01_Linear_Interpolation

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Linear Interpolation

This Markdown is filling the missing data for BMI and media exposure at asynchronous time points using linear interpolation. The project is supervised by Professor Marc Scott and Professor Daphna Harel. The data is from the Belle Lab at the Bellevue Hospital. More details of the project scope is in the repository under lit folder.

R Libraries

This code block has all the needed R libraries

```
#For the dta raw files
library(foreign)
```

```
## Warning: package 'foreign' was built under R version 3.3.2
```

```
#For importing different types of data set without specification
library(rio)
```

```
## Warning: package 'rio' was built under R version 3.3.2
```

```
#For processing long form data
library(dplyr)
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
#GTools library for ordering numeric variables
library(gtools)
```

Uploading Raw data

In this code chunk, we are uploading raw .dta data and converting to it a csv. This will then be saved to a processing data folder to protect the integrity of the raw data.

```
#The BMI data extract
bmi <- read.dta("../../data/raw/MASextract1.dta")
#The Media data extract
media <- read.dta("../../data/raw/MASextract2.dta")
#Writing the BMI data to processing file
write.csv(bmi, "../../data/processing/bmi.csv")
#Writing the media data to processing file
write.csv(media, "../../data/processing/media.csv")
```

Loading the Data back from Processing Folder

This code chunk is loading the working version of the data extra to be used throughout the document.

```
#processing bmi data
p_bmi <- import("../../data/processing/bmi.csv")
p_media <- import("../../data/processing/media.csv")
```

Data Exploration

This code chunks examine the two data sets. In particular, the focus here is on the key variables and the time intervals they are recorded. At the end of each code block for each data set, there is a short summary of what the data consists of.

The BMI data set overview

```
head(p_bmi)
```

```
##   V1 ID_    AgeMos       zBMI
## 1  1   1 0.0000000 -3.5407891
## 2  2   1 0.1314168 -3.1878707
## 3  3   1 0.5585216 -0.2831618
## 4  4   1 1.5441478 -1.2716171
## 5  5   1 4.3039017 -1.1837007
## 6  6   1 6.3737168 -2.5585830
```

```
tail(p_bmi)
```

```
##          V1   ID_    AgeMos       zBMI
## 10321 10321 91008 0.9199179  1.4600797
## 10322 10322 91008 1.2813141  1.8749880
## 10323 10323 91118 0.0000000 -0.9925033
## 10324 10324 91118 0.5913758  1.3112072
## 10325 10325 91118 1.5112936  1.9073267
## 10326 10326 91118 3.9096510  2.6738663
```

```
dim(p_bmi) #10326, 4
```

```
## [1] 10326     4
```

```
#check the number of unique subjects
length(unique(p_bmi$ID_)) #667
```

```
## [1] 667
```

```
length(unique(p_bmi$AgeMos)) #1951
```

```
## [1] 1951
```

```
print(sum(is.na(p_bmi$ID_))) #0 no values are missing here
```

```
## [1] 0
```

```
print(sum(is.na(p_bmi$AgeMos))) #0 no values are missing here
```

```
## [1] 0
```

Each subject has different time points. For subject 1, months may be 0, 0.5, 1.0 while subject 2 has months in 0, 0.7, 1.2 etc.

