

# *Drug legalization in Latin America*

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## *Introduction*

This document presents the analysis of the PELA-USAL surveys dealing with drug legalization in Latin America.

## *Data preparation*

```
## [1] "No model selected"
```

## *Data description*

Country / Year cases, and the proportion they represent to the total amount of data.

```
desc.cases <- d %>%
  group_by(Country, Year) %>%
  summarize(N = n()) %>%
  ungroup() %>%
  mutate(Prop = N / sum(N))

kable(desc.cases)
```

Country	Year	N	Prop
Argentina	2013	67	0.0337
Bolivia	2015	93	0.0468
Brazil	2014	123	0.0618
Brazil	2018	109	0.0548
Chile	2014	68	0.0342
Colombia	2014	84	0.0422
Colombia	2018	69	0.0347
Costa Rica	2014	55	0.0277
Costa Rica	2018	44	0.0221
Dominican Republic	2017	61	0.0307
Ecuador	2013	94	0.0473
Ecuador	2017	88	0.0442
El Salvador	2012	62	0.0312
El Salvador	2015	57	0.0287
Guatemala	2016	78	0.0392
Honduras	2014	82	0.0412
Honduras	2018	92	0.0463
Mexico	2012	90	0.0452
Mexico	2015	100	0.0503
Mexico	2018	103	0.0518
Nicaragua	2017	59	0.0297
Panama	2014	47	0.0236
Paraguay	2013	55	0.0277
Peru	2018	73	0.0367
Uruguay	2015	69	0.0347
Venezuela	2016	67	0.0337

```
#length(levels(d$Country))
#d %>%
#  select(Country) %>%
#  unique() %>%
#  kable("latex", longtable = TRUE) %>%
##  kable_styling(font_size = 7, latex_options = c("repeat_header"))
kable(desc.cases, "latex", longtable = TRUE,
      caption = "Description of the number of surveys in each legislature (Country * Year)",
      label = "surveys") %>%
kableExtra::kable_styling(font_size = 7, latex_options = c("repeat_header")) %>%
cat(file = "description_surveys.tex")
```

### Missing data

Missing data distribution.

```
# Overall NA
length(which(is.na(d$Drugs))) / length(d$Drugs)

## [1] 0.0362

d %>%
  mutate(missing = ifelse(is.na(Drugs), TRUE, FALSE)) %>%
  group_by(Country, Year) %>%
  summarize(N = n(), N.missing = length(which(missing))) %>%
  ungroup() %>%
  mutate(Prop.missing = N.missing / N) %>%
  arrange(desc(Prop.missing)) %>%
  kable()
```

Country	Year	N	N.missing	Prop.missing
El Salvador	2015	57	8	0.1404
Colombia	2014	84	10	0.1190
Guatemala	2016	78	8	0.1026
Argentina	2013	67	5	0.0746
Peru	2018	73	5	0.0685
Mexico	2012	90	6	0.0667
El Salvador	2012	62	4	0.0645
Paraguay	2013	55	3	0.0545
Dominican Republic	2017	61	3	0.0492
Chile	2014	68	3	0.0441
Colombia	2018	69	3	0.0435
Mexico	2015	100	4	0.0400
Brazil	2014	123	3	0.0244
Ecuador	2017	88	2	0.0227
Bolivia	2015	93	2	0.0215
Costa Rica	2014	55	1	0.0182
Venezuela	2016	67	1	0.0149
Brazil	2018	109	1	0.0092
Costa Rica	2018	44	0	0.0000
Ecuador	2013	94	0	0.0000
Honduras	2014	82	0	0.0000
Honduras	2018	92	0	0.0000
Mexico	2018	103	0	0.0000
Nicaragua	2017	59	0	0.0000
Panama	2014	47	0	0.0000
Uruguay	2015	69	0	0.0000

### Drug legalization

Distribution of drug legalization approval.

```
d %>%
  ggplot(aes(x = Drugs)) + geom_bar() +
  facet_grid(Country ~ Year)
```

Distribution of drug legalization approval by parties.

```
d %>%
  ggplot(aes(x = Drugs, fill = Party, color = Party)) + geom_bar() +
  guides(fill = FALSE, color = FALSE) +
  facet_grid(Country ~ Year)
```

Distribution of drug legalization approval against covariates.

```
d %>%
  gather(Covariate, value, -Country, -Year, -Party, -Drugs) %>%
  ggplot(aes(x = jitter(value), y = jitter(Drugs))) + geom_point() +
  facet_grid(Country + Year ~ Covariate, scales = "free")
```

```
d %>%
  gather(Covariate, value, -Country, -Year, -Party, -Drugs) %>%
  ggplot(aes(x = jitter(value), y = jitter(Drugs))) + geom_point() +
  facet_grid(Country + Year ~ Covariate, scales = "free") +
  geom_smooth()
```

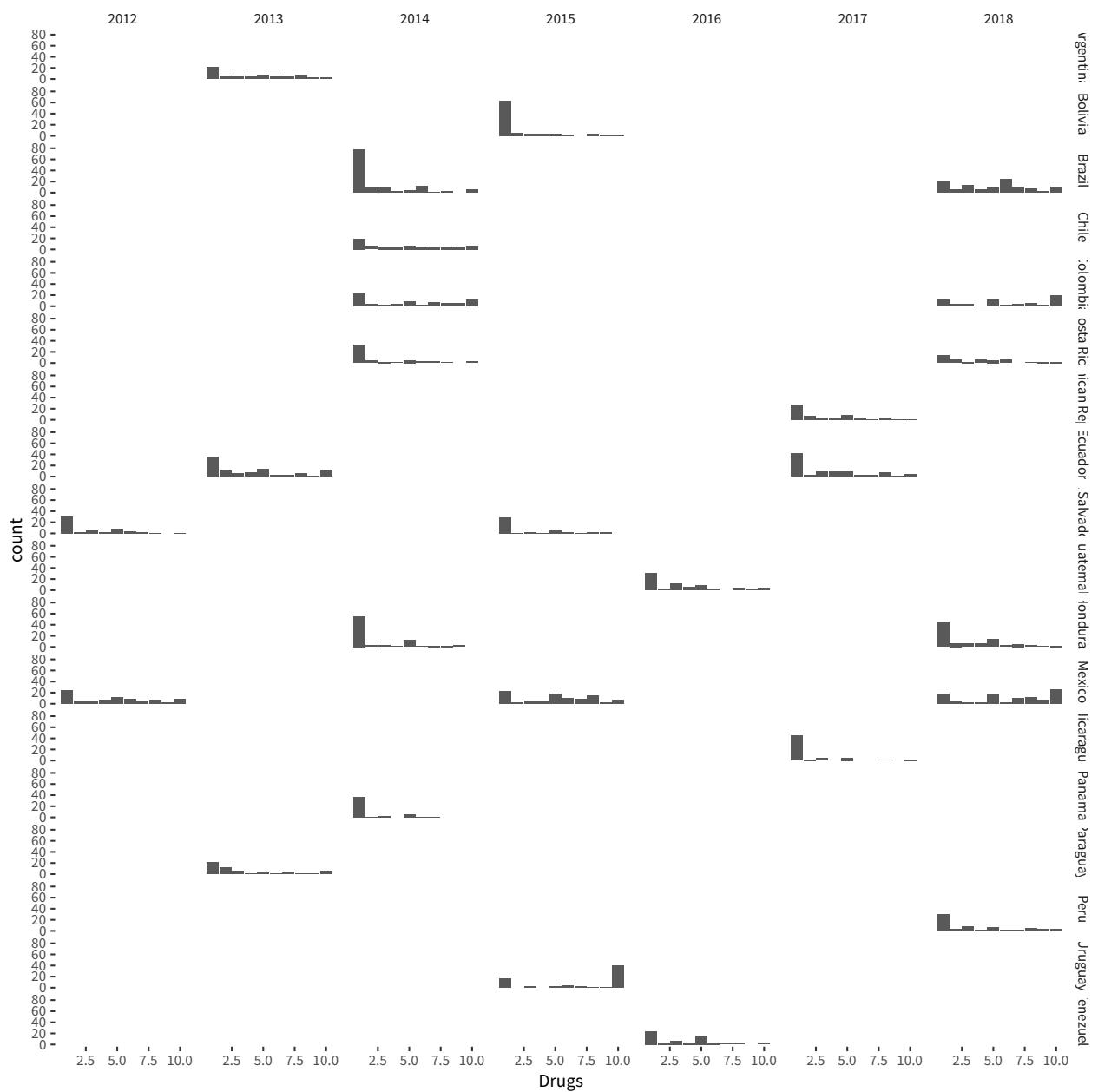


Figure 1: Distribution of drug legalization approval by sample.

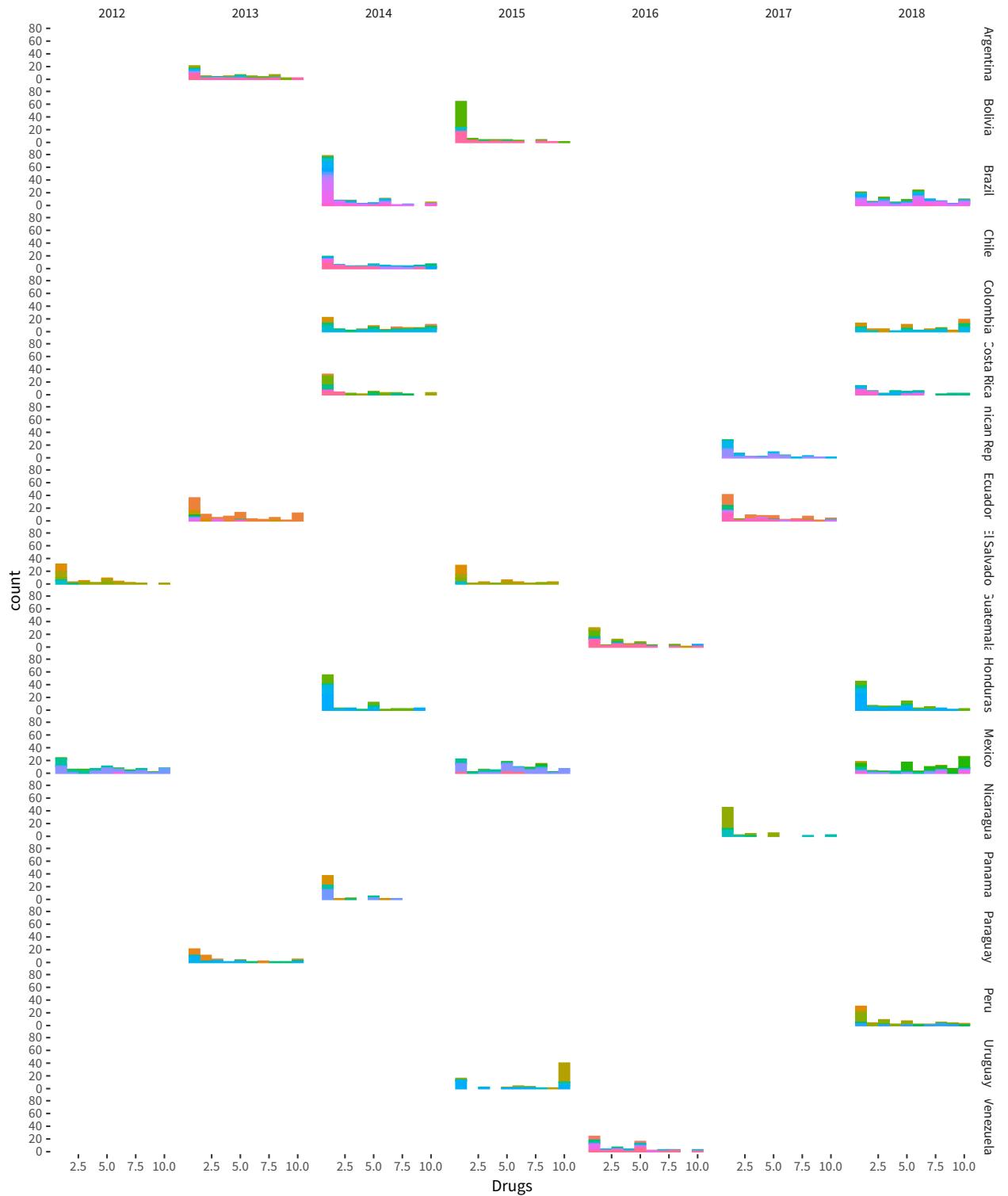


Figure 2: Distribution of drug legalization approval by party (and therefore country).

