10_lmm_aic

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```r
load("R/train_test.rda")
all <- rbind(train, test) %>%
  as.data.frame()
```

```r
ctrl <- lmeControl(opt = 'optim')
```

```r
fit1 <-  lme(ht ~ bs(time, degree = 3, knots = 10) * sex + genotype - 1,
             random = ~ 1| id,
             control = ctrl,
             data = all)
glance1 <- broom.mixed::glance(fit1) %>%
  mutate(fixed = "bs(time, knots = 10, degree = 3) * sex + genotype",
         random = "1 | id")

fit2 <-  lme(ht ~ bs(time, degree = 3, knots = 10) * sex + genotype - 1,
             random = ~ 1 + time| id,
             control = ctrl,
             data = all)
glance2 <- broom.mixed::glance(fit2) %>%
  mutate(fixed = "bs(time, knots = 10, degree = 3) * sex + genotype",
         random = "1 + time| id")

fit3 <-  lme(ht ~ bs(time, degree = 3, knots = c(5, 10)) * sex + genotype - 1,
             random = ~ 1| id,
             control = ctrl,
             data = all)
glance3 <- broom.mixed::glance(fit3) %>%
  mutate(fixed = "bs(time, knots = c(5, 10), degree = 3) * sex + genotype",
         random = "1 | id")

fit4 <-  lme(ht ~ bs(time, degree = 3, knots = c(5, 10)) * sex + genotype - 1,
             random = ~ 1 + time| id,
             control = ctrl,
             data = all)
glance4 <- broom.mixed::glance(fit4) %>%
  mutate(fixed = "bs(time, knots = c(5, 10), degree = 3) * sex + genotype",
         random = "1 + time| id")

fit5 <-  lme(ht ~ bs(time, degree = 3, knots = c(5, 10, 15)) * sex + genotype - 1,
             random = ~ 1| id,
             control = ctrl,
```

```r
              data = all)
glance5 <- broom.mixed::glance(fit5) %>%
  mutate(fixed = "bs(time, knots = c(5, 10, 15), degree = 3) * sex + genotype",
         random = "1 + time| id")

fit6 <-  lme(ht ~ bs(time, degree = 3, knots = c(5, 10, 15)) * sex + genotype - 1,
             random = ~ 1 + bs(time, df = 4, degree = 3, intercept = FALSE)| id,
             control = ctrl,
             data = all)
glance6 <- broom.mixed::glance(fit6) %>%
  mutate(fixed = "bs(time, knots = c(5, 10, 15), degree = 3) * sex + genotype",
         random = "1 + bs(time, df = 4, degree = 3)|id")

fit7 <-  lme(ht ~ bs(time, knots = c(10, 12, 15), degree = 3) * sex + genotype - 1,
             random = ~ 1 + bs(time, df = 5, degree = 3, intercept = FALSE)| id,
             control = ctrl,
             data = all)
glance7 <- broom.mixed::glance(fit7) %>%
  mutate(fixed = "bs(time, knots = c(10, 12, 15), degree = 3) * sex + genotype",
         random = "1 + bs(time, df = 5, degree = 3)| id")

# df 3 = intercept 0 + knots 3
fit8 <-  lme(ht ~ bs(time, knots = c(10, 12, 15), degree = 3) * sex + genotype - 1,
             random = ~ 1 + bs(time, df = 4, degree = 2, intercept = FALSE)| id,
             control = ctrl,
             data = all)
glance8 <- broom.mixed::glance(fit8) %>%
  mutate(fixed = "bs(time, knots = c(10, 12, 15), degree = 3) * sex + genotype",
         random = "1 + bs(time, df = 4, degree  = 2)|id")

## df 4 = linear 0 + knots 3
fit9 <-  lme(ht ~ bs(time, knots = c(10, 12, 15), degree = 3) * sex + genotype - 1,
             random = ~ 1 + bs(time, df = 4, degree = 1, intercept = FALSE)| id,
             control = ctrl,
             data = all)
glance9 <- broom.mixed::glance(fit9) %>%
  mutate(fixed = "bs(time, knots = c(10, 12, 15), degree = 3) * sex + genotype",
         random = "1 + bs(time, df = 4, degree = 1)| id")

