Foundations for Bayesian Analysis

This document provides an introduction *(or review, depending on prereqs)* to the concepts and skills foundational for Bayesian Analysis. There are two major sections: **Understanding Conditional Probability** and **Foundations for Optimization**:

Understanding Conditional Probability

Before getting into Conditional Probability, let's level-set on a few assumptions about regression:

- Regression assumes a relationship between dependent and independent variables with a wide range of distributions.
- Independent variables (x) can be any distribution, but the residuals ($y - \hat{y}$) should be normally distributed **after the model has been applied (e.g., $a + bx$ in a simple linear case)**. That said, dependent variables (y) in transaction environments are seldom normally distributed. But there are approaches for transforming variables, and designing models *(either in the equation or model distributions)*, that can address a wide range of distributions. So, this should not be a problem and it's **not** OK to *assume the data are normally distributed based on the Central Limit Theorem*. See EndNote[1].
- There is also an assumption about homoscedasticity *(or homogeneity of variance)*, which relates to the distribution of y.

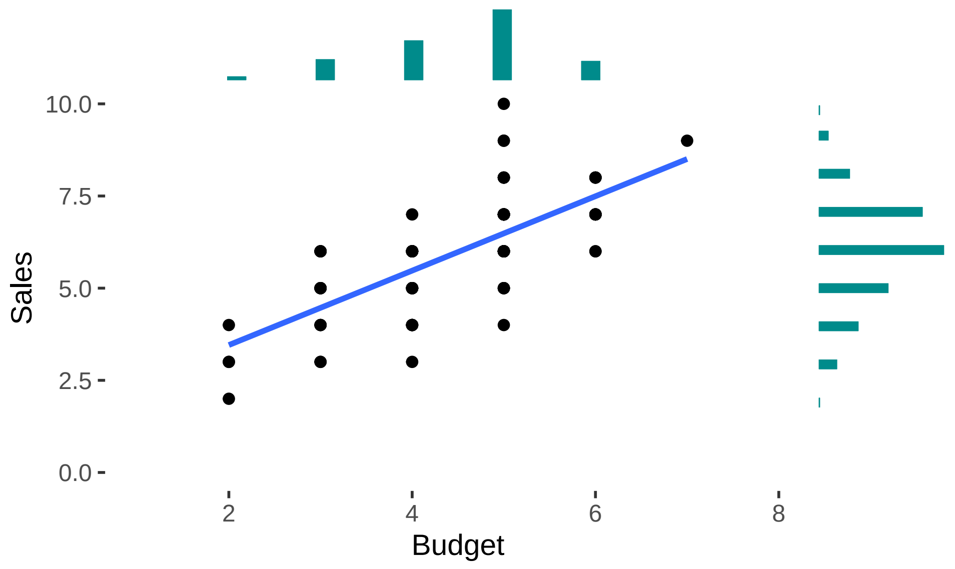
So, with those in mind, let's look at this how the distribution of y changes when we set conditions on x *(with a Bayesian twist)*

Load the following libraries:

```r
library(tidyverse)
library(stringr)
library(lubridate)
library(kableExtra)
library(cowplot)
library(ggExtra)
library(sfsmisc)
library(janitor)
```

.. and generate some data *(using discrete variables here to add a little clarity)*, and create a plot where we can see both the regression and the distributions:

```r
set.seed(222)

intercept = 2
slope = 1
N = 100

# generate discrete data
ExampleData1 = data.frame(x = as.integer((rnorm(N, 5, sd = 1)))) %>%
  mutate(y = as.integer((intercept + (slope * x)) + rnorm(N, 0, sd = 1)))

# plot using ggextra format
plot_center = ggplot(ExampleData1, aes(x=x,y=y)) +
  geom_point(width = .05) +
  geom_smooth(method="lm", se = F) +
  theme(panel.background = element_rect(fill = "white")) +
  xlim(1, 8) + ylim(0, 10) +
  ylab("Sales") + xlab("Budget")
p1 = ggMarginal(plot_center, type="histogram", fill = "cyan4", color = "white")
p1
```



..and gathering some measures we'll use later:

```
mod = lm(y~x, data = ExampleData1)
muX = mean(ExampleData1$x)
muY = round(mean(ExampleData1$y),1)
sigmaX = round(sd(ExampleData1$x),1)
sigmaY = round(sd(ExampleData1$y),1)
```

