

## 04\_model\_fit

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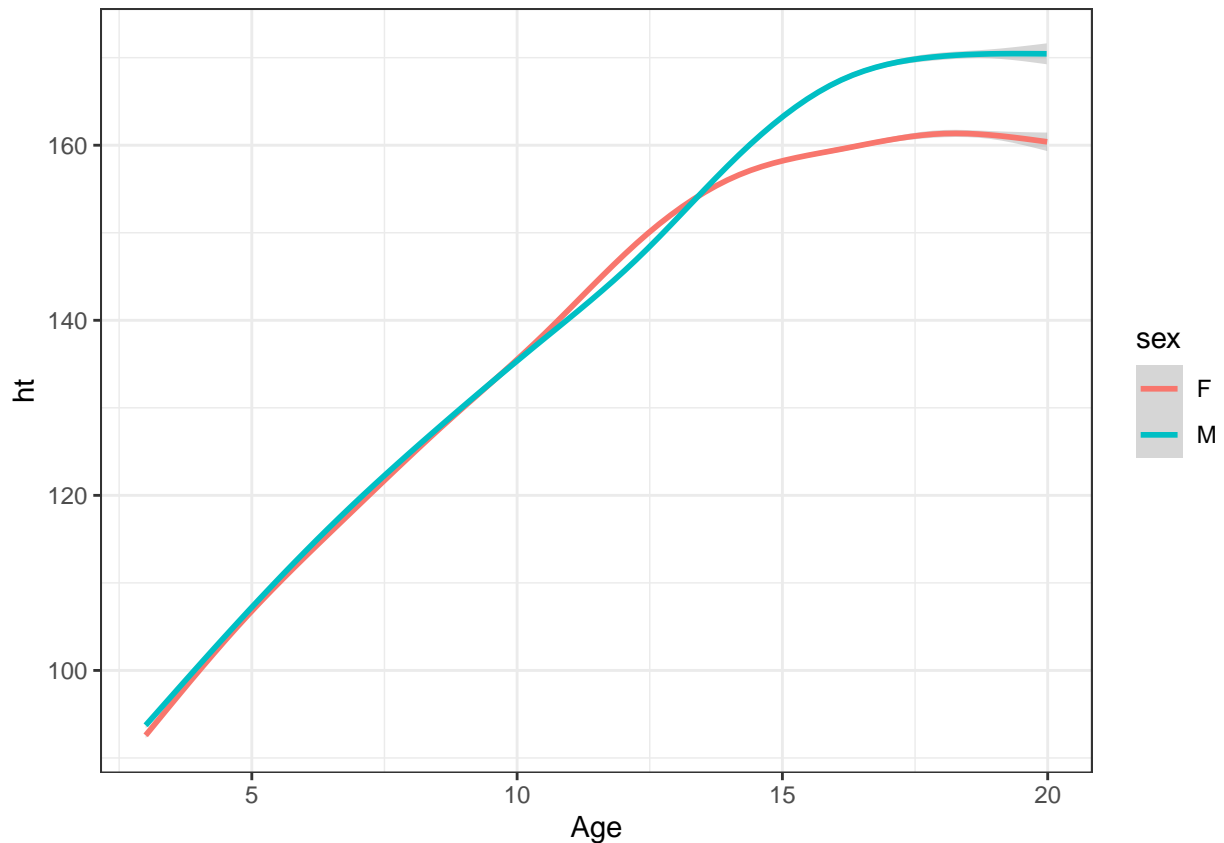
```
data <- here::here("data", "epic_clean_randy.csv") %>%  
  read.csv(row.names = 1)
```

```
# View(data)
```

```
plot1 <- data %>%  
  ggplot(aes(age, ht,  
             group = sex,  
             color = sex)) +  
  geom_smooth() +  
  xlab("Age") +  
  theme_bw()
```

```
plot1
```

```
## 'geom_smooth()' using method = 'gam' and formula 'y ~ s(x, bs = "cs")'
```



```
mod1_1_1 <- lme(ht ~ bs(age, knots = c(15), degree = 1,
                        intercept = FALSE) +
               sex + genotype - 1,
               random = ~ 1 | id,
               data = data)
tidy1_1_1 <- broom.mixed::tidy(mod1_1_1)
glance1_1_1 <- broom.mixed::glance(mod1_1_1) %>%
  mutate(model = "mod1_1_1")

mod1_1_2 <- lme(ht ~ bs(age, knots = c(10, 15), degree = 1) +
               sex + genotype - 1,
               random = ~ 1 | id,
               data = data)
glance1_1_2 <- broom.mixed::glance(mod1_1_2) %>%
  mutate(model = "mod1_1_2")

mod1_1_3 <- lme(ht ~ bs(age, knots = c(10, 15), degree = 1) +
               sex + genotype - 1,
               random = ~ 1 | id,
               data = data)
glance1_1_3 <- broom.mixed::glance(mod1_1_3) %>%
  mutate(model = "mod1_1_3")

mod1_1_4 <- lme(ht ~ bs(age, knots = c(10, 15), degree = 1) +
               sex + genotype - 1,
```

```

      random = ~ 1 + age | id,
      data = data)
glance1_1_4 <- broom.mixed::glance(mod1_1_4) %>%
  mutate(model = "mod1_1_4")

mod1_1_0 <- lme(ht ~ bs(age, degree = 1) +
  sex + genotype - 1,
  random = ~ 1 | id,
  data = data)
glance1_1_0 <- broom.mixed::glance(mod1_1_0) %>%
  mutate(model = "mod1_1_0")

