ON THE NECESSITY OF HUMAN DECISION-MAKING ERRORS TO EXPLAIN VACCINATION RATES FOR COVID-19: AN AGENT-BASED MODELING STUDY

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ABSTRACT

COVID-19 vaccines are important for individuals to avoid severe illness and collectively to prevent significant societal disruptions from uncontrolled disease spread. Vaccine adoption depends both on objective data about vaccine efficiency and on perceptions, which are shaped by individual characteristics and peer influences. Despite the abundance of Agent-Based Models (ABMs) models for COVID-19 and the long-term need for booster doses, ABMs have not yet accounted for the interplay of individual and collective drivers of vaccine adoption. In this explanatory study, we modify the validated COVASIM framework such that agents observe their peers' characteristics (derived from several datasets), use machine learning to reflect and then take decisions based on their own characteristics. We show that specific decision-making errors are necessary to replicate the real-world prevalence of COVID-19 vaccine coverage in the USA. Specifically, agents must only observe simple features of their peers (e.g., age, sex) rather than personal information (e.g., comorbidities).

Keywords: Agent-Based Model, COVASIM, COVID-19, Explanatory Model, Machine Learning.

1 INTRODUCTION

COVID-19 is an infection caused by the SARS-CoV-2 virus and responsible for almost 7M deaths worldwide by December 2022 (Google News 2022). COVID-19 is currently classified as a *pandemic*, which signifies that it is spread worldwide, as was the case for other viral respiratory diseases such as the H1N1 influenza pandemic or SARS (Noor and Maniha 2020). The immunity (albeit temporary) acquired from natural infections or one of the 33 approved COVID-19 vaccines (Machado et al. 2022) is contributing to a transition from a pandemic into an *endemic* status, which means that overall infection rates will become static. Concretely, it signifies that the virus will become a constant presence and will make a resurgence in regions with low cases (Phillips et al. 2021). Several reminders, such as Katzourakis (2022), have been issued to stress the implications of an endemic status. For example, "there can still be disruptive waves from endemic infections". In addition, an endemic state only means that the number of deaths will become more predictable, not necessarily lower: when authors forecast COVID-19 to turn into an influenza-like endemic disease, they note that there are 290,000 to 650,000 influenza-related deaths per year (Machado et al. 2022). One of the most striking illustrations comes from China, where a sudden transition into the endemic phase from the 'Zero Covid' (Liu, Leng, Yu, and McMorrow 2022) has visible consequences for the healthcare system (Master and Stanway 2022). It is thus essential to prevent unconstrained spread and focus on a low-incidence strategy (Czypionka et al. 2022), in particular by using vaccines. For instance, the high vaccination rate of Singapore has resulted in an endemic state for COVID-19, with fewer disruptions on the economy or the social fabric of society (Al-Tawfiq et al. 2022).

Surveys offer widely different takes (e.g., from 41% to 93% in Abdelmoneim et al. 2022) regarding the percentage of the US populations that would take additional vaccine doses (i.e., 'booster doses'). One of the largest cross-sectional survey studies concluded than half of US individuals would take boosters (Agaku et al. 2022). These numbers are potentially problematic, since a low-incidence strategy may require the yearly administration of an updated vaccine (Torjesen 2021, Marks, Woodcock, and Califf 2022). Responses are also highly heterogeneous since they are shaped by geographical, occupational, and sociodemographical factors (Terry et al. 2022, Agaku et al. 2022). The variety of factors involved demonstrate that a successful vaccination campaign is not merely a matter of vaccine efficacy or access: it also strongly depends on public compliance, where *perceptions* are important determinants of vaccine uptake (Iftekhar et al. 2021, Fan et al. 2022). While perception has been almost exclusively investigated at the individual level, a study released in November 2022 on a representative sample of the US population also examined predictors at the *collective* level (Hao 2022). The study found that perceptions are driven both by individual characteristics *and social networks*, measured as the percentage of friends and family that were vaccinated or contracted the virus.

Agent-Based Models (ABMs) allow to represent heterogeneous individuals (thus capturing variations in individual-level predictors) and their interactions through social networks. While early COVID-19 research employed compartmental models, ABMs have become about as prevalent as the tool of choice in recent studies (Zhang et al. 2022). Examples of ABMs for COVID-19 simulations have appeared at ANNSIM (Giabbanelli et al. 2021) and numerous other venues (Lorig et al. 2021, Ibrahim 2023). However, social networks have only served to model either the spread of the pathogen (Kerr et al. 2021, Li and Giabbanelli 2021b, Zhang et al. 2022) and/or contact tracing (Almagor and Picascia 2020). The present study thus seeks to address an urgent research gap by using ABMs to examine vaccine choices as a result of both individual- and collective-level factors. Our aim is *explanatory*, as we seek to build a model of individual decision-making processes which reproduces the observed pattern of 81% vaccination among US adults as of January 29, 2023. In sum, the contributions of our study are twofold:

- We extend the validated `COVASIM` framework (Kerr et al. 2021) by creating the first Agent-Based Model that combines individual demographic factors with social network influences to accurately reproduce the vaccination coverage observed in the USA.
- We demonstrate that specific individual decision-making *errors* are necessary to reproduce existing patterns, thus providing a model that can be reused for future COVID-19 ABMs that will need to account for yearly vaccine adoption.

