

Chapter 6 Sample Answers

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This page provides sample answers to the assignment at the end of Chapter 6 of Applied Statistics with R: A Practical Guide for the Life Sciences by Justin Touchon. Chapter 6 introduces you to *More Linear Models*, which is to say models like *linear regression*, *two-way ANOVA*, and *Analysis of Covariance*. We also continued practicing using the **tidyverse** to explore and manipulate our data. We saw how to do fun things like plot confidence intervals around non-linear regression lines and how to use the **predict()** function. There was **a lot** in this chapter.

There are three assignments to do to continue working on the skills you are building. As always, my hope is that you are here either because 1) you want to check the answers you got to make sure you completed the assignments correctly, or 2) you got stumped and need some help. Either way, you will learn much more if you have already spent some time working through the assignments on your own. If you haven't done that, close this page and go work on it! :) The first assignment at the end of Chapter 6 is straightforward, but the second and third are very open ended. I have tried to reasonably show some different options for what you might have come up with, but understand that your choices might have been different than what I show here.

Question 1

At the end of the Chapter 5, you analyzed the log of final mass by each of the three categorical predictors independently. What happens if you include all three predictors in the model at the same time? Does the significance of any of the individual predictors change when you include more variables? If so, what does that tell you about how your interpretation of one variable might change when you include other variables in the model?

As I did in Chapter 5, I'm going to load any packages I will need and create the "byTank" version of the data.

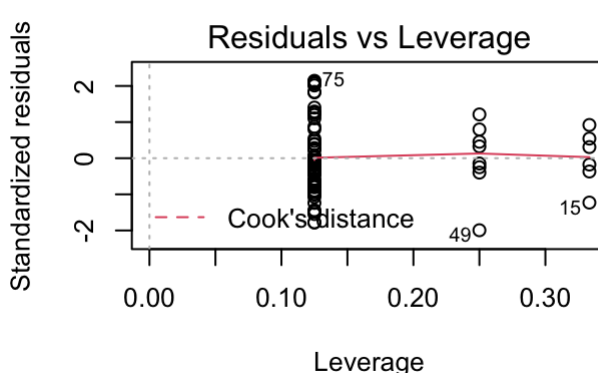
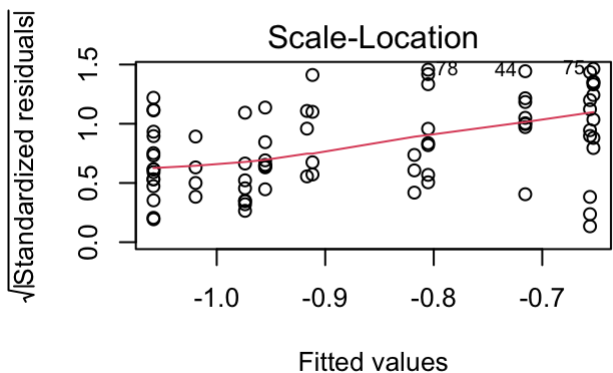
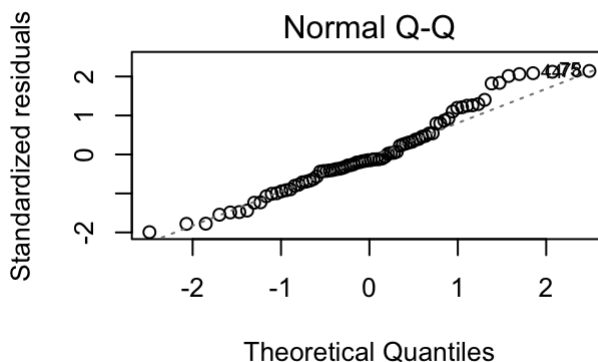
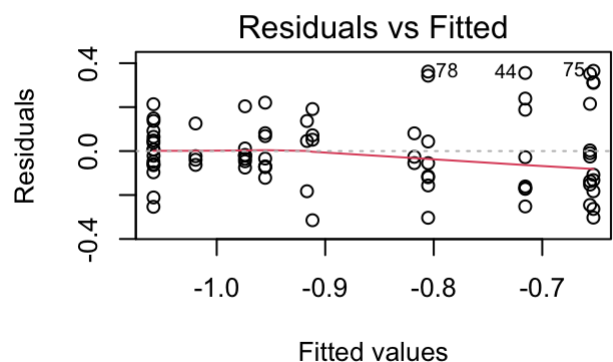
```
library(MASS)
library(car)
library(emmeans)
library(cowplot)
library(tidyverse)
```

```
## 'data.frame':    78 obs. of  16 variables:
## $ Tank.Unique      : int  1 2 3 4 5 6 7 8 9 10 ...
## $ Block           : int  1 1 1 1 1 1 1 1 1 1 ...
## $ Pred            : Factor w/ 3 levels "C","NL","L": 2 1 1 3 2 3 2 1 3 1 ...
## $ Hatch           : Factor w/ 2 levels "E","L": 2 1 2 2 1 1 2 1 2 2 ...
## $ Res             : Factor w/ 2 levels "Hi","Lo": 1 1 1 2 1 1 2 2 1 2 ...
## $ Age.DPO         : num  47.2 45.4 53.8 56.9 64.8 ...
## $ Age.FromEmergence : num  13.2 11.4 19.8 22.9 30.8 ...
## $ SVL.initial     : num  19.4 18.4 18.9 18.8 19.7 ...
## $ Tail.initial    : num  4.83 5.37 4.8 4.63 5.43 ...
## $ SVL.final       : num  19.7 19 19.1 19.1 20.1 ...
## $ Mass.final      : num  0.418 0.382 0.412 0.382 0.486 ...
## $ Resorb.days     : num  3.49 3.79 3.51 3.65 4.22 ...
## $ log.SVL.final   : num  2.98 2.94 2.95 2.95 3 ...
## $ log.Age.FromEmergence: num  2.58 2.43 2.99 3.13 3.43 ...
## $ log.Age.DPO     : num  3.85 3.82 3.99 4.04 4.17 ...
## $ log.Mass.final  : num  -0.873 -0.962 -0.887 -0.962 -0.721 ...
```

The model we need to create is hopefully straightforward to you. Instead of having just one predictor, such as *Pred* or *Res*, we will have all three of our predictors: *Pred*, *Hatch*, and *Res*. We will then use the **Anova()** function from the **car** package to assess statistical significance.

Before we make the model, recall that when we analyzed the variables individually there was a highly significant effect of predators, but no significant effect of resources or hatching age. What will happen when all three predictors are in the model together?

```
lm.PHR<-lm(log.Mass.final~Pred*Hatch*Res, data=RxP.byTank)
par(mfrow=c(2,2));plot(lm.PHR)
```



