UKCOGS survey: analysis

Last updated: 30th June 2020

Introduction

This notebook reproduces analysis presented in the paper

Prepare data

```
In [1]: ## Libraries
        library("xtable")
        library("ggplot2")
```

```
In [2]: mydta3 <- read.csv("200630-ukcogs-data.csv")
        head(mydta3)
```

A data.frame: 6 × 41

	X	ID	centre	name	staffreduced	staffJDCOVID	staffJDRedeploy	staffGOCOVID	staffG
	<int>	<dbl>	<fct>	<fct>	<fct>	<lgl>	<lgl>	<lgl>	
1	18	11593373277	Unit	site-1	No	FALSE	FALSE	FALSE	
2	30	11555988746	Unit	site-2	No	FALSE	FALSE	FALSE	
3	55	11550243631	Centre	site-3	Yes	FALSE	TRUE	FALSE	
4	13	11593709116	Unit	site-4	No	FALSE	FALSE	FALSE	
5	22	11563796810	Centre	site-5	Yes	FALSE	TRUE	FALSE	
6	9	11594652889	Centre	site-6	No	FALSE	FALSE	FALSE	

Analysis

Summary of hospitals

```
In [3]: ##############
        ## Basic summaries

        t.inc<-!duplicated(mydta3$newname)

        mynumberresp <- tapply(mydta3$ID, mydta3$newname, length)

        mydtasummary <- mydta3[t.inc,]

        mysummary <- cbind( mydtasummary$name,mynumberresp,as.character(mydtasummar
        y$centre))

        mysummary <- mysummary[order(mysummary[,3], mysummary[,1], mysummary[,2]),]

        colnames(mysummary) <- c("Site", "Number response", "Type")

        rownames(mysummary) <- rep("", nrow(mysummary))

        xtable(mysummary, align="llrc", include.rownames=FALSE)

        table(mysummary[,2], mysummary[,3])
```

A xtable: 51 × 3

	Site	Number response	Type
	<fct>	<fct>	<fct>
X	10	1	Centre
X.1	13	1	Centre
X.2	15	1	Centre
X.3	16	2	Centre
X.4	18	1	Centre
X.5	19	1	Centre
X.6	20	3	Centre
X.7	23	1	Centre
X.8	24	2	Centre
X.9	27	1	Centre
X.10	28	1	Centre
X.11	29	1	Centre
X.12	3	2	Centre
X.13	30	1	Centre
X.14	31	2	Centre
X.15	33	1	Centre
X.16	35	2	Centre
X.17	37	1	Centre
X.18	40	1	Centre
X.19	41	4	Centre
X.20	45	1	Centre
X.21	46	1	Centre
X.22	49	2	Centre
X.23	5	5	Centre
X.24	51	1	Centre
X.25	54	1	Centre
X.26	56	3	Centre
X.27	57	1	Centre
X.28	58	1	Centre
X.29	61	1	Centre
X.30	63	1	Centre
X.31	64	1	Centre
X.32	1	1	Unit
X.33	11	1	Unit
X.34	12	1	Unit
X.35	14	1	Unit
X.36	2	1	Unit
X.37	26	1	Unit
X.38	34	1	Unit
X.39	38	1	Unit

```
       Centre Unit
1        22   18
2         6    1
3         2    0
4         1    0
5         1    0
```

The sites that responded to the questionnaire are listed above, with information on the number of people who completed a form and site type (centre or unit).

In total there were 34 centres and 19 units

```
In [4]: table(mysummary[,3])

        Centre   Unit
            32     19
```

Regarding staffing, have you experienced significant reduction in staff numbers?

```
In [5]: ###############################################
        ## Discrepancy within some centre responses

        ##remove 11550771438 - not agreed with others
        mydta3 <- mydta3[!(mydta3$ID==11550771438),]

        ##remove 11561304662 - not agreed with others
        mydta3 <- mydta3[!(mydta3$ID==11561304662),]

        ##remove 11596521251 - not agreed with others
        mydta3 <- mydta3[!(mydta3$ID==11596521251),]

        ##remove 11549791528 - not agreed with others
        mydta3 <- mydta3[!(mydta3$ID==11549791528),]
```

Some centres had different answers regarding staffing reductions.

In what follows we assumed that a site had seen a reduction in staffing if one respondant said their had been.

```
In [6]: mystaffred <- tapply(as.character(mydta3$staffreduced), mydta3$newname, fun
        ction(ind) mean(ind=="Yes"))

        ##centres staff reduced
        centre.red <- mydta3$newname %in% names(mystaffred)[mystaffred>0]

        mydta4a <- mydta3[centre.red,]

        mydta4a$newname <- as.factor(as.character(mydta4a$newname))

        mydta4b <- mydta3[!centre.red,c(1,2,3,4,5,18:41)]

        mydta4b$newname <- as.factor(as.character(mydta4b$newname))

        ## Write CSV files for to separate by sites that saw a reduction and those
        that did not
        write.csv(mydta4a, file="output/staffred-all.csv")

        write.csv(mydta4b, file="output/staffOK-all.csv")

        ## summary unit / centre
        mydta4au <- mydta4a[!duplicated(mydta4a$newname),]

        mydta4bu <- mydta4b[!duplicated(mydta4b$newname),]

        print("Centre / Units with reduction in staff")

        mydta4au$name

        print("Centre / Units with NO reduction in staff")

        mydta4bu$name

        print("== summary ==")

        print("Centre / Units with reduction in staff")

        table(mydta4au$centre)

        print("Centre / Units with NO reduction in staff")

        table(mydta4bu$centre)
```

```
[1] "Centre / Units with reduction in staff"
```

site-3 ·   site-5 ·   site-10 ·   site-11 ·   site-20 ·   site-25 ·   site-28 ·   site-31 ·   site-32 ·   site-33 ·
site-36 ·   site-38 ·   site-43 ·   site-44 ·   site-46 ·   site-50 ·   site-53 ·   site-55 ·   site-56 ·   site-58 ·
site-60 ·   site-61 ·   site-63 ·   site-68 ·   site-69

▸ **Levels**:

```
[1] "Centre / Units with NO reduction in staff"
```

site-1 ·   site-2 ·   site-4 ·   site-6 ·   site-9 ·   site-13 ·   site-18 ·   site-19 ·   site-21 ·   site-22 ·
site-23 ·   site-26 ·   site-34 ·   site-35 ·   site-39 ·   site-40 ·   site-42 ·   site-45 ·   site-51 ·   site-57 ·
site-59 ·   site-62 ·   site-64 ·   site-65 ·   site-66 ·   site-67

▸ **Levels**:

```
[1] "== summary =="
[1] "Centre / Units with reduction in staff"

Centre    Unit
    17       8

[1] "Centre / Units with NO reduction in staff"

Centre    Unit
    15      11
```

```
In [7]:  ## Summary statistics. Take average within centre

         fn.sumstat.bin <- function(ind){
             min(sum(ind),1, na.rm=TRUE)
         }

         ## do opposite - sensititivty analysis
         ##fn.sumstat.bin <- function(ind){
         ##     floor(mean(ind, na.rm=TRUE))
         ##}

         mydta5a1 <- data.frame(sapply(6:13, function(idx) tapply(mydta4a[,idx], myd
         ta4a$newname, fn.sumstat.bin)))

         mydta5a2 <- data.frame(sapply(14:17, function(idx) tapply(mydta4a[,idx], my
         dta4a$newname, mean, na.rm=TRUE)))

         mydta5a <- cbind(mydta5a1, mydta5a2)

         colnames(mydta5a) <- colnames(mydta4a[,6:17])

         ## output CSV file with data
         write.csv(mydta5a, file="output/staffred-summarybycentre.csv")

         ##Look at individual results
         mydta5a
```