The remainder of this paper is structured as follows. In Section 2, we briefly cover the use of ABMs for vaccine hesitancy and the inclusion of decision-making errors in COVID-19 ABMs. We introduce our methods and US-focused datasets in Section 3 and present our results in Section 4, with an emphasis on identifying combinations of parameters that reproduce the target vaccination rate of 81.0%. The implications of these results are discussed in Section 5 with respect to policy implications and future ABM developments.

2 BACKGROUND

The percentage of individuals who have received at least one dose of any COVID-19 vaccine varies across nations (Table 1). In Western Europe, similarly to our setting of the USA, first dose coverage ranges from 70% to 80% (Fan et al. 2022). Although numerous determinants are involved in shaping individual decisions regarding vaccination (Terry, Cartledge, Damery, and Greenfield 2022), the majority of simulation models for COVID-19 do not represent how individuals arrive at a decision. Many models were developed *prior* to the availability of vaccines, hence they focus on non-pharmaceutical interventions such as mask wearing and social distance. As vaccines became available, newer ABMs starting incorporating mechanisms to assign vaccines to specific agents, but assignments tended to be based on priority categories such as the elderly (Li and Giabbanelli 2021a) or individuals in nursing homes (Sulis and Terna 2021), people at severe risk or healthcare workers (Jahn et al. 2021). These allocation mechanisms are perpetuated in more recent ABMs (Cattaneo et al. 2022). Such models have made it clear that vaccine hesitancy is harmful for public health, as it leads to slower vaccination rates and ultimately increases fatality (Bhattacharya et al. 2021).

In parallel, ABMs have been developed solely to study the spread of beliefs regarding vaccines. While ABMs of *disease spread* are often rooted in SEIR models from computational epidemiology, ABMs focused on individual beliefs resemble models of *rumor spread* (Ndii et al. 2018). For example, in Sobkowicz and Sobkowicz (2021), agents have an opinion (drawn from a normal distribution) and some agents whose opinions are constant will send up to five messages (or opinions) per step. The action of anti-vaccination messages may be countered as agents may be convinced to vaccinate if they visit a supportive doctor; otherwise they will be influenced by the circulating messages. A similar model was proposed in Naderi et al. (2021), where agents also had demographic attributes (age, sex, race, income, education). A more abstract approach was taken by Al Atiqi, Chang, and Deguchi (2022), who used an ABM to simulate how a person's sentiment towards vaccines may change when reading Facebook pages. In all three cases, the model only accounted for the spread of rumors, although in reality there is a strong *interplay* between disease spread and information spread. For example, personally knowing someone who died of COVID-19 increases the odds of getting a vaccine (Beerman, Beaumont, and Giabbanelli 2022), and getting a vaccine reduces the odds of dying from COVID-19. The need to *jointly* simulate disease spread and information spread is a core motivation for the present work.

Table 1: Sample of worldwide rates, sorted alphabetically by country (Mathieu et al. 2020).

Country	**Single-Vaccination**	**Full-Vaccination**
Argentina	92%	84%
Canada	92%	84%
China	94%	91%
Costa Rica	91%	85%
France	81%	79%
Mexico	78%	65%
Japan	83%	82%
Spain	88%	86%
United States	81%	68%

3 METHODS

While early ABMs for COVID-19 were developed from scratch or built on prior efforts by the same team, several frameworks have made it possible to instantiate an ABM by leveraging a validated model and adding relevant aspects for a given research problem. In particular, `COVASIM` "has become one of the most widely adopted COVID models, and is used by researchers and policymakers in dozens of countries" (Kerr et al.

2022). In several cases (Cattaneo et al. 2022, Li and Giabbanelli 2021a), two reasons explain the choice of `COVASIM` for a new study: the framework automatically embeds agents in multiple realistic synthetic social networks based on their age (home, community, work or school if age relevant) and handles the entire disease progression, including age-based disease severity. `COVASIM` also contains an immunity module, which handles vaccines and their efficacy against the different variants that may spread simultaneously. To use this framework in our study, the next two paragraphs detail how we (i) expand the attributes of the agents and initialize them for our target population of the USA; and (ii) redesign the agents' decision-making activities such that they can account for errors typical of human behavior and are shaped by both individual attributes and peers. For both (i) and (ii), we implement the recommendations recently formulated by (Beerman et al. 2022). The section concludes with the design of our experiments.

