20221209 - 2.mgm

2022-12-09

library(pacman)  
p\_load(tidyverse, here, sjlabelled, stringr, glue, EGAnet, janitor, haven,   
 ggpubr, gridExtra, dplyr, GGally, qgraph, sjmisc, igraph, sjPlot,  
 grid, psych, stargazer, mgm, backbone, ggplot2, tnet, ggrepel,  
 NetworkComparisonTest, Matrix, bootnet, matrixcalc, openxlsx, devtools, jtools)

# Input

W3 = readRDS((here("Input", "W3.rds")))

# Processing

## Network objects

## network objects  
type <-c("g","g","c","g","c","g","g","g","g","g","g","g","c","c","c","g","c",  
 "c","g","c","g","g","g")  
  
level <-c("1","1","2","1","2","1","1","1","1","1","1","1","2","2","2","1","2"  
 ,"2","1","2","1","1","1")  
  
shortnames <- c(  
"vac\_bad",  
"vac\_free",  
"low\_worry",  
"low\_risk",  
"conspiracy",  
"nat",  
"int\_locus",  
"low\_col\_resp",  
"PTV\_L",  
"PTV\_5SM",  
"PTV\_BOI",  
"distrust\_sci",  
"pray",  
"media",  
"female",  
"young",  
"low\_educ",  
"rural",  
"eco\_insec",  
"hesitancy",  
"low\_comp",  
"distrust\_gov",  
"distrust\_inst")  
  
longnames <- c(  
"Vaccine bad for health",  
"Against mandatory vaccination",  
"Low worry about infection",  
"Low risk perception",  
"Endorsing conspiracy theories",  
"Trust in alternative medicine",  
"Internal health locus of control",  
"Low sense of collective responsability",  
"Propensity to vote for L",  
"Propensity to vote for 5SM",  
"Propensity to vote for BOI",  
"Distrust of science",  
"Religion, pray",  
"Digital media diet",  
"Sex, female",  
"Age, young",  
"Educational level, low",  
"Living in a rural region",  
"Economic insecurity",  
"Vaccine hesitancy",  
"Low compliance with preventive behaviors",  
"Disapproval of Government",  
"Distrust of institutions")  
  
shapes <- c(  
"circle",   
"circle",  
"circle",  
"circle",  
"circle",  
"circle",  
"circle",  
"circle",  
"circle",  
"circle",  
"circle",  
"circle",  
"circle",  
"circle",  
"circle",  
"circle",  
"circle",  
"circle",  
"circle",  
"square",  
"circle",  
"circle",  
"circle")  
  
# Community detection function (modified to allow for iterations)  
communityStability <- function(data, type, level, iterations)  
{  
   
 communityMemberships <- list()  
   
 for (i in 1:iterations)  
 {  
 fitGraph <- mgm(data, type, level, k = 2, verbatim = TRUE)  
 iGraph<- graph\_from\_adjacency\_matrix(abs  
 (fitGraph$pairwise$wadj), "undirected", weighted =  
 TRUE)  
 communityMemberships[[i]] <- cluster\_walktrap(iGraph)$membership  
 }  
   
 communityOverlap <- matrix(NA, length(data), length(data))  
   
 for(j in 1:length(data))  
 {  
   
 overlapPerNode <- matrix(NA, iterations, ncol(communityOverlap))  
   
 for(k in 1: iterations)  
 {  
 overlapPerNode[k,] <- as.numeric(communityMemberships[[k]][j] == communityMemberships[[k]])  
 }  
   
 communityOverlap[j,] <- apply(overlapPerNode, 2, mean)  
 }  
   
 diag(communityOverlap) <- 0  
   
 return(list(communityMemberships = communityMemberships, communityOverlap = communityOverlap))  
   
}

## Fit model

set.seed(1)  
FitW3 <- mgm(W3, type, level, k = 2, binarySign = TRUE)

## | | | 0% | |--- | 4% | |------ | 9% | |--------- | 13% | |------------ | 17% | |--------------- | 22% | |------------------ | 26% | |--------------------- | 30% | |------------------------ | 35% | |--------------------------- | 39% | |------------------------------ | 43% | |--------------------------------- | 48% | |------------------------------------- | 52% | |---------------------------------------- | 57% | |------------------------------------------- | 61% | |---------------------------------------------- | 65% | |------------------------------------------------- | 70% | |---------------------------------------------------- | 74% | |------------------------------------------------------- | 78% | |---------------------------------------------------------- | 83% | |------------------------------------------------------------- | 87% | |---------------------------------------------------------------- | 91% | |------------------------------------------------------------------- | 96% | |----------------------------------------------------------------------| 100%  
## Note that the sign of parameter estimates is stored separately; see ?mgm

## Community stability (Supplement S1)

#LOAD THE OBJECT down below TO SAVE TIME:  
#CommunityStabTotal<-communityStability(W3, type, level, it=1000)  
  
#load the object instead:  
CommunityStabTotal = readRDS(here("Input", "CommunityStabTotal.rds"))

# Visualize community stability   
pdf(file = '../Output/Supplement/community\_stability.pdf',paper = "USr",  
 height = 9, width = 12)  
qgraph(CommunityStabTotal$communityOverlap, layout = "spring",   
 theme = "Borkulo", labels = shortnames,  
 nodeNames = longnames,vsize=4.0,  
 edge.labels=FALSE, legend = TRUE, legend.cex = 0.3)  
dev.off()

## quartz\_off\_screen   
## 2

# Vizualise detected communities   
inputCommDetection\_total<-CommunityStabTotal$communityOverlap  
inputCommDetection\_total[which(inputCommDetection\_total <= .90)] <- 0  
  
pdf(file = '../Output/Supplement/detected\_communities.pdf',paper = "USr",  
 height = 9, width = 12)  
qgraph(inputCommDetection\_total, layout = "spring", theme = "Borkulo",  
 labels = shortnames, nodeNames = longnames, vsize=4.0,  
 edge.labels=FALSE, legend = TRUE, legend.cex = 0.3)  
dev.off()

## quartz\_off\_screen   
## 2

Totalgroup\_comm <- list(  
 " "=c(1,2,12,20),  
 " "=c(3,4),  
 " "=c(5,8),  
 " "=c(6,7,21),  
 " "=c(9,11),  
 " "=c(10,22,23),  
 " "=c(13:19))  
  
# define nice colors  
Totalgroup\_cols <- c("#BDE6F1","#E96479","#3FA796","#B4CFB0",  
 "#DF7861","#C3ACD0","#FFD56F")

## Plot no minimum (Supplement S1)

#enables theme colorblind because we don't need to specify edge.color  
inputGraphMGM <- FitW3$pairwise$wadj  
signsGraphMGM <- FitW3$pairwise$signs  
signsGraphMGM[which(is.na(signsGraphMGM))] <- 1  
inputGraphMGM <- inputGraphMGM\*signsGraphMGM  
  
# Plot   
set.seed(1)  
pdf(file = '../Output/Supplement/MGM\_nomin.pdf',paper = "USr", height = 9, width = 12)  
GraphMGM<-qgraph(inputGraphMGM,   
 layout = "spring", theme = "Borkulo",   
 labels = shortnames, nodeNames = longnames,  
 cut = 0.10, maximum = 1,   
 details = FALSE, vsize=6.0, shape = shapes,  
 groups=Totalgroup\_comm, color= Totalgroup\_cols,  
 legend = TRUE, legend.cex = 0.4, borders = FALSE)  
dev.off()

## quartz\_off\_screen   
## 2

### Plot with predictability (Article)

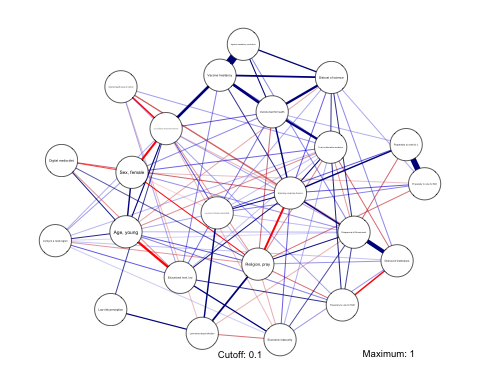
#Predicted values  
p\_obj <- predict(FitW3, W3, errorCat = c("CC","nCC","CCmarg"), errorCon = c("R2"))  
  
