Lab1

August 7, 2019

```
In [2]: #install.packages("psych")
        #install.packages("gpairs")
        #install.packages("gplots")
        #install.packages("coefplot")
        #install.packages("car")
        #install.packages("corrplot")
        #install.packages("alr3")
        #install.packaged("MASS")
        #install.packages("mlogit")
        library(MASS)
        library(alr3)
        require(car)
        require("psych")
        require(gpairs)
        require(corrplot)
        require(gplots)
        require(coefplot)
```

```
In [2]: setwd("C:\\Users\\armop\\Dropbox\\PHD\\Teaching\\AGBU505\\2019\\Lecture1") ##Start by 
        df=read.table("amus_park.csv",sep=",",header=TRUE)
```

After loading the data start the usual procedure to check the correctness of the loaded data. Check whether the loaded data has correct dimensions, print the first and last few observations.

```
In [3]: dim(df)
```

1. 500 2. 8

```
In [4]: head(df)
```

weekend	num.child	distance	rides	games	wait	clean	overall
yes	0	114.64826	82	68	64	86	49
yes	2	27.01410	82	73	80	84	68
no	1	63.30098	79	75	74	86	62
yes	0	25.90993	82	68	69	87	38
no	4	54.71831	78	83	78	84	69
no	5	22.67934	76	75	51	77	29

```
In [5]: tail(df)
```

	weekend	num.child	distance	rides	games	wait	clean	overall
495	no	5	41.47010	78	80	80	87	57
496	no	0	11.05258	85	67	72	87	48
497	yes	0	8.18774	86	79	85	89	48
498	no	2	45.17740	90	88	89	91	74
499	no	3	27.08838	78	79	84	86	57
500	no	1	38.40876	81	84	81	83	65

Check for NAN or missing values

```
In [6]: sum(is.na(df)) #Check for NAN or missing values
```

0

It is good idea to summerize your data and investigate it.

```
In [7]: describe(df)
```

	vars	n	mean	sd	median	trimmed	mad	min	max
weekend*	1	500	1.48200	0.5001763	1.00000	1.47750	0.00000	1.0000000	2.0000
num.child	2	500	1.73800	1.4959384	2.00000	1.61000	1.48260	0.0000000	5.0000
distance	3	500	31.04751	33.1454452	19.01909	24.64603	17.25512	0.5267228	239.1921
rides	4	500	80.38200	5.4150458	80.00000	80.35250	5.93040	67.0000000	94.0000
games	5	500	74.14400	8.1249797	74.00000	74.20000	8.89560	52.0000000	96.0000
wait	6	500	73.41600	10.7518439	74.00000	73.50500	11.86080	43.0000000	103.0000
clean	7	500	85.39200	5.1333262	85.00000	85.38750	5.93040	72.0000000	98.0000
overall	8	500	52.87200	16.0763339	52.00000	52.51000	16.30860	6.0000000	102.0000

or you can use different command

```
In [8]: summary(df)
```

```
 weekend      num.child         distance            rides            games
 no :259   Min.   :0.000   Min.   :  0.5267   Min.   :67.00   Min.   :52.00
 yes:241   1st Qu.:0.000   1st Qu.: 10.3181   1st Qu.:77.00   1st Qu.:68.00
           Median :2.000   Median : 19.0191   Median :80.00   Median :74.00
           Mean   :1.738   Mean   : 31.0475   Mean   :80.38   Mean   :74.14
           3rd Qu.:3.000   3rd Qu.: 39.5821   3rd Qu.:84.00   3rd Qu.:80.00
           Max.   :5.000   Max.   :239.1921   Max.   :94.00   Max.   :96.00
      wait            clean          overall
 Min.   : 43.00   Min.   :72.00   Min.   :  6.00
 1st Qu.: 65.75   1st Qu.:82.00   1st Qu.: 41.75
 Median : 74.00   Median :85.00   Median : 52.00
 Mean   : 73.42   Mean   :85.39   Mean   : 52.87
 3rd Qu.: 81.00   3rd Qu.:89.00   3rd Qu.: 63.00
 Max.   :103.00   Max.   :98.00   Max.   :102.00
```

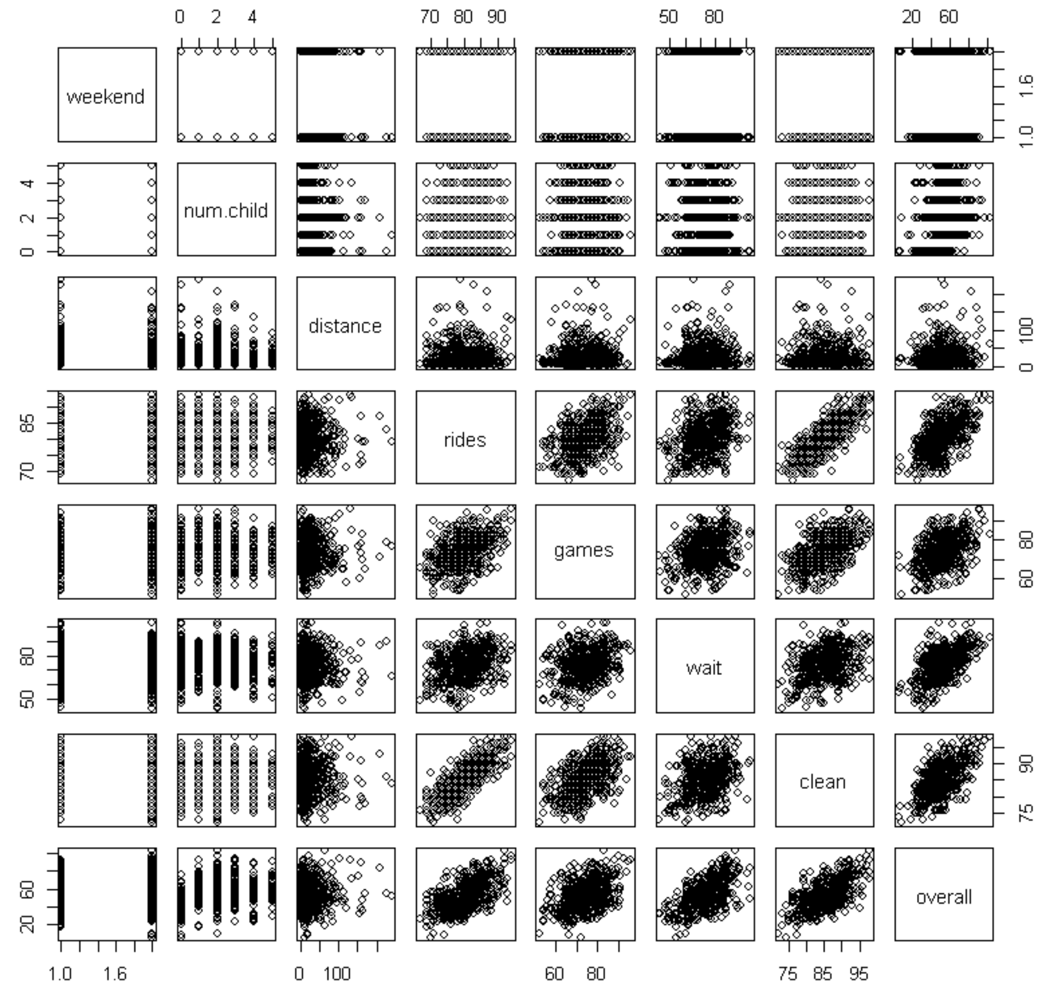
For summerizing discrete data use function *table()*

```
In [9]: table(df$weekend) #for discrete data
```

```
 no yes
259 241
```

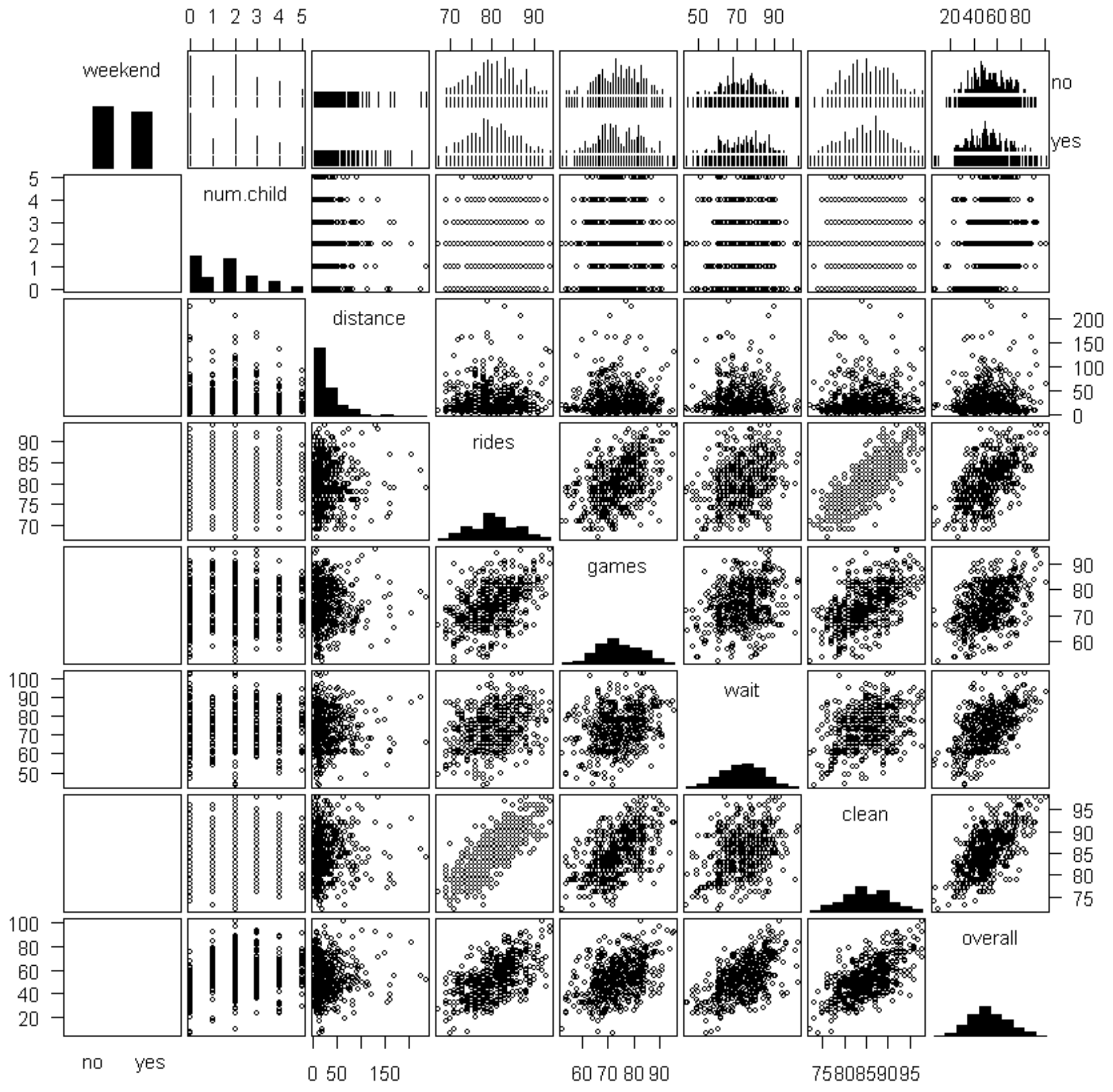
Before modeling, there are two important things to check: that each individual variable has a reasonable distribution, and that joint relationships among the variables are appropriate for modeling. Start by visualizing data.

```
In [10]: #Visualize the data
         pairs(formula =  weekend +  num.child + distance   +rides   + games + wait + clean
               + overall, data=df,main="")
```



```
In [11]: gpairs(df)
```

```
Loading required package: grid
Loading required package: lattice
```