```

```

mod1_2_1 <- lme(ht ~ bs(age, knots = c(15),
  degree = 3, intercept = FALSE) +
  sex + genotype - 1,
  random = ~ 1 | id,
  data = data)
tidy1_2_1 <- broom.mixed::tidy(mod1_2_1)
glance1_2_1 <- broom.mixed::glance(mod1_2_1) %>%
  mutate(model = "mod1_2_1")

mod1_2_2 <- lme(ht ~ bs(age, knots = c(10, 15), degree = 3, intercept = FALSE) +
  sex + genotype - 1,
  random = ~ 1 | id,
  data = data)
glance1_2_2 <- broom.mixed::glance(mod1_2_2) %>%
  mutate(model = "mod1_2_2")

mod1_2_3 <- lme(ht ~ bs(age, knots = c(10, 15), degree = 3, intercept = FALSE) +
  sex + genotype - 1,
  random = ~ 1 | id,
  data = data)
glance1_2_3 <- broom.mixed::glance(mod1_2_3) %>%
  mutate(model = "mod1_2_3")

mod1_2_4 <- lme(ht ~ bs(age, knots = c(10, 15), degree = 3, intercept = FALSE) +
  sex + genotype - 1,
  random = ~ 1 + age | id,
  data = data)
glance1_2_4 <- broom.mixed::glance(mod1_2_4) %>%
  mutate(model = "mod1_2_4")

mod1_2_0 <- lme(ht ~ bs(age, degree = 3, intercept = FALSE) +
  sex + genotype - 1,
  random = ~ 1 | id,
  data = data)
glance1_2_0 <- broom.mixed::glance(mod1_2_0) %>%
  mutate(model = "mod1_2_0")

```

```

mod1_3_1 <- lme(ht ~ ns(age, knots = c(10),
  intercept = FALSE) +
  sex + genotype - 1,

```

```

      random = ~ 1 | id,
      data = data)
tidy1_3_1 <- broom.mixed::tidy(mod1_3_1)
glance1_3_1 <- broom.mixed::glance(mod1_3_1) %>%
  mutate(model = "mod1_3_1")

mod1_3_2 <- lme(ht ~ ns(age, knots = c(10, 15),
      intercept = FALSE) +
      sex + genotype - 1,
      random = ~ 1 | id,
      data = data)
glance1_3_2 <- broom.mixed::glance(mod1_3_2) %>%
  mutate(model = "mod1_3_2")

mod1_3_3 <- lme(ht ~ ns(age, knots = c(10, 15), intercept = FALSE) +
      sex + genotype - 1,
      random = ~ 1 | id,
      data = data)
glance1_3_3 <- broom.mixed::glance(mod1_3_3) %>%
  mutate(model = "mod1_3_3")

mod1_3_4 <- lme(ht ~ ns(age, knots = c(10), intercept = FALSE) +
      sex + genotype - 1,
      random = ~ 1 + age | id,
      data = data)
glance1_3_4 <- broom.mixed::glance(mod1_3_4) %>%
  mutate(model = "mod1_3_4")

mod1_3_0 <- lme(ht ~ ns(age, intercept = FALSE) +
      sex + genotype - 1,
      random = ~ 1 | id,
      data = data)
glance1_3_0 <- broom.mixed::glance(mod1_3_0) %>%
  mutate(model = "mod1_3_0")