OK, in the plot above, we can see y *(lets call it Sales in M's to keep it real)* and x *(let's call it Advertising in K's)*, with a linear relationship determining the **mean** of y, defined by $b_0 + b_1x$ for each value of x. So, the model is **parameterized** with two coefficients (b_0, b_1). The overall distributions of x and y are shown on the margins *(keep in mind that values can repeat, so one point could include many observations - therefore, the points and histograms may not appear to match up - but they do).*

Knowing the **mean** for a specific value of x is a good start, and we can get the variance of the distribution of y from the standard error. But what if we want to know the *probability* for a range of y, given a specific value for x? For example: What's the probability that sales = 5M, given the advertising budget = 3k? *(do you think a business manager might ask this type of question?)*. This is a conditional probability, and can be written, generally, as a joint occurrence of random variables, or **joint probability density function**, which *(in continuous case)* can be defined as:

$P(y_1 \le y \le y_2, x_1 \le x \le x_2) = \int_{y_1}^{y_2} \int_{x_1}^{x_2} p(x, y)\, dx\, dy$

So in our example *(simplified by the discrete variables)*, the pdf could be stated as:

$P(y = 5|x = 3) = \Pi(y = 5|x = 3)$

And we can get a **conditional mean and variance** of y by **averaging** the conditional **mean** over the *marginal* distribution of x where the inner expectation averages over y, conditional on x, and the outer expectation averages over x *(BDA formula 1.8)*

$E(y) = E(E(y|x))$

This sounds fancy, but really, it's just a mean weighted by the joint probability of the variables, which, in R, can be estimated using a weighted.mean function:

$EY = weighted.mean(y, conditional.density)$

And similarly, the conditional variance can be determined by determining the mean of the conditional variance and the variance of the conditional mean, which can be estimated with another weighted mean with the densities:

$CV = weighted.mean((y - EY), conditional.density)$

(these are shortcuts to the precise methods outlined in BDA, which is painfully tedious. We really don't have to do this my hand, so just work trough this a few times, and we'll introduce other methods)

if we

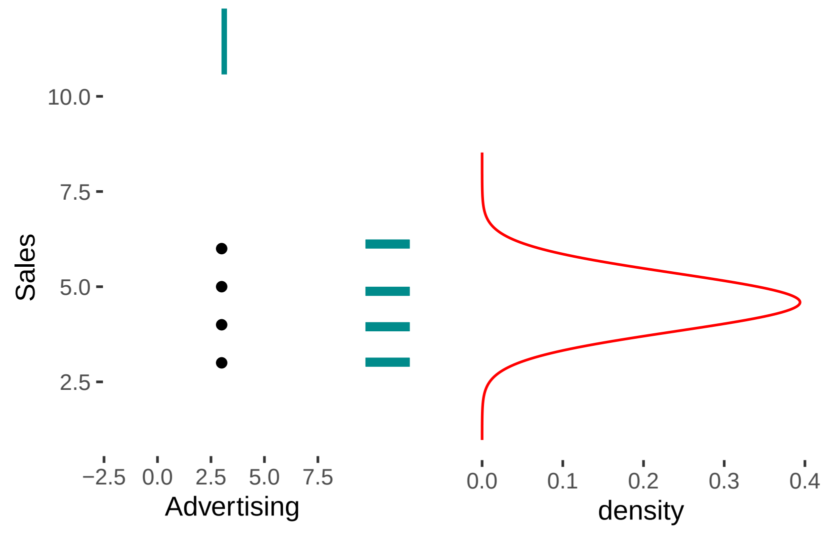
```r
AnalysisSummary1 = ExampleData1 %>% group_by(x,y) %>%
  summarise(Cnt = n(), Prob = round(Cnt/N,2))

MarAnalysis  = AnalysisSummary1 %>%
  select(y, x, Prob) %>%
  pivot_wider(names_from = x, values_from = Prob) %>%
  adorn_totals("row") %>%
  adorn_totals("col")

knitr::kable(MarAnalysis) %>%
  kable_styling(full_width = F, bootstrap_options = "striped", font_size = 9)
```

y	2	3	4	5	6	7	Total
2	0.01	NA	NA	NA	NA	NA	0.01
3	0.02	0.02	0.01	NA	NA	NA	0.05
4	0.01	0.03	0.05	0.01	NA	NA	0.10
5	NA	0.05	0.08	0.04	NA	NA	0.17
6	NA	0.04	0.10	0.14	0.02	NA	0.30
7	NA	NA	0.01	0.17	0.07	NA	0.25
8	NA	NA	NA	0.04	0.04	NA	0.08
9	NA	NA	NA	0.02	NA	0.01	0.03
10	NA	NA	NA	0.01	NA	NA	0.01
Total	0.04	0.14	0.25	0.43	0.13	0.01	1.00