#insert them in a list, and compute different metrics for cathegorical variables  
error\_list <- list()   
error\_list[[1]] = p\_obj$errors[1,2]  
error\_list[[2]] = p\_obj$errors[2,2]  
 beyondmarg <- p\_obj$errors[3,3]-p\_obj$errors[3,5]  
 error\_list[[3]] = c(p\_obj$errors[3,5],beyondmarg)  
error\_list[[4]] = p\_obj$errors[4,2]  
 beyondmarg <- p\_obj$errors[5,3]-p\_obj$errors[5,5]  
 error\_list[[5]] = c(p\_obj$errors[5,5],beyondmarg)  
error\_list[[6]] = p\_obj$errors[6,2]  
error\_list[[7]] = p\_obj$errors[7,2]  
error\_list[[8]] = p\_obj$errors[8,2]  
error\_list[[9]] = p\_obj$errors[9,2]  
error\_list[[10]] = p\_obj$errors[10,2]  
error\_list[[11]] = p\_obj$errors[11,2]  
error\_list[[12]] = p\_obj$errors[12,2]  
 beyondmarg <- p\_obj$errors[13,3]-p\_obj$errors[13,5]  
 error\_list[[13]] = c(p\_obj$errors[13,5],beyondmarg)  
 beyondmarg <- p\_obj$errors[14,3]-p\_obj$errors[14,5]  
 error\_list[[14]] = c(p\_obj$errors[14,5],beyondmarg)  
 beyondmarg <- p\_obj$errors[15,3]-p\_obj$errors[15,5]  
 error\_list[[15]] = c(p\_obj$errors[15,5],beyondmarg)  
error\_list[[16]] = p\_obj$errors[16,2]  
 beyondmarg <- p\_obj$errors[17,3]-p\_obj$errors[17,5]  
 error\_list[[17]] = c(p\_obj$errors[17,5],beyondmarg)  
 beyondmarg <- p\_obj$errors[18,3]-p\_obj$errors[18,5]  
 error\_list[[18]] = c(p\_obj$errors[18,5],beyondmarg)  
error\_list[[19]] = p\_obj$errors[19,2]  
 beyondmarg <- p\_obj$errors[20,3]-p\_obj$errors[20,5]  
 error\_list[[20]] = c(p\_obj$errors[20,5],beyondmarg)  
error\_list[[21]] = p\_obj$errors[21,2]  
error\_list[[22]] = p\_obj$errors[22,2]  
error\_list[[23]] = p\_obj$errors[23,2]  
  
# List for Colors   
color\_list <- list()  
color\_list[[1]] = "#90B4D4"  
color\_list[[2]] = "#90B4D4"  
color\_list[[3]] = c("#ffa500", "#ff4300")  
color\_list[[4]] = "#90B4D4"  
color\_list[[5]] = c("#ffa500", "#ff4300")  
color\_list[[6]] = "#90B4D4"  
color\_list[[7]] = "#90B4D4"  
color\_list[[8]] = "#90B4D4"  
color\_list[[9]] = "#90B4D4"  
color\_list[[10]] = "#90B4D4"  
color\_list[[11]] = "#90B4D4"  
color\_list[[12]] = "#90B4D4"  
color\_list[[13]] = c("#ffa500", "#ff4300")  
color\_list[[14]] = c("#ffa500", "#ff4300")  
color\_list[[15]] = c("#ffa500", "#ff4300")  
color\_list[[16]] = "#90B4D4"  
color\_list[[17]] = c("#ffa500", "#ff4300")  
color\_list[[18]] = c("#ffa500", "#ff4300")  
color\_list[[19]] = "#90B4D4"  
color\_list[[20]] = c("#ffa500", "#ff4300")  
color\_list[[21]] = "#90B4D4"  
color\_list[[22]] = "#90B4D4"  
color\_list[[23]] = "#90B4D4"

# The final plot  
set.seed(100)  
GraphMGM<-qgraph(inputGraphMGM, pie = error\_list, pieColor = color\_list,  
 layout = "spring", theme = "Borkulo",   
 labels = shortnames, nodeNames = longnames,  
 cut = 0.10, minimum = 0.06, maximum = 1,   
 details = FALSE, vsize=6.0, shape = shapes,  
 groups=Totalgroup\_comm, color= Totalgroup\_cols,  
 legend = TRUE, legend.cex = 0.35, borders = TRUE,   
 filetype="jpg", filename=here("Output", "Article", "MGM\_min\_06\_predictability"))

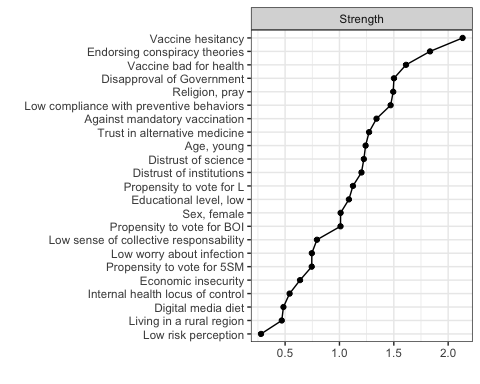
## Output stored in /Users/art/Documents/Github/lavori in corso/papers/vaccine/Processing//Users/art/Documents/Github/lavori in corso/papers/vaccine/Output/Article/MGM\_min\_06\_predictability.jpg

## Centrality estimates

#graph with complete labels for centrality plot  
GraphMGMCENT<-qgraph(inputGraphMGM,   
 layout = "spring", theme = "colorblind",  
 labels = longnames, minimum = 0,  
 cut = 0.10, maximum = 1, details = TRUE,  
 legend = FALSE)



#centrality Total  
centMGM <- centralityTable(GraphMGMCENT,standardized = FALSE, signed = FALSE)  
  
#CentralityPlot Total  
centrality\_table = centralityPlot(GraphMGMCENT, include = c("Strength"), scale = "raw",  
 orderBy = "Strength", signed = FALSE) + theme\_nice() + theme(axis.text.y=element\_text(hjust=1))



ggsave(here("Output", "Article", "Centrality\_Table.jpg"), centrality\_table)

## Saving 5 x 4 in image

### Degree centrality

#Convert to igraph  
igraph\_graph <- graph.adjacency(FitW3$pairwise$wadj, mode="undirected", weighted = TRUE)  
  
#Degree centrality  
degree\_cent = degree(igraph\_graph)   
  
#Merge vectors  
degree\_data <- data.frame(names(W3), degree\_cent)

## ASPL

#Shortest Path Lenght with tnet from opshal  
spl\_o = distance\_w(FitW3$pairwise$wadj, directed=NULL, subsample=1)  
spl\_o <- spl\_o[upper.tri(spl\_o)]  
aspl\_o <- mean(spl\_o)

ASPL = 1.563595

## Bootstrap (Supplement S1)

#### Edge accuracy

#edge weight accuracy: non parametric bootstrap with 8 cores  
#edgeacc = bootnet(W3, nBoots = 1000, nCores = 8, 'mgm')  
  
#load the object instead:  
edgeacc = readRDS(here("Input", "edgeacc.rds"))  
  
#plot 1  
pdf('../Output/Supplement/robustness/edge\_accuracy.pdf', height = 70, width = 50)  
plot(edgeacc, labels = longnames, order = "sample")  
dev.off()

## quartz\_off\_screen   
## 2

#Plot 2  
pdf('../Output/Supplement/robustness/edge\_accuracy\_CI.pdf', height = 70, width = 50)  
plot(edgeacc, plot = "interval", split0 = TRUE, order="sample", labels=longnames)  
dev.off()

## quartz\_off\_screen   
## 2

#summary  
saummary\_edgeacc = summary(edgeacc, statistics = c("edge", "strength"),   
 perNode = FALSE, rank = FALSE)

#### Centrality stability (Supplement S1)

# case dropping bootstrap  
#centstab = bootnet(W3, nBoots = 1000, 'mgm', type = "case", nCores = 8)  
  
#load the object instead:  
centstab = readRDS(here("Input", "centstab.rds"))  
  
#plot 1  
pdf('../Output/Supplement/robustness/Centrality\_stability.pdf', height = 70, width = 50)  
plot(centstab, "Strength", perNode = TRUE, labels = longnames,  
 subsetRange = c(100,50))  
dev.off()

## quartz\_off\_screen   
## 2

#Plot 2  
pdf('../Output/Supplement/robustness/Centrality\_stability\_CI.pdf', height = 70, width = 50)  
plot(centstab, "Strength", CIstyle = "quantiles")  
dev.off()

## quartz\_off\_screen   
## 2

#CS-coefficient (result should be above 0.25, better if above 0.5)  
corstab = corStability(centstab)

## === Correlation Stability Analysis ===   
##   
## Sampling levels tested:  
## nPerson Drop% n  
## 1 385 75.0 86  
## 2 505 67.2 111  
## 3 625 59.4 87  
## 4 744 51.7 99  
## 5 864 43.9 100  
## 6 984 36.1 99  
## 7 1104 28.3 97  
## 8 1223 20.6 105  
## 9 1343 12.8 94  
## 10 1463 5.0 122  
##   
## Maximum drop proportions to retain correlation of 0.7 in at least 95% of the samples:  
##   
## edge: 0.75 (CS-coefficient is highest level tested)  
## - For more accuracy, run bootnet(..., caseMin = 0.672, caseMax = 1)   
##   
## strength: 0.75 (CS-coefficient is highest level tested)  
## - For more accuracy, run bootnet(..., caseMin = 0.672, caseMax = 1)   
##   
## Accuracy can also be increased by increasing both 'nBoots' and 'caseN'.