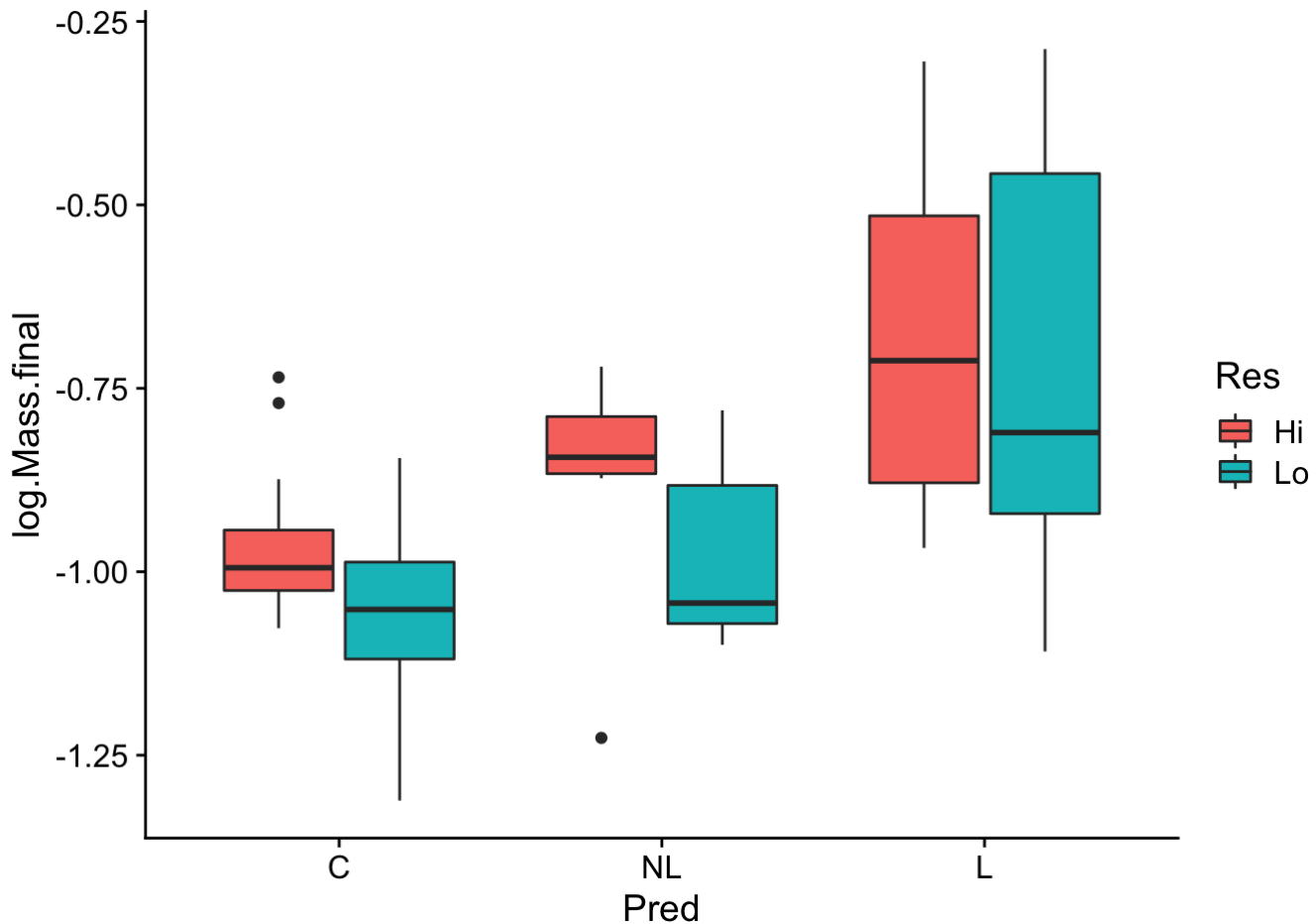
Notice that the QQ-plot looks particularly great now that we have more predictors in the model!

```
Anova(lm.PHR)
```

```
## Anova Table (Type II tests)
##
## Response: log.Mass.final
##           Sum Sq Df F value    Pr(>F)
## Pred           1.52168  2 22.9030 2.79e-08 ***
## Hatch           0.03198  1  0.9628  0.33006
## Res             0.10805  1  3.2527  0.07587 .
## Pred:Hatch      0.05866  2  0.8829  0.41843
## Pred:Res        0.01362  2  0.2051  0.81511
## Hatch:Res       0.03142  1  0.9457  0.33437
## Pred:Hatch:Res  0.01953  2  0.2939  0.74629
## Residuals      2.19252 66
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

So this is really interesting. Now that we have more predictors in the model, the estimate of statistical significance for our Resource treatment has gone from 0.14 when it was analyzed alone to 0.076. It's not below the generally accepted threshold of 0.05, but it is close enough that I think you could argue that *something* is going on. Resources are not having as big of an effect as predators, but they are clearly have some impact on final mass at metamorphosis. We can see this effect if we create a box-and-whisker plot of the data.

```
ggplot(data=RxP.byTank, x=Pred, y=log.Mass.final, fill=Res, geom="boxplot")+theme_cowplot  
( )
```



This clearly shows us that metamorphs emerging from the High resource treatment were generally larger than those emerging from the Low resource treatment, and that this effect is pretty consistent across the three predator treatments (although it is less pronounced in the Lethal predator treatment).

Question 2

Combine your knowledge of predict() and ggplot() to plot an ANCOVA different than that represented by lm5. Make sure it is plotted on the original scale of whatever variables you choose and that it has confidence intervals. Make sure to add interesting colors and useful axes, etc.

Okay, this is a very open ended question. You can pick whichever variables you want! As a reminder, the lm5 was a model that evaluated the effect of Predators on final SVL while controlling for variation in age at metamorphosis. This is known as an Analysis of Covariance, or ANCOVA for short.

```
lm5<-lm(log.SVL.final~log.Age.DPO*Pred, data=RxP.byTank)
```

The assignment has two steps.

1. You need to pick a pair of continuous variables, one to use as a response variable and one to use as your covariate, and one categorical variable. Now, you can't just pick any pair of continuous variables. You need to make sure that the pair make sense together. For example, it would not make much sense to use SVL as

a covariate for age at metamorphosis, since we would generally expect the relationship to go in the other direction (age should effect size, but size would not effect age).

2. You use `predict()` to plot it, like we did while working through the chapter.

I will provide one examples of a possible answer you might get and hopefully that will illuminate how to think about making a figure like this.

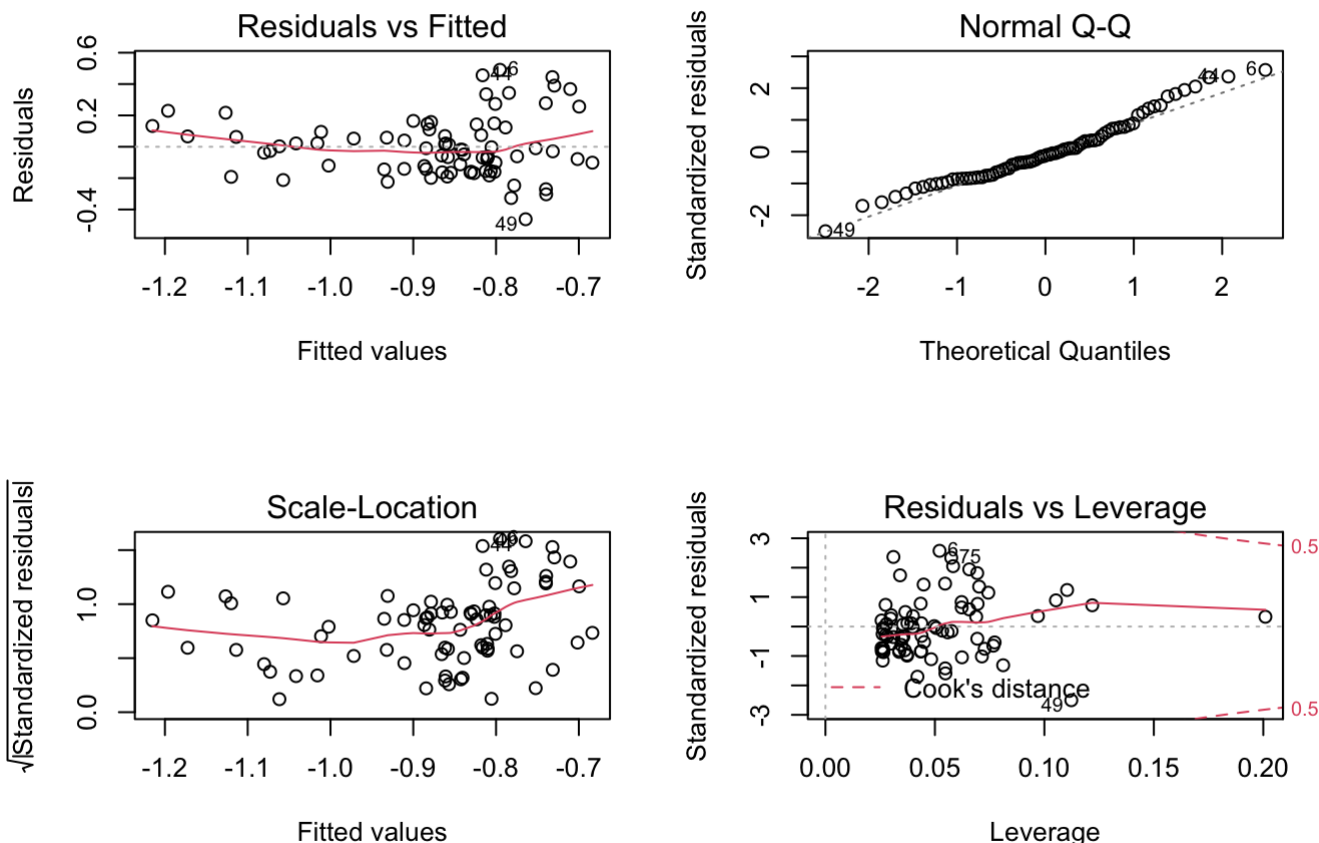
The effect of resources on final mass at metamorphosis, controlling for variation in age at metamorphosis

Perhaps the simplest thing you could do is just to change the response variable. Instead of looking at snout-vent length, let's examine mass. But, to make the example a little more interesting let's use *Res* as our categorical variable instead of *Pred*. The model would look like this. Recall that it is good practice to have your covariate coded before the categorical variable.