A data.frame: 25 × 12

	staffJDCOVID	staffJDRedeploy	staffGOCOVID	staffGORedeploy	staffConstCOVID	staffConstRedeploy
	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
13	0	0	0	0	1	(
17	1	0	0	0	1	(
19	1	1	0	1	0	(
20	0	1	0	1	0	(
21	1	0	0	0	1	(
22	1	0	1	0	1	(
24	1	0	0	0	1	(
26	1	0	1	0	1	(
3	0	1	0	0	1	(
30	1	1	0	1	1	(
31	0	1	0	0	0	(
33	1	0	0	0	1	(
34	0	1	0	0	1	(
36	0	1	0	0	1	(
37	0	0	0	0	1	(
38	1	1	0	1	1	(
40	0	1	0	0	0	(
42	0	1	0	0	0	(
43	1	0	0	0	1	(
45	1	1	0	0	0	(
5	0	1	0	1	0	-
50	1	0	0	0	1	(
51	1	1	0	0	1	(
8	0	0	0	0	1	(
9	1	1	0	1	0	-

```
In [8]: mysum.staffred <- list(summary(mydta5a$staffJDred),
                               summary(mydta5a$staffGOred),
                               summary(mydta5a$staffCONred),
                               summary(mydta5a$staffCNSred))

        myna.staffred <- unlist(lapply(mysum.staffred, function(ind) ind[7]))

        ##mylabname <- paste(c("Junior", "Gyn Onc", "Consultant", "CNS"), "\n (NA
        =", myna.staffred, ")", sep="")

        ##boxplot(list(mydta5a$staffJDred, mydta5a$staffGOred, mydta5a$staffCONred,
        mydta5a$staffCNSred), names=mylabname, ylab="Percentage reduction (%)")


        mylabname <- paste(c("Junior", "Gyn Onc", "Consultant", "CNS"), "\n (NA=",
        myna.staffred, ")", sep="")


        fn.format<-function(ind, ndigit=2)
        {
            format(round(ind,ndigit), nsmall=ndigit)
        }

        fn.sumstat1 <- function(ind, ndig=0){
                paste(sum(ind), " (", fn.format(round(sum(ind)/length(ind) * 100),n
        dig), "%)", sep="")
        }


        fn.summaryyes <- function(inyes1, inyes2, inperc){
            print(paste("Number yes Covid: ", sum(inyes1), "/", length(inyes1), "
        (", fn.format(sum(inyes1)/length(inyes1)*100,0), "%)", sep=""))
            print(paste("Number yes redeploy: ", sum(inyes2), "/", length(inyes2),
        " (", fn.format(sum(inyes2)/length(inyes2)*100,0), "%)", sep=""))
            print("cross tab")
            COVID<-inyes1; REDEPLOY <- inyes2
            print(addmargins(table(COVID, REDEPLOY)))

            print("individual responses: percentage reduction")
            print(sort(inperc[inyes1==1 | inyes2==1], na.last=TRUE))
            print("summary: percentage reduction")
            summary(inperc[inyes1==1 | inyes2==1])
            }

        print("== Junior doctors ==")
        fn.summaryyes(mydta5a$staffJDCOVID,mydta5a$staffJDRedeploy, mydta5a$staffJD
        red)

        print("== GO Sub-specialty Trainee == ")
        fn.summaryyes(mydta5a$staffGOCOVID, mydta5a$staffGORedeploy, mydta5a$staffG
        Ored)

        print("== Consultant ==")
        fn.summaryyes(mydta5a$staffConstCOVID,mydta5a$staffConstRedeploy, mydta5a$s
        taffCONred)

        print("== CNS ==")
        fn.summaryyes(mydta5a$staffCNSCOVID,mydta5a$staffCNSRedeploy, mydta5a$staff
        CNSred)
```

```
[1] "== Junior doctors =="
[1] "Number yes Covid: 14/25 (56%)"
[1] "Number yes redeploy: 14/25 (56%)"
[1] "cross tab"
      REDEPLOY
COVID  0  1 Sum
   0   3  8  11
   1   8  6  14
   Sum 11 14  25
[1] "individual responses: percentage reduction"
 [1]  10.0  15.0  15.0  20.0  22.5  25.0  25.0  30.0  30.0  40.0  40.0  40.0
[13]  40.0  50.0  60.0 100.0 100.0 100.0 100.0 100.0 100.0   NaN
[1] "summary: percentage reduction"

   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   10.0    25.0    40.0    50.6   100.0   100.0       1

[1] "== GO Sub-specialty Trainee == "
[1] "Number yes Covid: 2/25 (8%)"
[1] "Number yes redeploy: 6/25 (24%)"
[1] "cross tab"
      REDEPLOY
COVID  0  1 Sum
   0  17  6  23
   1   2  0   2
   Sum 19  6  25
[1] "individual responses: percentage reduction"
[1]   30 100 100 100 100 100 100 100
[1] "summary: percentage reduction"

   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  30.00  100.00  100.00   91.25  100.00  100.00

[1] "== Consultant =="
[1] "Number yes Covid: 17/25 (68%)"
[1] "Number yes redeploy: 2/25 (8%)"
[1] "cross tab"
      REDEPLOY
COVID  0  1 Sum
   0   6  2   8
   1  17  0  17
   Sum 23  2  25
[1] "individual responses: percentage reduction"
 [1]   0.0   1.0 16.5 20.0 20.0 20.0 20.0 25.0 25.0 30.0 30.0 30.0 33.0 40.0 5
0.0
[16] 50.0 50.0 70.0  NaN
[1] "summary: percentage reduction"

   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.00   20.00   27.50   29.47   38.25   70.00       1

[1] "== CNS =="
[1] "Number yes Covid: 9/25 (36%)"
[1] "Number yes redeploy: 14/25 (56%)"
[1] "cross tab"
      REDEPLOY
COVID  0  1 Sum
   0   9  7  16
   1   2  7   9
   Sum 11 14  25
[1] "individual responses: percentage reduction"
 [1]   1.0 16.5 20.0 20.0 20.0 25.0 30.0 30.0 40.0 50.0 50.0 62.5 75.0 80.0
NaN
[16]   NaN
[1] "summary: percentage reduction"

   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   1.00   20.00   30.00   37.14   50.00   80.00       2
```

```r
mygplotdta <- data.frame(reduction=c(mydta5a$staffJDred,mydta5a$staffGOred,
  mydta5a$staffCONred, mydta5a$staffCNSred), group=rep(c("Junior Doctors", "G
O Sub-specialty", "Consultant\
", "CNS"), each=nrow(mydta5a)))

##mygplotdta[is.na(mygplotdta[,1]),1] <- 0

p <- ggplot(mygplotdta, aes(x=group, y=reduction)) +
    geom_boxplot()+
  geom_dotplot(binaxis='y', stackdir='center', dotsize=.7)

p

## sub group
#mygplotdta1 <- data.frame(reduction=c(mydta5a1$staffJDred,mydta5a1$staffGO
red, mydta5a1$staffCONred, mydta5a1$staffCNSred), group=rep(c("Junior Docto
rs (Unit)", "GO Sub-specialty (Unit)", "Consultant (Unit)", "CNS (Unit)"),
each=nrow(mydta5a1)))

#mygplotdta0 <- data.frame(reduction=c(mydta5a0$staffJDred,mydta5a0$staffGO
red, mydta5a0$staffCONred, mydta5a0$staffCNSred), group=rep(c("Junior Docto
rs (Centre)", "GO Sub-specialty (Centre)", "Consultant (Centre)", "CNS (Cen
tre)"), each=nrow(mydta5a0)))

#mygplotdta01<-rbind(mygplotdta0, mygplotdta1)
#mygplotdta01  <-  mygplotdta01[order(as.character(mygplotdta01$group)),]
#mygplotdta01$group <- factor(as.character(mygplotdta01$group))
```

Warning message:
"Removed 26 rows containing non-finite values (stat_boxplot)."
`stat_bindot()` using `bins = 30`. Pick better value with `binwidth`.

