Bootstrap illustration

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Introduction

This vignette will show how to bootstrap the estimate of a `ddhazard` call. this vignette builds on the vignettes 'ddhazard' and 'Comparing methods for time varying logistic models'. Thus, it is suggest to read these first. You can get the version used to make this vignette by calling:'

```
current_version # The string you need to pass devtools::install_github
```

```
## [1] "boennecd/dynamichazard@4b91c16611d0acc9e873ef2b59b7cab4debfd9b9"
```

```
devtools::install_github(current_version)
```

PBC data set

We start by settings up the data set. We will use the pbc2 data set from the `survival` package as in the vignette 'Comparing methods for time varying logistic models':

```
# PBC data set from survival with time variying covariates
# Details of tmerge are not important in this scope. The code is included
# to make you able to reproduce the results
# See: https://cran.r-project.org/web/packages/survival/vignettes/timedep.pdf
library(survival)
temp <- subset(pbc, id <= 312, select=c(id, sex, time, status, edema, age))
pbc2 <- tmerge(temp, temp, id=id, death = event(time, status))
pbc2 <- tmerge(pbc2, pbcseq, id=id, albumin = tdc(day, albumin),
               protime = tdc(day, protime), bili = tdc(day, bili))
pbc2 <- pbc2[, c("id", "tstart", "tstop", "death", "sex", "edema",
                 "age", "albumin", "protime", "bili")]
```

Next, we fit the model as in the vignette 'Comparing methods for time varying logistic models':

```
library(dynamichazard)
```

```
## Loading required package: Rcpp
```

```
## Loading required package: boot
```

```
##
## Attaching package: 'boot'
```

```
## The following object is masked from 'package:survival':
##
##     aml
```

```
## Loading required package: stringr
```

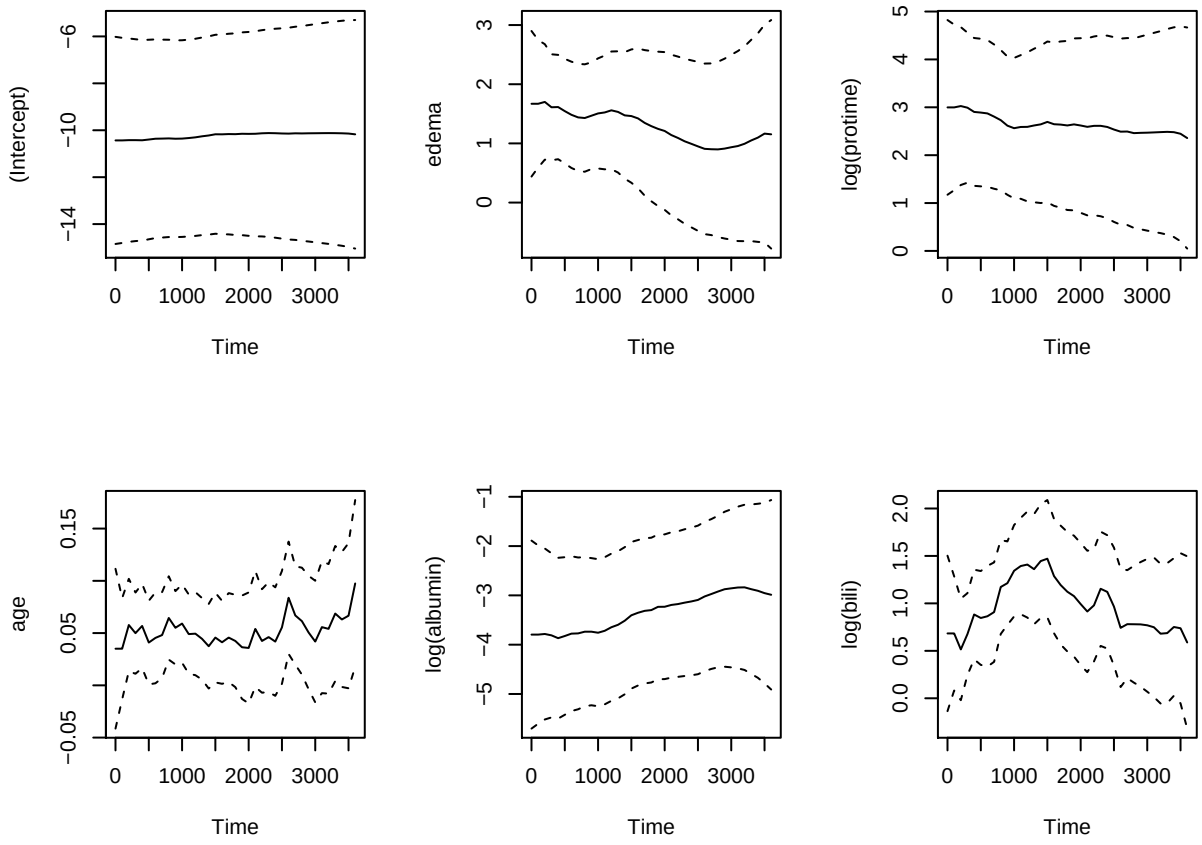
```
dd_fit <- ddhazard(Surv(tstart, tstop, death == 2) ~ age + edema +
                         log(albumin) + log(protime) + log(bili), pbc2,
                   id = pbc2$id, by = 100, max_T = 3600,
```

```
                    Q_0 = diag(rep(10000, 6)), Q = diag(rep(0.001, 6)),
                    control = list(save_risk_set = T, save_data = T, eps = .1))
```

```
## a_0 not supplied. One iteration IWLS of static glm model is used
```

