Table1

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library(knitr)  
library(data.table)  
data.before.psm <- readRDS('mito\_data\_before\_PSM')  
data.after.psm <- readRDS('caliper\_matched\_data')

table1.stats <- c('N', 'mean age', 'age range',  
 '%white', '%black', '%asian', '%other',  
 'median BMI', 'BMI range',  
 'median ALKP', 'ALKP range',  
 'median PSA', 'PSA range',  
 'num ECOG = 0', '% ECOG = 0', 'num ECOG = 1', '% ECOG = 1',  
 'median hgb', 'hgb range',  
 'num recent doce', '% recent doce',  
 'num w bone met', '% w bone met',  
 'num w visc met', '% w visc met',  
 'num w bone and vis met', '% w bone and visc met',  
 'num w bone or visc met', '% w bone or visc met')  
  
  
getSingleCohortStats <- function(data) {  
   
 return(c(nrow(data),  
 round(mean(data$age), 1),  
 paste0('(', paste(range(data$age), collapse = ', '), ')'),  
 round(100 \* mean(data$race == 'WHITE')),  
 round(100 \* mean(data$race == 'BLACK')),  
 round(100 \* mean(data$race == 'ASIAN')),  
 round(100 \* mean(data$race == 'OTHER')),  
 round(median(data$bmi)),  
 paste0('(', paste(round(range(data$bmi), 1), collapse = ', '), ')'),  
 round(median(data$alkp)),  
 paste0('(', paste(round(range(data$alkp), 1), collapse = ', '), ')'),  
 round(median(data$psa)),  
 paste0('(', paste(round(range(data$psa), 1), collapse = ', '), ')'),  
 sum(data$ecog == 0),  
 round(100 \* mean(data$ecog == 0)),  
 sum(data$ecog == 1),  
 round(100 \* mean(data$ecog == 1)),  
 round(median(data$hgb)),  
 paste0('(', paste(round(range(data$hgb), 1), collapse = ', '), ')'),  
 sum(data$recent.doce == 1),  
 round(100 \* mean(data$recent.doce == 1)),  
 sum(data$bone == 1),  
 round(100 \* mean(data$bone == 1)),  
 sum(data$visc == 1),  
 round(100 \* mean(data$visc == 1)),  
 sum(data$bone == 1 & data$visc == 1),  
 round(100 \* mean(data$bone == 1 & data$visc == 1)),  
 sum(data$bone == 1 | data$visc == 1),  
 round(100 \* mean(data$bone == 1 | data$visc == 1))))  
}  
  
getPValues <- function(data1, data2) {  
   
 return(c(NA,  
 t.test(data1$age, data2$age)$p.value,  
 NA,  
 prop.test(x = c(sum(data1$race == 'WHITE'), sum(data2$race == 'WHITE')),  
 n = c(nrow(data1), nrow(data2)))$p.value,  
 prop.test(x = c(sum(data1$race == 'BLACK'), sum(data2$race == 'BLACK')),  
 n = c(nrow(data1), nrow(data2)))$p.value,  
 prop.test(x = c(sum(data1$race == 'ASIAN'), sum(data2$race == 'ASIAN')),  
 n = c(nrow(data1), nrow(data2)))$p.value,  
 prop.test(x = c(sum(data1$race == 'OTHER'), sum(data2$race == 'OTHER')),  
 n = c(nrow(data1), nrow(data2)))$p.value,  
 t.test(data1$bmi, data2$bmi)$p.value,  
 NA,  
 t.test(data1$alkp, data2$alkp)$p.value,  
 NA,  
 t.test(data1$psa, data2$psa)$p.value,  
 NA,  
 prop.test(x = c(sum(data1$ecog == 1), sum(data2$ecog == 1)),  
 n = c(nrow(data1), nrow(data2)))$p.value,  
 NA, NA, NA,  
 t.test(data1$hgb, data2$hgb)$p.value,  
 NA,  
 prop.test(x = c(sum(data1$recent.doce == 1), sum(data2$recent.doce == 1)),  
 n = c(nrow(data1), nrow(data2)))$p.value,  
 NA,  
 prop.test(x = c(sum(data1$bone == 1), sum(data2$bone == 1)),  
 n = c(nrow(data1), nrow(data2)))$p.value,  
 NA,  
 prop.test(x = c(sum(data1$visc == 1), sum(data2$visc == 1)),  
 n = c(nrow(data1), nrow(data2)))$p.value,  
 NA,  
 prop.test(x = c(sum(data1$bone == 1 & data1$visc == 1),   
 sum(data2$bone == 1 & data2$visc == 1)),  
 n = c(nrow(data1), nrow(data2)))$p.value,  
 NA,  
 prop.test(x = c(sum(data1$bone == 1 | data1$visc == 1),   
 sum(data2$bone == 1 | data2$visc == 1)),  
 n = c(nrow(data1), nrow(data2)))$p.value,  
 NA))  
   
