

weekly_july4

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This is a RMDmarkdown to track and show progress between 20/07/22 ~ 27/07/22.

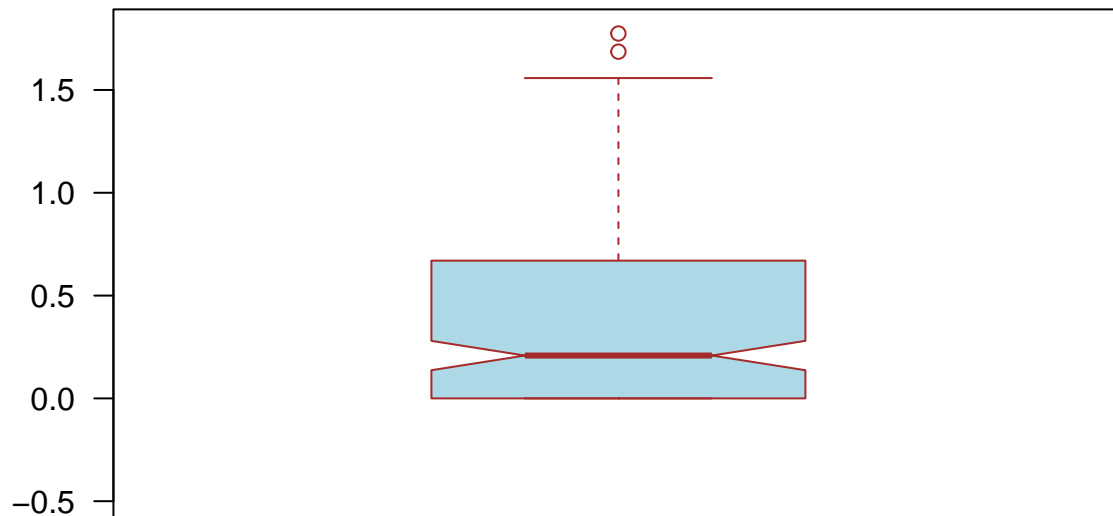
There are four things I would like to share with you.

1. I am now having most of my absolute subclonality estimations in the range [0,1].
2. Boxplot suggested by Oscar.
3. Timeplot of subclonality, purity and CT scan results mentioned by Solon.
4. liquidCNA vs ichorCNA (with results newly sent by Solon)

1. Absolute ratio [0,1]

```
boxplot(RECIST$rat,  
        ylim = c(-0.5, 1.8),  
        main = "Boxplot of all subclonality estimations",  
        las = 1,  
        col = c("lightblue"),  
        border = "brown",  
        horizontal = FALSE,  
        notch = TRUE)
```

Boxplot of all subclonality estimations



I was able to achieve this by changing the baseline samples; instead of always setting it to Sample1, I set the Sample with the lowest mean CNS to be the baseline.

2. Boxplot of subclonality for YES/NO Progression

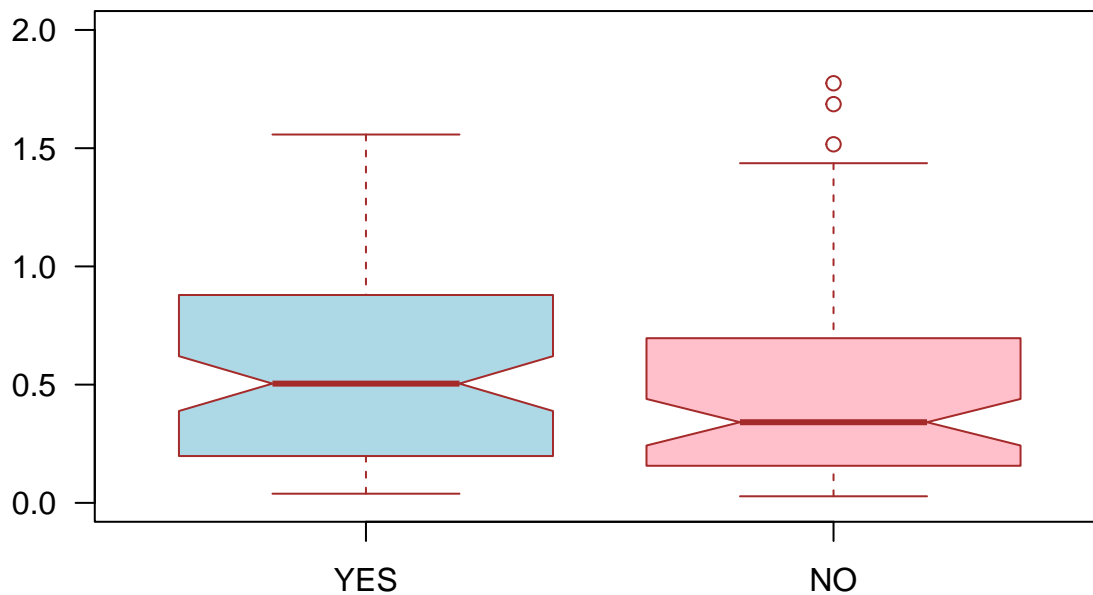
Subclonality:

```
#SUBCLONALITY X PROGRESSION!
na.or.base <- which(is.na(RECIST$rat) | RECIST$rat == 0)
RECIST.good <- RECIST[-na.or.base,]

yes.prog <- which(RECIST.good$Progression == "YES")

#
boxplot(RECIST.good[yes.prog,]$rat,
        RECIST.good[-yes.prog,]$rat,
        ylim = c(0, 2),
        main = "Subclonality estimation against progression",
        at = c(1,2),
        names = c("YES", "NO"),
        las = 1,
        col = c("lightblue", "pink"),
        border = "brown",
        horizontal = FALSE,
        notch = TRUE)
```