`COVASIM` creates agents with a distribution of age and sex. Given recent reviews on determinants of COVID-19 vaccination (Terry et al. 2022, Agaku et al. 2022), we *added six individual attributes*: race and ethnicity, income, educational attainment (whether a person has a bachelor degree), diabetes, hypertension, and political belief. These attributes are added through through consecutive steps. First, we use one data source to generate agents by jointly assigning age, sex, race and ethnicity, and income (Figure 1). This creates realistic demographics for the US instead of assigning each factor based on a single dependency (e.g., age given sex, income given age). Second, since no dataset contains all of our target attributes, we use recent datasets to initialize each of the remaining four constructs. In each case, the initialization depends on three existing attributes (e.g., diabetes given age, sex, race and ethnicity) to capture as much as possible the joint distributions in the population (Figure 1). Third, we import these features into `COVASIM` by matching agents created with the platform with a pool of synthetic agent created through our process. In addition to socio-demographic attributes, we initialize the simulation by ensuring that a small subset (5% at random) of agents are currently actively infectious and some are vaccinated. It is important to accurately assign vaccines to the right agents at baseline, since the spread of adoption will account for peer influences (as detailed in the next paragraph). We thus seed the simulation with 10% of individuals vaccinated, identified among those most likely to have received the first dose given their age, race and ethnicity.

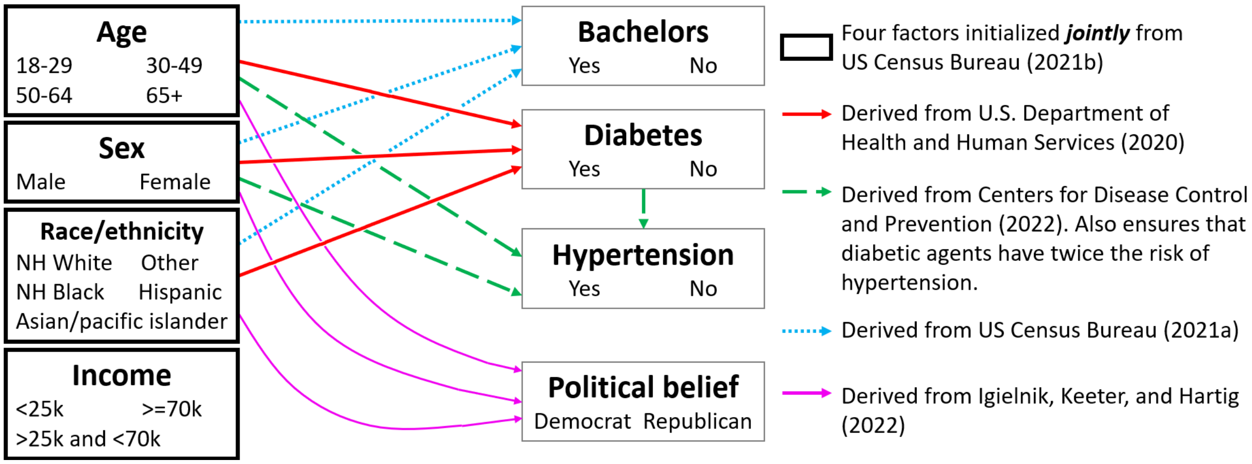


Figure 1: We first initialized four attributes jointly and then used a multitude of data sources to initialize additional (dependent) attributes. *Note: 'NH' means Non Hispanic.*

Every month each agent decides whether or not to vaccinate based on the knowledge accumulated about their peers (i.e., the cumulative observations up to the current month) and the decisions of their internal model. **First, agents observe** their peers. In reality, individuals may not know everything about others: for example, it is reasonable to know the age category of other agents, but we may not be aware of their political opinions or co-morbidities such as hypertension. We thus account for errors in decision-making by allowing agents to observe only a *percentage* of their peers and *a subset* of their attributes. The attributes are added gradually (Figure 3-left) to test the resemble the more information an individual learns about another as their relationship strengthens. For example, the first few attributes would be commonly known about an acquaintance (e.g., age, sex, whether they died), while the next set of attributes adds personal information (e.g., political views and income bracket) and the last attributes disclose medical information (the two co-morbidities of diabetes and hypertension). **Second, agents reflect** on their observations by deriving a model, similarly to how humans form generalizations from experiences. Each agent was equipped with a decision tree classifier, with observations from peers as input and whether to vaccinate as output. We chose decision trees because they can conveniently be visualized for debugging and constrained by a single parameter (the depth of the decision tree as in Figure 2) such that we can vary the sophistication of each agent's decision-making process. **Third, agents apply** the decision-tree classifier to themselves, given their own attributes. For example, they may have seen most of their older friends with co-morbidities taking the vaccine, but if they are young without co-morbidity then they do not feel concerned by their peers decisions. This mechanism replicates how individuals observe others' decisions and (partly) understand their motivations, but do not always feel personally concerned.

