An Online Application to Explain Community Immunity with Personalized Avatars: A Randomized Controlled Trial

Hina Hakim, Julie A Bettinger, Christine T. Chambers, S. Michelle Driedger, Eve Dubé, Teresa Gavaruzzi, Anik Giguere, Noah M. Ivers, Anne-Sophie Julien, Shannon E. MacDonald, Magniol Noubi, Rita Orji, Elizabeth Parent, Beate Sander, Aaron M. Scherer, Kumanan Wilson, Daniel Reinharz, Holly O. Witteman

Authors information:

Hina Hakim
Title: Dr.
Role : Research Associate
Qualifications: B.D.S, M.Sc, PhD
Affiliated institute: Department of Family and Emergency Medicine, Laval University, Quebec City, QC, Canada
VITAM Research Centre for Sustainable Health & Research Centre of the CHU de Québec-Université Laval.
Institutional address: 1050 avenue de la Médecine, Pavillon Ferdinand-Vandry 4204, Université Laval, Québec City, Québec, G1V 0A6, Canada,
Email: hina.hakim.1@ulaval.ca
ORCID: 0000-0003-0517-2621

Dr. Julie A Bettinger
Title : Dr.
Role : Professor
Qualifications: MPH PhD
Affiliated institute: Vaccine Evaluation Center, BC Children's Hospital, University of British Columbia
Institutional address: 950 West 28th Ave, Vancouver, BC V5Z 4H4
Email:jbettinger@bcchr.ubc.ca
ORCID:0000-0002-2118-4174

Christine T. Chambers
Title (Dr., Ms., Prof., etc.): Dr.
Role : Professor & Canada Research Chair
Qualifications (BSc, M.Sc, PhD, etc.): PhD
Affiliated institute: Departments of Psychology and Neuroscience and Pediatrics, Dalhousie University, Halifax, NS, Canada
Institutional address: IWK Health Centre, Centre for Pediatric Pain Research, 5850/5980 University Avenue, Halifax, Nova Scotia, B3K 6R8 Canada
Email:christine.chambers@dal.ca
ORCID: 0000-0002-7138-916X

S. Michelle Driedger
Title: Dr.
Role: Professor
Qualifications (BSc, M.Sc, PhD, etc.): PhD
Affiliated institute: Department of Community Health Sciences, University of Manitoba, Winnipeg, MB, Canada

Institutional address: S113-750 Bannatyne Avenue, Winnipeg, MB, R3E 0W3
Email: Michelle.Driedger@umanitoba.ca
ORCID: 0000-0003-3769-5785

Eve Dubé
Title: Dr.
Role: Adjunct Professor
Qualifications (BSc, M.Sc, PhD, etc.): PhD
Affiliated institute: Department of Anthropology, Laval University Quebec City, QC, Canada
Institutional address: 1030 Avenue des Sciences Humaines
Email: eve.dube@ant.ulaval.ca
ORCID: 0000-0003-1336-1510

Teresa Gavaruzzi
Title: Dr.
Role : Assistant Professor
Qualifications (BSc, M.Sc, PhD etc.): PhD
Affiliated institute: Department of Medical and Surgical Sciences, University of Bologna, Italy
Institutional address: PSYMED c/o Policlinico S. Orsola - Malpighi - PAD 21, 2° Piano
Via Massarenti 9 - 40138 Bologna- Italy
Email: teresa.gavaruzzi@unibo.it
ORCID: 0000-0001-6389-2550

Anik Giguere
Title: Dr
Role: Professor
Qualifications (BSc, M.Sc, PhD, etc.): PhD
Institutional address: VITAM Research Centre for Sustainable Health & Research Centre, 2480, chemin de la Canardière, bureau #139
Québec QC G1J 0A4
Email: anik.giguere@fmed.ulaval.ca
ORCID:0000-0001-9928-7395

Noah M. Ivers
Title: Dr
Role: Associate Professor
Qualifications (BSc, M.Sc, PhD, etc.): MD, PhD, CCFD
Institutional address: , Department of Family & Community Medicine, University of Toronto, 76 Grenville Street Toronto, ON M5S 1B2, Canada
Email: Noah.Ivers@wchospital.ca
ORCID: 0000-0003-2500-2435

Anne-Sophie Julien
Title: Ms
Role: Statistical Consultant
Qualifications (BSc, M.Sc, PhD, etc.): M.Sc
Institutional address: Université Laval, Pavillon Adrien-Pouliot, local 3102, 1050 avenue de la Médecine, Québec (QC), Canada, G1V 0A6
Email: Anne-Sophie.Julien@mat.ulaval.ca

ORCID:0000-0002-5578-1399

Shannon E. MacDonald
Title: Dr.
Role: Associate Professor
Qualifications: PhD, RN
Affiliated institute: Faculty of Nursing, University of Alberta, Edmonton, AB, Canada
Institutional address: Faculty of Nursing, University of Alberta, Edmonton, AB T6G 1C9
Email: smacdon@ualberta.ca
ORCID: 0000-0003-4675-4433

Magniol Noubi
Title: Mr.
Role : Research technician
Qualifications (BSc, M.Sc, PhD, etc.):
Affiliated institute: Department of Family and Emergency Medicine, Laval University, Quebec City, QC, Canada
Institutional address: 1050 avenue de la Médecine, Pavillon Ferdinand-Vandry 2881, Université Laval, Québec City, Québec, G1V 0A6, Canada
Email: magniol.noubi.1@ulaval.ca
ORCID: 0000-0002-3040-0326

Rita Orji
Title: Dr
Role: Professor
Qualifications (BSc, M.Sc, PhD, etc.): PhD
Affiliated institute: Faculty of Computer Science, Dalhousie University, Halifax, NS, Canada
Institutional address: 6050 University Ave. Halifax, NS, B3H 4R2, Canada
Email: rita.orji@dal.ca
ORCID: 0000-0001-6152-8034

Elizabeth Parent
Title: Ms.
Role : Research professional
Qualifications (BSc, M.Sc, PhD, etc.): M.A.
Affiliated institute: Department of Family and Emergency Medicine, Laval University, Quebec City, QC, Canada
Institutional address: 1050 avenue de la Médecine, Pavillon Ferdinand-Vandry 2881, Université Laval, Québec City, Québec, G1V 0A6, Canada
Email: elizabeth.parent@fmed.ulaval.ca
ORCID: 0000-0001-8332-9538

Beate Sander
Title : Dr.
Role : Senior Scientist and Professor
Qualifications (BSc, M.Sc, PhD, etc.): RN MBA MEcDev PhD
Affiliated institute:
Institutional address: University Health Network, Toronto General Hospital, Eaton Building, 10th Floor, Room 247, 200 Elizabeth Street, Toronto, ON M5G 2C4, Canada

Email: beate.sander@uhnresearch.ca
ORCID: 0000-0003-2128-9133

Aaron M. Scherer
Title: Dr.
Role: Assistant Professor of Internal Medicine
Qualifications (BSc, M.Sc, PhD, etc.): PhD
Affiliated institute: University of Iowa
Institutional address: 200 Hawkins Dr., Department of Internal Medicine, Iowa City, IA 52242
Email: aaron-scherer@uiowa.edu
ORCID: 0000-0002-4134-9300

Kumanan Wilson
Title: Dr.
Role: Senior Scientist and Professor
Qualifications (BSc, M.Sc, PhD, etc.): MD, MSc, FRCP(C)
Affiliated institute: Department of Medicine, University of Ottawa, Ottawa, Ontario, Canada
Bruyere Research Institute, Ottawa, Ontario, Canada
Email: kwilson@toh.ca
ORCID: 0000-0002-1741-7705

Daniel Reinharz
Title: Dr
Role: Professor
Qualifications (BSc, M.Sc, PhD, etc.): MD, PhD
Affiliated institute: Department of Social and Preventive Medicine, Laval University, Quebec City, QC, Canada
Institutional address: 1050 avenue de la Médecine, Pavillon Ferdinand-Vandry, Université Laval, Québec City, Québec, G1V 0A6, Canada
Email: daniel.reinharz@fmed.ulaval.ca
ORCID: 0000-0003-4433-059X

Holly O. Witteman
Title: Dr.
Role: Professor
Qualifications (BSc, M.Sc, PhD, etc.): PhD
Affiliated institute: VITAM Research Centre for Sustainable Health & Research Centre of the CHU de Québec-Université Laval.
Department of Family and Emergency Medicine, Laval University, Quebec City, QC, Canada
Institutional address: 1050 avenue de la Médecine, Pavillon Ferdinand-Vandry 4482, Université Laval, Québec City, Québec, G1V 0A6, Canada
Email: holly.witteman@fmed.ulaval.ca
ORCID: 0000-0003-4192-0682

Corresponding author:
Holly O. Witteman, 1050 avenue de la Médecine, Pavillon Ferdinand-Vandry, Université Laval, Québec City, Québec, G1V 0A6, Canada, telephone: 418.656.2131, fax: 418-656.2465, email: holly.witteman@fmed.ulaval.ca

Keywords: Community immunity; Herd immunity; Vaccination; Vaccination Hesitancy; Visualization; Data Visualization; Digital Health; Randomized Controlled Trial

Abstract

Background: To evaluate the effects of a web-based, personalized avatar intervention conveying the concept of community immunity (herd immunity) on risk perception (perceptions of the risk of infection spreading (to self, family, community, and vulnerable individuals)) and other cognitive and emotional responses across 4 vaccine-preventable disease contexts: measles, pertussis, influenza, and an unnamed “vaccine-preventable disease.”

Methods: Through a robust user-centered design process, we developed a web application, “*herdimm*,” showing how community immunity works. In our application, people personalize a virtual community by creating avatars (themselves, 2 vulnerable people in their community, and 6 other people around them; e.g., family members or co-workers.) *Herdimm* integrates these avatars in a 2-minute narrated animation showing visually how infections spread with and without the protection of community immunity. The present study was a 2x4 factorial randomized controlled trial to assess *herdimm*’s effects. We recruited 3883 adults via Qualtrics living in Canada who could complete an online study in English or French. We pre-registered our study, including depositing our questionnaire and pre-scripted statistical code on Open Science Framework (https://osf.io/hkysb/). The trial ran from March 1 to July 1, 2021. We compared the web application to no intervention (i.e. control) on primary outcome risk perception, divided into *objective risk perception* (accuracy of risk perception) and *subjective risk perception* (subjective sense of risk), and on secondary outcomes–emotions (worry, anticipated guilt), knowledge, and vaccination intentions–using analysis of variance for continuous outcomes and logistic regression for dichotomous outcomes. We conducted planned moderation analyses using participants’ scores on a validated scale of individualism and collectivism as moderators.

Results: Overall, *herdimm* had desirable effects on all outcomes. People randomized to *herdimm* were more likely to score high on objective risk perception (58.0%, 95% confidence interval 56.0%-59.9%) compared to those assigned to the control condition (38.2%, 95% confidence interval 35.5%-40.9%). *Herdimm* increased subjective risk perception from a mean of 5.30 on a scale from 1 to 7 among those assigned to the control to 5.54 among those assigned to *herdimm*. The application also increased emotions (worry, anticipated guilt) ($F(1,3875)=13.13$, $p<0.001$), knowledge ($F(1,3875)=36.37$, $p<0.001$) and vaccination intentions (Chi-squared(1)=9.4136, p=0.002). While objective risk perception did not differ by disease (Chi-squared(3)=6.94, p=0.074), other outcomes did (subjective risk perception $F(3,3875) = 5.6430$, $p<0.001$; emotions $F(3,3875)=78.54$, $p<0.001$; knowledge ($F(3,3875)=5.20$, p=0.001); vaccination intentions Chi-squared (3)=15.02, p=0.002). Moderation models showed that many findings were moderated by participants’ individualism and collectivism scores. Overall, whereas outcomes tended not to vary by individualism and collectivism among participants in the control condition, the positive effects of *herdimm* were larger among participants with more collectivist orientations and effects were sometimes negative among participants with more individualist orientations.

Conclusions: Conveying the concept of community immunity through a web application using personalized avatars increases objective and subjective risk perception and positively influences intentions to receive vaccines, particularly among people who have more collectivist worldviews. Including prosocial messages about the collective benefits of vaccination in public health campaigns may increase positive effects among people who are more collectivist while possibly backfiring among those who are more individualistic.

Introduction

Many vaccines protect against disease by not only preventing infection in those receiving the vaccine but also preventing the infection from being transmitted from one person to another [1,2]. Such transmission prevention can occur because the vaccines confer sterilizing immunity, because they lower viral load and therefore partially prevent transmission, and/or because, by lowering infection risk, they decrease the number of people within a population who are infected and thus lower the chances of interacting with an infectious individual [3].

The concept of community immunity, also known as herd immunity, refers to the indirect protection of unvaccinated or undervaccinated people by increasing the number of people around them who have immunity. Such an increase in immunity can break the chain of transmission by decreasing the overall probability of contact with an infectious agent, thereby preventing the spread of infectious agents within susceptible populations [1].

Despite the success of vaccines and immunization programs as public health measures, some people perceive such measures as unsafe or even unnecessary [4,5]. The reasons behind such perceptions include concerns about vaccine safety, a mistrust in healthcare agencies or pharmaceutical companies, unfamiliarity with vaccine-preventable diseases, and inaccurate mental models that ignore community immunity [6–9]. Providing accurate education about community immunity may be useful for increasing willingness to vaccinate, generating benefits both to individuals and communities, although the success of these efforts may depend on the extent the population of interest is more collectivist or more individualist [10,11].

The COVID-19 pandemic provided a salient example of the challenge of ensuring public understanding of individual and collective benefits of vaccines. On top of already-existing public health communication challenges regarding established vaccines, there was uncertainty about community immunity thresholds due to fluctuating estimates of the disease's reproductive number [12], new variants reducing vaccine effectiveness [13], the lack of sterilizing immunity offered by available vaccines, and evolving hybrid immunity due to widespread infection [14]. The Covid-19 pandemic therefore highlighted both the importance and the difficulty of communication strategies emphasizing individuals' roles in reducing transmission and protecting vulnerable people within communities [13].

In a previous systematic review, we identified graphic visualization as a potentially promising approach for achieving effective communication about community immunity [15]. Visualization is a powerful communication mechanism that uses pre-attentive processing to communicate large amounts of information rapidly in understandable and compelling ways [16]. While some visualizations about community immunity existed, few had been evaluated for their effects on vaccination intentions and uptake nor on vaccine uptake's precursors, namely knowledge, attitudes, beliefs and emotions. Furthermore, none had been evaluated in multiple disease contexts [15]. Because disease transmission dynamics and community immunity parameters (for example, vaccine effectiveness) differ across vaccine-preventable diseases, ideally, an effective means of conveying the concept of community immunity should be usable across multiple diseases. Finally, no existing visualizations used personalized avatars. Studies of the Proteus Effect have shown that people identify with a personalized avatar to the point that they change their behaviour according to their avatar's characteristics [17–19], suggesting that personalized avatars in a community immunity visualization may reinforce people's sense of actually being part of the community. This sense of community would ideally make the

visualization more salient and personally relevant, thus influencing risk perception, a key antecedent of vaccine uptake. [20,21]

Risk perception refers to the perceived severity and likelihood of an adverse event. Risk perception may draw on an individual's comprehension of the objective likelihood of events, and also on an individual's subjective feelings about the severity and likelihood of events. This latter subjective dimension of risk perception is referred to as the 'risk as feelings' framework [22] which aligns with observations of people's reactions to danger as instinctive and intuitive [23,24]. When people receive information about health risks, they may translate it intuitively into feelings of anxiety, worry, or distress, or a more vague feeling of 'badness' associated with the risk [25,26]. Risk perception influences vaccine decisions and behavior by shaping how individuals perceive and weigh the risks of vaccination against the risks of not getting vaccinated [27,28]. Therefore, when seeking to understand the impact of an educational intervention about community immunity, its effects on risk perception are of particular interest.

Objective

Our study objective was to evaluate a previously-developed web application, hereafter referred to as *herdimm*. The main purpose of *herdimm* was to clearly convey the concept of community immunity to people from various backgrounds, including varying levels of education. We developed it with attention to its potential effects on people's feelings relevant to their role in community immunity [29]. In the web application, people personalize a virtual community by creating avatars representing themselves, 2 vulnerable people in their community, and 6 other people around them; for example, family members or co-workers. The web application integrates these avatars in a 2-minute narrated animation explaining how community immunity works [30,31].

In this study, we aimed to evaluate the effects of *herdimm* on risk perception (that is, perceptions of the risk of spreading infection to oneself, one's family, one's community, and vulnerable individuals within one's community), and on known antecedents of decisions to get vaccinated across four vaccine-preventable disease contexts. Our research questions were therefore:

1. Does *herdimm* influence risk perception (meaning vaccine-preventable disease risk to oneself, family, community and vulnerable people) compared to a control (no intervention)?
2. Does *herdimm* influence other outcomes (vaccination intentions, emotion, knowledge, and trust in information) compared to a control (no intervention)?

Methods

Study design

We conducted a 2 (visualization: *herdimm*, no education about community immunity) x 4 (disease: measles, pertussis, flu, unnamed "vaccine-preventable disease" hereby referred to as "generic") factorial randomized controlled trial among adults in Canada using Qualtrics, an online survey platform. The study arms differed by the two independent variables (visualization and disease). In other words, participants in different arms saw either no intervention (control) or the herdimm intervention (*herdimm*) for one of four possible vaccine-preventable diseases. For efficient data collection, the present 2x4 trial (8 study arms) conducted in both English and

French was complemented by a head-to-head comparison of existing available interventions about community immunity, most of which were available only in English and none of which offered different versions for different diseases. This complementary study added 5 arms to the larger study and will be reported separately.

Interventions

The main intervention was the application named *herdimm*, developed in our previous study [29]; web development code available on GitHub (https://github.com/Witteman-Lab/herdimm). A version of *herdimm* (measles/generic, English) is shown here on YouTube for illustration: [30]. Links to sample visualizations of all possible *herdimm* versions are available in Appendix 1.

In the current study, we assessed the effects of *herdimm* across four possible diseases (measles, pertussis, flu/influenza, and generic). We tested the intervention across multiple diseases because disease transmission varies (including the number of new infections caused by the first infected person in a population) and community immunity parameters differ across vaccine-preventable diseases. Among other differences, for some diseases such as measles, a high vaccination rate can achieve a sufficient level of community immunity. For other diseases such as influenza, vaccines must be complemented by other protective measures to optimize protection of all members of a community. Therefore, it was important to assess whether any potential effects would be robust and would generalize across infectious diseases with different transmission characteristics. For the “generic” condition, we used the visualization for measles, but did not specify the disease and merely referred to, “a vaccine-preventable disease,” in all questions. For example, participants assigned to the measles condition were asked to indicate their level of agreement or disagreement with the statement, “I am worried about getting measles,” while the equivalent item for those assigned to the generic disease was, “I am worried about getting a vaccine preventable disease.” We developed *herdimm* in both official languages of Canada (English and French), and the trial was conducted in both languages.

Randomization and allocation

We used computerized randomization within Qualtrics [32] to automatically assign participants to study arms randomly. Each study arm was accessible in both languages and we pre-specified our sampling parameters such that 75% of the sample for each study arm would be people who elected to participate in English and 25% in French, based on the percentage of spoken languages within the Canadian population [33]. This was a single-blinded study because we could not mask participants to the fact that they have been randomized to a computer application including a visualization. However, participants did not know the purpose of the study arm to which they were assigned, and investigators were blinded to the study arm during the data collection and in the pre-scripted statistical code.

Ethics and trial registration

This study was approved by the ethics committee of Laval University. We pre-registered the trial at ClinicalTrials.gov (NCT04787913). We pre-planned all statistical analyses by developing our statistical code prior to beginning the trial using simulated data with the support of a statistician (ASJ). This pre-scripted statistical code was also peer-reviewed by an external

statistician. We pre-registered all study materials (protocol, study questionnaire, data dictionary, and pre-scripted statistical code) on Open Science Framework on February 26, 2021 (https://osf.io/hkysb/). We report the trial following the CONSORT guidelines [34]. The trial began on March 1, 2021 and ended on July 1, 2021.

Study participants

We conducted the online randomized controlled trial in Qualtrics among adults living in Canada. Participants were recruited using established survey panels subcontracted in Qualtrics. Participants were eligible if they were 18 years and above, residing in Canada, able to use a computer, could read and understand at least one of French or English, and were able to provide consent. Those who did not meet this criteria were excluded from the study. We used sampling quotas in an effort to represent key characteristics of the Canadian population in the most recent national census [35]. Specifically, we required that the overall sample population for the study consisted of 50% people who identified as female, 49% as male, and 1% as other (e.g., non-binary, two spirit). Regarding age, 30.5% of the study population were required to be within the age group 18-34 years old, 34.4% within 35-49 years old, and 35.2% within the group aged 50 years and older. For education level, we specified that 25-35% of the study population must report their highest education level as elementary school (completed or not) or high school diploma, 10-15% as apprenticeship or trade certificate or diploma, 20-25% as college or polytechnical school certificate or diploma, and 30-40% as university degree or above. Finally, we required a minimum of 22% of the study population to report their racial identity as other than white, and 25% of the study population to be French speakers. A small incentive (typically $1-1.50, depending on panel) was offered to the participants to complete the survey.

Outcomes

Our primary outcome was risk perception. We chose this as our primary outcome as people's decisions regarding vaccination depend on their perception of risks associated with diseases and vaccines, including vaccine safety and potential side effects. Such risk perceptions may be formed long before they are presented with a decision to vaccinate or not, suggesting that interventions that shape such perceptions may be important upstream influences on subsequent vaccine acceptance. High risk perception of vaccines can deter vaccination, resulting in lower vaccination rates, but building trust in vaccines, science and effective communication can alleviate risk perception and increase vaccination intentions [36]. We defined risk perception for this study as the participants' sense of risk posed by a vaccine-preventable disease to an individual, their family, their community, and vulnerable people in their community. Secondary outcomes were measures of emotions (worry, anticipated guilt), knowledge about community immunity, and vaccination intentions.

Measures

We measured our primary outcome using questions developed and pre-tested to assess risk perception (6 items, Figure 1 and Table 1). Based on this pre-testing, we were concerned that the first item might be measuring a different construct than the other five items. Our pre-scripted analyses (written prior to starting data collection, with this potential difference in mind) suggested this was indeed the case. Specifically, the scatter plot and Bland-Altman test (see Figures S1 S2 in Appendix 2) showed that the first item did not measure the same construct as the second through sixth items. We therefore divided the six items into *objective risk*

perception (Figure 1; item 1, which assessed how people perceived risk compared to actual risk) and *subjective risk perception* (Table1; items 2 to 6, which assessed people's subjective feelings of risk.) The Cronbach alpha for subjective risk perception was 0.76, which is acceptable for combining 5 items into a single measure.

Figure 1. Objective risk perception (condition: measles)

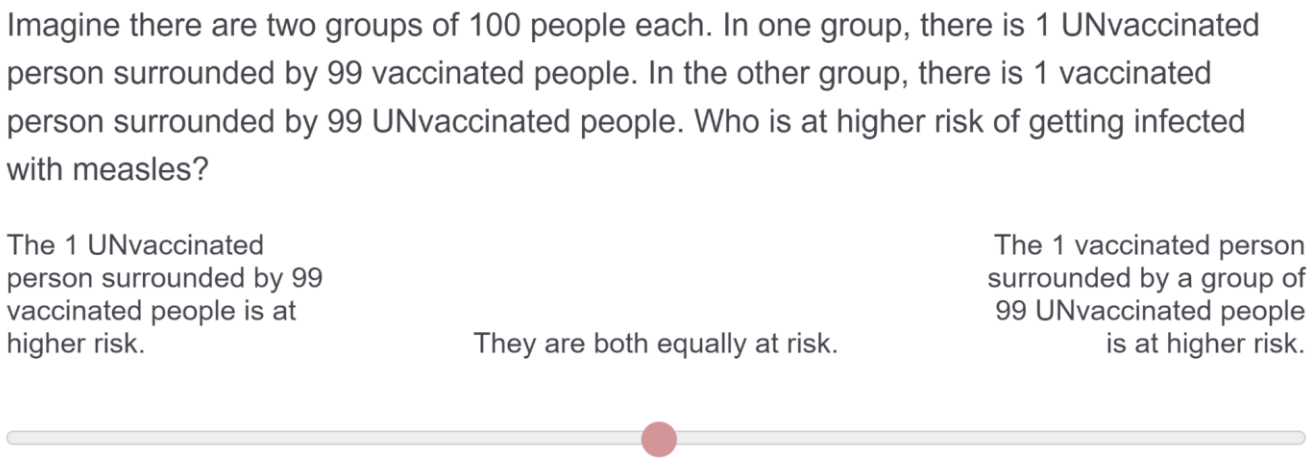


Table 1. Subjective risk perception

Please indicate the extent to which you agree or disagree with the following statements. (Response options: 1 = strongly disagree, 2 = moderately disagree, 3 = slightly disagree, 4 = neutral, 5 = slightly agree, 6 = moderately agree, 7 = strongly agree)
A person's decision to be vaccinated or not against {{measles/pertussis/the flu/a vaccine preventable disease}}* affects only them, individually.
People who are vaccinated against {{measles/pertussis/the flu/a vaccine preventable disease}} are less likely to pass it on to others.
My decision to be vaccinated against {{measles/pertussis/the flu/a vaccine preventable disease}} has no impact on anyone else's chances of catching {{measles/pertussis/the flu/that vaccine preventable disease}}
My decision NOT to be vaccinated against {{measles/pertussis/the flu/a vaccine preventable disease}} has no impact on anyone else's chances of catching {{measles/pertussis/the flu/that vaccine preventable disease}}
If I get vaccinated against {{measles/pertussis/the flu/a vaccine preventable disease}}, it lowers the risk of vulnerable people in my community (babies, young children, older people, cancer patients) getting sick.

*{{measles/pertussis/the flu/a vaccine preventable disease}} indicates all four possible conditions. Each participant in the study was randomly assigned to view the entire study, including all questions, with only one of these four.

We measured emotions by asking participants to indicate their level of agreement using a 7-point Likert-type scale from strongly agree to strongly disagree with 5 items including, for

example, “I am worried about people in my life (family, friends) getting {{measles/pertussis/flu/a vaccine preventable disease}},” and “I would feel guilty if someone in my life (a family member, a friend) got {{measles/pertussis/flu/a vaccine preventable disease}} from me”. We measured knowledge about community immunity by asking participants to respond to 15 items with response options that were either multiple choice or true/false/I don’t know. Items included, for example, ”A vaccine preventable disease can spread from one person to another person,” and, “Unvaccinated people in a population can be protected from infections when enough people in their community are vaccinated.” We measured vaccination intentions by asking people to indicate their likelihood of getting a free vaccine against the disease in question on a 100-point slider labeled “extremely unlikely, I would definitely NOT be vaccinated” at one end and “extremely likely, I would definitely BE vaccinated” at the other end. Specifically, the wording of the question was, “If you were eligible to receive a free vaccine against measles/pertussis/flu/a vaccine preventable disease, how likely would you be to get vaccinated?” Appendix 3 provides the complete questionnaire.

Covariates and Moderating Variables

Individualism and collectivism

We used validated measures of individualism and collectivism from the cultural orientation scale [37] as moderating variables. This scale measures four dimensions of individualism and collectivism: horizontal individualism, vertical individualism, horizontal collectivism, and vertical collectivism. Horizontal Individualism is about, “seeing the self as fully autonomous, and believing that equality between individuals is the ideal.” Vertical Individualism is about, “seeing the self as fully autonomous, but recognizing that inequality will exist among individuals [and] accepting this inequality.” Horizontal Collectivism is about, “seeing the self as part of a collective but perceiving all the members of that collective as equal”, while Vertical Collectivism is about, “seeing the self as a part of a collective and being willing to accept hierarchy and inequality within that collective.” [38] All questions are answered on a 9-point Likert-type scale, where 1 indicates, “never or definitely no,” and 9 indicates, “always or definitely yes.” We included this scale to assess whether a person's orientation towards individualism or collectivism might change the effects that *herdimm* might have on their risk perception, emotions, knowledge, and vaccination intentions.

Demographics

We used socio-demographic variables as covariates: born in Canada, age, gender, ethnicity, education level, income, disability, and preferred language. (All question wordings in English and French are available in Appendix 3.)

Sample size

To determine the sample size for a 2*4 factorial randomized controlled trial using a two-way analysis of variance, assuming a small effect size (Cohen’s f=0.10), power of 80% (beta = 0.80), 5% type 1 error (alpha = 0.05), we determined that we required n=302 participants per group. We increased this to n=320 per group to allow for a secondary analysis (study reported separately) in which we would be comparing five groups in a one-way analysis of variance using only the English-speaking participants. The sample size of *herdimm* arms was then doubled to enable an embedded study (secondary to this work, not reported in this manuscript) of male versus female voice for the narration. This enabled more precise estimates of the

effects of the herdimm intervention. We estimated the sample size by using G*power, version 3.1.9.2 [39] for a continuous outcome.

Statistical analysis

To determine the effects of *herdimm* compared to control, we performed a two-way analyses of variance using the two independent variables (visualization, disease) and their interaction (visualization*disease) for continuous outcomes (subjective risk perception, knowledge, emotions) and logistic regression for dichotomous outcomes (objective risk perception, vaccination intentions.)

As planned in our pre-scripted statistical analyses written prior to collecting data, we transformed outcomes from continuous to dichotomous whenever the distribution did not respect the assumptions of the models described below; for example, if there were ceiling effects. This was the case for two variables: objective risk perception and vaccination intentions. For objective risk perception, we had set a minimum value of 80 out of 100 as a cutoff indicating high risk perception because our pre-testing had suggested that we might observe ceiling effects on this variable. For vaccination intentions, we had pre-scripted a median threshold in the event of model assumption violations. We therefore dichotomized vaccination intentions as being at/above the median or below the median.

We analyzed 3 models for each outcome. We chose our primary model to examine overall effects, and subsequent models to examine the robustness of results when adjusted for covariates or in the presence of moderators. Accordingly, we first determined the effects of factors (visualization and disease) without any covariates on each outcome (Model 1). For Model 2, we first examined our planned covariates and collapsed categories containing less than 5% of participants (that is ethnicity, language, education levels, and disability.) We used Model 2 to determine the effects of factors (visualization and disease) with adjustment for covariates (socio-demographic characteristics, individualism and collectivism.) Next, we determined the moderating effects of individualism and collectivism with adjustment for socio-demographic covariates (Model 3). Our overall 3-model approach is summarized in table 2 below.

Table 2. Models used for analysis

Model	**Analytical goal**
Model 1 (primary model)	Check for effects of factors without any covariates
Model 2	Check for effects of factors with adjustment for covariates (individualism and collectivism, born in Canada, age, gender, ethnicity, education level, income, disability, and preferred language)
Model 3	Check for moderating effects of individualism & collectivism with adjustment for other covariates (born in Canada, age, gender,

	ethnicity, education level, income, disability, and preferred language)

For simplicity here, we report only Model 1 results when these results remained consistent after adjusting for covariates in Model 2. When inclusion of covariates affected the results, we also report the adjusted (Model 2) results. We report results from Models 3 when these showed statistically-significant interactions. We report group-based means with 95% confidence intervals for continuous variables (i.e., subjective risk perception, knowledge, emotions) and probabilities of being at or above the median with 95% confidence intervals for the dichotomous variables (i.e., objective risk perception, vaccination intentions.)

To address missing outcome data, we also repeated all the primary models after using data imputation for any missing outcome values. To do this, fifteen multiple imputation datasets were generated. The primary author (HH) and a statistician (ASJ) compared results, examining whether results from analyses of the imputed datasets replicated or contradicted analyses from the original dataset.

We performed all analyses using R version 4.1.0 [40]. We used the package *psych* (version 1.9.12.31) [41] for descriptive analyses, the packages *stats*, *car* (version 3.0-8) [42] and *emmeans* [43] for the analyses of variance and logistic regressions, and the package *mice* (version 3.11.0) [44] for multiple imputation. We developed statistical code with the support of a statistician (ASJ), using simulated data prior to collecting study data. An external statistician peer reviewed the R code prior to conducting the study. We preregistered the statistical code in Open Science Framework on February 26th, 2021 (https://osf.io/hkysb/).

Data collection methods

The trial ran from March 1 to July 1, 2021. After providing consent, each participant was randomized into a single study arm. All participants completed the same post-intervention questionnaire containing questions about risk perception, emotion, knowledge, vaccination intentions (see Appendix 3 for the complete questionnaire.)

Data management

In order to be considered as contributing valid data, participants randomly allocated to intervention arms were required to spend a predetermined amount of time viewing and/or interacting with the intervention. These time requirements were set based on the minimum time possible for each intervention: control = no minimum restrictions; *herdimm* = minimum 206 seconds. To determine the minimum length of time, we calculated the shortest possible interaction time with the narrated animation, assuming very high internet speed and near-instantaneous transitions between the survey and the web application. Participants whose timestamps on the survey page were less than the predetermined minimum were excluded from the dataset. All the information we collected was kept confidential and used for research purposes only. Data was stored on Qualtrics servers located in Canada and subject to Canadian data privacy laws. Anonymized data are available at Université Laval's Dataverse, Boréalis: https://doi.org/10.5683/SP3/41MWKO.

Results

Of 18509 participants who started the study, 3883 participants were eligible for the analysis. Most excluded participants (n=10724) were excluded because their timestamps showed that they did not view the complete *herdimm* intervention. Figure 2 shows the CONSORT flow diagram.

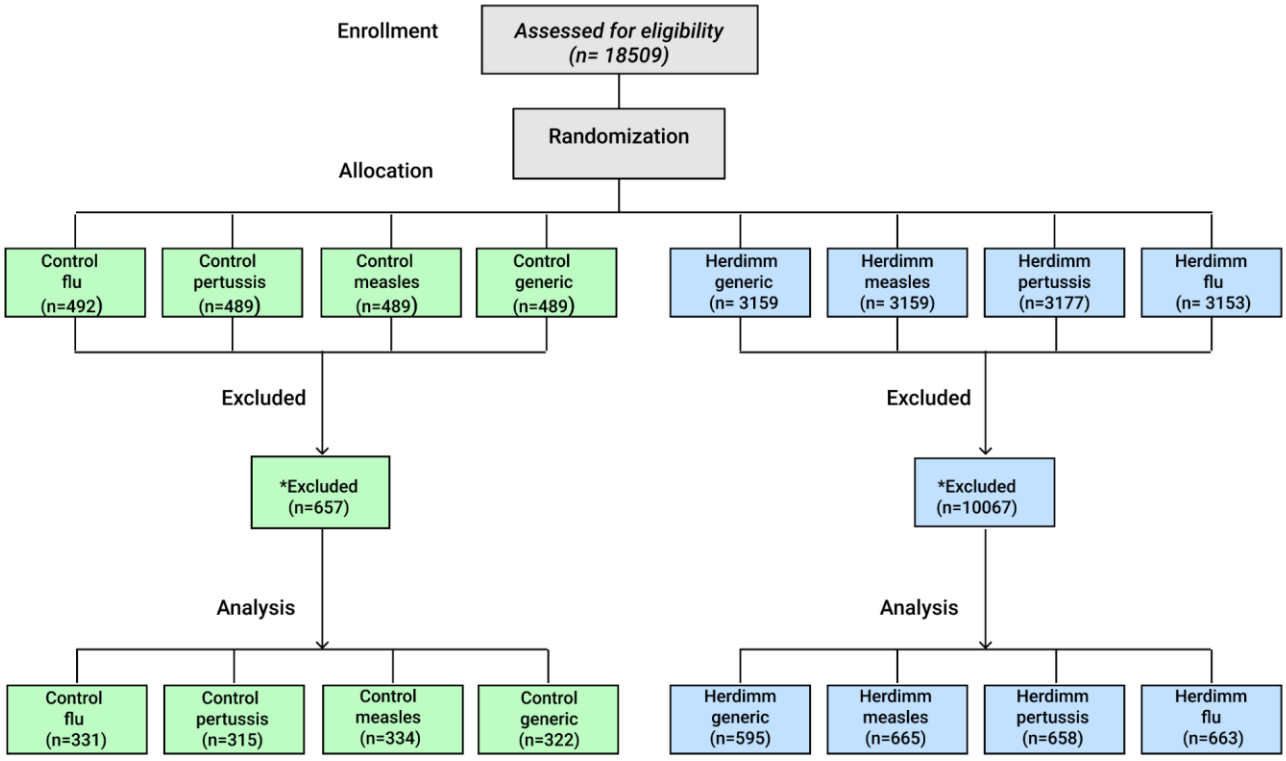


Figure 2. CONSORT flow diagram

Note: Non-applicable elements of the CONSORT template were removed. There was no time interval between intervention allocation and follow-up.

We collapsed covariate categories containing less than 5% of the total sample within that covariate. For example, when the people identifying as a particular ethnicity comprised less than 5% of the total sample, we collapsed that category with the closest other category within that covariate to facilitate analysis. Specifically, the covariate *ethnicity* (in which participants could select multiple options) was planned to have grouped categories Asian, Black, Indigenous, Maghrebian/Middle Eastern, white, and others (e.g., Latin American, self-reported "other"). However, because the Black, Indigenous, and Maghrebian/Middle Eastern groups each represented <5% of the total sample, categories were reduced to Asian, white, and others. Along the same lines, to account for low counts in some of the seven *education levels*, we recoded this covariate as *college degree and above* and *no college degree* (elementary

school, high school diploma, or apprenticeship or trade certificate or diploma.) Similarly, due to low counts of people identifying as having a disability that specifically affects their ability to use technology like computers, we merged this covariate with the larger group of people identifying as having any disability. In the new, merged covariate *disability*, anyone indicating a disability of any kind (technical or other) was coded as having a disability. When no other category was available or when merging with another category would be inappropriate, as was the case for *gender identity*, we coded those data as missing rather than assigning those participants to a larger gender group. Similarly, the covariate *language* was planned to include French, English and other languages, but due to low counts for other languages, only the French and English categories remained.

Of 3883 participants, 50% identified as female, 49% as male. Eighty-one percent were comfortable communicating in English with their healthcare professional, and 24% in French. Eighty-two percent of the participants identified themselves as white, a category including white North American and white European. Ten percent identified themselves as Asian, a category including East, Central, South, Southeast Asian. Twenty-three percent participants reported a disability, while 75% reported no disability. Sixty-one percent of the participants reported higher education (college degree or higher) and 39% lower education (no college degree). Eighty-five percent of participants indicated their place of birth as in Canada. Table 3 shows details of participants' characteristics across the study. Results per arm are shown in Appendix 4. Full results of all analyses using all models are available in Appendix 5.

Table 3. Participants' characteristics (N=3883)

Characteristic		**Study population***
Age: median (IQR)		42 (32-57)
Gender identity: n (%)		
	Male	1914 (49%)
	Female	1934 (50%)
	Not available**	35 (1%)
Language(s) spoken: n (%)		
English	Yes	3144 (81%)
	No	734 (19%)
	Not available	5 (0)
French	Yes	937 (24%)
	No	2946 (76%)
	Not available	-
Ethnicity: n (%)		

White	Yes	3172 (82%)
	No	645 (17%)
	Not available	66 (2%)
Asian	Yes	385 (10%)
	No	3432 (88%)
	Not available	66 (2%)
Other	Yes	269 (7%)
	No	3548 (91%)
	Not available	66 (2%)
Disability: n (%)	Yes	883 (23%)
	No	2924 (75%)
	Not available	76 (2%)
Education levels: n (%*)*		
	College degree and above	2361 (61%)
	No college degree (elementary school, high school, apprenticeship or trade certificate)	1497 (39%)
	Not available	25 (1%)
Born in Canada: n (%)	Yes	3303 (85%)
	No	536 (14%)
	Not available	44 (1%)
Individualism and collectivism: mean (SD)	Vertical individualism (e.g., “It is important that I do my job better than others.”)	5.12 (1.65)
	Horizontal individualism (e.g., “I rely on myself most of the time, I rarely rely on others.”)	7.22 (1.16)
	Vertical collectivism (e.g., “It is important to me that I respect the decisions made	6.83 (1.39)

	by my groups.")	
	Horizontal collectivism (e.g., "I feel good when I cooperate with others.")	6.85 (1.33)

*****Percentages may add up to +/-100% because of rounding.
**Data could be not available due to participants choosing another option (e.g., gender-nonconforming), choosing, "I prefer not to answer," or leaving the question unanswered.

