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Modelled Encounters with Public Health Risks: How Do We Predict the 'Unpredictable'?

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Contents

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Abstract

Encounters with risk, as Hutter and Power (2005, 11) clarify, are events of problematization that 'place in question existing attention to risk and its modes of identification, recognition and definition'. Infectious diseases, as a public health risk, call for new ways of encountering their continuously changing, uncertain nature. When a new, emerging infection appears, or when vaccination coverage fails to provide population-wide protection, the preventive and protective measures against risks need to be re-assessed and developed further. Computer-based modelling techniques provide a set of tools for encountering public health risks. What kinds of model-based predictions are utilised in public health decision-making processes and on what basis do we rely on these predictions? These questions are addressed through a notion of *modelled encounters* with public health risks.

The main focus is on two modes of predictive encounters with public health risks. First, by analysing the case of *Haemophilus influenzae* type b bacterial circulation and the effectiveness of vaccination interventions to reduce it, I will introduce the notion of *explanation-based* predictions. These predictions are capable of addressing short-term developments in the transmission of Hib by explaining its epidemiological mechanisms. Secondly, I will study *scenario-building* predictions that anticipate the course of a *pandemic influenza* outbreak. Through these cases, the nature of model-based prediction is discussed as *modelled encounters* with public health risks. These encounters provide an evidence-base for public health decision-making processes.

The study builds on a long-term ethnographic research project on mathematical modelling of infectious diseases with a research group from the National Institute for Health and Welfare, Helsinki (the *Hib* case). The data on the pandemic influenza preparedness planning is gathered from scientific publications and from policy documents of a national and international level.

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Introduction

Public health decision-makers face the challenges of renewing vaccination strategies and preparing for the potential threat of pandemics. In other words, public health risks are anticipated through surveillance and monitoring procedures[1] carried out by the national public health institutes[2]. However, in addition to these procedures, decision-makers search for alternative ways to process the information flow in order to gain evidence for public health interventions[3]. Evidence for developing the required preventive and protective measures for decision-making processes is produced and utilised by computer-based modelling techniques. Yet, we have only limited understanding of the ways in which these techniques provide reliable predictions for public health work in order to anticipate common risks from prevailing or emerging infections.

When we encounter risks and uncertainties, or predict a possible course of events, we develop and utilise various measurement devices, such as statistical methods, surveys and models. From a historical perspective, we can identify a shift away from 'informal expert judgment towards a greater reliance upon *quantifiable objects*[4]', as Porter (2000, 226) argues. The tendencies underlying this shift are addressed by the growing interest in the sociology of quantification – i.e. in the 'production and communication of numbers' (Espeland & Stevens, 2008, 402). How do we 'do things with numbers[5]'? This paper will focus on how micro-simulation methods are used for predicting risks in infectious disease epidemiology. By placing modelling in the context of measurement[6], we will learn the different ways in which trust, credibility and usability of the modelled predictions emerge and are communicated from research domain to decision-making processes.

How do we encounter the uncertainties? Modelling techniques provide a way to produce predictions, or in broader terms, evidence for decision-making processes, and, as such, they provide a new way of encountering public health risks. Modelled encounters with public health risks are approached in terms of studying the nature of model-based predictions. These predictions form the core of our attempts to control public health concerns, prepare for sudden outbreaks, or estimate population-wide effects of bacterial or viral transmissions. Modelled encounters with risk introduce two modes of predictions: those based on explanations and those that build scenarios

[1] Surveillance and monitoring procedures comprise, for example, keeping records of notifiable diseases (e.g. measles) or participating in international collaborations to govern outbreaks of emerging infections.
[2] Surveillance activities are carried out on various levels: on a national level by public health institutes, such as the Health Protection Agency in the UK and the Institute for Health and Welfare (THL) in Finland; on an international level by the European Disease Control Centre (ECDC) in Stockholm, and on an inter-governmental level by WHO, especially through GOARN, the Global Outbreak Alert and Response Network.
[3] Vaccinations are the most common public health interventions related to infectious disease epidemiology.
[4] In Porter's example, quantifiable objects are mortality statistics used in the life insurance industry.
[5] Espeland and Stevens elaborate on J.L.Austin's idea of speech acts (doing things with words) by applying them to the domain of quantification. They suggest that we can 'do things with numbers' and as with words, they argue that 'numbers often change as they travel across time and social space' (Espeland & Stevens, 2008: 406).
[6] Cf. Morgan and Morrison (1999), Boumans (1999), van den Bogaard (1999).

for future events or developments.