A plot of the estimates is given below. The dashed lines are 95% point-wise confidence intervals using the variances estimates from the Extended Kalman filter with smoothing:

```
plot(dd_fit)
```



Sampling individuals

We can bootstrap the estimates in the model by using `ddhazard_boot` function as done below:

```
set.seed(7451)
R <- 10000
boot_out <- ddhazard_boot(
  dd_fit,
  do_sample_weights = F,       # should re-sampeling be by weights or by
                               # sampling each individual discreetly
  do_stratify_with_event = F, # stratify on whether the individual is an event
                               # or not
  R = R                        # Number of bootstrap samples
```

```
  )
```

```
## Warning in ddhazard_boot(dd_fit, do_sample_weights = F,
## do_stratify_with_event = F, : Failed to estimate 330 times
```

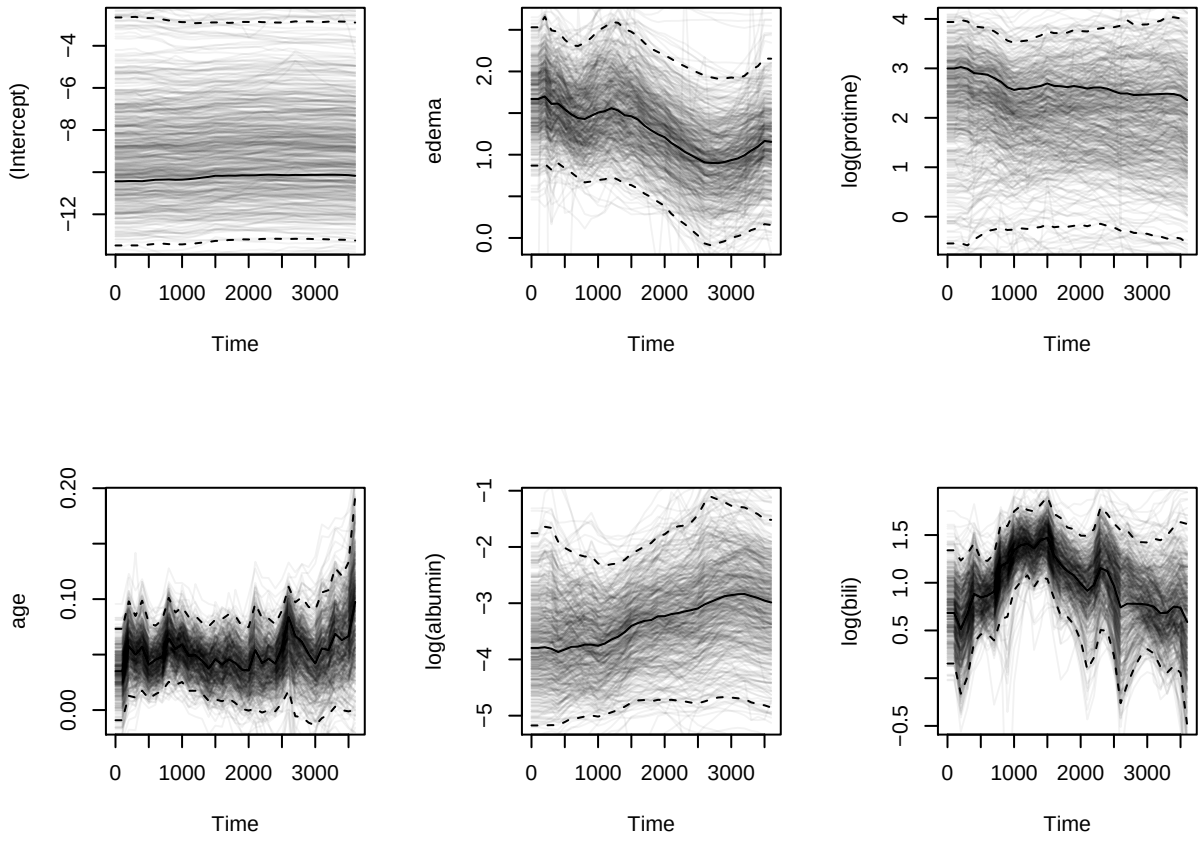
```
# The list has the same structure and class as the list returned by boot::boot
# Though, a few elements are added
class(boot_out)
```

```
## [1] "ddhazard_boot" "boot"
```