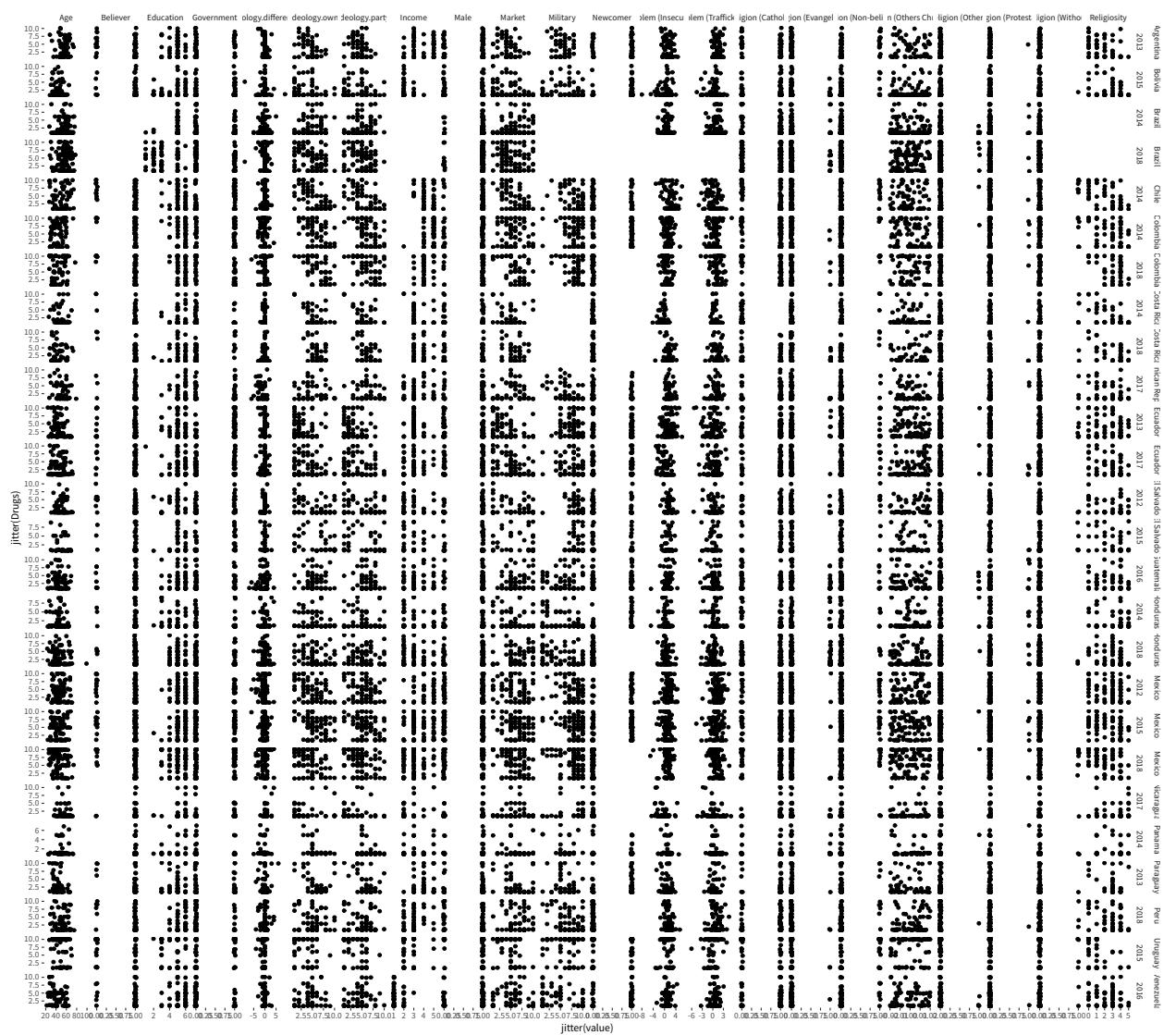


Figure 3: Distribution of drug legalization approval against covariates, by sample.

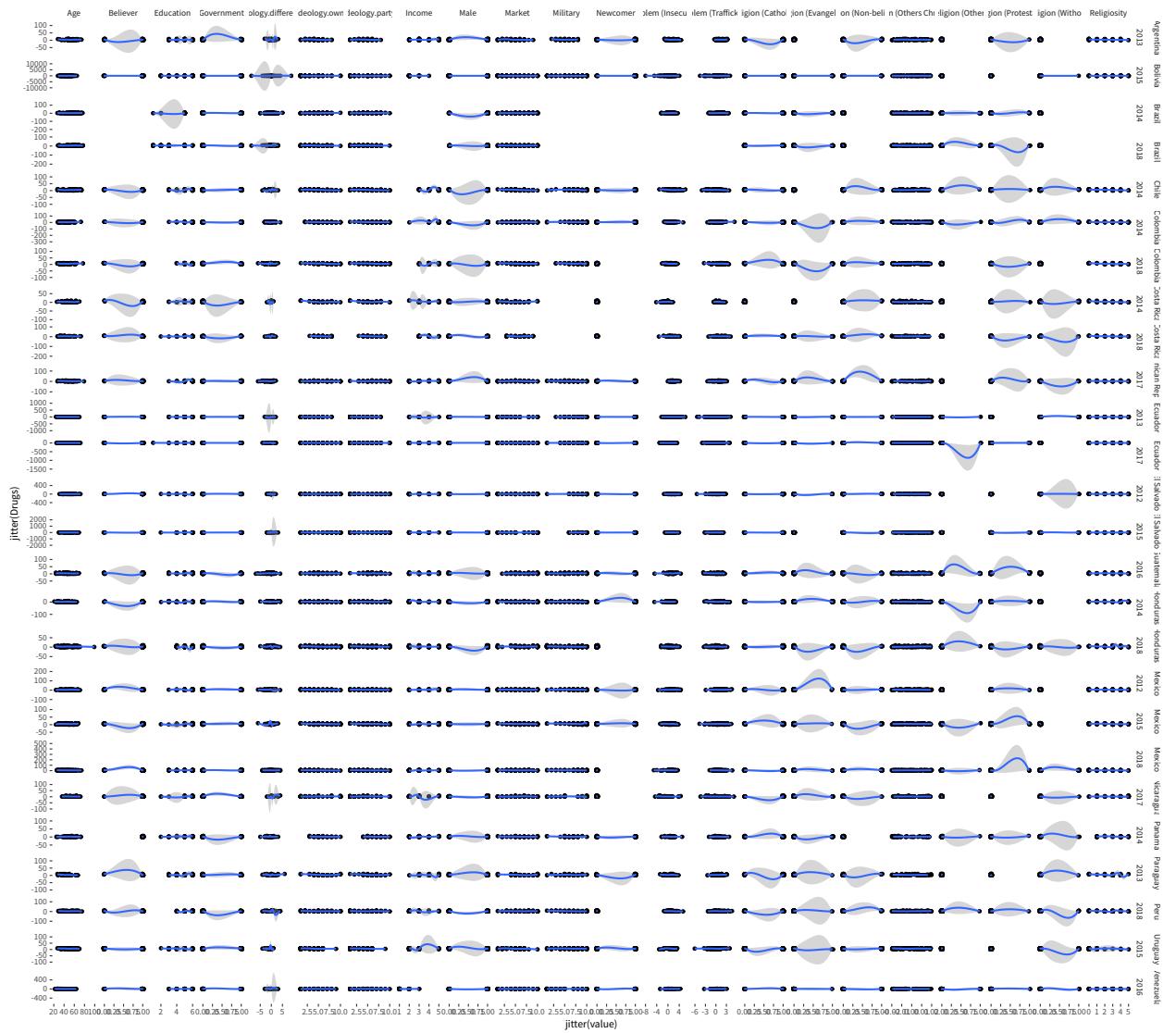


Figure 4: Distribution of drug legalization approval against covariates, by sample. Includes a loess smoother.

```
d %>%
gather(Covariate, value, -Country, -Year, -Party, -Drugs) %>%
ggplot(aes(x = jitter(value), y = jitter(Drugs))) + geom_point() +
facet_grid(Country ~ Covariate, scales = "free") +
geom_smooth(method = "lm")
```

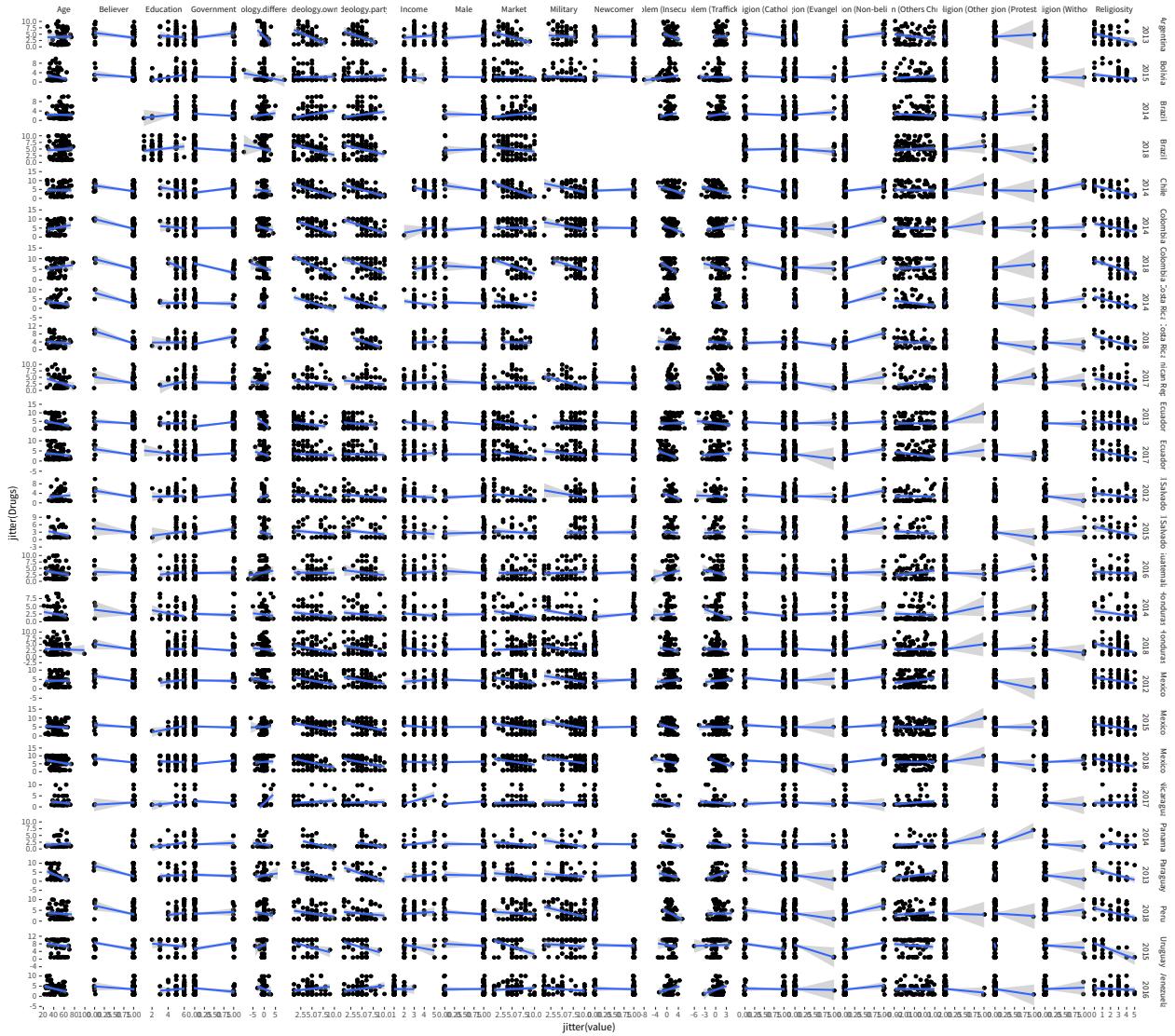


Figure 5: Distribution of drug legalization approval against covariates, by sample. Includes a smoothed linear model.

### Religion denominations

```
# This table excludes the NAs that are assigned anywhere
d %>%
select(Country, starts_with("Religion")) %>%
gather(Religion, value, -Country) %>%
filter(value == 1) %>%
group_by(Religion) %>%
summarize(N = n()) %>%
mutate(Prop = N / dim(d)[1])

## # A tibble: 6 x 3
##   Religion           N   Prop
##   <chr>         <int>  <dbl>
```

```
## 1 Religion (Catholic)      1315 0.661
## 2 Religion (Evangelical)   150 0.0754
## 3 Religion (Non-believer) 220 0.111
## 4 Religion (Others)       34 0.0171
## 5 Religion (Protestant)   58 0.0292
## 6 Religion (Without)      63 0.0317
```

### *Variable description*

```
vd <- d %>%
  select(Drugs, Age, Gender = Male, Education, Income,
         Ideology = Ideology.own, Military,
         `Problem (Trafficking)`, `Problem (Insecurity)`,
         Religiosity, Religion = `Religion (Catholic)`,
         Government) %>%
  mutate(Religion = as.factor(ifelse(Religion == 1, "Catholic", "Non-C")))) %>%
  mutate(Gender = as.factor(ifelse(Gender == 1 | is.na(Gender), "M", "F")))) %>%
  mutate(Government = as.factor(ifelse(Government == 1, "Gov", "Opp")))) %>%
  mutate(Drugs = ifelse(Drugs > 1, "OL", "FP")) %>%
  mutate(Drugs = ifelse(is.na(Drugs), "(M)", Drugs)) %>%
  mutate(Drugs = factor(Drugs, levels = c("FP", "OL", "(M"))))

p <- ggpairs(vd,
  legend = 1,
  upper = list(continuous = wrap("cor", size = 3, hjust=0.8)),
  diag = list(continuous = "barDiag", color = NULL, alpha = 0.3),
  lower = list(continuous = wrap("points", aes = 0.1, size = 0.1, position = position_jitter())),
  mapping = aes(color = Drugs)) +
  theme_minimal(base_size = 8) +
  theme(legend.position = "bottom",
        panel.grid.minor = element_blank(),
        panel.grid.major = element_blank())

# For a B&W version

for (i in 1:p$nrow) {
  for(j in 1:p$ncol){
    p[i,j] <- p[i,j] +
    #   scale_fill_manual(values=c("#00AFBB", "#E7B800", "#FC4E07")) +
    #   scale_color_manual(values=c("#00AFBB", "#E7B800", "#FC4E07"))
    scale_fill_grey() +
    scale_color_grey()
  }
}

library(compareGroups)
library(forcats)
vd.1 <- vd %>%
  mutate(Drugs = fct_recode(Drugs,
                            `Full prohibition` = "FP",
                            `Open to legalization` = "OL",
                            `(Missing response)` = "(M)"))

cg <- compareGroups(Drugs ~ ., data = vd.1)
tb <- createTable(cg, show.p.overall = FALSE)

tc <- "Description of individual level variables."
if (knitr::is_latex_output()) {
  export2html(tb, file = "table-descriptives-comparison.html")
  input(table-descriptives-comparison.html)
} else {
  export2latex(tb, file = "table-descriptives-comparison.tex")
  input(table-descriptives-comparison.tex)
}
```