Primary outcome (risk perception)

Objective risk perception

Compared to participants in the control condition, those in the *herdimm* condition had significantly higher odds of providing a correct objective risk perception response (Chi-squared (1) = 134.54, $p < 0.001$). More specifically, people who were assigned to *herdimm* were more likely to understand that 1 unvaccinated person surrounded by 99 vaccinated people is more protected from infection than 1 vaccinated person surrounded by 99 unvaccinated people (58.0%, 95% confidence interval 56.0%-59.9%) compared to those assigned to the control condition (38.2%, 95% confidence interval 35.5%-40.9%). There was no main effect of disease (measles, pertussis, flu, generic vaccine-preventable disease) (Chi-squared (3) = 6.94, $p = 0.074$), and no statistically-significant interaction between intervention and disease (Chi-squared (3) = 1.19, $p = 0.755$). These results did not change when including covariates (Model 2) or when testing for moderation effects (Model 3).

Subjective risk perception

Participants assigned to the *herdimm* condition had higher subjective risk perception compared to those assigned to the control condition ($F(1,3875) = 28.7856$, $p < 0.001$). Subjective risk perception also differed whether the disease was presented as measles, pertussis, flu, or a generic "vaccine preventable disease" ($F(3,3875) = 5.6430$, $p < 0.001$). We also observed an interaction between intervention and disease on subjective risk perception. More specifically, subjective risk perception was higher among people who were assigned to *herdimm* compared to those assigned to the control. Differences estimates for each disease showed that this effect was likely driven by the larger difference among people assigned to the flu condition (difference estimate = 0.456, standard error = 0.0869, $t(3875) = -5.243$, $p < 0.0001$; all difference estimates available in Appendix 5). Table 4 shows means and 95% confidence intervals for subjective risk perception for each combination of intervention and disease.

Table 4. Two way analysis of variance of subjective risk perception

	Intervention		
Disease	Control: mean (95% confidence interval)	Herdimm: mean (95% confidence interval)	
Generic	5.31 (5.17-5.45)	5.46 (5.36-5.56)	$F(3,3875) = 5.6430$, $p < 0.001$
Measles	5.44 (5.30-5.58)	5.61 (5.51-5.71)	

Pertussis	5.39 (5.25-5.54)	5.56 (5.46-5.66)	
Flu	5.06 (4.92-5.20)	5.52 (5.42-5.62)	
	F(1,3875) = 28.7856, p < 0.001		F(3,3875) = 2.8324, p = 0.037

***Abbreviations: p**, p-value; **F**, F-statistic*

Our second model showed that intervention and disease interaction continued to demonstrate the same effects on subjective risk perception after adjustment for covariates, and is driven by the effects of the *herdimm* intervention among participants assigned to measles, pertussis and flu. The third model suggested that the increase in subjective risk perception for *herdimm* versus control was somewhat driven by the responses of people who scored low on vertical individualism (i.e., who disagreed with statements like, “It is important that I do my job better than others,”) (see Figure 3) and low on horizontal collectivism (i.e., people who disagreed with statements like, “I feel good when I cooperate with others.”) The third model further suggested that the relationship between participants’ horizontal individualism scores (i.e., their agreement with statements like, “I rely on myself most of the time, I rarely rely on others,”) and subjective risk perception was negative among those randomized to the flu condition while it was positive among those randomized to other diseases.

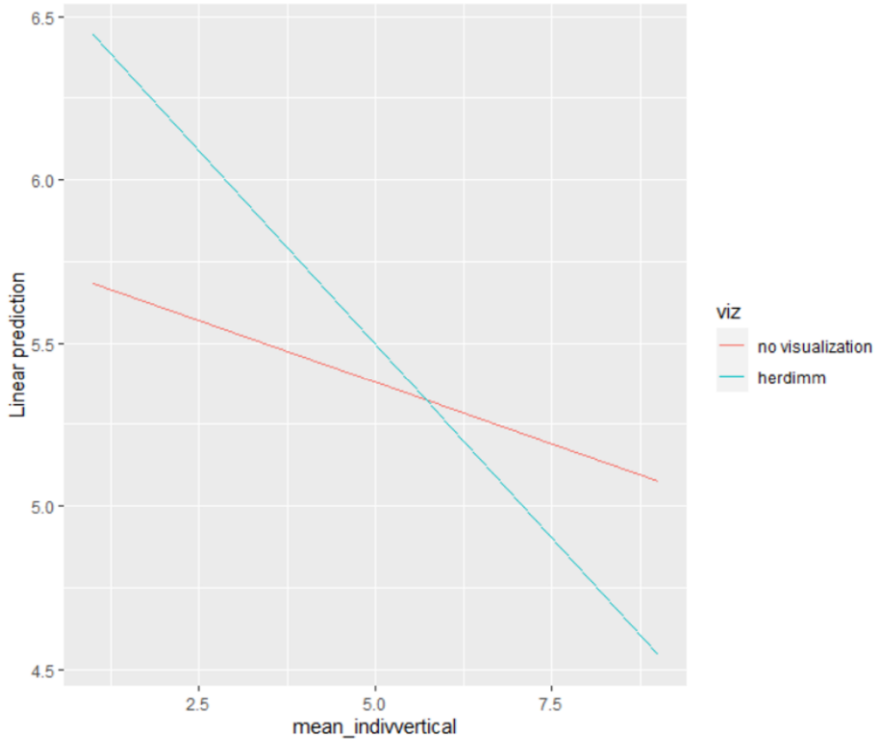


Figure 3. Subjective risk perception for *herdimm* versus control by participants’ vertical individualism

Secondary outcomes

For our second research question we assessed the effects of the *herdimm* intervention on other outcomes (namely, emotions, knowledge and vaccination intentions) compared to a control of no intervention.

Emotions

The primary model showed a statistically significant main effect of the intervention (*herdimm* or control) ($F(1,3875) = 13.13$, $p < 0.001$), main effect of disease (measles, pertussis, flu, generic vaccine-preventable disease) $F(3,3875) = 78.54$, $p < 0.001$), and no statistically significant interaction between intervention and disease on emotions $F(3,3875) = 1.49$, $p = 0.216$. More specifically, people who were assigned to *herdimm* reported stronger emotional responses (mean 5.07, 95% confidence interval 5.02-5.13) compared to those assigned to control (mean 4.90, 95% confidence interval 4.83-4.98). In other words, they were more likely to indicate higher levels of agreement with statements like, “I am worried about people in my life (family, friends) getting a vaccine-preventable disease,” and “I would feel guilty if someone in my life (a family member, a friend) got a vaccine-preventable disease from me.” People assigned to the generic ‘vaccine-preventable disease’ condition (mean 5.48, 95% confidence interval 5.39-5.57) had a higher mean score on emotions than those assigned to any specific diseases. People assigned to the measles (mean 4.59, 95% confidence interval 4.50-4.68) and pertussis conditions (mean 4.70, 95% confidence interval 4.6-4.79) had lower mean emotions than those assigned to flu (mean 5.18, 95% confidence interval 5.09-5.27).

The second model showed that inclusion of planned covariates, which required excluding 419 participants due to missing covariates, changed the results. The effect of the intervention became not significant ($F(1,3440) = 2.93$, $p = 0.087$) and the effect of disease remained significant ($F(3,3440) = 75.47$, $p < 0.001$), while the interaction between intervention and disease remained not significant. The third model suggested that the higher mean on emotions for *herdimm* was driven by the responses of people who scored low on horizontal collectivism (i.e., people who disagreed with statements like, “I feel good when I cooperate with others”) in the generic disease and who scored high on horizontal collectivism (i.e., people who agreed with the above statement) for measles and pertussis.

Knowledge

The primary model showed a statistically significant main effect of the interventions ($F(1,3875) = 36.37$, $p < 0.001$), main effect of disease (measles, pertussis, flu, generic vaccine-preventable disease) ($F(3,3875) = 5.20$, $p = 0.001$), and no statistically significant interaction between intervention and disease on knowledge ($F(3,3875) = 2.54$, $p = 0.055$). More specifically, people assigned to *herdimm* had higher mean knowledge (mean 9.12, 95% confidence interval 9.02-9.22) compared to those assigned to the control (mean 8.58, 95% confidence interval 8.44-8.73). People who were assigned to the generic vaccine-preventable disease had higher mean knowledge than those assigned to measles (difference estimate = 0.410, standard error = 0.127, $t(3875) = 3.239$, $p = 0.007$) and pertussis (difference estimate = 0.337, standard error = 0.128, $t(3875) = 2.631$, $p = 0.042$). Those assigned to disease flu also had higher mean knowledge than those assigned to measles (difference estimate = 0.357, standard error = 0.125, $t(3875) = 2.861$, $p = 0.022$).

The second model showed that, after inclusion of planned covariates (thus excluding 419 participants with missing covariate data), the effect of the interaction between intervention and disease became significant as well ($F(3,3440) = 3.2962$, $p = 0.0196$). After adjusting for covariates, people assigned to *herdimm* had higher mean knowledge than those assigned the control when they were also assigned to measles (difference estimate = 0.844, standard error = 0.182, $t(3440) = 4.627$, $p < 0.001$), pertussis (difference estimate = 0.508, standard error = 0.187, $t(3440) = 2.725$, $p = 0.007$) or flu (difference estimate = 0.680, standard error = 0.182,

t(3440) = 3.743, p < 0.001) but not when they were assigned to generic vaccine-preventable disease (difference estimate = 0.076, standard error = 0.184, t(3440) = 0.413, p = 0.680).

The third model suggested that the higher mean knowledge for *herdimm* was driven by the responses of people who scored low on vertical individualism (i.e., who disagreed with statements like, “It is important that I do my job better than others.”) To explore whether people who scored differently on individualism and collectivism subscales might have paid more or less attention to the information in *herdimm*, we conducted additional exploratory posthoc analyses on time spent away from the Qualtrics survey, when participants were supposed to be viewing *herdimm*. Overall, differences appeared to be minimal (Appendix 6)

Vaccination intentions

The primary logistic regression model showed a statistically significant main effect of the intervention (*herdimm* or control) (Chi-squared (1) = 9.41, p = 0.002), main effect of disease (measles, pertussis, flu, generic vaccine-preventable disease) (Chi-squared (3) = 15.02, p = 0.002), and no statistically significant interaction between intervention and disease on vaccination intentions (Chi-squared (3) = 3.72, p = 0.293). More specifically, people assigned to *herdimm* were more likely to score high on vaccination intentions (52.1%, 95% confidence interval 50.1%-54.0%) compared to those assigned to the control (46.9%, 95% confidence interval 44.1%-49.6%). People who were assigned to the flu (45.8%, 95% confidence interval 42.5% - 49.1%) were less likely to score high on vaccination intentions compared to those assigned to a generic ‘vaccine-preventable disease’ (52.7%, 95% confidence interval 49.3%-56.1%) and measles (52.9%, 95% confidence interval 49.5%-56.1%). Those assigned to measles were also more likely to score high on vaccination intentions compared to those assigned to pertussis (46.6%, 95% confidence interval 43.2%-49.9%).

The second model showed that inclusion of planned covariates (and its according exclusion of 419 participants who did not provide sociodemographic information) changed the results. The effect of the intervention became not significant (Chi-squared (1) = 2.69, p=0.10). The covariates with statistically significant effects at the 5% level on vaccination intentions were age (Chi-squared (1) = 56.646, p<0.001), collective horizontalism (Chi-squared (1) = 46.271, p<0.001), income (Chi-squared (3) = 42.401 , p<0.001), disability (Chi-squared (1) = 19.7276, p<0.001), vertical individualism (Chi-squared (1) = 6.422 , p= 0.011), horizontal individualism (Chi-squared (1) = 4.261 , p= 0.04), and education level (Chi-squared (1) = 4.141, p= 0.042). The third model suggested that the relationship between participants’ vertical individualism scores (i.e., their agreement with statements like, “I rely on myself most of the time, I rarely rely on others,”) and vaccination intentions was positive among those randomized to the flu condition while it was negative among those randomized to other diseases. In addition to moderation model results available above and in Appendix 5, Appendix 6 presents graphs of all outcome data, including vaccination intentions, by Collectivism and Individualism subscales.

Impact of missing outcome data

Comparing results from analyses with multiple imputation on missing outcome data to the analyses without, we observed no notable differences. Some outcomes (subjective risk perception, knowledge, and emotion) had no missing values, and there were no changes from original results for the primary model. The lack of missing data might be because these variables are a function of several items, and therefore, even if some items were missing, a mean or sum could still be calculated. For the other outcomes measured by a single item

(objective risk perception, vaccination intention) the rate of missing data was approximately 1%. After imputing these missing data points, there were no changes to the results of any analyses.

Discussion

This study offers 4 key findings. First, compared to the control condition of no education, the *herdimm* web app improved objective risk perception, increased subjective risk perception, improved knowledge about how herd immunity or community immunity works, increased emotions such as concern for vulnerable people, and increased intentions to receive vaccines. People often perceive risk based on their impressions of overall disease prevalence and severity [45,46]. By presenting epidemiological evidence about how vaccines protect whole communities in a way that allowed people across backgrounds, education levels, and disability statuses to understand it, the *herdimm* intervention led to improved understanding of levels of risk (objective risk perception) and increased subjective risk perception and associated emotions, indicating higher levels of concern for others in one's community and vulnerable people within it. This finding is consistent with the previous research in which risk perception and emotions influenced vaccine decisions [47–49] and similar web-based interventions improved vaccine knowledge, attitudes, and intentions to receive vaccines [10,50–52]. Our study therefore adds to previous research suggesting that communicating population-level benefits of vaccination may help encourage vaccine uptake, at least in some populations.

Second, our study showed that people with more collectivist orientations are more responsive to messages demonstrating collective benefits of widespread vaccination than people with more individualist orientations. Previous work by Betsch and colleagues analyzed the effects of a similar intervention across countries demonstrating more individualist and collectivist orientations at the population level. They found that their intervention had larger effects in encouraging vaccination intentions in countries with higher overall individualist scores (United States, Germany and the Netherlands) than in collectivist countries with higher overall collectivist scores (South Korea, Vietnam and Hong Kong) because baseline vaccine uptake was already high in the second group, and there was therefore less room for change [10]. Our study built on this finding by incorporating a validated scale of individualism and collectivism [37] to assess whether a person's orientation towards individualism or collectivism moderated how they responded to the intervention. Our study was conducted in Canada, a multicultural, Western country that was not represented in Betsch and colleagues' study but would typically be grouped with the United States, Germany and the Netherlands, rather than with South Korea, Vietnam and Hong Kong. Overall, our findings suggested that people with more collectivist orientations were more responsive to the community immunity idea than those with more individualist orientations. In other words, by conducting within-country rather than between-country analyses, we found that some people are more collectivist while others are more individualist, and these individual differences may influence how people respond to public health appeals to protect others. Other research by Amin and colleagues has similarly shown that individuals' orientations toward purity and liberty as moral foundations are associated with vaccine hesitancy, while the moral foundations of harm and fairness that are more commonly emphasized in messaging around vaccines were not associated with vaccine hesitancy or uptake [53]. Taken together, such findings emphasize the importance of potentially tailoring approaches to vaccine messaging according to individuals' broader values, worldviews, and orientations towards self and others [54].

Third, although most findings were consistent across the four disease conditions we used in our study, we did observe signals of potential disease-specific findings that offer potential implications or avenues for future work. One such signal occurred on the outcome of subjective risk perception, which was higher overall among people who were assigned to the *herdimm* intervention compared to those assigned to the control condition, but particularly so among people assigned to the influenza condition due to lower baseline subjective risk perception among people who completed the study in the context of influenza. Specifically, people assigned to the control condition in the context of influenza indicated lower subjective risk perception, meaning they were less likely to agree with statements like, “If I get vaccinated against the flu, it lowers the risk of vulnerable people in my community (babies, young children, older people, cancer patients) getting sick,” compared to those asked to indicate their level of agreement with those same statements but with terms measles, pertussis, or a vaccine-preventable disease in place of, “the flu.” This is consistent with lower uptake of influenza vaccines in many jurisdictions compared to uptake of vaccines against measles, pertussis, and many other diseases. Among those assigned to the *herdimm* intervention, however, subjective risk perception was similar across diseases. This may imply that helping people understand how community immunity works may be particularly useful in the context of influenza, a condition for which vaccine uptake is often lower, especially among those at lower risk of severe influenza [55].

Fourth and finally, our study also offers some methodological lessons for future evaluations of similar digital health interventions that may be useful to other research groups. Participants in our study assigned to the *herdimm* condition had to answer sociodemographic questions in Qualtrics, click on a link to visit a university-based website hosting the *herdimm* intervention, then return to their Qualtrics questionnaire to answer questions making up the outcome measures. We observed very high dropout rates due to people either abandoning the study at the point of visiting the university-based website, or completing the outcome questions with insufficient time in between to have actually visited the *herdimm* website. A related study our group conducted in which we adapted the *herdimm* intervention to show why social distancing was being recommended to help reduce COVID-19 transmission showed that the largest proportion of people who abandoned the university-based website in that study did so at the step of creating 8 additional avatars to represent the people around the individual [56]. For future research, we therefore added the option for people to auto-generate additional avatars. Additionally, rather than simply instructing participants to visit an external site and return to the questionnaire to complete the study, in future studies in which we need to ask participants to visit an external site, we plan to use individualized links containing the anonymized Qualtrics respondent IDs as parameters within the link, then provide an individualized link back to their Qualtrics questionnaire. Although this is a more complex procedure, it will ensure better intervention fidelity as well as allow the collection of data about people’s behaviour at the website (for example, time spent on each step, choice of avatars, etc.) for analysis. Additionally, our planned analyses for this study included plans for multiple imputation to account for missing outcome data. However, we did not pre-plan similar imputation for missing sociodemographic data, meaning that our adjusted analyses removed about 11% of participants while also adding variables, and therefore had lower statistical power. Future studies should include plans for addressing missing data among covariates to avoid such diminished statistical power.

Strengths and Limitations

Our study had five key limitations. First, some outcomes were evaluated with items developed specifically for this study due to the lack of validated scales in the context of communication about community immunity. While we pre-tested our measures and examined standard psychometric indicators of validity such as Cronbach alpha, full validation studies were outside the scope of this work. Second, as noted above, we observed high dropout rates in *herdimm* arms, likely because people had to visit the *herdimm* website in the middle of the questionnaire and then come back to finish the study. This means that the effects of the *herdimm* intervention may be either overestimated or underestimated. To explore this issue, we examined sociodemographic differences between people who did and did not complete the study. The largest difference we observed was among participants who self-identified as white, who were more populous among the group who completed the study (80% among completes versus 62% among incompletes.) Identifying as white was also associated with higher knowledge. This means that the observed effects of *herdimm* on knowledge may be overestimated because, in the final dataset, there were more people with a characteristic associated with higher knowledge in the intervention arms. Alternatively, effects may be underestimated if the higher knowledge scores are attributable to pre-existing knowledge. Third, some identity elements (e.g., some racial and ethnic groups) had to be merged due to low numbers. As a result, we do not know the influence of specific groups, e.g., Black Caribbean, as a covariate on our outcomes. This may be a limitation if such covariates are influential on our outcomes. However, given that the racial and ethnic groups that we did retain had little influence as covariates, it is unlikely that collapsing groups would have had a substantial influence. Fourth, the distribution of data on a number of continuous or quasi-continuous outcomes required establishing a cutoff to perform logistic regressions. Although we prepared our statistical code before collecting data and preregistered our analyses, we had little prior data to guide our choices for such cutoffs, meaning that the cutoffs were necessarily somewhat arbitrary. Fifth and finally, our study took place during early COVID-19 vaccination campaigns in Canada. We did not add COVID-19 as a named vaccine-preventable disease in our study for a number of reasons, including that it was not yet known whether the early COVID-19 vaccines would be able to produce robust community immunity. It is possible, and perhaps likely, that participants assigned to the generic, “vaccine-preventable disease,” condition may have been thinking of COVID-19 as they responded to the study questions, which may have influenced their responses in one direction or another. However, for the vast majority of our outcomes, we did not observe significant differences between people assigned to the generic disease and those assigned to measles, pertussis, and flu. This suggests that if participants were thinking of COVID-19, their responses were nonetheless similar to the responses of people thinking of other diseases.

Our study also had three key strengths. First, for methodological robustness, we preregistered the entire study, including all study materials and statistical code developed with simulated data. Such preregistration may have been particularly important for this study, given that we anticipated the need to divide risk perception into objective and subjective components and use logistic regressions for a number of continuous outcomes. Second, we evaluated the *herdimm* intervention across four disease conditions–three named diseases and an unnamed, “vaccine-preventable disease.” Much research on vaccine decision making is conducted on only one vaccine-preventable disease at a time or without ever naming a particular disease, thus limiting its generalizability. People may respond differently to a situation involving an abstract, unnamed disease than they do to a known, named disease, and yet we cannot

assume that responses to messaging about one specific disease will be applicable to messaging about another specific disease. Identifying approaches that work across diseases is important for achieving broader public health goals. Studies such as ours therefore offer findings that are more robust than they would have been had we used only a single disease. Third, the *herdimm* intervention offers insights about the potential applicability of personalization and tailoring to vaccine messaging. By having people create their own avatar, the avatars of people around them, and then using those avatars in an animation, the *herdimm* intervention aimed to help people literally see how their vaccination decisions could impact others around them. This message was more impactful among people with more collectivist orientations, underlining the idea that although public health messages are often universal, delivering them differently to different people may increase their impact.

Conclusions

Visually conveying the concept of community immunity using personalized avatars improves objective and subjective risk perception, emotions, knowledge and increases intentions to receive vaccines. Our work also contributes evidence of how community immunity messages may influence vaccine acceptance differently among people whose personal orientations are more collectivist versus those who are more individualist, which offers insights about how we might target messages to different people. Put another way, conveying the concept of community immunity in understandable ways may contribute to public health efforts to achieve adequate vaccine coverage. However, this needs to be done with care, as not everyone will respond to messages about protecting others in the same way.

DECLARATIONS

Ethics approval and consent to participate

This project is approved by the “Comité d’éthique de la recherche en sciences de la santé” ethics committee of Laval University (Approval No. 2017- 137 Phase II / 03-09-2019). All participants included in the study consented to participate in the study.

Consent for publication

Availability of data and materials

All study materials were pre-registered and are available on Open Science Framework (https://osf.io/hkysb/). Web development code is available on GitHub: https://github.com/Witteman-Lab/herdimm. Anonymized data are available at Université Laval’s Dataverse, Boréalis: https://doi.org/10.5683/SP3/41MWKO.

Conflict of interest

None

Acknowledgments

The authors gratefully acknowledge the contributions of Mehdi Aouami and Rosalie Baker for designing the first version of our prototype, and Ali Ben Charif for constructive comments on earlier versions of this paper.

Authors’ Contributions

Funding

This study was funded by the Canadian Institutes of Health Research (grant number FDN-148426, 2016-2021, PI: Witteman). The CIHR had no role in determining the study design, the plans for data collection or analysis, the decision to publish, nor the preparation of this manuscript. HOW is funded by a Tier 2 Canada Research Chair in Human-Centred Digital Health. Dr. Sander is funded by a Tier 1 Canada Research Chair in Economics of Infectious Diseases (CRC-2022-00362). Dr. Scherer was supported by the National Institute on Aging of the National Institutes of Health under Award Number K01AG065440. The content is solely the responsibility of the authors and does not necessarily represent the official views of NIH.

Appendices

Appendix 1. Links or video of herdimm intervention

Appendix 2. Scatterplot and bland-altman for risk perception

Appendix 3. *Herdimm* survey questionnaire

Appendix 4. Descriptive statistic per study arm

Appendix 5. Complete results of models

Appendix 6. Outcomes and timestamp versus Individualism and Collectivism subscales

Abbreviation

OSF Open Science Framework
(IQR) Interquartile range
CI, Confidence interval
Df, Degree of freedom
p, p-value;
F, F-statistic
LR Chisq, Likelihood ratio tests
ANOVA, Analysis of variance

Figures

Figure 1. Objective risk perception
Figure 2. CONSORT flow diagram
Figure 3. Subjective risk perception for *herdimm* versus control

Tables

Table 1. Subjective risk perception
Table 2. Model used for analysis
Table 3. Participants characteristics across the study (N=3883)
Table 4. Two way analysis of variance of subjective risk perception

References

1. Rashid H, Khandaker G, Booy R. Vaccination and herd immunity: what more do we know? Curr Opin Infect Dis. 2012;25: 243–249.

2. Metcalf CJE, Ferrari M, Graham AL, Grenfell BT. Understanding Herd Immunity. Trends Immunol. 2015;36: 753–755.

3. Mulberry N, Tupper P, Kirwin E, McCabe C, Colijn C. Vaccine rollout strategies: The case for vaccinating essential workers early. PLOS Glob Public Health. 2021;1: e0000020.

4. Alfredsson R, Svensson E, Trollfors B, Borres MP. Why do parents hesitate to vaccinate their children against measles, mumps and rubella? Acta Paediatr. 2004;93: 1232–1237.

5. Dube E, Bettinger JA, Halperin B, Bradet R, Lavoie F, Sauvageau C, et al. Determinants of parents' decision to vaccinate their children against rotavirus: results of a longitudinal study. Health Education Research. 2012. pp. 1069–1080. doi:10.1093/her/cys088

6. Downs JS, de Bruin WB, Fischhoff B. Parents' vaccination comprehension and decisions. Vaccine. 2008;26: 1595–1607.

7. Omer SB, Salmon DA, Orenstein WA, deHart MP, Halsey N. Vaccine refusal, mandatory immunization, and the risks of vaccine-preventable diseases. N Engl J Med. 2009;360: 1981–1988.

8. Salmon DA, Dudley MZ, Glanz JM, Omer SB. Vaccine hesitancy: Causes, consequences, and a call to action. Vaccine. 2015;33 Suppl 4: D66–71.

9. Smith LE, Amlôt R, Weinman J, Yiend J, Rubin GJ. A systematic review of factors affecting vaccine uptake in young children. Vaccine. 2017;35: 6059–6069.

10. Betsch C, Böhm R, Korn L, Holtmann C. On the benefits of explaining herd immunity in vaccine advocacy. Nature Human Behaviour. 2017;1: s41562–017–0056.

11. Logan J, Nederhoff D, Koch B, Griffith B, Wolfson J, Awan FA, et al. "What have you HEARD about the HERD?" Does education about local influenza vaccination coverage and herd immunity affect willingness to vaccinate? Vaccine. 2018;36: 4118–4125.

12. Al-Hatamleh MAI, Abusalah MA, Hatmal MM, Alshaer W, Ahmad S, Mohd-Zahid MH, et al. Understanding the challenges to COVID-19 vaccines and treatment options, herd immunity and probability of reinfection. J Taibah Univ Med Sci. 2023;18: 600–638.

13. She J, Hou D, Chen C, Bi J, Song Y. Challenges of vaccination and herd immunity in COVID-19 and management strategies. Clin Respir J. 2022;16: 708–716.

14. Skowronski DM, Kaweski SE, Irvine MA, Kim S, Chuang ESY, Sabaiduc S, et al. Serial cross-sectional estimation of vaccine-and infection-induced SARS-CoV-2 seroprevalence in British Columbia, Canada. CMAJ. 2022;194: E1599–E1609.

15. Hakim H, Provencher T, Chambers CT, Driedger SM, Dube E, Gavaruzzi T, et al. Interventions to help people understand community immunity: A systematic review. Vaccine. 2019;37: 235–247.

16. Healey CG, Enns JT. Attention and visual memory in visualization and computer graphics. IEEE Trans Vis Comput Graph. 2012;18: 1170–1188.

17. Yee N, Bailenson J. The Proteus Effect: The Effect of Transformed Self-Representation on

Behavior. Hum Commun Res. 2007;33: 271–290.

18. Yee N, Bailenson JN, Ducheneaut N. The Proteus Effect: Implications of Transformed Digital Self-Representation on Online and Offline Behavior. Communic Res. 2009;36: 285–312.

19. Yee N, Ducheneaut N, Yao M, Nelson L. Do men heal more when in drag? conflicting identity cues between user and avatar. Proceedings of the SIGCHI Conference on Human Factors in Computing Systems. New York, NY, USA: Association for Computing Machinery; 2011. pp. 773–776.

20. Wakefield JRH, Khauser A. Doing it for us: Community identification predicts willingness to receive a COVID-19 vaccination via perceived sense of duty to the community. J Community Appl Soc Psychol. 2021;31: 603–614.

21. Paul KT, Eberl J-M, Partheymüller J. Policy-Relevant Attitudes Toward COVID-19 Vaccination: Associations With Demography, Health Risk, and Social and Political Factors. Front Public Health. 2021;9: 671896.

22. Loewenstein GF, Weber EU, Hsee CK, Welch N. Risk as feelings. Psychol Bull. 2001;127: 267.

23. Slovic P, Finucane ML, Peters E, MacGregor DG. Risk as Analysis and Risk as Feelings: Some Thoughts about Affect, Reason, Risk, and Rationality. Risk Analysis. 2004. pp. 311–322. doi:10.1111/j.0272-4332.2004.00433.x

24. Slovic P, Peters E. Risk Perception and Affect. Curr Dir Psychol Sci. 2006;15: 322–325.

25. Reyna VF. How people make decisions that involve risk a dual-processes approach. Curr Dir Psychol Sci. 2004;13: 60–66.

26. Peters E, Lipkus I, Diefenbach MA. The Functions of Affect in Health Communications and in the Construction of Health Preferences. J Commun. 2006;56: S140–S162.

27. Du M, Tao L, Liu J. Association between risk perception and influenza vaccine hesitancy for children among reproductive women in China during the COVID-19 pandemic: a national online survey. BMC Public Health. 2022;22: 385.

28. Marzo RR, Ahmad A, Islam MS, Essar MY, Heidler P, King I, et al. Perceived COVID-19 vaccine effectiveness, acceptance, and drivers of vaccination decision-making among the general adult population: A global survey of 20 countries. PLoS Negl Trop Dis. 2022;16: e0010103.

29. Hakim H, Bettinger JA, Chambers CT, Driedger SM, Dubé E, Gavaruzzi T, et al. A Web Application About Herd Immunity Using Personalized Avatars: Development Study. J Med Internet Res. 2020;22: e20113.

30. Lab W. Community Immunity Demo Video. Youtube; 12 May 2021 [cited 16 Nov 2022]. Available: https://www.youtube.com/watch?v=PXzqXnZ-keQ

31. Lab W. Herdimm application. In: Design for better health - Community Immunity [Internet]. 2021. Available: http://wlab.fmed.ulaval.ca/projects/herdimm/#/?d=measles&v=male&lang=en

32. Online survey software. In: Qualtrics [Internet]. 30 Sep 2019 [cited 11 Sep 2023]. Available: https://www.qualtrics.com/core-xm/survey-software/

33. Canadian Heritage. Statistics on official languages in Canada. 26 Nov 2019 [cited 2 Jul 2021]. Available: https://www.canada.ca/en/canadian-heritage/services/official-languages-bilingualism/publications/statistics.html

34. The CONSORT Statement. [cited 26 Jan 2021]. Available: http://www.consort-statement.org/

35. Government of Canada, Canada S. Census Profile, 2016 Census - Canada [Country] and Canada [Country]. 8 Feb 2017 [cited 8 Nov 2023]. Available: https://www12.statcan.gc.ca/census-recensement/2016/dp-pd/prof/details/page.cfm?Lang=E&Geo1=PR&Code1=01&Geo2=&Code2=&SearchText=Canada&SearchType=Begins&SearchPR=01&B1=All&TABID=1&type=0

36. Osuji VC, Galante EM, Mischoulon D, Slaven JE, Maupome G. COVID-19 vaccine: A 2021 analysis of perceptions on vaccine safety and promise in a U.S. sample. PLoS One. 2022;17: e0268784.

37. Triandis HC, Gelfand MJ. Converging measurement of horizontal and vertical individualism and collectivism. J Pers Soc Psychol. 74: 118–128.

38. Fetzer Institute. INDIVIDUALISM AND COLLECTIVISM SCALE (also known as the Culture Orientation Scale). Available: https://fetzer.org/sites/default/files/images/stories/pdf/selfmeasures/CollectiveOrientation.pdf

39. Faul F, Erdfelder E, Lang A-G, Buchner A. G*Power 3: a flexible statistical power analysis program for the social, behavioral, and biomedical sciences. Behav Res Methods. 2007;39: 175–191.

40. R Development Core Team. R: A language and environment for statistical computing. Vienna, Austria: R Foundation for Statistical Computing; 2017. Available: https://www.R-project.org/

41. Revelle W. Procedures for personality and psychological research, Northwestern University, Evanston, Illinois, USA. 2017. Available: https://CRAN.R-project.org/package=psych Version = 2.0.12,.

42. Fox J, Weisberg S. An R Companion to Applied Regression. SAGE Publications; 2018.

43. Lenth RV. Emmeans: estimated marginal means, aka least-squares means. R package version 1.6. 1. 2021.

44. van Buuren S, Groothuis-Oudshoorn K. mice: Multivariate Imputation by Chained Equations in R. Journal of Statistical Software, Articles. 2011;45: 1–67.

45. Durham DP, Casman EA. Incorporating individual health-protective decisions into disease transmission models: a mathematical framework. J R Soc Interface. 2012;9: 562–570.

46. Funk S, Salathé M, Jansen VAA. Modelling the influence of human behaviour on the spread of infectious diseases: a review. J R Soc Interface. 2010;7: 1247–1256.

47. Chapman GB, Coups EJ. Emotions and preventive health behavior: worry, regret, and influenza vaccination. Health Psychol. 2006;25: 82–90.

48. Weinstein ND, Kwitel A, McCaul KD, Magnan RE, Gerrard M, Gibbons FX. Risk perceptions: assessment and relationship to influenza vaccination. Health Psychol. 2007;26: 146–151.

49. Caserotti M, Girardi P, Rubaltelli E, Tasso A, Lotto L, Gavaruzzi T. Associations of COVID-19 risk perception with vaccine hesitancy over time for Italian residents. Soc Sci Med. 2021;272: 113688.

50. Schmid P, Rauber D, Betsch C, Lidolt G, Denker M-L. Barriers of Influenza Vaccination Intention and Behavior – A Systematic Review of Influenza Vaccine Hesitancy, 2005 – 2016. PLOS ONE. 2017. p. e0170550. doi:10.1371/journal.pone.0170550

51. Vietri JT, Li M, Galvani AP, Chapman GB. Vaccinating to help ourselves and others. Med Decis Making. 2012;32: 447–458.

52. Kim M, Lee H, Kiang P, Aronowitz T, Sheldon LK, Shi L, et al. A Storytelling Intervention in a Mobile, Web-Based Platform: A Pilot Randomized Controlled Trial to Evaluate the Preliminary Effectiveness to Promote Human Papillomavirus Vaccination in Korean American College Women. Health Educ Behav. 2020;47: 258–263.

53. Amin AB, Bednarczyk RA, Ray CE, Melchiori KJ, Graham J, Huntsinger JR, et al. Association of moral values with vaccine hesitancy. Nature Human Behaviour. 2017;1: 873–880.

54. Hornsey MJ, Harris EA, Fielding KS. The psychological roots of anti-vaccination attitudes: A 24-nation investigation. Health Psychol. 2018;37: 307–315.

55. Yeung MPS, Lam FLY, Coker R. Factors associated with the uptake of seasonal influenza vaccination in adults: a systematic review. J Public Health . 2016;38: 746–753.

56. Etienne D, Archambault P, Aziaka D, Chipenda-Dansokho S, Dubé E, Fallon CS, et al. A Personalized Avatar-Based Web Application to Help People Understand How Social Distancing Can Reduce the Spread of COVID-19: Cross-sectional, Observational, Pre-Post Study. JMIR Form Res. 2023;7: e38430.