Warning message:
"Removed 26 rows containing non-finite values (stat_bindot)."

```
In [10]: ##########################
         ## centres vs units
         ##########################
         myord <- order(mydta4a$newname[!duplicated(mydta4a$newname)])
         t.inc <- mydta4a$centre[!duplicated(mydta4a$newname)][myord]=="Centre"
         mydta5a0 <- mydta5a[t.inc,]
         mydta5a1 <- mydta5a[!t.inc,]
         print("== Junior doctors ==")
         print("= Unit =")
         fn.summaryyes(mydta5a1$staffJDCOVID,mydta5a1$staffJDRedeploy, mydta5a1$staf
         fJDred)
         print("= Centre =")
         fn.summaryyes(mydta5a0$staffJDCOVID,mydta5a0$staffJDRedeploy, mydta5a0$staf
         fJDred)

         print("== GO Sub-specialty Trainee == ")
         print("= Unit =")
         fn.summaryyes(mydta5a1$staffGOCOVID, mydta5a1$staffGORedeploy, mydta5a1$sta
         ffGOred)
         print("= Centre =")
         fn.summaryyes(mydta5a0$staffGOCOVID, mydta5a0$staffGORedeploy, mydta5a0$sta
         ffGOred)

         print("== Consultant ==")
         print("= Unit =")
         fn.summaryyes(mydta5a1$staffGOCOVID,mydta5a1$staffGORedeploy, mydta5a1$staf
         fGOred)
         print("= Centre =")
         fn.summaryyes(mydta5a0$staffGOCOVID,mydta5a0$staffGORedeploy, mydta5a0$staf
         fGOred)
         print("== CNS ==")
         print("= Unit =")
         fn.summaryyes(mydta5a1$staffCNSCOVID,mydta5a1$staffCNSRedeploy, mydta5a1$st
         affCNSred)
         print("= Centre =")
         fn.summaryyes(mydta5a0$staffCNSCOVID,mydta5a0$staffCNSRedeploy, mydta5a0$st
         affCNSred)
```

```
[1] "== Junior doctors =="
[1] "= Unit ="
[1] "Number yes Covid: 5/8 (62%)"
[1] "Number yes redeploy: 4/8 (50%)"
[1] "cross tab"
     REDEPLOY
COVID 0 1 Sum
  0   2 1   3
  1   2 3   5
  Sum 4 4   8
[1] "individual responses: percentage reduction"
[1]  10  25  30  40  40 NaN
[1] "summary: percentage reduction"

  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    10      25      30      29      40      40       1

[1] "= Centre ="
[1] "Number yes Covid: 9/17 (53%)"
[1] "Number yes redeploy: 10/17 (59%)"
[1] "cross tab"
     REDEPLOY
COVID  0  1 Sum
  0    1  7   8
  1    6  3   9
  Sum  7 10  17
[1] "individual responses: percentage reduction"
 [1]  15.0  15.0  20.0  22.5  25.0  30.0  40.0  40.0  50.0  60.0 100.0 100.0
[13] 100.0 100.0 100.0 100.0
[1] "summary: percentage reduction"

  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 15.00   24.38   45.00   57.34  100.00  100.00

[1] "== GO Sub-specialty Trainee == "
[1] "= Unit ="
[1] "Number yes Covid: 0/8 (0%)"
[1] "Number yes redeploy: 1/8 (12%)"
[1] "cross tab"
     REDEPLOY
COVID 0 1 Sum
  0   7 1   8
  Sum 7 1   8
[1] "individual responses: percentage reduction"
[1] 30
[1] "summary: percentage reduction"

  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
    30      30      30      30      30      30

[1] "= Centre ="
[1] "Number yes Covid: 2/17 (12%)"
[1] "Number yes redeploy: 5/17 (29%)"
[1] "cross tab"
      REDEPLOY
COVID  0  1 Sum
  0   10  5  15
  1    2  0   2
  Sum 12  5  17
[1] "individual responses: percentage reduction"
[1] 100 100 100 100 100 100 100
[1] "summary: percentage reduction"

  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   100     100     100     100     100     100
```

```
[1] "== Consultant =="
[1] "= Unit ="
[1] "Number yes Covid: 0/8 (0%)"
[1] "Number yes redeploy: 1/8 (12%)"
[1] "cross tab"
     REDEPLOY
COVID 0 1 Sum
  0   7 1   8
  Sum 7 1   8
[1] "individual responses: percentage reduction"
[1] 30
[1] "summary: percentage reduction"

   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
     30      30      30      30      30      30

[1] "= Centre ="
[1] "Number yes Covid: 2/17 (12%)"
[1] "Number yes redeploy: 5/17 (29%)"
[1] "cross tab"
     REDEPLOY
COVID  0  1 Sum
  0   10  5  15
  1    2  0   2
  Sum 12  5  17
[1] "individual responses: percentage reduction"
[1] 100 100 100 100 100 100 100
[1] "summary: percentage reduction"

   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
    100     100     100     100     100     100

[1] "== CNS =="
[1] "= Unit ="
[1] "Number yes Covid: 4/8 (50%)"
[1] "Number yes redeploy: 6/8 (75%)"
[1] "cross tab"
     REDEPLOY
COVID 0 1 Sum
  0   1 3   4
  1   1 3   4
  Sum 2 6   8
[1] "individual responses: percentage reduction"
[1]  20  20  40  50  80 NaN NaN
[1] "summary: percentage reduction"

   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
     20      20      40      42      50      80       2

[1] "= Centre ="
[1] "Number yes Covid: 5/17 (29%)"
[1] "Number yes redeploy: 8/17 (47%)"
[1] "cross tab"
     REDEPLOY
COVID  0  1 Sum
  0    8  4  12
  1    1  4   5
  Sum  9  8  17
[1] "individual responses: percentage reduction"
[1]  1.0 16.5 20.0 25.0 30.0 30.0 50.0 62.5 75.0
[1] "summary: percentage reduction"

   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   1.00   20.00   30.00   34.44   50.00   75.00
```

```
In [11]:  # sub group
          mygplotdta1 <- data.frame(reduction=c(mydta5a1$staffJDred,mydta5a1$staffGOr
          ed, mydta5a1$staffCONred, mydta5a1$staffCNSred), group=rep(c("Junior Doctor
          s (Unit)", "GO Sub-specialty (\
          Unit)", "Consultant (Unit)", "CNS (Unit)"), each=nrow(mydta5a1)))

          mygplotdta0 <- data.frame(reduction=c(mydta5a0$staffJDred,mydta5a0$staffGOr
          ed, mydta5a0$staffCONred, mydta5a0$staffCNSred), group=rep(c("Junior Doctor
          s (Centre)", "GO Sub-specialty\
           (Centre)", "Consultant (Centre)", "CNS (Centre)"), each=nrow(mydta5a0)))


          mygplotdta01<-rbind(mygplotdta0, mygplotdta1)
          mygplotdta01  <-  mygplotdta01[order(as.character(mygplotdta01$group)),]
          mygplotdta01$group <- factor(as.character(mygplotdta01$group))

          p <- ggplot(mygplotdta01, aes(x=group, y=reduction)) +
              geom_boxplot()+
            geom_dotplot(binaxis='y', stackdir='center', dotsize=.7)

          p
```

Warning message:
"Removed 26 rows containing non-finite values (stat_boxplot)."
`stat_bindot()` using `bins = 30`. Pick better value with `binwidth`.

Warning message:
"Removed 26 rows containing non-finite values (stat_bindot)."
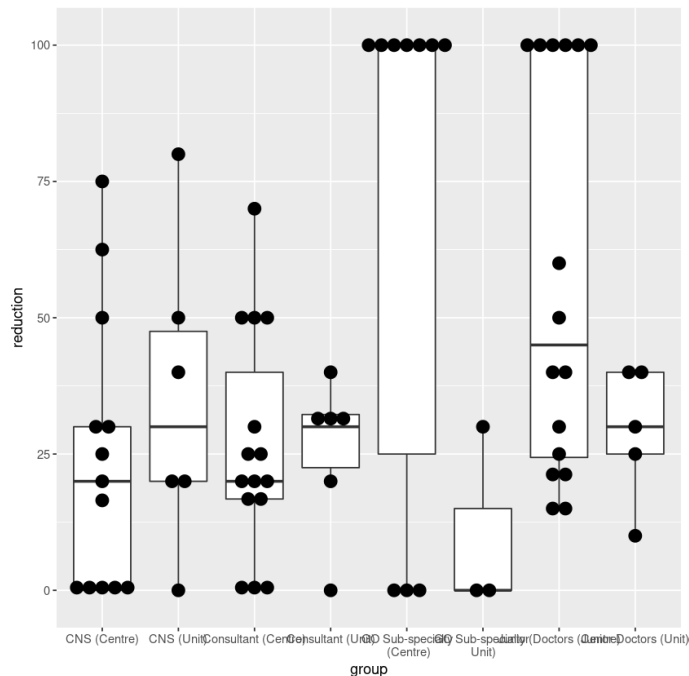
MDT changes

```
mymdtchange <- tapply(as.character(mydta3$MDTchange), mydta3$newname, funct
ion(ind) mean(ind=="Yes"))

print(paste("Number centres with change to MDT:", sum(mymdtchange), "/", le
ngth(mymdtchange)))

mycentre <- tapply(mydta3$centre, mydta3$newname, function(ind) ind[1])

mymdtchangevirtual <- tapply(mydta3$MDTvirual, mydta3$newname, mean) >0.1

mymdtchangevirtualF2F <- tapply(mydta3$MDTvirualF2F, mydta3$newname, mean)
>0.1

mymdtchangesuspend <- tapply(mydta3$MDTsuspend, mydta3$newname, mean) >0.1

mymdtchangeMDTlessfreq <- tapply(mydta3$MDTlessfreq, mydta3$newname, mean)
>0.1

mymdtchangeMDTlessattd <- tapply(mydta3$MDTlessattd, mydta3$newname, mean)
>0

##sensitivity analysis -- opposite
##mymdtchangevirtual <- tapply(mydta3$MDTvirual, mydta3$newname, mean) == 1

##mymdtchangevirtualF2F <- tapply(mydta3$MDTvirualF2F, mydta3$newname, mea
n) == 1

##mymdtchangesuspend <- tapply(mydta3$MDTsuspend, mydta3$newname, mean) ==
1

##mymdtchangeMDTlessfreq <- tapply(mydta3$MDTlessfreq, mydta3$newname, mea
n) == 1

##mymdtchangeMDTlessattd <- tapply(mydta3$MDTlessattd, mydta3$newname, mea
n) == 1

mysumdtaMDT <- data.frame(centre=mycentre, virtual=mymdtchangevirtual, virt
ualF2F=mymdtchangevirtualF2F, suspend=mymdtchangesuspend, lessfreq=mymdtcha
ngeMDTlessfreq, lessattd=mymdtchangeMDTlessattd)

fn.sumstatMDT1 <- function(mysumdtaMDT){

    paste(fn.format(colSums(mysumdtaMDT)[2:6],0), "/", nrow(mysumdtaMDT), "
(",
          fn.format(colMeans(mysumdtaMDT)[2:6]*100,0), "%)", sep="")

}

mysumMDT.all <- cbind(c("Virtual MDT", "Mixed virual F2F", "Less freq", "Su
spend", "Less Attd"), fn.sumstatMDT1(mysumdtaMDT))

##unit
mysumdtaMDT.unit <- mysumdtaMDT[mysumdtaMDT$centre==2,]

mysumMDT.unit <- cbind(c("Virtual MDT", "Mixed virual F2F", "Less freq", "S
uspend", "Less Attd"), fn.sumstatMDT1(mysumdtaMDT.unit))

##centre
mysumdtaMDT.centre <- mysumdtaMDT[mysumdtaMDT$centre==1,]

mysumMDT.centre <- cbind(c("Virtual MDT", "Mixed virual F2F", "Less freq",
"Suspend", "Less Attd"), fn.sumstatMDT1(mysumdtaMDT.centre))

mysumMDT.sum <- cbind(mysumMDT.all, mysumMDT.unit[,2], mysumMDT.centre[,2])

colnames(mysumMDT.sum) <- c("Type", "All", "Unit", "Centre")

mysumMDT.sum
```