To get a visual, we can then use these parameters to generate the conditional distribution of y, given $x = 3k$, as illustrated below:

```r
# filter for advertising budget of 3k
AnalysisSummary2 = AnalysisSummary1 %>%
  filter(x == 3)

# esimated expected value and variance
EY = round(weighted.mean(AnalysisSummary2$y, AnalysisSummary2$Prob),2)
CV = weighted.mean((AnalysisSummary2$y-EY)^2, AnalysisSummary2$Prob)


# summarize for unique values of x (eliminate recurring values which have the same densities)
AnalysisSummary3 = AnalysisSummary2 %>%
  group_by(x) %>% summarise(my = mean(y))
```

```r
# plot using ggextra format
plot_center = ggplot(AnalysisSummary2, aes(x=x,y=y)) +
  geom_point() +
  theme(panel.background = element_rect(fill = "white")) +
  xlim(-2, 9) + ylim(1, 10) +
  ylab("Sales") + xlab("Advertising")
p2 = ggMarginal(plot_center, type="histogram",
                fill = "cyan4", color = "white")
base <- data.frame(x = seq(0, 10, by = .01))
PF1 = ggplot(base, aes(xy)) +
  geom_line(aes(x,y= dnorm(x, mean = EY, sd = sqrt(CV))), color = "red") +
  theme(panel.background = element_rect(fill = "white"),
        axis.text.y = element_blank(),
        axis.ticks.y = element_blank()) +
  xlim(0, 14) +
  xlab("")+
  ylab("density") +
  coord_flip()

# bring all the plots together using cowplot
library(cowplot)
plot_grid(p2, PF1, nrow = 1, ncols = 2)
```

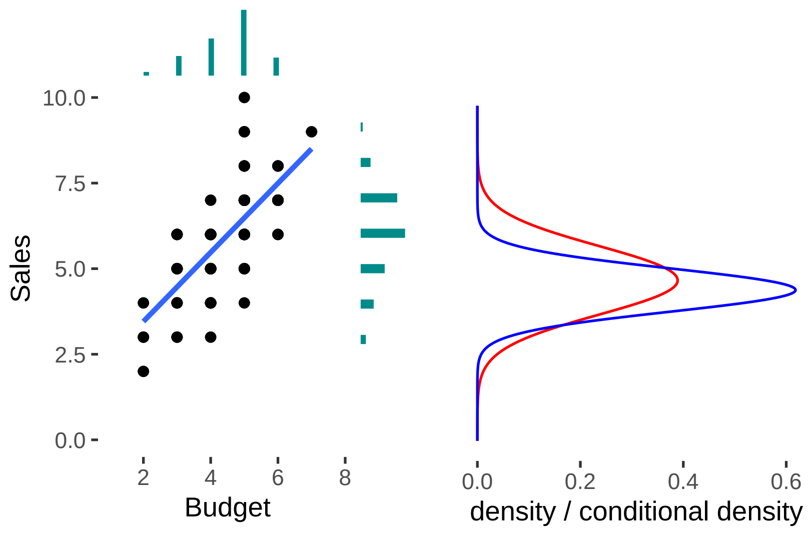


The conditional mean $E(E(y|x))$ is not the mean of y where $x = 3$, it is the conditional **mean** over the *marginal* distribution - and it won't be the same. Let's try to clear this up a bit. The conditional mean should be a little higher than just the distribution of y where $x = 3$ *(these plots are not precisely aligned, sorry about that)*. It will get "pulled" more towards the center of the marginal y.

Let's ignore conditional parameters, and just estimate the mean of y, if it were all we had was the data from $x = 3$:

```r
mod2 = lm(y~x, AnalysisSummary2)
y2 = predict(mod2, AnalysisSummary2)
EY2 = mean(y2)
CV2 = summary(mod2)$coefficient[,'Std. Error']
```

```
PF = ggplot(base, aes(x)) +
  geom_line(aes(x,y= dnorm(x, mean = EY, sd = CV)), color = "red") +
  geom_line(aes(x,y= dnorm(x, mean = EY2, sd = CV2)), color = "blue") +
  theme(panel.background = element_rect(fill = "white"),
        axis.text.y = element_blank(),
        axis.ticks.y = element_blank()) +
  xlim(0, 12) +
  xlab("") + ylab("density / conditional density") +
  coord_flip()

library(cowplot)
plot_grid(p1, PF, nrow = 1, ncols = 2)
```

