# Demographic data

Nathan Constantine-Cooke

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## Table of contents

## Introduction

```
source("Survival/utils.R")
library(forestplot)

# Setup analysis environment
analysis_setup <- setup_analysis()
paths <- analysis_setup$paths
demo <- analysis_setup$demo

flare.df <- readRDS(paste0(paths$outdir, "flares-controlled.RDS"))
flare.cd.df <- readRDS(paste0(paths$outdir, "flares-controlled-cd.RDS"))
flare.uc.df <- readRDS(paste0(paths$outdir, "flares-controlled-uc.RDS"))

cd.clin.forest <- readRDS(paste0(paths$outdir, "cd-clin-controlled.RDS"))
cd.hard.forest <- readRDS(paste0(paths$outdir, "cd-hard-controlled.RDS"))
uc.clin.forest <- readRDS(paste0(paths$outdir, "uc-clin-controlled.RDS"))
uc.hard.forest <- readRDS(paste0(paths$outdir, "uc-hard-controlled.RDS"))
```

This page describes associations between demographic data and time-to-flare. Sex and IMD
are not covered here as they are covered in the controlled variables section

The page describing demographic variables in a descriptive manner can be found here.

## Age

### Crohn's disease

### Patient-reported flare

```
# Categorize age
flare.cd.df <- categorize_variable(flare.cd.df, "Age",
                                   breaks = c(0, 18, 30, 45, 65, Inf),
                                   labels = c("Under 18", "18-29", "30-44", "45-64", "65+"))

# Generate survival plot and run Cox model
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "Age",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Age",
  plot_base_path = "plots/cd/soft-flare/demographics/age",
  break_time_by = 200
)

# Extract hazard ratio for Age (continuous variable)
fit.me <- coxph(
  Surv(softflare_time, softflare) ~ Sex + IMD + cat + Age + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

cd.clin.forest <- rbind(cd.clin.forest, get_HR(fit.me, "Age"))

# Display plot and model summary
analysis_result$plot
invisible(cox_summary(fit.me))
```

Cox model summary:

| Variable | HR | Lower 95% | Upper 95% | P-value |
|----------|------|-----------|-----------|---------|
| SexFemale | 1.9948 | 1.5719 | 2.5314 | 0.0000 |
| IMD2 | 0.9308 | 0.5932 | 1.4607 | 0.7552 |
| IMD3 | 0.8884 | 0.5615 | 1.4056 | 0.6131 |
| IMD4 | 0.9315 | 0.5990 | 1.4484 | 0.7527 |

| Variable | HR | Lower 95% | Upper 95% | P-value |
|---|---|---|---|---|
| IMD5 | 0.9621 | 0.6277 | 1.4748 | 0.8594 |
| catFC 50-250 | 1.5738 | 1.2191 | 2.0316 | 0.0005 |
| catFC > 250 | 2.4166 | 1.8207 | 3.2075 | 0.0000 |
| Age | 1.0049 | 0.9977 | 1.0121 | 0.1862 |

Diagnostics:

**Proportional hazards assumption test**

| | Chi-squared statistic | DF | P-value |
|---|---|---|---|
| Sex | 0.2901 | 0.9920 | 0.5868 |
| IMD | 5.8012 | 3.9466 | 0.2090 |
| cat | 2.3892 | 1.9800 | 0.2989 |
| Age | 2.7170 | 0.9659 | 0.0948 |
| GLOBAL | 12.3923 | 15.5406 | 0.6865 |

**DF betas**

Warning: `gather_()` was deprecated in tidyr 1.2.0.
i Please use `gather()` instead.
i The deprecated feature was likely used in the survminer package.
  Please report the issue at <https://github.com/kassambara/survminer/issues>.

`geom_smooth()` using formula = 'y ~ x'

**Martingale residuals**

`geom_smooth()` using formula = 'y ~ x'

**Objective flare**

```
# Generate survival plot and run Cox model for objective flare
analysis_result <- run_survival_analysis(
  data = flare.cd.df,
  var_name = "Age",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Age",
  plot_base_path = "plots/cd/hard-flare/demographics/age",
  break_time_by = 500
)

# Extract hazard ratio for Age (continuous variable)
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~ Sex + IMD + cat + Age + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

cd.hard.forest <- rbind(cd.hard.forest, get_HR(fit.me, "Age"))

# Display plot and model summary
analysis_result$plot
invisible(cox_summary(fit.me))
```

Cox model summary:

| Variable | HR | Lower 95% | Upper 95% | P-value |
|---|---|---|---|---|
| SexFemale | 1.4100 | 1.0742 | 1.8506 | 0.0133 |
| IMD2 | 0.9220 | 0.5371 | 1.5828 | 0.7684 |
| IMD3 | 0.9333 | 0.5377 | 1.6200 | 0.8061 |
| IMD4 | 0.9037 | 0.5282 | 1.5462 | 0.7117 |
| IMD5 | 0.9530 | 0.5672 | 1.6014 | 0.8559 |
| catFC 50-250 | 2.0702 | 1.5083 | 2.8414 | 0.0000 |
| catFC > 250 | 3.3191 | 2.3583 | 4.6712 | 0.0000 |
| Age | 0.9865 | 0.9779 | 0.9953 | 0.0026 |

Diagnostics:

**Proportional hazards assumption test**

| | Chi-squared statistic | DF | P-value |
|---|---|---|---|
| Sex | 0.2070 | 0.9856 | 0.6432 |
| IMD | 4.3372 | 3.9449 | 0.3546 |
| cat | 8.6873 | 1.9855 | 0.0128 |
| Age | 3.3245 | 0.9503 | 0.0635 |
| GLOBAL | 16.4294 | 18.2438 | 0.5790 |

**DF betas**

`geom_smooth()` using formula = 'y ~ x'