[1] "Number centres with change to MDT: 51 / 51"

A matrix: 5 × 4 of type chr

Type	All	Unit	Centre
Virtual MDT	20/51 (39%)	5/19 (26%)	15/32 (47%)
Mixed virual F2F	33/51 (65%)	13/19 (68%)	20/32 (62%)
Less freq	0/51 (0%)	0/19 (0%)	0/32 (0%)
Suspend	0/51 (0%)	0/19 (0%)	0/32 (0%)
Less Attd	21/51 (41%)	6/19 (32%)	15/32 (47%)

```
In [13]:  #### reduced percentage attendees
          mysumdtaMDT$redperc <- tapply(mydta3$redperc, mydta3$newname, mean, na.rm=T
          RUE)
          mysumdtaMDT$centre2<-as.factor(c("Centre", "Unit")[mysumdtaMDT$centre])
          mean(rowSums(mysumdtaMDT[,2:6])>0)

          p <- ggplot(mysumdtaMDT, aes(x=centre2, y=redperc)) +
              geom_boxplot()+
            geom_dotplot(binaxis='y', stackdir='center', dotsize=.7)

          tapply(mysumdtaMDT$redperc, mysumdtaMDT$centre2, summary)
          p
```

0.980392156862745

```
$Centre
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.00    0.00   15.00   24.35   50.00   75.00       5

$Unit
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  0.000   0.000   0.000   9.438  17.000  50.000       3
```

```
Warning message:
"Removed 8 rows containing non-finite values (stat_boxplot)."
`stat_bindot()` using `bins = 30`. Pick better value with `binwidth`.
```

```
Warning message:
"Removed 8 rows containing non-finite values (stat_bindot)."
```
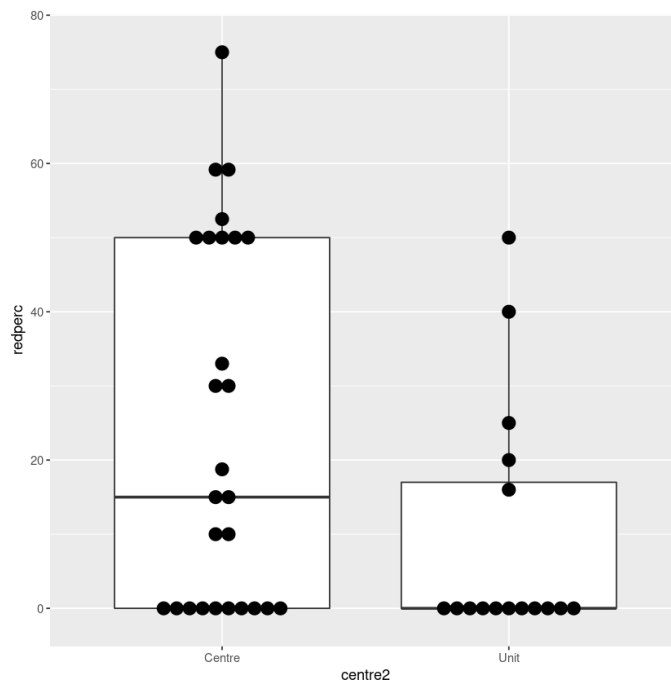
```
##What proportion of your out-patient clinic is remote consultation (teleph
one/ video)

mysumdtaMDT$outpatientremote <- tapply(mydta3$outpatientremote, mydta3$newn
ame, mean, na.rm=TRUE)

p <- ggplot(mysumdtaMDT, aes(x=centre2, y=outpatientremote)) +
    geom_boxplot()+
  geom_dotplot(binaxis='y', stackdir='center', dotsize=.7)

p

summary(mysumdtaMDT$outpatientremote)

tapply(mysumdtaMDT$outpatientremote, mysumdtaMDT$centre2, summary)
```

```
Warning message:
"Removed 2 rows containing non-finite values (stat_boxplot)."
`stat_bindot()` using `bins = 30`. Pick better value with `binwidth`.

Warning message:
"Removed 2 rows containing non-finite values (stat_bindot)."

   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   2.00   50.00   75.00   66.37   87.50   95.00       2

$Centre
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  25.00   50.00   74.38   68.51   86.88   95.00       2

$Unit
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
      2      50      75      63      85      95
```
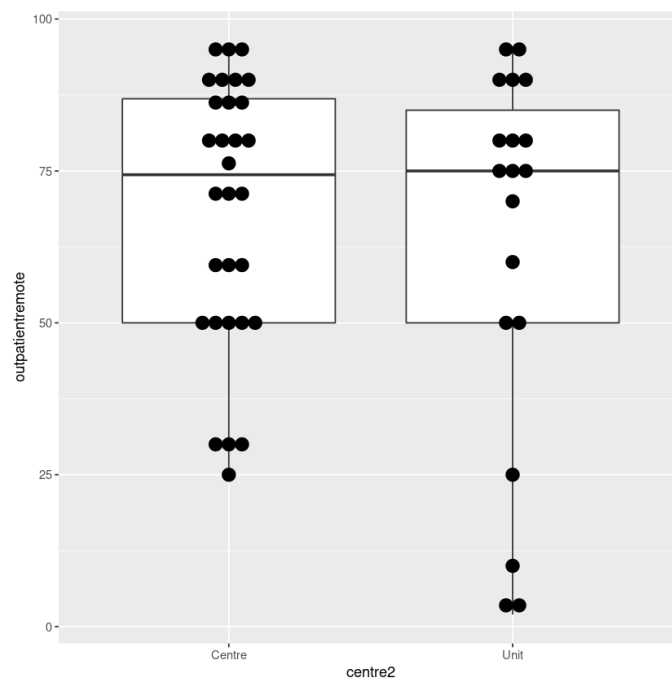

Re theatre time, how much reduction in theatre time has occurred? (If not reduced enter '0')

```r
In [15]: fn.sumpercavg <- function(colidx){

    thisstat <- tapply(mydta3[,colidx], mydta3$newname, mean, na.rm=TRUE)

    return(thisstat)

    }

fn.summarystat <- function(percentage, subgroup){
    p <- ggplot(mysumdtaMDT, aes(x=subgroup, y=percentage)) +
        geom_boxplot()+
        geom_dotplot(binaxis='y', stackdir='center', dotsize=.7)


    thissum <- summary(percentage)

    thissum2 <- tapply(percentage, subgroup, summary)

    return(list(p, thissum, thissum2))

}

mysumdtaMDT$theatrered <- fn.sumpercavg(26)

stat.theatrered <- fn.summarystat(mysumdtaMDT$theatrered, mysumdtaMDT$centr
e2)

stat.theatrered[[1]]

print("Summary overall")

stat.theatrered[[2]]

print("By centre / unit")

stat.theatrered[[3]]

 p <- ggplot(mysumdtaMDT, aes(x=centre2, y=theatrered)) +
        geom_boxplot()+
        geom_dotplot(binaxis='y', stackdir='center', dotsize=.7) +
        xlab("Site type")+
        ylab("Percentage reduced (%)")

tiff("output/theatretimereduced.tiff", units="in", width=5, height=5, res=2
00)
p
dev.off()

wilcox.test(split(mysumdtaMDT$theatrered,mysumdtaMDT$centre2)[[1]],split(my
sumdtaMDT$theatrered,mysumdtaMDT$centre2)[[2]])
```

Warning message:
"Removed 6 rows containing non-finite values (stat_boxplot)."
`stat_bindot()` using `bins = 30`. Pick better value with `binwidth`.

