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DISCRIMINATION AGAINST MOBILE EU CITIZENS BEFORE AND DURING THE FIRST COVID-19 LOCKDOWN: EVIDENCE FROM A CONJOINT EXPERIMENT IN GERMANY

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1

Introduction

This report presents the data analysis for “Discrimination against mobile EU citizens before and during the first Covid-19 lockdown: evidence from a conjoint experiment in Germany”, published in the *European Union Politics*.

2

Data arrangement and cleaning for covid infection rate (exposure)

```
source("load_packages.R")
library(readxl)
```

Generate a variable of exposure to COVID made up of the combination between:

- Region of the individual respondent
- Infection rate of the region at a specific moment in time

```
# Original data can be retrieved from:
# https://www.destatis.de/DE/Themen/Laender-Regionen/Regionales/Gemeindeverzeichnis/Administrativ/02-bundeslaender.xls
url.population <- "https://www.destatis.de/DE/Themen/Laender-Regionen/Regionales/Gemeindeverzeichnis/Administrativ/02-bundeslaender.xls"
#download.file(url.population, destfile = "02-bundeslaender.xlsx")

population <- read_excel("02-bundeslaender.xlsx",
                         sheet = 2, skip = 7,
                         col_names = FALSE) %>%
  select(Region = `...1`,
         Population = `...4`) %>%
  filter(!is.na(Population)) %>%
  filter(!is.na(Region)) %>%
  mutate(Region = str_sub(Region, 5, -1)) %>%
  mutate(Population = as.integer(Population))

source("load_packages.R")
url.covid.rki <- "https://opendata.arcgis.com/datasets/dd4580c810204019a7b8eb3e0b329dd6_0.csv"
# Uncomment the following line if you need to download the file automatically
#download.file(url.covid.rki, destfile = "dd4580c810204019a7b8eb3e0b329dd6_0.csv")
# or better yet, download it manually, as it is very large as of June 2021 (>300
# Mb), and download.file() may not handle it.
covid.orig <- read.csv("dd4580c810204019a7b8eb3e0b329dd6_0.csv")
head(covid.orig)

##   ObjectId IdBundesland      Bundesland    Landkreis Altersgruppe Geschlecht
## 1       1 Schleswig-Holstein SK Flensburg     A00-A04        M
## 2       2 Schleswig-Holstein SK Flensburg     A00-A04        M
## 3       3 Schleswig-Holstein SK Flensburg     A00-A04        M
## 4       4 Schleswig-Holstein SK Flensburg     A00-A04        M
## 5       5 Schleswig-Holstein SK Flensburg     A00-A04        M
## 6       6 Schleswig-Holstein SK Flensburg     A00-A04        M
##   AnzahlFall AnzahlTodesfall            Meldedatum IdLandkreis
## 1       1           0 2020/09/30 00:00:00+00       1001
## 2       1           0 2020/10/29 00:00:00+00       1001
```

```

## 3      1          0 2020/11/03 00:00:00+00      1001
## 4      1          0 2020/11/20 00:00:00+00      1001
## 5      1          0 2020/11/23 00:00:00+00      1001
## 6      1          0 2020/12/18 00:00:00+00      1001
##          Datenstand NeuerFall NeuerTodesfall      Refdatum
## 1 18.06.2021, 00:00 Uhr      0      -9 2020/09/30 00:00:00+00
## 2 18.06.2021, 00:00 Uhr      0      -9 2020/10/29 00:00:00+00
## 3 18.06.2021, 00:00 Uhr      0      -9 2020/11/03 00:00:00+00
## 4 18.06.2021, 00:00 Uhr      0      -9 2020/11/19 00:00:00+00
## 5 18.06.2021, 00:00 Uhr      0      -9 2020/11/18 00:00:00+00
## 6 18.06.2021, 00:00 Uhr      0      -9 2020/12/14 00:00:00+00
##      NeuGenesen AnzahlGenesen IstErkrankungsbeginn      Altersgruppe2
## 1      0           1          0 Nicht übermittelt
## 2      0           1          0 Nicht übermittelt
## 3      0           1          0 Nicht übermittelt
## 4      0           1          1 Nicht übermittelt
## 5      0           1          1 Nicht übermittelt
## 6      0           1          1 Nicht übermittelt

```

Only work with the data up to the maximum date in which sampling was done. Calculate a 5-days moving average for infection rates on 100,000 inhabitants.

```

load("sample-eup.RData")
dates.main <- range(I$DateCompleted[I$Sample=="Main"])
dates.crisis <- range(I$DateCompleted[I$Sample=="Crisis"])

# Original data contains entries by age group and sex, and at the Landkreis (local) level
# We remove that and group by region and by date
covid <- covid.orig %>%
  tibble() %>%
  select(Region = Bundesland,
         Date = Meldedatum,
         Infected = AnzahlFall,
         Death = AnzahlTodesfall) %>%
  mutate(Date = as.Date(str_sub(Date, start = 1, end = 10),
                        format = "%Y/%m/%d")) %>%
  # Avoid days greater than one month after the last day of sampling
  filter(Date <= (max(I$DateCompleted) + 30)) %>%
  # Filter Infected and Death with -1
  filter(Infected >= 0 & Death >= 0)

# Calculate total cases grouping age groups and sex
covid <- covid %>%
  group_by(Region, Date) %>%
  summarize(Infected = sum(Infected),
            Death = sum(Death)) %>%
  ungroup() %>%
  # Merge with population
  left_join(population)

# Calculate cumulative cases and infection rates
covid.cum <- covid %>%
  group_by(Region) %>%
  arrange(Region, Date) %>%
  mutate(Infected = cumsum(Infected),
        Death = cumsum(Death)) %>%
  mutate(`Infection rate` = Infected / Population * 1e5,
        `Death rate` = Death / Population * 1e5) %>%
  mutate(`Infection growth rate` = (Infected - lag(Infected)) / lag(Infected),
        `Death growth rate` = (Death - lag(Death)) / lag(Death)) %>%
  mutate(`Infection growth rate smoothed` = zoo::rollmean(`Infection growth rate`, k = 5, fill = NA),
        `Death growth rate smoothed` = zoo::rollmean(`Death growth rate`, k = 5, fill = NA))

```

```
covid.cum %>%
  ggplot(aes(x = Date, y = `Infection rate`, group = Region)) +
  geom_line()
```

```
covid.cum %>%
  ggplot(aes(x = Date, y = `Infection growth rate`, group = Region)) +
  geom_line()
```

```
covid.cum %>%
  ggplot(aes(x = Date, y = `Infection growth rate smoothed`, group = Region)) +
  geom_rect(inherit.aes = FALSE,
            aes(xmin = dates.main[1], xmax = dates.main[2],
                 ymin = -Inf, ymax = Inf),
            color = "transparent", fill = "gray", alpha = 0.1) +
  geom_rect(inherit.aes = FALSE,
            aes(xmin = dates.crisis[1], xmax = dates.crisis[2],
                 ymin = -Inf, ymax = Inf),
            color = "transparent", fill = "gray", alpha = 0.2) +
  geom_line()
```

```
f1 <- covid.cum %>%
  ggplot(aes(x = Date, y = (`Infection rate`))) +
  geom_rect(inherit.aes = FALSE,
            aes(xmin = dates.main[1], xmax = dates.main[2],
                 ymin = -Inf, ymax = Inf),
            color = "transparent", fill = "gray", alpha = 0.1) +
  geom_rect(inherit.aes = FALSE,
            aes(xmin = dates.crisis[1], xmax = dates.crisis[2],
                 ymin = -Inf, ymax = Inf),
            color = "transparent", fill = "gray", alpha = 0.2) +
  geom_line(aes(group = Region)) +
  scale_y_continuous(breaks = c(1, 10, 100, 300)) +
  coord_trans(y = "log2") +
  ylab("Infection rate\n(by 100,000 inhabitants)")
```

f1

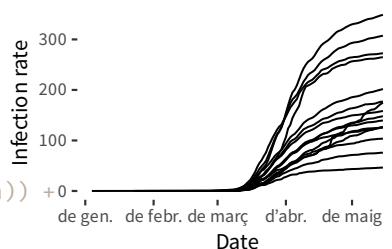
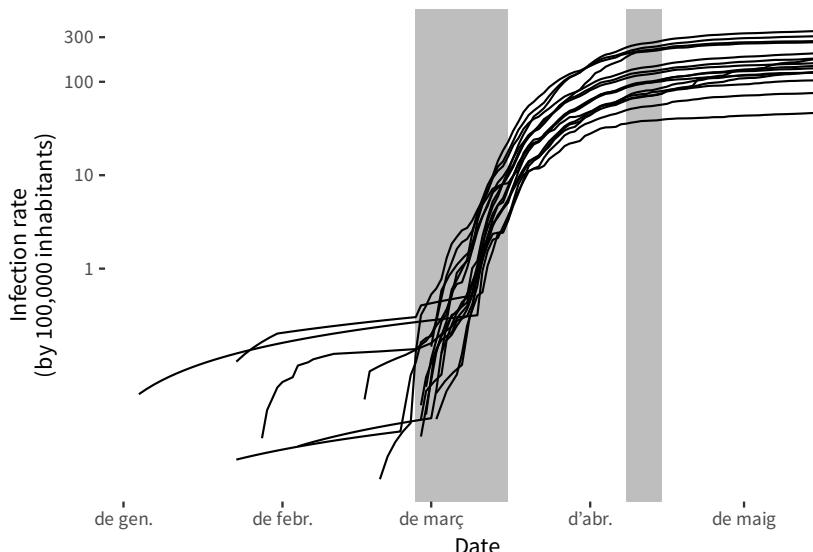


Figure 2.1: Infection rate by 100,000 inhabitants

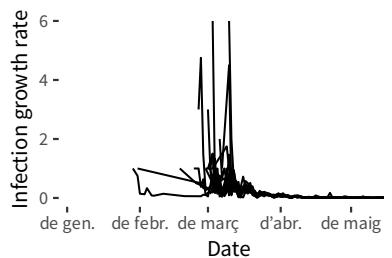


Figure 2.2: Infection rate daily growth rate

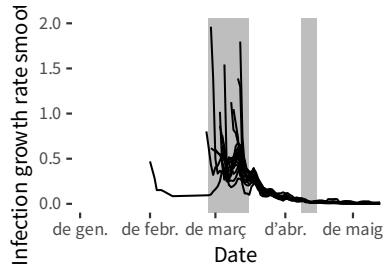


Figure 2.3: Infection rate daily growth rate

```
f2 <- covid.cum %>%
  filter(Date == dates.crisis[2]) %>%
  ggplot(aes(x = `Infection rate`, y = reorder(Region, `Infection rate`))) +
```

Figure 2.4: Infection rate by 100,000 inhabitants. Log scale.

```
geom_point() +
scale_x_continuous(breaks = c(50, 100, 300)) +
coord_trans(x = "log2") +
xlab("Infection rate\n(by 100,000 inhabitants)") +
ylab("Region") +
ggtitle(dates.crisis[2])
```

plot_grid(f1, f2)

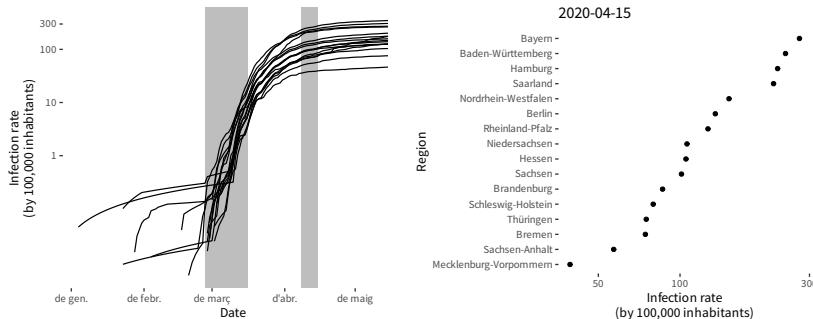


Figure 2.5: a) Temporal evolution of infection rate by 100,000 inhabitants (log scale); b) Dotplot of the infection rate by 100,000 inhabitants in the last day of the fieldwork (log scale)

```
plot_grid(f1 + theme_tufte(base_family = "Helvetica"),
          f2 + theme_tufte(base_family = "Helvetica"))
```

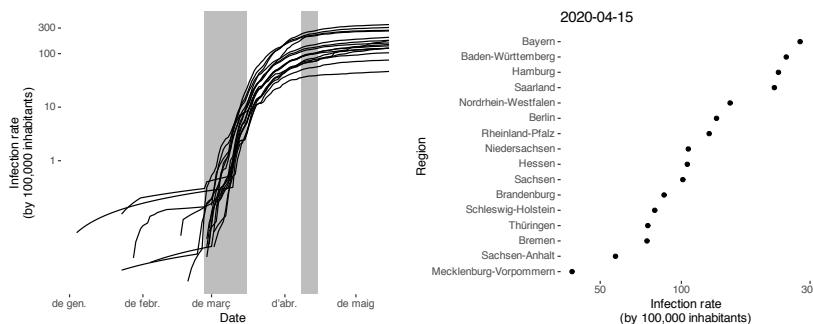


Figure 2.6: a) Temporal evolution of infection rate by 100,000 inhabitants (log scale); b) Dotplot of the infection rate by 100,000 inhabitants in the last day of the fieldwork (log scale)

```
ggsave("tmp.pdf", width = 10, height = 4)
```

Define exposure as:

- the average of the last 5 days' infection rate by german region.

```
# Calculate exposure
covid.exposure <- covid.cum %>%
  select(Region, Date, Exposure = `Infection rate`)

save(covid.exposure, file = "covid_exposure.RData")

source("load_packages.R")
load("sample-eup.RData")

std <- function(x) (x - mean(x, na.rm = TRUE)) / (2 * sd(x, na.rm = TRUE))
inv.logit <- function(x) return(1 / (1 + (exp(-(x)))))
logit <- function(x) return(log(x/(1-x)))
or <- function(x, significant = 2) {
  or <- as.character(signif((x - 1) * 100, significant))
  #or[or < 0] <- paste0("\u25bd ", str_replace(or[or < 0], "-", ""), "%")
  or[or < 0] <- paste0("\u25bd ", str_replace(or[or < 0], "-", ""), "%")
  #or[or > 0] <- paste0("\u25b2 ", or[or > 0], "%")
```

```
or[or > 0] ← paste0("\u25b3 ", or[or > 0], "%")
or[or == 0] ← "="
return(or)
}
# Add exposition data on covid
load("covid_exposure.RData")
I ← left_join(I, covid.exposure, by = c("Region" = "Region", "DateCompleted" = "Date"))
run.pcp ← TRUE
run.full.beta ← TRUE
```


3

Model: decision, individual, comprehensive (crisis/no crisis), attitudes, exposition/vulnerability (simplified)

The reference respondent has the following characteristics:

- German citizen
- Female
- Average age
- Average ideology
- Average openness
- Treatment not shown
- General population

Therefore, the values of the Intercept correspond to this individual.

```
d ← E %>%
  mutate(Observation = 1:n())
di ← I

Y ← d$Decision
n0 ← length(Y)

X ← d %>%
  mutate(`Nationality Netherlands` = ifelse(Nationality == "Netherlands", 1, 0)) %>%
  mutate(`Gender Male` = ifelse(Gender == "Male", 1, 0)) %>%
  mutate(`Profession Nurse` = ifelse(Profession == "Nurse", 1, 0)) %>%
  mutate(`Language Full` = ifelse(Language == "Full", 1, 0)) %>%
  mutate(`Age 25` = ifelse(Age == "25", 1, 0)) %>%
  mutate(`Age 55` = ifelse(Age == "55", 1, 0)) %>%
  mutate(`First shown` = ifelse(ProfileOrder == 1, 1, 0)) %>%
  select(`Nationality Netherlands`,
         `Gender Male`,
         `Profession Nurse`,
         `Language Full`,
         `Age 25`,
         `Age 55`,
         `First shown`) %>%
  as.matrix()
X ← cbind("(Intercept)" = 1, X)
nF ← dim(X)[[2]]
feature.label ← dimnames(X)[[2]]

b0 ← rep(0, nF)
B0 ← diag(nF)
diag(B0) ← 2.5^-2
diag(B0) ← 1^-2

id.outcome ← as.numeric(d$Outcome)
outcome.label ← levels(d$Outcome)
```

```
nOutcome ← length(outcome.label)

id.exercise ← d$Exercise
exercise.label ← sort(unique(d$Exercise))
nE ← length(exercise.label)

id.population ← as.numeric(d$Population)
population.label ← levels(d$Population)
nP ← length(population.label)
ind.id.population ← as.numeric(di$Population)

id.treatment ← as.numeric(d$Treatment)
treatment.label ← levels(d$Treatment)
nT ← length(treatment.label)

first.shown.profile ← ifelse(d$ProfileOrder = 1, 1, 0)

id.sample ← as.numeric(d$Sample)
sample.label ← levels(d$Sample)
nS ← length(sample.label)
ind.id.sample ← as.numeric(di$Sample)

id ← d$id
nId ← length(unique(d$id))

# Process the individual-level data with respondent characteristics
# and convert it into a matrix as the previous 'X'
C ← di %>%
  mutate(`Male` = ifelse(Gender == "Male", 1, 0)) %>%
  mutate(`Age (≥60)` = ifelse(Age ≥ 60, 1, 0)) %>%
  mutate(`Education (Primary)` = ifelse(Education == "Primary", 1, 0)) %>%
  mutate(`Ideology (right)` = std(Ideology)) %>%
  mutate(`Income (Low)` = ifelse(Income %in% c("unter EUR 500", "EUR 500 bis unter EUR 1.000"), 1, 0)) %>%
  mutate(Migrant = ifelse(Migration == "Yes", 1, 0)) %>%
  mutate(`Crisis sample` = ifelse(Sample == "Crisis", 1, 0)) %>%
  mutate(`Treatment_shown` = ifelse(Treatment == "Shown", 1, 0)) %>%
  # Exposure is standardized by each Sample
  group_by(Sample) %>%
  mutate(Exposure = std(Exposure)) %>%
  ungroup() %>%
  select(Male,
         `Age (≥60)` ,
         `Education (Primary)` ,
         `Ideology (right)` ,
         `Treatment_shown` ,
         `Income (Low)` ,
         Migrant,
         Exposure,
         ) %>%
  as.matrix()
C ← cbind("(Intercept)" = 1, C)
nCov ← dim(C)[2]
covariate.label ← dimnames(C)[[2]]
cov.missing ← which(apply(C, 2, function(x) ifelse(length(which(is.na(x))) > 0, TRUE, FALSE)))
c0 ← rep(0, nCov)
C0 ← diag(nCov)
diag(C0) ← 2.5^2

D ← list
n0 ← n0,
id_outcome ← id.outcome, nOutcome ← nOutcome,
id_exercise ← id.exercise , nE ← nE,
id_population ← id.population, nP ← nP,
ind_id_sample ← ind.id.sample, nS ← nS,
ind_id_population ← ind.id.population,
id_treatment ← id.treatment, nT ← nT,
first_shown_profile ← first.shown.profile,
X ← uname(x), nF ← nF, b0 ← b0, B0 ← B0,
C ← uname(C), nCov ← nCov, c0 ← c0, C0 ← C0,
cov.missing ← uname(cov.missing),
```

```

_id = id, nId = nId,
Y = Y)

# Arrange an object to prepare a table comparing samples
d.sample <- di %>%
  select(Sample,
         Gender, Age, Education, Ideology, Migration, Income) %>%
  mutate(`Income availability` = ifelse(is.na(Income), "Reported", "Not reported")) %>%
  mutate(`Income level (low)` = ifelse(Income %in% c("unter EUR 500",
                                                    "EUR 500 bis unter EUR 1.000",
                                                    "EUR 1.000 bis unter EUR 1.500"),
                                         "Below €1,500", "Above €1,500")) %>%
  mutate(`Income level (high)` = ifelse(Income %in% c("EUR 10.000 und mehr",
                                                    "EUR 5.000 bis unter EUR 10.000",
                                                    "EUR 4.500 bis unter EUR 5.000",
                                                    "EUR 4.000 bis unter EUR 4.500"),
                                         "Above €4,000", "Below €4,000")) %>%
  mutate(Income = as.character(Income)) %>%
  mutate(Income = str_replace_all(Income, "EUR ", "")) %>%
  mutate(Income = str_replace(Income, " bis unter ", "-")) %>%
  mutate(Income = ifelse(Income == "unter 500", "<500", Income)) %>%
  mutate(Income = ifelse(Income == "10.000 und mehr", ">10.000", Income)) %>%
  mutate(Income = str_replace_all(Income, "\\.", ",")) %>%
  mutate(Income = ifelse(is.na(Income), "Not reported", Income)) %>%
  mutate(Income = as.factor(Income)) %>%
  select(-Income)

library(compareGroups)
cg <- compareGroups(Sample ~ ., data = d.sample)
tb <- createTable(cg)

tc <- "Odds ratio of expected grand-effects, sorted by magnitude."
if (knitr::is_latex_output()) {
  export2html(tb, file = "table-descriptives-comparison-samples.html")
  input(table-descriptives-comparison-samples.html)
} else {
  export2latex(tb, file = "table-descriptives-comparison-samples.tex")
  input(table-descriptives-comparison-samples.tex)
}

cat('input{table-descriptives-comparison-samples}')

input{table-descriptives-comparison-samples}

cat("table-descriptives-comparison-samples.html")

```

Model description:

$Y_o \sim$	$\mathcal{B}(\pi_o)$	Main data component
$\pi_o =$	$\text{logit}(\beta_{i,O,f} F_{o,f})$	Linear relationship
$\beta_{i,O,f} \sim$	$\mathcal{MN}(\mu_{i,O,f}, \Sigma_{\beta_O})$	
$\Sigma_{\beta_O} \sim$	$\mathcal{IW}(0, 9)$	VCov for individual effects
$\mu_{i,O,f} =$	$(\theta_{O,f,s,v} C_{i,v})$	Explanation of individual behavior
$\theta_{O,f,s,v} \sim$	$\mathcal{N}(\omega_{O,f}, \sigma_\theta)$	Priors for explanatory variables of individual behavior
$\omega_{O,f} \sim$	$\mathcal{N}(0, 2.5)$	Prior for the effects shared by outcome
$\sigma_{\theta_{O,f,v}} \sim$	$\mathcal{U}(0, 1)$	Prior for SD of individual behavior

Where:

- Y : Outcome variable capturing whether a profile has been prioritized (1) or not (0).

- o : Observation
- o : Outcomes (Welfare/ Rights)
- s : Sample (Main / Crisis)
- t : Treatment (Shown / Not shown)
- F : Matrix with the observations of features (the discrimination sources, plus intercept and first shown profile), for each experimental data point.
- C : Matrix with the characteristics v of the respondents, including their population p and the treatment t .
- f : Feature
- $\theta_{O,f,s,v}$: Main parameters of interest capturing the individual variables affecting discrimination effects by outcome, sample and profiles' feature.
- $\omega_{O,f}$: Hyper-parameters capturing the shared effect of individual characteristics on features over outcomes and sample.
- Σ_{β_o} : Variance-covariance matrix of the individual effects prioritizing the different profiles, by outcome.
- σ_θ : Between outcome/sample and within feature/individual characteristic's standard deviations.