Encounters with risk, as Hutter and Power (2005, 11) clarify, are events of problematization that 'place in question existing attention to risk and its modes of identification, recognition and definition'. 'Risk identification', they continue, 'is socially organised by a wide variety of institutions which support prediction and related forms of intervention around the possibility of future events'. Smith (2006, 3114), in his analysis of the SARS[7] epidemic in 2002, underlines two approaches to risk. The 'realist' approach, according to him, regards risk[8] as an objective threat or danger that can be measured independently of the social context within which it occurs. He argues that the 'social constructivist' approach, by contrast, sees risk as a culturally or socially constructed threat that cannot be demonstrated independently of those processes. He then proposes a 'material-discursive' position, which is a mediatory one. In his terms, 'risk is both a materially measurable probability of an event and a socially constructed element of how that probability is perceived by the individual and society'.

The mediatory approach proposed by Smith is a useful conceptualisation when explaining the ways in which risk is represented, anticipated and processed in models. As this paper explicates, the two modes of prediction - explanation-based and scenario-building - provide two strategies: to produce evidence for the decision-making; and to translate the potential threat into a quantifiable, measurable risk, following it through the social process that tries to control and minimise it in society. In a way, Smith's mediatory approach seems to go beyond the numerical to the socially constructed, and, as I will discuss in this paper, this approach can be located within the modelling process.

One way to look at the *modelled encounters* with risk is to examine Dianne Vaughan's (2005) account of regulating risk in two modes or strategies. A compliance strategy is forward-looking and preventive, whereas a deterrent strategy is backward-looking. To some extent, the modelled encounters overlap with these categories, yet do not fully cover them. This paper will suggest that explanation-based predictions are not merely backward-looking, despite their mechanistic component. In a similar way, scenario-building predictions are preventive and forward-looking, but they carry some information from the earlier epidemics. What begins as an epistemic exercise to make sense of the potential threat of an outbreak, or to explain the population-level, indirect effects of immunity levels, may also fulfil social functions, as Oreskes (2007) suggests. Social functions, therefore, allow for the extrapolation of knowledge about the future development of an outbreak, or the potential effect of a vaccination intervention, through qualitative scenarios.

Research methods and data

The study analyses how an integrated simulation-model on Hib transmission in the Finnish population produces *explanation-based* predictions. This analysis builds on a long-term ethnographic research project on mathematical modelling of infectious

[7] Sudden Acute Respiratory Syndrome.

[8] The realist account of risk is close to Schlich's definition of risk and uncertainty. He says that 'one can speak of risk when the probability estimates of an event are known, or at least knowable while uncertainty, by contrast, implies that these probabilities are inestimable or unknown'. (Schlich, 2006)

diseases, especially Hib transmission in the Finnish population, with a research group from the National Public Health Institute, Helsinki[9]. I will keep the focus on a single, integrated model in order to allow for a detailed description of the ways in which the model is able to predict. The findings from the Hib case will be discussed in relation to a micro-simulation model on mitigating an influenzae pandemic. This example will show how micro-simulations produce *scenario-building* predictions. The analysis focuses on detailed micro-level observations and interpretations of the predictive capacities of micro-simulations. Both models are chosen, because they provide clear examples of the predictive capacities of simulations. I have chosen not to explore the vast literature on pandemic influenzae models, but to concentrate in detail on a single model. The analysis is informed by a practical course, 'Introduction to Infectious Disease Modelling', organised by the London School for Hygiene and Tropical Medicine, 2006, which gave me the tools to read the models and understand their core structure. As part of the coursework, myself and the group analysed the published pandemic simulation models[10] and prepared an exercise on national preparedness planning.