```

```

mod2_1_1 <- lme(ht ~ ns(age, knots = c(15),
      intercept = FALSE) * sex +
      genotype - 1,
      random = ~ 1 | id,
      data = data)
tidy2_1_1 <- broom.mixed::tidy(mod2_1_1)

glance2_1_1 <- broom.mixed::glance(mod2_1_1) %>%
  mutate(model = "mod2_1_1")

mod2_1_2 <- lme(ht ~ ns(age, knots = c(10, 15),
      intercept = FALSE) * sex +
      genotype - 1,
      random = ~ 1 | id,
      data = data)
glance2_1_2 <- broom.mixed::glance(mod2_1_2) %>%
  mutate(model = "mod2_1_2")

```

```

mod2_1_3 <- lme(ht ~ ns(age, knots = c(10, 15),
                        intercept = FALSE) * sex + genotype - 1,
               random = ~ 1 | id,
               data = data)
glance2_1_3 <- broom.mixed::glance(mod2_1_3) %>%
  mutate(model = "mod2_1_3")

mod2_1_4 <- lme(ht ~ ns(age, knots = c(10, 15),
                        intercept = FALSE) * sex + genotype - 1,
               random = ~ 1 + age | id,
               data = data)
glance2_1_4 <- broom.mixed::glance(mod2_1_4) %>%
  mutate(model = "mod2_1_4")

mod2_1_0 <- lme(ht ~ ns(age, intercept = FALSE) * sex + genotype - 1,
               random = ~ 1 | id,
               data = data)
glance2_1_0 <- broom.mixed::glance(mod2_1_0) %>%
  mutate(model = "mod2_1_0")

```

```

mod2_2_1 <- lme(ht ~ bs(age, knots = c(15),
                        degree = 3, intercept = FALSE) * sex +
               genotype - 1,
               random = ~ 1 | id,
               data = data)
tidy2_2_1 <- broom.mixed::tidy(mod2_2_1)

glance2_2_1 <- broom.mixed::glance(mod2_2_1) %>%
  mutate(model = "mod2_2_1")

mod2_2_2 <- lme(ht ~ bs(age, knots = c(10, 15),
                        degree = 3, intercept = FALSE) * sex +
               genotype - 1,
               random = ~ 1 | id,
               data = data)
glance2_2_2 <- broom.mixed::glance(mod2_2_1) %>%
  mutate(model = "mod2_2_2")

mod2_2_3 <- lme(ht ~ bs(age, knots = c(10, 15),
                        degree = 3, intercept = FALSE) * sex + genotype - 1,
               random = ~ 1 | id,
               data = data)
glance2_2_3 <- broom.mixed::glance(mod2_2_3) %>%
  mutate(model = "mod2_2_3")

mod2_2_4 <- lme(ht ~ bs(age, knots = c(10, 15),
                        degree = 3, intercept = FALSE) * sex + genotype - 1,
               random = ~ 1 + age | id,
               data = data)

glance2_2_4 <- broom.mixed::glance(mod2_2_4) %>%

```

```

mutate(model = "mod2_2_4")

mod2_2_0 <- lme(ht ~ bs(age, degree = 3, intercept = FALSE) * sex + genotype - 1,
               random = ~ 1 | id,
               data = data)
glance2_2_0 <- broom.mixed::glance(mod2_2_0) %>%
  mutate(model = "mod2_2_0")

# predict(mod2_2_4)

```

```
library(mgcv)
```

```
## This is mgcv 1.8-39. For overview type 'help("mgcv-package")'.
```

```

mod3_1_1<- gam(ht ~ s(age, bs = "cr") +
               s(id, bs = "re") + genotype + sex,
               data = data)

```

```

glance3_1_1 <- broom.mixed::glance(mod3_1_1) %>%
  mutate(model = "mod3_1_1") %>%
  select(sigma = deviance, logLik, AIC, BIC, model)

```

```

mod3_1_2<- gam(ht ~ s(age, bs = "cr", k =50) +
               s(id, bs = "re") + genotype + sex,
               data = data)
glance3_1_2 <- broom.mixed::glance(mod3_1_2) %>%
  mutate(model = "mod3_1_2") %>%
  select(sigma = deviance, logLik, AIC, BIC, model)