```
lm.Age_Res<-lm(log.Mass.final~log.Age.DPO*Res, data=RxP.byTank)
```

Let's look at the diagnostic plots to make sure everything looks okay.

```
par(mfrow=c(2,2));plot(lm.Age_Res)
```



Overall these look great. Next, let's look at the summary of the model and assess significance.

```
summary(lm.Age_Res)
```

```
##
## Call:
## lm(formula = log.Mass.final ~ log.Age.DPO * Res, data = RxP.byTank)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.46215 -0.14395 -0.02316  0.10666  0.49077
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.02029   0.71186   0.029   0.977
## log.Age.DPO   -0.21551   0.17950  -1.201   0.234
## ResLo         0.99534   0.80811   1.232   0.222
## log.Age.DPO:ResLo -0.23531   0.20050  -1.174   0.244
##
## Residual standard error: 0.1959 on 74 degrees of freedom
## Multiple R-squared:  0.2868, Adjusted R-squared:  0.2579
## F-statistic: 9.918 on 3 and 74 DF,  p-value: 1.421e-05
```

```
Anova(lm.Age_Res)
```

```
## Anova Table (Type II tests)
##
## Response: log.Mass.final
##              Sum Sq Df F value    Pr(>F)
## log.Age.DPO    0.98025  1 25.5352 3.037e-06 ***
## Res            0.03562  1  0.9279  0.3385
## log.Age.DPO:Res 0.05287  1  1.3773  0.2443
## Residuals      2.84073 74
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

This is really interesting. First, the summary output shows us that our adjusted R^2 is quite high, 0.2579. That tells us that our predictors collectively explain 25.79% of the variation in metamorph mass. That's not bad, but not nearly as high as when we included *Pred* in the model. Our model as a whole is also highly significant, with a p-value of 0.00001421. We could of course use the model coefficients (under the *Estimate* column) to figure out the intercepts and slopes for the regressions for each resource level, but we are going to use `predict` to do that for us. Let's do that, shall we?

First, let's figure out what the range should be for our x-variable. Recall that, as we did in Chapter 6, we can log-transform the values directly in next step where we create our blank data frame, so we want to know the range of the *raw* data values here.

```
range(RxP.byTank$Age.DPO)
```

```
## [1] 38.11111 140.90244
```

Okay, so the smallest average age at metamorphosis was 38.1 days and the largest was 140.9 days. We'll thus declare our x-axis range as 35–145 days (no harm in putting a little buffer around the data, right?). Next we need to make our “newdata” object for predict to use. We can use **expand.grid()** to make our lives easier.

```
lm.Age_Res.newdata<-expand.grid("log.Age.DPO"=log(35:145), Res=c("Lo","Hi"))
```

Next, use **predict()** to calculate the predicted values and their confidence intervals.

```
lm.Age_Res.predicted<-predict(lm.Age_Res, newdata=lm.Age_Res.newdata, se.fit=T)
str(lm.Age_Res.predicted)
```

```
## List of 4
## $ fit          : Named num [1:222] -0.587 -0.6 -0.612 -0.624 -0.636 ...
## ..- attr(*, "names")= chr [1:222] "1" "2" "3" "4" ...
## $ se.fit       : Named num [1:222] 0.0709 0.0687 0.0665 0.0644 0.0624 ...
## ..- attr(*, "names")= chr [1:222] "1" "2" "3" "4" ...
## $ df           : int 74
## $ residual.scale: num 0.196
```

Recall that since the variables in our model were log-transformed, the predicted fits we just generated are also on a log-scale. Since our goal here is to plot them on the original scale, we need to exponentiate them.

```
#First, exponentiate the fitted values
lm.Age_Res.newdata$predict.SVL<-exp(lm.Age_Res.predicted$fit)
#Next, calculate the upper and lower bounds of the CIs
lm.Age_Res.newdata$predict.SVL.CIupper<-exp(lm.Age_Res.predicted$fit+lm.Age_Res.predicted$se.fit)
lm.Age_Res.newdata$predict.SVL.CIlower<-exp(lm.Age_Res.predicted$fit-lm.Age_Res.predicted$se.fit)
#Lastly, exponentiate the age data so it is back on the original scale
lm.Age_Res.newdata$Age.DPO<-exp(lm.Age_Res.newdata$log.Age.DPO)
lm.Age_Res.newdata
```

##	log.Age.DPO	Res	predict.SVL	predict.SVL.CIupper	predict.SVL.CIlower	Age.DPO
## 1	3.555348	Lo	0.5558793	0.5967481	0.5178094	35
## 2	3.583519	Lo	0.5488642	0.5878942	0.5124254	36
## 3	3.610918	Lo	0.5421263	0.5794197	0.5072333	37
## 4	3.637586	Lo	0.5356476	0.5712995	0.5022205	38
## 5	3.663562	Lo	0.5294115	0.5635109	0.4973756	39
## 6	3.688879	Lo	0.5234033	0.5560334	0.4926880	40
## 7	3.713572	Lo	0.5176091	0.5488482	0.4881480	41
## 8	3.737670	Lo	0.5120163	0.5419381	0.4837466	42
## 9	3.761200	Lo	0.5066135	0.5352874	0.4794756	43
## 10	3.784190	Lo	0.5013900	0.5288818	0.4753272	44
## 11	3.806662	Lo	0.4963359	0.5227080	0.4712944	45
## 12	3.828641	Lo	0.4914422	0.5167540	0.4673703	46
## 13	3.850148	Lo	0.4867005	0.5110084	0.4635489	47
## 14	3.871201	Lo	0.4821029	0.5054611	0.4598241	48
## 15	3.891820	Lo	0.4776422	0.5001024	0.4561907	49
## 16	3.912023	Lo	0.4733117	0.4949237	0.4526434	50
## 17	3.931826	Lo	0.4691050	0.4899167	0.4491774	51
## 18	3.951244	Lo	0.4650163	0.4850738	0.4457882	52
## 19	3.970292	Lo	0.4610402	0.4803881	0.4424715	53
## 20	3.988984	Lo	0.4571714	0.4758529	0.4392233	54
## 21	4.007333	Lo	0.4534052	0.4714622	0.4360398	55
## 22	4.025352	Lo	0.4497370	0.4672102	0.4329173	56
## 23	4.043051	Lo	0.4461627	0.4630915	0.4298527	57
## 24	4.060443	Lo	0.4426782	0.4591012	0.4268426	58
## 25	4.077537	Lo	0.4392798	0.4552344	0.4238843	59
## 26	4.094345	Lo	0.4359639	0.4514865	0.4209750	60
## 27	4.110874	Lo	0.4327273	0.4478534	0.4181121	61
## 28	4.127134	Lo	0.4295667	0.4443307	0.4152933	62
## 29	4.143135	Lo	0.4264793	0.4409147	0.4125165	63
## 30	4.158883	Lo	0.4234621	0.4376013	0.4097797	64
## 31	4.174387	Lo	0.4205126	0.4343870	0.4070813	65
## 32	4.189655	Lo	0.4176282	0.4312681	0.4044196	66
## 33	4.204693	Lo	0.4148065	0.4282410	0.4017934	67
## 34	4.219508	Lo	0.4120452	0.4253024	0.3992013	68
## 35	4.234107	Lo	0.4093423	0.4224488	0.3966423	69
## 36	4.248495	Lo	0.4066956	0.4196770	0.3941156	70
## 37	4.262680	Lo	0.4041031	0.4169837	0.3916205	71
## 38	4.276666	Lo	0.4015632	0.4143657	0.3891562	72
## 39	4.290459	Lo	0.3990738	0.4118199	0.3867223	73
## 40	4.304065	Lo	0.3966335	0.4093434	0.3843183	74
## 41	4.317488	Lo	0.3942406	0.4069332	0.3819438	75
## 42	4.330733	Lo	0.3918935	0.4045865	0.3795987	76
## 43	4.343805	Lo	0.3895908	0.4023005	0.3772826	77
## 44	4.356709	Lo	0.3873311	0.4000726	0.3749953	78
## 45	4.369448	Lo	0.3851130	0.3979002	0.3727367	79
## 46	4.382027	Lo	0.3829353	0.3957809	0.3705065	80
## 47	4.394449	Lo	0.3807967	0.3937124	0.3683047	81
## 48	4.406719	Lo	0.3786961	0.3916924	0.3661309	82
## 49	4.418841	Lo	0.3766323	0.3897189	0.3639851	83
## 50	4.430817	Lo	0.3746043	0.3877898	0.3618671	84
## 51	4.442651	Lo	0.3726110	0.3859033	0.3597766	85
## 52	4.454347	Lo	0.3706515	0.3840574	0.3577135	86

