

# INTRO TO MLR

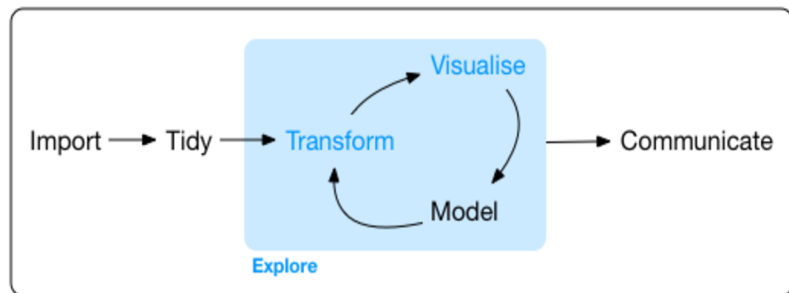
Research Methods in Psychology I & II • Department of Psychology • Colorado State University

## BY THE END OF THIS UNIT YOU WILL:

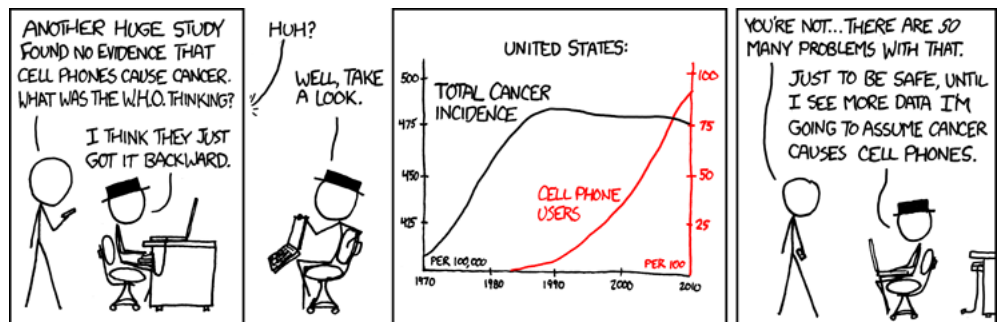
1. Understand the utility of including multiple predictor variables in a MLR model.
2. Know how to fit a Multiple Linear Regression model (MLR) in R.
3. Have an intuitive sense of what it means to control for variables when looking at the effect of others.
4. Be able to define partial and semi-partial correlation and understand the difference.
5. Know how to fit a series of nested models and be able to determine if one model fits significantly better than another.
6. Know how to plot the results of a MLR model.

## What is Multiple Linear Regression (MLR)?

MLR extends SLR to consider more than one predictor. We'll continue working with one continuously distributed dependent variable (i.e., outcome,  $y$ ), but now we'll consider multiple continuously distributed independent variables (i.e., predictors,  $x$ 's).



Wickham & Grolemund—R for Data Science



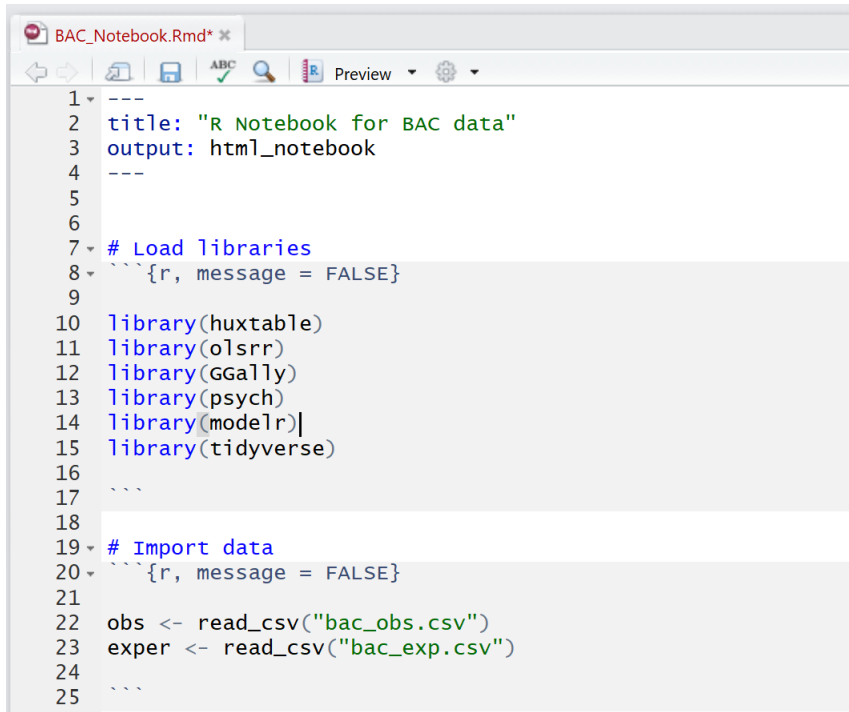
## **Dataset Description**

A research team sought to examine factors associated with 21st birthday drinking among female students at a large University. Female students who were nearing age 21 and self-classified as regular drinkers were eligible for the study. In total, 200 students were recruited and agreed to take part in the study. Students were instructed to report to the lab two weeks prior to their 21st birthday. During this lab session, students completed a brief survey that measured alcohol use during the past month (using the Timeline Follow Back Method) and their weight was recorded. One week prior to their 21st birthday, participants were sent a link for an online survey to measure positive alcohol expectancies for drinking on their 21st birthday. Within three days prior to their 21st birthday, students reported to the lab and were given a diary-based data collection form to record several items on their 21st birthday. Students were instructed to record the food that they consumed during the day, the degree to which they were in a partying mood just prior to the celebration, and the quantity and type of drinks that they consumed during the first two hours of the celebration. The students were also given a small breathalyzer machine to measure BAC 2 hours after consumption of their first drink.

The dataset called `bac_obs.csv` contains the data:

- `weight`: weight in kilograms
- `alcexp`: positive alcohol expectancy for drinking on the impending 21st birthday, a multi-item scale that ranges from 1-7, where a higher score indicates more positive expectations about the role alcohol will play
- `typ_drks`: the number of standard alcohol drinks consumed in the past 30 days
- `pmood`: a rating on a scale from 1-9 on the respondent's mood to party on the 21st birthday, where 1 means never been less in the mood to party, and 9 means never been more in the mood to party
- `absorb`: a score calculated from the food diaries to determine how full the participant was when they began drinking, the score ranges from 1 to 8, where 1 means a completely full stomach, and 8 means a completely empty stomach
- `alc_gm`: a score calculated from the drinking diary to estimate the grams of alcohol consumed on the 21st birthday
- `bac`: the participant's blood alcohol content, measured as grams of alcohol per deciliter of blood on the 21st birthday

## Set Up the Notebook



```
BAC_Notebook.Rmd* x
1 ---
2 title: "R Notebook for BAC data"
3 output: html_notebook
4 ---
5
6
7 # Load libraries
8 ```{r, message = FALSE}
9
10 library(huxtable)
11 library(olsrr)
12 library(GGally)
13 library(psych)
14 library(modelr)
15 library(tidyverse)
16
17 ```
18
19 # Import data
20 ```{r, message = FALSE}
21
22 obs <- read_csv("bac_obs.csv")
23 exper <- read_csv("bac_exp.csv")
24
25 ```
```

Please begin by setting up your notebook. Load the libraries (note that there is one new library—huxtable) and import the data. We will use the bac\_exp dataset later, but we'll import it now to have it handy.

