

Homework #6

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1

The Proactive Kids Foundation was founded in 2008 by Tony Burke as an early intervention and nonprofit organization with the mission of improving body composition, physical strength, body image and self-esteem in children. According to Burke, “kids alone can’t turn their lives around,” so it is necessary to involve the family as part of the intervention to change the child’s environment.

The PAK Program utilizes a three-tiered approach to make changes in the child’s environment; fitness, nutrition and lifestyle coaching with the goal of educating parents or caregivers along with the child on the topics of mental health coaching (i.e., lifestyle), fitness, and nutrition to impact variables affecting body composition for long-term sustainability. The ProActive kids data consists of 884 children. The data was collected between 2010 to 2017. All children were between 5 to 17 years of age and resided in four Illinois counties.

Body Composition: Height (inches), weight (pounds), body fat (percent), fat free mass (FFM) and BMI and were obtained during week 1 and week 8.

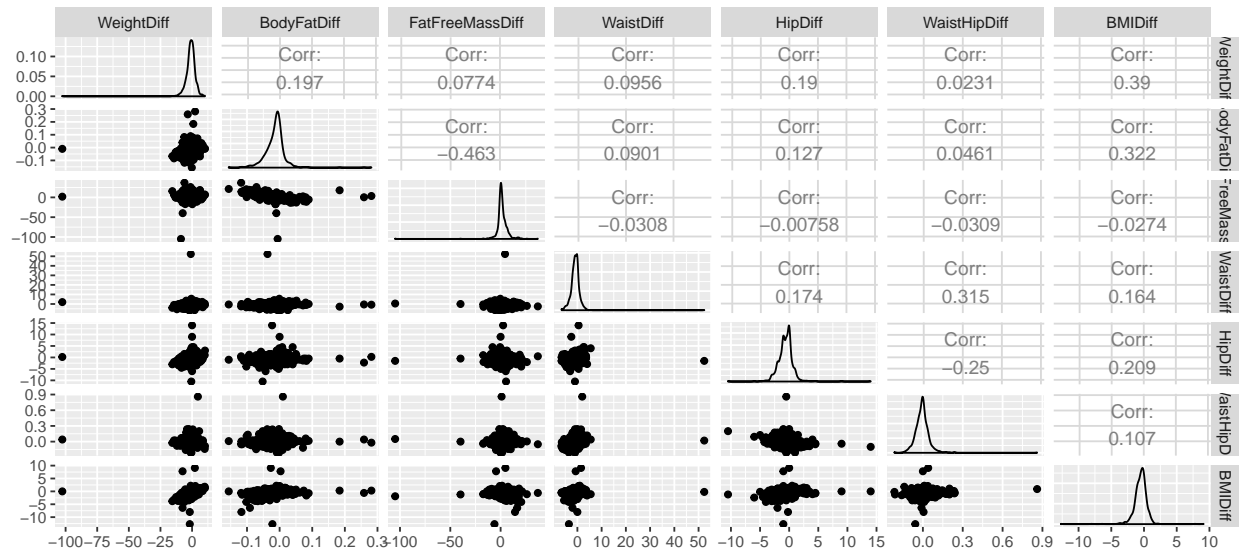
a

Does the program designed by the ProActive Kids Foundation improve the body composition of the children?

In order to visualize the change, the difference of week 8 to week 1 can be computed. Values that fall around 0 indicate that there was little or no change in measurements. Values less than 1 indicate that the Week 8 value was greater than Week 1, and vice versa.

```
kids <- read.csv("~/Downloads/kid_PAK.csv")
kids.plus <-
  kids %>%
  as_tibble() %>%
  mutate(
    WeightDiff = Week_8_Weight - Week_1_Weight,
    BodyFatDiff = Week_8_Body_Fat - Week_1_Body_Fat,
    FatFreeMassDiff = Week_8_Fat_Free_Mass - Week_1_Fat_Free_Mass,
    WaistDiff = Week_8_Waist - Week_1_Waist,
    HipDiff = Week_8_Hip - Week_1_Hip,
    WaistHipDiff = Week_8_Waist_Hip_Ratio - Week_1_Waist_Hip_Ratio,
    BMIDiff = Ending_BMI - Starting_BMI,
    Sex = toupper(Sex)
  )

kids.plus %>%
  select(WeightDiff, BodyFatDiff, FatFreeMassDiff, WaistDiff, HipDiff, WaistHipDiff, BMIDiff) %>%
  ggpairs()
```