## 53	4.465908	Lo	0.3687247	0.3822506	0.3556774	87
## 54	4.477337	Lo	0.3668298	0.3804812	0.3536682	88
## 55	4.488636	Lo	0.3649659	0.3787476	0.3516856	89
## 56	4.499810	Lo	0.3631321	0.3770485	0.3497293	90
## 57	4.510860	Lo	0.3613277	0.3753825	0.3477990	91
## 58	4.521789	Lo	0.3595517	0.3737483	0.3458945	92
## 59	4.532599	Lo	0.3578036	0.3721446	0.3440153	93
## 60	4.543295	Lo	0.3560826	0.3705704	0.3421611	94
## 61	4.553877	Lo	0.3543879	0.3690246	0.3403317	95
## 62	4.564348	Lo	0.3527189	0.3675061	0.3385266	96
## 63	4.574711	Lo	0.3510749	0.3660139	0.3367456	97
## 64	4.584967	Lo	0.3494553	0.3645472	0.3349881	98
## 65	4.595120	Lo	0.3478595	0.3631051	0.3332540	99
## 66	4.605170	Lo	0.3462870	0.3616868	0.3315428	100
## 67	4.615121	Lo	0.3447371	0.3602915	0.3298542	101
## 68	4.624973	Lo	0.3432093	0.3589184	0.3281877	102
## 69	4.634729	Lo	0.3417030	0.3575669	0.3265430	103
## 70	4.644391	Lo	0.3402179	0.3562362	0.3249198	104
## 71	4.653960	Lo	0.3387533	0.3549258	0.3233177	105
## 72	4.663439	Lo	0.3373088	0.3536350	0.3217363	106
## 73	4.672829	Lo	0.3358840	0.3523633	0.3201753	107
## 74	4.682131	Lo	0.3344783	0.3511102	0.3186343	108
## 75	4.691348	Lo	0.3330914	0.3498750	0.3171129	109
## 76	4.700480	Lo	0.3317229	0.3486573	0.3156109	110
## 77	4.709530	Lo	0.3303722	0.3474567	0.3141278	111
## 78	4.718499	Lo	0.3290391	0.3462726	0.3126634	112
## 79	4.727388	Lo	0.3277232	0.3451046	0.3112172	113
## 80	4.736198	Lo	0.3264241	0.3439524	0.3097890	114
## 81	4.744932	Lo	0.3251413	0.3428154	0.3083785	115
## 82	4.753590	Lo	0.3238747	0.3416934	0.3069853	116
## 83	4.762174	Lo	0.3226238	0.3405859	0.3056091	117
## 84	4.770685	Lo	0.3213883	0.3394926	0.3042496	118
## 85	4.779123	Lo	0.3201680	0.3384131	0.3029065	119
## 86	4.787492	Lo	0.3189624	0.3373472	0.3015795	120
## 87	4.795791	Lo	0.3177713	0.3362944	0.3002684	121
## 88	4.804021	Lo	0.3165944	0.3352546	0.2989728	122
## 89	4.812184	Lo	0.3154314	0.3342273	0.2976925	123
## 90	4.820282	Lo	0.3142820	0.3332124	0.2964271	124
## 91	4.828314	Lo	0.3131461	0.3322095	0.2951765	125
## 92	4.836282	Lo	0.3120232	0.3312184	0.2939404	126
## 93	4.844187	Lo	0.3109132	0.3302388	0.2927184	127
## 94	4.852030	Lo	0.3098157	0.3292705	0.2915105	128
## 95	4.859812	Lo	0.3087307	0.3283132	0.2903162	129
## 96	4.867534	Lo	0.3076578	0.3273668	0.2891354	130
## 97	4.875197	Lo	0.3065968	0.3264309	0.2879679	131
## 98	4.882802	Lo	0.3055475	0.3255053	0.2868133	132
## 99	4.890349	Lo	0.3045096	0.3245900	0.2856716	133
## 100	4.897840	Lo	0.3034831	0.3236845	0.2845424	134
## 101	4.905275	Lo	0.3024675	0.3227889	0.2834255	135
## 102	4.912655	Lo	0.3014629	0.3219028	0.2823208	136
## 103	4.919981	Lo	0.3004688	0.3210261	0.2812280	137
## 104	4.927254	Lo	0.2994853	0.3201585	0.2801470	138
## 105	4.934474	Lo	0.2985121	0.3193000	0.2790775	139
## 106	4.941642	Lo	0.2975489	0.3184504	0.2780193	140