## Descriptive Statistics

describe(obs)

	vars	n	mean	sd	median	trimmed	mad	min	max	range	skew	kurtosis	se
id	1	200	100.50	57.88	100.50	100.50	74.13	1.00	200.00	199.00	0.00	-1.22	4.09
weight	2	200	68.46	9.92	68.90	68.52	9.56	37.60	91.40	53.80	-0.18	0.16	0.70
typ_drks	3	200	46.86	14.67	46.50	47.11	14.08	4.00	79.00	75.00	-0.15	-0.29	1.04
alcexp	4	200	4.09	0.78	4.13	4.11	0.77	2.01	6.06	4.05	-0.26	-0.07	0.06
pmood	5	200	5.12	1.40	5.00	5.09	1.48	1.00	9.00	8.00	0.18	-0.05	0.10
absorb	6	200	4.69	0.91	4.64	4.68	0.95	2.67	6.80	4.13	0.11	-0.60	0.06
alc_gm	7	200	32.79	7.73	33.00	32.76	8.90	8.00	58.00	50.00	0.04	0.43	0.55
bac	8	200	0.08	0.02	0.08	0.08	0.02	0.02	0.15	0.13	0.22	0.40	0.00

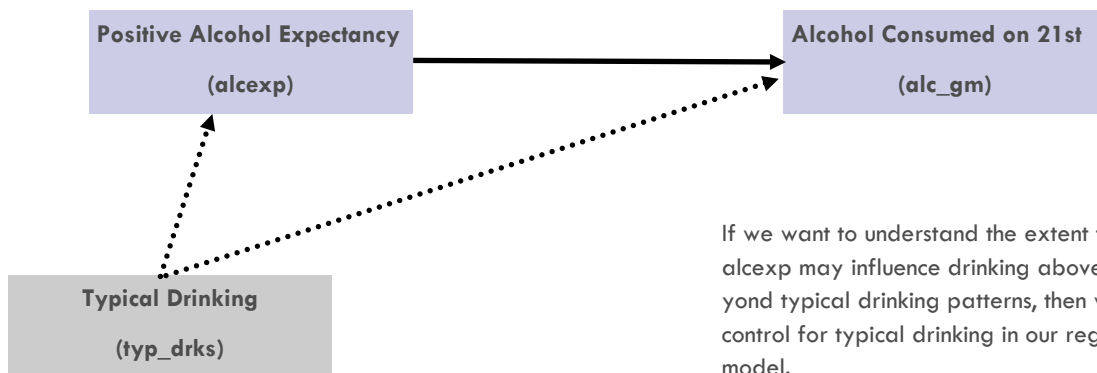
## Initial Research Question

Let's begin with a simple research question:

Does a positive alcohol expectancy predict more drinking on a female's 21st birthday?

This is an important research question that considers the role positive alcohol expectancies may play in influencing drinking on the 21st birthday. If it were found that holding positive alcohol expectancies is causally associated with drinking, then an intervention designed to challenge these expectancies might be an effective strategy to reduce risky drinking in this setting. While only an experiment can prove cause and effect, we can attempt to better understand the potential causal effect of expectancies on consumption if we think carefully about common causes of these two constructs and control for them.

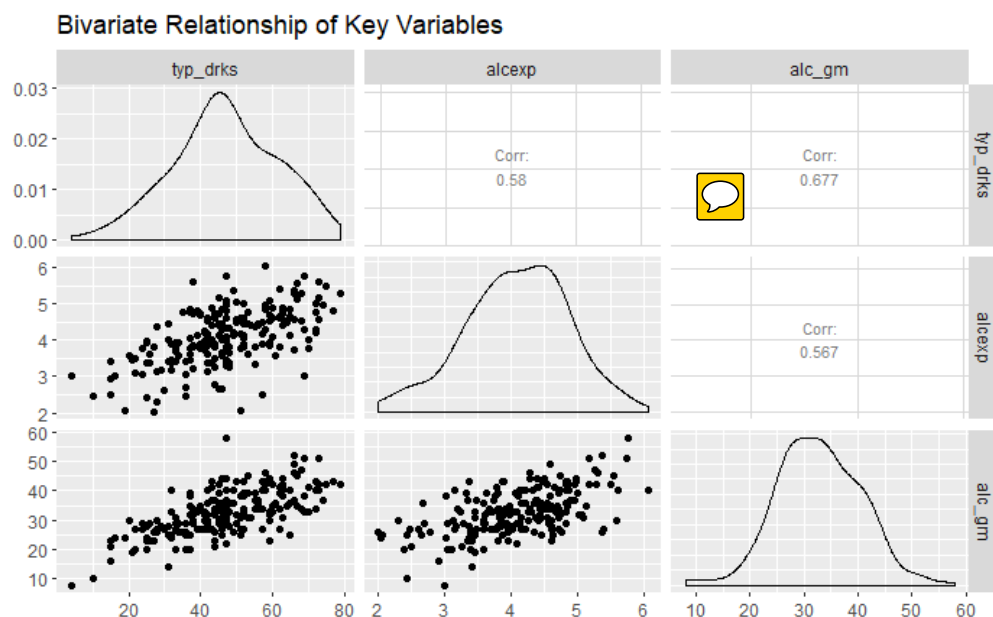
These common causes are potential confounders. A confounder is a pre-exposure variable that causes the exposure, and conditional on the exposure, the outcome. In our example, alcohol expectancy is the exposure and typical drinking is the potential confounder. If `typ_drks` is a confounder and is left out of the equation, the observed effect of `alcexp` on `alc_gm` is spurious. A spurious association is a relationship between two variables that does not result from any direct relation between them, but rather because they are both caused by another variable (or set of variables).



## Scatterplot Matrix

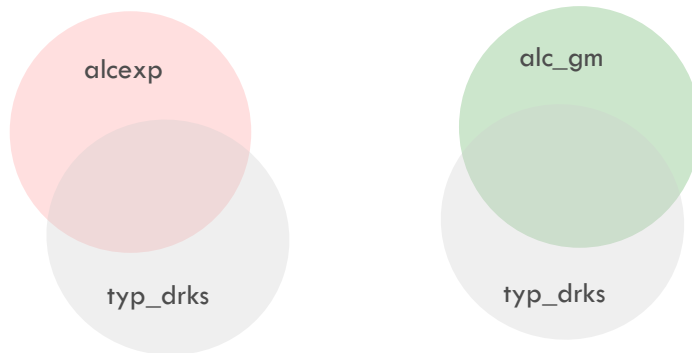
Let's take a look at a scatterplot matrix of the three variables of interest.

```
scatterplot <- ggpairs(obs, columns = c("typ_drks", "alcexp", "alc_gm"),
  upper = list(continuous = wrap("cor", size=3)),
  title = "Bivariate Relationship of Key Variables")
print(scatterplot, progress=FALSE )
```

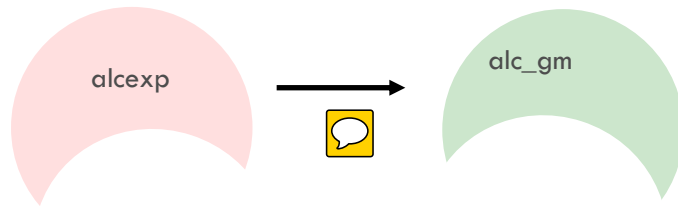


## Partialling Out the Effect of a Potential Confounder

We desire to partial out the effect of typical drinking and estimate the independent effect of alcohol expectancies on alcohol consumption on the 21st birthday. From the correlation matrix, we see that 34% of the variability in alcexp is associated with typ\_drks ( $.580^2$ ) and 46% of the variability in alc\_gm is associated with typ\_drks ( $.677^2$ ).



Imagine that we could pull out the variability in alc\_gm and alcexp associated with typ\_drks, then we'd be able to assess the association of alcexp on alc\_gms, independent of the effect of typ\_drks. That is, the part of the relationship between alcexp and alc\_gm that isn't associated with typ\_drks.