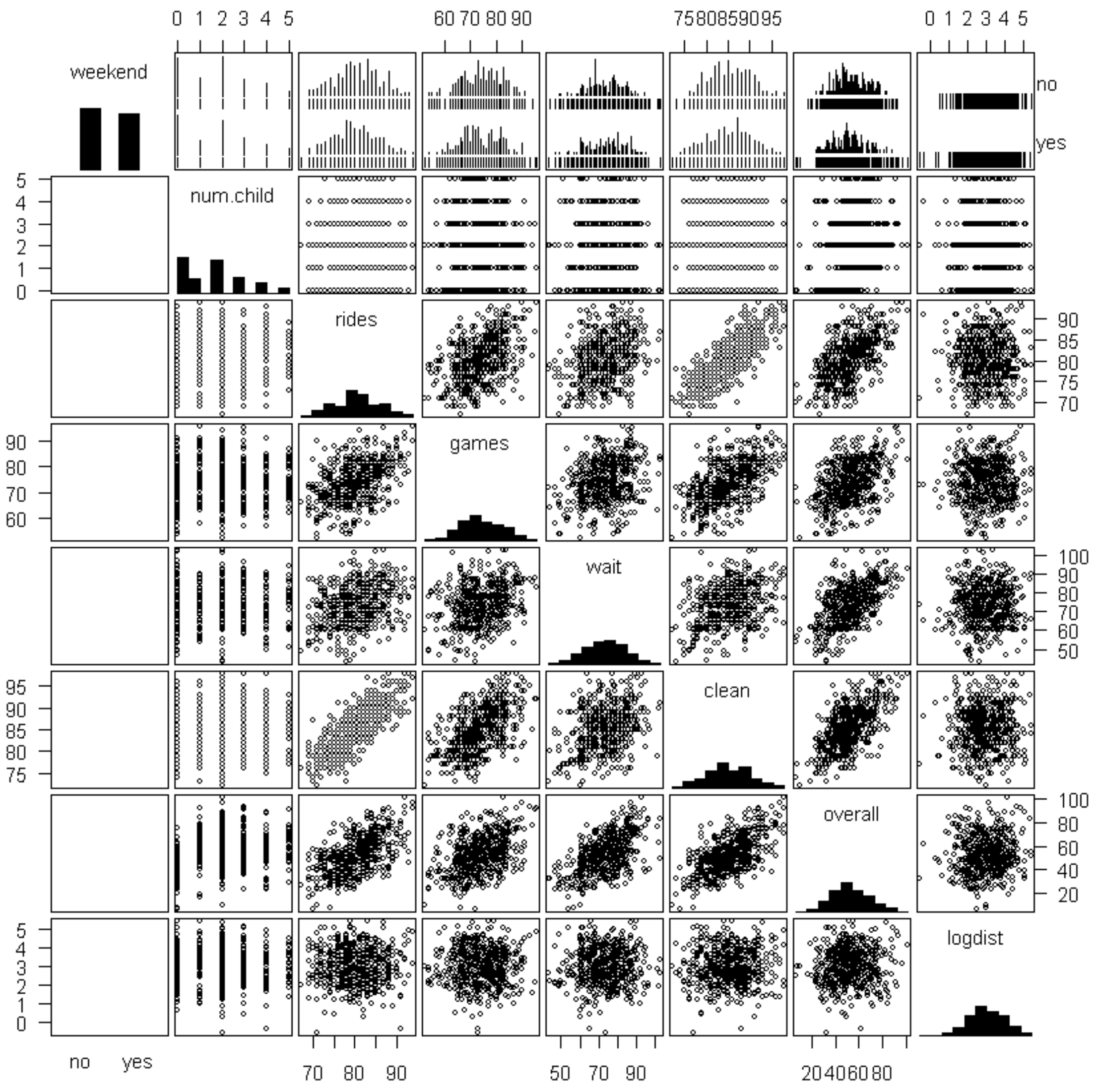


The difference of the above two function is on how they handle the discrete values.

To check the relationships among variables, we examine the bivariate scatterplots shown Figure above. They show few concerns apart from the need to transform distance. For example, the pairwise scatterplots of our continuous measures are generally elliptical in shape, which is a good indication that they are appropriate to use in a linear model. One question, however, concerns the fact that the variables in the lower right of figure are positively correlated.

```
In [12]: df$logdist=log(df$distance)
```

```
In [13]: gpairs(df[,-3])
```



```
In [14]: head(df)
```

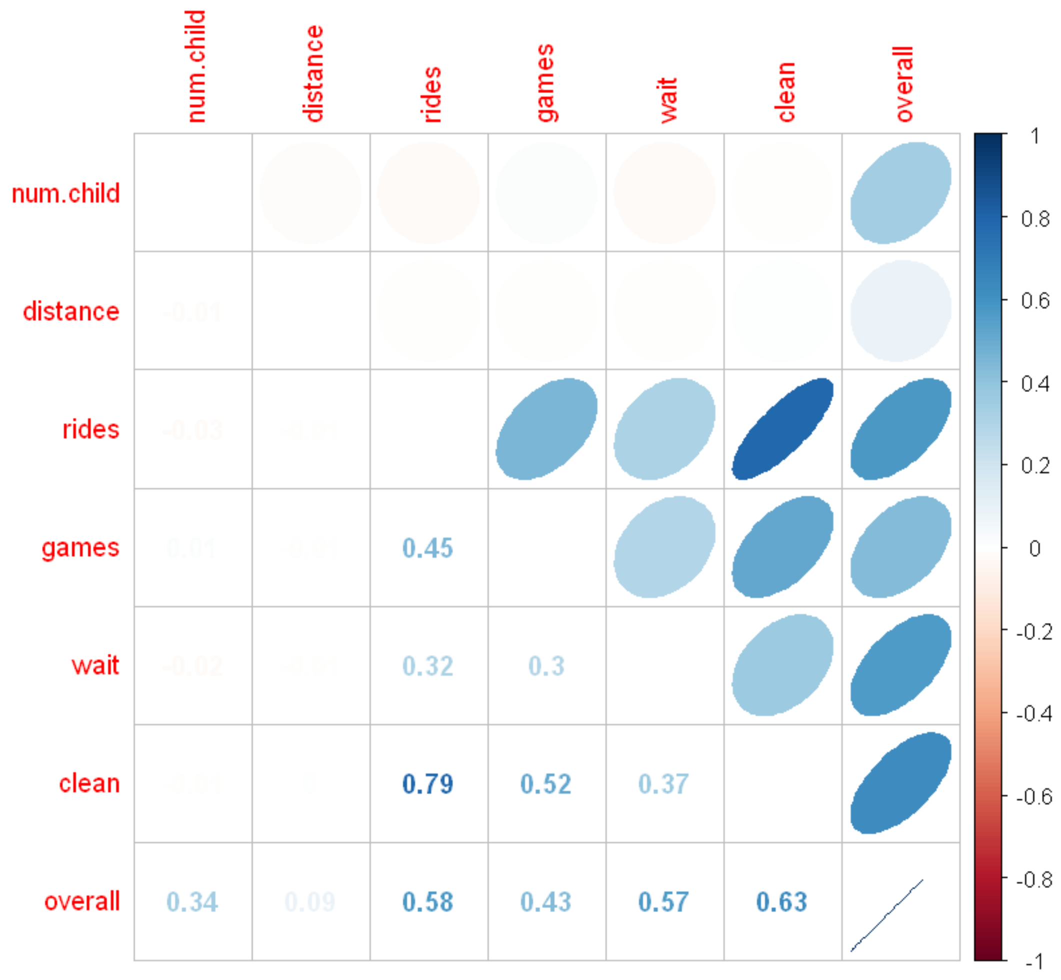
weekend	num.child	distance	rides	games	wait	clean	overall	logdist
yes	0	114.64826	82	68	64	86	49	4.741869
yes	2	27.01410	82	73	80	84	68	3.296359
no	1	63.30098	79	75	74	86	62	4.147901
yes	0	25.90993	82	68	69	87	38	3.254626
no	4	54.71831	78	83	78	84	69	4.002198
no	5	22.67934	76	75	51	77	29	3.121454

Although scatterplots provide a lot of visual information, when there are more than a few variables, it can be helpful to assess the relationship between each pair with a single number.

```
In [15]: cor(df[,2:8])
```

	num.child	distance	rides	games	wait	clean	overa
num.child	1.00000000	-0.012136454	-0.027697383	0.012343448	-0.020994861	-0.007998140	0.342
distance	-0.01213645	1.000000000	-0.008598235	-0.008036711	-0.005848262	0.002919032	0.088
rides	-0.02769738	-0.008598235	1.000000000	0.453413358	0.315824769	0.789004748	0.577
games	0.01234345	-0.008036711	0.453413358	1.000000000	0.299620997	0.516460748	0.433
wait	-0.02099486	-0.005848262	0.315824769	0.299620997	1.000000000	0.366849504	0.565
clean	-0.00799814	0.002919032	0.789004748	0.516460748	0.366849504	1.000000000	0.628
overall	0.34242021	0.088297655	0.577726856	0.433254206	0.565395275	0.628146742	1.000

```
In [16]: corrplot.mixed(corr=cor(df[ , 2:8], use="complete.obs"),upper="ellipse", tl.pos="lt")
```



A correlation plot produced using corrplot.mixed() from the corrplot package is an easy way to visualize all of the correlations in the data. Numeric values of r are shown in the lower triangle of the matrix. The upper triangle displays ellipses (because we used the argument upper="ellipse").