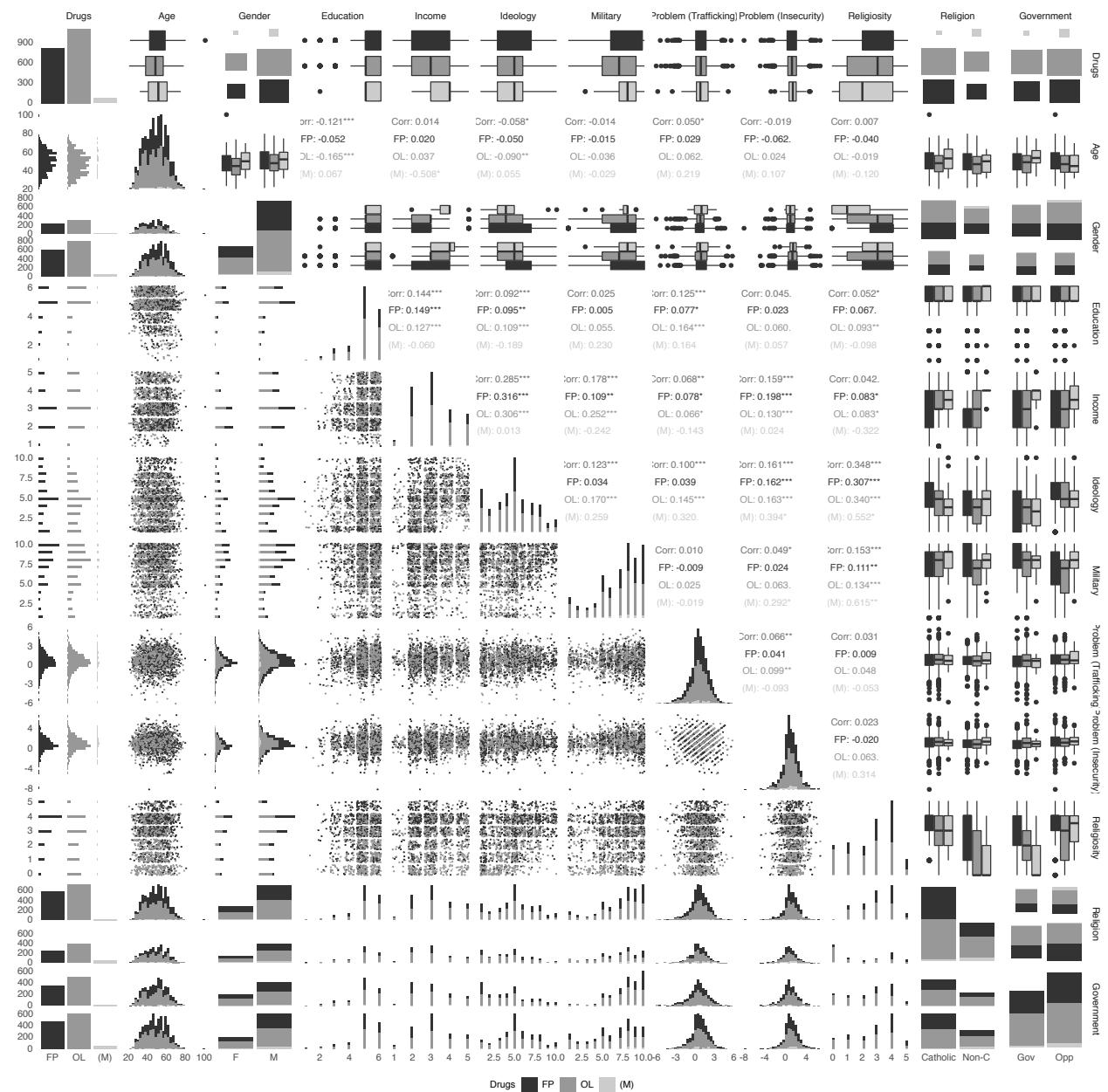


Figure 6: Description of the variables involved in the analysis. The main variable Drugs has values FP=Full prohibition, OL=Open to legalization and (M)=missing value.

```

load("pela-drugs-country-variables.RData")
# Copied and Pasted from the data transformations in the data arrangement
# section following
vdc <- left_join(vdem, hdi) %>%
  left_join(wgi) %>%
  left_join(unsafety) %>%
  left_join(threat.traffickers) %>%
  select(
    `Democracy` = Electoral,
    `Wealth` = `GDP per capita (2011 PPP $)` ,
    `Violence` = `Homicide rate (per 100,000 people)` ,
    `Health` = `Mortality rate, infant (per 1,000 live births)` ,
    `Education` = `Mean years of schooling (years)` ,
    `Effectiveness` = `Government effectiveness` ,
    `Unsafety` = `Unsafety` ,
    `Threat by traffickers` = Threat.Traffickers) %>%
# Transformations
  mutate(Wealth = log(Wealth))

p <- ggpairs(vdc) +
  # legend = 1,
  # upper = list(continuous = wrap("cor", size = 3, hjust=0.8)),
  # diag = list(continuous = "barDiag", color = NULL, alpha = 0.3),
  # lower = list(continuous = wrap("points", aes = 0.1, size = 0.1, position = position_jitter())))) +
  # theme_minimal(base_size = 10) +
  theme(
    panel.grid.minor = element_blank(),
    panel.grid.major = element_blank())

```

p

### Data preparation for analysis

#### Data cleaning and preparation

```

std <- function(x) (x - mean(x, na.rm = TRUE)) / (2 * sd(x, na.rm = TRUE))
or <- function(x, significant = 2) {
  or <- as.character(signif((x - 1) * 100, significant))
  #or[or < 0] <- paste0("▼ ", str_replace(or[or < 0], "-", ""))
  #or[or < 0] <- paste0("\U25Bd ", str_replace(or[or < 0], "-", ""))
  #or[or > 0] <- paste0("▲ ", or[or > 0], "%")
  or[or > 0] <- paste0("\U25B3 ", or[or > 0], "%")
  or[or == 0] <- "="
  return(or)
}
d <- mutate(d, id = 1:dim(d)[1])
y <- as.integer(ifelse(d$Drugs == 1, 0, 1))
y.cont <- d$Drugs
y.cont <- log(y.cont)
y.cont <- y.cont - mean(y.cont, na.rm = TRUE)
n0 <- length(y)

id.country <- as.integer(as.factor(d$Country))
countries.labels <- levels(as.factor(d$Country))
nC <- length(countries.labels)

id.time <- as.integer(as.factor(d$Year))
time.labels <- levels(as.factor(d$Year))
nT <- length(time.labels)

if (length(which(d$`Religion (Others Christian)` == 1)) != 0) {
  stop("There are now cases of 'Others Christian' that you may want to assign somewhere\n. Right now they are excluded a few lines")
}

X <- d %>%
  # left_join(decriminalized) %>%
  select(-Country, -Year, -Party, -Drugs) %>%
  select(-id) %>%

```

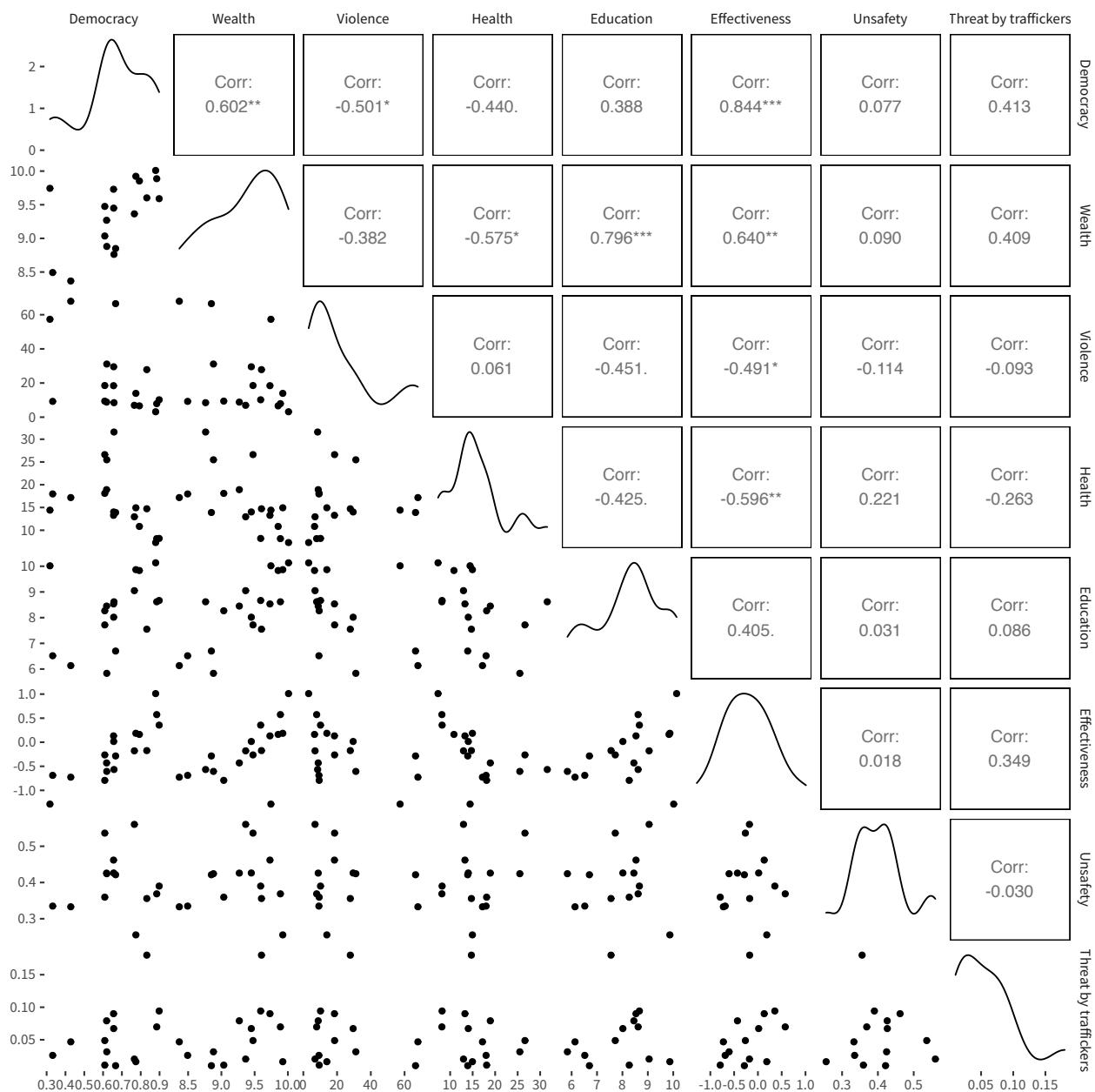


Figure 7: Description of the variables at the country level involved in the analysis.

```

select(-Newcomer) %>%
select(-Ideology.difference, -Ideology.party) %>%
select(-Market) %>%
select(-Believer) %>%
select(-`Religion (Catholic)` %>% # Reference category
      select(-`Religion (Others Christian)` %>% # there are no cases
# Not picking a religion means that NAs are reference category
      rename(`Ideology (right)` = Ideology.own)

#nv <- c("Age", "Male", "Income", "Education", "Government")
nv <- c("Age", "Male", "Income", "Government")
nv <- c(nv, dimnames(x)[[2]][str_detect(dimnames(x)[[2]], "Religion ")])

# Add binary country identifier for decriminalization
# as an individual level variable
#nv <- c(nv, "Decriminalized")

XNV <- X %>%          # Non varying covariates
  select(nv) %>%
  as.matrix()
covariates.labels.nv <- dimnames(XNV)[[2]]
X <- X %>%
  select(-nv) %>%
  as.matrix()
covariates.labels <- dimnames(X)[[2]]

XC <- left_join(vdem, hdi) %>%
  left_join(wgi) %>%
  left_join(unsafety) %>%
  left_join(threat.traffickers) %>%
  left_join(state.capacity) %>%
  select(Country,
#       `Democracy (Electoral)` = Electoral,
#       Democracy = Electoral,
#       `GDP per capita` = `GDP per capita (2011 PPP $)`,
#       Wealth = `GDP per capita (2011 PPP $)`,
#       `Homicide rate` = `Homicide rate (per 100,000 people)`,
#       Violence = `Homicide rate (per 100,000 people)`,
#       `Life expectancy` = `Life expectancy at birth (years)`,
#       Health = `Life expectancy at birth (years)`,
#       Health = `Mortality rate, infant (per 1,000 live births)`,
#       Education = `Mean years of schooling (years)`,
#       Effectiveness = `Government effectiveness`,
#       `Administrative capacity` = `Administrative capacity`,
#       Unsafety = `Unsafety`,
#       Threat by traffickers = Threat.Traffickers) %>%
# Transformations
  mutate(Wealth = log(Wealth)) %>%
  mutate(Health = -Health) %>%
# Standardize
  gather(Variable, value, -Country) %>%
  group_by(Variable) %>%
  mutate(value = std(value)) %>%
  spread(Variable, value) %>%
  left_join(decriminalized) %>%
  arrange(Country) %>%
  select(-Country)
#   mutate(`(Intercept)` = 1) %>%
#XC <- cbind(1, XC) # Add intercept
#dimnames(XC)[[2]][1] <- "(Intercept)"

XC.non.contextual <- XC %>%
  as.matrix()
covariates.countries.labels.non.contextual <- dimnames(XC.non.contextual)[[2]]
nCovCnc <- dim(XC.non.contextual)[2]

XC <- XC %>%
  # Remove variable that does not vary by context
  select(-Decriminalized) %>%
  as.matrix()