Warning message:
"Removed 6 rows containing non-finite values (stat_bindot)."

[1] "Summary overall"

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.00   20.00   40.00   43.62   70.00  100.00       6
```

[1] "By centre / unit"

```
$Centre
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.00   12.50   30.00   34.64   55.00   92.00       5

$Unit
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.00   32.50   60.00   57.08   87.50  100.00       1
```

Warning message:
"Removed 6 rows containing non-finite values (stat_boxplot)."
`stat_bindot()` using `bins = 30`. Pick better value with `binwidth`.

Warning message:
"Removed 6 rows containing non-finite values (stat_bindot)."

png: 2

Warning message in wilcox.test.default(split(mysumdtaMDT$theatrered, mysumdt
aMDT$centre2)[[1]], :
"cannot compute exact p-value with ties"

```
        Wilcoxon rank sum test with continuity correction

data:  split(mysumdtaMDT$theatrered, mysumdtaMDT$centre2)[[1]] and split(mys
umdtaMDT$theatrered, mysumdtaMDT$centre2)[[2]]
W = 145, p-value = 0.02314
alternative hypothesis: true location shift is not equal to 0
```
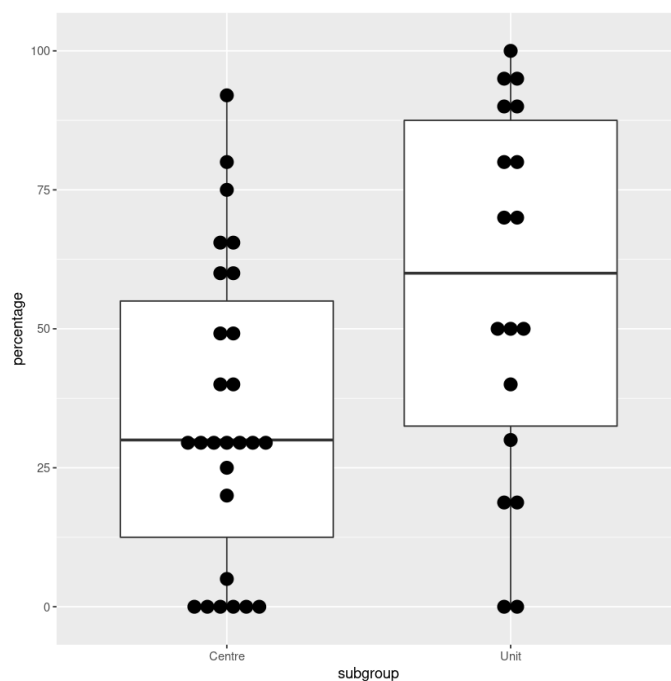
What is the proportion of surgical cases postponed (if no cases postponed, enter '0')

In [16]:
```
mysumdtaMDT$surgcasered <- fn.sumpercavg(27)

stat.surgcasered <- fn.summarystat(mysumdtaMDT$surgcasered, mysumdtaMDT$cen
tre2)

stat.surgcasered[[1]]

print("Overall")

stat.surgcasered[[2]]

print("Centre / Unit")

stat.surgcasered[[3]]
```

```
Warning message:
"Removed 9 rows containing non-finite values (stat_boxplot)."
`stat_bindot()` using `bins = 30`. Pick better value with `binwidth`.

Warning message:
"Removed 9 rows containing non-finite values (stat_bindot)."

[1] "Overall"
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.00   16.25   30.00   37.54   56.75  100.00       9

[1] "Centre / Unit"

$Centre
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.00   16.25   30.00   35.06   50.00  100.00       6

$Unit
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.00   16.25   35.00   41.56   72.50  100.00       3
```
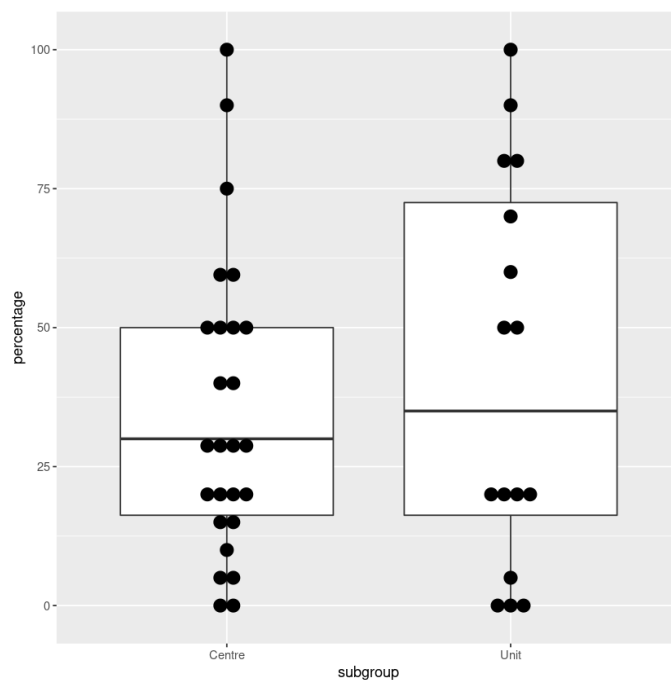
Re Medical Oncology access/capacity, how much is this reduced by? (If not reduced enter '0', If unknown enter NK)

In [17]:
```
mysumdtaMDT$medoncred <- fn.sumpercavg(28)

stat.medoncred <- fn.summarystat(mysumdtaMDT$medoncred, mysumdtaMDT$centre
2)

stat.medoncred[[1]]

print("Overall")

stat.medoncred[[2]]

print("Centre / Unit")

stat.medoncred[[3]]
```

```
Warning message:
"Removed 28 rows containing non-finite values (stat_boxplot)."
`stat_bindot()` using `bins = 30`. Pick better value with `binwidth`.

Warning message:
"Removed 28 rows containing non-finite values (stat_bindot)."

[1] "Overall"
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.00    0.00    0.00   10.14    0.00   90.00      28

[1] "Centre / Unit"

$Centre
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.00    0.00    0.00   14.10   13.33   90.00      19

$Unit
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
      0       0       0       5       0      50       9
```
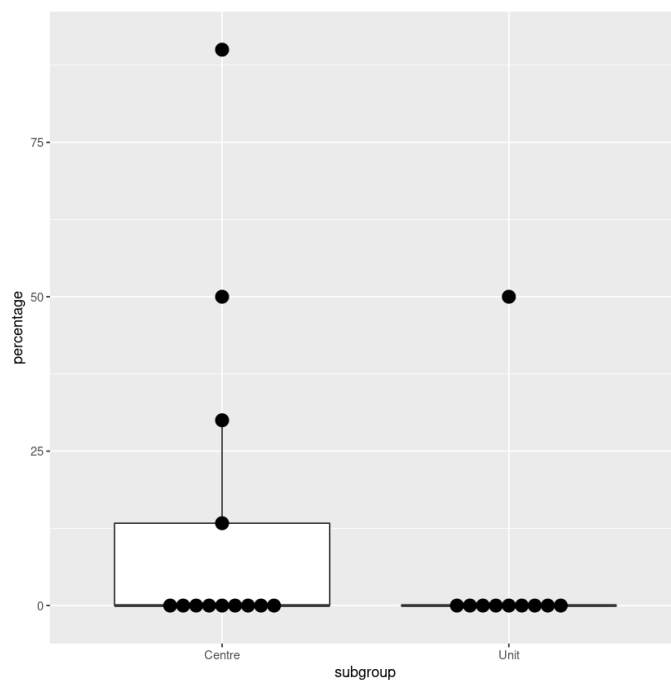
Re Clinical Oncology access/capacity, how much is this reduced by? (If not reduced enter '0', If unknown enter NK)

In [18]:
```
mysumdtaMDT$clinoncred <- fn.sumpercavg(29)

stat.clinoncred <- fn.summarystat(mysumdtaMDT$clinoncred, mysumdtaMDT$centr
e2)

stat.clinoncred[[1]]

print("Overall")

stat.clinoncred[[2]]

print("Centre / Unit")

stat.clinoncred[[3]]
```

```
Warning message:
"Removed 27 rows containing non-finite values (stat_boxplot)."
`stat_bindot()` using `bins = 30`. Pick better value with `binwidth`.