This model estimates the following number of parameters:

```
# beta
(nId * nOutcome * nF) +
# theta
(nOutcome * nF * nS * nCov) +
# omega
(nF * nCov) +
# sigma_theta
(nF * nS * nCov)

## [1] 65096

M <- "Decision, Individual (Crisis comprehensive), attitudes, vulnerability/exposure, simplified"
M.lab <- "crisis-decision-individual-comprehensive-attitudes-vulnerability-exposure-simplified"
m <-
model {
  for (o in 1:nO) {
    Y[o] ~ dbern(p[o])
    logit(p[o]) <- inprod(beta[id[o],id_outcome[o],1:nF], X[o,1:nF])
  }
  # Priors for effects
  #
  for (ocm in 1:nOutcome) {
    for (id in 1:nId) {
      for (f in 1:nF) {
        beta[id,ocm,f] ~ dnorm(mu[id,ocm,f], 2.5^-2)
      }
    }
  }
  for (f in 1:nF) {
    for (ocm in 1:nOutcome) {
      for (id in 1:nId) {
        mu[id,ocm,f] <- inprod(theta[ocm,f,ind_id_sample[id],1:nCov], C[id,1:nCov])
      }
      for (cov in 1:nCov) {
        for (s in 1:nS) {
          theta[ocm,f,s,cov] ~ dnorm(omega[f,cov], tau_theta[f,cov])
        }
      }
    }
    for (cov in 1:nCov) {
      omega[f,cov] ~ dnorm(0, 2.5^-2)
      tau_theta[f,cov] <- pow(sigma_theta[f,cov], -2)
      sigma_theta[f,cov] ~ dt(0, 0.5^-2, 3)T(0,)
    }
  }
}
```

```

# Missing data
#
for (id in 1:nId) {
    for (v in cov.missing) {
        C[id,v] ~ dnorm(0, 1^-2)
    }
}
write(m, file = paste("models/model-", M.lab, ".bug", sep = ""))
par <- NULL
par <- c(par, "theta")
par <- c(par, "sigma_theta")
par <- c(par, "omega")
par.beta <- c("beta")
par.pcp <- c("p")

adapt <- 2e2 # 7h
burnin <- 1e4 # 5e4 # 1h 30'
burnin <- 1e3
run <- 2e3
run <- 5e3
run.beta <- 100
run.p <- 100
chains <- 1
method <- "parallel"
thin <- 20
thin <- 1

t0 <- proc.time()
#rj <- run.jags(model = paste("models/model-", M.lab, ".bug", sep = ""),
#                 data = dump.format(D, checkvalid = FALSE),
##                 inits = inits,
#                 modules = "glm",
#                 n.chains = chains,
#                 adapt = adapt,
#                 burnin = burnin, sample = run,
#                 thin = 1, #thin,
#                 monitor = par, method = method, summarise = FALSE)
#s <- as.mcmc.list(rj)

my.jags <- function(seed, model, data, inits = inits, n.adapt, n.burnin, n.samples, thin) {
    require(rjags)
    load.module('glm')
    load.module('lecuyer')
    load.module('dic')
    tic()
    print(paste("Starting with seed", seed))
    toc()
    tic()
    data$seed <- seed
    print(data$seed)
    jm <- jags.model(model, n.chains = 1, n.adapt = n.adapt,
                      inits = list(list(.RNG.name = "base::Super-Duper", .RNG.seed = seed)),
                      data = data)
    print(paste("Initialization complete for seed", seed, ", updating ..."))
    toc()
    tic()
    update(jm, n.iter = burnin)
    print(paste("Update complete for seed", seed, ", sampling main parameters ..."))
    toc()
    tic()
    s <- coda.samples(jm, variable.names = par, n.iter = run * thin, thin = thin)
    print(paste("Main samples completed for seed", seed, ", sampling for beta ..."))
    toc()
    tic()
    s.beta <- coda.samples(jm, variable.names = par.beta, n.iter = run.beta * thin, thin = thin)
    print(paste("Beta samples completed for seed", seed, ", sampling for pcp ..."))
    toc()
    tic()
    s.pcp <- coda.samples(jm, variable.names = par.pcp, n.iter = run.p, thin = 1)
    print(paste("PCP samples completed for seed", seed, ", all OK"))
    toc()
    return(list(s, s.beta, s.pcp))
}

```

```

}

s.both <- mclapply(
  X = seq_len(chains),
  FUN = my.jags,
  model = paste("models/model-", M.lab, ".bug", sep = ""),
  data = D,
  n.adapt = adapt, n.burnin = burnin, n.samples = run, thin = thin,
  mc.preschedule = FALSE,
  mc.cores = chains)
save(s.both, file = "sboth.RData")

# Not very elegant, but works now. Must be improved
s <- as.mcmc.list(list(s.both[[1]][[1]][[1]]))
s.beta <- as.mcmc.list(list(s.both[[1]][[2]][[1]]))
s.p <- as.mcmc.list(list(s.both[[1]][[3]][[1]]))
save(s, file = paste("samples-", M.lab, ".RData", sep = ""))
save(s.beta, file = paste("samples-beta-", M.lab, ".RData", sep = ""))
save(s.p, file = paste("samples-p-", M.lab, ".RData", sep = ""))
proc.time() - t0

load(file = paste("samples-", M.lab, ".RData", sep = ""))
load(file = paste("samples-beta-", M.lab, ".RData", sep = ""))

ggmcmc(ggs(s.beta, family = "beta\\[.,", sort = FALSE),
        file = paste0("ggmcmc-beta-some-", M.lab, ".pdf"),
        plot = c("traceplot", "crosscorrelation", "caterpillar"))

ggmcmc(ggs(s, family = "omega", sort = FALSE),
        file = paste0("ggmcmc-omega-", M.lab, ".pdf"),
        plot = c("traceplot", "crosscorrelation", "caterpillar"))

ggmcmc(ggs(s, family = "theta\\[1,", sort = FALSE),
        file = paste0("ggmcmc-theta-", M.lab, ".pdf"),
        plot = c("traceplot", "crosscorrelation", "caterpillar"))

ggmcmc(ggs(s, family = "omega", sort = FALSE),
        file = paste0("ggmcmc-publication-omega-", M.lab, ".pdf"))

ggmcmc(ggs(s, family = "theta\\[]^omega", sort = FALSE),
        file = paste0("ggmcmc-publication-theta-omega-", M.lab, ".pdf"))

ggmcmc(ggs(s, family = "sigma_theta", sort = FALSE),
        file = paste0("ggmcmc-sigma_theta-", M.lab, ".pdf"),
        plot = c("traceplot", "crosscorrelation", "caterpillar"))

ggmcmc(ggs(s, family = "sigma"),
        file = paste0("ggmcmc-sigma-", M.lab, ".pdf"),
        plot = c("traceplot", "crosscorrelation", "caterpillar"))

L.sigma.theta <- plab("sigma_theta", list(Feature = feature.label,
                                             Covariate = covariate.label))
S.sigma.theta <- ggs(s, family = "sigma_theta", par_labels = L.sigma.theta)
ggs_caterpillar(S.sigma.theta, label = "Feature") +#, comparison = "Sample") +
  facet_wrap(~ Covariate)
ggs_caterpillar(S.sigma.theta, label = "Covariate", comparison = "Sample") +
  facet_wrap(~ Feature)

```

3.1 Part-worth contributions

Figure 3.1 shows the slopes for the effect of “Nationality Netherlands” on Rights, for each individual in the sample, sorted by the strength of their effect.

Individual 70 is the one more likely to discriminate favouring Dutch citizens, and individual 47 is the one more likely to discriminate against them.

Higher uncertainties imply that the information in the 6 experiments is less conclusive. It may be because the signal they sent when prioritizing is less clear, or because by chance the profiles shown were less relevant to extract such signal (indeed, individual 33 is qualified as “poor quality”).

```
L.beta <- plab("beta", list(id = 1:nId,
  Outcome = outcome.label,
  Feature = feature.label)) %>%
  mutate(id = as.numeric(as.character(id))) %>%
  left_join(select(di, id, Sample, Treatment))
S.beta <- ggs(s.beta, family = "beta\\\[", par_labels = L.beta, sort = FALSE) %>%
  select(-c(dim.1, dim.2, dim.3))

# Save memory and remove the objects once the ggs() has been applied
rm(s.beta)
invisible(gc())

S.beta %>%
  filter(Outcome = "Rights" &
         Feature = "Nationality Netherlands") %>%
  ggs_caterpillar(label = "id") +
  ylab("Individual id") +
  aes(color = Sample) +
  geom_vline(xintercept = 0, col = "red") +
  theme(axis.text = element_text(size = rel(0.5))) +
  scale_color_discrete_qualitative(palette = "Dynamic")

ggs_caterpillar(S.beta %>%
  filter(Outcome = "Rights" &
         Feature = "Language Full"),
  label = "id") +
  ylab("Individual id") +
  aes(color = Sample) +
  geom_vline(xintercept = 0, col = "red") +
  theme(axis.text = element_text(size = rel(0.5))) +
  scale_color_discrete_qualitative(palette = "Dynamic")

ggs_caterpillar(S.beta %>%
  filter(Outcome = "Welfare" &
         Feature = "Age 25"),
  label = "id") +
  ylab("Individual id") +
  aes(color = Sample) +
  geom_vline(xintercept = 0, col = "red") +
  theme(axis.text = element_text(size = rel(0.5))) +
  scale_color_discrete_qualitative(palette = "Dynamic")

ci.beta <- S.beta %>%
  ci() %>%
  filter(Feature != "(Intercept)") %>%
  select(id, Outcome, Feature, median)

order.beta.mean <- ci.beta %>%
  group_by(Feature) %>%
  summarize(Mean = mean(median)) %>%
  arrange(desc(Mean)) %>%
  mutate(Feature = as.character(Feature)) %>%
  select(Feature) %>%
  unlist(use.names = FALSE)

ci.beta.bins <- ci.beta %>%
  mutate(interval = cut(median, breaks = seq(-8, 9, 0.1))) %>%
  group_by(Outcome, Feature, interval) %>%
  count() %>%
  mutate(value = ifelse(str_detect(interval, "-"), "Negative", "Positive")) %>%
```

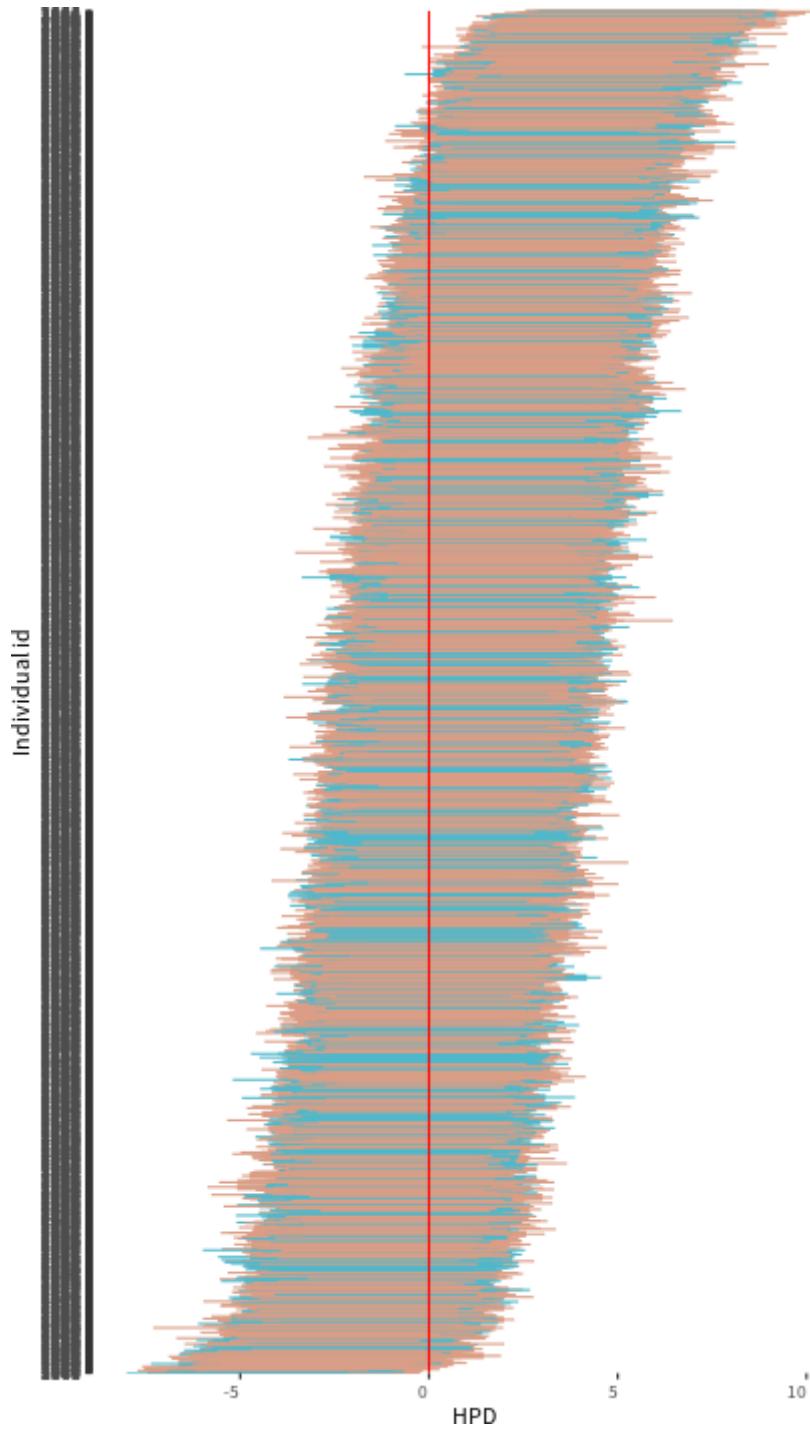


Figure 3.1: Discrimination on Nationality (Netherlands) on rights, by each individual in the sample.

```
ungroup() %>%
mutate(Feature = factor(as.character(Feature), levels = order.beta.mean))
ggplot(ci.beta.bins, aes(x = interval, y = n, color = value, fill = value)) +
geom_bar(stat = "identity") +
facet_grid(Feature ~ Outcome) +
xlab("Utility") + ylab(NULL) +
guides(color = "none", fill = "none") +
theme(axis.ticks = element_blank(), axis.text = element_blank(),
strip.text.y = element_text(angle = 0))
```

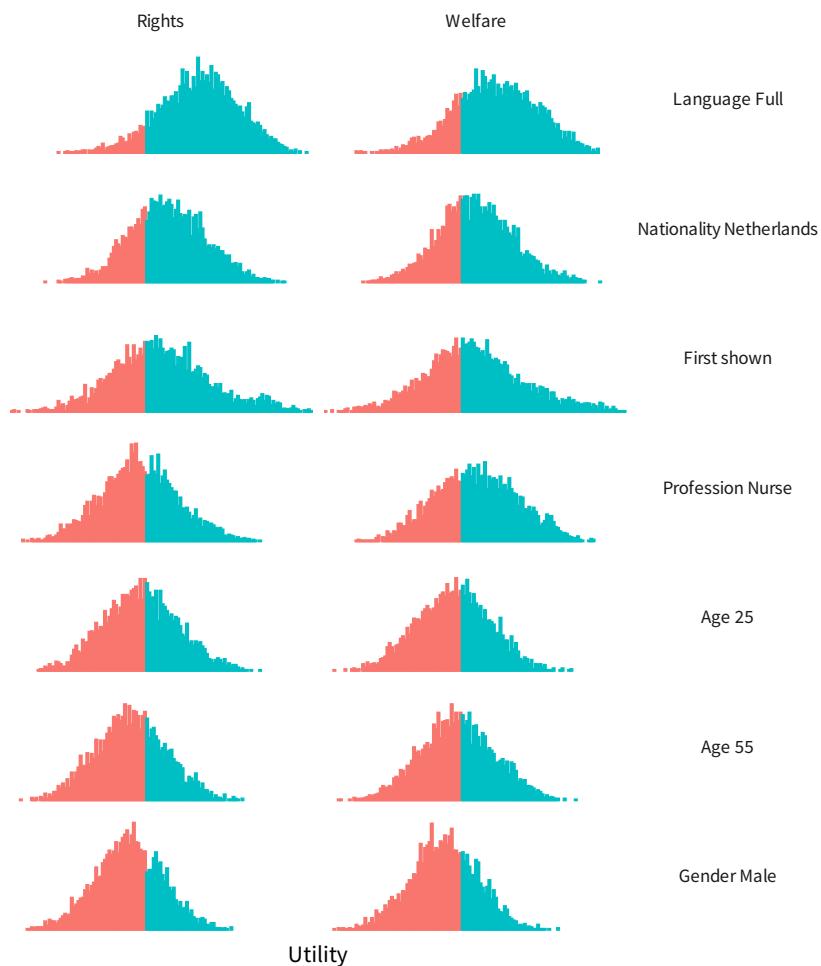


Figure 3.2: Distribution of the mean values for each individuals' utilities. Colors represent positive/negative utilities.

```
ci.beta %>%
ggplot(aes(x = median, color = Outcome, fill = Outcome)) +
geom_density(alpha = 0.6, color = NA) +
facet_grid(Feature ~ .) +
xlab("Utility") + ylab(NULL) +
geom_vline(xintercept = 0, lty = 3) +
theme(axis.ticks = element_blank(), axis.text = element_blank(),
strip.text.y = element_text(angle = 0)) +
scale_fill_discrete_qualitative(palette = "Dark 2")

ci.beta %>%
left_join(select(di, id, Sample)) %>%
filter(Feature != "First shown") %>%
ggplot(aes(x = median, y = ..density..)) +
geom_histogram(data = . %>% filter(Sample == "Main")) +
geom_density(data = . %>% filter(Sample == "Crisis")) +
```

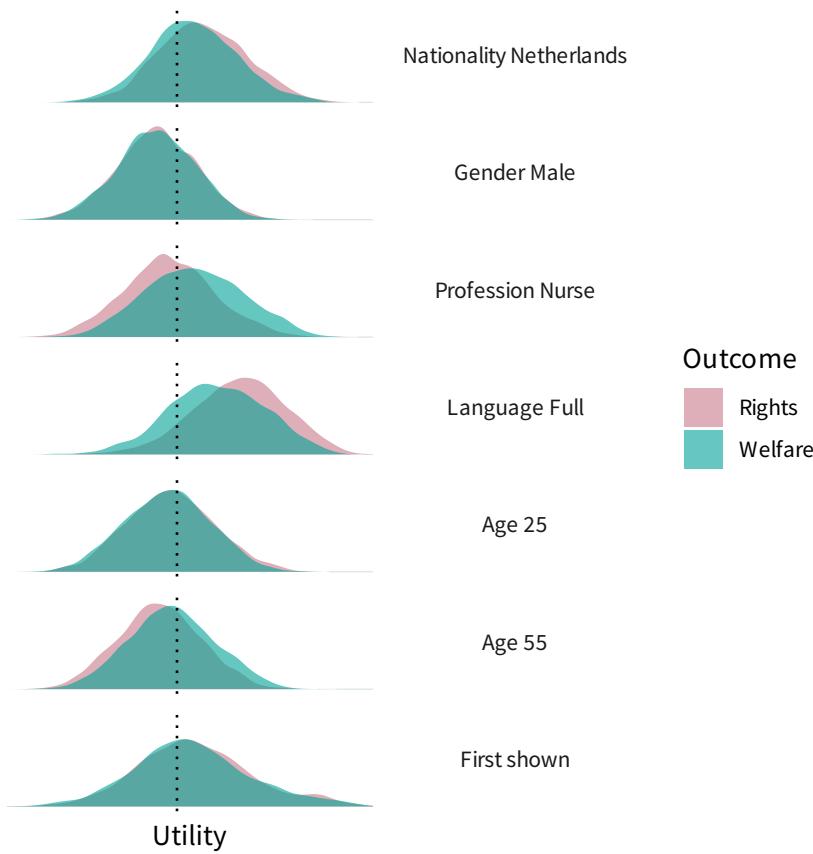


Figure 3.3: Distribution of the mean values for each individuals' utilities, by outcome.

```

facet_grid(Feature ~ Outcome) +
  xlab("Utility") + ylab(NULL) +
  geom_vline(xintercept = 0, lty = 3) +
  theme(axis.ticks = element_blank(), axis.text = element_blank(),
        strip.text.y = element_text(angle = 0))

ci.beta %>%
  left_join(select(di, id, Sample)) %>%
  filter(Feature != "First shown") %>%
  mutate(Feature = factor(as.character(Feature), levels = order.beta.mean)) %>%
  ggplot(aes(x = median, y = ..density..)) +
  geom_histogram(data = . %>% filter(Sample = "Main"),
                 binwidth = 0.1) +
  geom_density(data = . %>% filter(Sample = "Crisis"),
               lwd = 1.5) +
  facet_grid(Feature ~ Outcome) +
  xlab("Utility") + ylab(NULL) +
  geom_vline(xintercept = 0, lty = 3) +
  scale_x_continuous(breaks = logit(c(0.01, 0.1, 0.5, 0.9, 0.99)),
                     labels = paste(c(0.01, 0.1, 0.5, 0.9, 0.99) * 100, "%", sep = "")) +
  theme(axis.ticks.y = element_blank(),
        axis.text.y = element_blank(),
        strip.text.y = element_text(angle = 0))

ci.beta %>%
  left_join(select(di, id, Sample)) %>%
  filter(Feature != "First shown") %>%
  ggplot(aes(x = median, y = ..density..)) +
  geom_density(data = . %>% filter(Sample = "Main"), lwd = 1) +
  geom_density(data = . %>% filter(Sample = "Crisis"), color = "grey70", lwd = 1) +
  facet_grid(Feature ~ Outcome) +

```

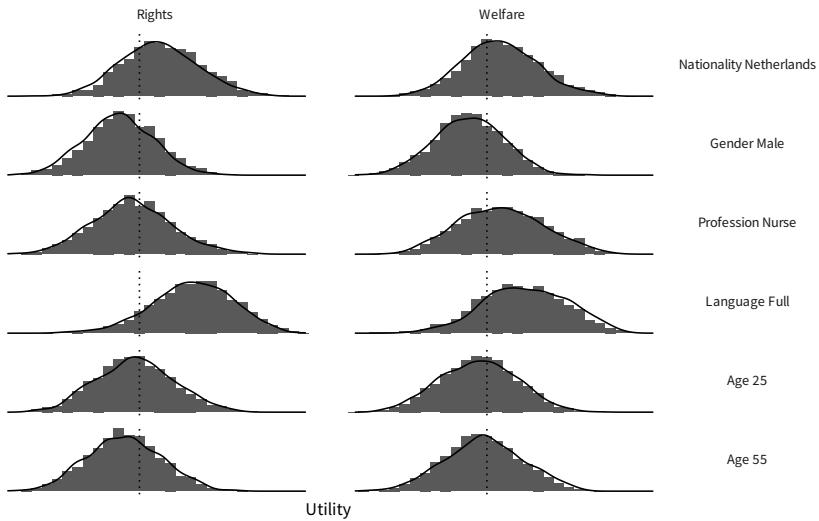


Figure 3.4: Distribution of the mean values for each individuals' utilities, by sample and outcome.