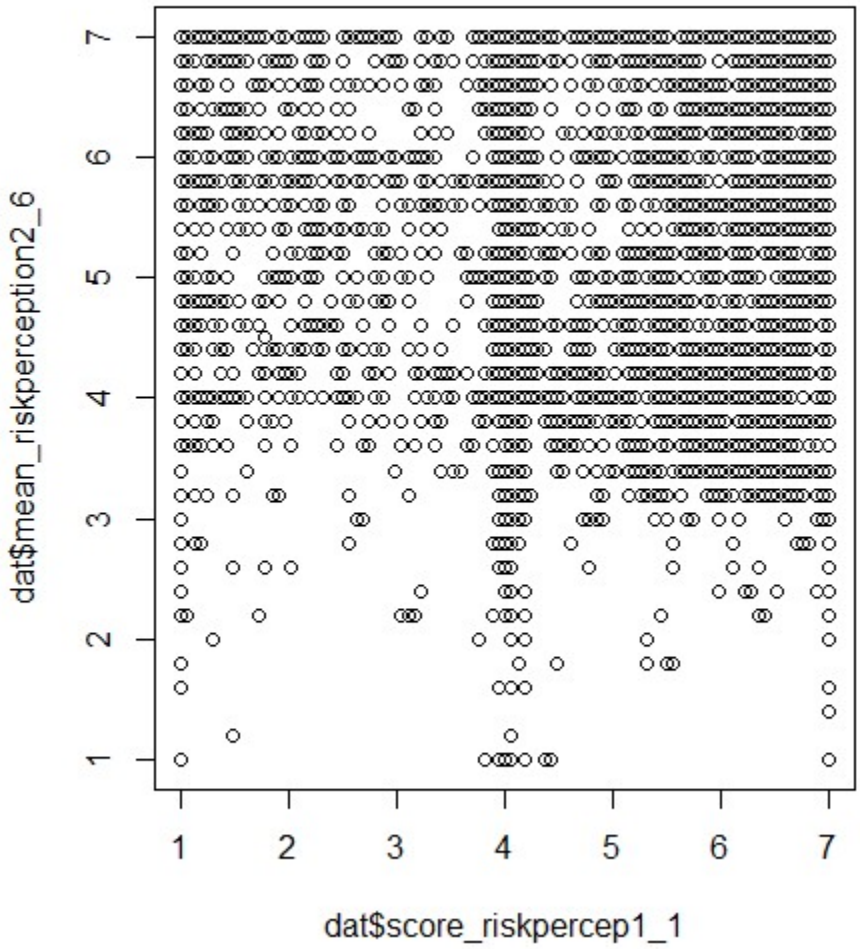
Appendix 1 : Links or video of herdimm intervention

Visualization	Link or video
Herdimm demo video (English)	https://www.youtube.com/watch?v=PXzqXnZ-keQ
Herdimm demo video (French)	https://www.youtube.com/watch?v=F8ZjQTcihjg
Herdimm: generic vaccine preventable disease & measles (English-Male)	http://wlab.fmed.ulaval.ca/projects/herdimm/#/?d=measles&v=male&lang=en
Herdimm: generic vaccine preventable disease & measles (English-Female)	http://wlab.fmed.ulaval.ca/projects/herdimm/#/?d=measles&v=female&lang=en
Herdimm: generic vaccine preventable disease & measles (French -Male)	http://wlab.fmed.ulaval.ca/projects/herdimm/#/?d=measles&v=male&lang=fr
Herdimm: generic vaccine preventable disease & measles (French-Female)	http://wlab.fmed.ulaval.ca/projects/herdimm/#/?d=measles&v=female&lang=fr
Herdimm- pertussis (English- Male)	http://wlab.fmed.ulaval.ca/projects/herdimm/#/?d=pertussis&v=male&lang=en
Herdimm- pertussis (English- Female)	http://wlab.fmed.ulaval.ca/projects/herdimm/#/?d=pertussis&v=female&lang=en
Herdimm- pertussis (French- Male)	http://wlab.fmed.ulaval.ca/projects/herdimm/#/?d=pertussis&v=male&lang=fr
Herdimm- pertussis (French- Female)	http://wlab.fmed.ulaval.ca/projects/herdimm/#/?d=pertussis&v=female&lang=fr
Herdimm-flu (English Male)	http://wlab.fmed.ulaval.ca/projects/herdimm/#/?d=flu&v=male&lang=en
Herdimm-flu (English Female)	http://wlab.fmed.ulaval.ca/projects/herdimm/#/?d=flu&v=female&lang=en
Herdimm-flu (French Male)	http://wlab.fmed.ulaval.ca/projects/herdimm/#/?d=flu&v=male&lang=fr

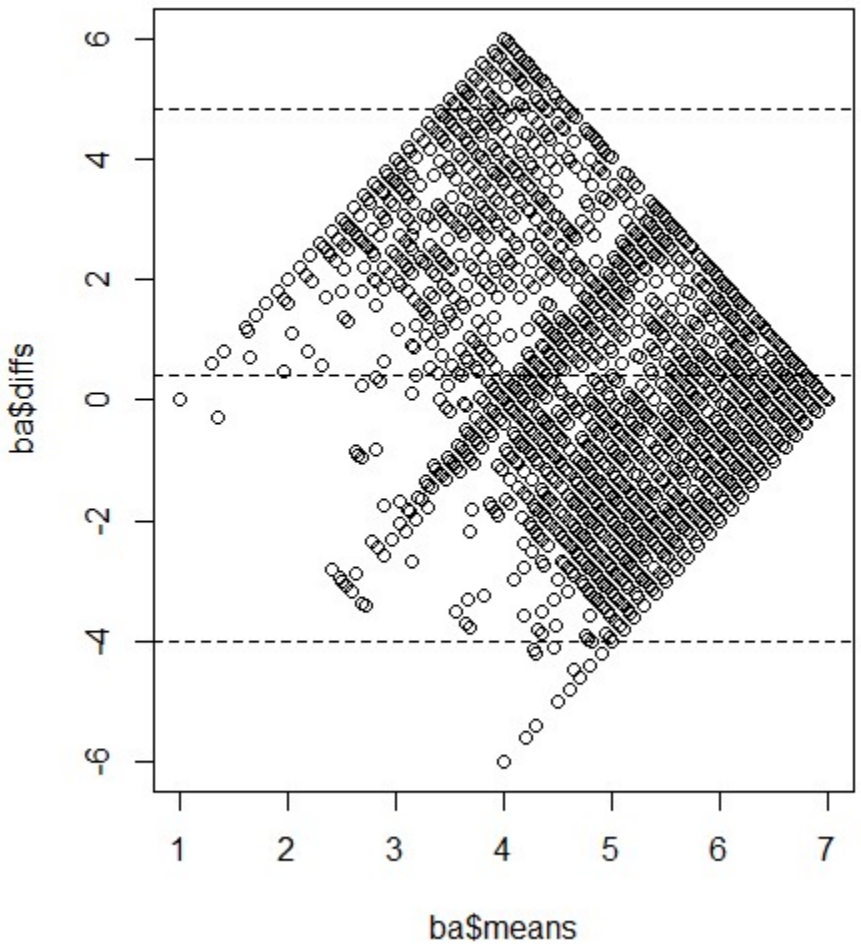
Herdimm-flu (French Female)	http://wlab.fmed.ulaval.ca/projects/herdimm/#/?d=flu&v=female&lang=fr

Appendix 2:

S1: Scatter plot to see if the item risk percep_1 (objective risk perception) and risk percept_2 to 6 (subjective risk perception) are all measuring the same thing



S2: Bland altman to see if the item risk percep_1 and risk percept_2 to 6 are all measuring the same thing



contag_phase3b

Start of Block: Introduction

Intro **Project Description**

Project Description

Introduction
Thank you for participating in this study. This project is a collaboration with University Laval, Public Health Ontario (PHO) and The National Institute of Public Health of Quebec (INSPQ).

In this study, we will first give you some information to do with contagious diseases and then ask you to answer some questions.

The survey will take about 15 to 20 minutes. Your name will not be recorded anywhere in this survey. Researchers will not be able to associate your name with your answers. If you choose to leave the study, you can stop at any time. You may choose not to answer any questions you don't want to answer. If, for some reason, you cannot complete the survey, you may **restart** the survey at a later time by clicking on the survey link in your email invitation. You will have to **restart** the survey from the beginning.

If you become worried about your health while taking this survey, please talk to a healthcare provider.

About the researchers
This study is a PhD project conducted by Ms. Hina Hakim, PhD student, supervised by Holly O. Witteman, PhD, professor and researcher in the Faculty of Medicine at Laval University. Ms. Hakim is co-supervised by Dr. Daniel Reinharz, professor and researcher in the Faculty of Medicine at Laval University.

Purpose of the study
The purpose of this study is to evaluate the effects of information to do with contagious diseases on risk perception, knowledge, emotions, attitudes, beliefs, and behavioural intentions.

What your participation entails
Participating in this study will involve following:

- Answering survey questions.
- You may be asked to view or listen to information, which will require either the ability to read or hear.

- You may be asked to briefly visit another website in the middle the survey.

Risks and benefits
The risks associated with participating in the study, specifically:

- Information and questions, we ask may make you feel uncomfortable or anxious. We suggest you to consult your healthcare professional, as the case may be;
- You may feel some discomfort having to focus on a computer screen.
- You may feel some fatigue from concentrating throughout the survey.

There is no personal benefit to participate in this study, however, the information we gather will help us to evaluate the effects of the information, which may help in improving the way health information is shared, and population health.

Your help means a lot to us. We thank you again for taking the time to complete this survey.

Confidentiality and data protection
All information we collect will be confidential and used only for research purposes.
In other words:

- Participant credentials will not be associated with the results of the study and no individual information will be presented in reports, publications or presentations.
- All data will be presented in aggregate form without individual identifiers.
- Data will be stored on Qualtrics servers located in Canada. When we work with data, the only people who will have access to our Qualtrics account will be the investigators and our team members who have complete and relevant ethics training. When the data is stored on our computers, each of our computers will be protected by a password. The data will be stored on a secure server, to which access is maintained and reserved for the members of the team (members of the team affiliated with Université Laval).

After the end of the study:

- Anonymized data (answers to questions in the survey including socio-demographic information) will be deposited in a public repository (Dataverse de l'Université Laval (Laval University)) which will allow data sharing with the scientific community. No information that would allow anyone to identify a person will be deposited in this public repository.
- Any other electronic data will be destroyed in June 2027.

Contact people
If you have any questions about the research study, or if you experience a problem as a result of participating in the study, please contact:

Holly Witteman
Laval University
Tel: (418) 656-2131 ext: 403981
Email: holly.witteman@fmed.ulaval.ca

If you have concerns about your rights as a participant in this study or any complaints, you can communicate with the University Laval Ombudsman at:

Pavillon Alphonse-Desjardins
2325, rue de l'Université, Local 3320
Québec, QC G1V 0A6
Tel: 418-656-3081
Toll free: 1-866-323-2271
Email: info@ombudsman.ulaval.ca

This project has been approved by Laval University Research Ethics Board: Approval No. 2017-137 Phase II A-6/ 10-09-2020

Start of Block: Consent for participation:

Consent

1. I have been informed about the nature and purpose of this study and the research procedures.
2. I was informed in English which is a language I understand fluently.
3. I understand that my participation in this study is voluntary and that I can withdraw at any time without penalty or consequences of any kind.
4. I understand that the information collected is confidential and will only be used for research purposes.
5. I have read the project description and informed consent form and I voluntarily agree to participate in this study.

O Yes I Consent (1)

O No I do not Consent (0)

Skip To: End of Survey If I have been informed about the nature and purpose of this study and the research procedures. I wa... = No I do not Consent

t_consent Timing
First Click (1)
Last Click (2)
Page Submit (3)
Click Count (4)

t_consent Durée
First Click (1)
Last Click (2)
Page Submit (3)
Click Count (4)

Page Break

End of Block: Consent for participation:

Start of Block: Standard Sociodemo Canada

yearofbirth In what year were you born?

▼ Prefer not to answer (888) ... 2010 (2010)

bornincanada Were you born in Canada? (Check one only.)

O Prefer not to answer (888)

O Yes (1)

O No - What year did you arrive in Canada? (0) _____

Display This Question:

If If False

hp Were you born outside North America? (Check one only.)

O Prefer not to answer (888)

O Yes (1)

O No - What year did you arrive in North America? (0)

_____

X→

language What language would you feel most comfortable speaking in with your healthcare provider? (doctor, nurse, dentist, pharmacist)? (Check all that apply.)

☐ Prefer not to answer (888)

☐ English (1)

☐ French (2)

☐ Other, please specify: (3)

_____

ethnicity Which of the following best describes your racial or ethnic group(s)? (Check all that apply.)

- ☐ Prefer not to answer (888)
- ☐ Asian - East (e.g., Chinese, Japanese, Korean) (1)
- ☐ Asian - Central (e.g., Kazakhstani, Uzbekistani) (2)
- ☐ Asian - South (e.g., Indian, Pakistani, Sri Lankan) (3)
- ☐ Asian - South-East (e.g., Malaysian, Filipino, Vietnamese) (4)
- ☐ Black - African (e.g., Ghanaian, Kenyan, Somali) (13)
- ☐ Black - Caribbean (e.g., Barbadian, Jamaican) (14)
- ☐ Black - North American (e.g., Canadian, American) (15)
- ☐ First Nations (16)
- ☐ Indigenous or aboriginal person from outside of North America (e.g., Maori, Quechua) (5)
- ☐ Inuit (8)
- ☐ Latin American (e.g., Chilean, Mexican, Salvadorian) (9)
- ☐ Metis (Metis Nation in Canada) (10)
- ☐ Middle Eastern (e.g., Egyptian, Iranian, Lebanese) (12)
- ☐ North African (e.g., Moroccan, Tunisian) (11)
- ☐ White - European (e.g., English, Italian, Portuguese, Russian) (6)
- ☐ White - North American (e.g., Canadian, American) (7)

☐ Other, please specify: (17)

_____

disability Do you consider yourself to have a disability (e.g, physical disability, sensory disability (e.g., hearing or vision loss), chronic illness, learning disability, mental illness, developmental disability or other)? (Check one only.)

- O Prefer not to answer (888)
- O No disability (0)
- O Yes, at least one disability (1)

techdisability Do you have a disability that limits your access to technology and computer based tools (p.ex. : computer, tablet, interactive terminal)? (Check one only.)

- O Prefer not to answer (888)
- O No (0)
- O Yes (1)

sexatbirth What sex were you assigned at birth, meaning on your original birth certificate? (Check one only.)

- O Prefer not to answer (888)
- O Female (1)
- O Male (2)

genderidentity Do you consider yourself: (Check one only.)

- O Female (1)
- O Male (2)
- O Indigenous or other cultural gender minority identity (e.g., two-spirit) (3)
- O Something else (e.g. non-binary, gender fluid) (4)
- O Prefer not to answer (888)

X→

income What was your total family income before taxes last year? (Check one only.)

- O □Prefer not to answer (888)
- O □24 999 or less (1)
- O □25 000 to 49 999 (2)
- O □50 000 to 99 999 (3)
- O □100 000 or more (4)
- O □Do not know (5)

supportedbyincome How many people does this income support?

O Number of people: (1) _____

O Prefer not to answer (888)

educationlevel What is the highest level of education you have completed? (Check one only.)

- O □ Prefer not to answer (888)
- O □ Elementary School (completed or not) (1)
- O □ High School Diploma (2)
- O □ Apprenticeship or trade certificate or diploma (3)
- O □ College or polytechnical school certificate or diploma (4)
- O □ University degree, bachelor level or below (5)
- O □ University graduate degree (Master's level) (6)
- O □ University graduate degree (Doctorate level) (7)
- O □ Do not know (8)

t_sociodemographic Timing
First Click (1)
Last Click (2)
Page Submit (3)
Click Count (4)

t_sociodemographic Durée
First Click (1)
Last Click (2)
Page Submit (3)
Click Count (4)

End of Block: Standard Sociodemo Canada

Start of Block: Individualism and Collectivism Scale - Triandis1998 - EN/FR

ih1 **Evaluate how well each of the following statements applies to you:**

I'd rather depend on myself rather than others.

- O Never or definitely not =1 (1)
- O 2 (2)
- O 3 (3)
- O 4 (4)
- O 5 (5)
- O 6 (6)
- O 7 (7)
- O 8 (8)
- O Always or definitely yes = 9 (9)

ih2 I rely on myself most of the time, I rarely rely on others.

- O Never or definitely not = 1 (1)
- O 2 (2)
- O 3 (3)
- O 4 (4)
- O 5 (5)
- O 6 (6)
- O 7 (7)
- O 8 (8)
- O Always or definitely yes = 9 (9)

ih3 I often do “my own thing.”

- O Never or definitely not = 1 (1)
- O 2 (2)
- O 3 (3)
- O 4 (4)
- O 5 (5)
- O 6 (6)
- O 7 (7)
- O 8 (8)
- O Always or definitely yes = 9 (9)

ih4 My personal identity, independent of others, is very important to me.

- O Never or definitely not = 1 (1)
- O 2 (2)
- O 3 (3)
- O 4 (4)
- O 5 (5)
- O 6 (6)
- O 7 (7)
- O 8 (8)
- O Always or definitely yes = 9 (9)

iv1 It is important that I do my job better than others.

- O Never or definitely not = 1 (1)
- O 2 (2)
- O 3 (3)
- O 4 (4)
- O 5 (5)
- O 6 (6)
- O 7 (7)
- O 8 (8)
- O Always or definitely yes = 9 (9)

iv2 Winning is everything.

- O Never or definitely not = 1 (1)
- O 2 (2)
- O 3 (3)
- O 4 (4)
- O 5 (5)
- O 6 (6)
- O 7 (7)
- O 8 (8)
- O Always or definitely yes = 9 (9)

iv3 Competition is the law of nature.

- O Never or definitely not = 1 (1)
- O 2 (2)
- O 3 (3)
- O 4 (4)
- O 5 (5)
- O 6 (6)
- O 7 (7)
- O 8 (8)
- O Always or definitely yes = 9 (9)

iv4 When another person does better than I do, I get tense and aroused.

- O Never or definitely not = 1 (1)
- O 2 (2)
- O 3 (3)
- O 4 (4)
- O 5 (5)
- O 6 (6)
- O 7 (7)
- O 8 (8)
- O Always or definitely yes = 9 (9)

ch1 If a coworker gets a prize, I would feel proud.

- O Never or definitely not = 1 (1)
- O 2 (2)
- O 3 (3)
- O 4 (4)
- O 5 (5)
- O 6 (6)
- O 7 (7)
- O 8 (8)
- O Always or definitely yes = 9 (9)

ch2 The well-being of my coworkers is important to me.

- O Never or definitely not = 1 (1)
- O 2 (2)
- O 3 (3)
- O 4 (4)
- O 5 (5)
- O 6 (6)
- O 7 (7)
- O 8 (8)
- O Always or definitely yes = 9 (9)

ch3 To me, pleasure is spending time with others.

- O Never or definitely not = 1 (1)
- O 2 (2)
- O 3 (3)
- O 4 (4)
- O 5 (5)
- O 6 (6)
- O 7 (7)
- O 8 (8)
- O Always or definitely yes = 9 (9)

ch4 I feel good when I cooperate with others.

- O Never or definitely not = 1 (1)
- O 2 (2)
- O 3 (3)
- O 4 (4)
- O 5 (5)
- O 6 (6)
- O 7 (7)
- O 8 (8)
- O Always or definitely yes = 9 (9)

cv1 Parents and children must stay together as much as possible.

- O Never or definitely not = 1 (1)
- O 2 (2)
- O 3 (3)
- O 4 (4)
- O 5 (5)
- O 6 (6)
- O 7 (7)
- O 8 (8)
- O Always or definitely yes = 9 (9)

cv2 It is my duty to take care of my family, even when I have to sacrifice what I want.

- O Never or definitely not = 1 (1)
- O 2 (2)
- O 3 (3)
- O 4 (4)
- O 5 (5)
- O 6 (6)
- O 7 (7)
- O 8 (8)
- O Always or definitely yes = 9 (9)

cv3 Family members should stick together, no matter what sacrifices are required.

- O Never or definitely not = 1 (1)
- O 2 (2)
- O 3 (3)
- O 4 (4)
- O 5 (5)
- O 6 (6)
- O 7 (7)
- O 8 (8)
- O Always or definitely yes = 9 (9)

cv4 It is important to me that I respect the decisions made by my groups.

- O Never or definitely not = 1 (1)
- O 2 (2)
- O 3 (3)
- O 4 (4)
- O 5 (5)
- O 6 (6)
- O 7 (7)
- O 8 (8)
- O Always or definitely yes = 9 (9)

t_ic Timing
First Click (1)
Last Click (2)
Page Submit (3)
Click Count (4)

t_ic Durée
First Click (1)
Last Click (2)
Page Submit (3)
Click Count (4)

End of Block: Individualism and Collectivism Scale - Triandis1998 - EN/FR

Start of Block: media

Display This Question:
If viz = 0

control Now we need your answers to some questions about contagious diseases.

Display This Question:
If viz = 1
Or viz = 2

robertkochgeneric Now you will visit another website with some information about contagious diseases.

When you are done, **please come back here to finish the survey.**

Display This Question:

If viz = 1

And disease = 0

And voice = 1

herdimmgenericmale Please click here to go to the other website

---

Display This Question:

If viz = 1

And disease = 0

And voice = 2

herdimmgenericfemale Please click here to go to the other website

---

Display This Question:

If viz = 1

And disease = 1

And voice = 1

herdimmmeaslesmale Please click here to go to the other website

---

Display This Question:

If viz = 1

And disease = 1

And voice = 2

herdimmmeaslesfemale Please click here to go to the other website

---

Display This Question:

If viz = 1

And disease = 2

And voice = 1

herdimmpertussismale Please click here to go to the other website

---

Display This Question:

If viz = 1

And disease = 2

And voice = 2

herdimmpertussisfema Please click here to go to the other website

---

Display This Question:

If viz = 1

And disease = 3

And voice = 1

herdimmflumale Please click here to go to the other website

Display This Question:

If viz = 1

And disease = 3

And voice = 2

herdimmflufemale Please click here to go to the other website

---

Display This Question:

If Q_Language = EN

And viz = 2

robertkoch Please click here to go to the other website

Display This Question:

If Q_Language = EN

And viz = 3

sbsnewsgeneric Now we ask you to please watch the video below with some information to do with contagious diseases and then continue the survey.

Display This Question:

If Q_Language = EN

And viz = 5

guardianmeasles
Now we ask you to please watch the video below with some information to do with contagious diseases and then continue the survey.

Display This Question:

If Q_Language = EN

And viz = 6

theotheredmundmeasle Now we ask you to please watch the video below with some information to do with contagious diseases and then continue the survey.

Display This Question:

If viz = 7

publichealthagencyca Now we ask you to please watch the video below with some information to do with contagious diseases and then continue the survey.

t_media Timing
First Click (1)
Last Click (2)
Page Submit (3)
Click Count (4)

t_media Durée
First Click (1)
Last Click (2)
Page Submit (3)
Click Count (4)

End of Block: media

Start of Block: Risk Perception

riskpercep1 Imagine there are two groups of 100 people each. In one group, there is 1 UNvaccinated person surrounded by 99 vaccinated people. In the other group, there is 1 vaccinated person surrounded by 99 UNvaccinated people. Who is at higher risk of getting infected with ${e://Field/diseasedescEN}?

	The 1 UNvaccinated person surrounded by 99 vaccinated people is at higher risk.	They are both equally at risk.	The 1 vaccinated person surrounded by a group of 99 UNvaccinated people is at higher risk.
1 ()			

riskpercep2 A person's decision to be vaccinated or not against ${e://Field/diseasedescEN} affects only them, individually.

- O strongly disagree (1)
- O moderately disagree (2)
- O slightly disagree (3)
- O neutral (4)
- O slightly agree (5)
- O moderately agree (6)
- O strongly agree (7)

riskpercep3 People who are vaccinated against ${e://Field/diseasedescEN} are less likely to pass it on to others.

- O strongly disagree (1)
- O moderately disagree (2)
- O slightly disagree (3)
- O neutral (4)
- O slightly agree (5)
- O moderately agree (6)
- O strongly agree (7)

riskpercep4 My decision to be vaccinated against ${e://Field/diseasedescEN} has **no impact** on anyone else's chances of catching ${e://Field/diseasedescEN}.

- O strongly disagree (1)
- O moderately disagree (2)
- O slightly disagree (3)
- O neutral (4)
- O slightly agree (5)
- O moderately agree (6)
- O strongly agree (7)

riskpercep5 My decision NOT to be vaccinated against ${e://Field/diseasedescEN} has **no impact** on anyone else's chances of catching ${e://Field/diseasedescEN}.

- O strongly disagree (1)
- O moderately disagree (2)
- O slightly disagree (3)
- O neutral (4)
- O slightly agree (5)
- O moderately agree (6)
- O strongly agree (7)

riskpercep6 If I get vaccinated against ${e://Field/diseasedescEN}, it lowers the risk of vulnerable people in my community (babies, young children, older people, cancer patients) getting sick.

- O strongly disagree (1)
- O moderately disagree (2)
- O slightly disagree (3)
- O neutral (4)
- O slightly agree (5)
- O moderately agree (6)
- O strongly agree (7)

t-riskpercp Timing
First Click (1)
Last Click (2)
Page Submit (3)
Click Count (4)

t-riskpercp Durée
First Click (1)
Last Click (2)
Page Submit (3)
Click Count (4)

End of Block: Risk Perception

Start of Block: 5CScale

confidence1 I am completely confident that vaccines are safe.

- O strongly disagree (1)
- O moderately disagree (2)
- O slightly disagree (3)
- O neutral (4)
- O slightly agree (5)
- O moderately agree (6)
- O strongly agree (7)

confidence2 Vaccinations are effective.

- O strongly disagree (1)
- O moderately disagree (2)
- O slightly disagree (3)
- O neutral (4)
- O slightly agree (5)
- O moderately agree (6)
- O strongly agree (7)

confidence3 Regarding vaccines, I am confident that public authorities decide in the best interest of the community.

- O strongly disagree (1)
- O moderately disagree (2)
- O slightly disagree (3)
- O neutral (4)
- O slightly agree (5)
- O moderately agree (6)
- O strongly agree (7)

complacency1 Vaccination is unnecessary because vaccine-preventable diseases are not common anymore.

- O strongly disagree (1)
- O moderately disagree (2)
- O slightly disagree (3)
- O neutral (4)
- O slightly agree (5)
- O moderately agree (6)
- O strongly agree (7)

complacency2 My immune system is so strong, it also protects me against diseases.

- O strongly disagree (1)
- O moderately disagree (2)
- O slightly disagree (3)
- O neutral (4)
- O slightly agree (5)
- O moderately agree (6)
- O strongly agree (7)

complacency3 Vaccine-preventable diseases are not so severe that I should get vaccinated.

- O strongly disagree (1)
- O moderately disagree (2)
- O slightly disagree (3)
- O neutral (4)
- O slightly agree (5)
- O moderately agree (6)
- O strongly agree (7)

constraints1 Everyday stress prevents me from getting vaccinated.

- O strongly disagree (1)
- O moderately disagree (2)
- O slightly disagree (3)
- O neutral (4)
- O slightly agree (5)
- O moderately agree (6)
- O strongly agree (7)

constraints2 For me, it is inconvenient to receive vaccinations.

- O strongly disagree (1)
- O moderately disagree (2)
- O slightly disagree (3)
- O neutral (4)
- O slightly agree (5)
- O moderately agree (6)
- O strongly agree (7)

constraints3 Visiting the doctor's makes me feel uncomfortable; this keeps me from getting vaccinated.

- O strongly disagree (1)
- O moderately disagree (2)
- O slightly disagree (3)
- O neutral (4)
- O slightly agree (5)
- O moderately agree (6)
- O strongly agree (7)

calculation1 When I think about getting vaccinated, I weigh benefits and risks to make the best decision possible.

- O strongly disagree (1)
- O moderately disagree (2)
- O slightly disagree (3)
- O neutral (4)
- O slightly agree (5)
- O moderately agree (6)
- O strongly agree (7)

calculation2 For each and every vaccination, I closely consider whether it is useful for me.

- O strongly disagree (1)
- O moderately disagree (2)
- O slightly disagree (3)
- O neutral (4)
- O slightly agree (5)
- O moderately agree (6)
- O strongly agree (7)

calculation3 It is important for me to fully understand the topic of vaccination, before I get vaccinated.

- O strongly disagree (1)
- O moderately disagree (2)
- O slightly disagree (3)
- O neutral (4)
- O slightly agree (5)
- O moderately agree (6)
- O strongly agree (7)

collectiverespon1 When everyone else is vaccinated, I don't have to get vaccinated, too.

- O strongly disagree (1)
- O moderately disagree (2)
- O slightly disagree (3)
- O neutral (4)
- O slightly agree (5)
- O moderately agree (6)
- O strongly agree (7)

collectiverespon2 I get vaccinated because I can also protect people with a weaker immune system.

- O strongly disagree (1)
- O moderately disagree (2)
- O slightly disagree (3)
- O neutral (4)
- O slightly agree (5)
- O moderately agree (6)
- O strongly agree (7)

collectiverespon3 Vaccination is a collective action to prevent the spread of diseases.

- O strongly disagree (1)
- O moderately disagree (2)
- O slightly disagree (3)
- O neutral (4)
- O slightly agree (5)
- O moderately agree (6)
- O strongly agree (7)

t_5Cscale Timing
First Click (1)
Last Click (2)
Page Submit (3)
Click Count (4)

t_5Cscale Durée
First Click (1)
Last Click (2)
Page Submit (3)
Click Count (4)

End of Block: 5CScale

Start of Block: Emotion

emotion1 I am worried about getting ${e://Field/diseasedescEN}.

- O strongly disagree (1)
- O moderately disagree (2)
- O slightly disagree (3)
- O neutral (4)
- O slightly agree (5)
- O moderately agree (6)
- O strongly agree (7)

emotion2 I am worried about people in my life (family, friends) getting ${e://Field/diseasedescEN}.

- O strongly disagree (1)
- O moderately disagree (2)
- O slightly disagree (3)
- O neutral (4)
- O slightly agree (5)
- O moderately agree (6)
- O strongly agree (7)

emotion3 I am worried about vulnerable people in my community (babies, young children, older people, cancer patients) getting ${e://Field/diseasedescEN}.

- O strongly disagree (1)
- O moderately disagree (2)
- O slightly disagree (3)
- O neutral (4)
- O slightly agree (5)
- O moderately agree (6)
- O strongly agree (7)

emotion4 I would feel guilty if someone in my life (a family member, a friend) got the ${e://Field/diseasedescEN} from me.

- O strongly disagree (1)
- O moderately disagree (2)
- O slightly disagree (3)
- O neutral (4)
- O slightly agree (5)
- O moderately agree (6)
- O strongly agree (7)

emotion5 I would feel guilty if a vulnerable person (a baby, a young child, an older person, a cancer patient) got ${e://Field/diseasedescEN} from me.

- O strongly disagree (1)
- O moderately disagree (2)
- O slightly disagree (3)
- O neutral (4)
- O slightly agree (5)
- O moderately agree (6)
- O strongly agree (7)

---

t_emotion Timing
First Click (1)
Last Click (2)
Page Submit (3)
Click Count (4)

t_emotion Durée
First Click (1)
Last Click (2)
Page Submit (3)
Click Count (4)

End of Block: Emotion

Start of Block: Knowledge

know01 When a person gets vaccinated, it can help protect: (check one)

- O The person (1)
- O The people around them (2)
- O Vulnerable people in their community (3)
- O All of the above (4)

know02 Which people are considered more vulnerable to contagious diseases, either because they can catch them more easily, or the diseases can make them sicker? (check all that apply)

- ☐ People who are very old (1)
- ☐ People who are very young (babies, etc.) (2)
- ☐ People who are athletes (3)
- ☐ People who have cancer (4)
- ☐ People who are healthy adults (5)

statement For the following statements, please indicate whether they are true, false, or you don't know:

	True (1)	False (0)	I don't know (77)
${e://Field/diseasedescEN_CAP} can spread from one person to another person. (know03)	O	O	O
When you come into contact with someone who is infected with ${e://Field/diseasedescEN}, there is a chance you could get the disease. (know04)	O	O	O
The only way to get ${e://Field/diseasedescEN} is to touch someone who has the disease. (know05)	O	O	O
${e://Field/diseasedescEN_CAP} always spread through groups of people at the same speed. (know07)	O	O	O
Some vaccines provide less protection than others. (know08)	O	O	O
Every vaccine provides full protection from a single dose (one needle/shot, one dose of drops in the mouth, or a one spray up the nose). (know10)	O	O	O
Some vaccines only provide partial protection after one dose and require multiple doses to get protected. (know11)	O	O	O
Some vaccines become less effective over time and need booster doses. (know12)	O	O	O
Community protection (or herd immunity) means everyone in the community has been vaccinated. (know13)	O	O	O
Unvaccinated people in a population can be protected from infections when enough people in their community are vaccinated. (know14)	O	O	O

Every person in a community (100%) must be vaccinated to achieve community protection. (know15)	O	O	O
The percentage of people (that is, how many members of a community) who must be vaccinated for the community to achieve community protection depends on the disease and the vaccine. (know16)	O	O	O
An individual's decision to get vaccinated or not affects only that individual. (know17)	O	O	O

t_know Durée
First Click (1)
Last Click (2)
Page Submit (3)
Click Count (4)

End of Block: Knowledge

Start of Block: Trust

trustinfo ${e://Field/trustq_EN}

- O not at all trustworthy (1)
- O moderately untrustworthy (2)
- O slightly untrustworthy (3)
- O neutral (4)
- O slightly trustworthy (5)
- O moderately trustworthy (6)
- O strongly trustworthy (7)

t_trustinfo Timing
First Click (1)
Last Click (2)
Page Submit (3)
Click Count (4)

t_trustinfo Durée
First Click (1)
Last Click (2)
Page Submit (3)
Click Count (4)

End of Block: Trust

Start of Block: Behavioural intentions

Display This Question:
If disease = 1
Or disease = 2
Or disease = 3

immune To the best of your knowledge, are you already immune to ${e://Field/diseasedescEN}?

O Yes (1)

O No (0)

O I don't know (77)

Display This Question:

If To the best of your knowledge, are you already immune to ${e://Field/diseasedescEN}? = Yes

Or If

disease = 0

Q For the next question, imagine you were **not** already immune to ${e://Field/diseasedescEN}.

---

vaxintention If you were eligible to receive a free vaccine against ${e://Field/diseasedescEN}, how likely would you be to get vaccinated?

	Extremely unlikely, I would definitely NOT be vaccinated	Extremely likely, I would definitely BE vaccinated
1 ()		

---

t_vaxintention Timing
First Click (1)
Last Click (2)
Page Submit (3)
Click Count (4)

c19vax Have you already received a COVID-19 vaccine (between Dec 2020 and now)?

- O Yes (1)
- O No (0)
- O I don't know (77)

---

t_c19vax Timing
First Click (1)
Last Click (2)
Page Submit (3)
Click Count (4)

t_c19vax Durée
First Click (1)
Last Click (2)
Page Submit (3)
Click Count (4)

Page Break

Display This Question:

If Have you already received a COVID-19 vaccine (between Dec 2020 and now)? = No

Or Have you already received a COVID-19 vaccine (between Dec 2020 and now)? = I don't know

c19vaxintention Assuming you will be eligible to get a COVID-19 vaccine this year, how likely are you to get the vaccine?

	Extremely unlikely, I will definitely NOT get a COVID-19 vaccine	Extremely likely, I will definitely get a COVID-19 vaccine
1 ()		

t_c19vaxintention Timing
First Click (1)
Last Click (2)
Page Submit (3)
Click Count (4)

t_c19vaxintention Durée
First Click (1)
Last Click (2)
Page Submit (3)
Click Count (4)

End of Block: Behavioural intentions

Appendix 4: Descriptive analysis per arm):

		control generic*	**control measles***	**control pertussis***	**control flu***	**herdimm generic***	**herdimm measles***	**herdimm pertussis***	**herdimm flu***
Age: median (IQR)		45 (27)	44 (29)	45 (28)	46 (28)	40 (21)	41(25)	41(24)	40 (22)
Gender identity: n (%)	Male	158 (49)	163 (49)	156 (50)	163 (50)	289 (49)	320 (49)	320 (49)	345 (53)
	Female	164 (51)	171 (51)	156 (50)	168 (51)	304 (51)	345 (52)	335 (51)	317 (48)
	Not available**	0 (0)	1 (0)	5 (2)	2 (1)	6 (1)	6 (1)	7 (1)	8 (1)
Language(s) spoken: n (%)									
English	Yes	235 (73)	244 (73)	232 (74)	238 (72)	502 (85)	555 (84)	559 (85)	579 (88)
	No	86 (27)	90 (27)	83 (26)	93 (28)	92 (16)	109 (16)	98 (15)	83 (13)
	Not available	1 (0)	0 (0)	0 (0)	0 (0)	1 (0)	1 (0)	1 (0)	1 (0)
French	Yes	101 (31)	107 (32)	99 (31)	109 (33)	114 (19)	141 (21)	137 (21)	129 (20)
	No	221 (69)	227 (68)	216 (69)	222 (67)	481 (81)	524 (79)	521 (79)	534 (81)
	Not available	-	-	-	-	-	-	-	-

		control generic*	control measles*	control pertussis*	control flu*	herdimm generic*	herdimm measles*	herdimm pertussis*	herdimm flu*
Ethnicity: n (%)									
White	Yes	235 (75)	255 (78)	248 (81)	253 (78)	490 (84)	558 (85)	570 (88)	563 (86)
	No	80 (25)	74 (22)	59 (19)	71 (22)	95 (16)	99 (15)	77 (12)	90 (14)
	Not available	7 (2)	5 (2)	8(3)	7 (2)	10 (2)	8 (1)	11 (2)	10 (2)
Asian	Yes	49 (16)	43 (13)	36 (12)	44 (14)	53 (9)	59 (9)	43 (7)	58 (9)
	No	266 (84)	286 (87)	271 (88)	280 (86)	532 (91)	598 (91)	604 (93)	595 (91)
	Not available	7 (2)	5 (2)	8 (3)	7 (2)	10 (2)	8 (1)	11 (2)	10 (2)
Other	Yes	29 (9)	36 (11)	28 (9)	29 (9)	41(7)	39 (6)	35 (5)	32 (5)
	No	286 (89)	293 (88)	279 (89)	295 (89)	544 (91)	618 (93)	612 (93)	621 (94)
	Not available	7 (2)	5 (2)	8 (3)	7 (2)	10 (2)	8 (1)	11 (2)	10 (2)
Disability if any: n (%)	Yes	75 (24)	71 (22)	67(22)	72 (22)	130 (22)	155 (24)	164 (25)	149 (23)
	No	244 (76)	253 (78)	240 (78)	251 (78)	453 (78)	501 (76)	482 (75)	500 (77)

		control generic*	control measles*	control pertussis*	control flu*	herdimm generic*	herdimm measles*	herdimm pertussis*	herdimm flu*
	Not available	3 (1)	10 (3)	8 (3)	8 (2)	12 (2)	9 (1)	12 (2)	14 (2)
Education levels: n (%)	College degree and above	173 (54)	158 (48)	167 (54)	174 (53)	399 (67)	440 (66)	431 (66)	419 (63)
	No college degree (elementary school, high school, apprenticeship or trade certificate)	145 (46)	171 (52)	144 (46)	155 (47)	195 (33)	224 (34)	222 (34)	241 (37)
	Not available	4 (1)	5 (2)	4 (1)	2 (1)	1 (0)	1 (0)	5 (1)	3 (1)
Place of birth (Canada): n (%)	Yes	254 (79)	280 (84)	266 (86)	274 (84)	518 (88)	573 (87)	569 (87)	569 (87)
	No	66 (21)	52 (16)	45 (14)	51 (16)	70 (12)	85 (13)	83 (13)	84 (13)
	Not available	2 (1)	2 (1)	4 (1)	6 (2)	7 (2)	7 (1)	6 (1)	10 (2)
Individualism and	Vertical individualis	46.34 (16.43)	45.5 (17.13)	46.15 (16.69)	47.52 (17.48)	42.61 (14.58)	43.86 (15.78)	44.09 (15.26)	43.28 (15.24)

		control generic*	control measles*	control pertussis*	control flu*	herdimm generic*	herdimm measles*	herdimm pertussis*	herdimm flu*
collectivism: mean (SD)	m (e.g., “It is important that I do my job better than others.”)								
	Horizontal individualism (e.g., “I rely on myself most of the time, I rarely rely on others.”)	7.21 (1.19)	7.25 (1.16)	7.31 (1.13)	7.2 (1.24)	7.1 (1.16)	7.28 (1.11)	7.22 (1.16)	7.2 (1.15)
	Vertical collectivism (e.g., “It is important to me that I respect the decisions made by my groups.”)	6.86 (1.31)	6.84 (1.4)	6.95 (1.45)	6.97 (1.37)	6.75 (1.36)	6.78 (1.4)	6.76 (1.37)	6.85 (1.42)
	Horizontal collectivism (e.g., “I feel good when I cooperate with others.”)	6.82 (1.37)	6.69 (1.36)	6.84 (1.46)	6.95 (1.26)	6.82 (1.33)	6.86 (1.29)	6.82 (1.3)	6.92 (1.3)

*****Percentages may add up to +/-100% because of rounding.
**Data could be not available due to participants choosing another option (e.g., gender-nonconforming), choosing, “I prefer not to answer,” or leaving the question unanswered.

