

Friday, January 31

## Marginal Means

A *marginal mean* is effectively an average of expected responses. The **emmeans** package is particularly useful for making inferences about marginal means. It can also be done using **contrast** but it is not a documented feature.

```
library(trtools)
library(emmeans)
```

Welcome to emmeans.

Caution: You lose important information if you filter this package's results.  
See '? untidy'

Attaching package: 'emmeans'

The following objects are masked from 'package:trtools':

contrast, neuralgia

**Warning:** The **emmeans** package contains a function called **contrast** which is not the same as the function of the same name in the **trtools** package, resulting in a namespace conflict if both packages are loaded. If you have both packages loaded in a given session, use **trtools::contrast** and **emmeans::contrast** to refer to a given function.

**Example:** Consider again the data from the platyfish study.

```
m <- lm(Percentage ~ Pair, data = Sleuth3::case0602)
summary(m)$coefficients
```

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	56.406	3.864	14.5965	5.208e-24
PairPair2	4.479	5.657	0.7919	4.308e-01
PairPair3	6.023	5.384	1.1187	2.667e-01
PairPair4	10.594	5.657	1.8727	6.485e-02
PairPair5	7.805	6.441	1.2118	2.292e-01
PairPair6	6.929	5.657	1.2250	2.243e-01

We see that there are indicator variables for male pairs 2-6. The model can be written as

$$E(Y_i) = \begin{cases} \beta_0, & \text{if the } i\text{-th observation was from the first male pair,} \\ \beta_0 + \beta_1, & \text{if the } i\text{-th observation was from the second male pair,} \\ \beta_0 + \beta_2, & \text{if the } i\text{-th observation was from the third male pair,} \\ \beta_0 + \beta_3, & \text{if the } i\text{-th observation was from the fourth male pair,} \\ \beta_0 + \beta_4, & \text{if the } i\text{-th observation was from the fifth male pair,} \\ \beta_0 + \beta_5, & \text{if the } i\text{-th observation was from the sixth male pair.} \end{cases}$$

We can use **contrast** to estimate the expected response for each pair.

```
trtools::contrast(m, a = list(Pair = paste("Pair", 1:6, sep = "")),
  cnames = paste("Pair", 1:6, sep = ""))
```

Note how I used a shortcut to specify the pairs.

```
paste("Pair", 1:6, sep = "")
```

```
[1] "Pair1" "Pair2" "Pair3" "Pair4" "Pair5" "Pair6"
```

This can also be done using the `emmeans` function from the package `emmeans`.

```
library(emmeans)
emmeans(m, ~ Pair)
```

Pair	emmean	SE	df	lower.CL	upper.CL
Pair1	56.4	3.86	78	48.7	64.1
Pair2	60.9	4.13	78	52.7	69.1
Pair3	62.4	3.75	78	55.0	69.9
Pair4	67.0	4.13	78	58.8	75.2
Pair5	64.2	5.15	78	54.0	74.5
Pair6	63.3	4.13	78	55.1	71.6

Confidence level used: 0.95

Denote the six expected responses (one for each pair) as

$$\begin{aligned}\mu_1 &= \beta_0, \\ \mu_2 &= \beta_0 + \beta_1, \\ \mu_3 &= \beta_0 + \beta_2, \\ \mu_4 &= \beta_0 + \beta_3, \\ \mu_5 &= \beta_0 + \beta_4, \\ \mu_6 &= \beta_0 + \beta_5.\end{aligned}$$

One marginal mean would be the average expected response across the pairs. This could be written as

$$\mu = \frac{\mu_1 + \mu_2 + \mu_3 + \mu_4 + \mu_5 + \mu_6}{6} = \beta_0 + \frac{1}{6}\beta_1 + \frac{1}{6}\beta_2 + \frac{1}{6}\beta_3 + \frac{1}{6}\beta_4 + \frac{1}{6}\beta_5.$$

We can estimate this quantity with `lincon`.

```
lincon(m, a = c(1,1/6,1/6,1/6,1/6,1/6))
```

	estimate	se	lower	upper	tvalue	df	pvalue
(1,1/6,1/6,1/6,1/6,1/6),0	62.38	1.722	58.95	65.81	36.23	78	1.501e-50

We can also use `emmeans`.

```
emmeans(m, ~ 1)
```

	emmean	SE	df	lower.CL	upper.CL
1 overall	62.4	1.72	78	59	65.8

Results are averaged over the levels of: Pair

Confidence level used: 0.95

Note that we can use the confidence interval to test the null hypothesis that  $\mu = 50$ . For a test statistic and p-value for this test we could write this as

$$\mu = 50 \Leftrightarrow \beta_0 + \frac{1}{6}\beta_1 + \frac{1}{6}\beta_2 + \frac{1}{6}\beta_3 + \frac{1}{6}\beta_4 + \frac{1}{6}\beta_5 = 50 \Leftrightarrow \beta_0 + \frac{1}{6}\beta_1 + \frac{1}{6}\beta_2 + \frac{1}{6}\beta_3 + \frac{1}{6}\beta_4 + \frac{1}{6}\beta_5 - 50 = 0.$$