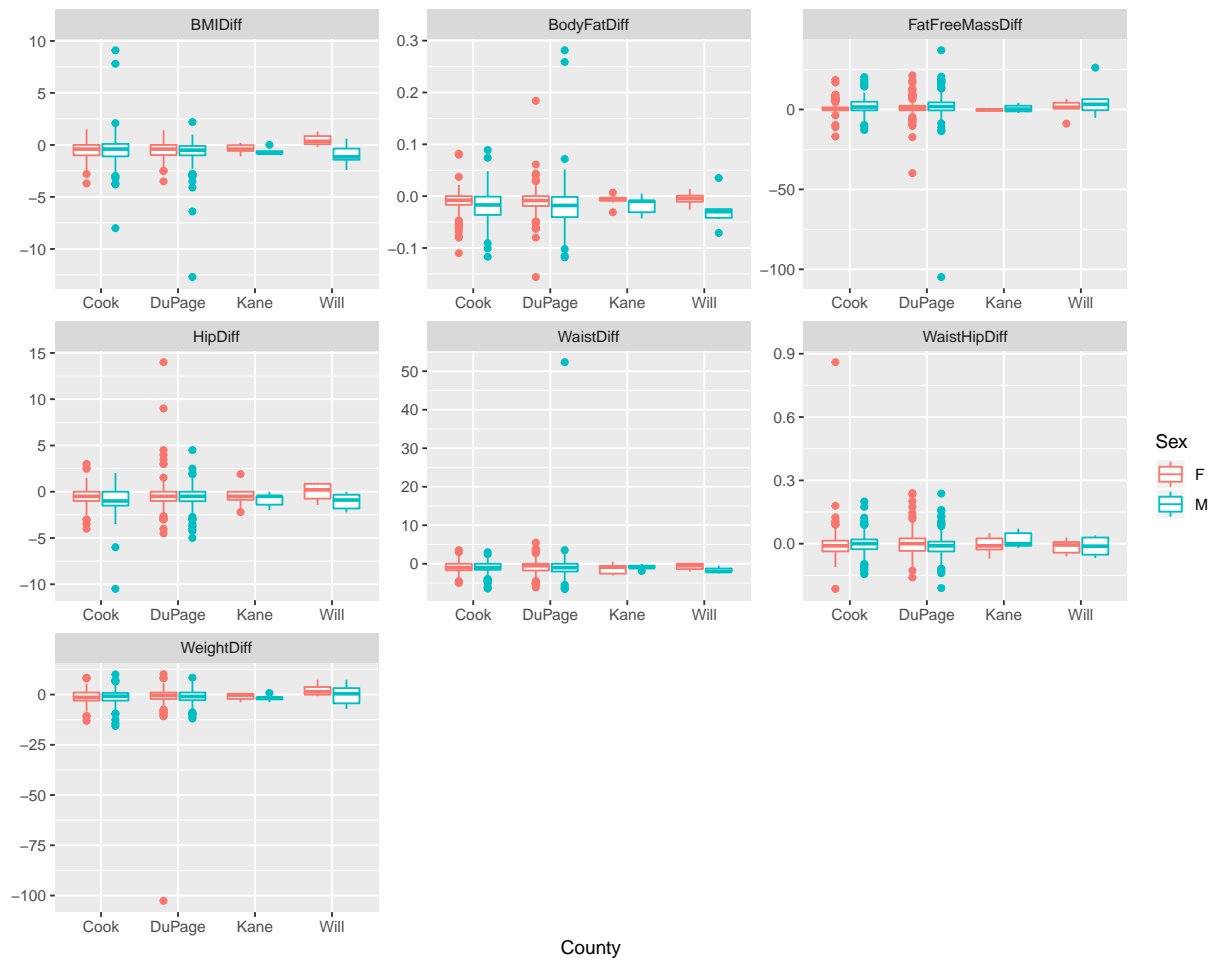
The scatterplots generally appear clustered around 0 with Body Fat differences having the largest variability. The cluster of observations appears to be generally evenly distributed around 0. The shifts in the density plots as well as the scatterplots show that there are a handful of outliers for each value in this dataset.

boxplots for each difference variable

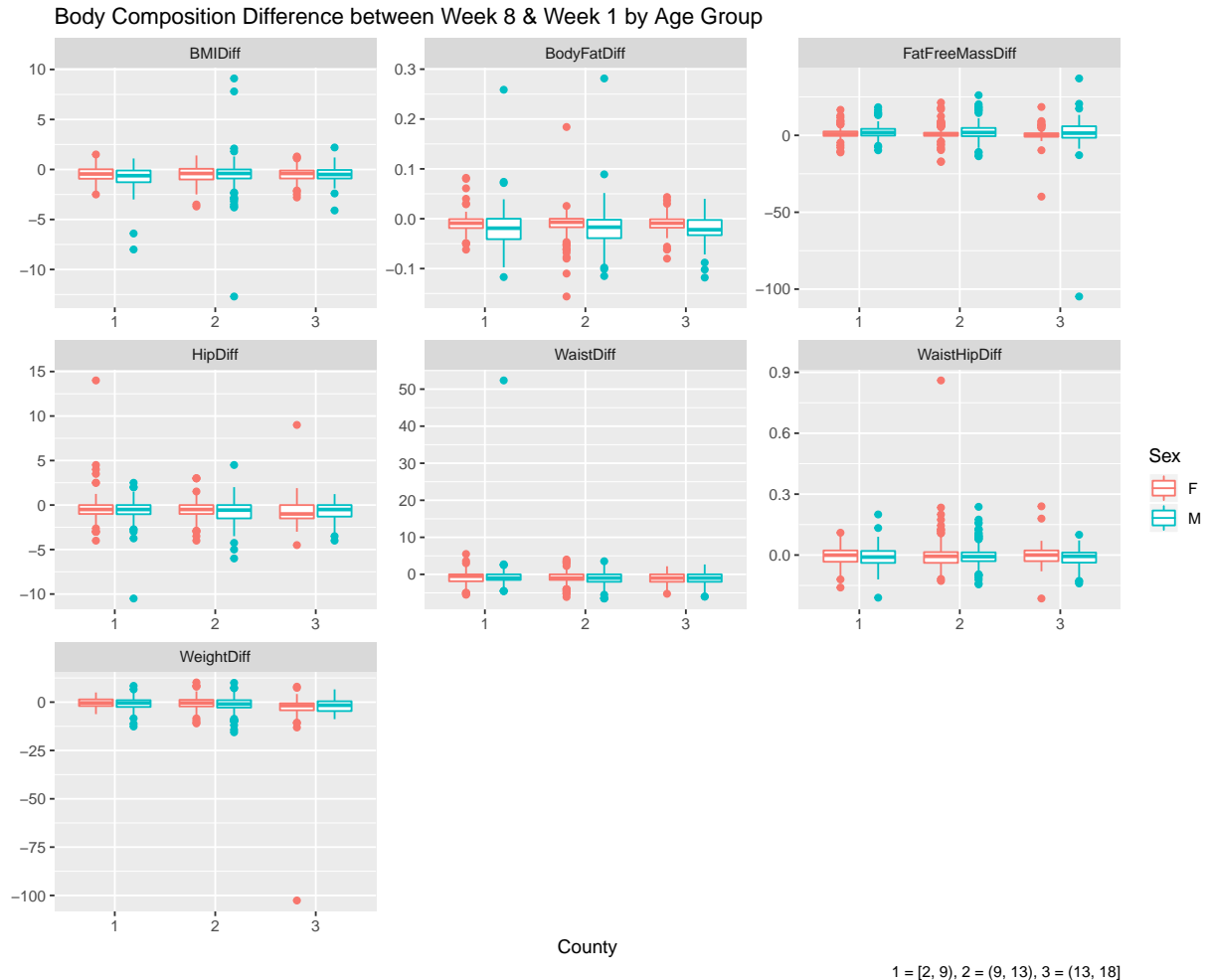
kids.plus %>%

```
select(WeightDiff, BodyFatDiff, FatFreeMassDiff, WaistDiff, HipDiff, WaistHipDiff, BMIDiff, Sex, County_in_IL) %>%
gather(c(-Sex, -County_in_IL), key = "variable", value = "value") %>%
ggplot(aes(y = value, x = County_in_IL, color = Sex)) +
  geom_boxplot() +
  facet_wrap(~ variable, ncol = 3, scales = "free") +
  ylab("") +
  xlab("County") +
  ggtitle("Body Composition Difference between Week 8 & Week 1 by County")
```