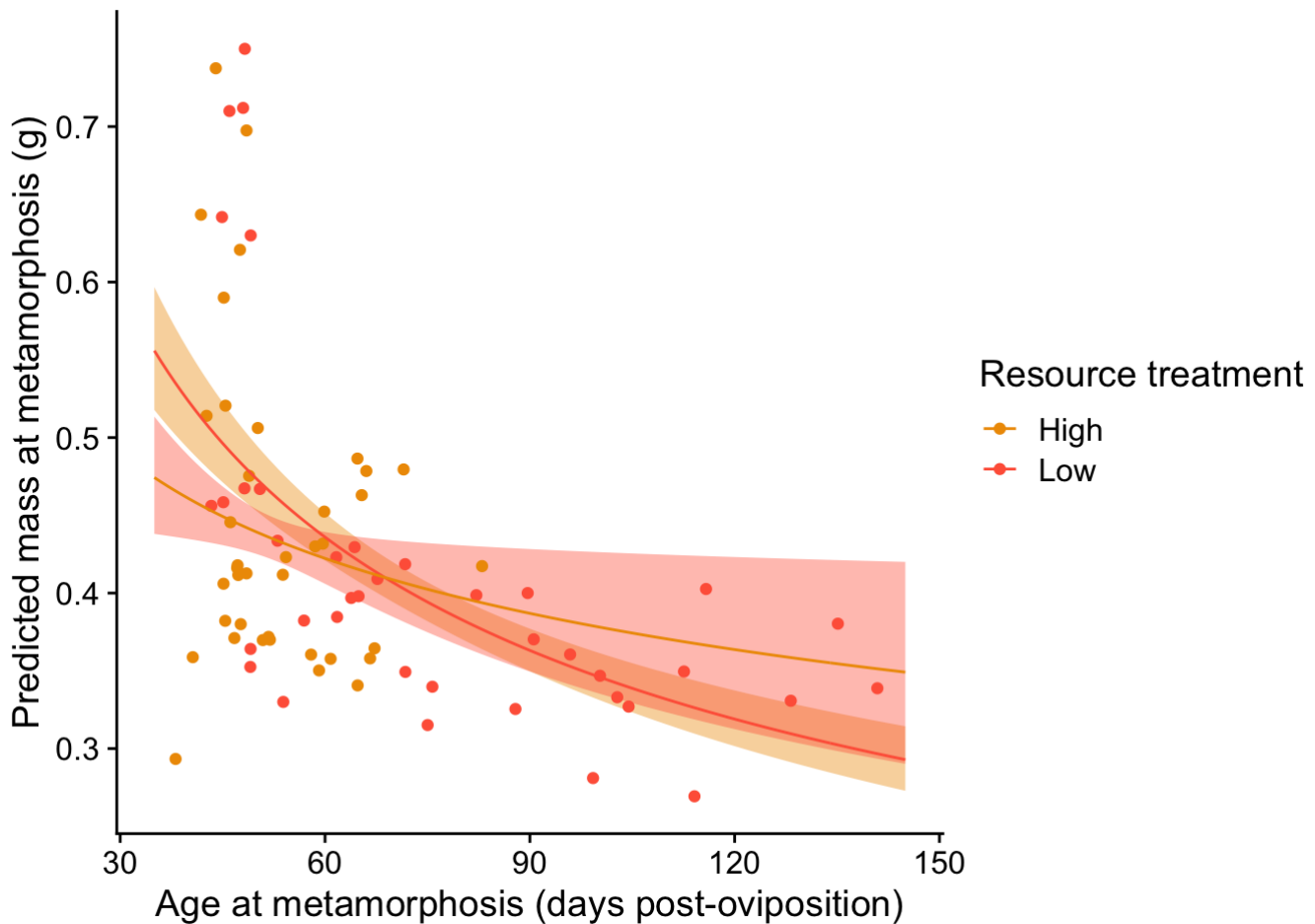
## 107	4.948760	Lo	0.2965957	0.3176094	0.2769722	141
## 108	4.955827	Lo	0.2956522	0.3167770	0.2759362	142
## 109	4.962845	Lo	0.2947184	0.3159530	0.2749109	143
## 110	4.969813	Lo	0.2937939	0.3151371	0.2738962	144
## 111	4.976734	Lo	0.2928787	0.3143294	0.2728919	145
## 112	3.555348	Hi	0.4742884	0.5134944	0.4380758	35
## 113	3.583519	Hi	0.4714176	0.5080343	0.4374400	36
## 114	3.610918	Hi	0.4686421	0.5028086	0.4367973	37
## 115	3.637586	Hi	0.4659564	0.4978067	0.4361439	38
## 116	3.663562	Hi	0.4633552	0.4930195	0.4354757	39
## 117	3.688879	Hi	0.4608338	0.4884401	0.4347879	40
## 118	3.713572	Hi	0.4583880	0.4840629	0.4340749	41
## 119	3.737670	Hi	0.4560136	0.4798845	0.4333301	42
## 120	3.761200	Hi	0.4537069	0.4759029	0.4325461	43
## 121	3.784190	Hi	0.4514645	0.4721185	0.4317142	44
## 122	3.806662	Hi	0.4492833	0.4685331	0.4308243	45
## 123	3.828641	Hi	0.4471602	0.4651506	0.4298655	46
## 124	3.850148	Hi	0.4450924	0.4619762	0.4288257	47
## 125	3.871201	Hi	0.4430775	0.4590160	0.4276924	48
## 126	3.891820	Hi	0.4411129	0.4562759	0.4264538	49
## 127	3.912023	Hi	0.4391965	0.4537605	0.4251000	50
## 128	3.931826	Hi	0.4373261	0.4514713	0.4236241	51
## 129	3.951244	Hi	0.4354998	0.4494055	0.4220244	52
## 130	3.970292	Hi	0.4337156	0.4475551	0.4203041	53
## 131	3.988984	Hi	0.4319720	0.4459072	0.4184722	54
## 132	4.007333	Hi	0.4302671	0.4444448	0.4165416	55
## 133	4.025352	Hi	0.4285995	0.4431484	0.4145283	56
## 134	4.043051	Hi	0.4269677	0.4419977	0.4124489	57
## 135	4.060443	Hi	0.4253704	0.4409730	0.4103198	58
## 136	4.077537	Hi	0.4238062	0.4400562	0.4081562	59
## 137	4.094345	Hi	0.4222738	0.4392313	0.4059711	60
## 138	4.110874	Hi	0.4207722	0.4384844	0.4037755	61
## 139	4.127134	Hi	0.4193003	0.4378039	0.4015787	62
## 140	4.143135	Hi	0.4178569	0.4371798	0.3993881	63
## 141	4.158883	Hi	0.4164411	0.4366039	0.3972094	64
## 142	4.174387	Hi	0.4150519	0.4360695	0.3950474	65
## 143	4.189655	Hi	0.4136885	0.4355709	0.3929055	66
## 144	4.204693	Hi	0.4123500	0.4351033	0.3907865	67
## 145	4.219508	Hi	0.4110355	0.4346629	0.3886924	68
## 146	4.234107	Hi	0.4097443	0.4342463	0.3866248	69
## 147	4.248495	Hi	0.4084757	0.4338508	0.3845847	70
## 148	4.262680	Hi	0.4072289	0.4334739	0.3825728	71
## 149	4.276666	Hi	0.4060032	0.4331138	0.3805896	72
## 150	4.290459	Hi	0.4047981	0.4327687	0.3786353	73
## 151	4.304065	Hi	0.4036129	0.4324372	0.3767099	74
## 152	4.317488	Hi	0.4024470	0.4321179	0.3748134	75
## 153	4.330733	Hi	0.4012998	0.4318099	0.3729455	76
## 154	4.343805	Hi	0.4001709	0.4315120	0.3711060	77
## 155	4.356709	Hi	0.3990596	0.4312236	0.3692946	78
## 156	4.369448	Hi	0.3979655	0.4309438	0.3675109	79
## 157	4.382027	Hi	0.3968881	0.4306720	0.3657544	80
## 158	4.394449	Hi	0.3958270	0.4304077	0.3640246	81
## 159	4.406719	Hi	0.3947816	0.4301503	0.3623211	82
## 160	4.418841	Hi	0.3937517	0.4298993	0.3606435	83