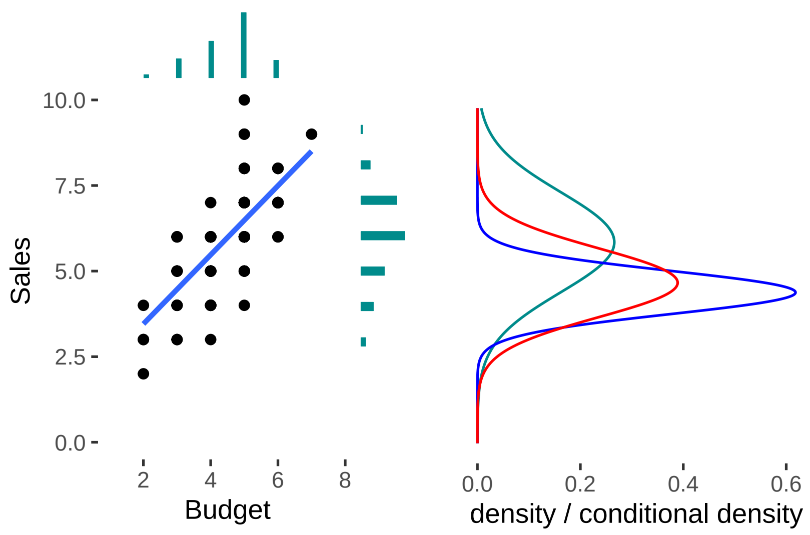


Now let's compare these. Notice that the conditional mean is closer to the overall mean of y. It's *weighted* by the marginal population. Let's talk about how this works.

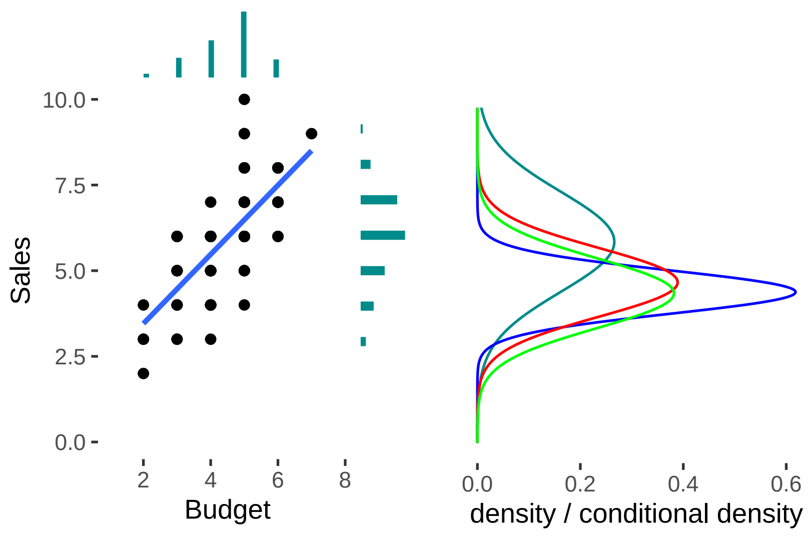
The second estimate ignores that there is a bigger market for y, with a tendency to "pull" y up, towards the mean *(central tendency)*.

Which one do you think is the better estimate? Now, let's pull everything together and compare:

```
base <- data.frame(x = seq(0, 10, by = .01))
PF = ggplot(base, aes(x)) +
  geom_line(aes(x,y= dnorm(x, mean = muY, sd = sigmaY)), color = "cyan4") +
  geom_line(aes(x,y= dnorm(x, mean = EY2, sd = CV2)), color = "blue") +
  geom_line(aes(x,y= dnorm(x, mean = EY, sd = CV)), color = "red") +
  theme(panel.background = element_rect(fill = "white"),
        axis.text.y = element_blank(),
        axis.ticks.y = element_blank()) +
  xlim(0, 12) +
  xlab("") + ylab("density / conditional density") +
  coord_flip()

library(cowplot)
plot_grid(p1, PF, nrow = 1, ncols = 2)
```



```
# and adding lm's prediciton

lmPred = predict(mod, newdata = AnalysisSummary2)

PF = PF +
  geom_line(aes(x,y= dnorm(x, mean = as.numeric(lmPred[1]), sd = as.numeric(summary(mod)[6]))), color =
plot_grid(p1, PF, nrow = 1, ncols = 2)
```