These ellipses are tighter, progressively closer to being lines, for larger values of r, and are rounder, more like circles for r near zero. They are also shaded blue for positive direction, and red for negative (and show corresponding positive or negative slope).

Correlation coefficient r measures the linear association between two variables. If the relationship between two variables is not linear, it would be misleading to interpret r.

1 Modeling

Now we are ready for model selection and validation process. We start with the Linear Model with a Single Predictor.

The goal of a satisfaction drivers analysis is to discover relationships between customers' satisfaction with features of the service (or product) and their overall experience. For example, to what extent is satisfaction with the park's rides related to overall experience? Is the relationship strong or weak?

Like most other R functions, *lm()* returns an object that we can save and use for other purposes. Typically, we assign the result of *lm()* to an object that is used in subsequent lines of code. For example, we can assign the result of *lm()* to a new object *m1*:

```
In [17]: m1=lm(overall  rides, data=df)
```

In the output, R repeats the model for reference and reports two coefficients, which are the intercept and the slope of the fitted line. Those can be used to determine the best estimate for any respondent's report of overall based on knowing his or her value for rides.

```
In [18]: m1$coefficients
```

(Intercept) -84.9968794504225 **rides** 1.71517105136004

```
In [19]: typeof(m1$coefficients)
```

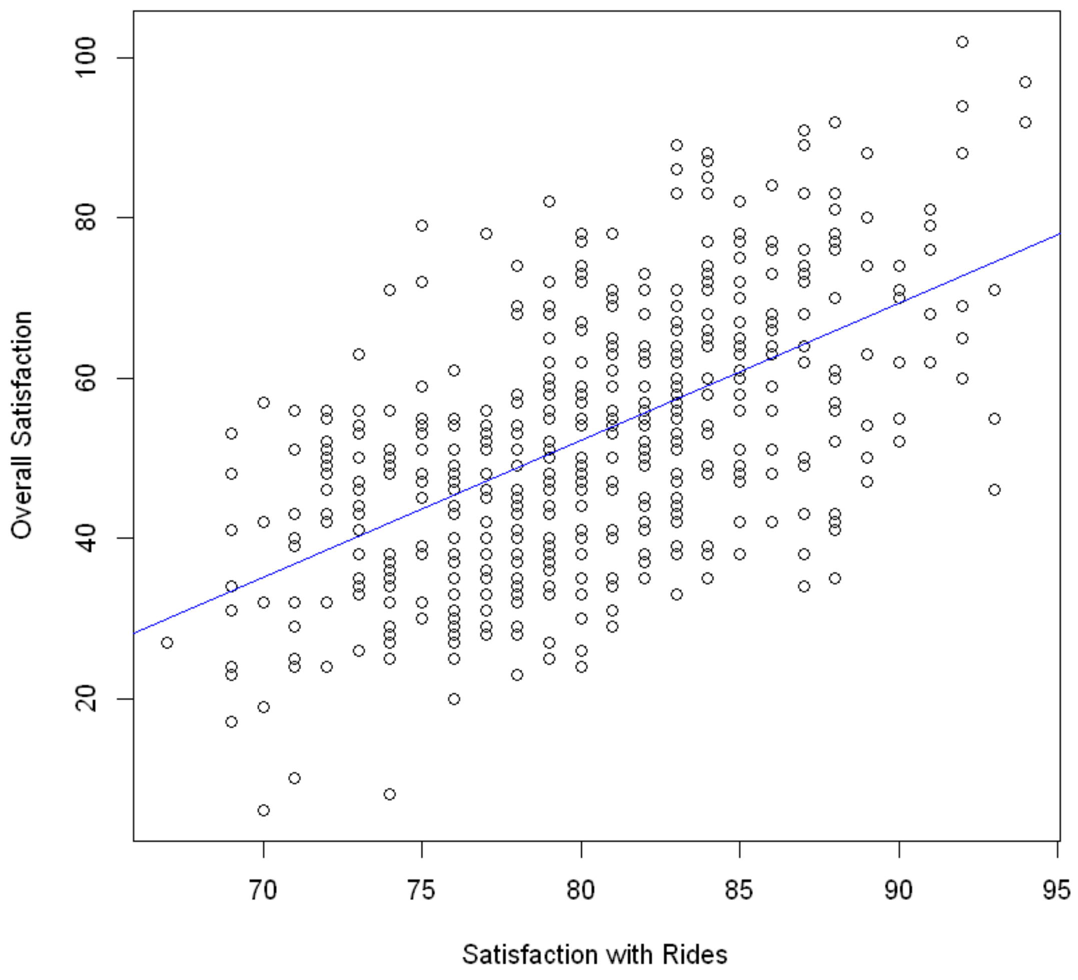
'double'

For example, from this model we would expect that a customer who gives a rating of 90 for satisfaction with rides would give an overall rating of:

```
In [20]: m1$coefficients[1]+m1$coefficients[2]*90
```

(Intercept): 69.3685151719808

```
In [21]: plot(overall  rides, data=df,xlab="Satisfaction with Rides", ylab="Overall Satisfacti
         abline(m1, col="blue")
```



The result is shown in *abline()* recognizes that it is dealing with an lm object and uses the slope and the intercept from m1 to draw the line.

If you want more details about output

```
In [22]: summary(m1)
```

```
Call:
lm(formula = overall ~ rides, data = df)

Residuals:
    Min      1Q  Median      3Q     Max
-33.926 -10.358   0.635   8.964  35.359
```

```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -84.9969     8.7483  -9.716   <2e-16 ***
rides         1.7152     0.1086  15.795   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 13.14 on 498 degrees of freedom
Multiple R-squared:  0.3338,Adjusted R-squared:  0.3324
F-statistic: 249.5 on 1 and 498 DF,  p-value: < 2.2e-16
```

```
In [23]: t_value <- 1.7146/ 0.1085
         print(t_value)
```

```
[1] 15.80276
```

```
In [24]: p_value<-1-pt(t_value, df=498)
         print(p_value)
```

```
[1] 0
```

```
In [25]: alpha=0.05
         conf_int_l<-1.7146  -qt(alpha/2,498)*0.1085
         conf_int_u<-1.7146  + qt(alpha/2,498)*0.1085
         round(conf_int_l,3)
         round(conf_int_u,3)
```

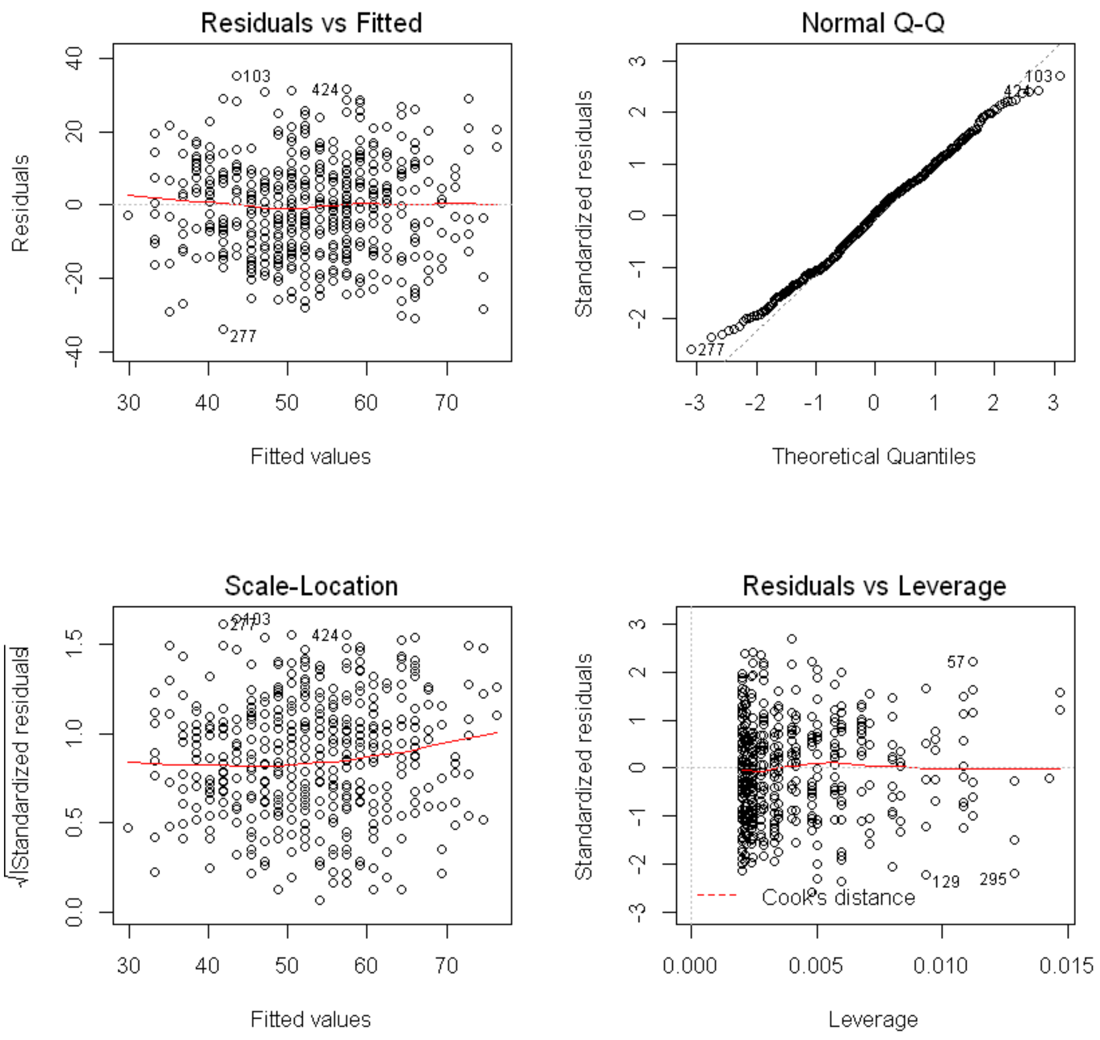
1.928
1.501

```
In [26]: round(confint(m1),3)
```

	2.5 %	97.5 %
(Intercept)	-102.185	-67.809
rides	1.502	1.929

Cecking Model Validity and Model Fit

```
In [27]: par(mfrow=c(2,2))
         plot(m1)
```



1. The first plot (in the upper left corner) shows the fitted values versus residuals for $m1$. There is no obvious pattern between the fitted values for overall satisfaction and the residuals; this is consistent with the idea that **the residuals are due to random error**, and supports the notion that the model is adequate.
2. The second plot in the lower left of figure is similar to the first, except that instead of plotting the raw residual value, it plots the square root of the standardized residual. Again, there should be no clear pattern; if there were it might indicate a nonlinear relationship. Observations with high residuals are flagged as potential outliers, and R labels them with row numbers in case we wish to inspect them in the data frame. A common pattern in residual plots is a **cone or funnel**, where the range of errors gets progressively **larger for larger fitted values**. This is called **heteroskedasticity** and is a violation of linear model assumptions. Sometimes a transformation of the predictor or outcome variable will resolve heteroskedasticity.