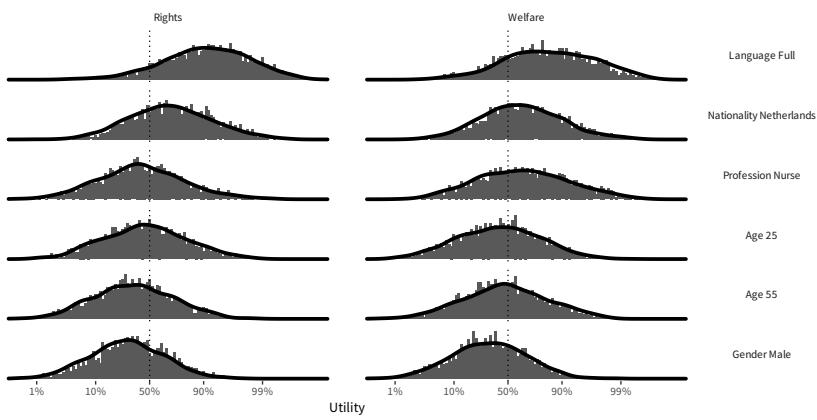


Figure 3.5: Distribution of the mean values for each individuals' utilities, by sample and outcome.

```
xlab("Utility") + ylab(NULL) +
geom_vline(xintercept = 0, lty = 3) +
theme(axis.ticks = element_blank(), axis.text = element_blank(),
strip.text.y = element_text(angle = 0))
```

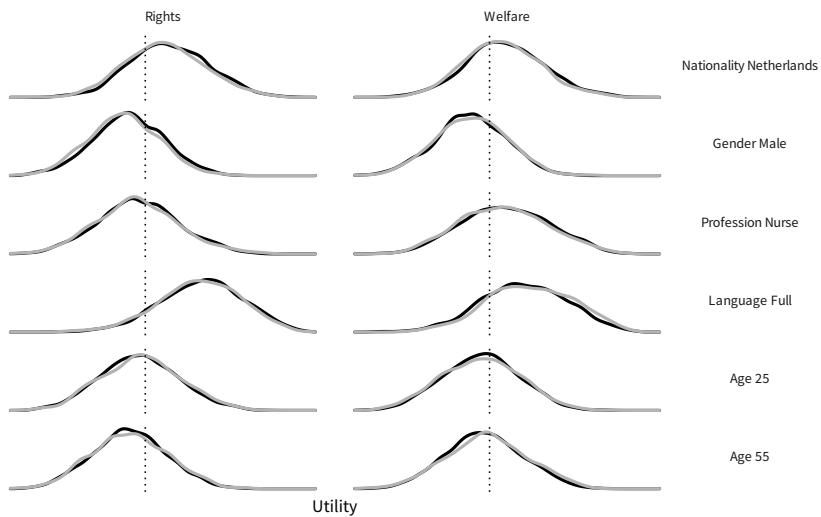


Figure 3.6: Distribution of the mean values for each individuals' utilities, by sample and outcome.

```
ci_beta %>%
  left_join(select(di, id, Sample)) %>%
  ggplot(aes(x = median, fill = Sample)) +
  geom_density(alpha = 0.6, color = NA) +
  facet_grid(Feature ~ Outcome) +
  xlab("Utility") + ylab(NULL) +
  geom_vline(xintercept = 0, lty = 3) +
  theme(axis.ticks = element_blank(), axis.text = element_blank(),
  strip.text.y = element_text(angle = 0)) +
  scale_fill_discrete_qualitative(palette = "Dynamic")
```

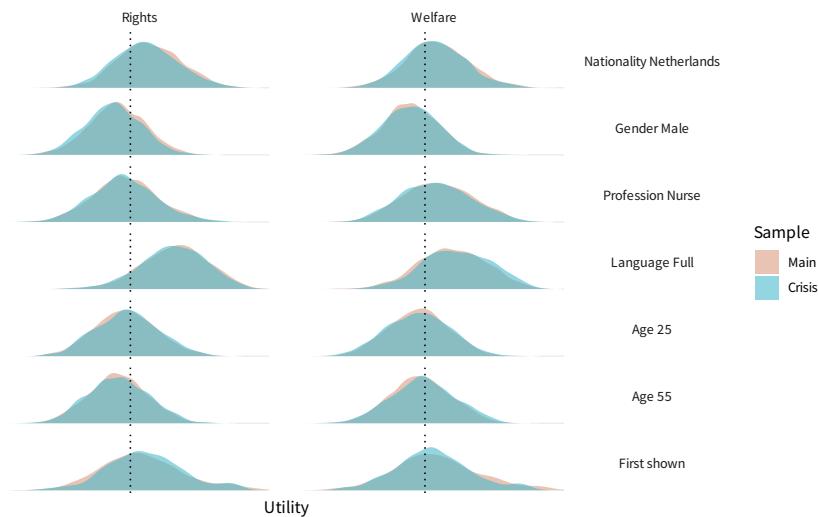


Figure 3.7: Distribution of the mean values for each individuals' utilities, by sample.

```
ci_beta %>%
  left_join(select(I, id, Treatment)) %>%
  ggplot(aes(x = median, fill = Treatment)) +
  geom_density(alpha = 0.6, color = NA) +
```

```
facet_grid(Feature ~ Outcome) +
  xlab("Utility") + ylab(NULL) +
  geom_vline(xintercept = 0, lty = 3) +
  theme(axis.ticks = element_blank(), axis.text = element_blank(),
    strip.text.y = element_text(angle = 0)) +
  scale_fill_discrete_qualitative(palette = "Harmonic")
```

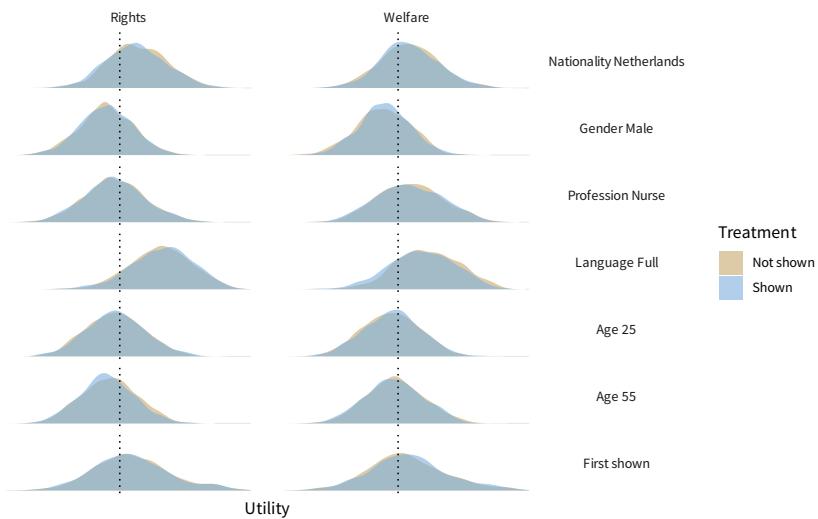


Figure 3.8: Distribution of the mean values for each individuals' utilities, by treatment.

```
ci_beta %>%
  left_join(select(I, id, Migration)) %>%
  ggplot(aes(x = median, fill = Migration)) +
  geom_density(alpha = 0.6, color = NA) +
  facet_grid(Feature ~ Outcome) +
  xlab("Utility") + ylab(NULL) +
  geom_vline(xintercept = 0, lty = 3) +
  theme(axis.ticks = element_blank(), axis.text = element_blank(),
    strip.text.y = element_text(angle = 0)) +
  scale_fill_discrete_qualitative(palette = "Warm")
```

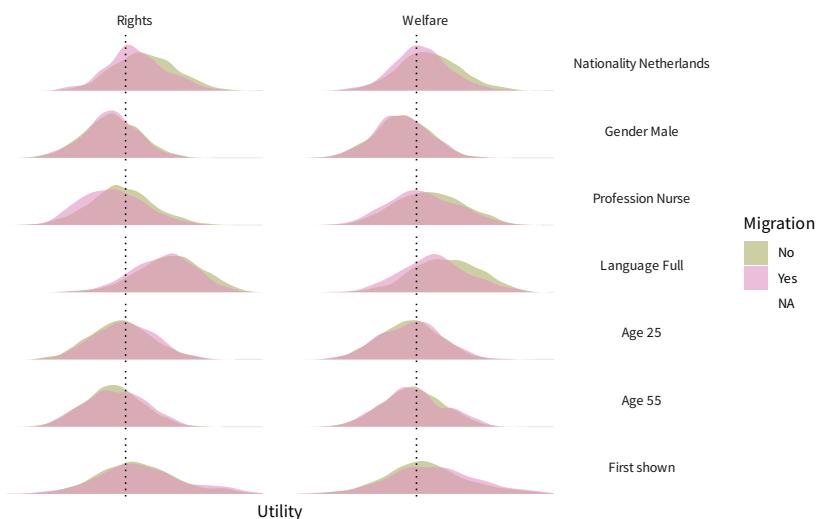


Figure 3.9: Distribution of the mean values for each individuals' utilities, by migrant.

```
ci_beta %>%
  left_join(select(I, id, Gender)) %>%
```

```
ggplot(aes(x = median, fill = Gender)) +
  geom_density(alpha = 0.6, color = NA) +
  facet_grid(Feature ~ Outcome) +
  xlab("Utility") + ylab(NULL) +
  geom_vline(xintercept = 0, lty = 3) +
  theme(axis.ticks = element_blank(), axis.text = element_blank(),
    strip.text.y = element_text(angle = 0)) +
  scale_fill_discrete_qualitative(palette = "Warm")
```

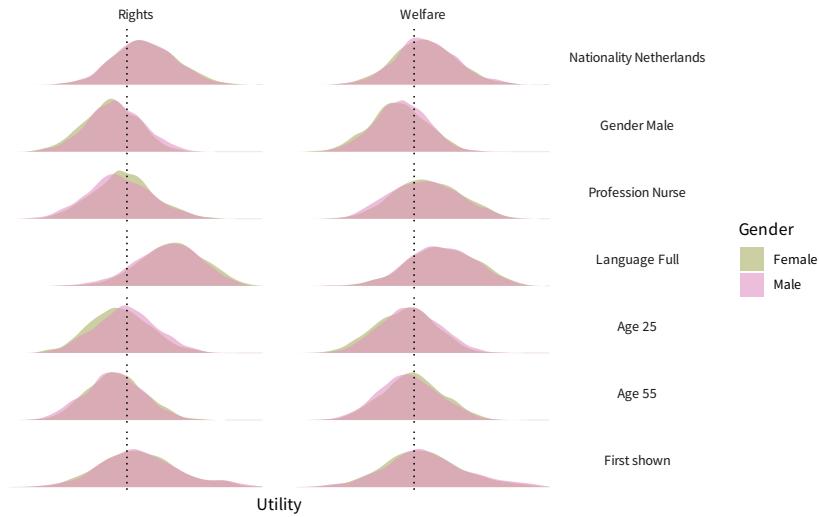


Figure 3.10: Distribution of the mean values for each individuals' utilities, by gender.

```
ci.beta %>%
  left_join(select(I, id, Education)) %>%
  ggplot(aes(x = median, fill = Education)) +
  geom_density(alpha = 0.6, color = NA) +
  facet_grid(Feature ~ Outcome) +
  xlab("Utility") + ylab(NULL) +
  geom_vline(xintercept = 0, lty = 3) +
  theme(axis.ticks = element_blank(), axis.text = element_blank(),
    strip.text.y = element_text(angle = 0)) +
  scale_fill_discrete_qualitative(palette = "Warm")
```

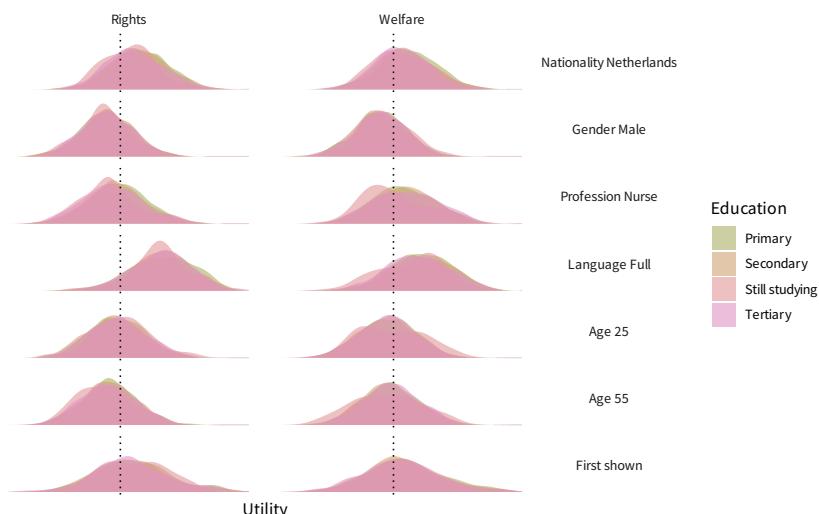


Figure 3.11: Distribution of the mean values for each individuals' utilities, by gender.

```
ci.beta %>%
  left_join(select(I, id, Age)) %>%
  mutate(`Age group` = cut(Age, breaks = c(-Inf, 30, 50, Inf))) %>%
  ggplot(aes(x = median, fill = `Age group`)) +
  geom_density(alpha = 0.6, color = NA) +
  facet_grid(Feature ~ Outcome) +
  xlab("Utility") + ylab(NULL) +
  geom_vline(xintercept = 0, lty = 3) +
  theme(axis.ticks = element_blank(), axis.text = element_blank(),
        strip.text.y = element_text(angle = 0)) +
  scale_fill_discrete_qualitative(palette = "Warm")
```

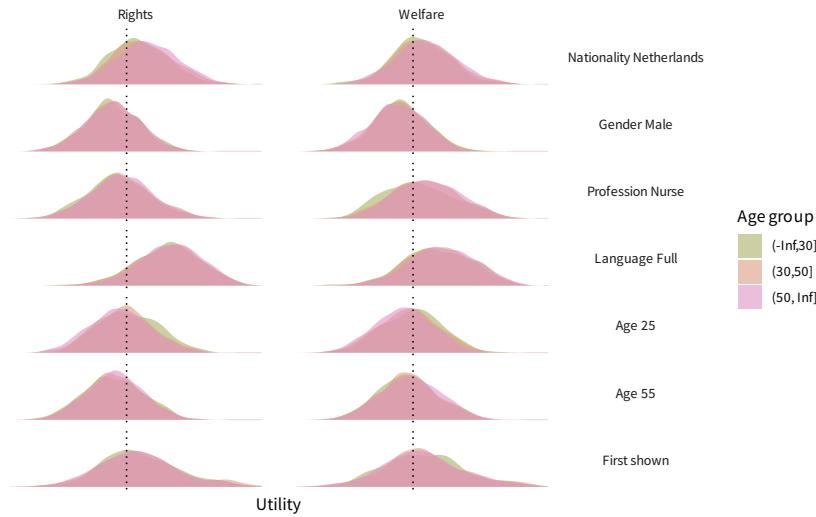


Figure 3.12: Distribution of the mean values for each individuals' utilities, by age group.

```
ci.beta %>%
  left_join(select(I, id, Ideology)) %>%
  mutate(`Ideology group` = cut(Ideology, breaks = c(-Inf, 2, 4, 5, 7, Inf))) %>%
  ggplot(aes(x = median, fill = `Ideology group`)) +
  geom_density(alpha = 0.6, color = NA) +
  facet_grid(Feature ~ Outcome) +
  xlab("Utility") + ylab(NULL) +
  geom_vline(xintercept = 0, lty = 3) +
  theme(axis.ticks = element_blank(), axis.text = element_blank(),
        strip.text.y = element_text(angle = 0)) +
  scale_fill_discrete_diverging(palette = "Blue-Red", rev = TRUE)

ci.beta %>%
  left_join(select(I, id, Income)) %>%
  mutate(`Income data` = ifelse(is.na(Income), "Missing", "Available")) %>%
  ggplot(aes(x = median, fill = `Income data`)) +
  geom_density(alpha = 0.6, color = NA) +
  facet_grid(Feature ~ Outcome) +
  xlab("Utility") + ylab(NULL) +
  geom_vline(xintercept = 0, lty = 3) +
  theme(axis.ticks = element_blank(), axis.text = element_blank(),
        strip.text.y = element_text(angle = 0)) +
  scale_fill_discrete_qualitative(palette = "Warm")

ci.beta %>%
  left_join(select(I, id, Income)) %>%
  ggplot(aes(x = median, fill = Income)) +
  geom_density(alpha = 0.6, color = NA) +
  facet_grid(Feature ~ Outcome) +
```

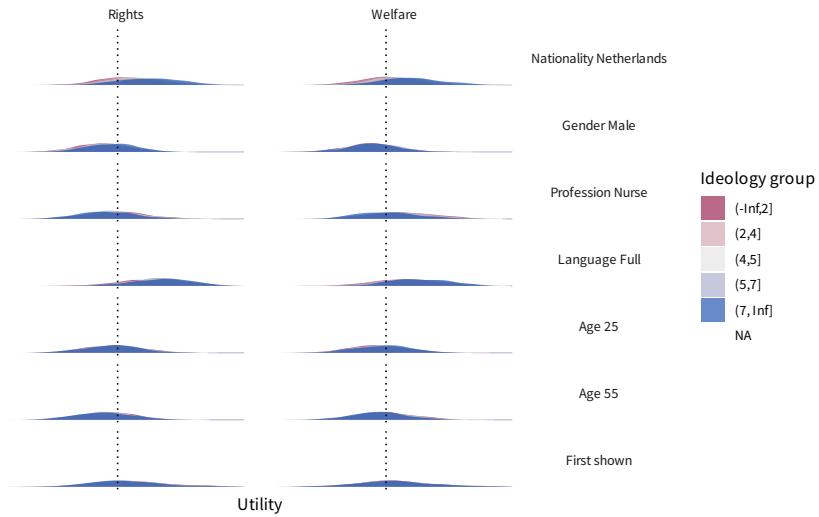


Figure 3.13: Distribution of the mean values for each individuals' utilities, by ideology group.

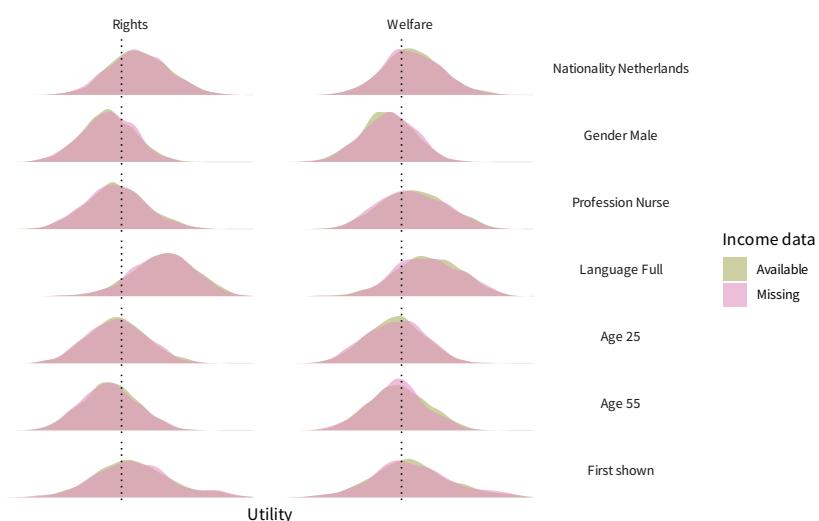


Figure 3.14: Distribution of the mean values for each individuals' utilities, by income data availability.

```
xlab("Utility") + ylab(NULL) +
geom_vline(xintercept = 0, lty = 3) +
theme(axis.ticks = element_blank(), axis.text = element_blank(),
strip.text.y = element_text(angle = 0)) +
scale_fill_discrete_sequential(palette = "Oranges", rev = TRUE)
```

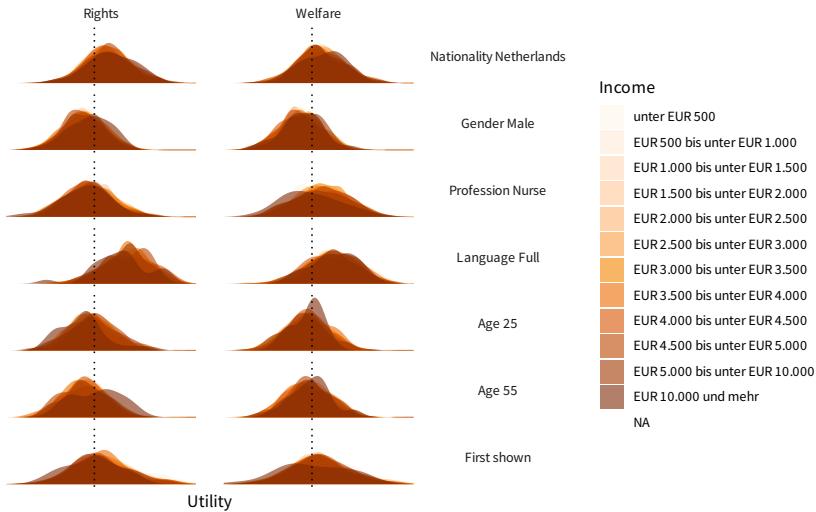


Figure 3.15: Distribution of the mean values for each individuals' utilities, by income.

Figure 3.16 presents the summary of the relationships between individual utilities in each feature.

```
ci.beta.w <- ci.beta %>%
pivot_wider(c(id, Outcome), names_from = Feature, values_from = median)

my_dens <- function(data, mapping, ... , low = "#132B43", high = "#56B1F7") {
  ggplot(data = data, mapping=mapping) +
    geom_density( ... , alpha=0.3)
}

ggpairs(select(ci.beta.w, -id),
lower = list(continuous = wrap("points", alpha = 0.1)),
diag = list(continuous = my_dens),
mapping = aes(color = Outcome))

ci.beta.w <- ci.beta %>%
filter(Outcome == "Rights") %>%
filter(Feature != "First shown") %>%
left_join(select(di, id, Sample)) %>%
pivot_wider(c(id, Sample), names_from = Feature, values_from = median)

my_dens <- function(data, mapping, ... ) {
  ggplot(data = data, mapping=mapping) +
    geom_density( ... , alpha=0.3)
}

my_sc <- function(data, mapping, ... ) {
  ggplot(data = data, mapping = mapping) +
    geom_point(alpha = 0.1) +
    geom_smooth(method = "loess")
}

ggplot <- function( ... ) ggplot2::ggplot( ... ) + scale_color_discrete_qualitative(palette = "Dynamic") + scale_color_discrete_sequential(palette = "Oranges")

unlockBinding("ggplot", parent.env(asNamespace("GGally")))
assign("ggplot", ggplot, parent.env(asNamespace("GGally")))

gpd <- select(ci.beta.w, -c(id))
ggpairs(gpd,
columns = 2:ncol(gpd),
title = "Rights",
```

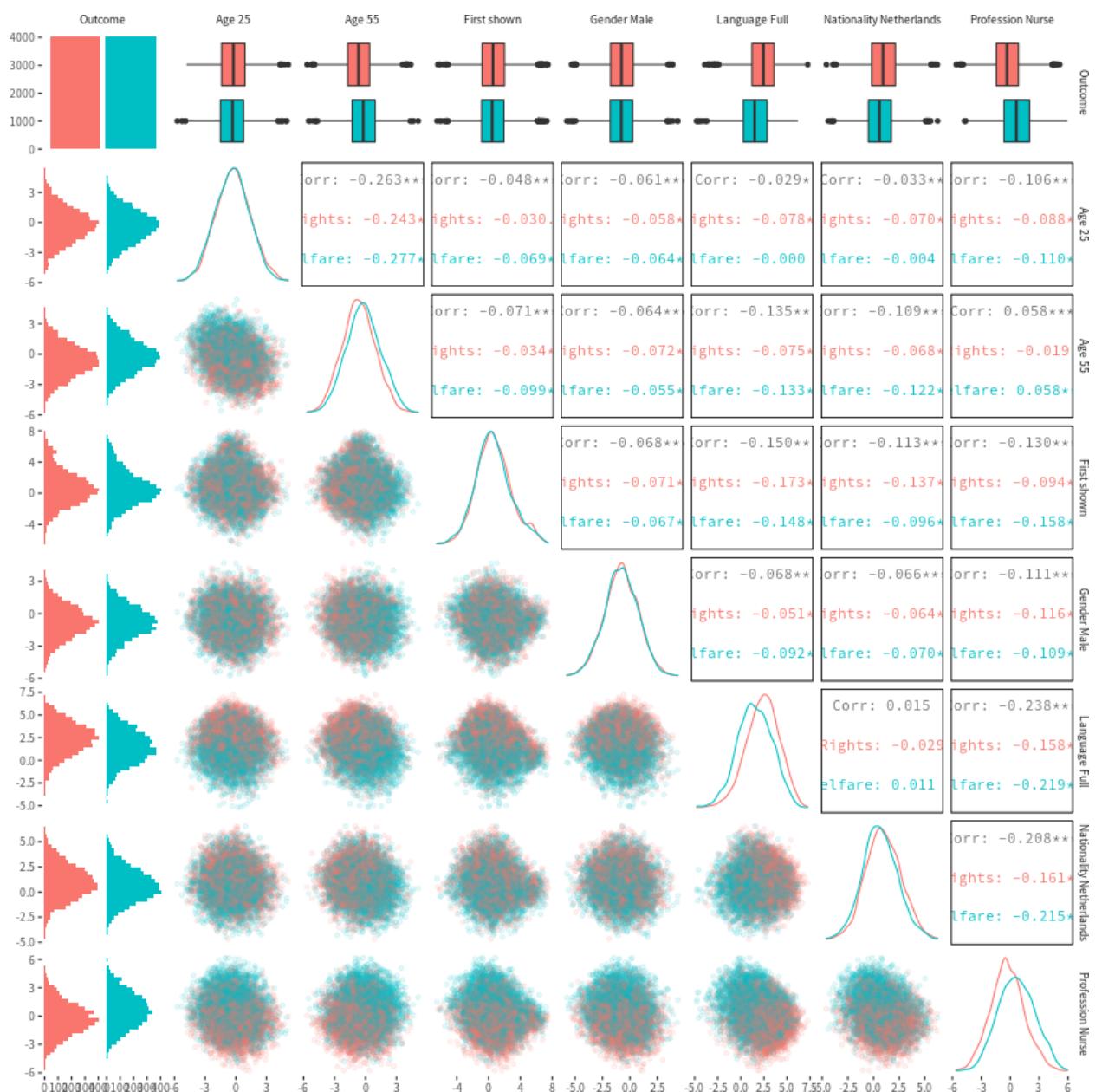


Figure 3.16: Comparison of median expected individual effects of every feature, by outcome.

```
legend = c(2, 1),
lower = list(continuous = my_sc),
diag = list(continuous = my_dens),
mapping = aes(color = Sample)) +
theme(legend.position = "bottom")
```