**Martingale residuals**

`geom_smooth()` using formula = 'y ~ x'

**Ulcerative colitis**

**Patient-reported flare**

```
# Categorize age
flare.uc.df <- categorize_variable(flare.uc.df, "Age",
                                   breaks = c(0, 18, 30, 45, 65, Inf),
                                   labels = c("Under 18", "18-29", "30-44", "45-64", "65+"))

# Generate survival plot and run Cox model
analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "Age",
  outcome_time = "softflare_time",
  outcome_event = "softflare",
  legend_title = "Age",
  plot_base_path = "plots/uc/soft-flare/demographics/age",
  break_time_by = 200
)

# Extract hazard ratio for Age (continuous variable)
fit.me <- coxph(
  Surv(softflare_time, softflare) ~ Sex + IMD + cat + Age + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
```

```
  data = flare.uc.df
)

uc.clin.forest <- rbind(uc.clin.forest, get_HR(fit.me, "Age"))

# Display plot and model summary
analysis_result$plot
invisible(cox_summary(fit.me))
```

Cox model summary:

| Variable | HR | Lower 95% | Upper 95% | P-value |
|---|---|---|---|---|
| SexFemale | 1.5135 | 1.2220 | 1.8747 | 0.0001 |
| IMD2 | 1.2074 | 0.7621 | 1.9129 | 0.4220 |
| IMD3 | 1.0923 | 0.6966 | 1.7126 | 0.7006 |
| IMD4 | 1.4407 | 0.9378 | 2.2131 | 0.0955 |
| IMD5 | 1.2134 | 0.7953 | 1.8512 | 0.3695 |
| catFC 50-250 | 1.5856 | 1.2399 | 2.0277 | 0.0002 |
| catFC > 250 | 2.1185 | 1.6228 | 2.7658 | 0.0000 |
| Age | 0.9928 | 0.9857 | 0.9998 | 0.0449 |

Diagnostics:

**Proportional hazards assumption test**

| | Chi-squared statistic | DF | P-value |
|---|---|---|---|
| Sex | 1.2765 | 0.9891 | 0.2555 |
| IMD | 3.9850 | 3.9439 | 0.3998 |
| cat | 5.7478 | 1.9712 | 0.0549 |
| Age | 0.2636 | 0.9656 | 0.5931 |
| GLOBAL | 11.8199 | 19.6624 | 0.9132 |

**DF betas**

```
`geom_smooth()` using formula = 'y ~ x'
```

**Martingale residuals**

`geom_smooth()` using formula = 'y ~ x'

**Objective flare**

```r
# Generate survival plot and run Cox model for objective flare
analysis_result <- run_survival_analysis(
  data = flare.uc.df,
  var_name = "Age",
  outcome_time = "hardflare_time",
  outcome_event = "hardflare",
  legend_title = "Age",
  plot_base_path = "plots/uc/hard-flare/demographics/age",
  break_time_by = 500
)

# Extract hazard ratio for Age (continuous variable)
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~ Sex + IMD + cat + Age + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)

uc.hard.forest <- rbind(uc.hard.forest, get_HR(fit.me, "Age"))

# Display plot and model summary
analysis_result$plot
invisible(cox_summary(fit.me))
```

Cox model summary:

| Variable | HR | Lower 95% | Upper 95% | P-value |
|---|---|---|---|---|
| SexFemale | 1.2937 | 0.9958 | 1.6807 | 0.0538 |
| IMD2 | 1.3555 | 0.7565 | 2.4289 | 0.3067 |
| IMD3 | 1.3777 | 0.7842 | 2.4203 | 0.2650 |
| IMD4 | 1.7536 | 1.0168 | 3.0242 | 0.0434 |
| IMD5 | 1.3509 | 0.7875 | 2.3173 | 0.2747 |
| catFC 50-250 | 2.0872 | 1.5288 | 2.8495 | 0.0000 |
| catFC > 250 | 3.1867 | 2.3015 | 4.4124 | 0.0000 |
| Age | 0.9882 | 0.9794 | 0.9971 | 0.0094 |

| Variable | HR | Lower 95% | Upper 95% | P-value |
|---|---|---|---|---|

Diagnostics:

**Proportional hazards assumption test**

|  | Chi-squared statistic | DF | P-value |
|---|---|---|---|
| Sex | 0.1150 | 0.9847 | 0.7285 |
| IMD | 2.7089 | 3.9421 | 0.5986 |
| cat | 4.0990 | 1.9687 | 0.1255 |
| Age | 0.3529 | 0.9656 | 0.5381 |
| GLOBAL | 7.4819 | 23.1362 | 0.9991 |

**DF betas**

`geom_smooth()` using formula = 'y ~ x'

**Martingale residuals**

`geom_smooth()` using formula = 'y ~ x'

**BMI**

**Crohn's disease**

**Patient-reported flare**

```
p <- generate_survival_plot(
  data = flare.cd.df,
  formula = Surv(softflare_time, softflare) ~ BMIcat,
  legend_title = "BMI",
  legend_labs = c("Underweight", "Normal", "Overweight", "Obese"),
  palette = c("#1A8FE3", "#E76D83", "#5FB49C", "#FED766"),
  xlab = "Time from study recruitment (days)",
  title = "Time to clinical flare",
  break_time_by = 200,
  plot_path = "plots/cd/soft-flare/demographics/bmi"
```

```
)

print(p, newpage = FALSE)

fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + IMD + cat + BMI + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

cd.clin.forest <- rbind(
  cd.clin.forest,
  get_HR(fit.me, c("BMI"))
)

invisible(cox_summary(fit.me))
```

