R plotting

Zhuyu Qiu

11/12/2019

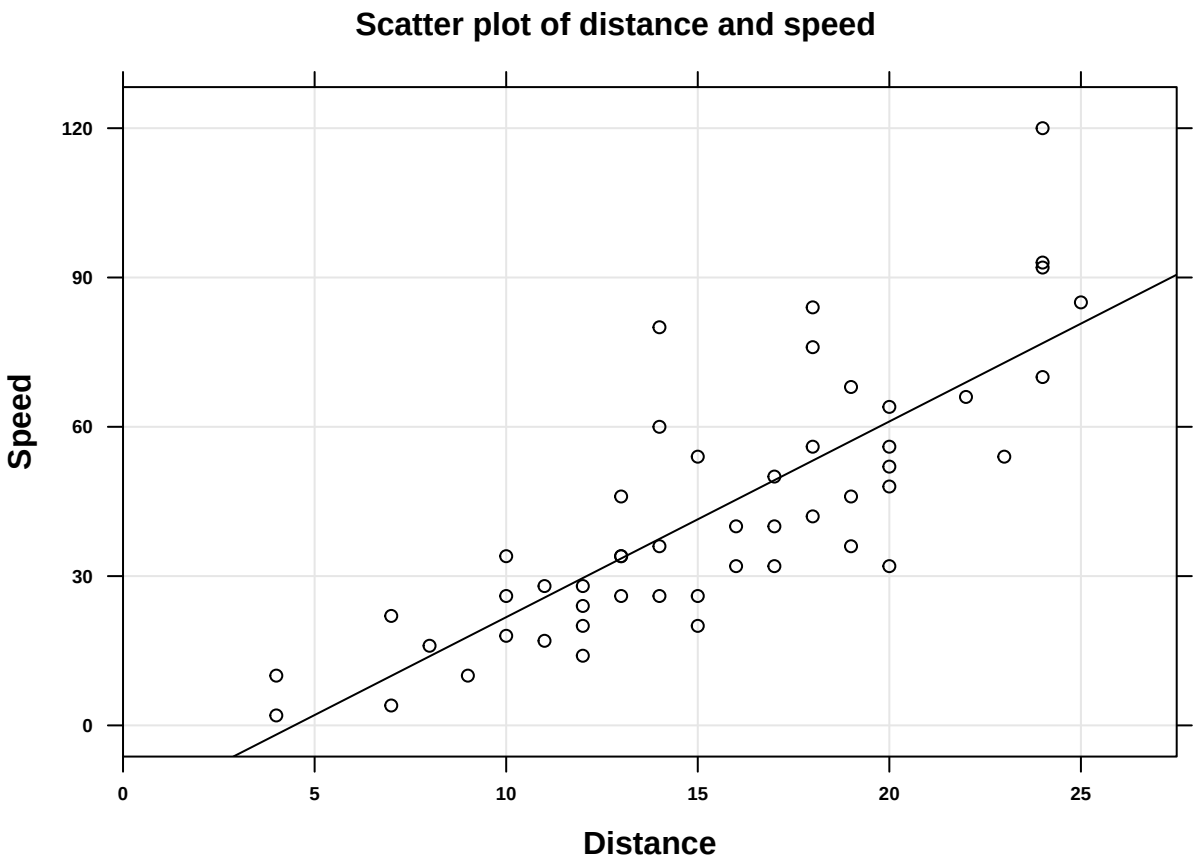
Question 2

2a. Create a simple scatterplot using BoutrosLab.plotting.general

```
cars <- datasets::cars;
summary(cars);
```

```
##      speed           dist
##  Min.   : 4.0   Min.   :  2.00
##  1st Qu.:12.0   1st Qu.: 26.00
##  Median :15.0   Median : 36.00
##  Mean   :15.4   Mean   : 42.98
##  3rd Qu.:19.0   3rd Qu.: 56.00
##  Max.   :25.0   Max.   :120.00
```

