

Biostatistics I: Linear Regression

Effect Plots

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The Multiple Linear Regression Model

$$y_i = f(\mathbf{x}_i)^\top \boldsymbol{\beta} + \varepsilon_i \quad E(\varepsilon_i) = \mathbf{0}, \quad \text{var}(\varepsilon) = \sigma^2 \mathbf{I}$$

Interpretation:

β_j is the expected change in y that is associated with an increase in x_j (or $f(x_j)$) of 1 unit **while all other covariates are kept constant.**

⇒ The interpretation of the coefficients of each of the covariate terms is **independent of all other covariate terms.**

But:

When the model includes **interaction terms** or **non-linear effects** that involve multiple coefficients for the same variable, the corresponding regression coefficients **cannot be interpreted independently.**

Example: Child Growth

```
library("splines")
mod1 <- lm(weight ~ ns(age, df = 3) * sex + height + race + kcal_sd, data = child)
```

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```
library("splines")
mod1 <- lm(weight ~ ns(age, df = 3) * sex + height + race + kcal_sd, data = child)
```

```
summary(mod1)
```

```
## [...]
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t| )
## (Intercept)                 8.8194   5.0408   1.75   0.081 .
## ns(age, df = 3)1            32.0575   4.1071   7.81  5.6e-14 ***
## ns(age, df = 3)2            50.0534   7.2659   6.89  2.3e-11 ***
## ns(age, df = 3)3            51.2129   4.2022  12.19 < 2e-16 ***
## sexgirl                     -2.3740   2.1136  -1.12   0.262
## height                      0.0862   0.0539   1.60   0.111
## raceasian                   0.5653   0.7585   0.75   0.457
## raceother                   -0.7135   0.7314  -0.98   0.330
## kcal_sd                     0.2140   0.3046   0.70   0.483
## ns(age, df = 3)1:sexgirl    3.2505   2.5435   1.28   0.202
## ns(age, df = 3)2:sexgirl   -6.3503   5.3730  -1.18   0.238
## ns(age, df = 3)3:sexgirl   -15.5742  2.3841  -6.53  2.0e-10 ***
## [...]
```

Fitted Values & Confidence Intervals

We obtain the **fitted values** from a linear regression model by multiplying a **design matrix \mathbf{X}** with the vector of **parameter estimates** for the regression coefficients $\hat{\beta}$:

$$\hat{\mathbf{y}} = \mathbf{X}\hat{\beta}.$$

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A $(1 - \alpha) \times 100\%$ **confidence interval** for $\hat{\mathbf{y}}$ can be obtained as

$$\hat{\mathbf{y}} \pm z_{1-\alpha/2} \text{se}(\hat{\mathbf{y}}),$$

where

$$\text{se}(\hat{\mathbf{y}}) = \sqrt{\text{var}(\hat{\mathbf{y}})} = \sqrt{\text{diag} \left(\mathbf{X} \text{var}(\hat{\beta}) \mathbf{X}^\top \right)}.$$

Example: Effects of Race

Create data containing the (hypothetical) observations:

```
effectDF <- data.frame(  
  race = levels(child$race),  
  age = 14,  
  height = 160,  
  sex = "boy",  
  kcal_sd = 0  
)
```

```
##           race age height sex kcal_sd  
## 1 caucasian 14    160 boy     0  
## 2      asian 14    160 boy     0  
## 3    other   14    160 boy     0
```

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)
```

```
##          race  age height sex kcal_sd  
## 1 caucasian 14    160 boy      0  
## 2      asian 14    160 boy      0  
## 3     other 14    160 boy      0
```

Create the design matrix:

```
X <- model.matrix(~ ns(age, df = 3) * sex + height + race + kcal_sd, data = effectDF)
```

Problem: Knots are positioned based on the new data.

⇒ The coefficients have a different interpretation!

Example: Effects of Race

Create the **design matrix** via the `terms`-object:

```
Terms <- terms(mod1)
X <- model.matrix(delete.response(Terms),
                  data = effectDF,
                  xlev = mod1$xlevels)
```

Example: Effects of Race

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```
Terms <- terms(mod1)
X <- model.matrix(delete.response(Terms),
                  data = effectDF,
                  xlev = mod1$xlevels)
```

Extract the **parameter estimates**:

```
betas <- coef(mod1)
```

Extract the **variance-covariance matrix** of the regression coefficients:

```
V <- vcov(mod1)
```

Example: Effects of Race

Calculate the fitted values, standard errors, and confidence intervals:

```
fit <- X %*% betas  
se <- sqrt(diag(X %*% V %*% t(X)))  
  
lwr <- fit - qnorm(0.975) * se  
upr <- fit + qnorm(0.975) * se
```

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Combine the input data with the fitted values, etc.:

```
effectDF <- data.frame(effectDF, fit = fit, se = se, lwr = lwr, upr = upr)
```

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Combine the input data with the fitted values, etc.:

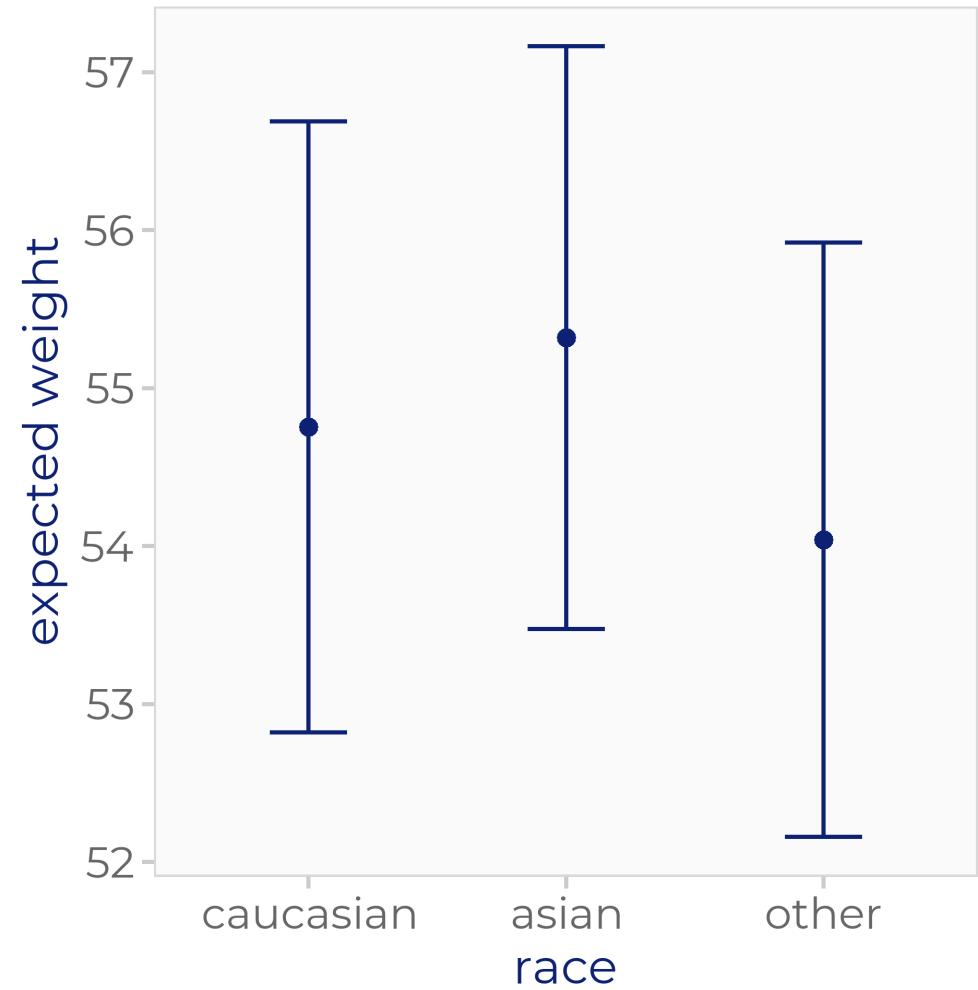
```
effectDF <- data.frame(effectDF, fit = fit, se = se, lwr = lwr, upr = upr)
```

Alternatively:

```
pred <- predict(mod1, newdata = effectDF, interval = "confidence")  
effectDF <- cbind(effectDF, pred)
```

Effect Plot for Race

```
library("ggplot2")  
  
ggplot(effectDF,  
       aes(x = race, y = fit)) +  
  geom_point() +  
  geom_errorbar(aes(ymin = lwr, ymax = upr)) +  
  ylab("expected weight")
```

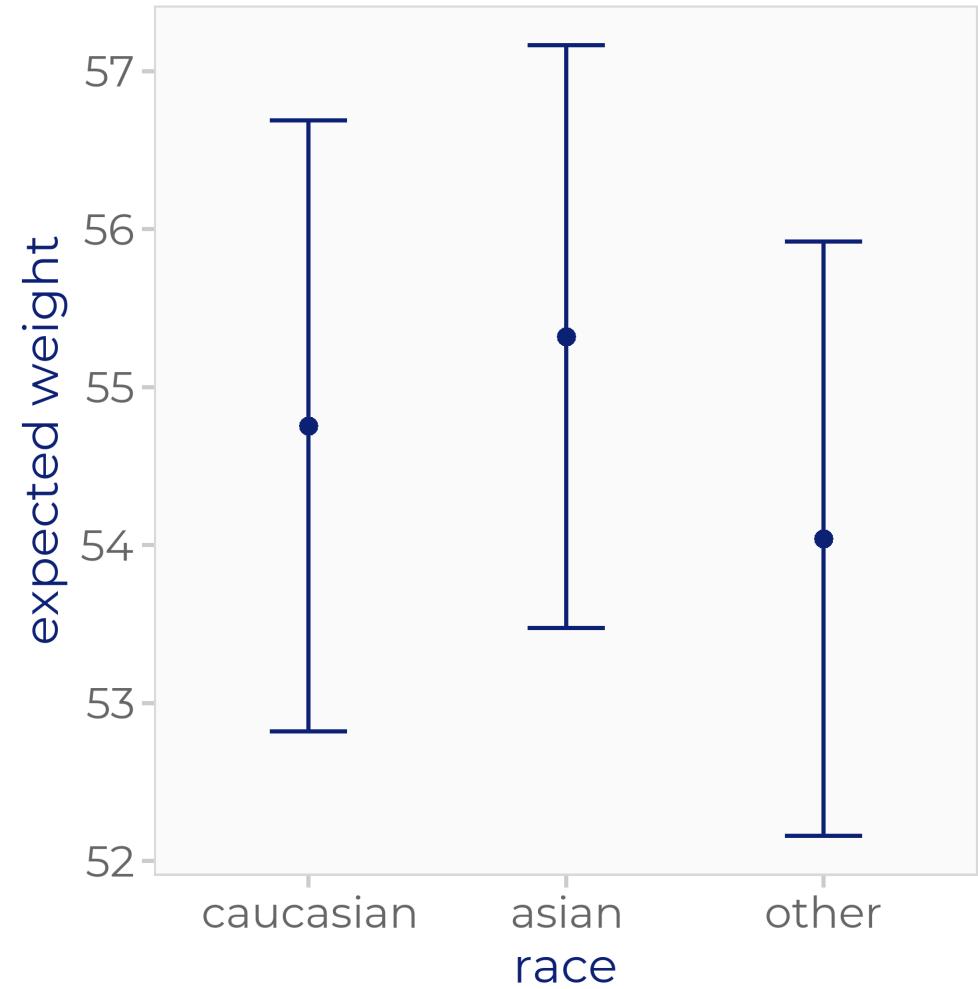


Effect Plot for Race

