Adapting the "Networking during Infectious Diseases Model" (NIDM) for Science Communication using Julia and Genie

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Abstract. Scientific publications can be challenging for non-experts due to their complex concepts, technical terminology, and detailed descriptions of results. Interactive simulations can be used as a powerful way to communicate scientific progress to non-experts, providing a more engaging and hands-on experience that can help users understand complex processes. In this paper, we present a prototype of an interactive simulation for the "Networking during Infectious Diseases Model" (NIDM), which integrates theory from sociology, health psychology, and epidemiology to explore the interplay between social networks and the spread of infectious diseases. The prototype was developed using user-centered design and formatively evaluated. The goal of the contribution is to open the discussion on the evaluation of the prototype and to enhance the intuitive understanding of self-protective behavior and distancing measures following the outbreak of COVID-19. The results highlight the potential of interactive simulations as a tool for science communication and public engagement.

Keywords: Social Networks · Infectious Diseases · Risk Perception · Agent-based Models · Science Communication · Julia

1 Introduction

It can be challenging for non-experts to understand scientific publications for several reasons. That is, scientific publications tend to present intricate concepts and theories that necessitate in-depth knowledge of the underlying subject. In addition, scientists frequently employ specialized and technical terminology

that may be unfamiliar to individuals outside the respective field. Furthermore, scientific publications frequently describe results and discoveries in a highly detailed and technical manner, particularly when involving extensive statistical analysis and data.

A powerful way to communicate scientific progress to non-experts is by using interactive simulations, allowing users to manipulate variables and observe the resulting outcomes in real-time. This form of interaction provides a more hands-on and engaging experience compared to traditional forms of communication such as lectures or texts. Furthermore, interactive simulations can foster a sense of curiosity and encourage users to ask questions and form hypotheses about how different variables may affect the system. This can be especially useful when complex and dynamic processes are challenging to understand and visualize.

Take the interplay between social networks and infectious diseases, for example. It is known that social networks play a crucial role in the spread of infectious diseases. If, for example, a social network is highly connected, the disease is more likely to spread quickly through the network. Clusters within the network, on the other hand, highly connected areas with only a few connecting relations in between, tend to slow down disease spread [1,10,14]. Although this effect can be described with only a few words, true comprehension of the time-dependent interplay between social networks and the spread of infections is challenging.

This paper presents a prototype of an interactive simulation for the "Networking during Infectious Diseases Model" (NIDM) [16]. The NIDM is a previously developed individual-based mathematical model framework and agent-based simulation that integrates theory from sociology, health psychology, and epidemiology. Networking decisions in the NIDM are a trade-off between the benefits, costs, and potential harms of infections created by a social relationship. The degree to which agents avoid infectious others depends on individual risk perceptions regarding personal susceptibility to, and the severity of, an infectious disease. Simulations based on the NIDM give rise to complex interdependencies between individual behavior, network properties, and the spread of infections.

The goal of this contribution is two-fold. On the one hand, we aim to open the discussion on our method of evaluation and how to proceed in turning our prototype into a valuable tool for science communication. On the other hand, with the provision of our prototype, we aim to lay the foundation for enhancing the intuitive understanding of the efficacy of self-protective behavior and distancing measures following the outbreak of COVID-19. This way, we want to contribute to the discourse and arouse interest in the importance of science in the public domain.

2   Background

To fully understand the background of this paper, it is critical to understand the project's key purpose. For this, we discuss the aim of the prototype—science communication—and the content being communicated—the networking during infectious disease model.

2.1   Science communication

Classical methods of publishing scientific research, such as papers in peer-reviewed journals, chapters in textbooks, and presentations at scientific conferences remain arguably among the most popular channels to communicate and discuss scientific progress. A vast body of literature covers how to communicate scientific findings in the best possible way [4,6,9,15]. Over time, science communication has become a topic of increasing interest. Technological advances, especially the internet, have made it easier to gain access to even the most specialized information, whether in the form of open-access papers, science podcasts, social media, online lectures, or science slams. The success and ever-increasing number of such publications demonstrate the popularity both among the scientists presenting their results and among an audience that no longer necessarily consists only of experts.