Here is how we can do that with `lincon`.

```
lincon(m, a = c(1,1/6,1/6,1/6,1/6,1/6), b = -50)
```

```

              estimate    se lower upper tvalue df    pvalue
(1,1/6,1/6,1/6,1/6,1/6),-50  12.38 1.722  8.95 15.81  7.189 78 3.439e-10

```

Here is how we do it with `emmeans`.

```
emmeans(m, ~ 1, offset = -50, infer = TRUE)
```

```

 1      emmean  SE df lower.CL upper.CL t.ratio p.value
overall  12.4 1.72 78    8.95    15.8   7.189 <.0001

```

Results are averaged over the levels of: Pair

Confidence level used: 0.95

By *not* listing an explanatory variable on the right-hand side of `~`, we are asking that `emmeans` average over that explanatory variable. Also note that the argument `infer = TRUE` makes the `emmeans` function provide both confidence intervals as well as tests.

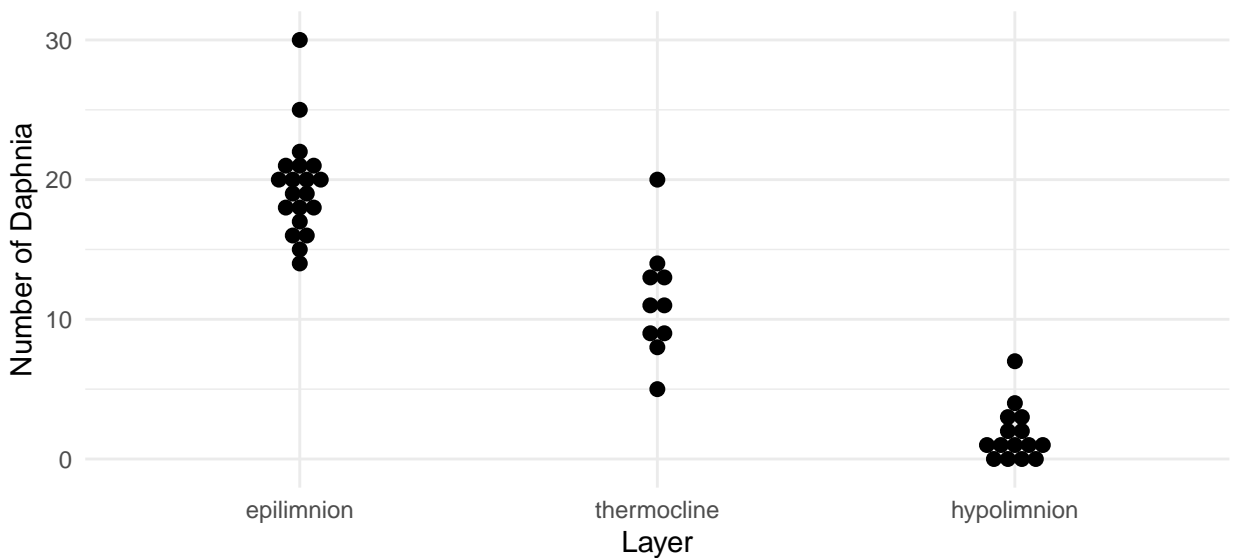
**Note:** If we just want to know whether or not we would reject the null hypothesis that  $\mu = 50$  we can also just look at the confidence interval for  $\mu$ .

**Example:** Consider the following data from a survey of water fleas.

```

library(ggplot2)
p <- ggplot(daphniastrat, aes(x = layer, y = count)) +
  geom_dotplot(binaxis = "y", stackdir = "center") +
  labs(x = "Layer", y = "Number of Daphnia") + theme_minimal()
plot(p)

```



We might model these data using the following linear model.

```

m <- lm(count ~ layer, data = daphniastrat)
summary(m)$coefficients

```

```

              Estimate Std. Error t value Pr(>|t|)
(Intercept)    19.50     0.7271  26.820 4.727e-28
layerthermocline  -8.20     1.2593  -6.512 7.293e-08
layerhypolimnion -17.77     1.1106 -15.997 1.784e-19

```

So our model can be written as

$$E(Y_i) = \begin{cases} \beta_0, & \text{if the } i\text{-th observation is from the epilimnion layer,} \\ \beta_0 + \beta_1, & \text{if the } i\text{-th observation is from the thermocline layer,} \\ \beta_0 + \beta_2, & \text{if the } i\text{-th observation is from the hypolimnion layer.} \end{cases}$$

Let  $\mu_e$ ,  $\mu_t$ , and  $\mu_h$  denote the expected number of daphnia per liter for the epilimnion, thermocline, and hypolimnion layers, respectively (i.e., the density of daphnia in each layer). So

$$\mu_e = \beta_0, \quad \mu_t = \beta_0 + \beta_1, \quad \mu_h = \beta_0 + \beta_2.$$

It is known that the volumes of the epilimnion, thermocline, and hypolimnion layers are 100, 200, and 400 kL, respectively. The density for the entire lake is then

$$\mu = \frac{100}{700}\mu_e + \frac{200}{700}\mu_t + \frac{400}{700}\mu_h = \beta_0 + \frac{2}{7}\beta_1 + \frac{4}{7}\beta_2.$$