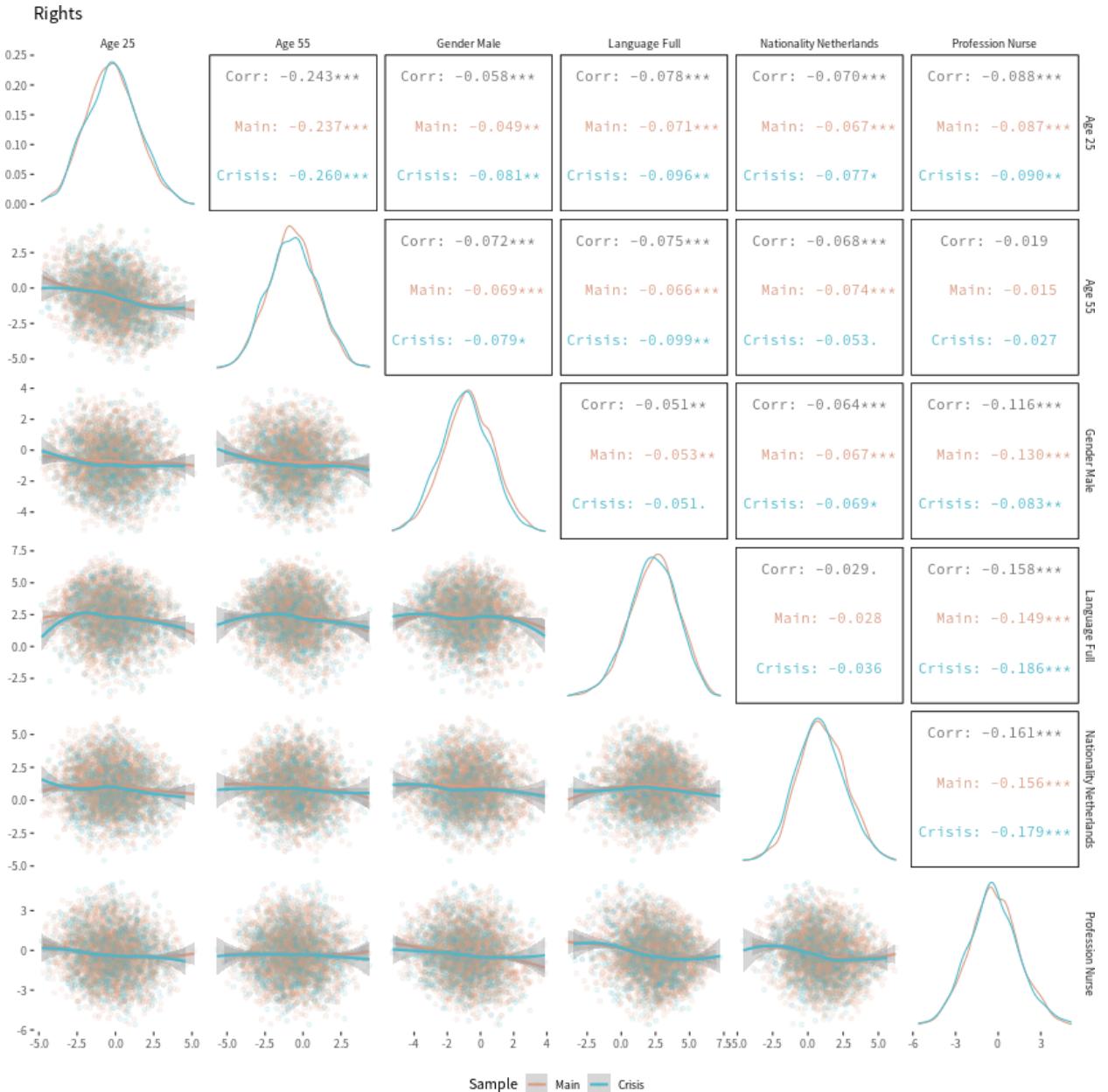


Figure 3.17: Comparison of median expected individual effects of every feature, by sample. Only rights.

```
ci.beta.w <- ci.beta %>%
filter(Outcome == "Welfare") %>%
filter(Feature != "First shown") %>%
left_join(select(di, id, Sample)) %>%
pivot_wider(c(id, Sample), names_from = Feature, values_from = median)

my_dens <- function(data, mapping, ...) {
  ggplot(data = data, mapping=mapping) +
    geom_density(..., alpha=0.3)
}
```

```

my_sc <- function(data, mapping, ...) {
  ggplot(data = data, mapping = mapping) +
    geom_point(alpha = 0.1) +
    geom_smooth(method = "lm")
}

ggplot <- function(...) ggplot2::ggplot(...) + scale_color_discrete_qualitative(palette = "Dynamic") + scale
unlockBinding("ggplot", parent.env(asNamespace("GGally")))
assign("ggplot", ggplot, parent.env(asNamespace("GGally")))

gpd <- select(ci.beta.w, -c(id))
gpairs(gpd,
  columns = 2:ncol(gpd),
  title = "Welfare",
  legend = c(2, 1),
  lower = list(continuous = my_sc),
  diag = list(continuous = my_dens),
  mapping = aes(color = Sample)) +
  theme(legend.position = "bottom")

```

3.2 Attribute importance

```

importance <- function(x) {
  if (length(x) == 1) {
    return(abs(x))
  } else {
    return(max(x) - min(x))
  }
}

S.importance <- S.beta %>%
  filter(!Feature %in% c("First shown", "(Intercept")) %>%
  ci() %>%
  select(id, Outcome, Feature, value = median) %>%
  separate(Feature, " ", into = c("Attribute", "Level")) %>%
  group_by(id, Outcome, Attribute) %>%
  summarize(Importance = importance(value))

S.relative.importance <- S.importance %>%
  group_by(id, Outcome) %>%
  mutate(`Relative importance` = Importance / sum(Importance)) %>%
  group_by(id, Outcome, Attribute) %>%
  mutate(SumRelativeImportance = sum(`Relative importance`)) %>%
  left_join(select(di, id, Sample))

S.relative.importance.nationality.order <- S.relative.importance %>%
  group_by(id, Outcome) %>%
  filter(Attribute = "Nationality") %>%
  arrange(desc(SumRelativeImportance)) %>%
  ungroup() %>%
  mutate(order = 1:n()) %>%
  select(id, Outcome, order)

S.relative.importance <- S.relative.importance %>%
  left_join(S.relative.importance.nationality.order)
save(S.relative.importance, file = paste("relative-importance-", M.lab, "-beta-relative_importance", ".RData"))

fo1 <- ggplot(filter(S.relative.importance, Outcome == outcome.label[1]),
  aes(x = reorder(id, order),
      y = `Relative importance`,
      fill = Attribute)) +
  geom_bar(position = "fill", stat = "identity") +
  xlab("Id") + ggtitle(outcome.label[1]) +
  scale_fill_brewer(type = "qual", palette = "Set1")

fo2 <- ggplot(filter(S.relative.importance, Outcome == outcome.label[2]),
  aes(x = reorder(id, order),
      y = `Relative importance`,
      fill = Attribute)) +
  geom_bar(position = "fill", stat = "identity") +

```

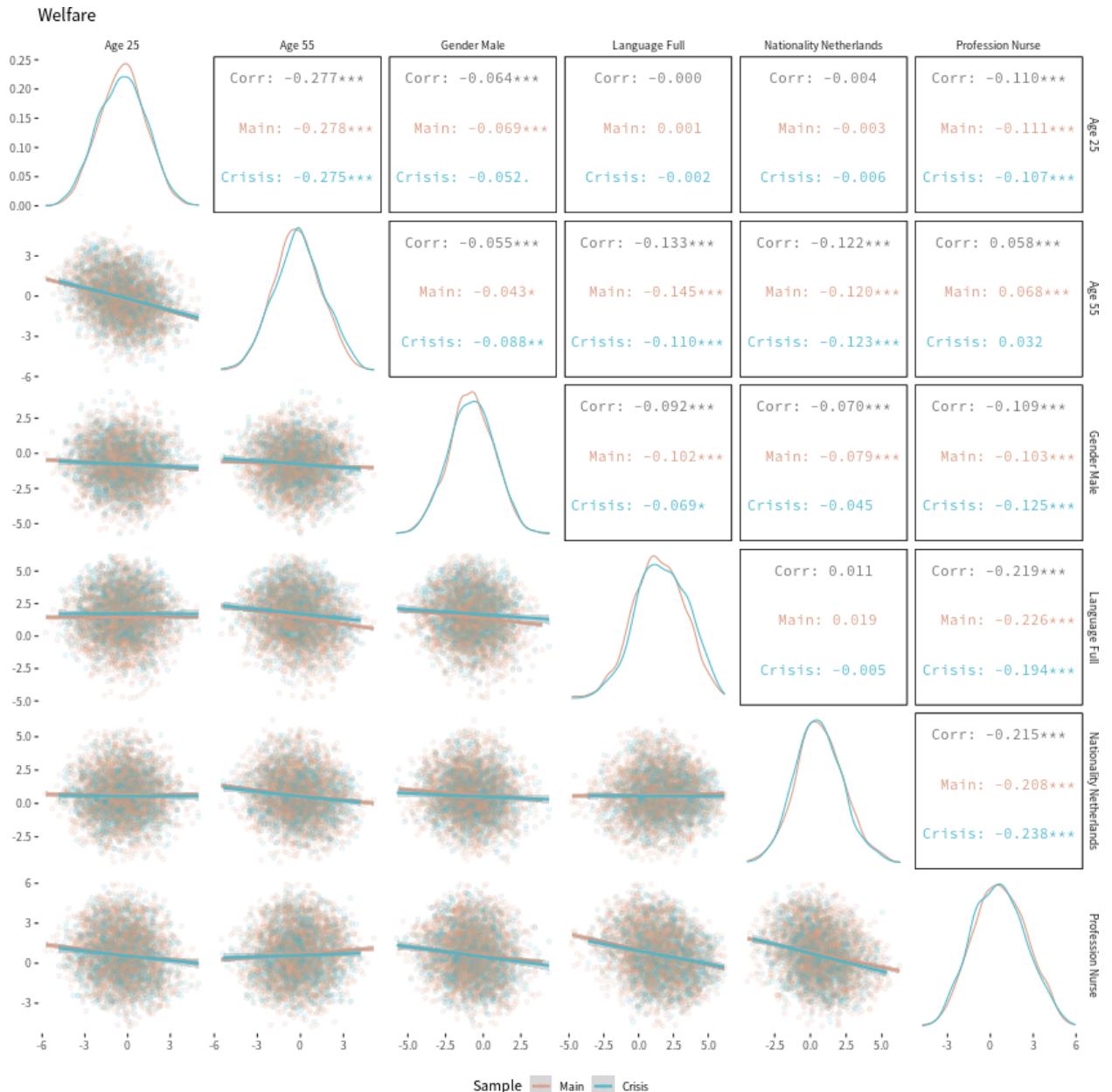


Figure 3.18: Comparison of median expected individual effects of every feature, by sample. Only welfare.

```
xlab("Id") + ggtitle(outcome.label[2]) +
  scale_fill_brewer(type = "qual", palette = "Set1")
grid.arrange(f01, f02, nrow = 2)
```

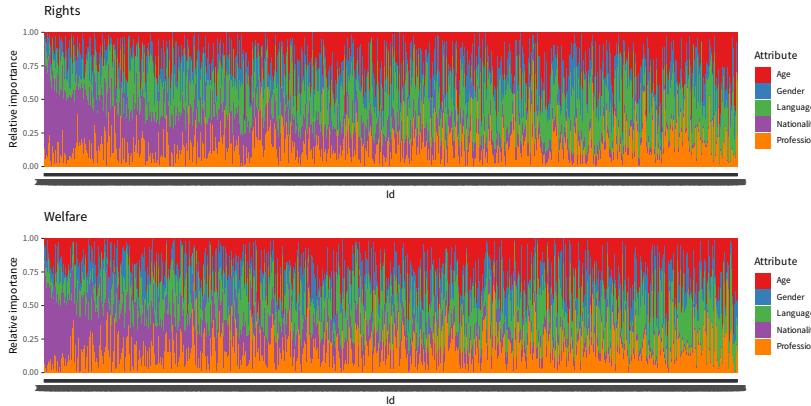


Figure 3.19: Relative importances assigned to each attribute by every individual, by outcome.

```
qtl <- seq(0, 1, by = 0.05)
ri.quantiles <- S.relative.importance %>%
  group_by(Outcome, Attribute, Sample) %>%
  # This summarize() requires dplyr-1.0 as of 200419
  summarize(q = qtl,
            quantiles = quantile(`Relative importance`, qtl))

ggplot(ri.quantiles,
       aes(x = q, y = quantiles, color = Attribute, lty = Sample)) +
  geom_line() +
  facet_grid(~ Outcome) +
  scale_fill_brewer(type = "qual", palette = "Set1") +
  xlab("Individuals (percentile, ordered)") + ylab("Relative importance") +
  ggtitle("Individual Relative importances")
```

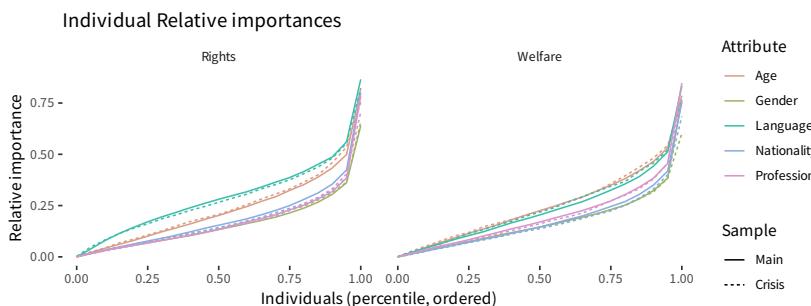


Figure 3.20: Comparison of relative importances for each sample.

```
ggplot(ri.quantiles,
       aes(x = q, y = quantiles, color = Outcome, lty = Sample)) +
  geom_line() +
  facet_grid(~ Attribute) +
  scale_color_discrete_qualitative(palette = "Dark 2") +
  xlab("Individuals (percentile, ordered)") + ylab("Relative importance") +
  ggtitle("Individual Relative importances")

ggplot(ri.quantiles,
       aes(x = q, y = quantiles, color = Sample)) +
  geom_line()
```

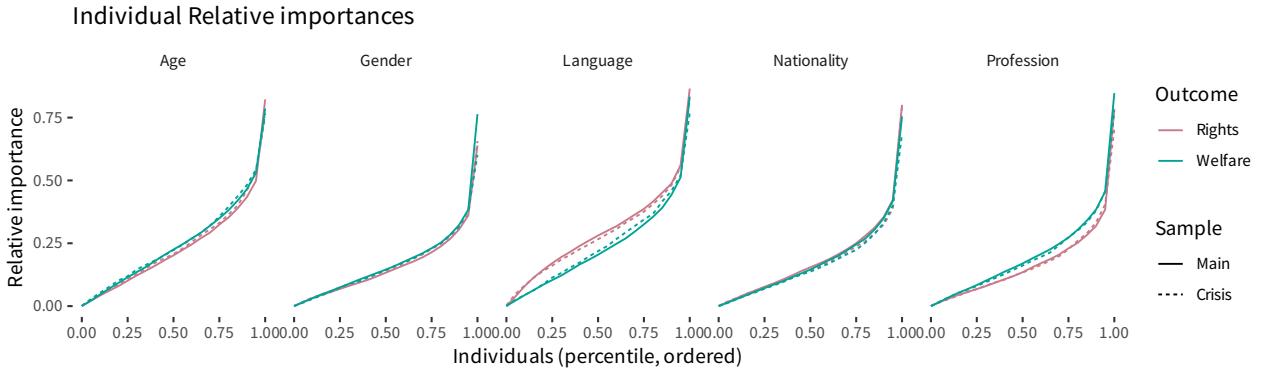


Figure 3.21: Comparison of relative importances for each sample.

```
facet_grid(Outcome ~ Attribute) +
  scale_color_discrete_qualitative(palette = "Dark 2") +
  xlab("Individuals (percentile, ordered)") + ylab("Relative importance") +
  ggtitle("Individual Relative importances")
```

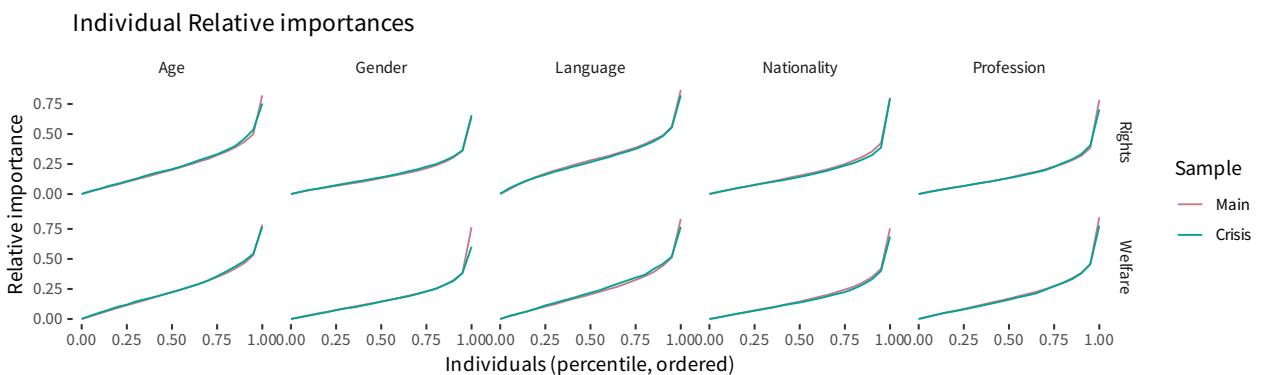


Figure 3.22: Comparison of relative importances for each sample.

```
pairs.S.relative.importance <- S.relative.importance %>%
  ungroup() %>%
  select(id, Outcome, Attribute, `Relative importance`) %>%
  mutate(id = as.numeric(as.character(id))) %>%
  left_join(select(di, id, Sample, Treatment)) %>%
  pivot_wider(names_from = Attribute, values_from = `Relative importance`)

my_dens <- function(data, mapping, ... , low = "#132B43", high = "#56B1F7") {
  ggplot(data = data, mapping=mapping) +
    geom_density(..., alpha=0.3)
}

ggpairs(select(pairs.S.relative.importance, -id),
  lower = list(continuous = wrap("points", alpha = 0.1)),
  diag = list(continuous = my_dens),
  mapping = aes(color = Outcome))
```

3.3 Explanatory variables for individual discriminations

```
L.theta <- plab("theta", list(Outcome = outcome.label,
  Feature = feature.label,
  Sample = sample.label,
  Covariate = covariate.label))

S.theta <- ggs(s, family = "theta\\[", par_labels = L.theta) %>%
  mutate(Model = M) %>%
```

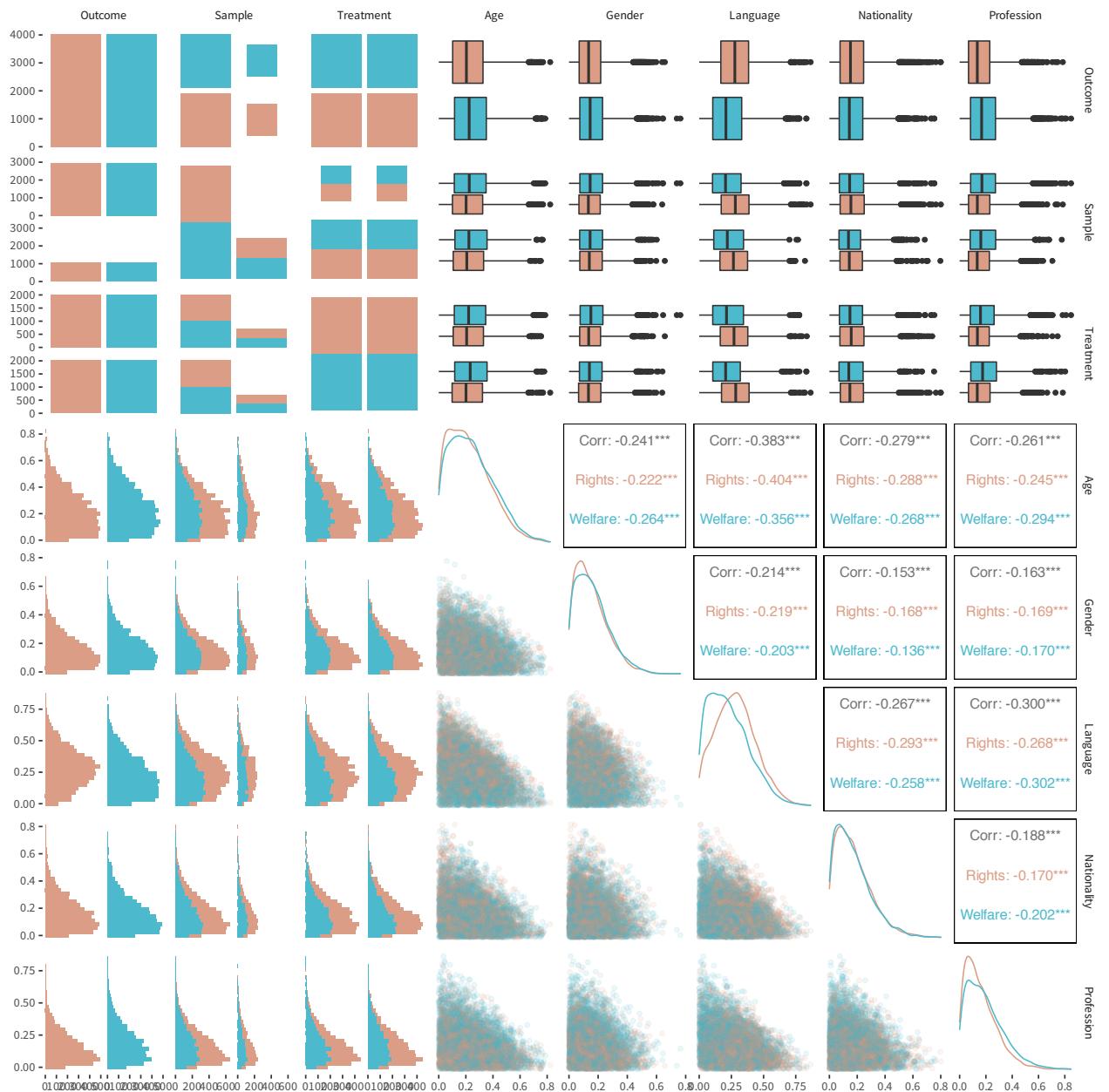


Figure 3.23: Comparison of individual relative importances, by outcome.

```
filter(Feature != "First shown")
save(S.theta, file = paste("samples-", M.lab, "-theta", ".RData", sep = ""))
ci.theta <- ci(S.theta)
```

Figure 3.24 allows to compare the difference in the effects of each sample (main/crisis) for each individual characteristic, by outcome (welfare/rights).