From the scientists' perspective, communicating scientific research to a broader audience has not only promotional benefits. Including the general public in scientific discourse can be beneficial on various levels. For example, by making science more accessible to a broader audience, researchers can improve scientific literacy and promote a positive perception of science among the general public. In addition, the involvement of the general public can help to ensure that scientific research is conducted in an ethical and responsible manner. Including non-experts can help to identify potential risks and ethical concerns associated with research. Furthermore, this can provide valuable input on how to mitigate these risks and ensure that research is conducted in a socially responsible manner. Including the general public can also improve the relevance and impact of scientific research. By incorporating the perspectives and experiences of non-experts, scientists can identify research questions that are relevant to society and that address real-world problems. This can lead to the development of more impactful and relevant solutions.

Although there is no universal answer to how results should be communicated to a non-specialist audience, research has shown that different methods are effective in different contexts and for different goals. That is, visual elements, such as graphs, diagrams, and animations, can help to understand complex scientific relationships [11,13,18]. Incorporating storytelling into science communication can increase engagement and retention of information [7]. Interactive simulations, on the other hand, allow users to manipulate variables and see the effects of those changes in real-time. This can help users develop a more profound understanding of complex systems and their underlying mechanisms. A study among postgraduate science teachers by Zacharia [22], for example, showed that the use of computer simulations had a positive effect on the quality of explanations regarding physical phenomena in Mechanics, Waves/Optics, and Thermal Physics. Another study among elementary school students by Evagorou et al. [5] indicates that an interactive simulation of the ecosystem of a marsh can support the development of system thinking skills.

2.2   The networking during infectious diseases model (NIDM)

A complex system that is typically studied using computer simulations is the relationship between network structures and disease dynamics. A previously developed model framework to study the interdependencies between individual health behavior, social network properties, and spread of infections is the "Networking during Infectious Diseases Model" (NIDM) [16]. Realizations of the NIDM are individual-based models for infectious disease transmission [2,21,19], that assume an agent (i) to myopically optimize individual utility (U_i) composed of the benefits of social relationships (B_i), the costs to maintain these relationships (C_i), and the potential harm of infectious contacts (D_i):

$$U_i = B_i - C_i - D_i. \tag{1}$$

The realization of the NIDM used for this study is the "Small-worlds during Infectious Diseases Model" (SWIDM) [17]. The SWIDM allows studying the effect of small-world properties (i.e., clusters of densely connected areas within a network) on the spread of infections. To realize the incentive of clustering, the benefits of social relationships:

$$B_i = b_1 \cdot t_i + b_2 \cdot \left(1 - 2 \cdot \frac{|x_i - \alpha|}{\max(\alpha, 1 - \alpha)}\right) \tag{2}$$

are defined as the combination of the benefits (b_1)[1] for the number of social relationships (t_i) and the weighted (b_2) proportion of closed triads[2] (x_i) an agent i is part of. α defines the preferred proportion of closed triads and thus allows to control the degree of clustering in the network.

The costs of maintaining social relationships

$$C_i = c_1 \cdot t_i + c_2 \cdot t_i^2 \tag{3}$$

are defined as marginally increasing costs (c_1, c_2) dependent on the number of social relations an agent i has (t_i). These costs, in combination with the benefits for the number of social relationships ($b_1 \cdot t_i$), allow controlling the actual number of social relationships an agent i has.

The potential harm of infectious contacts

$$D_i = p_i \cdot s_i. \tag{4}$$

is the combination of the *perceived* probability to acquire and infection (p_i) and the *perceived* severity of the disease (s_i). That means an agent i transforms the actual probability to get infected

$$\pi_i = 1 - (1 - \gamma)^{t_{i_I}}, \tag{5}$$

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[1] See Table 1 for an overview of all model parameters and state variables.
[2] A closed triad is a group of three nodes in a network where each pair of nodes (here: agents) is directly connected by an edge (here: social relation), forming a triangle shape.

with γ being the probability to get infected per single contact and t_{i_I} the number of infected social relations the agent has, into a subjective perception, depending on the agent's disease state:

$$p_i = \begin{cases} \pi_i^{2-r}, \text{ if } i \text{ is susceptible,} \\ 1, \text{ if } i \text{ is infected,} \\ 0, \text{ if } i \text{ is recovered.} \end{cases} \tag{6}$$

Finally, the actual severity of the disease (σ) is transformed into a subjective perception, depending on agent i's disease state:

$$s_i = \begin{cases} \sigma^r, \text{ if } i \text{ is susceptible,} \\ \sigma, \text{ if } i \text{ is infected,} \\ 0, \text{ if } i \text{ is recovered.} \end{cases} \tag{7}$$

As a result, risk perception values (r) above 1 cause agents to overestimate the probability of acquiring infections and disease severity. Consequently, these *risk averse* agents tend to dissolve infectious relationships quicker than agents with risk perception values (r) below 1.