```

```

covariates.countries.labels <- dimnames(XC)[[2]]
nCovC <- dim(XC)[2]

# Standardize only non-binary variables (manually check!)
covariates.labels

## [1] "Education"           "Ideology (right)"      "Religiosity"
## [4] "Military"            "Problem (Insecurity)" "Problem (Trafficking)"

#cv.cont <- c("Ideology (right)", "Religiosity", "Military",
# "Problem (Violence)", "Problem (Trafficking)")
X.std <- X
#for (l in c(1, 2, 3, 4, 5)) X.std[,l] <- std(X.std[,l]) # w/o education
for (l in c(1, 2, 3, 4, 5, 6)) X.std[,l] <- std(X.std[,l]) # w/ education
covariates.labels.nv

## [1] "Age"                  "Male"
## [3] "Income"               "Government"
## [5] "Religion (Protestant)" "Religion (Evangelical)"
## [7] "Religion (Non-believer)" "Religion (Without)"
## [9] "Religion (Others)"

#cv.nv.cont <- c("Age", "Income", "Education")
XNV.std <- XNV
#for (l in c(1, 3, 4, 5)) XNV.std[,l] <- std(XNV.std[,l]) # w/o education
for (l in c(1, 3, 4)) XNV.std[,l] <- std(XNV.std[,l]) # w/ education

# Create interactions
#X.std <- cbind(X.std, X.std[,dimnames(X.std)[[2]] == "Ideology (right)"] *
#                 X.std[,dimnames(X.std)[[2]] == "Military"])
#dimnames(X.std)[[2]][length(dimnames(X.std)[[2]])] <- "Ideology * Military"
#X.std <- cbind(X.std, X.std[,dimnames(X.std)[[2]] == "Ideology (right)"] *
#                 X.std[,dimnames(X.std)[[2]] == "Age"])
#dimnames(X.std)[[2]][length(dimnames(X.std)[[2]])] <- "Ideology * Age"
#X.std <- cbind(X.std, X.std[,dimnames(X.std)[[2]] == "Ideology (right)"] *
#                 X.std[,dimnames(X.std)[[2]] == "Government"])
#dimnames(X.std)[[2]][length(dimnames(X.std)[[2]])] <- "Ideology * Government"

# Re-specify covariates numbers and labels
covariates.labels <- dimnames(X.std)[[2]]
nCov <- dim(X.std)[2]

covariates.labels.nv <- dimnames(XNV.std)[[2]]
nCovNV <- dim(XNV.std)[2]

b0 <- rep(0, nCov)
B0 <- diag(nCov)
diag(B0) <- 2.5^-2
#diag(B0) <- 1^-2

b0c <- rep(0, nCovC)
B0c <- diag(nCovC)
diag(B0c) <- 2.5^-2
#diag(B0c) <- 1^-2

b0c.nc <- rep(0, nCovCnc)
B0c.nc <- diag(nCovCnc)
diag(B0c.nc) <- 2.5^-2
#diag(B0c.nc) <- 1^-2

# List covariates with missing values
(apply(X, 2, function(x) length(which(is.na(x)))))

##          Education Ideology (right)      Religiosity
##             134                64              346
##          Military Problem (Insecurity) Problem (Trafficking)
##             359                118              122

(apply(XNV, 2, function(x) length(which(is.na(x)))))

```

```

##          Age           Male        Income
##      97             36         364
## Government Religion (Protestant) Religion (Evangelical)
##          0              0             0
## Religion (Non-believer) Religion (Without) Religion (Others)
##          0              0             0

(apply(XC, 2, function(x) length(which(is.na(x)))))

##          Democracy       Education Effectiveness
##          0                  0                 0
## Health Threat by traffickers          Unsafety
##          0                  4                 4
## Violence           Wealth
##          0                  0

```

```

D <- list(
  y = y, y.cont = y.cont,
  id.country = id.country, nC = nC,
  X.std = unname(X.std), nCov = nCov,
  XNV.std = unname(XNV.std), nCovNV = nCovNV,
  XC = unname(XC), nCovC = nCovC,
  XC.non.contextual = unname(XC.non.contextual), nCovCnc = nCovCnc,
# b0 = b0, B0 = B0,
  id.time = id.time, nT = nT,
  b0 = b0, B0 = B0,
  b0c = b0c, B0c = B0c,
  b0c.nc = b0c.nc, B0c.nc = B0c.nc,
  n0 = n0)

```

### *Model description*

The model is build up in different components:

- Binary logistic regression with two hierarchical components.
- The outcome to explain ( $y$ ) is the individual response to the degree of support to drug legalization. Originally measured in a scale between 1 (no legalization at all) and 10 (full legalization), almost half the cases correspond to the response “1” for full prohibition. Therefore we opt for dichotomizing the original variable into “Full prohibition” (corresponding to the original variable 1) and “Open to legalization” (corresponding to values from 2 to 10 in the original scale).
- An alternative model specification using a zero-inflated normal distribution is available in the online appendix.
- The main hierarchical component includes varying intercepts and varying slopes.
- Varying intercepts allow us to capture country specific legislator predisposition to be favourable to some sort of drug legalization.
- Varying slopes allow us to capture how contextual effects (associated to country characteristics) can mediate the effect of individual-level variables.
- In addition to varying intercepts and varying slopes we add a non-nested hierarchical component that accounts for the temporal evolution of the support for drug legalization.

Based on this, the model description is as follows:

$y_i \sim$	$\mathcal{B}(\pi_i)$	Main data component
$\text{logit}(\pi_i) = \alpha_y + \omega_c + \lambda F_i + \delta_c X_i$		Main logistic model
$\omega_c \sim$	$\mathcal{N}(\Omega + \gamma, \sigma_\omega)$	Prior for varying intercepts
$\alpha_y \sim$	$\mathcal{N}(\alpha_{y-1}, \sigma_\alpha)$	Kalman filter for temporal component
$\sigma_\alpha \sim$	$\mathcal{N}(0, 0.1)$	Prior for year-to-year change on overall legalization.
$\lambda \sim$	$\mathcal{T}(0, 2.5, 5)$	Prior for non-varying control variables
$\delta_c \sim$	$\mathcal{N}(\Delta + \theta Z_c, \sigma_\delta)$	Prior for varying slopes
$\gamma \sim$	$\mathcal{N}(0, 2.5)$	Prior for effects of country characteristics on varying intercepts
$\theta \sim$	$\mathcal{N}(0, 2.5)$	Prior for effects of country characteristics on varying slopes
$\Omega, \Delta \sim$	$\mathcal{T}(0, 2.5, 5)$	Priors for the grand means
$\sigma_\omega, \sigma_\delta \sim$	$\mathcal{G}(2, 1)$	Priors for variances (sd)

Where:

- $i$ : Individual.
- $c$ : Country.
- $y$ : Year.
- $X$ : Matrix of covariates for the explanatory variables at the individual level that are allowed to vary by country.
- $F$ : Matrix of covariates for the control variables at the individual level that are non-varying for all countries.
- $Z$ : Matrix of covariates for the explanatory variables at the country level.
- $\omega$ : Varying intercepts.
- $\Omega$ : Overall mean over countries of all legislator propensity to some sort of drug legalization, for the reference legislator.
- $\alpha$ : Temporal evolution of overall support to drug legalization.
- $\gamma$ : Parameters accounting for country-level variables explaining varying intercepts.
- $\delta$ : Parameters for the control variables.
- $\theta$ : Main parameters of interest accounting for country-level variables explaining individual-level attitudes.

Write the model.

```
m <- ''
m <- paste(m, '
model {
  # Data part
  for (o in 1:n0) {
    y[o] ~ dbern(p[o])
    logit(p[o]) <-
      omega[id.country[o]] +
      alpha[id.time[o]] +
      inprod(lambda, XNV.std[o,]) +
      inprod(delta[id.country[o],], X.std[o,])
  }
  #
  # Priors for country varying intercepts
  #
  for (c in 1:nC) {
    omega[c] ~ dnorm(mu.omega[c], sigma.omega^-2)
    mu.omega[c] <- Omega + inprod(gamma, XC.non.contextual[c,])
  }
}
```

```

#
# Priors for grand mean of the varying intercepts
#
Omega ~ dt(0, 2.5^-2, 3)

#
# Priors for the group-level predictors of the varying intercepts
#
gamma ~ dnorm(b0c.nc, B0c.nc)

#
# Priors for between-region standard deviation
#
sigma.omega ~ dgamma(2, 1)

#
# Priors for the group-level predictors of the varying intercepts
#
for (l in 1:nCovNV) {
  lambda[l] ~ dt(0, 2.5^-2, 3)
}

## Priors for temporal effects, Kalman filter
##
## for (t in 2:nT) {
##   alpha[t] ~ dnorm(alpha[t-1], sigma.alpha^-2)
## }
## sigma.alpha ~ dnorm(0, 0.1^-2)T(0,)
## alpha[1] <- 0
##
## Priors for temporal effects, varying intercepts
##
for (t in 1:nT) {
  alpha[t] ~ dnorm(0, 1^-2)
}

##
# Priors for varying slopes
#
for (cov in 1:nCov) {
  for (c in 1:nC) {
    delta[c,cov] ~ dnorm(mu.delta[c,cov], sigma.delta[cov]^2)
    mu.delta[c,cov] <- Delta[cov] + inprod(theta[,cov], XC[c,])
  }
  Delta[cov] ~ dt(0, 2.5^-2, 3)
  sigma.delta[cov] ~ dgamma(2, 1)
}

#
# Priors for group level predictors of varying slopes
#
for (cov in 1:nCov) {
  theta[1:nCovC,cov] ~ dnorm(b0c, B0c)
}

#
# Missing data (individual level variables)
#
for (o in 1:nO) {
  for (cov in 1:nCov) {
    #X.std[o,cov] ~ dnorm(0, 0.5^-2)
    X.std[o,cov] ~ dunif(-1, 1)
  }
  #for (covnv in c(1, 3, 4)) { # age, education, income
  #  for (covnv in c(1, 3)) { # age, income
  #    XNV.std[o,covnv] ~ dunif(-1, 1)
  #  }
  #  XNV.std[o,2] ~ dbern(0.5) # male
}
#
# Missing data (country level variables)
#
for (c in 1:nC) {

```

```

for (covC in 1:nCovC) {
  #XC[c,covC] ~ dnorm(0, 0.5^-2)
  XC[c,covC] ~ dunif(-1, 1)
  XC.non.contextual[c,covC] ~ dnorm(XC[c,covC], 100)
}
}, sep = "")

write(m, file = paste("models/model-", M, ".bug", sep = ""))
adapt <- 3e2
burnin <- 1e3
runs <- 2e3
thin <- 1
chains <- 1

adapt <- 3e2
burnin <- 5e3
runs <- 2e3
thin <- 20
chains <- 1

par <- NULL
par <- c(par, "delta", "omega")
par <- c(par, "alpha")
par <- c(par, "gamma")
par <- c(par, "lambda")
par <- c(par, "theta")
par <- c(par, "sigma.alpha")
par <- c(par, "Delta", "Omega")
par <- c(par, "sigma.delta", "sigma.omega")
if (runFit) par <- c(par, "p")
if (runFitCont) par <- c(par, "resid")

## Initial values for ordinal variables
#inits.lambda <- array(0, dim = c(nV, 2))
#inits.lambda[,2] <- 1
#inits.lambda[,1] <- NA
#for (io in 1:nV) {
#  nC <- nCat[io]
#  #assign(paste("alpha", io, ".0", sep = ""), seq(-10, 10, length.out = nC - 1))
#  assign(paste("alpha", io, ".0", sep = ""), seq(-4, 4, length.out = nC - 1))
#}
#
#inits <- list(
#  list(.RNG.seed=14718, .RNG.name="base :: Mersenne-Twister",
#    alpha1.0 = alpha1.0,
#    alpha2.0 = alpha2.0,
#    alpha3.0 = alpha3.0,
#    alpha4.0 = alpha4.0,
#    alpha5.0 = alpha5.0,
#    beta = inits.beta,
#    lambda = inits.lambda),
#    gamma = inits.gamma),
#  list(.RNG.seed=14719, .RNG.name="base :: Mersenne-Twister",
#    alpha1.0 = alpha1.0,
#    alpha2.0 = alpha2.0,
#    alpha3.0 = alpha3.0,
#    alpha4.0 = alpha4.0,
#    alpha5.0 = alpha5.0,
#    beta = inits.beta,
#    lambda = inits.lambda)),
#    gamma = inits.gamma))

```

Sample

```

t0 <- proc.time()
rj <- run.jags(
  model = paste("models/model-", M, ".bug", sep = ""),
  # inits = inits,
  data = dump.format(D, checkvalid = FALSE),
  n.chains = chains, adapt = adapt, burnin = burnin, sample = runs, thin = thin,
  # monitor = par, method = "rjparallel", summarise = FALSE, silent.jags = FALSE)
  monitor = par, method = "parallel", summarise = FALSE, silent.jags = FALSE)
# monitor = par, method = "bgparallel", summarise = FALSE, silent.jags = FALSE)

```

```

S <- as.mcmc.list(rj)
save(s, file = paste("sample-", M, ".RData", sep = ""))
print(proc.time() - t0)

S <- ggs(s, family = "omega|Omega|alpha|delta|Delta|gamma|theta")
ggmcmc(S, file = paste("ggmcmc-", M, ".pdf", sep = ""), param_page = 8,
plot = c("traceplots", "crosscorrelation", "geweke", "Rhat", "caterpillar"))

S <- ggs(s, family = "theta\\\[3,6\\]|theta")
ggmcmc(S, file = paste("ggmcmc-theta_3_6-", M, ".pdf", sep = ""), param_page = 8,
plot = c("crosscorrelation"))

S <- ggs(s, family = "omega|Omega|alpha|delta|Delta|gamma|theta")
ggmcmc(S, file = paste("ggmcmc-", M, "-full.pdf", sep = ""), param_page = 10,
plot = c("traceplot", "density",
"running",
"autocorrelation",
"crosscorrelation",
"geweke", "Rhat"))

ggmcmc(S, file = paste("ggmcmc-", M, ".html", sep = ""), param_page = 8,
dev_type_html = "png",
plot = c("traceplots", "crosscorrelation", "geweke", "Rhat", "caterpillar"))

ggmcmc(ggs(s, family = "^beta"),
file = paste("ggmcmc-beta-", M, ".pdf", sep = ""),
param_page = 7,
plot = c("crosscorrelation", "caterpillar"))

S <- ggs(s, family = "nu")
ggmcmc(S, file = paste("ggmcmc-nu-", M, ".pdf", sep = ""), param_page = 8,
plot = c("traceplots", "crosscorrelation", "geweke", "Rhat", "caterpillar"))

```

### Temporal evolution

```

L.alpha <- plab("alpha", list(time = 1:nT)) %>%
  mutate(Year = as.integer(time.labels))
S.alpha <- ggs(s, family = "^alpha", par_labels = L.alpha)
ggplot(ci(S.alpha), aes(x = Year, y = median, ymin = Low, ymax = High)) +
  geom_point(size = 2) +
  geom_linerange(size = 1.2) +
  geom_linerange(aes(ymin = low, ymax = high), size = 0.7) +
  ylab("HPD")

ggs_histogram(ggs(s, family = "sigma\\\.alpha"))

```

### Country effects

```

L.omega <- plab("omega", list(Country = countries.labels))
S.omega <- ggs(s, family = "^omega", par_labels = L.omega)
ggs_caterpillar(S.omega)

L.omega <- plab("omega", list(Country = countries.labels))
S.omega <- ggs(s, family = "^omega", par_labels = L.omega) %>%
  left_join(decriminalized) %>%
  mutate(Decriminalized = as.factor(ifelse(Decriminalized == 1,
                                         "Decriminalized", "Criminalized")))

ggs_caterpillar(S.omega) +
  aes(color = Decriminalized) +
  scale_color_colorblind() +
  theme(legend.position = "right")

```

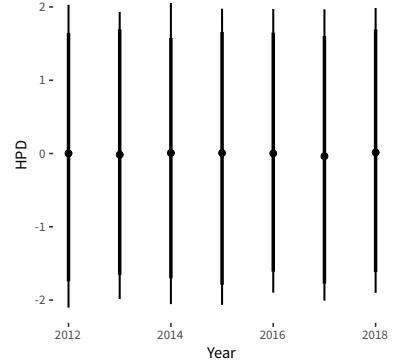


Figure 8: Temporal evolution.

