Categorical Predictors

Chapter 5 of ALR4, Chapter 14, 15 of LMWR2

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Categorical Predictors

A **categorical variable** is a variable that can take on one of a limited, usually fixed, number of possible values, assigning each individual or other unit of observation to a particular group or nominal category on the basis of some qualitative property.

Categorical predictors are often called **factors**

Example: UN Data

Consider data from 199 localities (mostly members of the United Nations, but a few areas such as Hong Kong). The measured variables include:

- `ppgdp` – the gross national product per person in U.S. dollars
- `fertility` – average number of children per woman
- `lifeExpF` – female life expectancy, years
- `pctUrban` – percentage of population living in urban areas
- `group` – a factor with level `oecd` for countries that are members of the Organization for Economic Cooperation and Development (OECD) as of May 2012, `africa` for countries on the African continent, and other for all other countries. No OECD countries are located in Africa.

Exploring Data for One-Factor Models

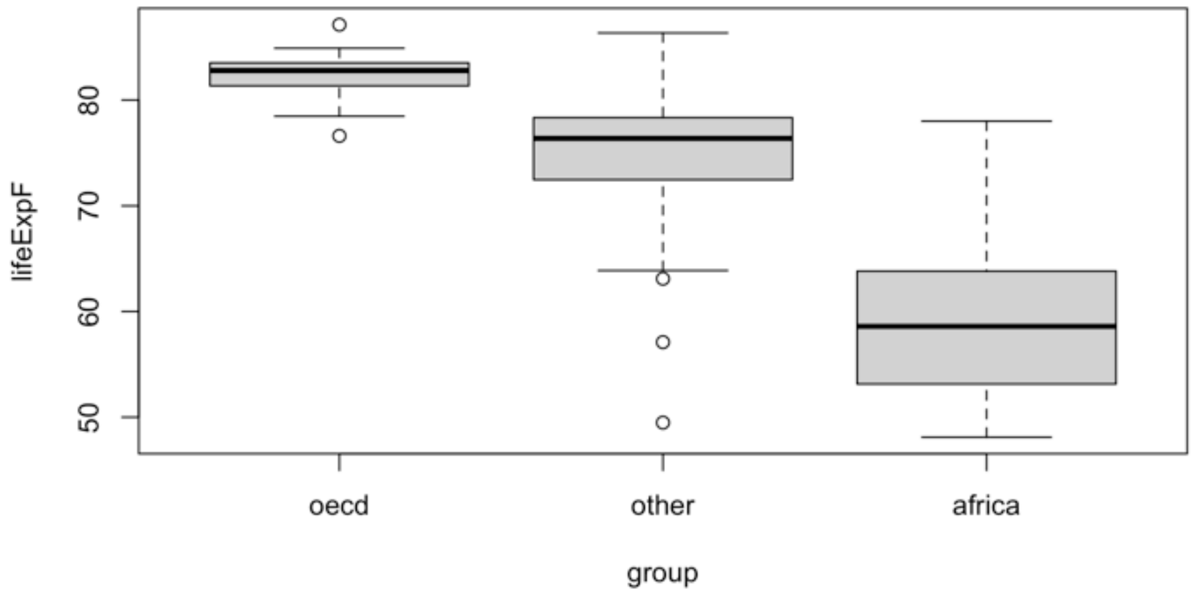
If the only predictor is a factor, then the regression model is called a one-factor or one-way design.

Boxplots of a one-factor model are useful for comparing different levels of each factor.

- The thick middle line indicates the median value.
- The box extends to the 25th and 75th percentiles. The distance between the quartiles is known as the **interquartile range (IQR)**.
- The **whiskers** generally extend to the most extreme values that are within 1.5 IQRs from the **quartiles**.
- Values outside the whiskers are outliers and are indicated by a dot or star.