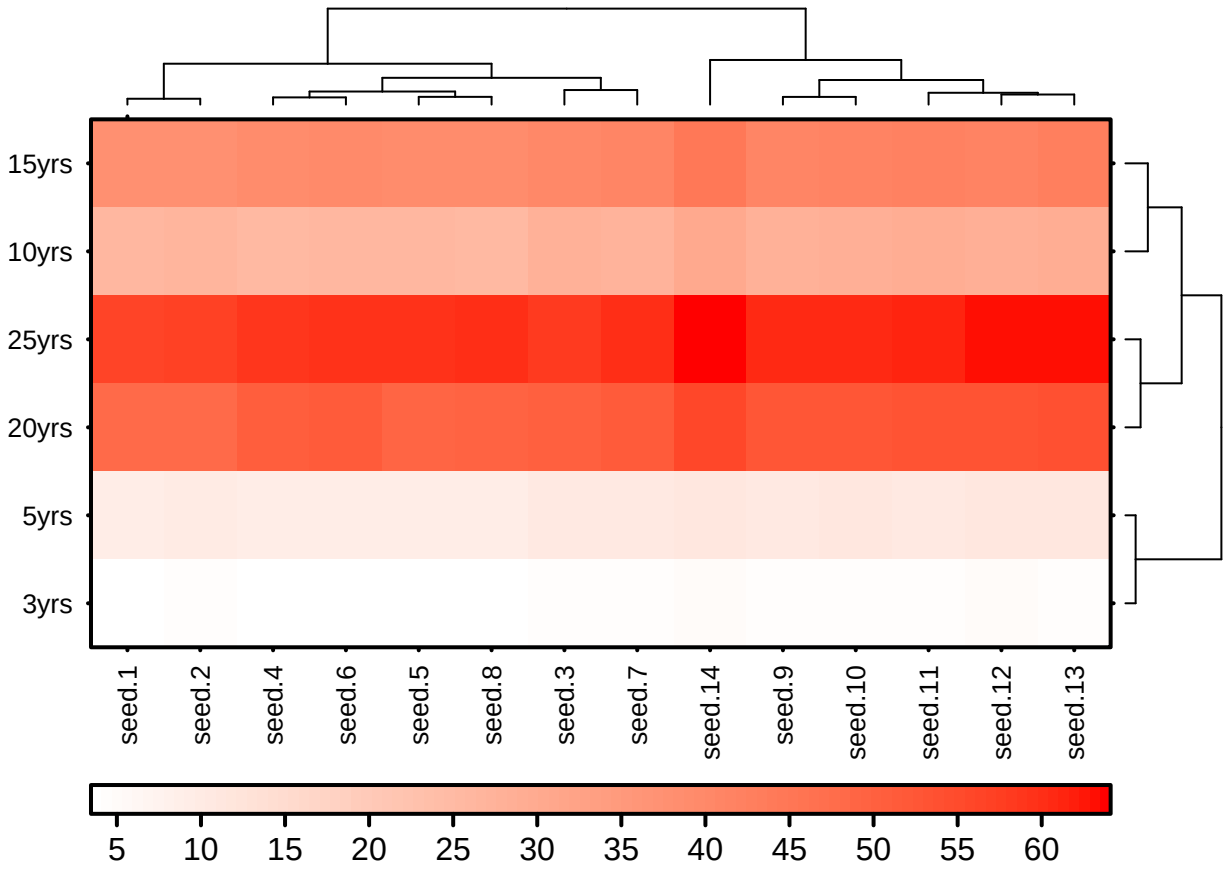
```
create.scatterplot(
  formula = dist ~ speed,
  data = cars,
  main = "Scatter plot of distance and speed",
  xlab.label = "Distance",
  ylab.label = "Speed",
  yat = seq(0,150,30),
  xaxis.cex = 0.6,
  yaxis.cex = 0.6,
  xlab.cex = 1,
  ylab.cex = 1,
  main.cex = 1,
  pch = 1,
  col=  "black",
  type =  c  (  "p" , "g" , "r" )
)
```



2b. Create a heatmap displaying data found in the 'Loblolly' dataset

```
loblolly <- datasets::Loblolly;
loblolly <- reshape(data = loblolly, idvar = "Seed",
                    v.names = "height",
                    timevar = "age",
                    direction = "wide");

loblolly$Seed <- as.numeric(loblolly$Seed);
loblolly.sort <- loblolly[order(loblolly$Seed),];
loblolly.matrix <- as.matrix(loblolly.sort[,-1]);
row.names(loblolly.matrix) <- paste("seed", 1:14, sep = ".");
colnames(loblolly.matrix) <- c("3yrs", "5yrs", "10yrs", "15yrs", "20yrs", "25yrs");

create.heatmap(
  x = loblolly.matrix,

  # format the colour key
  colourkey.cex = 1,
  colourkey.labels.at = seq(0, 70, 5),

  # set labels to NA -- results in default labels
  xaxis.lab = NA,
  yaxis.lab = NA,
  xaxis.cex = 0.8,
  yaxis.cex = 0.8,
```

```
  # set font style (default is bold, 1 is roman)
  xaxis.fontface = 1,
  yaxis.fontface = 1,

  # specify clustering method
  # if no clustering is desired, set this to "none"
  clustering.method = "complete",

  # select distance measure
  rows.distance.method = "euclidean",
  cols.distance.method = "manhattan"
);
```

