# 06\_update

# randy

# 2022-04-19

## 1. Redo table 1 with final sample

### table0

Variable	$N = 1,370^1$	
Genotype		
One allele F508del	477 (35%)	
Others or Unknown	150 (11%)	
Two alleles F508del	del 743 (54%)	
Gender		
Female	693~(51%)	
Male	677 (49%)	
Race		
Other	62~(4.5%)	
White	1,308 (95%)	
Ethnicity		
Hispanic	43 (3.3%)	
Non-Hispanic	1,274 (97%)	
Unknown	53	
$Visit\ number$	45 (32, 60)	
$Age\ at\ registration,\ years$	$3.13 \ (3.06, \ 3.22)$	
Age at end of follow-up, years	$12.8\ (10.2,\ 16.0)$	
$Follow-up,\ years$	9.6 (7.0, 12.7)	
$Height\ at\ registration,\ cm$	94.0 (91.4, 97.0)	
$Weight\ at\ registration,\ kg$	$14.10 \ (13.10, \ 15.30)$	

<sup>&</sup>lt;sup>1</sup>n (%); Median (IQR)

Variable	testing, $N = 457^1$	training, $N = 913^1$
Genotype		
One allele F508del	151 (33%)	326 (36%)
Others or Unknown	58 (13%)	$92\ (10\%)$
Two alleles F508del	248 (54%)	495 (54%)
Gender		
Female	224~(49%)	469~(51%)
Male	233~(51%)	444 (49%)
Race		
Other	$21\ (4.6\%)$	41 (4.5%)
White	436~(95%)	872 (96%)
Ethnicity		
Hispanic	18 (4.1%)	25~(2.8%)
Non-Hispanic	419~(96%)	855 (97%)
Unknown	20	33
$Visit \ number$	44 (32, 61)	45 (31, 59)
$Age\ at\ registration,\ years$	$3.14 \ (3.07, \ 3.23)$	$3.13 \ (3.05, \ 3.22)$
Age at end of follow-up, years	$13.1\ (10.3,\ 15.9)$	$12.7\ (10.2,\ 16.0)$
$Follow ext{-}up,\ years$	9.9 (7.2, 12.7)	9.4 (7.0, 12.9)
Height at registration, cm	94.0 (91.7, 97.2)	94.0 (91.2, 96.8)
$Weight\ at\ registration,\ kg$	$14.10 \ (13.20, \ 15.30)$	14.10 (13.10, 15.30)

<sup>&</sup>lt;sup>1</sup>n (%); Median (IQR)

```
## save pptx -----
## flextable can be saved directly to powerpoints
flextable::save_as_pptx(
  table0,
  path = "figure/01_table0.pptx")
flextable::save_as_pptx(
  table1,
  path = "figure/01_table1.pptx")
```

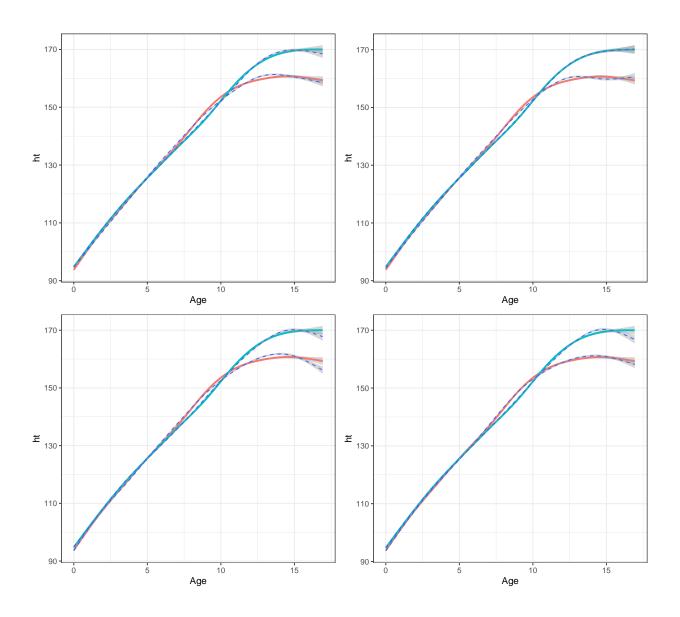
2. Refine spline model for training dataset.