Body Composition Difference between Week 8 & Week 1 by County



```
kids.plus %>%
  select(WeightDiff, BodyFatDiff, FatFreeMassDiff, WaistDiff, HipDiff, WaistHipDiff, BMIDiff, Sex, age_group) %>%
  gather(c(-Sex, -age_group), key = "variable", value = "value") %>%
  ggplot(aes(y = value, x = factor(age_group), color = Sex)) +
    geom_boxplot() +
    facet_wrap(~ variable, ncol = 3, scales = "free") +
    ylab("") +
    xlab("County") +
    ggtitle("Body Composition Difference between Week 8 & Week 1 by Age Group") +
    labs(caption = "1 = [2, 9), 2 = (9, 13), 3 = (13, 18]")
```



By county, males have a larger range of composition differences compared to Females for Body Fat, Fat Free Mass, and Hip. The genders are similar in spread for Waist, Waist Hip, BMI, and Weight differences. The counties don't appear to have any noticeable effect on body composition differences.

By Age Group, Males have a larger spread in Body Fat change compared to females. However, the spread and center values appear to be similar across age ranges. This indicates that Age Group is likely not a significant contributing factor to body composition loss.

Based on the above graphs, I suspect that the program does not have a significant effect on body composition for most individuals.

Assumptions

The data are multi-level. One level was removed by calculating the difference between Week 1 and Week 8 (thus removing the longitudinal portion of the model). The levels are as follows:

Level 1

- Body Composition Differences
- Gender
- Age

Level 2

- County
- age_group

The boxplots hint at the variances between genders differing but it can be confirmed with Levene's Test.

```
levene.test(kids.plus$BodyFatDiff, group = kids.plus$Sex)
```

```
##
## Modified robust Brown-Forsythe Levene-type test based on the absolute
## deviations from the median
##
## data: kids.plus$BodyFatDiff
## Test Statistic = 54.114, p-value = 4.319e-13
```

While only one variable is shown, all body composition differences result in heteroscedascity. When modeling, Sex will be modeled with heteroscedastic variances.

Since each participant comes from a county, this will be represented as a *Random Effect* within the models. Age, Sex, and their interaction will be treated as *Fixed Effects* as those are the primary independent variables of interest.

Weight

```
kids.m.weight1 <- lme(WeightDiff ~ Age * Sex, random = ~1 | County_in_IL, kids.plus, method = "REML", w
kids.m.weight1 %>% summary
```

```
## Linear mixed-effects model fit by REML
## Data: kids.plus
##      AIC      BIC    logLik
## 5162.848 5196.323 -2574.424
##
## Random effects:
## Formula: ~1 | County_in_IL
##      (Intercept) Residual
## StdDev: 0.0001805634 5.685343
##
## Variance function:
## Structure: Different standard deviations per stratum
## Formula: ~1 | Sex
## Parameter estimates:
##      F      M
## 1.0000000 0.6038167
## Fixed effects: WeightDiff ~ Age * Sex
##      Value Std.Error DF   t-value p-value
## (Intercept)  3.207723 1.1199111 879   2.864266  0.0043
## Age        -0.411073 0.1047923 879  -3.922745  0.0001
## SexM       -3.293791 1.3022163 879  -2.529373  0.0116
## Age:SexM    0.304470 0.1220874 879   2.493870  0.0128
## Correlation:
##      (Intr) Age    SexM
## Age      -0.970
## SexM     -0.860  0.834
## Age:SexM  0.833 -0.858 -0.970
##
## Standardized Within-Group Residuals:
```

```
##           Min           Q1           Med           Q3           Max
## -17.50148991  -0.36877229   0.04189108   0.46395725   3.30686808
##
## Number of Observations: 886
## Number of Groups: 4
```

```
kids.m.weight2 <- lme(WeightDiff ~ Age * Sex, random = ~1 | County_in_IL, kids.plus, method = "REML")
anova(kids.m.weight1, kids.m.weight2) %>% as_tibble() %>% select(-call) %>% kable %>% kable_styling(ful
```