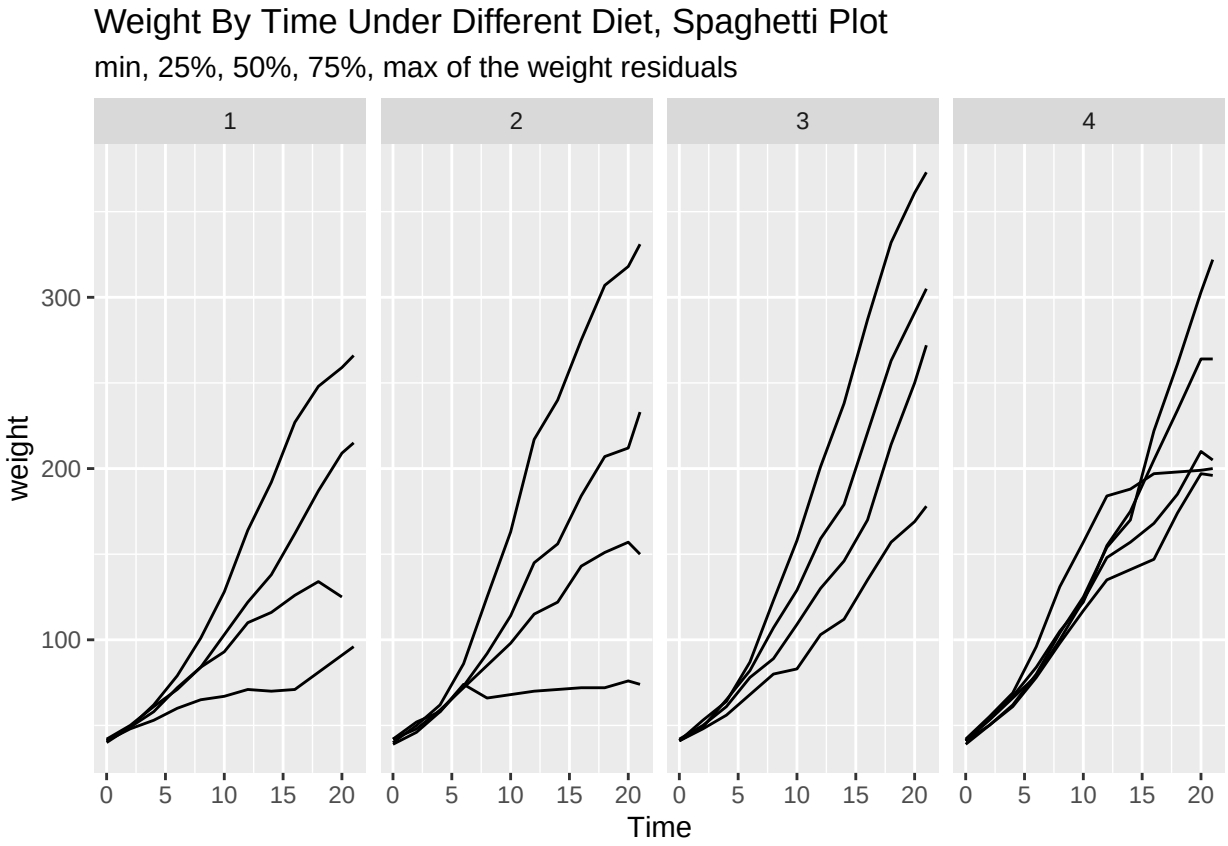


2c. Take a look at the 'ChickWeight' dataset

```
chickweight <- datasets::ChickWeight;

# chicken weight by time, spaghetti plot

ggplot(data = chickweight,
       aes(x = Time, y = weight, group = Chick))+
  geom_line()+ facet_grid(.~ Diet, scales = 'free')+
  ggtitle("Chicken Weight By Time Under Different Diet, Spaghetti Plot");
```


```
# From the spaghetti plot, chicken tend to have a bigger increasement in weight under Diet 3.


chick.residual <- chickweight %>%
  group_by(Time,Diet) %>%
  mutate(meanweight = mean(weight)) %>%
  ungroup() %>%
  mutate(residual = weight - meanweight) %>%
  group_by(Chick,Diet) %>%
  mutate(median.residual = median(residual)) %>%
  ungroup();

chick.stat <- chick.residual %>%
  group_by(Diet) %>%
  mutate(min = min(median.residual),
         q1 = quantile(median.residual,c(.25)),
         q2 = quantile(median.residual,c(.5)),
         q3 = quantile(median.residual,c(.75)),
        max = max(median.residual)) %>%
  ungroup()%>%
  select(Diet,min, q1, q2, q3, max) %>%
  unique();

chick.id <- chick.residual %>%
  filter(median.residual %in% as.matrix(chick.stat[,-1]));

ggplot(chick.id, aes(x = Time, y = weight, group = Chick)) +
```

```
  geom_line()+facet_grid(.~ Diet, scales='free') +
  ggtitle("Weight By Time Under Different Diet, Spaghetti Plot",
          subtitle = "min, 25%, 50%, 75%, max of the weight residuals");
```



- Chicken tend to have higher vairation in weight as time goes by under Diet2. Least variation in weight was shown in chicken under diet4.

```
### Function 1 ########################################################################
##Input variables:
#number of row, number of columns, column data type, and column names
#Output variables:
#empty dataset
#Description:
#Function that create empty dataframe

emptydf <- function(numrow, numcol, type, name){
  df <- data.frame(matrix(NA, nrow <- numrow, ncol <- numcol));
  for (i in 1:numcol){
    print(type[i])
    if('numeric' == type[i]) {df[,i] <- as.numeric(df[,i])
    colnames(df)[i] <- name[i]};
    if('character' == type[i]) {df[,i] <- as.character(df[,i])
    colnames(df)[i] <- name[i]};
    if('logical' == type[i]) {df[,i] <- as.logical(df[,i])
    colnames(df)[i] <- name[i]};
    if('factor' == type[i]) {df[,i] <- as.factor(df[,i])
    colnames(df)[i] <- name[i]};
```

```
  }
  return(df);
}
```

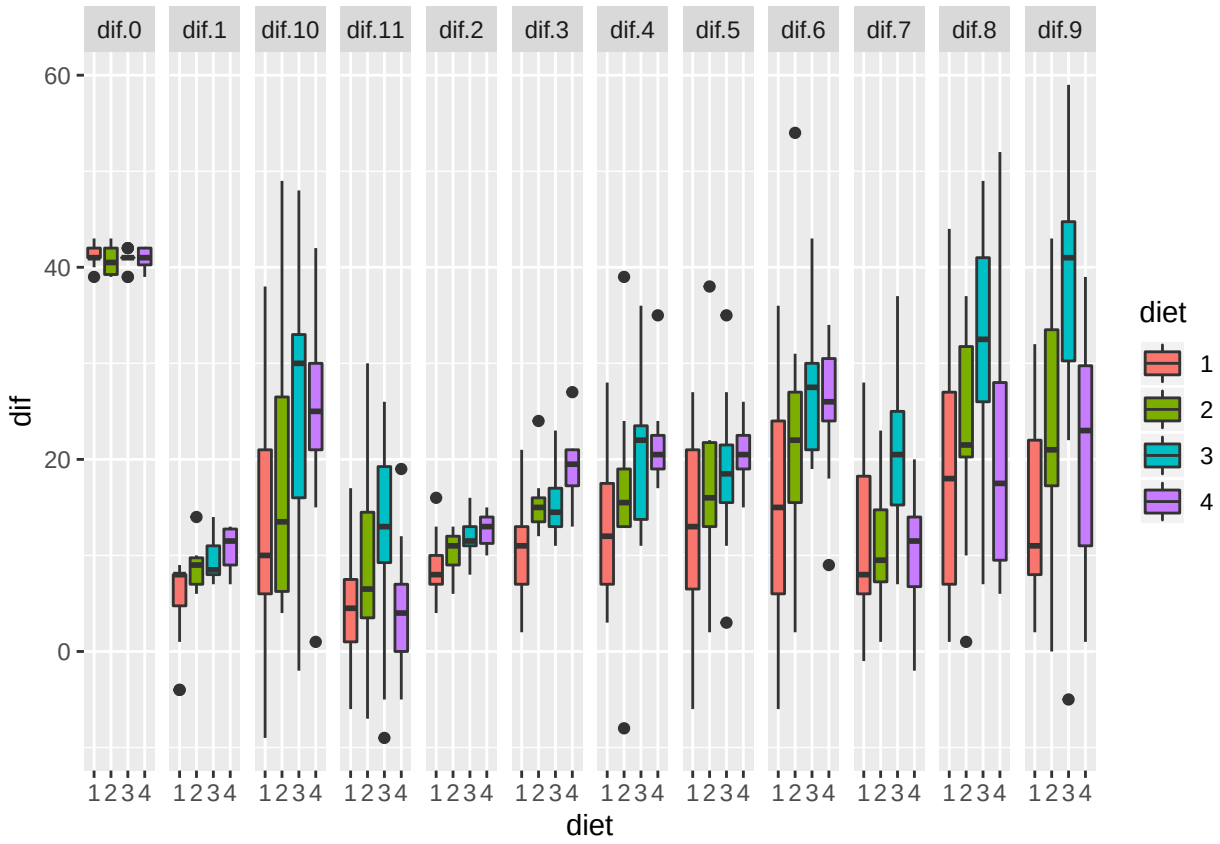
```
# chicken weight difference by time, box plot
chickweight.dif <- emptydf(nlevels(as.factor(chickweight$Chick)),
                           nlevels(as.factor(chickweight$Time))+2 ,
                       c('character', 'character', rep('numeric',nlevels(as.factor(chickweight$Time)) ))
                         c('chick', 'diet', paste("dif", 0 : nlevels(as.factor(chickweight$Time)) , sep =
```

```
## [1] "character"
## [1] "character"
## [1] "numeric"
## [1] "numeric"
## [1] "numeric"
## [1] "numeric"
## [1] "numeric"
## [1] "numeric"
## [1] "numeric"
## [1] "numeric"
## [1] "numeric"
## [1] "numeric"
## [1] "numeric"
```