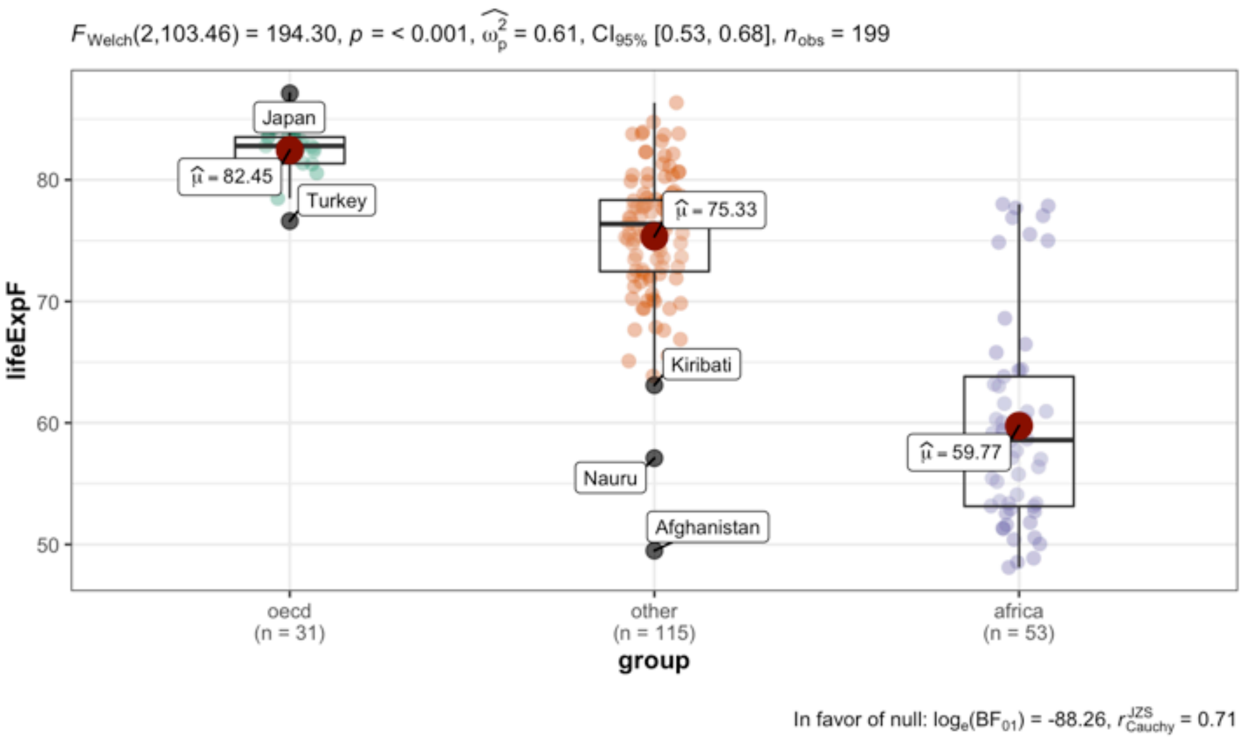
Boxplot Example

```
data(UN11, package = 'alr4')
boxplot(lifeExpF ~ group, data = UN11)
```



More Details

```
library(ggstatsplot)
UN11$country = row.names(UN11)
ggbetweenstats(data = UN11, plot.type = 'box',x = group, y = lifeExpF, outlier.tagging = T, out
```



What we get?

-The oecd countries generally have the largest female life expectancy, with africa having the lowest.

- Nauru and Afghanistan have unusually low female life expectancy for the other group.
- Japan has high female life expectancy, and Turkey has low life expectancy, compared to the other members of the oecd.
- The variation of female life expectancy in oecd is smallest, but in africa is largest.

Defining Factors as Regressors

Defining Factors as Regressors

Dummy or **indicator** variables are used to include categorical predictors in a regression model.

A dummy variable U_j for factor level j is 1 if an observation has level j, but 0 otherwise.

- -1 and 1, or 1 and 2, are sometimes used, but this is less common and more difficult to interpret.
- Assignment labels are mostly arbitrary and do not affect the results.

Since group has $d = 3$ levels, the jth dummy variable U_j for the factor $j = 1, 2, \ldots, d$ has ith value u_ij, for $i = 1, 2, \ldots, n$, given by

$$u_{ij} = \begin{cases} 1 & \text{if group}_i = j\text{th category of group} \\ 0 & \text{otherwise} \end{cases}$$

Try in R

```
levels(UN11$group)
```

```
## [1] "oecd"   "other"  "africa"
```

```
U1 = with(UN11, (group == levels(group)[1])+0)
U2 = with(UN11, (group == levels(group)[2])+0)
U3 = with(UN11, (group == levels(group)[3])+0)
head(data.frame(group = UN11$group, U1, U2, U3))
```

```
##    group U1 U2 U3
## 1  other  0  1  0
## 2  other  0  1  0
## 3 africa  0  0  1
## 4 africa  0  0  1
## 5  other  0  1  0
## 6  other  0  1  0
```

U_1 is the dummy variable for oecd, U_2 is the dummy variable for other, and U_3 for africa.