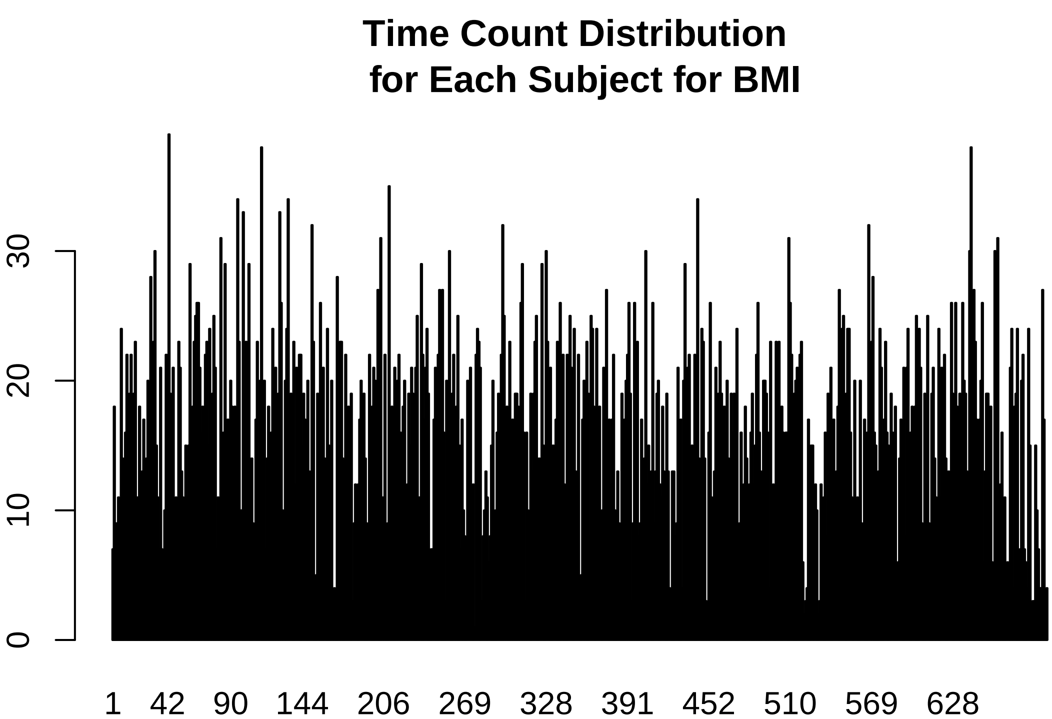
This is to explore the number of time intervals each subject has.

```r
#This uses dplyr to group by each subject and count their instances. This effectively counts the number
bmi_timed <- p_bmi %>%
  group_by(ID_) %>%
  summarize(n = n())
print(bmi_timed)
```

```
## # A tibble: 667 × 2
##      ID_     n
##    <int> <int>
## 1      1     7
## 2      2    18
## 3      3     9
## 4      4     9
## 5      5    11
## 6      6     5
## 7      7    24
## 8      8    14
## 9      9    10
## 10    10    16
## # ... with 657 more rows
```

We will do a quick barplot to see the distribution of time points for each subject has

```r
#Using the table function and barplot to draw the distribution of time.
barplot(table(bmi$ID_), main = "Time Count Distribution \n for Each Subject for BMI")
```



Check the Minimum/Maximum time intervals. This is to see if we have to explore edge cases later down the road for Last Value Carried forward at the end for each subject

```r
min(bmi_timed$n) #1
```

```
## [1] 1
```

```r
max(bmi_timed$n) #39
```

```
## [1] 39
```

At least 1 subject has only 1 time interval for BMI. These **singletons** will be applied **LOCF** or **LOCB**.

Media exposure data set overview

```r
head(p_media)
```

```
##   V1 ID_    AgeMos lnmediatimespent sqrtmediatimespent
## 1  1   1 15.244353         4.948760          11.832160
## 2  2   1  7.786448         5.463832          15.329710
## 3  3   2 24.147844         4.795791          10.954452
## 4  4   2 42.940453         3.433987           5.477226
## 5  5   2  6.735113         4.330733           8.660254
## 6  6   2 60.714581         4.795791          10.954452
```

```r
tail(p_media)
```

```
##        V1   ID_   AgeMos lnmediatimespent sqrtmediatimespent
## 1634 1634 90372 16.09856         5.602119          16.431677
## 1635 1635 90406 50.43121         5.198497          13.416408
## 1636 1636 90425 23.65503         3.433987           5.477226
## 1637 1637 90448 36.66530         4.510859           9.486833
## 1638 1638 90448 27.92608         4.110874           7.745967
## 1639 1639 90448 59.79466         5.198497          13.416408
```

```r
dim(p_media) #1639, 5
```

```
## [1] 1639    5
```

```r
#check the number of unique subjects
length(unique(p_media$ID_)) #542
```

```
## [1] 542
```

```r
length(unique(p_media$AgeMos)) #745
```

```
## [1] 745
```

```r
print(sum(is.na(p_media$ID_))) #0
```

```
## [1] 0
```

```r
print(sum(is.na(p_media$AgeMos))) #0
```

```
## [1] 0
```

This is to explore the number of time intervals each subject has.