In addition to the mathematical model, the NIDM defines an agent-based simulation. In the most basic form, the simulation consists of two processes that are computed consecutively for a number of discrete time steps, infectious disease dynamics, and ego-centered network formation:

```
% computation of discrete time steps
ts = 0
While ts < ts_max:
    Compute disease dynamics.
    Compute ego-centered network formation.
    ts++.
```

Table 1. Scales for model parameters and state variables.

	Scale
I. Model parameters	
I.I. Social benefits	
Benefit of neighbors	$b_1 \in \mathbb{R}_0^+$
Benefit of closed triads	$b_2 \in \mathbb{R}_0^+$
Preferred proportion of closed triads	$0 \leq \alpha \leq 1$
I.II. Social costs	
Cost per neighbor	$c_1 \in \mathbb{R}_0^+$
Marginal cost per neighbor	$c_2 \in \mathbb{R}_0^+$
I.III. Disease properties	
Disease severity	$\sigma > 1$
Infectivity[*]	$0 \leq \gamma \leq 1$
Recovery time in time steps	$\tau > 0$
I.IV. Individual level properties	
Risk perception	$0 \leq r \leq 2$
I.V. Simulation / network properties	
Number of agents	$N \in \mathbb{N}_0$
Number of offered agents per time step	$0 < \phi \leq N$
Proportion of ϕ as neighbors	$0 \leq \psi \leq 1$
Proportion of ϕ as neighbors' neighbors	$0 \leq \xi \leq 1$
II. State variables	
Number of neighbors of agent i	$0 \leq t_i \leq N$
Number of infected neighbors of agent i	$0 \leq t_{i_I} \leq t_i$
Proportion of closed triads of agent i	$0 \leq x_i \leq 1$
Time steps since infection of agent i	$ts_{i_I} \in \mathbb{R}_0^+$

[*]: Infectivity is operationalized as transmission probability per contact and time step.

Disease dynamics is realized as an update process of the agents' individual disease states (susceptible, infected, recovered):

```
% disease dynamics
Repeat until all agents have been processed:

    Randomly select an unprocessed agent i.
    If i is susceptible:

        If ∼ U[0,1] ≤ πᵢ    % for πᵢ, see Equation 5
        Infect i.

    If i is infected:

        If tsᵢ_I ≥ τ
        Recover i.
```

Ego-centered network formation is realized as an update process of the agents' individual social relations. That is, agents myopically seek to maximize their individual utility based on the agents offered to them by the simulation.[3]:

```
% ego-centered network formation
Repeat until all agents have been processed:
    Randomly select an unprocessed agent i.
    Create an empty set of agents J⁴.
    Add to J until J consists of φ agents:
        With probability ψ:
            a random neighbor of i.
        With probability ψ + ξ:
            a random neighbor's neighbor of i.
        With probability 1 − (ψ + ξ):
            a random agent from the entire population.
    Repeat until all agents in J have been processed:
        If relation ij exists:
            If Uᵢ−ij > Uᵢ+ij:
                Dissolve relation ij.
        If relation ij not exists:
            If Uᵢ+ij ≥ Uᵢ−ij && Uⱼ+ij ≥ Uᵢ−ij:
                Create relation ij.
```

Simulation studies based on the SWIDM have shown that the co-evolution of social networks and infectious diseases produces outcomes that are hard to foresee, even for well-studied properties, such as clustering. In static networks, sparse connections between clusters can slow disease spread [1,10,14], while relations between clusters can facilitate disease spread through the entire network [20]. In networks with agents adapting their social behavior according to perceived risks of infection, the existence of only a few relations bridging two clusters, however, requires severing only a few relations for the disease to die out quickly [17].

3   Method

During the user-centered design approach, several user interface artifacts were developed at different levels of fidelity. These artifacts were used to formatively evaluate the ideas. We next present both artifacts and the processes to attain these artifacts.

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[3] Offers can be considered the number of contacts an agent has on a given time step. This can be, for example, an individual meeting 12 other individuals throughout a single day.