Multiple linear regression (MLR) allows us to accomplish this task. The slope for each variable in the MLR will represent the unique effect of that variable holding constant/adjusting for/partialing out (these all mean the same thing) the effect of all other variables in the model.

## Explore the Meaning of Partial Regression Coefficients in a MLR

The regression slopes in a MLR are called partial regression coefficients because the effect of the other variables has been partialled out. Let's explore what that means.

```
# step 1 - regress alc_gm (y) on variable(s) we want to partial out (typ_drks)
ry <- lm(data = obs, alc_gm ~ typ_drks)

# step 2 - regress alcexp (key predictor) on variable(s) we want to partial out (typ_drks)
rx <- lm(data = obs, alcexp ~ typ_drks)

# gather residuals from step 1 and 2, and add them to our dataset
obs1 <- obs %>%
  add_residuals(ry, var = "resid_ry") %>%
  add_residuals(rx, var = "resid_rx")
```

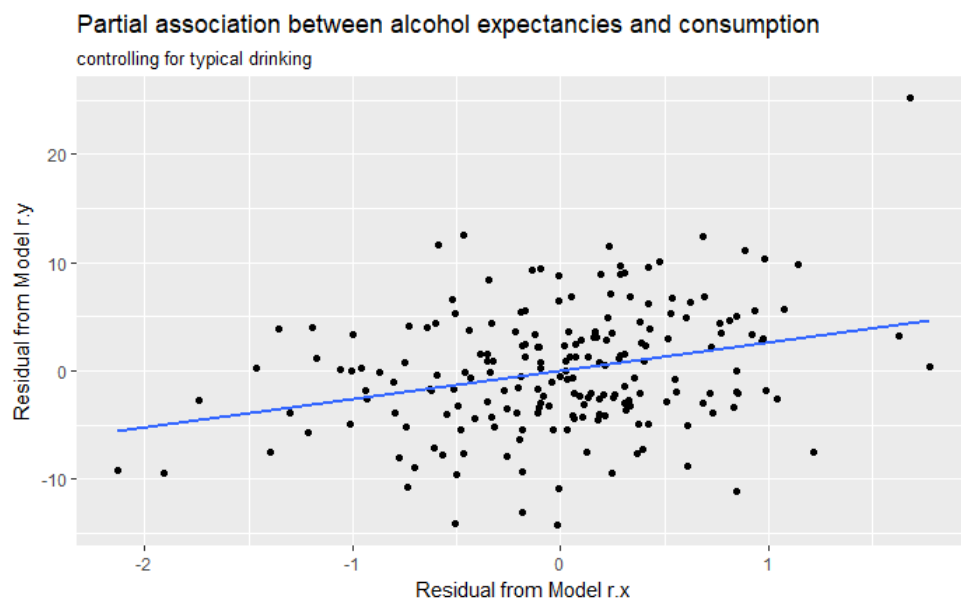
↑  
Name of the model used  
to calculate the residuals

↑  
Name of the new variable that  
contains the residuals.

BAC_Notebook.Rmd* x obs1 x										
	id	weight	typ_drks	alcexp	pmood	absorb	alc_gm	bac	resid_ry	resid_rx
1	1	64.9	36	2.69	5	4.80	29	0.073	0.08214694	-1.060712219
2	2	62.6	42	3.61	4	5.05	32	0.085	0.94283924	-0.325512098
3	3	71.1	64	4.50	5	4.79	35	0.081	-3.90128900	-0.113111654
4	4	67.6	25	2.40	4	4.99	20	0.052	-4.99578894	-1.011912441
5	5	70.2	59	3.95	3	4.02	23	0.052	-14.11853258	-0.509111755
6	6	74.0	67	5.13	5	6.09	35	0.087	-4.97094285	0.424488406
7	7	57.2	15	2.92	4	4.63	16	0.041	-5.43027611	-0.183912643
8	8	69.8	69	4.30	3	4.77	33	0.082	-7.68404542	-0.467111553
9	9	69.8	52	5.01	6	5.90	39	0.095	4.37732640	0.766488104
10	10	59.2	42	3.13	5	5.17	30	0.081	-1.05716076	-0.805512098
11	11	71.6	63	4.41	7	5.84	41	0.085	2.45526228	-0.172311674
12	12	59.3	47	4.82	4	4.24	29	0.086	-3.83991718	0.730488003
13	13	74.4	66	5.30	4	6.09	46	0.097	6.38560843	0.625288386

## Scatterplot of Residuals

```
# step 3 - plot residual from step 1 (on y) and residual from step 2 (on x) on a scattergram  
ggplot(data=obs1, aes(x = resid_rx, y = resid_ry)) +  
  geom_point() +  
  geom_smooth(method = "lm", se = FALSE) +  
  labs(title = "Partial association between alcohol expectancies and consumption",  
        subtitle = "controlling for typical drinking",  
        x = "Residual from Model r.x", y = "Residual from Model r.y")
```



Even after partialling out the effect of typical drinking, we still see a positive relationship between alcohol expectancies and alcohol consumption.



## Regression of alc\_gm residual on alcexp residual

```
# step 4 - regress residual from step 1 on residual from step 2
```

```
ryx <- lm(data = obs1, resid_ry ~ resid_rx)
```

```
ols_regress(ryx)
```

Model Summary

R	0.292	RMSE	5.454
R-Squared	0.085	Coef. Var	-3.301718e+16
Adj. R-Squared	0.080	MSE	29.751
Pred R-Squared	0.063	MAE	4.302

RMSE: Root Mean Square Error  
MSE: Mean Square Error  
MAE: Mean Absolute Error

ANOVA

	Sum of Squares	DF	Mean Square	F	Sig.
Regression	547.609	1	547.609	18.407	0.0000
Residual	5890.633	198	29.751		
Total	6438.243	199			

Parameter Estimates

model	Beta	Std. Error	Std. Beta	t	Sig.	lower	upper
(Intercept)	0.000	0.386		0.000	1.000	-0.761	0.761
resid_rx	2.611	0.609	0.292	4.290	0.000	1.411	3.811

```
cor(obs1$resid_ry, obs1$resid_rx)
```

```
[1] 0.2916431
```

The regression coefficient for resid\_rx is positive, indicating that partialling out typ\_drks, a one-unit increase in alcexp is associated with a 2.611 unit increase in alcohol consumption. Note that the correlation is .29 (which of course is the same as the standardized beta) and the  $R^2$  is .085, indicating that a little more than 8% of the remaining variability in alcohol consumption (after partialling out typical drinking) can be predicted by the remaining variability in alcohol expectancies (after partialling out typical drinking). We won't worry about the inference aspects of the model for now.