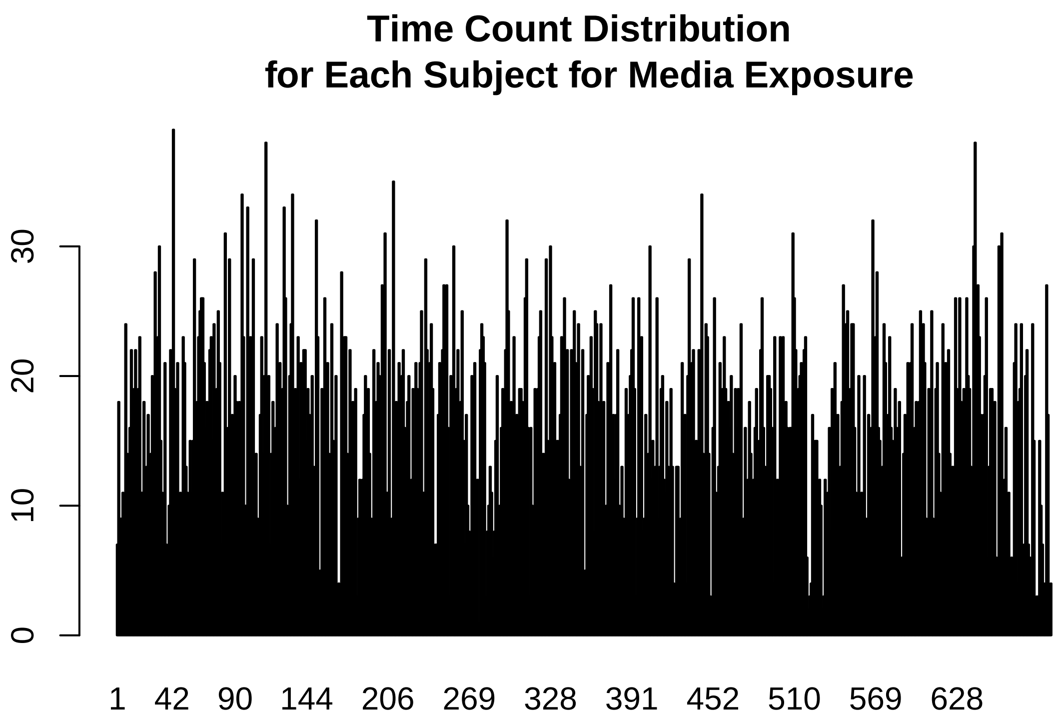
```r
#This uses dplyr to group by each subject and count their instances. This effectively counts the number
media_timed <- p_media %>%
  group_by(ID_) %>%
  summarize(n = n())
print(media_timed)
```

```
## # A tibble: 542 × 2
##      ID_     n
##    <int> <int>
```

```
## 1       1     2
## 2       2     4
## 3       3     1
## 4       4     2
## 5       5     5
## 6       6     3
## 7       7     3
## 8       8     4
## 9       9     2
## 10     10     3
## # ... with 532 more rows
```

Like the BMI from before, each subject has different count of time as well as time intervals where the data is collected.

```r
#Using the table function and barplot to draw the distribution of time.
barplot(table(bmi$ID_), main = "Time Count Distribution \n for Each Subject for Media Exposure")
```



Cleaning data

In this section, I will attempt to discover the subjects that only have 1 data point for the BMI data set or the Media exposure data set. [**EDIT**]These will have to be removed from the working data set as Linear interpolation cannot happen unless we have more than 1 data point. Those subjects will be noted down and saved in a separate file.[**EDIT**]

[**UPDATE_1**] The singletons will **NOT** be removed from the file. Instead, LOCF and LOCB will be applied. This will be done once, the interpolation function has been tested.

[**UPDATE_2**] The singletons *MUST* be removed from the file or be expanded. The approx function cannot handle a case where there is only 1 single point. Addendum markdown has been added to explore the Singleton case. The question is to which time points does the singleton value has to be applied to. It must have a corresponding subject ID match from media at least to get another valid time point.