3. The third result of *plot()* for *lm* objects is a *Normal QQ plot*. A QQ plot helps you see whether the **residuals follow a normal distribution**, another key assumption. It compares the values that residuals would be expected to take if they are normally distributed, versus their actual values. When the model is appropriate, these points are similar and fall close to a diagonal line; when the relationship between the variables is nonlinear or otherwise does not match the assumption, the points deviate from the diagonal line. In the present case, the QQ plot suggests that the data fits the assumption of the model.
4. The final plot in the lower right panel of figure again helps to **identify potential outliers**, observations that may come from a different distribution than the others. Outliers are a problem because, if they are far from other points, they unduly influence the fitted line. We do not want one or a very few observations to have a large effect on the coefficients. The lower right plot plots the leverage of each point, a measure of how much influence the point has on the model coefficients. When a point has a high residual and high leverage,b**it indicates that the point has both a different pattern (residual) and undue influence (leverage)**. One measure of the leverage of a data point is Cook's distance, an estimate of how much predicted (y) values would change if the model were re-estimated with that point eliminated from the data. If you have observations with **high Cook's distance, this chart would show dotted lines for the distances**; in the present case, there are none. Still, in the lower right of figure, three points are automatically labeled with row numbers because they are potentially problematic outliers based on high standardized residual distance and leverage on the model.

1.1 Dealing with Outliers

I do not recommend routinely remove outliers yet I do recommend to inspect them and determine whether there is a problem with the data. Let inspect the identified points by selecting those rows:

```
In [28]: df[c(57, 129, 295),]
```

	weekend	num.child	distance	rides	games	wait	clean	overall	logdist
57	yes	2	63.29248	92	83	93	98	102	4.147767
129	yes	0	11.89550	70	72	54	74	6	2.476161
295	no	0	11.74474	93	78	67	89	46	2.463406

In this case, none of the data points is obviously invalid (for instance, with values below 1 or greater than 100). Overall, figure looks good and suggests that the model relating overall satisfaction to satisfaction with rides is reasonable.

Now that we've covered the basics of linear models using just one predictor, we turn to the problem of assessing multiple drivers of satisfaction. Our goal is to sort through all of the features of the park—rides, games, wait times, and cleanliness—to determine which ones are most closely related to overall satisfaction.

1.2 Including Variables

```
In [29]: m2 <- lm(overall  rides + games + wait + clean, data=df)
         summary(m2)
```

```
Call:
lm(formula = overall ~ rides + games + wait + clean, data = df)
```

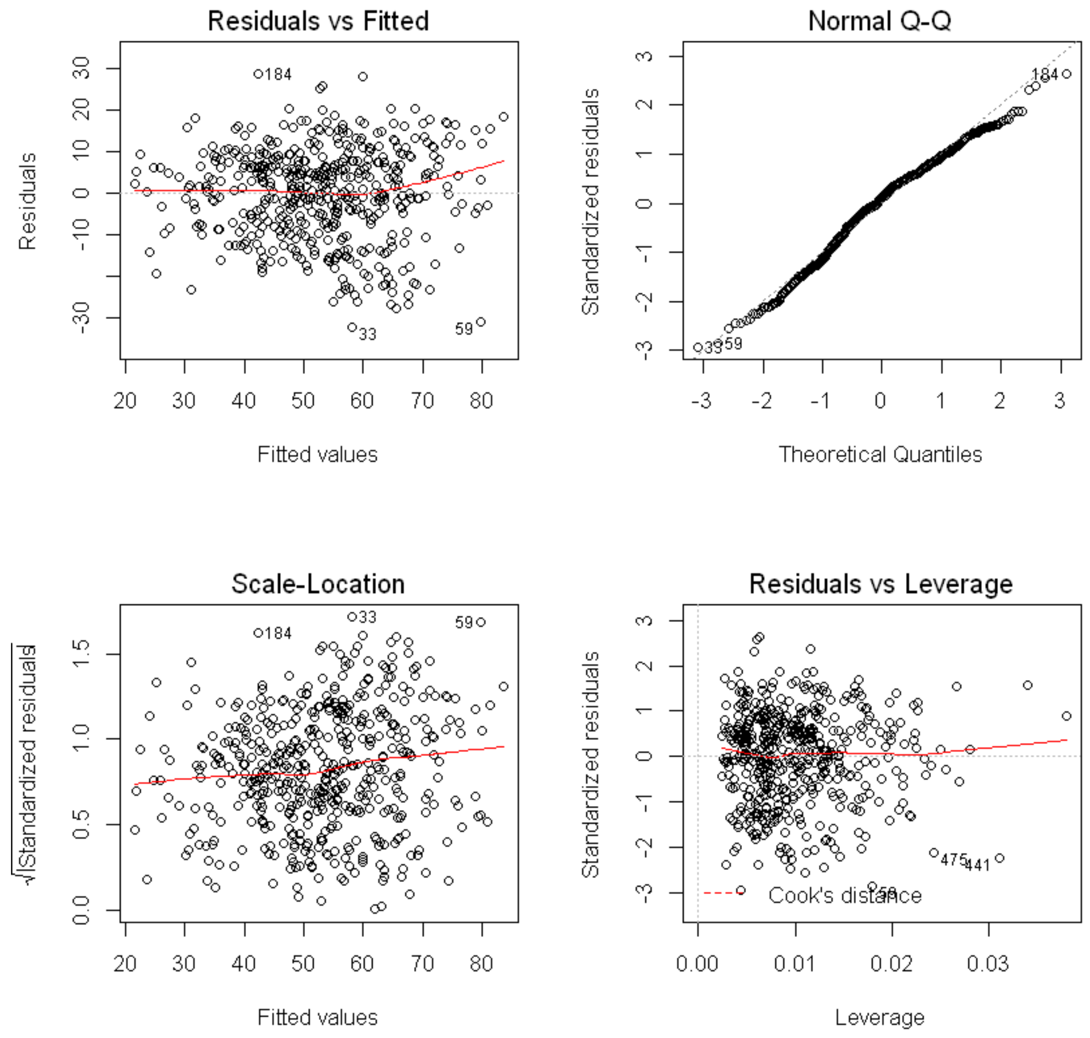
```
Residuals:
    Min      1Q  Median      3Q     Max 
-32.101  -7.266   1.274   7.582  28.695 

Coefficients:
              Estimate Std. Error t value Pr(>|t|)    
(Intercept) -125.16246    8.26476 -15.144  < 2e-16 ***
rides          0.53948    0.14753   3.657 0.000283 ***
games          0.16085    0.07115   2.261 0.024218 *  
wait           0.55497    0.04936  11.244  < 2e-16 ***
clean          0.96028    0.16394   5.858 8.57e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 10.92 on 495 degrees of freedom
Multiple R-squared:  0.5427,Adjusted R-squared:  0.539 
F-statistic: 146.8 on 4 and 495 DF,  p-value: < 2.2e-16
```

The R-squared increased to 0.5586, meaning that about half of the variation in overall ratings is explained by the ratings for specific features. The residual standard error is now 10.59, meaning that the predictions are more accurate. Our residuals also appear to be symmetric.

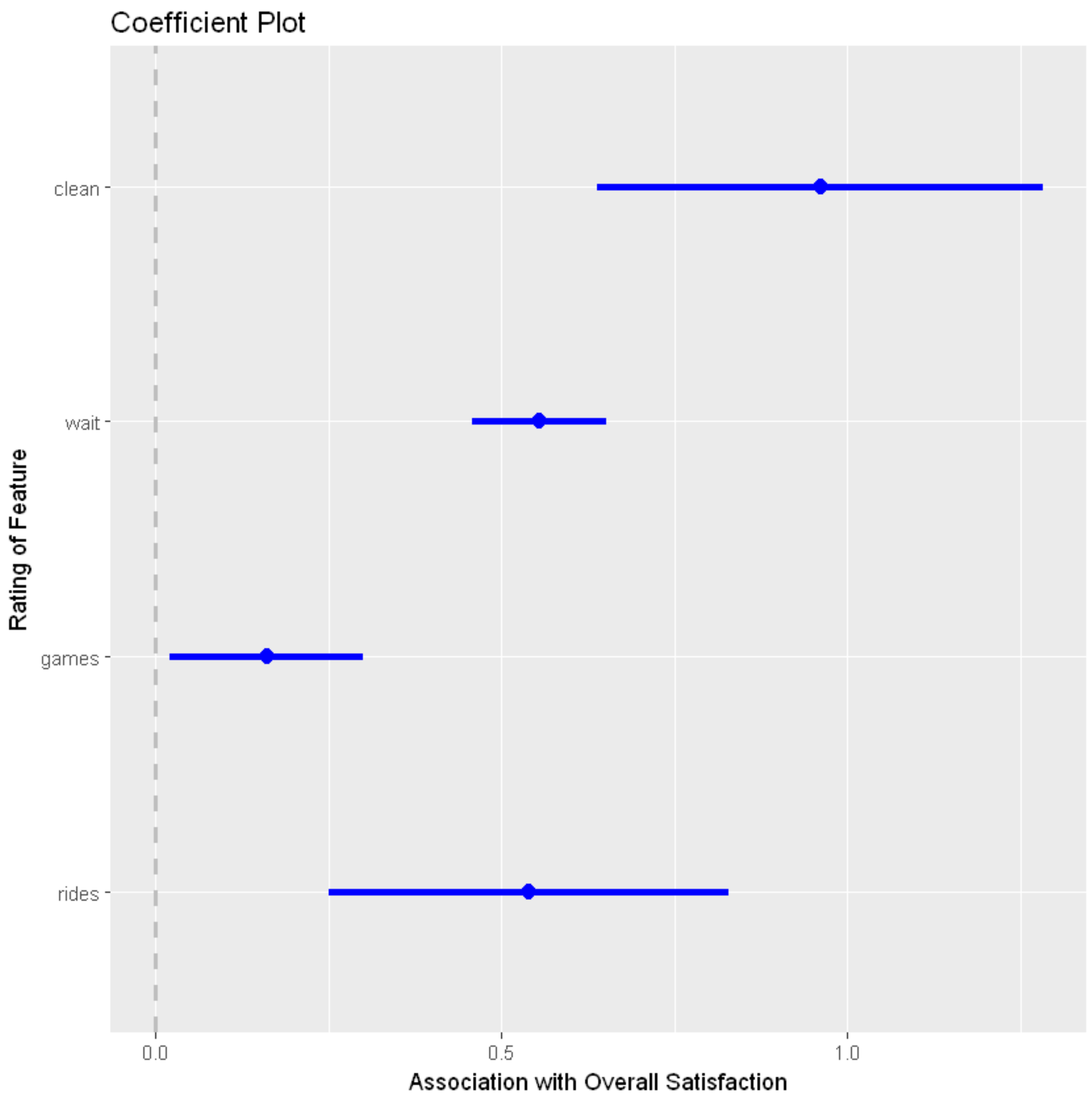
```
In [30]: par(mfrow=c(2,2))
         plot(m2)
```