Above, we bootstrap the model by sampling the individuals discreetly. I.e. individuals will have weights of $0, 1, 2, \ldots$. We can plot 95% confidence bounds from the bootstrap estimates as follows:

```
plot(dd_fit, ddhazard_boot = boot_out)
```

```
## Only plotting 500 of the boot sample estimates
```



The completely black line are the estimates, the dashed lines are 2.5% and 97.5% quantiles of the bootstrap estimates taken at each point and the transparent black lines each represent a bootstrap estimate. We can check if it affects the results if we perform stratified sampling between those individuals who has an event and those who does not as follows:

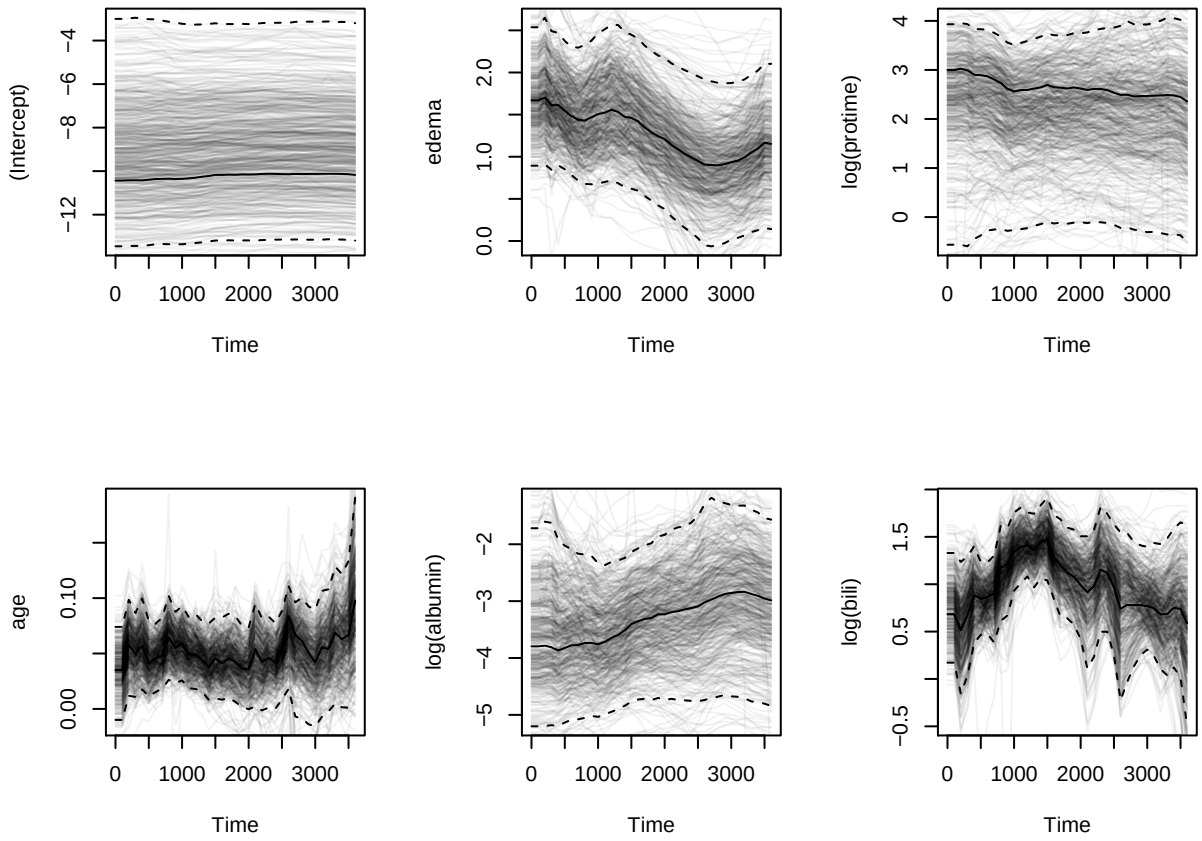
```
set.seed(8524)
boot_out_stratify_by_events <- ddhazard_boot(
  dd_fit,
```

```
  do_sample_weights = F,
  do_stratify_with_event = T, # changed
  R = R)
```

```
## Warning in ddhazard_boot(dd_fit, do_sample_weights = F,
## do_stratify_with_event = T, : Failed to estimate 332 times
```

```
plot(dd_fit, ddhazard_boot = boot_out_stratify_by_events)
```

```
## Only plotting 500 of the boot sample estimates
```