Note that location and scale shifts for each estimate. But which one is most realistic for $x = 3$? Also consider that often, we don't have the full marginal distribution of y.

```
knitr::kable(MarAnalysis) %>%
  kable_styling(full_width = F, bootstrap_options = "striped", font_size = 9)
```

y	2	3	4	5	6	7	Total
2	0.01	NA	NA	NA	NA	NA	0.01
3	0.02	0.02	0.01	NA	NA	NA	0.05
4	0.01	0.03	0.05	0.01	NA	NA	0.10
5	NA	0.05	0.08	0.04	NA	NA	0.17
6	NA	0.04	0.10	0.14	0.02	NA	0.30
7	NA	NA	0.01	0.17	0.07	NA	0.25
8	NA	NA	NA	0.04	0.04	NA	0.08
9	NA	NA	NA	0.02	NA	0.01	0.03
10	NA	NA	NA	0.01	NA	NA	0.01
Total	0.04	0.14	0.25	0.43	0.13	0.01	1.00

From a classic Bayes Theorem perspective:

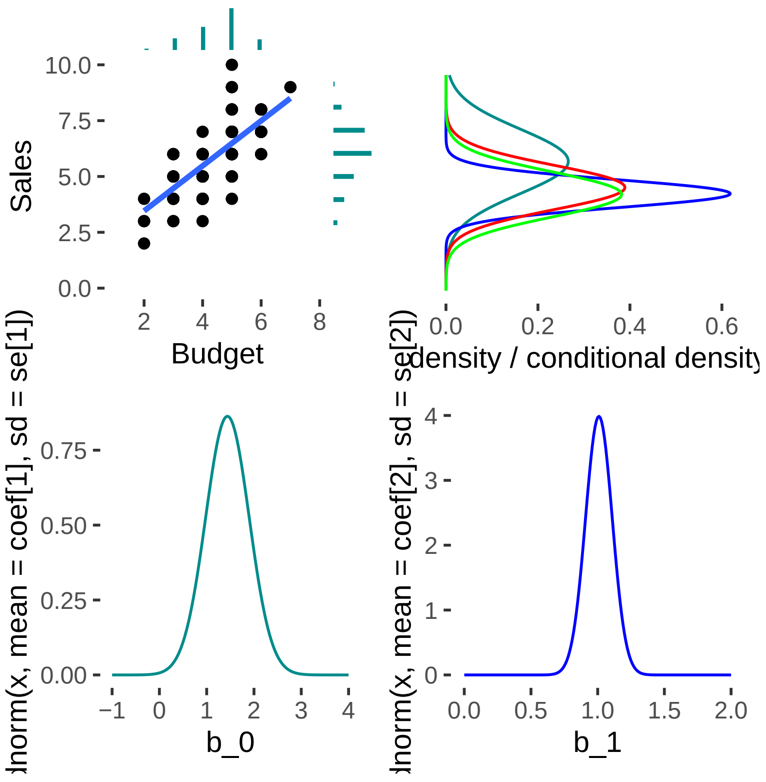
$P(Sales = 5|Budget = 3) = \frac{P(Budget=3|Sales=5)*P(Sales=5)}{P(Budget=3)}$

$P(Sales = 5|Budget = 3) = \frac{.30x.17}{.14} = .36$

Note $P(Budget = 3|Sales = 5)$ is determined from the condition distribution Sales, so the probability of Budget = 3 in that distribution *()*

We're not done yet. There are few other distributions that are important in our analysis - those of the parameters. We'll just pull those for awareness:

```r
coef = summary(mod)$coeff[, "Estimate"]
se = summary(mod)$coeff[, "Std. Error"]

dfData <- data.frame(x = seq(-1, 4, by = .01))
pp1 <- ggplot(dfData) +
  geom_line(aes(x,y= dnorm(x, mean = coef[1], sd = se[1])), color = "cyan4") +
  theme(panel.background = element_rect(fill = "white")) +
  xlab("b_0")

dfData <- data.frame(x = seq(0, 2, by = .01))
pp2 <- ggplot(dfData) +
  geom_line(aes(x,y= dnorm(x, mean = coef[2], sd = se[2])), color = "blue") +
  theme(panel.background = element_rect(fill = "white")) +
  xlab("b_1")

plot_grid(p1, PF, pp1, pp2, rows = 2, cols = 2)
```



This is a fairly complete picture for conditional analysis, and a good start on understanding Bayesian analysis. For now, let's set this aside and look some skills we'll need for model optimization *(which is a big deal in the transaction space)*.