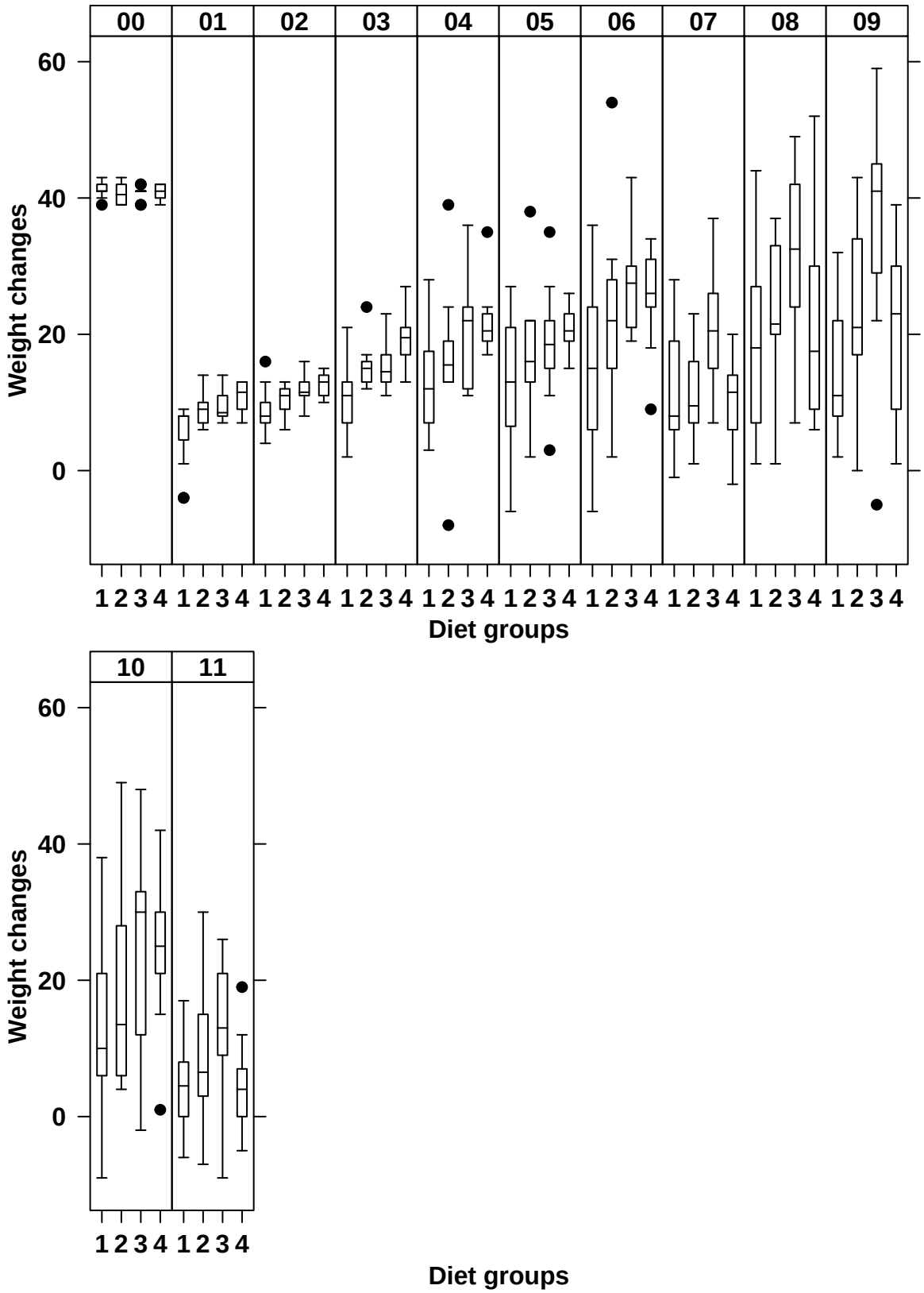
```
chickweight$Time <- as.character(chickweight$Time);
chickweight.wide <- chickweight %>%
  group_by(Chick, Diet) %>%
  spread(Time,weight, fill=NA, sep = ".");

chickweight.wide  <- chickweight.wide[, c(01,02,03,09,12,13,14,04,05,06,07,08,10,11)];

# Calculate weight difference between each measurement
for(i in 1: (nlevels(as.factor(chickweight$Time))-1) ){
  chickweight.dif [,i+3]<- chickweight.wide[,i+3]-chickweight.wide[,i+2];
}

chickweight.dif[,1:3] <- chickweight.wide[,1:3];

chickweight.dif.long <- chickweight.dif %>%
  gather(interval,dif,dif.0:dif.11 );


create.violinplot(formula = dif.0 ~ diet,
                data = chickweight.dif,
                ylimits =  c(35,50)
);
```


```
ggplot(data = chickweight.dif.long,
       aes(x = diet, y =dif, fill = diet)) +
  geom_boxplot()+
  facet_grid(.~ interval);
```

```
## Warning: Removed 22 rows containing non-finite values (stat_boxplot).
```




```
chickweight.dif.long = chickweight.dif.long %>%
  mutate ( interval.num = sprintf("%02d", as.numeric(substr(interval,5,6))));

diet.colour <- recode.vector(
    chickweight.dif.long$diet,
    list(
        blue = 1,
        hazel = 2,
       green = 3,
       brown = 4
        )
    );

create.boxplot(formula = dif ~ diet | interval.num,
    data = chickweight.dif.long,
    xaxis.cex = 1,
    yaxis.cex = 1,
    ylab.label = "Weight changes",
    xlab.label = "Diet groups",
    xlab.cex = 1,
    ylab.cex = 1,
    layout = c(10,1)
    );
```