## df 5 = quadratic 2 + knots 3
fit10 <-  lme(ht ~ bs(time, knots = c(10, 12, 15), degree = 3) * sex + genotype - 1,
             random = ~ 1 + bs(time, df = 5, degree = 2, intercept = FALSE)| id,
             control = ctrl,
             data = train)
glance10 <- broom.mixed::glance(fit10) %>%
  mutate(fixed = "bs(time, knots = c(10, 12, 15), degree = 3) * sex + genotype",
         random = "1 + bs(time, df = 5, degree = 2)| id")

fit11 <-  lme(ht ~ bs(time, knots = c(5, 10, 15), degree = 3) * sex + genotype - 1,
             random = ~ 1 + bs(time, df = 5, degree = 2, intercept = FALSE)| id,
             control = ctrl,
             data = all)
glance11 <- broom.mixed::glance(fit11) %>%
```

```r
  mutate(fixed = "bs(time, knots = c(5, 10, 15), degree = 3) * sex + genotype",
         random = "1 + bs(time, df = 5, degree = 2)| id")

fit12 <-  lme(ht ~ bs(time, knots = c(5, 10, 15), degree = 3) * sex + genotype - 1,
              random = ~ 1 + bs(time, df = 4, degree = 1, intercept = FALSE)| id,
              control = ctrl,
              data = all)
glance12 <- broom.mixed::glance(fit11) %>%
  mutate(fixed = "bs(time, knots = c(5, 10, 15), degree = 3) * sex + genotype",
         random = "1 + bs(time, df = 4, degree = 1)| id")
```

```r
result <- rbind(glance1, glance2, glance3,
                glance4, glance5, glance6,
                glance7, glance8, glance9,
                glance10, glance11, glance12) %>%
  as.data.frame() %>%
  dplyr::select(-nobs, -sigma, -logLik) %>%
  dplyr::select(fixed, random, everything()) %>%
  arrange(AIC)

library(xtable)

result
```

```
#>                                                             fixed
#> 1   bs(time, knots = c(10, 12, 15), degree = 3) * sex + genotype
#> 2   bs(time, knots = c(10, 12, 15), degree = 3) * sex + genotype
#> 3    bs(time, knots = c(5, 10, 15), degree = 3) * sex + genotype
#> 4    bs(time, knots = c(5, 10, 15), degree = 3) * sex + genotype
#> 5   bs(time, knots = c(10, 12, 15), degree = 3) * sex + genotype
#> 6   bs(time, knots = c(10, 12, 15), degree = 3) * sex + genotype
#> 7    bs(time, knots = c(5, 10, 15), degree = 3) * sex + genotype
#> 8         bs(time, knots = c(5, 10), degree = 3) * sex + genotype
#> 9               bs(time, knots = 10, degree = 3) * sex + genotype
#> 10   bs(time, knots = c(5, 10, 15), degree = 3) * sex + genotype
#> 11       bs(time, knots = c(5, 10), degree = 3) * sex + genotype
#> 12             bs(time, knots = 10, degree = 3) * sex + genotype
#>                             random      AIC      BIC
#> 1   1 + bs(time, df = 5, degree = 2)| id 145323.9 145653.9
#> 2   1 + bs(time, df = 5, degree = 3)| id 220137.5 220483.3
#> 3   1 + bs(time, df = 5, degree = 2)| id 221241.6 221587.4
#> 4   1 + bs(time, df = 4, degree = 1)| id 221241.6 221587.4
#> 5   1 + bs(time, df = 4, degree  = 2)|id 226128.2 226419.4
#> 6   1 + bs(time, df = 4, degree = 1)| id 229121.0 229412.2
#> 7    1 + bs(time, df = 4, degree = 3)|id 229273.9 229565.1
#> 8                          1 + time| id 276004.3 276168.1
#> 9                          1 + time| id 280094.9 280240.5
#> 10                         1 + time| id 314642.4 314806.2
#> 11                               1 | id 315240.1 315385.7
#> 12                               1 | id 317322.2 317449.6
```

```r
print(xtable(result, type = "latex"),
      file = paste0("figure/S10_model_selection_aic", Sys.Date(), ".tex"))
```

```r
plot <- all %>%
  ggplot(aes(x = time, y = ht, group = id, color = sex)) +
  geom_line(alpha = 0.2, color = "grey") +
  geom_smooth(aes(group = sex)) +
  theme_bw() +
  labs(x = "Time (yr)") +
  labs(y = "Height (cm)") +
  # ggthemes::scale_fill_tableau("Jewel Bright") +
  ## so far the best color composition
  scale_color_manual(values = c("#eb1e2c", "#00A9FF")) +
  ## facet_wrap("group") +
  theme(axis.text.x = element_text(size = 15),
        axis.text.y = element_text(size = 15),
        axis.title = element_text(size = 16)) +
  theme(legend.position = "none")


ggsave(paste0("figure/S10_supp_figure_overall", Sys.Date(), ".png"))
```

this is the linear mixed model for the analysis