##	161	4.430817	Hi	0.3927367	0.4296544	0.3589911	84
##	162	4.442651	Hi	0.3917363	0.4294152	0.3573635	85
##	163	4.454347	Hi	0.3907501	0.4291813	0.3557602	86
##	164	4.465908	Hi	0.3897778	0.4289525	0.3541807	87
##	165	4.477337	Hi	0.3888189	0.4287285	0.3526244	88
##	166	4.488636	Hi	0.3878732	0.4285090	0.3510909	89
##	167	4.499810	Hi	0.3869403	0.4282937	0.3495797	90
##	168	4.510860	Hi	0.3860199	0.4280826	0.3480903	91
##	169	4.521789	Hi	0.3851118	0.4278753	0.3466223	92
##	170	4.532599	Hi	0.3842156	0.4276717	0.3451750	93
##	171	4.543295	Hi	0.3833310	0.4274717	0.3437482	94
##	172	4.553877	Hi	0.3824577	0.4272750	0.3423414	95
##	173	4.564348	Hi	0.3815956	0.4270816	0.3409541	96
##	174	4.574711	Hi	0.3807443	0.4268914	0.3395858	97
##	175	4.584967	Hi	0.3799037	0.4267041	0.3382363	98
##	176	4.595120	Hi	0.3790734	0.4265196	0.3369050	99
##	177	4.605170	Hi	0.3782532	0.4263380	0.3355916	100
##	178	4.615121	Hi	0.3774429	0.4261590	0.3342957	101
##	179	4.624973	Hi	0.3766423	0.4259826	0.3330170	102
##	180	4.634729	Hi	0.3758512	0.4258087	0.3317549	103
##	181	4.644391	Hi	0.3750694	0.4256372	0.3305093	104
##	182	4.653960	Hi	0.3742967	0.4254680	0.3292798	105
##	183	4.663439	Hi	0.3735329	0.4253011	0.3280659	106
##	184	4.672829	Hi	0.3727777	0.4251363	0.3268675	107
##	185	4.682131	Hi	0.3720311	0.4249736	0.3256841	108
##	186	4.691348	Hi	0.3712929	0.4248130	0.3245155	109
##	187	4.700480	Hi	0.3705628	0.4246544	0.3233613	110
##	188	4.709530	Hi	0.3698408	0.4244977	0.3222213	111
##	189	4.718499	Hi	0.3691266	0.4243429	0.3210952	112
##	190	4.727388	Hi	0.3684202	0.4241900	0.3199827	113
##	191	4.736198	Hi	0.3677213	0.4240388	0.3188835	114
##	192	4.744932	Hi	0.3670298	0.4238893	0.3177973	115
##	193	4.753590	Hi	0.3663456	0.4237415	0.3167240	116
##	194	4.762174	Hi	0.3656685	0.4235954	0.3156632	117
##	195	4.770685	Hi	0.3649984	0.4234508	0.3146147	118
##	196	4.779123	Hi	0.3643352	0.4233078	0.3135783	119
##	197	4.787492	Hi	0.3636787	0.4231664	0.3125537	120
##	198	4.795791	Hi	0.3630289	0.4230264	0.3115407	121
##	199	4.804021	Hi	0.3623855	0.4228879	0.3105391	122
##	200	4.812184	Hi	0.3617485	0.4227508	0.3095488	123
##	201	4.820282	Hi	0.3611178	0.4226151	0.3085693	124
##	202	4.828314	Hi	0.3604932	0.4224807	0.3076007	125
##	203	4.836282	Hi	0.3598747	0.4223477	0.3066426	126
##	204	4.844187	Hi	0.3592621	0.4222159	0.3056949	127
##	205	4.852030	Hi	0.3586553	0.4220855	0.3047573	128
##	206	4.859812	Hi	0.3580543	0.4219563	0.3038298	129
##	207	4.867534	Hi	0.3574589	0.4218283	0.3029121	130
##	208	4.875197	Hi	0.3568691	0.4217015	0.3020040	131
##	209	4.882802	Hi	0.3562847	0.4215758	0.3011055	132
##	210	4.890349	Hi	0.3557057	0.4214513	0.3002162	133
##	211	4.897840	Hi	0.3551319	0.4213280	0.2993361	134
##	212	4.905275	Hi	0.3545633	0.4212057	0.2984649	135
##	213	4.912655	Hi	0.3539998	0.4210845	0.2976026	136
##	214	4.919981	Hi	0.3534413	0.4209644	0.2967490	137

##	215	4.927254	Hi	0.3528878	0.4208453	0.2959040	138
##	216	4.934474	Hi	0.3523391	0.4207272	0.2950673	139
##	217	4.941642	Hi	0.3517952	0.4206102	0.2942389	140
##	218	4.948760	Hi	0.3512560	0.4204941	0.2934185	141
##	219	4.955827	Hi	0.3507214	0.4203790	0.2926062	142
##	220	4.962845	Hi	0.3501914	0.4202648	0.2918017	143
##	221	4.969813	Hi	0.3496658	0.4201516	0.2910049	144
##	222	4.976734	Hi	0.3491447	0.4200393	0.2902158	145

Okay, now we are ready to plot these data and visualize the effects (or lack thereof) of resources and age on mass at metamorphosis. We will use **ggplot2** here, specifically plotting with the **ggplot()** function. The code below follows the exact same logic as that from Chapter 6. We first define the basic aesthetics of the figure with the **ggplot()** function, then customize what all we want to add to the figure (the ribbon, the points, the lines, the fills and colors, the x-axis and y-axis labels, and that we want to apply the cowplot theme). Easy peasy!

```
ggplot(data=RxP.byTank, aes(x=Age.DPO, y=Mass.final, col=Res))+
  geom_ribbon(data=lm.Age_Res.newdata, inherit.aes=F, aes(x=Age.DPO, ymax=predict.SVL.CI
upper, ymin=predict.SVL.CIlower, fill=Res), alpha=0.4)+
  geom_point()+
  geom_line(data=lm.Age_Res.newdata, inherit.aes=F, aes(x=Age.DPO, y=predict.SVL, col=Re
s))+
  scale_fill_manual(values=c("orange2","tomato1"), guide="none")+
  scale_color_manual(values=c("orange2","tomato1"), labels=c("High","Low"), name="Resour
ce treatment")+
  ylab("Predicted mass at metamorphosis (g)")+
  xlab("Age at metamorphosis (days post-oviposition)")+
  theme_cowplot()
```



Doesn't that figure look nice! I think so.

Question 3

Explore the statistical analyses shown here but with different interactions. Pick two different questions to ask. There are lots of questions you can ask! Just make sure that you are clear about what question you are asking and then conduct the analysis to answer it.

There are many different questions you could ask here, so this is once again a very open ended assignment. Here are just two possibilities.

Do Hatching age and Predator treatment effect the length of the tail remaining when froglets crawl out of the water?

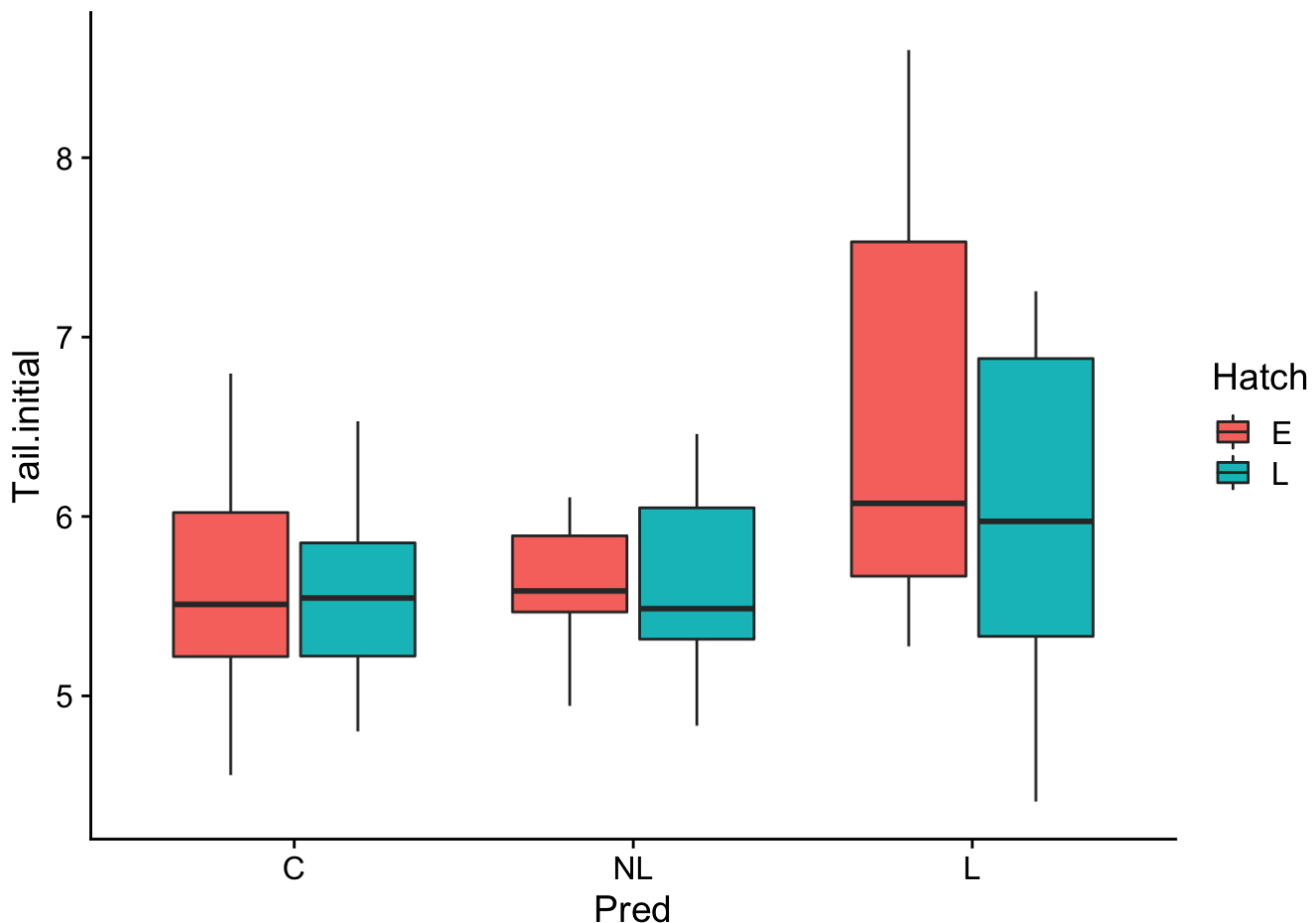
To understand this question, let's think a little bit about the biology of an amphibian. When a tadpole is turning into a frog (what we call metamorphosis) one of the changes it goes through is that it resorbs the tail into the body. The tail essentially serves as energy for completing all of the morphological changes that are occurring during this time. Since the tail is generally long, it takes a little while for the froglet to resorb it and the transforming froglet can make a choice (to a certain degree) about when to crawl out of the water. As soon as the tadpole develops arms, its ability to swim is greatly hampered. Thus, staying in the water is a dangerous proposition. However, having a long tail on land is also dangerous, because it means the new little froglet will be less able to jump and avoid predators. Thus, you might predict that if the water is safe, you should stay put as