The structure of the paper

The structure of the paper is as follows. Firstly, I will analyse how micro-simulations are used for predictions and will study *explanation-based* predictions in the case of an integrated transmission model on *Haemophilus influenzae* type b bacteria. Secondly, I will discuss the factors that form and sustain reliability of model-based predictions. Thirdly, I will discuss an example of scenario-building predictions produced in a simulation model of mitigation strategies for a pandemic. Finally, I will discuss the ways in which these two predictive modes are useful for encountering public health risks.

Predicting through micro-simulations

Technologies form an integral part of the procedures through which organisations and individuals try to control risks they encounter. These technologies range from software systems to visualisations and representations, from advanced technological structures (e.g. air traffic control) to models (Hutter and Power, 2005). Models, or broadly speaking, computer-based tools and techniques, have become commonly used in various scientific and policy-making contexts. Yet they have the potential to 'legitimate a range of possible social futures', as Evans (2000) describes the capacity of economic models. Den Butter and Morgan (2000) seem to suggest that models that are engaged with policy-making processes in economics actually build a bridge between research and policies, or between 'positive theory and normative practice'. In their account, these models form a part of the 'value chain' through which knowledge

[9] The case study was conducted during 2002-2004 at the University of Helsinki. I observed modelling practices in 22 work meetings (recorded and transcribed, duration of a meeting app. 2 hours) at the National Public Health Institute and conducted 28 thematic, semi-structured interviews (transcribed for analysis) with mathematical modellers, epidemiologists and computer scientists working as members of the interdisciplinary team. The models were published in Auranen 1996, 1999, 2000a, 2000b and 2004; Leino 2000, 2002, 2004 and Mäkelä 2003.

[10] A set of published models were analysed and studied in small groups in June 2006. I have chosen one of these as an example of a scenario-building modelling exercise.

is created, stored and transmitted in organisations.

One of the main reasons for developing modelling techniques is to overcome uncertainties relating to complex phenomena, such as climate, economy or infectious diseases. Establishing modelling practices also helps form a network that integrates and communicates available knowledge. Paul Edwards (1999, 439) argues that:

> Uncertainties exist not only because of quantifiable, reducible empirical and computational limits, but also because of unquantifiable, irreducible epistemological limits related to inductive reasoning and modelling.

His argument seems to suggest that due to the very nature of the modelled phenomenon itself, uncertainties remain as a part of the process. As Shackley and Wynne (1996, 276) emphasise, scientific knowledge, or the 'authority' of it, is limited in policy making, since it restricts decision-making and action. Van den Bogaard (1999, 323) shows, on the contrary, that the first macro-econometric model, developed by Tinbergen in the 1930s for the Dutch Central Planning Bureau, was a 'liberation both from the uncertainties caused by the whimsical nature of the economy and the woolly theories of the economists'. One form of uncertainty remains within the models, as MacKenzie's (2005, 186) study on financial economics shows: 'models affect the reality they analyse'. According to him, this 'reflexive connection serves to increase the veracity of finance theory's assumptions and the accuracy of its models' predictions', but it may also function in a counterproductive way (as in his case, the exploitation of arbitrage opportunities by using mathematical models leads to instability of the system). It seems to me that when modelling complex, open-ended systems, such as climate or ecological systems, there will remain uncertainties, because of limited computational capacity, biased reflection of the reality, or the unpredictable nature of the phenomena themselves[11]. In public health decision-making, however, prediction is a key motivation for developing modelling techniques. What kinds of model-based predictions are we able to identify in infectious disease studies?

Generally speaking, computer-based models (including simulation techniques) in infectious disease epidemiology share the following characteristics: firstly, they have a three-part elementary structure, comprised of the data element, the mathematical method and computational techniques, and the element of substantial knowledge, or the epidemiological component. Secondly, they are 'tailor-made', usually addressing a specified research question, which to some extent limits their applicability. Thirdly, the majority of these models rely on currently available data. And it is precisely the need to re-use and re-analyse the data that partially motivates the model-building exercise. Fourthly, micro-practices that are independent of the context of application, for example the pathogen studied, can be identified within the modelling process. A detailed analysis of the eight consecutive steps in the modelling process is documented by Habbema et. al. (1996, 167):

1) Identification of questions to be addressed

[11] Petersen (2006, 176) argues that even though 'simulation models of ecological systems may give an impression of the scope of behavioural possibilities of such systems, and as such may contribute reasons for taking policy measures, cannot predict future states of these open and unpredictable systems'.