Next we examine the model coefficients. Each coefficient represents the strength of the relationship between satisfaction with that feature and overall satisfaction, conditional on the values of the other predictors. All four features are identified as being statistically significant.

```
In [31]: coefplot(m2, intercept=FALSE, outerCI=1.96, lwdOuter=1.5, ylab="Rating of Feature",xla
```

```
Warning message:
"Ignoring unknown aesthetics: xmin, xmax"
```



We use coefplot() arguments to set the outer confidence interval to a width of 1.96 standard errors (using outerCI=1.96, which corresponds to a 95% confidence interval) and to increase the size of the plotted lines slightly with lwdOuter=1.5. The result is shown in Figure, where we see that **satisfaction with cleanliness is estimated to be the most important feature** associated with overall satisfaction, followed by satisfaction with the rides and wait times. Satisfaction with games is estimated to be relatively less important. A plot of coefficients is often a key output from a satisfaction drivers analysis. Sorting the plot so that the coefficients are in order based on their estimated coefficient may make it easier to quickly identify the features that are most closely related to overall satisfaction if you have a large number of predictors.

Now that we have two model objects, m1 and m2 we might ask which one is better. One way to evaluate models is to compare their R-squared values.

```
In [32]: summary(m1)$adj.r.squared
         summary(m2)$adj.r.squared
```

0.332430505598762
0.538966781918842
and AIC criterion, which is given by:

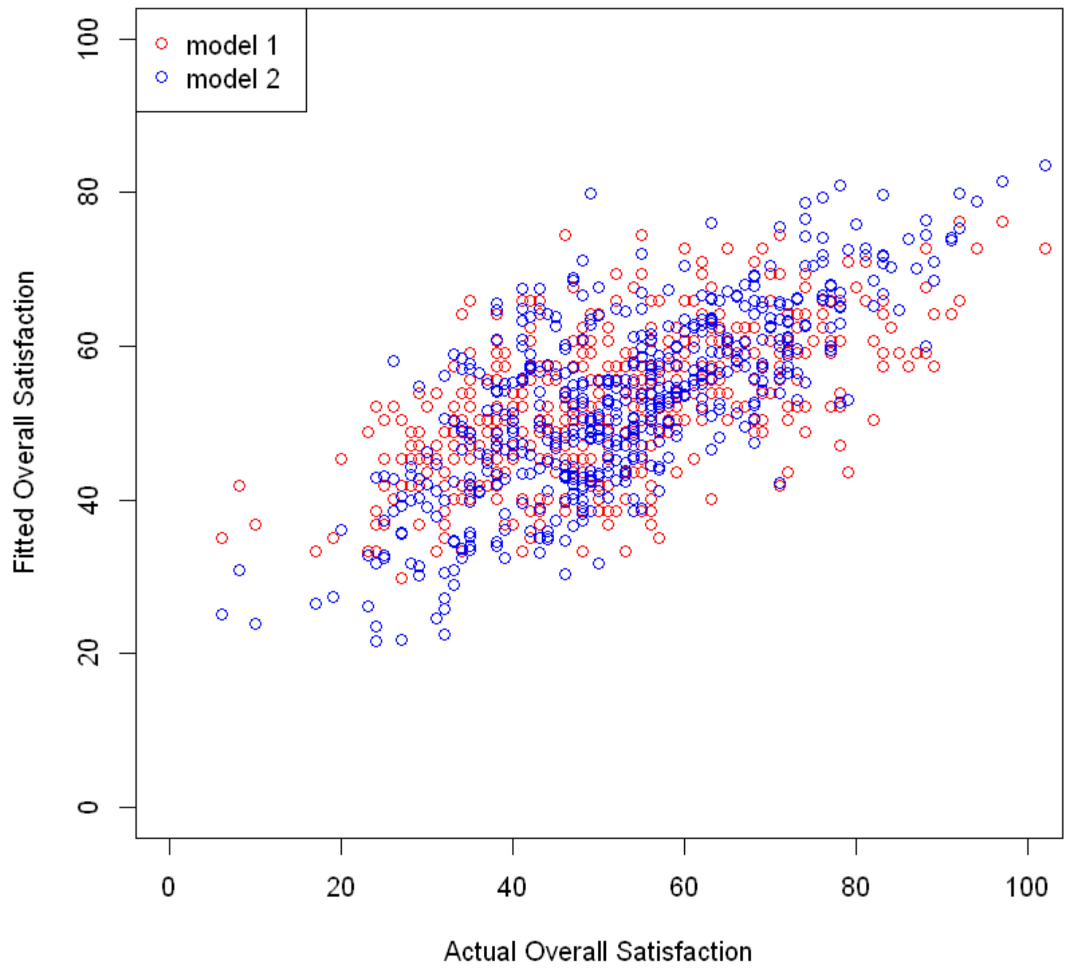
$$AIC = -2\log L + k \times edf,$$

where L is likelihood function (in our case based on normal distribution) and edf is the number of free parameters for regression model. In OLS it is equal number of independent variables.

```
In [33]: extractAIC(m1,k=2)
         extractAIC(m2,k=2)
```

1. 2 2. 2577.28834706684
1. 5 2. 2395.18049016794
To compare the predictions of the models visually, we plot the fitted versus actual values for each:

```
In [34]: plot(df$overall, fitted(m1), col="red",xlim=c(0,100), ylim=c(0,100), xlab="Actual Ove
         points(df$overall, fitted(m2), col="blue")
         legend("topleft", legend=c("model 1", "model 2"),col=c("red", "blue"), pch=1)
```



If the model fits the data perfectly, it would **fall along a 45 line in this plot**, but, of course, it is nearly impossible to fit customer satisfaction data perfectly. By comparing the red and the blue points in the resulting plot in figure, you can see that the **blue cloud of points is more tightly clustered along a diagonal line**, which shows that m2 explains more of the variation in the data than m1.

2 Comparing Nested Models

For a more formal test, which is possible because the models here are nested. We can use anova() function to determine whether m2 explains more of the variation than m1:

```
In [35]: anova(m1, m2)
```

Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
498	85921.11	NA	NA	NA	NA
495	58980.91	3	26940.2	75.36562	3.641831e-40

The low p-value indicates that the additional predictors in m2 significantly improve the fit of the model. If these two models were the only ones under consideration, we would interpret m2 instead of m1.

Thus far, we have interpreted raw coefficients in order to evaluate the contributions of ratings on the shared 100-point scale. However, if the variables have different scales, such as a survey where rides is rated on a 1–10 scale while cleanliness is rated 1–5 scale, then their coefficient values would not be directly comparable. In the present data, this occurs with the distance and logdist variables, which are not on a 100-point scale. When you wish to **compare coefficients, it can be helpful to standardize data on a common scale before fitting a model** (and after transforming any variables to a more normal scale). The most common standardization converts values to zero-centered units of standard deviation. This subtracts a variable's mean from each observation and then divides by the standard deviation (sd()). This could be done by:

```
In [36]: df.std <- df[ , -3] # sat but remove distance
         df.std[ , 3:8] <- scale(df.std[ , 3:8])
```

```
In [37]: head(df.std)
```

weekend	num.child	rides	games	wait	clean	overall	logdist
yes	0	0.2987971	-0.7561865	-0.87575676	0.1184417	-0.2408509	1.7886823
yes	2	0.2987971	-0.1408004	0.61236008	-0.2711692	0.9410106	0.3226360
no	1	-0.2552148	0.1053541	0.05431626	0.1184417	0.5677911	1.1862757
yes	0	0.2987971	-0.7561865	-0.41072025	0.3132472	-0.9250865	0.2803106
no	4	-0.4398855	1.0899720	0.42634547	-0.2711692	1.0032138	1.0385034
no	5	-0.8092268	0.1053541	-2.08485169	-1.6348075	-1.4849157	0.1452467

2.1 Model 3

For the next step, we wonder whether satisfaction is different for customers who come on the weekend, travel farther, or have more children.We add these predictors to the model using the standardized data:

```
In [38]: m3 <- lm(overall  rides + games + wait + clean + weekend + logdist + num.child, data =
         summary(m3)
```

```
Call:
lm(formula = overall ~ rides + games + wait + clean + weekend +
    logdist + num.child, data = df.std)

Residuals:
     Min       1Q   Median       3Q      Max
-1.60258 -0.39978  0.02281  0.41053  1.70036

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
```

```
(Intercept) -0.39447    0.04675  -8.438 3.63e-16 ***
rides        0.20641    0.04210   4.903 1.29e-06 ***
games        0.07134    0.03041   2.346   0.0194 *
wait         0.37871    0.02792  13.566  < 2e-16 ***
clean        0.29033    0.04431   6.553 1.43e-10 ***
weekendyes  -0.04370    0.05167  -0.846   0.3981
logdist      0.06557    0.02585   2.537   0.0115 *
num.child    0.23909    0.01720  13.904  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.5739 on 492 degrees of freedom
Multiple R-squared:  0.6752,Adjusted R-squared:  0.6706
F-statistic: 146.1 on 7 and 492 DF,  p-value: < 2.2e-16
```