Sampling weights

We can also sample the weights. This is done as follows: within each stratum j (e.g. those who have an event and those who do not) let r_j denote the number of individuals. Then we sample r_j uniform variables $l_i \sim \text{Unif}(0, 1)$ for $i = 1, \dots, r_j$ and normalize with a constant c such that $\sum_{i=1}^{r_j} l_i / c = r_j$. The code below will sample the weights as described above:

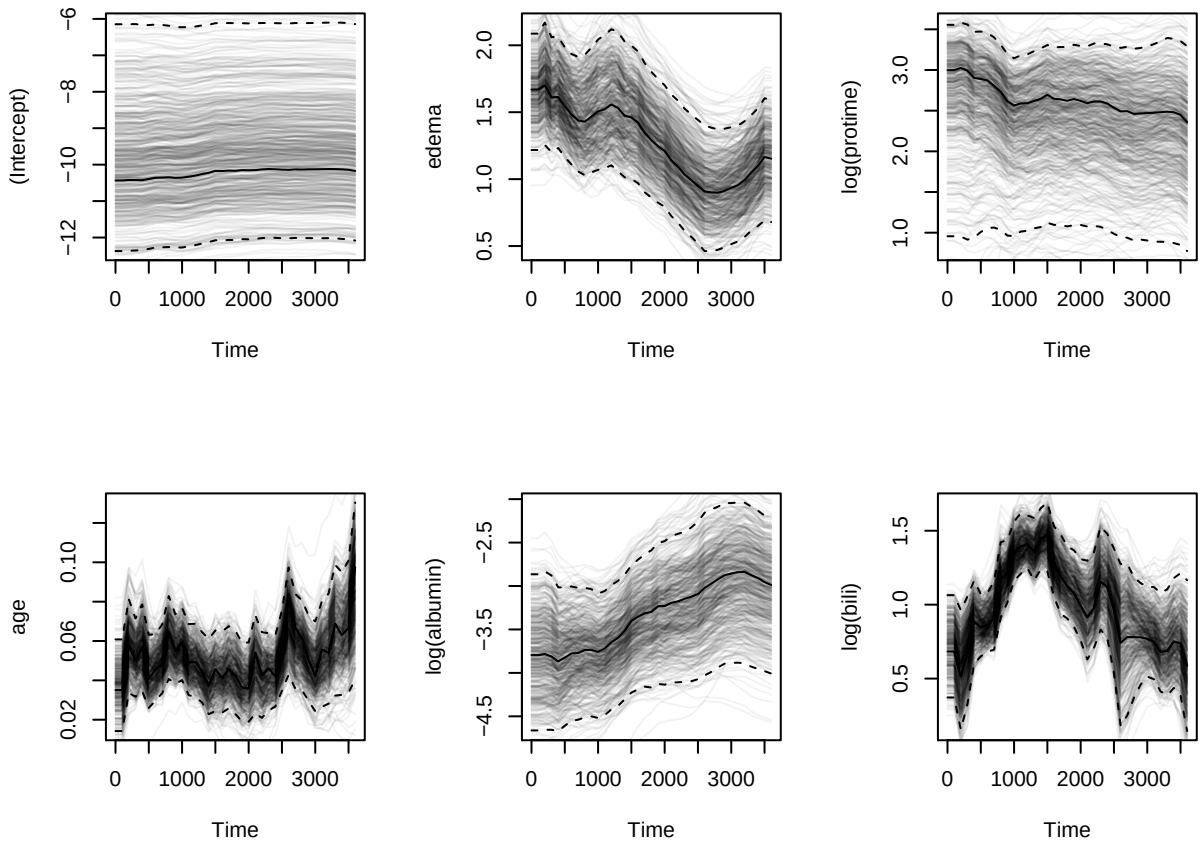
```
set.seed(401)
boot_out_by_weights <- ddhazard_boot(
  dd_fit,
  do_sample_weights = T,       # changed
  do_stratify_with_event = F, # set back to false
```

```
  R = R)
```

```
## Warning in ddhazard_boot(dd_fit, do_sample_weights = T,
## do_stratify_with_event = F, : Failed to estimate 1 times
```

```
plot(dd_fit, ddhazard_boot = boot_out_by_weights)
```

```
## Only plotting 500 of the boot sample estimates
```