One-Factor Model

Regression coefficients are generally called effects in this setting.

How can we build a model using the form y=X+ϵ?

What would happen if we fit the model

$$E(lifeExpF \mid group) = \beta_0 + \beta_1 U_1 + \beta_2 U_2 + \beta_3 U_3?$$

Why?

This is why!

In that case, X would be rank deficient since $U_1 + U_2 + U_3 = 1$, which will always match the intercept.

- The columns of X would be linearly dependent.

We only need $d - 1$ dummy variables to represent d levels because the last level represented when all the other dummy variables were 0.

- Any of the d dummy variables could be excluded, though generally it is the first or last level.
- `R` drops the first level by default.
- The level dropped is known as the **reference** or **baseline** level.
- In `R`, this method for creating the dummy variables is known as the **treatment contrast**.

A different solution

Other possibilities for avoiding linear dependence are:

- Drop β_0 from the model.
- Assume $\sum_{i=1}^{p-1} \beta_i = 0$.
- This is known as a **sum contrast** and does NOT use dummy variables.
- Interpretation is generally more difficult.

Models

Using a treatment contrast with the first level of `group` as the reference level (`oecd`), our model becomes

$$E(lifeExpF \mid group) = \beta_0 + \beta_2 U_2 + \beta_3 U_3.$$

Since `group = oecd` implies $U_2 = U_3 = 0$,

$$E(lifeExpF \mid group = oecd) = \beta_0 + \beta_2 0 + \beta_3 0 = \beta_0.$$

Since `group = other` implies $U_2 = 1$ and $U_3 = 0$,

$$E(lifeExpF \mid group = other) = \beta_0 + \beta_2 1 + \beta_3 0 = \beta_0 + \beta_2.$$

Since `group = africa` implies $U_2 = 0$ and $U_3 = 1$,

$$E(lifeExpF \mid group = africa) = \beta_0 + \beta_2 0 + \beta_3 1 = \beta_0 + \beta_3.$$

Fit in R

- Method 1

```r
lm(lifeExpF ~ U2 + U3, data = UN11)
```

```
##
## Call:
## lm(formula = lifeExpF ~ U2 + U3, data = UN11)
##
## Coefficients:
## (Intercept)           U2           U3
##       82.45        -7.12       -22.67
```

- Method 2

```r
lm(lifeExpF ~ group, data = UN11)
```

```
##
## Call:
## lm(formula = lifeExpF ~ group, data = UN11)
##
## Coefficients:
## (Intercept)   groupother  groupafrica
##       82.45        -7.12       -22.67
```

`LifeExpF` of different groups

- $\hat{E}(Lifeexpf \mid group = oecd) = \hat{\beta}_0 = 82.45.$
- $\hat{E}(Lifeexpf \mid group = other) = \hat{\beta}_0 + \hat{\beta}_2 = 82.45 - 7.12 = 75.33.$
- $\hat{E}(Lifeexpf \mid group = africa) = \hat{\beta}_0 + \hat{\beta}_3 = 82.45 - 22.67 = 59.79.$

Interpretation

```
lm(lifeExpF ~ group, data = UN11)
```

```
##
## Call:
## lm(formula = lifeExpF ~ group, data = UN11)
##
## Coefficients:
## (Intercept)   groupother  groupafrica
##       82.45        -7.12       -22.67
```

Interpretation

```
lm(lifeExpF ~ group, data = UN11)
```

```
##
## Call:
## lm(formula = lifeExpF ~ group, data = UN11)
##
## Coefficients:
## (Intercept)   groupother  groupafrica
##       82.45        -7.12       -22.67
```

- The expected female life expectancy for OECD nations is 82.45 years.
- The expected female life expectancy for other nations is 7.12 years less than nations in OECD.
- The expected female life expectancy for African nations is 22.67 years less than nations in OECD.