A simulation runs for a a full year starting at February 3, 2021 to October 3, 2022. This time period was selected to follow the timeline of the collected data for the United States vaccination total (Table 1). We initialize the `COVASIM` model, add agent attributes, seed the infection and vaccines, and run ML models on each agent as four variants of increasing strength emerge over a year. At initialization we seeded 10% of the population to be vaccinated by randomly selecting agents from the pool of agents who should have been vaccinated given the data. During the simulation, every agent (including those that were vaccinated at the start) records all attributes of the peers with whom they interact. Then, at each month, the agents train their own decision tree with their cumulative list of observations and finally predict whether or not they will vaccinate based on their own attributes. Note that the creation of the synthetic population (attributes and social ties) ensures that there is assortativity, hence an agent cannot decline the vaccine in perpetuity solely because it never finds its peers relatable.

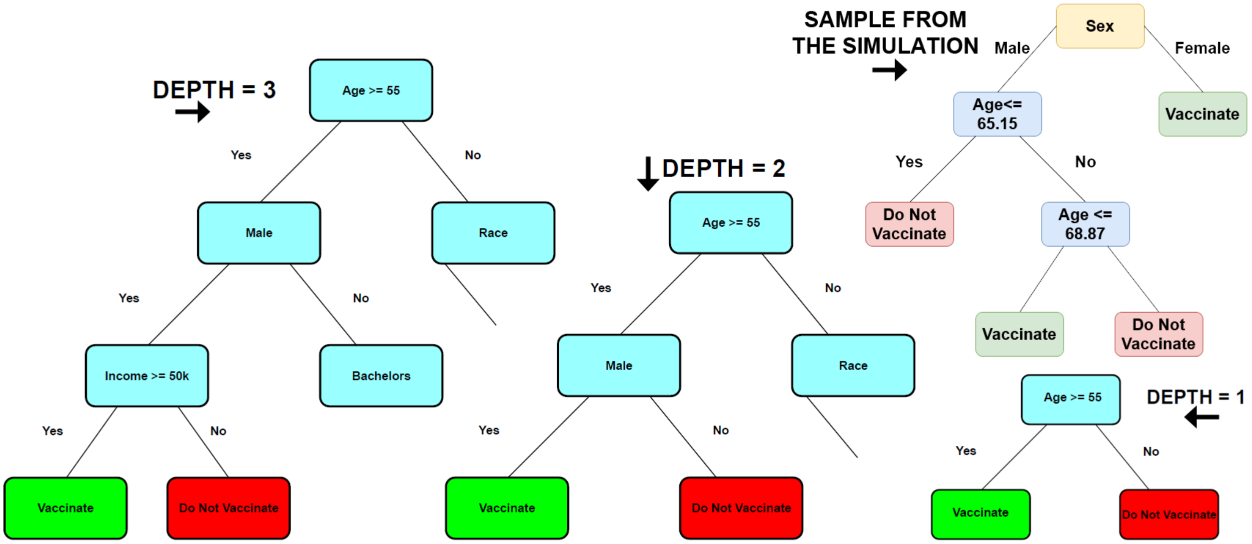


Figure 2: Each agent has a decision tree classifier, where the output is whether to vaccinate. The *depth* of the decision tree is a key parameter. As the depth of a decision tree increases, the vaccination decision of an individual may depend on a larger number of factors and/or revisit some factors to refine their choices. The agent's decision tree produced by our simulation (top-right) was obtained for the following parameters: Depth = 4, Attributes: {Sex, Age, Race}, Percentage of Observations: 100%).

In our experiments, we varied three model parameters as follows: decision tree depth from 1 to 4 (to examine the consequences of agents making simpler decisions); the amount of peers observed from 10, 25, 50, 75, or 100%; and the ten increasingly detailed subsets of peer information that were available to each agent (Figure 3-left). We ran each combination of parameter values ten times to account for the stochastic behavior of the model. Our experiments used the following software ecosystem: `COVASIM` 3.1.2 and `Numpy` 1.20.3 for the simulation of disease spread, `scikit-learn` 1.1.1 for the machine learning activities of each agent, and `Pandas` 1.3.3 for data analysis.