}  
  
pred.before.psm <- getSingleCohortStats(data.before.psm[treatment == 0,])  
mito.before.psm <- getSingleCohortStats(data.before.psm[treatment == 1,])  
pred.after.psm <- getSingleCohortStats(data.after.psm[treatment == 0,])  
mito.after.psm <- getSingleCohortStats(data.after.psm[treatment == 1,])  
  
before.p <- getPValues(data.before.psm[treatment == 0,],   
 data.before.psm[treatment == 1,])  
after.p <- getPValues(data.after.psm[treatment == 0,],   
 data.after.psm[treatment == 1,])

kable(data.frame(pred.before.psm,   
 mito.before.psm,  
 before.p,  
 pred.after.psm,   
 mito.after.psm,  
 after.p,  
 row.names = table1.stats),  
 row.names = TRUE)

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | pred.before.psm | mito.before.psm | before.p | pred.after.psm | mito.after.psm | after.p |
| N | 257 | 303 | NA | 198 | 198 | NA |
| mean age | 67.8 | 66.4 | 0.0403 | 67.6 | 67.4 | 0.7786 |
| age range | (47, 86) | (47, 85) | NA | (47, 85) | (49, 85) | NA |
| %white | 75 | 83 | 0.0317 | 77 | 82 | 0.2128 |
| %black | 5 | 6 | 0.6330 | 4 | 6 | 0.3470 |
| %asian | 9 | 8 | 0.7612 | 8 | 9 | 0.8537 |
| %other | 11 | 3 | 0.0003 | 12 | 3 | 0.0012 |
| median BMI | 27 | 28 | 0.0206 | 28 | 28 | 0.7696 |
| BMI range | (18.2, 54) | (17.6, 46.8) | NA | (18.2, 54) | (17.6, 46.8) | NA |
| median ALKP | 136 | 124 | 0.2434 | 140 | 126 | 0.3497 |
| ALKP range | (36, 3485) | (2.4, 3418) | NA | (36, 3485) | (2.4, 3418) | NA |
| median PSA | 153 | 109 | 0.5108 | 166 | 119 | 0.8722 |
| PSA range | (0.2, 5927) | (1.7, 11220) | NA | (0.6, 5927) | (1.7, 11220) | NA |
| num ECOG = 0 | 129 | 101 | 0.0001 | 81 | 84 | 0.8385 |
| % ECOG = 0 | 50 | 33 | NA | 41 | 42 | NA |
| num ECOG = 1 | 128 | 202 | NA | 117 | 114 | NA |
| % ECOG = 1 | 50 | 67 | NA | 59 | 58 | NA |
| median hgb | 12 | 12 | 0.0006 | 12 | 12 | 0.6944 |
| hgb range | (8.3, 16) | (7.6, 16) | NA | (8.4, 16) | (7.6, 15.4) | NA |
| num recent doce | 169 | 217 | 0.1612 | 138 | 140 | 0.9125 |
| % recent doce | 66 | 72 | NA | 70 | 71 | NA |
| num w bone met | 229 | 262 | 0.4140 | 175 | 172 | 0.7602 |
| % w bone met | 89 | 86 | NA | 88 | 87 | NA |
| num w visc met | 101 | 135 | 0.2424 | 82 | 96 | 0.1891 |
| % w visc met | 39 | 45 | NA | 41 | 48 | NA |
| num w bone and vis met | 83 | 112 | 0.2862 | 66 | 82 | 0.1192 |
| % w bone and visc met | 32 | 37 | NA | 33 | 41 | NA |
| num w bone or visc met | 247 | 285 | 0.3605 | 191 | 186 | 0.3470 |
| % w bone or visc met | 96 | 94 | NA | 96 | 94 | NA |