```
library("ggplot2")  
  
ggplot(effectDF,  
       aes(x = race, y = fit)) +  
  geom_point() +  
  geom_errorbar(aes(ymin = lwr, ymax = upr)) +  
  ylab("expected weight")
```

Expected weight for

- boys, who are
- 14 years of age and
- 160 cm tall,
- with a standardized kcal intake of 0.



Example: Race and Sex

Specify the new (hypothetical) data:

```
effectDF2 <- expand.grid(  
  race = levels(child$race),  
  age = 14,  
  height = 160,  
  sex = levels(child$sex),  
  kcal_sd = 0  
)
```

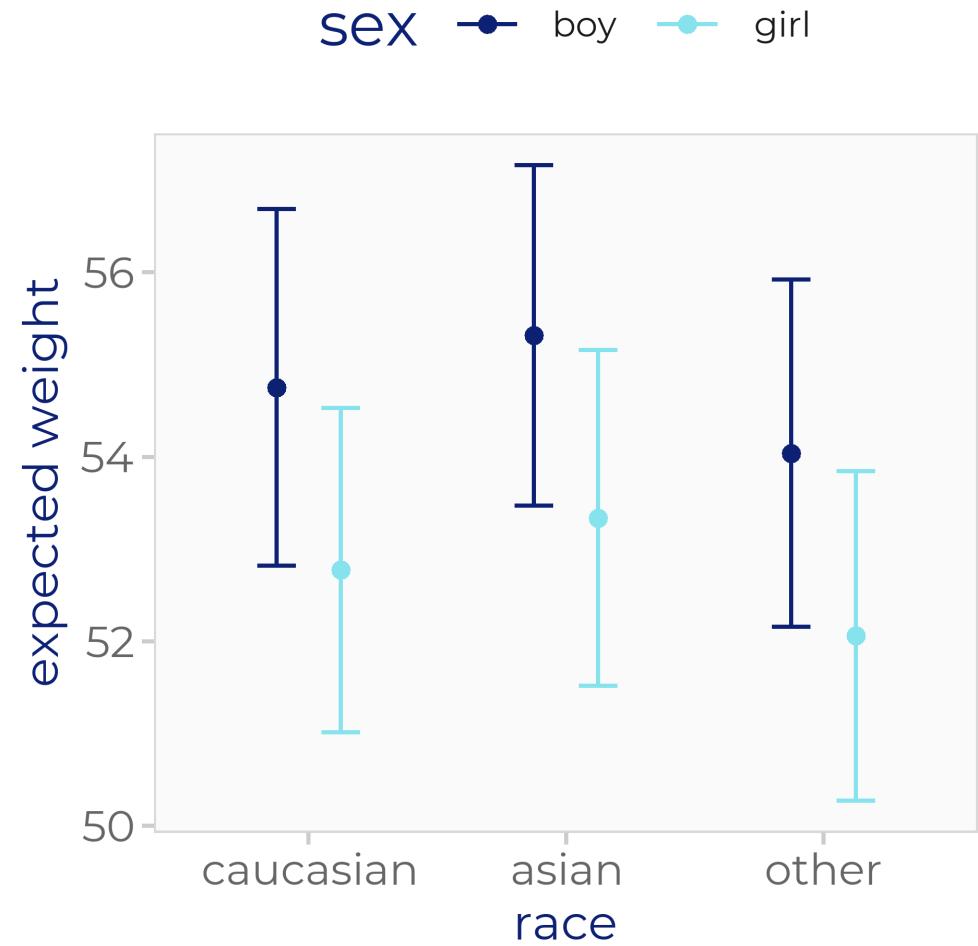
	##	race	age	height	sex	kcal_sd
	## 1	caucasian	14	160	boy	0
	## 2	asian	14	160	boy	0
	## 3	other	14	160	boy	0
	## 4	caucasian	14	160	girl	0
	## 5	asian	14	160	girl	0
	## 6	other	14	160	girl	0

Obtain fitted values and confidence intervals:

```
pred2 <- predict(mod1, newdata = effectDF2,  
                  interval = "confidence")  
effectDF2 <- cbind(effectDF2, pred2)
```

Example: Race and Sex