[4] J allows prioritization of neighbors for selection.

3.1   Sketches

To determine the optimal initial user interface, we employed an iterative approach. As a first step, we created various sketches of user interfaces (see Fig. 1) using paper prototyping [8]. The advantage of hand-drawn sketches is that they can be produced quickly and in large numbers so that many ideas can be captured and compared in a short time. The goal of creating these sketches was to identify the most important functions of the simulation and the UI elements best suited for them.

Our focus was on making the model as simple and understandable as possible. For this reason, the sketches were prepared by the members of our research group who had the least experience with the NIDM, as in-depth knowledge of the model could be a hindrance to identifying the minimal and essential elements.

To identify critical aspects of the design, the members of the sketch group evaluated the sketches and identified core elements of the user interface using a heuristic evaluation approach. Among these core elements of the user interface, we identified the following aspects in order of importance.

First, a visually delineated menu that includes all the elements for controlling the model. This should be conducive to the clarity of the controls. Second, the use of sliders, rather than number inputs, for setting parameter values. Third, parameter sliders should be supplemented with info tags with explanations that allow first-time users to operate them. Fourth, the selection of different diseases with preset parameter settings should be provided to allow for interesting and plausible scenarios to be observed. Fifth, nodes should be supplemented with hover effects, communicating status information such as disease states quickly and easily. Sixth, a click on a network node should infect it with the disease. Seventh, a static legend with color information, shall be used to explain health states. Eighth, users shall be able to switch between different representations of health states of nodes. Here, color codings, but also the use of emojis, are conceivable, promoting intuitive and accessible use. Ninth, a button should make it possible to add more nodes. Tenth, diagrams should provide information about the historical course of disease spread to make a better impression of the course of epidemics. Eleventh, it should be possible to speed up and slow down the simulation. Twelfth, it should be possible to switch between an expert and a lay mode, which differ in complexity and configuration options of the model.

3.2   Static prototypes

After evaluating the sketches and identifying the most important elements, we started implementing a prototype. The backend logic, i.e., the implementation of the mathematical model, the simulation loop consisting of disease dynamics, and ego-centered network formation was implemented in Julia [3]. Julia is a programming language that was designed to address some of the shortcomings of existing languages, particularly in the domain of scientific and technical computing. Specifically, Julia's JIT (Just-In-Time) compiler is designed to generate highly optimized machine code on the fly, which makes it much faster than many other
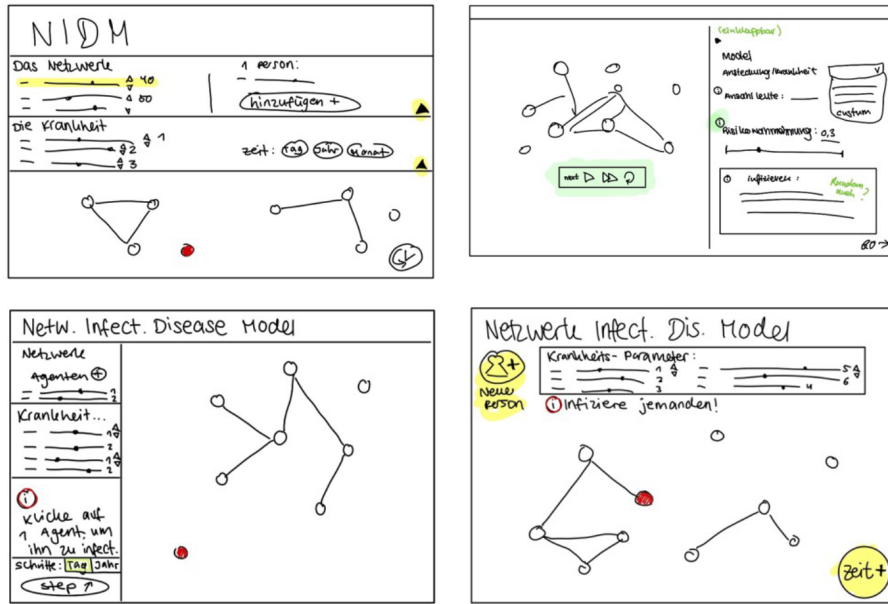
Fig. 1. Selected sketches of user interfaces. A common feature of all sketches is the visually delimited menu that includes all the elements for controlling the model. Furthermore, we quickly realized that sliders provide a more intuitive way to set the model parameters than numeric inputs. A large visual output of the network is also an element that appears in each of the sketches. However, it remained unclear where the menu should be placed and whether the elements to control simulation steps should be part of the model parameter menu. Since the user interface was designed for German-speaking users, the elements are labeled with German names: *Agenten+* = *agents+*, *Ansteckung* = *infection*, *Anzahl Leute* = *number of persons*, *das Netzwerk* = *the network*, *die Krankheit* = *the disease*, *einklappbar* = *collapsible*, *hinzufügen* = *add*, *Infiziere jemanden!* = *infect someone!*, *infizieren* = *infect*, *Klicke auf 1 Agent um ihn zu infect.* = *click on 1 agent to infect it*, *Krankheits-Parameter* = *disease parameter*, *Neue Person* = *new person*, *Person* = *person*, *Risikowahrnehmung* = *risk perception*, *Schritte: Tag Jahr* = *steps: day year*, *Zeit+* = *time+*, *Zeit: Tag Jahr Monat* = *time: day year month*.