Model	df	AIC	BIC	logLik	Test	L.Ratio	p-value
1	7	5162.848	5196.323	-2574.424		NA	NA
2	6	5268.852	5297.545	-2628.426	1 vs 2	108.0045	0

```
intervals(kids.m.weight1)
```

```
## Approximate 95% confidence intervals
##
## Fixed effects:
##           lower           est.           upper
## (Intercept)  1.00971127  3.2077231  5.4057350
## Age         -0.61674558 -0.4110733 -0.2054011
## SexM        -5.84960735 -3.2937911 -0.7379749
## Age:SexM     0.06485322  0.3044701  0.5440870
## attr("label")
## [1] "Fixed effects:"
##
## Random Effects:
## Level: County_in_IL
##           lower           est.           upper
## sd((Intercept)) 4.546314e-51 0.0001805634 7.171333e+42
##
## Variance function:
##           lower           est.           upper
## M 0.5499922 0.6038167 0.6629087
## attr("label")
## [1] "Variance function:"
##
## Within-group standard error:
##           lower           est.           upper
## 5.321017 5.685343 6.074614
```

The model accounting for heroscedasticity in Sex and without. The AIC and BIC values indicate that accounting the heterosceastic model is a better fit. County doesnt appear to affect the model due to its small intercept value but the fixed effects are all significant.

Body Fat

```
kids.m.bfat1 <- lme(BodyFatDiff ~ Age * Sex, random = ~1 | County_in_IL, kids.plus, method = "REML", we
kids.m.bfat1 %>% summary
```

```
## Linear mixed-effects model fit by REML
## Data: kids.plus
##           AIC           BIC      logLik
```

```
## -3732.056 -3698.581 1873.028
##
## Random effects:
## Formula: ~1 | County_in_IL
## (Intercept) Residual
## StdDev: 2.534778e-07 0.0222665
##
## Variance function:
## Structure: Different standard deviations per stratum
## Formula: ~1 | Sex
## Parameter estimates:
## F M
## 1.000000 1.630617
## Fixed effects: BodyFatDiff ~ Age * Sex
## Value Std.Error DF t-value p-value
## (Intercept) -0.007682595 0.004386104 879 -1.7515762 0.0802
## Age -0.000216930 0.000410416 879 -0.5285605 0.5972
## SexM -0.010642338 0.008284482 879 -1.2846112 0.1993
## Age:SexM 0.000166755 0.000779347 879 0.2139672 0.8306
## Correlation:
## (Intr) Age SexM
## Age -0.970
## SexM -0.529 0.514
## Age:SexM 0.511 -0.527 -0.970
##
## Standardized Within-Group Residuals:
## Min Q1 Med Q3 Max
## -6.57327466 -0.44569013 0.07054434 0.44570512 8.70136921
##
## Number of Observations: 886
## Number of Groups: 4

kids.m.bfat2 <- lme(BodyFatDiff ~ Age * Sex, random = ~1 | County_in_IL, kids.plus, method = "REML")

anova(kids.m.bfat1, kids.m.bfat2) %>% as_tibble() %>% select(-call) %>% kable %>% kable_styling(full_wi
```

Model	df	AIC	BIC	logLik	Test	L.Ratio	p-value
1	7	-3732.056	-3698.581	1873.028		NA	NA
2	6	-3632.791	-3604.098	1822.395	1 vs 2	101.2655	0

```
intervals(kids.m.bfat1)

## Approximate 95% confidence intervals
##
## Fixed effects:
## lower est. upper
## (Intercept) -0.016291054 -0.007682595 0.0009258639
## Age -0.001022440 -0.0002169298 0.0005885804
## SexM -0.026902013 -0.0106423382 0.0056173367
## Age:SexM -0.001362843 0.0001667546 0.0016963524
## attr(,"label")
## [1] "Fixed effects:"
##
## Random Effects:
## Level: County_in_IL
```

```
##               lower      est.      upper
## sd((Intercept)) 2.386278e-74 2.534778e-07 2.692519e+60
##
## Variance function:
##      lower      est.      upper
## M 1.485318 1.630617 1.79013
## attr("label")
## [1] "Variance function:"
##
## Within-group standard error:
##      lower      est.      upper
## 0.02083979 0.02226650 0.02379089
```

Again the model accounting for variance is superior. Going forward only this model will be used. None of the fixed terms are significant in this context so theres nothing that can be gleaned from this model.