Ohter strata

You can also provide your own strata to perform stratified sampling with. This is done by setting the `strata` argument in the call to `ddhazard_boot`. Notice that this has to be on an individual level (one indicator variable per individual) not observation level (not one indicator variable per row in the design matrix). Further, you can use the `unique_id` argument to match the individual entries with the entries in `strata`. As an example, we stratify by the `age` at the start of the study period with the code below:

```
# Individuals have different number of rows in the dataset
xtabs(~xtabs(~pbc2$id))
```

```
## xtabs(~pbc2$id)
##  1  2  3  4  5  6  7  8  9 10 11 12 13 14
## 27 27 34 48 32 30 18 22 21 22  9  9  8  5
```

```r
# Though all the individual have the same age for all periods
# This age is the age at the start of the study
unique(tapply(pbc2$age, pbc2$id, function(x) length(unique(x))))
```

```
## 1
## 1
```

```r
# Next, we find the age for each individual
unique_id <- unique(pbc2$id)
age <- sapply(unique_id, function(x) pbc2$age[pbc$id == x][1])
summary(age)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   33.63   44.52   52.04   50.69   56.22   70.56
```

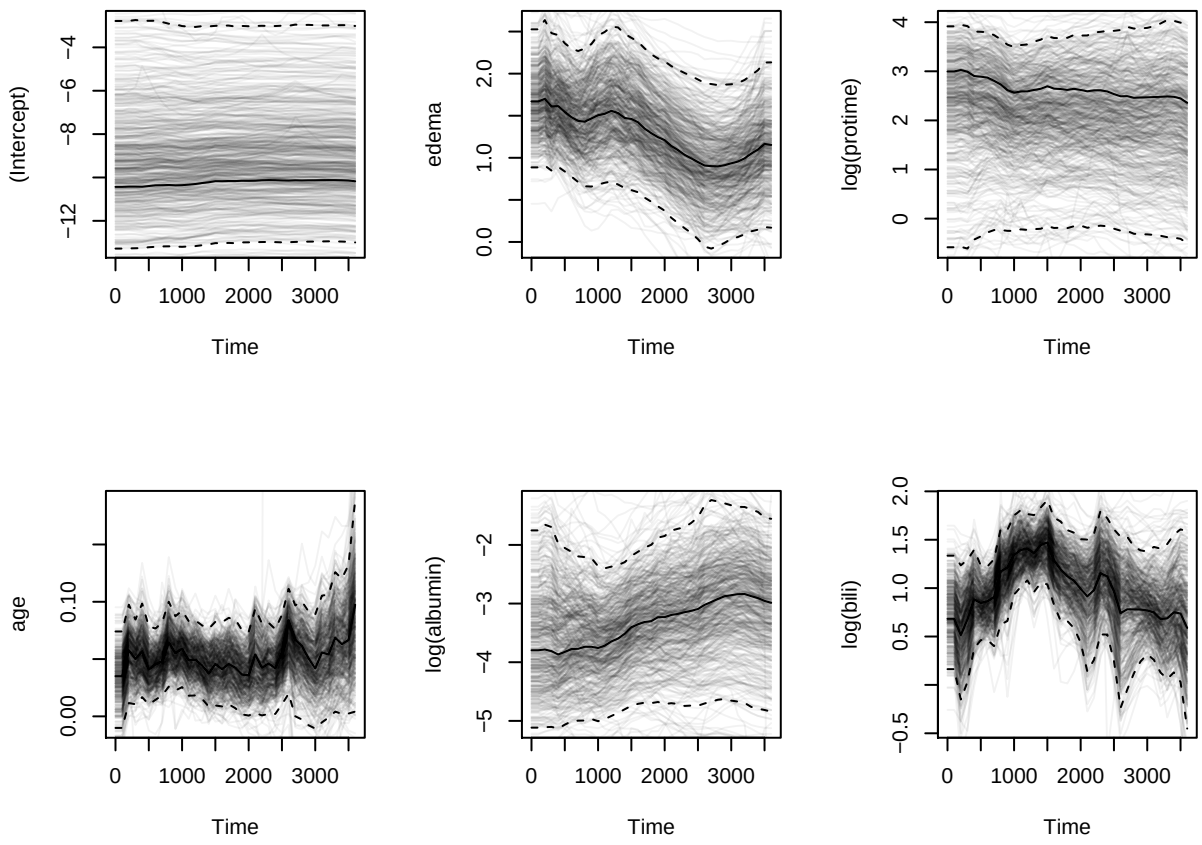
```r
# We define a strata variable for those less than age 50
is_less_than_50 <- age < 50

# We perform stratified sampling over this variable as follows
set.seed(101)
boot_out_with_strata <- ddhazard_boot(
  dd_fit,
  unique_id = unique_id,
  strata = is_less_than_50,
  R = R)
```

```
## Warning in ddhazard_boot(dd_fit, unique_id = unique_id, strata =
## is_less_than_50, : Failed to estimate 309 times
```

```r
plot(dd_fit, ddhazard_boot = boot_out_with_strata)
```

```
## Only plotting 500 of the boot sample estimates
```