```
ggplot(effectDF2,  
       aes(x = race, y = fit, color = sex)) +  
  
  geom_point(  
    position = position_dodge(width = 0.5)) +  
  
  geom_errorbar(  
    aes(ymin = lwr, ymax = upr),  
    position = position_dodge(width = 0.5)) +  
  
  ylab("expected weight") +  
  
  theme(legend.position = "top")
```



Choosing Reference Values

Any variable not of interest is set to a "reference" value, for example,

- the median,
- the reference category, or
- the largest category.

The "reference" values should be representative / typical values.

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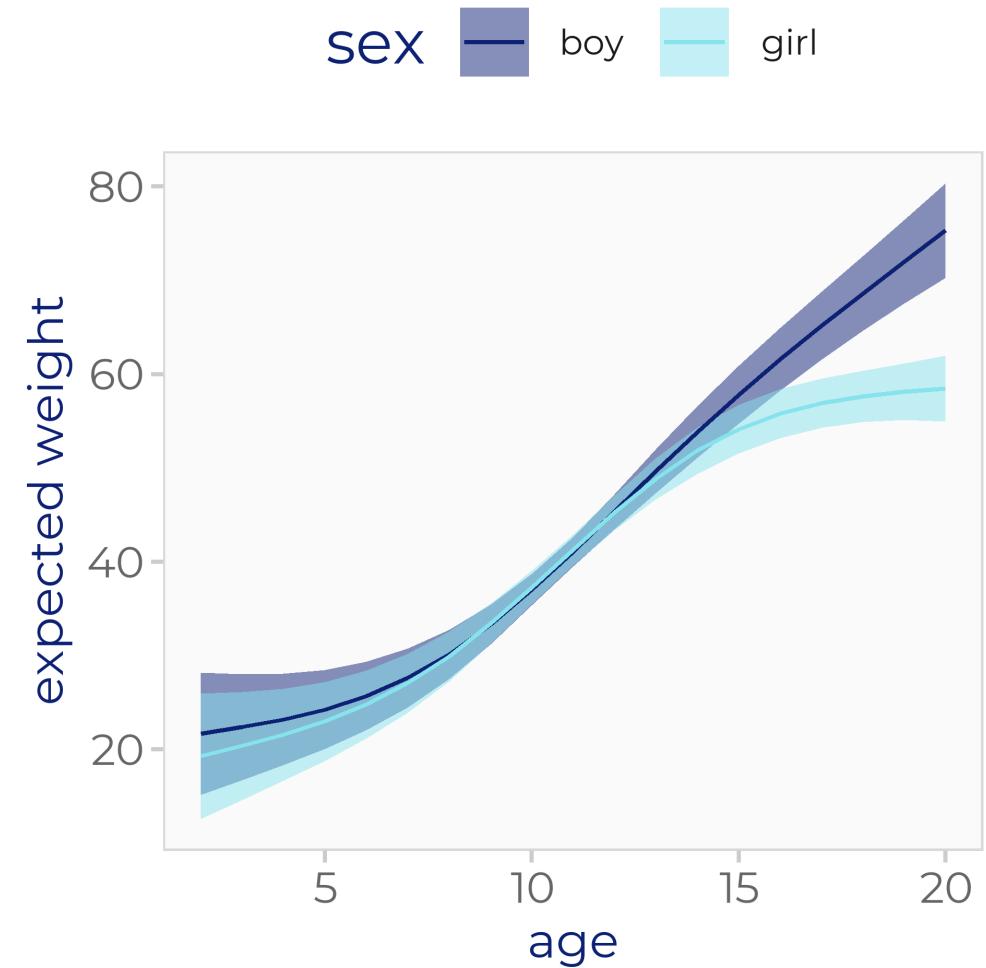
Example: Age and Sex

```
effectDF3 <- expand.grid(  
  age = 2:20,  
  sex = levels(child$sex),  
  height = median(child$height),  
  race = "asian",  
  kcal_sd = 0  
)
```

	##	age	sex	height	race	kcal_sd
## 1	2	boy	143.1	asian	0	
## 2	3	boy	143.1	asian	0	
## 3	4	boy	143.1	asian	0	
## ...						
## 19	20	boy	143.1	asian	0	
## 20	2	girl	143.1	asian	0	
## 21	3	girl	143.1	asian	0	
## ...						

Effect Plot for Sex and Age

```
ggplot(effectDF3,  
       aes(x = age, y = fit, color = sex)) +  
  
  geom_ribbon(  
    aes(ymin = lwr, ymax = upr, fill = sex),  
    alpha = 0.5, color = NA) +  
  