dynamic languages. This makes Julia a great choice for computationally intensive tasks, such as numerical simulations.

We used Genie for the technical implementation of the user interface. Genie is a web framework for the Julia programming language that allows developing high-performance web applications. One of the main advantages of using Genie with Julia is the performance benefits that Julia provides. Julia's JIT compiler and built-in support for parallelism and distributed computing make it well-suited for building high-performance web applications that can handle large amounts

of data and high traffic loads, making it a suitable candidate for interactive simulations for a large audience through a web-based user interface.

Despite the benefits of Julia and Genie, we encountered some delays and setbacks, especially due to communication issues between the backend and the user interface. Consequently, we decided to perform a preliminary evaluation of a static prototype with limited functionality. That is, we created a detailed hand-drawn (see Figure 2) and a web-based user interface (see Figure 2) with sliders to set a minimal set of parameters, a legend to explain the different disease states, and a timeline for modifying the simulation speed. Furthermore, we dropped both the expert mode and the function of displaying the historical course of disease spread via a diagram.

3.3   Evaluation

The preliminary evaluation was conducted as formative usability testing using semi-structured interviews with three subjects. As a first step, the interview procedure was explained to the subjects. They were told that the goal of the study was to design a suitable and appealing user interface for a scientific model. Furthermore, it was explained that the goal of the scientific model is to explore how fast diseases can spread in a social network and that disease spread depends on various parameters both in terms of the disease (e.g., how contagious it is) and the people in the network (e.g., the strength of risk perception). Subjects were also asked to speak aloud any thoughts they had while viewing the prototypes (*Thinking Aloud* [12]) and to share both criticisms, ambiguities, and positive features.

Following these explanations, subjects were presented with our prototypes. After the subjects were given enough time to familiarize themselves with the prototypes and to verbalize their impressions, they were further asked to describe for each element whether it was clear without additional help what it was for, how to start a simulation, how to modify a simulation, and what conclusions could be drawn from the model. Finally, each respondent was asked which elements would be additionally necessary or should be modified to improve the user experience and understanding of the model.

4   Results

In the following, the impressions of the subjects are first discussed in detail. Subsequently, the combined findings are discussed, and how they influenced the design of our interactive prototype.