The above code is only provide for illustrative purposes. There is no reason to do stratified sampling over the age (as far as I can see). However, it may be useful if you have e.g. categorical variables in your model and want to ensure that each bootstrap sample has a given amount of observation in each categori. Lastly, setting `do_stratify_with_event = T` will yield an interaction factor between the passed `strata` and whether or not the given individual has an event. Stratified sampling will then be performed over this variable

Fixed effects

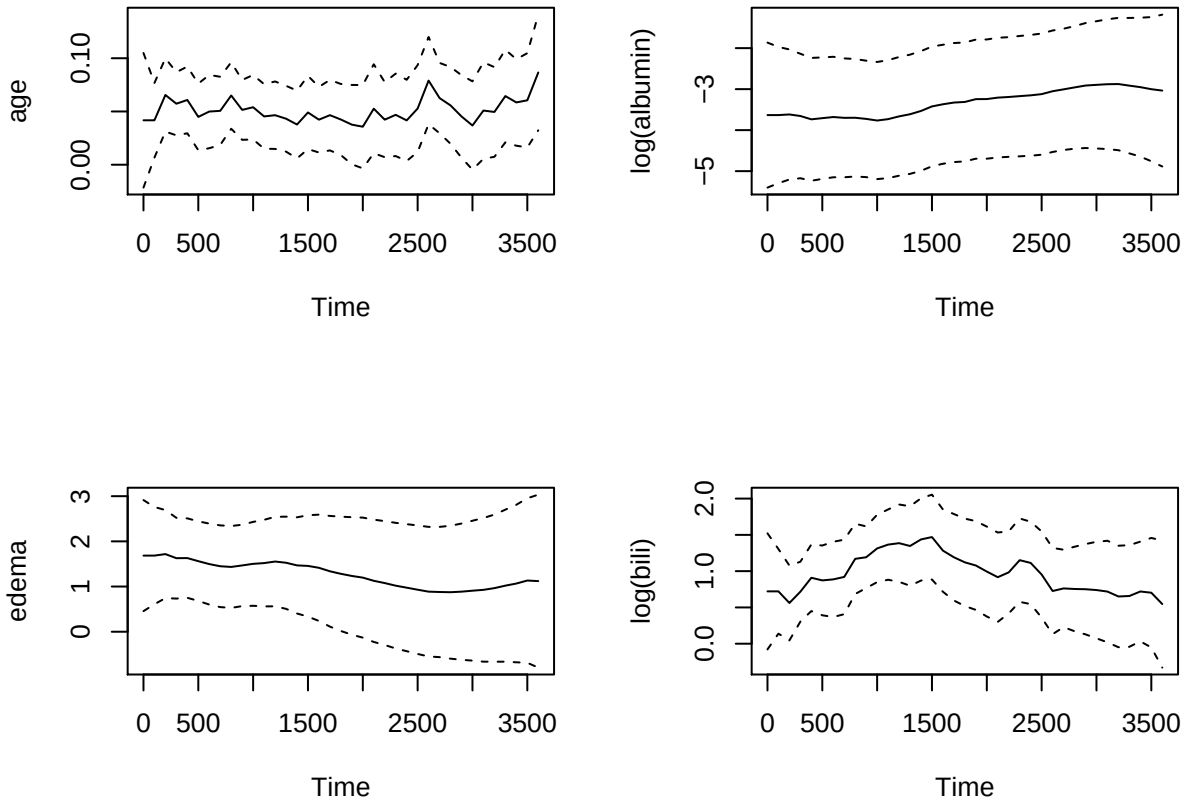
Fixed effects (time invariant effects) can also be bootstrap estimated. The fixed effects bootstrap estimates are added as the last entries of the element `t` of the returned object by `ddhazard_boot`. As an example we will estimate a model below where `log(protime)` and the intercept are fixed

```
dd_fit <- ddhazard(Surv(tstart, tstop, death == 2) ~
                     ddFixed(1) + ddFixed(log(protime)) # changed to fixed
                     + age + edema + log(albumin) +  + log(bili), pbc2,
                   id = pbc2$id, by = 100, max_T = 3600,
                   Q_0 = diag(rep(10000, 4)), Q = diag(rep(0.001, 4)),
                   control = list(
                     save_risk_set = T, save_data = T, eps = .1,
                     fixed_terms_method = "E_step")      # Fixed effects are
                                                         # esimated in E-step
                   )
```

```
## a_0 not supplied. One iteration IWLS of static glm model is used
```

