Birth weight analysis

```
run_birthweight1 <- TRUE
run_birthweight2 <- TRUE
run_birthweight_mcmc <- TRUE


library(inlamisclass)
library(ggplot2)
```

Across all cases, we will use the same misclassification matrix and number of iterations, so we define these.

```
MC_matrix <- matrix(c(0.95, 0.05, 0.2, 0.8), nrow = 2, byrow = T)
# Number of iterations for importance sampling:
niter <- 100000


birthweight_naive <- INLA::inla(bwt ~ lwt + smoke, data = birthweight)
```

Birth weight analysis, case 1

In this case, we assume that the proportion of smokers in the study is 0.4, and that the probability of a woman smoking is independent of other covariates. That means that the exposure model will only have an intercept, and this we set to be $\alpha_0 = \log(\frac{p}{1-p})$, where $p = 0.4$.

```
p <- 0.4

start_time <- Sys.time()
birthweight_model1 <- inla_is_misclass(formula_moi = bwt ~ smoke + lwt,
                                       formula_imp = smoke ~ 1,
                                       alpha = log(p/(1-p)),
                                       MC_matrix = MC_matrix,
                                       data = birthweight, niter = niter)
end_time <- Sys.time()

birthweight_results1 <- list(runtime = end_time - start_time, model = birthweight_model1,
                             summary = make_results_df(birthweight_model1, niter = niter))

saveRDS(list(model1 = birthweight_results1,
             niter = niter, nburnin = 0, rundate = Sys.time()),
        file = "results/birthweight_results1.rds")


birthweight_results1 <- readRDS("results/birthweight_results1.rds")
```

Birth weight analysis, case 2

In this case, we let the prbability that a person is smoking depend on their weight according to a logistic exposure model with $\alpha_0 = -0.3$ and $\alpha_z = 0.02$, meaning that higher body weight leads to a higher probability of smoking.

```r
start_time <- Sys.time()
birthweight_model2 <- inla_is_misclass(formula_moi = bwt ~ smoke + lwt,
                                       formula_imp = smoke ~ lwt,
                                       alpha = c(-3, 0.02),
                                       MC_matrix = MC_matrix,
                                       data = birthweight, niter = niter)
end_time <- Sys.time()

birthweight_results2 <- list(runtime = end_time - start_time, model = birthweight_model2,
                             summary = make_results_df(birthweight_model2, niter = niter))



# Save results ----
saveRDS(list(model2 = birthweight_results2,
             niter = niter, nburnin = 0, rundate = Sys.time()),
        file = "results/birthweight_results2.rds")


birthweight_results2 <- readRDS("results/birthweight_results2.rds")


plot_compare_inlamisclass(list(birthweight_results1$model1$model,
                               birthweight_results2$model2$model),
                          naive_mod = birthweight_naive,
                          niter = niter, num_inlamisclass_models = 2)
```
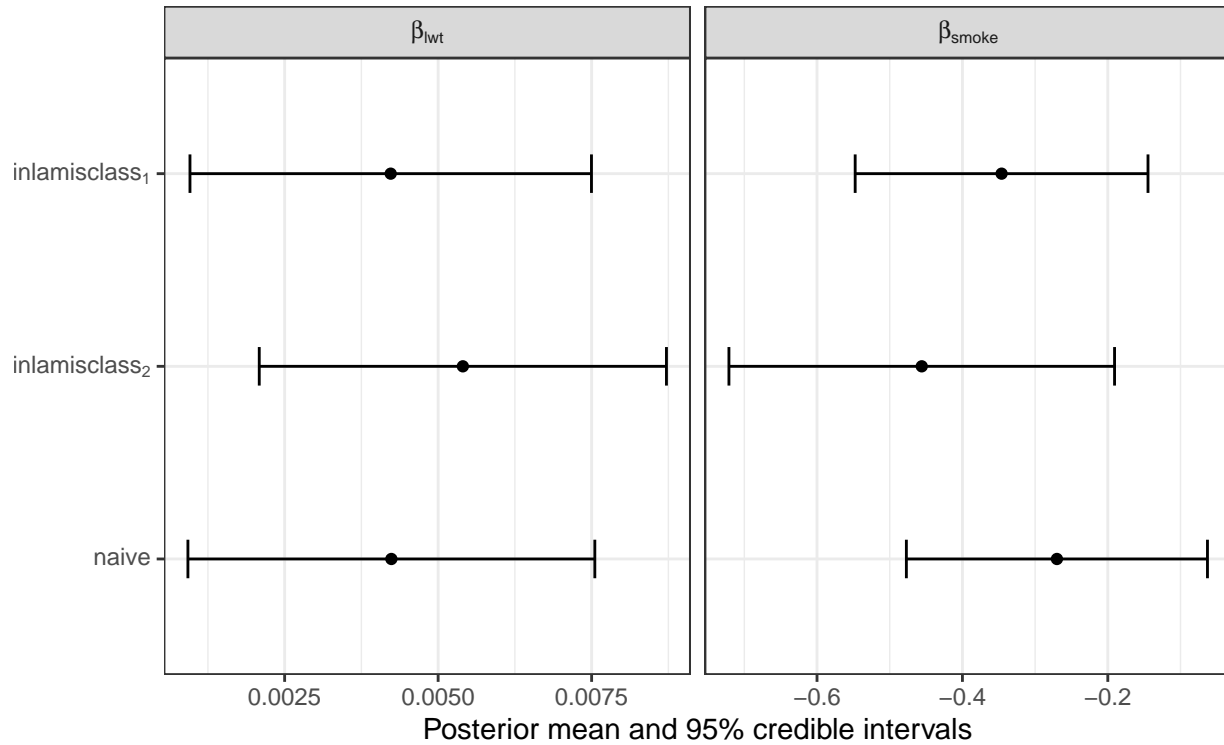
Posterior mean and 95% credible intervals