Try spline model with 3 inner knots set at percentiles (quartiles) too and compare to the splines you had tried before.

```
train <- here::here("data", "epic_clean_randy.csv") %>%
  read.csv(row.names = 1) %>%
  mutate(id = as.factor(id)) %>%
  filter(group == "training")
test <- here::here("data", "epic_clean_randy.csv") %>%
  read.csv(row.names = 1) %>%
  filter(group == "testing")
baseline <- train %>%
  group_by(id) %>%
  arrange(time) %>%
  slice(1L) %>%
  rename(ht_base = ht,
         time_base = time) %>%
 dplyr::select(id, ht_base, time_base)
# lmeControl
ctrl <- lmeControl(opt = 'optim')</pre>
## the original mod2_2_4 in file "04_model_fit.Rmd"
fit2_0 \leftarrow lme(ht \sim bs(time, knots = c(10, 15),
                       degree = 3,
                       intercept = FALSE) * sex + genotype - 1,
              control = ctrl,
              random = ~ 1| id,
              data = train)
fit2_1 \leftarrow lme(ht \sim bs(time, knots = c(10, 12),
                       degree = 3,
                       intercept = FALSE) * sex + genotype - 1,
              control = ctrl,
              random = ~1|id,
              data = train)
fit2_2 \leftarrow lme(ht \sim bs(time, df = 5,
                       degree = 3,
                       intercept = FALSE) * sex + genotype - 1,
               control = ctrl,
              random = ~1|id,
              data = train)
fit3_0 \leftarrow lme(ht \sim bs(time, df = 6,
                       degree = 3,
                       intercept = FALSE) * sex + genotype - 1,
               control = ctrl,
              random = ~1 | id,
              data = train)
get_tag <- function(fit, data1 = train) {</pre>
  tidy <- broom.mixed::tidy(fit)</pre>
  glance <- broom.mixed::glance(fit)</pre>
  augment <- broom.mixed::augment(fit) %>%
```

```
dplyr::select(time, .fitted, sex) %>%
    unique()
  plot1 <- ggplot() +</pre>
        geom_smooth(data = data1,
                     aes(x = time,
                         y = ht,
                         group = sex,
                         color = sex)) +
        geom_smooth(data = augment,
                     aes(x = time, y = .fitted,
                         group = sex),
                     linetype = 2,
                     size = 0.5) +
        xlab("Age") +
        theme_bw() +
    theme(legend.position = "none")
  return(list(tidy = tidy,
              glance = glance,
              augment = augment,
              plot = plot1))
}
tag2_0 \leftarrow get_tag(fit = fit2_0)
tag2_1 <- get_tag(fit = fit2_1)</pre>
tag2_2 <- get_tag(fit = fit2_2)</pre>
tag3_0 \leftarrow get_tag(fit = fit3_0)
glance_all <- map_dfr(list(tag2_0, tag2_1,</pre>
                     tag2_2, tag3_0),
                   "glance") %>%
  mutate(model = c("fit2_0", "fit2_1",
                    "fit2_2", "fit3_0")) %>%
  dplyr::select(model, everything())
glance_all
## # A tibble: 4 x 5
     model sigma logLik
                                AIC
                                         BIC
##
     <chr> <dbl>
                     <dbl>
                             <dbl>
                                       <dbl>
## 1 fit2_0 2.52 -104694. 209421. 209560.
## 2 fit2_1 2.49 -104297. 208626. 208765.
## 3 fit2_2 2.50 -104488. 209008. 209147.
## 4 fit3_0 2.49 -104178. 208393. 208549.
```

3. plot the predicted/expected means.