The time varying effects are plotted below:

```
plot(dd_fit)
```



The fixed effects are estimated to:

```
dd_fit$fixed_effects
```

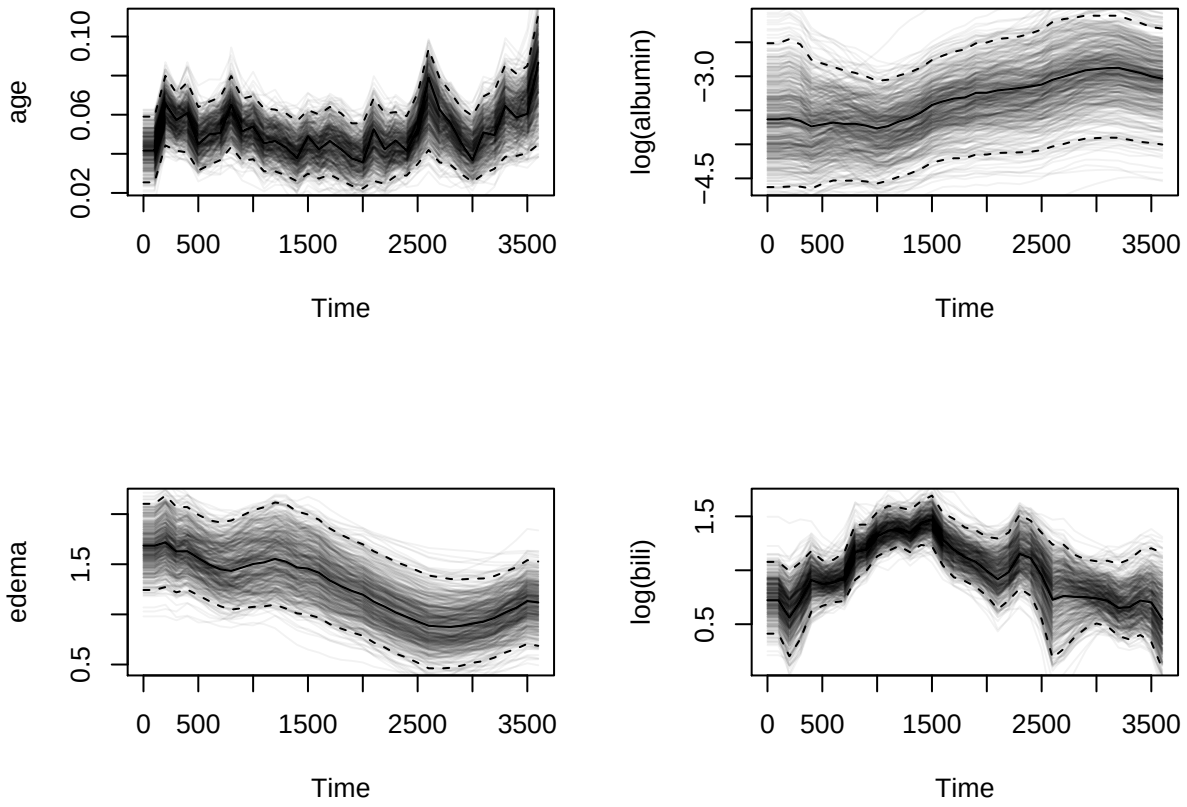
```
##  (Intercept) log(protime)
##   -10.406120     2.725937
```

