R Notebook

1. P_housing

1a.graph change in house prices

1b.look for an inflection point -

?? any evidence of a slowdown in price appreciation ??

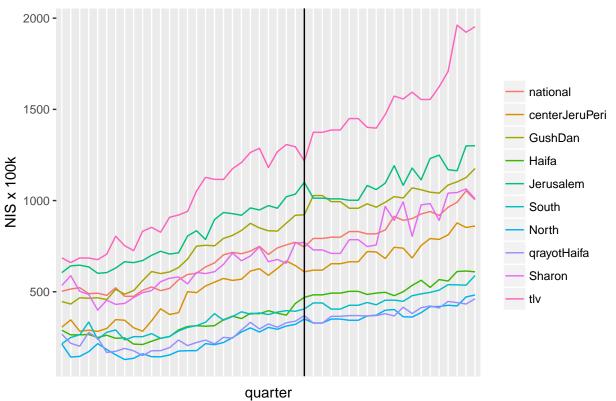
2. try to say something about renters vs. owners

2a.?? any difference ??

2b.?? are they like Tokyo renters or San Francisco renters ??

Here I have added a vertical line where it seems that housing prices, at least in some areas began to slow their ascent. It looks like after my line at least Gush Dan and Haifa prices grow at a slower rate. I now attempt to find this inflection point.



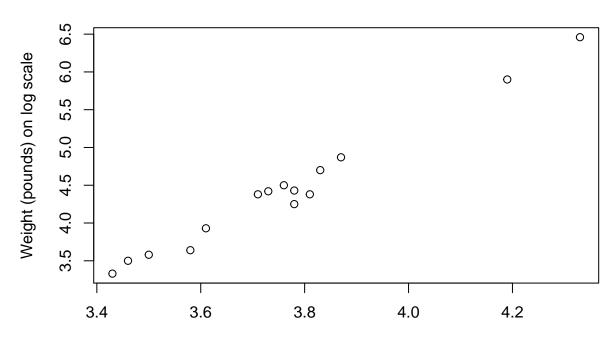


```
library(inflection)
#ede(p1.5$quarter,p1.$value,1)
#func = splinefun(x=p1.5$quarter,y=p1.5$value, method="fmm",ties=mean)
#zzz <-spline(x=p1.5$quarter,y=p1.5$value, method="fmm",ties=mean)
#qplot(spline)
#dValue <-diff(p1.5$value)
#dValue1<-c(NA,dValue)
#p1.5$dValue <-dValue1
#ggplot(data=p1.5,aes(x=quarter, y=dValue))
#qplot(func)
#lm(data=p1.5, formula=log(quarter) ~ log(value))</pre>
```

try the lm code alli. $mod1 = lm(lnWeight \sim lnLength, data = alligator)$.

```
alligator = data.frame(
  lnLength = c(3.87, 3.61, 4.33, 3.43, 3.81, 3.83, 3.46, 3.76,
     3.50, 3.58, 4.19, 3.78, 3.71, 3.73, 3.78),
  lnWeight = c(4.87, 3.93, 6.46, 3.33, 4.38, 4.70, 3.50, 4.50,
     3.58, 3.64, 5.90, 4.43, 4.38, 4.42, 4.25)
)
plot(lnWeight ~ lnLength, data = alligator,
     xlab = "Snout vent length (inches) on log scale",
     ylab = "Weight (pounds) on log scale",
     main = "Alligators in Central Florida"
)
```

Alligators in Central Florida



Snout vent length (inches) on log scale

```
alli.mod1 = lm(lnWeight ~ lnLength, data = alligator)
summary(alli.mod1)
```

```
##
## lm(formula = lnWeight ~ lnLength, data = alligator)
## Residuals:
                 1Q
                      Median
  -0.24348 -0.03186 0.03740 0.07727
##
## Coefficients:
              Estimate Std. Error t value Pr(>|t|)
##
               -8.4761
                           0.5007
                                  -16.93 3.08e-10 ***
## (Intercept)
## lnLength
                                    25.80 1.49e-12 ***
                3.4311
                           0.1330
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 0.1229 on 13 degrees of freedom
## Multiple R-squared: 0.9808, Adjusted R-squared: 0.9794
## F-statistic: 665.8 on 1 and 13 DF, p-value: 1.495e-12
```