Combination	Attribute added
1	age
2	+sex
3	+race
4	+dead
5	+bachelors
6	+income
7	+political
8	+diagnosed
9	+diabetes
10	+hypertension

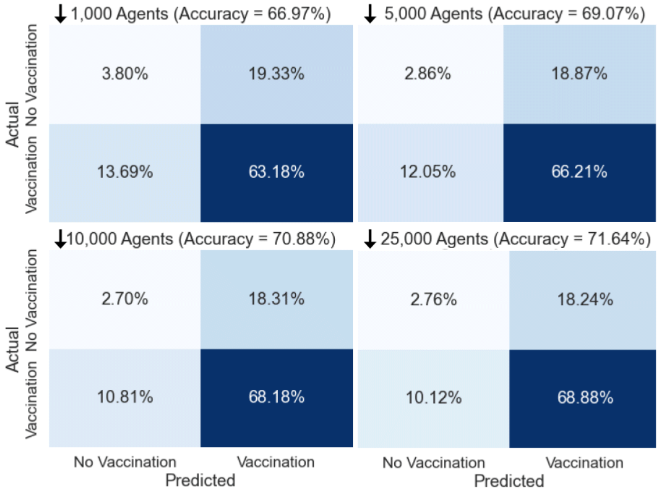


Figure 3: Left: Our 10 combinations (or simulation scenarios) add one factor at a time, from most to least potentially important based on prior reviews. For example, combination 3 has three factors: age, sex, race. Right: Confusion matrices for various populations where *Actual* represents the agents we determined would actually vaccinate and *Predicted* represents the agents that were predicted to vaccinate during the simulation. Parameters: Depth = 4, Attributes: $\{$Sex, Age, Race$\}$, Percentage of Observations: 100%.

Before interpreting the results from an ABM, we must ensure that (i) the model is sufficiently accurate for its purpose and (ii) the population size is sufficient to provide consistent results. We determine accuracy through a *confusion matrix* (Figure 3-right) by using our data to calculate which agents will vaccinate prior to simulation and then we compare those expectations with the simulation outcomes. Regarding the population size, it should not be too small as results may be incorrect and subject to significant variations, even as only a few hundred agents are added; this is exemplified in works such as Gibson et al. (2022). The population should not be too large either, as computationals cost may become prohibitive and force us to compromise the number of combinations examined (i.e., reduction in search space) and/or the number of repeats (Robinson 2014). Consequently, we perform simulations at increasingly large population sizes ($10,000$ agents, $25,000$ agents and $50,000$ agents) while looking for stability in the confusion matrix and the percentage of vaccinated agents.

4 RESULTS

For full disclosure, our data is permanently hosted on a third-party repository at https://doi.org/10.5281/zenodo.7582642. The data consists of two files: supplementary online material S1 provides the percentage of vaccinated population for each simulation run (i.e., each combination and each repeat) while supplementary online material S2 provides the average vaccination percentage across repeats for analysis. Our analysis of the average vaccination percentage at different population sizes confirms that we have enough agents. Specifically, results across population sizes differ by 0.45 ± 0.84 *percentage points* on average, or a

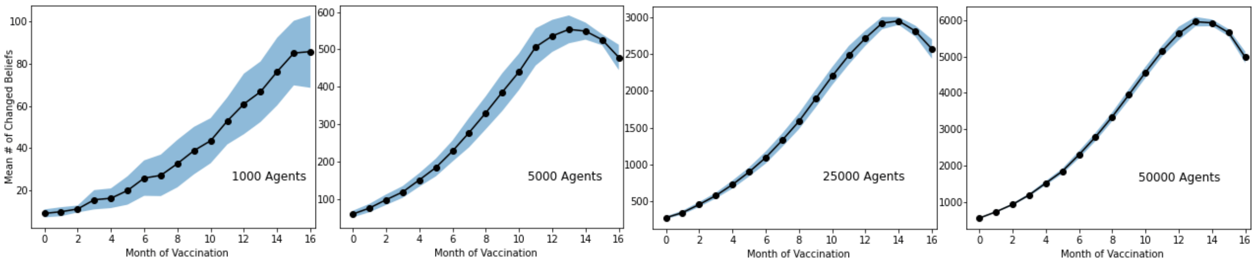


Figure 4: Agents changing their beliefs on vaccination over time.