 $4.\ \,$  For broken stick model try time for a anchoring of and 

```
group = train$id)
est1_all <- predict(bks1,
                   group = train$id)
bks2 <- brokenstick(formula = ht ~ time | id,</pre>
                    data = train,
                    subjid = train$id,
                    knots = c(10, 12))
est2_knots <- predict(bks2,
                     x = "knots",
                     group = train$id)
est2_all <- predict(bks2,
                   group = train$id)
bks31 <- brokenstick(formula = ht ~ time | id,
                    data = train,
                    subjid = train$id,
                    knots = c(10, 12, 15))
bks32 <- brokenstick(formula = ht ~ time | id,
                    data = train,
                    knots = c(10, 12, 15),
                    seed = 555)
est31_knots <- predict(bks31,
                     x = "knots",
                     group = train$id)
est31_all <- predict(bks31,
                   group = train$id)
est32_knots <- predict(bks32,
                     x = "knots",
                     group = train$id)
est32_all <- predict(bks32,
                   group = train$id)
```

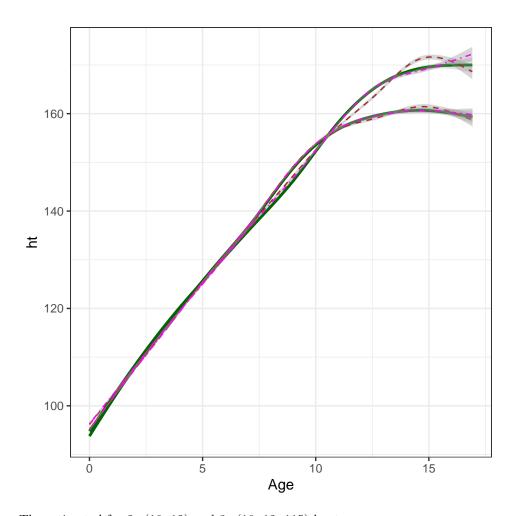
#### summary(bks31)

```
## Class
               brokenstick (kr)
## Variables
               ht (outcome), time (predictor), id (group)
## Data
               43645 (n), 0 (nmis), 913 (groups)
## Parameters 22 (total), 5 (fixed), 5 (variance), 10 (covariance), 2 (error)
## Knots
              0 10 12 15 16.93
## Means
               95.70756 155.5789 163.3136 165.4726 164.6041
## Residuals 0.2482916 0.8770755 1.37863 2.204521 31.63544 (min, P25, P50, P75, max)
## Mean resid 1.94943
## R-squared
              0.995773
##
## Variance-covariance matrix
                                     time_12
                                              time 15 time 16.93
                 time 0
                          time_10
            19.5582961
## time_0
```

```
## time 10
             24.3589089 82.8971499
          18.0994146 51.9116584 82.1773243
## time 12
## time 15 19.0925951 23.9096542 66.5183404 91.5442478
## time_16.93 16.2139215 27.1723183 66.5902829 81.2333102 82.523759
summary(bks32)
## Class
               brokenstick (kr)
## Variables ht (outcome), time (predictor), id (group)
## Data
          43645 (n), 0 (nmis), 913 (groups)
## Parameters 22 (total), 5 (fixed), 5 (variance), 10 (covariance), 2 (error)
             0 10 12 15 16.93
## Knots
             95.71299 155.5664 163.2632 165.3464 164.0733
## Means
## Residuals 0.2440794 0.878987 1.387723 2.208051 30.83667 (min, P25, P50, P75, max)
## Mean resid 1.948516
## R-squared
             0.9957725
##
## Variance-covariance matrix
                          time_10 time_12 time_15 time_16.93
##
                 time 0
## time 0
           19.5935051
## time_10 24.2353492 82.6316341
## time_12
          17.8177299 50.6881557 81.118866
          18.9074014 23.210069 65.3710932 91.3853125
## time 15
## time_16.93 16.5900516 22.8482092 61.3250568 83.4066696 81.9589513
```

