https://www.youtube.com/watch?v=1keotmoOWo4 (https://www.youtube.com/watch?v=1keotmoOWo4)

Ch4. Exploring data with graphs

The art of presenting data

Packages used in this chapter

#install.packages("ggplot2")library(ggplot2)

Introducing ggplot2

The anatomy of a plot

In ggplot2, a plot is made up of layers



The anatomy of a graph



Geometric objects (geoms)

https://www.rstudio.com/wp-content/uploads/2015/03/ggplot2-cheatsheet.pdf (https://www.rstudio.com/wp-content/uploads/2015/03/ggplot2-cheatsheet.pdf)

http://docs.gaplot2.org/current/ (http://docs.gaplot2.org/current/)

geom_....()

Aesthetics

Linetype, Size, Shape, Colour, Alpha



The anatomy of the ggplot() function

myGraph <- ggplot(myData, aes(variable for x axis, variable for y axis))myGraph <- ggplot(myData, aes(variable for x axis, variable for y axis, colour = gender))+ ops(title = "Title") => ggtitle("New Plot Title")



myGraph + geom_bar()myGraph + geom_bar() + geom_point()myGraph <- ggplot(myData, aes(variable for x axis, variable for y axis, colour = gender))myGraph + geom_point(colour = "Blue")myGraph + geom_point(shape = 17, colour = "Blue")myGraph + geom_bar() + geom_point() + labels(x = "Text", y = "Text")

```
In [ ]:
```

Stats and geoms

```
In [ ]:
myHistogram <- ggplot(myData, aes(variable))

In [ ]:
myHistogram + geom_histogram()

In [ ]:
myHistogram + geom_histogram(aes(y = ..count..))

In [ ]:
myHistogram + geom_histogram(aes(y = ..density..))

In [ ]:
myHistogram + geom_histogram(aes(y = ..count..), binwidth = 0.4)

In [ ]:</pre>
```

Avoiding overplotting

1. position adjustment



2. faceting





```
In [ ]:
```

```
+ facet_wrap( ~ y, nrow = integer, ncol = integer)
```

```
In [ ]:
```

```
+ facet_grid( x ~ y )
```

```
In [ ]:
```

```
facet_grid(gender ~ extroversion)
```

```
In [ ]:
```

```
+ facet_wrap( ~ Rating_Type)
```

```
In [ ]:
```

```
+ facet_wrap( ~ Rating_Type, ncol = 2)
```

```
In [ ]:
```

```
+ facet_wrap( ~ Rating_Type, nrow = 2)
```

Saving graphs



```
In [ ]:
```

```
ggsave(filename)
```

```
In [ ]:
```

```
ggsave("Outlier Amazon.png")
```

```
In [ ]:
    ggsave("Outlier Amazon.tiff")

In [ ]:
    ggsave("Outlier Amazon.tiff", width = 2, height = 2)

In [ ]:
    In [ ]:
    In [ ]:
```

FacebookNarcissism.dat

```
In [3]:
```

facebookData <- read.delim("FacebookNarcissism.dat", header = TRUE)</pre>

In [4]:

head(facebookData)

Out[4]:

	id	NPQC_R_Total	Rating_Type	Rating
1	1	31	Attractive	2
2	1	31	Fashionable	2
3	1	31	Glamourous	2
4	1	31	Cool	2
5	2	37	Attractive	2
6	2	37	Fashionable	2

In [5]:

```
'data.frame': 776 obs. of 4 variables:

$ id : int 1 1 1 1 2 2 2 2 5 5 ...
```

```
$ id : int 1 1 1 1 2 2 2 2 5 5 ...

$ NPQC_R_Total: num 31 31 31 37 ...

$ Rating_Type : Factor w/ 4 levels "Attractive", "Cool",..: 1 3
4 2 1 3 4 2 1 3 ...

$ Rating : int 2 2 2 2 2 2 2 3 3 ...
```

In [6]:

```
summary(facebookData)
```

Out[6]:

id	NPQC_R_Total	Rating_Type	Rating
Min. : 1.0	Min. :14.00	Attractive :194	Min. :1.00
0			
1st Qu.: 78.0	1st Qu.:27.44	Cool :194	1st Qu.:2.00
0			
Median :139.0	Median :33.00	Fashionable:194	Median :3.00
0			
Mean :141.9	Mean :33.16	Glamourous :194	Mean :2.88
8			
3rd Qu.:208.0	3rd Qu.:38.00		3rd Qu.:3.00
0			
Max. :275.0	Max. :52.00		Max. :5.00
0			

contents of the dataframe

- 1. id: a number indicating from which participant the profile photo came
- 2. NPQC_R_Total: the total score on the narcissism questionnaire.
- 3. Rating_Type: whether the rating was for coolness, glamour, fashion or atttractiveness (stored as strings of text)
- 4. Rating: the rating given (on a scale from 1 to 5)