#### Testing Edge and centrality differences (Supplement S1)

# Test: difference of weight ties 2-3 vs 4-5  
differenceTest(edgeacc, 2--3, 3--4, "strength")

## Expected significance level given number of bootstrap samples is approximately: 0.05

## id1 id2 measure lower upper significant  
## 1 conspiracy h\_locus strength -1.400756 -0.5711839 TRUE

# Plot test results for every edge weight in the network  
pdf('../Output/Supplement/robustness/test\_edges.pdf', height = 70, width = 50)  
plot(edgeacc, "edge", plot = "difference", onlyNonZero = TRUE, order = "sample",   
 labels = T)

## Expected significance level given number of bootstrap samples is approximately: 0.05

dev.off()

## quartz\_off\_screen   
## 2

# Test: difference of strength of node 5 [conspiracy] vs 20 [hesitancy] (if the bootstrapped CI include 0, they do not differ)  
test\_conspiracy\_vs\_hesitancy = differenceTest(edgeacc, 5, 20, "strength")

## Expected significance level given number of bootstrap samples is approximately: 0.05

#test\_conspiracy\_vs\_distrust\_gov = differenceTest(edgeacc, 5, 22, "strength")  
#test\_conspiracy\_vs\_vac\_bad = differenceTest(edgeacc, 5, 1, "strength")  
#test\_conspiracy\_vs\_pray = differenceTest(edgeacc, 5, 13, "strength")  
  
# Plot test results for every edge weight in the network  
pdf('../Output/Supplement/robustness/test\_strenghts.pdf', height = 70, width = 50)  
plot(edgeacc, "strength", order = "mean", labels = T)

## Expected significance level given number of bootstrap samples is approximately: 0.05

dev.off()

## quartz\_off\_screen   
## 2

## Additional robustness check (Supplement S1)

#Creating serial number for each row  
W3\_robustness = W3  
W3\_robustness$id = 1:nrow(W3)  
  
#Splitting randomly the original data frame in two partitions  
W3\_robustness\_a = W3\_robustness %>% dplyr::sample\_frac(.50)   
W3\_robustness\_b = dplyr::anti\_join(W3\_robustness, W3\_robustness\_a, by = 'id')   
  
#Remove id variable  
W3\_robustness\_a = W3\_robustness\_a %>% dplyr::select(-id)  
W3\_robustness\_b = W3\_robustness\_b %>% dplyr::select(-id)  
  
#Fitting two mgm  
set.seed(1)  
FitW3\_robustness\_a <- mgm(W3\_robustness\_a, type, level, k = 2, binarySign = TRUE)

## | | | 0% | |--- | 4% | |------ | 9% | |--------- | 13% | |------------ | 17% | |--------------- | 22% | |------------------ | 26% | |--------------------- | 30% | |------------------------ | 35% | |--------------------------- | 39% | |------------------------------ | 43% | |--------------------------------- | 48% | |------------------------------------- | 52% | |---------------------------------------- | 57% | |------------------------------------------- | 61% | |---------------------------------------------- | 65% | |------------------------------------------------- | 70% | |---------------------------------------------------- | 74% | |------------------------------------------------------- | 78% | |---------------------------------------------------------- | 83% | |------------------------------------------------------------- | 87% | |---------------------------------------------------------------- | 91% | |------------------------------------------------------------------- | 96% | |----------------------------------------------------------------------| 100%  
## Note that the sign of parameter estimates is stored separately; see ?mgm

set.seed(1)  
FitW3\_robustness\_b <- mgm(W3\_robustness\_b, type, level, k = 2, binarySign = TRUE)

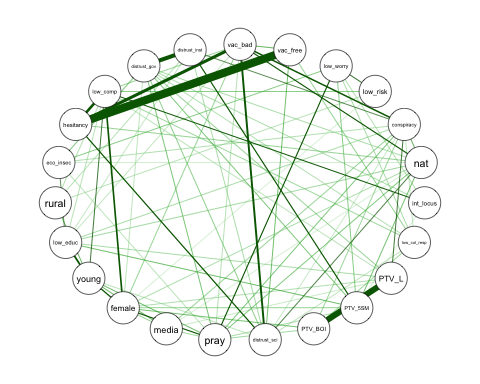
## | | | 0% | |--- | 4% | |------ | 9% | |--------- | 13% | |------------ | 17% | |--------------- | 22% | |------------------ | 26% | |--------------------- | 30% | |------------------------ | 35% | |--------------------------- | 39% | |------------------------------ | 43% | |--------------------------------- | 48% | |------------------------------------- | 52% | |---------------------------------------- | 57% | |------------------------------------------- | 61% | |---------------------------------------------- | 65% | |------------------------------------------------- | 70% | |---------------------------------------------------- | 74% | |------------------------------------------------------- | 78% | |---------------------------------------------------------- | 83% | |------------------------------------------------------------- | 87% | |---------------------------------------------------------------- | 91% | |------------------------------------------------------------------- | 96% | |----------------------------------------------------------------------| 100%  
## Note that the sign of parameter estimates is stored separately; see ?mgm

#Network Comparison Test between the two mgm   
set.seed(1)  
robustness\_a\_b = NCT(W3\_robustness\_a, W3\_robustness\_b, it = 1000,  
 test.edges=TRUE, edges="all",   
 progressbar=FALSE, p.adjust.methods= c("bonferroni"),   
 test.centrality=TRUE,   
 centrality=c("strength"),nodes="all")

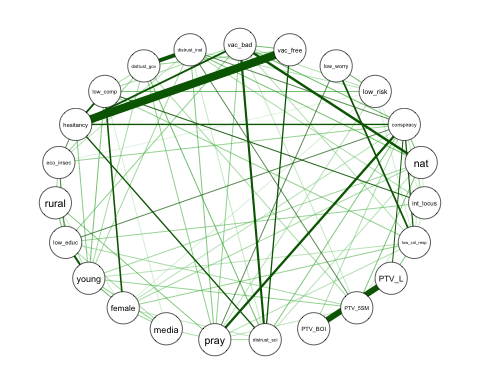
#Visualize results of edge tests   
inputNCTgraph <- FitW3\_robustness\_a$pairwise$wadj - FitW3\_robustness\_b$pairwise$wadj  
inputNCTgraph[upper.tri(inputNCTgraph)][which(robustness\_a\_b$einv.pvals$`p-value` >= .05)] <- 0  
inputNCTgraph <- forceSymmetric(inputNCTgraph)  
  
pdf(here("Output", "Supplement", "nct.pdf"))  
nct\_plot = qgraph(inputNCTgraph, labels = shortnames, edge.labels = TRUE)  
dev.off()

## quartz\_off\_screen   
## 2

#Visualize results of centrality tests  
#Calculate strength  
Graph\_robustness\_a <-qgraph(FitW3\_robustness\_a$pairwise$wadj, labels = shortnames)



cent\_robustness\_a <- centralityTable(Graph\_robustness\_a)  
  
Graph\_robustness\_b <-qgraph(FitW3\_robustness\_b$pairwise$wadj, labels = shortnames)



cent\_robustness\_b <- centralityTable(Graph\_robustness\_b)  
  
#isolate what is statistically different  
robustness\_a\_b$diffcen.pval #no differences are statistically significant

## strength  
## vac\_bad 1.000  
## vac\_ob 1.000  
## worry 1.000  
## risk 1.000  
## conspiracy 1.000  
## nat 1.000  
## h\_locus 1.000  
## he\_eco 1.000  
## PTV\_L 1.000  
## PTV\_5SM 1.000  
## PTV\_BOI 1.000  
## tr\_sci 1.000  
## pray 1.000  
## media 1.000  
## sex 1.000  
## age 0.046  
## educ 1.000  
## reg 0.184  
## eco\_insec 1.000  
## hesitancy 1.000  
## low\_comp 1.000  
## distrust\_gov 1.000  
## distrust\_inst 1.000

robustness\_a\_b$diffcen.real #raw differences in centrality

## strength  
## vac\_bad 0.133839956  
## vac\_ob 0.008350283  
## worry 0.098534698  
## risk 0.146727652  
## conspiracy -0.026317984  
## nat 0.184549079  
## h\_locus 0.148037506  
## he\_eco -0.094034582  
## PTV\_L -0.027806009  
## PTV\_5SM 0.176776702  
## PTV\_BOI 0.140999444  
## tr\_sci 0.086101789  
## pray 0.258077991  
## media 0.189061865  
## sex 0.097210152  
## age 0.420278912  
## educ 0.168005877  
## reg 0.123570893  
## eco\_insec 0.161828352  
## hesitancy 0.092382804  
## low\_comp 0.191480095  
## distrust\_gov 0.004318075  
## distrust\_inst 0.162524112