**SLR: typ\_drks → alc\_gm**

Before we fit the full MLR, let's take a look at the two SLR models, one for each predictor. Here's the first.

```
m1 <- lm(data = obs, alc_gm ~ typ_drks)
ols_regress(m1)
```

Model Summary

R	0.677	RMSE	5.702
R-Squared	0.458	Coef. Var	17.390
Adj. R-Squared	0.455	MSE	32.516
Pred R-Squared	0.448	MAE	4.441

RMSE: Root Mean Square Error

MSE: Mean Square Error

MAE: Mean Absolute Error

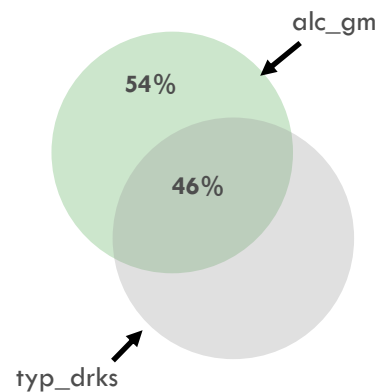
ANOVA

	Sum of Squares	DF	Mean Square	F	Sig.
Regression	5444.937	1	5444.937	167.452	0.0000
Residual	6438.243	198	32.516		
Total	11883.180	199			

Parameter Estimates

model	Beta	Std. Error	Std. Beta	t	Sig	lower	upper
(Intercept)	16.082	1.353		11.889	0.000	13.415	18.749
typ_drks	0.357	0.028	0.677	12.940	0.000	0.302	0.411

If a participant reports no drinking in the past 30 days (a typ\_drks score of 0), we predict their alc\_gm score to be 16.1. A standard drink is 14 grams of alcohol, so this equates to a little more than one drink. Now, recall that the sample represents drinkers, and the lowest typ\_drks score is 4 — so a score of 0 is a bit outside of our data. Centering would be wise, and we will do this moving forward to the MLR. The slope for typ\_drks equals .36; therefore, for each additional drink that a participant reported consuming during the prior 30 days, we predict that she will consume .36 additional grams of alcohol on her 21st birthday. This is a sizeable effect (the correlation is .68, and about 46% of the variability in alcohol consumed is predicted by drinking pattern during the past 30 days. The slope is significantly different from 0.



## SLR: alcexp → alc\_gm

Here's the second.

```
m2 <- lm(data = obs, alc_gm ~ alcexp)
ols_regress(m2)
```

Model Summary

R	0.567	RMSE	6.380
R-Squared	0.322	Coef. Var	19.457
Adj. R-Squared	0.318	MSE	40.703
Pred R-Squared	0.306	MAE	5.105

RMSE: Root Mean Square Error  
MSE: Mean Square Error  
MAE: Mean Absolute Error

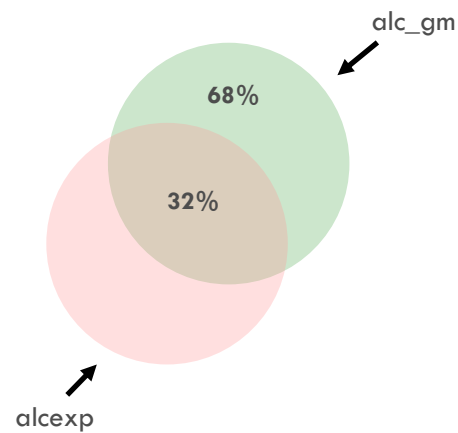
ANOVA

	Sum of Squares	DF	Mean Square	F	Sig.
Regression	3823.957	1	3823.957	93.947	0.0000
Residual	8059.223	198	40.703		
Total	11883.180	199			

Parameter Estimates

model	Beta	Std. Error	Std. Beta	t	Sig.	lower	upper
(Intercept)	9.819	2.412		4.070	0.000	5.062	14.577
alcexp	5.623	0.580	0.567	9.693	0.000	4.479	6.767

How do you interpret this model?



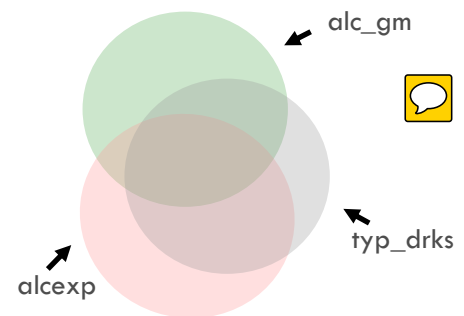
## Fit the MLR: $\text{alcexp} + \text{typ\_drks} \rightarrow \text{alc\_gm}$

```
obs <- obs %>%
  mutate(alcexp_m = alcexp - mean(alcexp),
         typ_drks_m = typ_drks - mean(typ_drks))
m3 <- lm(data = obs, alc_gm ~ typ_drks_m + alcexp_m)
ols_regress(m3)
```



First, we will center our predictors at the mean, and then fit the MLR. To add multiple predictors, simply list each x variable on the right hand side of the tilde, separated by a + sign.

Model Summary					
R	0.710	RMSE	5.468		
R-Squared	0.504	Coef. Var	16.677		
Adj. R-Squared	0.499	MSE	29.902		
Pred R-Squared	0.487	MAE	4.302		
RMSE: Root Mean Square Error					
MSE: Mean Square Error					
MAE: Mean Absolute Error					
ANOVA					
	Sum of Squares	DF	Mean Square	F	Sig.
Regression	5992.547	2	2996.273	100.204	0.0000
Residual	5890.633	197	29.902		
Total	11883.180	199			
Parameter Estimates					
model	Beta	Std. Error	Std. Beta	t	Sig
(Intercept)	32.790	0.387		84.802	0.000
typ_drks_m	0.276	0.032	0.524	8.516	0.000
alcexp_m	2.611	0.610	0.263	4.279	0.000



The venn diagram is for illustrative purposes and not drawn to perfect scale.

Let's begin digging into the parameter estimates. The intercept is 32.790, this is the predicted alcohol consumed for a female who reported average typical drinking and held average alcohol expectancies. Now consider our key predictor —  $\text{alc\_exp}$ . In the SLR, the slope for  $\text{alc\_exp}$  was 5.623, in the MLR it is 2.611. How are these effects interpreted across the two models?

In SLR: Each one unit increase in  $\text{alc\_exp}$  is associated with a 5.6 unit increase in  $\text{alc\_gm}$ .

In MLR: Holding constant/adjusting for/partialling out  $\text{typ\_drks}$ , each one unit increase in  $\text{alcexp}$  is associated with a 2.6 unit increase in  $\text{alc\_gm}$ .

In a MLR, the slope of each variable captures the unique effect of that particular variable, holding constant or partialling out the effect of the other predictors in the model. Notice that the regression coefficient for  $\text{alcexp}$  is the same as what we obtained using the residuals in our previous exercise.

Each regression slope is interpreted in the same manner, it's the expected change in  $y$  for a one-unit increase in  $x$ , holding constant all other predictors.

$$\text{alc\_gm}_i = 32.79 + .28\text{typ\_drks\_m}_i + 2.61\text{alcexp\_m}_i + e_i$$

## Predicted Scores

$$\text{alc\_gm}_i = 32.79 + .28\text{typ\_drks\_m}_i + 2.61\text{alcexp\_m}_i + e_i$$

```
predgrid_demo <- data_grid(obs,
  alcexp_m = c(-1, 0, 1),
  typ_drks_m = c(1, 1, 1)) %>%
  add_predictions(m3)

predgrid_demo
```

Here we create a prediction matrix where alcexp\_m varies, but typ\_drks\_m is held constant.

	alcexp_m	typ_drks_m	pred
1	-1	1	30.45496
2	0	1	33.06613
3	1	1	35.67729

$$33.06613 - 30.45496 = 2.61$$

$$35.67729 - 33.06613 = 2.61$$

Holding constant typ\_drks, our predicted values of alc\_gm demonstrate that each 1 unit increase in alcexp is associated with a 2.61 unit increase in alc\_gm.