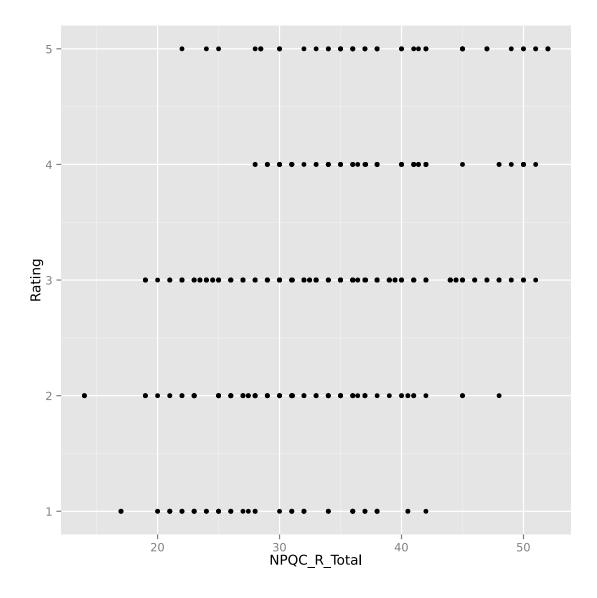
In [10]:

```
graph <- ggplot(facebookData, aes(NPQC_R_Total, Rating))</pre>
```

In [11]:

```
graph + geom_point()
```

Error in if (args[[1]]\$name == "C_title" && !is.null(arg
s[[2]])) {: missing value where TRUE/FALSE needed

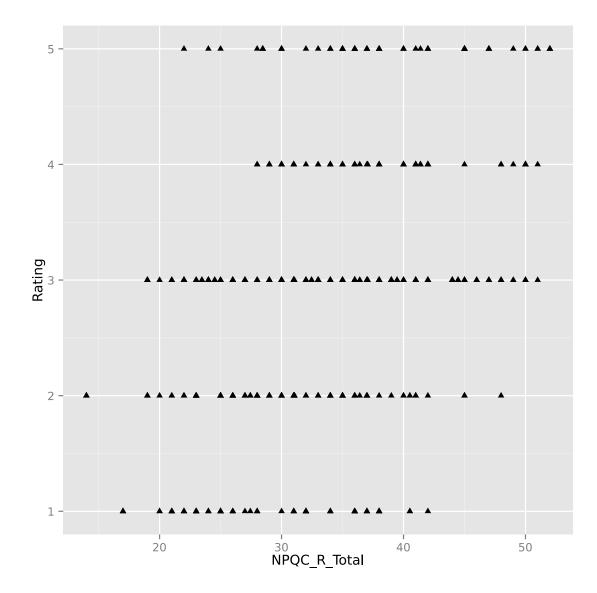


In [13]:

change the shape of point

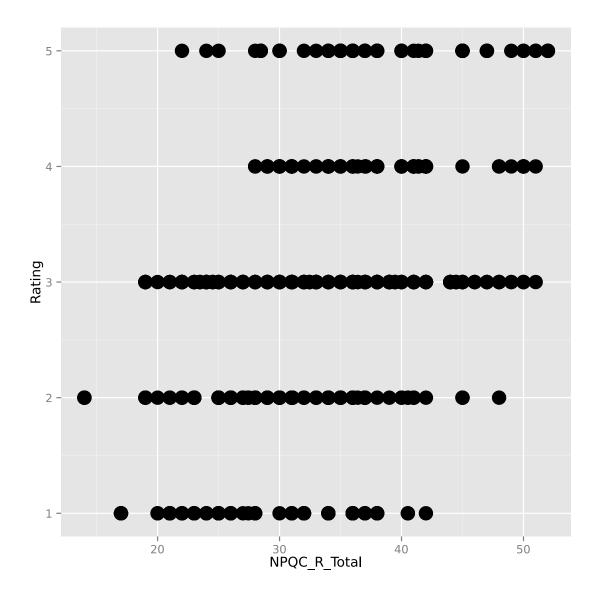
In [15]:

```
graph + geom_point(shape = 17)
```



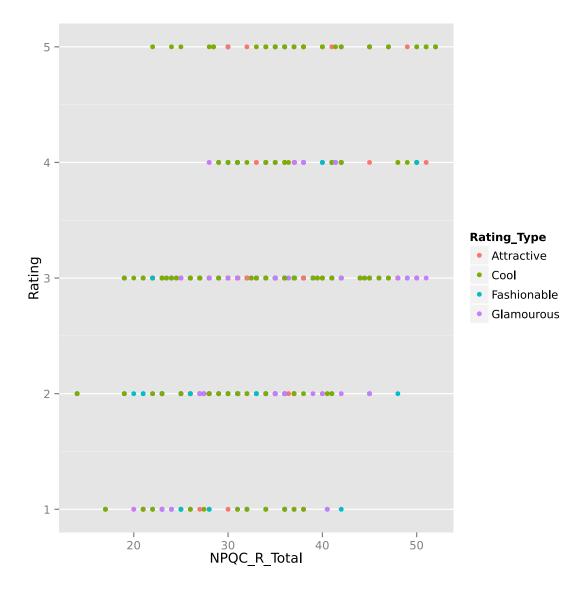
In [16]:

```
graph + geom_point(size = 6)
```



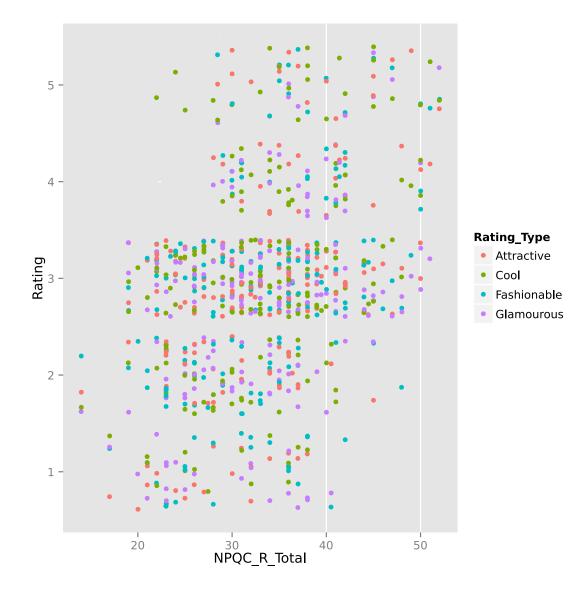
In [17]:

```
graph + geom_point(aes(colour = Rating_Type))
```