It can be read as follows: the last row of each panel, containing the “(Intercept)” is the baseline effect of prioritizing one individual over another. The two “(Intercept)” effects in the first column represent the reference category which, in both outcomes, is less preferred than other features. If we would observe differences between the two samples in the last two rows, for the features (nationality, gender, profession, language and age), then we would have to conclude that during crisis the overall effect of prioritization would have changed. But this is not happening in any feature, neither for welfare nor for rights. Therefore, we must conclude that the crisis has not altered, overall, the society response to prioritization requests. The population keeps having the same aggregatide patterns of discrimination.

On the other hand, if we would found differences in crisis/main sample for the individual effects altering the likelihood of prioritizing, then we would have to conclude that what has changed is how individual characteristics realing the sources of discrimination. For instance, if the intercept (lower row) is positive (implying that this concrete feature is prioritized over the reference category) and an effect that was zero now is positive, this would mean that that specific individual characteristic increases the discrimination during crisis. Likewise, if the main effect (last row) is positive and the individual effect is negative, it would imply that the source of discrimination is lower during crisis, for that specific individual characteristic.

```
ci.theta %>%
ggplot(aes(ymin = low, ymax = high, y = median,
           x = Covariate,
           group = Sample, color = Sample)) +
coord_flip() +
geom_point(position = position_dodge(width = 0.3)) +
geom_linerange(position = position_dodge(width = 0.3)) +
geom_linerange(aes(ymin = Low, ymax = High), size = 1, position = position_dodge(width = 0.3)) +
facet_grid(Outcome ~ Feature, scales = "free") +
geom_hline(aes(yintercept = 0), lty = 3) +
xlab("Covariates") +
scale_color_discrete_qualitative(palette = "Dynamic")

p90relevant <- S.theta %>%
  select(Iteration, Chain, Outcome, Feature, Sample, Covariate, value) %>%
  group_by(Outcome, Sample, Feature, Covariate) %>%
  summarize(prob = length(which(value > 0)) / n()) %>%
  mutate(relevant = ifelse(prob > 0.9 | prob < 0.1, 1, 0.2))

ci.theta %>%
  left_join(p90relevant) %>%
  ggplot(aes(ymin = low, ymax = high, y = median,
             x = Covariate,
             group = Sample, color = Sample, alpha = relevant)) +
  coord_flip() +
  geom_point(position = position_dodge(width = 0.3)) +
  geom_linerange(position = position_dodge(width = 0.3)) +
  geom_linerange(aes(ymin = Low, ymax = High), size = 1, position = position_dodge(width = 0.3)) +
  facet_grid(Outcome ~ Feature, scales = "free") +
```

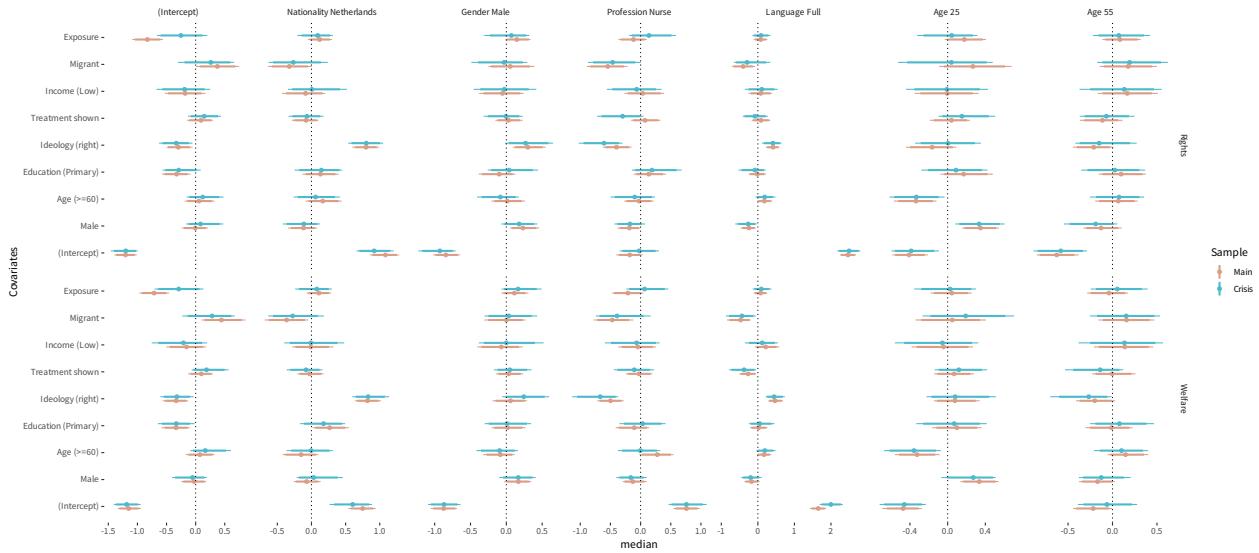


Figure 3.24: Discrimination for each attribute, with its effect by individual covariates, by outcome.

```

geom_hline(aes(yintercept = 0), lty = 3) +
xlab("Covariates") +
guides(alpha = FALSE) +
scale_color_discrete_qualitative(palette = "Dynamic")

comparison.relevant <- S.theta %>%
  select(Iteration, Chain, Outcome, Feature, Sample, Covariate, value) %>%
  pivot_wider(names_from = Sample, values_from = value) %>%
  group_by(Outcome, Feature, Covariate) %>%
  summarize(prob = length(which(Crisis > Main)) / n()) %>%
  mutate(relevant = ifelse(prob > 0.90 | prob < 0.10, 1, 0.2))

ci.theta %>%
  left_join(comparison.relevant) %>%
  ggplot(aes(ymin = low, ymax = high, y = median,
             x = Covariate,
             group = Sample, color = Sample, alpha = relevant)) +
  coord_flip() +
  geom_point(position = position_dodge(width = 0.3)) +
  geom_linerange(position = position_dodge(width = 0.3)) +
  geom_linerange(aes(ymin = Low, ymax = High), size = 1, position = position_dodge(width = 0.3)) +
  facet_grid(Outcome ~ Feature, scales = "free") +
  geom_hline(aes(yintercept = 0), lty = 3) +
  xlab("Covariates") +
  guides(alpha = FALSE) +
  scale_color_discrete_qualitative(palette = "Dynamic")

ci.theta %>%
  ggplot(aes(ymin = low, ymax = high, y = median,
             x = Feature,
             group = Sample, color = Sample)) +
  coord_flip() +
  geom_point(position = position_dodge(width = 0.3)) +
  geom_linerange(position = position_dodge(width = 0.3)) +
  geom_linerange(aes(ymin = Low, ymax = High), size = 1, position = position_dodge(width = 0.3)) +
  facet_grid(Covariate ~ Outcome, scales = "free") +
  geom_hline(aes(yintercept = 0), lty = 3) +
  xlab("Covariates") +
  scale_color_discrete_qualitative(palette = "Dynamic")

```

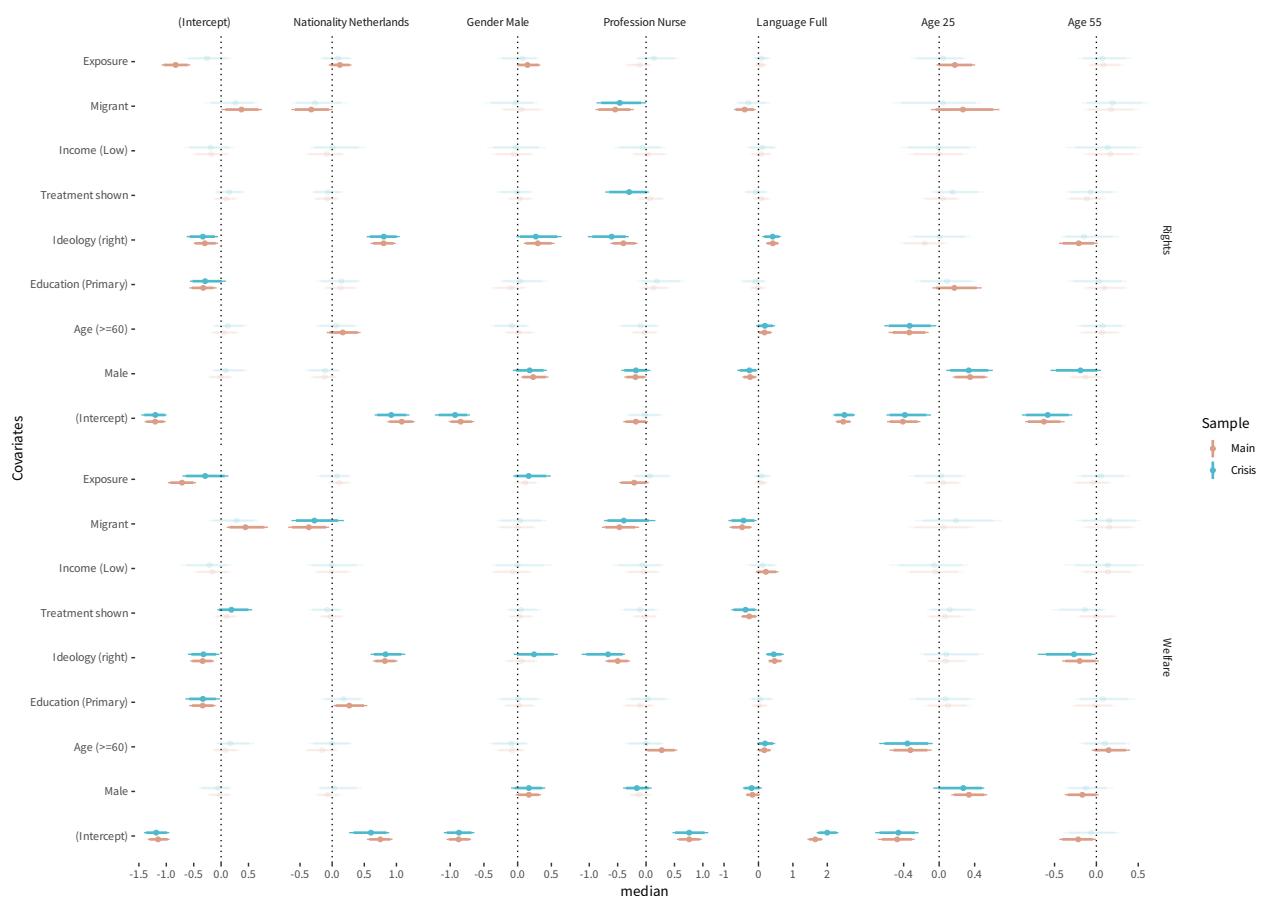


Figure 3.25: Discrimination for each attribute, with its effect by individual covariates, by outcome. Highlighted effects correspond to parameters with density not overlapping zero by 10 percent or more.

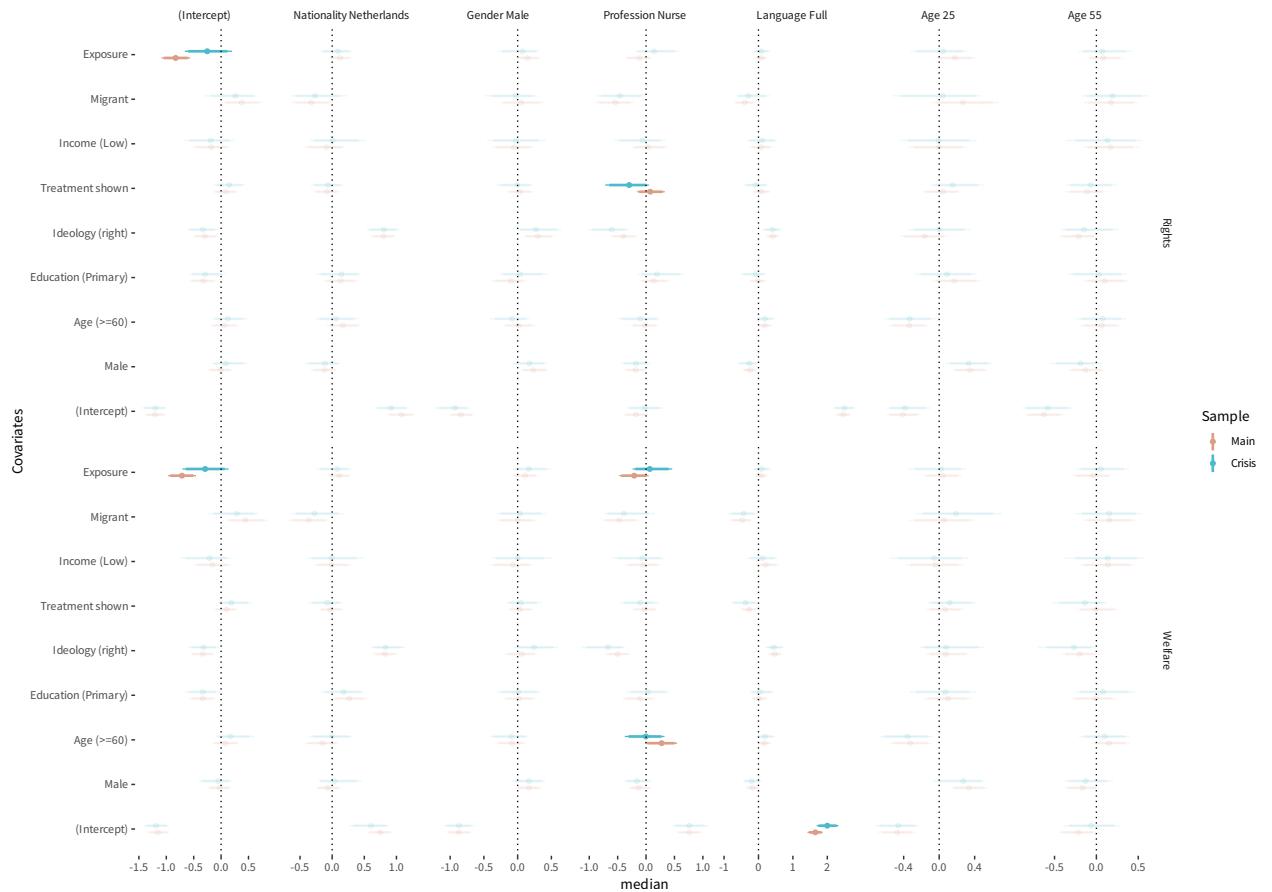


Figure 3.26: Discrimination for each attribute, with its effect by individual covariates, by outcome. The effects highlighted correspond to pre-post covid effects being different with probability higher than 99%.

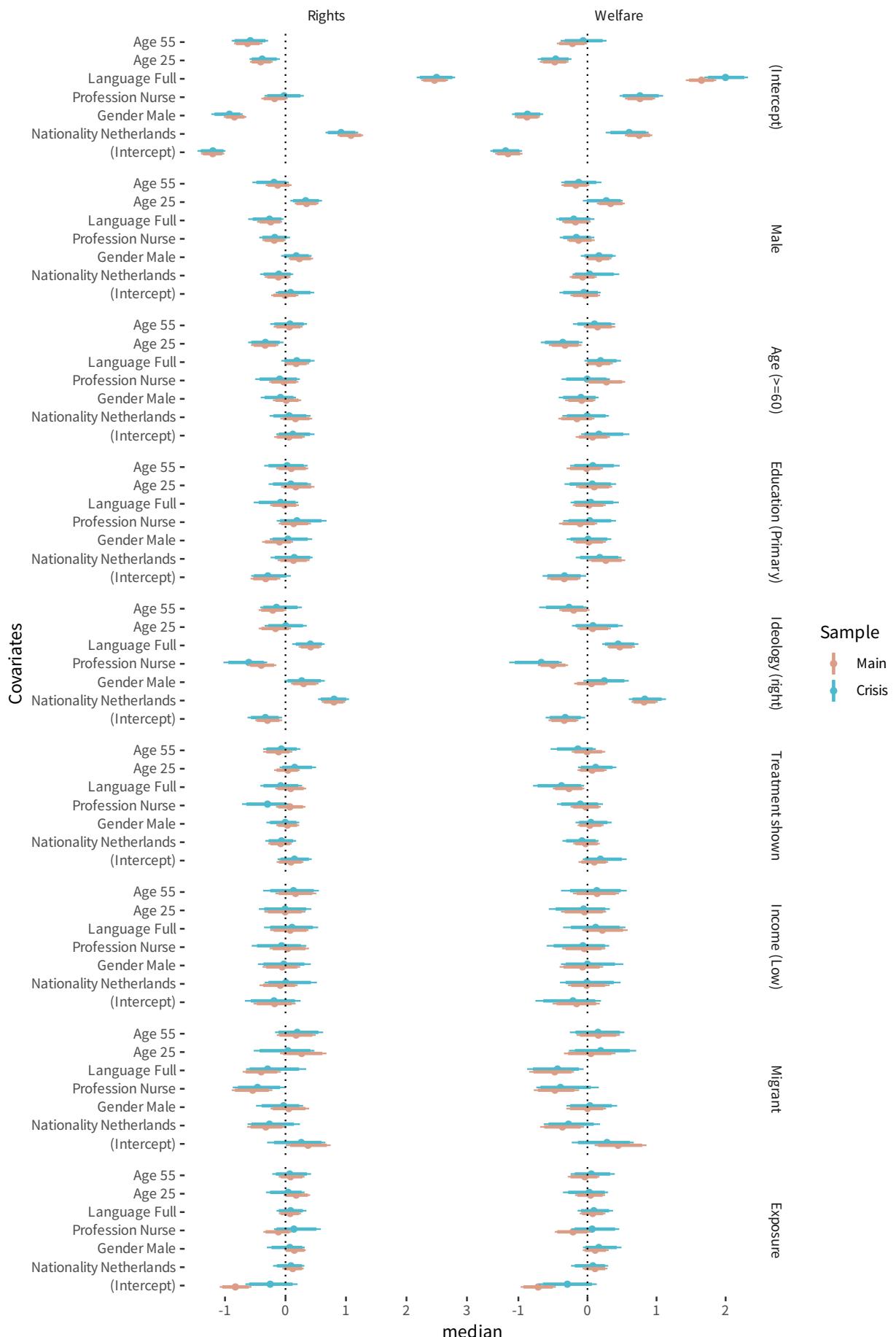


Figure 3.27: Discrimination for each attribute, with its effect by individual covariates, by outcome and sample

```
ci.theta %>%
  ggplot(aes(ymin = low, ymax = high, y = median,
             x = Covariate,
             group = Sample, color = Sample)) +
  coord_flip() +
  geom_point(position = position_dodge(width = 0.3)) +
  geom_linerange(position = position_dodge(width = 0.3)) +
  geom_linerange(aes(ymin = Low, ymax = High), size = 1, position = position_dodge(width = 0.3)) +
  facet_grid(Feature ~ Outcome, scales = "free") +
  geom_hline(aes(yintercept = 0), lty = 3) +
  xlab("Covariates") +
  scale_color_discrete_qualitative(palette = "Dynamic")
```

Interpretation of the magnitude of the individual-level effects on the likelihood of preference for different profiles can be seen at ??.

```
pp <- S.theta %>%
  select(Iteration, Chain, Outcome, Feature, Sample, Covariate, value) %>%
  filter(Feature != "First shown") %>%
  filter(Covariate != "Treatment shown") %>%
  spread(Feature, value) %>%
  gather(Feature, value, -c(Iteration, Chain, Outcome, Sample, Covariate, `^`((Intercept)`))) %>%
  mutate(`0` = inv.logit(`^`((Intercept)`))) %>%
  mutate(`1` = inv.logit(`^`((Intercept)` + value))) %>%
  select(-c(`^`((Intercept)`), value))

pp %>%
  filter(Outcome == "Rights") %>%
  sample_frac(0.02) %>%
  filter(Covariate != "(Intercept)") %>%
  ggplot(aes(x = 0, y = `0`,
             xend = 1, yend = `1`,
             color = Sample)) +
  geom_segment(alpha = 0.2) +
  facet_grid(Feature ~ Covariate) +
  xlab("Variable range") + ylab("Predicted probability") +
  ggtitle("Rights") +
  geom_hline(yintercept = 0.5, lty = 3) +
  theme(axis.text.x = element_blank(),
        axis.ticks.x = element_blank()) +
  guides(colour = guide_legend(override.aes = list(alpha = 1))) +
  scale_color_discrete_qualitative(palette = "Dynamic")

pp <- S.theta %>%
  select(Iteration, Chain, Outcome, Feature, Sample, Covariate, value) %>%
  filter(Feature != "First shown") %>%
  filter(Covariate != "Treatment shown") %>%
  spread(Feature, value) %>%
  gather(Feature, value, -c(Iteration, Chain, Outcome, Sample, Covariate, `^`((Intercept)`))) %>%
  mutate(`0` = inv.logit(`^`((Intercept)`))) %>%
  mutate(`1` = inv.logit(`^`((Intercept)` + value))) %>%
  select(-c(`^`((Intercept)`), value))

pp %>%
  filter(Outcome == "Welfare") %>%
  sample_frac(0.02) %>%
  filter(Covariate != "(Intercept)") %>%
  ggplot(aes(x = 0, y = `0`,
             xend = 1, yend = `1`,
             color = Sample)) +
  geom_segment(alpha = 0.2) +
  facet_grid(Feature ~ Covariate) +
  xlab("Variable range") + ylab("Predicted probability") +
  ggtitle("Welfare") +
  geom_hline(yintercept = 0.5, lty = 3) +
```