We can estimate this with `lincon` or `emmeans` using the `weights` option.

```
lincon(m, a = c(1, 2/7, 4/7))
```

```
      estimate      se lower upper tvalue df    pvalue
(1,2/7,4/7),0  7.005 0.572  5.85 8.159  12.25 42 1.907e-15
```

```
emmeans(m, ~ 1, weights = c(1/7, 2/7, 4/7))
```

```
  1      emmean    SE df lower.CL upper.CL
overall      7 0.572 42    5.85    8.16
```

Results are averaged over the levels of: layer

Confidence level used: 0.95

Note that when using `emmeans` it is important to put the weights in the correct order. We can verify the order using `level` (if the variable is a factor) or by using `weights = "slow.levels"`.

```
levels(daphniastrat$layer)
```

```
[1] "epilimnion" "thermocline" "hypolimnion"
```

```
emmeans(m, ~ 1, weights = "show.levels")
```

`emmeans` are obtained by averaging over these factor combinations

```
      layer
  1 epilimnion
  2 thermocline
  3 hypolimnion
```

We can estimate the expected number of daphnia per liter for each layer.

```
emmeans(m, ~ layer)
```

```
      layer      emmean    SE df lower.CL upper.CL
epilimnion  19.50 0.727 42    18.033    20.97
thermocline  11.30 1.030 42     9.225    13.38
hypolimnion   1.73 0.840 42     0.039     3.43
```

Confidence level used: 0.95

```
trtools::contrast(m, a = list(layer = c("epilimnion", "thermocline", "hypolimnion")),
  cnames = c("epilimnion", "thermocline", "hypolimnion"))
```

	estimate	se	lower	upper	tvalue	df	pvalue
epilimnion	19.500	0.7271	18.03274	20.967	26.820	42	4.727e-28
thermocline	11.300	1.0282	9.22498	13.375	10.990	42	6.221e-14
hypolimnion	1.733	0.8395	0.03909	3.428	2.065	42	4.517e-02

We can also do inferences concerning the differences between pairs of layers.

```
pairs(emmeans(m, ~ layer), adjust = "none")
```

contrast	estimate	SE	df	t.ratio	p.value
epilimnion - thermocline	8.20	1.26	42	6.512	<.0001
epilimnion - hypolimnion	17.77	1.11	42	15.997	<.0001
thermocline - hypolimnion	9.57	1.33	42	7.207	<.0001

```
trtools::contrast(m,
  a = list(layer = c("epilimnion", "epilimnion", "thermocline")),
  b = list(layer = c("thermocline", "hypolimnion", "hypolimnion")),
  cnames = c("E-T", "E-H", "T-H"))
```

	estimate	se	lower	upper	tvalue	df	pvalue
E-T	8.200	1.259	5.659	10.74	6.512	42	7.293e-08
E-H	17.767	1.111	15.525	20.01	15.997	42	1.784e-19
T-H	9.567	1.327	6.888	12.25	7.207	42	7.363e-09

The `adjust = "none"` option for `pairs` specifies that no adjustment be made to confidence intervals or tests for the family-wise Type I error rate.<sup>1</sup>

Something to note when using the `weights` argument with the `emmeans` function is that the weights that are used must sum to one, and if they do not they will be normalized so that they do. For example, the following provide the same result.

```
emmeans(m, ~ 1, weights = c(1/7, 2/7, 4/7))
```

1	emmean	SE	df	lower.CL	upper.CL
overall	7	0.572	42	5.85	8.16

Results are averaged over the levels of: layer

Confidence level used: 0.95

```
emmeans(m, ~ 1, weights = c(1, 2, 4)) # original weights multiplied by 7
```

1	emmean	SE	df	lower.CL	upper.CL
overall	7	0.572	42	5.85	8.16

Results are averaged over the levels of: layer

Confidence level used: 0.95

If you want to use weights that do not sum to one, you can use the `contrast` function from the `emmeans` package (different from the function of the same name from `trtools`).

<sup>1</sup>The family-wise Type I error rate is the probability of making *at least one* Type I error. If it is desired that the family-wise Type I error rate be no greater than  $\alpha$  (default is 0.05), then some adjustment can be made. This adjustment is seen in the p-values and confidence intervals. The most general method is to use `adjust = "mvt"`. Some special cases are more widely known such as Tukey (`adjust = "tukey"`) and Bonferroni (`adjust = "bonferroni"`), but the adjustment based on the multivariate *t*-distribution (`adjust = "mvt"`) is the most general and accurate. Note that an adjustment will produce “simultaneous” confidence intervals. A method of producing simultaneous confidence intervals has the property that the probability that *all* of the confidence intervals will contain the quantities being estimated is equal to the specified confidence level (95% by default). The multivariate *t*-distribution adjustment is perhaps not as well known, so a reference that you can cite is Edwards, D. & Berry, J. T. (1987). The efficiency of simulation-based multiple comparisons. *Biometrics*, 43(4), 913–928.

```
emmeans(m, ~1, weights = c(1/7, 2/7, 4/7))
```