  geom_line() +  
  
  ylab("expected weight") +  
  
  theme(legend.position = "top")
```

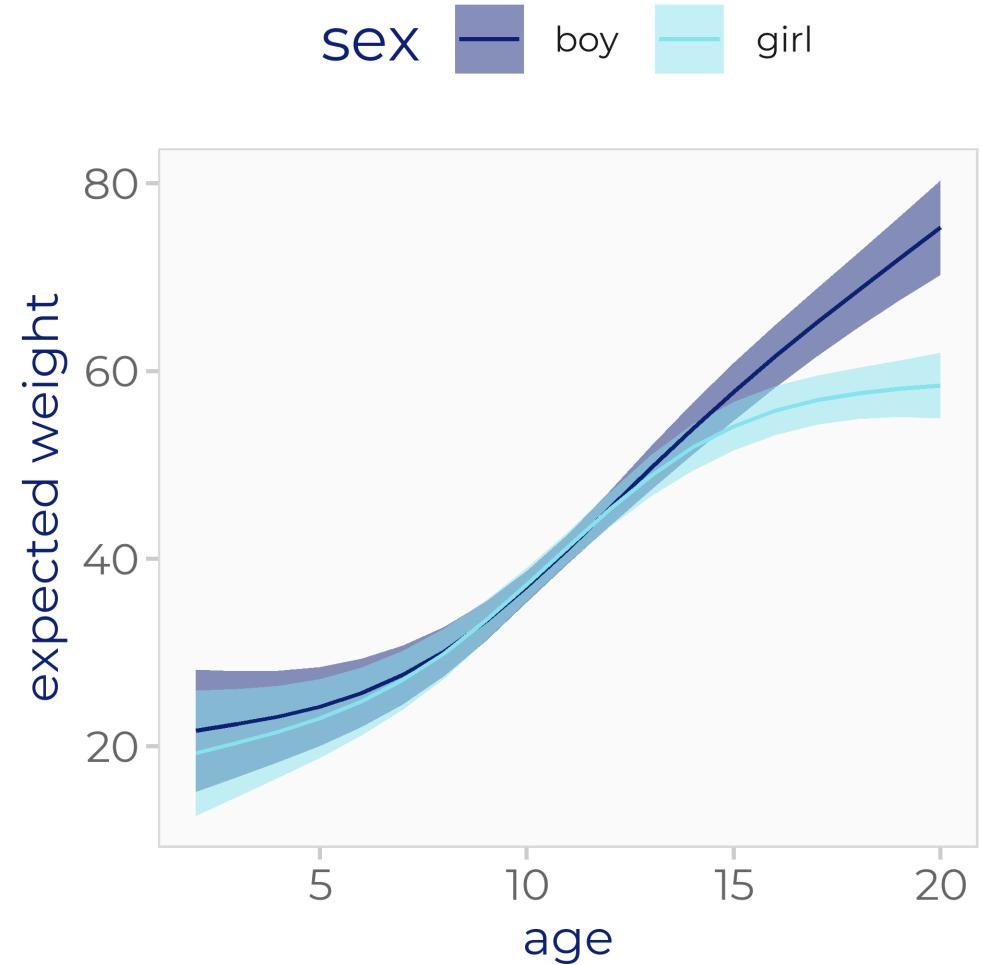


Effect Plot for Sex and Age

```
ggplot(effectDF3,  
       aes(x = age, y = fit, color = sex)) +  
  
  geom_ribbon(  
    aes(ymin = lwr, ymax = upr, fill = sex),  
    alpha = 0.5, color = NA) +  
  
  geom_line() +  
  
  ylab("expected weight") +  
  
  theme(legend.position = "top")
```

Expected weight for boys and girls, all

- 143.1 cm tall,
- asian,
- with a standardized kcal intake of 0.



Effect Plot for Sex and Age

Note:

Due to the strong association between age and height, some combinations of covariate values are **not realistic**.