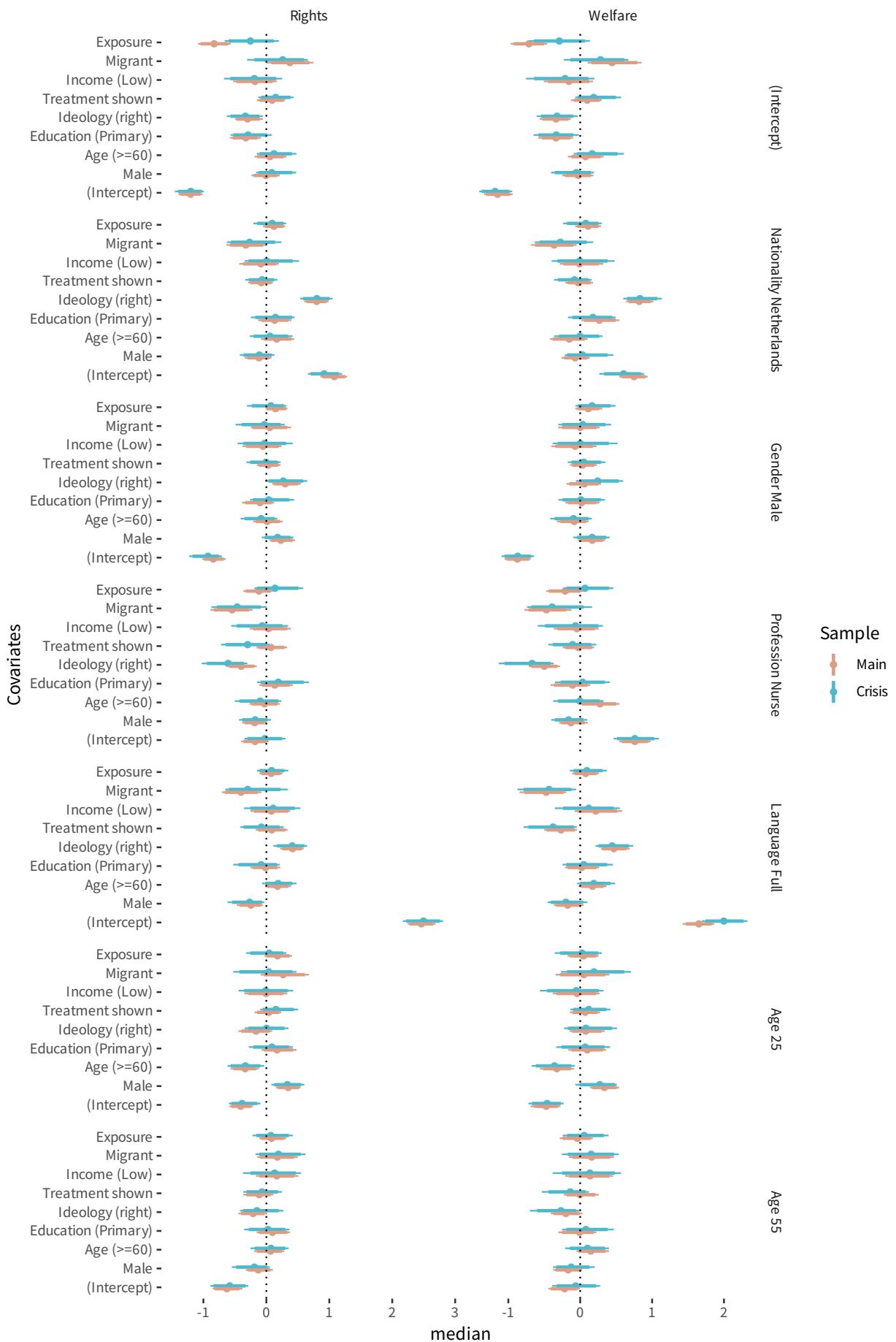
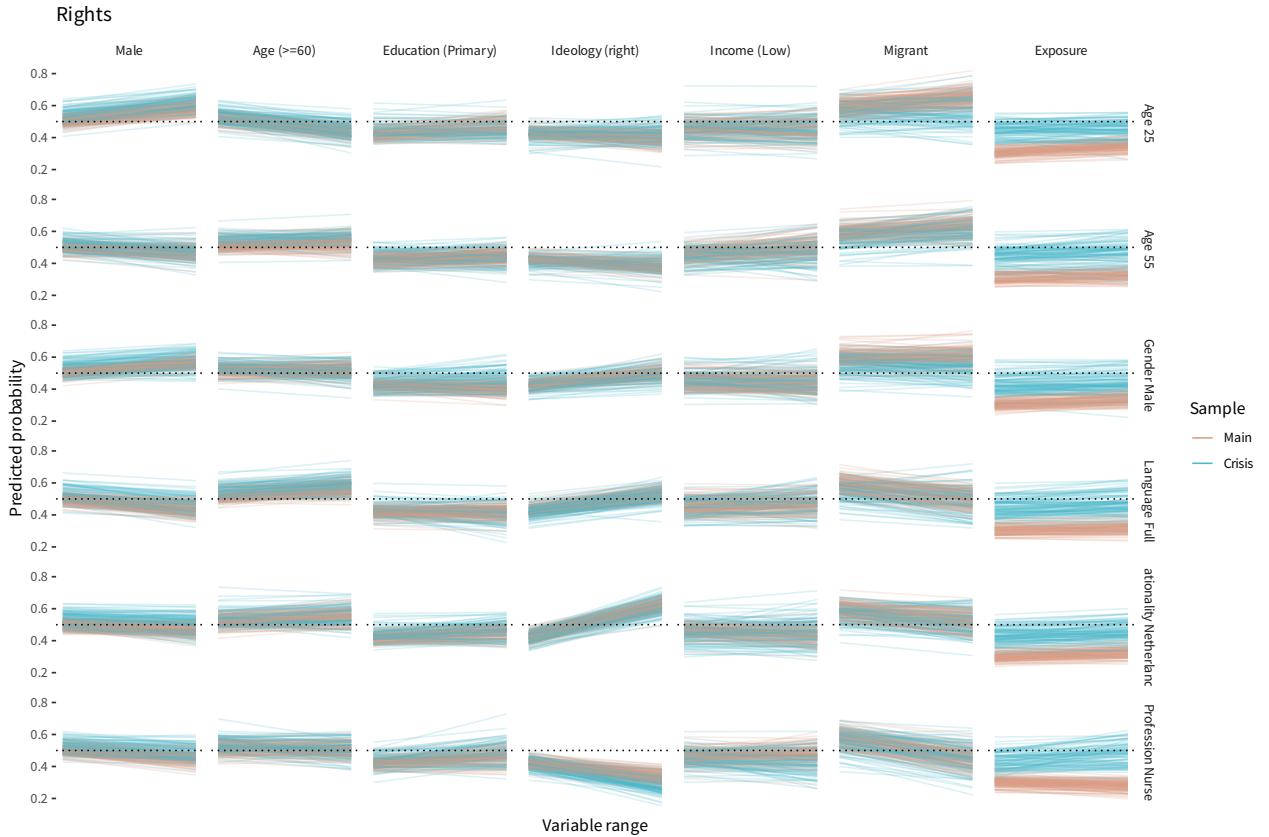


Figure 3.28: Discrimination for each attribute, with its effect by individual covariates, by outcome and sample



```

theme(axis.text.x = element_blank(),
      axis.ticks.x = element_blank()) +
guides(colour = guide_legend(override.aes = list(alpha = 1))) +
scale_color_discrete_qualitative(palette = "Dynamic")

pp <- S.theta %>%
  select(Iteration, Chain, Outcome, Feature, Sample, Covariate, value) %>%
  filter(Feature != "First shown") %>%
  filter(Covariate != "Treatment shown") %>%
  spread(Feature, value) %>%
  gather(Feature, value, -c(Iteration, Chain, Outcome, Sample, Covariate)) %>%
  mutate(`0` = inv.logit(`(Intercept)`)) %>%
  mutate(`1` = inv.logit(`(Intercept)` + value)) %>%
  select(-c(`(Intercept)`), value) %>%
  gather(x, `Predicted probability`, `0`, `1`) %>%
  group_by(Outcome, Sample, Covariate, Feature, x) %>%
  summarize(`Predicted probability` = median(`Predicted probability`)) %>%
  spread(x, `Predicted probability`)

pp %>%
  filter(Outcome == "Rights") %>%
  filter(Covariate != "(Intercept)") %>%
  ggplot(aes(x = 0, y = `0`,
             xend = 1, yend = `1`,
             color = Sample)) +
  geom_segment() +
  facet_grid(Feature ~ Covariate) +
  xlab("Variable range") + ylab("Predicted probability") +
  ggtitle("Rights") +
  geom_hline(yintercept = 0.5, lty = 3) +
  theme(axis.text.x = element_blank(),
        axis.ticks.x = element_blank())

```

Figure 3.29: Predicted probability of prioritizing any given profile, by the change in each of the individual-level covariates, ranging from their standardized values. Only rights. The figure can be interpreted as follows: the slopes of the graph in the first row, first column are positive, which means that compared to females (low value in the horizontal axis), males (high value in the horizontal axis) have higher preference for younger individuals (because of the positive slopes). For the first row, second column the interpretation is that as age increases, individuals are have lower preferences for younger profiles, indistinctively in the main sample or in the crisis sample.

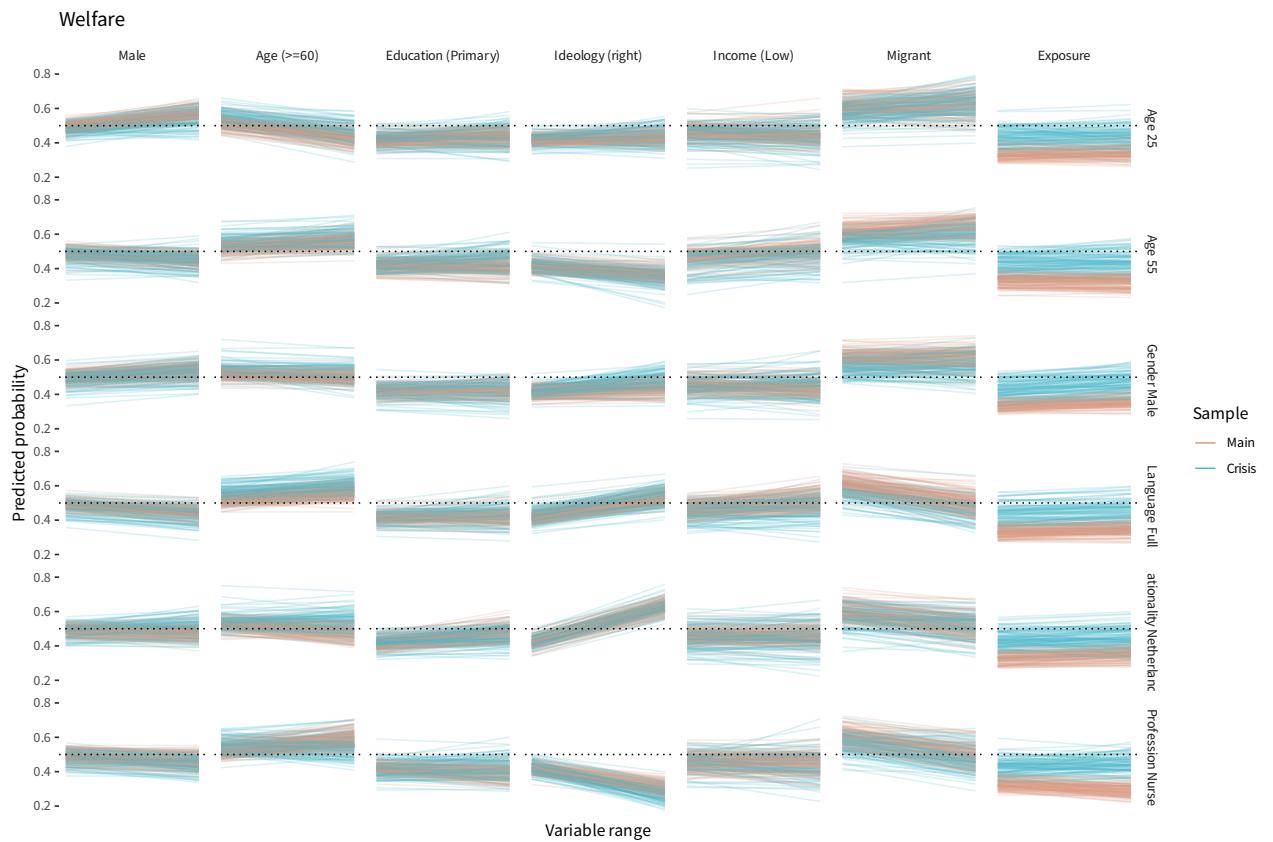


Figure 3.30: Predicted probability of prioritizing any given profile, by the change in each of the individual-level covariates, ranging from their standardized values. Only welfare.

```
axis.ticks.x = element_blank() +
guides(colour = guide_legend(override.aes = list(alpha = 1))) +
scale_color_discrete_qualitative(palette = "Dynamic")
```

```
pp <- S.theta %>%
  select(Iteration, Chain, Outcome, Feature, Sample, Covariate, value) %>%
  filter(Feature != "First shown") %>%
  filter(Covariate != "Treatment shown") %>%
  spread(Feature, value) %>%
  gather(Feature, value, -c(Iteration, Chain, Outcome, Sample, Covariate, `^`((Intercept)`))) %>%
  mutate(`_0` = inv.logit(`^`((Intercept)`))) %>%
  mutate(`_1` = inv.logit(`^`((Intercept)` + value))) %>%
  select(-c(`^`((Intercept)`), value)) %>%
  gather(x, `Predicted probability`, `_0`, `_1`) %>%
  group_by(Outcome, Sample, Covariate, Feature, x) %>%
  summarize(`Predicted probability` = median(`Predicted probability`)) %>%
  spread(x, `Predicted probability`)

pp %>%
  filter(Outcome == "Welfare") %>%
  filter(Covariate != "(Intercept)") %>%
  ggplot(aes(x = 0, y = `0`,
             xend = 1, yend = `1`,
             color = Sample)) +
  geom_segment() +
  facet_grid(Feature ~ Covariate) +
  xlab("Variable range") + ylab("Predicted probability") +
  ggtitle("Welfare") +
  geom_hline(yintercept = 0.5, lty = 3) +
  theme(axis.text.x = element_blank(),
        axis.ticks.x = element_blank()) +
```

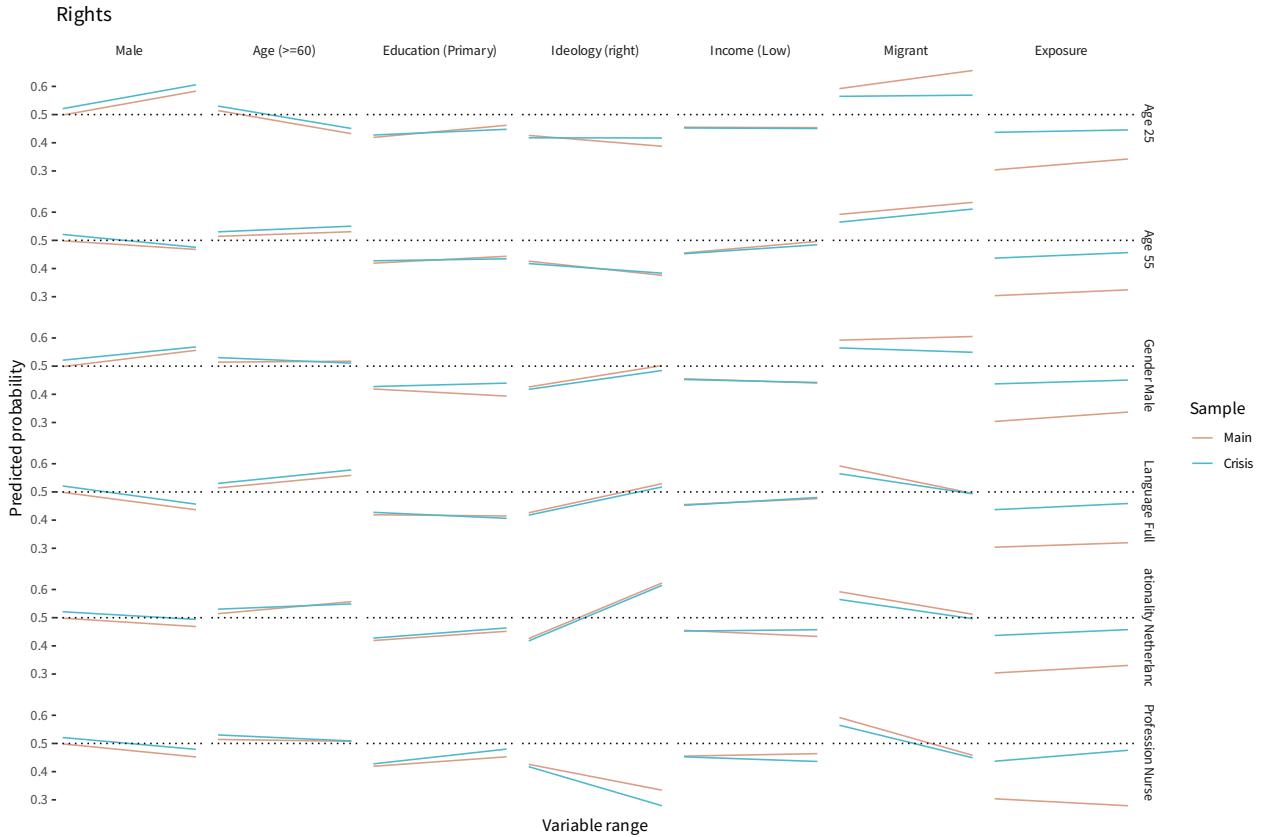


Figure 3.31: Predicted probability of prioritizing any given profile, by the change in each of the individual-level covariates, ranging from their standardized values. Only rights.

```
guides(colour = guide_legend(override.aes = list(alpha = 1))) +
scale_color_discrete_qualitative(palette = "Dynamic")
```

```
L.omega <- plab("omega", list(Feature = feature.label,
                                Covariate = covariate.label))
S.omega <- ggs(s, family = "^\omega\omega\\[", par_labels = L.omega)
ggplot(ci(S.omega), aes(ymin = low, ymax = high,
                         y = median, x = Covariate)) +
  coord_flip() +
  geom_point(position = position_dodge(width = 0.3)) +
  geom_linerange(position = position_dodge(width = 0.3)) +
  geom_linerange(aes(ymin = Low, ymax = High), size = 1, position = position_dodge(width = 0.3)) +
  facet_grid(~ Feature) +
  geom_hline(aes(yintercept = 0), lty = 3) +
  xlab("Parameter") + ylab("HPD") +
  ggtitle("Grand-grand-means for prioritization")
```

List median expected effects, by magnitude.

```
tb <- S.omega %>%
  filter(Feature != "(Intercept)") %>%
  ci() %>%
  arrange(desc(abs(median))) %>%
  mutate(`Odds Ratio` = exp(median)) %>%
  mutate(`Expected effect` = or(`Odds Ratio`)) %>%
  select(Feature, Covariate, `Odds Ratio`, `Expected effect`)

tc <- "Odds ratio of expected grand-effects, sorted by magnitude."
if (knitr::is_latex_output()) {
  kable(tb, format = "latex", caption = tc, longtable = TRUE, booktabs = TRUE) %>%
    kable_styling(font_size = 10)
```

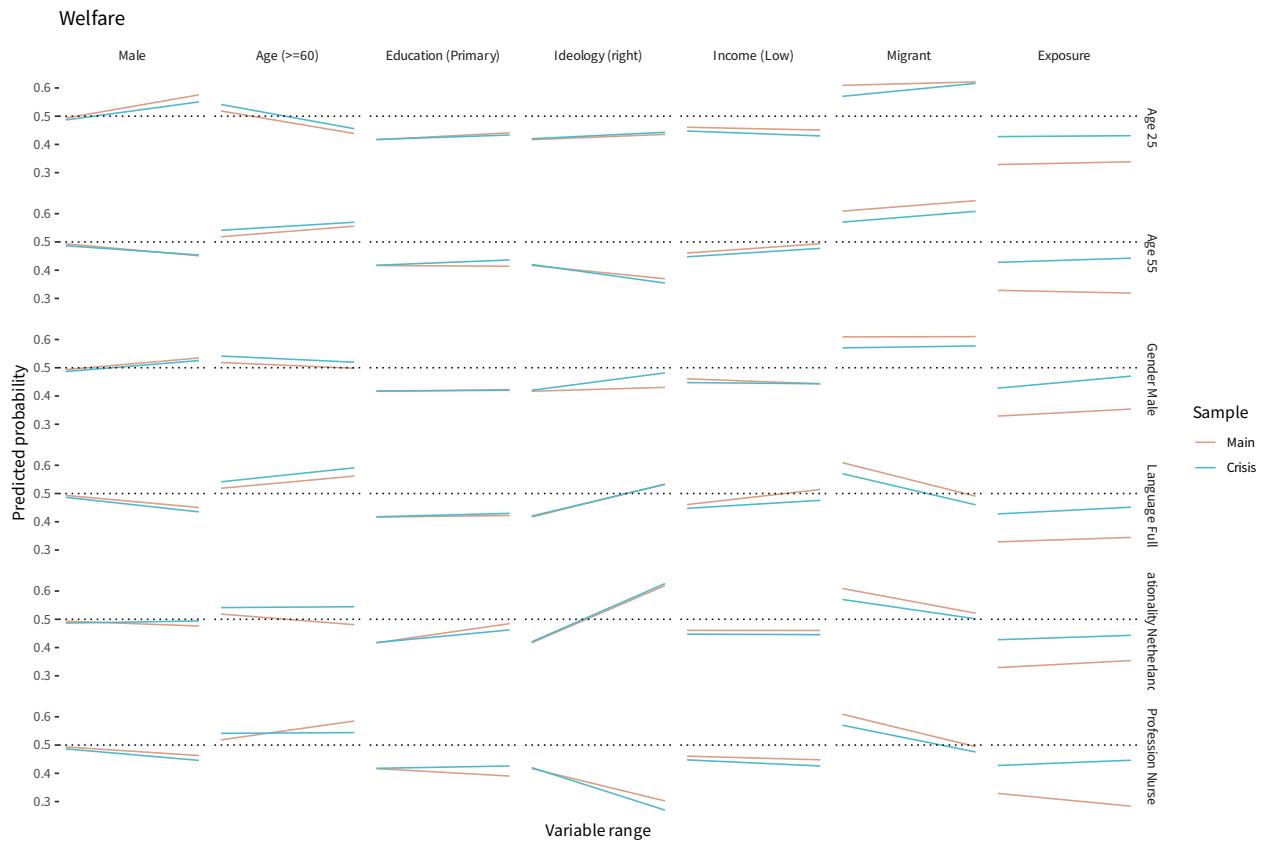


Figure 3.32: Predicted probability of prioritizing any given profile, by the change in each of the individual-level covariates, ranging from their standardized values. Only welfare.

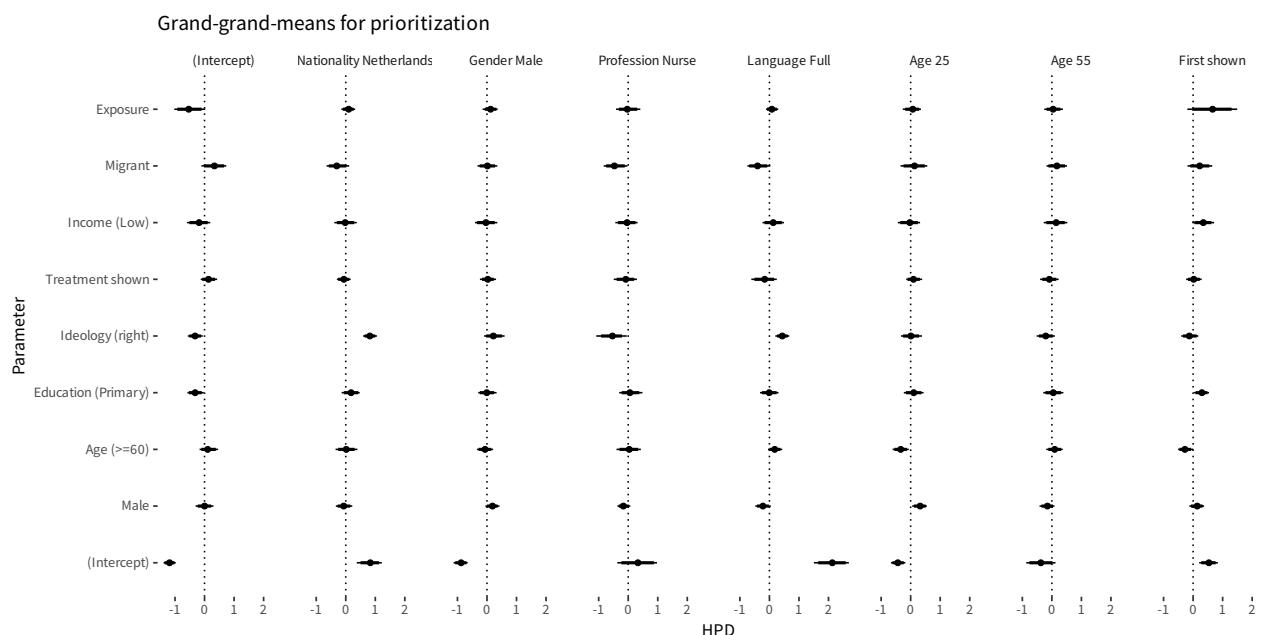


Figure 3.33: Prioritization of features (grand-grand mean).

```
} else {
  kable(tb, format = "html", caption = tc, booktabs = TRUE) %>%
    kable_styling(font_size = 10, position = "center", bootstrap_options = "striped", full_width = T)
}
```

Table 3.1: Odds ratio of expected grand-effects, sorted by magnitude.