When your data **includes factors**, you must be careful about the data type. For example, *num.child* is a numeric variable, ranging 0–5, but it doesn't necessarily make sense to treat it as a number, as we did in m3. In doing so, we **implicitly assume that satisfaction goes up or down linearly as a function of the number of children**, and that the effect is the same for each additional child. (Anyone who has taken a group of children to an amusement park might guess that this is an unreasonable assumption.) We correct this by converting *num.child* to a **factor** and re-estimating the model:

```
In [39]: df.std$num.child.factor <- factor(df.std$num.child)
```

```
In [40]: m4 <- lm(overall  rides + games + wait + clean + weekend + logdist + num.child.factor
         summary(m4)
```

```
Call:
lm(formula = overall ~ rides + games + wait + clean + weekend +
    logdist + num.child.factor, data = df.std)

Residuals:
     Min       1Q   Median       3Q      Max
-1.25150 -0.32994 -0.00513  0.31409  1.44218

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
(Intercept)       -0.72670    0.04437 -16.378  < 2e-16 ***
rides              0.22188    0.03496   6.347 5.01e-10 ***
games              0.04299    0.02521   1.705   0.0888 .
wait               0.38241    0.02312  16.537  < 2e-16 ***
clean              0.29755    0.03675   8.097 4.52e-15 ***
weekendyes        -0.01880    0.04273  -0.440   0.6602
logdist            0.03154    0.02148   1.468   0.1426
num.child.factor1  1.06124    0.07049  15.056  < 2e-16 ***
num.child.factor2  1.08519    0.05575  19.465  < 2e-16 ***
num.child.factor3  1.03091    0.06946  14.841  < 2e-16 ***
num.child.factor4  0.98893    0.07943  12.450  < 2e-16 ***
num.child.factor5  1.04293    0.10253  10.172  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4742 on 488 degrees of freedom
Multiple R-squared:  0.7801,Adjusted R-squared:  0.7751
F-statistic: 157.4 on 11 and 488 DF,  p-value: < 2.2e-16
```

A striking thing about m4 is that **the increase in overall satisfaction is about the same regardless of how many children there are** in the party—about one standard deviation higher for any number of children. This suggests that we don't actually need to estimate a different increase for each number of children. In fact, if the increase is the same for one child as for five children, attempting to fit a model that scales increasingly per child would result in a less accurate estimate. Instead, we declare a new variable called *has.child* that is TRUE when the party has children in it and FALSE when the party does not have children. We then estimate the model using that new factor variable. **We also drop weekend from the model because it doesn't seem to be a significant predictor**:

```
In [41]: df.std$has.child <- factor(df.std$num.child > 0)
         m5 <- lm(overall  rides + games + wait + clean + logdist + has.child,data=df.std)
         summary(m5)
```

```
Call:
lm(formula = overall ~ rides + games + wait + clean + logdist +
    has.child, data = df.std)

Residuals:
     Min       1Q   Median       3Q      Max
-1.26183 -0.33269 -0.00197  0.32233  1.43605

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)   -0.73590    0.03861 -19.058  < 2e-16 ***
rides          0.22082    0.03466   6.370 4.33e-10 ***
games          0.04424    0.02509   1.763   0.0785 .
wait           0.38335    0.02299  16.674  < 2e-16 ***
clean          0.29785    0.03648   8.164 2.73e-15 ***
logdist        0.03443    0.02124   1.621   0.1056
has.childTRUE  1.05429    0.04629  22.774  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Residual standard error: 0.4727 on 493 degrees of freedom
Multiple R-squared:  0.7792,Adjusted R-squared:  0.7765
F-statistic:   290 on 6 and 493 DF,  p-value: < 2.2e-16
```

We can include an interaction of two terms by using the : operator between variables in a formula. For instance, to estimate overall as a function of rides plus the interaction of wait and has.child, we could write the formula as overall *rides + wait:no.child*.

```
In [42]: m6 <- lm(overall  rides + games + wait + clean + weekend + logdist + has.child + ride
                  games:has.child + wait:has.child + clean:has.child + rides:weekend + games:w
         + wait:weekend + clean:weekend, data=df.std)

In [43]: summary(m6)
```

```
Call:
lm(formula = overall ~ rides + games + wait + clean + weekend +
    logdist + has.child + rides:has.child + games:has.child +
    wait:has.child + clean:has.child + rides:weekend + games:weekend +
    wait:weekend + clean:weekend, data = df.std)

Residuals:
     Min       1Q   Median       3Q      Max
-1.20612 -0.29683  0.00697  0.30788  1.45325

Coefficients:
                     Estimate Std. Error t value Pr(>|t|)
(Intercept)         -0.714619   0.042563 -16.790  < 2e-16 ***
rides                0.146551   0.067344   2.176 0.030026 *
games                0.073642   0.048821   1.508 0.132103
wait                 0.132772   0.043923   3.023 0.002637 **
clean                0.304566   0.078835   3.863 0.000127 ***
weekendyes          -0.015968   0.040826  -0.391 0.695880
logdist              0.026443   0.020480   1.291 0.197261
has.childTRUE        1.044456   0.044397  23.525  < 2e-16 ***
rides:has.childTRUE  0.054988   0.072208   0.762 0.446719
games:has.childTRUE -0.057629   0.052324  -1.101 0.271275
wait:has.childTRUE   0.341793   0.046910   7.286 1.31e-12 ***
clean:has.childTRUE  0.001811   0.078638   0.023 0.981640
rides:weekendyes     0.072338   0.066973   1.080 0.280637
games:weekendyes     0.021666   0.048577   0.446 0.655779
wait:weekendyes      0.033464   0.044053   0.760 0.447846
clean:weekendyes    -0.043026   0.070224  -0.613 0.540366
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4477 on 484 degrees of freedom
```

```
Multiple R-squared:  0.8056,Adjusted R-squared:  0.7996
F-statistic: 133.7 on 15 and 484 DF,  p-value: < 2.2e-16
```

The model object m6 now includes eight interaction terms between ratings for features of the park and no.child and weekend. Only **one of these interactions is significant: the wait:no.child interaction**. This suggests we could drop the non-significant interactions to create a new model m7:

```
In [44]: m7 <- lm(overall  rides + games + wait + clean + logdist + has.child + wait:has.child
         summary(m7)
```

```
Call:
lm(formula = overall ~ rides + games + wait + clean + logdist +
    has.child + wait:has.child, data = df.std)

Residuals:
     Min       1Q   Median       3Q      Max
-1.18731 -0.30473 -0.00076  0.32601  1.41957

Coefficients:
                   Estimate Std. Error t value Pr(>|t|)
(Intercept)        -0.72769    0.03647 -19.952  < 2e-16 ***
rides               0.21439    0.03274   6.549 1.46e-10 ***
games               0.04875    0.02370   2.057   0.0402 *
wait                0.15182    0.03674   4.133 4.21e-05 ***
clean               0.28936    0.03446   8.396 4.96e-16 ***
logdist             0.02890    0.02006   1.440   0.1504
has.childTRUE       1.04753    0.04372  23.962  < 2e-16 ***
wait:has.childTRUE  0.33970    0.04348   7.813 3.42e-14 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4463 on 492 degrees of freedom
Multiple R-squared:  0.8036,Adjusted R-squared:  0.8008
F-statistic: 287.6 on 7 and 492 DF,  p-value: < 2.2e-16
```

In these results, we see that **attending the park with children is a predictor of higher satisfaction, and waiting time is more important predictor among those with children (wait:has.childTRUE) than those without children.** We don't know the reason for this, but perhaps children go on more rides and their parents are therefore more influenced by wait times.

One might further tune the model by considering whether logdist is still needed; I'll leave that you to verify that and assume that **model m7 is the final model**.

2.1.1 What to do with results?

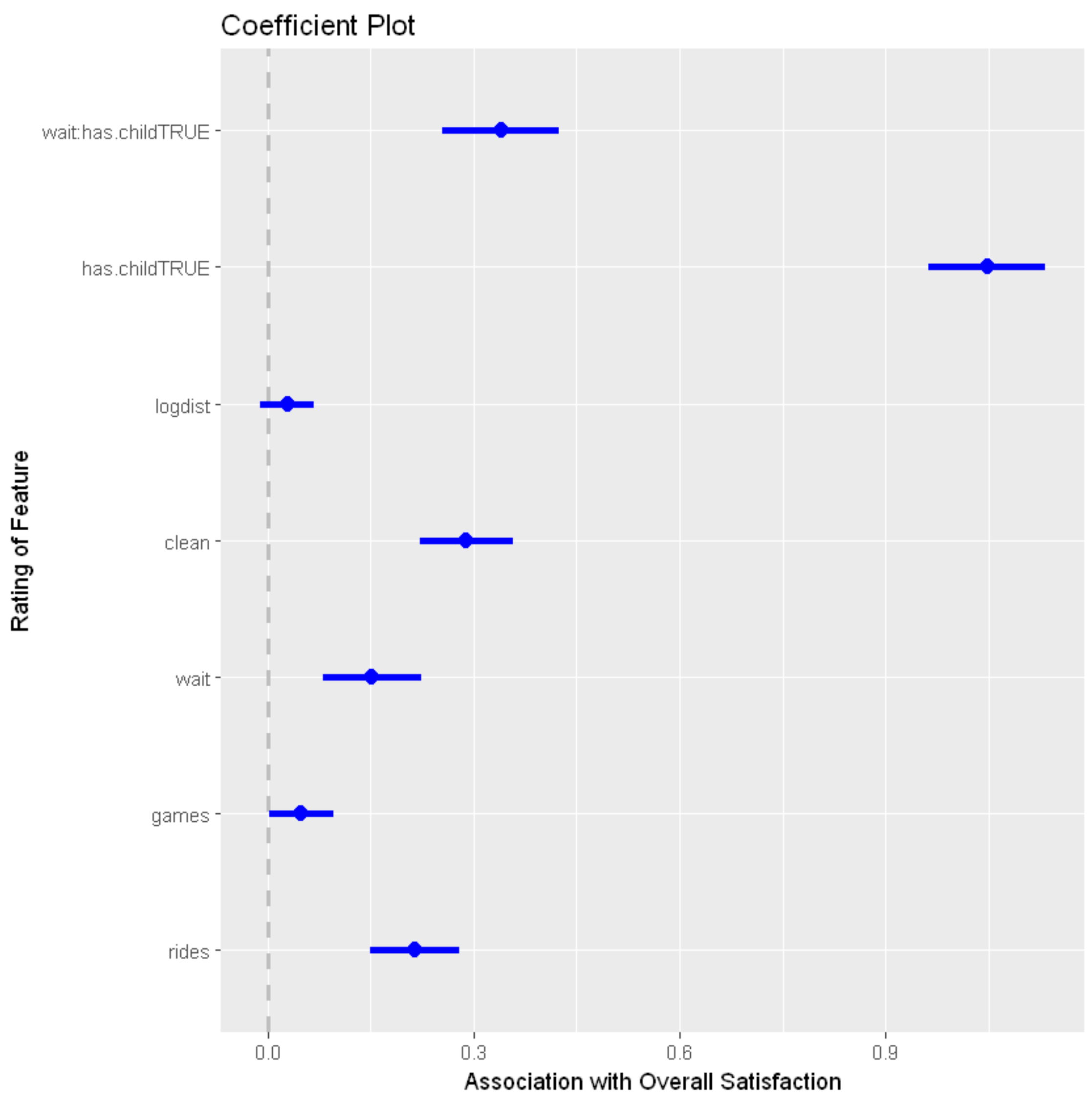
What do we do with these results as marketers? We identify several possible marketing interventions. 1. If we want to increase satisfaction overall, we could perhaps do so by trying to increase the number of visitors with children. 2. Alternatively, if we want to appeal to visitors without children, we might engage in further research to understand why their ratings are lower. 3. If we are allocating budget to personnel, the importance of cleanliness suggests continuing to allocate resources there (as opposed, say, to games). 4. We might also want to learn more about the association between children and waiting time, and whether there are things we could do to make waiting less frequent or more enjoyable.