Fat Free Mass

```
kids.m.ffreemass1 <- lme(FatFreeMassDiff ~ Age * Sex, random = ~1 | County_in_IL, kids.plus, method = "REML")
kids.m.ffreemass1 %>% summary
```

```
## Linear mixed-effects model fit by REML
## Data: kids.plus
##      AIC      BIC    logLik
## 5557.137 5590.612 -2771.569
##
## Random effects:
## Formula: ~1 | County_in_IL
##      (Intercept) Residual
## StdDev: 0.0002049374 4.146103
##
## Variance function:
## Structure: Different standard deviations per stratum
## Formula: ~1 | Sex
## Parameter estimates:
##      F      M
## 1.000000 1.762465
## Fixed effects: FatFreeMassDiff ~ Age * Sex
##      Value Std.Error DF   t-value p-value
## (Intercept) 2.1063479 0.8167083 879 2.5790699 0.0101
## Age      -0.1147639 0.0764210 879 -1.5017334 0.1335
## SexM      1.9024794 1.6333301 879 1.1647856 0.2444
## Age:SexM  -0.0751178 0.1536867 879 -0.4887719 0.6251
## Correlation:
##      (Intr) Age    SexM
## Age      -0.970
## SexM     -0.500 0.485
## Age:SexM 0.482 -0.497 -0.970
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -14.45914738 -0.34112896 -0.07744787 0.28533771 4.88341821
##
```



```
## Number of Observations: 886
## Number of Groups: 4
intervals(kids.m.ffreemass1, which = "fixed")

## Approximate 95% confidence intervals
##
## Fixed effects:
##           lower      est.      upper
## (Intercept) 0.5034218 2.10634791 3.70927401
## Age        -0.2647529 -0.11476395 0.03522496
## SexM       -1.3032027  1.90247939 5.10816153
## Age:SexM    -0.3767536 -0.07511776 0.22651804
## attr("label")
## [1] "Fixed effects:"
```

The fixed effects are not significant and the standard error of the random effects is very small.

Waist

```
kids.m.waist1 <- lme(WaistDiff ~ Age * Sex, random = ~1 | County_in_IL, kids.plus, method = "REML", wei
kids.m.waist1 %>% summary
```

```
## Linear mixed-effects model fit by REML
## Data: kids.plus
##      AIC      BIC    logLik
## 3913.345 3946.82 -1949.672
##
## Random effects:
## Formula: ~1 | County_in_IL
##      (Intercept) Residual
## StdDev: 0.09407075 1.587838
##
## Variance function:
## Structure: Different standard deviations per stratum
## Formula: ~1 | Sex
## Parameter estimates:
##      F      M
## 1.000000 1.861468
## Fixed effects: WaistDiff ~ Age * Sex
##           Value Std.Error DF   t-value p-value
## (Intercept) -0.5402435 0.3209685 879 -1.683167 0.0927
## Age        -0.0312176 0.0292982 879 -1.065512 0.2869
## SexM       0.9518384 0.6521699 879  1.459494 0.1448
## Age:SexM    -0.0974129 0.0613801 879 -1.587044 0.1129
## Correlation:
##      (Intr) Age      SexM
## Age      -0.951
## SexM     -0.468  0.465
## Age:SexM  0.451 -0.476 -0.970
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.368347583 -0.412603892  0.005273475  0.439070858 17.777234100
```

```
##
## Number of Observations: 886
## Number of Groups: 4
intervals(kids.m.waist1)

## Approximate 95% confidence intervals
##
## Fixed effects:
##           lower      est.      upper
## (Intercept) -1.17019764 -0.54024348 0.08971067
## Age          -0.08872024 -0.03121760 0.02628504
## SexM         -0.32815362  0.95183842 2.23183045
## Age:SexM     -0.21788145 -0.09741286 0.02305574
## attr("label")
## [1] "Fixed effects:"
##
## Random Effects:
## Level: County_in_IL
##           lower      est.      upper
## sd((Intercept)) 0.007579042 0.09407075 1.167602
##
## Variance function:
##           lower      est.      upper
## M 1.695524 1.861468 2.043653
## attr("label")
## [1] "Variance function:"
##
## Within-group standard error:
##           lower      est.      upper
## 1.485999 1.587838 1.696657
```

The fixed effects are not significant and the standard error of the random effects is very small.

Hip

```
kids.m.hip1 <- lme(HipDiff ~ Age * Sex, random = ~1 | County_in_IL, kids.plus, method = "REML", weights
kids.m.hip1 %>% summary
```

```
## Linear mixed-effects model fit by REML
## Data: kids.plus
##           AIC      BIC      logLik
## 3016.305 3049.78 -1501.153
##
## Random effects:
## Formula: ~1 | County_in_IL
##           (Intercept) Residual
## StdDev: 0.1465308 1.373747
##
## Variance function:
## Structure: Different standard deviations per stratum
## Formula: ~1 | Sex
## Parameter estimates:
##           F           M
```

```
## 1.0000000 0.9022917
## Fixed effects: HipDiff ~ Age * Sex
##           Value Std.Error   DF    t-value p-value
## (Intercept) -0.0426223  0.2899281  879  -0.1470098  0.8832
## Age         -0.0437615  0.0253708  879  -1.7248755  0.0849
## SexM        -0.7382503  0.3618720  879  -2.0400866  0.0416
## Age:SexM     0.0458963  0.0339827  879   1.3505768  0.1772
## Correlation:
##      (Intr) Age    SexM
## Age      -0.918
## SexM     -0.702  0.724
## Age:SexM  0.679 -0.744 -0.970
##
## Standardized Within-Group Residuals:
##      Min          Q1          Med          Q3          Max
## -7.75281273 -0.50228992  0.05761278  0.52277392 10.31635858
##
## Number of Observations: 886
## Number of Groups: 4
```

```
intervals(kids.m.hip1)
```

```
## Approximate 95% confidence intervals
##
## Fixed effects:
##           lower      est.      upper
## (Intercept) -0.61165443 -0.04262228  0.526409872
## Age         -0.09355605 -0.04376155  0.006032958
## SexM        -1.44848442 -0.73825030 -0.028016177
## Age:SexM    -0.02080049  0.04589630  0.112593097
## attr("label")
## [1] "Fixed effects:"
##
## Random Effects:
## Level: County_in_IL
##           lower      est.      upper
## sd((Intercept)) 0.04263793 0.1465308 0.5035725
##
## Variance function:
##           lower      est.      upper
## M 0.8219528 0.9022917 0.9904832
## attr("label")
## [1] "Variance function:"
##
## Within-group standard error:
##           lower      est.      upper
## 1.285804 1.373747 1.467705
```

Sex is the only parameter that is considered moderately significant.