```r
load("results/results_lmm_2023-10-19.Rdata")
mae <- mean(abs(lmm_test$bias)); mae
```

```
#> [1] 3.04425
```

```r
rmse <- mean(abs(lmm_test$bias)^2) %>% sqrt(); rmse
```

```
#> [1] 4.166886
```

```r
cov50 <- mean(abs(lmm_test$coverage50)); cov50
```

```
#> [1] 0.6144895
```

```r
cov80 <- mean(abs(lmm_test$coverage80)); cov80
```

```
#> [1] 0.8819561
```

```r
cov90 <- mean(abs(lmm_test$coverage90)); cov90
```

```
#> [1] 0.9465248
```

```
sessionInfo()
```

```
#> R version 4.2.2 (2022-10-31)
#> Platform: aarch64-apple-darwin20 (64-bit)
#> Running under: macOS 14.0
#>
#> Matrix products: default
#> BLAS:   /Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/lib/libRblas.0.dylib
#> LAPACK: /Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/lib/libRlapack.dylib
#>
#> locale:
#> [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
#>
#> attached base packages:
#> [1] splines   stats     graphics  grDevices utils     datasets  methods
#> [8] base
#>
#> other attached packages:
#>  [1] xtable_1.8-4    nlme_3.1-162    flextable_0.9.2 gtsummary_1.7.1
#>  [5] lubridate_1.9.2 forcats_1.0.0  stringr_1.5.0   dplyr_1.1.2
#>  [9] purrr_1.0.1     readr_2.1.4     tidyr_1.3.0     tibble_3.2.1
#> [13] ggplot2_3.4.3   tidyverse_2.0.0 here_1.0.1
#>
#> loaded via a namespace (and not attached):
#>  [1] fontquiver_0.2.1      rprojroot_2.0.3      tools_4.2.2
#>  [4] backports_1.4.1       utf8_1.2.3           R6_2.5.1
#>  [7] mgcv_1.8-42           colorspace_2.1-0     withr_2.5.0
#> [10] tidyselect_1.2.0      curl_5.0.1           compiler_4.2.2
#> [13] textshaping_0.3.6     cli_3.6.1            gt_0.9.0
#> [16] xml2_1.3.5            officer_0.6.2        fontBitstreamVera_0.1.1
#> [19] labeling_0.4.2        scales_1.2.1         askpass_1.1
#> [22] systemfonts_1.0.4     digest_0.6.33        rmarkdown_2.23
#> [25] gfonts_0.2.0          pkgconfig_2.0.3      htmltools_0.5.5
#> [28] parallelly_1.36.0     fastmap_1.1.1        rlang_1.1.1
#> [31] rstudioapi_0.15.0     httpcode_0.3.0       shiny_1.7.4.1
#> [34] farver_2.1.1          generics_0.1.3       jsonlite_1.8.7
#> [37] broom.mixed_0.2.9.4   zip_2.3.0            magrittr_2.0.3
#> [40] Matrix_1.5-3          Rcpp_1.0.11          munsell_0.5.0
#> [43] fansi_1.0.4           gdtools_0.3.3        lifecycle_1.0.3
#> [46] furrr_0.3.1           stringi_1.7.12       yaml_2.3.7
#> [49] grid_4.2.2            parallel_4.2.2       listenv_0.9.0
#> [52] promises_1.2.0.1      crayon_1.5.2         lattice_0.21-8
#> [55] hms_1.1.3             knitr_1.43           pillar_1.9.0
#> [58] uuid_1.1-0            codetools_0.2-19     crul_1.4.0
#> [61] glue_1.6.2            freshr_1.0.2         evaluate_0.21
#> [64] fontLiberation_0.1.0  data.table_1.14.8    broom.helpers_1.13.0
#> [67] vctrs_0.6.3           tzdb_0.4.0           httpuv_1.6.11
#> [70] gtable_0.3.3          openssl_2.1.0        future_1.33.0
#> [73] xfun_0.39             mime_0.12            broom_1.0.5
#> [76] later_1.3.1           ragg_1.2.5           timechange_0.2.0
#> [79] globals_0.16.2        ellipsis_0.3.2
```