Assignment2_210034046

```
#importing baldy.csv data
PROC import out= Najmi050.baldy
dbms=csv replace
file="/home/u59691081/sasuser.v94/SasFolder/New Folder3/Baldy.csv";
getnames=yes;
datarow=2;
run;
DATA najmi050.baldy_mm;
SET najmi050.baldy;
Luxuriant=luxuriant*25.4;
placebo=placebo*25.4;
baldbegone=baldbegone*25.4;
skinheadnomore=skinheadnomore*25.4;
RUN;
#/*checking contents*/
proc contents data=najmi050.baldy_mm;
run;
#/*checking numeric variable*/
proc univariate data=najmi050.baldy_mm;
run;


data najmi050.LuxuriantVsPlacebo;
set najmi050.baldy_mm;
keep luxuriant placebo;
run;




proc transpose data=najmi050.luxuriantvsplacebo out=temp;
by rows:;
var luxuriant placebo;
run;
proc transpose data=temp out=want;
   by _name_;
   var col:;
run;
proc print data=want;
run;
data najmi050.LuxuriantVsPlacebo;
set work.want;
rename _name_=LUXorPlacebo col1=growth_mm;
run;
proc print data=najmi050.LuxuriantVsPlacebo;
run;
```

```
proc ttest alpha=0.05 data=najmi050.luxuriantvsplacebo sided=2;
class LUXorPlacebo;
var growth_mm;
run;
#The F-stat for equality variance (F<0.0001) shows that the null hypothesis that the variance of the tw
#groups lux or placebo is not the same. Therefore, options are to either use the unpooled Satterthwaite

proc univariate data=najmi050.luxuriantvsplacebo normaltest;
run;
#According to Shapiro-wilk test, the assumption that data is normal, doesn't satisfy.
#To this end, we use non-parametric tests to test growths are equal.
proc npar1way wilcoxon data=najmi050.luxuriantvsplacebo;
class luxorplacebo;
var growth_mm;
exact;
run;
#/*pvalue <0.0001 which is lower than the 0.05 significance level.
#Therefore, we conclude that the placebo and luxuriant have significantly different growth rates.*/
proc univariate data=najmi050.baldy_mm;
run;



Data Najmi050.LUXVSALLBRANDS;
set najmi050.baldy_mm;
keep luxuriant baldbegone skinheadnomore;
run;

proc transpose data=najmi050.luxvsallbrands out=temp;
by rows:;
var luxuriant baldbegone skinheadnomore;
run;
proc sort data= temp;
by _name_;
run;
proc transpose data=work.temp out=need;
by _name_;
var col:;
run;
data najmi050.luxvsallbrands;
set need;
run;
data najmi050.luxvsallbrands;
set najmi050.luxvsallbrands;
rename _name_=Brand col1=Growth_mm;
run;

proc anova data=najmi050.luxvsallbrands;
class brand;
model growth_mm=brand;
means brand/tukey cldiff;
run;
```

```
#pvalue<0.0001 for anova shows that our null
#hypothesis should be rejected and there is a significant difference,
#between the growth rate of atleast one brand compared to the others.

data najmi050.Growths_set;
set najmi050.baldy_mm;
keep luxuriant placebo baldbegone skinheadnomore;
run;
proc transpose data=najmi050.growths_set out=temp;
by rows:;
var luxuriant placebo baldbegone skinheadnomore;
run;
proc sort data=temp;
by _name_;
run;
proc transpose data=temp out=need;
by _name_;
var col:;
run;
data najmi050.Growths_set;
set need;
rename _name_=brand col1=growth_mm;
run;
data najmi050.age_set;
set najmi050.baldy_mm;
drop luxuriant placebo baldbegone skinheadnomore;
run;
data najmi050.age_set;
set najmi050.age_set;
rename ageluxuriant=luxuriant ageplacebo=placebo agebaldbegone=baldbegone ageskinheadnomore=skinheadnom
run;
proc transpose data=najmi050.age_set out=temp;
by rows:;
var luxuriant placebo baldbegone skinheadnomore;
run;

proc sort data=temp;
by _name_;
run;
proc transpose data=temp out=need;
by _name_;
var col:;
run;
data najmi050.ages_set;
set need;
rename _name_=brand col1=ages;
run;

data najmi050.Merged_Growth_Ages;
merge najmi050.growths_set najmi050.ages_set;
run;
proc glm data=najmi050.merged_growth_ages;
class brand;
```

```
model growth_mm=ages/solution clparm;
run;
proc print data=najmi050.merged_growth_ages;
```

R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see http://rmarkdown.rstudio.com.

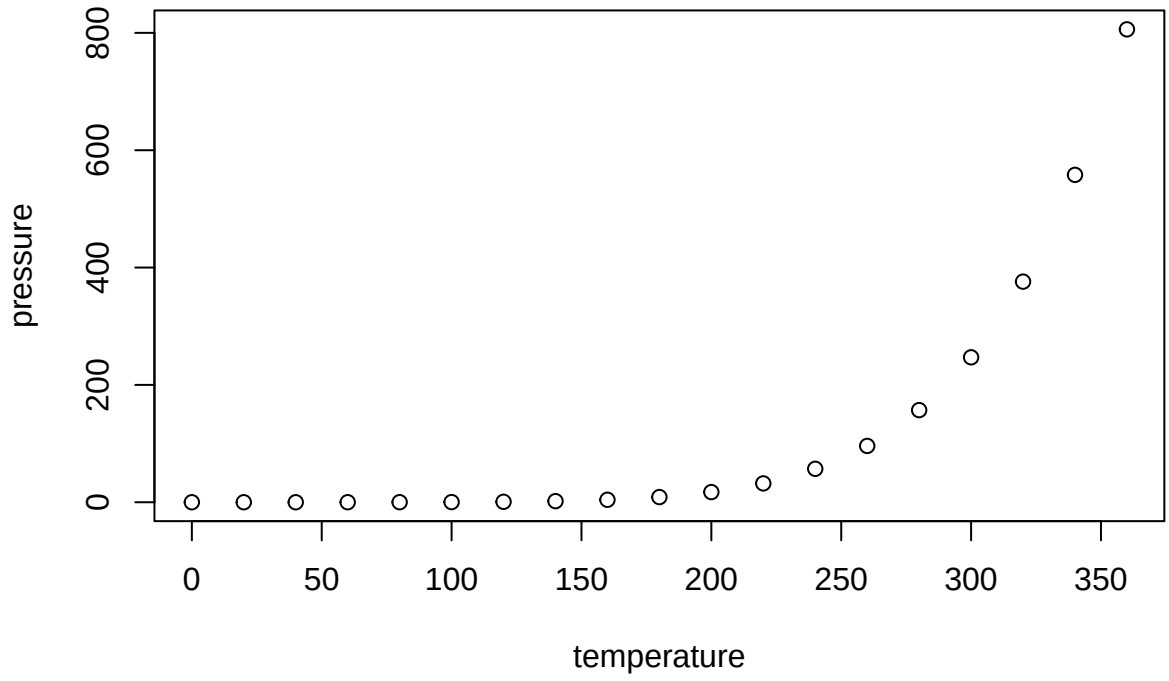
When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
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
```

Including Plots

You can also embed plots, for example:



Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.