Foundations for Optimization

When I interviewed job applicants for analyst and data science positions, I focused on generalization and optimization - that quickly told me if they were an experienced resource.

Optimization is especially important in Bayesian modeling because the approach uses Markov Chain Monte Carlo *(MCMC)* sampling. MCMC is really the only practical approach to defining probabilities in complex, multi-distribution, multilevel spaces, but it requires a significant amount of computational resources *and time* to wander through those spaces and find parameters. This is partly because of the way the sampler works:

High performance computing *(clusters)* helps a lot, but it won't compensate for poor model design. Transformation, Factorization and Reparametrization are essential skills in model design. You may have touched on these topics in prerequisite courses, for example:

- **Transformation** includes scaling *(and centering)*, log transforms, and vectorization *(using vectors instead of iterative operations)*.
- **Factorization** includes QR *(the method utilized by lm)* and Cholesky matrix decomposition *(you practiced factoring quadratics in high school, hopefully - it's the same idea)*.
- **Reparameterization**, as a general term, includes factorization, and adds other techniques. We'll introduce these as needed during exercises.

Many optimization approaches are intended to reduce the total data and the total variance *(keeping in mind that we have to leave breadcrumbs so we can get back to the original scale)*, and we'll explore these later. But fist, we need to build a foundation to understand this all better. We'll fist look at some alternative ways to get the parameters of the regression distributions μ, σ, b_0, b_1. We want to know this because

We'll break this into two sections I'll call variance and decomposition:

Variance

Let's start with the familiar. Taking our model from above *(mod)*, let's summarize:

```r
summary(mod)
```

```
##
## Call:
## lm(formula = y ~ x, data = ExampleData1)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.4846 -0.4846  0.0200  0.5246  3.5154
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.4387     0.4622   3.113  0.00243 **
## x             1.0092     0.1001  10.086  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.045 on 98 degrees of freedom
## Multiple R-squared:  0.5093, Adjusted R-squared:  0.5043
## F-statistic: 101.7 on 1 and 98 DF,  p-value: < 2.2e-16
```

You should be familiar with rmse as a measure of model fit *(1.03 here)*. We often used the following function to calculate rmse for out-of-sample data *(feeding residuals to the function and we used to evaluate model fit)*:

```r
rmse <- function(error)
{
  sqrt(mean(error^2))
}
```

We now need to drill down more on what it means and how it's calculated *(we'll use a normal equation the rest of the way so we can break up the components)*. Recall that the normal equation is: $\beta = (X^TX)^{-1}(X^TY)$, $\hat{y} = \beta(X^T)$, and error is $\sum(y-\hat{y})^2/df$ where df is degrees of freedom *(number of observations - estimated coefficients)*. So, if we have std error $\sqrt{\sum(y-\hat{y})^2/df}$, we can compute the covariance matrix $Var(\beta|X) = \sigma^2(X^TX)^{-1}$. Let's compute these values and compare to lm.

First, come manual covariance calculations:

```r
mX = model.matrix(y ~ x, ExampleData1)
vY = ExampleData1$y
vBeta2 <- solve(t(mX)%*%mX) %*% t(mX) %*% vY

# degrees of freedom (just getting technical here - n is fine in transaction environments)
df = nrow(mX) - ncol(mX)
# calculate mean error
sigmaSq = sum((vY - (t(as.vector(vBeta2)%*%t(mX))))^2)/df
# and standardize
rmse = sqrt(sigmaSq)
# so the variance-covariance is:
vCv = solve(t(mX)%*%mX) * sigmaSq
# check with lm
vCvlm = vcov(mod)
# create std error
vStdErr <- sqrt(diag(vCv))
```

```
knitr::kable(vCv) %>%
  kable_styling(full_width = F, bootstrap_options = "striped", font_size = 9)
```

	(Intercept)	x
(Intercept)	0.2136614	-0.0450551
x	-0.0450551	0.0100122

Comparing with covariance from lm:

	(Intercept)	x
(Intercept)	0.2136614	-0.0450551
x	-0.0450551	0.0100122

Manual Std. Error:

	x
(Intercept)	0.4622352
x	0.1000612

And if we don't have b *(and se)*, we can determine those parameters just from the contrivance of (x, y):

$Cov(x, y) = \frac{\sum(x-\bar{x})*(y-\bar{y})}{n-1}$, and $b_1 = \frac{Cov(x,y)}{var(x)}$,

So, b_1 can be estimated as follows:

```
# doing this the long way (so you can see)
CovXY2 = sum(((ExampleData1$x - mean(ExampleData1$x))* (ExampleData1$y - mean(ExampleData1$y))))/(nrow(

varX = var(ExampleData1$x)

b1 = CovXY2/varX
round(b1,2)
```

```
## [1] 1.01
```

Pretty cool huh?

