0.0691 0.1163 0.3206  
## depression1 0.0458 0.0805 0.2722  
## cancer1 0.2033 0.2456 0.4305  
## transferedin1 0.1497 0.0943 0.2923  
## nolifesupportorderYes 0.0710 0.1405 0.3476  
## insurancetypeMedicare 0.2340 0.2667 0.4423  
## insurancetypeMedicare & Medicaid 0.0563 0.0707 0.2563  
## insurancetypeNo insurance 0.0623 0.0524 0.2228  
## insurancetypePrivate 0.3347 0.2723 0.4452  
## insurancetypePrivate & Medicare 0.2244 0.2101 0.4074  
*## Sample sizes:  
## Control Treated  
## All 3551 2184  
## Matched 2184 2184  
## Unmatched 1367 0  
## Discarded 0 0*

# so optimal is matching better so will go by optimal matching  
#Analysis where ## Matched 2184 2184 for control and treated  
readydata <- match.data(optimal)  
analysis <- svydesign(ids = ~1, weights = ~weights, data = readydata)  
  
model <- svyglm(died ~ factor(surgerytype), analysis, family = gaussian())  
  
summary(model)

##   
## Call:  
## svyglm(formula = died ~ factor(surgerytype), design = analysis,   
## family = gaussian())  
##   
## Survey design:  
## svydesign(ids = ~1, weights = ~weights, data = readydata)  
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -0.05027 0.02171 -2.316 0.020591 \*   
## factor(surgerytype)1 0.11607 0.03014 3.851 0.000119 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.9917798)  
##   
## Number of Fisher Scoring iterations: 2

model2 <- svyglm(died ~ factor(surgerytype) + bloodpressure + temperature + creatinelevels + sodiumlevels + urineweight + kg + severe + cognitivedecline + depression + cancer + transferedin + nolifesupportorder + insurancetype + resp + infection + trauma, analysis, family = gaussian())  
  
summary(model2)

##   
## Call:  
## svyglm(formula = died ~ factor(surgerytype) + bloodpressure +   
## temperature + creatinelevels + sodiumlevels + urineweight +   
## kg + severe + cognitivedecline + depression + cancer + transferedin +   
## nolifesupportorder + insurancetype + resp + infection + trauma,   
## design = analysis, family = gaussian())  
##   
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -0.151194 0.057362 -2.636 0.00842 \*\*   
## factor(surgerytype)1 0.122280 0.028825 4.242 2.26e-05 \*\*\*  
## bloodpressure -0.045465 0.016809 -2.705 0.00686 \*\*   
## temperature -0.065006 0.014813 -4.389 1.17e-05 \*\*\*  
## creatinelevels 0.061865 0.014061 4.400 1.11e-05 \*\*\*  
## sodiumlevels 0.005563 0.014315 0.389 0.69761   
## urineweight -0.004063 0.014244 -0.285 0.77547   
## kg -0.051328 0.015640 -3.282 0.00104 \*\*   
## severe1 0.056581 0.038002 1.489 0.13659   
## cognitivedecline1 0.155399 0.053165 2.923 0.00349 \*\*   
## depression1 -0.042938 0.068140 -0.630 0.52863   
## cancer1 0.387022 0.033470 11.563 < 2e-16 \*\*\*  
## transferedin1 -0.131510 0.044261 -2.971 0.00298 \*\*   
## nolifesupportorderYes 0.367552 0.041074 8.949 < 2e-16 \*\*\*  
## insurancetypePrivate & Medicare -0.035237 0.064036 -0.550 0.58216   
## respYes -0.023589 0.031503 -0.749 0.45402   
## infectionYes 0.039036 0.035749 1.092 0.27492   
## traumaYes -0.372381 0.141303 -2.635 0.00844 \*\*   
#**surgerytype 1** appears to have a significant impact with surgerytype 1 leading to a .0123 SD decrease in death.   
#many covariates also seem to impact

***FINAL SUMMARY :***

*We analyzed data to find the surgery type 1 or 0 which has better survival chances for patient. I we did all three matching , stratified and weighing and we saw that weighing and stratified were almost same when it comes to balance. Matching did result is loss of data.*

*Of those three weighting didn’t result in any data loss. Based on these analyses we would suggest that there is likely a negative effect of surgery type 1 on death, which means by taking surgery type 1 the patient is less likely to die but also note that the size/significance of the effect is likely smaller than we found. We would also suggest that the weighting method is doing the best overall job (reducing covariate imbalance and using all observations).*

*Weighing(b=0.142 t= 5.09 p < 0.001) as it is having negative effect.*

*Other covariates which also impacted the surgery type in turn impacted the death counts are p< 0.001*

Estimate t value

|  |
| --- |
| (Intercept) -0.19951 -9.221  factor(surgerytype)1 0.14179 5.094  bloodpressure -0.05575 -3.921  temperature -0.07955 -5.690  creatinelevels 0.04553 2.836  kg -0.03087 -2.138  cognitivedecline 0.23898 5.605  cancer 0.39961 13.395  transferedin -0.12606 -2.722  nolifesupportorder 0.44069 12.995  trauma -0.56678 -4.091 |

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