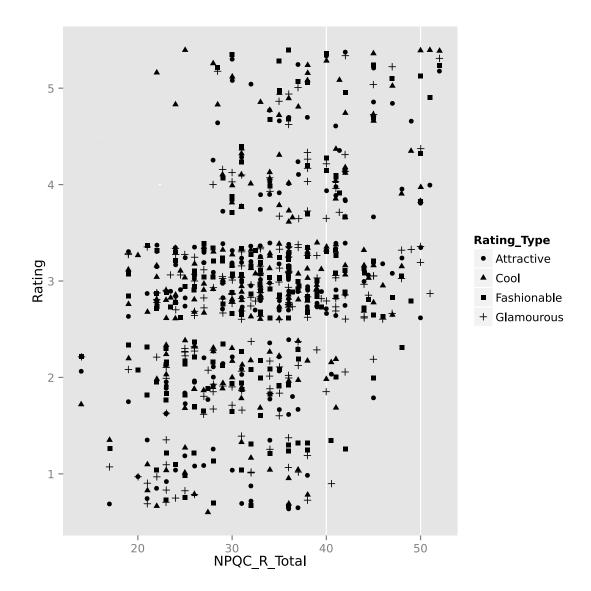
In [18]:

```
graph + geom_point(aes(colour = Rating_Type), position = "jitter")
```



In [19]:

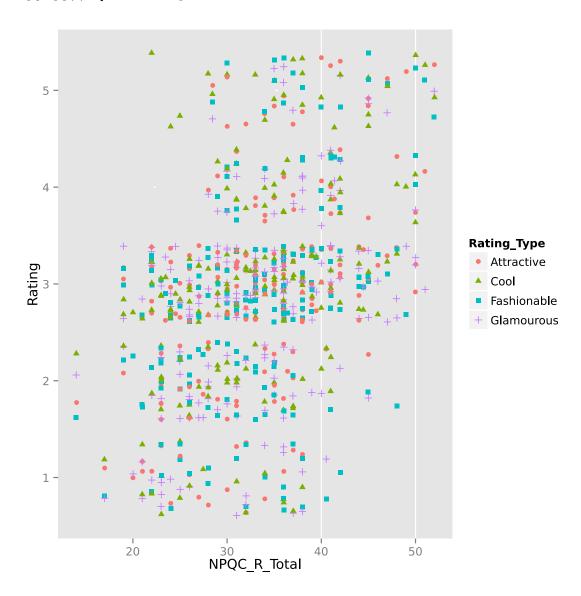
```
graph + geom_point(aes(shape = Rating_Type), position = "jitter")
```



In [20]:

```
graph + geom_point(aes(colour = Rating_Type, shape = Rating_Type), position
= "jitter")
```

Error in if (args[[1]]\$name == "C_title" && !is.null(arg
s[[2]])) {: missing value where TRUE/FALSE needed



Graphing relationships: the scatterplot

Simple scatterplot

```
In [39]:
```

examData <- read.delim("Exam Anxiety.dat", header = TRUE)</pre>

In [40]:

```
head(examData); str(examData); summary(examData)
```

Out[40]:

	Code	Revise	Exam	Anxiety	Gender
1	1	4	40	86.298	Male
2	2	11	65	88.716	Female
3	3	27	80	70.178	Male
4	4	53	80	61.312	Male
5	5	4	40	89.522	Male
6	6	22	70	60.506	Female

```
'data.frame': 103 obs. of 5 variables:
$ Code : int 1 2 3 4 5 6 7 8 9 10 ...
$ Revise : int 4 11 27 53 4 22 16 21 25 18 ...
$ Exam : int 40 65 80 80 40 70 20 55 50 40 ...
$ Anxiety: num 86.3 88.7 70.2 61.3 89.5 ...
$ Gender : Factor w/ 2 levels "Female", "Male": 2 1 2 2 2 1 1 1 1 ...
```

Out[40]:

Code	Revise	Exam	Anxiety
Gender			
Min. : 1.0	Min. : 0.00	Min. : 2.00	Min. : 0.05
6 Female:51			
1st Qu.: 26.5	1st Qu.: 8.00	1st Qu.: 40.00	1st Qu.:69.77
5 Male :52			
Median : 52.0	Median :15.00	Median : 60.00	Median :79.04
4			
Mean : 52.0	Mean :19.85	Mean : 56.57	Mean :74.34
4			
3rd Qu.: 77.5	3rd Qu.:23.50	3rd Qu.: 80.00	3rd Qu.:84.68
6			
Max. :103.0	Max. :98.00	Max. :100.00	Max. :97.58
2			

