Two Lines, Different Slopes (Crocodiles Continued)

We have measurements of the head length (cm) and total body length (cm) of 32 crocodiles of two different species:

```
head(crocs, 3)
##
     Body Head
                  Species
## 1 338 52.0
                   Indian
## 2 333 48.0 Australian
## 3 202 38.3
                   Indian
2 lines by filtering to create separate data sets
aus_crocs <- crocs %>% filter(Species == "Australian")
aus_fit <- lm(Head ~ Body, data = aus_crocs)</pre>
summary(aus_fit)
##
## Call:
## lm(formula = Head ~ Body, data = aus_crocs)
## Residuals:
##
                1Q Median
                                3Q
      \mathtt{Min}
                                       Max
## -2.3529 -0.9968 0.0824 0.7419
                                    2.7973
##
## Coefficients:
##
               Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.463022
                          1.523732
                                     2.273
                                            0.0407 *
## Body
               0.125344
                          0.004819 26.010 1.35e-12 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.504 on 13 degrees of freedom
## Multiple R-squared: 0.9811, Adjusted R-squared: 0.9797
## F-statistic: 676.5 on 1 and 13 DF, p-value: 1.35e-12
ind crocs <- crocs %>% filter(Species == "Indian")
ind_fit <- lm(Head ~ Body, data = ind_crocs)</pre>
summary(ind_fit)
##
## Call:
## lm(formula = Head ~ Body, data = ind_crocs)
##
## Residuals:
##
       Min
                1Q Median
                                ЗQ
                                       Max
  -4.5756 -1.6627 -0.0904 1.2208
##
## Coefficients:
##
                Estimate Std. Error t value Pr(>|t|)
## (Intercept) 10.538438
                           1.861787
                                       5.66 4.53e-05 ***
## Body
                0.131304
                           0.005791
                                      22.68 5.08e-13 ***
##
  ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 2.503 on 15 degrees of freedom
## Multiple R-squared: 0.9717, Adjusted R-squared: 0.9698
## F-statistic: 514.2 on 1 and 15 DF, p-value: 5.08e-13
```

1 model, 2 lines (different slopes)

ggplot(data = crocs) +

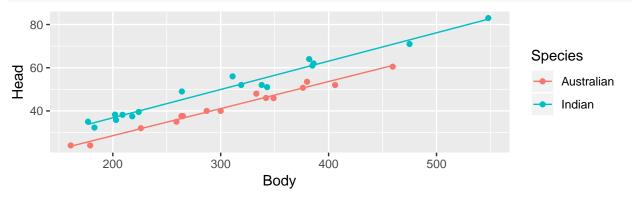
• Last class we used this code to fit 2 lines with the same slope:

```
parallel_lines_fit <- lm(Head ~ Body + Species, data = crocs)</pre>
```

• To allow for different slopes, use * instead of +

```
two_lines_fit <- lm(Head ~ Body * Species, data = crocs)
summary(two_lines_fit)</pre>
```

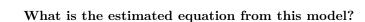
```
##
## Call:
## lm(formula = Head ~ Body * Species, data = crocs)
## Residuals:
##
      Min
                1Q Median
  -4.5756 -1.3294 -0.0040 0.9646
                                    4.6261
##
##
  Coefficients:
##
                      Estimate Std. Error t value Pr(>|t|)
## (Intercept)
                      3.463022
                                 2.126572
                                            1.628
                                                    0.1146
## Body
                      0.125344
                                 0.006726
                                           18.637
                                                    <2e-16 ***
## SpeciesIndian
                      7.075415
                                 2.638253
                                            2.682
                                                    0.0121 *
## Body:SpeciesIndian 0.005959
                                 0.008296
                                            0.718
                                                    0.4785
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.099 on 28 degrees of freedom
## Multiple R-squared: 0.9775, Adjusted R-squared: 0.975
## F-statistic: 404.6 on 3 and 28 DF, p-value: < 2.2e-16
crocs <- crocs %>%
  mutate(
   fitted = predict(two_lines_fit)
```

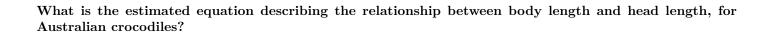


• Recall that SpeciesIndian is an indicator variable defined as:

geom_point(mapping = aes(x = Body, y = Head, color = Species)) +
geom_line(mapping = aes(x = Body, y = fitted, color = Species))

$${\tt SpeciesIndian} = \begin{cases} 1 & \text{if the species for crocodile i is Indian.} \\ 0 & \text{otherwise (in this case, the species is Australian)} \end{cases}$$





What is the estimated equation describing the relationship between body length and head length, for Indian crocodiles?

What is the interpretation of $\widehat{\beta}_0 = 3.463$?

What is the interpretation of
$$\widehat{\beta}_1 = 7.075$$
?

What is the interpretation of
$$\hat{\beta}_2 = 0.125$$
?

What is the interpretation of $\hat{\beta}_3 = 0.006$?

Using the output from the summary function, conduct a test of the claim that the slope of the line describing the relationship between body length and head length in the population of all Australian crocodiles is the same as the slope of the line describing the relationship between body length and head length in the population of all Indian crocodiles.