There are many more such questions one could pose from results like these; **a crucial step in analysis is to think carefully about the implications and where one might be able to make a product or market intervention**.

Important to remember that the model assesses **association, not causation**. Possible changes in outcome should be viewed as hypotheses suggested by the model, to be confirmed separately.

```
In [45]: coefplot(m7, intercept=FALSE, outerCI=1.96, lwdOuter=1.5,ylab="Rating of Feature",xlal
```

```
Warning message:
"Ignoring unknown aesthetics: xmin, xmax"
```

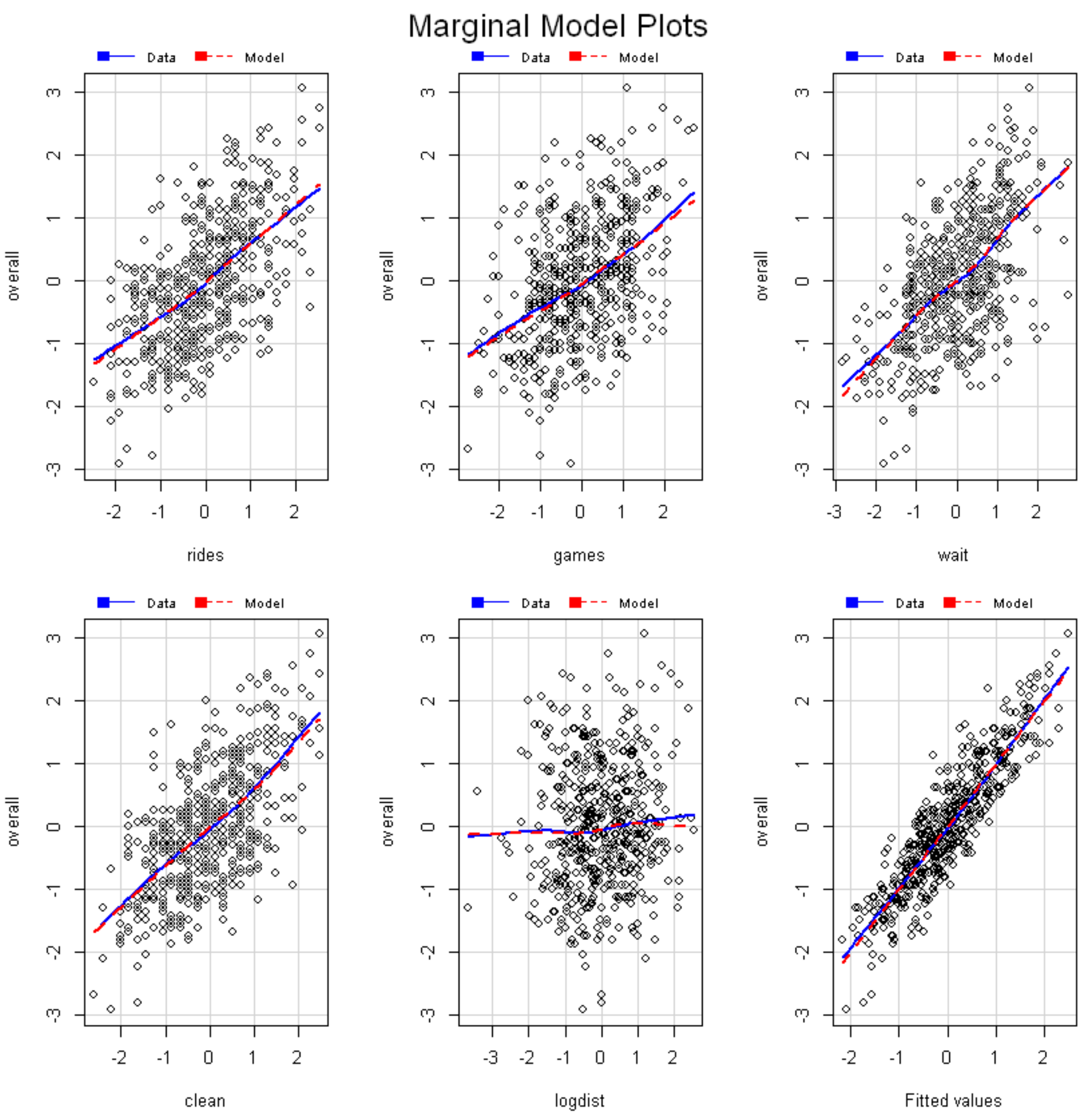


3 Marginal Plot

Marginal Plots provide cool way to validate the functional form of the features.

```
In [46]: mmps(m7,layout=c(2,3))
```

```
Warning message in mmps(m7, layout = c(2, 3)):
"Interactions and/or factors skipped"
```

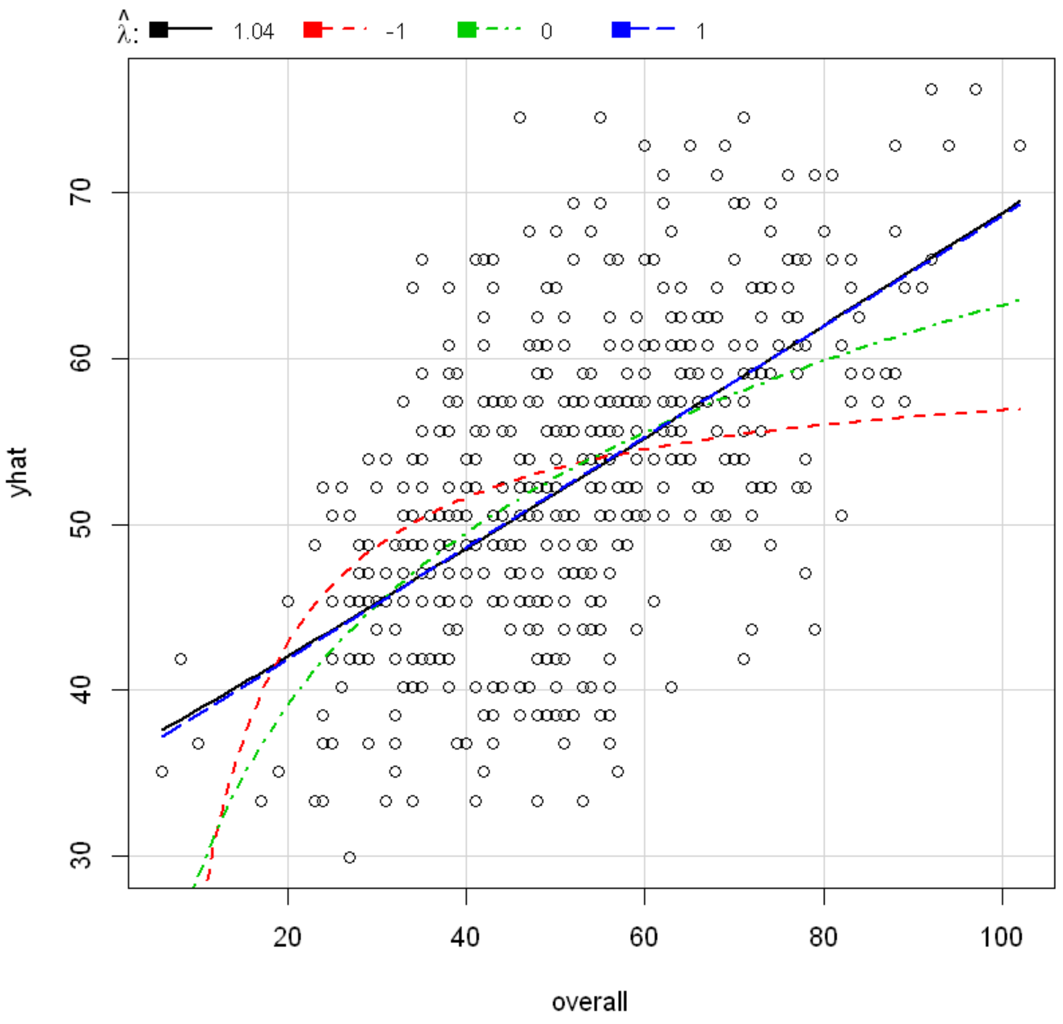


4 Inverse Response Plot

```
In [47]: par(mfrow=c(1,1))
         inverse.response.plot(m1,key=TRUE)

Warning message:
"'inverse.response.plot' is deprecated.
Use 'inverseResponsePlot' instead.
See help("Deprecated") and help("alr3-deprecated")."
```