long as possible and complete as much of metamorphosis as possible before entering the scary new terrestrial world. On the flip side, if there is eminent danger in the water, you probably want to get out and take your chances on land. Let's see how the different predator treatments (remember, one of the treatments is a real live lethal predator swimming around in the tank) and hatching age might affect the size of the tail when we collected froglets the morning after they had crawled out of the water. Longer tails would imply that they left the water earlier in the window of metamorphosis, whereas shorter tails would imply they stayed put longer.

```
lm.tail<-lm(Tail.initial~Hatch*Pred, data=RxP.byTank)
Anova(lm.tail)
```

```
## Anova Table (Type II tests)
##
## Response: Tail.initial
##           Sum Sq Df F value    Pr(>F)
## Hatch      0.920  1  1.5241 0.2210101
## Pred      9.298  2  7.7018 0.0009309 ***
## Hatch:Pred 1.334  2  1.1054 0.3366458
## Residuals 43.459 72
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
qplot(data=RxP.byTank, x=Pred, y=Tail.initial, fill=Hatch, geom="boxplot")+theme_cowplot
()
```



Very interesting. The **Anova()** results show us that there is a highly significant effect of predator treatment, but no effect of hatching age, on tail length at metamorphosis. By looking at the boxplots, we can see (even without running the necessary post-hoc tests) that this is being driven by the lethal predator treatment. As we might have expected, froglets collected from tanks with lethal predators had longer tails than froglets from either control tanks or tanks with caged, nonlethal predators. That last point is also particularly interesting, since it implies that the metamorphosing froglets in the tank are not sensing the nonlethal predators to be as big a risk as the lethal predators.

Is the amount of time needed to resorb the tail influenced by how long the tail was when froglets crawled out of the water and the Predator or Resource treatment?

We certainly might expect that there would be a positive relationship between how long a froglets tail is when it leaves the water and how long it takes to resorb that tail into the body. But is there an effect of predators or resources? We might imagine that an animal that is “skinnier” or has fewer fat reserves would resorb the tail faster, whereas an animal that is more robust would resorb it more slowly. We know that predators affect the size of froglets at metamorphosis (presumably because they eat some of the tadpoles in the tank, thereby leaving more food for the survivors) and so it is possible that they might affect the energy reserves of the animals too.

Below I’ve made an ANCOVA with two categorical predictors, which allows us to see if there are effects of predators, resources, or if they interact, as well if any of them interact with the size of the tail when we first caught the froglets.

```
lm.resorb<-lm(Resorb.days~Tail.initial*Pred*Res, data=RxP.byTank)
Anova(lm.resorb)
```

```
## Anova Table (Type II tests)
##
## Response: Resorb.days
##
##           Sum Sq Df F value    Pr(>F)
## Tail.initial  11.1528  1  78.2841 8.106e-13 ***
## Pred           0.3255  2   1.1423 0.3253039
## Res           2.3333  1  16.3783 0.0001386 ***
## Tail.initial:Pred  0.5246  2   1.8411 0.1667014
## Tail.initial:Res  0.7083  1   4.9719 0.0291689 *
## Pred:Res        0.2546  2   0.8936 0.4140563
## Tail.initial:Pred:Res  0.0279  2   0.0981 0.9067010
## Residuals      9.4027 66
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The **Anova()** results demonstrate that the time needed to resorb the tail is affected by the size of the tail at emergence, the resource treatment of the tadpoles, and the interaction between them. There is clearly no effect of predator treatment, so if we wanted we could reduce the model to what is known as the *minimal adequate model*, an idea popularized by Michael Crawley in his excellent book, *The R Book*. This will give us the most accurate estimates of predictor significance. To do so, we would remove the nonsignificant predictor (in this case, *Pred*) from the model, like so.

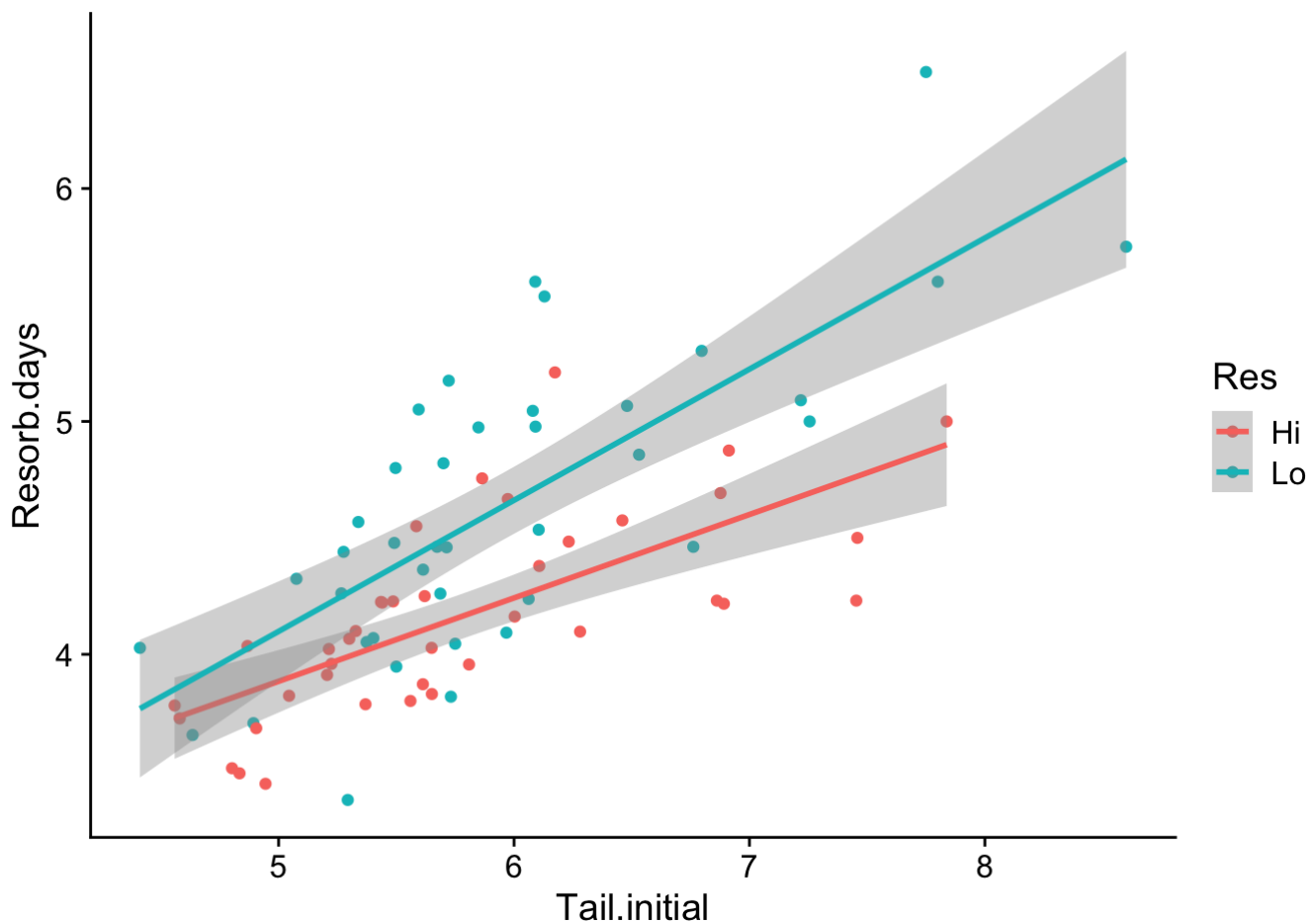
```
lm.resorb<-lm(Resorb.days~Tail.initial*Res, data=RxP.byTank)
Anova(lm.resorb)
```