Waist-Hip Ratio

```
kids.m.waisthip1 <- lme(WaistHipDiff ~ Age * Sex, random = ~1 | County_in_IL, kids.plus, method = "REML")
kids.m.waisthip1 %>% summary
```

```
## Linear mixed-effects model fit by REML
## Data: kids.plus
##      AIC      BIC    logLik
## -2515.156 -2481.681 1264.578
##
## Random effects:
## Formula: ~1 | County_in_IL
##      (Intercept)  Residual
## StdDev: 7.066454e-06 0.06535221
##
## Variance function:
## Structure: Different standard deviations per stratum
## Formula: ~1 | Sex
## Parameter estimates:
##      F      M
## 1.0000000 0.7561438
## Fixed effects: WaistHipDiff ~ Age * Sex
##      Value Std.Error DF   t-value p-value
## (Intercept) -0.019116144 0.012873220 879 -1.4849543 0.1379
## Age          0.001547237 0.001204572 879  1.2844703 0.1993
## SexM         0.013660886 0.016037946 879  0.8517852 0.3946
## Age:SexM     -0.001703553 0.001504680 879 -1.1321697 0.2579
## Correlation:
##      (Intr) Age    SexM
## Age      -0.970
## SexM     -0.803  0.779
## Age:SexM  0.777 -0.801 -0.970
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -4.11937028 -0.48056948 -0.02735479  0.39874188 13.15586811
##
## Number of Observations: 886
## Number of Groups: 4
```

```
intervals(kids.m.waisthip1, which = "fixed")
```

```
## Approximate 95% confidence intervals
##
## Fixed effects:
##      lower      est.      upper
## (Intercept) -0.0443819813 -0.019116144 0.006149694
## Age          -0.0008169362  0.001547237 0.003911411
## SexM         -0.0178162537  0.013660886 0.045138025
## Age:SexM     -0.0046567371 -0.001703553 0.001249632
## attr(,"label")
## [1] "Fixed effects:"
```

There are no significant parameters.

BMI

```
kids.m.bmi1 <- lme(BMIDiff ~ Age * Sex, random = ~1 | County_in_IL, kids.plus, method = "REML", weights
kids.m.bmi1 %>% summary
```

```
## Linear mixed-effects model fit by REML
## Data: kids.plus
##      AIC      BIC    logLik
## 2538.461 2571.936 -1262.23
##
## Random effects:
## Formula: ~1 | County_in_IL
##      (Intercept) Residual
## StdDev: 0.007208256 0.7721343
##
## Variance function:
## Structure: Different standard deviations per stratum
## Formula: ~1 | Sex
## Parameter estimates:
##      F      M
## 1.000000 1.658794
## Fixed effects: BMIDiff ~ Age * Sex
##      Value Std.Error DF   t-value p-value
## (Intercept) -0.2933702 0.15220524 879 -1.927465 0.0542
## Age          -0.0147116 0.01423253 879 -1.033658 0.3016
## SexM          -0.7307012 0.29086459 879 -2.512170 0.0122
## Age:SexM       0.0566014 0.02736404 879  2.068460 0.0389
## Correlation:
##      (Intr) Age    SexM
## Age      -0.970
## SexM     -0.523  0.507
## Age:SexM  0.504 -0.520 -0.970
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -9.5394582 -0.4832522  0.0710996  0.5090557  7.5626362
##
## Number of Observations: 886
## Number of Groups: 4
intervals(kids.m.bmi1, which = "fixed")
```

```
## Approximate 95% confidence intervals
##
## Fixed effects:
##      lower      est.      upper
## (Intercept) -0.592098375 -0.29337024  0.005357887
## Age          -0.042645289 -0.01471157  0.013222139
## SexM          -1.301571376 -0.73070119 -0.159831003
## Age:SexM       0.002894941  0.05660143  0.110307922
## attr("label")
## [1] "Fixed effects:"
```

The interaction between Age and Sex is significant, as well as Sex. The standard error associated with the Random Effect of County is small indicating that it hardly effects the model.