```
##   age  sex height race kcal_sd fit lwr upr
## 1   2 boy    143 asian     0 21.7 15.2 28.2
## 19  20 boy    143 asian     0 75.3 70.3 80.4
## 20  2 girl   143 asian     0 19.3 12.6 26.0
## 38  20 girl   143 asian     0 58.5 55.0 62.0
```

Effect Plot for Sex and Age

Note:

Due to the strong association between age and height, some combinations of covariate values are **not realistic**.

##	age	sex	height	race	kcal_sd	fit	lwr	upr
## 1	2	boy	143	asian	0	21.7	15.2	28.2
## 19	20	boy	143	asian	0	75.3	70.3	80.4
## 20	2	girl	143	asian	0	19.3	12.6	26.0
## 38	20	girl	143	asian	0	58.5	55.0	62.0

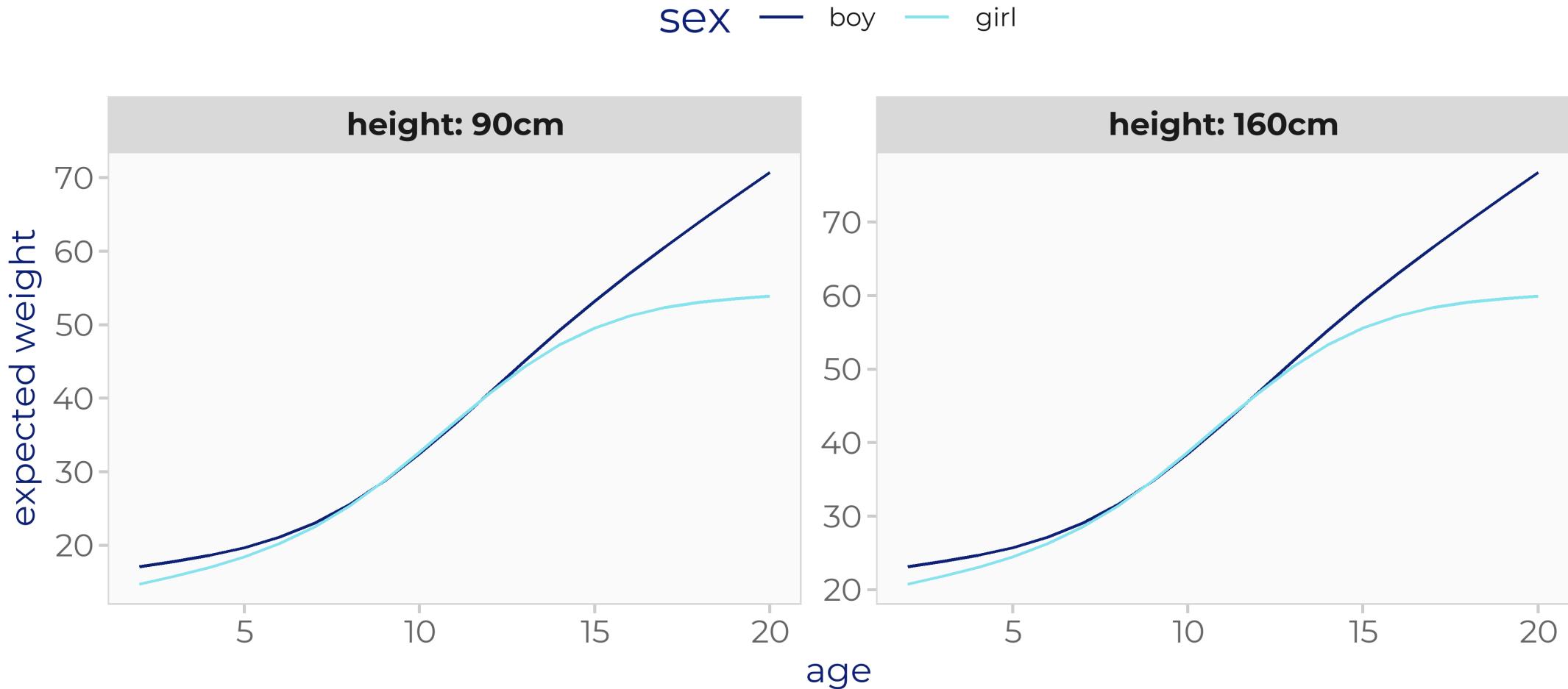
Because the model **does not include an interaction** of height different choices for height only cause a **shift on the y-axis**.

- The **shape** of the age-sex-weight relationship remains the same, irrespective of height.
- The **width of the confidence band** may change with height.

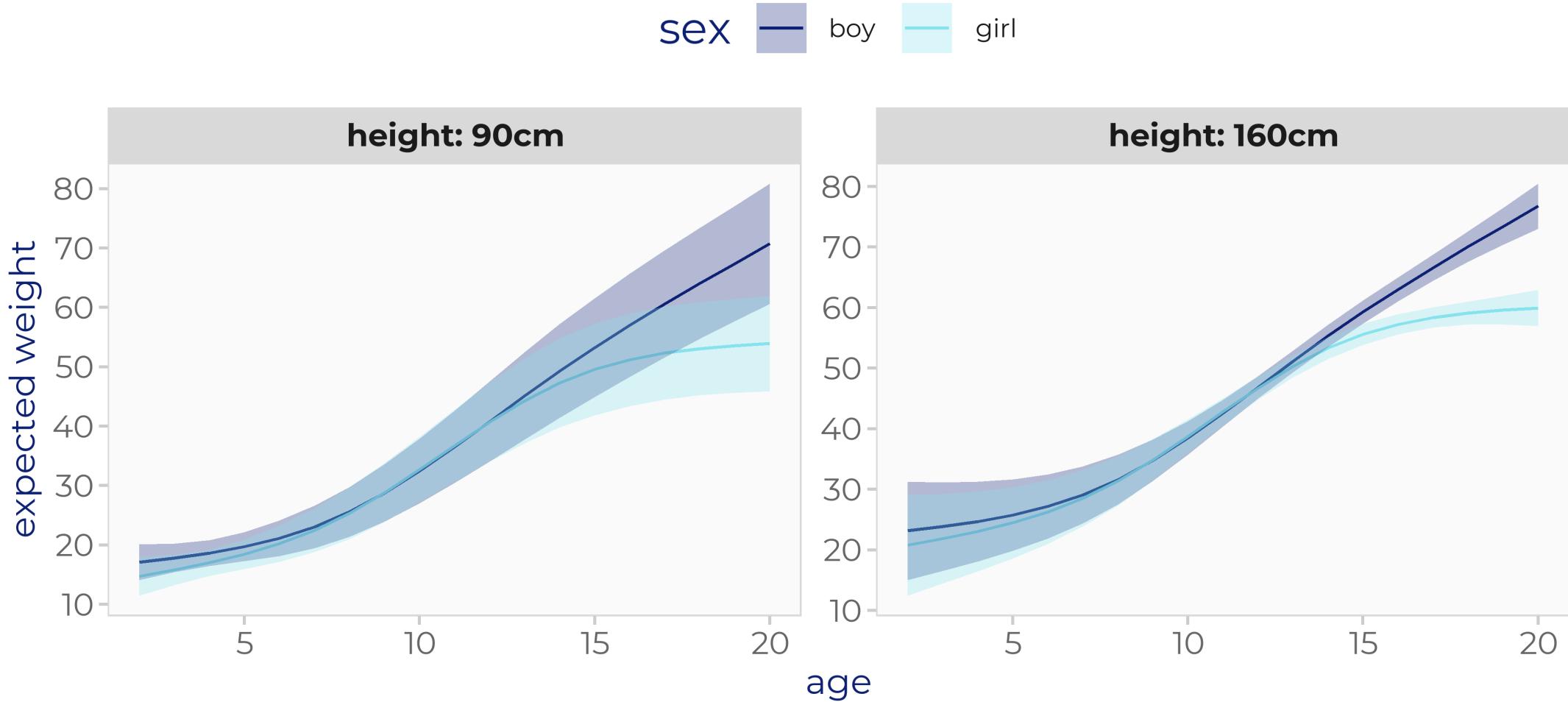
⇒ **Interpretation of the shape or differences** in expected weight between boys and girls is possible.

⇒ Interpretation of the **absolute values** of expected weight may not be meaningful.

Effect Plot for Sex and Age



Effect Plot for Sex and Age



Uncertainty is Important!

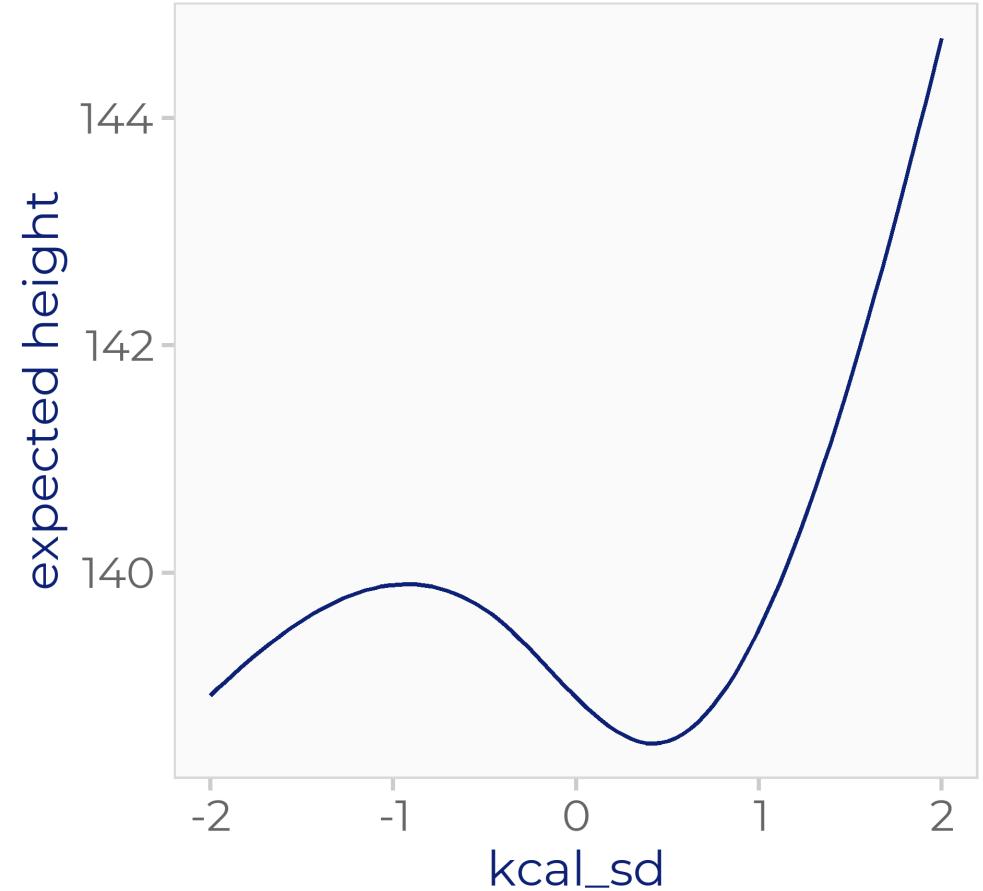
Why are confidence intervals/bands so important for interpretation of effect plots?