Cox model summary:

| Variable | HR | Lower 95% | Upper 95% | P-value |
|----------|------|-----------|-----------|---------|
| SexFemale | 2.1473 | 1.6736 | 2.7550 | 0.0000 |
| IMD2 | 0.8998 | 0.5671 | 1.4279 | 0.6542 |
| IMD3 | 0.8895 | 0.5555 | 1.4243 | 0.6258 |
| IMD4 | 0.9343 | 0.5951 | 1.4667 | 0.7676 |
| IMD5 | 0.9772 | 0.6332 | 1.5081 | 0.9171 |
| catFC 50-250 | 1.5540 | 1.1972 | 2.0170 | 0.0009 |
| catFC > 250 | 2.2569 | 1.6787 | 3.0342 | 0.0000 |
| BMI | 1.0122 | 0.9911 | 1.0337 | 0.2594 |

Diagnostics:

**Proportional hazards assumption test**

| | Chi-squared statistic | DF | P-value |
|-----|-----------------------|--------|---------|
| Sex | 0.1734 | 0.9925 | 0.6740 |
| IMD | 6.5777 | 3.9477 | 0.1556 |
| cat | 1.5900 | 1.9797 | 0.4468 |
| BMI | 2.3144 | 0.9900 | 0.1265 |

| | Chi-squared statistic | DF | P-value |
|---|---|---|---|
| GLOBAL | 10.2401 | 14.8159 | 0.7941 |

**DF betas**

`` `geom_smooth()` using formula = 'y ~ x' ``

**Martingale residuals**

`` `geom_smooth()` using formula = 'y ~ x' ``

**Objective flare**

```
p <- generate_survival_plot(
  data = flare.cd.df,
  formula = Surv(hardflare_time, hardflare) ~ BMIcat,
  legend_title = "BMI",
  legend_labs = c("Underweight", "Normal", "Overweight", "Obese"),
  palette = c("#1A8FE3", "#E76D83", "#5FB49C", "#FED766"),
  xlab = "Time from study recruitment (days)",
  title = "Time to objective flare",
  break_time_by = 500,
  plot_path = "plots/cd/hard-flare/demographics/bmi"
)

print(p, newpage = FALSE)

fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + IMD + cat + BMI + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

cd.hard.forest <- rbind(
  cd.hard.forest,
  get_HR(fit.me, c("BMI"))
)

invisible(cox_summary(fit.me))
```

Cox model summary:

| Variable | HR | Lower 95% | Upper 95% | P-value |
|----------|-----|-----------|-----------|---------|
| SexFemale | 1.5011 | 1.1295 | 1.9950 | 0.0051 |
| IMD2 | 0.9513 | 0.5451 | 1.6599 | 0.8604 |
| IMD3 | 0.9658 | 0.5454 | 1.7103 | 0.9050 |
| IMD4 | 0.8451 | 0.4830 | 1.4788 | 0.5556 |
| IMD5 | 0.9334 | 0.5478 | 1.5906 | 0.8001 |
| catFC 50-250 | 2.0103 | 1.4508 | 2.7857 | 0.0000 |
| catFC > 250 | 3.1451 | 2.1945 | 4.5074 | 0.0000 |
| BMI | 1.0200 | 0.9949 | 1.0456 | 0.1187 |

Diagnostics:

**Proportional hazards assumption test**

| | Chi-squared statistic | DF | P-value |
|-----|-----------------------|------|---------|
| Sex | 0.8263 | 0.9880 | 0.3591 |
| IMD | 3.6654 | 3.9453 | 0.4448 |
| cat | 7.2453 | 1.9854 | 0.0263 |
| BMI | 3.8299 | 0.9886 | 0.0495 |
| GLOBAL | 15.1563 | 17.4781 | 0.6169 |

**DF betas**

`geom_smooth()` using formula = 'y ~ x'

**Martingale residuals**

`geom_smooth()` using formula = 'y ~ x'

**Ulcerative colitis**

**Patient-reported flare**

```
p <- generate_survival_plot(
  data = flare.uc.df,
  formula = Surv(softflare_time, softflare) ~ BMIcat,
  legend_title = "BMI",
  legend_labs = c("Underweight", "Normal", "Overweight", "Obese"),
  palette = c("#1A8FE3", "#E76D83", "#5FB49C", "#FED766"),
  xlab = "Time from study recruitment (days)",
  title = "Time to clinical flare",
  break_time_by = 200,
  plot_path = "plots/uc/soft-flare/demographics/bmi"
)

print(p, newpage = FALSE)

fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex + IMD + cat + BMI + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)
uc.clin.forest <- rbind(
  uc.clin.forest,
  get_HR(fit.me, c("BMI"))
)
invisible(cox_summary(fit.me))
```

Cox model summary:

| Variable | HR | Lower 95% | Upper 95% | P-value |
|----------|-----|-----------|-----------|---------|
| SexFemale | 1.5667 | 1.2601 | 1.9478 | 0.0001 |
| IMD2 | 1.2357 | 0.7747 | 1.9711 | 0.3743 |
| IMD3 | 1.0037 | 0.6340 | 1.5890 | 0.9873 |
| IMD4 | 1.4156 | 0.9159 | 2.1878 | 0.1177 |
| IMD5 | 1.1137 | 0.7241 | 1.7128 | 0.6240 |
| catFC 50-250 | 1.6181 | 1.2586 | 2.0803 | 0.0002 |
| catFC > 250 | 2.1566 | 1.6473 | 2.8235 | 0.0000 |
| BMI | 0.9686 | 0.9481 | 0.9896 | 0.0035 |

Diagnostics:

**Proportional hazards assumption test**

|  | Chi-squared statistic | DF | P-value |
|---|---|---|---|
| Sex | 1.3437 | 0.9904 | 0.2438 |
| IMD | 3.8474 | 3.9456 | 0.4189 |
| cat | 4.7128 | 1.9726 | 0.0925 |
| BMI | 0.4838 | 0.9851 | 0.4807 |
| GLOBAL | 10.4559 | 17.3504 | 0.8958 |