Appendix 5: Complete results of models

Non Descriptive labels	labels
disease1	Measles
disease2	Pertussis
disease3	Flu
viz1	herdimm
language_1	English
language_2	French
edhi	We recoded this covariate as college degree and above and no college degree (elementary school, high school diploma, or apprenticeship or trade certificate or diploma.)
mean_indivhorz	Mean horizontal individualism
mean_indivvertical	Mean vertical individualism
mean_collhorz	Mean horizontal collectivism
mean_collvertical	Mean vertical collectivism

Risk perception 1 (Objective risk perception)

Two-way

Model 1: Check for direct effects of factors without any covariates ####

```
> options(contrasts=c("contr.sum", "contr.poly"))

> rlog_RP1_1 <- glm(relevel(RP1_dicho,ref="Low")  ~ viz * disease,
data = datMain,family=binomial("logit"))

> options(contrasts=c("contr.sum", "contr.poly"))

> rlog_RP1_1 <- glm(relevel(RP1_dicho,ref="Low")  ~ viz * disease,
data = datMain,family=binomial("logit"))

> Anova(rlog_RP1_1,type="III")
```

```
Analysis of Deviance Table (Type III tests)

Response: relevel(RP1_dicho, ref = "Low")

           LR Chisq Df Pr(>Chisq)

viz        134.537  1    < 2e-16 ***

disease          6.941  3    0.07379 .

viz:disease      1.193  3    0.75470

---

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> summary(rlog_RP1_1)

Call:

glm(formula = relevel(RP1_dicho, ref = "Low") ~ viz * disease,

     family = binomial("logit"), data = datMain)

Deviance Residuals:

     Min        1Q    Median      3Q     Max

-1.3974  -1.2660    0.9724    1.0755    1.4395

Coefficients:

                Estimate Std. Error z value Pr(>|z|)

(Intercept)   -0.0800911  0.0350116  -2.288   0.0222 *

viz1       -0.4011403  0.0350116 -11.457   <2e-16 ***

disease1   -0.0148705  0.0610799  -0.243   0.8076

disease2   -0.0110067  0.0601345  -0.183   0.8548

disease3   -0.1158617  0.0613271  -1.889   0.0589 .

viz1:disease1  0.0617254  0.0610799   1.011   0.3122

viz1:disease2 -0.0201992  0.0601345  -0.336   0.7369
```

```
viz1:disease3 -0.0007439  0.0613271  -0.012   0.9903

---

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

 Null deviance: 5341.2  on 3854  degrees of freedom

Residual deviance: 5196.2  on 3847  degrees of freedom

  (28 observations effacées parce que manquantes)

AIC: 5212.2

Number of Fisher Scoring iterations: 4

> # Interpretation of model 1

> mRP1_v <- emmeans(rlog_RP1_1,~viz,type = "response") #proportions

NOTE: Results may be misleading due to involvement in interactions

> mRP1_v

 viz             response   SE  df asymp.LCL asymp.UCL

 no visualization     0.382 0.01355 Inf     0.355     0.409

 herdimm              0.580 0.00977 Inf     0.560     0.599

Results are averaged over the levels of: disease

Unknown transformation "relevel": no transformation done

Confidence level used: 0.95

> plot(mRP1_v)

> confint(pairs(mRP1_v,reverse = TRUE)) #Odds ratios

 contrast                  odds.ratio SE  df asymp.LCL asymp.UCL

 herdimm / no visualization      2.23 0.156 Inf   1.92      2.54
```

```
Results are averaged over the levels of: disease

Unknown transformation "relevel": no transformation done

Confidence level used: 0.95

> mRP1_d <- emmeans(rlog_RP1_1,  ~ disease, type = "response")
#proportions

NOTE: Results may be misleading due to involvement in interactions

> mRP1_d

 disease   response     SE  df asymp.LCL asymp.UCL

 Generic   0.476 0.0177 Inf      0.442     0.511

 Measles   0.477 0.0172 Inf      0.443     0.511

 Pertussis 0.451 0.0176 Inf      0.417     0.486

 Flu       0.515 0.0172 Inf      0.482     0.549


Results are averaged over the levels of: viz

Unknown transformation "relevel": no transformation done

Confidence level used: 0.95

> plot(mRP1_d)

> confint(pairs(mRP1_d,reverse = FALSE)) #Odds ratios

 contrast             odds.ratio      SE  df asymp.LCL asymp.UCL

Measles / Generic     1.004 0.0993 Inf      0.749      1.26

 Pertussis / Generic       0.904 0.0908 Inf      0.671      1.14

 Pertussis / Measles       0.900 0.0894 Inf      0.671      1.13

 Flu / Generic             1.170 0.1156 Inf      0.873      1.47

 Flu / Measles             1.165 0.1137 Inf      0.873      1.46
```

```
 Flu / Pertussis           1.294 0.1282 Inf      0.964      1.62

Results are averaged over the levels of: viz

Unknown transformation "relevel": no transformation done

Confidence level used: 0.95

Conf-level adjustment: tukey method for comparing a family of 4
estimates
```

Model 2: Check for direct effects of factors with adjustment for other covariates

```
> rlog_RP1_2 <-

+   glm(relevel(RP1_dicho,ref="Low")  ~ viz * disease +

+     mean_indivhorz +

+     mean_indivvertical +

+     mean_collhorz +

+     mean_collvertical +

+     bornincanada +

+     language_1 +

+     language_2 +

+     Asian_group +

+     White_group +

+     disability_any +

+     genderidentity +

+     income +

+     edhi +

+     age,

+     data = datMain,family=binomial("logit")
```

```
+   )
> Anova(rlog_RP1_2, type = "III")
Analysis of Deviance Table (Type III tests)
Response: relevel(RP1_dicho, ref = "Low")
                 LR Chisq Df Pr(>Chisq)
viz                99.145  1  < 2.2e-16 ***
disease             4.503  3  0.2119784
mean_indivhorz      0.941  1  0.3319641
mean_indivvertical  0.744  1  0.3882938
mean_collhorz      14.842  1  0.0001169 ***
mean_collvertical   1.214  1  0.2704943
bornincanada        0.030  1  0.8628115
language_1          0.568  1  0.4509358
language_2          2.082  1  0.1490280
Asian_group         3.852  1  0.0496760 *
White_group         2.451  1  0.1174442
disability_any      0.000  1  0.9876937
genderidentity      2.371  1  0.1236102
income             17.023  3  0.0006991 ***
edhi                1.668  1  0.1964689
age                 0.814  1  0.3669477
viz:disease         2.054  3  0.5611757
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
> summary(rlog_RP1_2)

Call:

glm(formula = relevel(RP1_dicho, ref = "Low") ~ viz * disease +

     mean_indivhorz + mean_indivvertical + mean_collhorz +
mean_collvertical +

     bornincanada + language_1 + language_2 + Asian_group +
White_group + disability_any + genderidentity + income + edhi + age,
family = binomial("logit"), data = datMain)

 Deviance Residuals:

     Min        1Q    Median      3Q     Max

-1.6602  -1.1533   0.8341   1.0694   1.7111

Coefficients:

                     Estimate Std. Error z value Pr(>|z|)

(Intercept)      -1.2372706  0.3035918  -4.075 4.59e-05 ***

viz1             -0.3843823  0.0390175  -9.852  < 2e-16 ***

disease1         -0.0040396  0.0652813  -0.062 0.950658

disease2         -0.0353700  0.0652503  -0.542 0.587772

disease3         -0.0886128  0.0664177  -1.334 0.182147

mean_indivhorz   0.0328459  0.0338591   0.970 0.332008

mean_indivvertical -0.0205122  0.0237844  -0.862 0.388454

mean_collhorz    0.1269786  0.0331068   3.835 0.000125 ***

mean_collvertical   0.0353344  0.0320666   1.102 0.270502

bornincanada1    0.0099776  0.0577401   0.173 0.862807

language_11      -0.0616265  0.0817918  -0.753 0.451176

language_21      -0.1076321  0.0746361  -1.442 0.149277
```

```
Asian_group1     0.1715646  0.0875834   1.959 0.050128 .
White_group1     0.1133617  0.0725047   1.564 0.117933
disability_any1  0.0006842  0.0443622   0.015 0.987694
genderidentity1 -0.0561817  0.0364970  -1.539 0.123719
income1         -0.2487811  0.0840148  -2.961 0.003065 **
income2         -0.0709786  0.0664042  -1.069 0.285121
income3          0.0696654  0.0564833   1.233 0.217434
edhi1           -0.0504610  0.0390503  -1.292 0.196285
age             -0.0021782  0.0024144  -0.902 0.366961
viz1:disease1    0.0916958  0.0651595   1.407 0.159353
viz1:disease2   -0.0295778  0.0652268  -0.453 0.650217
viz1:disease3   -0.0170697  0.0663730  -0.257 0.797042
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
(Dispersion parameter for binomial family taken to be 1)
 Null deviance: 4775.3  on 3447  degrees of freedom
Residual deviance: 4575.5  on 3424  degrees of freedom
  (435 observations effacées parce que manquantes)
AIC: 4623.5
Number of Fisher Scoring iterations: 4
> # Interpretation of model 2
> mRP1_2_v <- emmeans(rlog_RP1_2,~viz,type = "response")
NOTE: Results may be misleading due to involvement in interactions
> mRP1_2_v
```

```
 viz             response    SE  df asymp.LCL asymp.UCL

 no visualization     0.384 0.0215 Inf      0.342     0.426

 herdimm              0.573 0.0217 Inf      0.531     0.616

Results are averaged over the levels of: disease, bornincanada,
language_1, language_2, Asian_group, White_group, disability_any,
genderidentity, income, edhi

Unknown transformation "relevel": no transformation done

Confidence level used: 0.95

> plot(mRP1_2_v)

> confint(pairs(mRP1_2_v,reverse = TRUE))

 contrast                  odds.ratio SE  df asymp.LCL asymp.UCL

 herdimm / no visualization      2.16 0.168 Inf   1.83      2.49

Results are averaged over the levels of: disease, bornincanada,
language_1, language_2, Asian_group, White_group, disability_any,
genderidentity, income, edhi

Unknown transformation "relevel": no transformation done

Confidence level used: 0.95

> mRP1_2_d <- emmeans(rlog_RP1_2,  ~ disease, type = "response")

NOTE: Results may be misleading due to involvement in interactions

> mRP1_2_d

 disease   response     SE  df asymp.LCL asymp.UCL

 Generic   0.477 0.0257 Inf      0.426     0.527

 Measles   0.469 0.0258 Inf      0.418     0.520

 Pertussis 0.456 0.0262 Inf      0.404     0.507

 Flu       0.510 0.0258 Inf      0.459     0.560
```

```
Results are averaged over the levels of: viz, bornincanada,
language_1, language_2, Asian_group, White_group, disability_any,
genderidentity, income, edhi

Unknown transformation "relevel": no transformation done

Confidence level used: 0.95

> plot(mRP1_2_d)

> confint(pairs(mRP1_2_d,reverse = TRUE))

 contrast             odds.ratio      SE  df asymp.LCL asymp.UCL

 Measles / Generic         0.969 0.1032 Inf      0.704      1.23

 Pertussis / Generic       0.919 0.0992 Inf      0.664      1.17

 Pertussis / Measles       0.948 0.1022 Inf      0.686      1.21

 Flu / Generic             1.141 0.1206 Inf      0.831      1.45

 Flu / Measles             1.177 0.1245 Inf      0.858      1.50

 Flu / Pertussis           1.242 0.1330 Inf      0.900      1.58

Results are averaged over the levels of: viz, bornincanada,
language_1, language_2, Asian_group, White_group, disability_any,
genderidentity, income, edhi

Unknown transformation "relevel": no transformation done

Confidence level used: 0.95

Conf-level adjustment: tukey method for comparing a family of 4
estimates
```

Model 3: Check for moderating effects of individualism & collectivism with adjustment for other covariates

```
> rlog_RP1_3 <-

+   glm(relevel(RP1_dicho,ref="Low")  ~

+     viz * disease * mean_indivhorz +

+     viz * disease * mean_indivvertical +
```

```
+     viz * disease * mean_collhorz +
+     viz * disease * mean_collvertical +
+     bornincanada +
+     language_1 +
+     language_2 +
+     Asian_group +
+     White_group +
+     disability_any +
+     genderidentity +
+     income +
+     edhi +
+     age,
+     data = datMain,family=binomial("logit")
+   )
> Anova(rlog_RP1_3, type = "III")
Analysis of Deviance Table (Type III tests)
Response: relevel(RP1_dicho, ref = "Low")
                            LR Chisq Df Pr(>Chisq)
viz                           0.7868  1  0.3750784
disease                       0.3022  3  0.9596235
mean_indivhorz                0.4402  1  0.5070139
mean_indivvertical            0.0518  1  0.8199333
mean_collhorz                12.8300  1  0.0003411 ***
mean_collvertical             0.9290  1  0.3351292
```

bornincanada	0.0279	1	0.8674032	
language_1	0.7579	1	0.3839776	
language_2	2.4752	1	0.1156556	
Asian_group	3.9343	1	0.0473122	*
White_group	2.6661	1	0.1025044	
disability_any	0.0002	1	0.9887741	
genderidentity	2.2450	1	0.1340512	
income	17.1811	3	0.0006486	***
edhi	1.5977	1	0.2062323	
age	0.9055	1	0.3413121	
viz:disease	0.3926	3	0.9417634	
viz:mean_indivhorz	0.6121	1	0.4339999	
disease:mean_indivhorz	3.1340	3	0.3714283	
viz:mean_indivvertical	1.6252	1	0.2023618	
disease:mean_indivvertical	0.9590	3	0.8111732	
viz:mean_collhorz	0.0371	1	0.8471999	
disease:mean_collhorz	0.4709	3	0.9252262	
viz:mean_collvertical	0.0134	1	0.9078471	
disease:mean_collvertical	1.1954	3	0.7540962	
viz:disease:mean_indivhorz	1.3141	3	0.7257980	
viz:disease:mean_indivvertical	1.6541	3	0.6471908	
viz:disease:mean_collhorz	1.6143	3	0.6561498	
viz:disease:mean_collvertical	1.0509	3	0.7889304	

```
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> summary(rlog_RP1_3)

Call:

glm(formula = relevel(RP1_dicho, ref = "Low") ~ viz * disease *

     mean_indivhorz + viz * disease * mean_indivvertical + viz *

     disease * mean_collhorz + viz * disease * mean_collvertical +

     bornincanada + language_1 + language_2 + Asian_group +
White_group +

     disability_any + genderidentity + income + edhi + age, family =
binomial("logit"),

     data = datMain)

 Deviance Residuals:

     Min        1Q    Median      3Q     Max

-1.6729  -1.1513   0.8305   1.0642   1.7068

 Coefficients:

                                  Estimate Std. Error z value Pr(>|z|)

(Intercept)                     -1.220066   0.331571  -3.680 0.000234
***

viz1                            -0.273334   0.308566  -0.886 0.375715

disease1                        -0.264449   0.515026  -0.513 0.607624

disease2                         0.024359   0.551847   0.044 0.964792

disease3                         0.193246   0.549988   0.351 0.725315

mean_indivhorz                   0.024186   0.036459   0.663 0.507086

mean_indivvertical              -0.005925   0.026027  -0.228 0.819913

mean_collhorz                    0.125924   0.035397   3.557 0.000374
***
```

mean_collvertical	0.033474	0.034761	0.963	0.335572
bornincanada1	0.009706	0.058134	0.167	0.867399
language_11	-0.071511	0.082192	-0.870	0.384274
language_21	-0.117862	0.074964	-1.572	0.115894
Asian_group1	0.173873	0.087836	1.980	0.047759 *
White_group1	0.119056	0.073001	1.631	0.102913
disability_any1	0.000629	0.044705	0.014	0.988774
genderidentity1	-0.055069	0.036764	-1.498	0.134158
income1	-0.252880	0.084649	-2.987	0.002814 **
income2	-0.072620	0.066955	-1.085	0.278099
income3	0.073967	0.056857	1.301	0.193282
edhi1	-0.049780	0.039367	-1.264	0.206053
age	-0.002319	0.002437	-0.952	0.341332
viz1:disease1	0.279651	0.515453	0.543	0.587450
viz1:disease2	-0.250393	0.553360	-0.452	0.650912
viz1:disease3	0.037273	0.550251	0.068	0.945994
viz1:mean_indivhorz	-0.027963	0.035734	-0.783	0.433905
disease1:mean_indivhorz	0.032513	0.061886	0.525	0.599329
disease2:mean_indivhorz	0.044438	0.062685	0.709	0.478382
disease3:mean_indivhorz	-0.113597	0.064417	-1.763	0.077821 .
viz1:mean_indivvertical	0.031819	0.024988	1.273	0.202899
disease1:mean_indivvertical	0.022073	0.042855	0.515	0.606503

```
disease2:mean_indivvertical       0.012209   0.043235   0.282 0.777651

disease3:mean_indivvertical       0.006216   0.042493   0.146 0.883689

viz1:mean_collhorz               -0.006752   0.035027  -0.193 0.847143

disease1:mean_collhorz            0.025793   0.061596   0.419 0.675399

disease2:mean_collhorz           -0.032992   0.059849  -0.551 0.581464

disease3:mean_collhorz            0.019632   0.060708   0.323 0.746410

viz1:mean_collvertical           -0.003986   0.034431  -0.116 0.907833

disease1:mean_collvertical       -0.039039   0.060984  -0.640 0.522075

disease2:mean_collvertical       -0.031763   0.059356  -0.535 0.592556

disease3:mean_collvertical        0.055172   0.060415   0.913 0.361122

viz1:disease1:mean_indivhorz     -0.005886   0.061841  -0.095 0.924178

viz1:disease2:mean_indivhorz      0.069124   0.062627   1.104 0.269705

viz1:disease3:mean_indivhorz     -0.038323   0.064451  -0.595 0.552100

viz1:disease1:mean_indivvertical -0.044082   0.042850  -1.029 0.303596

viz1:disease2:mean_indivvertical  0.042412   0.043270   0.980 0.327002

viz1:disease3:mean_indivvertical  0.014027   0.042503   0.330 0.741388

viz1:disease1:mean_collhorz       0.054583   0.061646   0.885 0.375932

viz1:disease2:mean_collhorz      -0.054661   0.059842  -0.913 0.361020

viz1:disease3:mean_collhorz      -0.031210   0.060773  -0.514 0.607563

viz1:disease1:mean_collvertical  -0.043031   0.060990  -0.706 0.480474

viz1:disease2:mean_collvertical  -0.018040   0.059462  -0.303 0.761596

viz1:disease3:mean_collvertical   0.054549   0.060450   0.902 0.366857

---

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
(Dispersion parameter for binomial family taken to be 1)

     Null deviance: 4775.3  on 3447  degrees of freedom

Residual deviance: 4562.3  on 3396  degrees of freedom

  (435 observations effacées parce que manquantes)

AIC: 4666.3

Number of Fisher Scoring iterations: 4

## Interpretation of model 3 : no interaction with moderator to
interpret
```

Risk perception 2-6 (Subjective risk perception)

Two-way

Model 1: Check for direct effects of factors without any covariates (for risk perception 2 to 6)

```
> options(contrasts=c("contr.sum", "contr.poly")) # CHANGELOG: The
statement below is added to calculate properly the type III sum of
squares with lm 2021-07-27

> mRP1_2_6 <- lm(mean_riskperception2_6  ~ viz * disease, data =
datMain)

> Anova(mRP1_2_6,type="III")

Anova Table (Type III tests)

Response: mean_riskperception2_6

            Sum Sq   Df    F value     Pr(>F)

(Intercept) 101523    1 60871.3300 < 2.2e-16 ***

viz             48    1    28.7856 8.558e-08 ***

disease         28    3     5.6430  0.000743 ***

viz:disease     14    3     2.8324  0.036917 *

Residuals  6463 3875
```

```
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> summary(mRP1_2_6)
Call:
lm(formula = mean_riskperception2_6 ~ viz * disease, data = datMain)
Residuals:
     Min   1Q  Median      3Q    Max
-4.6087 -1.0622  0.2419  1.2063  1.9378
Coefficients:
           Estimate Std. Error t value Pr(>|t|)
(Intercept)     5.41839    0.02196 246.721  < 2e-16 ***
viz1       -0.11783   0.02196  -5.365 8.56e-08 ***
disease1   -0.03458   0.03847  -0.899  0.36875
disease2         0.10543    0.03768   2.798  0.00517 **
disease3         0.05746    0.03822   1.503  0.13286
viz1:disease1  0.04147     0.03847   1.078  0.28112
viz1:disease2  0.03293     0.03768   0.874  0.38226
viz1:disease3  0.03563     0.03822   0.932  0.35135
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 1.291 on 3875 degrees of freedom
Multiple R-squared:  0.01293,         Adjusted R-squared:  0.01115
F-statistic:  7.25 on 7 and 3875 DF,  p-value: 1.175e-08
```

```
> mRP1_2_6_vd <- emmeans(mRP1_2_6,~viz|disease)

> mRP1_2_6_vd

disease = Generic:

 viz             emmean     SE   df lower.CL upper.CL

 no visualization   5.31 0.0720 3875  5.17     5.45

 herdimm         5.46 0.0529 3875      5.36     5.56


disease = Measles:

 viz             emmean     SE   df lower.CL upper.CL

 no visualization   5.44 0.0707 3875  5.30     5.58

 herdimm         5.61 0.0501 3875      5.51     5.71

disease = Pertussis:

 viz             emmean     SE   df lower.CL upper.CL

 no visualization   5.39 0.0728 3875  5.25     5.54

 herdimm         5.56 0.0503 3875      5.46     5.66

disease = Flu:

 viz             emmean     SE   df lower.CL upper.CL

 no visualization   5.06 0.0710 3875  4.92     5.20

 herdimm         5.52 0.0502 3875      5.42     5.62

Confidence level used: 0.95

> pairs(mRP1_2_6_vd) # Only do multiple comparisons if type 3 test is
significant

disease = Generic:

 contrast                   estimate   SE   df t.ratio p.value
```

```
 no visualization - herdimm   -0.153 0.0893 3875  -1.709  0.0875

disease = Measles:

 contrast                   estimate   SE   df t.ratio p.value

 no visualization - herdimm   -0.170 0.0866 3875  -1.960  0.0500

disease = Pertussis:

 contrast                   estimate   SE   df t.ratio p.value

 no visualization - herdimm   -0.164 0.0885 3875  -1.858  0.0632


disease = Flu:

 contrast                   estimate   SE   df t.ratio p.value

 no visualization - herdimm   -0.456 0.0869 3875  -5.243  <.0001

> plot(mRP1_2_6_vd)

> mRP1_2_6_dv <- emmeans(mRP1_2_6,~disease|viz)

> mRP1_2_6_dv

viz = no visualization:

 disease   emmean     SE   df lower.CL upper.CL

 Generic   5.31 0.0720 3875      5.17     5.45

 Measles   5.44 0.0707 3875      5.30     5.58

 Pertussis   5.39 0.0728 3875    5.25     5.54

 Flu       5.06 0.0710 3875      4.92     5.20

viz = herdimm:

 disease   emmean     SE   df lower.CL upper.CL

 Generic   5.46 0.0529 3875      5.36     5.56

 Measles   5.61 0.0501 3875      5.51     5.71
```

```
 Pertussis    5.56 0.0503 3875     5.46      5.66

 Flu        5.52 0.0502 3875       5.42      5.62

Confidence level used: 0.95

> pairs(mRP1_2_6_dv) # Only do multiple comparisons if type 3 test is
significant

viz = no visualization:

 contrast              estimate   SE    df t.ratio p.value

 Generic - Measles     -0.1315 0.1009 3875  -1.303  0.5607

 Generic - Pertussis   -0.0862 0.1023 3875  -0.842  0.8343

 Generic - Flu         0.2452 0.1011 3875   2.426  0.0724

 Measles - Pertussis    0.0453 0.1014 3875   0.446  0.9703

 Measles - Flu         0.3767 0.1002 3875   3.761  0.0010

 Pertussis - Flu       0.3314 0.1017 3875   3.260  0.0062

viz = herdimm:

 contrast              estimate   SE    df t.ratio p.value

 Generic - Measles     -0.1486 0.0729 3875  -2.038  0.1741

 Generic - Pertussis   -0.0979 0.0731 3875  -1.340  0.5375

 Generic - Flu         -0.0578 0.0729 3875  -0.792  0.8580

 Measles - Pertussis    0.0507 0.0710 3875   0.713  0.8918

 Measles - Flu         0.0908 0.0709 3875   1.281  0.5753

 Pertussis - Flu       0.0401 0.0711 3875   0.564  0.9426

P value adjustment: tukey method for comparing a family of 4 estimates
```

Model 2: Check for direct effects of factors with adjustment for other covariates

```
> #CHANGELOG ASJ: change list of covariates after recoding and
deletion for <5% categories, 2021-08-04

>

> mRP2_2_6 <-

+   lm(

+     mean_riskperception2_6  ~ viz * disease +

+     mean_indivhorz +

+     mean_indivvertical +

+     mean_collhorz +

+     mean_collvertical +

+     bornincanada +

+     language_1 +

+     language_2 +

+     Asian_group +

+     White_group +

+     disability_any +

+     genderidentity +

+     income +

+     edhi +

+     age,

+     data = datMain

+   )

> Anova(mRP2_2_6, type = "III")

Anova Table (Type III tests)
```

Response: mean_riskperception2_6

	Sum Sq	Df	F value	Pr(>F)	
(Intercept)	1290.0	1	869.5460	< 2.2e-16	***
viz	57.5	1	38.7881	5.295e-10	***
disease	36.0	3	8.0840	2.302e-05	***
mean_indivhorz	23.0	1	15.4788	8.508e-05	***
mean_indivvertical	275.6	1	185.7474	< 2.2e-16	***
mean_collhorz	18.5	1	12.4731	0.0004183	***
mean_collvertical	12.2	1	8.1899	0.0042379	**
bornincanada	3.8	1	2.5749	0.1086604	
language_1	4.7	1	3.2001	0.0737206	.
language_2	2.7	1	1.7957	0.1803165	
Asian_group	0.4	1	0.2369	0.6264830	
White_group	0.3	1	0.1924	0.6609294	
disability_any	55.4	1	37.3121	1.119e-09	***
genderidentity	6.4	1	4.3079	0.0380105	*
income	36.0	3	8.0944	2.268e-05	***
edhi	3.8	1	2.5492	0.1104447	
age	121.6	1	81.9744	< 2.2e-16	***
viz:disease	23.6	3	5.3036	0.0012021	**
Residuals	5103.5	3440			

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

```
> summary(mRP2_2_6)


Call:

lm(formula = mean_riskperception2_6 ~ viz * disease + mean_indivhorz +

     mean_indivvertical + mean_collhorz + mean_collvertical +

     bornincanada + language_1 + language_2 + Asian_group +
White_group +

     disability_any + genderidentity + income + edhi + age, data =
datMain)



Residuals:

     Min   1Q  Median      3Q    Max

-5.3125 -0.9019  0.1312  0.9893  2.6108



Coefficients:

                Estimate Std. Error t value Pr(>|t|)

(Intercept)     5.252126   0.178110  29.488  < 2e-16 ***

viz1            -0.142931   0.022950  -6.228 5.29e-10 ***

disease1        -0.016014   0.038546  -0.415 0.677831

disease2        0.125488   0.038175   3.287 0.001022 **

disease3        0.056686   0.038801   1.461 0.144118

mean_indivhorz  0.078372   0.019920   3.934 8.51e-05 ***

mean_indivvertical -0.190610   0.013986 -13.629  < 2e-16 ***

mean_collhorz   0.068661   0.019441   3.532 0.000418 ***

mean_collvertical  -0.054212   0.018943  -2.862 0.004238 **
```

```
bornincanada1    -0.054658   0.034062  -1.605 0.108660

language_11      0.086412   0.048305   1.789 0.073721 .

language_21      0.059010   0.044035   1.340 0.180316

Asian_group1     0.025106   0.051580   0.487 0.626483

White_group1     -0.018771   0.042791  -0.439 0.660929

disability_any1  0.159688   0.026143   6.108 1.12e-09 ***

genderidentity1  0.044696   0.021535   2.076 0.038010 *

income1          -0.203629   0.049311  -4.129 3.72e-05 ***

income2          0.016673   0.039208   0.425 0.670679

income3          0.140941   0.033363   4.225 2.46e-05 ***

edhi1            0.036862   0.023088   1.597 0.110445

age              0.012870   0.001421   9.054  < 2e-16 ***

viz1:disease1    0.057247   0.038468   1.488 0.136802

viz1:disease2    0.049503   0.038170   1.297 0.194755

viz1:disease3    0.044842   0.038774   1.156 0.247561

---

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1


Residual standard error: 1.218 on 3440 degrees of freedom

  (419 observations effacées parce que manquantes)

Multiple R-squared:  0.1369,          Adjusted R-squared:  0.1312

F-statistic: 23.73 on 23 and 3440 DF,  p-value: < 2.2e-16


> > mRP2_2_6_vd <- emmeans(mRP2_2_6,~viz|disease)
```

```
> mRP2_2_6_vd

disease = Generic:

 viz             emmean     SE   df lower.CL upper.CL

 no visualization   5.42 0.0809 3440   5.26     5.58

 herdimm         5.59 0.0698 3440      5.45     5.73


disease = Measles:

 viz             emmean     SE   df lower.CL upper.CL

 no visualization   5.55 0.0827 3440   5.39     5.71

 herdimm         5.74 0.0671 3440      5.61     5.87


disease = Pertussis:

 viz             emmean     SE   df lower.CL upper.CL

 no visualization   5.48 0.0848 3440   5.31     5.64

 herdimm         5.67 0.0681 3440      5.54     5.81


disease = Flu:

 viz             emmean     SE   df lower.CL upper.CL

 no visualization   5.06 0.0822 3440   4.90     5.22

 herdimm         5.65 0.0676 3440      5.52     5.78


Results are averaged over the levels of: bornincanada, language_1,
language_2, Asian_group, White_group, disability_any, genderidentity,
income, edhi

Confidence level used: 0.95
```

```
> pairs(mRP2_2_6_vd) # Only do multiple comparisons if type 3 test is
significant

disease = Generic:

 contrast                  estimate   SE   df t.ratio p.value

 no visualization - herdimm   -0.171 0.0897 3440  -1.910  0.0563



disease = Measles:

 contrast                  estimate   SE   df t.ratio p.value

 no visualization - herdimm   -0.187 0.0887 3440  -2.106  0.0353



disease = Pertussis:

 contrast                  estimate   SE   df t.ratio p.value

 no visualization - herdimm   -0.196 0.0908 3440  -2.162  0.0307



disease = Flu:

 contrast                  estimate   SE   df t.ratio p.value

 no visualization - herdimm   -0.589 0.0884 3440  -6.661  <.0001



Results are averaged over the levels of: bornincanada, language_1,
language_2, Asian_group, White_group, disability_any, genderidentity,
income, edhi

> plot(mRP2_2_6_vd) # Explore options for less ugly plot for
publication/thesis

>

> mRP2_2_6_dv <- emmeans(mRP2_2_6,~disease|viz)

> mRP2_2_6_dv
```

viz = no visualization:

disease	emmean	SE	df	lower.CL	upper.CL
Generic	5.42	0.0809	3440	5.26	5.58
Measles	5.55	0.0827	3440	5.39	5.71
Pertussis	5.48	0.0848	3440	5.31	5.64
Flu	5.06	0.0822	3440	4.90	5.22

viz = herdimm:

disease	emmean	SE	df	lower.CL	upper.CL
Generic	5.59	0.0698	3440	5.45	5.73
Measles	5.74	0.0671	3440	5.61	5.87
Pertussis	5.67	0.0681	3440	5.54	5.81
Flu	5.65	0.0676	3440	5.52	5.78

Results are averaged over the levels of: bornincanada, language_1, language_2, Asian_group, White_group, disability_any, genderidentity, income, edhi

Confidence level used: 0.95

> pairs(mRP2_2_6_dv) # Only do multiple comparisons if type 3 test is significant

viz = no visualization:

contrast	estimate	SE	df	t.ratio	p.value
Generic - Measles	-0.1338	0.1020	3440	-1.311	0.5560
Generic - Pertussis	-0.0603	0.1038	3440	-0.581	0.9378
Generic - Flu	0.3590	0.1016	3440	3.533	0.0024

```
 Measles - Pertussis    0.0735 0.1042 3440    0.705  0.8951

 Measles - Flu         0.4927 0.1022 3440    4.820  <.0001

 Pertussis - Flu       0.4193 0.1039 3440    4.035  0.0003


viz = herdimm:

 contrast              estimate    SE    df t.ratio p.value

 Generic - Measles     -0.1492 0.0725 3440  -2.059  0.1668

 Generic - Pertussis   -0.0851 0.0727 3440  -1.171  0.6452

 Generic - Flu         -0.0587 0.0725 3440  -0.810  0.8499

 Measles - Pertussis    0.0641 0.0705 3440   0.910  0.7995

 Measles - Flu         0.0906 0.0703 3440   1.287  0.5710

 Pertussis - Flu       0.0264 0.0705 3440   0.375  0.9821


Results are averaged over the levels of: bornincanada, language_1,
language_2, Asian_group, White_group, disability_any, genderidentity,
income, edhi

P value adjustment: tukey method for comparing a family of 4 estimates
```

Model 3: Check for moderating effects of individualism & collectivism with adjustment for other covariates

```
> mRP3_2_6 <-

+   lm(

+     mean_riskperception2_6  ~

+     viz * disease * mean_indivhorz +
```

```
+     viz * disease * mean_indivvertical +
+     viz * disease * mean_collhorz +
+     viz * disease * mean_collvertical +
+     bornincanada +
+     language_1 +
+     language_2 +
+     Asian_group +
+     White_group +
+     disability_any +
+     genderidentity +
+     income +
+     edhi +
+     age,
+     data = datMain
+   )
> Anova(mRP3_2_6, type = "III")
Anova Table (Type III tests)
Response: mean_riskperception2_6
                            Sum Sq   Df  F value  Pr(>F)
(Intercept)                 1047.9  1 716.6940 < 2.2e-16 ***
viz                            3.2  1   2.1952 0.1385346
disease                       23.7  3   5.3948 0.0010573 **
mean_indivhorz                17.8  1  12.1958 0.0004851 ***
mean_indivvertical           157.9  1 108.0030 < 2.2e-16 ***
```

mean_collhorz	21.5	1	14.7221	0.0001268	***
mean_collvertical	13.7	1	9.3499	0.0022472	**
bornincanada	4.5	1	3.0785	0.0794237	.
language_1	4.8	1	3.2494	0.0715364	.
language_2	2.3	1	1.5555	0.2124109	
Asian_group	0.3	1	0.1850	0.6671728	
White_group	0.0	1	0.0117	0.9137622	
disability_any	51.8	1	35.4543	2.876e-09	***
genderidentity	7.2	1	4.9324	0.0264237	*
income	36.1	3	8.2197	1.896e-05	***
edhi	3.0	1	2.0294	0.1543757	
age	108.5	1	74.2377	< 2.2e-16	***
viz:disease	2.9	3	0.6691	0.5709438	
viz:mean_indivhorz	5.5	1	3.7357	0.0533429	.
disease:mean_indivhorz	30.6	3	6.9784	0.0001118	***
viz:mean_indivvertical	45.6	1	31.2066	2.501e-08	***
disease:mean_indivvertical	2.7	3	0.6081	0.6097023	
viz:mean_collhorz	5.6	1	3.8465	0.0499299	*
disease:mean_collhorz	1.1	3	0.2592	0.8548273	
viz:mean_collvertical	5.6	1	3.8335	0.0503207	.
disease:mean_collvertical	3.1	3	0.7043	0.5493584	
viz:disease:mean_indivhorz	8.0	3	1.8299	0.1394644	
viz:disease:mean_indivvertical	6.5	3	1.4882	0.2156734	
viz:disease:mean_collhorz	6.2	3	1.4027	0.2400508	

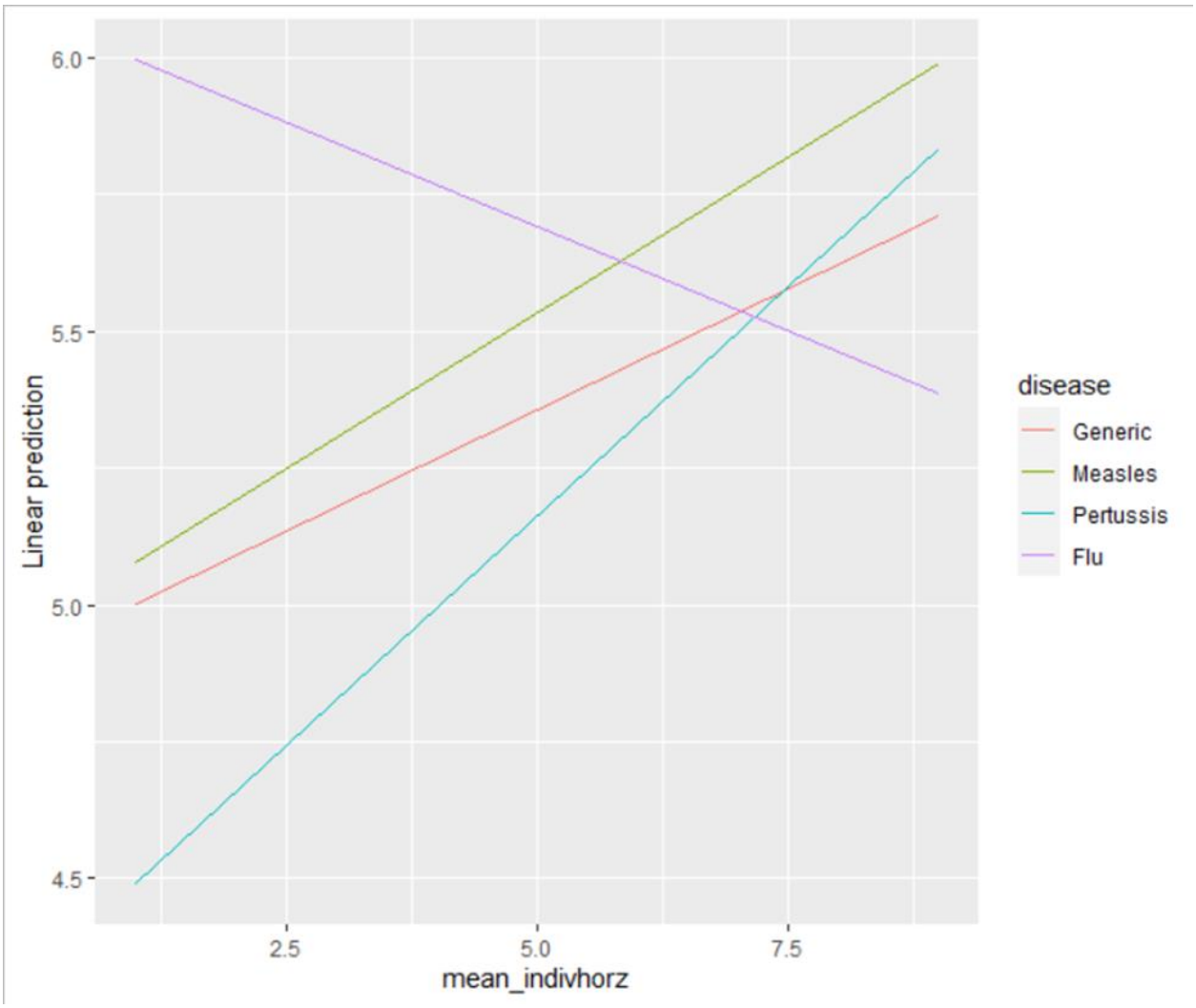
```
viz:disease:mean_collvertical     7.3  3   1.6614 0.1731695

Residuals                      4988.8 3412

---

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> summary(mRP3_2_6)

Call:

lm(formula = mean_riskperception2_6 ~ viz * disease * mean_indivhorz +

     viz * disease * mean_indivvertical + viz * disease *
mean_collhorz +

     viz * disease * mean_collvertical + bornincanada + language_1 +

     language_2 + Asian_group + White_group + disability_any +

     genderidentity + income + edhi + age, data = datMain)

Residuals:

     Min   1Q  Median      3Q    Max

-5.5146 -0.9026  0.1188  0.9901  2.6264

Coefficients:

                                Estimate Std. Error t value Pr(>|t|)

(Intercept)                     5.119656   0.191238  26.771  < 2e-16
***

viz1                           -0.262906   0.177445  -1.482 0.138535

disease1                       -0.207575   0.298125  -0.696 0.486307

disease2                        0.018653   0.315541   0.059 0.952864

disease3                       -0.890051   0.314521  -2.830 0.004684
**

mean_indivhorz                  0.073631   0.021084   3.492 0.000485
***
```

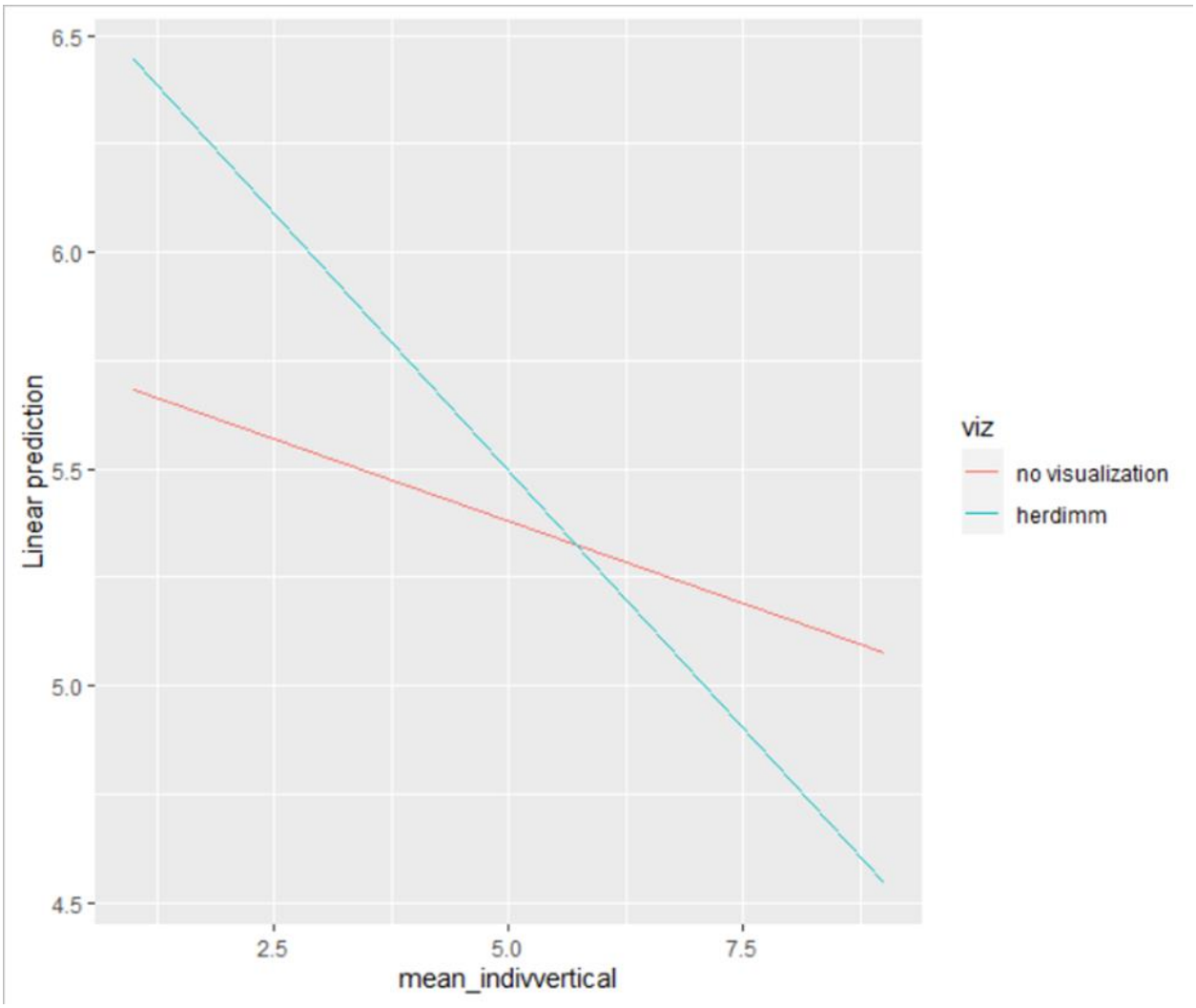
mean_indivvertical	-0.156605	0.015069	-10.392	< 2e-16 ***
mean_collhorz	0.077808	0.020279	3.837	0.000127 ***
mean_collvertical	-0.061468	0.020102	-3.058	0.002247 **
bornincanada1	-0.059627	0.033984	-1.755	0.079424 .
language_11	0.086694	0.048093	1.803	0.071536 .
language_21	0.054667	0.043832	1.247	0.212411
Asian_group1	0.022077	0.051334	0.430	0.667173
White_group1	0.004630	0.042751	0.108	0.913762
disability_any1	0.155111	0.026050	5.954	2.88e-09 ***
genderidentity1	0.047724	0.021489	2.221	0.026424 *
income1	-0.204520	0.049157	-4.161	3.25e-05 ***
income2	0.007103	0.039110	0.182	0.855887
income3	0.141228	0.033260	4.246	2.23e-05 ***
edhi1	0.032852	0.023061	1.425	0.154376
age	0.012247	0.001421	8.616	< 2e-16 ***
viz1:disease1	0.084059	0.298389	0.282	0.778184
viz1:disease2	-0.368701	0.316511	-1.165	0.244144
viz1:disease3	-0.048925	0.314674	-0.155	0.876453
viz1:mean_indivhorz	-0.039969	0.020679	-1.933	0.053343 .