## Backbone (Article)

#model selection  
backbone.suggest(FitW3$pairwise$wadj)

## The disparity filter is suggested. Type "?disparity" for more information.

# application of the disparity filter  
backbone\_matrix <- disparity(  
 inputGraphMGM,  
 alpha = 0.05,  
 signed = FALSE,  
 mtc = "none",  
 class = "original",  
 narrative = TRUE)

##

## === Suggested manuscript text and citations ===

## We used the backbone package for R (v2.1.2; Neal, 2022) to extract the unweighted backbone of a weighted and undirected unipartite network containing 23 nodes. An edge was retained in the backbone if its weight was statistically significant (alpha = 0.05) using the disparity filter (Serrano et al., 2009). This reduced the number of edges by 82%, and reduced the number of connected nodes by 26.1%.

##

## Neal, Z. P. 2022. backbone: An R Package to Extract Network Backbones. PLOS ONE, 17, e0269137. https://doi.org/10.1371/journal.pone.0269137

##

## Serrano, M. A., Boguna, M., & Vespignani, A. (2009). Extracting the multiscale backbone of complex weighted networks. Proceedings of the National Academy of Sciences, 106(16), 6483-6488. https://doi.org/10.1073/pnas.0808904106

#plot  
set.seed(100)  
GraphMGM<-qgraph(backbone\_matrix,   
 layout = "spring", theme = "Borkulo",   
 labels = shortnames,nodeNames = longnames,  
 details = FALSE, vsize=6.0, shape = shapes,  
 groups=Totalgroup\_comm, color= Totalgroup\_cols,  
 legend = TRUE, legend.cex = 0.35, borders = FALSE,   
 filetype="jpg", filename=here("Output", "Article", "backbone.jpg"))

## Output stored in /Users/art/Documents/Github/lavori in corso/papers/vaccine/Processing//Users/art/Documents/Github/lavori in corso/papers/vaccine/Output/Article/backbone.jpg.jpg

## Regressions (Supplement S1)

#Fitting logistic regressions  
model\_vac\_bad <- glm( hesitancy ~ vac\_bad + sex + age + educ + reg + eco\_insec,   
 data = W3, family = binomial)  
  
model\_vac\_ob <- glm( hesitancy ~ vac\_ob + sex + age + educ + reg + eco\_insec,   
 data = W3, family = binomial)  
  
model\_worry <- glm( hesitancy ~ worry + sex + age + educ + reg + eco\_insec,   
 data = W3, family = binomial)  
  
model\_risk <- glm( hesitancy ~ risk + sex + age + educ + reg + eco\_insec,   
 data = W3, family = binomial)  
  
model\_conspiracy <- glm( hesitancy ~ conspiracy + sex + age + educ + reg + eco\_insec,   
 data = W3, family = binomial)  
  
model\_nat <- glm( hesitancy ~ nat + sex + age + educ + reg + eco\_insec,   
 data = W3, family = binomial)  
  
model\_h\_locus <- glm( hesitancy ~ h\_locus + sex + age + educ + reg + eco\_insec,   
 data = W3, family = binomial)  
  
model\_he\_eco <- glm( hesitancy ~ he\_eco + sex + age + educ + reg + eco\_insec,   
 data = W3, family = binomial)  
  
model\_PTV\_L <- glm( hesitancy ~ PTV\_L + sex + age + educ + reg + eco\_insec,   
 data = W3, family = binomial)  
  
model\_PTV\_5SM <- glm( hesitancy ~ PTV\_5SM + sex + age + educ + reg + eco\_insec,   
 data = W3, family = binomial)  
  
model\_PTV\_BOI <- glm( hesitancy ~ PTV\_BOI + sex + age + educ + reg + eco\_insec,   
 data = W3, family = binomial)  
  
model\_tr\_sci <- glm( hesitancy ~ tr\_sci + sex + age + educ + reg + eco\_insec,   
 data = W3, family = binomial)  
  
model\_pray <- glm( hesitancy ~ pray + sex + age + educ + reg + eco\_insec,   
 data = W3, family = binomial)  
  
model\_media <- glm( hesitancy ~ media + sex + age + educ + reg + eco\_insec,   
 data = W3, family = binomial)  
  
model\_low\_comp <- glm( hesitancy ~ low\_comp + sex + age + educ + reg + eco\_insec,   
 data = W3, family = binomial)  
  
model\_distrust\_gov <- glm( hesitancy ~ distrust\_gov + sex + age + educ + reg + eco\_insec,   
 data = W3, family = binomial)  
  
model\_distrust\_inst <- glm( hesitancy ~ distrust\_inst + sex + age + educ + reg + eco\_insec,   
 data = W3, family = binomial)  
  
#Additional model for final table  
model\_educ <- glm( hesitancy ~ educ + sex + age + reg + eco\_insec,   
 data = W3, family = binomial)  
 #coeff  
 coeff\_educ = exp(extract\_numeric(model\_educ$coefficients[2]))

## extract\_numeric() is deprecated: please use readr::parse\_number() instead

#significance  
 summary(model\_educ)$coeff[-1,4] < 0.05

## educ sex age reg eco\_insec   
## TRUE TRUE FALSE FALSE TRUE

## Export regression table for additional material (Supplement S1)

#model\_vac\_bad  
tab\_model(list(model\_vac\_bad),  
 show.p = TRUE,  
 p.style = "stars",  
 p.threshold = c(0.1, 0.05, 0.01),  
 dv.labels = c("vac\_bad"),  
 collapse.ci = TRUE,  
 show.aic = TRUE,  
 title = "Logit regression model on vaccine hesitancy",  
 string.pred = " ",  
 auto.label = FALSE,   
 file = here("Output", "Supplement", "regressions", "model\_vac\_bad.doc")  
)

Logit regression model on vaccine hesitancy

vac\_bad

Odds Ratios

(Intercept)

0.00 \*\*\*(0.00 – 0.01)

vac\_bad

3.39 \*\*\*(2.95 – 3.93)

sex

1.04 (0.75 – 1.44)

age

1.01 \*\*(1.00 – 1.02)

educ

1.28 (0.90 – 1.83)

reg

1.12 (0.80 – 1.55)

eco\_insec

1.06 (0.82 – 1.35)

Observations

1540

R2 Tjur

0.319

AIC

986.178

* p<0.1   \*\* p<0.05   \*\*\* p<0.01

#model\_vac\_ob  
tab\_model(list(model\_vac\_ob),  
 show.p = TRUE,  
 p.style = "stars",  
 p.threshold = c(0.1, 0.05, 0.01),  
 dv.labels = c("vac\_ob"),  
 collapse.ci = TRUE,  
 show.aic = TRUE,  
 title = "Logit regression model on vaccine hesitancy",  
 string.pred = " ",  
 auto.label = FALSE,   
 file = here("Output", "Supplement", "regressions", "model\_vac\_ob.doc")  
)

Logit regression model on vaccine hesitancy

vac\_ob

Odds Ratios

(Intercept)

0.00 \*\*\*(0.00 – 0.00)

vac\_ob

5.67 \*\*\*(4.71 – 6.94)

sex

0.98 (0.67 – 1.43)

age

1.01 \*(1.00 – 1.03)

educ

1.61 \*\*(1.07 – 2.43)

reg

1.09 (0.74 – 1.60)

eco\_insec

0.79 (0.58 – 1.07)

Observations

1540

R2 Tjur

0.509

AIC

736.441

* p<0.1   \*\* p<0.05   \*\*\* p<0.01

#model\_worry  
tab\_model(list(model\_worry),  
 show.p = TRUE,  
 p.style = "stars",  
 p.threshold = c(0.1, 0.05, 0.01),  
 dv.labels = c("worry"),  
 collapse.ci = TRUE,  
 show.aic = TRUE,  
 title = "Logit regression model on vaccine hesitancy",  
 string.pred = " ",  
 auto.label = FALSE,   
 file = here("Output", "Supplement", "regressions", "model\_worry.doc")  
)