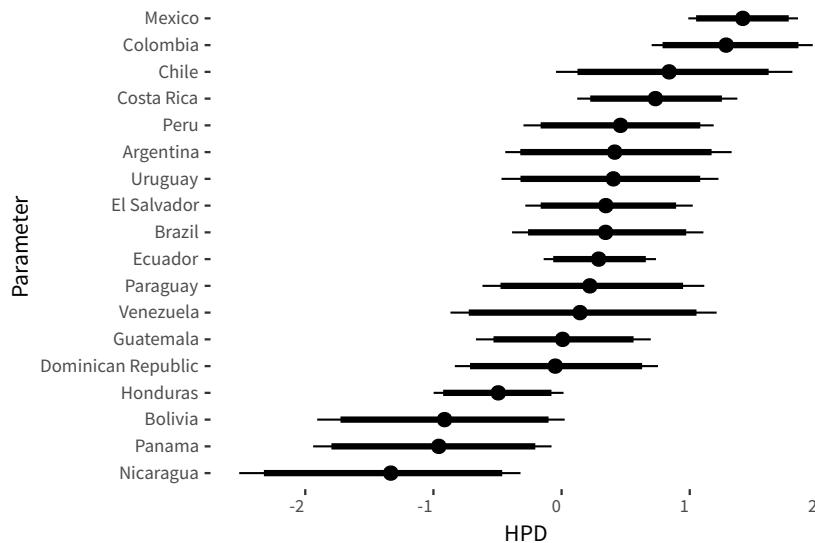


Figure 9: Country differences (logged odds).

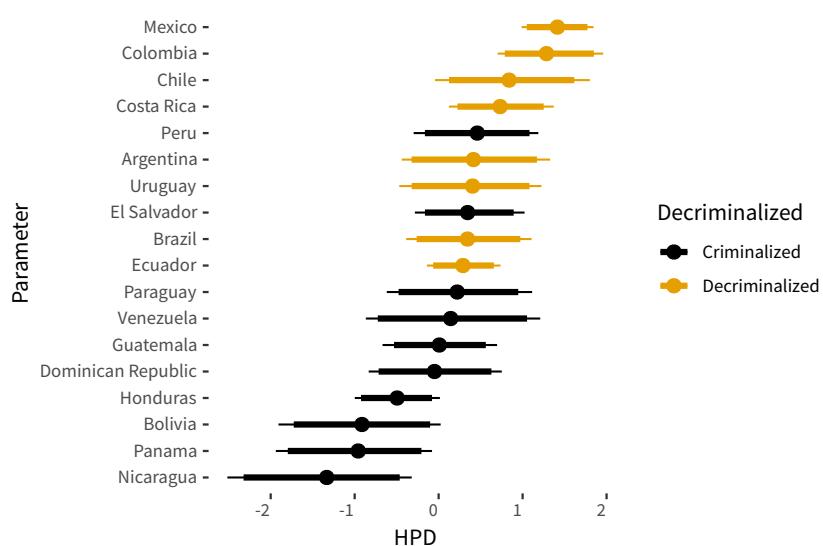


Figure 10: Country differences (logged odds).

```
L.omega <- plab("omega", list(Country = countries.labels))
S.omega.prob <- ggs(s, family = "omega", par_labels = L.omega) %>%
  mutate(value = inv.logit(value))
ggs_caterpillar(S.omega.prob) +
  expand_limits(x = c(0, 1))
```

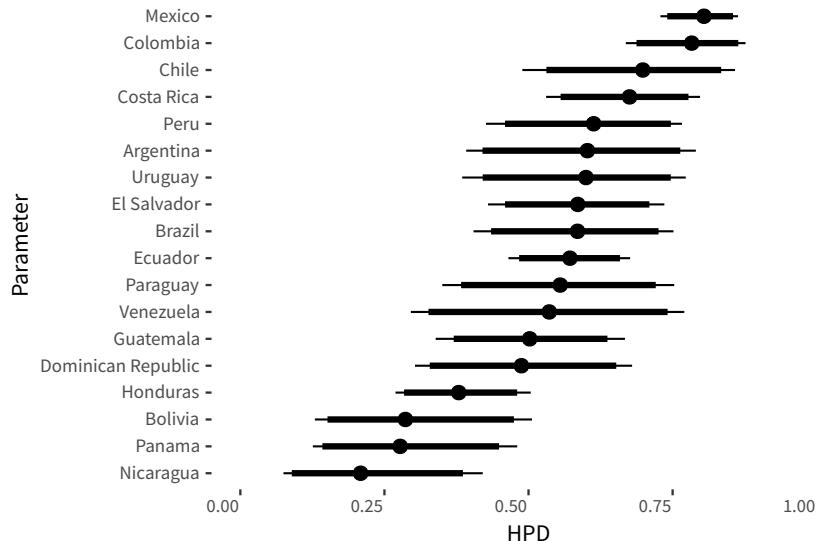


Figure 11: Country differences (expected probabilities for a mean legislator).

```
L.omega <- plab("omega", list(Country = countries.labels))
S.omega.prob <- ggs(s, family = "omega", par_labels = L.omega) %>%
  mutate(value = inv.logit(value)) %>%
  left_join(decriminalized) %>%
  mutate(Decriminalized = as.factor(ifelse(Decriminalized = 1,
                                             "Decriminalized", "Criminalized")))

ggs_caterpillar(S.omega.prob) +
  expand_limits(x = c(0, 1)) +
  scale_color_colorblind() +
  theme(legend.position = "right")
```

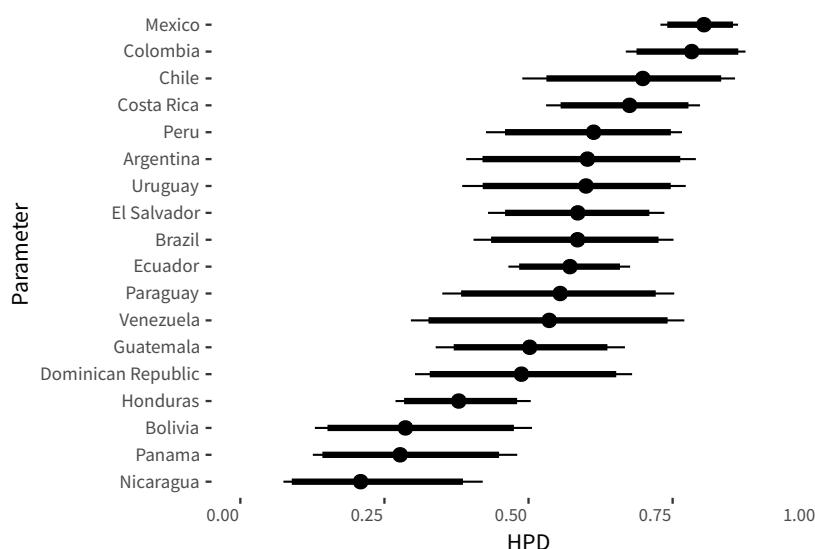


Figure 12: Country differences (expected probabilities for a mean legislator).

```
S.Omega <- ggs(s, family = "Omega")
ggs_histogram(S.Omega) +
  geom_vline(xintercept = 0, lty = 3)
```

### Individual-level covariates effects

```
L.lambda <- plab("lambda", list(Covariate = covariates.labels.nv))
S.lambda <- ggs(s, family = "lambda", par_labels = L.lambda)
ggs_caterpillar(S.lambda) +
  geom_vline(xintercept = 0, lty = 3)
```

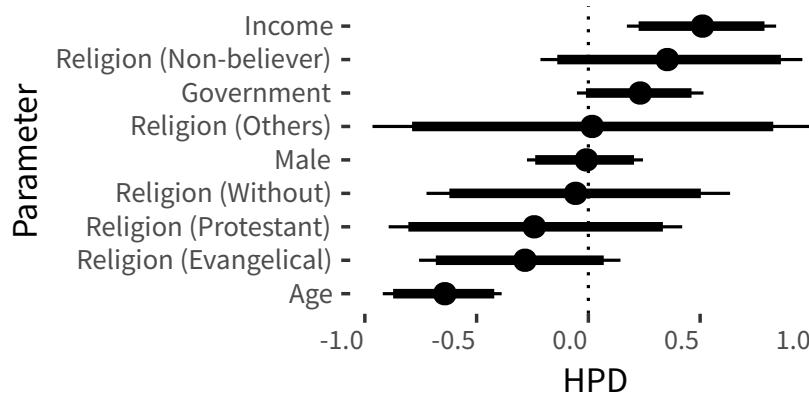


Figure 14: Covariate effects at the individual level, for the variables whose effect does not vary by country.

```
L.Delta <- plab("Delta", list(Covariate = covariates.labels))
S.Delta <- ggs(s, family = "Delta", par_labels = L.Delta)
ggs_caterpillar(S.Delta) +
  geom_vline(xintercept = 0, lty = 3)
```

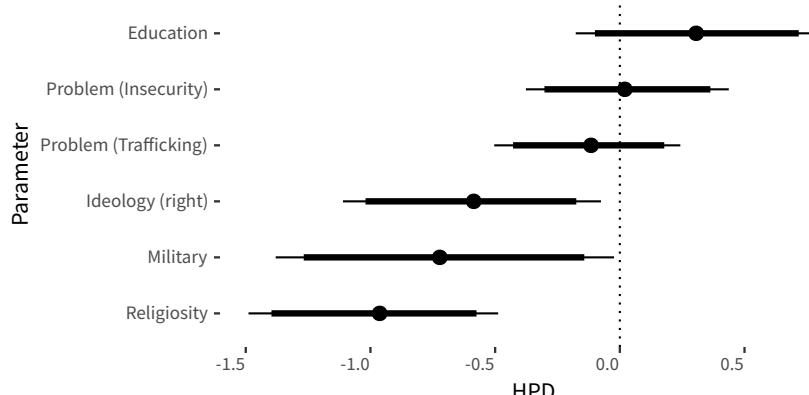


Figure 15: Covariate effects at the individual level. Shared associations by countries.

```
S.lambda.Delta <- bind_rows(mutate(S.lambda, Fixed = "Yes"),
                           mutate(S.Delta, Fixed = "No, varying"))

ggs_caterpillar(S.lambda.Delta) +
  geom_vline(xintercept = 0, lty = 3) +
  aes(color = Fixed) +
  scale_color_grey()
```

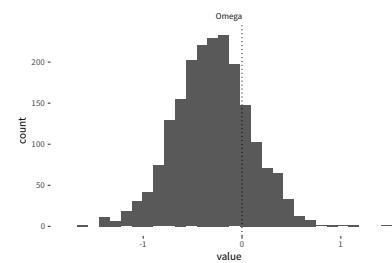


Figure 13: Overall intercept. Grand mean.

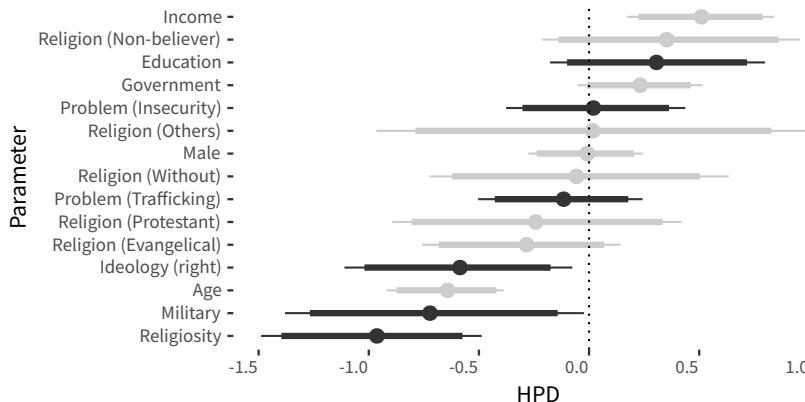


Figure 16: Covariate effects at the individual level. Shared associations by countries (black) and non-varying variables (grey).

```
S.lambda.Delta <- bind_rows(mutate(S.lambda, Fixed = "Yes"),
                           mutate(S.Delta, Fixed = "No, varying")) %>%
  mutate(value = exp(value))

f1 <- ggs_caterpillar(S.lambda.Delta) +
  geom_vline(xintercept = 1, lty = 3) +
  aes(color = Fixed) +
  scale_color_grey() +
  xlab("Odds of drug legalization (HPD)") +
  ylab("Covariate") +
  scale_x_continuous(trans = "log2",
                     breaks = c(0.25, 0.5, 1, 2),
                     labels = c("0.25", "0.5", "1", "2")) +
  ggtitle("Individual-level effects") +
  theme(text = element_text(size = 8))
print(f1)
```

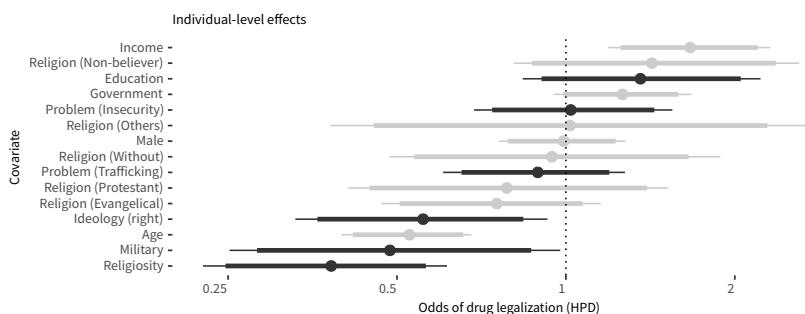


Figure 17: Covariate effects at the individual level. Shared associations by countries (black) and non-varying variables (grey).