BMI cleaning

Figuring out the 1 data point subjects and saving it them to an output file.

```
#Recalling the count by ID dataset from above for BMI.
head(bmi_timed)
```

```
## # A tibble: 6 × 2
##     ID_     n
##   <int> <int>
## 1     1     7
## 2     2    18
## 3     3     9
## 4     4     9
## 5     5    11
## 6     6     5
```

```
#Getting the indexes for which n = 1
#An assumption has been that for each row, there is no missing corresponding time value or bmi value. T
bmi_exclude <- bmi_timed[bmi_timed$n==1,]
print(bmi_exclude)
```

```
## # A tibble: 3 × 2
##     ID_     n
##   <int> <int>
## 1   276     1
## 2   550     1
## 3   626     1
```

```
write.csv(bmi_exclude, "../../data/final/bmisubjects_withonedatap.csv")
```

There are 3 subjects with 1 data point and has been saved to an output file.

Removing the 3 subjects from the processing BMI file by their ID.

```
dim(p_bmi)#checking the dimensions of p_bmi before removing
```

```
## [1] 10326     4
```

```
p_bmi <- p_bmi[!(p_bmi$ID_ %in% bmi_exclude$ID_), ] #removing by a logical vector where we want all the
dim(p_bmi)
```

```
## [1] 10323     4
```

```
#This is the Singleton File of BMI
p_bmi_singleton <- p_bmi[(p_bmi$ID_ %in% bmi_exclude$ID_),]
write.csv(p_bmi_singleton, "../../data/processing/bmi_subject_singleton.csv")
```

Media exposure cleaning

Figuring out the 1 data point subjects and saving it them to an output file.

```
#Recalling the count by ID dataset from above for Media exposure.
head(media_timed)
```

```
## # A tibble: 6 × 2
##     ID_     n
##   <int> <int>
## 1     1     2
## 2     2     4
## 3     3     1
## 4     4     2
```

```
## 5      5      5
## 6      6      3
```

```
#Getting the indexes for which n = 1
#An assumption has been that for each row, there is no missing corresponding time value or media value.
media_exclude <- media_timed[media_timed$n==1,]
print(media_exclude)
```

```
## # A tibble: 100 × 2
##       ID_     n
##     <int> <int>
## 1       3     1
## 2      21     1
## 3      38     1
## 4      40     1
## 5      49     1
## 6      66     1
## 7      70     1
## 8      79     1
## 9      94     1
## 10     98     1
## # ... with 90 more rows
```

```
write.csv(media_exclude, "../../data/final/mediasubjects_withonedatap.csv")
```

There are 100 subjects in media exposure file that only has 1 data point.

Removing the 100 subjects from the processing BMI file by their ID.

```
dim(p_media)#checking the dimensions of p_bmi before removing
```

```
## [1] 1639    5
```

```
p_media <- p_media[!(p_media$ID_ %in% media_exclude$ID_), ] #removing by a logical vector where we want
dim(p_media)
```

```
## [1] 1539    5
```

```
#This is the media Singleton Output
p_media_singleton <- p_media[(p_media$ID_ %in% media_exclude$ID_),]
write.csv(p_media_singleton, "../../data/processing/media_subject_singleton.csv")
```

Output

This is to build redundancy of data sets should code be accidentally changed etc. The data will be saved in the final data folder.

Output

bmi_clean_1 has removed 3 subjects with 1 data point media_clean_1 has removed 100 subjects with 1 data point

```
#write.csv(p_bmi,"../../data/final/bmi_clean_1.csv")
#write.csv(p_media, "../../data/final/media_clean_1.csv")
```

Merging the two data sets

Check the number of ID matches between the two files

The two ids to merge across the data sets are not of equal length. We will use the smaller one as base and see how much more are missing.

[**EDIT**] Need to document how many matches are in each data set and both data sets. [**EDIT**]

[**UPDATE_1**] This matching issue has been handled in 01_Addendum.Rmd file.

```
#Writing in the Media Exposure Smaller one first to fill in
matched_index <- match(p_media$ID_, p_bmi$ID_)
#Checking the number of non matches using is.na
non_matches <- sum(is.na(matched_index))
print(non_matches) #19
```

```
## [1] 19
```

```
#Checking total matches by substracting from maximum unique ID of smaller set to the missing ones
total_matches <- length(unique(p_media$ID_)) - non_matches
print(total_matches) #423
```

```
## [1] 423
```

```
#This is not perfect total number. The best way is to match it to match the IDs by innerjoin and captur
```

Join the two tables to fill in missing Xs and missing Ys for Each Subject

There are 10 steps in this section. At the end, we come out with an entirely interpolated data set. An Appendix section goes through the concept of Linear Interpolation as well as testing the Approx function that has been used extensively in this section. Other tests of the custom function that is written has been removed. Should it need to be in the Appendix, we can easily provide.