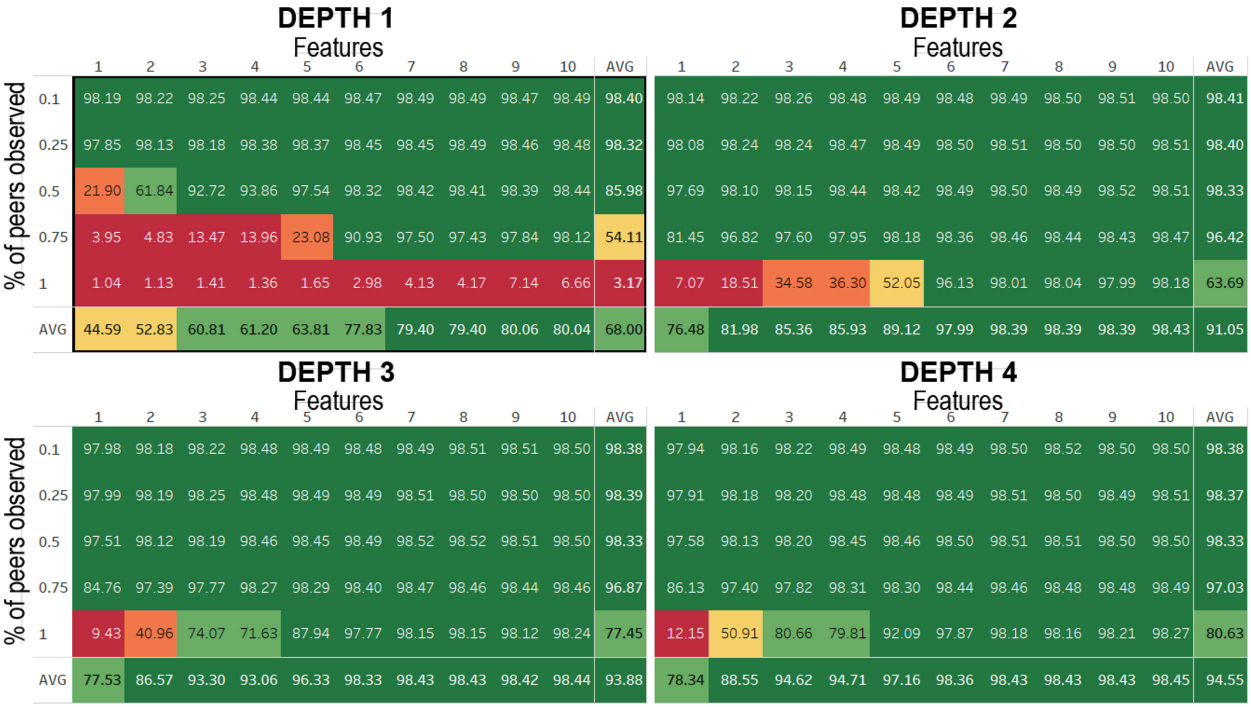
relative average difference of 1.55 ± 3.82. For example, for a decision tree depth of 2, the first combination of features (age only), and 75% of peers observed, we have the following vaccination rates: 81.45% for $10,000$ agents, 84.00% for $25,000$ agents, and 85.71% for $50,000$ agents. The widest difference is 4.25 percentage points (85.71 - 81.45) or a relative difference of 5.23%. The fact that most results are very close is further observed as 174 out of 200 combinations have a difference of less than 0.5 percentage points.

Heatmaps in Figure 5 summarizes the impact of the percentage of available data (i.e., observations) for the agent's internal models and the combination of attributes (Figure 3-left) at various depths of the decision tree. Overall, results show that the real-world coverage of 81% in the U.S.A. can only be obtained if agents observe enough of their peers. That is, if agents ignored most of their peers and decisions were not subject to social influences, the simulations suggest that almost the entire population would have been vaccinated. The best parameter combination to reproduce the target coverage of 81% consists of a decision tree depth of 4, 100% of observations, and three attributes (age, sex, race and ethnicity). Using this combination produced an accuracy over 70% when using a sufficient population size, per the confusion matrices (Figure 3-right). The second best combination is a decision tree depth of 2, 75% of observations, and only one attribute (age). If agents observe fewer peers, then they almost all get vaccinated. If agents have a very limited ability to reflect on the evidence (i.e., lower depths of the decision tree), then too few of them get vaccinated. The sensitivity of the model to the parameters is further visualized in Figure 6. We also analyzed the number of agents changing their mind regarding vaccination. Figure 4 shows that most agents change their belief after one year of simulation (i.e., between months 12 and 14).

5 DISCUSSION

A recent study showed that perceptions (and ultimately adoption) regarding the COVID-19 vaccine were driven by both individual characteristics and the social influences conveyed by peers (Hao 2022). Although many ABMs have been developed to study COVID-19, none of them has so far accounted for the interplay of individual and collective influences on vaccine decisions. Using machine learning to operationalize the decision-making module of agents, we found that few combinations of individual and collective features could accurately replicate the real-world coverage in the USA. Since a model is a *simplification* of reality, our results *should not be literally interpreted* to mean that only the two combinations found here explain the real-world vaccine coverage. Rather, the trends and high sensitivity of our model suggest that real-world patterns can be explained by the ability to observe most neighbors and derive sufficient rules from observations. These rules are based on commonly low-level observed features (e.g., age, sex) rather than very personal information (e.g., co-morbidities). In other words, individuals are not blind to their peers, unable to make judgments, or engaged in complex rules that take into account intimate details about their peers. Rather, they take into account simple features about most people around them.