- From the boxplot, we can find out that there is not a big difference in weight between 4 groups at time0.
- Chicken on Diet 1 tend to have the least weight changes, while chicken on Diet 3 have the most weight

changes during the time.
- Chicken on Diet 3 tend to have the most weight changes in the last few weeks.
- In the last few weeks the weight changes tend to have higher vairance among diet groups.

Question 3

```
seq.control <- read.table("/cloud/project/Q3_SeqControl_data", header = T);

# Ste 1 Reorder data
seq.control1 <- seq.control[order(seq.control$yes.votes, decreasing = T),];

# Step 2 Create the CPCG bars
colour.scheme.large <- c(
  'rosybrown1',
  'rosybrown4',
  'red',
  'darkred',
  'darkorange',
  'gold',
  'darkolivegreen3',
  'darkgreen',
  'aquamarine',
  'cyan4',
  'dodgerblue',
  'darkblue',
  'plum',
  'magenta',
  'darkorchid',
  'purple4',
  'gray70',
  'gray30'
);
```

```
### Function 2 ########################################################################
##Input variables:
# data that need to create a bar plot, colour scheme
#Output variables:
# covariate bars
#Description:
#Function that create covariate bars

heatmap <- function(data,colour){
  plot <- create.heatmap(
    x <- t(as.matrix(as.numeric(data))),
    clustering.method = "none",
    scale.data = FALSE,
    colour.scheme = colour,
    total.col = 12,
    force.grid.col = TRUE,
    grid.col = TRUE,
    print.colour.key = FALSE,

    # remove y-axis ticks
```

```
    yaxis.tck = 0,
    height = 1,
    xaxis.lab = NULL,
    yaxis.lab = NULL,
    yat = 1,
    yaxis.cex = 1);
  return(plot);
};
```

```
gene.heatmap <- heatmap(
  data = seq.control1$CPCG,
  colour = colour.scheme.large[1:12]);

average.reads.start.heatmap <- heatmap(
  data = seq.control1$Average.reads.start,
  colour = c("white", "deeppink"));

unique.start.points.heatmap <- heatmap(
  data = seq.control1$Unique.start.points,
  colour = c("white", "darkblue"));

x.base.0.quality.heatmap   <- heatmap(
  data = seq.control1$X..Bases...0.quality,
          colour = c("white", "darkorange"));


#  Create FFPE bar
seq.control1 <- seq.control1 %>%
  dplyr::mutate(FFPE =  ifelse("CPCG0102P" == CPCG | "CPCG0103P" == CPCG,1,0) );

FFPE.heatmap <- heatmap(data = seq.control1$FFPE,
                        colour = c("white", "darkslategrey"));

# Step 5 Create the barplot
barplot.colour.choice <- c("grey", "black");
barplot.colour <- barplot.colour.choice[factor(seq.control1$outcome, levels <- c(0,1))];

yes.votes.barplot <- create.barplot(
  formula = yes.votes ~ c(1:72),
  border.col = 'transparent',
  data = seq.control1,
  col = barplot.colour,
  right.padding = 2,
  xaxis.cex = 0.5,
  abline.h = 0.5,
  abline.lty = 2,
  abline.col = 'darkgrey'
);

# Step 6 Create a legend for each of the covariates

# create legend for cpcgene sample heatmap
  sample.legend <- list(
    legend = list(
```

```
    colours = colour.scheme.large[1:12],
    title = expression(underline("Sample")),
    labels = levels(seq.control1$CPCG),
    continuous = FALSE
 )
);


# create legend for outcome heatmap
  prep.legend <- list(
    legend = list(
      colours = c('white', 'black'),
      labels = c('Frozen', 'FFPE'),
      title = expression(bold(underline('Sample preparation'))),
      continuous = FALSE
    )
);


# create legend for x..base....0.quality heatmap
qual.legend <- list(
  legend = list(
  colours =  c("white", "darkorange"),
  labels = c("97.0", "83.0"),
  title = expression(bold(underline('%Base > 0 quality'))),
  continuous = TRUE
  )
);

# create legend for unique.start.point.heatmap
l.s <- scientific.notation(x=min(seq.control1$Unique.start.points),digits=2);
h.s <- scientific.notation(x=max(seq.control1$Unique.start.points),digits=2);

  uni.start.legend <- list(
    legend = list(
      colours =  c("white", "darkblue"),
      labels = c(h.s, l.s),
      title = expression(bold(underline('Unique start point'))),
      continuous = TRUE
    )
  );


# create legend for average.reads.start.heatmap
l.r <- round(min(seq.control1$Average.reads.start),2);
h.r <-  round(max(seq.control1$Average.reads.start),2);

  ave.start.legend <- list(
    legend <- list(
      colours <-  c("white", "deeppink"),
      labels <- c(h.r, l.r),
      title <- expression(bold(underline('Unique start point'))),
      continuous <- TRUE
```

```
    )
  );


#combine all covariates legends
covariate.legends <- c(
  sample.legend,
  prep.legend,
  qual.legend,
  uni.start.legend,
  ave.start.legend
);

legends1 <- BoutrosLab.plotting.general::legend.grob(
  legends = covariate.legends,
  title.cex = 0.75,
  title.just = 'left',
  label.cex = 0.65,
  size = 1.5,
  between.row = 1.0,
  between.col = 0.5,
 layout = c(1,6)
);
```

```
## Warning in FUN(X[[i]], ...): 'x' is NULL so the result will be NULL

## Warning in FUN(X[[i]], ...): 'x' is NULL so the result will be NULL
```