**DF betas**

`geom_smooth()` using formula = 'y ~ x'

**Martingale residuals**

`geom_smooth()` using formula = 'y ~ x'

**Objective flare**

```
p <- generate_survival_plot(
  data = flare.uc.df,
  formula = Surv(hardflare_time, hardflare) ~ BMIcat,
  legend_title = "BMI",
  legend_labs = c("Underweight", "Normal", "Overweight", "Obese"),
  palette = c("#1A8FE3", "#E76D83", "#5FB49C", "#FED766"),
  xlab = "Time from study recruitment (days)",
  title = "Time to objective flare",
  break_time_by = 500,
  plot_path = "plots/uc/hard-flare/demographics/bmi"
)

print(p, newpage = FALSE)

fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex + IMD + cat + BMI + frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.uc.df
)
```

```
uc.hard.forest <- rbind(
  uc.hard.forest,
  get_HR(fit.me, "BMI")
  )
invisible(cox_summary(fit.me))
```

Cox model summary:

| Variable | HR | Lower 95% | Upper 95% | P-value |
|---|---|---|---|---|
| SexFemale | 1.3542 | 1.0359 | 1.7703 | 0.0265 |
| IMD2 | 1.4226 | 0.7804 | 2.5931 | 0.2499 |
| IMD3 | 1.3567 | 0.7598 | 2.4225 | 0.3024 |
| IMD4 | 1.7491 | 0.9986 | 3.0636 | 0.0506 |
| IMD5 | 1.2764 | 0.7316 | 2.2270 | 0.3902 |
| catFC 50-250 | 2.0568 | 1.4948 | 2.8299 | 0.0000 |
| catFC > 250 | 3.2137 | 2.3058 | 4.4790 | 0.0000 |
| BMI | 0.9808 | 0.9558 | 1.0065 | 0.1415 |

Diagnostics:

**Proportional hazards assumption test**

| | Chi-squared statistic | DF | P-value |
|---|---|---|---|
| Sex | 0.1486 | 0.9850 | 0.6938 |
| IMD | 2.5015 | 3.9358 | 0.6345 |
| cat | 3.5648 | 1.9672 | 0.1640 |
| BMI | 0.1512 | 0.9853 | 0.6915 |
| GLOBAL | 6.9035 | 22.4944 | 0.9993 |

**DF betas**

`geom_smooth()` using formula = 'y ~ x'

**Martingale residuals**

`geom_smooth()` using formula = 'y ~ x'

```
saveRDS(flare.df, paste0(paths$outdir, "flares-demographics.RDS"))
saveRDS(flare.cd.df, paste0(paths$outdir, "flares-demographics-cd.RDS"))
saveRDS(flare.uc.df, paste0(paths$outdir, "flares-demographics-uc.RDS"))

saveRDS(cd.clin.forest, paste0(paths$outdir, "cd-clin-demographics.RDS"))
saveRDS(cd.hard.forest, paste0(paths$outdir, "cd-hard-demographics.RDS"))
saveRDS(uc.clin.forest, paste0(paths$outdir, "uc-clin-demographics.RDS"))
saveRDS(uc.hard.forest, paste0(paths$outdir, "uc-hard-demographics.RDS"))
```

Control for additional covariates

Crohn's disease

Patient-reported flare

```
fit.me <- coxph(
  Surv(softflare_time, softflare) ~
    Sex +
    IMD +
    cat +
    `IBD Duration` +
    BMI +
    Treatment +
    Age +
    frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

invisible(cox_summary(fit.me))
```

Cox model summary:

| Variable | HR | Lower 95% | Upper 95% | P-value |
| --- | ---: | ---: | ---: | ---: |
| SexFemale | 2.1585 | 1.6671 | 2.7947 | 0.0000 |
| IMD2 | 0.8389 | 0.5280 | 1.3326 | 0.4569 |
| IMD3 | 0.8199 | 0.5074 | 1.3247 | 0.4172 |
| IMD4 | 0.8984 | 0.5702 | 1.4156 | 0.6442 |
| IMD5 | 0.9268 | 0.5991 | 1.4337 | 0.7327 |
| catFC 50-250 | 1.4944 | 1.1441 | 1.9521 | 0.0032 |
| catFC > 250 | 2.1836 | 1.6127 | 2.9566 | 0.0000 |
| IBD Duration | 0.9942 | 0.9829 | 1.0056 | 0.3152 |