Interesting Facts

- $\hat{\beta}_0$ is simply the sample mean of the responses in the oecd group.
- $\hat{\beta}_2$ is the difference between the sample mean of the responses for the other group and the oecd group.
- $\hat{\beta}_3$ is the difference between the sample mean of the responses for the africa group and the oecd group.

```r
with(UN11, tapply(lifeExpF, group, mean))
```

```
##     oecd    other   africa
## 82.44645 75.32674 59.77226
```

Effect Plot

```
library(effects)
```

```
## Loading required package: carData
```

```
## lattice theme set by effectsTheme()
## See ?effectsTheme for details.
```

```
lmod1 = lm(lifeExpF ~ group, data = UN11)
plot(predictorEffect('group',lmod1))
```

Factors and Quantitative Predictors

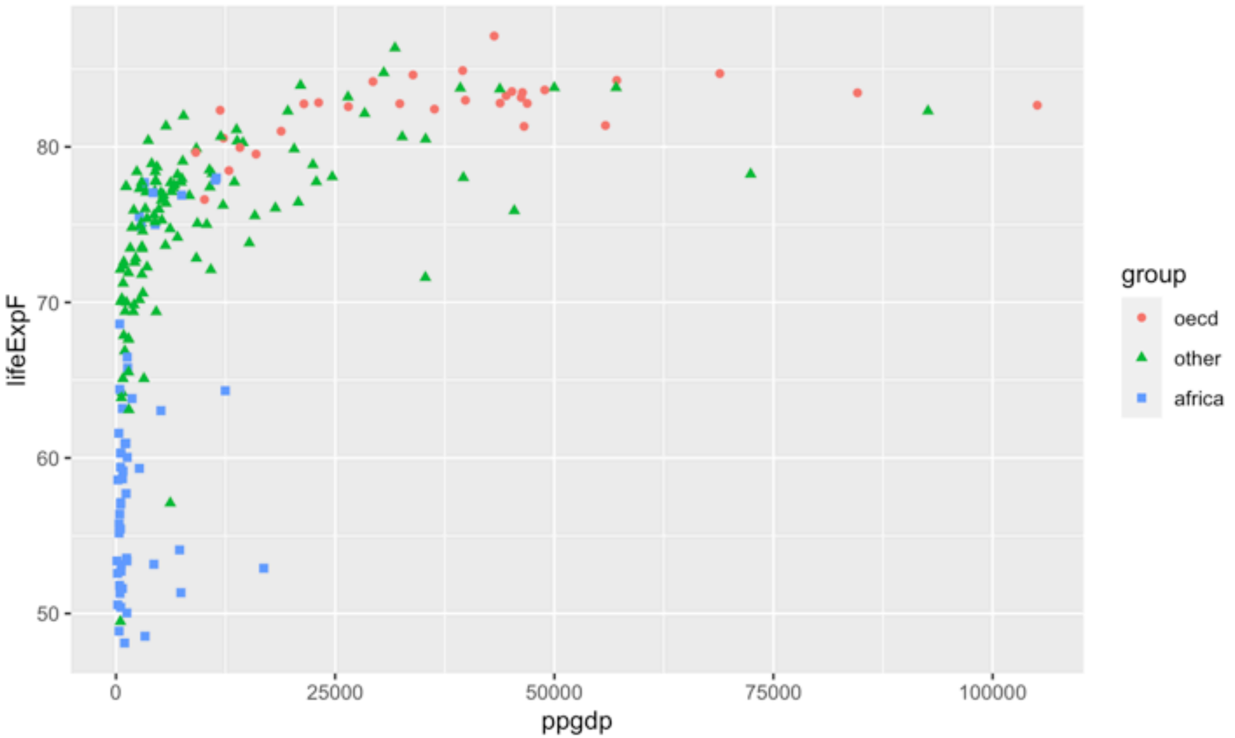
It is common to study the effect of a factor AFTER adjusting for one or more other quantitative regressors.

If we have a mixture of factors and quantitative variables in our data, it's useful to create a scatterplot of the response versus the covariate that distinguishes the observations for each level.

- This helps us assess whether the relationship between the response and quantitative regressor differs for the levels of the factor.