Conclusion

There is evidence that given a child's age and gender, the PAK program does improve both BMI and Weight. A majority of the differences are negative indicating that there was a decrease between Week 1 and Week

8. This dataset contains many outliers and they were not dealt with in this case. Further analysis should mitigate them.

```
kids.m.bmi1$fitted[,2] %>% enframe() %>% mutate(is_effective = value <= 0) %>% group_by(is_effective) %>
```

is_effective	n
TRUE	886

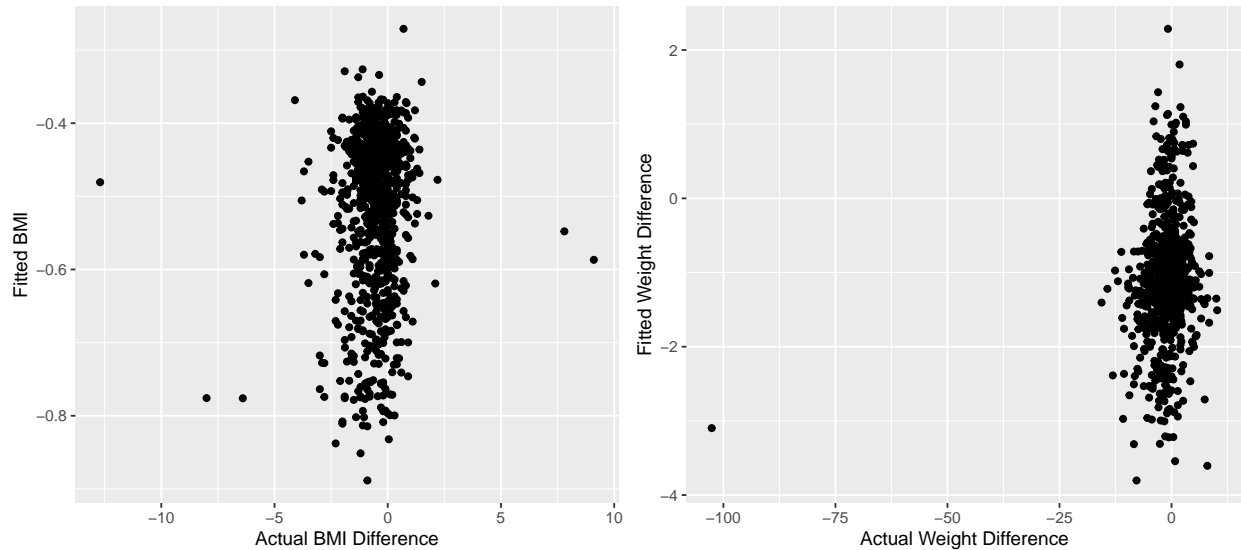
```
plot1 <- qplot(kids.m.bmi1$data$BMIDiff, kids.m.bmi1$fitted[,1]) + xlab("Actual BMI Difference") + ylab("Fitted BMI")
```

```
kids.m.weight1$fitted[,2] %>% enframe() %>% mutate(is_effective = value <= 0) %>% group_by(is_effective) %>
```

is_effective	n
FALSE	69
TRUE	817

```
plot2 <- qplot(kids.m.weight1$data$WeightDiff, kids.m.weight1$fitted[,1]) + xlab("Actual Weight Difference") + ylab("Fitted Weight Difference")
```

```
grid.arrange(plot1, plot2, ncol = 2)
```



b

Is there any significant difference among the four counties?

There is no significant difference between the four counties. The Boxplots show them to be fairly similar and all models showed that the coefficients associated with the four counties were very small.

II

The data used in this exercise were originally reported by Douglas et al (2004) and the data was reproduced by West et al (2012). The main goal of their experiment was to examine nucleotide activation (guanine nucleotide bonding) in seven different brain nuclei (i.e. brain regions) among five adults male rats. The basal nucleotide activation, measured after treatment with saline solution,

was compared to activation in the same region after treatment with the drug carbachol. Activation was measured as the mean optical density produced by autoradiography.

We want to compare activation in a subset of three of the original seven brain regions studied by the authors: the bed nucleus of the stria terminals (BST), the lateral septum (LS), and the diagonal band of Broca (VDB). The original data layout for this study is shown below. Use an appropriate statistical model to examine the nucleotide activation.

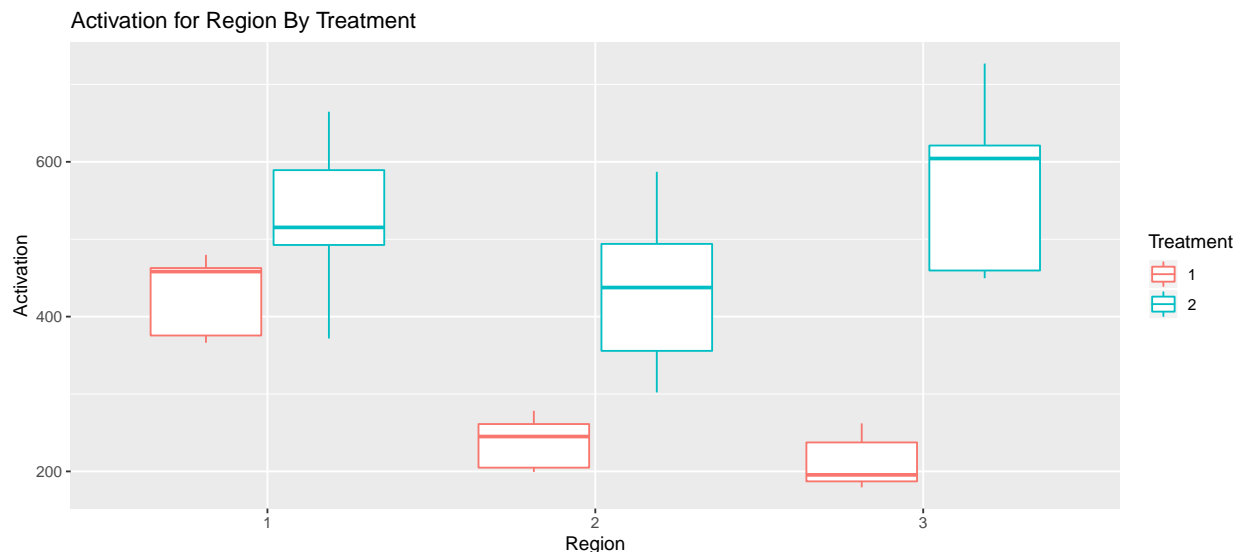
```
activate <- read.table("~/Downloads/ratbrain.txt", header = TRUE)

activate %>% head %>% kable %>% kable_styling(full_width = F, bootstrap_options = "striped", latex_opti
```

animal	treatment	region	activate
R111097	1	1	366.19
R111097	1	2	199.31
R111097	1	3	187.11
R111097	2	1	371.71
R111097	2	2	302.02
R111097	2	3	449.70