| Variable | HR | Lower 95% | Upper 95% | P-value |
|---|---|---|---|---|
| BMI | 1.0040 | 0.9821 | 1.0264 | 0.7231 |
| TreatmentMono biologic | 0.9820 | 0.6903 | 1.3971 | 0.9197 |
| TreatmentCombo therapy | 0.7083 | 0.4599 | 1.0909 | 0.1175 |
| Treatment5-ASA | 1.3322 | 0.7502 | 2.3657 | 0.3276 |
| TreatmentNone reported | 0.9726 | 0.7007 | 1.3502 | 0.8683 |
| Age | 1.0046 | 0.9957 | 1.0136 | 0.3112 |
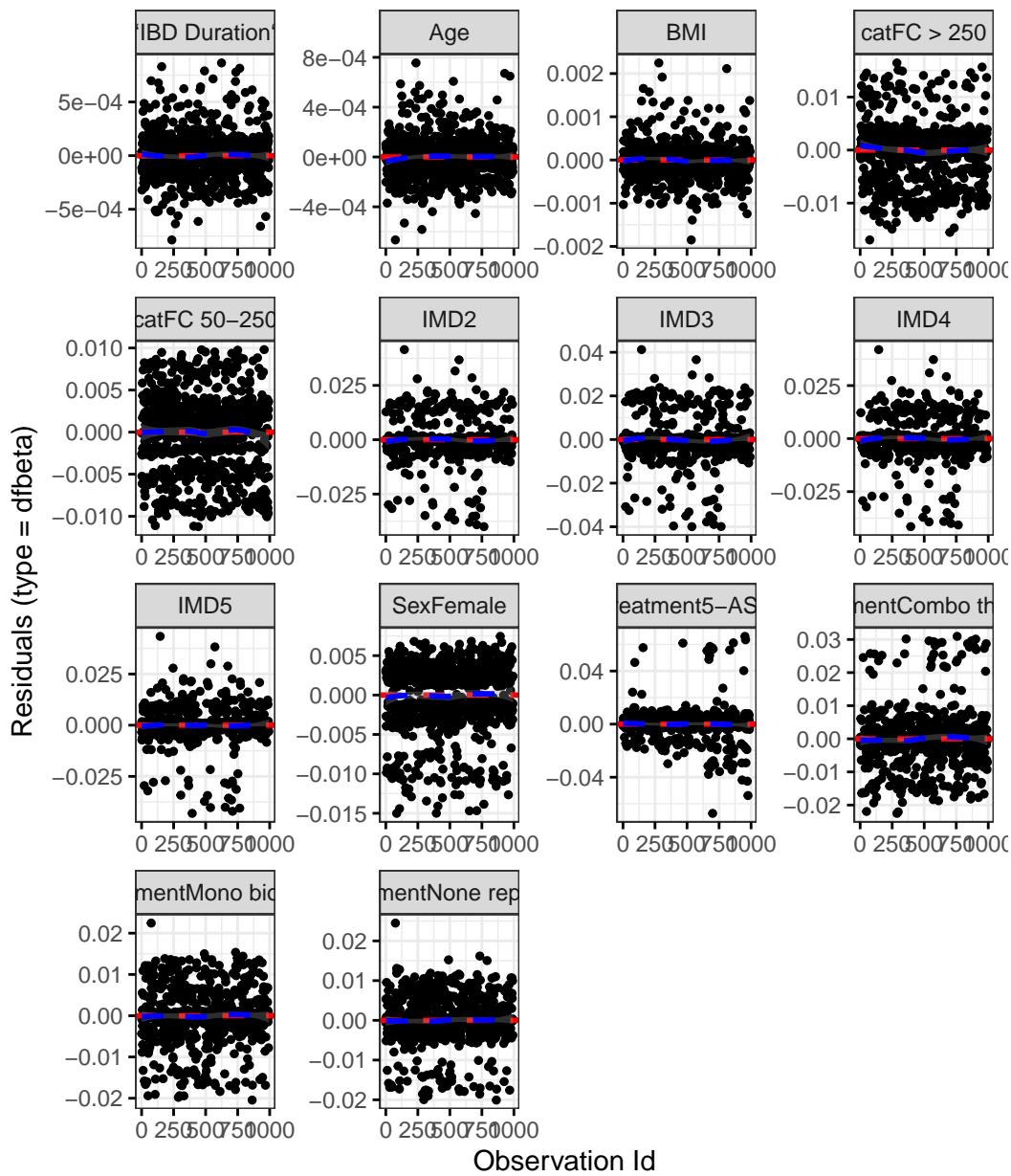
Diagnostics:

**Proportional hazards assumption test**

| | Chi-squared statistic | DF | P-value |
|---|---|---|---|
| Sex | 0.4811 | 0.9924 | 0.4849 |
| IMD | 5.6223 | 3.9577 | 0.2246 |
| cat | 1.4933 | 1.9842 | 0.4702 |
| IBD Duration | 3.5316 | 0.9957 | 0.0598 |
| BMI | 2.1568 | 0.9913 | 0.1404 |
| Treatment | 3.4530 | 3.9163 | 0.4721 |
| Age | 2.1438 | 0.9913 | 0.1416 |
| GLOBAL | 18.1663 | 18.5875 | 0.4840 |