```

```

rbind(glance1_1_0, glance1_1_1, glance1_1_2, glance1_1_3, glance1_1_4,
      glance1_2_0, glance1_2_1, glance1_2_2, glance1_2_3, glance1_2_4,
      glance1_3_0, glance1_3_1, glance1_3_2, glance1_3_3, glance1_3_4,
      glance2_1_0, glance2_1_1, glance2_1_2, glance2_1_3, glance2_1_4,
      glance2_2_0, glance2_2_1, glance2_2_2, glance2_2_3, glance2_2_4,
      glance3_1_1, glance3_1_2) %>%
  as.data.frame() %>%
  select(model, everything()) %>%
  arrange(AIC) %>%
  knitr::kable()

```

model	sigma	logLik	AIC	BIC
mod2_2_4	1.757194e+00	-137580.2	275196.3	275360.1
mod2_1_4	1.894312e+00	-142386.5	284800.9	284928.3
mod1_2_4	1.988080e+00	-145524.6	291075.2	291193.5
mod1_1_4	2.040270e+00	-147206.5	294435.1	294535.2
mod1_3_4	2.324777e+00	-155491.4	311002.7	311093.7
mod2_2_3	2.469911e+00	-157462.8	314957.6	315103.2
mod2_2_1	2.545388e+00	-159411.3	318850.7	318978.1

model	sigma	logLik	AIC	BIC
mod2_2_2	2.545388e+00	-159411.3	318850.7	318978.1
mod2_1_3	2.570794e+00	-160056.1	320136.3	320245.5
mod2_2_0	2.610822e+00	-161055.2	322134.4	322243.6
mod2_1_1	2.675200e+00	-162632.7	325285.4	325376.4
mod2_1_2	2.675200e+00	-162632.7	325285.4	325376.4
mod1_2_2	2.777831e+00	-165071.1	330164.3	330264.4
mod1_2_3	2.777831e+00	-165071.1	330164.3	330264.4
mod1_1_2	2.827718e+00	-166226.4	332470.8	332552.7
mod1_1_3	2.827718e+00	-166226.4	332470.8	332552.7
mod1_3_2	2.837113e+00	-166439.3	332896.6	332978.5
mod1_3_3	2.837113e+00	-166439.3	332896.6	332978.5
mod1_2_1	2.838455e+00	-166468.8	332957.6	333048.6
mod1_2_0	2.867249e+00	-167122.8	334263.6	334345.5
mod1_1_1	2.886363e+00	-167556.8	335129.6	335202.4
mod1_3_1	3.057375e+00	-171282.8	342581.7	342654.5
mod2_1_0	3.786998e+00	-185167.8	370351.6	370424.4
mod1_3_0	3.838961e+00	-186049.8	372113.5	372177.2
mod1_1_0	3.838961e+00	-186050.0	372113.9	372177.6
mod3_1_2	2.552443e+06	-214786.1	429610.7	429785.2
mod3_1_1	2.552849e+06	-214791.4	429612.4	429747.0

```
mod2_2_4 <- lme(ht ~ bs(time, knots = c(15),
                      degree = 3, intercept = FALSE) * sex +
               genotype - 1,
               random = ~ 1 | id,
               data = data)

glance2_2_4 <- broom.mixed::glance(mod2_2_4) %>%
  mutate(model = "mod2_2_4")
glance2_2_4
```

```
## # A tibble: 1 x 5
##   sigma logLik   AIC   BIC model
##   <dbl>   <dbl> <dbl> <dbl> <chr>
## 1  2.59 -160675. 321377. 321504. mod2_2_4
```