4.1   Insights from the evaluation

With regard to the numeric inputs, subject 1 suggested omitting them or replacing them with other elements, since they bear no meaning for a layperson. Furthermore, subject 1 suggested that the sliders be colored so that setting such
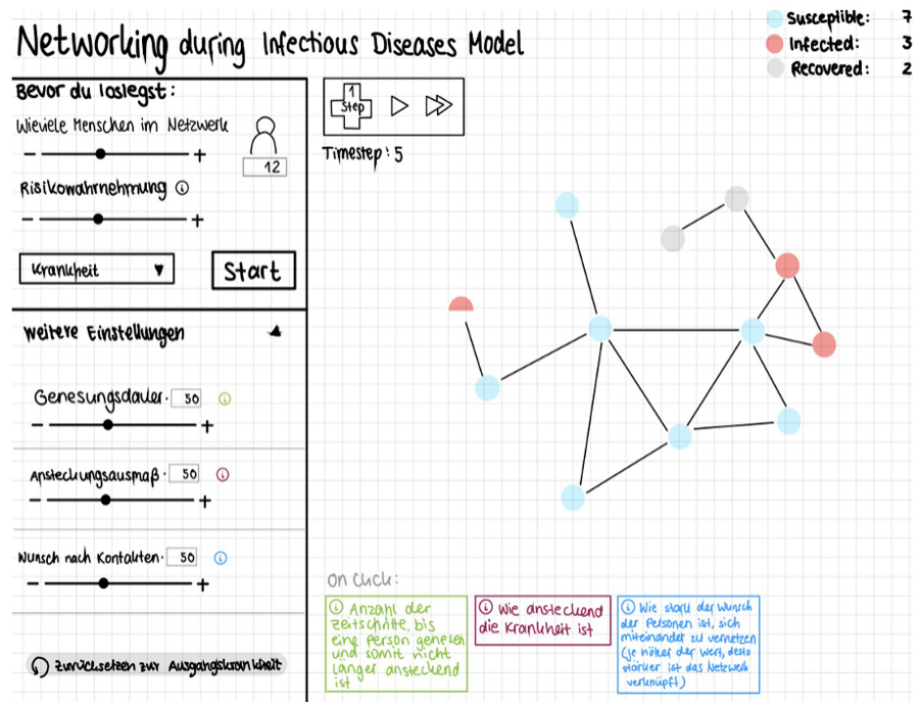
Fig. 2.   Hand-drawn static prototype. The figure shows one of the two static user interfaces used for a preliminary evaluation of our designs. Both designs have a similar layout (e.g., a visually delimited menu that includes all the elements for controlling the model on the left, a panel to control the progression of time steps at the top, a legend describing the color codes for disease states). In comparison to the design in Fig. 3, this design is somewhat slimmed-down and uses a more playful language. Since the prototype was designed for German-speaking users, the elements are labeled with German names: ***Bevor du loslegst:*** *= before you start:*, ***Wieviele Menschen im Netzwerk*** *= how many individuals in the network*, ***Risikowahrnehmung*** *= risk perception*, ***Krankheit*** *= disease*, ***Start*** *= start*, ***weitere Einstellungen*** *= additional settings*, ***Genesungsdauer*** *= recovery time*, ***Ansteckungsausmaß*** *= infection level*, ***Wunsch nach Kontakten*** *= desire for contact*, ***Zurücksetzen zur Ausgangskrankheit*** *= Reset to initial disease*, ***Anzahl der Zeitschritte bis eine Person genesen und somit nicht länger ansteckend ist.*** *= Number of time steps until a person recovers and is therefore no longer contagious.*, ***Wie ansteckend die Krankheit ist.*** *= How contagious the disease is.*, ***Wie stark der Wunsch der Personen ist, sich miteinander zu vernetzen (je höher der Wert, desto stärker ist das Netzwerk verknüpft)*** *= How strong the desire of individuals is to connect with each other (the higher the value, the more connected the network).*