Subclonality estimation against progression



Fortunately, the boxplot shows an increase in sub-clonality with progression. However, this is less apparent for purity.

Purity:

```
#PURITY X PROGRESSION!
yes.prog <- which(RECIST.good$Progression == "YES")

#draw
```

```

boxplot(RECIST[yes.prog,]$purity_mean,
        RECIST[-yes.prog,]$purity_mean,
        ylim = c(0, 0.6),
        main = "Purity estimation against progression",
        at = c(1,2),
        names = c("YES", "NO"),
        las = 1,
        col = c("lightblue", "pink"),
        border = "brown",
        horizontal = FALSE,
        notch = TRUE)

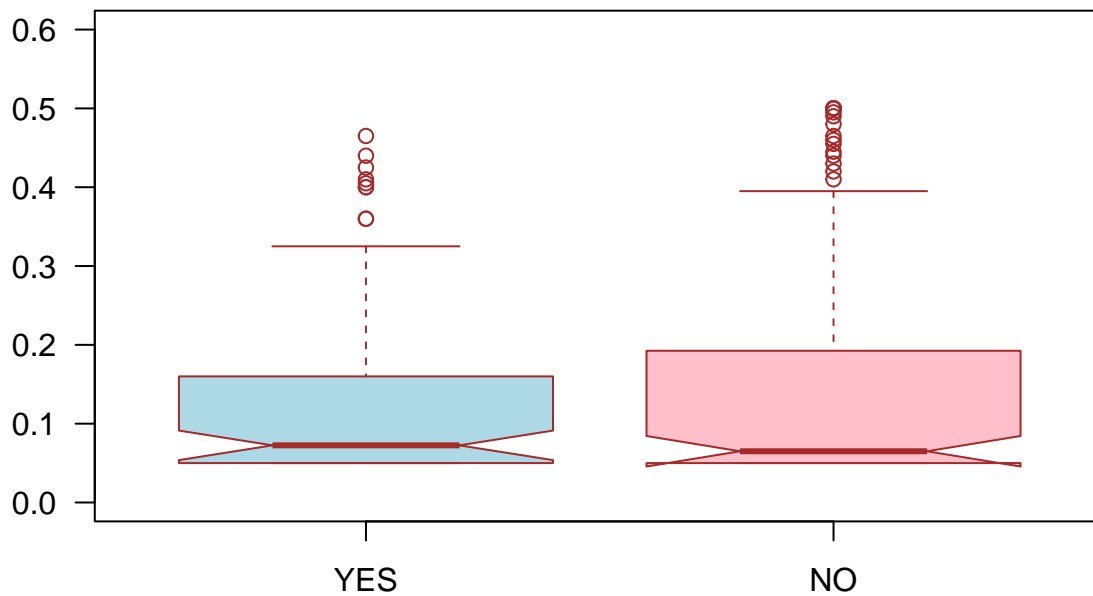
```

```

## Warning in (function (z, notch = FALSE, width = NULL, varwidth = FALSE, : some
## notches went outside hinges ('box'): maybe set notch=FALSE