1	emmean	SE	df	lower.CL	upper.CL
overall	7	0.572	42	5.85	8.16

Results are averaged over the levels of: layer

Confidence level used: 0.95

```
emmeans::contrast(emmeans(m, ~layer), method = list(layer = c(1/7, 2/7, 4/7)), infer = TRUE)
```

contrast	estimate	SE	df	lower.CL	upper.CL	t.ratio	p.value
layer	7	0.572	42	5.85	8.16	12.245	<.0001

Confidence level used: 0.95

But suppose we wanted to estimate the *number* of daphnia in the lake ( $\tau$ ). It can be shown that this is

$$\tau = 700000\mu = 700000 \left( \frac{1}{7}\mu_e + \frac{2}{7}\mu_t + \frac{4}{7}\mu_h \right) = 100000\mu_e + 200000\mu_t + 400000\mu_h.$$

Note that there are 700kL in the lake, which is 700000L (which is the scale used for the observations). This can be estimated as follows.

```
emmeans::contrast(emmeans(m, ~layer),  
  method = list(layer = 700000 * c(1/7, 2/7, 4/7)), infer = TRUE)
```

contrast	estimate	SE	df	lower.CL	upper.CL	t.ratio	p.value
layer	4903333	4e+05	42	4095230	5711437	12.245	<.0001

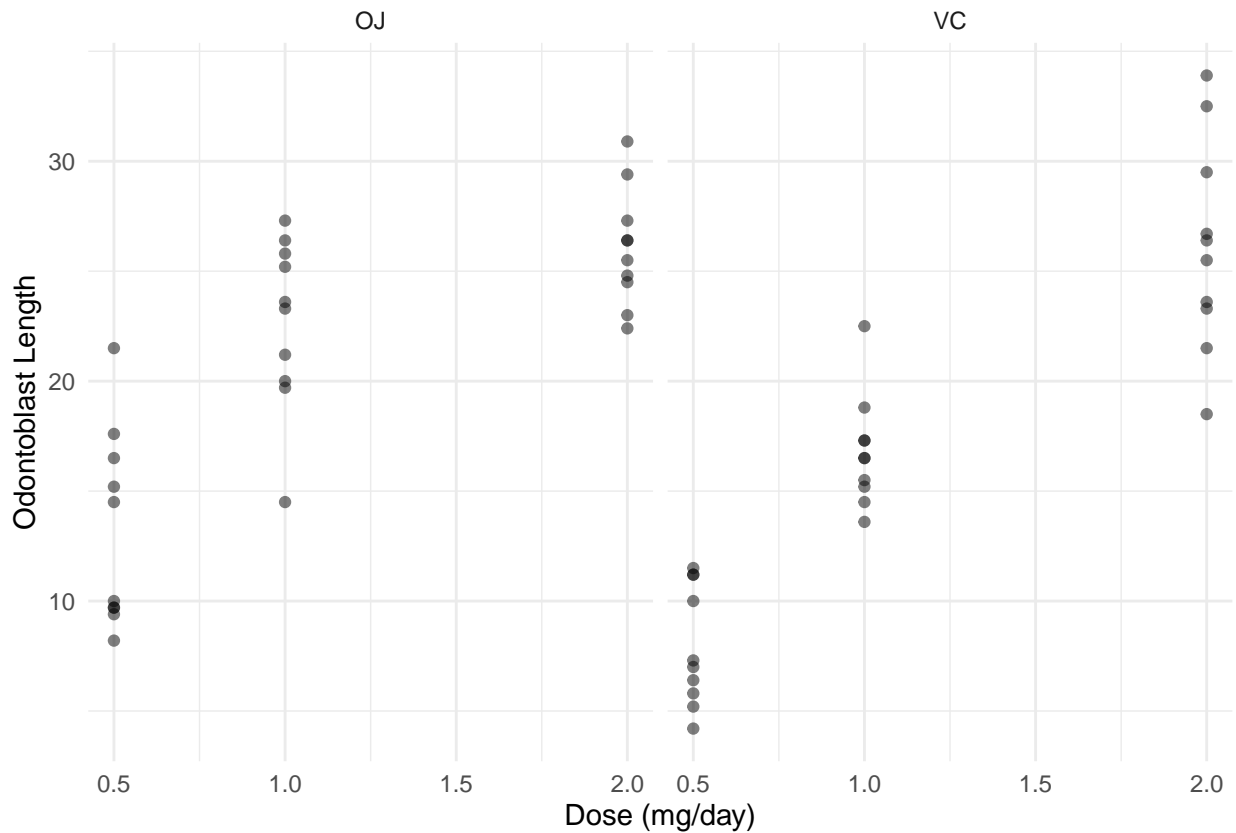
Confidence level used: 0.95

Another approach is to use `lincon` but your weights/coefficients will be different since they are applied to  $\beta_0$ ,  $\beta_1$ , and  $\beta_2$ .