Feature	Covariate	Odds Ratio	Expected effect
Language Full	(Intercept)	8.4098	△ 740%
Gender Male	(Intercept)	0.4163	▽ 58%
Nationality Netherlands	(Intercept)	2.2992	△ 130%
Nationality Netherlands	Ideology (right)	2.2602	△ 130%
First shown	Exposure	1.9339	△ 93%
First shown	(Intercept)	1.7083	△ 71%
Profession Nurse	Ideology (right)	0.5861	▽ 41%
Profession Nurse	Migrant	0.6265	▽ 37%
Language Full	Ideology (right)	1.5458	△ 55%
Age 25	(Intercept)	0.6477	▽ 35%
Language Full	Migrant	0.6684	▽ 33%
Age 55	(Intercept)	0.6883	▽ 31%
First shown	Income (Low)	1.4122	△ 41%
Age 25	Age (>=60)	0.7151	▽ 28%
Profession Nurse	(Intercept)	1.3882	△ 39%
Age 25	Male	1.3778	△ 38%
Nationality Netherlands	Migrant	0.7373	▽ 26%
First shown	Education (Primary)	1.3470	△ 35%
First shown	Age (>=60)	0.7577	▽ 24%
First shown	Migrant	1.2487	△ 25%
Language Full	Male	0.8026	▽ 20%
Gender Male	Ideology (right)	1.2414	△ 24%
Age 55	Ideology (right)	0.8118	▽ 19%
Gender Male	Male	1.2047	△ 20%
Nationality Netherlands	Education (Primary)	1.1978	△ 20%
Language Full	Age (>=60)	1.1959	△ 20%
Age 55	Migrant	1.1853	△ 19%
Profession Nurse	Male	0.8488	▽ 15%
Language Full	Treatment shown	0.8511	▽ 15%
Age 55	Male	0.8592	▽ 14%
Age 55	Income (Low)	1.1572	△ 16%
First shown	Male	1.1492	△ 15%
Age 25	Migrant	1.1407	△ 14%
Language Full	Income (Low)	1.1373	△ 14%
First shown	Ideology (right)	0.8821	▽ 12%
Gender Male	Exposure	1.1300	△ 13%
Age 25	Education (Primary)	1.1095	△ 11%
Nationality Netherlands	Exposure	1.1051	△ 11%
Age 25	Treatment shown	1.1007	△ 10%
Age 55	Age (>=60)	1.0999	△ 10%
Age 55	Treatment shown	0.9187	▽ 8.1%
Profession Nurse	Treatment shown	0.9212	▽ 7.9%
Language Full	Exposure	1.0850	△ 8.5%
Age 25	Exposure	1.0746	△ 7.5%
Nationality Netherlands	Male	0.9324	▽ 6.8%

Gender Male	Age (>=60)	0.9371	▽ 6.3%
Nationality Netherlands	Treatment shown	0.9389	▽ 6.1%
Profession Nurse	Education (Primary)	1.0592	△ 5.9%
Age 55	Education (Primary)	1.0479	△ 4.8%
Age 55	Exposure	1.0416	△ 4.2%
Profession Nurse	Income (Low)	0.9619	▽ 3.8%
Gender Male	Income (Low)	0.9651	▽ 3.5%
Profession Nurse	Age (>=60)	1.0362	△ 3.6%
Profession Nurse	Exposure	0.9682	▽ 3.2%
Age 25	Income (Low)	0.9717	▽ 2.8%
Gender Male	Treatment shown	1.0287	△ 2.9%
First shown	Treatment shown	1.0220	△ 2.2%
Nationality Netherlands	Income (Low)	0.9803	▽ 2%
Nationality Netherlands	Age (>=60)	1.0168	△ 1.7%
Gender Male	Migrant	1.0147	△ 1.5%
Language Full	Education (Primary)	0.9917	▽ 0.83%
Gender Male	Education (Primary)	0.9927	▽ 0.73%
Age 25	Ideology (right)	1.0059	△ 0.59%

3.4 Differential discrimination

Figure 3.34 shows the differential discrimination that welfare outcomes have over rights. Histograms show the distribution of the values of the differential discrimination in each simulation. Therefore, a histogram that clearly overlaps 0.5 indicates that there is no trace of differential discrimination. When the histogram barely overlaps zero it indicates evidence of a differential discrimination, either welfare effects being greater than rights (right to the zero) or rights effects being greater than welfare (left to the zero).

```
dd.outcome <- S.theta %>%
  select(Iteration, Chain, Outcome, Covariate, Feature, Sample, value) %>%
  spread(Outcome, value) %>%
  mutate(`Differential discrimination on welfare` = Rights - Welfare)
tb <- dd.outcome %>%
  group_by(Covariate, Feature, Sample) %>%
  summarize(`Prob Welfare > Rights` = length(which(`Differential discrimination on welfare` > 0)) / n()) %>%
  arrange(desc(`Prob Welfare > Rights`))
fig.labels <- tb %>%
  mutate(P = paste0(100 * signif(`Prob Welfare > Rights`, 2), "%")) %>%
  mutate(P = str_replace(P, "^0\\.\\.", "\\."))

ggplot(filter(dd.outcome, Sample == "Crisis"),
       aes(x = `Differential discrimination on welfare`)) +
  geom_histogram(binwidth = 0.01) +
  facet_grid(Covariate ~ Feature) +
  geom_text(data = fig.labels, #filter(fig.labels, Population == "General population"),
            aes(x = -Inf, y = Inf, label = P), size = rel(0.8),
            hjust = -0.5, vjust = +1.5) +
  geom_vline(xintercept = 0, lty = 3) +
  xlim(c(-1, 1)) +
  ggtitle("Differential discrimination on welfare")

tb <- dd.outcome %>%
  mutate(Covariate = str_replace(Covariate, "^\\\\(", "\\\\(")) %>%
  group_by(Covariate, Feature) %>%
  summarize(`Prob Welfare > Rights` = length(which(`Differential discrimination on welfare` > 0)) / n()) %>%
  arrange(desc(`Prob Welfare > Rights`))
```

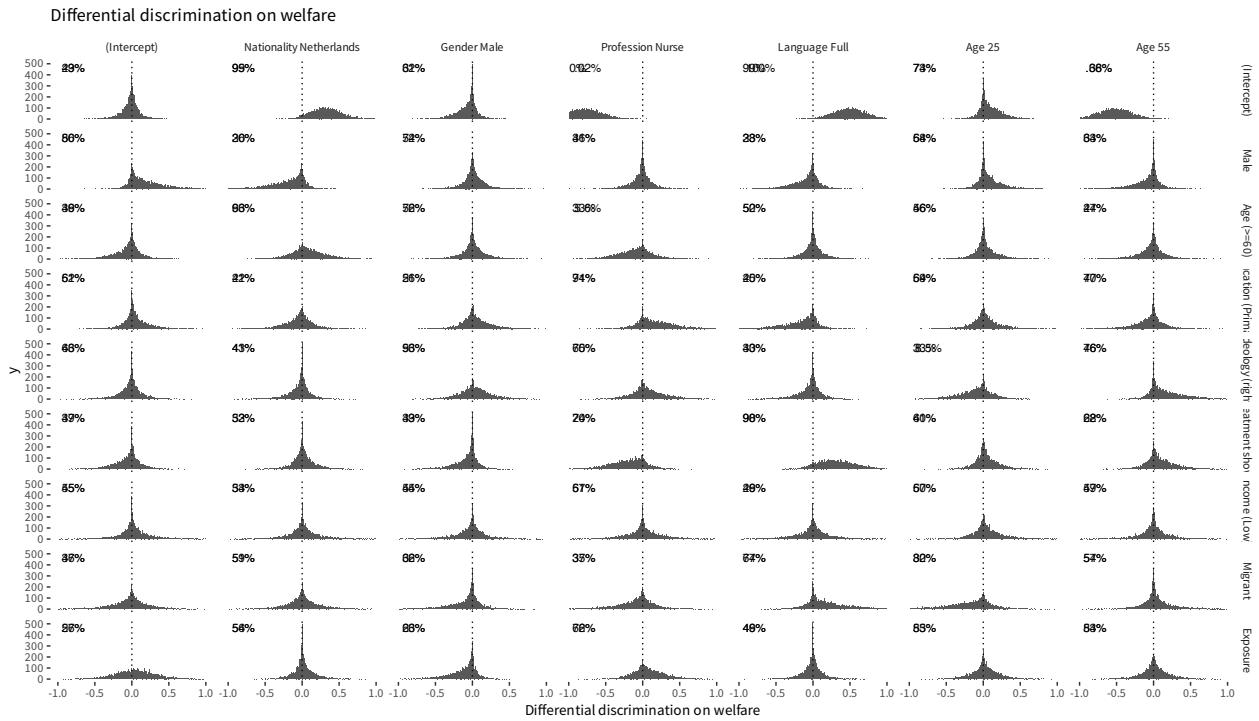


Figure 3.34: Differential discrimination on welfare over rights. Only crisis sample is shown. Values indicate the probability of having found a differential discrimination favouring welfare.

```
tc <- "Probability of finding a differential discrimination on welfare over rights"
if (knitr::is_latex_output()) {
  kable(tb, format = "latex", caption = tc, longtable = TRUE, booktabs = TRUE) %>%
    kable_styling(font_size = 8)
} else {
  kable(tb, format = "html", caption = tc, booktabs = TRUE) %>%
    kable_styling(font_size = 8, position = "center", bootstrap_options = "striped", full_width = T)
}
```

Table 3.2: Probability of finding a differential discrimination on welfare over rights.

Covariate	Feature	Prob Welfare > Rights
\(\text{(Intercept)} \)	Language Full	0.9960
\(\text{(Intercept)} \)	Nationality Netherlands	0.9715
Treatment shown	Language Full	0.9376
Education (Primary)	Profession Nurse	0.8243
Age (>=60)	Nationality Netherlands	0.7951
Ideology (right)	Gender Male	0.7452
\(\text{(Intercept)} \)	Age 25	0.7327
Migrant	Language Full	0.7086
Exposure	Age 25	0.6882
Exposure	Profession Nurse	0.6873
Exposure	Age 55	0.6842
Male	(Intercept)	0.6824
Ideology (right)	Profession Nurse	0.6751
Age (>=60)	Gender Male	0.6388
Male	Gender Male	0.6266
Education (Primary)	Age 25	0.6134
Ideology (right)	Age 55	0.6110
Male	Age 25	0.6097
Income (Low)	Profession Nurse	0.5903
Income (Low)	Age 25	0.5858
Education (Primary)	Age 55	0.5813
Education (Primary)	(Intercept)	0.5665

Migrant	Age 25	0.5612
Migrant	Age 55	0.5563
Migrant	Nationality Netherlands	0.5535
Exposure	Nationality Netherlands	0.5489
Ideology (right)	(Intercept)	0.5467
Income (Low)	Age 55	0.5302
Age (>=60)	Age 25	0.5108
Age (>=60)	Language Full	0.5057
Treatment shown	Age 25	0.5032
Income (Low)	(Intercept)	0.5027
Income (Low)	Gender Male	0.4965
Migrant	Gender Male	0.4917
Male	Age 55	0.4862
Exposure	Language Full	0.4790
Treatment shown	Profession Nurse	0.4734
\(Intercept)	Gender Male	0.4658
Treatment shown	Age 55	0.4471
Exposure	Gender Male	0.4467
Income (Low)	Nationality Netherlands	0.4331
Treatment shown	(Intercept)	0.4324
Treatment shown	Nationality Netherlands	0.4275
Age (>=60)	(Intercept)	0.4235
Ideology (right)	Nationality Netherlands	0.4174
Exposure	(Intercept)	0.4160
Migrant	(Intercept)	0.4158
Treatment shown	Gender Male	0.4123
Education (Primary)	Gender Male	0.3868
Male	Profession Nurse	0.3820
Income (Low)	Language Full	0.3744
Ideology (right)	Language Full	0.3689
\(Intercept)	(Intercept)	0.3616
Migrant	Profession Nurse	0.3583
Age (>=60)	Age 55	0.3540
Education (Primary)	Language Full	0.3268
Education (Primary)	Nationality Netherlands	0.3142
Male	Language Full	0.3022
Male	Nationality Netherlands	0.2760
Ideology (right)	Age 25	0.2085
Age (>=60)	Profession Nurse	0.1917
\(Intercept)	Age 55	0.0052
\(Intercept)	Profession Nurse	0.0001

```

dd.sample <- S.theta %>%
  select(Iteration, Chain, Outcome, Covariate, Feature, Sample, value) %>%
  spread(Sample, value) %>%
  mutate(`Differential discrimination on crisis` = Crisis - Main)
tb <- dd.sample %>%
  group_by(Covariate, Feature, Outcome) %>%
  summarize(`Prob Crisis > Main` = length(which(`Differential discrimination on crisis` < 0)) / n()) %>%
  arrange(desc(`Prob Crisis > Main`))

fig.labels <- tb %>%
  mutate(P = paste0(100 * signif(`Prob Crisis > Main`, 2), "%")) %>%
  mutate(P = str_replace(P, "\^0\\.\\.", "\\.")) %>%
  mutate(HighlightP = ifelse(abs(`Prob Crisis > Main` - 0.5) > 0.45, "Highlight", "Plain"))

fig.labels.Xpercent <- dd.sample %>%
  group_by(Covariate, Feature, Outcome) %>%
  summarize(`Prob Crisis > Main Xpercent` = length(which(`Differential discrimination on crisis` > log(1.05))) / n(),
            `Prob Crisis < Main Xpercent` = length(which(`Differential discrimination on crisis` < -log(1.05))) / n())
  mutate(P.pos = `Prob Crisis > Main Xpercent`) %>%
  mutate(P.neg = `Prob Crisis < Main Xpercent`) %>%
  mutate(P = ifelse(P.pos > P.neg, P.pos, P.neg)) %>%
  mutate(HighlightP = ifelse(abs(P - 0.5) > 0.45, "Highlight", "Plain")) %>%
  mutate(P.pos = str_replace(paste0(100 * signif(P.pos, 2), "%"), "\^0\\.\\.", "\\.")) %>%
  mutate(P.neg = str_replace(paste0(100 * signif(P.neg, 2), "%"), "\^0\\.\\.", "\\.")) %>%
  
```

```

  mutate(P.neg = str_replace(paste0(100 * signif(P.neg, 2), "%"), "\^0\\.", "\\.")) %>%
  mutate(P = str_replace(paste0(100 * signif(P, 2), "%"), "\^0\\.", "\\."))

tb ← dd.sample %>%
  mutate(Covariate = str_replace(Covariate, "\^\\(( ", "\\(\\(")) %>%
  group_by(Outcome, Covariate, Feature) %>%
  summarize(`Prob Crisis > Main` = length(which(`Differential discrimination on crisis` < 0)) / n()) %>%
  arrange(desc(`Prob Crisis > Main`))

tc ← "Probability of finding a differential discrimination on crisis over regular period."
if (knitr::is_latex_output()) {
  kable(tb, format = "latex", caption = tc, longtable = TRUE, booktabs = TRUE) %>%
    kable_styling(font_size = 8)
} else {
  kable(tb, format = "html", caption = tc, booktabs = TRUE) %>%
    kable_styling(font_size = 8, position = "center", bootstrap_options = "striped", full_width = T)
}

```

Table 3.3: Probability of finding a differential discrimination on crisis over regular period.

Outcome	Covariate	Feature	Prob Crisis > Main
Rights	Treatment shown	Profession Nurse	0.9520
Welfare	Age (>=60)	Profession Nurse	0.9004
Rights	Ideology (right)	Profession Nurse	0.8674
Rights	\(Intercept)	Nationality Netherlands	0.8532
Welfare	Ideology (right)	Profession Nurse	0.8174
Welfare	Treatment shown	Age 55	0.8092
Rights	Migrant	Age 25	0.8086
Welfare	\(Intercept)	Nationality Netherlands	0.8078
Rights	Treatment shown	Language Full	0.8064
Rights	Exposure	Age 25	0.7924
Rights	\(Intercept)	Gender Male	0.7754
Welfare	Migrant	(Intercept)	0.7572
Rights	Age (>=60)	Gender Male	0.7390
Rights	Exposure	Gender Male	0.7278
Welfare	Treatment shown	Language Full	0.7142
Rights	Age (>=60)	Nationality Netherlands	0.7116
Rights	Education (Primary)	Age 25	0.6948
Rights	Migrant	(Intercept)	0.6904
Rights	Male	Age 55	0.6870
Welfare	Education (Primary)	Nationality Netherlands	0.6866
Welfare	Ideology (right)	Age 55	0.6854
Welfare	Male	Age 25	0.6806
Rights	Income (Low)	Profession Nurse	0.6750
Rights	Migrant	Gender Male	0.6708
Rights	Male	Gender Male	0.6666
Welfare	Income (Low)	Language Full	0.6630
Welfare	Treatment shown	Nationality Netherlands	0.6622
Rights	Education (Primary)	Age 55	0.6598
Rights	Education (Primary)	Language Full	0.6592
Welfare	Treatment shown	Profession Nurse	0.6580
Rights	Age (>=60)	Profession Nurse	0.6510
Rights	Treatment shown	Gender Male	0.6236
Welfare	\(Intercept)	(Intercept)	0.6218
Welfare	Age (>=60)	Age 55	0.6186
Welfare	Exposure	Nationality Netherlands	0.6180
Rights	Exposure	Nationality Netherlands	0.6140
Welfare	Income (Low)	(Intercept)	0.6042
Rights	Ideology (right)	(Intercept)	0.6018
Welfare	Male	Profession Nurse	0.6016
Welfare	Male	(Intercept)	0.5946
Welfare	Age (>=60)	Age 25	0.5842
Welfare	Male	Language Full	0.5752

Rights	Male	Language Full	0.5696
Rights	Income (Low)	Age 55	0.5654
Welfare	Exposure	Age 25	0.5634
Welfare	Education (Primary)	Age 25	0.5612
Welfare	Ideology (right)	Language Full	0.5576
Rights	Ideology (right)	Gender Male	0.5562
Welfare	Income (Low)	Profession Nurse	0.5506
Welfare	Income (Low)	Age 25	0.5372
Rights	Male	Age 25	0.5310
Rights	Exposure	Age 55	0.5278
Welfare	Age (>=60)	Gender Male	0.5266
Welfare	Education (Primary)	Gender Male	0.5252
Rights	Ideology (right)	Language Full	0.5160
Welfare	Income (Low)	Age 55	0.5154
Rights	Income (Low)	(Intercept)	0.5070
Welfare	Migrant	Age 55	0.5042
Rights	Income (Low)	Age 25	0.5028
Welfare	\(Intercept)	Profession Nurse	0.5012
Welfare	Education (Primary)	(Intercept)	0.4996
Welfare	Income (Low)	Nationality Netherlands	0.4972
Rights	Male	Nationality Netherlands	0.4950
Welfare	Male	Gender Male	0.4936
Rights	Ideology (right)	Nationality Netherlands	0.4924
Rights	Education (Primary)	Nationality Netherlands	0.4912
Welfare	\(Intercept)	Gender Male	0.4868
Rights	Age (>=60)	Age 25	0.4856
Rights	\(Intercept)	(Intercept)	0.4854
Rights	Male	Profession Nurse	0.4766
Rights	Age (>=60)	Age 55	0.4724
Rights	Migrant	Age 55	0.4714
Rights	Exposure	Language Full	0.4654
Rights	Age (>=60)	Language Full	0.4618
Welfare	Ideology (right)	Age 25	0.4612
Welfare	Ideology (right)	Nationality Netherlands	0.4590
Rights	Treatment shown	Nationality Netherlands	0.4556
Welfare	Ideology (right)	(Intercept)	0.4538
Rights	Income (Low)	Language Full	0.4532
Rights	Income (Low)	Gender Male	0.4524
Welfare	Age (>=60)	Language Full	0.4438
Welfare	\(Intercept)	Age 25	0.4402
Welfare	Treatment shown	Gender Male	0.4382
Welfare	Migrant	Language Full	0.4342
Welfare	Exposure	Language Full	0.4320
Welfare	Education (Primary)	Language Full	0.4308
Rights	\(Intercept)	Language Full	0.4292
Welfare	Migrant	Gender Male	0.4186
Rights	\(Intercept)	Age 25	0.4062
Rights	\(Intercept)	Age 55	0.4012
Rights	Education (Primary)	(Intercept)	0.4006
Rights	Migrant	Nationality Netherlands	0.3944
Rights	Treatment shown	Age 55	0.3854
Rights	Education (Primary)	Profession Nurse	0.3830
Welfare	Male	Age 55	0.3750
Welfare	Income (Low)	Gender Male	0.3692
Welfare	Treatment shown	Age 25	0.3606
Welfare	Exposure	Gender Male	0.3496
Rights	Treatment shown	(Intercept)	0.3474
Rights	Migrant	Profession Nurse	0.3472
Welfare	Migrant	Nationality Netherlands	0.3412
Welfare	Migrant	Profession Nurse	0.3358
Rights	Ideology (right)	Age 55	0.3314
Rights	Age (>=60)	(Intercept)	0.3214

Rights	Income (Low)	Nationality Netherlands	0.3180
Welfare	Education (Primary)	Age 55	0.3064
Rights	Migrant	Language Full	0.2998
Welfare	Migrant	Age 25	0.2934
Welfare	Age (>=60)	(Intercept)	0.2744
Welfare	Exposure	Age 55	0.2672
Welfare	Treatment shown	(Intercept)	0.2654
Rights	Male	(Intercept)	0.2548
Welfare	Male	Nationality Netherlands	0.2428
Welfare	Education (Primary)	Profession Nurse	0.2388
Welfare	Age (>=60)	Nationality Netherlands	0.2216
Rights	Treatment shown	Age 25	0.2128
Rights	Education (Primary)	Gender Male	0.2120
Rights	\(Intercept)	Profession Nurse	0.2096
Rights	Ideology (right)	Age 25	0.1968
Welfare	\(Intercept)	Age 55	0.1850
Welfare	Ideology (right)	Gender Male	0.1522
Rights	Exposure	Profession Nurse	0.1132
Welfare	Exposure	Profession Nurse	0.0910
Welfare	Exposure	(Intercept)	0.0376
Welfare	\(Intercept)	Language Full	0.0244
Rights	Exposure	(Intercept)	0.0124

```
dd.sample %>%
  filter(Outcome == "Welfare") %>%
  left_join(fig.labels) %>%
  mutate(Highlight = abs(`Prob Crisis > Main` - 0.5)) %>%
  ggplot(aes(x = `Differential discrimination on crisis`)) +
  geom_histogram(binwidth = 0.01, aes(color = Highlight)) +
  facet_grid(Covariate ~ Feature) +
  geom_text(data = filter(fig.labels, Outcome == "Welfare"),
            aes(x = -Inf, y = Inf, label = P),
            size = rel(0.8),
            hjust = -0.5, vjust = +1.5) +
  geom_vline(xintercept = 0, lty = 3) +
  xlim(c(-1.5, 1.5)) +
  ggtitle("Differential discrimination on crisis. Welfare") +
  scale_color_continuous_sequential(palette = "Grays") +
  theme(strip.text.y = element_text(angle = 0)) +
  guides(color = FALSE)

dd.sample %>%
  filter(Outcome == "Rights") %>%
  left_join(fig.labels) %>%
  mutate(Highlight = abs(`Prob Crisis > Main` - 0.5)) %>%
  ggplot(aes(x = `Differential discrimination on crisis`)) +
  geom_histogram(binwidth = 0.01, aes(color = Highlight)) +
  facet_grid(Covariate ~ Feature) +
  geom_text(data = filter(fig.labels, Outcome == "Rights"),
            aes(x = -Inf, y = Inf, label = P),
            size = rel(0.8),
            hjust = -0.5, vjust = +1.5) +
  geom_vline(xintercept = 0, lty = 3) +
  xlim(c(-1.5, 1.5)) +
  ggtitle("Differential discrimination on crisis. Rights") +
  scale_color_continuous_sequential(palette = "Grays") +
  theme(strip.text.y = element_text(angle = 0)) +
  guides(color = FALSE)

dd.sample %>%
  filter(Outcome == "Welfare") %>%
  left_join(fig.labels.Xpercent) %>%
  mutate(Highlight = ifelse(HighlightP == "Highlight", 0.9, 0.1)) %>%
```

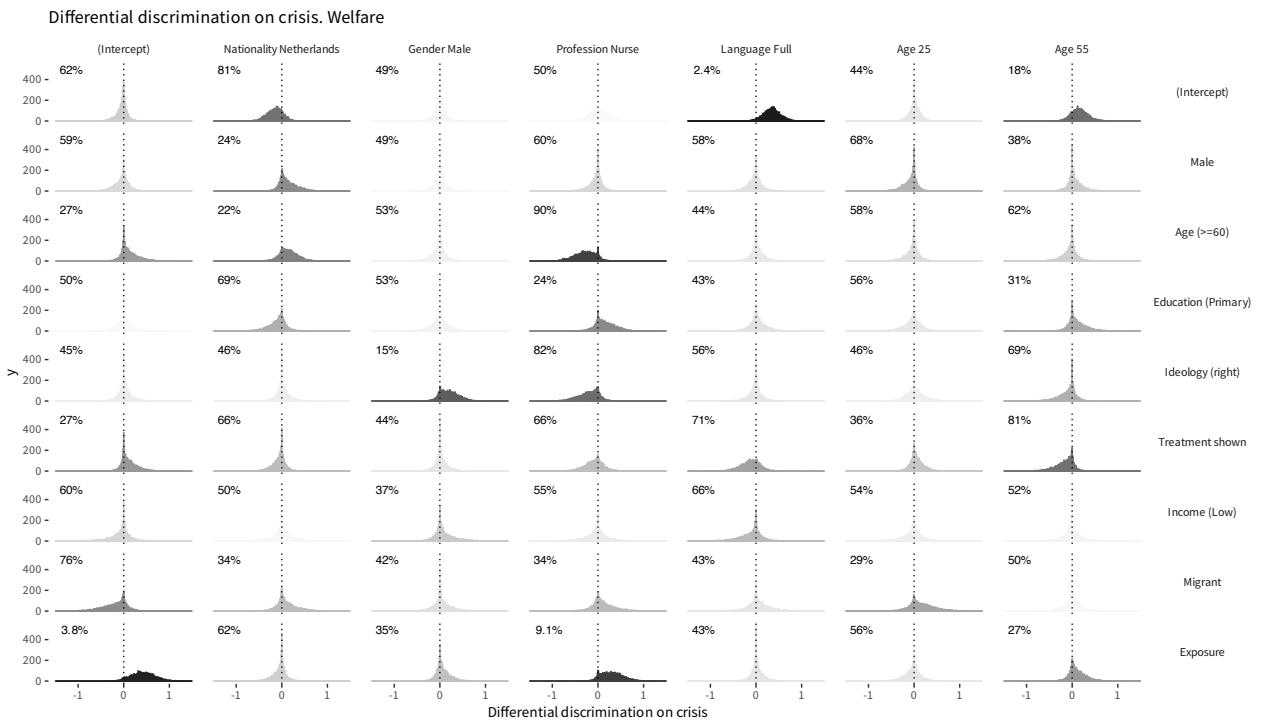


Figure 3.35: Differential discrimination on crisis time over the regular main sample. Only welfare is shown. Values indicate the probability of having found a differential discrimination stronger in crisis.