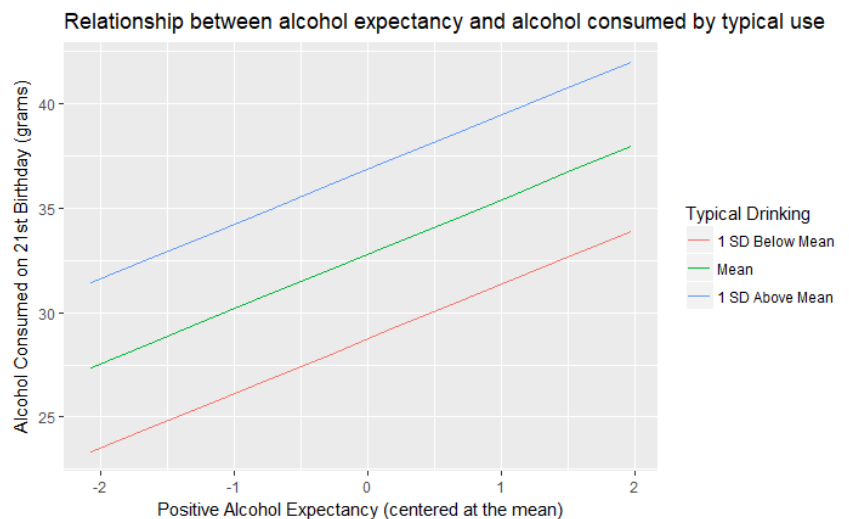
## Make a Plot of the Fitted Model

Now we create a prediction matrix that spans the whole range of `alcexp_m` (that is what `seq_range` does) with 10 evenly spaced values of `alcexp_m` between the min and max values. We specify 3 prototypical values of weight. The `data_grid` function then produces all possible combos of our specification—so, the range of `alcexp_m` for each of the three prototypical weights.

```
predgrid_plot <- data_grid(obs,
  alcexp_m = seq_range(alcexp_m, 10),
  typ_drks_m = c(-14.67, 0, 14.67)) %>%
  mutate(typ_drks_m.f = factor(typ_drks_m,
    levels = c(-14.67, 0, 14.67),
    labels = c("1 SD Below Mean", "Mean", "1 SD Above Mean"))) %>%
  add_predictions(m3)

ggplot(data = predgrid_plot, aes(x = alcexp_m, y = pred, group = typ_drks_m.f, color = typ_drks_m.f)) +
  geom_line() +
  guides(color=guide_legend("Typical Drinking")) +
  labs(title = "Relationship between alcohol expectancy and alcohol consumed by typical use",
    x = "Positive Alcohol Expectancy (centered at the mean)", y = "Alcohol Consumed on 21st Birthday (grams)")
```

	alcexp_m	typ_drks_m	typ_drks_m.f	pred	alcexp
1	-2.0752	-14.67	1 SD Below Mean	23.32052	2.01
2	-2.0752	0.00	Mean	27.37131	2.01
3	-2.0752	14.67	1 SD Above Mean	31.42210	2.01
4	-1.6252	-14.67	1 SD Below Mean	24.49554	2.46
5	-1.6252	0.00	Mean	28.54633	2.46
6	-1.6252	14.67	1 SD Above Mean	32.59712	2.46
7	-1.1752	-14.67	1 SD Below Mean	25.67057	2.91
8	-1.1752	0.00	Mean	29.72136	2.91
9	-1.1752	14.67	1 SD Above Mean	33.77215	2.91
10	-0.7252	-14.67	1 SD Below Mean	26.84559	3.36
11	-0.7252	0.00	Mean	30.89638	3.36
12	-0.7252	14.67	1 SD Above Mean	34.94717	3.36



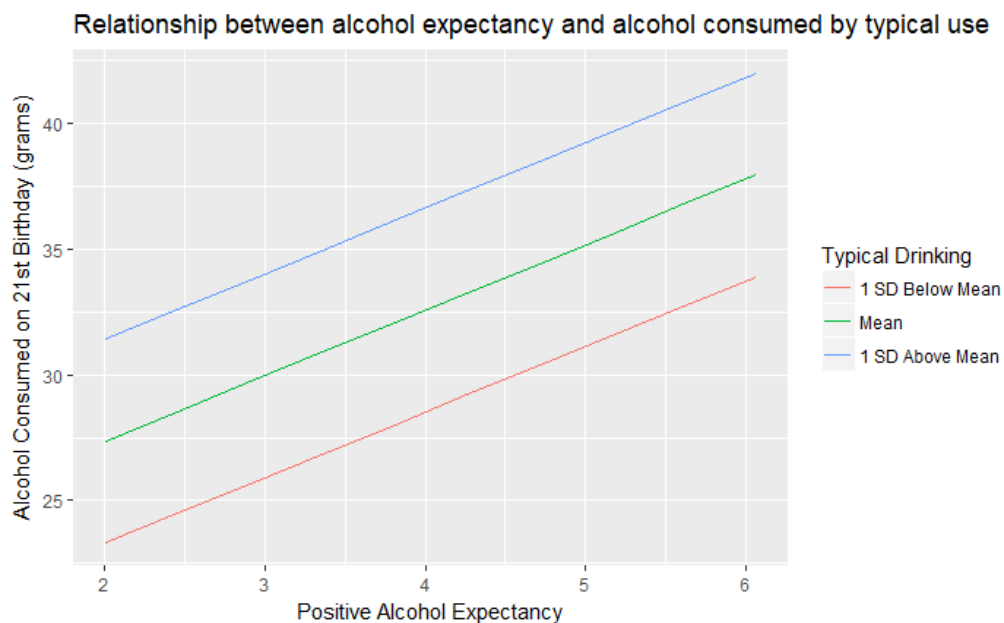
## Modify Plot to Put x-axis on Original Scale

```

predgrid_plot <- data_grid(obs,
  alcexp_m = seq_range(alcexp_m, 10),
  typ_drks_m = c(-14.67, 0, 14.67)) %>%
mutate(typ_drks_m.f = factor(typ_drks_m,
  levels = c(-14.67, 0, 14.67),
  labels = c("1 SD Below Mean", "Mean", "1 SD Above Mean"))) %>%
add_predictions(m3) %>%
mutate (alcexp = alcexp_m + mean(obs$alcexp))

ggplot(data = predgrid_plot, aes(x = alcexp, y = pred, group = typ_drks_m.f, color = typ_drks_m.f)) +
  geom_line() +
  guides(color=guide_legend("Typical Drinking")) +
  labs(title = "Relationship between alcohol expectancy and alcohol consumed by typical use",
    x = "Positive Alcohol Expectancy", y = "Alcohol Consumed on 21st Birthday (grams)")

```



## One Last Advanced Graph with Confidence Intervals

```

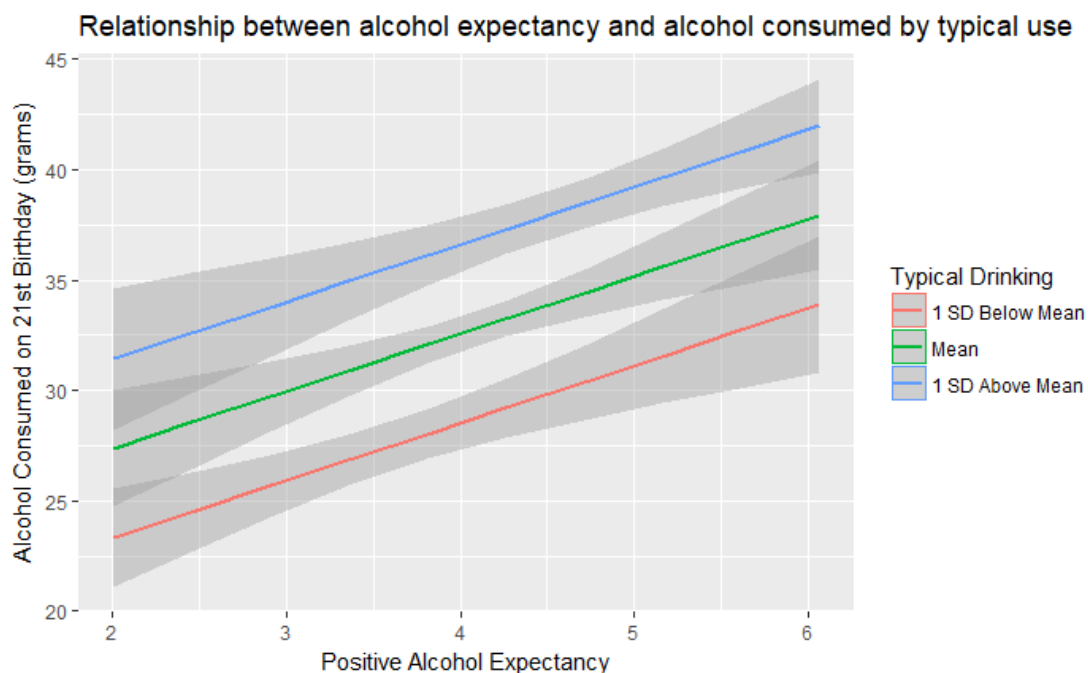
pred1 <- data_grid(obs,
  alcexp_m = seq_range(alcexp_m, 10),
  typ_drks_m = c(-14.67, 0, 14.67)) %>%
mutate(typ_drks_m.f = factor(typ_drks_m,
  levels = c(-14.67, 0, 14.67),
  labels = c("1 SD Below Mean", "Mean", "1 SD Above Mean")))

pred2 <- predict(m3, pred1, interval = "confidence") %>%
  as_data_frame()

pred3 <- cbind(pred1, pred2) %>%
  mutate (alcexp = alcexp_m + mean(obs$alcexp))

ggplot(data = pred3, aes(x = alcexp, y = fit, group = typ_drks_m.f, color = typ_drks_m.f)) +
  geom_ribbon(aes(ymin = lwr, ymax = upr, color = NULL), alpha = .4, fill = "grey60") +
  geom_line(size = 1) +
  guides(color=guide_legend("Typical Drinking")) +
  labs(title = "Relationship between alcohol expectancy and alcohol consumed by typical use",
    x = "Positive Alcohol Expectancy", y = "Alcohol Consumed on 21st Birthday (grams)")