Now plot something from the linear model of the alligators against the original data.

```
# plot(resid(alli.mod1) ~ fitted(alli.mod1),
# xlab = "Fitted Values",
# ylab = "Residuals",
# main = "Residual Diagnostic Plot",
# panel = function(x, y, ...)
# {
# panel.grid(h = -1, v = -1)
```

```
# panel.abline(h = 0)
# panel.xyplot(x, y, ...)
# }
# )
```

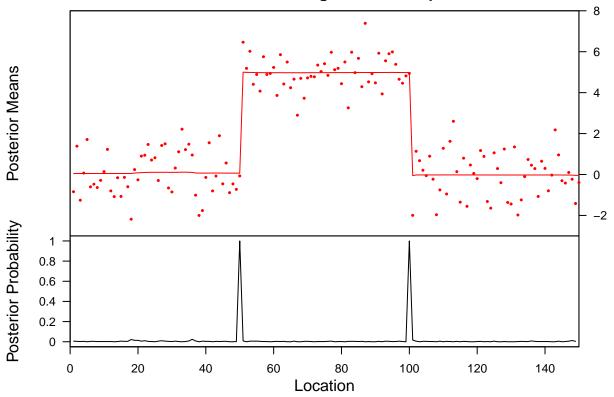
try the R package bcp, work an example from the pdf

```
library(bcp)
```

```
## Loading required package: grid
##### univariate sequential data #####
# an easy problem with 2 true change points

set.seed(5)
x <- c(rnorm(50), rnorm(50, 5, 1), rnorm(50))
bcp.1a <- bcp(x)
plot(bcp.1a, main="Univariate Change Point Example")</pre>
```

Univariate Change Point Example

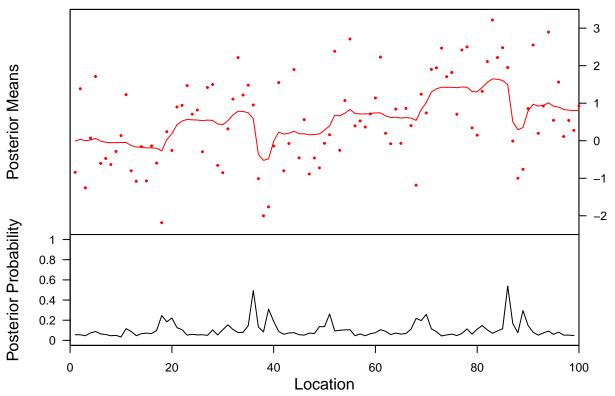


#legacyplot(bcp.1a)

I think that only has frequencies of X. Let's see if the 2nd example actually has some Ys.

```
# a hard problem with 1 true change point
set.seed(5)
x <- rep(c(0,1), each=50)
y <- x + rnorm(50, sd=1)
bcp.1b <- bcp(y)
plot(bcp.1b, main="Univariate Change Point Example")</pre>
```

Univariate Change Point Example



don't know what that was, but it still doesn't look right. I will try the 3rd example from the bcp manual. https://cran.r-project.org/web/packages/bcp/bcp.pdf

```
##### multivariate sequential data #####
# an easy problem in k=3 dimensions
set.seed(5)
x <- rnorm(6, sd=3)
y <- rbind(cbind(rnorm(50, x[1]), rnorm(50, x[2]), rnorm(50, x[3])),
cbind(rnorm(50, x[4]), rnorm(50, x[5]), rnorm(50, x[6])))
bcp.2a <- bcp(y)
plot(bcp.2a, main="Multivariate (k=3) Change Point Example")</pre>
```