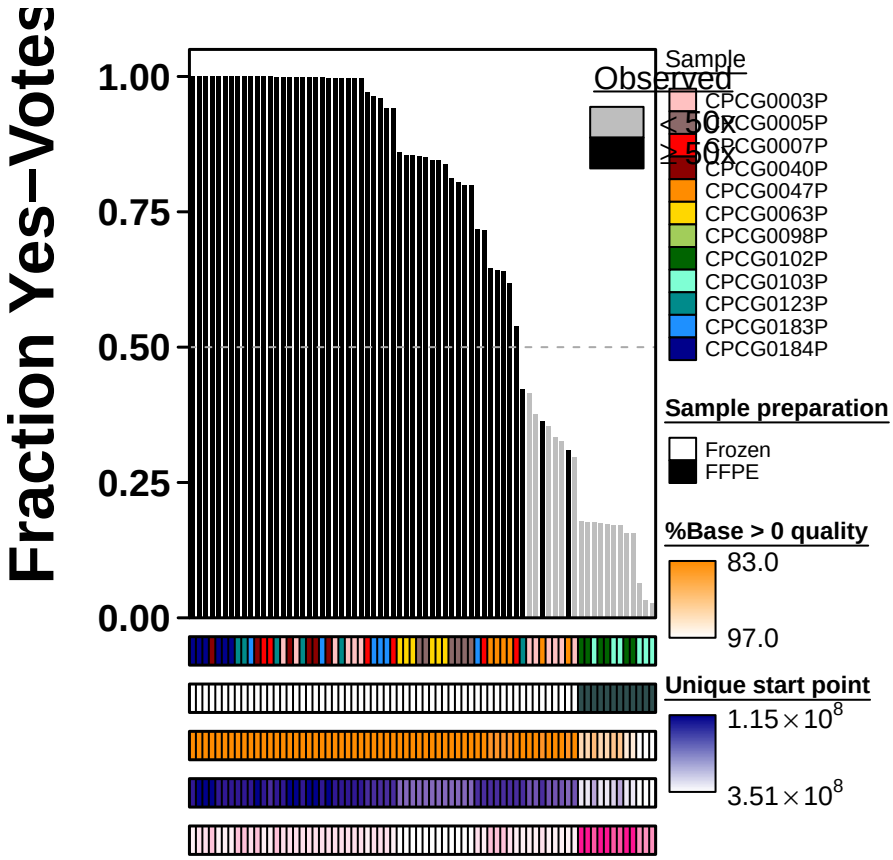
```
# create legend for barplot
barplot.legend <- list(
legend = list(
    colours = c('grey', 'black'),
    labels = c(
      as.expression(substitute(x < '50x',list(x = ''))),
      as.expression(substitute(x >= '50x',list(x = '')))
    ),
    title = expression(underline('Observed'))
  )
);

legends2 <- BoutrosLab.plotting.general::legend.grob(barplot.legend);
```

```
## Warning in FUN(X[[i]], ...): 'x' is NULL so the result will be NULL
```

```
# Multiplot

  plot.objects <- list(
    average.reads.start.heatmap,
    unique.start.points.heatmap,
    x.base.0.quality.heatmap,
    FFPE.heatmap,
    gene.heatmap,
    yes.votes.barplot
  );
```

```
# identify where plotting objects should be placed in the multiplot
  yat.vals <- list();
  for (n in 1:(length(plot.objects)-1)) {
    yat.vals <- c(yat.vals, list(NULL));
  }

# combine plots
  create.multiplot(
    plot.objects = plot.objects,
    #filename = 'testing_votes.tiff',
    panel.heights = c(1, rep(0.05, length(plot.objects)-1)),
    yat = c(yat.vals, list(seq(0,1,0.25))),
    yaxis.cex = 1.15,
    ylab.label = c(' ', 'Fraction Yes-Votes', ' ', ' ', ' '),
    ylab.padding = 6.5,
    right.padding = 35,
    bottom.padding = -5,
    xat = NULL,
    y.spacing = 0.5,
    ylimits = list(c(0.9,1), c(0.9,1), c(0.9,1), c(0.9,1), c(0.9,1), c(0.00,1.05)),
    legend = list(
      inside = list(
        fun = legends1,
        x = 1.02,
        y = 1
      ),
      inside = list(
        x = 0.85,
        y = 0.98,
        fun = legends2
      )
    ),
      print.new.legend = TRUE,
    width = 12,
    height = 6,
    resolution = 1200,
  );
```

```
## Warning in formals(fun): argument is not a function
## Warning in formals(fun): argument is not a function
## Warning in formals(fun): argument is not a function
## Warning in formals(fun): argument is not a function
## Warning in formals(fun): argument is not a function
```