```





## R<sup>2</sup> for MLR Model

The R<sup>2</sup> for this MLR is 50.4% (obtained by SSR/SST) meaning that half of the variability in alc\_gm can be predicted by alcexp and typ\_drks. Notice that some of the explained variability is predicted just by typ\_drks, some just by alcexp, and some can be predicted by both alcexp and typ\_drks. MLR allows us to divvy up this variability and determine how much each variable uniquely contributes, as well as how the variables come together to predict the overall variability in the outcome.

Model Summary

R	0.710	RMSE	5.468
R-Squared	0.504	Coef. var	16.677
Adj. R-Squared	0.499	MSE	29.902
Pred R-Squared	0.487	MAE	4.302

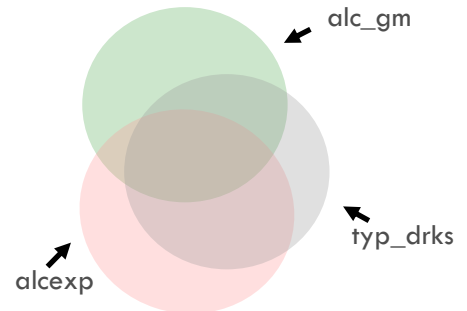
RMSE: Root Mean Square Error  
MSE: Mean Square Error  
MAE: Mean Absolute Error

ANOVA

	Sum of Squares	DF	Mean Square	F	Sig.
Regression	5992.547	2	2996.273	100.204	0.0000
Residual	5890.633	197	29.902		
Total	11883.180	199			

Parameter Estimates

model	Beta	Std. Error	Std. Beta	t	Sig	lower	upper
(Intercept)	32.790	0.387		84.802	0.000	32.027	33.553
typ_drks_m	0.276	0.032	0.524	8.516	0.000	0.212	0.340
alcexp_m	2.611	0.610	0.263	4.279	0.000	1.408	3.814



The venn diagram is for illustrative purposes and not drawn to perfect scale.

The **adjusted R<sup>2</sup>** corrects for a problem with regular R<sup>2</sup> – that is, in R<sup>2</sup> the denominator (SST) is fixed (unchanging) and the numerator (SSR) can ONLY increase. Therefore, each additional variable used in the equation will, at least, not decrease the numerator and will probably increase the numerator (at least to a small extent), resulting in a higher R<sup>2</sup>, even when the added variable(s) adds nothing to the model. On the other hand, the adjusted R<sup>2</sup> can decline in value if the contribution to the explained variance by the additional variable(s) is less than the impact on the degrees of freedom. ADJUSTED R<sup>2</sup> REWARDS PARSIMONY.

While the R<sup>2</sup> can be interpreted as a proportion, the Adjusted R<sup>2</sup> CANNOT – so please don't interpret it in this way.

$$Adj\_R^2 = 1 - \left( (1 - R^2) \frac{(n-1)}{(n-k-1)} \right) \quad \text{Where } n \text{ is the sample size and } k \text{ is the number of predictors.}$$

**Predicted R<sup>2</sup>** also attempts to prevent overfitting. It indicates how well a regression model predicts responses for new observations. It is calculated by systematically removing each observation from the data set, estimating the regression equation, and determining how well the model predicts the removed observation. Both adjusted and predicted R<sup>2</sup> can be negative and are always smaller than R<sup>2</sup>.

A key benefit of adjusted and predicted R-squared is that it can prevent you from overfitting a model.

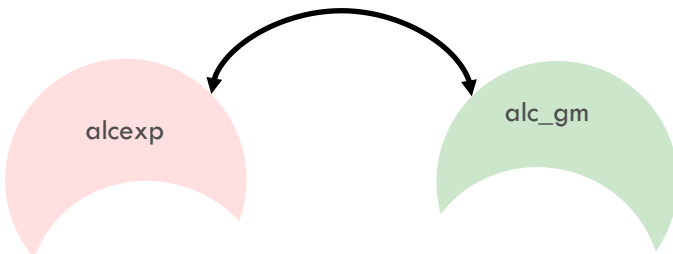
## Partial and Semi-Partial (Part) Correlations

```
cor(obs1$resid_ry, obs1$resid_rx)
cor(obs1$alc_gm, obs1$resid_rx)
```

```
[1] 0.2916431
[1] 0.2146688
```

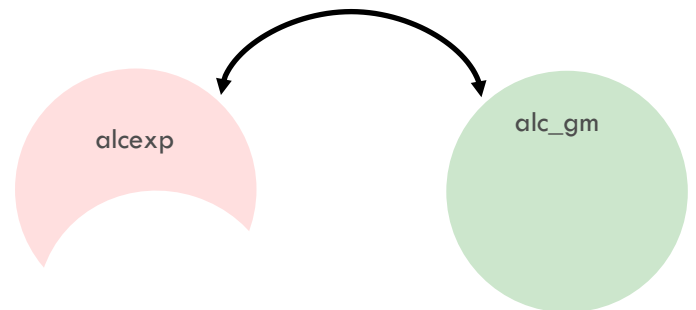
### Partial Correlation

For a predictor (alcexp) and outcome (alc\_gm) of interest, partial correlation first removes from both alcexp and alc\_gm all variance which may be accounted for by the other predictors (in this case, just one, typ\_drks), then correlates the remaining variance of alcexp (the residual) with the remaining variance of alc\_gm (the residual). Here, the partial correlation between alcexp and alc\_gm is .292. Notice that this is the correlation of the two residuals that we obtained in our previous activity.