**DF betas**
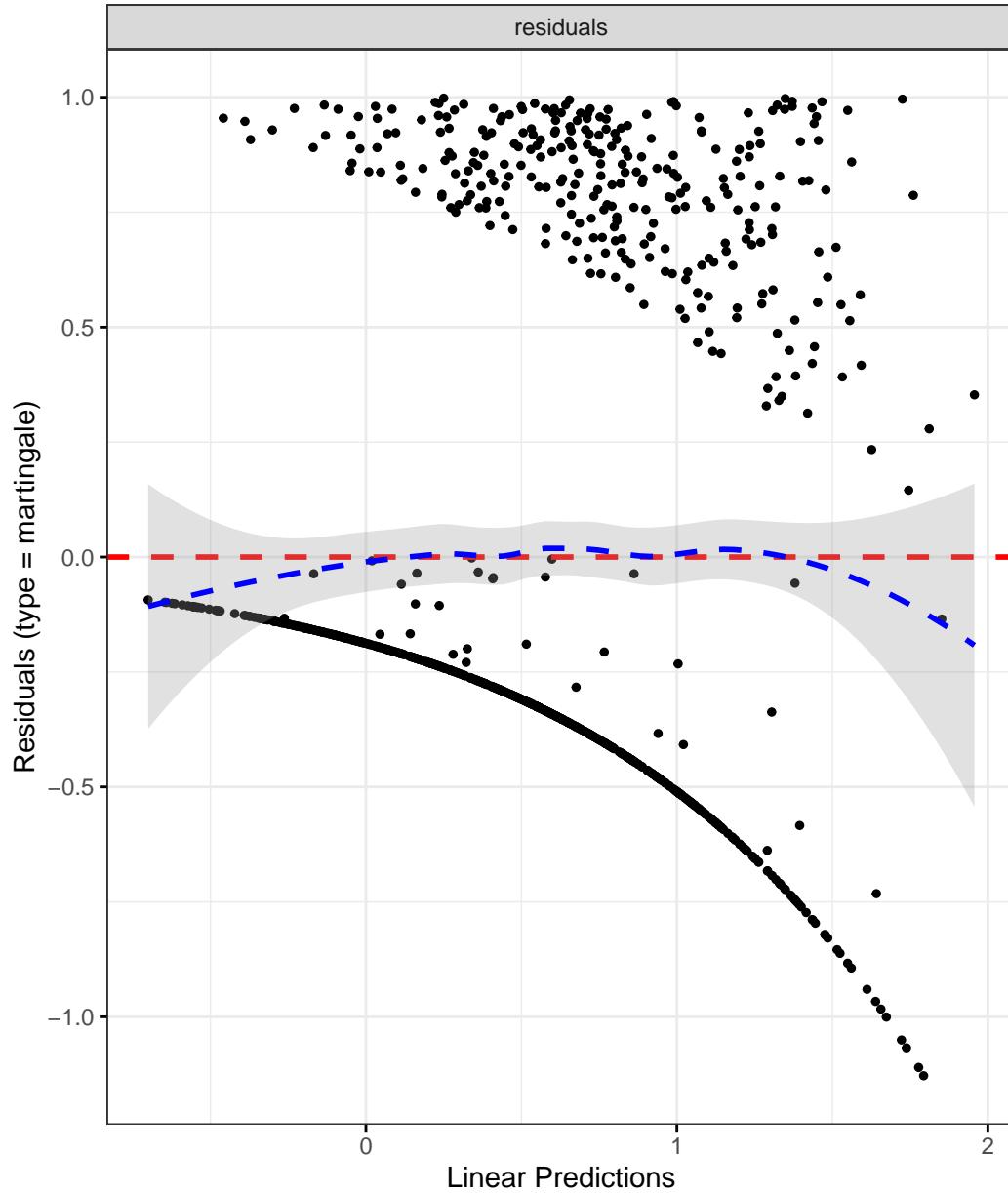
`geom_smooth()` using formula = 'y ~ x'

Residuals (type = dfbeta)

Observation Id

Martingale residuals

`geom_smooth()` using formula = 'y ~ x'

######

Objective flare

```
fit.me <- coxph(
  Surv(hardflare_time, hardflare) ~
    Sex +
    IMD +
    cat +
```

```
    `IBD Duration` +
    BMI +
    Treatment +
    Age +
    frailty(SiteNo),
  control = coxph.control(outer.max = 20),
  data = flare.cd.df
)

invisible(cox_summary(fit.me))
```

Cox model summary:

| Variable | HR | Lower 95% | Upper 95% | P-value |
|---|---|---|---|---|
| SexFemale | 1.7096 | 1.2650 | 2.3103 | 0.0005 |
| IMD2 | 0.9875 | 0.5574 | 1.7494 | 0.9656 |
| IMD3 | 0.8917 | 0.4907 | 1.6203 | 0.7068 |
| IMD4 | 0.9573 | 0.5384 | 1.7022 | 0.8819 |
| IMD5 | 1.0963 | 0.6346 | 1.8936 | 0.7417 |
| catFC 50-250 | 2.0382 | 1.4550 | 2.8550 | 0.0000 |
| catFC > 250 | 3.2590 | 2.2523 | 4.7158 | 0.0000 |
| IBD Duration | 0.9861 | 0.9714 | 1.0009 | 0.0659 |
| BMI | 1.0172 | 0.9912 | 1.0439 | 0.1964 |
| TreatmentMono biologic | 0.9700 | 0.6482 | 1.4516 | 0.8824 |
| TreatmentCombo therapy | 0.6422 | 0.3867 | 1.0667 | 0.0872 |
| Treatment5-ASA | 1.2541 | 0.5732 | 2.7438 | 0.5708 |
| TreatmentNone reported | 0.7334 | 0.4971 | 1.0822 | 0.1183 |
| Age | 0.9883 | 0.9777 | 0.9991 | 0.0331 |