### Magnitudes:

```
S.lambda.Delta <- bind_rows(mutate(S.lambda, Fixed = "Yes"),
                           mutate(S.Delta, Fixed = "No, varying"))
tb <- S.lambda.Delta %>%
  mutate(value = exp(value)) %>%
  ci() %>%
  rename(`Expected OR` = median) %>%
  select(Parameter, `Expected OR`) %>%
  mutate(`Expected effect` = or(`Expected OR`)) %>%
  arrange(desc(`Expected OR`))

tc <- "Odds ratio of expected effects. For variables varying by country
characteristics, they are the average expected effects (over the countries)."
if (knitr::is_latex_output()) {
  kable(tb, format = "latex", caption = tc, longtable = TRUE, booktabs = TRUE) %>%
  kable_styling(font_size = 10)
```

```

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

```

Table 1: Odds ratio of expected effects. For variables varying by country characteristics, they are the average expected effects (over the countries).

Parameter	Expected OR	Expected effect
Income	1.6664	△ 67%
Religion (Non-believer)	1.4235	△ 42%
Education	1.3580	△ 36%
Government	1.2612	△ 26%
Problem (Insecurity)	1.0201	△ 2%
Religion (Others)	1.0169	△ 1.7%
Male	0.9913	▽ 0.87%
Religion (Without)	0.9445	▽ 5.5%
Problem (Trafficking)	0.8910	▽ 11%
Religion (Protestant)	0.7849	▽ 22%
Religion (Evangelical)	0.7531	▽ 25%
Ideology (right)	0.5566	▽ 44%
Age	0.5263	▽ 47%
Military	0.4858	▽ 51%
Religiosity	0.3817	▽ 62%

The values can be interpreted as follows: one unit increase in the income of the legislator (corresponding to a 2 standard deviations increase in the variable, or roughly a move from its minimum value to its mean, or from its mean to its maximum value, or more generally from a low to a high value) is expected to increase the probability of the legislator to being favourable to drug legislation by 90 percent.

For binary variables the interpretation is performed using Catholics as the base reference. In this case, then, non-believers are 90 percent more likely than catholics to favour drug legalization, and evangelical are  $1 - 0.58 = 42$  percent more likely.

```

L.sigma.delta <- plab("sigma.delta", list(Covariate = covariates.labels))
S.sigma.delta <- ggs(s, family = "sigma.delta", par_labels = L.sigma.delta)
ggs_caterpillar(S.sigma.delta) +
  expand_limits(x = 0)

```

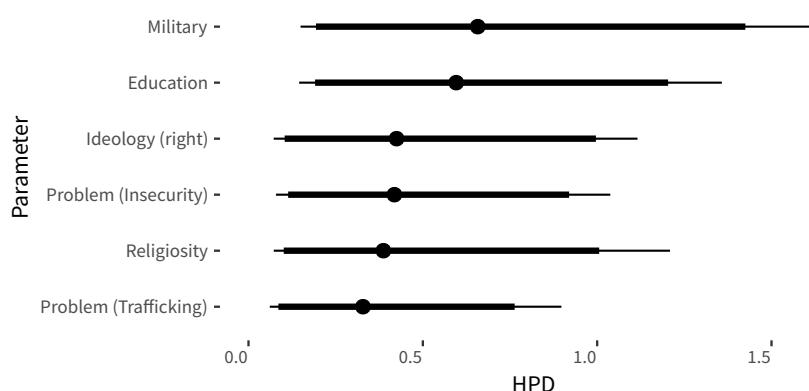


Figure 18: Error components of each covariate at the individual level. How much variation exists between countries.

```
L.delta <- plab("delta", list(Covariate = countries.labels, Covariate =
  covariates.labels))
S.delta <- ggs(s, family = "delta", par_labels = L.delta)
ggs_caterpillar(S.delta, label = "Country") +
  geom_vline(xintercept = 0, lty = 3) +
  facet_wrap(~ Covariate, ncol = 3, scale = "free")
```

### *Country-level covariates effects*

```
L.gamma <- plab("gamma", list(CCovariate = covariates.countries.labels.non.contextual)) %>%
  rename(`Covariate (country level)` = CCovariate)
S.gamma <- ggs(s, family = "gamma", par_labels = L.gamma)
ggs_caterpillar(S.gamma) +
  geom_vline(xintercept = 0, lty = 3) +
  ylab("Country")

L.theta <- plab("theta", list(CCovariate = covariates.countries.labels,
  Covariate = covariates.labels))
# rename(`Covariate (country level)` = CCovariate)
S.theta <- ggs(s, family = "theta", par_labels = L.theta)
ggs_caterpillar(S.theta, label = "CCovariate") +
  geom_vline(xintercept = 0, lty = 3) +
  facet_wrap(~ Covariate, ncol = 4, scale = "free")

L.theta <- plab("theta", list(CCovariate = covariates.countries.labels,
  Covariate = covariates.labels))
# rename(`Covariate (country level)` = CCovariate)
S.theta <- ggs(s, family = "theta", par_labels = L.theta)
f2 <- ggs_caterpillar(S.theta, label = "CCovariate") +
  geom_vline(xintercept = 0, lty = 3) +
  xlab("Logged odds (HPD)") +
  ylab("Country-level covariate") +
  facet_wrap(~ Covariate, ncol = 3, scale = "free_x") +
  ggtitle("Context-mediated effects") +
  theme(text = element_text(size = 8))
print(f2)

L.theta <- plab("theta", list(CCovariate = covariates.countries.labels,
  Covariate = covariates.labels))
# rename(`Covariate (country level)` = CCovariate)
S.theta <- ggs(s, family = "theta", par_labels = L.theta)
ggs_caterpillar(S.theta, label = "Covariate") +
  geom_vline(xintercept = 0, lty = 3) +
  facet_wrap(~ CCovariate, ncol = 5, scale = "free")

f1t <- f1 + ggtitle("Individual-level effects")
f2t <- f2 + ggtitle("Context-mediated effects")
cowplot::plot_grid(f1t, f2t, ncol = 2, rel_widths = c(1/3, 2/3), labels = "auto")

#ggsave("tmp.pdf", width = 12, height = 6)
```

Report the interactions between individual level effects and the context according to their expected strength that have a probability arbitrarily larger than 80 percent of being either positive or negative.

```
threshold <- 0.8
tb <- S.theta %>%
  group_by(Covariate, CCovariate) %>%
  summarize(MeanExpectedEffect = mean(value),
```

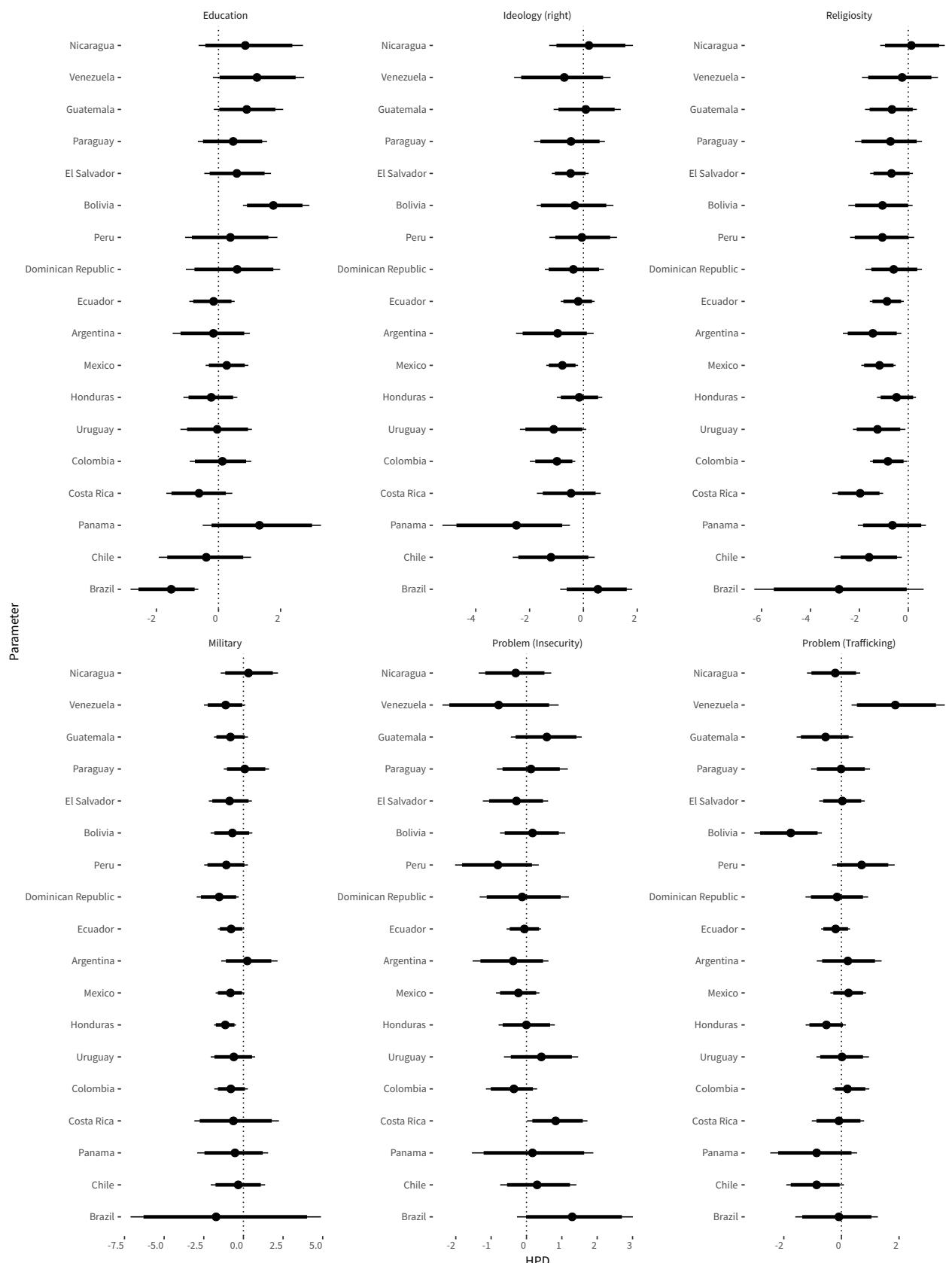


Figure 19: Covariate effects at the individual level.

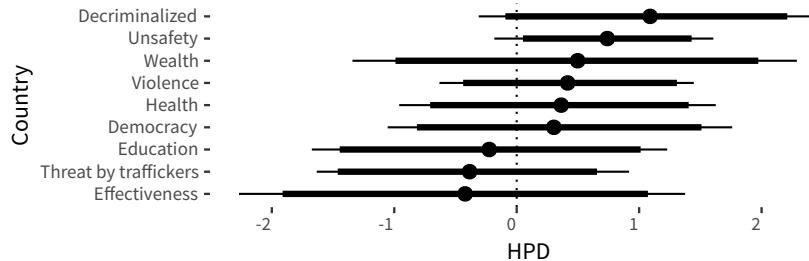


Figure 20: Effects at the country level on the varying intercepts.

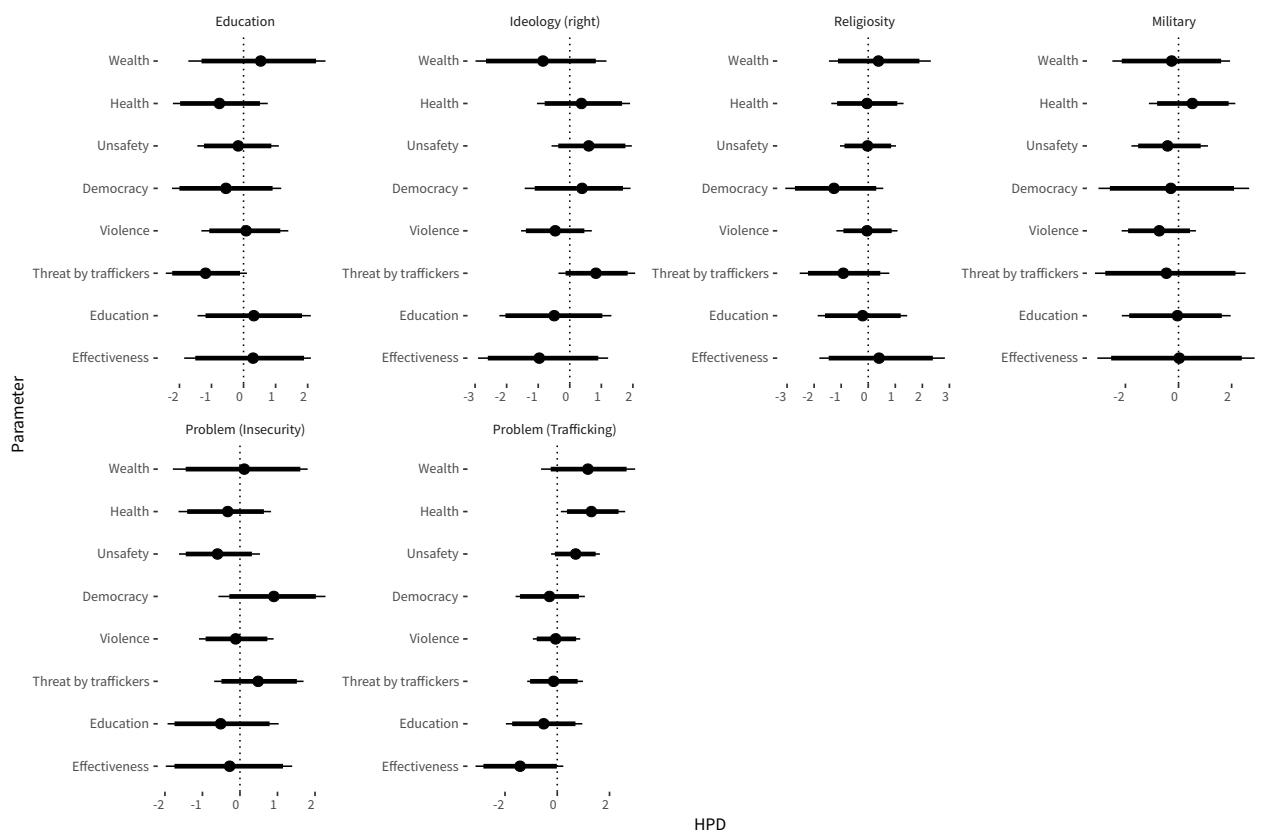


Figure 21: Effects at the country level on the varying slopes.