```
mod_kcal <- lm(height ~ ns(kcal_sd, df = 3),  
                 data = child)  
  
predDF <- data.frame(  
  kcal_sd = seq(-2, 2, length = 100)  
)  
  
predDF <- cbind(  
  predDF,  
  predict(mod_kcal, newdata = predDF,  
          interval = "confidence"))  
)  
  
p_naive <- ggplot(predDF,  
                    aes(x = kcal_sd, y = fit)) +  
  geom_line() +  
  ylab("expected height")  
  
p_naive
```

Uncertainty is Important!

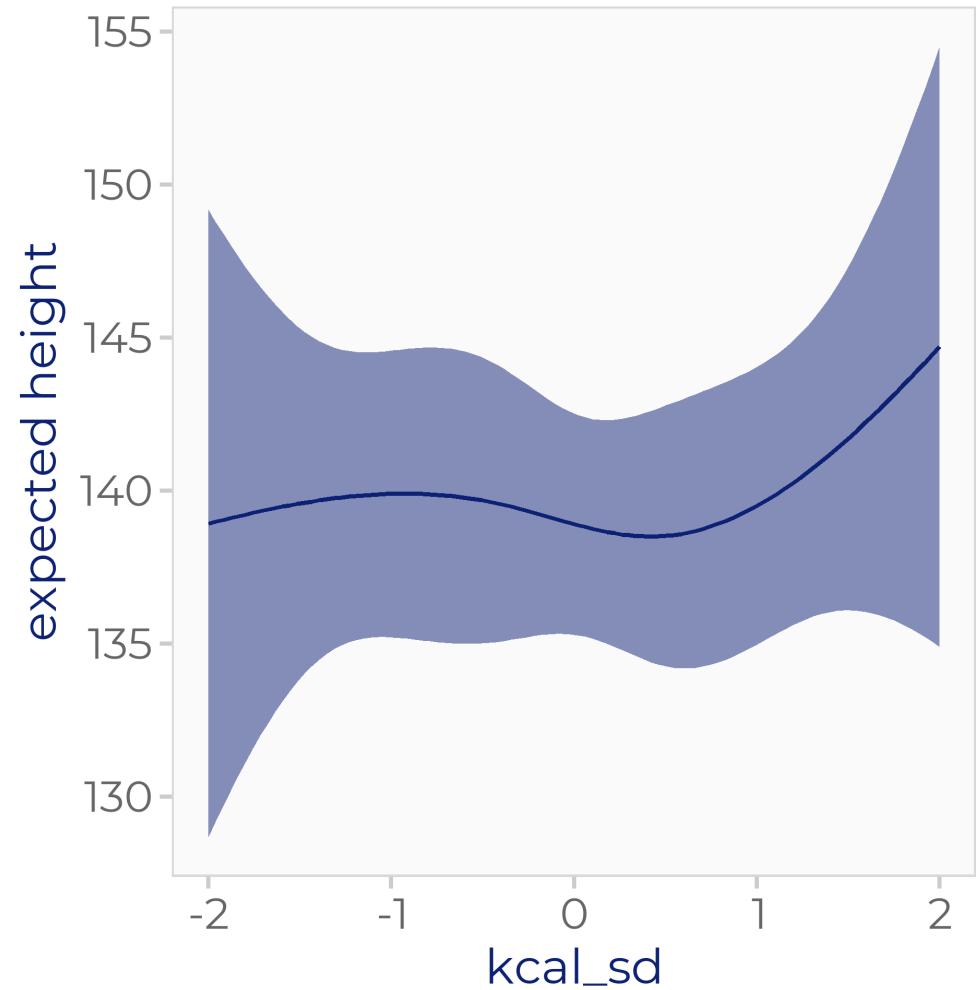
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mod_kcal <- lm(height ~ ns(kcal_sd, df = 3),  
                 data = child)  
  
predDF <- data.frame(  
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)  
  
predDF <- cbind(  
  predDF,  
  predict(mod_kcal, newdata = predDF,  
          interval = "confidence"))  
  
p_naive <- ggplot(predDF,  
                    aes(x = kcal_sd, y = fit)) +  
  geom_line() +  
  ylab("expected height")  
  
p_naive
```