Diagnostics:
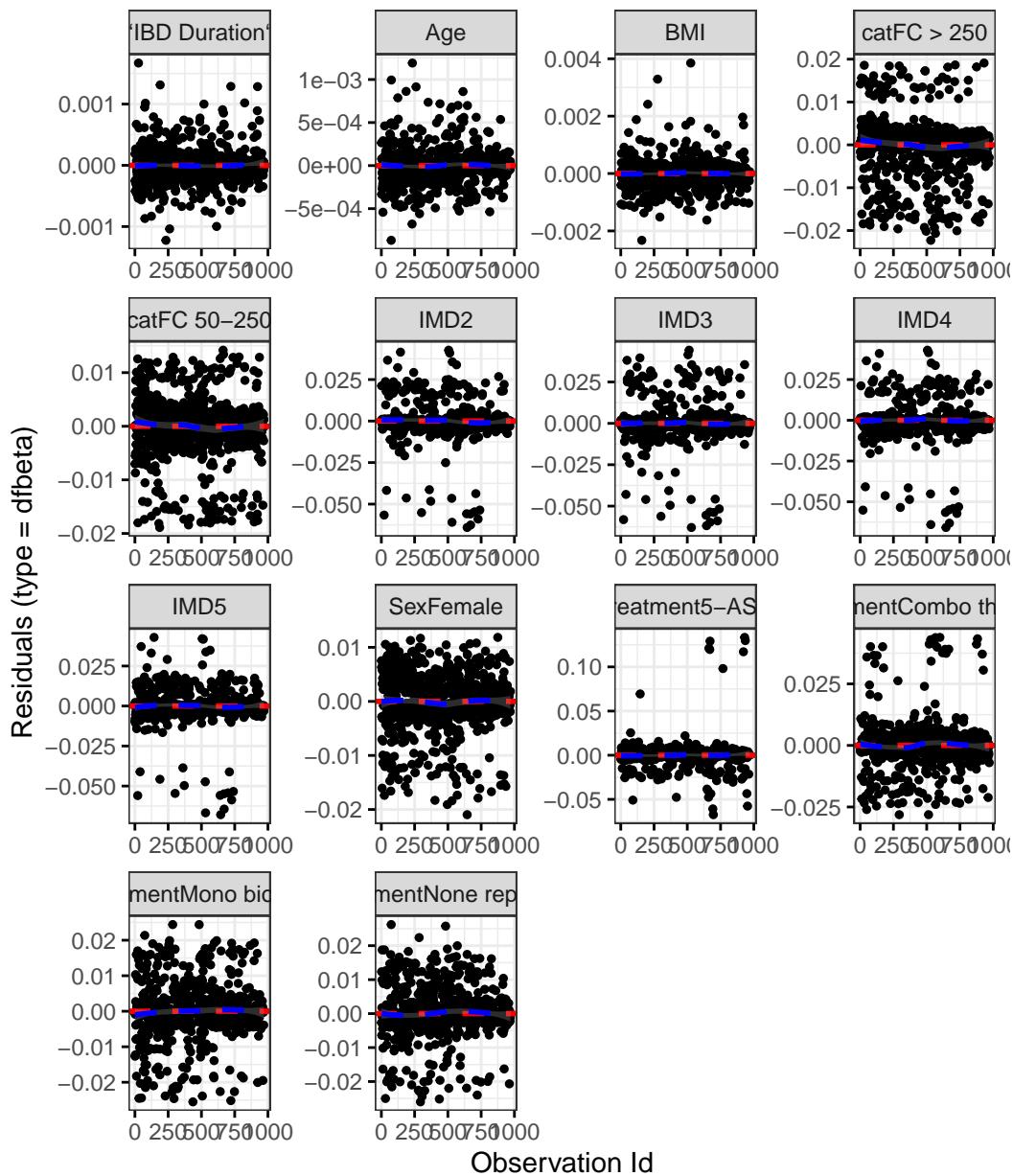
**Proportional hazards assumption test**

| | Chi-squared statistic | DF | P-value |
|---|---|---|---|
| Sex | 0.3823 | 0.9866 | 0.5308 |
| IMD | 2.0716 | 3.9513 | 0.7157 |
| cat | 7.1574 | 1.9870 | 0.0275 |
| IBD Duration | 0.1161 | 0.9959 | 0.7317 |
| BMI | 4.6695 | 0.9901 | 0.0302 |

|  | Chi-squared statistic | DF | P-value |
|---|---|---|---|
| Treatment | 3.4118 | 3.8994 | 0.4757 |
| Age | 4.6542 | 0.9917 | 0.0306 |
| GLOBAL | 21.4207 | 20.1145 | 0.3796 |