And then we can back into b_0: $b_0 = \bar{y} - b\bar{x}$

We're not done yet! Another way to get the covariance is *(it's just a little different, but you may find it easier at times)*:

$Cov(x, y) = \frac{n(\bar{x}\bar{y}-\bar{x}*\bar{y})}{n-1}$

The code below uses this approach and compares the covariances:

```
CovXY3 = nrow(ExampleData1)*(mean(ExampleData1$x*ExampleData1$y) -  mean(ExampleData1$x)* mean(ExampleD

bo = data.frame(Description = c("covXY2","covXY3", "b1"), Value = c(CovXY2, CovXY3, b1))
bo$Value = round(bo$Value,2)

knitr::kable(bo) %>%
  kable_styling(full_width = F, bootstrap_options = "striped", font_size = 9)
```

Description	Value
covXY2	1.11
covXY3	1.11
b1	1.01

You can also use solve and treat the covariance matrices as a system of equations:

```r
b0 <- cov(as.matrix(ExampleData1$x))
b1 <- cov(as.matrix(ExampleData1$x),as.matrix(ExampleData1$y))

vBeta1 <- solve(b0, b1)[, 1]  # Coefficients from the covariance matrix

vBeta1
```

```
## [1] 1.009174
```

Let's take a look at the full covariance matrix from the model:

```r
Out <- data.frame(vcov(mod))
knitr::kable(Out) %>%
  kable_styling(full_width = F, bootstrap_options = "striped", font_size = 9)
```

	X.Intercept.	x
(Intercept)	0.2136614	-0.0450551
x	-0.0450551	0.0100122

Just to review, the covariance matrix provides the variance of each variable on the diagonal, and the covariances outside *(which is why it's really called a variance-covariance matrix - I just use covariance for expediency)*.

Another way to get the vcv is using Cholesky decomposition *(we'll look at Cholesky soon)*

```r
mX = model.matrix(y ~ x, ExampleData1)
vY = ExampleData1$y
vBeta2 <- solve(t(mX)%*%mX, t(mX)%*%vY)
y_hat = t(as.numeric(vBeta2)%*%t(mX))
# estimate of sigma-squared
dSigmaSq <- sum((vY - mX%*%vBeta2)^2)/(nrow(mX)-ncol(mX))
# variance covariance matrix
mVarCovar <- dSigmaSq*chol2inv(chol(t(mX)%*%mX))
mVarCovar
```

```
##             [,1]        [,2]
## [1,]  0.21366136 -0.04505511
## [2,] -0.04505511  0.01001225
```

```r
# coeff. est. standard errors
vStdErr <- sqrt(diag(mVarCovar))
vStdErr
```

```
## [1] 0.4622352 0.1000612
```

Factorization

QR

QR decomposition factors the model matrix into a Q and a R matrix *(which by definition, can be multiplied to yield the original matrix)*. The R is rectangular, and the bottom row is all zeros except the last column -

which will align with a beta value. The we just have to back-solve to get the beta values *(we don't actually have to back solve ourselves, we can use matrix algebra to do it)*.

How come we can do this? Let's start with a normal equation and assume we can factor X into Q and R. Then, see how it can used to solve the beta values:

$(X^TX)\beta = X^TY$, so:
$(QR^TQR)\beta = (QR)^TY$
$(R^TQ^TQ)R\beta = R^TQ^TY$
$(R^T)^{-1}R^TR\beta = (R^T)^{-1}R^TQ^TY$
$R\beta = Q^TY$