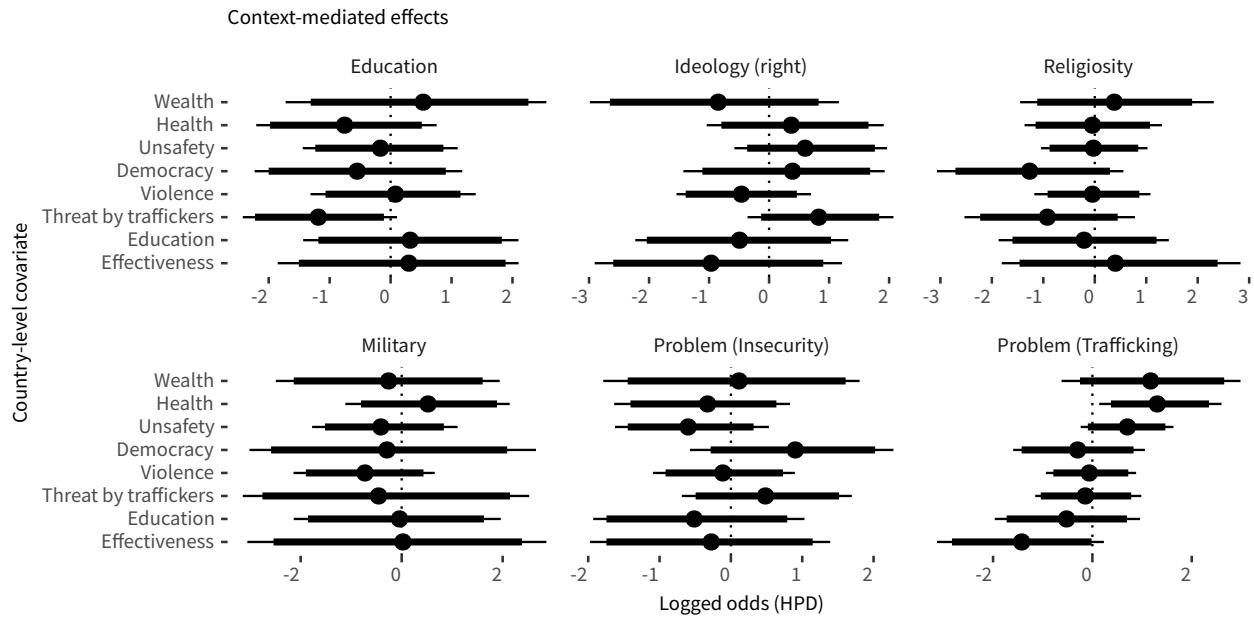


Figure 22: Effects at the country level on the varying slopes.

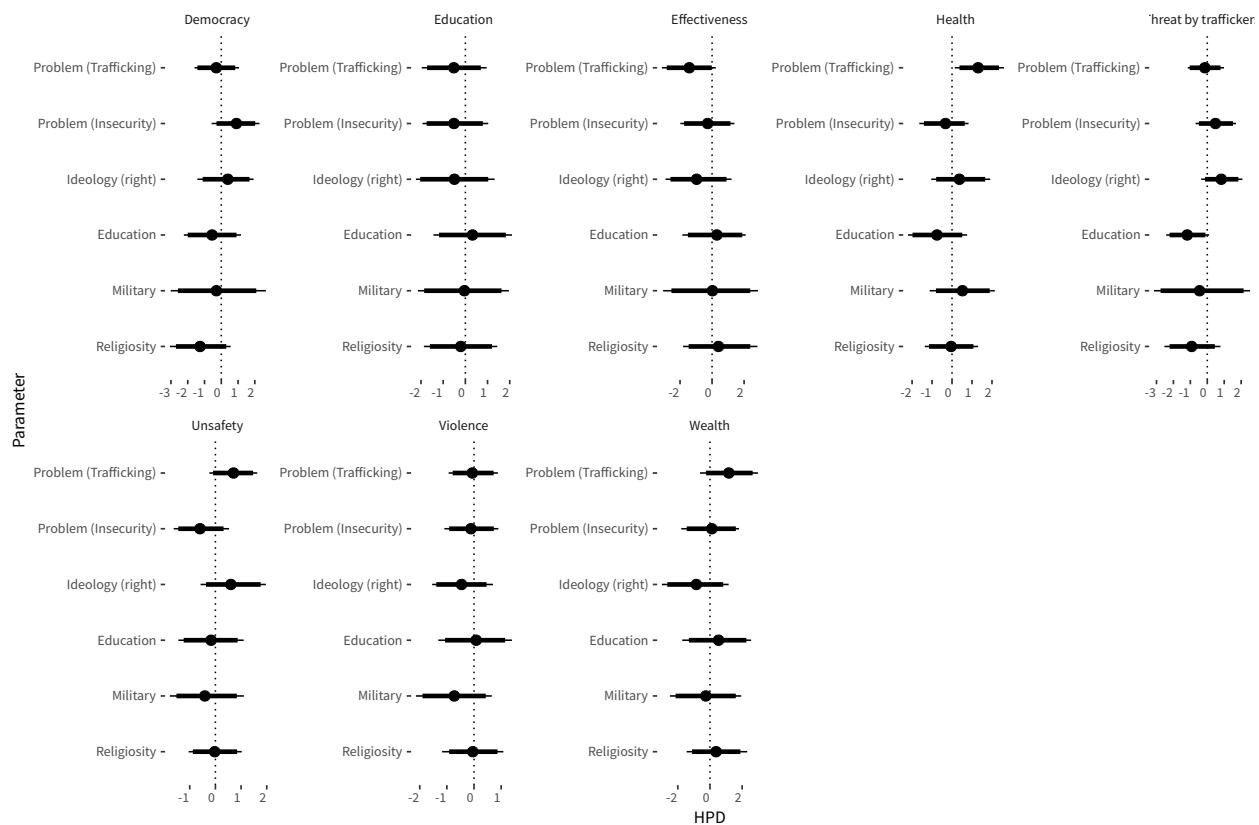


Figure 23: Effects at the country level on the varying slopes.

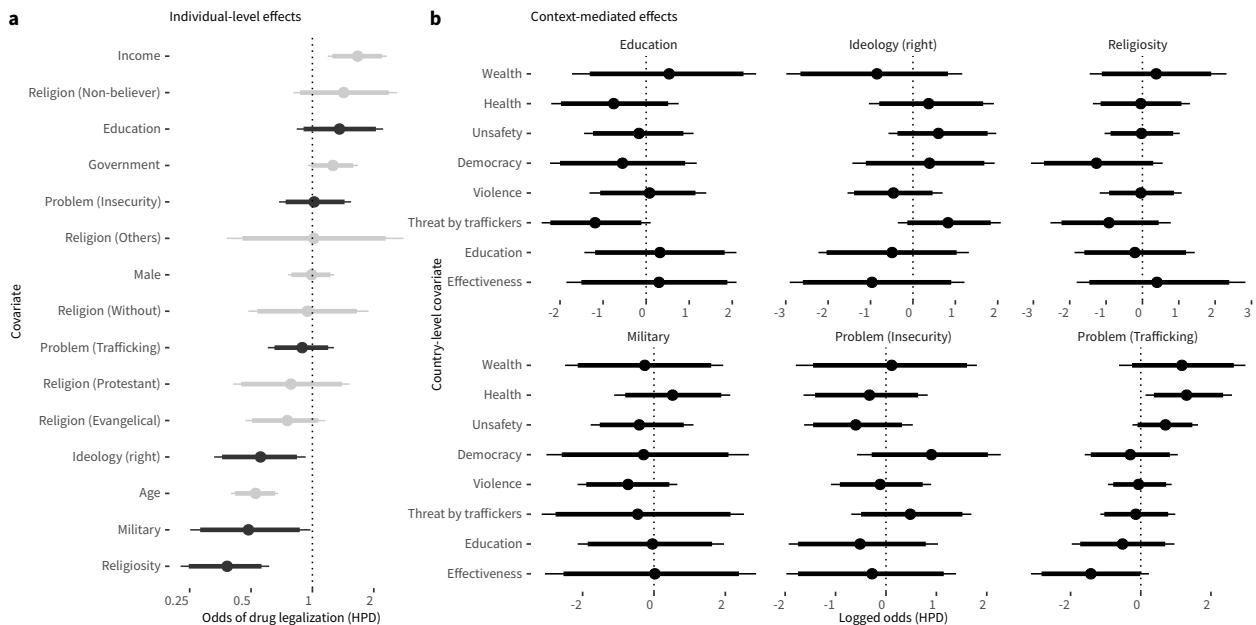


Figure 24: a) Covariate effects at the individual level. Shared associations by countries (black) and non-varying variables (grey); b) effects at the country level on the varying slopes.

```

`P > 0` = length(which(value > 0)) / n(),
`P < 0` = length(which(value < 0)) / n() %>%
  arrange(desc(abs(MeanExpectedEffect))) %>%
  filter(`P > 0` > threshold | `P < 0` > threshold) %>%
  rename(`Individual-level covariate` = Covariate) %>%
  rename(`Contextual covariate` = CCovariate) %>%
  mutate(`Expected OR` = exp(MeanExpectedEffect)) %>%
  mutate(`Mean expected effect` = or(`Expected OR`)) %>%
  mutate(`P > 0` = ifelse(`P > 0` > threshold, paste0(round(`P > 0` * 100, 1), "%"), ""))
  mutate(`P < 0` = ifelse(`P < 0` > threshold, paste0(round(`P < 0` * 100, 1), "%"), ""))
  select(-MeanExpectedEffect)

```

```

tc <- "Contextual and individual effects' relationship, with degree of evidence
and magnitude of effects, for variables varying by country characteristics."
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 2: Contextual and individual effects' relationship, with degree of evidence and magnitude of effects, for variables varying by country characteristics.

Individual-level covariate	Contextual covariate	P > 0	P < 0	Expected OR	Mean expected effect
Problem (Trafficking)	Effectiveness		95.3 %	0.2430	▽ 76%
Problem (Trafficking)	Health	98.4 %		3.7474	△ 270%
Religiosity	Democracy		90.8 %	0.2861	▽ 71%
Problem (Trafficking)	Wealth	91.2 %		3.2401	△ 220%
Education	Threat by traffickers		96.2 %	0.3103	▽ 69%
Ideology (right)	Effectiveness		82.6 %	0.3903	▽ 61%
Religiosity	Threat by traffickers		87.8 %	0.4046	▽ 60%
Problem (Insecurity)	Democracy	88.8 %		2.4142	△ 140%
Ideology (right)	Threat by traffickers	91.8 %		2.3044	△ 130%
Education	Health		84 %	0.4698	▽ 53%
Military	Violence		86.2 %	0.4803	▽ 52%
Problem (Trafficking)	Unsafty	92.7 %		2.0188	△ 100%

Ideology (right) Problem (Insecurity)	Unsafety Unsafety	83.9 % 85.5 %	1.8911 0.5612	$\Delta$ 89% $\nabla$ 44%
--	----------------------	------------------	------------------	------------------------------

In this case the interpretation would be as follows: one unit increase in government effectiveness (which means moving from the lower to the mean value, or from the mean to the higher) in a country makes that a legislator that considers that trafficking is a problem is less likely to support prohibition by 82 percent.