```

Purity estimation against progression



3. Timeplot of subclonality, purity and CT scan result

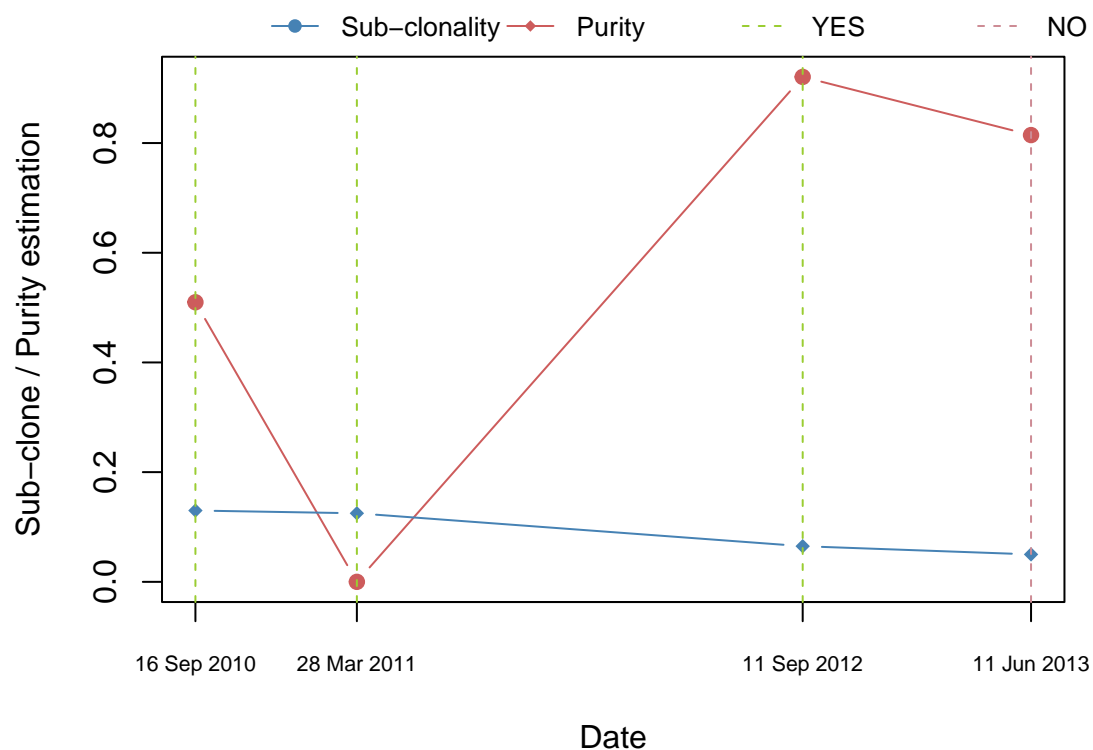
Here are two examples:

```

plot.estimation.w.RECIST(2)

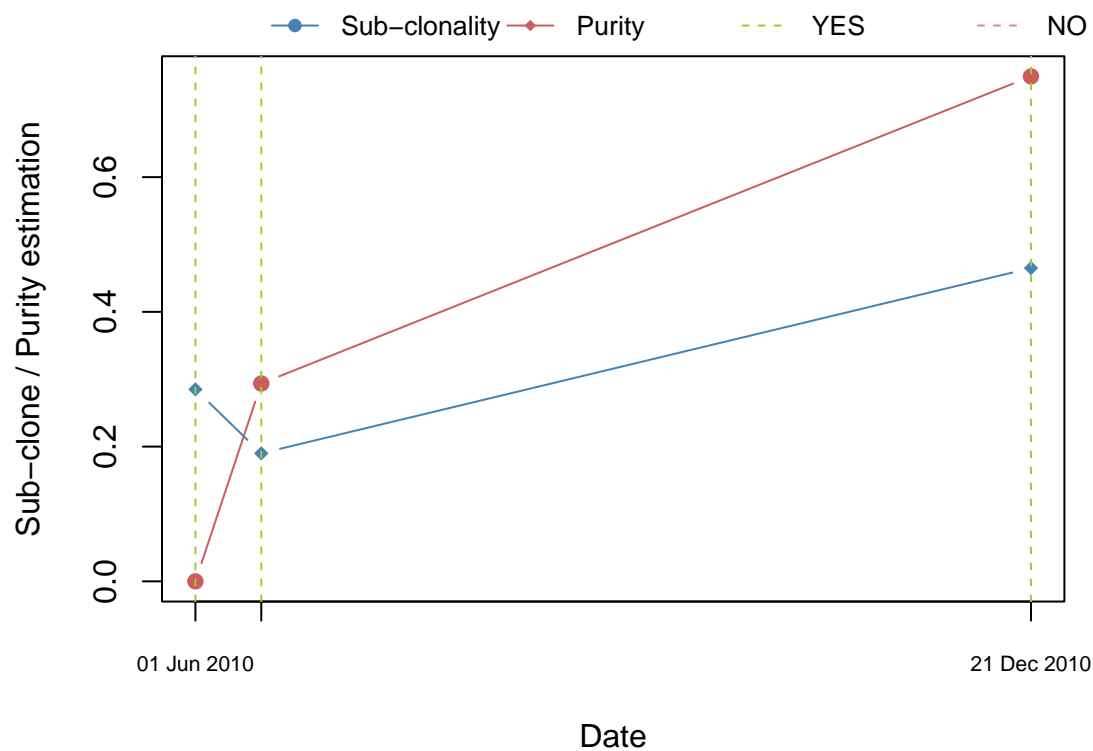
```

Patient 388 | LiquidCNA estimations with RECIST



```
plot.estimation.w.RECIST(7)
```

Patient 1005 | LiquidCNA estimations with RECIST



4. IchorCNA vs liquidCNA

There still aren't any apparent correlations between purity estimations of liquidCNA and ichorCNA.

For ichorCNA, I am using the values under the column ichorCNA. Is this correct? What are the columns ACE, rascal & tMAD?

```
#get liquidCNA purities
purities <- unlist(sapply(1:length(liquidCNA_results),
                          function(x) as.numeric(liquidCNA_results[[x]]$purity_mean)))

plot(purities, unlist(ichor.purities), xlab = "liquidCNA", ylab = "ichorCNA",
     main = "purity | liquidCNA vs ichorCNA")
```