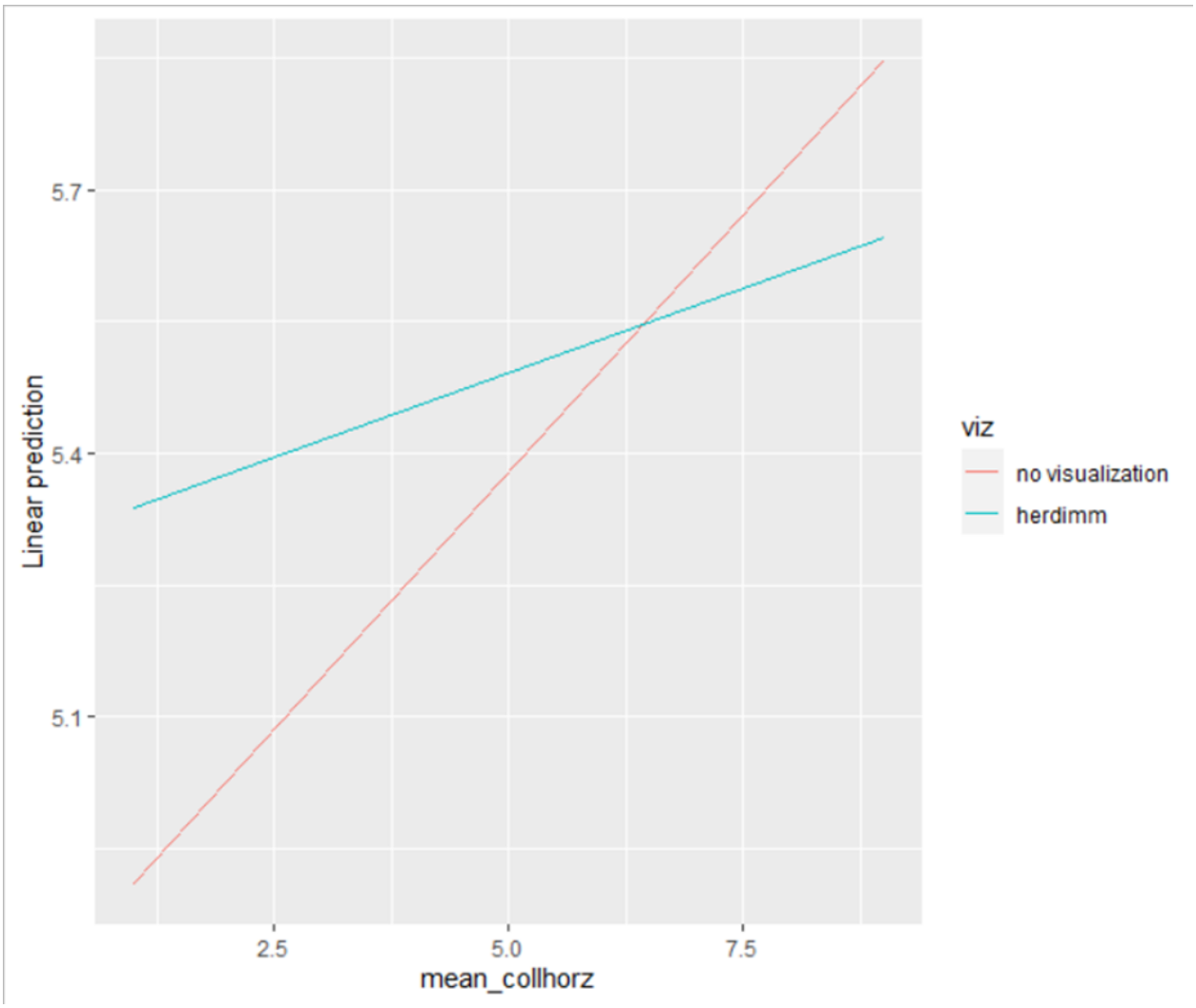
```
disease1:mean_indivhorz            0.015116   0.036099   0.419 0.675428

disease2:mean_indivhorz            0.040223   0.036070   1.115 0.264878

disease3:mean_indivhorz            0.094139   0.036966   2.547 0.010921
*

viz1:mean_indivvertical            0.080747   0.014455   5.586 2.50e-08
***

disease1:mean_indivvertical       -0.004002   0.024912  -0.161 0.872371

disease2:mean_indivvertical        0.005490   0.024827   0.221 0.824990

disease3:mean_indivvertical       -0.027332   0.024440  -1.118 0.263500

viz1:mean_collhorz                 0.039367   0.020072   1.961 0.049930
*

disease1:mean_collhorz             0.025438   0.035229   0.722 0.470297

disease2:mean_collhorz            -0.018287   0.034516  -0.530 0.596277

disease3:mean_collhorz             0.007966   0.034184   0.233 0.815740

viz1:mean_collvertical            -0.038973   0.019905  -1.958 0.050321
.

disease1:mean_collvertical        -0.010672   0.035616  -0.300 0.764467

disease2:mean_collvertical        -0.011774   0.034393  -0.342 0.732123

disease3:mean_collvertical         0.048407   0.034326   1.410 0.158572

viz1:disease1:mean_indivhorz      -0.011523   0.036071  -0.319 0.749410

viz1:disease2:mean_indivhorz       0.013563   0.036027   0.376 0.706593

viz1:disease3:mean_indivhorz       0.065112   0.036980   1.761 0.078370
.

viz1:disease1:mean_indivvertical   0.039675   0.024903   1.593 0.111205

viz1:disease2:mean_indivvertical   0.009363   0.024849   0.377 0.706335

viz1:disease3:mean_indivvertical  -0.043781   0.024448  -1.791 0.073418
.
```

```
viz1:disease1:mean_collhorz       0.053518   0.035268   1.517 0.129241

viz1:disease2:mean_collhorz       0.007187   0.034511   0.208 0.835035

viz1:disease3:mean_collhorz      -0.061586   0.034224  -1.799 0.072033
.

viz1:disease1:mean_collvertical  -0.076700   0.035625  -2.153 0.031391
*

viz1:disease2:mean_collvertical   0.033591   0.034451   0.975 0.329611

viz1:disease3:mean_collvertical   0.037282   0.034339   1.086 0.277695

---

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1


Residual standard error: 1.209 on 3412 degrees of freedom

  (419 observations effacées parce que manquantes)

Multiple R-squared:  0.1563,          Adjusted R-squared:  0.1437

F-statistic:  12.4 on 51 and 3412 DF,  p-value: < 2.2e-16

> > mRP3_2_6_d <- emmeans(mRP3_2_6,  ~ disease)

NOTE: Results may be misleading due to involvement in interactions

> mRP3_2_6_d

 disease   emmean     SE   df lower.CL upper.CL

 Generic   5.50 0.0607 3412      5.38     5.61

 Measles   5.64 0.0610 3412      5.52     5.76

 Pertussis   5.55 0.0622 3412    5.43     5.67

 Flu       5.36 0.0611 3412      5.24     5.48

Results are averaged over the levels of: viz, bornincanada,
language_1, language_2, Asian_group, White_group, disability_any,
genderidentity, income, edhi
```

```
Confidence level used: 0.95

> pairs(mRP3_2_6_d) # Only do multiple comparisons if type 3 test is
significant

 contrast             estimate   SE   df t.ratio p.value

 Generic - Measles    -0.1492 0.0629 3412  -2.374  0.0823

 Generic - Pertussis  -0.0550 0.0635 3412  -0.866  0.8226

 Generic - Flu         0.1355 0.0626 3412   2.163  0.1340

 Measles - Pertussis   0.0942 0.0637 3412   1.480  0.4499

 Measles - Flu         0.2847 0.0628 3412   4.533  <.0001

 Pertussis - Flu       0.1905 0.0634 3412   3.003  0.0143

Results are averaged over the levels of: viz, bornincanada,
language_1, language_2, Asian_group, White_group, disability_any,
genderidentity, income, edhi

P value adjustment: tukey method for comparing a family of 4 estimates

> plot(mRP3_2_6_d)
```







Emotions

Two-way

Model 1: Check for direct effects of factors without any covariates

```
> mEmotions_1 <- lm(mean_emotion  ~ viz * disease, data = datMain)

> Anova(mEmotions_1,type="III")

Anova Table (Type III tests)

Response: mean_emotion

             Sum Sq    Df     F value     Pr(>F)
```

```
(Intercept)   86042    1 45899.2910 < 2.2e-16 ***
viz              25    1    13.1273 0.0002948 ***
disease         442    3    78.5368 < 2.2e-16 ***
viz:disease       8    3     1.4856 0.2163553
Residuals      7264 3875
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> summary(mEmotions_1)
Call:
lm(formula = mean_emotion ~ viz * disease, data = datMain)
Residuals:
    Min      1Q  Median      3Q     Max
-4.4808 -0.8808  0.1842  1.0791  2.5311
Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    4.98820    0.02328 214.241  < 2e-16 ***
viz1          -0.08436    0.02328  -3.623 0.000295 ***
disease1       0.49228    0.04079  12.069  < 2e-16 ***
disease2      -0.39332    0.03995  -9.845  < 2e-16 ***
disease3      -0.28728    0.04052  -7.089 1.59e-12 ***
viz1:disease1  0.08400    0.04079   2.059 0.039518 *
viz1:disease2 -0.04166    0.03995  -1.043 0.297091
viz1:disease3 -0.03053    0.04052  -0.753 0.451277
---
```

```
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 1.369 on 3875 degrees of freedom

Multiple R-squared:  0.06262,    Adjusted R-squared:  0.06093

F-statistic: 36.98 on 7 and 3875 DF,  p-value: < 2.2e-16

> mEmotions_1_v <- emmeans(mEmotions_1,~viz)

NOTE: Results may be misleading due to involvement in interactions

> mEmotions_1_v

 viz              emmean    SE   df lower.CL upper.CL

 no visualization   4.90 0.038 3875     4.83     4.98

 herdimm            5.07 0.027 3875     5.02     5.13

Results are averaged over the levels of: disease

Confidence level used: 0.95

> plot(mEmotions_1_v)

> mEmotions_1_d <- emmeans(mEmotions_1,  ~ disease)

NOTE: Results may be misleading due to involvement in interactions

> mEmotions_1_d

 disease   emmean     SE   df lower.CL upper.CL

 Generic     5.48 0.0474 3875     5.39     5.57

 Measles     4.59 0.0459 3875     4.50     4.68

 Pertussis   4.70 0.0469 3875     4.61     4.79

 Flu         5.18 0.0461 3875     5.09     5.27

Results are averaged over the levels of: viz

Confidence level used: 0.95
```

```
> pairs(mEmotions_1_d) # Only do multiple comparisons if type 3 test
is significant

 contrast            estimate     SE   df t.ratio p.value

 Generic - Measles      0.886 0.0660 3875  13.426  <.0001

 Generic - Pertussis    0.780 0.0667 3875  11.695  <.0001

 Generic - Flu          0.304 0.0661 3875   4.600  <.0001

 Measles - Pertussis   -0.106 0.0656 3875  -1.616  0.3699

 Measles - Flu         -0.582 0.0650 3875  -8.943  <.0001

 Pertussis - Flu       -0.476 0.0657 3875  -7.234  <.0001

Results are averaged over the levels of: viz

P value adjustment: tukey method for comparing a family of 4 estimates
```

Model 2: Check for direct effects of factors with adjustment for other covariates

```
> mEmotions_2 <-

+   lm(

+     mean_emotion  ~ viz * disease +

+       mean_indivhorz +

+       mean_indivvertical +

+       mean_collhorz +

+       mean_collvertical +

+       bornincanada + #CHANGELOG ASJ: covariate list shortened 2021-
08-04

+       language_1 +

+       language_2 +

+       Asian_group +

+       White_group +
```

```
+       disability_any +
+       genderidentity +
+       income +
+       edhi +
+       age,
+     data = datMain
+   )
> Anova(mEmotions_2, type = "III")
Anova Table (Type III tests)
Response: mean_emotion
                   Sum Sq   Df  F value    Pr(>F)
(Intercept)         477.1    1 282.7357 < 2.2e-16 ***
viz                   4.9    1   2.9305  0.087009 .
disease             382.0    3  75.4663 < 2.2e-16 ***
mean_indivhorz       16.0    1   9.4949  0.002077 **
mean_indivvertical   43.3    1  25.6527 4.302e-07 ***
mean_collhorz       105.4    1  62.4423 3.663e-15 ***
mean_collvertical    47.3    1  28.0367 1.265e-07 ***
bornincanada          0.6    1   0.3840  0.535521
language_1            4.1    1   2.4494  0.117661
language_2            0.1    1   0.0365  0.848408
Asian_group           2.4    1   1.4398  0.230253
White_group           1.5    1   0.8640  0.352682
disability_any       40.6    1  24.0744 9.698e-07 ***
```

```
genderidentity       52.9    1  31.3216 2.357e-08 ***
income               20.0    3   3.9542  0.007937 **
edhi                  8.6    1   5.0942  0.024069 *
age                   4.6    1   2.7296  0.098596 .
viz:disease           8.9    3   1.7638  0.151878
Residuals          5804.7 3440
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> summary(mEmotions_2)
Call:
lm(formula = mean_emotion ~ viz * disease + mean_indivhorz +
    mean_indivvertical + mean_collhorz + mean_collvertical +
    bornincanada + language_1 + language_2 + Asian_group + White_group
+
    disability_any + genderidentity + income + edhi + age, data =
datMain)
Residuals:
    Min      1Q  Median      3Q     Max
-5.0215 -0.8450  0.1745  0.9612  3.1640
Coefficients:
                    Estimate Std. Error t value Pr(>|t|)
(Intercept)         3.194016   0.189953  16.815  < 2e-16 ***
viz1               -0.041900   0.024476  -1.712  0.08701 .
disease1            0.497976   0.041109  12.114  < 2e-16 ***
disease2           -0.398729   0.040713  -9.794  < 2e-16 ***
```

```
disease3           -0.269408   0.041381  -6.510 8.58e-11 ***
mean_indivhorz     -0.065463   0.021245  -3.081  0.00208 **
mean_indivvertical  0.075545   0.014916   5.065 4.30e-07 ***
mean_collhorz       0.163841   0.020734   7.902 3.66e-15 ***
mean_collvertical   0.106974   0.020203   5.295 1.26e-07 ***
bornincanada1       0.022510   0.036327   0.620  0.53552
language_11         0.080627   0.051517   1.565  0.11766
language_21         0.008978   0.046963   0.191  0.84841
Asian_group1        0.066008   0.055010   1.200  0.23025
White_group1       -0.042421   0.045637  -0.930  0.35268
disability_any1     0.136799   0.027881   4.907 9.70e-07 ***
genderidentity1     0.128534   0.022967   5.597 2.36e-08 ***
income1            -0.170171   0.052590  -3.236  0.00122 **
income2             0.023860   0.041815   0.571  0.56829
income3             0.037599   0.035581   1.057  0.29072
edhi1              -0.055574   0.024623  -2.257  0.02407 *
age                 0.002505   0.001516   1.652  0.09860 .
viz1:disease1       0.092047   0.041026   2.244  0.02492 *
viz1:disease2      -0.049539   0.040708  -1.217  0.22371
viz1:disease3      -0.018986   0.041353  -0.459  0.64618
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
Residual standard error: 1.299 on 3440 degrees of freedom
  (419 observations effacées parce que manquantes)
```

```
Multiple R-squared:  0.1448,     Adjusted R-squared:  0.139

F-statistic: 25.31 on 23 and 3440 DF,  p-value: < 2.2e-16

> mEmotions_2_v <- emmeans(mEmotions_2,~viz)

NOTE: Results may be misleading due to involvement in interactions

> mEmotions_2_v

 viz               emmean     SE   df lower.CL upper.CL

 no visualization   5.04 0.0570 3440     4.93     5.15

 herdimm            5.12 0.0557 3440     5.01     5.23

Results are averaged over the levels of: disease, bornincanada,
language_1, language_2, Asian_group, White_group, disability_any,
genderidentity, income, edhi

Confidence level used: 0.95

> plot(mEmotions_2_v)

> mEmotions_2_d <- emmeans(mEmotions_2,  ~ disease)

NOTE: Results may be misleading due to involvement in interactions

> mEmotions_2_d

 disease   emmean     SE   df lower.CL upper.CL

 Generic     5.58 0.0648 3440     5.45     5.71

 Measles     4.68 0.0649 3440     4.55     4.81

 Pertussis   4.81 0.0662 3440     4.68     4.94

 Flu         5.25 0.0649 3440     5.12     5.38

Results are averaged over the levels of: viz, bornincanada,
language_1, language_2, Asian_group, White_group, disability_any,
genderidentity, income, edhi

Confidence level used: 0.95
```

```
> pairs(mEmotions_2_d) # Only do multiple comparisons if type 3 test
is significant

 contrast            estimate     SE   df t.ratio p.value

 Generic - Measles      0.897 0.0668 3440  13.429  <.0001

 Generic - Pertussis    0.767 0.0676 3440  11.347  <.0001

 Generic - Flu          0.328 0.0666 3440   4.923  <.0001

 Measles - Pertussis   -0.129 0.0671 3440  -1.928  0.2165

 Measles - Flu         -0.569 0.0662 3440  -8.596  <.0001

 Pertussis - Flu       -0.440 0.0670 3440  -6.565  <.0001

Results are averaged over the levels of: viz, bornincanada,
language_1, language_2, Asian_group, White_group, disability_any,
genderidentity, income, edhi

P value adjustment: tukey method for comparing a family of 4 estimates
```

Model 3: Check for moderating effects of individualism & collectivism with adjustment for other covariates

```
> mEmotions_3 <-

+   lm(

+     mean_emotion  ~

+       viz * disease * mean_indivhorz +

+       viz * disease * mean_indivvertical +

+       viz * disease * mean_collhorz +

+       viz * disease * mean_collvertical +

+       bornincanada + #CHANGELOG ASJ: covariate list shortened 2021-
08-04

+       language_1 +

+       language_2 +
```

```
+       Asian_group +
+       White_group +
+       disability_any +
+       genderidentity +
+       income +
+       edhi +
+       age,
+     data = datMain
+   )
> Anova(mEmotions_3, type = "III")
Anova Table (Type III tests)
Response: mean_emotion
                            Sum Sq   Df  F value    Pr(>F)
(Intercept)                  435.5    1 260.4980 < 2.2e-16 ***
viz                            3.6    1   2.1566 0.1420470
disease                       19.3    3   3.8388 0.0093137 **
mean_indivhorz                13.3    1   7.9560 0.0048206 **
mean_indivvertical            29.2    1  17.4907 2.960e-05 ***
mean_collhorz                 89.0    1  53.2458 3.643e-13 ***
mean_collvertical             36.9    1  22.0572 2.751e-06 ***
bornincanada                   0.3    1   0.2018 0.6532923
language_1                     3.4    1   2.0067 0.1566974
language_2                     0.0    1   0.0089 0.9248792
Asian_group                    2.1    1   1.2604 0.2616512
```

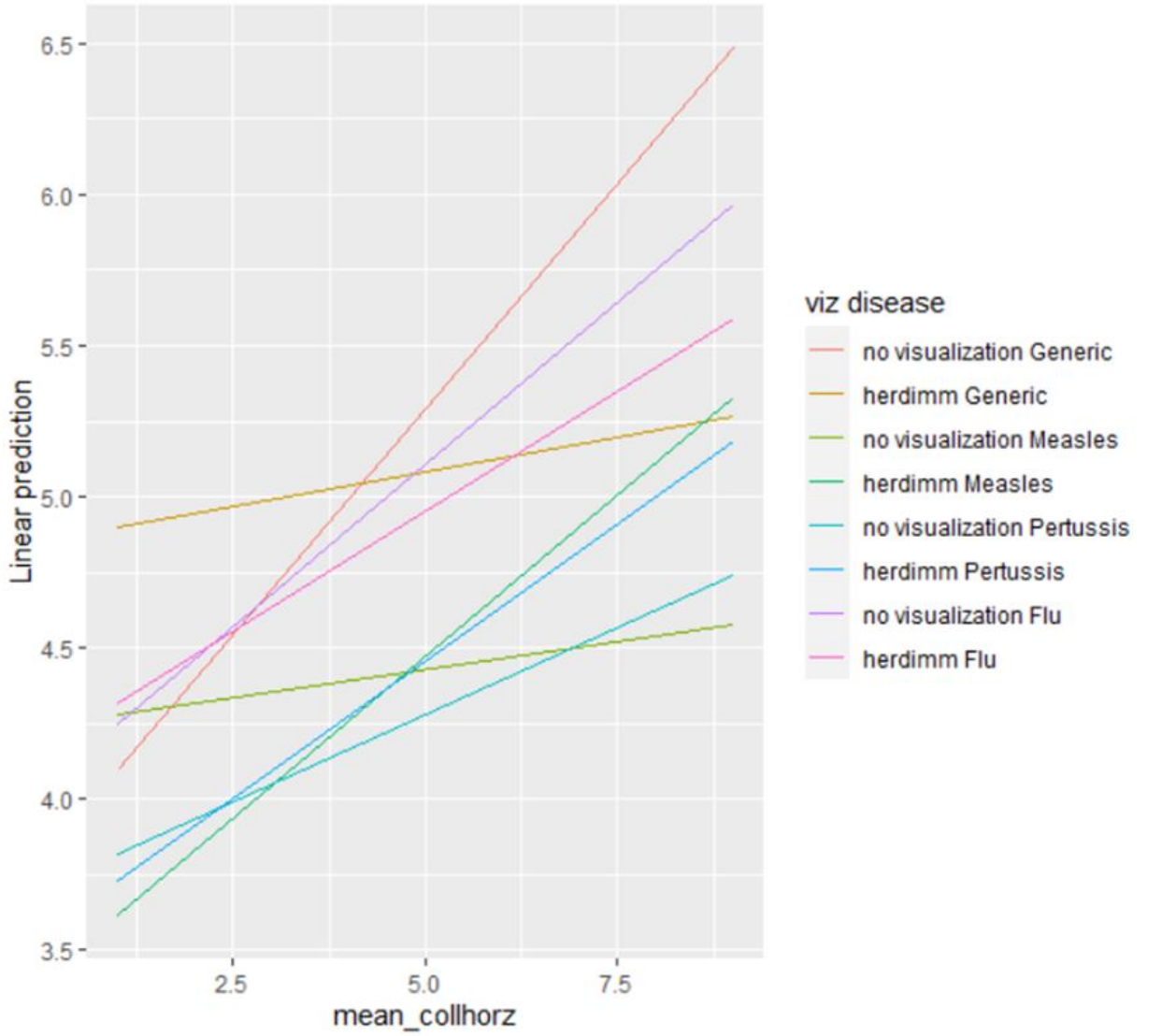
```
White_group                          1.8    1   1.1036 0.2935579
disability_any                      41.8    1  25.0122 5.984e-07 ***
genderidentity                      55.1    1  32.9685 1.019e-08 ***
income                              19.5    3   3.8955 0.0086106 **
edhi                                 7.9    1   4.7368 0.0295918 *
age                                  5.2    1   3.1294 0.0769792 .
viz:disease                          0.3    3   0.0691 0.9763966
viz:mean_indivhorz                   1.4    1   0.8542 0.3554259
disease:mean_indivhorz               8.5    3   1.7030 0.1641963
viz:mean_indivvertical               3.8    1   2.2624 0.1326437
disease:mean_indivvertical          29.0    3   5.7740 0.0006187 ***
viz:mean_collhorz                    0.2    1   0.1425 0.7058583
disease:mean_collhorz                1.9    3   0.3885 0.7612813
viz:mean_collvertical                1.0    1   0.6117 0.4341908
disease:mean_collvertical            2.7    3   0.5388 0.6557366
viz:disease:mean_indivhorz          10.5    3   2.0840 0.1001869
viz:disease:mean_indivvertical       4.6    3   0.9163 0.4320920
viz:disease:mean_collhorz           22.7    3   4.5229 0.0035968 **
viz:disease:mean_collvertical        5.3    3   1.0570 0.3661375
Residuals                         5704.5 3412
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> summary(mEmotions_3)
Call:
```

```
lm(formula = mean_emotion ~ viz * disease * mean_indivhorz +

    viz * disease * mean_indivvertical + viz * disease * mean_collhorz
+

    viz * disease * mean_collvertical + bornincanada + language_1 +

    language_2 + Asian_group + White_group + disability_any +

    genderidentity + income + edhi + age, data = datMain)

Residuals:

    Min      1Q  Median      3Q     Max

-4.8307 -0.8326  0.1854  0.9500  3.1323

Coefficients:

                                Estimate Std. Error t value Pr(>|t|)

(Intercept)                     3.300575   0.204497  16.140  < 2e-16
***

viz1                            0.278655   0.189748   1.469 0.142047

disease1                        0.741100   0.318795   2.325 0.020147
*

disease2                       -0.385695   0.337419  -1.143 0.253088

disease3                       -0.846124   0.336328  -2.516 0.011923
*

mean_indivhorz                 -0.063594   0.022546  -2.821 0.004821
**

mean_indivvertical              0.067392   0.016114   4.182 2.96e-05
***

mean_collhorz                   0.158233   0.021685   7.297 3.64e-13
***

mean_collvertical               0.100957   0.021496   4.697 2.75e-06
***

bornincanada1                   0.016325   0.036340   0.449 0.653292
```

language_11	0.072852	0.051428	1.417	0.156697
language_21	0.004420	0.046871	0.094	0.924879
Asian_group1	0.061627	0.054893	1.123	0.261651
White_group1	-0.048025	0.045716	-1.051	0.293558
disability_any1	0.139315	0.027856	5.001	5.98e-07 ***
genderidentity1	0.131940	0.022979	5.742	1.02e-08 ***
income1	-0.167638	0.052565	-3.189	0.001440 **
income2	0.019546	0.041822	0.467	0.640265
income3	0.038619	0.035566	1.086	0.277627
edhi1	-0.053671	0.024660	-2.176	0.029592 *
age	0.002689	0.001520	1.769	0.076979 .
viz1:disease1	-0.008251	0.319077	-0.026	0.979372
viz1:disease2	0.102371	0.338456	0.302	0.762316
viz1:disease3	-0.138933	0.336492	-0.413	0.679716
viz1:mean_indivhorz	-0.020438	0.022113	-0.924	0.355426
disease1:mean_indivhorz	0.057945	0.038602	1.501	0.133426
disease2:mean_indivhorz	-0.050536	0.038571	-1.310	0.190216
disease3:mean_indivhorz	0.040915	0.039530	1.035	0.300720
viz1:mean_indivvertical	-0.023249	0.015457	-1.504	0.132644
disease1:mean_indivvertical	-0.102503	0.026639	-3.848	0.000121 ***

```
disease2:mean_indivvertical       0.064341   0.026549   2.424 0.015423
*

disease3:mean_indivvertical       0.041311   0.026134   1.581 0.114034

viz1:mean_collhorz                0.008102   0.021464   0.377 0.705858

disease1:mean_collhorz            0.013902   0.037672   0.369 0.712122

disease2:mean_collhorz           -0.032382   0.036909  -0.877 0.380358

disease3:mean_collhorz           -0.009992   0.036554  -0.273 0.784610

viz1:mean_collvertical           -0.016648   0.021285  -0.782 0.434191

disease1:mean_collvertical       -0.031870   0.038086  -0.837 0.402768

disease2:mean_collvertical        0.033988   0.036777   0.924 0.355476

disease3:mean_collvertical        0.018906   0.036706   0.515 0.606545

viz1:disease1:mean_indivhorz     -0.046718   0.038572  -1.211 0.225903

viz1:disease2:mean_indivhorz      0.043263   0.038525   1.123 0.261528

viz1:disease3:mean_indivhorz      0.065099   0.039544   1.646 0.099801
.

viz1:disease1:mean_indivvertical  0.011224   0.026629   0.422 0.673412

viz1:disease2:mean_indivvertical -0.018731   0.026572  -0.705 0.480902

viz1:disease3:mean_indivvertical -0.028146   0.026143  -1.077 0.281728

viz1:disease1:mean_collhorz       0.117797   0.037714   3.123 0.001802
**

viz1:disease2:mean_collhorz      -0.096573   0.036903  -2.617 0.008912
**

viz1:disease3:mean_collhorz      -0.041413   0.036597  -1.132 0.257890

viz1:disease1:mean_collvertical  -0.063272   0.038095  -1.661 0.096824
.

viz1:disease2:mean_collvertical   0.043736   0.036840   1.187 0.235238
```

```
viz1:disease3:mean_collvertical   0.010858   0.036720   0.296 0.767476

---

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 1.293 on 3412 degrees of freedom

  (419 observations effacées parce que manquantes)

Multiple R-squared:  0.1595,     Adjusted R-squared:  0.147

F-statistic:  12.7 on 51 and 3412 DF,  p-value: < 2.2e-16
```



Knowledge

Two-way

Model 1: Check for direct effects of factors without any covariates

```
> mKnowledge_1 <- lm(sum_knowledge  ~ viz * disease, data = datMain)

> Anova(mKnowledge_1,type="III")

Anova Table (Type III tests)


Response: sum_knowledge

            Sum Sq    Df     F value      Pr(>F)

(Intercept) 270957     1 39192.6506 < 2.2e-16 ***

viz            251     1     36.3666 1.788e-09 ***

disease        108     3     5.1982   0.001392 **

viz:disease     53     3     2.5345   0.055118 .

Residuals   26790 3875

---

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> summary(mKnowledge_1)

Call:

lm(formula = sum_knowledge ~ viz * disease, data = datMain)

Residuals:

     Min       1Q   Median   3Q      Max

-9.2670 -1.9627   0.0015   1.9203   5.5683

Coefficients:

            Estimate Std. Error t value Pr(>|t|)
```

```
(Intercept)      8.85194    0.04471 197.971  < 2e-16 ***
viz1       -0.26964   0.04471  -6.030 1.79e-09 ***
disease1         0.20002    0.07833   2.554  0.01070 *
disease2   -0.21029   0.07672  -2.741  0.00615 **
disease3   -0.13683   0.07782  -1.758  0.07879 .
viz1:disease1  0.18042    0.07833   2.303  0.02131 *
viz1:disease2 -0.16841     0.07672  -2.195  0.02822 *
viz1:disease3 -0.01373     0.07782  -0.176  0.86001
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Residual standard error: 2.629 on 3875 degrees of freedom
Multiple R-squared:  0.01425,    Adjusted R-squared:  0.01247
F-statistic: 8.003 on 7 and 3875 DF,  p-value: 1.106e-09
> mKnowledge_1_v
 viz             emmean     SE   df lower.CL upper.CL
 no visualization   8.58 0.0729 3875   8.44  8.73
 herdimm         9.12 0.0518 3875      9.02     9.22
Results are averaged over the levels of: disease
Confidence level used: 0.95
> plot(mKnowledge_1_v)
> mKnowledge_1_d <- emmeans(mKnowledge_1,  ~ disease)
NOTE: Results may be misleading due to involvement in interactions
> mKnowledge_1_d
 disease    emmean     SE   df lower.CL upper.CL
```

```
 Generic   9.05 0.0910 3875      8.87     9.23

 Measles   8.64 0.0882 3875      8.47     8.81

 Pertussis   8.72 0.0901 3875    8.54     8.89

 Flu       9.00 0.0885 3875      8.83     9.17

Results are averaged over the levels of: viz

Confidence level used: 0.95

> pairs(mKnowledge_1_d) # Only do multiple comparisons if type 3 test
is significant

 contrast             estimate   SE   df t.ratio p.value

 Generic - Measles    0.4103 0.127 3875   3.239  0.0066

 Generic - Pertussis   0.3368 0.128 3875   2.631  0.0424

 Generic - Flu        0.0529 0.127 3875   0.417  0.9756

 Measles - Pertussis  -0.0735 0.126 3875  -0.583  0.9373

 Measles - Flu        -0.3574 0.125 3875  -2.861  0.0220

 Pertussis - Flu      -0.2839 0.126 3875  -2.249  0.1105

Results are averaged over the levels of: viz

P value adjustment: tukey method for comparing a family of 4 estimates
```