### the estimated c(10, 12) and c(10, 15)

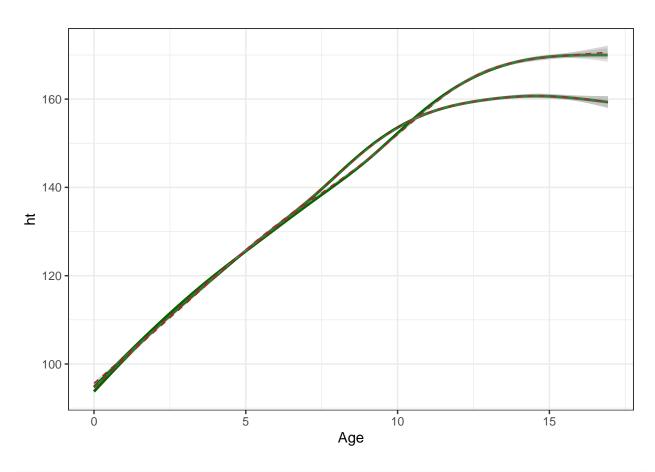
```
plot_bks1 <- ggplot() +</pre>
  geom_smooth(data = train,
              aes(x = time, y = ht,
                  group = sex),
              alpha = 0.3,
              size = 1,
              color = "darkgreen") +
  geom_smooth(data = est1_all,
              aes(x = time, y = .pred,
                  group = sex),
              color = "brown",
              linetype = 2,
              size = 0.5) +
  geom_smooth(data = est2_all,
                    aes(x = time, y = .pred,
                         group = sex),
              color = "magenta",
              linetype = 4,
              size = 0.5) +
  xlab("Age") +
  theme_bw()
plot_bks1
```



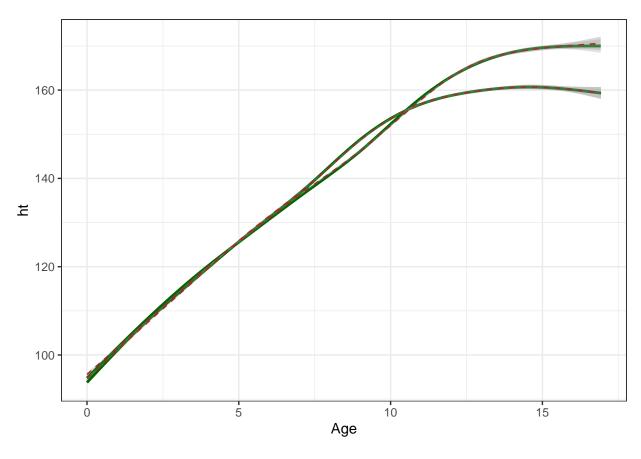
The estimated for 2 c(10, 12) and 3 c(10, 12, 115) knots