Logit regression model on vaccine hesitancy

worry

Odds Ratios

(Intercept)

0.05 \*\*\*(0.02 – 0.11)

worry

1.12 (0.84 – 1.50)

sex

1.41 \*\*(1.08 – 1.85)

age

1.00 (0.99 – 1.01)

educ

1.77 \*\*\*(1.32 – 2.39)

reg

1.07 (0.82 – 1.40)

eco\_insec

1.26 \*\*(1.02 – 1.56)

Observations

1540

R2 Tjur

0.021

AIC

1394.191

* p<0.1   \*\* p<0.05   \*\*\* p<0.01

#model\_risk  
tab\_model(list(model\_risk),  
 show.p = TRUE,  
 p.style = "stars",  
 p.threshold = c(0.1, 0.05, 0.01),  
 dv.labels = c("risk"),  
 collapse.ci = TRUE,  
 show.aic = TRUE,  
 title = "Logit regression model on vaccine hesitancy",  
 string.pred = " ",  
 auto.label = FALSE,   
 file = here("Output", "Supplement", "regressions", "model\_risk.doc")  
)

Logit regression model on vaccine hesitancy

risk

Odds Ratios

(Intercept)

0.02 \*\*\*(0.01 – 0.06)

risk

1.31 \*\*\*(1.10 – 1.57)

sex

1.40 \*\*(1.07 – 1.84)

age

1.00 (0.99 – 1.01)

educ

1.76 \*\*\*(1.31 – 2.38)

reg

1.05 (0.80 – 1.38)

eco\_insec

1.28 \*\*(1.04 – 1.58)

Observations

1540

R2 Tjur

0.027

AIC

1385.843

* p<0.1   \*\* p<0.05   \*\*\* p<0.01

#model\_conspiracy  
tab\_model(list(model\_conspiracy),  
 show.p = TRUE,  
 p.style = "stars",  
 p.threshold = c(0.1, 0.05, 0.01),  
 dv.labels = c("conspiracy"),  
 collapse.ci = TRUE,  
 show.aic = TRUE,  
 title = "Logit regression model on vaccine hesitancy",  
 string.pred = " ",  
 auto.label = FALSE,   
 file = here("Output", "Supplement", "regressions", "model\_conspiracy.doc")  
)

Logit regression model on vaccine hesitancy

conspiracy

Odds Ratios

(Intercept)

0.03 \*\*\*(0.01 – 0.07)

conspiracy

5.18 \*\*\*(3.79 – 7.17)

sex

1.31 \*(0.99 – 1.74)

age

1.01 (1.00 – 1.02)

educ

1.44 \*\*(1.06 – 1.96)

reg

1.05 (0.79 – 1.39)

eco\_insec

1.12 (0.90 – 1.38)

Observations

1540

R2 Tjur

0.095

AIC

1273.608

* p<0.1   \*\* p<0.05   \*\*\* p<0.01

#model\_nat  
tab\_model(list(model\_nat),  
 show.p = TRUE,  
 p.style = "stars",  
 p.threshold = c(0.1, 0.05, 0.01),  
 dv.labels = c("nat"),  
 collapse.ci = TRUE,  
 show.aic = TRUE,  
 title = "Logit regression model on vaccine hesitancy",  
 string.pred = " ",  
 auto.label = FALSE,   
 file = here("Output", "Supplement", "regressions", "model\_nat.doc")  
)

Logit regression model on vaccine hesitancy

nat

Odds Ratios

(Intercept)

0.02 \*\*\*(0.01 – 0.04)

nat

1.32 \*\*\*(1.26 – 1.39)

sex

1.17 (0.88 – 1.55)

age

1.01 \*\*(1.00 – 1.02)

educ

1.48 \*\*(1.09 – 2.03)

reg

1.00 (0.75 – 1.33)

eco\_insec

1.18 (0.94 – 1.47)

Observations

1540

R2 Tjur

0.119

AIC

1251.696

* p<0.1   \*\* p<0.05   \*\*\* p<0.01

#model\_h\_locus  
tab\_model(list(model\_h\_locus),  
 show.p = TRUE,  
 p.style = "stars",  
 p.threshold = c(0.1, 0.05, 0.01),  
 dv.labels = c("h\_locus"),  
 collapse.ci = TRUE,  
 show.aic = TRUE,  
 title = "Logit regression model on vaccine hesitancy",  
 string.pred = " ",  
 auto.label = FALSE,   
 file = here("Output", "Supplement", "regressions", "model\_h\_locus.doc")  
)

Logit regression model on vaccine hesitancy

h\_locus

Odds Ratios

(Intercept)

0.29 \*\*\*(0.13 – 0.65)

h\_locus

0.78 \*\*\*(0.74 – 0.82)

sex

1.47 \*\*\*(1.11 – 1.95)

age

1.00 (0.99 – 1.01)

educ

1.92 \*\*\*(1.41 – 2.62)

reg

1.07 (0.81 – 1.42)

eco\_insec

1.17 (0.94 – 1.45)

Observations

1540

R2 Tjur

0.095

AIC

1295.937

* p<0.1   \*\* p<0.05   \*\*\* p<0.01

#model\_he\_eco  
tab\_model(list(model\_he\_eco),  
 show.p = TRUE,  
 p.style = "stars",  
 p.threshold = c(0.1, 0.05, 0.01),  
 dv.labels = c("he\_eco"),  
 collapse.ci = TRUE,  
 show.aic = TRUE,  
 title = "Logit regression model on vaccine hesitancy",  
 string.pred = " ",  
 auto.label = FALSE,   
 file = here("Output", "Supplement", "regressions", "model\_he\_eco.doc")  
)

Logit regression model on vaccine hesitancy

he\_eco

Odds Ratios

(Intercept)

0.02 \*\*\*(0.01 – 0.05)

he\_eco

1.24 \*\*\*(1.17 – 1.31)

sex

1.49 \*\*\*(1.13 – 1.96)

age

1.00 (0.99 – 1.01)

educ

1.67 \*\*\*(1.23 – 2.26)

reg

1.06 (0.80 – 1.39)

eco\_insec

1.22 \*(0.98 – 1.50)

Observations

1540

R2 Tjur

0.065

AIC

1332.312

* p<0.1   \*\* p<0.05   \*\*\* p<0.01

#model\_PTV\_L  
tab\_model(list(model\_PTV\_L),  
 show.p = TRUE,  
 p.style = "stars",  
 p.threshold = c(0.1, 0.05, 0.01),  
 dv.labels = c("PTV\_L"),  
 collapse.ci = TRUE,  
 show.aic = TRUE,  
 title = "Logit regression model on vaccine hesitancy",  
 string.pred = " ",  
 auto.label = FALSE,   
 file = here("Output", "Supplement", "regressions", "model\_PTV\_L.doc")  
)

Logit regression model on vaccine hesitancy

PTV\_L

Odds Ratios

(Intercept)

0.04 \*\*\*(0.02 – 0.08)

PTV\_L

1.13 \*\*\*(1.09 – 1.17)

sex

1.37 \*\*(1.04 – 1.80)

age

1.01 (1.00 – 1.02)

educ

1.60 \*\*\*(1.19 – 2.17)

reg

1.02 (0.77 – 1.35)

eco\_insec

1.29 \*\*(1.05 – 1.60)

Observations

1540

R2 Tjur

0.047

AIC

1350.314

* p<0.1   \*\* p<0.05   \*\*\* p<0.01

#model\_PTV\_5SM  
tab\_model(list(model\_PTV\_5SM),  
 show.p = TRUE,  
 p.style = "stars",  
 p.threshold = c(0.1, 0.05, 0.01),  
 dv.labels = c("PTV\_5SM"),  
 collapse.ci = TRUE,  
 show.aic = TRUE,  
 title = "Logit regression model on vaccine hesitancy",  
 string.pred = " ",  
 auto.label = FALSE,   
 file = here("Output", "Supplement", "regressions", "model\_PTV\_5SM.doc")  
)

Logit regression model on vaccine hesitancy

PTV\_5SM

Odds Ratios

(Intercept)

0.06 \*\*\*(0.03 – 0.12)

PTV\_5SM

0.98 (0.94 – 1.02)

sex

1.41 \*\*(1.08 – 1.84)

age

1.00 (0.99 – 1.01)

educ

1.79 \*\*\*(1.33 – 2.42)

reg

1.07 (0.82 – 1.41)

eco\_insec

1.26 \*\*(1.02 – 1.55)