Model 2: Check for direct effects of factors with adjustment for other covariates

```
> mKnowledge_2 <-

+   lm(

+     sum_knowledge  ~ viz * disease +

+     mean_indivhorz +

+     mean_indivvertical +

+     mean_collhorz +
```

```
+     mean_collvertical +
+     bornincanada + #CHANGELOG ASJ: covariate list shortened 2021-08-
04
+     language_1 +
+     language_2 +
+     Asian_group +
+     White_group +
+     disability_any +
+     genderidentity +
+     income +
+     edhi +
+     age,
+     data = datMain
+   )
> Anova(mKnowledge_2, type = "III")
Anova Table (Type III tests)
Response: sum_knowledge
                 Sum Sq   Df  F value  Pr(>F)
(Intercept)      3845.9     1 613.7038 < 2.2e-16 ***
viz                 195.7  1  31.2254 2.476e-08 ***
disease             101.9  3   5.4199  0.001020 **
mean_indivhorz       138.3    1  22.0687 2.734e-06 ***
mean_indivvertical   613.3    1  97.8697 < 2.2e-16 ***
mean_collhorz         12.6    1   2.0119  0.156161
```

```
mean_collvertical     176.6    1  28.1776 1.177e-07 ***
bornincanada           0.2   1   0.0306  0.861181
language_1             0.5   1   0.0728  0.787382
language_2             0.1   1   0.0087  0.925645
Asian_group           29.6  1   4.7163  0.029945 *
White_group           51.6  1   8.2395  0.004124 **
disability_any        27.9  1   4.4558  0.034855 *
genderidentity        19.4    1   3.0930  0.078718 .
income               154.2  3   8.2021 1.943e-05 ***
edhi                  12.9  1   2.0513  0.152163
age                  319.0  1  50.9008 1.179e-12 ***
viz:disease           62.0  3   3.2962  0.019652 *
Residuals        21557.7 3440
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> summary(mKnowledge_2)
Call:
lm(formula = sum_knowledge ~ viz * disease + mean_indivhorz +
     mean_indivvertical + mean_collhorz + mean_collvertical +
     bornincanada + language_1 + language_2 + Asian_group +
White_group +
     disability_any + genderidentity + income + edhi + age, data =
datMain)
Residuals:
     Min      1Q  Median   3Q     Max
```

```
-9.5302 -1.6472  0.1765  1.8945  6.0874

Coefficients:

                 Estimate Std. Error t value Pr(>|t|)

(Intercept)      9.068508   0.366064  24.773  < 2e-16 ***

viz1             -0.263572   0.047168  -5.588 2.48e-08 ***

disease1         0.254299   0.079222   3.210  0.00134 **

disease2         -0.166158   0.078460  -2.118  0.03427 *

disease3         -0.185772   0.079746  -2.330  0.01989 *

mean_indivhorz   0.192331   0.040941   4.698 2.73e-06 ***

mean_indivvertical -0.284364   0.028744  -9.893  < 2e-16 ***

mean_collhorz    0.056675   0.039957   1.418  0.15616

mean_collvertical  -0.206670   0.038934  -5.308 1.18e-07 ***

bornincanada1    -0.012243   0.070006  -0.175  0.86118

language_11      0.026779   0.099279   0.270  0.78738

language_21      0.008447   0.090504   0.093  0.92565

Asian_group1         0.230226   0.106011   2.172  0.02995 *

White_group1         0.252449   0.087948   2.870  0.00412 **

disability_any1      0.113416   0.053730   2.111  0.03486 *

genderidentity1  -0.077839   0.044259  -1.759  0.07872 .

income1             -0.414060   0.101348  -4.086 4.50e-05 ***

income2          -0.056751   0.080582  -0.704  0.48132

income3          0.132385   0.068569   1.931  0.05360 .

edhi1            -0.067962   0.047451  -1.432  0.15216

age                  0.020844   0.002922   7.134 1.18e-12 ***
```

```
viz1:disease1    0.225499   0.079063   2.852  0.00437 **
viz1:disease2   -0.158270   0.078450  -2.017  0.04373 *
viz1:disease3    0.009383   0.079691   0.118  0.90628
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Residual standard error: 2.503 on 3440 degrees of freedom
  (419 observations effacées parce que manquantes)
Multiple R-squared:  0.08506,    Adjusted R-squared:  0.07894
F-statistic:  13.9 on 23 and 3440 DF,  p-value: < 2.2e-16
> mKnowledge_2_vd <- emmeans(mKnowledge_2,~viz|disease)
> mKnowledge_2_vd
disease = Generic:
 viz             emmean     SE   df lower.CL upper.CL
 no visualization   9.13 0.166 3440    8.80     9.45
 herdimm         9.20 0.144 3440  8.92  9.48
disease = Measles:
 viz             emmean     SE   df lower.CL upper.CL
 no visualization   8.32 0.170 3440    7.99     8.66
 herdimm         9.17 0.138 3440  8.90     9.44
disease = Pertussis:
 viz             emmean     SE   df lower.CL upper.CL
 no visualization   8.47 0.174 3440    8.13     8.81
 herdimm         8.98 0.140 3440  8.70     9.25
disease = Flu:
```

```
 viz             emmean     SE   df lower.CL upper.CL

 no visualization   8.67 0.169 3440    8.34     9.00

 herdimm         9.35 0.139 3440  9.08  9.62

Results are averaged over the levels of: bornincanada, language_1,
language_2, Asian_group, White_group, disability_any, genderidentity,
income, edhi

Confidence level used: 0.95

> pairs(mKnowledge_2_vd) # Only do multiple comparisons if type 3 test
is significant

disease = Generic:

 contrast                  estimate   SE   df t.ratio p.value

 no visualization - herdimm  -0.0761 0.184 3440  -0.413  0.6797

disease = Measles:

 contrast                  estimate   SE   df t.ratio p.value

 no visualization - herdimm  -0.8437 0.182 3440  -4.627  <.0001

disease = Pertussis:

 contrast                  estimate   SE   df t.ratio p.value

 no visualization - herdimm  -0.5084 0.187 3440  -2.725  0.0065

disease = Flu:

 contrast                  estimate   SE   df t.ratio p.value

 no visualization - herdimm  -0.6804 0.182 3440  -3.743  0.0002

Results are averaged over the levels of: bornincanada, language_1,
language_2, Asian_group, White_group, disability_any, genderidentity,
income, edhi

> plot(mKnowledge_2_vd)

> mKnowledge_2_dv <- emmeans(mKnowledge_2,~disease|viz)
```

```
> mKnowledge_2_dv

viz = no visualization:

 disease   emmean     SE   df lower.CL upper.CL

 Generic     9.13 0.166 3440     8.80  9.45

 Measles     8.32 0.170 3440     7.99  8.66

 Pertussis   8.47 0.174 3440     8.13  8.81

 Flu         8.67 0.169 3440     8.34  9.00

viz = herdimm:

 disease   emmean     SE   df lower.CL upper.CL

 Generic     9.20 0.144 3440     8.92  9.48

 Measles     9.17 0.138 3440     8.90  9.44

 Pertussis   8.98 0.140 3440     8.70  9.25

 Flu         9.35 0.139 3440     9.08  9.62

Results are averaged over the levels of: bornincanada, language_1,
language_2, Asian_group, White_group, disability_any, genderidentity,
income, edhi

Confidence level used: 0.95

> pairs(mKnowledge_2_dv) # Only do multiple comparisons if type 3 test
is significant

viz = no visualization:

 contrast             estimate   SE   df t.ratio p.value

 Generic - Measles    0.8042 0.210 3440   3.835  0.0007

 Generic - Pertussis   0.6562 0.213 3440   3.076  0.0113

 Generic - Flu        0.4588 0.209 3440   2.197  0.1243

 Measles - Pertussis  -0.1480 0.214 3440  -0.691  0.9004
```

```
 Measles - Flu        -0.3454 0.210 3440  -1.644  0.3540

 Pertussis - Flu      -0.1974 0.214 3440  -0.924  0.7919

viz = herdimm:

 contrast             estimate   SE   df t.ratio p.value

 Generic - Measles    0.0367 0.149 3440   0.246  0.9948

 Generic - Pertussis   0.2240 0.149 3440   1.499  0.4380

 Generic - Flu        -0.1454 0.149 3440  -0.976  0.7630

 Measles - Pertussis   0.1873 0.145 3440   1.293  0.5675

 Measles - Flu        -0.1821 0.145 3440  -1.260  0.5886

 Pertussis - Flu      -0.3694 0.145 3440  -2.549  0.0528

Results are averaged over the levels of: bornincanada, language_1,
language_2, Asian_group, White_group, disability_any, genderidentity,
income, edhi

P value adjustment: tukey method for comparing a family of 4 estimates
```

Model 3: Check for moderating effects of individualism & collectivism with adjustment for other covariates

```
> mKnowledge_3 <-

+   lm(

+     sum_knowledge  ~

+     viz * disease * mean_indivhorz +

+     viz * disease * mean_indivvertical +

+     viz * disease * mean_collhorz +

+     viz * disease * mean_collvertical +

+     bornincanada + #CHANGELOG ASJ: covariate list shortened 2021-08-
04

+     language_1 +
```

```
+     language_2 +
+     Asian_group +
+     White_group +
+     disability_any +
+     genderidentity +
+     income +
+     edhi +
+     age,
+     data = datMain
+   )
> Anova(mKnowledge_3, type = "III")
Anova Table (Type III tests)
Response: sum_knowledge
                              Sum Sq   Df  F value  Pr(>F)
(Intercept)                   3098.9     1 496.4341 < 2.2e-16 ***
viz                           14.2  1   2.2730 0.1317400
disease                       48.8  3   2.6083 0.0499439 *
mean_indivhorz                113.9 1  18.2538 1.986e-05 ***
mean_indivvertical            379.4 1  60.7743 8.437e-15 ***
mean_collhorz                 15.5  1   2.4797 0.1154176
mean_collvertical             144.8 1  23.1948 1.528e-06 ***
bornincanada                  0.1   1   0.0091 0.9241715
language_1                    0.3   1   0.0472 0.8281107
language_2                    0.0   1   0.0074 0.9312850
```

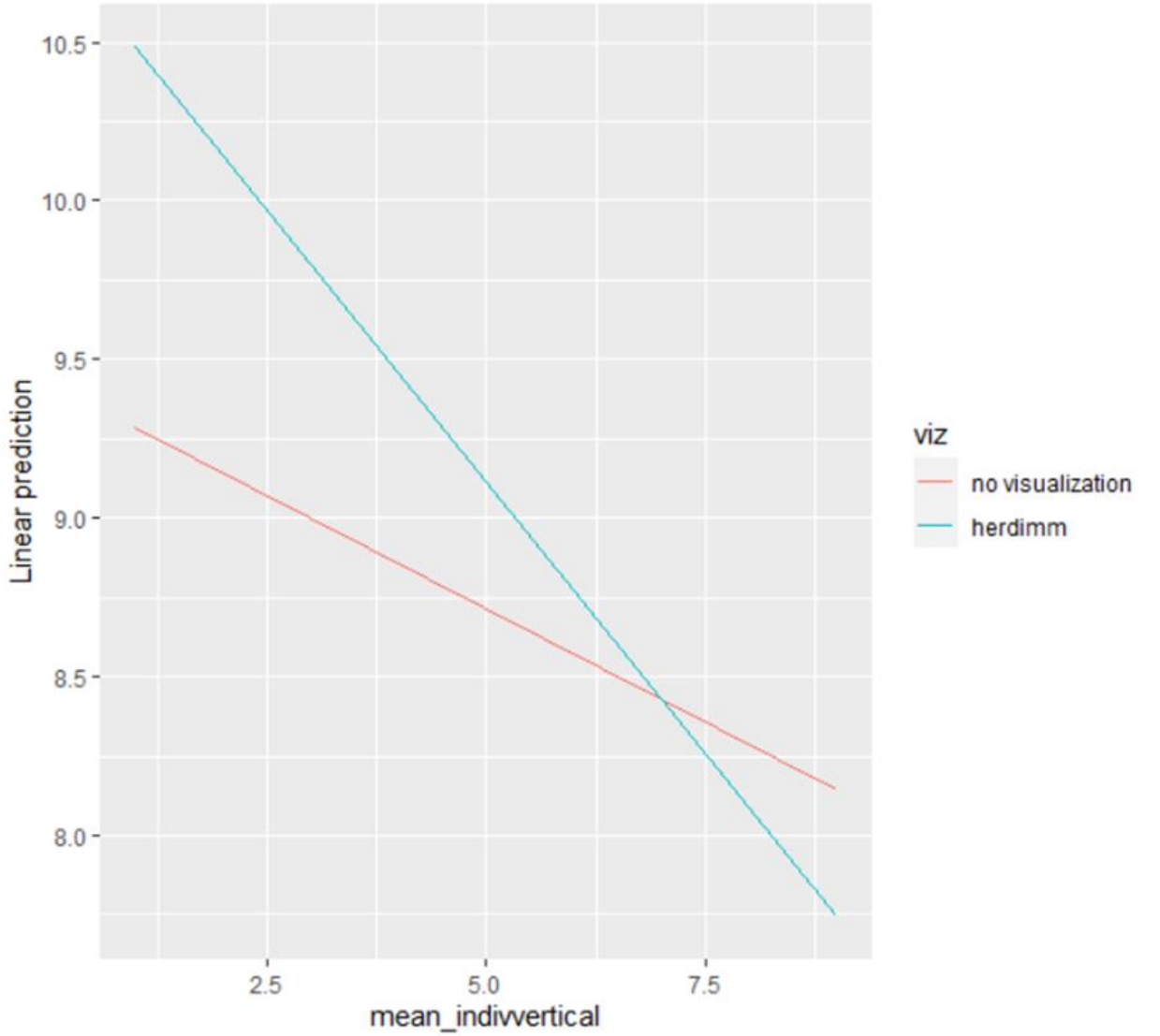
```
Asian_group                        29.0  1   4.6501 0.0311214 *
White_group                        60.4  1   9.6746 0.0018837 **
disability_any                     24.1  1   3.8588 0.0495671 *
genderidentity                     16.4  1   2.6291 0.1050123
income                            165.2  3   8.8199 8.012e-06 ***
edhi                               12.2  1   1.9594 0.1616648
age                               291.3  1  46.6646 9.933e-12 ***
viz:disease                        77.4  3   4.1346 0.0061797 **
viz:mean_indivhorz                 10.2  1   1.6331 0.2013679
disease:mean_indivhorz             22.8  3   1.2169 0.3019200
viz:mean_indivvertical             69.3  1  11.1059 0.0008697 ***
disease:mean_indivvertical         15.0    3   0.8009 0.4932355
viz:mean_collhorz                  9.0   1   1.4338 0.2312218
disease:mean_collhorz              13.6  3   0.7286 0.5348361
viz:mean_collvertical              2.1   1   0.3386 0.5606861
disease:mean_collvertical          20.1    3   1.0740 0.3588160
viz:disease:mean_indivhorz         10.9    3   0.5827 0.6263226
viz:disease:mean_indivvertical     5.8    3   0.3082 0.8194584
viz:disease:mean_collhorz          2.4    3   0.1260 0.9447159
viz:disease:mean_collvertical      43.9    3   2.3466 0.0708305 .
Residuals                     21299.1 3412
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> summary(mKnowledge_3)
```

```
Call:

lm(formula = sum_knowledge ~ viz * disease * mean_indivhorz +

     viz * disease * mean_indivvertical + viz * disease *
mean_collhorz +

     viz * disease * mean_collvertical + bornincanada + language_1 +

     language_2 + Asian_group + White_group + disability_any +

     genderidentity + income + edhi + age, data = datMain)

Residuals:

     Min       1Q   Median   3Q      Max

-9.4256 -1.6255  0.1538  1.8771  5.9932

Coefficients:

                                Estimate Std. Error t value Pr(>|t|)

(Intercept)                     8.804181   0.395147  22.281  < 2e-16
***

viz1                            -0.552772   0.366648  -1.508 0.131740

disease1                        0.832961   0.616002   1.352 0.176399

disease2                        -0.315740   0.651989  -0.484 0.628224

disease3                        -1.546495   0.649880  -2.380 0.017383
*

mean_indivhorz                  0.186130   0.043565   4.272 1.99e-05
***

mean_indivvertical              -0.242735   0.031137  -7.796 8.44e-15
***

mean_collhorz                   0.065982   0.041901   1.575 0.115418

mean_collvertical               -0.200044   0.041537  -4.816 1.53e-06
***

bornincanada1                   -0.006684   0.070220  -0.095 0.924171
```

language_11	0.021578	0.099373	0.217	0.828111
language_21	-0.007810	0.090567	-0.086	0.931285
Asian_group1	0.228727	0.106069	2.156	0.031121 *
White_group1	0.274759	0.088335	3.110	0.001884 **
disability_any1	0.105735	0.053826	1.964	0.049567 *
genderidentity1	-0.071995	0.044402	-1.621	0.105012
income1	-0.424961	0.101570	-4.184	2.94e-05 ***
income2	-0.068079	0.080812	-0.842	0.399601
income3	0.139800	0.068723	2.034	0.042004 *
edhi1	-0.066700	0.047650	-1.400	0.161665
age	0.020063	0.002937	6.831	9.93e-12 ***
viz1:disease1	2.089741	0.616548	3.389	0.000708 ***
viz1:disease2	-0.989636	0.653993	-1.513	0.130316
viz1:disease3	-1.043932	0.650197	-1.606	0.108463
viz1:mean_indivhorz	-0.054603	0.042728	-1.278	0.201368
disease1:mean_indivhorz	-0.111898	0.074590	-1.500	0.133661
disease2:mean_indivhorz	0.067611	0.074531	0.907	0.364387
disease3:mean_indivhorz	0.090626	0.076382	1.186	0.235517
viz1:mean_indivvertical	0.099532	0.029867	3.333	0.000870 ***
disease1:mean_indivvertical	0.053314	0.051474	1.036	0.300395
disease2:mean_indivvertical	0.027883	0.051299	0.544	0.586793

```
disease3:mean_indivvertical      -0.013011   0.050499  -0.258 0.796700

viz1:mean_collhorz                0.049663   0.041475   1.197 0.231222

disease1:mean_collhorz           -0.022577   0.072792  -0.310 0.756457

disease2:mean_collhorz           -0.085513   0.071319  -1.199 0.230604

disease3:mean_collhorz            0.027768   0.070632   0.393 0.694245

viz1:mean_collvertical           -0.023932   0.041129  -0.582 0.560686

disease1:mean_collvertical        0.015869   0.073592   0.216 0.829289

disease2:mean_collvertical        0.016401   0.071064   0.231 0.817494

disease3:mean_collvertical        0.082808   0.070927   1.168 0.243082

viz1:disease1:mean_indivhorz     -0.083871   0.074531  -1.125 0.260538

viz1:disease2:mean_indivhorz      0.075909   0.074442   1.020 0.307943

viz1:disease3:mean_indivhorz      0.014277   0.076409   0.187 0.851791

viz1:disease1:mean_indivvertical -0.032055   0.051455  -0.623 0.533344

viz1:disease2:mean_indivvertical  0.031742   0.051344   0.618 0.536473

viz1:disease3:mean_indivvertical  0.024596   0.050516   0.487 0.626364

viz1:disease1:mean_collhorz       0.006155   0.072873   0.084 0.932690

viz1:disease2:mean_collhorz      -0.021965   0.071308  -0.308 0.758081

viz1:disease3:mean_collhorz      -0.023475   0.070717  -0.332 0.739945

viz1:disease1:mean_collvertical  -0.166587   0.073610  -2.263 0.023692
*

viz1:disease2:mean_collvertical   0.040229   0.071185   0.565 0.572025

viz1:disease3:mean_collvertical   0.142723   0.070954   2.011 0.044353
*

---

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
Residual standard error: 2.498 on 3412 degrees of freedom
  (419 observations effacées parce que manquantes)
Multiple R-squared:  0.09603,    Adjusted R-squared:  0.08252
F-statistic: 7.107 on 51 and 3412 DF,  p-value: < 2.2e-16
```



Vax intention

Two-way

Model 1

```
> options(contrasts=c("contr.sum", "contr.poly"))

> rlog_vi_1 <- glm(vaxintentRel  ~ viz * disease, data =
datMain,family=binomial("logit"))

> Anova(rlog_vi_1,type="III")

Analysis of Deviance Table (Type III tests)



Response: vaxintentRel

             LR Chisq Df Pr(>Chisq)

viz         9.4136  1   0.002154 **

disease    15.0225  3   0.001798 **

viz:disease   3.7223  3   0.293055

---

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> summary(rlog_vi_1)

Call:

glm(formula = vaxintentRel ~ viz * disease, family =
binomial("logit"),

      data = datMain)

Deviance Residuals:

   Min      1Q  Median      3Q     Max

-1.303  -1.161   1.057   1.194   1.279

Coefficients:

                Estimate Std. Error z value Pr(>|z|)

(Intercept)   -0.021170   0.034217  -0.619  0.53612

viz1        -0.104892   0.034217  -3.066  0.00217 **
```

```
disease1         0.128075   0.059932   2.137  0.03260 *

disease2         0.135581   0.058819   2.305  0.02116 *

disease3   -0.116625   0.059511  -1.960  0.05003 .

viz1:disease1 -0.039518   0.059932  -0.659  0.50965

viz1:disease2 -0.070144   0.058819  -1.193  0.23305

viz1:disease3  0.006676   0.059511   0.112  0.91068

---

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 5362.1  on 3867  degrees of freedom

Residual deviance: 5327.2  on 3860  degrees of freedom

  (15 observations effacées parce que manquantes)

AIC: 5343.2

Number of Fisher Scoring iterations: 3

> # Interpretation of model 1

> mvi_1_v <- emmeans(rlog_vi_1,~viz,type = "response") #proportions

NOTE: Results may be misleading due to involvement in interactions

> mvi_1_v

 viz             prob       SE  df asymp.LCL asymp.UCL

 no visualization 0.469 0.01388 Inf    0.441     0.496

 herdimm         0.521 0.00991 Inf     0.501     0.540

Results are averaged over the levels of: disease

Confidence level used: 0.95

Intervals are back-transformed from the logit scale
```

```
> plot(mvi_1_v)

> confint(pairs(mvi_1_v,reverse = TRUE)) #Odds ratios

 contrast                  odds.ratio      SE  df asymp.LCL asymp.UCL

 herdimm / no visualization      1.23 0.0844 Inf       1.08      1.41


Results are averaged over the levels of: disease

Confidence level used: 0.95

Intervals are back-transformed from the log odds ratio scale

> mvi_1_d <- emmeans(rlog_vi_1,  ~ disease, type = "response")
#proportions

NOTE: Results may be misleading due to involvement in interactions

> mvi_1_d

 disease    prob      SE  df asymp.LCL asymp.UCL

 Generic   0.527 0.0173 Inf      0.493      0.561

 Measles   0.529 0.0169 Inf      0.495      0.561

 Pertussis 0.466 0.0171 Inf      0.432     0.499

 Flu       0.458 0.0168 Inf      0.425      0.491

Results are averaged over the levels of: viz

Confidence level used: 0.95

Intervals are back-transformed from the logit scale

> plot(mvi_1_d)

> pairs(mvi_1_d,reverse = TRUE,type = "response")

 contrast             odds.ratio      SE  df null z.ratio p.value

 Measles / Generic         1.008 0.0978 Inf 1   0.077  0.9998
```

```
 Pertussis / Generic       0.783 0.0766 Inf 1  -2.500  0.0600

 Pertussis / Measles       0.777 0.0750 Inf 1  -2.613  0.0445

 Flu / Generic             0.759 0.0737 Inf 1  -2.836  0.0237

 Flu / Measles             0.754 0.0721 Inf 1  -2.955  0.0165

 Flu / Pertussis           0.970 0.0936 Inf 1  -0.315  0.9892

Results are averaged over the levels of: viz

P value adjustment: tukey method for comparing a family of 4 estimates

Tests are performed on the log odds ratio scale

> confint(pairs(mvi_1_d,reverse = TRUE)) #Odds ratios

 contrast             odds.ratio       SE  df asymp.LCL asymp.UCL

 Measles / Generic         1.008 0.0978 Inf      0.785     1.293

 Pertussis / Generic       0.783 0.0766 Inf      0.609     1.007

 Pertussis / Measles       0.777 0.0750 Inf      0.606     0.996

 Flu / Generic             0.759 0.0737 Inf      0.592     0.974

 Flu / Measles             0.754 0.0721 Inf      0.590     0.964

 Flu / Pertussis           0.970 0.0936 Inf      0.757     1.243

Results are averaged over the levels of: viz

Confidence level used: 0.95

Conf-level adjustment: tukey method for comparing a family of 4
estimates

Intervals are back-transformed from the log odds ratio scale
```

Model 2: Check for direct effects of factors with adjustment for other covariates

```
> rlog_vi_2 <-

+   glm(vaxintentRel  ~ viz * disease +
```

```
+           mean_indivhorz +
+           mean_indivvertical +
+           mean_collhorz +
+           mean_collvertical +
+           bornincanada +
+           language_1 +
+           language_2 +
+           Asian_group +
+           White_group +
+           disability_any +
+           genderidentity +
+           income +
+           edhi +
+           age,
+     data = datMain,family=binomial("logit")
+   )
> Anova(rlog_vi_2, type = "III")
Analysis of Deviance Table (Type III tests)

Response: vaxintentRel
                LR Chisq Df Pr(>Chisq)
viz                2.693  1   0.100809
disease           15.778  3   0.001259 **
mean_indivhorz     4.261  1   0.039000 *
```

```
mean_indivvertical    6.422  1   0.011274 *

mean_collhorz         46.271  1  1.030e-11 ***

mean_collvertical     0.018  1   0.894372

bornincanada          1.294  1   0.255327

language_1            0.177  1   0.673708

language_2            3.476  1   0.062282 .

Asian_group           1.005  1   0.316029

White_group           0.321  1   0.571114

disability_any        19.727  1  8.935e-06 ***

genderidentity        0.524  1   0.469012

income                42.401  3  3.299e-09 ***

edhi                  4.141  1   0.041860 *

age                   56.646  1  5.217e-14 ***

viz:disease           1.170  3   0.760313

---

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> summary(rlog_vi_2)


Call:

glm(formula = vaxintentRel ~ viz * disease + mean_indivhorz +

      mean_indivvertical + mean_collhorz + mean_collvertical +

      bornincanada + language_1 + language_2 + Asian_group +
White_group +

      disability_any + genderidentity + income + edhi + age, family =
binomial("logit"),
```

```
      data = datMain)

Deviance Residuals:

      Min        1Q    Median        3Q       Max

-1.8868  -1.1331   0.6937   1.0939   2.1065


Coefficients:

                 Estimate Std. Error z value Pr(>|z|)

(Intercept)      -2.626498   0.311119  -8.442  < 2e-16 ***

viz1             -0.064457   0.039289  -1.641  0.10088

disease1         0.114874   0.065946   1.742  0.08152 .

disease2         0.174135   0.065398   2.663  0.00775 **

disease3         -0.098568   0.066185  -1.489  0.13642

mean_indivhorz   0.070515   0.034187   2.063  0.03915 *

mean_indivvertical -0.060564   0.023932  -2.531  0.01138 *

mean_collhorz    0.226951   0.033798   6.715 1.88e-11 ***

mean_collvertical   0.004319   0.032525   0.133  0.89437

bornincanada1    0.066158   0.058170   1.137  0.25541

language_11      -0.034958   0.083058  -0.421  0.67384

language_21      -0.141268   0.075946  -1.860  0.06287 .

Asian_group1     0.088213   0.088028   1.002  0.31630

White_group1     0.041390   0.073103   0.566  0.57126

disability_any1  0.200115   0.045293   4.418 9.95e-06 ***

genderidentity1  0.026611   0.036750   0.724  0.46900

income1          -0.463243   0.086078  -5.382 7.38e-08 ***
```

```
income2          0.082026   0.067168   1.221  0.22201

income3          0.011847   0.057075   0.208  0.83556

edhi1           -0.080337   0.039490  -2.034  0.04191 *

age              0.018277   0.002451   7.457 8.83e-14 ***

viz1:disease1   -0.017027   0.065787  -0.259  0.79577

viz1:disease2   -0.056351   0.065360  -0.862  0.38860

viz1:disease3    0.021626   0.066135   0.327  0.74368

---

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

 Null deviance: 4786.9  on 3453  degrees of freedom

Residual deviance: 4529.3  on 3430  degrees of freedom

  (429 observations effacées parce que manquantes)

AIC: 4577.3

Number of Fisher Scoring iterations: 4

> # Interpretation of model 2

> mvi_2_v <- emmeans(rlog_vi_2,~viz,type = "response")

NOTE: Results may be misleading due to involvement in interactions

> mvi_2_v

 viz             prob  SE  df asymp.LCL asymp.UCL

 no visualization 0.480 0.0228 Inf     0.436     0.525

 herdimm         0.513 0.0223 Inf      0.469     0.556

Results are averaged over the levels of: disease, bornincanada,
language_1, language_2, Asian_group, White_group, disability_any,
genderidentity, income, edhi
```

```
Confidence level used: 0.95

Intervals are back-transformed from the logit scale

> plot(mvi_2_v)

> confint(pairs(mvi_2_v,reverse = TRUE))

 contrast                   odds.ratio      SE  df asymp.LCL asymp.UCL

 herdimm / no visualization      1.14 0.0894 Inf  0.975      1.33

Results are averaged over the levels of: disease, bornincanada,
language_1, language_2, Asian_group, White_group, disability_any,
genderidentity, income, edhi

Confidence level used: 0.95

Intervals are back-transformed from the log odds ratio scale

> mvi_2_d <- emmeans(rlog_vi_2,  ~ disease, type = "response")

NOTE: Results may be misleading due to involvement in interactions

> mvi_2_d

 disease    prob      SE  df asymp.LCL asymp.UCL

 Generic   0.525 0.0259 Inf      0.474      0.576

 Measles   0.540 0.0259 Inf      0.489      0.590

 Pertussis 0.472 0.0264 Inf      0.421     0.524

 Flu       0.449 0.0258 Inf      0.399      0.500

Results are averaged over the levels of: viz, bornincanada,
language_1, language_2, Asian_group, White_group, disability_any,
genderidentity, income, edhi

Confidence level used: 0.95

Intervals are back-transformed from the logit scale

> plot(mvi_2_d)

> confint(pairs(mvi_2_d,reverse = TRUE))
```

contrast	odds.ratio	SE	df	asymp.LCL	asymp.UCL
Measles / Generic	1.061	0.1138	Inf	0.806	1.398
Pertussis / Generic	0.808	0.0875	Inf	0.612	1.067
Pertussis / Measles	0.761	0.0819	Inf	0.578	1.004
Flu / Generic	0.737	0.0787	Inf	0.560	0.969
Flu / Measles	0.694	0.0738	Inf	0.529	0.912
Flu / Pertussis	0.912	0.0976	Inf	0.693	1.201

Results are averaged over the levels of: viz, bornincanada, language_1, language_2, Asian_group, White_group, disability_any, genderidentity, income, edhi

Confidence level used: 0.95

Conf-level adjustment: tukey method for comparing a family of 4 estimates

Intervals are back-transformed from the log odds ratio scale

```
> pairs(mvi_2_d,reverse=TRUE,type="response")
```

contrast	odds.ratio	SE	df	null	z.ratio	p.value
Measles / Generic	1.061	0.1138	Inf	1	0.553	0.9459
Pertussis / Generic	0.808	0.0875	Inf	1	-1.971	0.1992
Pertussis / Measles	0.761	0.0819	Inf	1	-2.536	0.0545
Flu / Generic	0.737	0.0787	Inf	1	-2.860	0.0220
Flu / Measles	0.694	0.0738	Inf	1	-3.433	0.0033
Flu / Pertussis	0.912	0.0976	Inf	1	-0.858	0.8263

Results are averaged over the levels of: viz, bornincanada, language_1, language_2, Asian_group, White_group, disability_any, genderidentity, income, edhi

P value adjustment: tukey method for comparing a family of 4 estimates

```
Tests are performed on the log odds ratio scale
```

Model 3: Check for moderating effects of individualism & collectivism with adjustment for other covariates

```
> rlog_vi_3 <-
+   glm(vaxintentRel  ~
+          viz * disease * mean_indivhorz +
+          viz * disease * mean_indivvertical +
+          viz * disease * mean_collhorz +
+          viz * disease * mean_collvertical +
+          bornincanada +
+          language_1 +
+          language_2 +
+          Asian_group +
+          White_group +
+          disability_any +
+          genderidentity +
+          income +
+          edhi +
+          age,
+     data = datMain,family=binomial("logit")
+   )
> Anova(rlog_vi_3, type = "III")
Analysis of Deviance Table (Type III tests)
Response: vaxintentRel
```

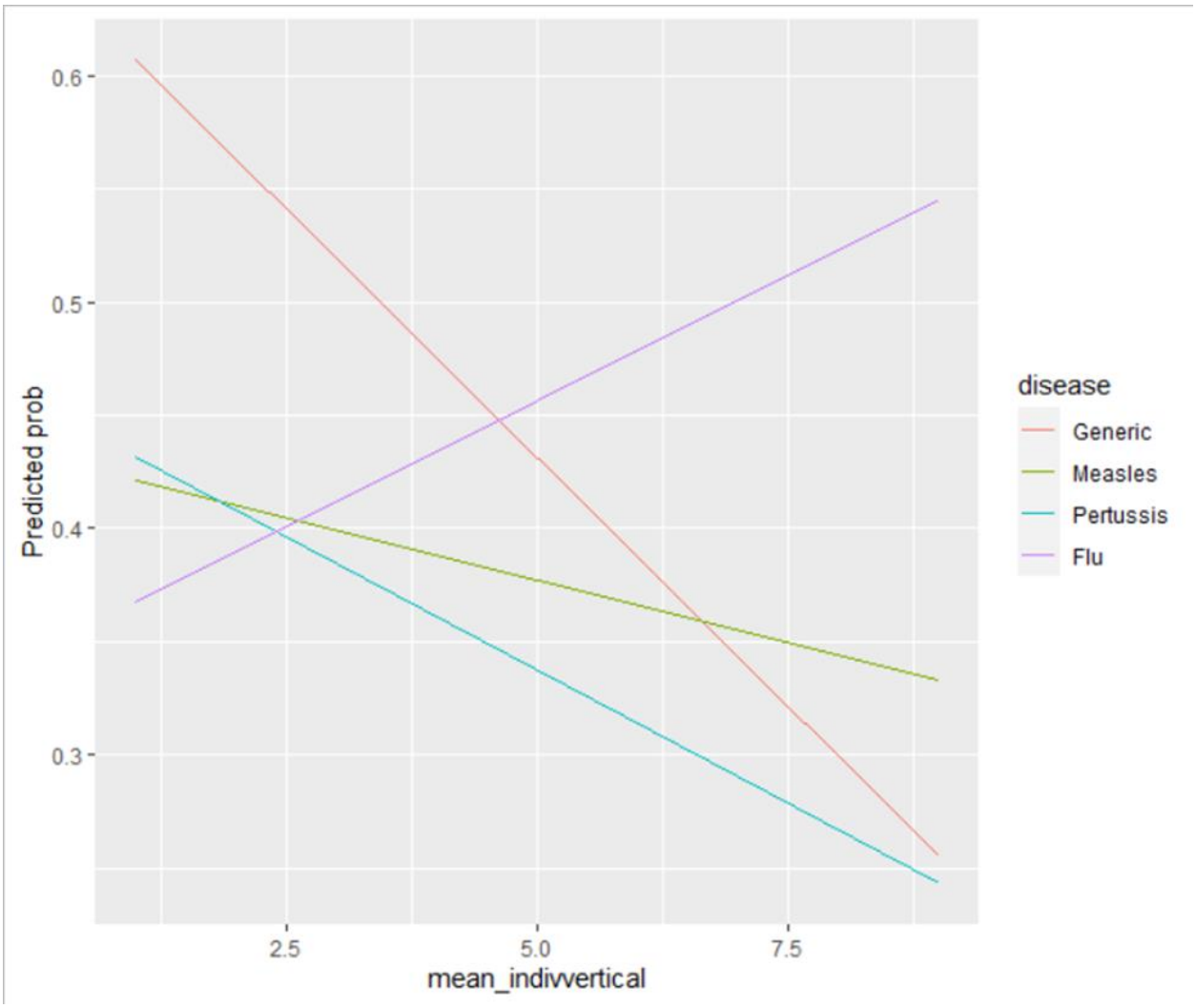
	LR Chisq	Df	Pr(>Chisq)	
viz	0.073	1	0.7867666	
disease	4.314	3	0.2294804	
mean_indivhorz	4.417	1	0.0355838	*
mean_indivvertical	5.727	1	0.0167020	*
mean_collhorz	44.802	1	2.181e-11	***
mean_collvertical	0.301	1	0.5830358	
bornincanada	0.908	1	0.3405692	
language_1	0.059	1	0.8084048	
language_2	2.835	1	0.0922474	.
Asian_group	0.916	1	0.3383970	
White_group	0.322	1	0.5702079	
disability_any	20.025	1	7.643e-06	***
genderidentity	0.676	1	0.4110133	
income	42.826	3	2.680e-09	***
edhi	4.128	1	0.0421857	*
age	57.220	1	3.897e-14	***
viz:disease	1.451	3	0.6936517	
viz:mean_indivhorz	0.119	1	0.7299379	
disease:mean_indivhorz	2.670	3	0.4452902	
viz:mean_indivvertical	0.005	1	0.9419263	
disease:mean_indivvertical	16.801	3	0.0007764	***
viz:mean_collhorz	0.939	1	0.3325764	
disease:mean_collhorz	2.031	3	0.5659568	

```
viz:mean_collvertical            3.667  1  0.0555092 .

disease:mean_collvertical        3.033  3  0.3865716

viz:disease:mean_indivhorz       0.840  3  0.8399763

viz:disease:mean_indivvertical   2.481  3  0.4786469

viz:disease:mean_collhorz        0.129  3  0.9881121

viz:disease:mean_collvertical    1.471  3  0.6890145

---

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> summary(rlog_vi_3)

Call:

glm(formula = vaxintentRel ~ viz * disease * mean_indivhorz +

     viz * disease * mean_indivvertical + viz * disease *
mean_collhorz +

     viz * disease * mean_collvertical + bornincanada + language_1 +

     language_2 + Asian_group + White_group + disability_any +

     genderidentity + income + edhi + age, family = binomial("logit"),

     data = datMain)

Deviance Residuals:

     Min       1Q   Median       3Q      Max

-2.0072  -1.1176   0.6401   1.0911   2.2031

Coefficients:

                                 Estimate Std. Error z value Pr(>|z|)

(Intercept)                      -2.579532   0.339262  -7.603 2.89e-14
***

viz1                             0.084661   0.312834   0.271  0.78668
```

disease1	0.736750	0.523299	1.408	0.15916
disease2	-0.757207	0.565249	-1.340	0.18038
disease3	-0.524349	0.556100	-0.943	0.34573
mean_indivhorz	0.077555	0.036947	2.099	0.03581 *
mean_indivvertical	-0.062966	0.026352	-2.389	0.01688 *
mean_collhorz	0.237841	0.036120	6.585	4.56e-11 ***
mean_collvertical	-0.019425	0.035406	-0.549	0.58326
bornincanada1	0.056059	0.058825	0.953	0.34060
language_11	-0.020293	0.083708	-0.242	0.80845
language_21	-0.128395	0.076417	-1.680	0.09292 .
Asian_group1	0.084929	0.088768	0.957	0.33869
White_group1	0.041991	0.073990	0.568	0.57036
disability_any1	0.203942	0.045822	4.451	8.56e-06 ***
genderidentity1	0.030525	0.037130	0.822	0.41101
income1	-0.469615	0.087148	-5.389	7.10e-08 ***
income2	0.075218	0.067879	1.108	0.26781
income3	0.016099	0.057684	0.279	0.78018
edhi1	-0.081161	0.039957	-2.031	0.04223 *
age	0.018615	0.002484	7.493	6.75e-14 ***
viz1:disease1	-0.184935	0.523603	-0.353	0.72394

```
viz1:disease2                    -0.471708   0.566570  -0.833  0.40509

viz1:disease3                    0.597600   0.556309   1.074  0.28272

viz1:mean_indivhorz              0.012505   0.036233   0.345  0.72999

disease1:mean_indivhorz          0.057972   0.063535   0.912  0.36153

disease2:mean_indivhorz          0.037503   0.063299   0.592  0.55354

disease3:mean_indivhorz          -0.007697   0.065240  -0.118  0.90608

viz1:mean_indivvertical          -0.001844   0.025310  -0.073  0.94193

disease1:mean_indivvertical      -0.124739   0.043899  -2.842  0.00449
**

disease2:mean_indivvertical      0.015600   0.043446   0.359  0.71954

disease3:mean_indivvertical      -0.044564   0.042916  -1.038  0.29909

viz1:mean_collhorz               0.034582   0.035764   0.967  0.33357

disease1:mean_collhorz           -0.022534   0.062831  -0.359  0.71986

disease2:mean_collhorz           0.077252   0.061773   1.251  0.21109

disease3:mean_collhorz           0.006502   0.061534   0.106  0.91585

viz1:mean_collvertical           -0.066983   0.035049  -1.911  0.05599
.

disease1:mean_collvertical       -0.036034   0.063185  -0.570  0.56848

disease2:mean_collvertical       0.005388   0.060436   0.089  0.92896

disease3:mean_collvertical       0.095008   0.060594   1.568  0.11690

viz1:disease1:mean_indivhorz     0.044599   0.063497   0.702  0.48244

viz1:disease2:mean_indivhorz     0.017629   0.063222   0.279  0.78037

viz1:disease3:mean_indivhorz     -0.026671   0.065266  -0.409  0.68279

viz1:disease1:mean_indivvertical  0.014022   0.043861   0.320  0.74919

viz1:disease2:mean_indivvertical -0.011519   0.043491  -0.265  0.79111
```