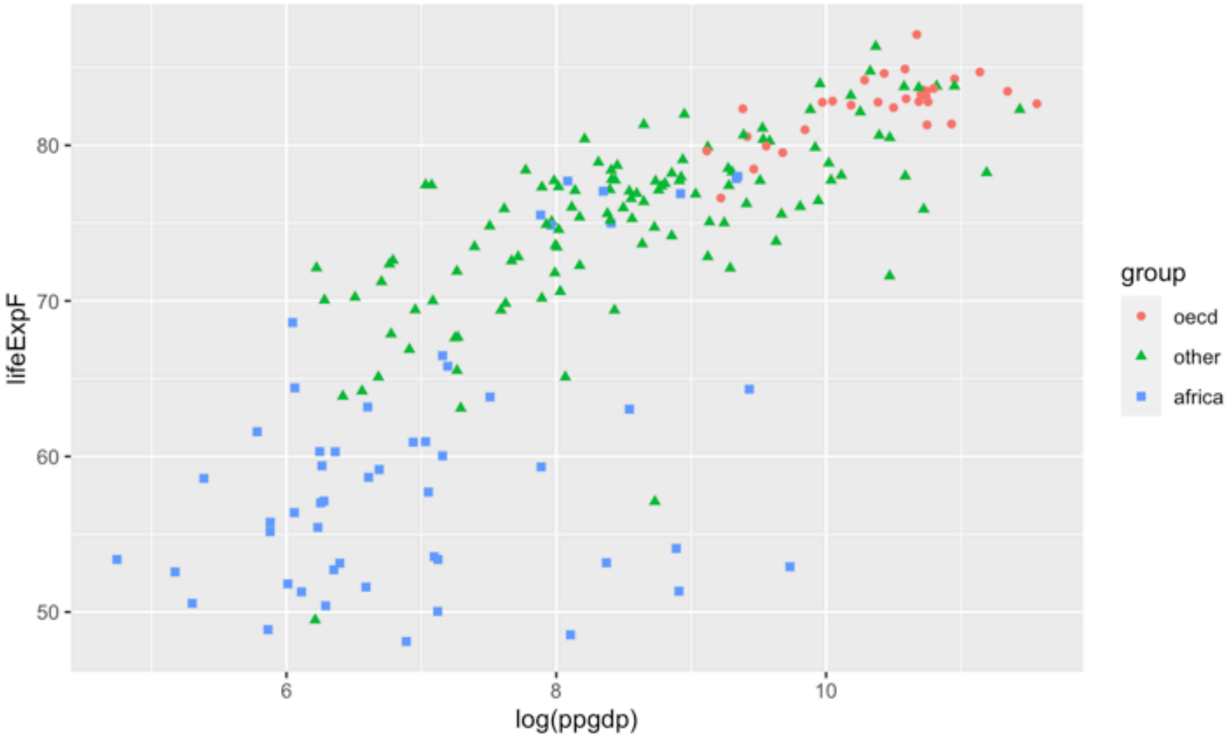
Scatter Plot

```
library(ggplot2)
ggplot(data = UN11, aes(x = ppgdp, y = lifeExpF, col = group, shape = group))+
  geom_point()
```



Helpful One

```
ggplot(data = UN11, aes(x = log(ppgdp), y = lifeExpF, col = group, shape = group))+
  geom_point()
```



What we see?

- The linear relationship between lifeExpF and log(ppgdp) is fairly weak for the africa locations
- The linear relationship is reasonably strong for the other locations
- The linear relationship is reasonably strong for oecd locations.
- It's unclear whether the average rate of change between lifeExpF and log(ppgdp) (the slope) is the same for the three factor levels.
- The average lifeExpF seems to differ vertically for the same levels of log(ppgdp) for the different factor levels.

Different Models to Consider

Suppose we have a response y, a quantitative regressor x, and a two-level factor variable represented by a dummy variable u:

$$u = \begin{cases} 0 & \text{for the reference level} \\ 1 & \text{for the treatment level.} \end{cases}$$

Consider several possible regression models:

- The same regression line for both levels, $y=\beta_0+\beta_1 x+\epsilon$.
- In R: `y ~ x`
- A factor predictor but no quantitative predictor, $y=\beta_0+\beta_2 u+\epsilon$.
- In R: `y ~ u`
- This is a **one-way model**.

Different Models to Consider

- Separate regression lines for each group having the same slope, $y = \beta_0 + \beta_1 x + \beta_2 u + \epsilon$.

- In R: $y\ x + u$.

- This is known as a parallel lines or main effects model.

- β_2 represents the vertical distance between the regression lines (the effect of the treatment).

- Separate lines for each group with different slopes, y=β_0+β_1 x+β_2 u+β_3 xu+ϵ.