We can bootstrap the estimates with a call similar to those we made before:

```
set.seed(9001)
boot_out <- ddhazard_boot(
  dd_fit,
  do_sample_weights = T,       # sample weights
  do_stratify_with_event = F, # dont stratify by event
  R = R)

# Plot time varying effects
plot(dd_fit, ddhazard_boot = boot_out)
```

```
## Only plotting 500 of the boot sample estimates
```



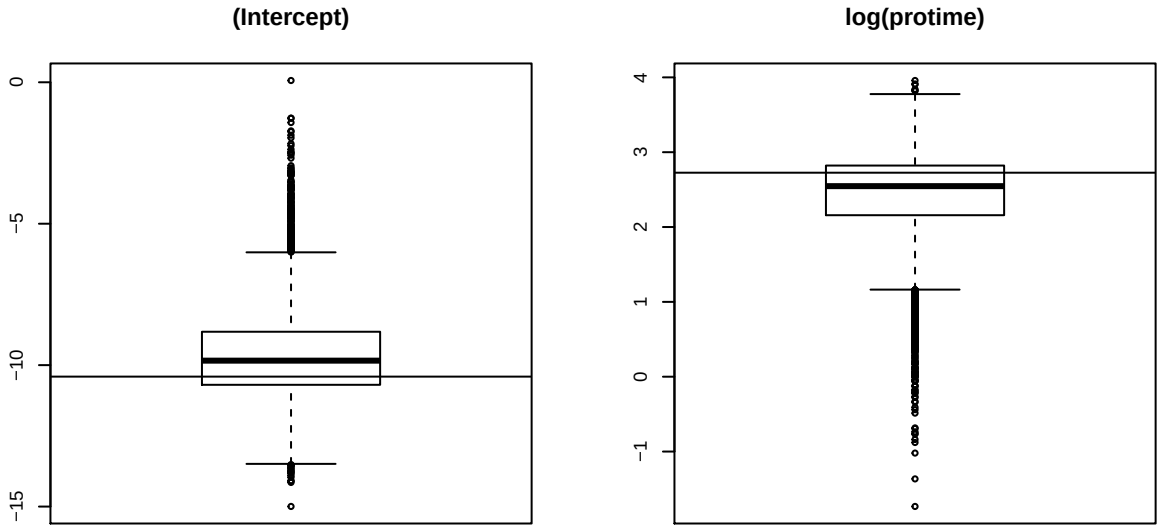
We then turn the bootstrap estimates of the fixed effects. Below, we first slice out the fixed effects, print a few of the bootstrap sample estimates and then make a box plot of the all the sample estimates. Lastly, we add a continuous horizontal line for the initial estimates:

```
# Print some of bootstrap estimates of the fixed effects
fixed_effects_ests <- t(tail(t(boot_out$t), 2))
head(fixed_effects_ests)
```

```
##      (Intercept) log(protime)
## [1,]   -7.605845     1.381172
## [2,]   -9.885875     2.096563
## [3,]   -6.312162     1.029886
## [4,]   -9.949000     2.664229
## [5,]   -9.816320     2.415881
## [6,]   -9.657463     2.724311
```

```
# Make a boxplot of the fixed effects
par(mfcol = c(1, 2), cex = .6)
for(i in 1:ncol(fixed_effects_ests)){
  boxplot(fixed_effects_ests[, i], main = colnames(fixed_effects_ests)[i])

  # Add a horisontal line at the estimates with the whole sample
  abline(h = dd_fit$fixed_effects[i])
}
```


(Intercept)
log(protime)
0
−5
−10
−15
4
3
2
1
0
−1