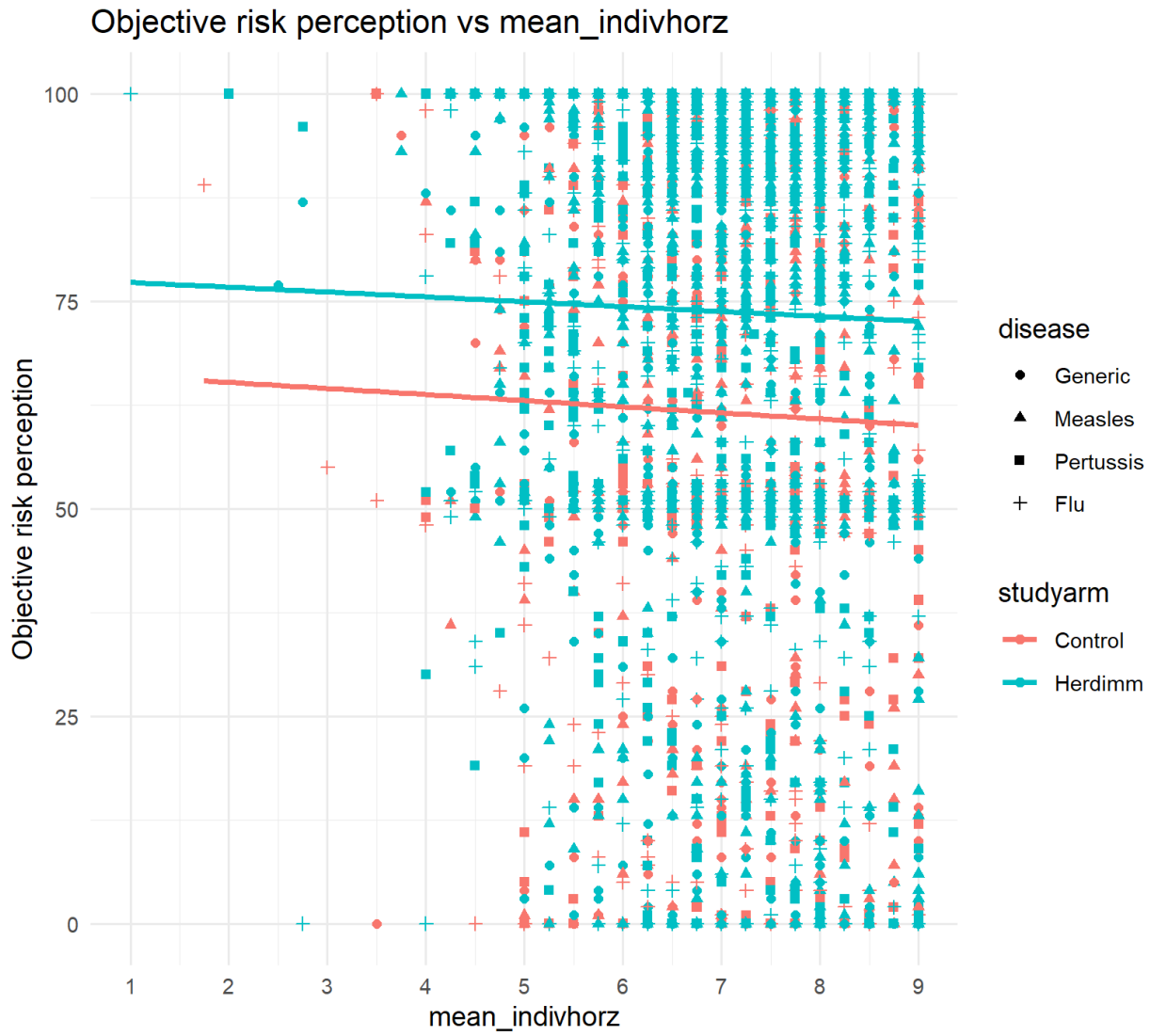
```
viz1:disease3:mean_indivvertical -0.054534   0.042933  -1.270  0.20401

viz1:disease1:mean_collhorz      0.003405   0.062885   0.054  0.95682

viz1:disease2:mean_collhorz      -0.016792   0.061754  -0.272  0.78569

viz1:disease3:mean_collhorz      0.018311   0.061609   0.297  0.76630

viz1:disease1:mean_collvertical  -0.038982   0.063198  -0.617  0.53735

viz1:disease2:mean_collvertical   0.067116   0.060529   1.109  0.26751

viz1:disease3:mean_collvertical  -0.035333   0.060604  -0.583  0.55988

---

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 4786.9  on 3453  degrees of freedom

Residual deviance: 4491.9  on 3402  degrees of freedom

  (429 observations effacées parce que manquantes)

AIC: 4595.9

Number of Fisher Scoring iterations: 4

 # Interpretation of model 3

> emmip(rlog_vi_3, disease ~ mean_indivvertical, cov.reduce = range,
type = "response")

NOTE: Results may be misleading due to involvement in interactions
```



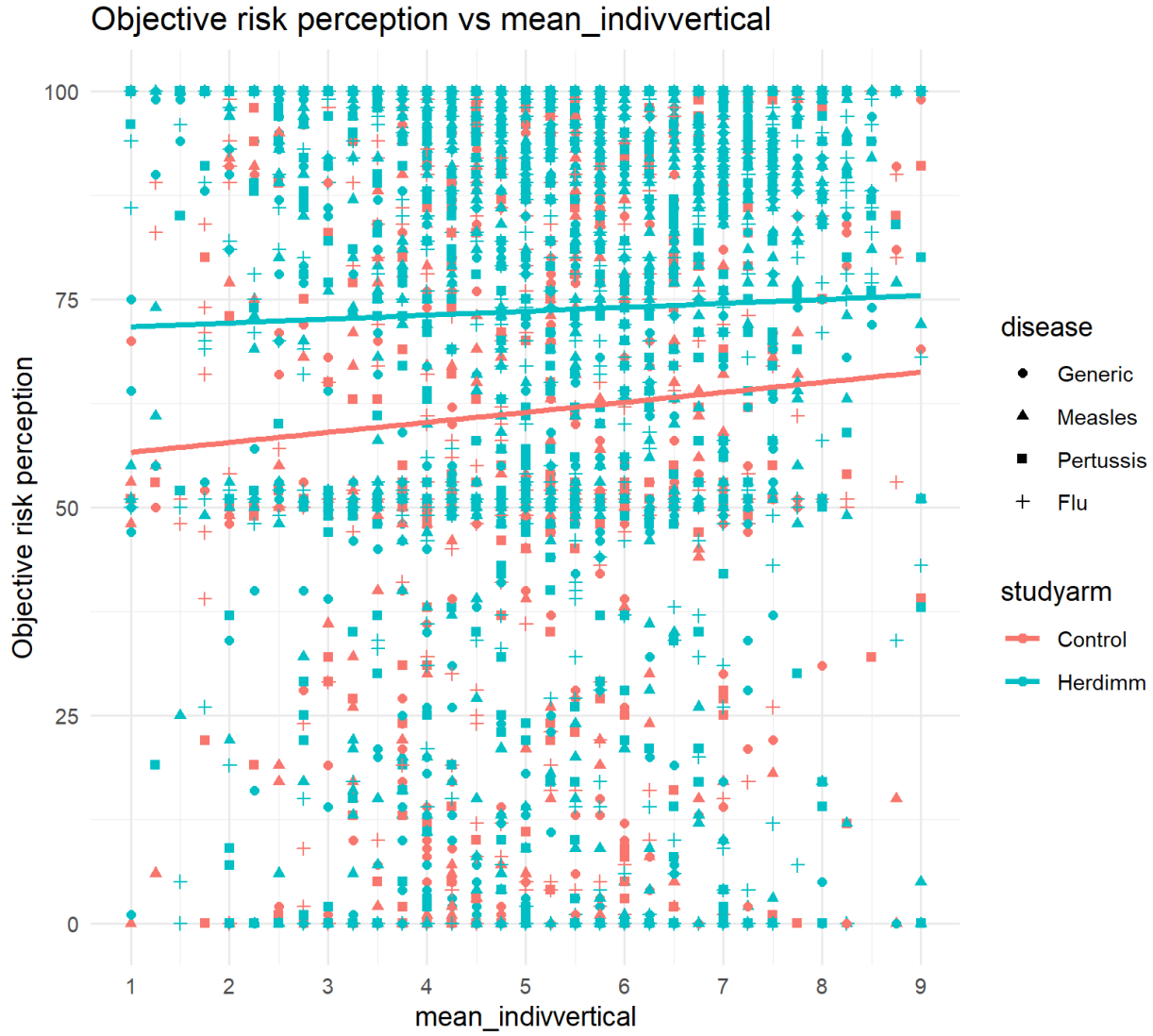
Appendix 6:
Outcomes versus Individualism and Collectivism subscales

Objective risk perception (risk percep_1)

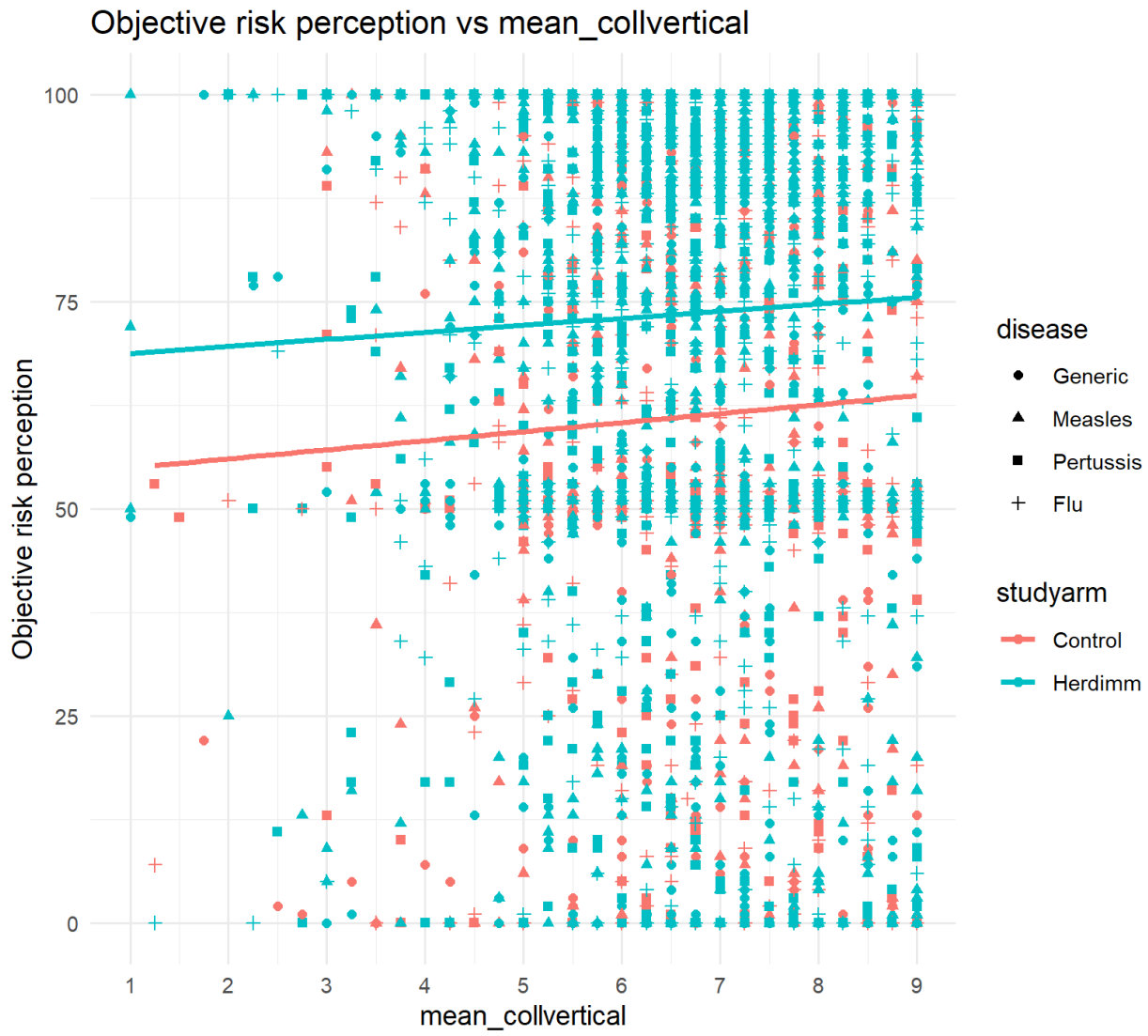
S1: objective risk perception vs mean horizontal individualism



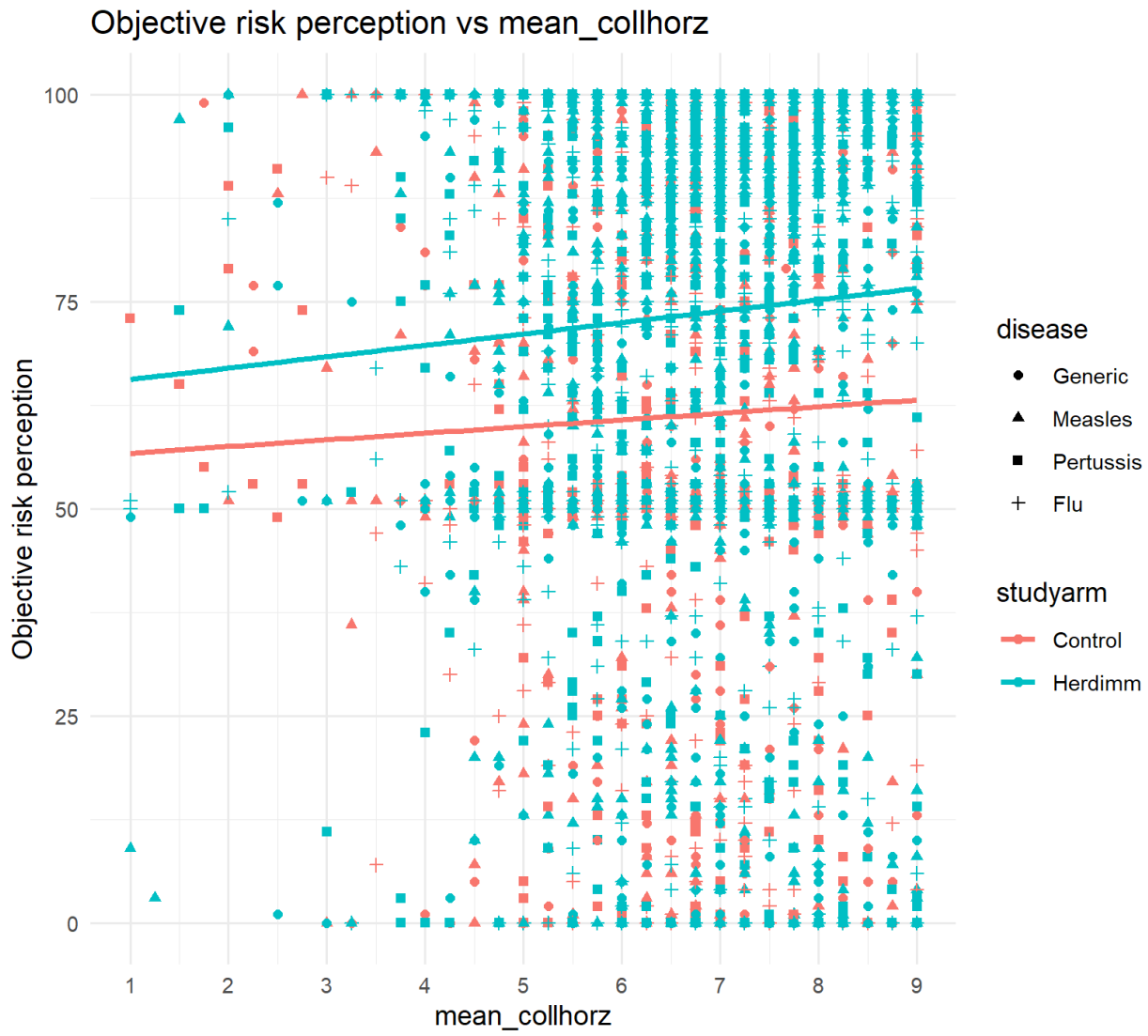
S2: objective risk perception vs mean vertical individualism



S3: objective risk perception vs mean vertical collectivism

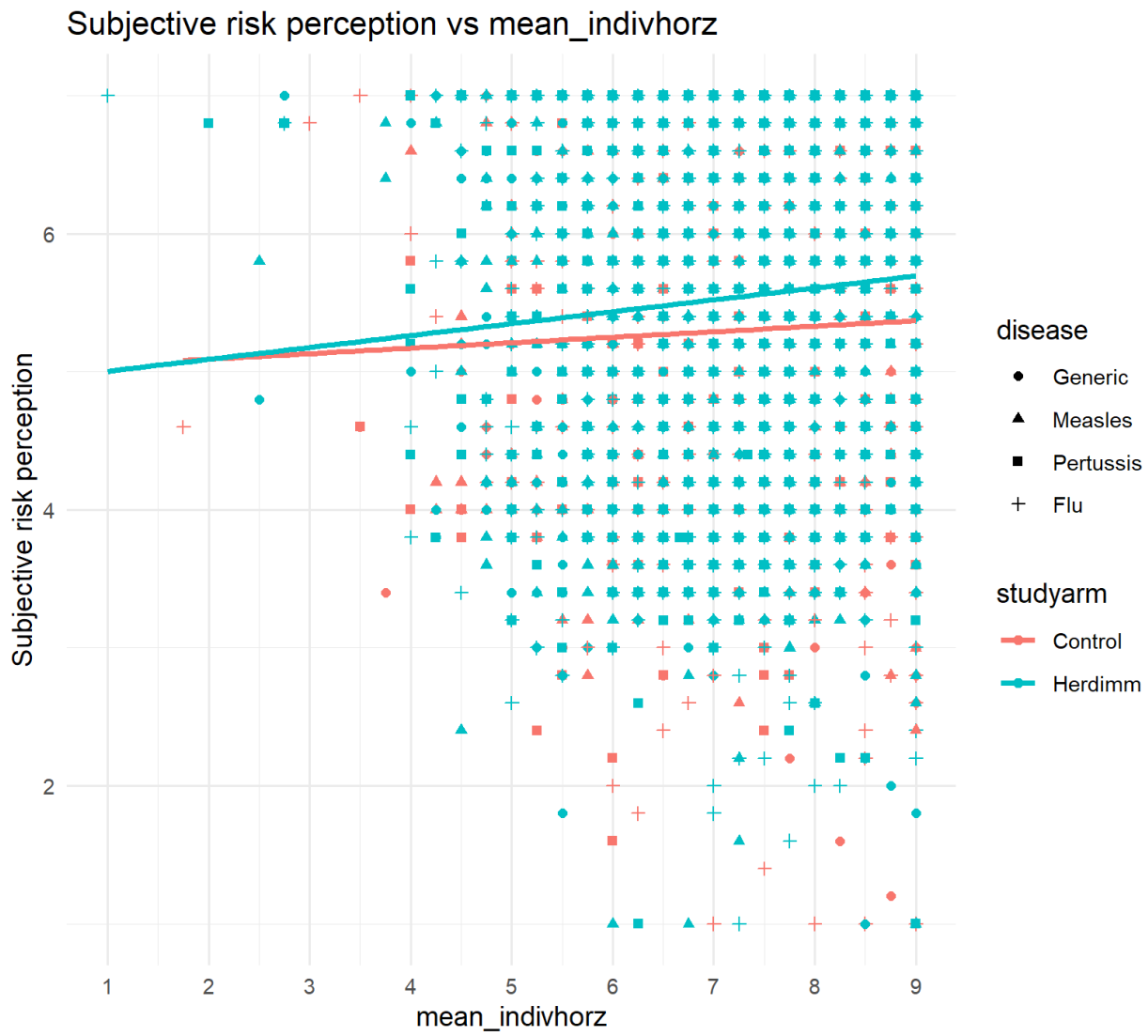


S4: objective risk perception vs mean horizontal collectivism

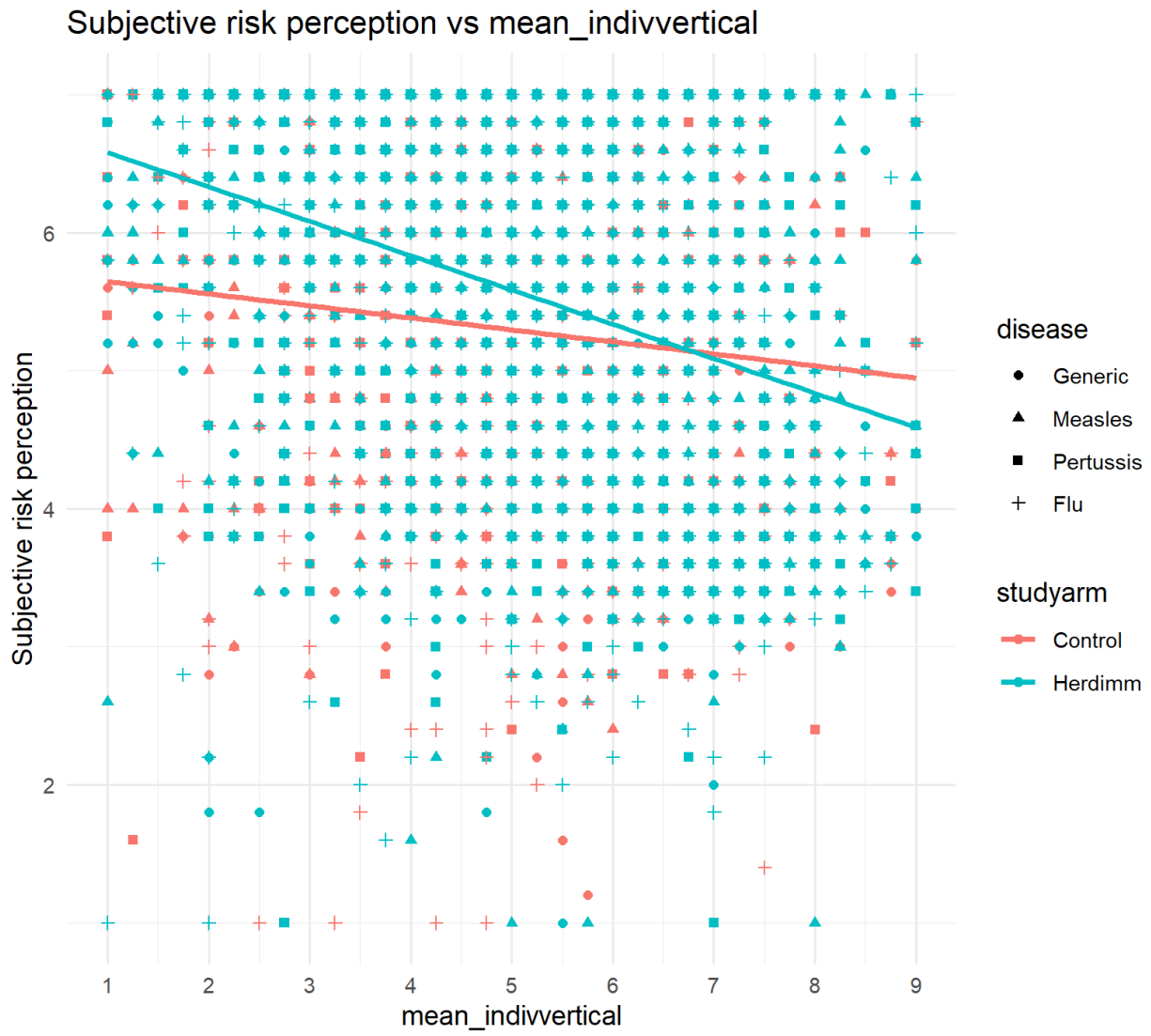


Subjective risk perception (risk percept_2 to 6)

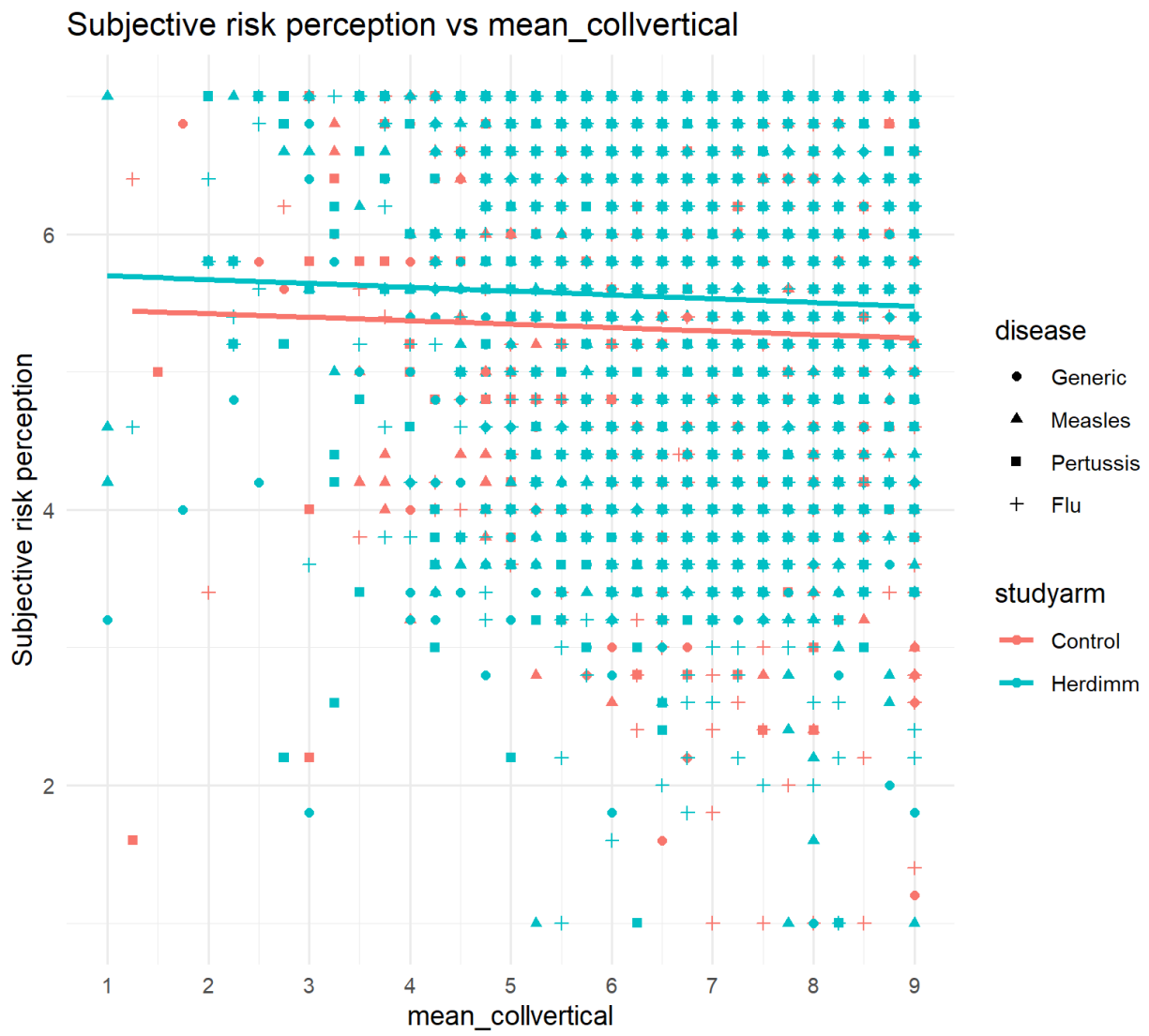
S5: subjective risk perception vs mean horizontal individualism



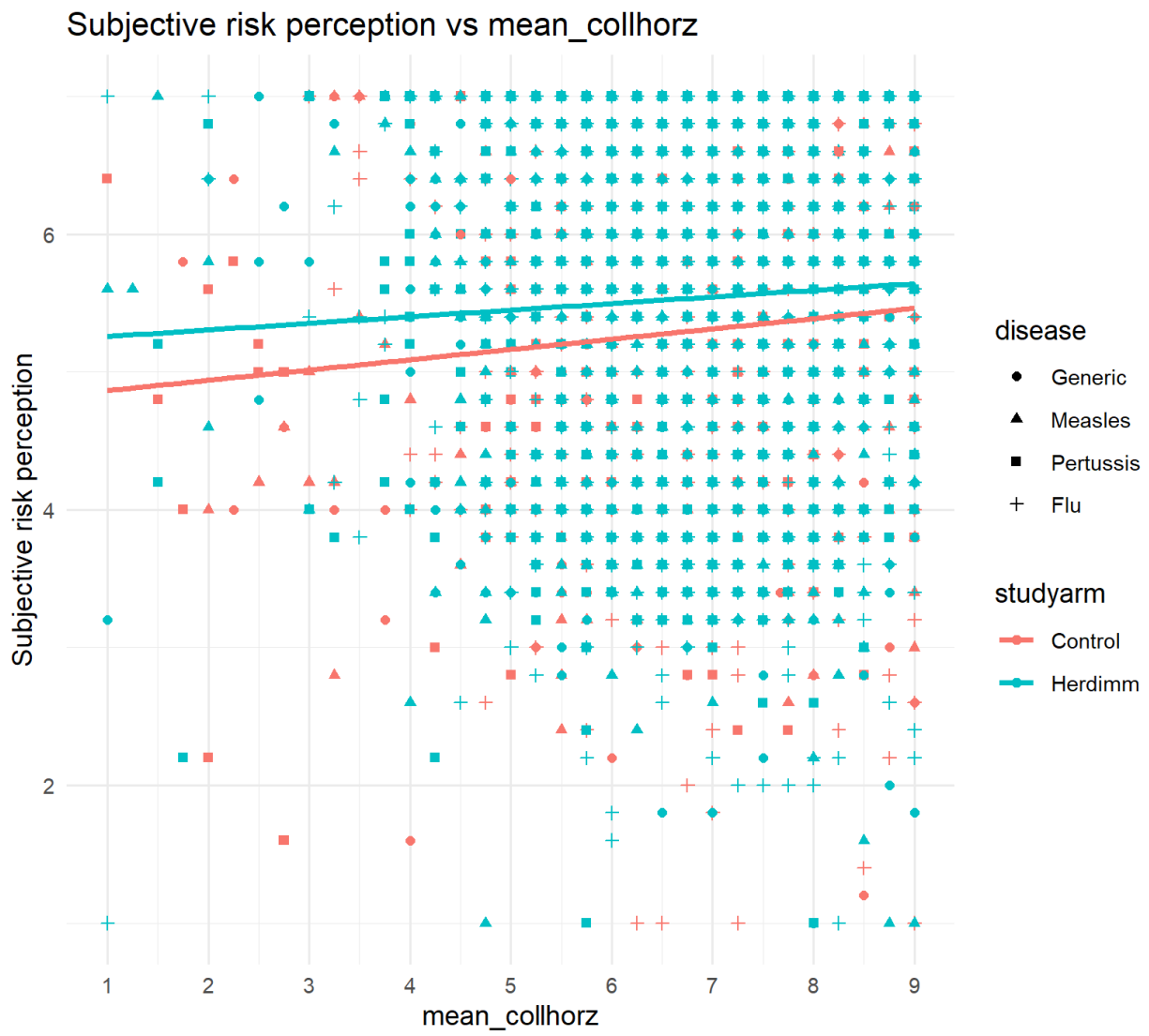
S6: subjective risk perception vs mean vertical individualism



S7: subjective risk perception vs mean vertical collectivism

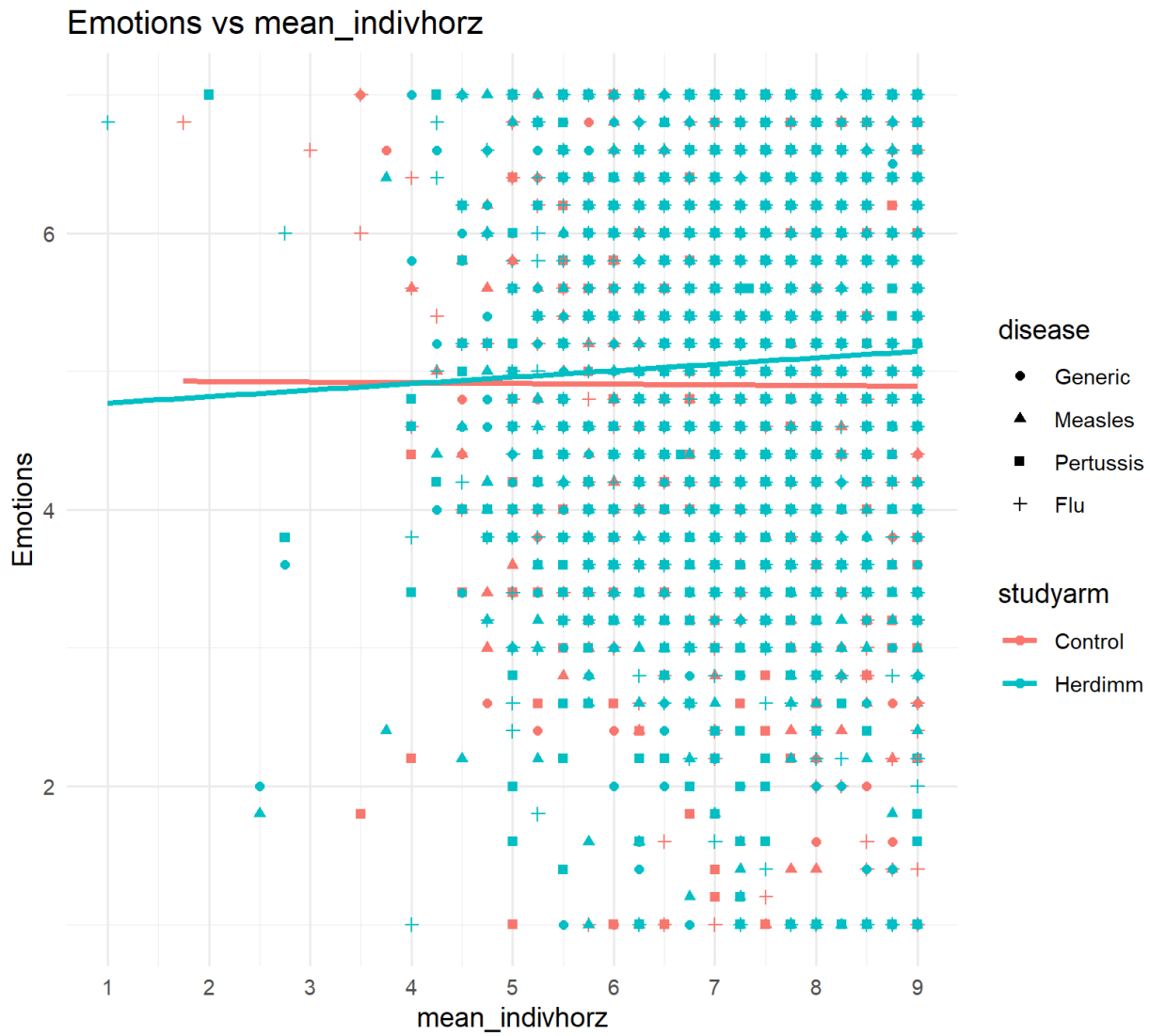


S8: subjective risk perception vs mean horizontal collectivism

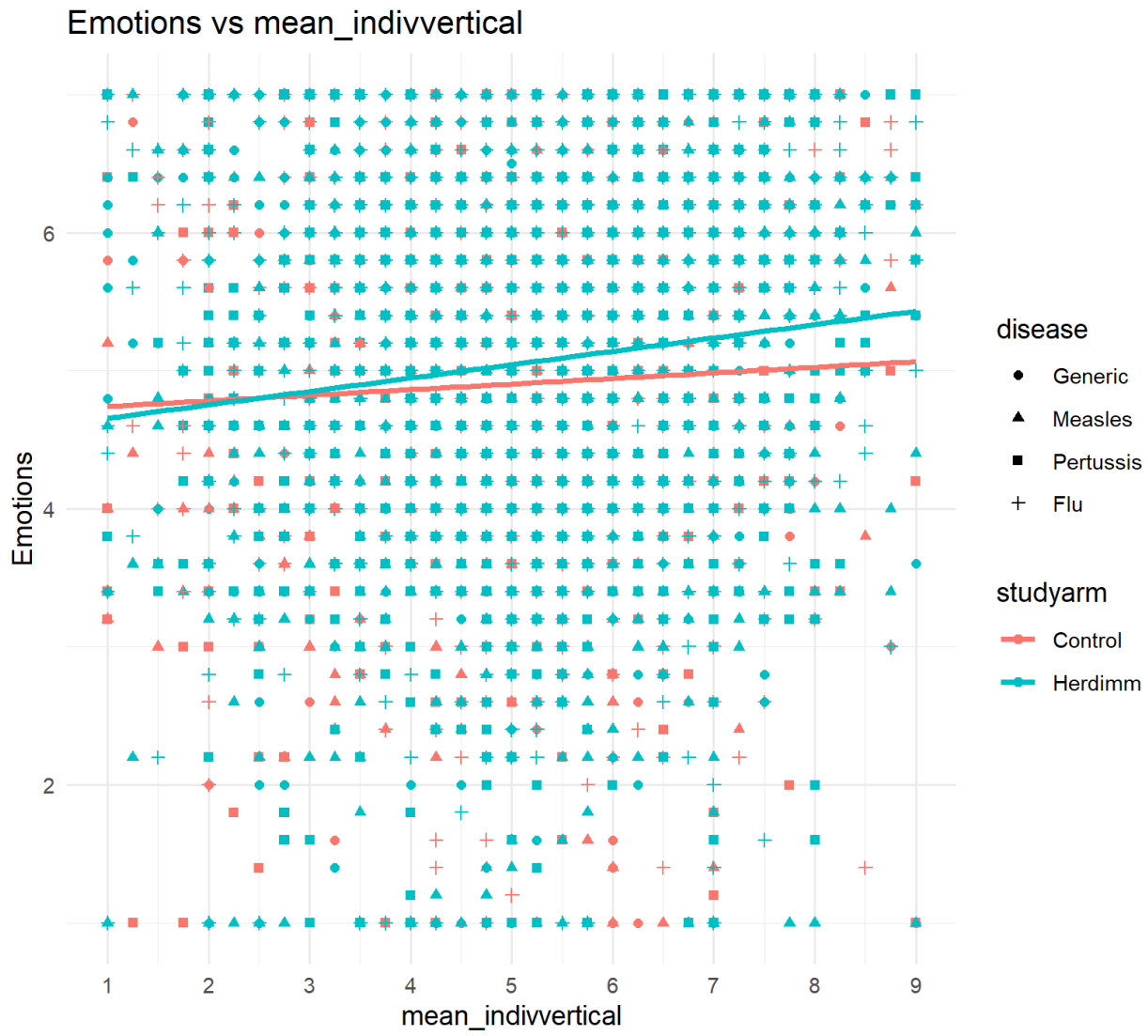


Emotions

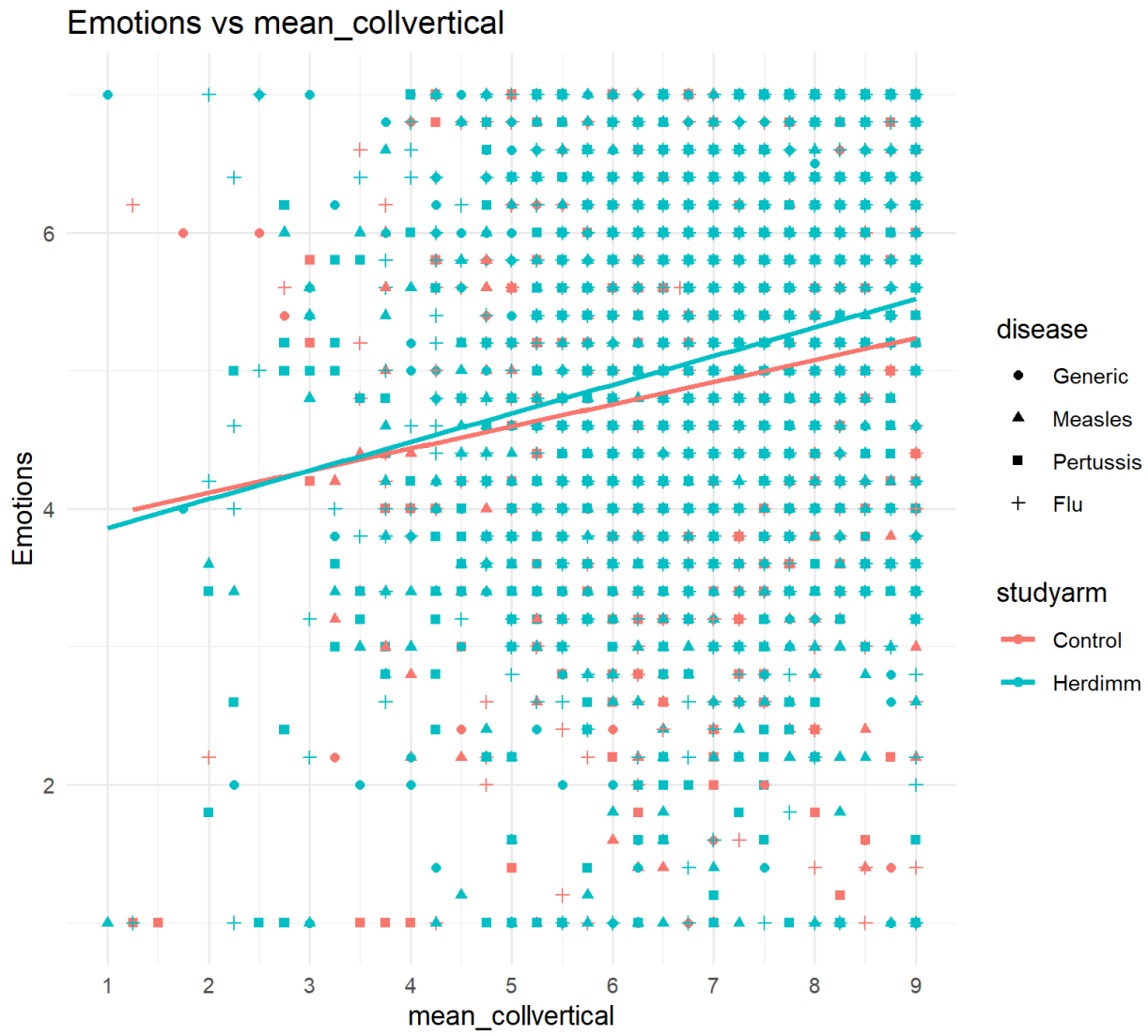
S9: emotions vs mean horizontal individualism