Observations

1540

R2 Tjur

0.021

AIC

1393.970

* p<0.1   \*\* p<0.05   \*\*\* p<0.01

#model\_PTV\_BOI  
tab\_model(list(model\_PTV\_BOI),  
 show.p = TRUE,  
 p.style = "stars",  
 p.threshold = c(0.1, 0.05, 0.01),  
 dv.labels = c("PTV\_BOI"),  
 collapse.ci = TRUE,  
 show.aic = TRUE,  
 title = "Logit regression model on vaccine hesitancy",  
 string.pred = " ",  
 auto.label = FALSE,   
 file = here("Output", "Supplement", "regressions", "model\_PTV\_BOI.doc")  
)

Logit regression model on vaccine hesitancy

PTV\_BOI

Odds Ratios

(Intercept)

0.03 \*\*\*(0.02 – 0.07)

PTV\_BOI

1.15 \*\*\*(1.11 – 1.19)

sex

1.43 \*\*(1.09 – 1.89)

age

1.01 (1.00 – 1.02)

educ

1.59 \*\*\*(1.18 – 2.16)

reg

1.03 (0.78 – 1.36)

eco\_insec

1.29 \*\*(1.05 – 1.60)

Observations

1540

R2 Tjur

0.054

AIC

1340.696

* p<0.1   \*\* p<0.05   \*\*\* p<0.01

#model\_tr\_sci  
tab\_model(list(model\_tr\_sci),  
 show.p = TRUE,  
 p.style = "stars",  
 p.threshold = c(0.1, 0.05, 0.01),  
 dv.labels = c("tr\_sci"),  
 collapse.ci = TRUE,  
 show.aic = TRUE,  
 title = "Logit regression model on vaccine hesitancy",  
 string.pred = " ",  
 auto.label = FALSE,   
 file = here("Output", "Supplement", "regressions", "model\_tr\_sci.doc")  
)

Logit regression model on vaccine hesitancy

tr\_sci

Odds Ratios

(Intercept)

0.00 \*\*\*(0.00 – 0.01)

tr\_sci

3.37 \*\*\*(2.93 – 3.91)

sex

1.22 (0.89 – 1.68)

age

1.01 \*\*(1.00 – 1.03)

educ

1.58 \*\*(1.11 – 2.25)

reg

0.96 (0.69 – 1.32)

eco\_insec

1.04 (0.81 – 1.34)

Observations

1540

R2 Tjur

0.300

AIC

1015.488

* p<0.1   \*\* p<0.05   \*\*\* p<0.01

#model\_pray  
tab\_model(list(model\_pray),  
 show.p = TRUE,  
 p.style = "stars",  
 p.threshold = c(0.1, 0.05, 0.01),  
 dv.labels = c("pray"),  
 collapse.ci = TRUE,  
 show.aic = TRUE,  
 title = "Logit regression model on vaccine hesitancy",  
 string.pred = " ",  
 auto.label = FALSE,   
 file = here("Output", "Supplement", "regressions", "model\_pray.doc")  
)

Logit regression model on vaccine hesitancy

pray

Odds Ratios

(Intercept)

0.06 \*\*\*(0.03 – 0.13)

pray

0.79 \*(0.60 – 1.04)

sex

1.37 \*\*(1.05 – 1.80)

age

1.00 (1.00 – 1.01)

educ

1.75 \*\*\*(1.30 – 2.37)

reg

1.06 (0.81 – 1.40)

eco\_insec

1.25 \*\*(1.01 – 1.54)

Observations

1540

R2 Tjur

0.022

AIC

1391.908

* p<0.1   \*\* p<0.05   \*\*\* p<0.01

#model\_media  
tab\_model(list(model\_media),  
 show.p = TRUE,  
 p.style = "stars",  
 p.threshold = c(0.1, 0.05, 0.01),  
 dv.labels = c("media"),  
 collapse.ci = TRUE,  
 show.aic = TRUE,  
 title = "Logit regression model on vaccine hesitancy",  
 string.pred = " ",  
 auto.label = FALSE,   
 file = here("Output", "Supplement", "regressions", "model\_media.doc")  
)

Logit regression model on vaccine hesitancy

media

Odds Ratios

(Intercept)

0.06 \*\*\*(0.03 – 0.12)

media

0.99 (0.75 – 1.30)

sex

1.41 \*\*(1.07 – 1.84)

age

1.00 (0.99 – 1.01)

educ

1.76 \*\*\*(1.31 – 2.38)

reg

1.07 (0.82 – 1.41)

eco\_insec

1.26 \*\*(1.02 – 1.55)

Observations

1540

R2 Tjur

0.020

AIC

1394.798

* p<0.1   \*\* p<0.05   \*\*\* p<0.01

#model\_low\_comp  
tab\_model(list(model\_low\_comp),  
 show.p = TRUE,  
 p.style = "stars",  
 p.threshold = c(0.1, 0.05, 0.01),  
 dv.labels = c("low\_comp"),  
 collapse.ci = TRUE,  
 show.aic = TRUE,  
 title = "Logit regression model on vaccine hesitancy",  
 string.pred = " ",  
 auto.label = FALSE,   
 file = here("Output", "Supplement", "regressions", "model\_low\_comp.doc")  
)

Logit regression model on vaccine hesitancy

low\_comp

Odds Ratios

(Intercept)

0.03 \*\*\*(0.02 – 0.07)

low\_comp

1.57 \*\*\*(1.45 – 1.69)

sex

1.98 \*\*\*(1.47 – 2.69)

age

0.99 (0.98 – 1.00)

educ

1.81 \*\*\*(1.32 – 2.50)

reg

0.97 (0.72 – 1.30)

eco\_insec

1.29 \*\*(1.03 – 1.61)

Observations

1540

R2 Tjur

0.152

AIC

1234.701

* p<0.1   \*\* p<0.05   \*\*\* p<0.01

#model\_distrust\_gov  
tab\_model(list(model\_distrust\_gov),  
 show.p = TRUE,  
 p.style = "stars",  
 p.threshold = c(0.1, 0.05, 0.01),  
 dv.labels = c("distrust\_gov"),  
 collapse.ci = TRUE,  
 show.aic = TRUE,  
 title = "Logit regression model on vaccine hesitancy",  
 string.pred = " ",  
 auto.label = FALSE,   
 file = here("Output", "Supplement", "regressions", "model\_distrust\_gov.doc")  
)

Logit regression model on vaccine hesitancy

distrust\_gov

Odds Ratios

(Intercept)

0.02 \*\*\*(0.01 – 0.04)

distrust\_gov

1.43 \*\*\*(1.34 – 1.52)

sex

1.39 \*\*(1.04 – 1.84)

age

1.00 (0.99 – 1.01)

educ

1.78 \*\*\*(1.30 – 2.43)

reg

0.98 (0.73 – 1.31)

eco\_insec

0.98 (0.78 – 1.22)

Observations

1540

R2 Tjur

0.125

AIC

1254.662

* p<0.1   \*\* p<0.05   \*\*\* p<0.01

#model\_distrust\_inst  
tab\_model(list(model\_distrust\_inst),  
 show.p = TRUE,  
 p.style = "stars",  
 p.threshold = c(0.1, 0.05, 0.01),  
 dv.labels = c("distrust\_inst"),  
 collapse.ci = TRUE,  
 show.aic = TRUE,  
 title = "Logit regression model on vaccine hesitancy",  
 string.pred = " ",  
 auto.label = FALSE,   
 file = here("Output", "Supplement", "regressions", "model\_distrust\_inst.doc")  
)

Logit regression model on vaccine hesitancy

distrust\_inst

Odds Ratios

(Intercept)

0.01 \*\*\*(0.01 – 0.03)

distrust\_inst

1.38 \*\*\*(1.30 – 1.47)

sex

1.46 \*\*\*(1.10 – 1.93)

age

1.01 (1.00 – 1.02)

educ

1.66 \*\*\*(1.22 – 2.26)

reg

1.00 (0.75 – 1.32)

eco\_insec

1.02 (0.82 – 1.27)

Observations

1540

R2 Tjur

0.112

AIC

1271.741

* p<0.1   \*\* p<0.05   \*\*\* p<0.01

#model\_vac\_bad  
tab\_model(list(model\_vac\_bad),  
 show.p = TRUE,  
 p.style = "stars",  
 p.threshold = c(0.1, 0.05, 0.01),  
 dv.labels = c("vac\_bad"),  
 collapse.ci = TRUE,  
 show.aic = TRUE,  
 title = "Logit regression model on vaccine hesitancy",  
 string.pred = " ",  
 auto.label = FALSE,   
 file = here("Output", "Supplement", "regressions", "model\_vac\_bad.doc")  
)

Logit regression model on vaccine hesitancy

vac\_bad

Odds Ratios

(Intercept)