Question 4

```
het <- read.table("/cloud/project/Q4_HetStudy_data.txt", header=T);

# create covariate table
covariate <-as.data.frame(colnames(het[,1:28]));
names(covariate) <- c("id");
covariate$sample <- substr(covariate$id, 1,8);
covariate$cohort <- c(rep("Bx",5),rep("Sx",23));

# convert gleason score 3+4 as 1, 4+3 as 2, 4+4 as 3
covariate$gleason.score <- c(1,1,2,1,2,1,2,2,3,3,1,1,1,1,1,2,1,2,2,2,1,1,1,3,2,2,2,1);
covariate$gleason.score.plus <- c(1,rep(NA,14),rep(1,4),rep(NA,9));

covariate$tissue.type <- substr(covariate$id, 9,10);

# create matrix for gleason score positive
gleason.score.plus.matrix <- data.frame(matrix(NA, nrow <- 28, ncol <- 2));
gleason.score.plus.matrix <- cbind(gleason.score.plus.matrix,covariate$gleason.score.plus);
gleason.score.plus.matrix <- cbind(gleason.score.plus.matrix,data.frame(matrix(NA, nrow <- 28, ncol <-

covariate.numeric <- data.frame(lapply(covariate, as.character),stringsAsFactors = FALSE);
covariate.numeric <- covariate.numeric[,2:6];
covariate.numeric <- covariate.numeric %>%
  dplyr::select(-c("gleason.score.plus"));
```

```
# convert covariate data to numeric
# create sample id
covariate.numeric <- covariate.numeric %>%
  dplyr::mutate(sample.id = as.integer(as.factor(sample)));
covariate.numeric$sample <- as.character(covariate.numeric$sample.id);
covariate.numeric <- covariate.numeric[,-5];

#convert Bx (biopsy) as 11, and Sx (surgery) as 12
covariate.numeric$cohort["Bx" == covariate.numeric$cohort] = 11;
covariate.numeric$cohort["Sx" == covariate.numeric$cohort] = 12;

#convert gleason score
covariate.numeric$gleason.score[1 == covariate.numeric$gleason.score] <- 13;
covariate.numeric$gleason.score[2 == covariate.numeric$gleason.score] <- 14;
covariate.numeric$gleason.score[3 == covariate.numeric$gleason.score] <- 15;

# concert  "F0" samples are Frozen(2), while all other samples are FPPE(1)
covariate.numeric$tissue.type["F0" != covariate.numeric$tissue.type] <- 17;
covariate.numeric$tissue.type["F0" == covariate.numeric$tissue.type] <- 16;

# set colour scheme
sample.colour <- c( 'blue','purple','green','orange','yellow','black','wheat4','green4','grey','red4');
cohort.colour <- c('royalblue', 'pink');
gleason.score.colour <- c("yellow1", "orange","red");
tissue.type.colour <- c('Frozen' = colours()[532],'FFPE' = colours()[557]);

# create covairate bar on the right
covariate.bar  <- create.heatmap(x = t(data.matrix(covariate.numeric)),
                                 clustering.method = "none",
                                 print.colour.key = FALSE,
                                 total.colours = 17,
                                 colour.scheme = c(sample.colour,cohort.colour,gleason.score.colour,tissu
                                 at=seq(0.5,17.5,1),
                                 # add row lines
                                 force.grid.col = TRUE,
                                 grid.col = TRUE,
                                 grid.row = TRUE,
                                 row.colour = "black",
                                 col.colour = "black",
                                 row.pos = which(1 == t(gleason.score.plus.matrix[1:28,1:4]), arr.ind =
                                 col.pos = which(1 == t(gleason.score.plus.matrix[1:28,1:4]), arr.ind =
                                 cell.text =rep("+", 5),
                                 text.cex = 1,
                                 xaxis.tck = 0,
                                 yaxis.tck = 0
);

#  create fraction plot
het.frac <- het %>%
  dplyr::select(-Baca, -Berger, -Weischenfeldt);
het.frac$frac <- rowSums(het.frac != 0)/28;

het.frac <- het.frac%>%
```

```
  dplyr::mutate(
    ends = sapply( strsplit(rownames(het),"-", fixed = TRUE),tail, 1),
    chr = sapply( strsplit(rownames(het),":", fixed = TRUE),head, 1),
    number = c(1:3113));

het.frac<- het.frac%>%
  dplyr::mutate(chr.num = gsub("chr", "", chr));

frac.plot <- create.barplot(formula = frac ~ number,
                            data = het.frac,
                            main = NULL,
                            stack = FALSE,
                            xlab.top.label = NULL,
                            xlab.label = NULL,
                            ylab.label = "Fraction",
                            ylab.cex = 0.8,
                            xaxis.tck = 0,
                            xaxis.lab = rep('',3113),
                            ylimits = c(0, 0.5),
                            yat = seq(0,0.6,0.25),
                            yaxis.cex = 0.6,
                            yaxis.tck = c(1,0)
);

# create literature covariate bars
het.literature <- cbind(het.frac[,30:32],het[,29:31]);

het.literature <- data.frame(lapply(het.literature, as.character),stringsAsFactors = FALSE);

# set colour scheme
literature.colour <- c('white', 'darkred', 'cornflowerblue', 'darkolivegreen4');

# create
publication.bar  <- create.heatmap(x =data.matrix(het.literature[,4:6]),
                                   clustering.method = "none",
                                   print.colour.key = FALSE,
                                   #otal.colours = 4,
                                   colour.scheme = c( literature.colour ),
                                   # add row lines
                                   at=seq(-0.5,3.5,1),

                                   col.lines = which("1000000" == het.literature$ends),
                                   force.grid.col = TRUE,
                                   grid.col = TRUE,
                                   force.grid.row = TRUE,
                                   grid.row = TRUE,
                                   row.colour = "black",