2) Investigation of existing knowledge
3) Model design
4) Model quantification
5) Model validation
6) Prediction and optimization
7) Decision making
8) Transfer of simulation program

The importance of setting the question follows the idea of *tailoring* a model to address particular interests. The investigation of existing knowledge is a process in which existing literature, laboratory results, experiences of existing models, and data from surveillance programmes are integrated as a part of assumptions about models. Morgan (2002, 42) aligns model-building to similar steps mentioned by Habbema et. al. (1996), although her focus is on economic models. The main difference is that in her account the model is built firstly to represent the world, then subjected to questions and manipulation in order to receive the answers to such questions, then these answers are related to real-world phenomena.

Model design follows the existing understanding of how the phenomenon of interest behaves and is often represented through a compartmental[12] structure. Model quantification is the process of estimating the optimal parameter values, and setting the algorithms to run the simulations. In Habbema's et. al. (1996) account, model validation means checking the model against data from a control program. However, model validation is a broad question and I will address it by asking why we rely on model-based predictions later in this paper. The particular interest in this paper is to analyse how the step from prediction and optimization to decision-making is taken.

By transfer of a simulation program, Habbema et. al. refer to the generalizability of the computer program in other infectious diseases. This step-wise characterisation of the micro-practices of modelling highlight that modelling is an *iterative*[13] practice, which builds upon and re-confirms previous steps throughout the process. Importantly, these models are not only scientific exercises for developing better computational algorithms, they are built first and foremost to explain, understand and predict the infectious disease phenomena of interest. The major application of this group of models (including simulations) is to design, for example, reliable and cost-effective vaccination strategies or to predict the course of an influenza pandemic (Mattila, 2006a,b,c).

Morgan (2002) characterises this process as 'story-telling', in which a model is a narrative device. I suggest that scenario-building predictions could be related to this aspect of model-building: 'story-telling' through processes of manipulation, as we will learn through pandemic modelling. The idea of model-building as a stepwise procedure invites us to focus on the steps of validation, prediction, and decision-making (steps 5-7 in Habbema's list).

[12] A compartmental structure of the model means that the population is divided into subgroups or sections according to, say, the impact on immunity, susceptibility and potential recovery from the modelled infection.
[13] Iterative practice is also recognised as an epistemic strategy in which 'successive stages of knowledge, each building on the proceeding one, are created in order to enhance the achievement of certain epistemic goals' (Chang, 2004: 226).

Two cases analysed in this study allow us to compare different types of model-based predictions. Firstly, as an example of a prediction that facilitates the renewal of vaccination strategies, a case of a population-level transmission model of *Haemophilus influenzae* type b bacteria is analysed. This case introduces us to *explanation-based* predictions that produce 'what would happen if'-scenarios. These scenarios derive their predictive capabilities from the available datasets, and help with short-term predictions that are beneficial when predicting outbreaks within a particular area. Therefore, the development of preventive measures in public health can be informed by *explanation-based* predictions.

Secondly, by analysing a micro-simulation model on mitigation strategies for a pandemic influenza, we will learn about *scenario-building* predictions. Typical for these predictions is that the data utilised in them is derived from past pandemics. Hence, these predictions are not capable of explaining a possible future pandemic, but they produce reliable scenarios for its potential development, and thus facilitate the distribution of protective measures. Hence, in order to assess the reliability and usability of model-based predictions, it is beneficial to increase the transparency of evidence throughout the production and utilisation process. This allows the different groups involved in the decision-making processes to evaluate the predictive scenarios and make well-informed decisions.