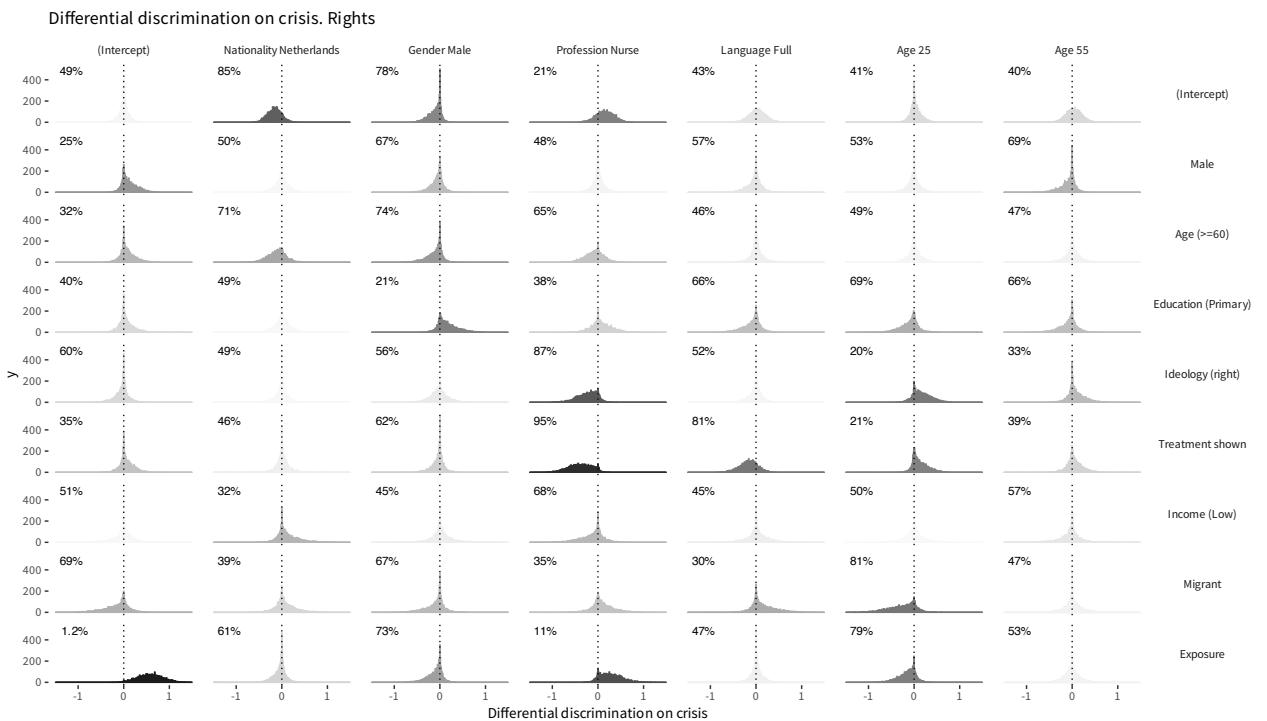


Figure 3.36: Differential discrimination on crisis time over the regular main sample. Only rights is shown. Values indicate the probability of having found a differential discrimination stronger in crisis.

```
ggplot(aes(x = `Differential discrimination on crisis`)) +
  geom_histogram(binwidth = 0.01, aes(color = Highlight)) +
  facet_grid(Covariate ~ Feature) +
  geom_text(data = filter(fig.labels, Outcome = "Welfare"),
            aes(x = -Inf, y = Inf, label = P),
            size = rel(0.8),
            hjust = -0.5, vjust = +1.5) +
  geom_vline(xintercept = 0, lty = 3) +
  xlim(c(-1.5, 1.5)) +
  ggtitle("Differential discrimination on crisis > 5%. Welfare") +
  scale_color_continuous_sequential(palette = "Grays") +
  theme(strip.text.y = element_text(angle = 0)) +
  guides(color = FALSE)
```

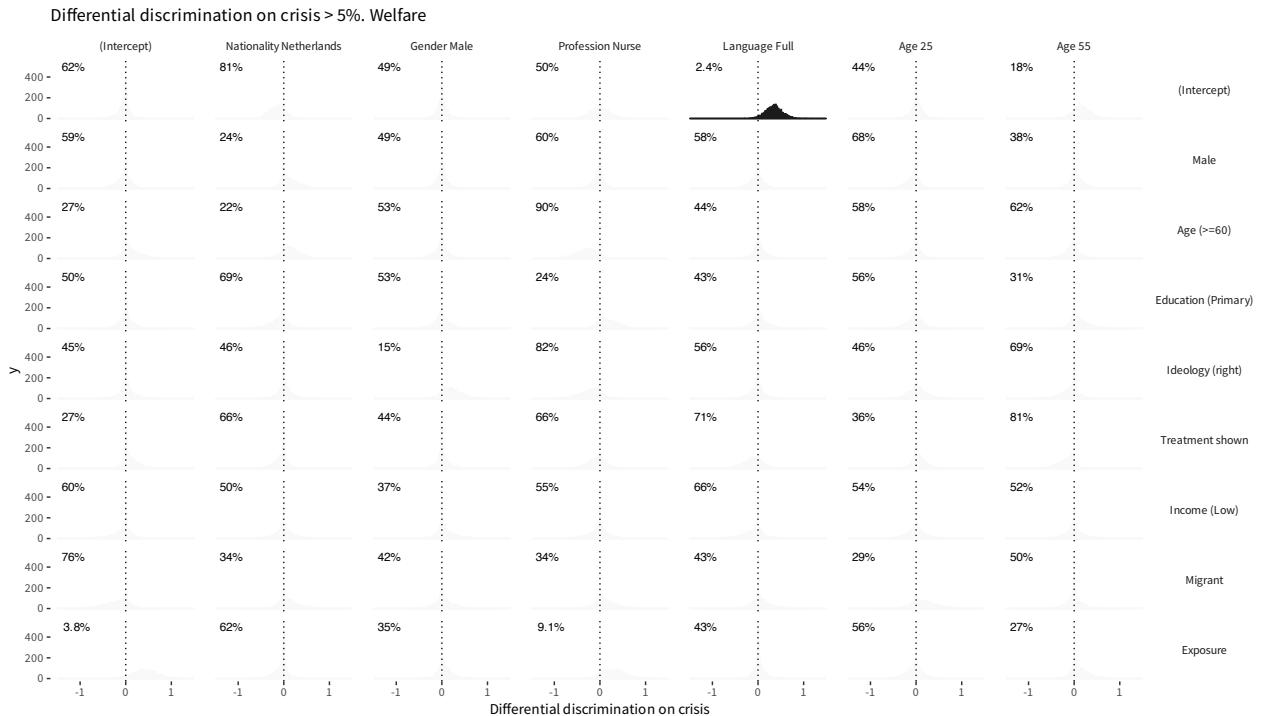


Figure 3.37: Differential discrimination on crisis time over the regular main sample. Only welfare is shown. Values indicate the probability of having found a differential discrimination stronger in crisis.

```
dd.sample %>
  filter(Outcome = "Rights") %>%
  left_join(fig.labels.Xpercent) %>%
  mutate(Highlight = ifelse(HighlightP = "Highlight", 0.9, 0.1)) %>%
  ggplot(aes(x = `Differential discrimination on crisis`)) +
  geom_histogram(binwidth = 0.01, aes(color = Highlight)) +
  facet_grid(Covariate ~ Feature) +
  geom_text(data = filter(fig.labels, Outcome = "Rights"),
            aes(x = -Inf, y = Inf, label = P),
            size = rel(0.8),
            hjust = -0.5, vjust = +1.5) +
  geom_vline(xintercept = 0, lty = 3) +
  xlim(c(-1.5, 1.5)) +
  ggtitle("Differential discrimination on crisis > 5%. Rights") +
  scale_color_continuous_sequential(palette = "Grays") +
  theme(strip.text.y = element_text(angle = 0)) +
  guides(color = FALSE)
```

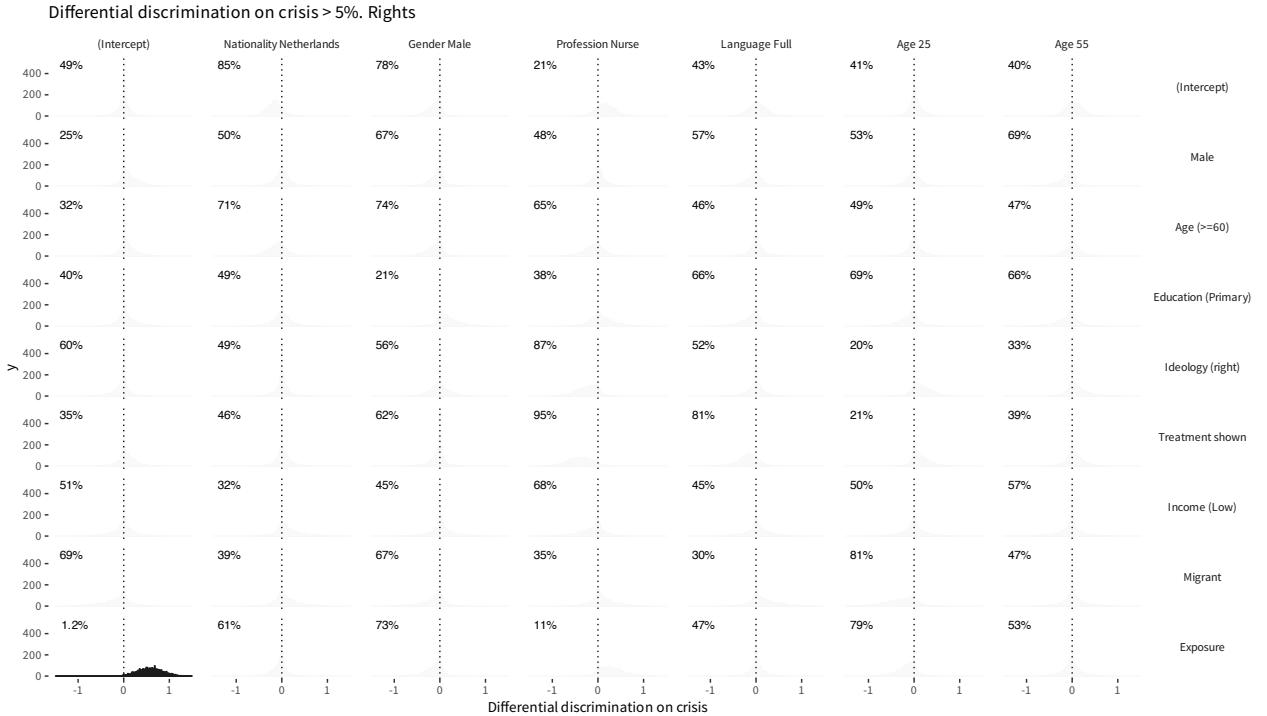


Figure 3.38: Differential discrimination on crisis time over the regular main sample. Only rights is shown. Values indicate the probability of having found a differential discrimination stronger in crisis.

3.5 Model fit

```

load(file = paste("samples-p-", M.lab, ".RData", sep = ""))
threshold <- d %>%
  group_by(Outcome, Sample, Treatment) %>%
  summarize(Threshold = length(which(Decision == 1)) / n())
L.p <- plab("p", list(Observation = 1:n0)) %>%
  mutate(Observation = as.integer(as.numeric(as.character(Observation))))
S.full <- ggs(s.p, family = "p\\[", par_labels = L.p, sort = FALSE) %>%
  select(Iteration, Chain, Observation, value) %>%
  left_join(select(d, Observation, Sample, Treatment, Outcome, Decision)) %>%
  left_join(threshold) %>%
  mutate(Correct = if_else( (value < Threshold & Decision == 0) |
                           (value > Threshold & Decision == 1),
                           TRUE, FALSE))
S <- S.full %>%
  group_by(Outcome, Sample, Treatment, Iteration, Chain) %>%
  summarize(PCP = length(which(Correct)) / n())
S.full <- S.full %>%
  select(Observation, Decision, value)

ggplot(S, aes(x = PCP, color = Sample)) +
  geom_density() +
  facet_grid(Treatment ~ Outcome) +
  expand_limits(x = c(0, 1)) +
  geom_vline(xintercept = 0, lty = 3) +
  scale_color_discrete_qualitative(palette = "Dynamic")

t.pcp <- S %>%
  group_by(Sample, Treatment, Outcome) %>%
  summarize(`Average PCP` = paste0(round(mean(PCP) * 100, digits = 1), "%"))
tc <- "Posterior median percent correctly predicted, by outcome, treatment and sample."
tc.oa <- "Model fit using posterior average of percent correctly predicted, by outcome, treatment and sample"
if (knitr::is_latex_output()) {

```

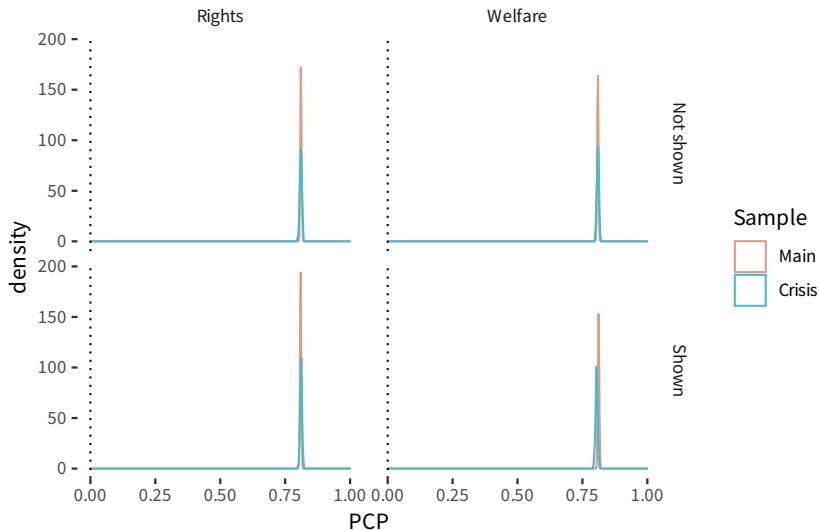


Figure 3.39: Model fit: Percent correctly predicted.

```

kable(t.pcp, format = "latex", caption = tc, booktabs = TRUE) %>%
  kable_styling(font_size = 10)
print(xtable(t.pcp, caption = tc.oa, label = "tab:main-pcp"),
      file = "table-main-pcp.tex", include.rownames = FALSE)
} else {
  kable(t.pcp, format = "html", caption = tc, booktabs = TRUE) %>%
    kable_styling(font_size = 10, position = "center", bootstrap_options = "striped", full_width = F)
}

```

3.6 Hypothesis 1: Dutch/Full language are treated more favourably in crisis.

These results aggregate individual behaviour.

```

tb <- S.theta %>%
  filter(Feature %in% c("Nationality Netherlands", "Language Full")) %>%
  filter(Covariate = "(Intercept)") %>%
  droplevels() %>%
  select(Iteration, Chain, Outcome, Feature, Sample, value) %>%
  pivot_wider(names_from = Sample, values_from = value) %>%
  group_by(Outcome, Feature) %>%
  summarize(`Prob H1` = paste0(round(length(which(Crisis > Main)) / n() * 100, digits = 1), "%")) %>%
  arrange(desc(`Prob H1`))

tc <- "Evidence for Hypothesis 1."
if (knitr::is_latex_output()) {
  kable(tb, format = "latex", caption = tc, longtable = TRUE, booktabs = TRUE) %>%
    kable_styling(font_size = 10)
  print(xtable(tb, caption = tc, label = "tab:main-h1"),
        file = "table-main-h1.tex", include.rownames = FALSE)
} else {
  kable(tb, format = "html", caption = tc, booktabs = TRUE) %>%
    kable_styling(font_size = 10, position = "center", bootstrap_options = "striped", full_width = F)
}

```

- 3.7 *Hypothesis 2 (exposure): respondents will prioritise applicants with Dutch nationality and excellent language skills the more they are/were exposed to the outbreak of COVID-19.*

```
tb ← S.theta %>%
  filter(Feature %in% c("Nationality Netherlands", "Language Full")) %>%
  filter(Covariate = "Exposure") %>%
  droplevels() %>%
  select(Iteration, Chain, Outcome, Feature, Sample, value) %>%
  pivot_wider(names_from = Sample, values_from = value) %>%
  group_by(Outcome, Feature) %>%
  summarize(`Prob H2` = paste0(round(length(which(Crisis > Main)) / n() * 100, digits = 1), "%")) %>%
  arrange(desc(`Prob H2`))

tc ← "Evidence for Hypothesis 2."
if (knitr::is_latex_output()) {
  kable(tb, format = "latex", caption = tc, longtable = TRUE, booktabs = TRUE) %>%
    kable_styling(font_size = 10)
  print(xtable(tb, caption = tc, label = "tab:main-h2"),
        file = "table-main-h2.tex", include.rownames = FALSE)
} else {
  kable(tb, format = "html", caption = tc, booktabs = TRUE) %>%
    kable_styling(font_size = 10, position = "center", bootstrap_options = "striped", full_width = F)
}
```

- 3.8 *Hypothesis 3 (vulnerability): Individuals who were most affected by the crisis (or are most likely to feel threatened by COVID-19) – low income, older - will show more discriminatory behaviour.*

```
tb ← S.theta %>%
  filter(Feature %in% c("Nationality Netherlands",
                        "Language Full",
                        "Gender Male",
                        "Profession Nurse",
                        "Age 25",
                        "Age 55")) %>%
  filter(Covariate %in% c("#"Male",
                           "#"Migrant",
                           "Age (≥60)",
                           "#Education (Primary)",
                           "Income (Low)",
                           "#Ideology (right)")) %>%
  select(Iteration, Chain, Outcome, Covariate, Sample, value) %>%
  pivot_wider(names_from = Sample, values_from = value) %>%
  mutate(MoreDiscrimination = ifelse((Main > 0 & Crisis > Main) |
                                       (Main < 0 & Crisis < Main), TRUE, FALSE)) %>%
  group_by(Outcome, Feature, Covariate) %>%
  summarize(`Prob H3` = paste0(round(length(which(MoreDiscrimination)) / n() * 100, digits = 1), "%")) %>%
  arrange(desc(`Prob H3`))

tb_sub ← tb %>%
  filter(Feature %in% c("Nationality Netherlands", "Language Full"))

tc ← "Evidence for Hypothesis 3."
if (knitr::is_latex_output()) {
  kable(tb, format = "latex", caption = tc, booktabs = TRUE) %>%
    kable_styling(font_size = 10)
  print(xtable(tb_sub, caption = tc, longtable = TRUE, label = "tab:main-h3"),
        file = "table-main-h3.tex", include.rownames = FALSE)
} else {
  kable(tb, format = "html", caption = tc, booktabs = TRUE) %>%
    kable_styling(font_size = 10, position = "center", bootstrap_options = "striped", full_width = F)
```


Programming environment

```
sessionInfo()

## R version 4.0.5 (2021-03-31)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Gentoo/Linux
##
## Matrix products: default
## BLAS:    /usr/lib64blas/blis/libblas.so.3
## LAPACK:  /usr/lib64/libopenblas_haswellp-r0.3.14.so
##
## locale:
## [1] LC_CTYPE=ca_AD.UTF-8      LC_NUMERIC=C
## [3] LC_TIME=ca_AD.UTF-8      LC_COLLATE=ca_AD.UTF-8
## [5] LC_MONETARY=ca_AD.UTF-8   LC_MESSAGES=ca_AD.UTF-8
## [7] LC_PAPER=ca_AD.UTF-8     LC_NAME=C
## [9] LC_ADDRESS=C              LC_TELEPHONE=C
## [11] LC_MEASUREMENT=ca_AD.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] parallel  grid      stats     graphics  grDevices utils      datasets
## [8] methods   base
##
## other attached packages:
## [1] readxl_1.3.1      tictoc_1.0.1      xtable_1.8-4
## [4]forcats_0.5.1     cowplot_1.1.1     scales_1.1.1
## [7] colorspace_2.0-1   stringr_1.4.0     GGally_2.1.1
## [10] ggmcmc_1.5.1.1   runjags_2.2.0-2   rjags_4-10
## [13] coda_0.19-4       ggthemes_4.2.4    extrafont_0.17
## [16] gridExtra_2.3      ggplot2_3.3.4     tidyverse_1.1.3
## [19] dplyr_1.0.6       kableExtra_1.3.4   tikzDevice_0.12.3.1
## [22] rmarkdown_2.9       knitr_1.33       colorout_1.2-2
##
## loaded via a namespace (and not attached):
## [1] httr_1.4.2        tufte_0.10       viridisLite_0.4.0  splines_4.0.5
## [5] assertthat_0.2.1   cellranger_1.1.0  yaml_2.2.1       Rttf2pt1_1.3.8
## [9] pillar_1.6.1       lattice_0.20-44   glue_1.4.2       extrafontdb_1.0
## [13] digest_0.6.27     RColorBrewer_1.1-2 rvest_1.0.0     Matrix_1.3-4
## [17] htmltools_0.5.1.1 plyr_1.8.6       pkgconfig_2.0.3   magick_2.7.2
## [21] bookdown_0.22     purrr_0.3.4     webshot_0.5.2   svglite_2.0.0
## [25] tibble_3.1.2      mgcv_1.8-36     generics_0.1.0   farver_2.1.0
## [29] ellipsis_0.3.2    withr_2.4.2     magrittr_2.0.1   crayon_1.4.1
## [33] evaluate_0.14     fansi_0.5.0     nlme_3.1-152   xml2_1.3.2
## [37] textshaping_0.3.5 tools_4.0.5      lifecycle_1.0.0  munsell_0.5.0
## [41] compiler_4.0.5    systemfonts_1.0.2 rlang_0.4.11   rstudioapi_0.13
## [45] filehash_2.4-2    labeling_0.4.2   gtable_0.3.0   DBI_1.1.1
## [49] reshape_0.8.8     R6_2.5.0       zoo_1.8-9     utf8_1.2.1
## [53] ragg_1.1.3       stringi_1.6.2   Rcpp_1.0.6     vctrs_0.3.8
## [57] tidyselect_1.1.1  xfun_0.24
```