- In R: `y ~ x + u + x:u` or `y ~ x*u`
  - This is known as a separate lines or interaction model.
  - `x:u` means the interaction between x and u.
  - `x*u` means the cross between x and u (x, u, and the interaction between x and u).

Example

```
lmodi = lm(lifeExpF ~ group*log(ppgdp), data = UN11)
head(model.matrix(lmodi))
```

```
##             (Intercept) groupother groupafrica log(ppgdp) groupother:log(ppgdp)
## Afghanistan           1          1           0   6.212606             6.212606
## Albania               1          1           0   8.209907             8.209907
## Algeria               1          0           1   8.405815             0.000000
## Angola                1          0           1   8.371450             0.000000
## Anguilla              1          1           0   9.528801             9.528801
## Argentina             1          1           0   9.122831             9.122831
##             groupafrica:log(ppgdp)
## Afghanistan               0.000000
## Albania                   0.000000
## Algeria                   8.405815
## Angola                    8.371450
## Anguilla                  0.000000
## Argentina                 0.000000
```

Example

```
library(knitr)
kable(summary(lmodi)$coefficients)
```

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	59.2136614	15.220345	3.8904284	0.0001377
groupother	-11.1731029	15.594836	-0.7164617	0.4745723
groupafrica	-22.9848394	15.783786	-1.4562310	0.1469536
log(ppgdp)	2.2425354	1.466444	1.5292337	0.1278438
groupother:log(ppgdp)	0.9294372	1.517667	0.6124117	0.5409862
groupafrica:log(ppgdp)	1.0949810	1.578460	0.6937019	0.4887032

Example

```
lm(lifeExpF ~ log(ppgdp), data = UN11[UN11$group=='oecd',])$coefficients
```

```
## (Intercept)  log(ppgdp)
##   59.213661    2.242535
```

```
lm(lifeExpF ~ log(ppgdp), data = UN11[UN11$group=='other',])$coefficients
```

```
## (Intercept)  log(ppgdp)
##   48.040558    3.171973
```

```
lm(lifeExpF ~ log(ppgdp), data = UN11[UN11$group=='africa',])$coefficients
```

```
## (Intercept)  log(ppgdp)
##   36.228822    3.337516
```

Example

$$\hat{E}(lifeExpF \,\big|\, ppgdp = x, group = oecd) =$$

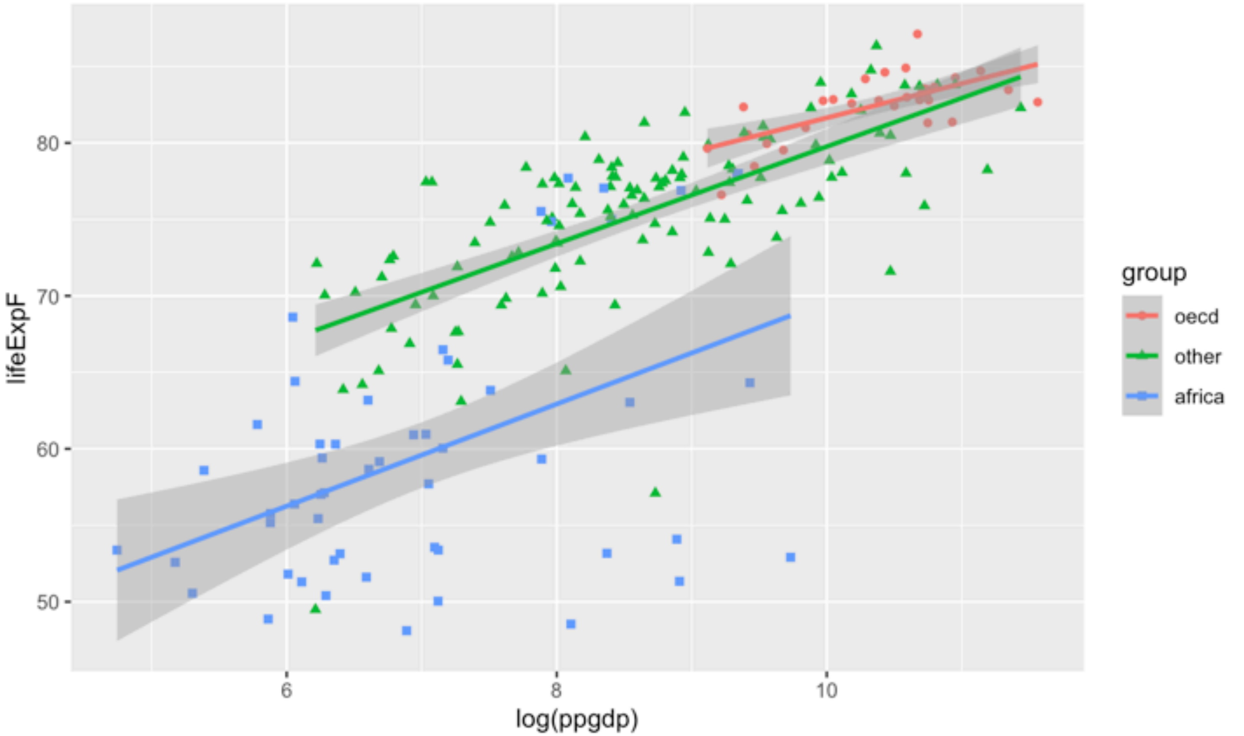
$$\hat{E}(lifeExpF \,\big|\, ppgdp = x, group = other) =$$