0.00 \*\*\*(0.00 – 0.01)

vac\_bad

3.39 \*\*\*(2.95 – 3.93)

sex

1.04 (0.75 – 1.44)

age

1.01 \*\*(1.00 – 1.02)

educ

1.28 (0.90 – 1.83)

reg

1.12 (0.80 – 1.55)

eco\_insec

1.06 (0.82 – 1.35)

Observations

1540

R2 Tjur

0.319

AIC

986.178

* p<0.1   \*\* p<0.05   \*\*\* p<0.01

#Additional model for final table  
tab\_model(list(model\_educ),  
 show.p = TRUE,  
 p.style = "stars",  
 p.threshold = c(0.1, 0.05, 0.01),  
 dv.labels = c("educ"),  
 collapse.ci = TRUE,  
 show.aic = TRUE,  
 title = "Logit regression model on vaccine hesitancy",  
 string.pred = " ",  
 auto.label = FALSE,   
 file = here("Output", "Supplement", "regressions", "model\_educ.doc")  
)

Logit regression model on vaccine hesitancy

educ

Odds Ratios

(Intercept)

0.06 \*\*\*(0.03 – 0.12)

educ

1.76 \*\*\*(1.31 – 2.38)

sex

1.41 \*\*(1.07 – 1.84)

age

1.00 (0.99 – 1.01)

reg

1.07 (0.82 – 1.41)

eco\_insec

1.26 \*\*(1.02 – 1.55)

Observations

1540

R2 Tjur

0.020

AIC

1392.803

* p<0.1   \*\* p<0.05   \*\*\* p<0.01

## Scatterplot data

#Gathering coefficients  
coeff = extract\_numeric(model\_vac\_bad$coefficients[2])

## extract\_numeric() is deprecated: please use readr::parse\_number() instead

coeff[2] = extract\_numeric(model\_vac\_ob$coefficients[2])

## extract\_numeric() is deprecated: please use readr::parse\_number() instead

coeff[3] = extract\_numeric(model\_worry$coefficients[2])

## extract\_numeric() is deprecated: please use readr::parse\_number() instead

coeff[4] = extract\_numeric(model\_risk$coefficients[2])

## extract\_numeric() is deprecated: please use readr::parse\_number() instead

coeff[5] = extract\_numeric(model\_conspiracy$coefficients[2])

## extract\_numeric() is deprecated: please use readr::parse\_number() instead

coeff[6] = extract\_numeric(model\_nat$coefficients[2])

## extract\_numeric() is deprecated: please use readr::parse\_number() instead

coeff[7] = extract\_numeric(model\_h\_locus$coefficients[2])

## extract\_numeric() is deprecated: please use readr::parse\_number() instead

coeff[8] = extract\_numeric(model\_he\_eco$coefficients[2])

## extract\_numeric() is deprecated: please use readr::parse\_number() instead

coeff[9] = extract\_numeric(model\_PTV\_L$coefficients[2])

## extract\_numeric() is deprecated: please use readr::parse\_number() instead

coeff[10] = extract\_numeric(model\_PTV\_5SM$coefficients[2])

## extract\_numeric() is deprecated: please use readr::parse\_number() instead

coeff[11] = extract\_numeric(model\_PTV\_BOI$coefficients[2])

## extract\_numeric() is deprecated: please use readr::parse\_number() instead

coeff[12] = extract\_numeric(model\_tr\_sci$coefficients[2])

## extract\_numeric() is deprecated: please use readr::parse\_number() instead

coeff[13] = extract\_numeric(model\_pray$coefficients[2])

## extract\_numeric() is deprecated: please use readr::parse\_number() instead

coeff[14] = extract\_numeric(model\_media$coefficients[2])

## extract\_numeric() is deprecated: please use readr::parse\_number() instead

coeff[15] = extract\_numeric(model\_low\_comp$coefficients[2])

## extract\_numeric() is deprecated: please use readr::parse\_number() instead

coeff[16] = extract\_numeric(model\_distrust\_gov$coefficients[2])

## extract\_numeric() is deprecated: please use readr::parse\_number() instead

coeff[17] = extract\_numeric(model\_distrust\_inst$coefficients[2])

## extract\_numeric() is deprecated: please use readr::parse\_number() instead

#Transform in odds ratio  
 coeff\_exp = unlist(lapply(coeff, exp))

#Significance  
summary(model\_vac\_bad)$coeff[-1,4] < 0.05

## vac\_bad sex age educ reg eco\_insec   
## TRUE FALSE TRUE FALSE FALSE FALSE

summary(model\_vac\_ob)$coeff[-1,4] < 0.05

## vac\_ob sex age educ reg eco\_insec   
## TRUE FALSE FALSE TRUE FALSE FALSE

summary(model\_worry)$coeff[-1,4] < 0.05 #not significant

## worry sex age educ reg eco\_insec   
## FALSE TRUE FALSE TRUE FALSE TRUE

summary(model\_risk)$coeff[-1,4] < 0.05

## risk sex age educ reg eco\_insec   
## TRUE TRUE FALSE TRUE FALSE TRUE

summary(model\_conspiracy)$coeff[-1,4] < 0.05

## conspiracy sex age educ reg eco\_insec   
## TRUE FALSE FALSE TRUE FALSE FALSE

summary(model\_nat)$coeff[-1,4] < 0.05

## nat sex age educ reg eco\_insec   
## TRUE FALSE TRUE TRUE FALSE FALSE

summary(model\_h\_locus)$coeff[-1,4] < 0.05

## h\_locus sex age educ reg eco\_insec   
## TRUE TRUE FALSE TRUE FALSE FALSE

summary(model\_he\_eco)$coeff[-1,4] < 0.05

## he\_eco sex age educ reg eco\_insec   
## TRUE TRUE FALSE TRUE FALSE FALSE

summary(model\_PTV\_L)$coeff[-1,4] < 0.05

## PTV\_L sex age educ reg eco\_insec   
## TRUE TRUE FALSE TRUE FALSE TRUE

summary(model\_PTV\_5SM)$coeff[-1,4] < 0.05 #not significant

## PTV\_5SM sex age educ reg eco\_insec   
## FALSE TRUE FALSE TRUE FALSE TRUE

summary(model\_PTV\_BOI)$coeff[-1,4] < 0.05

## PTV\_BOI sex age educ reg eco\_insec   
## TRUE TRUE FALSE TRUE FALSE TRUE

summary(model\_tr\_sci)$coeff[-1,4] < 0.05

## tr\_sci sex age educ reg eco\_insec   
## TRUE FALSE TRUE TRUE FALSE FALSE

summary(model\_pray)$coeff[-1,4] < 0.05 #not significant

## pray sex age educ reg eco\_insec   
## FALSE TRUE FALSE TRUE FALSE TRUE

summary(model\_media)$coeff[-1,4] < 0.05 #not significant

## media sex age educ reg eco\_insec   
## FALSE TRUE FALSE TRUE FALSE TRUE

summary(model\_low\_comp)$coeff[-1,4] < 0.05

## low\_comp sex age educ reg eco\_insec   
## TRUE TRUE FALSE TRUE FALSE TRUE

summary(model\_distrust\_gov)$coeff[-1,4] < 0.05

## distrust\_gov sex age educ reg eco\_insec   
## TRUE TRUE FALSE TRUE FALSE FALSE

summary(model\_distrust\_inst)$coeff[-1,4] < 0.05

## distrust\_inst sex age educ reg   
## TRUE TRUE FALSE TRUE FALSE   
## eco\_insec   
## FALSE

#vector for significance  
 Significance = rep(c("Significant"),17)  
 Significance[3] = "Not significant"  
 Significance[10] = "Not significant"  
 Significance[13] = "Not significant"  
 Significance[14] = "Not significant"

#Gatering strength scores  
strength = centMGM %>%  
 filter(measure=="Strength") %>%   
 dplyr::select(value) %>%  
 filter(!row\_number() %in% c(15:20))  
  
cent\_all = centMGM %>%  
 filter(measure=="Strength") %>%   
 dplyr::select(value, node) %>%   
 mutate\_if(is.numeric, ~round(., 2))

#Gatering degree  
degree\_cent\_graph = degree\_cent[-c(15:20)]

#Gathering names  
names = shortnames  
names = names[-c(15:20)]

#Merging into a df1 (Reported in Supplement S1)  
scatterplot = data.frame(names, coeff\_exp, strength, Significance) %>%   
 rename(strength = value)  
scatterplot$names = as.factor(scatterplot$names)  
scatterplot$coeff\_exp = as.numeric(scatterplot$coeff\_exp)  
scatterplot$strength = as.numeric(scatterplot$strength)  
scatterplot$Significance = as.factor(scatterplot$Significance)  
  