Warning message:
"Removed 27 rows containing non-finite values (stat_bindot)."

[1] "Overall"
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  0.000   0.000   0.000   9.771   8.125 100.000      27

[1] "Centre / Unit"

$Centre
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.00    0.00    0.00   14.88   10.00  100.00      19

$Unit
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  0.000   0.000   0.000   3.727   0.500  30.000       8
```
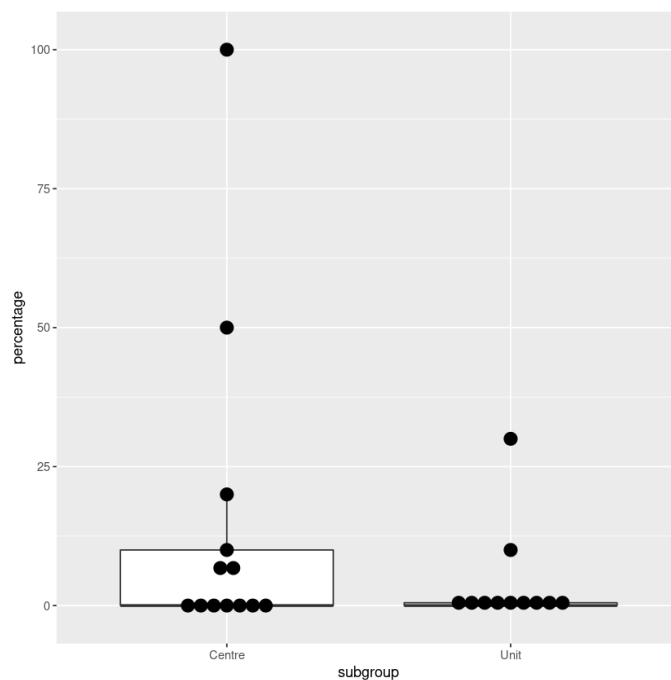
Re Radiology access/capacity, how much is this reduced by? (If not reduced enter '0', If unknown enter NK)

In [19]:
```
##
mysumdtaMDT$radiored <- fn.sumpercavg(30)

stat.radiored <- fn.summarystat(mysumdtaMDT$radiored, mysumdtaMDT$centre2)

stat.radiored[[1]]

print("Overall")

stat.radiored[[2]]

print("Centre / Unit")

stat.radiored[[3]]
```

```
Warning message:
"Removed 19 rows containing non-finite values (stat_boxplot)."
`stat_bindot()` using `bins = 30`. Pick better value with `binwidth`.

Warning message:
"Removed 19 rows containing non-finite values (stat_bindot)."

[1] "Overall"

  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
 0.000   0.000   0.000   9.375  10.000 100.000      19

[1] "Centre / Unit"

$Centre
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  0.00    0.00    0.00   14.74   17.50  100.00      13

$Unit
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
 0.000   0.000   0.000   1.538   0.000  20.000       6
```
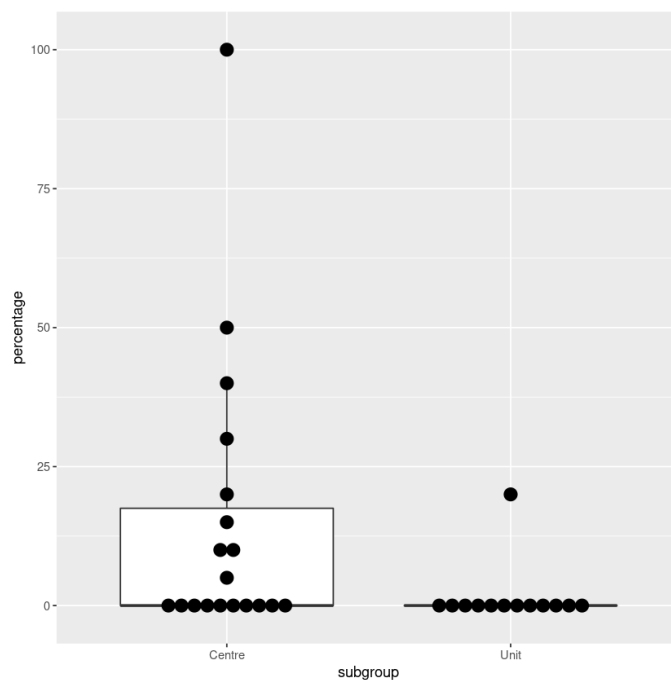
Re Pathology access/capacity, how much is this reduced by? (If not reduced enter '0', If unknown enter NK)

In [20]:
```
##
mysumdtaMDT$pathred <- fn.sumpercavg(31)

stat.pathred <- fn.summarystat(mysumdtaMDT$pathred, mysumdtaMDT$centre2)

stat.pathred[[1]]

print("Overall")

stat.pathred[[2]]

print("Centre / Unit")

stat.pathred[[3]]
```

```
Warning message:
"Removed 15 rows containing non-finite values (stat_boxplot)."
`stat_bindot()` using `bins = 30`. Pick better value with `binwidth`.

Warning message:
"Removed 15 rows containing non-finite values (stat_bindot)."

[1] "Overall"

   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  0.000   0.000   0.000   4.306   0.000 100.000      15

[1] "Centre / Unit"

$Centre
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  0.000   0.000   0.000   5.952   0.000 100.000      11

$Unit
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
      0       0       0       2       0      30       4
```
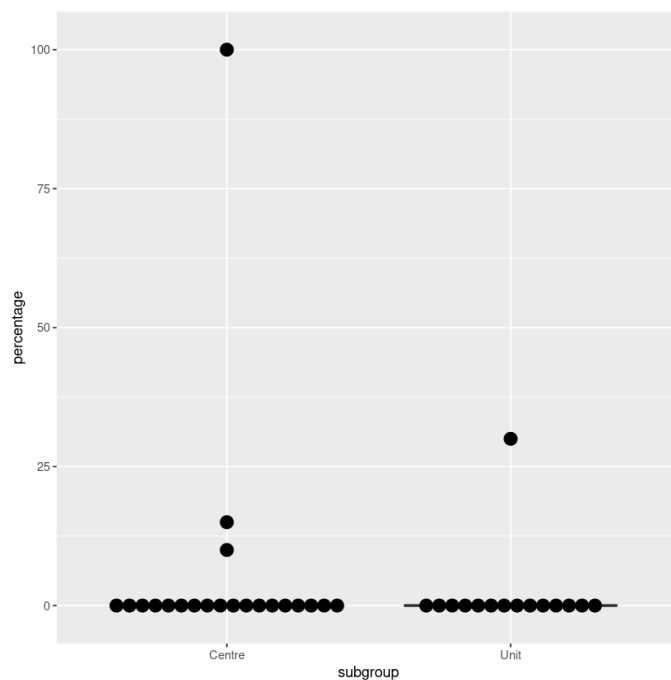
Re Palliative care access/capacity, how much is this reduced by? (If not reduced enter '0', If unknown enter NK)

```
In [21]: mysumdtaMDT$pallcapred <- fn.sumpercavg(32)

         stat.pallcapred <- fn.summarystat(mysumdtaMDT$pallcapred, mysumdtaMDT$centr
         e2)

         stat.pallcapred[[1]]

         print("Overall")

         stat.pallcapred[[2]]

         print("Centre / Unit")

         stat.pallcapred[[3]]
```

```
Warning message:
"Removed 28 rows containing non-finite values (stat_boxplot)."
`stat_bindot()` using `bins = 30`. Pick better value with `binwidth`.

Warning message:
"Removed 28 rows containing non-finite values (stat_bindot)."