Step 1: Finding the Common ID

```
common_ID <- intersect(p_bmi$ID_, p_media$ID_) # intersection works like in Set theory
length(common_ID) #436 common subject IDs
```

```
## [1] 436
```

Step 2: Extracting BMI and Media Data set based on shared ID

```
#Matched BMI
m_bmi <- p_bmi[(p_bmi$ID_ %in% common_ID), ]
#Matched Media
m_media <- p_media [(p_media$ID_ %in% common_ID),]
```

Step 3: Generating NAs for each of the data set This is referencing Professor Harel's code of spliting and merging data

```
#BMI data table first!
#First removing column V1 if it exists
if("V1" %in% colnames(m_bmi)){
  m_bmi <- m_bmi[,2:ncol(m_bmi)]
}
#Adding NAs in the BMI table by expanding the column
m_bmi <- cbind(m_bmi[,c(1,2)], NA, m_bmi[,3])
colnames(m_bmi) <- c("ID_", "AgeMos", "NA", "zBMI")

#MEDIA data table second!
if("V1" %in% colnames(m_media)){
```

```
 m_media <- m_media[,2:ncol(m_media)]
}
#Adding NAs in the MEDIA table by expanding the column
m_media <- cbind(m_media, NA)
#Also need to drop squrt time spent as it can be generated by the linear Time
m_media <- m_media[,-4]
```

Step 4: Merging the two data sets together

```
#The Column Names have to match for the data set to match together
colnames(m_bmi) <- c("ID", "Months", "Media", "zBMI")
colnames(m_media) <- c("ID", "Months", "Media", "zBMI")
#Combined Data Set
c_data <- rbind(m_bmi, m_media)
#Ordering to observe missing gaps in each data set
c_data <- c_data[order(c_data[,1]),]
#Convert all the time variables into numeric for later sorting
c_data$Months <- as.numeric(as.character(c_data$Months))
```

Step 4.5: Arrange the data set of each SubjectID by Time

```
#dplyr command that does the arrange by the Group ID then within the groups
#arrange it by Months
c_data_arr<- c_data %>% arrange(ID,Months)
View(c_data_arr)
```

Step 5: Checking # of duplicated values for each time value within each subject

```
#This is to check if BMI and Media has been recorded at the same time.
#If so, we want to merge those two rows in the data set.
dup_count <- c_data_arr %>% group_by(ID, Months) %>% summarise(n=n())
#View a subset of all the duplicate rows
v_dup <- dup_count[dup_count$n >1,]
print(head(v_dup))
```

```
## Source: local data frame [6 x 3]
## Groups: ID [5]
##
##      ID    Months     n
##   <int>     <dbl> <int>
## 1     2  6.735113     2
## 2     4  5.848049     2
## 3     7  6.340862     2
## 4     8  5.749486     2
## 5     9  7.129364     2
## 6     9 24.344969     2
```

```
print(dim(v_dup))
```

```
## [1] 317   3
```

Step 6: Merging duplicated row into 1 unit

For merging rows, we are essentially saying between two values in both rows, do not pick NA, pick the value. Below is a custom-built function that achieves that. Said function will be applied to the dplyr summarize_each (which is essentially, apply this function to each row of each column).

```
#The ifelse commands literally says, if not all of the x vector is NA, pick the maximum after removing
my.max <- function(x) ifelse(!all(is.na(x)),max(x, na.rm = T), NA)
```

```
#If BMI and Media are recorded at the same time month, there should not be two separate rows for it.
c_data_arr_mer <- c_data_arr %>% group_by(ID,Months) %>% summarise_each(funs(my.max))
#View(c_data_arr_mer)
write.csv(c_data_arr_mer, "../../data/processing/merged_arranged_data.csv")
```

Step 7: Split the data set by the Subject ID

Here we are spliting the data set by subject ID so that we can apply the interpolation function to each of the Subject ID

```
#Split the data by subject ID
c_data_split <- split(c_data_arr_mer, c_data_arr_mer[,1])
```