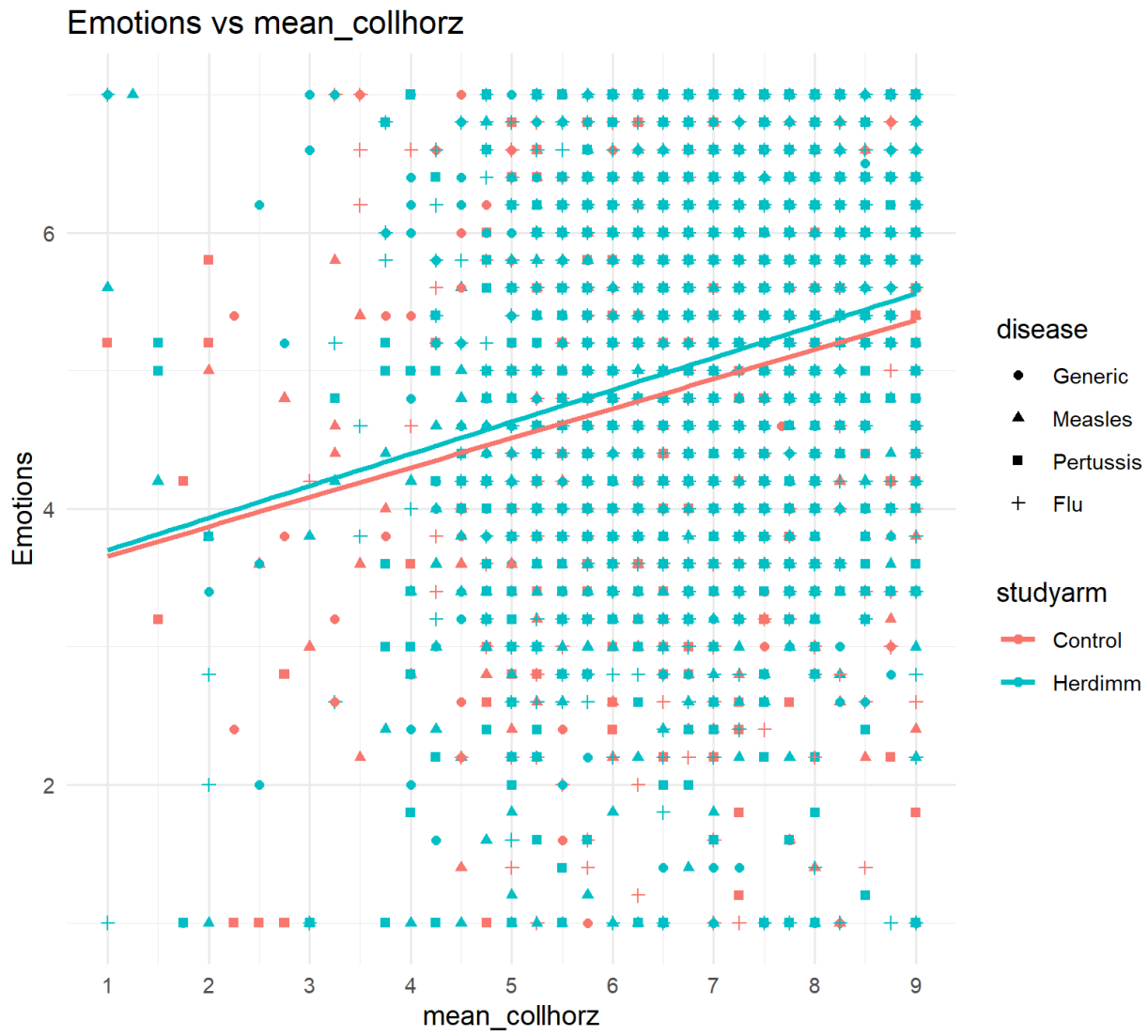
S10: emotions vs mean vertical individualism



S11: emotions vs mean vertical collectivism

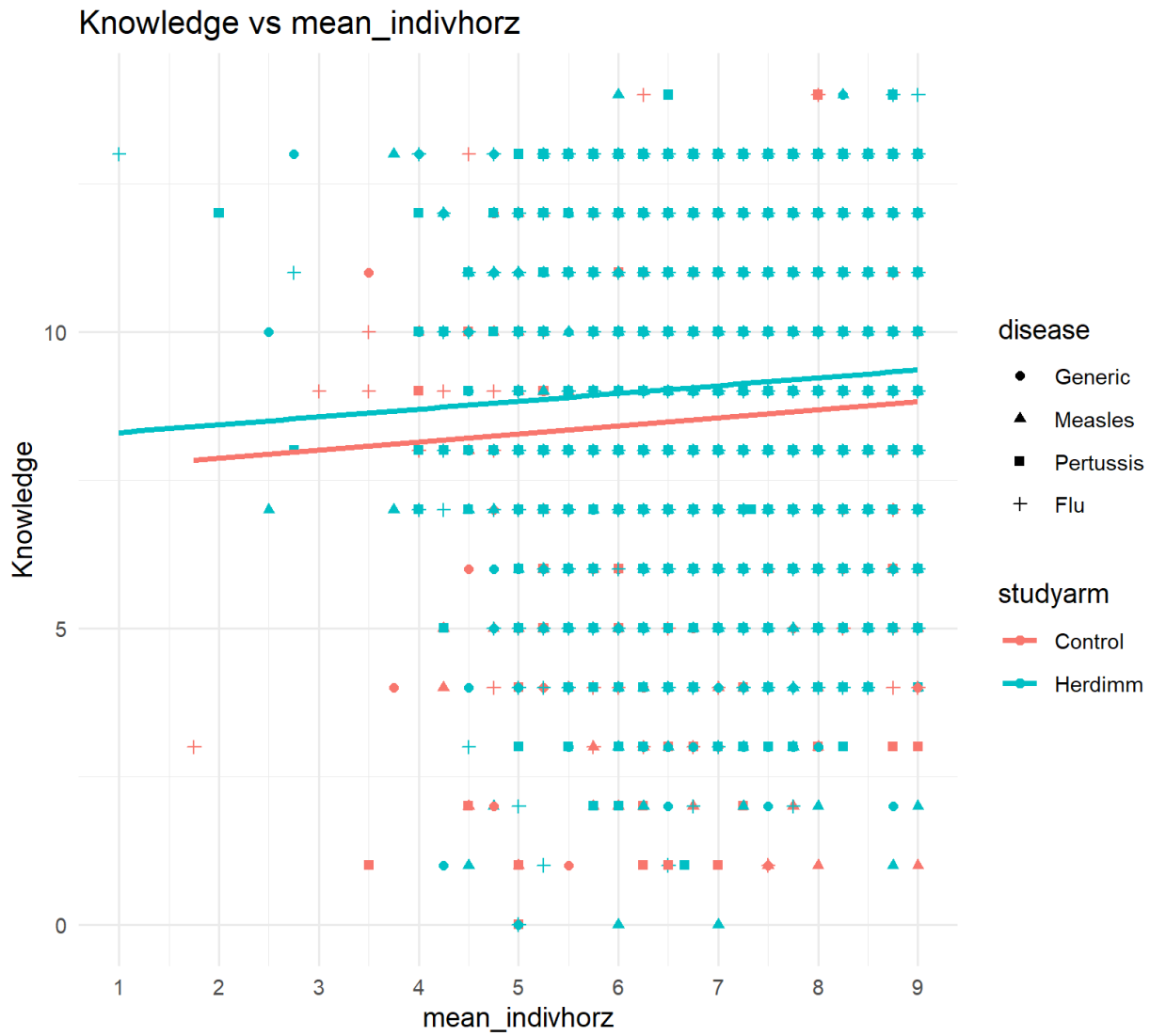


S12: emotions vs mean horizontal collectivism

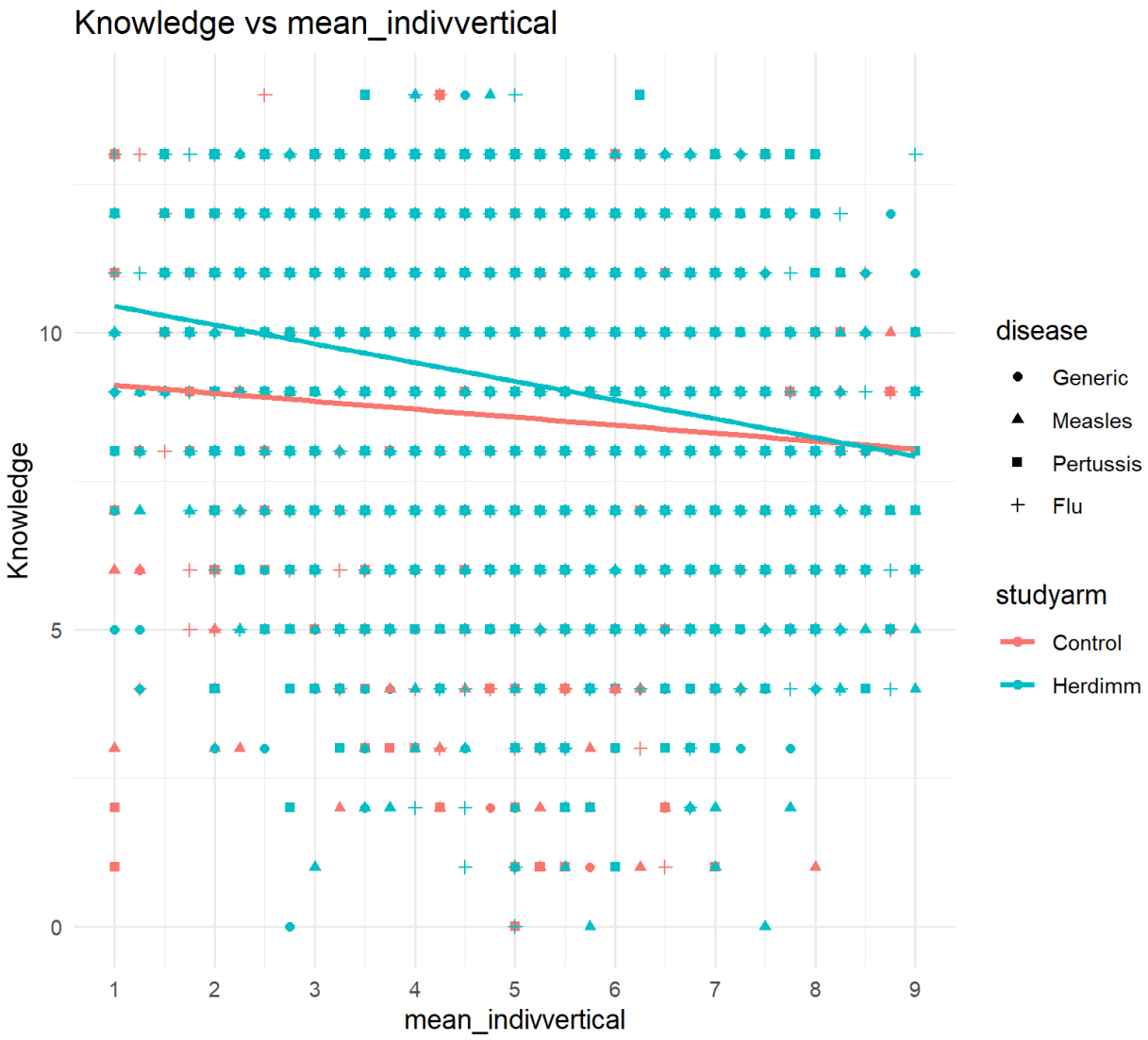


Knowledge

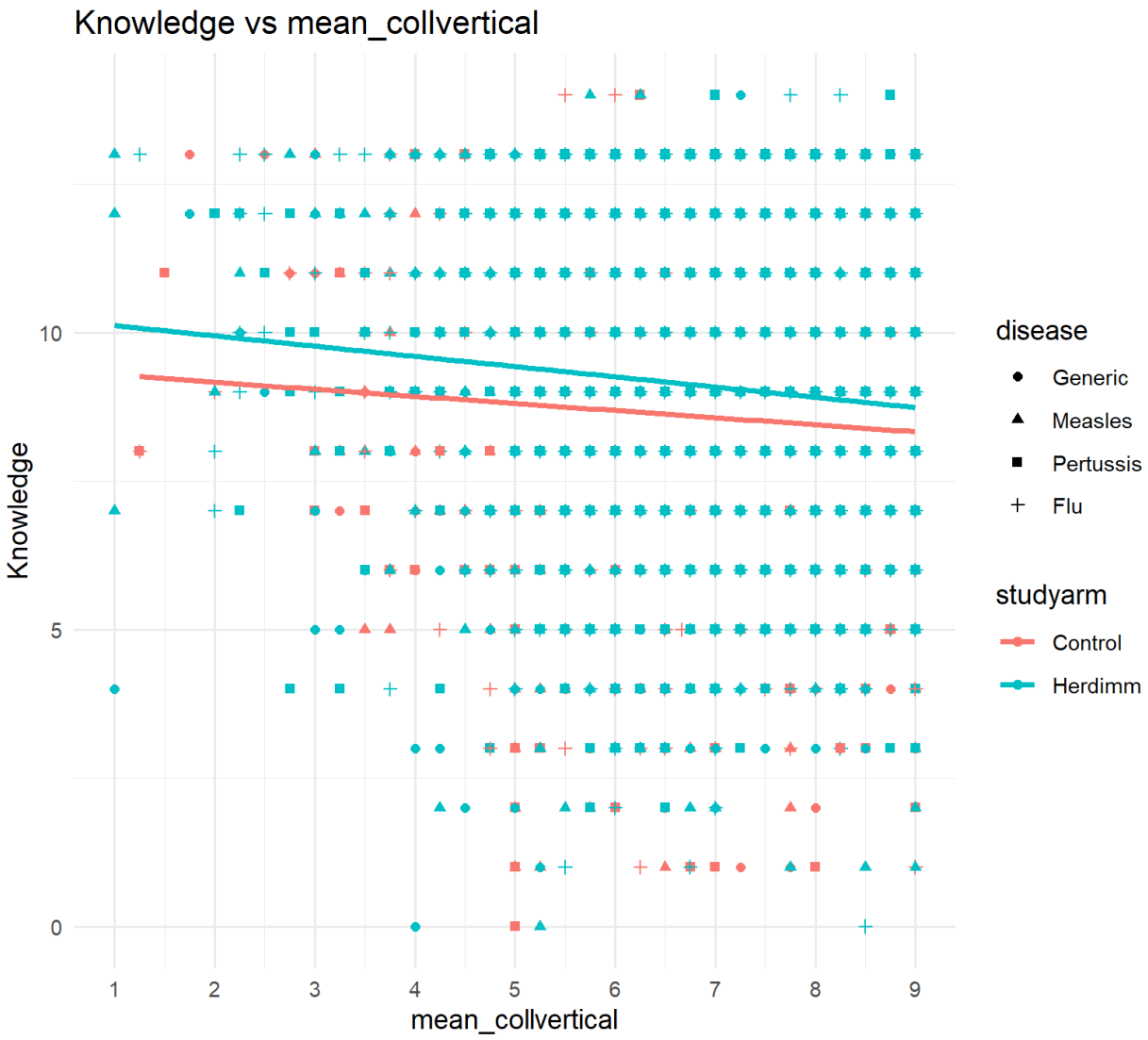
S13: knowledge vs mean horizontal individualism



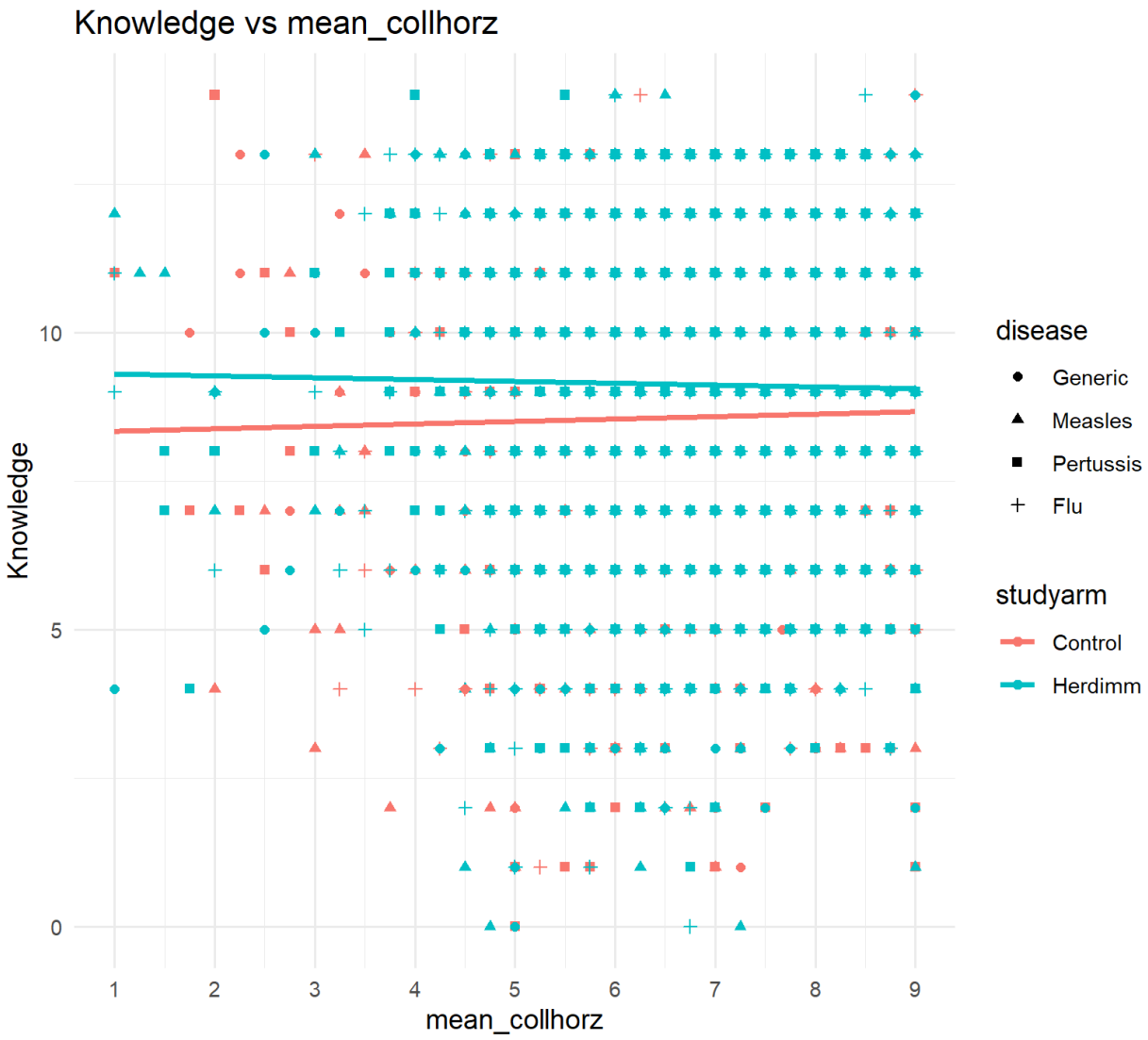
S14: knowledge vs mean vertical individualism



S15: knowledge vs mean vertical collectivism



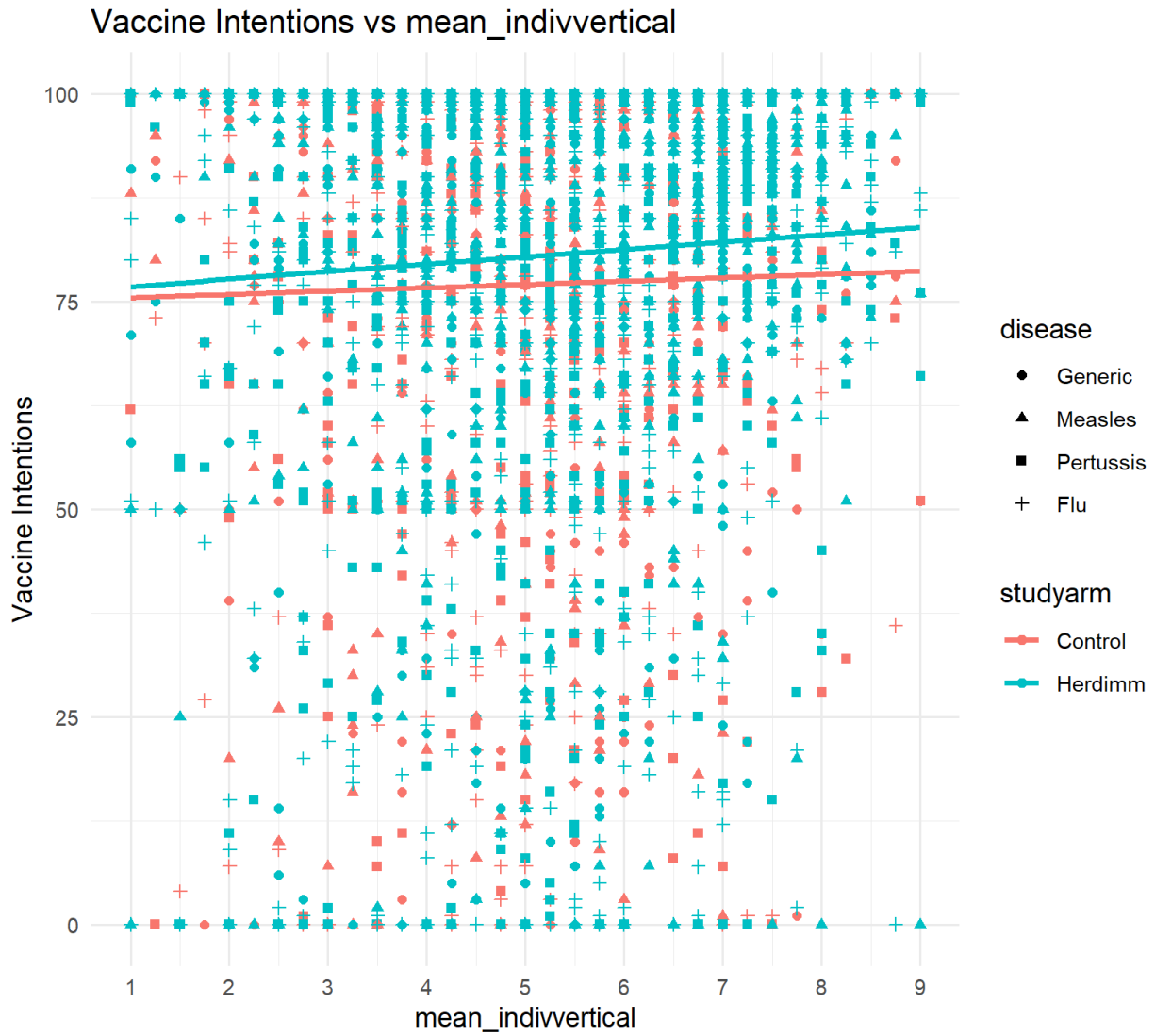
S16: knowledge vs mean horizontal collectivism



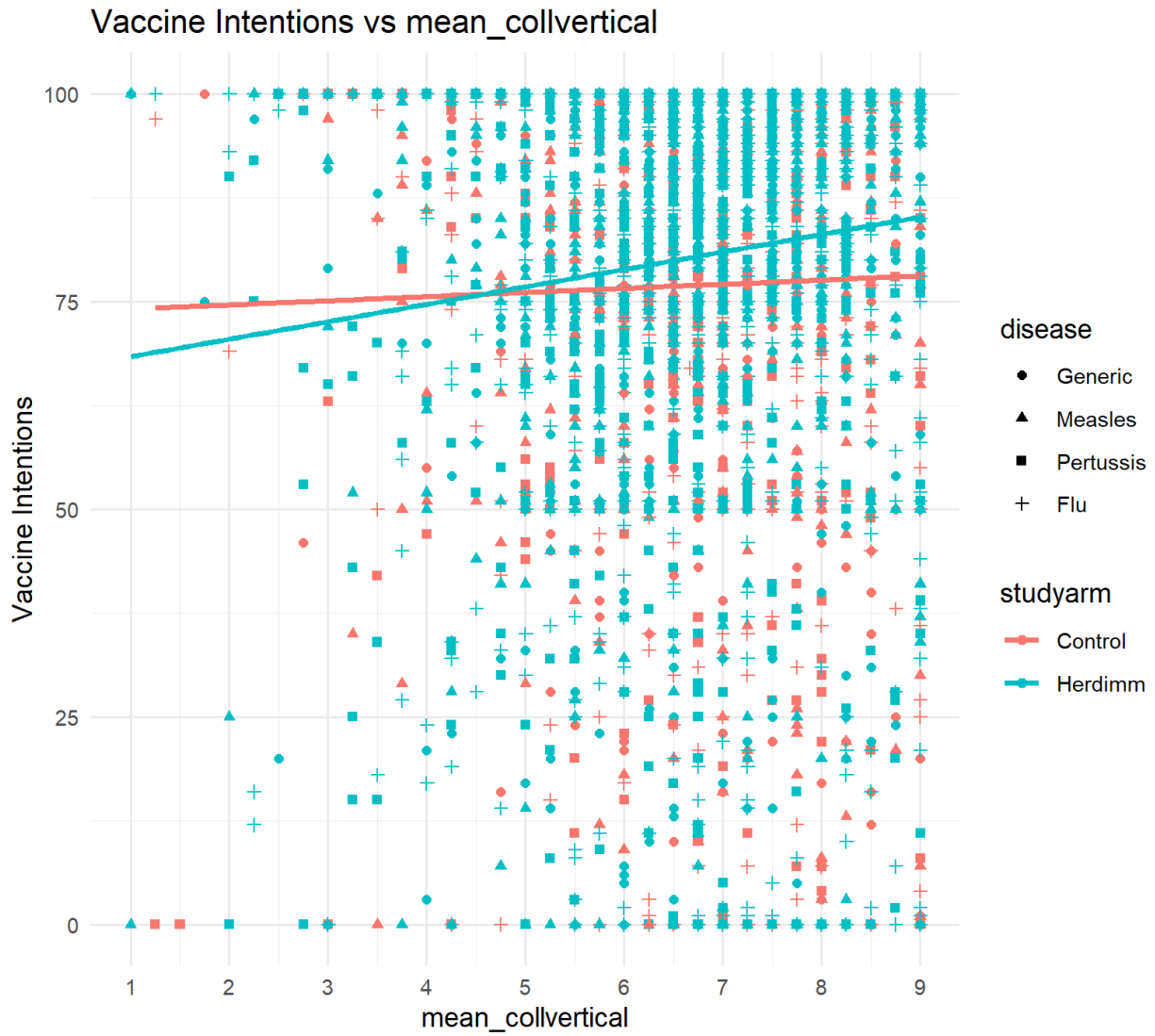
Vaccine intentions

S17: vaccine intentions vs mean horizontal individualism

S18: vaccine intentions vs mean vertical individualism



S19: vaccine intentions vs mean vertical collectivism

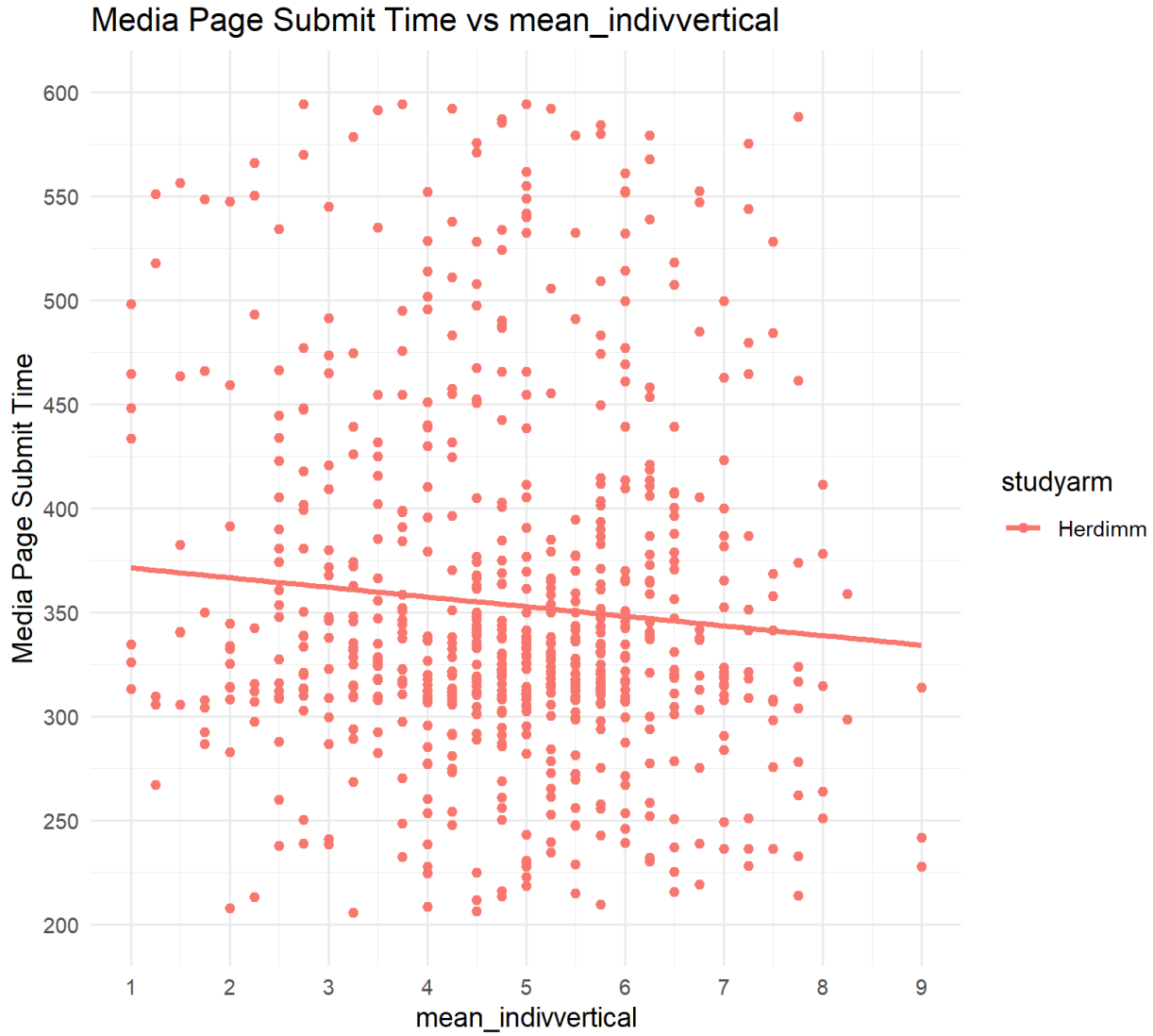


S20: vaccine intentions vs mean horizontal collectivism

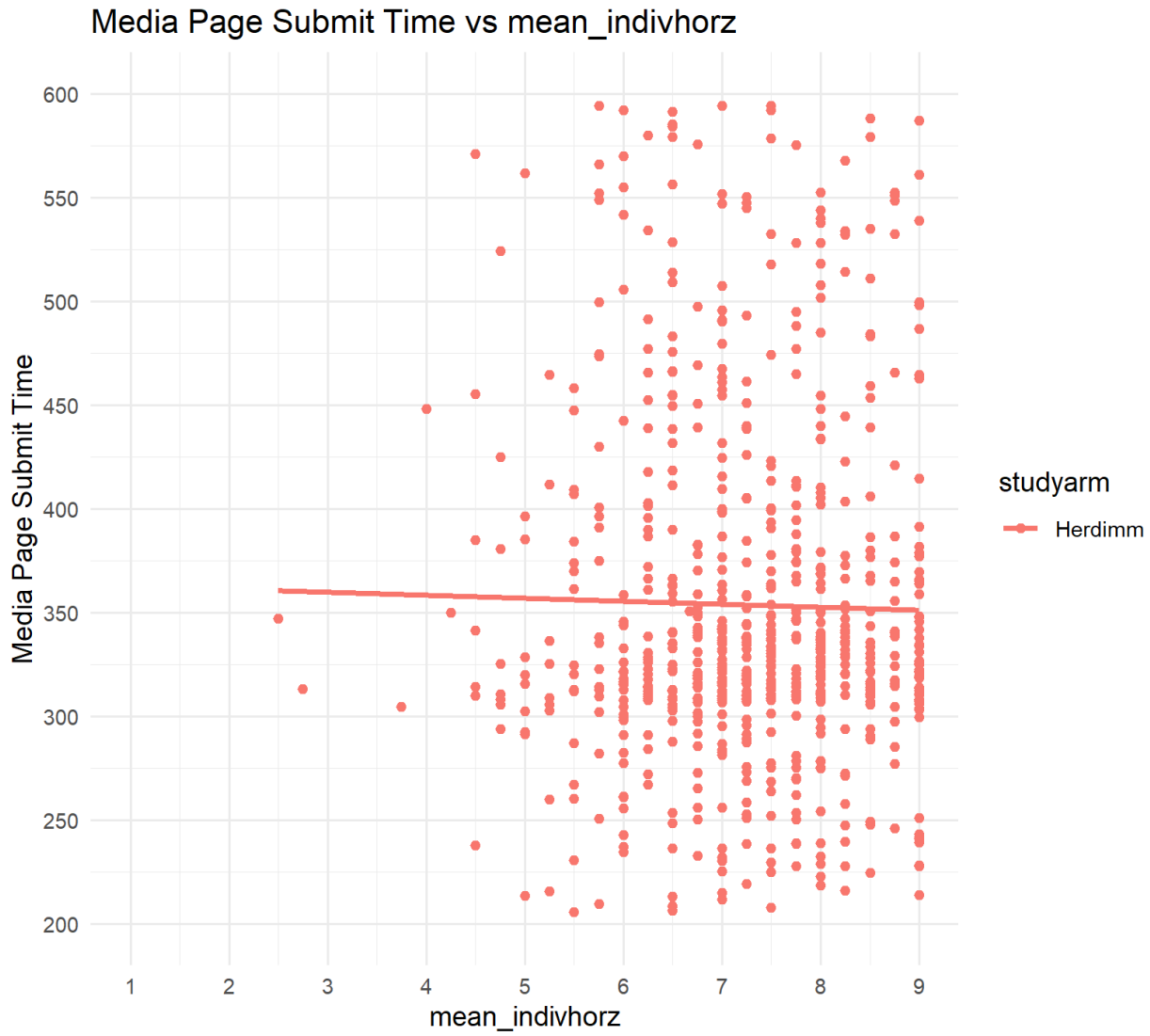
Timestamp for *herdimm* versus Individualism and Collectivism subscales (for participants assigned to *herdimm*)

Timestamp = seconds between reaching the page in which participants were directed to the *herdimm* intervention and returning to the page and clicking submit

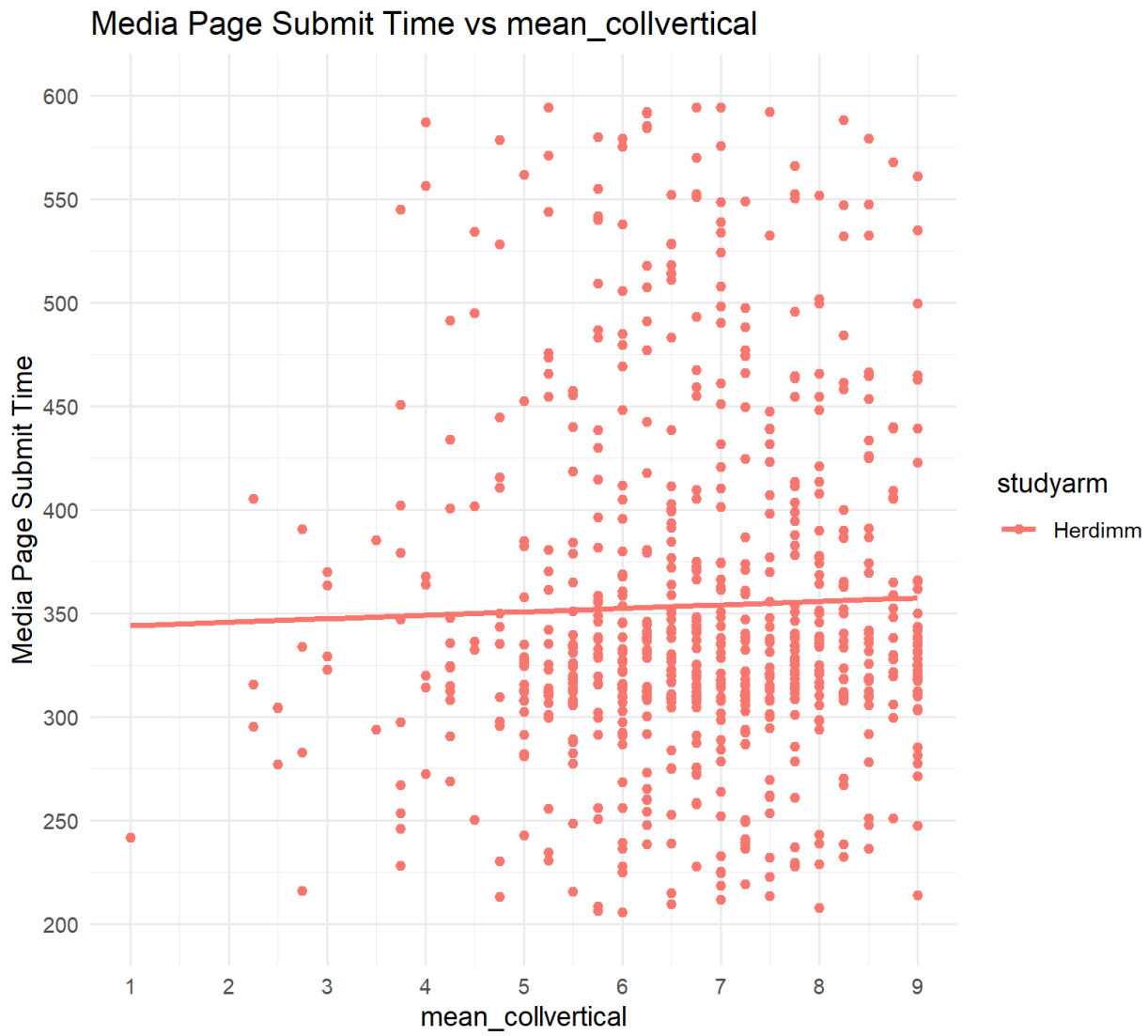
S21: Timestamp submitted for *herdimm* versus mean vertical individualism



S22: Timestamp submitted for *herdimm* versus mean horizontal individualism



S23: Timestamp submitted for *herdimm* versus mean vertical collectivism



S24: Timestamp submitted for *herdimm* versus mean horizontal collectivism