### Semi-Partial (Part) Correlation

For a predictor (alcexp) and outcome (alc\_gm) of interest, semi-partial correlation first removes from the predictor (alcexp) all variance which may be accounted for by the other predictors (in this case typ\_drks), then correlates the remaining variance of alcexp (the residual) with y. Here the semi-partial (part) correlation between alcexp and alc\_gm is .215.



```
ols_correlations(m3)
```

Correlations			
Variable	Zero order	Partial	Part
typ_drks_m	0.677	0.519	0.427
alcexp_m	0.567	0.292	0.215

## Squared Partial and Semi-Partial (Part) Correlations

`ols_correlations(m3)^2`

	Zero-order	Partial	Part
typ_drks_m	0.4582054	0.26908172	0.18249236
alcexp_m	0.3217958	0.08505568	0.04608271

### Squared Partial Correlation

The square of the partial correlation indicates what proportion of the residualized  $y$  (residual of alc\_gm) is predicted by the residualized  $x_1$  (residual of alcexp). In our example, 8.5% of the residual variability in alc\_gm is predicted by the residual variables of alcexp.

### Squared Semi-Partial (Part) Correlation

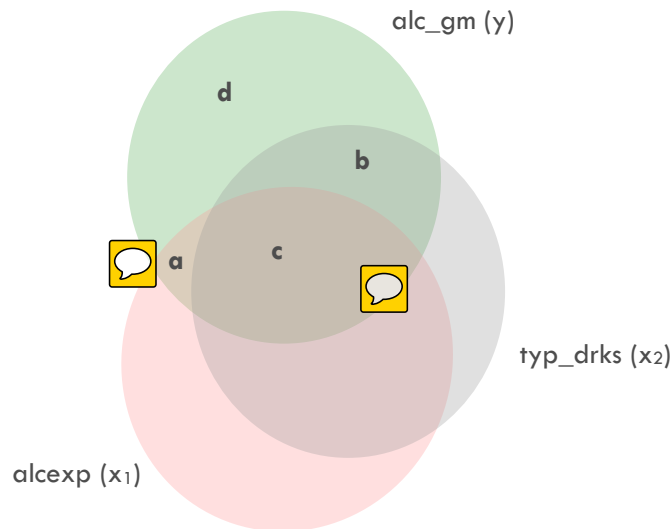
The square of the semi-partial correlation indicates the increment in  $R^2$  that is achieved when we add our  $x$  of interest ( $x_1$ , alcexp) to a model that already includes all other predictors (e.g.,  $x_2$ , typ\_drks). In our example, 4.6% of the **total** variability of alc\_gm is uniquely predicted by alcexp.

### Squared Partial Correlation

$$R^2_{yx_1|x_2} = \frac{a}{a + d}$$

### Squared Semi-Partial Correlation

$$R^2_{y(x_1|x_2)} = \frac{a}{a + b + c + d}$$



### Squared Zero-Order (Simple) Correlation

$$R^2_{yx_1} = \frac{a + c}{a + b + c + d}$$



## Hierarchical Regression: Model Building

In a hierarchical regression, we build a series of nested regression models. Nested means that one smaller model is a subset of a larger model. To explore this technique, let's consider two models to predict blood alcohol content in the `bac_obs` dataset.

1. Model 1: Regress blood alcohol content (`bac`) on alcohol expectancies (`alcexp`) and typical drinking (`typ_drks`). We call this the reduced model in the hierarchical set.
2. Model 2: Build on Model 1, add three variables that are directly related to `bac` — the participants weight (`weight`), the absorption rate based on food consumed during the day (`absorb`), and alcohol consumed (`alc_gm`). We call this the full model in the hierarchical set.

We specify a hierarchical regression, a set of sequential models, to determine if the full model significantly adds to our ability to predict the outcome over our reduced model. The null hypothesis is that the full model (e.g., Model 2) doesn't explain any additional variability over our reduced model (Model 1). The alternative hypothesis is that Model 2 explains significantly more variability than Model 1.

To test the hypothesis, we calculate a partial F-test. The formula for the partial F-test is below.

First, we need to calculate the critical value of F for the partial F-test. The *df* for the numerator of the critical F is equal to the difference in the number of predictors between the full and reduced models, and the *df* for the denominator of our critical F is equal to the *SSE* for the full model ( $n - 1 - \# \text{ of predictors}$ ).

```
qf(.95, df1 = 3, df2 = 194)
```

```
[1] 2.651153
```

$$Partial\ F^* = \frac{\frac{SSE_{Reduced} - SSE_{Full}}{df_{Reduced} - df_{Full}}}{\frac{SSE_{Full}}{df_{Full}}}$$

## Hierarchical Regression Syntax

### Model 1

```
# bac is a very small number -- we will multiply it by 100 so it's easier to read the output,
# we will also center all of the predictors at the mean
obs <- obs %>%
  mutate(bac100 = bac*100,
         alc_gm_m = alc_gm - mean(alc_gm),
         weight_m = weight - mean(weight),
         absorb_m = absorb - mean(absorb),
         alcexp_m = alcexp - mean(alcexp),
         typ_drks_m = typ_drks - mean(typ_drks))

mod1 <- lm(data = obs, bac100 ~ alcexp_m + typ_drks_m)
ols_regress(mod1)
```

### Model 2

```
mod2 <- lm(data = obs, bac100 ~ alcexp_m + typ_drks_m + absorb_m + weight_m + alc_gm_m)
ols_regress(mod2)
```

### Compare Models 1 and 2

```
anova(mod1, mod2, test = "F")
```



List the reduced model first, then the full model second

## Hierarchical Regression Results

Model Summary

R	0.683	RMSE	1.587
R-Squared	0.467	Coef. Var	19.158
Adj. R-Squared	0.461	MSE	2.520
Pred R-Squared	0.449	MAE	1.277

RMSE: Root Mean Square Error  
MSE: Mean Square Error  
MAE: Mean Absolute Error

ANOVA

	Sum of Squares	DF	Mean Square	F	Sig.
Regression	434.411	2	217.205	86.204	0.0000
Residual	496.377	197	2.520		
Total	930.788	199			

Parameter Estimates

model	Beta	Std. Error	Std. Beta	t	sig	lower	upper
(Intercept)	8.286	0.112		73.818	0.000	8.064	8.507
alcexp_m	0.907	0.177	0.327	5.119	0.000	0.557	1.256
typ_drks_m	0.065	0.009	0.440	6.886	0.000	0.046	0.083

Model Summary

R	0.961	RMSE	0.607
R-Squared	0.923	Coef. Var	7.325
Adj. R-Squared	0.921	MSE	0.368
Pred R-Squared	0.918	MAE	0.447

RMSE: Root Mean Square Error  
MSE: Mean Square Error  
MAE: Mean Absolute Error

ANOVA

	Sum of Squares	DF	Mean Square	F	Sig.
Regression	859.335	5	171.867	466.635	0.0000
Residual	71.452	194	0.368		
Total	930.788	199			

Parameter Estimates

model	Beta	Std. Error	Std. Beta	t	sig	lower	upper
(Intercept)	8.286	0.043		193.075	0.000	8.201	8.370
alcexp_m	0.023	0.073	0.008	0.320	0.749	-0.120	0.167
typ_drks_m	0.003	0.004	0.019	0.675	0.501	-0.005	0.011
absorb_m	-0.010	0.048	-0.004	-0.206	0.837	-0.104	0.084
weight_m	-0.090	0.005	-0.414	-20.062	0.000	-0.099	-0.081
alc_gm_m	0.252	0.008	0.899	31.057	0.000	0.236	0.268

### Analysis of Variance Table

Model 1: bac100 ~ alcexp\_m + typ\_drks\_m

Model 2: bac100 ~ alcexp\_m + typ\_drks\_m + absorb\_m + weight\_m + alc\_gm\_m

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	197	496.38				
2	194	71.45	3	424.92	384.57	< 2.2e-16 ***

---

signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

### Results of Model 1

### Results of Model 2

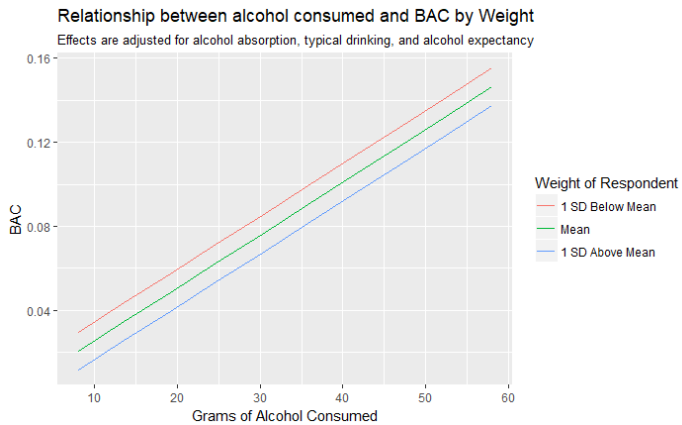
Comparison of Models.  $F^* = 384.57$ , this greatly exceeds our critical value of  $F$ , therefore we reject the null hypothesis. Model 2 predicts significantly more variance in bac than Model 1.