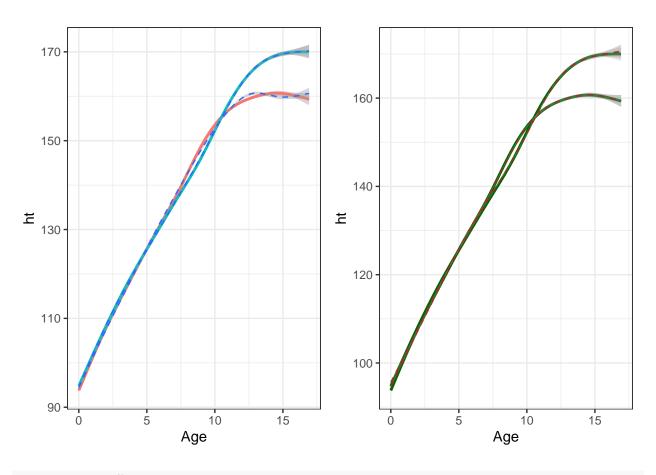
```
plot_bks2 <- ggplot() +</pre>
  geom_smooth(data = train,
              aes(x = time, y = ht,
                  group = sex),
              alpha = 0.3,
              size = 1,
              color = "darkgreen") +
  geom_smooth(data = est32_all,
              aes(x = time, y = .pred,
                  group = sex),
              color = "brown",
              linetype = 2,
              size = 0.5) +
  geom_smooth(data = est2_all,
                    aes(x = time, y = .pred,
                        group = sex),
              color = "magenta",
              linetype = 4,
              size = 0.5) +
  xlab("Age") +
  theme_bw()
```

```
Kk \leftarrow c(5, 10, 12, 15)
Kplot <- function(K,</pre>
                   seed = 555,
                   form = "ht ~ time | id") {
  bks3n <- brokenstick(formula = as.formula(form),</pre>
                     data = train,
                     knots = Kk,
                     method = "lmer")
  # ?brokenstick
  est_knots <- predict(bks3n,</pre>
                      x = "knots",
                      group = train$id)
  est_all <- predict(bks3n,</pre>
                    group = train$id)
  plot_bks <- ggplot() +</pre>
    geom_smooth(data = train,
                 aes(x = time, y = ht,
                     group = sex),
                 alpha = 0.3,
                 size = 1,
                 color = "darkgreen") +
    geom_smooth(data = est_all,
                 aes(x = time, y = .pred,
                     group = sex),
                 color = "brown",
                 linetype = 2,
                 size = 0.5) +
    xlab("Age") +
    theme_bw()
  return(list(model = bks3n,
               est.knot = est_knots,
               est.all = est_all,
               plot = plot_bks))
}
bksn <- Kplot(K = Kk)</pre>
bksn$plot
```

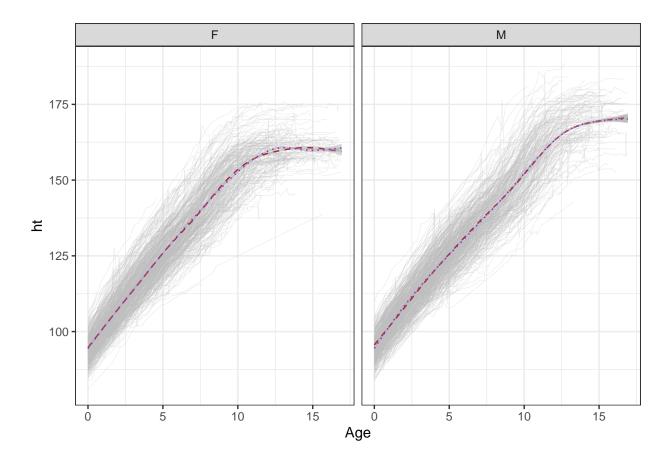


```
tag2_1 <- get_tag(fit = fit2_1)
bks2_1 <- Kplot(K = c(10, 12))
bks2_1$plot</pre>
```





```
plot <- ggplot() +</pre>
  geom_line(data = train,
              aes(x = time,
                  y = ht,
                  group = id),
            color = "grey",
              alpha = 0.3,
              size = 0.2) +
  geom_smooth(data = bks2_1$est.all,
                aes(x = time, y = .pred),
                color = "brown",
                linetype = 2,
                size = 0.5) +
        geom_smooth(data = tag2_1$augment,
                    aes(x = time, y = .fitted,
                        group = sex),
                    linetype = 3,
                    color = "purple",
                    size = 0.5) +
 xlab("Age") +
  theme_bw()
plot + facet_wrap("sex")
```



5. Make progress, as able with the latex file of the paper.

Start drafting a description of the dataset using Moss and Rice's papers: one paragraph to describe the study and a second to include descriptive statistics.

```
# install.packages("IrregLong")
library(IrregLong)

abacus.plot(n = 10,
    time = "time",
    id = "id",
    data = train,
    tmin = 0,
    tmax = 16,
    # xlab.abacus = "Time",
    # ylab.abacus = "Subject",
    pch.abacus = 16,
    col.abacus = 1)
```