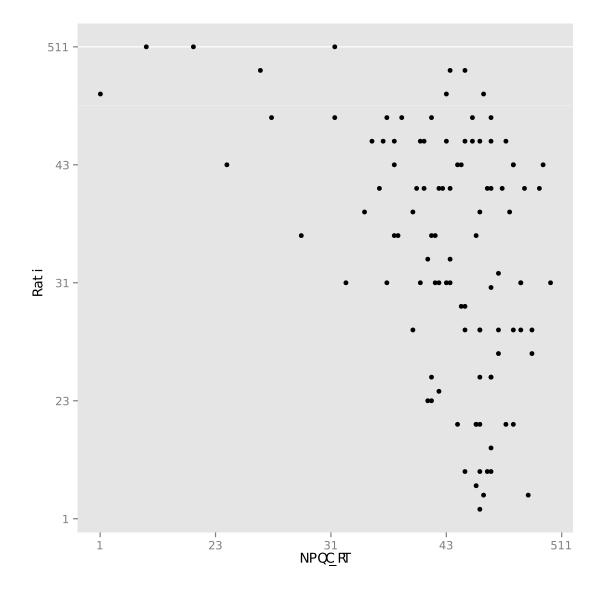
- 1. Code: a number indication from which participant the scores came.
- 2. Revise: the total hours spent revising.
- 3. Exam: mark on the exam as a percentage.
- 4. Anxiety: the score on the EAQ.
- 5. Gender: whether the participant was male or female (stored as strings of text).

In [41]:

```
scatter <- ggplot(examData, aes(Anxiety, Exam))</pre>
```

In [42]:

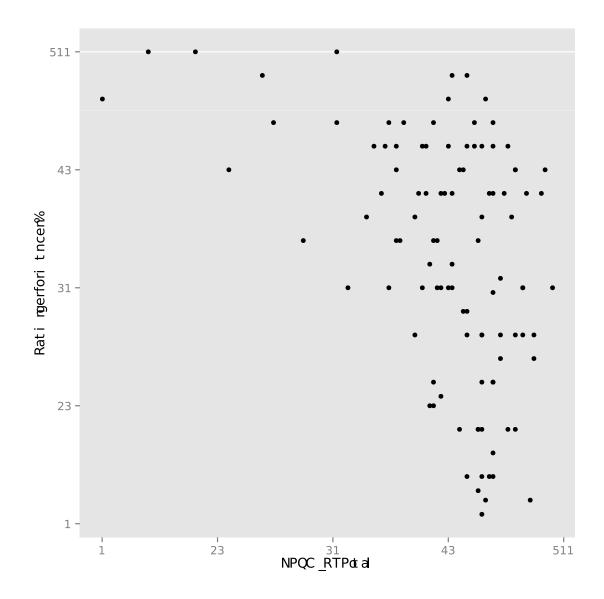
```
scatter + geom_point()
```



```
In [43]:
```

```
scatter + geom_point() + labs(x = "Exam Anxiety", y = "Exam Performance %")
```

Error in if (args[[1]]\$name == "C_title" && !is.null(arg
s[[2]])) {: missing value where TRUE/FALSE needed

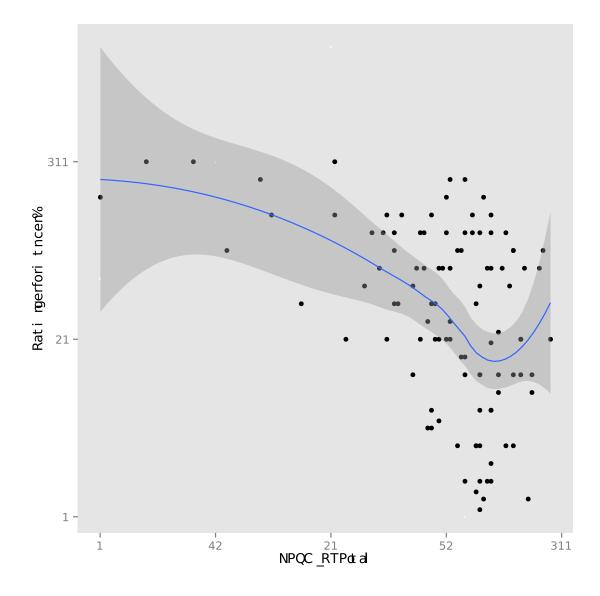


Adding a funky line: regression line

In [44]:

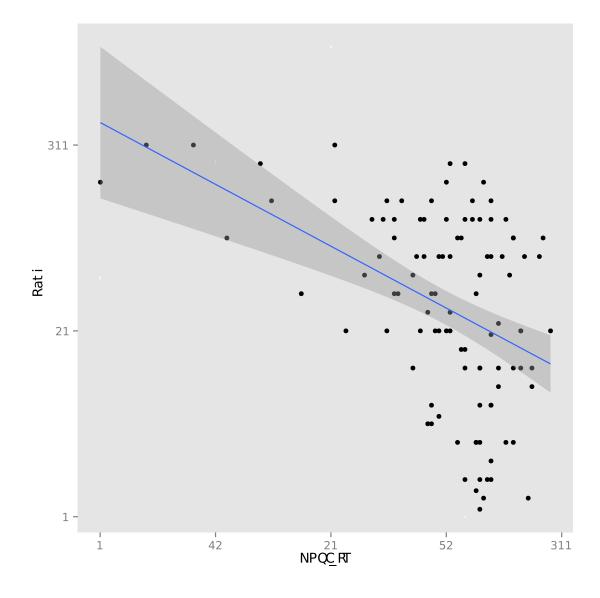
```
\label{eq:cont_point}  \mbox{scatter + geom\_point() + geom\_smooth() + labs(x = "Exam Anxiety", y = "Exam Performance %")}
```

geom_smooth: method="auto" and size of largest group is <1000, so using loess. Use 'method = x' to change the smoothing method.