## Marginal Means and “Main Effects”

Consider data from a randomized experiment with guinea pigs administered one of three doses of vitamin C (0.5, 1, or 2 mg/day) via one of two supplement methods: orange juice (OJ) or ascorbic acid (VC).

```
p <- ggplot(ToothGrowth, aes(x = dose, y = len)) +  
  geom_point(alpha = 0.5) + facet_wrap(~supp) +  
  labs(x = "Dose (mg/day)", y = "Odontoblast Length") + theme_minimal()  
plot(p)
```



Here we are going to model dose as a categorical variable so we need to coerce it to a factor. Perhaps the safest approach is to create a new variable.

```
ToothGrowth$dosef <- factor(ToothGrowth$dose)
```

Note: Whether a variable is a numeric, a factor, or something else can be seen use `str` (for “structure”).

```
str(ToothGrowth)
```

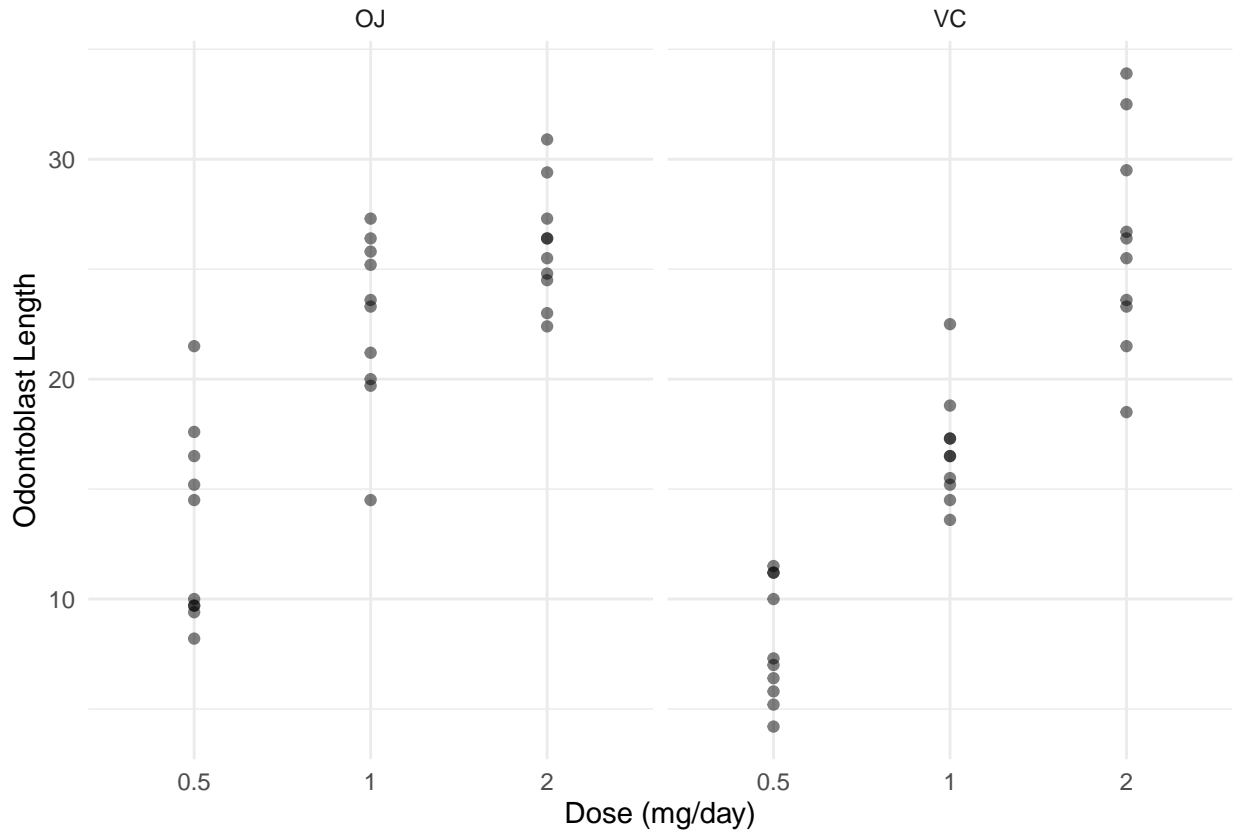
```
'data.frame': 60 obs. of 4 variables:
 $ len : num 4.2 11.5 7.3 5.8 6.4 10 11.2 11.2 5.2 7 ...
 $ supp : Factor w/ 2 levels "OJ","VC": 2 2 2 2 2 2 2 2 2 2 ...
 $ dose : num 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 ...
 $ dosef: Factor w/ 3 levels "0.5","1","2": 1 1 1 1 1 1 1 1 1 1 ...
```

Notice that `ggplot` responds differently.

```
summary(ToothGrowth)
```

	len	supp	dose	dosef
Min.	: 4.2	OJ:30	Min. :0.50	0.5:20
1st Qu.:	13.1	VC:30	1st Qu.:0.50	1 :20
Median	:19.2		Median :1.00	2 :20
Mean	:18.8		Mean :1.17	
3rd Qu.:	25.3		3rd Qu.:2.00	
Max.	:33.9		Max. :2.00	

```
p <- ggplot(ToothGrowth, aes(x = dosef, y = len)) +
  geom_point(alpha = 0.5) + facet_wrap(~supp) +
  labs(x = "Dose (mg/day)", y = "Odontoblast Length") + theme_minimal()
plot(p)
```