```
## Anova Table (Type II tests)
##
## Response: Resorb.days
##           Sum Sq Df F value    Pr(>F)
## Tail.initial  11.8299  1  83.2142 9.782e-14 ***
## Res           2.9483  1  20.7391 2.029e-05 ***
## Tail.initial:Res  0.5698  1  4.0082  0.04894 *
## Residuals     10.5200 74
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We can see that all three effects are still significant, and that the p-value for the interaction has increased a bit. FYI, these are the numbers you would want to publish if you were doing so. Now, let's visualize these effects!

```
qplot(data=RxP.byTank, x=Tail.initial, y=Resorb.days, col=Res, geom="point")+geom_smooth(
method="lm")+theme_cowplot()
```

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



So this implies that as expected, longer initial tails take more days to resorb but that frogs from Low resource treatments resorb them more slowly than do froglets from High resource treatments, and that the slopes of the regressions are not the same (which is what the interaction tells us). How interesting!

But wait! Oh no, we never checked our variables *Tail.initial* and *Resorb.days* for normality!! We better do so before we draw any hard conclusions about our data.

```
#Check normality of Tail.initial with a Shapiro-Wilks test
shapiro.test(RxP.byTank$Tail.initial)
```

```
##
## Shapiro-Wilk normality test
##
## data: RxP.byTank$Tail.initial
## W = 0.93824, p-value = 0.0009202
```

```
shapiro.test(log(RxP.byTank$Tail.initial))
```

```
##
## Shapiro-Wilk normality test
##
## data: log(RxP.byTank$Tail.initial)
## W = 0.96978, p-value = 0.06045
```

```
#Check normality of Resorb.days with a Shapiro-Wilks test
shapiro.test(RxP.byTank$Resorb.days)
```

```
##
## Shapiro-Wilk normality test
##
## data: RxP.byTank$Resorb.days
## W = 0.95378, p-value = 0.006556
```

```
shapiro.test(log(RxP.byTank$Resorb.days))
```

```
##
## Shapiro-Wilk normality test
##
## data: log(RxP.byTank$Resorb.days)
## W = 0.98023, p-value = 0.2668
```

In both cases, the data are significantly not normal and log-transforming the data makes them normal. Let's see what effect that has on our model and interpretation. Remember that you can just log-transform a variable directly in the model without actually coding it into the data frame.

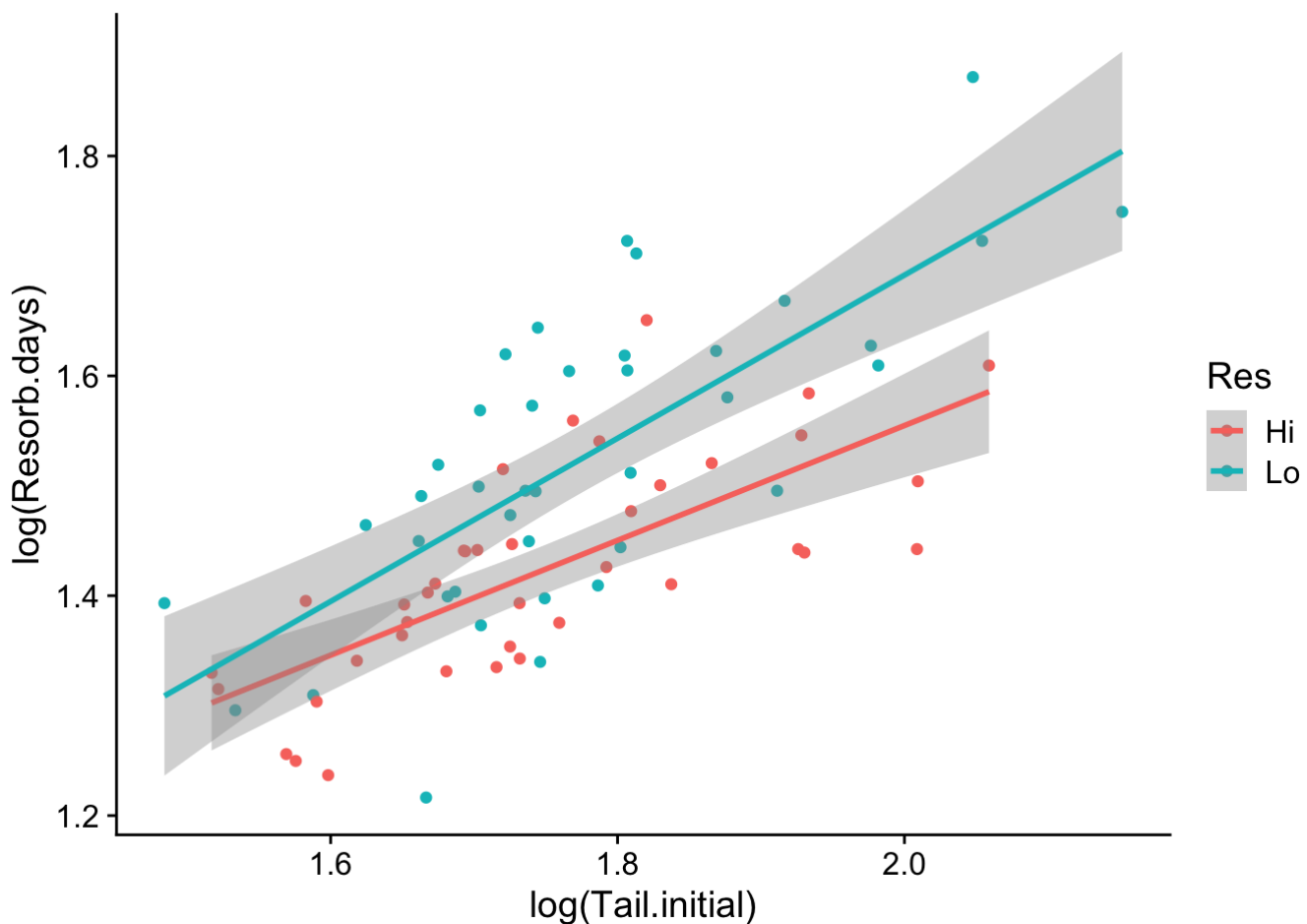
```
lm.resorb2<-lm(log(Resorb.days)~log(Tail.initial)*Res, data=RxP.byTank)
Anova(lm.resorb2)
```

```
## Anova Table (Type II tests)
##
## Response: log(Resorb.days)
##           Sum Sq Df F value    Pr(>F)
## log(Tail.initial)  0.58309  1  84.7679 6.771e-14 ***
## Res                0.13602  1  19.7735 3.014e-05 ***
## log(Tail.initial):Res 0.01754  1  2.5504  0.1145
## Residuals         0.50903  74
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Log-transforming the continuous variables clearly had effect. The interaction between initial tail length and resource treatment is no longer significant. We can visualize these effects quite easily.

```
qplot(data=RxP.byTank, x=log(Tail.initial), y=log(Resorb.days), col=Res, geom="point")+g
eom_smooth(method="lm")+theme_cowplot()
```

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



Taking together the statistical results and the figure, we can interpret this to mean that there is an effect of initial tail length on tail to resorb the tail (longer tails take longer to resorb) and that froglets from low resource tanks resorb their tails more slowly across the board (the slopes are not significantly different between the low and high resource animals).