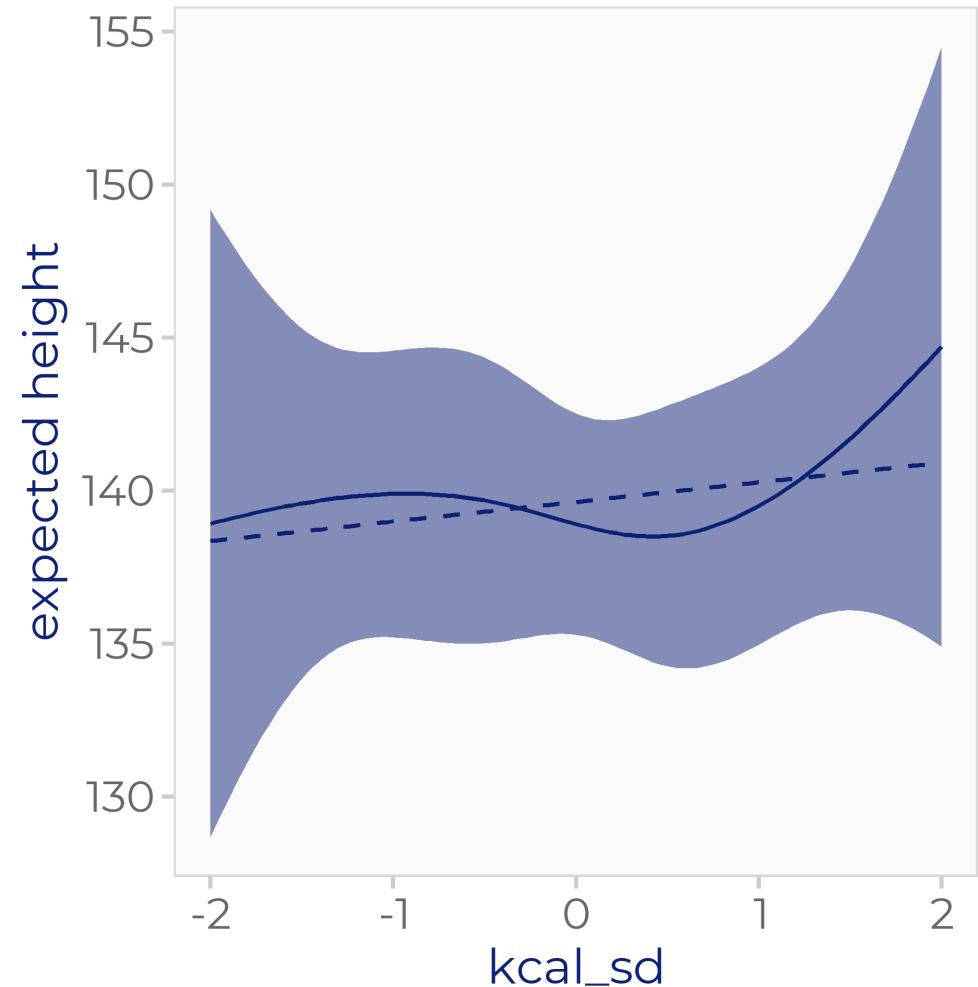
Uncertainty is Important!

```
p_naive +  
  geom_ribbon(aes(ymin = lwr, ymax = upr),  
              alpha = 0.5)
```



Uncertainty is Important!

```
mod_kcal_lin <- lm(height ~ kcal_sd,  
                     data = child)  
  
predDF <- cbind(  
  predDF,  
  fit_lin = predict(mod_kcal_lin,  
                     newdata = predDF)  
)  
  
p_naive %>% predDF +  
  geom_ribbon(aes(ymin = lwr, ymax = upr),  
              alpha = 0.5) +  
  geom_line(aes(y = fit_lin), lty = 2)
```



Effect Plots

- Are often necessary to be able to interpret **complex associations**.
- Can help to evaluate the **clinical relevance** of effects.
- Should use **meaningful** (combinations of) "**reference**" **values** for the covariates.

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Interpretation:

Expected response for a particular (hypothetical) observation that has a particular combination of covariate values.

- No categorization of continuous variables.
- No stratification.

Effect plots show a **visualization of the model**, not of the original data.

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- No stratification.

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There are **R packages** to facilitate creation of effect plots, for example, "visreg", "effects", "ggeffects", ...