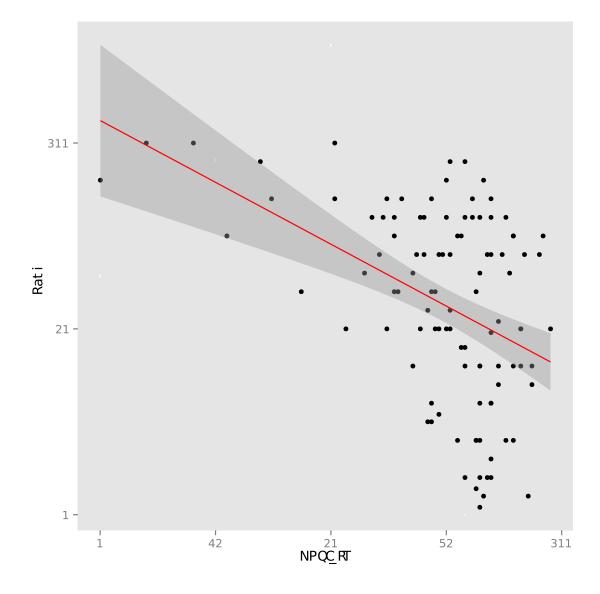
In [45]:

```
scatter + geom_point() + geom_smooth(method = "lm")
```



In [46]:

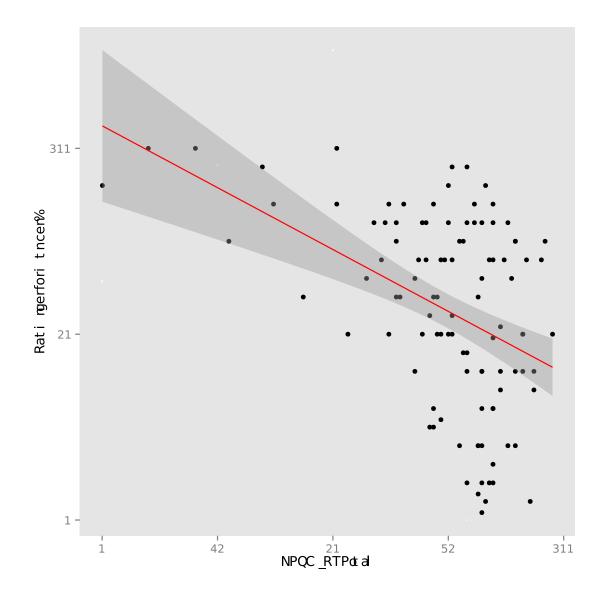
```
scatter + geom_point() + geom_smooth(method = "lm", colour = "Red")
```



In [47]:

```
scatter <- ggplot(examData, aes(Anxiety, Exam))
scatter + geom_point() + geom_smooth(method = "lm", colour = "Red") + lab
s(x = "Exam Anxiety")</pre>
```

Error in if (args[[1]]\$name == "C_title" && !is.null(arg
s[[2]])) {: missing value where TRUE/FALSE needed

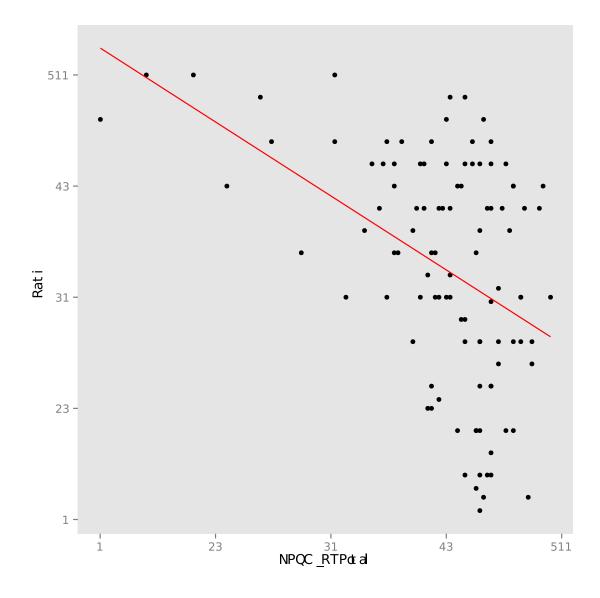


In [49]:

se = F : standard error = false

In [48]:

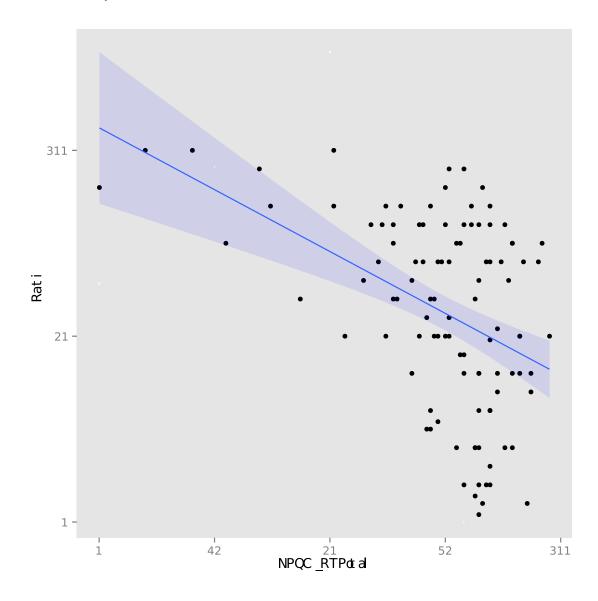
```
scatter <- ggplot(examData, aes(Anxiety, Exam))
scatter + geom_point() + geom_smooth(method = "lm",se = F, colour = "Red")
+ labs(x = "Exam Anxiety")</pre>
```