Step 8: Build Custom Function to Handle Interpolation

Main Custom function that interpolates our data frame

```
#The function will take in a data frame as well as an input vector that specifies which column indexes

#df refers to the data frame of interest
#par is a vector that specifies the TWO indexes: 1 being time in this case and the other being the miss

mdz_interpolate <- function(df, par){
  #Saving the data frame in a local variable
  x <- df
  #Pulling out the index for X vector (In our case Time)
  x_1 <- par[1]
  #Pulling out the index for Y Vector 1 (In our case BMI)
  y_1 <- par[2]
  #Pulling out the index for Y Vector 2 (In our case Media)
  y_2 <- par[3]
  #Pulling out x and y vectors for the interpolation
  #They are in data frame format.You have to unlist and make it a numeric vector.
  xx <- as.numeric(unlist(x[,x_1])) # X vector
  yy_1 <- as.numeric(unlist(x[,y_1])) # Y vector 1
  yy_2 <- as.numeric(unlist(x[,y_2])) # Y vector 2
  #Specifying indexes where we had to fill with the missing NA for y Vector 1
  xout_1 <- which(is.na(yy_1))
  #specifying indexes where we had to fill with the missing NA for y Vector 2
  xout_2 <- which(is.na(yy_2))
  #Specifying the minimum and maximum values for Last Value Carried Backward/Forward
  #Get the non-missing indexes first
  y_nmis_1 <- which(!is.na(yy_1))
  y_nmis_2 <- which(!is.na(yy_2))
  #Get the value from the furthest left index of Y (LOCB)
  y_min_1 <- yy_1[min(y_nmis_1)]
  y_min_2 <- yy_2[min(y_nmis_2)]
  #Get the value from the furthest right index of Y (LOCF)
  y_max_1 <- yy_1[max(y_nmis_1)]
  y_max_2 <- yy_2[max(y_nmis_2)]
  #Apply this to the interpolation function (Explanations of the function are in Appendix section)
  #The interpolation for the first vector
  out_1 <- approx(xx, yy_1, xout = xout_1,  method = "linear", yleft = y_min_1, yright = y_max_1, rule =
```

```
  #The interpolation for the second vector
  out_2 <- approx(xx, yy_2, xout = xout_2, method = "linear", yleft = y_min_2, yright = y_max_2, rule =
  #The missing values replaced data frame 1 of replaced Vector 1
  outframe_1 <- d_replace(x, out_1, 3)
  #The missing values replaced data frame 2 of replaced Vector 2
  outframe_2 <- d_replace(x, out_2, 4)
  outframe_1[,4] <- outframe_2[,4]
  return(outframe_1)
}
```

Helper Function that puts missing values back into the data frame.

```
#The function takes in an actual data frame (df), an Robject of the interpolation function which contai
d_replace <- function(df, robj, rcol){

  #saving the local data frame
  df <- df
  #saving the local robject
  robj <- robj
  #specifying the rows and the columns to replace the R values by
  df[robj$x,rcol] <- robj$y
  return(df)
}
```

Step 9: Applies the Custom Interpolation Function to the Split data set

```
#The split data is put in and then, the time column: 2, the BMI column: 3 and the media column 4 are ap
c_data_interp <- lapply(c_data_split, mdz_interpolate, par=c(2,3,4))
```

Step 10: Collapse the Split Data Into 1 Data Frame

```
#Use dplyr bind_rows to recompose the split data together
#http://dplyr.tidyverse.org/reference/bind.html
c_data_interp_bind <- bind_rows(c_data_interp)
write.csv(c_data_interp_bind, "../../data/final/final_interp_data.csv")
```

APPENDIX:

Section I: Theorectical Explanation

Base Linear Interpolation Function

The linear interpolation equation to be used in the base function is below. The y_0 and y_1 would be either BMI or Media exposure variable. The x_0 and x_1 would be the time variable.

The y variable is the missing value we are looking for at time x. For BMI variable, the x corresponds to time from Media exposure that is missing between the x_0 and the x_1 intervals. The converse can be said of the Media Exposure variable to BMI as well.

Source: Linear Interpolation, Wikipedia

$$y = y_0 + (x - x_0)\frac{y_1 - y_0}{x_1 - x_0}$$

This section deals with testing out functions and other stuffs

Use ApproxFun: https://stat.ethz.ch/R-manual/R-devel/library/stats/html/approxfun.html

Section II: Testing the Approx Function

START: Testing Out Linear Interpolation approx/approxfun

Both approx and approxfun looks fairly similar. There are a couple of **key parameters** to consider * x,y => input vectors * xout => we specify which indexes we want to interpolate values for * yleft => this is specifying the last value to be carried to the left or backward if x values are less than min(x)

- yright => this is specifying the last value to be carried to the right or forward if x values are more than max(x)
- rule => Two options. 1 is to get NA for yleft, yright case. 2 is to output yleft, yright cases

Test Case 1

This is a simple case of some missing Ys with X values. A manual calculation is done below to verify the answer.