Now consider the following linear model.

```
m <- lm(len ~ dosef + supp + dosef:supp, data = ToothGrowth)
summary(m)$coefficients
```

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	13.23	1.148	11.5208	3.603e-16
dosef1	9.47	1.624	5.8312	3.176e-07
dosef2	12.83	1.624	7.9002	1.430e-10
suppVC	-5.25	1.624	-3.2327	2.092e-03
dosef1:suppVC	-0.68	2.297	-0.2961	7.683e-01
dosef2:suppVC	5.33	2.297	2.3207	2.411e-02

The model is

$$E(Y_i) = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \beta_3 x_{i3} + \beta_4 x_{i4} + \beta_5 x_{i5},$$

where

$$x_{i1} = \begin{cases} 1, & \text{if dose is 1 mg/day,} \\ 0, & \text{otherwise,} \end{cases}$$

$$x_{i2} = \begin{cases} 1, & \text{if dose is 2 mg/day,} \\ 0, & \text{otherwise,} \end{cases}$$

$$x_{i3} = \begin{cases} 1, & \text{if supplement type is VC} \\ 0, & \text{otherwise,} \end{cases}$$

$$x_{i4} = x_{i1} x_{i3} = \begin{cases} 1, & \text{if dose is 1 mg/day and supplement type is VC,} \\ 0, & \text{otherwise,} \end{cases}$$



$$x_{i5} = x_{i2}x_{i3} = \begin{cases} 1, & \text{if dose is 2 mg/day and supplement type is VC,} \\ 0, & \text{otherwise.} \end{cases}$$

We can write this model case-wise.

$$E(Y_i) = \begin{cases} \beta_0, & \text{if dose is 0.5 mg/day and supplement type is OJ,} \\ \beta_0 + \beta_1, & \text{if dose is 1 mg/day and supplement type is OJ,} \\ \beta_0 + \beta_2, & \text{if dose is 2 mg/day and supplement type is OJ,} \\ \beta_0 + \beta_3, & \text{if dose is 0.5 mg/day and supplement type is VC,} \\ \beta_0 + \beta_1 + \beta_3 + \beta_4, & \text{if dose is 1 mg/day and supplement type is VC,} \\ \beta_0 + \beta_2 + \beta_3 + \beta_5, & \text{if dose is 2 mg/day and supplement type is VC.} \end{cases}$$

Note that if we omitted the interaction term so that the model formula is `len ~ dosef + supp`, then we would have the model