This is a Multi-level dataset with three levels: Region, Treatment, and animal respectively.

```
activate %>%
  ggplot(aes(y = activate, x = factor(region), color = factor(treatment))) +
  geom_boxplot() +
  ylab("Activation") +
  xlab("Region") +
  ggtitle("Activation for Region By Treatment") +
  # This is strange but it changes the legend text
  labs(color = "Treatment")
```



Activation is higher in all regions in Treatment 2 compared to Treatment 1. Treatment 2 also seems to have a greater spread than Treatment 1. Thus the treatments can be treated as separate variances. Though this should be compared to a model where region is treated with separate variances. Region, Treatment, and their interaction will be treated as fixed effects since we most interested in them. The animal itself should be treated as a random effect since there will be some measure of correlation between observations on the same animal.

```
activate.m.t1 <- lme(activate ~ factor(region) * factor(treatment), random = ~1 | animal, activate, method="REML")
summary(activate.m.t1)
```

```
## Linear mixed-effects model fit by REML
## Data: activate
##      AIC      BIC    logLik
## 285.187 295.7895 -133.5935
##
## Random effects:
## Formula: ~1 | animal
##      (Intercept) Residual
## StdDev:      40.1177 21.25381
##
## Variance function:
## Structure: Different standard deviations per stratum
## Formula: ~1 | factor(treatment)
## Parameter estimates:
##      1      2
## 1.000000 3.896054
## Fixed effects: activate ~ factor(region) * factor(treatment)
##
##              Value Std.Error DF   t-value p-value
## (Intercept)    428.506   20.30347 20   21.105062  0.0000
## factor(region)2   -190.762   13.44209 20  -14.191395  0.0000
## factor(region)3   -216.212   13.44209 20  -16.084701  0.0000
## factor(treatment)2    98.204   38.23234 20    2.568611  0.0183
## factor(region)2:factor(treatment)2  99.322   54.06869 20    1.836960  0.0811
## factor(region)3:factor(treatment)2 261.822   54.06869 20    4.842396  0.0001
## Correlation:
##              (Intr) fctr(r)2 fct()3 fctr(t)2 f()2:(
## factor(region)2   -0.331
## factor(region)3   -0.331  0.500
## factor(treatment)2 -0.116  0.176  0.176
## factor(region)2:factor(treatment)2  0.082 -0.249  -0.124 -0.707
## factor(region)3:factor(treatment)2  0.082 -0.124  -0.249 -0.707  0.500
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -1.5941411 -0.6358639  0.0947552  0.2780940  1.6094257
##
## Number of Observations: 30
## Number of Groups: 5
```

All the variables are considered significant except for the interaction between treatment 2 and region 2. The standard error associated with the animal ranges between 18.7665 and 85.7607 with 95% confidence. This indicates that the animal a treatment is applied may have a noticeable effect on the level of activation.

```
activate.m.t2 <- lme(activate ~ factor(region) * factor(treatment), random = ~1 | animal, activate, method="REML")
anova(activate.m.t1, activate.m.t2) %>% as_tibble %>% select(-call) %>% kable %>% kable_styling(full_width = TRUE)
```

Model	df	AIC	BIC	logLik	Test	L.Ratio	p-value
1	9	285.1870	295.7895	-133.5935		NA	NA
2	10	295.1756	306.9561	-137.5878	1 vs 2	7.988565	0.0047074


```
intervals(activate.m.t1)
```

```
## Approximate 95% confidence intervals
##
## Fixed effects:
##               lower    est.    upper
## (Intercept)    386.15370  428.506  470.8583
## factor(region)2 -218.80171 -190.762 -162.7223
## factor(region)3 -244.25171 -216.212 -188.1723
## factor(treatment)2  18.45274   98.204  177.9553
## factor(region)2:factor(treatment)2 -13.46331   99.322  212.1073
## factor(region)3:factor(treatment)2 149.03669  261.822  374.6073
## attr("label")
## [1] "Fixed effects:"
##
## Random Effects:
## Level: animal
##               lower    est.    upper
## sd((Intercept)) 18.76651  40.1177  85.76073
##
## Variance function:
##      lower    est.    upper
## 2 2.0228 3.896054 7.504073
## attr("label")
## [1] "Variance function:"
##
## Within-group standard error:
##      lower    est.    upper
## 13.18499 21.25381 34.26050
```

There is convincing evidence that the first model is a better fit.

Conclusion

Region 2 is estimated to be 190.762 points lower compared to Region 1. Region 3 is estimated to be 216.212 points lower than Region 1. Treatment 2 is estimated to increase activation by 98.204 assuming that all other variables are held constant. When Treatment 2 is applied to Region 2 and 3, there is an estimated increase in activation by 99.322 and 261.822 respectively.