In [50]:

```
scatter <- ggplot(examData, aes(Anxiety, Exam))
scatter + geom_point() + geom_smooth(method = "lm",alpha = 0.1, fill= "Blu
e") + labs(x = "Exam Anxiety")</pre>
```

Error in if (args[[1]]\$name == "C_title" && !is.null(arg
s[[2]])) {: missing value where TRUE/FALSE needed



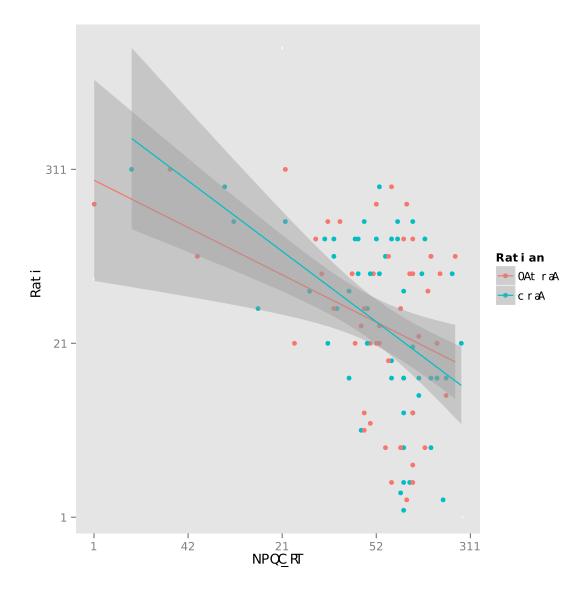
Grouped scatterplot

```
In [51]:
```

```
scatter <- ggplot(examData, aes(Anxiety, Exam, colour = Gender))</pre>
```

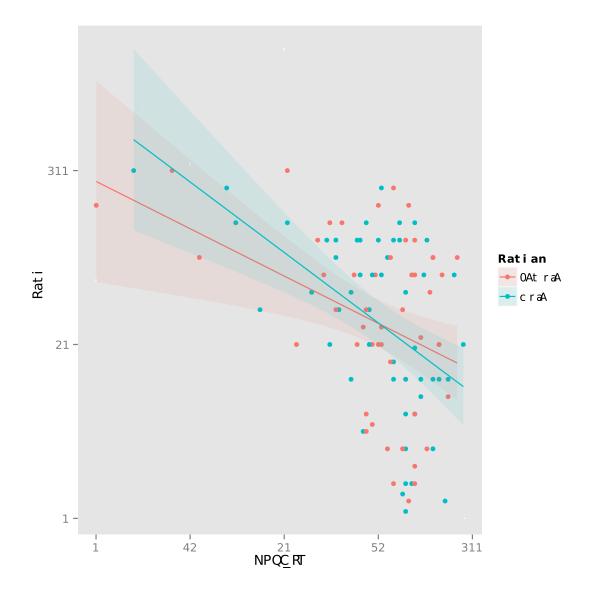
In [53]:

```
scatter + geom_point() + geom_smooth(method = "lm")
```



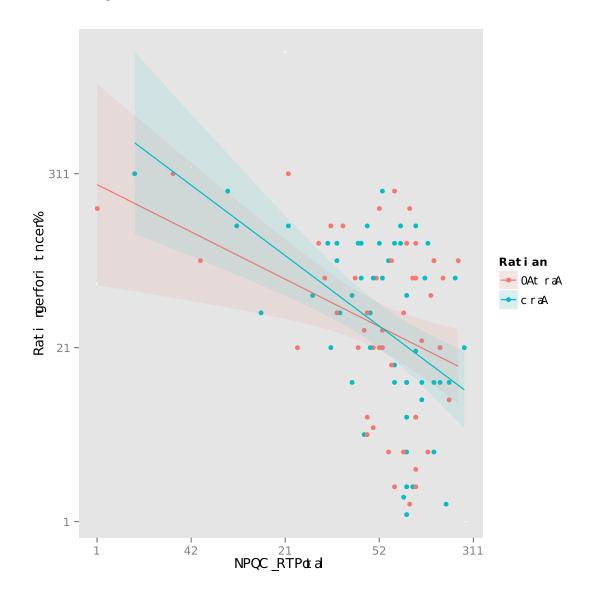
In [54]:

```
scatter + geom_point() + geom_smooth(method = "lm", aes(fill = Gender), alp
ha = 0.1)
```



In [55]:

Error in if (args[[1]]\$name == "C_title" && !is.null(arg
s[[2]])) {: missing value where TRUE/FALSE needed



Histograms: a good way to spot obvious problems

In [56]:

festivalData <- read.delim("DownloadFestival.dat", header = TRUE)</pre>

In [57]:

```
festival
Histogram <- ggplot(festival
Data, aes(day1)) + opts(legend.positio n="none")   
# not working
```

Error: Use 'theme' instead. (Defunct; last used in version 0.9.1)

In [58]:

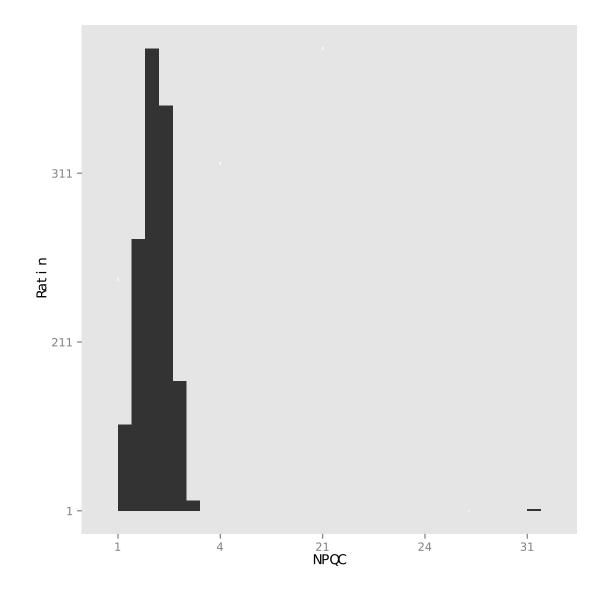
festivalHistogram <- ggplot(festivalData, aes(day1)) + theme(legend.positio n="none")



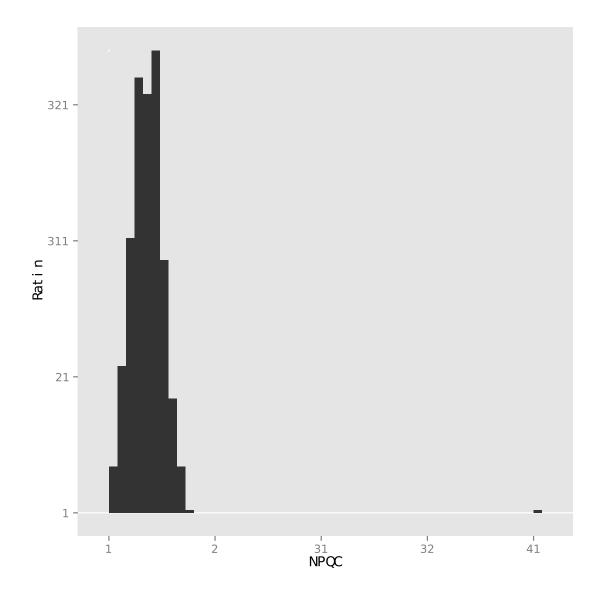
In [59]:

festivalHistogram + geom_histogram()

stat_bin: binwidth defaulted to range/30. Use 'binwidth = x' to adjust this.



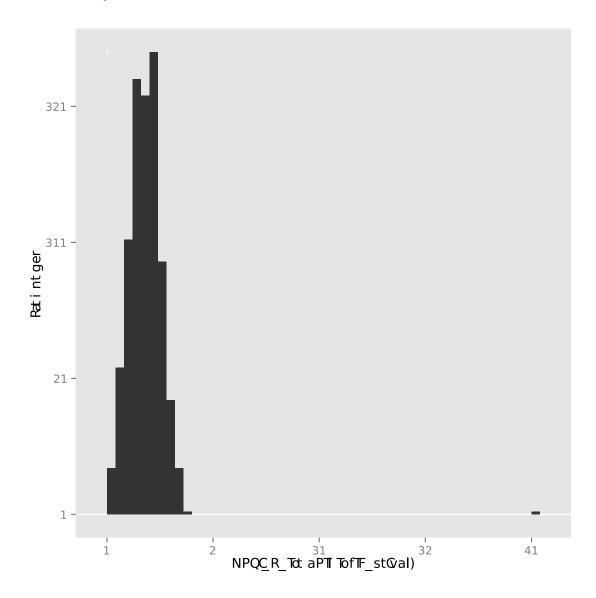
In [61]:
festivalHistogram + geom_histogram(binwidth = 0.4)



In [62]:

```
festivalHistogram + geom_histogram(binwidth = 0.4) + labs(x = "Hygiene (Day 1 of Festival)", y = "Frequency")
```

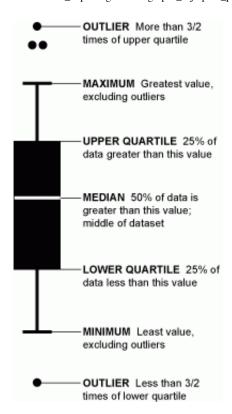
Error in if (args[[1]]\$name == "C_title" && !is.null(arg
s[[2]])) {: missing value where TRUE/FALSE needed



Boxplots (box-whisker disgrams)

Box plot 정확히 상자와 수염 그림(box and whisker plot)은 두 개 이상의 집단의 상대적 비교를 위해서 각 집단의 최대값(max)과 최소값(min) 그리고 중앙값(자료를 크기순으로 나열했을 때 가운데 위치하는 값: median) 및 사분위수(자료를 크기 순서에 따라 늘어놓은 자료를 4등분 했을 때 위치하는 값을 의미함) 제 1사분위수(아래에서 25% 백분위점에 위치하는 수: Q1), 제 3사분위수(아래에서 75% 백분위점에 위치하는 수: Q3)등 다섯 숫자를 요약하여 그 래프로 나타내는 방법으로 John W. Tukey가 제안한 탐색적 데이터 분석 방법입니다. 출처:

http://wsyang.com/2013/07/add-more-info-to-the-boxplot/ (http://wsyang.com/2013/07/add-more-info-to-the-boxplot/)



http://flowingdata.com/2008/02/15/how-to-read-and-use-a-box-and-whisker-plot/ (http://flowingdata.com/2008/02/15/how-to-read-and-use-a-box-and-whisker-plot/)