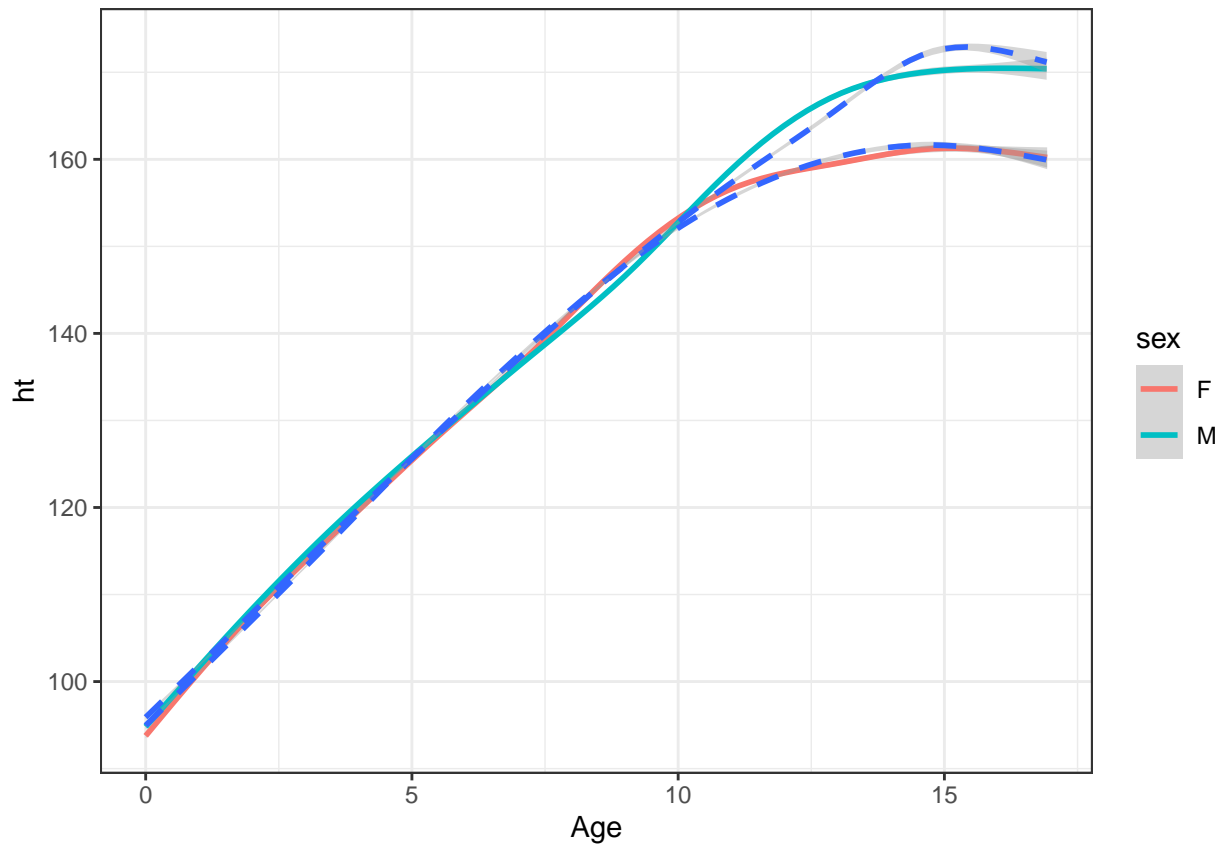
```
augment2_2_4 <- broom.mixed::augment(mod2_2_4) %>%
  mutate(model = "mod2_2_4")
```

```
fitted <- augment2_2_4 %>%
  select(time, .fitted, sex) %>%
  unique()
```

```
plot1 <-
  ggplot() +
  geom_smooth(data = data, aes(x = time, y = ht, group = sex, color = sex)) +
  geom_smooth(data = fitted, aes(x = time, y = .fitted, group = sex), linetype = 2) +
  xlab("Age") +
  theme_bw()

plot1
```

```
## 'geom_smooth()' using method = 'gam' and formula 'y ~ s(x, bs = "cs")'
## 'geom_smooth()' using method = 'gam' and formula 'y ~ s(x, bs = "cs")'
```



```
mod2_2_4 <- lme(ht ~ bs(time, knots = c(10, 15),
                    degree = 3, intercept = FALSE) * sex + genotype - 1,
               random = ~ 1 | id,
               data = data)

glance2_2_4 <- broom.mixed::glance(mod2_2_4) %>%
  mutate(model = "mod2_2_4")
glance2_2_4
```

```
## # A tibble: 1 x 5
##   sigma logLik    AIC    BIC model
##   <dbl>   <dbl> <dbl>   <dbl> <chr>
## 1  2.50 -158167. 316366. 316511. mod2_2_4
```

```
augment2_2_4 <- broom.mixed::augment(mod2_2_4) %>%
  mutate(model = "mod2_2_4")

fitted <- augment2_2_4 %>%
  select(time, .fitted, sex) %>%
  unique()

plot1 <-
```



```
ggplot() +
  geom_smooth(data = data, aes(x = time, y = ht, group = sex, color = sex)) +
  geom_smooth(data = fitted, aes(x = time, y = .fitted, group = sex), linetype = 2) +
  xlab("Age") +
  theme_bw()
```

plot1

```
## 'geom_smooth()' using method = 'gam' and formula 'y ~ s(x, bs = "cs")'
## 'geom_smooth()' using method = 'gam' and formula 'y ~ s(x, bs = "cs")'
```