                                   yaxis.tck = 0
);

# create main heatmap
literature.colour <- c('white', 'cornflowerblue','darkolivegreen4','darkred');
```

```
# create x axis location
het.frac.plot <- het.frac%>%
  dplyr::group_by(chr.num) %>%
  dplyr::mutate(x.location = ifelse (number == round(mean(number),digits = 0),1,0));

het.frac.plot <- data.frame(lapply(het.frac.plot, as.character),stringsAsFactors = FALSE);

# create y axis location
covariate <- covariate %>%
  dplyr::group_by(sample) %>%
  dplyr::mutate(first = row_number() == min( row_number() ));

# create main heat map
main.heatmap <- create.heatmap(x = data.matrix(het.frac.plot[,1:28]),
                               clustering.method = "none",
                               print.colour.key = FALSE,

                               total.colours = 4,
                               colour.scheme = c(literature.colour),
                               at = seq(-0.5, 3.5, 1),
                               # add row lines
                               row.lines = which(TRUE == covariate$first)+0.5,
                               grid.row = TRUE,

                               # add col lines
                               col.lines = which("1000000" == het.literature$ends),
                               force.grid.col = TRUE,
                               grid.col = TRUE,

                               #set labels for x and y axis
                               xaxis.lab =  c(1:22,"X", "Y"),
                               xat = which(1 == het.frac.plot$x.location),
                               xaxis.cex = 0.6,
                               xaxis.rot = 0,
                               yaxis.lab =  covariate$tissue.type,
                               yaxis.tck = c(1,0),
                               yaxis.cex = 0.6

                               #row.colour = "black",
                               #col.colour = "black"
);


# create the bottom notation heatmap
notation <- matrix(1:4, nrow = 1);
notation.heatmap <- create.heatmap(x = notation,
                                   clustering.method = "none",
                                   print.colour.key = FALSE,
                                   total.colours = 4,
                                   colour.scheme = c('white', 'cornflowerblue','darkolivegreen4','darkre
                                   at = seq(0.5,4.5,1),
                                   force.grid.col = TRUE,
                                   grid.col = TRUE,
```

```
                                    xaxis.lab =  c("", "None", "CTX", "ITX","INV"),
                                    xaxis.cex = 0.6,
                                    xaxis.rot = 0,
                                    yaxis.lab =  NULL,
                                    yaxis.cex = 0.6,
                                    yaxis.tck = 0,
                                    right.padding = 0
);


#create legend on the left
# create legend for samples
pid.legend <- list(
  legend = list(
    colours =  c( 'blue','purple','green','orange','yellow','black','wheat4','green4','grey','red4'),
    labels = unique(covariate$sample),
    title = expression(bold(underline('Patient ID'))),
    continuous = FALSE
  )
);

# create legend for cohort
cohort.legend <- list(
  legend = list(
    colours =  c('pink', 'royalblue' ),
    labels = c('Sx', 'Bx'),
    title = expression(bold(underline('Cohort'))),
    continuous = FALSE
  )
);

# create legend for Gleason score
gs.legend <- list(
  legend = list(
    colours =  c('yellow', 'orange','red' ),
    labels = c('3+4', '4+3', '4+4'),
    title = expression(bold(underline('Gleason score'))),
    continuous = FALSE
  )
);

# create legend for Tissue type

tissue.legend <- list(
  legend = list(
    colours =  c(colours()[532],colours()[557]),
    labels = c('FFPE', 'Frozen'),
    title = expression(bold(underline('Tissue type'))),
    continuous = FALSE
  )
);

# create legend for Publication
```

```
pub.legend <- list(
  legend = list(
    colours =  c('darkred', 'cornflowerblue','darkolivegreen4'),
    labels = c('Baca', 'Berger',"Weischenfeldt"),
    title = expression(bold(underline('Publication'))),
    continuous = FALSE
  )
);

left.legends <- legend.grob(
  legends = c(pid.legend, cohort.legend, gs.legend, tissue.legend, pub.legend),
  title.cex = 0.75,
  title.just = 'left',
  label.cex = 0.65,
  size = 1,
  between.row = 1.0,
  between.col = 0.5
);
```

```
## Warning in FUN(X[[i]], ...): 'x' is NULL so the result will be NULL

## Warning in FUN(X[[i]], ...): 'x' is NULL so the result will be NULL

## Warning in FUN(X[[i]], ...): 'x' is NULL so the result will be NULL

## Warning in FUN(X[[i]], ...): 'x' is NULL so the result will be NULL

## Warning in FUN(X[[i]], ...): 'x' is NULL so the result will be NULL
```

```
# create multiplot
plot.objects <- list(frac.plot,publication.bar, main.heatmap,covariate.bar,notation.heatmap );

create.multipanelplot(
  plot.objects = plot.objects,
  #filename = 'HetStudy.tiff',
  plot.objects.heights = c(0.6,0.3,1.4,0.2),
  plot.objects.widths = c(1.1, 0.1),
  layout.skip = c(FALSE, TRUE, FALSE, TRUE, FALSE, FALSE, FALSE, TRUE),
  layout.height = 4,
  layout.width = 2,

  #yaxis.cex = 1.15,
  ylab.axis.padding = 3.5,
  y.spacing = c(-1,-1,-1),
  x.spacing = 0,

  legend = list(
    left = list(
      fun = left.legends,
      x = 1.02,
      y = 1
    )
  ),
```

```
  left.legend.padding = 2,

  width = 12,
  height = 6,
  resolution = 1200

);
```

```
## Warning in rbind(plot.objects.heights, y.spacing): number of columns of
## result is not a multiple of vector length (arg 2)
```