## Plot Model 2

Let's plot Model 2 to see how we plot the fitted model relating alc\_gm to BAC by three prototypical weights. We will hold all of the other variables constant at the mean.

```
predgrid <- data_grid(obs,
  alc_gm_m = seq_range(alc_gm_m, 10),
  weight_m = c(-9.92, 0, 9.92),
  absorb_m = 0,
  alcexp_m = 0,
  typ_drks_m = 0) %>%
mutate(weight_m.f = factor(weight_m, levels = c(-9.92, 0, 9.92),
  labels = c("1 SD Below Mean", "Mean", "1 SD Above Mean"))) %>%
add_predictions(mod2) %>%
mutate (bac = pred/100, alc_gm = alc_gm_m + mean(obs$alc_gm))

ggplot(data = predgrid, aes(x = alc_gm, y = bac, group = weight_m.f, color = weight_m.f)) +
  geom_line() +
  guides(color=guide_legend("Weight of Respondent")) +
  labs(title = "Relationship between alcohol consumed and BAC by Weight",
    subtitle = "Effects are adjusted for alcohol absorption, typical drinking, and alcohol expectancy",
    x = "Grams of Alcohol Consumed", y = "BAC")
```





## Partial F for Model Trimming

We can also use a Partial F-test for modeling trimming, that is, to determine if removing variables is warranted. This is a desirable approach if one seeks to arrive at the most parsimonious, yet most predictive model possible. The models still must be nested. With this approach, a full model is compared to a subset model in which some of the predictors in the full model have been removed. Let's consider an example. In Model 2 that we just estimated, two of the variables are significant predictors (alc\_gm and weight), but the remaining predictors (alcexp, typ\_drks, and absorb) are not. We can determine if removing these predictors makes sense. In this example the critical value for the Partial F-test just happens to be the same as the critical value of F calculated to compare Model 1 to Model 2. The numerator df is the difference in the number of predictors between the two models (3), and the denominator df is the df for the SSE for the full model (194). Therefore, the critical value of F remains 2.65.

### Model 3

```
mod3 <- lm(data = obs, bac100 ~ weight_m + alc_gm_m)
ols_regress(mod3)
```

### Compare Models 2 and 3

```
anova(mod3, mod2, test = "F")
```

Model Summary

R	0.961	RMSE	0.604
R-Squared	0.923	Coef. Var	7.284
Adj. R-Squared	0.922	MSE	0.364
Pred R-Squared	0.920	MAE	0.449

RMSE: Root Mean Square Error  
MSE: Mean Square Error  
MAE: Mean Absolute Error

ANOVA

	Sum of Squares	DF	Mean Square	F	Sig.
Regression	859.029	2	429.514	1179.142	0.0000
Residual	71.759	197	0.364		
Total	930.788	199			

Parameter Estimates

model	Beta	Std. Error	Std. Beta	t	Sig.	lower	upper
(Intercept)	8.286	0.043		194.146	0.000	8.201	8.370
weight_m	-0.091	0.004	-0.418	-20.953	0.000	-0.100	-0.082
alc_gm_m	0.257	0.006	0.918	46.056	0.000	0.246	0.268

### Analysis of Variance Table

```
Model 1: bac100 ~ weight_m + alc_gm_m
Model 2: bac100 ~ alcexp_m + typ_drks_m + absorb_m + weight_m + alc_gm_m
Res.Df  RSS Df Sum of Sq    F Pr(>F)
1    197 71.759
2    194 71.452  3    0.30674 0.2776 0.8415
```

$F^* = .2776$ , this does not exceed critical value of F, therefore we do not reject the null hypothesis. Removing alcexp, typ\_drks and absorb doesn't significantly erode our ability to predict bac.

## Describe Results

Make a table of the results from all three models

```
huxreg("Model 1" = mod1, "Model 2" = mod2, "Model 3" = mod3, error_format = "{std.error}",
       statistics = c("N" = "nobs", "R-Squared" = "r.squared", "F statistic" = "statistic", "P value" = "p.value"))
```

	Model 1	Model 2	Model 3
(Intercept)	8.286 *** (0.112)	8.286 *** (0.043)	8.286 *** (0.043)
alcexp_m	0.907 *** (0.177)	0.023 (0.073)	
typ_drks_m	0.065 *** (0.009)	0.003 (0.004)	
absorb_m		-0.010 (0.048)	
weight_m		-0.090 *** (0.005)	-0.091 *** (0.004)
alc_gm_m		0.252 *** (0.008)	0.257 *** (0.006)
N	200	200	200
R-Squared	0.467	0.923	0.923
F statistic	86.204	466.635	1179.142
P value	0.000	0.000	0.000

\*\*\*  $p < 0.001$ ; \*\*  $p < 0.01$ ; \*  $p < 0.05$ .

The purpose of our analysis was to predict blood alcohol content (BAC) measured 2 hours after the start of female student's 21st birthday celebration. We used a hierarchical regression to examine two models. The first considered two predictors measured prior to the student's 21st birthday: typical drinking (measured as the number of standard drinks consumed during the 30 prior days) and positive expectancies for the role alcohol would play in the 21st birthday celebration. The second model added three additional variables measured on the day of the 21st birthday and highly relevant to BAC: the predicted absorption rate of the alcohol based on the amount of food consumed during the day, the participant's weight, and the grams of alcohol consumed. The two models were compared using a Partial F-test. The results of each model are presented in the Table 1. Model 1 predicted 46.7% of the variance in BAC ( $F(2,197)=86.20, p<.001$ ). Model 2 predicted 92.3% of the variance in BAC ( $F(5,194)=466.64, p<.001$ ). A Partial F-test indicated substantial improvement in the prediction of BAC for Model 2 over Model 1 ( $F(3,194) = 384.57, p<.001$ ).

Assessment of the parameter estimates in Model 2 revealed that only 2 of the variables independently predicted BAC (weight and alcohol consumed on the 21st birthday). Moreover, while typical drinking and alcohol expectancies predicted BAC in Model 1, once the additional variables in Model 2 were added, neither variable independently predicted BAC. We elected to examine a final model that trimmed the three non-significant predictors from the model. The results are presented in Table 1, Model 3. A Partial F-test was used to compare Model 2 and 3 ( $F(3, 194)=.28, NS$ ), the non-significant F-test indicates that the removal of these three variables did not significantly erode the overall model fit. Therefore, we consider Model 3 to be our final model.

\*We will build on this model in future Units to consider a potential interaction between alc\_gm and weight (i.e., perhaps the effect of each additional gram of alcohol is different depending on how much the student weighs), and whether alcohol consumption may mediate (i.e., explain) the effect of typical drinking and alcohol expectancies on BAC (i.e., the indirect effect).