as severe and less severe are visually supported. In general, subject 1 found the terms described in a sufficient manner to acquire a general understanding of the model and the user interface. However, additional explanations were required
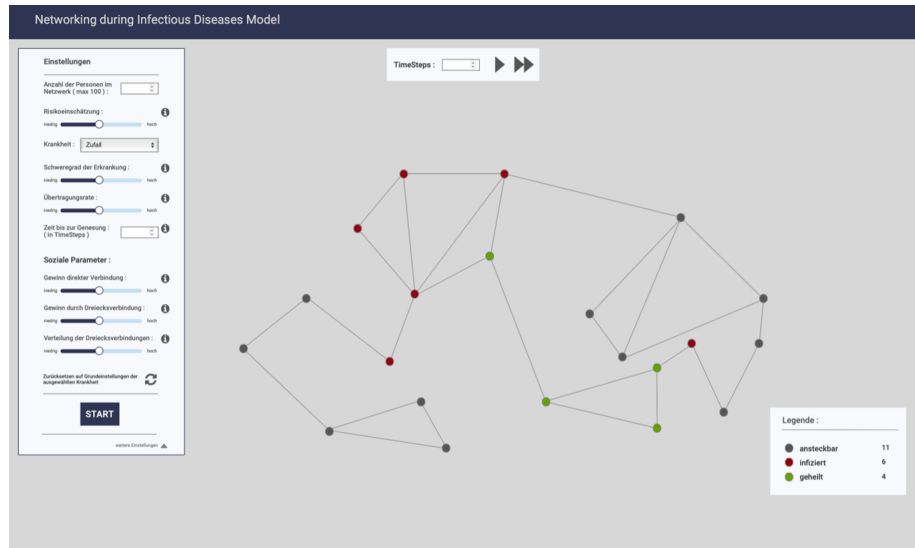
Fig. 3. Digital static prototype. The figure shows the other of the two static user interfaces used for a preliminary evaluation of our designs. Both designs have a similar layout (e.g., a visually delimited menu that includes all the elements for controlling the model on the left, a panel to control the progression of time steps at the top, a legend describing the color codes for disease states). In comparison to the design in Fig. 2, this design has a more technical/scientific approach in the way the parameters are presented and described. Since the prototype was designed for German-speaking users, the elements are labeled with German names: ***Einstellungen*** = *settings*, ***Anzahl der Personen im Netzwerk*** = *number of individuals in the network*, ***Risikoeinschätzung*** = *risk assessment*, ***niedrig*** = *low*, ***hoch*** = *high*, ***Krankheit: Zufall*** = *disease: random*, ***Übertragungsrate*** = *transmission rate*, ***Zeit bis zur Genesung*** = *time to recover*, ***Soziale Parameter*** = *social parameters*, ***Gewinn direkter Verbindung*** = *benefit of direct connection*, ***Gewinn durch Dreiecksverbindung*** = *benefit of triadic connection*, ***Verteilung der Dreiecksverbindung*** = *distribution of the triadic connection*,***Zurücksetzen auf Grundeinstellungen der ausgewählten Krankheit*** = *Reset to basic settings of the selected disease*, ***weitere Einstellungen*** = *additional settings*, ***Legende*** = *legend*, ***ansteckbar*** = *susceptible*, ***infiziert*** = *infected*, ***geheilt*** = *recovered*.

regarding risk perception. Subject 1 also noted that information about how to infect a person and what happens during a single time step is missing. Finally, subject 1 suggested providing pre-defined diseases.

Subject 2 showed great problems in understanding the model and the individual parameters. According to subject 2, the parameters were not labeled clearly enough and required additional information for a sufficient understanding. Additionally, subject 2 did not understand what the model does, its background, how the model is started, and how a network node is infected. A suggestion to simplify the handling of the user interface was the use of colors to visually support sliders.

Subject 3 reported that the interfaces were confusing. In addition, subject 3 showed major problems in understanding the model, the parameters, and the influence of the model parameters on the model behavior. According to subject 3, a meaningful example could be helpful to promote understanding. Subject 3 liked the neutral design without many colors and preferred the design with fewer elements.

In summary, the preliminary evaluation shows that the user interface alone is not sufficient to understand the model and its parameters. It follows that an introduction with basic information about the functionality and operation is indispensable. In addition, subjects asked for formal guidelines specifying the sequence of operation. Such a sequence, however, could also be achieved implicitly by the arrangement of the menu and the controls. Furthermore, two subjects pointed out that colors can support the sliders in their expressiveness.

4.2   Interactive prototype

Based on the findings from our preliminary evaluation, we created an interactive prototype (see Fig. 4). This prototype has a clear and simple structure that promotes focus on the essential elements of the user interface. The menu is now divided into two separate sections: network settings (top left) and disease settings (bottom left). Through this thematic division, we intend to create a structure that suggests an implicit sequence of actions.

Where appropriate, color coding is used. To indicate the risk of highly infectious diseases, we use red as a signal color. Diseases with a very low probability of transmission, on the other hand, are coded green. As the number of people in the network has no such positive or negative associations, it is presented in a neutral shade of gray.

To facilitate a better understanding, we have revised the wording. Labels describe outright the purpose of interaction elements (e.g., start new simulation). In addition, the most important information for interaction outside the menu is highlighted and placed at the top of the network view (i.e., double-click on individuals to infect them).

The interactive prototype has full functionality and can thus be configured via the control elements and can perform and display simulations.