[1] "Overall"

   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  0.000   0.000   0.000   4.348   0.000 100.000      28

[1] "Centre / Unit"

$Centre
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  0.000   0.000   0.000   6.667   0.000 100.000      17

$Unit
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
      0       0       0       0       0       0      11
```
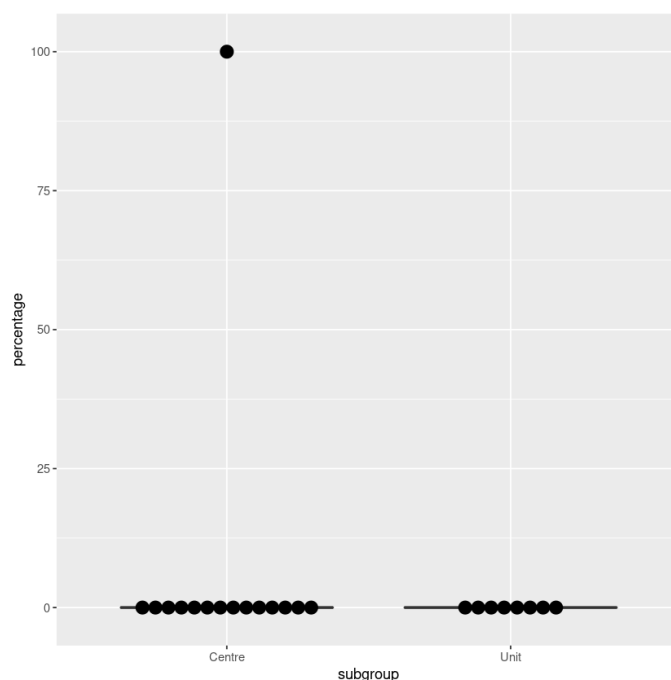
How much have your gynaecological oncology rapid access referrals dropped by (%)? (If not reduced enter '0')

In [22]:
```
mysumdtaMDT$gonvrred <- fn.sumpercavg(33)

stat.gonvrred <- fn.summarystat(mysumdtaMDT$gonvrred, mysumdtaMDT$centre2)

stat.gonvrred[[1]]

print("Overall")

stat.gonvrred[[2]]

print("Centre / Unit")

stat.gonvrred[[3]]
```

```
Warning message:
"Removed 10 rows containing non-finite values (stat_boxplot)."
`stat_bindot()` using `bins = 30`. Pick better value with `binwidth`.

Warning message:
"Removed 10 rows containing non-finite values (stat_bindot)."
```

```
[1] "Overall"

   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.00   25.00   50.00   46.22   70.00   80.00      10

[1] "Centre / Unit"

$Centre
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    0.0    30.0    50.0    48.4    70.0    80.0       7

$Unit
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  10.00   17.50   45.00   42.81   62.50   80.00       3
```
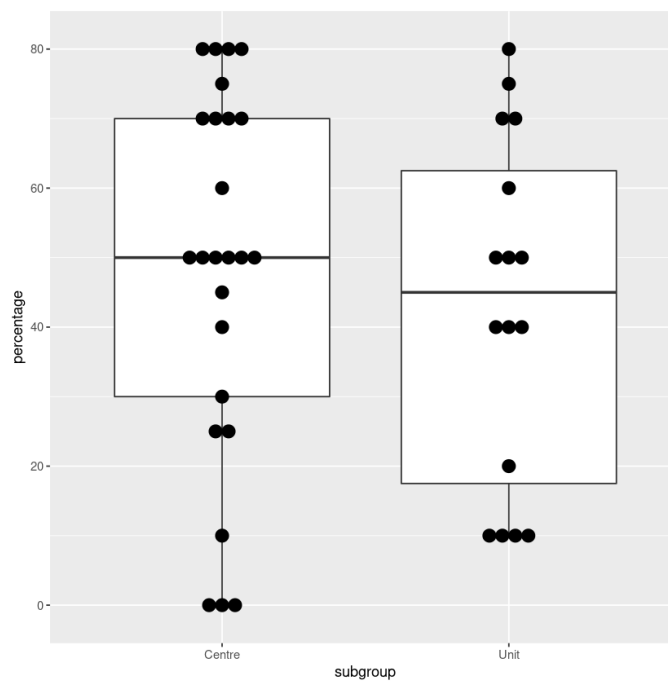
How much has your weekly MDT list/workload reduced by? (If not reduced enter '0')

```
In [23]: mysumdtaMDT$mdtworkred <- fn.sumpercavg(34)

stat.mdtworkred <- fn.summarystat(mysumdtaMDT$mdtworkred, mysumdtaMDT$centr
e2)

stat.mdtworkred[[1]]

print("Overall")

stat.mdtworkred[[2]]

print("Centre / Unit")

stat.mdtworkred[[3]]
```

```
Warning message:
"Removed 5 rows containing non-finite values (stat_boxplot)."
`stat_bindot()` using `bins = 30`. Pick better value with `binwidth`.

Warning message:
"Removed 5 rows containing non-finite values (stat_bindot)."
```

```
[1] "Overall"

   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.00    2.50   22.50   25.35   47.50   80.00       5

[1] "Centre / Unit"

$Centre
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.00   14.06   27.50   28.62   50.00   80.00       4

$Unit
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.00    0.00   20.00   20.28   30.00   50.00       1
```
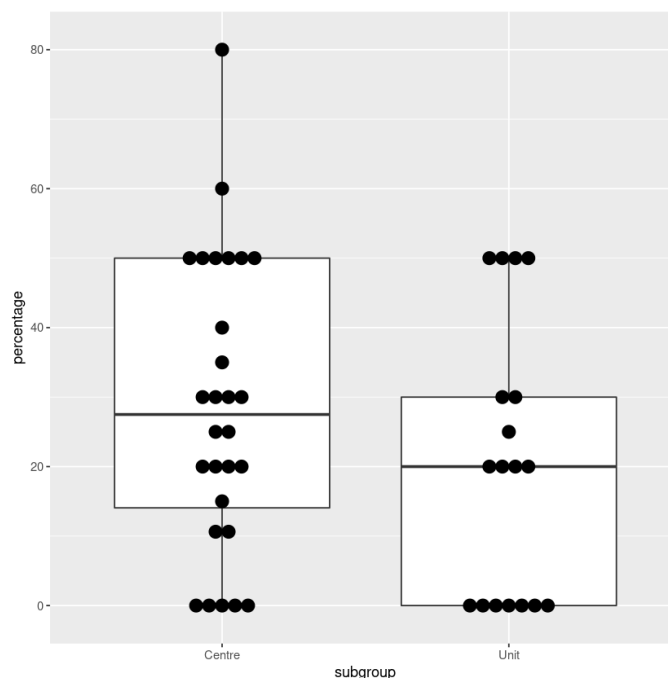
Have you needed to move activity off site to another hospital (e.g. Independent sector)

```r
mysumdtaMDT$movepperlist <- tapply(mydta3$movepperlist, mydta3$newname, mean) >0.1

mysumdtaMDT$moveclinic <- tapply(mydta3$moveclinic, mydta3$newname, mean) > 0.1

mysumdtaMDT$moveotheractivity <- tapply(mydta3$moveotheractivity, mydta3$newname, mean) >0.1

mysumdtaMDT$movenotyet <- tapply(mydta3$movenotyet, mydta3$newname, mean) > 0.1

mysumdtaMDT$centralhub <- tapply(mydta3$centralhub, mydta3$newname, mean) > 0.1

mysumdtaMDT$minaccesssurg <- tapply(mydta3$minaccesssurg, mydta3$newname, mean) >0.1

##sensitivity analysis -- do other way around (no is dominant)
##mysumdtaMDT$movepperlist <- tapply(mydta3$movepperlist, mydta3$newname, mean) ==1

##mysumdtaMDT$moveclinic <- tapply(mydta3$moveclinic, mydta3$newname, mean) ==1

##mysumdtaMDT$moveotheractivity <- tapply(mydta3$moveotheractivity, mydta3$newname, mean) ==1

##mysumdtaMDT$movenotyet <- tapply(mydta3$movenotyet, mydta3$newname, mean) == 1

##mysumdtaMDT$centralhub <- tapply(mydta3$centralhub, mydta3$newname, mean) == 1

##mysumdtaMDT$minaccesssurg <- tapply(mydta3$minaccesssurg, mydta3$newname, mean) ==1


fn.sumstatMDT2 <- function(mysumdtaMDT){

    paste(fn.format(colSums(mysumdtaMDT[,19:24], na.rm=TRUE),0), "/",
        colSums(!is.na(mysumdtaMDT[,19:24])), " (",
        fn.format(colMeans(mysumdtaMDT[,19:24], na.rm=TRUE)*100,0), "%)",
sep="")

}

mysumMDT.all2 <- cbind(c("Move Op list", "Move clinic", "Move other", "Not yet moved", "Central hub", "Min access surgery"), fn.sumstatMDT2(mysumdtaMDT))

##unit
mysumdtaMDT2.unit <- mysumdtaMDT[mysumdtaMDT$centre==2,]

mysumMDT.unit2 <- cbind(c("Move Op list", "Move clinic", "Move other", "Not yet moved", "Central hub", "Min access surgery"), fn.sumstatMDT2(mysumdtaMDT2.unit))