The implications for the development of ABMs going forward is that accounting for individual and collective drivers of vaccine choices can be achieved by letting agents observe all peers at each round and run relatively light models (decision tree). The characteristics of peers that are needed for decision-making are



DEPTH 1

Features

% of peers observed	1	2	3	4	5	6	7	8	9	10	AVG
0.1	98.19	98.22	98.25	98.44	98.44	98.47	98.49	98.49	98.47	98.49	98.40
0.25	97.85	98.13	98.18	98.38	98.37	98.45	98.45	98.49	98.46	98.48	98.32
0.5	21.90	61.84	92.72	93.86	97.54	98.32	98.42	98.41	98.39	98.44	85.98
0.75	3.95	4.83	13.47	13.96	23.08	90.93	97.50	97.43	97.84	98.12	54.11
1	1.04	1.13	1.41	1.36	1.65	2.98	4.13	4.17	7.14	6.66	3.17
AVG	44.59	52.83	60.81	61.20	63.81	77.83	79.40	79.40	80.06	80.04	68.00

DEPTH 2

Features

% of peers observed	1	2	3	4	5	6	7	8	9	10	AVG
0.1	98.14	98.22	98.26	98.48	98.49	98.48	98.49	98.50	98.51	98.50	98.41
0.25	98.08	98.24	98.24	98.47	98.49	98.50	98.51	98.50	98.50	98.51	98.40
0.5	97.69	98.10	98.15	98.44	98.42	98.49	98.50	98.49	98.52	98.51	98.33
0.75	81.45	96.82	97.60	97.95	98.18	98.36	98.46	98.44	98.43	98.47	96.42
1	7.07	18.51	34.58	36.30	52.05	96.13	98.01	98.04	97.99	98.18	63.69
AVG	76.48	81.98	85.36	85.93	89.12	97.99	98.39	98.39	98.39	98.43	91.05

DEPTH 3

Features

% of peers observed	1	2	3	4	5	6	7	8	9	10	AVG
0.1	97.98	98.18	98.22	98.48	98.49	98.48	98.49	98.51	98.51	98.50	98.38
0.25	97.99	98.19	98.25	98.48	98.49	98.49	98.51	98.50	98.50	98.50	98.39
0.5	97.51	98.12	98.19	98.46	98.45	98.49	98.52	98.52	98.51	98.50	98.33
0.75	84.76	97.39	97.77	98.27	98.29	98.40	98.47	98.46	98.44	98.46	96.87
1	9.43	40.96	74.07	71.63	87.94	97.77	98.15	98.15	98.12	98.24	77.45
AVG	77.53	86.57	93.30	93.06	96.33	98.33	98.43	98.43	98.42	98.44	93.88

DEPTH 4

Features

% of peers observed	1	2	3	4	5	6	7	8	9	10	AVG
0.1	97.94	98.16	98.22	98.49	98.48	98.49	98.50	98.52	98.50	98.50	98.38
0.25	97.91	98.18	98.20	98.48	98.48	98.49	98.51	98.50	98.49	98.51	98.37
0.5	97.58	98.13	98.20	98.45	98.46	98.50	98.51	98.51	98.50	98.50	98.33
0.75	86.13	97.40	97.82	98.31	98.30	98.44	98.46	98.48	98.48	98.49	97.03
1	12.15	50.91	80.66	79.81	92.09	97.87	98.18	98.16	98.21	98.27	80.63
AVG	78.34	88.55	94.62	94.71	97.16	98.36	98.43	98.43	98.43	98.45	94.55

Figure 5: Vaccination rate as a function of the depth of the decision tree, simulation combination (x-axis), and percentage of peers observed (y-axis). Values close or above the observed vaccination rate are in green, while values below are in red.

already used in many ABMs (many of which use age in their disease severity module), hence minor to no modifications are needed in terms of agent features.

We focused on vaccine engagement as a product of a *local* social context, but it is also impacted by community- and societal-level factors (e.g., conceptions of health, encounters with the healthcare system) (Pickersgill et al. 2022). For instance, our study setting of the USA is different from western European countries in terms of legal system and policy choices. Although article 8 of the European Court of Human Rights considers that compulsory vaccination may interfere with private rights, vaccination can legally be mandatory if treatment is not dangerous and can help others (Vergallo et al. 2022). Austria was the only nation to introduce a vaccination mandate and it abandoned it a few months later, but other countries use COVID-19 Vaccination Certificates (known in EU Regulation 2021/953 as ‘Green Digital Certificate’) as incentives (Vergallo et al. 2022). As a result, societal-level drivers for vaccination may be higher in these countries than in the USA. In addition, the individual-level constructs most strongly associated with vaccine intention are different across places (Limbu, Gautam, and Zhou 2022). Consequently, if our model is re-calibrated to a different location, simulation results may show that a different combination of variables best explains the current rate in the location of interest.