$$\hat{E}(lifeExpF \,\big|\, ppgdp = x, group = africa) =$$

Example

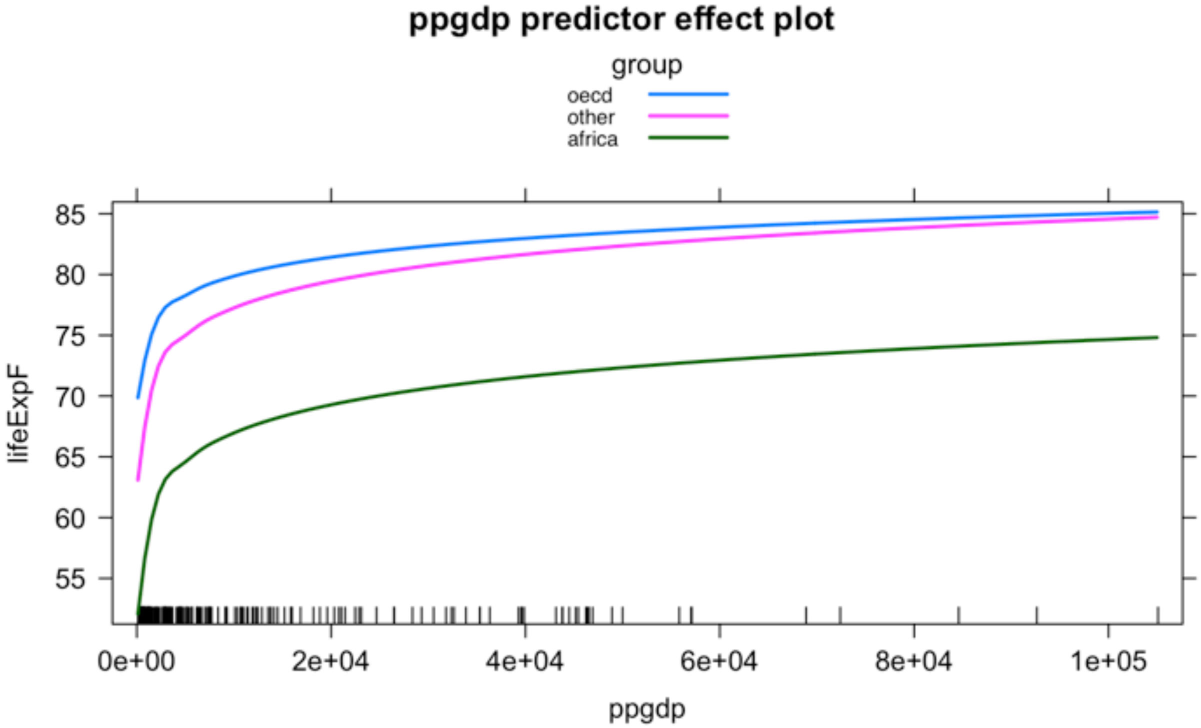
```
ggplot(data = UN11, aes(x = log(ppgdp), y = lifeExpF, col = group, shape = group))+
  geom_point() + geom_smooth(method = 'lm')
```

```
## `geom_smooth()` using formula 'y ~ x'
```