lambda	RSS
1.037404	28676.85
-1.000000	35249.13
0.000000	29794.01
1.000000	28677.74



```
In [48]: #Model=1
         n <- length(m1$residuals)
         npar <- length(m1$coefficients) +1
         #Calculate adjusted R_Square
         R_sq_m1<-summary(m1)$adj.r.squared
         #Calculate AICc
         AIC_m1<-extractAIC(m1,k=2)+2*npar*(npar+1)/(n-npar-1)
```

```
        #Calculate BIC
        BIC_m1<-extractAIC(m1,k=log(n))
        #Model=2
        npar <- length(m2$coefficients) +1
        #Calculate adjusted R_Square
        R_sq_m2<-summary(m2)$adj.r.squared
        #Calculate AICc
        AIC_m2<-extractAIC(m2,k=2)+2*npar*(npar+1)/(n-npar-1)
        #Calculate BIC
        BIC_m2<-extractAIC(m2,k=log(n))
        #Model=5
        npar <- length(m5$coefficients) +1
        #Calculate adjusted R_Square
        R_sq_m5<-summary(m5)$adj.r.squared
        #Calculate AICc
        AIC_m5<-extractAIC(m5,k=2)+2*npar*(npar+1)/(n-npar-1)
        #Calculate BIC
        BIC_m5<-extractAIC(m5,k=log(n))
        #Model=6
        npar <- length(m6$coefficients) +1
        #Calculate adjusted R_Square
        R_sq_m6<-summary(m6)$adj.r.squared
        #Calculate AICc
        AIC_m6<-extractAIC(m6,k=2)+2*npar*(npar+1)/(n-npar-1)
        #Calculate BIC
        BIC_m6<-extractAIC(m6,k=log(n))
        #Model=6
        npar <- length(m7$coefficients) +1
        #Calculate adjusted R_Square
        R_sq_m7<-summary(m7)$adj.r.squared
        #Calculate AICc
        AIC_m7<-extractAIC(m7,k=2)+2*npar*(npar+1)/(n-npar-1)
        #Calculate BIC
        BIC_m7<-extractAIC(m7,k=log(n))
```

```
In [49]: R_square<-cbind(R_sq_m1,R_sq_m2,R_sq_m5,R_sq_m6,R_sq_m7)
         AIC<-cbind(AIC_m1[2],AIC_m2[2],AIC_m5[2],AIC_m6[2],AIC_m7[2])
         BIC<-cbind(BIC_m1[2],BIC_m2[2],BIC_m5[2],BIC_m6[2],BIC_m7[2])
         table<-rbind(R_square,AIC,BIC)
```

```
In [50]: table
```

R_sq_m1	R_sq_m2	R_sq_m5	R_sq_m6	R_sq_m7
0.3324305	0.5389668	0.7765439	0.799596	0.8008016
2577.3367342	2395.3508756	-742.0264129	-786.701850	-798.4242080
2585.7175633	2416.2535307	-712.8174352	-720.537830	-765.0746901

4.1 Measuring the quality of fit

Suppose now you want to choose the model based on the measure how good is your model predicting. In the regression setting, the most commonly-use measure is the **mean squared error**(MSE), given by

$$MSE = \frac{1}{n}\sum_{i=1}^{n}(y_i - \hat{f}(x_i))^2,$$

where $\hat{f}(x_i)$ is the prediction that $hatf$ gives for the ith observation. The MSE will be small if the predicted responses are very close to the true responses and vice versa.

Important If you compute estimate to previously seen data set (**training data**), then it should be comparably small. But in general, we do not really care how well the method works on the training data. Rather, *we are interested in the accuracy of the predictions that we obtain when we apply out method to previously unseen test data*. When your dataset is small and you do not have luxury to divide your data into two parts. One of the recommended method is $K-$fold crossvalidation

4.1.1 Cross Validation

In this case we randomly divide the set of observations into k groups, or folds, of approximately equal size. Tje first fold is treated as a validation set, and the method is fit on the remaining $k-1$ folds. The MSE_1 is them computed on the observations in the held-out fold. This procedure is repeated k times; each time, a different group of observations is treated as a validation set. This process results in k estimates of the error, $MSE_1, MSE_2, \ldots, MSE_k$. The $k-$fold CV is computed by averaging values,

$$CV_{(k)} = \frac{1}{k}\sum_{i=1}^{k} MSE_i$$

```
In [51]: dim(df)
         MSE_m5<-deviance(m5)/nobs(m5)
         print(MSE_m5)
         MSE_m6<-deviance(m6)/nobs(m6)
         print(MSE_m6)
         MSE_m7<-deviance(m7)/nobs(m7)
         print(MSE_m7)
```

1. 500 2. 9

```
[1] 0.2203277
[1] 0.1939911
[1] 0.1960113
```

```
In [68]: cvlm<-function(n_folds=5,model,df)
             {
             data<-df
             K<-n_folds
             model<-model
             form<-formula(model)
             formtxt <- deparse(form)
```

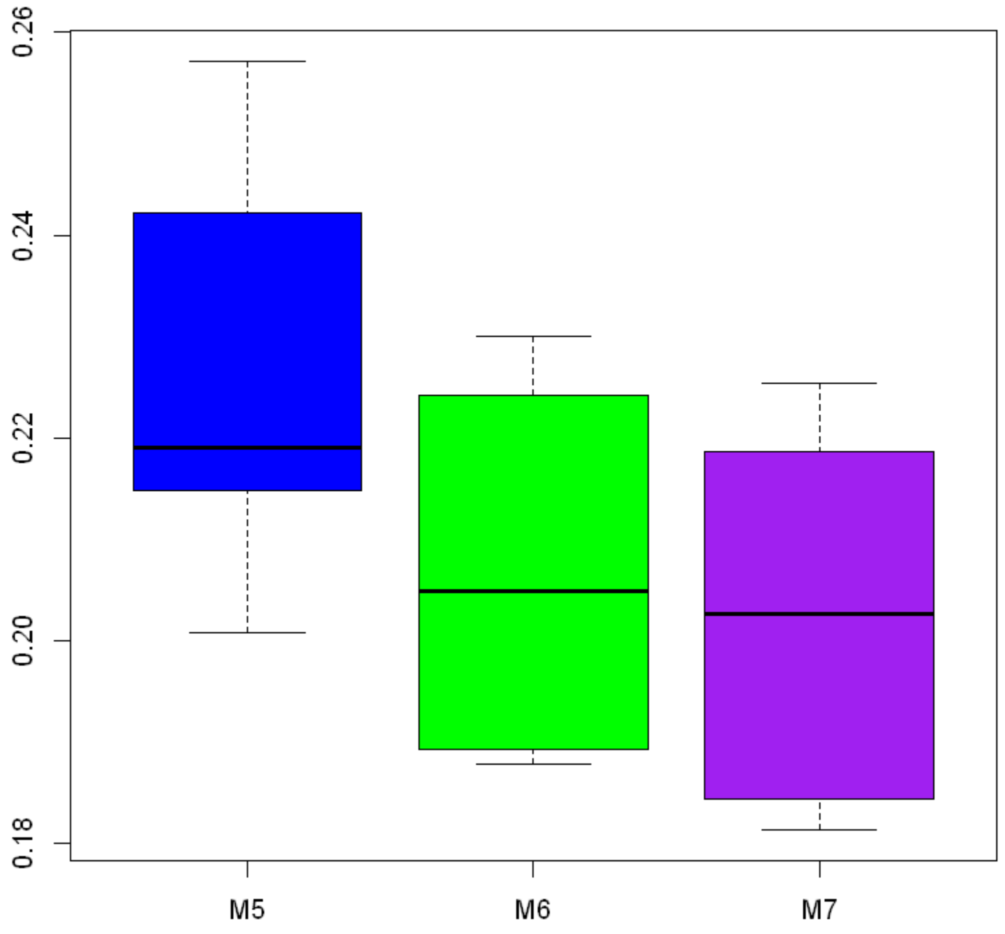
```
            mf <- model.frame(form, data = data)
            ynam <- attr(mf, "names")[attr(attr(mf, "terms"), "response")]
            n_fold<-5
            sum.sq<-numeric(n_fold)
            fold_i <-rep(1:n_fold,length.out=dim(data)[1])
            for ( i in 1:n_fold)
            {
              test_i <-which(fold_i==i)
              n<-length(test_i)[1]
              test<-data[test_i,]
              train<-data[-test_i,]
              test_x<-mf[test_i,]
              model_i<-lm(form,data=train)
              sum.sq[i]<-sum((test$overall-predict(model_i,newdata=test_x))^2)/n
             }
            SSE<-sum.sq
            MSE<-sum(sum.sq)/K
            return<-list("MSE"=MSE,"SSE"=SSE)
            return(return)
            }
```

```
In [69]: MSE.m5<-cvlm(5,m5,df.std)$MSE
         MSE.m6<-cvlm(5,m6,df.std)$MSE
         MSE.m7<-cvlm(5,m7,df.std)$MSE
         c(MSE.m5,MSE.m6,MSE.m7)
```

1. 0.226783083734997 2. 0.207219794257526 3. 0.202444613178952

```
In [70]: SSE.m5<-cvlm(5,m5,df.std)$SSE
         SSE.m6<-cvlm(5,m6,df.std)$SSE
         SSE.m7<-cvlm(5,m7,df.std)$SSE
```

```
In [72]: boxplot(SSE.m5,SSE.m6,SSE.m7,names=c("M5","M6","M7"),col=c("blue","green","purple"))
```



4.2 Recommended Procedure for Linear Model Fitting

We followed a lengthy process to arrive at the final model m7, and it is helpful to recount the general steps we recommend in creating such a linear model. 1. Inspect the data to make sure it is clean and has the structure you expect. 2. Check the distributions of the variables to make sure they are not highly skewed If one is skewed, consider transforming it. 3. Examine the bivariate scatterplots and correlation matrix to see whether there are any extremely correlated variables (such as r > 0.9, or several with r > 0.8). If so, omit some variables or consider transforming them if needed. 4. If you wish to estimate coefficients on a consistent scale, standardize the data with scale() (Sect. 7.3.3). 5. After fitting a model, check the residual quantiles in the output. The residuals show how well the model accounts for the individual observations (Sect. 7.2.4). 6. Check the standard model plots using plot(), which will help you judge whether a linear model is appropriate or whether there is nonlinearity, and will identify potential outliers in the data

(Sect. 7.2.4). 7. Try several models and compare them for overall interpretability and model fit by inspecting the residuals' spread and overall R2 (Sect. 7.3.1). If the models are nested, you could also use anova() for comparison (Sect. 6.5.1) . 8. Report the confidence intervals of the estimates with your interpretation and recommendations (Sect. 7.3).