**DF betas**
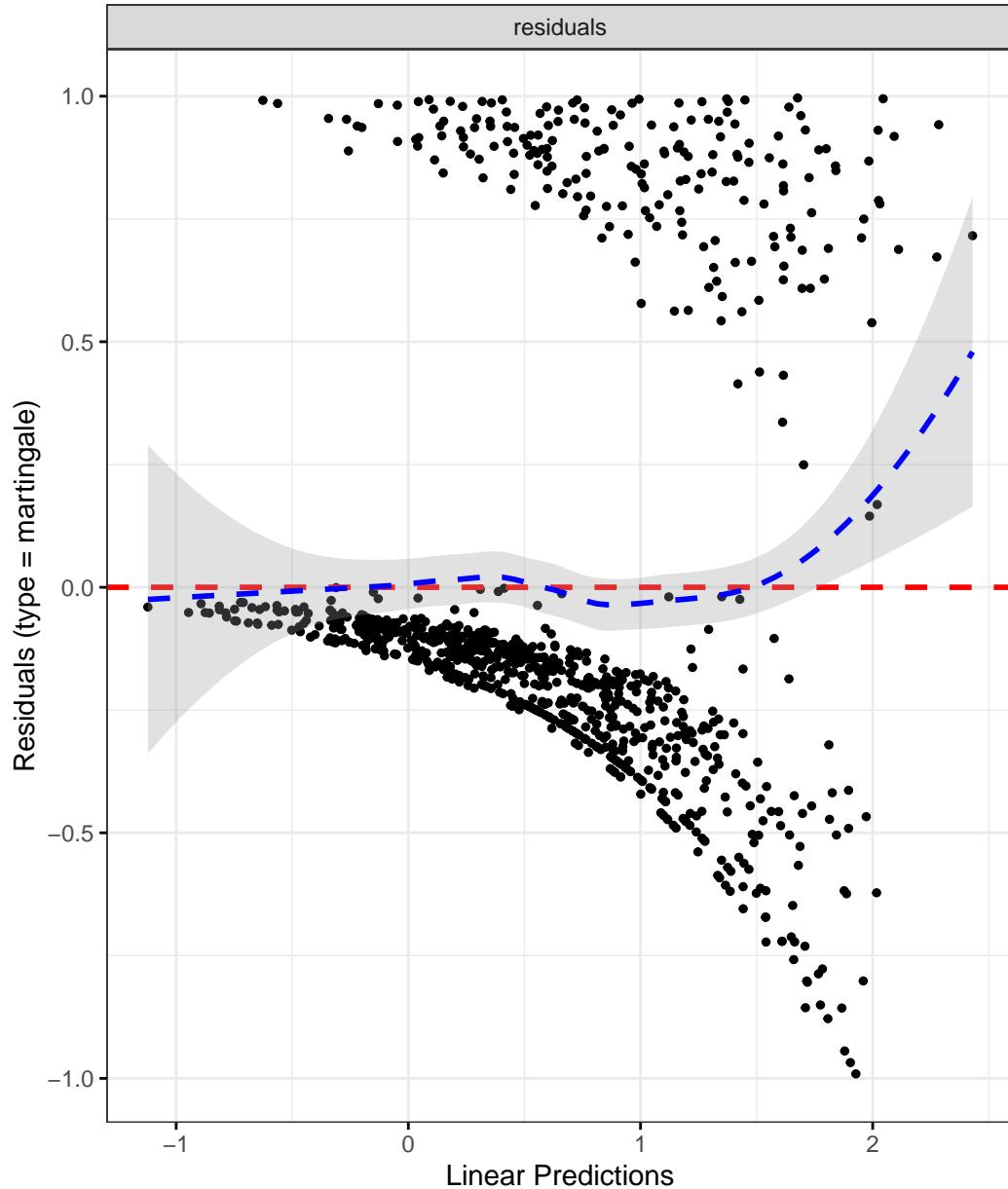
```
`geom_smooth()` using formula = 'y ~ x'
```

Martingale residuals

`geom_smooth()` using formula = 'y ~ x'

Ulcerative colitis

**Reproduction and reproducibility**

Session info

**R version 4.4.0 (2024-04-24)**

**Platform:** aarch64-unknown-linux-gnu

**locale:** *LC_CTYPE=en_US.UTF-8, LC_NUMERIC=C, LC_TIME=en_US.UTF-8, LC_COLLATE=en_US.UTF-8, LC_MONETARY=en_US.UTF-8, LC_MESSAGES=en_US.UTF-8, LC_PAPER=en_US.UTF-8, LC_NAME=C, LC_ADDRESS=C, LC_TELEPHONE=C, LC_MEASUREMENT=en_US.UTF-8* and *LC_IDENTIFICATION=C*

**attached base packages:** *grid, stats, graphics, grDevices, utils, datasets, methods* and *base*

**other attached packages:** *gtsummary(v.1.7.2), DescTools(v.0.99.54), finalfit(v.1.0.7), coxme(v.2.2-20), bdsmatrix(v.1.3-7), pander(v.0.6.5), survminer(v.0.4.9), ggpubr(v.0.6.0), survival(v.3.5-8), datefixR(v.1.6.1), lubridate(v.1.9.3), forcats(v.1.0.0), stringr(v.1.5.1), dplyr(v.1.1.4), purrr(v.1.0.2), readr(v.2.1.5), tidyr(v.1.3.1), tibble(v.3.2.1), ggplot2(v.3.5.1), tidyverse(v.2.0.0), readxl(v.1.4.3), forestplot(v.3.1.6), abind(v.1.4-5)* and *checkmate(v.2.3.2)*

**loaded via a namespace (and not attached):** *gridExtra(v.2.3), gld(v.2.6.6), rlang(v.1.1.3), magrittr(v.2.0.3), e1071(v.1.7-14), compiler(v.4.4.0), mgcv(v.1.9-1), vctrs(v.0.6.5), pkg-config(v.2.0.3), shape(v.1.4.6.1), fastmap(v.1.2.0), backports(v.1.5.0), labeling(v.0.4.3), KMsurv(v.0.1-5), utf8(v.1.2.4), rmarkdown(v.2.27), markdown(v.1.12), tzdb(v.0.4.0), nloptr(v.2.0.3), xfun(v.0.44), glmnet(v.4.1-8), jomo(v.2.7-6), jsonlite(v.1.8.8), pan(v.1.9), broom(v.1.0.6), R6(v.2.5.1), stringi(v.1.8.4), car(v.3.1-2), boot(v.1.3-30), rpart(v.4.1.23), cellranger(v.1.1.0), Rcpp(v.1.0.12), iterators(v.1.0.14), knitr(v.1.47), zoo(v.1.8-12), Matrix(v.1.7-0), splines(v.4.4.0), nnet(v.7.3-19), timechange(v.0.3.0), tidyselect(v.1.2.1), rstudioapi(v.0.16.0), yaml(v.2.3.8), ggtext(v.0.1.2), codetools(v.0.2-20), lattice(v.0.22-6), withr(v.3.0.0), evaluate(v.0.23), proxy(v.0.4-27), xml2(v.1.3.6), survMisc(v.0.5.6), pillar(v.1.9.0), carData(v.3.0-5), mice(v.3.16.0), foreach(v.1.5.2), generics(v.0.1.3), hms(v.1.1.3), commonmark(v.1.9.1), munsell(v.0.5.1), scales(v.1.3.0), rootSolve(v.1.8.2.4), minqa(v.1.2.7), xtable(v.1.8-4), class(v.7.3-22), glue(v.1.7.0), lmom(v.3.0), tools(v.4.4.0), data.table(v.1.15.4), lme4(v.1.1-35.3), ggsignif(v.0.6.4), Exact(v.3.2), mvtnorm(v.1.2-5), colorspace(v.2.1-0), nlme(v.3.1-164), cli(v.3.6.2), km.ci(v.0.5-6), fansi(v.1.0.6), expm(v.0.999-9), broom.helpers(v.1.15.0), gt(v.0.10.1), gtable(v.0.3.5), rstatix(v.0.7.2), digest(v.0.6.35), farver(v.2.1.2), htmltools(v.0.5.8.1), lifecycle(v.1.0.4), httr(v.1.4.7), mitml(v.0.4-5), gridtext(v.0.1.5)* and *MASS(v.7.3-60.2)*