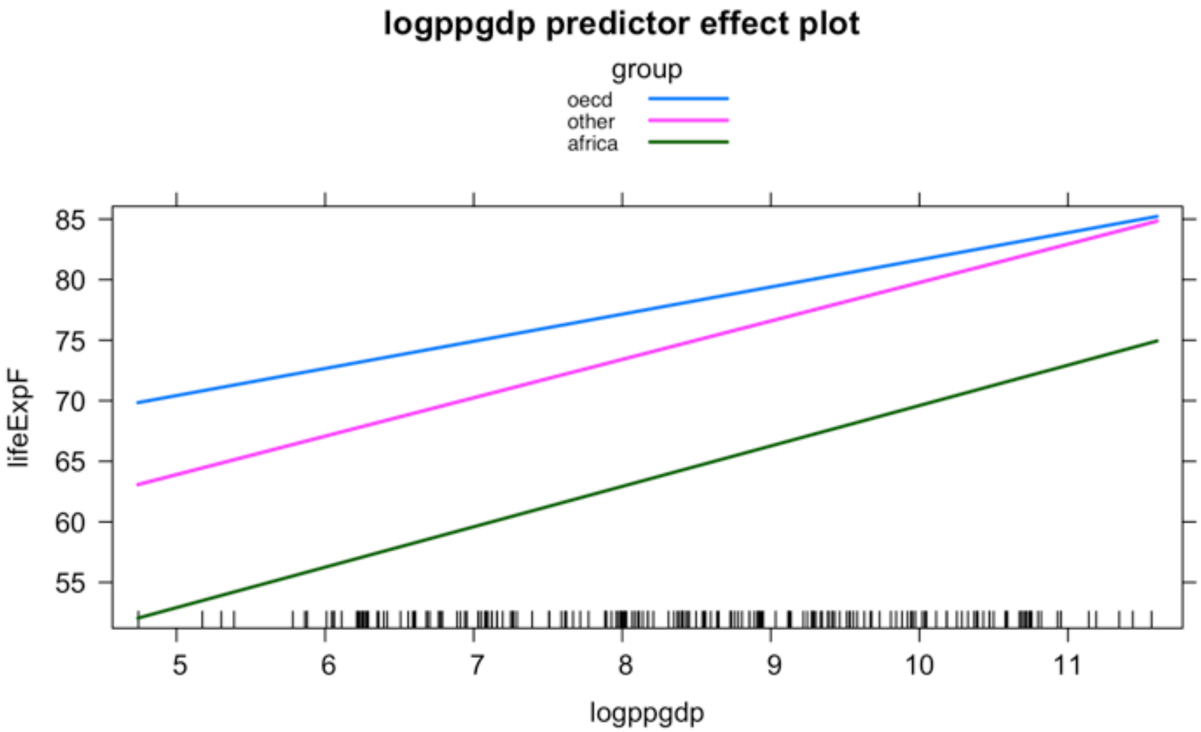
Effect Plot

```
par(mfrow = c(1,2))
plot(predictorEffect('ppgdp',lmodi), lines = list(multiline = T))
```



Effect Plot with Transformation

```
UN11$logppgdp = log(UN11$ppgdp)
plot(predictorEffect('logppgdp',lm(lifeExpF ~ group*logppgdp, data = UN11)), lines = list(mult:
```



Main Effect Model

Examining the fit of the interaction model to the data suggests that the slope might be the same for all groups.

A **main effects model** assumes the slope is the same for all factor levels but allows each group to have its own intercept.

- Main effects models are easier to interpret since the effect of the quantitative regressor is the same for all levels of the factor.
- This model is called the **Analysis of Covariance (ANCOVA)** when the factor levels indicate a randomly assigned treatment for subjects.

Example

```
lmodm = lm(lifeExpF ~ log(ppgdp) + group, UN11)
kable(summary(lmodm)$coefficients)
```

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	49.529241	3.3995539	14.569335	0.0000000
log(ppgdp)	3.177320	0.3159597	10.056092	0.0000000
groupother	-1.534683	1.1736824	-1.307579	0.1925556
groupafrica	-12.170365	1.5574486	-7.814297	0.0000000

Plot

```
ggplot(data = UN11, aes(x = log(ppgdp), y = lifeExpF, col = group, shape = group))+
  geom_point() + geom_smooth(method = 'lm', mapping= aes(y = predict(lmodm, UN11)))
```

```
## `geom_smooth()` using formula 'y ~ x'
```