$$E(Y_i) = \beta_0 + \beta_1x_{i1} + \beta_2x_{i2} + \beta_3x_{i3},$$

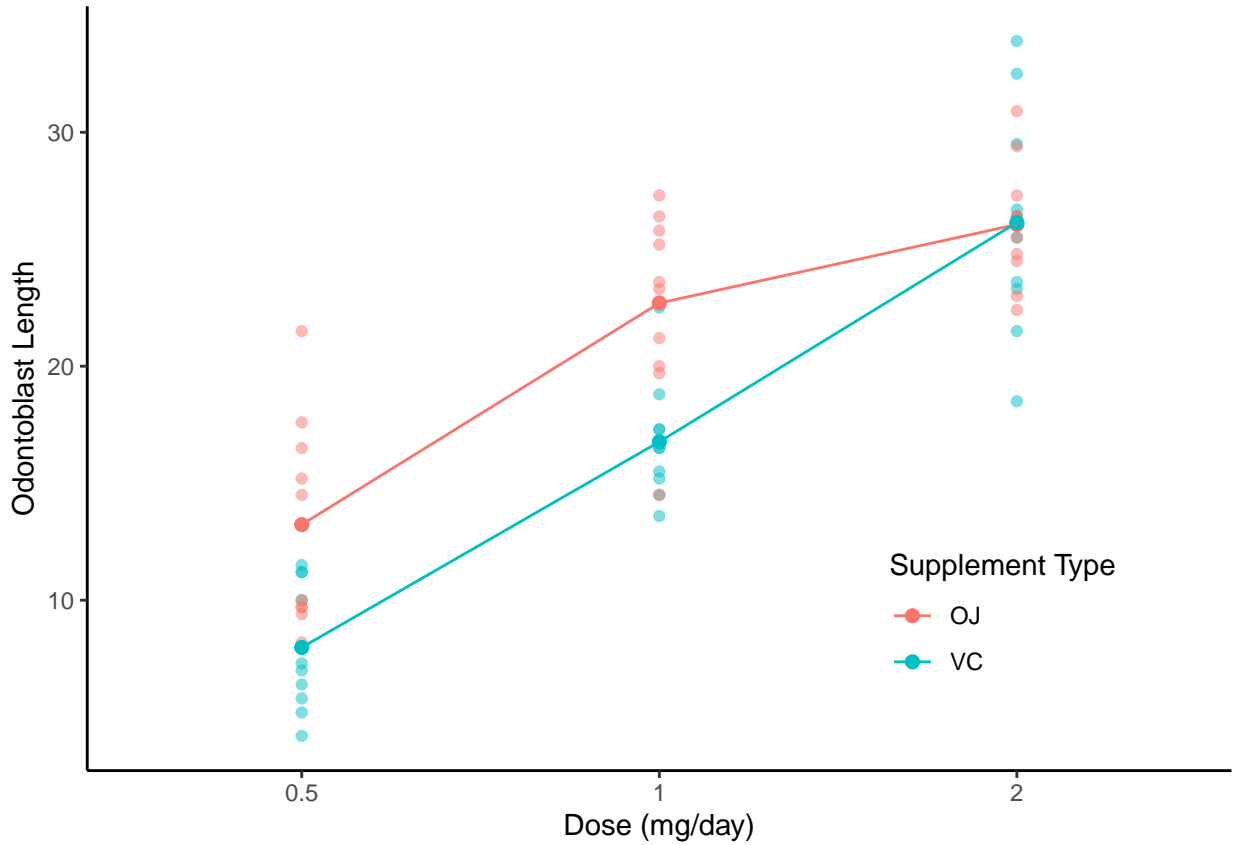
which can be written case-wise as

$$E(Y_i) = \begin{cases} \beta_0, & \text{if dose is 0.5 mg/day and supplement type is OJ,} \\ \beta_0 + \beta_1, & \text{if dose is 1 mg/day and supplement type is OJ,} \\ \beta_0 + \beta_2, & \text{if dose is 2 mg/day and supplement type is OJ,} \\ \beta_0 + \beta_3, & \text{if dose is 0.5 mg/day and supplement type is VC,} \\ \beta_0 + \beta_1 + \beta_3 & \text{if dose is 1 mg/day and supplement type is VC,} \\ \beta_0 + \beta_2 + \beta_3 & \text{if dose is 2 mg/day and supplement type is VC.} \end{cases}$$

Here is a visualization of the data and the model *with* the interaction.

```
d <- expand.grid(dosef = levels(ToothGrowth$dosef), supp = levels(ToothGrowth$supp))
d$yhat <- predict(m, newdata = d)

p <- ggplot(ToothGrowth, aes(x = dosef, y = len, color = supp)) +
  geom_point(alpha = 0.5) + theme_classic() +
  theme(legend.position = "inside", legend.position.inside = c(0.8,0.2)) +
  geom_point(aes(y = yhat), size = 2, data = d) +
  geom_line(aes(y = yhat, group = supp), data = d) +
  labs(x = "Dose (mg/day)", y = "Odontoblast Length", color = "Supplement Type")
plot(p)
```



Consider again the model with the interaction so that

$$E(Y_i) = \begin{cases} \beta_0, & \text{if dose is 0.5 mg/day and supplement type is OJ,} \\ \beta_0 + \beta_1, & \text{if dose is 1 mg/day and supplement type is OJ,} \\ \beta_0 + \beta_2, & \text{if dose is 2 mg/day and supplement type is OJ,} \\ \beta_0 + \beta_3, & \text{if dose is 0.5 mg/day and supplement type is VC,} \\ \beta_0 + \beta_1 + \beta_3 + \beta_4, & \text{if dose is 1 mg/day and supplement type is VC,} \\ \beta_0 + \beta_2 + \beta_3 + \beta_5, & \text{if dose is 2 mg/day and supplement type is VC.} \end{cases}$$

The “cell means” are

$$\mu_{\text{OJ},0.5} = \beta_0, \tag{1}$$

$$\mu_{\text{OJ},1.0} = \beta_0 + \beta_1, \tag{2}$$

$$\mu_{\text{OJ},2.0} = \beta_0 + \beta_2, \tag{3}$$

$$\mu_{\text{VC},0.5} = \beta_0 + \beta_3, \tag{4}$$

$$\mu_{\text{VC},1.0} = \beta_0 + \beta_1 + \beta_3 + \beta_4, \tag{5}$$

$$\mu_{\text{VC},2.0} = \beta_0 + \beta_2 + \beta_3 + \beta_5. \tag{6}$$

The “marginal means” for supplement type are

$$\mu_{\text{OJ}} = \frac{\mu_{\text{OJ},0.5} + \mu_{\text{OJ},1.0} + \mu_{\text{OJ},2.0}}{3} = \beta_0 + \frac{1}{3}\beta_1 + \frac{1}{3}\beta_2,$$

and

$$\mu_{\text{VC}} = \frac{\mu_{\text{VC},0.5} + \mu_{\text{VC},1.0} + \mu_{\text{VC},2.0}}{3} = \beta_0 + \frac{1}{3}\beta_1 + \frac{1}{3}\beta_2 + \beta_3 + \frac{1}{3}\beta_4 + \frac{1}{3}\beta_5.$$

We can estimate them using `lincon`.

```
lincon(m, a = c(1,1/3,1/3,0,0,0))
```

	estimate	se	lower	upper	tvalue	df	pvalue
(1,1/3,1/3,0,0,0),0	20.66	0.663	19.33	21.99	31.17	54	3.359e-36

```
lincon(m, a = c(1,1/3,1/3,1,1/3,1/3))
```

	estimate	se	lower	upper	tvalue	df	pvalue
(1,1/3,1/3,1,1/3,1/3),0	16.96	0.663	15.63	18.29	25.59	54	7.306e-32