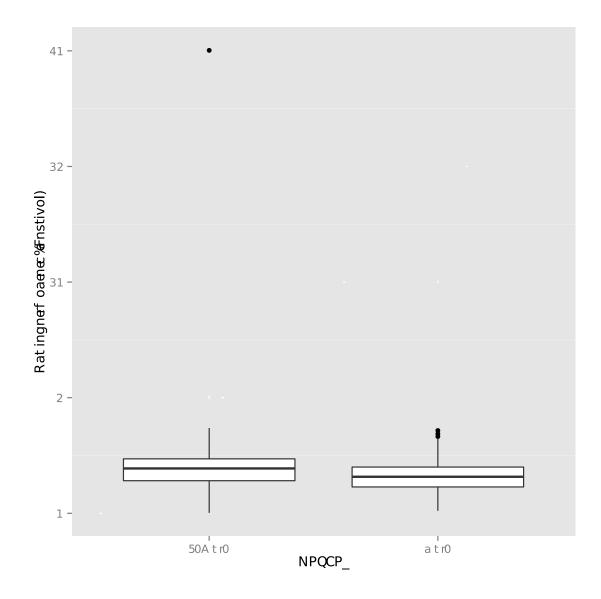
In [66]:

```
festivalBoxplot <- ggplot(festivalData, aes(gender, day1))</pre>
```

In [67]:

```
festivalBoxplot + geom_boxplot() + labs(x = "Gender", y = "Hygiene (Day 1 o f Festival)")
```

Error in if (args[[1]]\$name == "C_title" && !is.null(arg
s[[2]])) {: missing value where TRUE/FALSE needed



In [68]:

festivalData <- festivalData[order(festivalData\$day1),]</pre>

In [71]:

tail(festivalData)

Out[71]:

	ticknumb	gender	day1	day2	day3
774	4564	Female	3.38	3.44	3.41
300	3371	Female	3.41	NA	NA
657	4264	Male	3.44	NA	NA
303	3374	Male	3.58	3.35	NA
574	4016	Female	3.69	NA	NA
611	4158	Female	20.02	2.44	NA



Density plots

In [77]:

festivalData <- read.delim("DownloadFestival(No Outlier).dat", header = TRU
E)</pre>

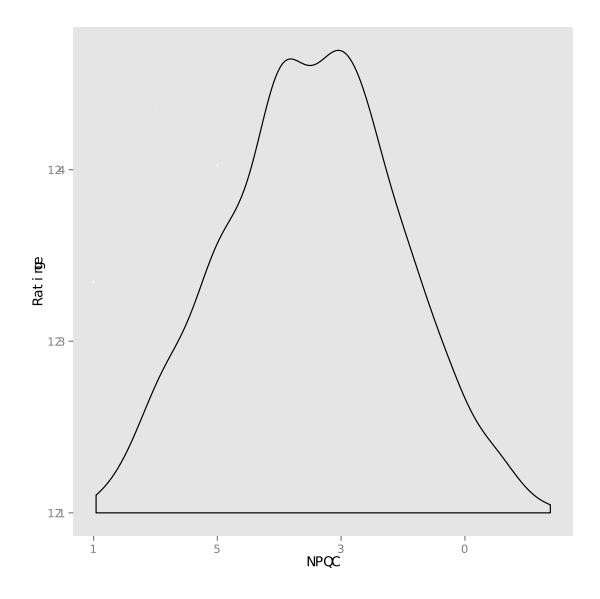
In [78]:

density <- ggplot(festivalData, aes(day1))</pre>

In [79]:

density + geom_density()

Error in if (args[[1]]\$name == "C_title" && !is.null(arg
s[[2]])) {: missing value where TRUE/FALSE needed



Graphing means

```
In [81]:
```

chickFlick <- read.delim("ChickFlick.dat", header = TRUE)</pre>

```
In [82]:
```

```
head(chickFlick); summary(chickFlick);str(chickFlick)
```

Out[82]:

	gender	film	arousal
1	Male	Bridget Jones' Diary	22
2	Male	Bridget Jones' Diary	13
3	Male	Bridget Jones' Diary	16
4	Male	Bridget Jones' Diary	10
5	Male	Bridget Jones' Diary	18
6	Male	Bridget Jones' Diary	24

Out[82]:

```
gender
                               film
                                          arousal
                                             : 3.00
Female:20
             Bridget Jones' Diary:20
                                       Min.
Male :20
            Memento
                                       1st Qu.:14.00
                                 :20
                                       Median :19.50
                                       Mean
                                              :20.02
                                       3rd Qu.:24.25
                                              :37.00
                                       Max.
'data.frame': 40 obs. of 3 variables:
 $ gender : Factor w/ 2 levels "Female", "Male": 2 2 2 2 2 2 2 2
2 2 ...
 $ film
          : Factor w/ 2 levels "Bridget Jones' Diary",..: 1 1 1
1 1 1 1 1 1 1 ...
 $ arousal: int 22 13 16 10 18 24 13 14 19 23 ...
```

Bar charts for one independent variable

```
In [83]:
bar <- ggplot(chickFlick, aes(film, arousal))</pre>
```

In [84]:

```
bar + stat_summary(fun.y = mean, geom = "bar", fill = "White", colour = "Bl
ack") + stat_summary(fun.data = mean_cl_normal, geom = "pointrange") + lab
s(x = "Film", y = "Mean Arousal")
```

Error: Hmisc package required for this functionality. Please in stall and try again.

```
In [ ]:
```