Figure for paper

```r
results1 <- make_results_df(birthweight_results1$model1$model)$moi
results2 <- make_results_df(birthweight_results2$model2$model)$moi
results_naive <- birthweight_naive$summary.fixed
results_naive$variable <- rownames(results_naive)

all_res <- dplyr::bind_rows(Ex1 = results1, Ex2 = results2, Naive = results_naive, .id = "Model")
all_res$labels <- paste0("beta", "[", c(0, "z", "x"), "]")
all_res$Model <- factor(all_res$Model, levels = c("Naive", "Ex1", "Ex2"))
all_res$Model <- plyr::revalue(all_res$Model,
                          c("Naive" = "Model with no adjustment",
                            "Ex1" = "Case 1: Smoking status is independent",
                            "Ex2" = "Case 2: Smoking status depends on weight"))

ggplot(dplyr::filter(all_res, variable != "(Intercept)"), aes(y = Model)) +
  geom_point(aes(x = mean)) +
  geom_errorbarh(aes(xmin = .data$"0.025quant", xmax = .data$"0.975quant"), height = .2) +
  scale_y_discrete(limits = rev) +
  facet_wrap(vars(labels), scales = "free_x", labeller = label_parsed) +
  theme_bw() +
  theme(axis.title = element_blank())
```
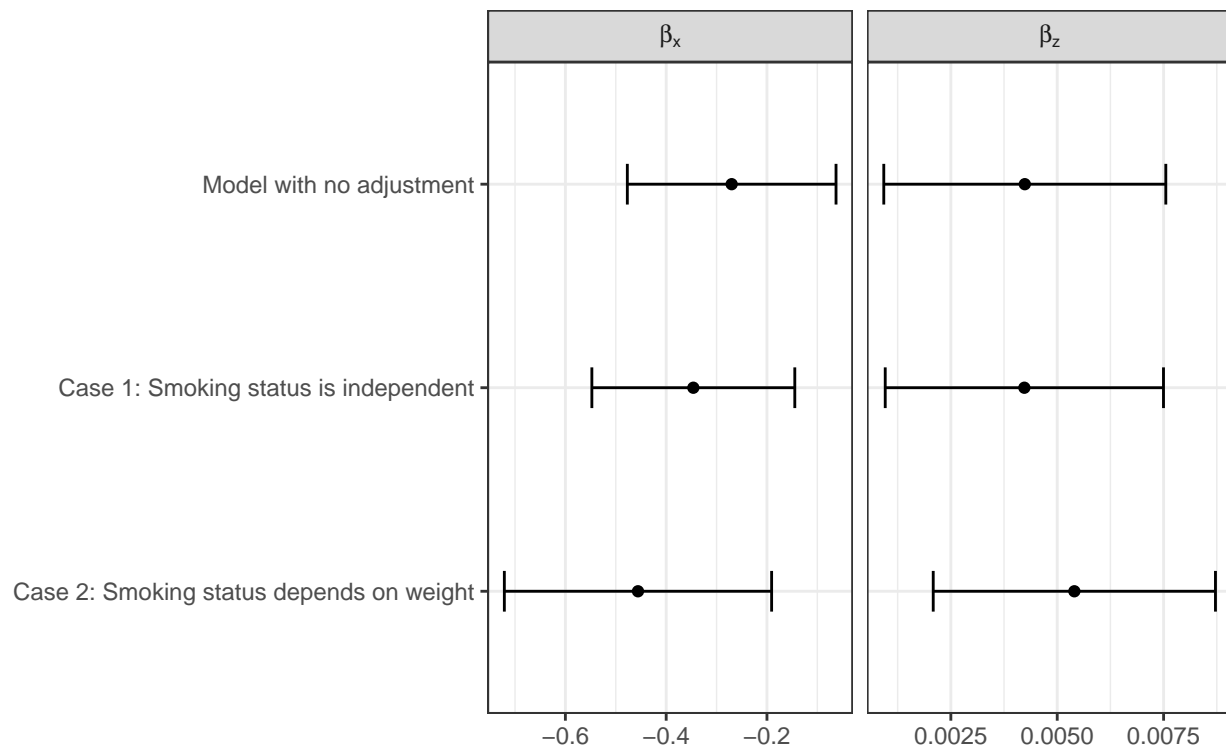
```
ggsave("figures/birthweight.pdf", height = 2.3, width = 7)
```