But we can also do it using emmeans.

```
emmeans(m, ~supp)
```

supp	emmean	SE	df	lower.CL	upper.CL
OJ	20.7	0.663	54	19.3	22.0
VC	17.0	0.663	54	15.6	18.3

Results are averaged over the levels of: dosef  
Confidence level used: 0.95

Now suppose we want to estimate the “main effect” which is

$$\mu_{OJ} - \mu_{VC} = \frac{\mu_{OJ,0.5} + \mu_{OJ,1.0} + \mu_{OJ,2.0}}{3} - \frac{\mu_{VC,0.5} + \mu_{VC,1.0} + \mu_{VC,2.0}}{3} = -\beta_3 - \frac{1}{3}\beta_4 - \frac{1}{3}\beta_5.$$

We can do this using lincon.

```
lincon(m, a = c(0,0,0,-1,-1/3,-1/3))
```

	estimate	se	lower	upper	tvalue	df	pvalue
(0,0,0,-1,-1/3,-1/3),0	3.7	0.9376	1.82	5.58	3.946	54	0.0002312

But we can also use functions from the emmeans package.

```
pairs(emmeans(m, ~supp), infer = TRUE)
```

contrast	estimate	SE	df	lower.CL	upper.CL	t.ratio	p.value
OJ - VC	3.7	0.938	54	1.82	5.58	3.946	0.0002

Results are averaged over the levels of: dosef  
Confidence level used: 0.95

The main effect of dose concerns differences among the marginal means of dose defined as  $\mu_{0.5}$ ,  $\mu_1$  and  $\mu_2$  where

$$\mu_{0.5} = \frac{\mu_{OJ,0.5} + \mu_{VC,0.5}}{2}, \quad \mu_1 = \frac{\mu_{OJ,1} + \mu_{VC,1}}{2}, \quad \mu_2 = \frac{\mu_{OJ,2} + \mu_{VC,2}}{2}.$$

```
emmeans(m, ~ dosef)
```

dosef	emmean	SE	df	lower.CL	upper.CL
0.5	10.6	0.812	54	8.98	12.2
1	19.7	0.812	54	18.11	21.4
2	26.1	0.812	54	24.47	27.7

Results are averaged over the levels of: supp  
Confidence level used: 0.95

```
pairs(emmeans(m, ~ dosef), adjust = "none")
```

contrast	estimate	SE	df	t.ratio	p.value
dosef0.5 - dosef1	-9.13	1.15	54	-7.951	<.0001

```
dosef0.5 - dosef2  -15.49 1.15 54 -13.493 <.0001
dosef1 - dosef2    -6.37 1.15 54  -5.543 <.0001
```

Results are averaged over the levels of: supp

## Main Effects in Anova Tables

In ANOVA tables the test of the “main effect” is the (joint) null hypothesis that all pairwise differences are zero. For the variable dose the null hypothesis is  $\mu_{0.5} = \mu_1 = \mu_2$ . This can be done using the `test` function.

```
test(pairs(emmeans(m, ~ dosef)), joint = TRUE)
```

```
df1 df2 F.ratio p.value note
  2  54  92.000 <.0001  d
```

d: df1 reduced due to linear dependence

This is the traditional main effect that is sometimes reported in an “ANOVA table” such as that produced by `Anova` from the `car` package.

```
library(car)
m <- lm(len ~ dosef + supp + dosef:supp, data = ToothGrowth,
        contrast = list(dosef = contr.sum, supp = contr.sum))
Anova(m, type = 3)
```

Anova Table (Type III tests)

```
Response: len
          Sum Sq Df F value  Pr(>F)
(Intercept) 21236  1 1610.39 < 2e-16 ***
dosef        2426  2   92.00 < 2e-16 ***
supp         205  1   15.57 0.00023 ***
dosef:supp   108  2    4.11 0.02186 *
Residuals   712 54
```

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The option `contrast = list(dosef = contr.sum, supp = contr.sum)` is necessary here for the `Anova` function to do the correct calculations.<sup>2</sup>

The test of the main effect of supplement method was given by

```
pairs(emmeans(m, ~ supp), infer = TRUE)
```

```
contrast estimate    SE df lower.CL upper.CL t.ratio p.value
OJ - VC         3.7 0.938 54    1.82    5.58   3.946 0.0002
```

Results are averaged over the levels of: dosef  
Confidence level used: 0.95

We do not need a joint test here since there are only two marginal means, but here it is anyway.

```
test(pairs(emmeans(m, ~ supp)), joint = TRUE)
```

```
df1 df2 F.ratio p.value
```

<sup>2</sup>I am demonstrating here what is sometimes called inferences based on Type III sums of squares. Another common approach is to use what is called Type II sums of squares. This can be done with the `Anova` function with `type = 2`. For inferences based on Type II sums of squares with the functions from the `emmeans` package an extra step is needed (email me for an example if you really want to know how to do it).

1 54 15.572 0.0002