Furthermore, future works could conduct these simulations at a smaller geographical scale to capture precise demographics which may produce more accurate results. For example, we may focus on a location such as New York City and only initialize attributes from data sets accordingly. These data sets could change our demographic variables. The New York City Community Health Survey (Survey 2020) (CHS) depicts age groupings to be the following: 0-17 (21%) 18-24 (8%), 25-44 (30%), 45-64 (25%), 65+ (16%). The American Community Survey (U.S. Census Bureau 2020) would switch our race percentages to the following: Asian (15%), Black (22%), Latino (29%), White (32%). Ultimately, a specific geographical location and its associated demographic data could change the vaccination rate.

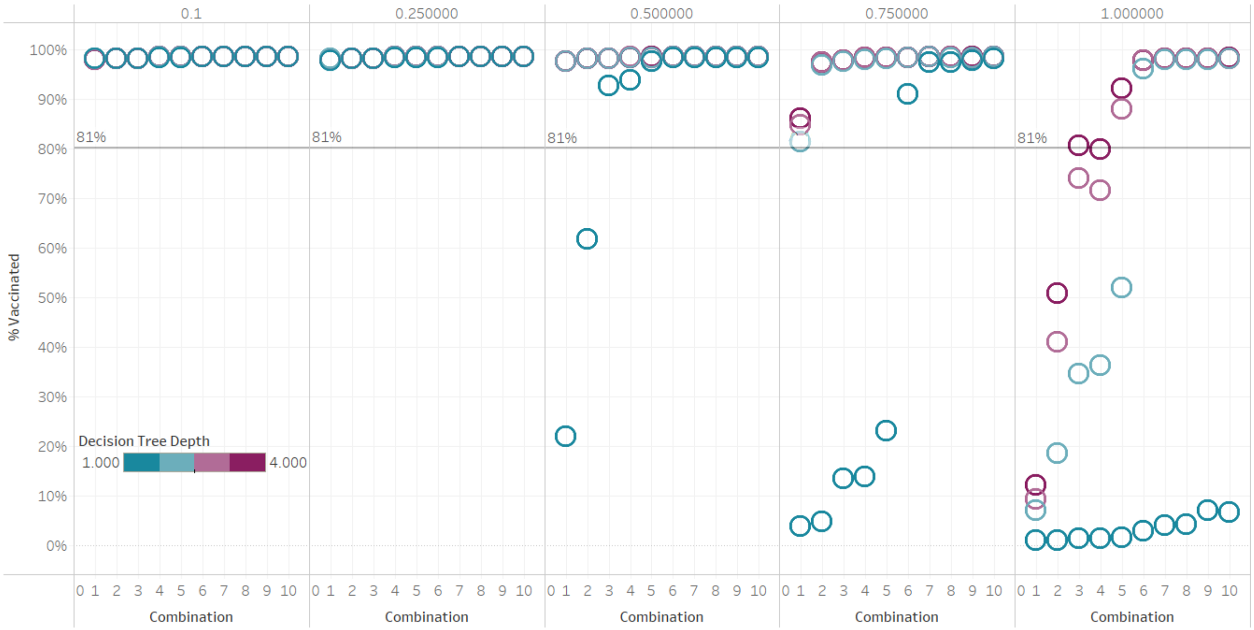


Figure 6: Effect of the percentage of observations, depth of the decision tree, and attribute combination onto the vaccination rate.

Since it is a simplification, future works could extend our model in numerous ways. Our results suggest that extensions may not be as necessary when it comes to agent features, since accounting for a few of them suffices to replicate core results. However, extensions may be beneficial to examine how agents deal with their memories. Indeed, the observations of each agent are strictly cumulative, hence there is a perfect recollection of every that was observed previously. This may artificially reduce the possibility that agents make a different decision later in the simulation, since their new observations become diluted among their extensive records of the past. In practice, it is likely that people 'forget' some of these past observations. A simple approach adopted in other ABMs would be to express that the probability of forgetting a past observation increases as time advances (Ding and Xie 2023). Most interestingly, computational models of cognitive science offer different approaches to handle *reconsolidation*, which deals with updating, distorting, or even erasing past observations (Ecker and Lewandowsky 2012). As we shift our focus from a mechanical model of disease progression onto an investigation of human health behaviors, opportunities abound to incorporate cognitive models into ABMs for COVID-19.

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