##centre
mysumdtaMDT2.centre <- mysumdtaMDT[mysumdtaMDT$centre==1,]

mysumMDT.centre2 <- cbind(c("Move Op list", "Move clinic", "Move other", "Not yet moved", "Central hub", "Min access surgery"), fn.sumstatMDT2(mysumdtaMDT2.centre))


mysumMDT.sum2 <- cbind(mysumMDT.all2, mysumMDT.unit2[,2], mysumMDT.centre2
```

A matrix: 6 × 4 of type chr

Type	All	Unit	Centre
Move Op list	23/41 (56%)	9/19 (47%)	14/22 (64%)
Move clinic	6/40 (15%)	2/19 (11%)	4/21 (19%)
Move other	8/38 (21%)	5/18 (28%)	3/20 (15%)
Not yet moved	3/29 (10%)	2/16 (12%)	1/13 (8%)
Central hub	15/39 (38%)	5/18 (28%)	10/21 (48%)
Min access surgery	30/41 (73%)	11/19 (58%)	19/22 (86%)

```
In [25]:  write.csv(file="output/centrelevelsummary.csv", mysumdtaMDT)
```

```
fn.nperc <- function(in1, in2, ndig=0){
    paste(in1, "/", in2, " (", fn.format(in1/in2*100,ndig), "%)", sep="")
}

fn.summaryyes.2 <- function(inyes1, inyes2, inperc){

    out1 <- paste(sum(inyes1), "/", length(inyes1), " (", fn.format(sum(iny
es1)/length(inyes1)*100,0), "%)", sep="")

    out2 <- paste(sum(inyes2), "/", length(inyes2), " (", fn.format(sum(iny
es2)/length(inyes2)*100,0), "%)", sep="")

    out3.i <- c(median(inperc[inyes1==1 | inyes2==1], na.rm=TRUE), quantile
(inperc[inyes1==1 | inyes2==1], c(0.25, 0.75), na.rm=TRUE))

    out3 <- paste(round(out3.i[1],0), "% (", round(out3.i[2],0), "-", round
(out3.i[3]), ")[", sum(is.na(inperc[inyes1==1 | inyes2==1])), "]", sep="")

    c(out1, out2, out3)

    }

tab1.redstaff <- c(table(mydta4au$centre), table(mydta4bu$centre))

t1.row1 <- c(fn.nperc(tab1.redstaff[1]+tab1.redstaff[2], sum(tab1.redstaf
f)),"", "",
            fn.nperc(tab1.redstaff[2], tab1.redstaff[2]+tab1.redstaff[4]),
"", "",
            fn.nperc(tab1.redstaff[1], tab1.redstaff[1]+tab1.redstaff
[3]),"", "")

##junior docs
t1.row2 <- c(fn.summaryyes.2(mydta5a$staffJDCOVID,mydta5a$staffJDRedeploy,
mydta5a$staffJDred),
fn.summaryyes.2(mydta5a1$staffJDCOVID,mydta5a1$staffJDRedeploy, mydta5a1$st
affJDred), ##unit
fn.summaryyes.2(mydta5a0$staffJDCOVID,mydta5a0$staffJDRedeploy, mydta5a0$st
affJDred)) ##centre

##GO subspec
t1.row3 <- c(fn.summaryyes.2(mydta5a$staffGOCOVID,mydta5a$staffGORedeploy,
mydta5a$staffGOred),
fn.summaryyes.2(mydta5a1$staffGOCOVID,mydta5a1$staffGORedeploy, mydta5a1$st
affGOred), ##unit
fn.summaryyes.2(mydta5a0$staffGOCOVID,mydta5a0$staffGORedeploy, mydta5a0$st
affGOred)) ##centre

## consultant
##Const subspec
t1.row4 <- c(fn.summaryyes.2(mydta5a$staffConstCOVID,mydta5a$staffConstRede
ploy, mydta5a$staffCONred),
fn.summaryyes.2(mydta5a1$staffConstCOVID,mydta5a1$staffConstRedeploy, mydta
5a1$staffCONred), ##unit
fn.summaryyes.2(mydta5a0$staffConstCOVID,mydta5a0$staffConstRedeploy, mydta
5a0$staffCONred)) ##centre

##CNS
t1.row5 <- c(fn.summaryyes.2(mydta5a$staffCNSCOVID,mydta5a$staffCNSRedeplo
y, mydta5a$staffCNSred),
fn.summaryyes.2(mydta5a1$staffCNSCOVID,mydta5a1$staffCNSRedeploy, mydta5a
1$staffCNSred), ##unit
fn.summaryyes.2(mydta5a0$staffCNSCOVID,mydta5a0$staffCNSRedeploy, mydta5a
0$staffCNSred)) ##centre

t1a<-rbind(t1.row1, t1.row2, t1.row3, t1.row4, t1.row5)

t1a.labels <- c("Reduction staff", "Junior doc", "GO Sub-spec", "Consultan
t", "CNS")
```

A matrix: 5 × 10 of type chr

	Item	COVID (All)	Redeployment (All)	% Reduced (All)	COVID (Unit)	Redeployment (Unit)	% Reduced (Unit)	COVID (Centre)	Redep
t1.row1	Reduction staff	25/51 (49%)			8/19 (42%)			17/32 (53%)	
t1.row2	Junior doc	14/25 (56%)	14/25 (56%)	40% (25-100)[1]	5/8 (62%)	4/8 (50%)	30% (25-40)[1]	9/17 (53%)	10/
t1.row3	GO Sub-spec	2/25 (8%)	6/25 (24%)	100% (100-100)[0]	0/8 (0%)	1/8 (12%)	30% (30-30)[0]	2/17 (12%)	5/
t1.row4	Consultant	17/25 (68%)	2/25 (8%)	28% (20-38)[1]	6/8 (75%)	0/8 (0%)	30% (30-33)[1]	11/17 (65%)	2/
t1.row5	CNS	9/25 (36%)	14/25 (56%)	30% (20-50)[2]	4/8 (50%)	6/8 (75%)	40% (20-50)[2]	5/17 (29%)	8/

A matrix: 26 × 4 of type chr

	Type	All	Unit	Centre
	(a) MDT functioning			
t2.row1	Implement change	51/51 (100%)	19/19 (100%)	32/32 (100%)
	Virtual MDT	20/51 (39%)	5/19 (26%)	15/32 (47%)
	Mixed virual F2F	33/51 (65%)	13/19 (68%)	20/32 (62%)
	Less freq	0/51 (0%)	0/19 (0%)	0/32 (0%)
	Suspend	0/51 (0%)	0/19 (0%)	0/32 (0%)
	Less Attd	21/51 (41%)	6/19 (32%)	15/32 (47%)
tab2.rednum	- how much less	40% (17-50)[2]	50% (16-52)[1]	25% (20-40)[1]
	Remote consulatation	75% (50-88)[2]	75% (50-85)[0]	74% (50-87)[2]
	(b) Reductions			
tab3.row2	Reduction theatre time	40% (20-70)[6]	60% (32-88)[1]	30% (12-55)[5]
tab3.row3	Postponed surgery	30% (16-57)[9]	35% (16-72)[3]	30% (16-50)[6]
tab3.row4	Med oncology	0% (0-0)[28]	0% (0-0)[9]	0% (0-13)[19]
tab3.row5	Clinical oncology	0% (0-8)[27]	0% (0-0)[8]	0% (0-10)[19]
tab3.row6	Radiology	0% (0-10)[19]	0% (0-0)[6]	0% (0-18)[13]
tab3.row7	Pathology	0% (0-0)[15]	0% (0-0)[4]	0% (0-0)[11]
tab3.row8	Palliative care	0% (0-0)[28]	0% (0-0)[11]	0% (0-0)[17]
tab3.row9	GO rapid access referrals	50% (25-70)[10]	45% (18-62)[3]	50% (30-70)[7]
tab3.row10	Weekly MDT list	22% (2-48)[5]	20% (0-30)[1]	28% (14-50)[4]
	(c) Move activity			
	Move Op list	23/41 (56%)	9/19 (47%)	14/22 (64%)
	Move clinic	6/40 (15%)	2/19 (11%)	4/21 (19%)
	Move other	8/38 (21%)	5/18 (28%)	3/20 (15%)
	Not yet moved	3/29 (10%)	2/16 (12%)	1/13 (8%)
	Central hub	15/39 (38%)	5/18 (28%)	10/21 (48%)
	Min access surgery	30/41 (73%)	11/19 (58%)	19/22 (86%)