5   Conclusion

In this paper, we have presented our approach to designing an interactive simulation for the complex co-evolution of social networks and infectious diseases. One of our goals is to receive valuable feedback on the method of our approach. That is, we started with sketches to identify the most important elements for an interactive simulation. We then created two static designs for user interfaces and performed formative usability testing using semi-structured interviews. Although we had only three subjects, we received important feedback. Most notably, the participants considered the prototypes and the model too complex to understand
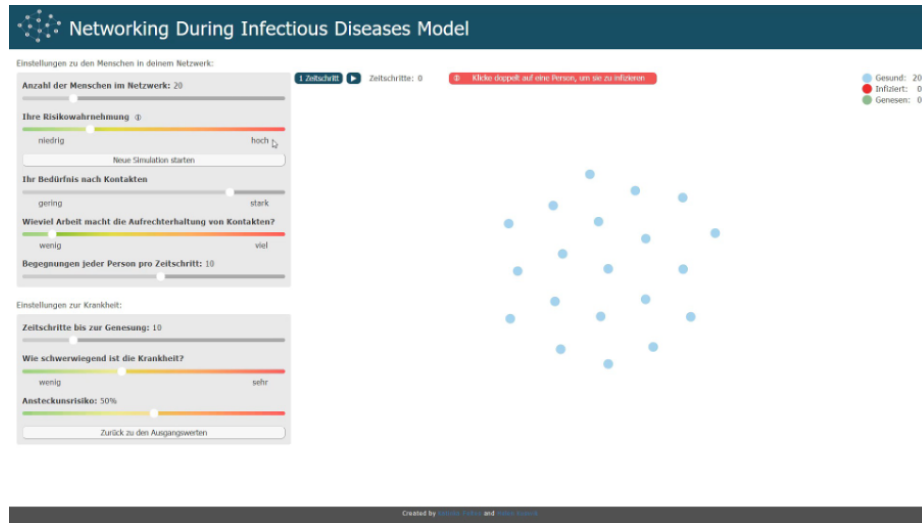
Fig. 4.   Interactive prototype. The figure shows the interactive prototype of our user interface design. The design considers the most important feedback from the preliminary evaluation: more precise labeling of the parameters, a simple and structured layout, and where appropriate color codings to support the sliders' expressiveness. Since the prototype was designed for German-speaking users, the elements are labeled with German names: ***Einstellungen zu den Menschen in deinem Netzwerk*** = *settings for the individuals in your network*, ***Anzahl der Menschen im Netzwerk*** = *number of individuals in the network*, ***Ihre Risikowahrnehmung*** = *your risk perception*, ***niedrig*** = *low*, ***hoch*** = *high*, ***Neue Simulation starten*** = *start new simulation*, ***Ihr Bedürfnis nach Kontakten*** = *your desire for contacts*, ***gering*** = *low*, ***stark*** = *high*, ***Wieviel Arbeit macht die Aufrechterhaltung von Kontakten?*** = *how much effort is involved in maintaining contacts*, ***wenig*** = *not much*, ***viel*** = *much*, ***Begegnungen jeder Person pro Zeitschritt*** = *contacts per individual and time step*, ***Einstellungen zur Krankheit*** = *disease settings*, ***Zeitschritte bis zur Genesung*** = *time steps until recovery*, ***Wie schwerwiegend ist die Krankheit?*** = *how severe is the disease?*, ***wenig*** = *not very*, ***sehr*** = *very*, ***Ansteckungsrisiko*** = *risk of infection*, ***Zurück zu den Ausgangswerten*** = *reset to initial values*, ***Zeitschritt*** = *time step*, ***Klicke doppelt auf eine Person, um die infizieren*** = *double-click on individuals to infect them*, ***Gesund*** = *susceptible*, ***Infiziert*** = *infected*, ***Genesen*** = *recovered*.

without further explanation or some other form of guidance. Based on the findings from the interviews, we designed a fully functional interactive prototype.

The other goal of our work is to lay the foundation for enhancing the intuitive understanding of the efficacy of self-protective behavior and distancing measures following the outbreak of COVID-19. Although we believe the foundation was successfully laid, further work needs to be done before our simulation can be an effective tool for science communication. The next step in our work involves technically refining the prototype to facilitate surveying of a larger sample. This will enable the development of a two-pronged approach. Firstly, we will

evaluate the scientific and technical validity of the simulation. Secondly, evaluating with individuals from the general population will inform us whether people can comprehend the spread of infectious diseases on social networks when playing with such a model. This investigation could be used to explore various phenomena of network theoretical infection epidemiology, such as clustering, which could aid in curbing the spread. To accomplish this, an evaluation concept must be created and coordinated with the domain experts and the simulation must be transformed to enable summative evaluation with end-users.

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