And there are two ways to solve using QR - fat and thin. The thin way is faster *(I have included some thin QR functions in this document for illustration - you don't need to know them - just understand the benefits outlined below)*. Being faster is what we're after!! Let's look at it:

```r
# functions
# ------------  Don't worry about these functions - just here for reference  ----#

inner_prod = function(v1, v2) {
  stopifnot(length(v1) == length(v2))
  len = length(v1)
  res = vector("numeric", length = len)
  for (i in 1:len) {
    res[i] = v1[i] * v2[i]
  }
  return(sum(res))
}
inner = function(v1, v2) {
  stopifnot(length(v1) == length(v2))
  return(sum(v1 * v2))
}

# thin QR

thinQR = function(x) {
  n = nrow(x)
  p = ncol(x)
  q1 = matrix(0, nrow = n, ncol = p)
  r1 = matrix(0, nrow = p, ncol = p)
  u = matrix(0, nrow = n, ncol = p)
  u[, 1] = x[, 1]
  for (k in 2:ncol(x)) {
    u[, k] = x[, k]
    # successive orthogonalization
    for (ctr in seq(1, (k - 1), 1)) {
      u[, k] = u[, k] - ((inner(u[, ctr], u[, k]) / inner(u[, ctr], u[, ctr])) * (u[, ctr]))
    }
  }
  q1 = apply(u, 2, function(x) { x / sqrt(inner(x, x)) })
  r1 = crossprod(q1, x) # t(q1) %*% x
  return(list(q = q1, r = r1, u = u))
}
```

The following sets up the data and solves the equation using lm first *(just for a baseline)*. Next, we use the qr function in R to get the Q matrix and the R matrix, and then solve using the equation above. Finally, we solve using thin QR *(from the functions above)*.

As you can see, we get the same answers for each method *(which shouldn't be a big surprise because lm also uses QR)*. First the lm beta:

```r
modQR = lm(y~x, ExampleData1)
lmBeta  = coef(modQR)

fatQRBeta <- solve(qr.R(qr(mX))) %*% t(qr.Q(qr(mX))) %*% vY

res = thinQR(mX)
thinQRBeta <- solve(res$r) %*% t(res$q) %*% vY

knitr::kable(lmBeta) %>%
  kable_styling(full_width = F, bootstrap_options = "striped", font_size = 9)
```

	x
(Intercept)	1.438716
x	1.009174

The Fat QR beta:

```r
knitr::kable(fatQRBeta) %>%
  kable_styling(full_width = F, bootstrap_options = "striped", font_size = 9)
```

(Intercept)	1.438716
x	1.009174

and Thin QR:

```r
knitr::kable(thinQRBeta) %>%
  kable_styling(full_width = F, bootstrap_options = "striped", font_size = 9)
```

(Intercept)	1.438716
x	1.009174

OK, so they get the same answer - so what's the big deal?

Keep in mind that an algorithm to solve a regression equation is going to try to minimize error, and most of the algorithms that solve the more complex regressions, do so using derivative based methods and maximum likelihood. The Bayesian world uses sampling to find parameters, but it samples derivatives of the log probability of the joint distributions *(which can be hundreds or even thousands - especially in multilevel cases)*. And the magnitude and variances of the parameters and data has a **BIG** effect on performance. With that in mind, let's just look at magnitude and variance of the data vs the thin Q and R:

```r
var(mX)
```

```
##             (Intercept)       x
## (Intercept)           0 0.00000
## x                     0 1.10101
```

```r
var(res$q)
```

```
##      [,1]       [,2]
## [1,]    0 0.00000000
## [2,]    0 0.01010101
```

Winner! Thin QR. That's the idea anyway.

Cholesky

One more tool. Cholesky decomp works the same way as QR, but it handles sparse matrices better *(sparse matrices are ones with lots of zeros and it's very common in transaction analysis - think of ERP tables, and how that translates into a model matrix with indicator variables - lots of them)*. We'll just run a simple example:

```
#use Cholesky to esimate beta
vBeta3 = chol2inv(chol(t(mX)%*%mX)) %*% t(mX)%*% vY
vBeta3
```

```
##           [,1]
## [1,] 1.438716
## [2,] 1.009174
```

chol produces the Cholesky decomposition and chol2inv produces the inverse, so we're back to $\beta = (X^TX)^{-1}(X^tY)$!! but in a process that can deal with LARGE datasets.

EndNotes:

1. A significant portion of our masters students are joining large consulting, risk management and assurance practices. Be aware that there's a common misconception about distributions: The "central limit theorem" doesn't transform a distribution. Most transaction distributions are not normal and increasing the number samples *(or sample size)* isn't going to magically transform the distribution to normal so you can apply the probabilities from intro statistics. It's true that, if we increase samples or sample size, the **means** of the samples will be normally distributed - but this doesn't provide any value in modeling or projecting transactions *(the mean is not a parameter in non-normal distributions, so it's rather useless)*. Maybe this explains why Audit firms practices around projects are so poor *(see "Insights into Large Audit Firm Sampling Policies" Brant E. Christensen, Randal J. Elder - AAA Journal)*. And "Big Data" isn't going to solve the problem.

Homework Assignment

No Homework this session - just groundwork and tools.