This helper function puts back the output to the actual data frame.

Simulated data 1

```
x_1 <- c(1,2,3,4,5,6)
y_1 <- c(3,NA,5,NA,NA,10)
xout_1 <- which(is.na(y_1)) #which returns the indexes where y_1 vector has NA values
```

Specifying y__left and y__right

This code chunk will tackle the case of last carried left/backward and last carried right/forward. The goal is to find the furthest left y index that is not NA and save the value. The same goes for the furthest right.

```
y_nmis_1 <- which(!is.na(y_1)) #indexes of non-missing y values
y_min_1 <- y_1[min(y_nmis_1)] #get the value from the furtherest left index of y
y_max_1 <- y_1[max(y_nmis_1)] #get the value from the furthest right index of y
```

Applying the function

This code chunk applies the function

```
out_1 <- approx(x_1, y_1, xout = xout_1,  method = "linear", yleft = y_min_1, yright = y_max_1, rule = 
```

Interpolated results

```
print(out_1$y)
```

```
## [1] 4.000000 6.666667 8.333333
```

Manual calculation to confirm it.

Notetoself: In the future, helper functions should be in a separate source file. Seek permission from MS/DH.

Base interpolation helper function

```
#Note: Come back and write more comments later.

#The function takes in two pairs of point and the point you want to interpolate
lin_interpol <- function(y0,y1,x0,x1,x){
  y <- y0 + (x-x0) * ((y1-y0)/(x1-x0))
  return(y)
}
```

Manually outputting the three NA values from above

```r
res_1_1 <- lin_interpol(3,5,1,3,2)
print(res_1_1)
```

```
## [1] 4
```

```r
res_2_1 <- lin_interpol(5,10,3,6,4)
print(res_2_1)
```

```
## [1] 6.666667
```

```r
res_3_1 <- lin_interpol(5,10,3,6,5)
print(res_3_1)
```

```
## [1] 8.333333
```

All the results matches up. We only have a case of Last Value Carried forward and backward to test

Test Case 2

Simulated data 2

We are testing the case of last value carried forward with 1 value missing on the left and 2 values missing on the right

```r
x_2 <- c(1,2,3,4,5,6)
y_2 <- c(NA,3,5,10,NA,NA)
xout_2 <- which(is.na(y_2)) #which returns the indexes where y_1 vector has NA values
```

Same as above (Comments to merge or fill in later)

```r
y_nmis_2 <- which(!is.na(y_2)) #indexes of non-missing y values
y_min_2 <- y_2[min(y_nmis_2)] #get the value from the furtherest left index of y
y_max_2 <- y_2[max(y_nmis_2)] #get the value from the furthest right index of y
```

This code chunk applies the function

```r
out_2 <- approx(x_2, y_2, xout = xout_2,  method = "linear", yleft = y_min_2, yright = y_max_2, rule = 2
```

Interpolated results

```r
print(out_2$y)
```

```
## [1]  3 10 10
```

Perfect. Left value carried forward and right value carried forward works like a charm.

END: Testing Out Linear Interpolation approx/approxfun

To Be Archived as R function is working as it should

Filling using Base Function above Function

```r
#Parameters, X and Y values of each subject with missing NAs for the Y values

#Within function
## skip the first time point
## from the second time point and onwards
### if a missing NA is encountered for Y, go to the non-missing X and Y pair and the next one before.
### Calculate the time points in between.
```

```
#This could be much easily done if I use indexes of missing and non-missing.
##Have an index vector with the two X and Ys.
## Missing indexes can be two types
### It could be an index of count 1 and multiple
### For either case, pick the x0 and y0 and fill it up
```

Applying for Last Value Carried Forward Function

```
#Apply Last Value Carried Forward/Backward for the values
```

Applying to all the subjects function

Execution of the Functions

```
#All BMI subjects
```

```
#All Media Exposure subjects
```