#Merging into a df2  
scatterplot\_degree = data.frame(names, coeff\_exp, degree\_cent\_graph, Significance)  
scatterplot\_degree$degree\_cent\_graph = as.numeric(scatterplot\_degree$degree\_cent\_graph)  
  
print(scatterplot\_degree)

## names coeff\_exp degree\_cent\_graph Significance  
## 1 vac\_bad 3.3883357 10 Significant  
## 2 vac\_free 5.6708848 4 Significant  
## 3 low\_worry 1.1215813 6 Not significant  
## 4 low\_risk 1.3108932 2 Significant  
## 5 conspiracy 5.1779681 15 Significant  
## 6 nat 1.3207578 15 Significant  
## 7 int\_locus 0.7773671 8 Significant  
## 8 low\_col\_resp 1.2379600 11 Significant  
## 9 PTV\_L 1.1313915 5 Significant  
## 10 PTV\_5SM 0.9810478 7 Not significant  
## 11 PTV\_BOI 1.1476554 6 Significant  
## 12 distrust\_sci 3.3740932 10 Significant  
## 13 pray 0.7902768 15 Not significant  
## 14 media 0.9895658 5 Not significant  
## 15 low\_comp 1.5665293 12 Significant  
## 16 distrust\_gov 1.4257922 16 Significant  
## 17 distrust\_inst 1.3790392 9 Significant

## Scatterplots

#Strength (Article)  
graph\_strength = ggplot(scatterplot, aes(x=strength, y=coeff\_exp, label = names)) +   
 geom\_point((aes(color=Significance))) + theme\_nice() +   
 geom\_smooth(method=lm, se = FALSE, linetype = "dotted", color = "#DCDCDC") +  
 geom\_text\_repel(size = 3) +  
 xlab("Strength centrality") + ylab("Regression coefficient") +   
 scale\_fill\_discrete(labels=c('label1', 'label2'))  
  
ggsave(here("Output", "Article", "graph\_strength.jpg"), graph\_strength, height = 5, width = 8)

## `geom\_smooth()` using formula = 'y ~ x'

## Warning: The following aesthetics were dropped during statistical transformation: label  
## ℹ This can happen when ggplot fails to infer the correct grouping structure in  
## the data.  
## ℹ Did you forget to specify a `group` aesthetic or to convert a numerical  
## variable into a factor?

#Degree (Supplement S1)  
graph\_degree = ggplot(scatterplot\_degree, aes(x=degree\_cent\_graph, y=coeff\_exp, label = names)) +   
 geom\_point((aes(color=Significance))) + theme\_nice() +   
 geom\_smooth(method=lm, se = FALSE, linetype = "dotted", color = "#DCDCDC") +  
 geom\_text\_repel(size = 3) +  
 xlab("Degree centrality") + ylab("Regression coefficient") +   
 scale\_fill\_discrete(labels=c('label1', 'label2'))  
  
ggsave(here("Output", "Supplement", "graph\_degree.jpg"), graph\_degree, height = 5, width = 8)

## `geom\_smooth()` using formula = 'y ~ x'

## Warning: The following aesthetics were dropped during statistical transformation: label  
## ℹ This can happen when ggplot fails to infer the correct grouping structure in  
## the data.  
## ℹ Did you forget to specify a `group` aesthetic or to convert a numerical  
## variable into a factor?

## Final table empirical predictors (Article)

#Df with variables that (1) are tied to hesitancy, (2) are in the backbone  
final\_tab = scatterplot %>%   
 mutate(degree = scatterplot\_degree$degree\_cent\_graph) %>%   
 add\_row(names = "educ", coeff\_exp = 1.764247, strength = 1.0869328,   
 Significance = "Significant", degree = 10) %>%   
 filter(names %in% c("vac\_free","vac\_bad","low\_comp","conspiracy","nat","educ")) %>%   
 mutate(edge\_weight=c(0.34, 0.95, 0.12, 0.07, 0.34, 0.07)) %>% #adding edge weights  
 relocate(Significance, .after = edge\_weight)   
  
 #conversion of type  
 final\_tab$names = as.factor(final\_tab$names)  
 final\_tab$coeff\_exp = as.numeric(final\_tab$coeff\_exp)  
 final\_tab$strength = as.numeric(final\_tab$strength)  
 final\_tab$degree = as.numeric(final\_tab$degree)  
 final\_tab$edge\_weight = as.numeric(final\_tab$edge\_weight)  
 final\_tab$Significance = as.factor(final\_tab$Significance)  
  
#Z scores  
final\_tab\_z = final\_tab %>%   
 mutate(coeff\_exp = (coeff\_exp - mean(coeff\_exp))/sd(coeff\_exp),   
 strength = (strength - mean(strength))/sd(strength),  
 degree = (degree - mean(degree))/sd(degree),  
 edge\_weight = (edge\_weight - mean(edge\_weight))/sd(edge\_weight)) %>%   
 mutate\_if(is.numeric, ~round(., 2)) %>%   
 arrange(desc(coeff\_exp)) %>%   
 dplyr::select(names, coeff\_exp, edge\_weight, strength, degree, Significance)  
  
final\_tab

## names coeff\_exp strength degree edge\_weight Significance  
## 1 vac\_bad 3.388336 1.612156 10 0.34 Significant  
## 2 vac\_free 5.670885 1.340933 4 0.95 Significant  
## 3 conspiracy 5.177968 1.833237 15 0.12 Significant  
## 4 nat 1.320758 1.272407 15 0.07 Significant  
## 5 low\_comp 1.566529 1.470828 12 0.34 Significant  
## 6 educ 1.764247 1.086933 10 0.07 Significant

final\_tab\_z

## names coeff\_exp edge\_weight strength degree Significance  
## 1 vac\_free 1.32 1.89 -0.36 -1.71 Significant  
## 2 conspiracy 1.06 -0.58 1.51 0.98 Significant  
## 3 vac\_bad 0.13 0.07 0.67 -0.24 Significant  
## 4 educ -0.72 -0.73 -1.32 -0.24 Significant  
## 5 low\_comp -0.83 0.07 0.13 0.24 Significant  
## 6 nat -0.96 -0.73 -0.62 0.98 Significant

#Table strength and degree centrality of each node (Supplement)  
table\_cent = cent\_all  
table\_cent[,3]= degree\_data[,2]  
table\_cent = table\_cent %>% dplyr::select(node, value, V3) %>%   
 rename(Strength = value, Degree = V3)  
  
table\_cent

## node Strength Degree  
## 1 Vaccine bad for health 1.61 10  
## 2 Against mandatory vaccination 1.34 4  
## 3 Low worry about infection 0.75 6  
## 4 Low risk perception 0.28 2  
## 5 Endorsing conspiracy theories 1.83 15  
## 6 Trust in alternative medicine 1.27 15  
## 7 Internal health locus of control 0.54 8  
## 8 Low sense of collective responsability 0.79 11  
## 9 Propensity to vote for L 1.12 5  
## 10 Propensity to vote for 5SM 0.74 7  
## 11 Propensity to vote for BOI 1.01 6  
## 12 Distrust of science 1.22 10  
## 13 Religion, pray 1.49 15  
## 14 Digital media diet 0.48 5  
## 15 Sex, female 1.01 10  
## 16 Age, young 1.24 11  
## 17 Educational level, low 1.09 10  
## 18 Living in a rural region 0.47 9  
## 19 Economic insecurity 0.64 9  
## 20 Vaccine hesitancy 2.13 7  
## 21 Low compliance with preventive behaviors 1.47 12  
## 22 Disapproval of Government 1.50 16  
## 23 Distrust of institutions 1.20 9

# Output

## Export heavy objects

#communities  
saveRDS(CommunityStabTotal, here("Input", "CommunityStabTotal.rds"))  
#bootnet  
saveRDS(edgeacc, here("Input","edgeacc.rds"))  
saveRDS(centstab, here("Input", "centstab.rds"))  
#final tab  
saveRDS(final\_tab, here("Input", "final\_tab.rds"))  
saveRDS(final\_tab\_z, here("Input", "final\_tab\_z.rds"))

## Edge weight to excel (Supplement S1)

##only upper triangle without edge weigths 0 for readability  
EdgeWeight\_Total\_half<-upper.triangle(inputGraphMGM)  
EdgeWeight\_Total\_half[EdgeWeight\_Total\_half == 0] <- NA  
EdgeWeightsExcel\_half<- list("mgm" = EdgeWeight\_Total\_half)  
write.xlsx(EdgeWeightsExcel\_half, "../Output/Supplement/EdgeWeightsExcel\_half.xlsx",  
 colWidths = "auto", rowNames = TRUE)