```
L.theta <- plab("theta", list(CCovariate = covariates.countries.labels,
                                Covariate = covariates.labels))
# rename(`Covariate (country level)` = CCovariate)
S.theta.pub <- ggs(s, family = "theta", par_labels = L.theta) %>%
  filter(!str_detect(Parameter, "Religion"))

ggs_caterpillar(S.theta.pub, label = "CCovariate") +
  geom_vline(xintercept = 0, lty = 3) +
  ylab("") +
  facet_wrap(~ Covariate, ncol = 3, scale = "free")
```

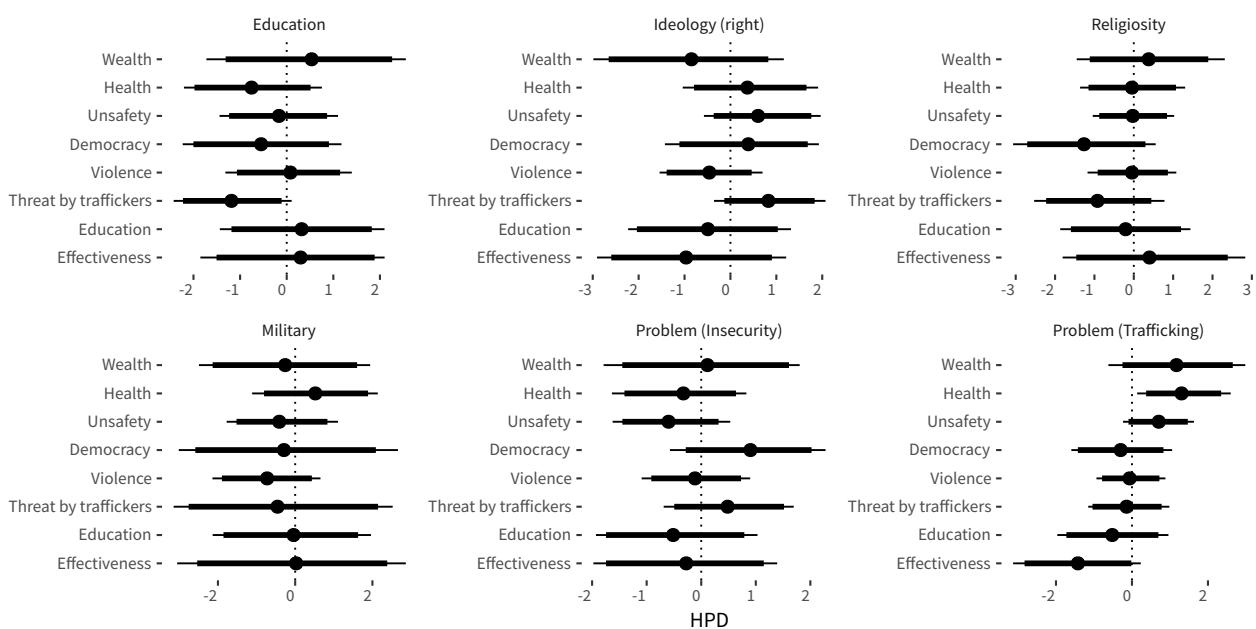


Figure 25: Effects at the country level on the varying slopes. Or, in other words, country-level variables mediating the effect of individual-level covariates.

### Model fit

```
L.p <- plab("p", list(id = 1:n0))
S.p <- ggs(s, family = "p\\[", par_labels = L.p) %>%
  mutate(id = as.integer(as.character(id)))
y.threshold <- length(which(y == 1)) / length(y)

# Percent correctly predicted.
ggs_pcp(S.p, outcome = D$y)

# Posterior mean of PCP
ggs_pcp(S.p, outcome = D$y)$data %>%
  summarize(`Mean of PCP` = mean(`Percent correctly predicted`))

## Mean of PCP
## 1      0.6887
```

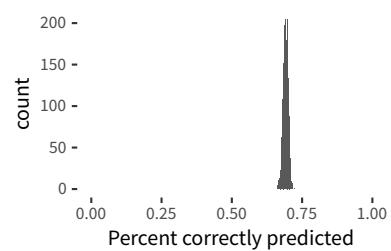


Figure 26: Percent correctly predicted.

```
# Pseudo-R2
S.resid <- ggs(s, family = "resid")
S.R2 <- S.resid %>%
  group_by(Iteration, Chain) %>%
  summarize(RSD = sd(value))

ggplot(S.R2, aes(x = RSD)) + geom_histogram() +
  geom_vline(xintercept = sd(D$y.cont, na.rm = TRUE)) +
  expand_limits(x = 0)

# Separation plot.
ggs_separation(S.p, outcome = D$y)
```

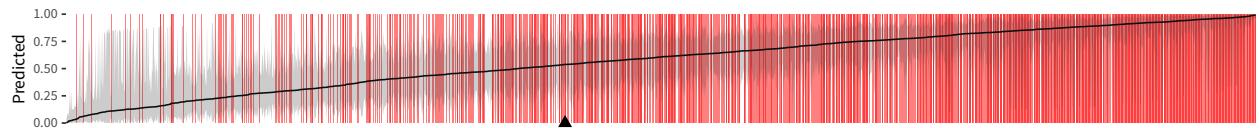


Figure 27: Model fit: separation plot.

Report worstly predicted cases.

```
d.fit <- bind_cols(d, y) %>%
  left_join(ci(S.p)) %>%
  rename(`Predicted probability` = median)
```

List of cases *predicted* to be likely to be *favourable* to drugs and currently *observing not favourable*.

```
d.fit %>%
  filter(y == 1) %>%
  arrange(`Predicted probability`) %>%
  select(id, Country, Year, Party, Drugs, y, `Predicted probability`) %>%
  slice(1:20) %>%
  kable()
```

id	Country	Year	Party	Drugs	y	Predicted probability
864	Panama	2014	CAMBIO DEMOCRÁTICO	3	1	0.0371
1146	Bolivia	2015	MAS	2	1	0.0622
198	El Salvador	2012	ARENA	6	1	0.0782
1793	Honduras	2018	PNH	4	1	0.1106
168	El Salvador	2012	ARENA	5	1	0.1238
1100	Bolivia	2015	MAS	3	1	0.1277
1104	Bolivia	2015	MAS	4	1	0.1363
1278	Dominican Republic	2017	PRSC	5	1	0.1395
1605	Nicaragua	2017	FSLN	5	1	0.1569
1710	Costa Rica	2018	Otros partidos	4	1	0.1575
714	Honduras	2014	PNH	3	1	0.1599
1251	Venezuela	2016	Otros partidos	3	1	0.1807
1569	Nicaragua	2017	FSLN	5	1	0.1815
838	Panama	2014	CAMBIO DEMOCRÁTICO	6	1	0.1816
1139	Bolivia	2015	MAS	2	1	0.1824
755	Honduras	2014	PNH	5	1	0.1948
1782	Honduras	2018	PNH	4	1	0.2044
759	Honduras	2014	PNH	3	1	0.2064
1803	Honduras	2018	Otros partidos hondureños	3	1	0.2130
207	El Salvador	2012	GANA	5	1	0.2263

List of cases *predicted* to be likely to be *unfavourable* to drugs and currently *observing favourable*.

```
d.fit %>%
  filter(y == 0) %>%
  arrange(desc(`Predicted probability`)) %>%
  select(id, Country, Year, Party, Drugs, y, `Predicted probability`) %>%
  slice(1:20) %>%
  kable()
```

id	Country	Year	Party	Drugs	y	Predicted probability
409	Mexico	2015	PRI	1	0	0.9672
1938	Mexico	2018	MORENA	1	0	0.9537
336	Mexico	2012	PRI	1	0	0.9467
1057	Uruguay	2015	FA	1	0	0.9298
1010	Chile	2014	PPD	1	0	0.9208
1233	Venezuela	2016	UNT	1	0	0.9186
449	Mexico	2015	PRI	1	0	0.9000
1898	Mexico	2018	MORENA	1	0	0.8995
933	Colombia	2014	CD	1	0	0.8978
940	Colombia	2014	P de la U	1	0	0.8970
497	Ecuador	2013	Alianza País	1	0	0.8897
1079	Uruguay	2015	Otros partidos	1	0	0.8849
919	Colombia	2014	PL	1	0	0.8817
1247	Venezuela	2016	AD	1	0	0.8807
1031	Uruguay	2015	PN	1	0	0.8760
83	Argentina	2013	Proyecto Sur	1	0	0.8722
381	Mexico	2015	PRI	1	0	0.8679
1022	Chile	2014	Otros	1	0	0.8666
728	Honduras	2014	LIBRE	1	0	0.8626
364	Mexico	2015	PRI	1	0	0.8622

```
d.fit %>%
  mutate(Correct = ifelse(`Predicted probability` < y.threshold & y == 0) | (`Predicted probability` > y.threshold & y == 1), TRUE,
  Error = y - `Predicted probability`) %>%
  select(-y, -`Predicted probability`, -id, -Parameter, -low, -Low, -High, -high, -ParameterOriginal, -dim.1) %>%
  select(-Ideology.difference, -Ideology.party) %>%
  gather(Covariate, value, -Country, -Year, -Party, -Drugs, -Error, -Correct) %>%
  filter(!is.na(Correct)) %>%
  ggplot(aes(x = value, y = Error, color = Correct)) +
  geom_point() +
  facet_wrap(~ Covariate, ncol = 5, scales = "free")
```

### Summary of results

- Weak evidence of temporal evolution, with increasing likelihood of favourable positions to legalization, but only when comparing 2012 against 2018.
- Discarding legislator (individual) effects, countries have different underlying values for drug legalization. For the median legislator, Mexico, Colombia and Chile being the most open to it, and Nicaragua and Bolivia the least likely.
- The expected probabilities for a median legislator to be in favour to drug legalization ranges between a bit less than 25 percent in Nicaragua and slightly more than 75 percent in Mexico.

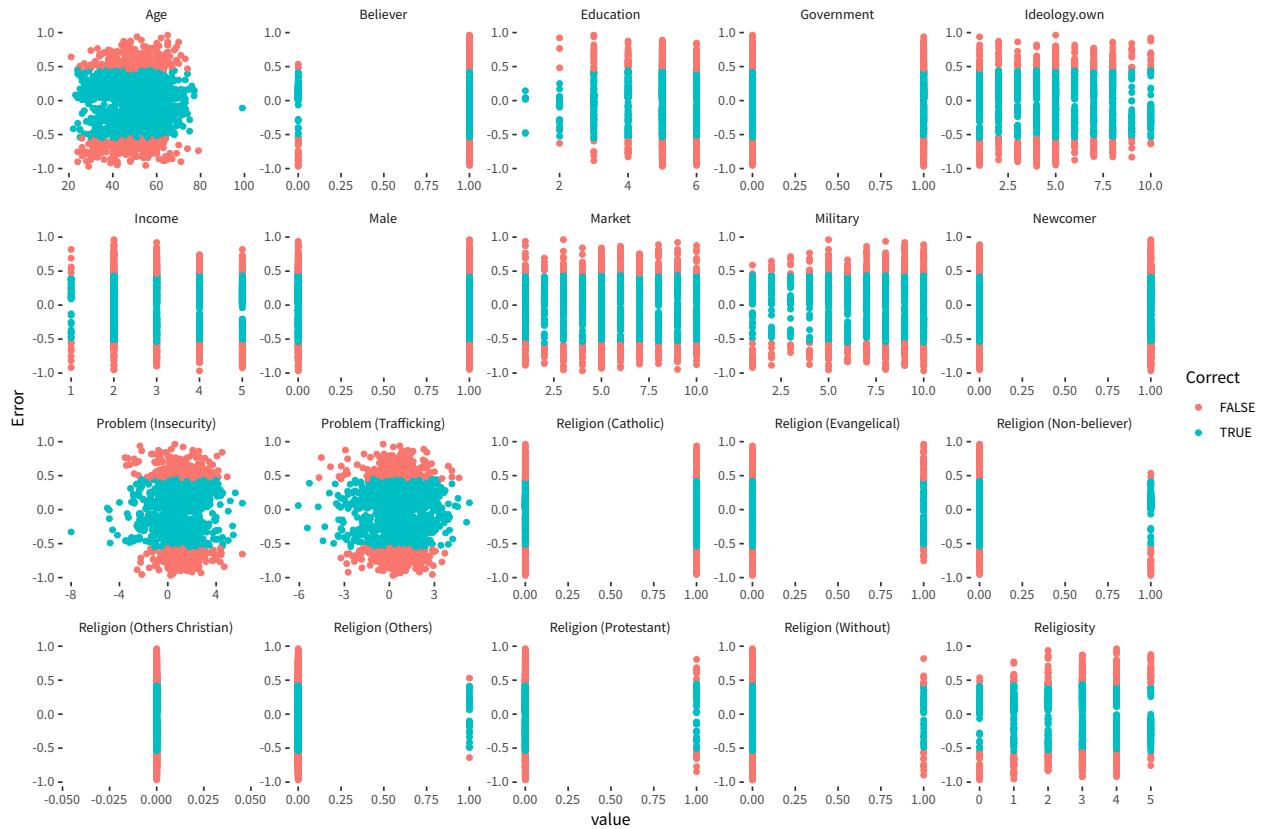


Figure 28: Covariate values against the difference between the observed value and the predicted value. Positive errors correspond to cases where a pro-legalization legislator is predicted to be non-favourable whereas negative values correspond to anti-legalization legislators being predicted as highly favourable.

- Control variables: except for gender, the rest of the control variables are associated with differential propensity to drug legalization. Income and belonging to the party in government positively, whereas age negatively.
- Individual variables that are generally aligned with drug legalization are education and religion (non-believers and others against catholics).
- Individual variables that are associated with more likelihood of being against drugs are religiosity, being in favour of military, religiosity. Also, compared to catholic legislators evangelical are more likely to be against drug legalization, but with low certainty.
- There is evidence of a mediated effects between country-level characteristics and the following individual-level variables:
  - Problem (trafficking). In healthier countries with low government effectiveness and low health, when legislators consider that trafficking is a problem are more likely to support drug legalization. Other ways to report it. In wealthier countries, legislators with higher consideration of trafficking being a problem are more likely to favour drug legalization. In countries with lower health and/or lower government effectiveness, legislators with higher consideration of trafficking being a problem are less likely to favour drug legalization.
  - Religiosity. In more democratic countries, the effect of religiosity decreases (the higher the religiosity of the legislator, the lower its propensity to drug legalization, but with lower effect than in non-democracies).

- Education. In countries where the perception of traffickers being a problem is greater, the more educated the legislator, the less likely to favour drug legalization.
- Variables at the country level do not explain at all the baseline support to drug legalization in the different countries.
- Contextual covariates also play a role in shaping different concrete religious effects (unsafety on those without religion; education on not-believers and threat by traffickers on education).
- The model is able to correctly predict slightly more than 2/3 of the legislators (69.7%).
- The worstly predicted cases of favourable legislators but the model predicting them low probability are Honduras (PNH, 3), Bolivia (MAS, 2), Panama (Cambio Democrático, 1) and El Salvador (ARENA, 2).
- The worstly predicted cases of unfavourable legislators but the model predicting them high probability are Venezuela (AD 1, UNT 1), Mexico (MORENA, 2, PRI 3).