However, within infectious disease studies, one of the major public health concerns is our limited capability to predict the emergence of outbreaks and peoples' behaviour in such an event. Outbreaks could be regarded either as 'small', when they occur say in closed populations such as army units, or 'large', such as the anticipated pandemic outbreak. Small outbreaks, for example the transmission of bacterial meningitis caused by Hib in a military garrison, may not receive broad media coverage, but are nevertheless important to the core tasks of public health officials. Protecting public health demands that we are prepared for, or capable of, controlling and managing these outbreaks. Dynamic transmission models provide a rather flexible tool in order to do that – they form a base from which anticipatory 'what would happen if'-type questions can be addressed. Larger, unexpected outbreaks that are capable of causing wider devastation easily gain significant attention. Preparedness plans are conducted both on national and international levels. Large-scale simulation models that utilise data on travel patterns and population density from past pandemics produce part of the scientific evidence-base. One example of these models focuses on mitigation strategies and provides estimates of their effectiveness. So, the two cases analysed in this study exemplify the two distinct modes of prediction represented through the models.

Explanation-based predictions in the case of an integrated simulation-model of Haemophilus influenzae type b transmission

Infections that mainly affect children's health are a mundane public health concern. One of the main threats is considered to be bacterial meningitis, because of its life-threatening nature. However, most of these infections are vaccine preventable, as in our case example, *Haemophilus influenzae* type b bacterial transmission. The main effort is still to reduce the risk of these severe disease forms in a population. So the need to predict potential public health risks is met by developing sophisticated

transmission models. Evidence of potential outbreaks, indirect effects of vaccinations, and estimates of herd immunity are assessed by models. What kinds of predictions are useful when forming the evidence-base for vaccine-preventable infections? Amy Dahan Dalmenico (2007) argues that there is a continuous tension between the explanatory and predictive functions of models. According to her, this tension is seen as a source of conflict and compromise:

> Modelling practices […] should they be first and foremost predictive and operational or cognitive and explanatory? Tension between explanatory and predictive capacities, between understanding and forecasting, is a source of conflict and compromise in modelling. (Dahan Dalmenico, 2007:126)

However, by analysing the capacity to form short-term, *explanation-based* predictions, in the case of Hib transmission models, I will show that the conflict suggested by Dahan Dalmenico could be overcome.

Hib colonises the human nasopharynx and is transmitted in droplets of saliva. The public health concern is related to its severe disease forms (Ladhani et. al. 2009). Hib is capable of causing severe and often life-threatening diseases, such as meningitis and pneumonia in young children (of which there are an estimated 3 million cases of serious illness and 400,000 deaths each year in children under 5 years of age worldwide). A part of the incentive to produce model-based predictions lies in the cost of vaccines. Hib vaccine is not yet a part of national vaccination strategies in developing countries, for example in Africa and Asia. Polysaccharide vaccines were on the market in the 70s and conjugates in the 80s. The main difference is that polysaccharides protect against the disease forms whereas the conjugates are capable of reducing the carriage of the bacteria and hence have an effect on population-level circulation of the bacteria. If considered from an economic point of view, polysaccharide vaccines are older and somewhat cheaper to produce, while the conjugates are more expensive. As clarified by Hib Initiative[14], Hib infections are difficult to treat in developing countries due to the lack of access to antibiotics, which are proven to be effective when treating the severe disease forms. Because of this, the Hib Initiative presents an estimation that 20% of children in developing countries with meningitis caused by Hib will die, and 15-20% of children suffering from the infection will develop life-long disabilities. As an epidemiologist from the Helsinki modelling group argues:

> While WHO and GAVI (the Global Alliance of Vaccinations and Inoculations) advocate Hib conjugate vaccines, the major question remains whether universal vaccination will be at all feasible in the poorest economies. Will it be cost-effective, and will it be an appropriate use of resources among other possible health interventions? Schedules optimising the age of vaccination and the number of doses are crucial for the acceptance of the expensive vaccines. (Leino, 2003).

These general concerns are translated into an integrated simulation-model in order to

[14] The Hib Initiative is a collaboration between the Centre for Disease Control (CDC, the US), John Hopkins University, the London School for Hygiene and Tropical Medicine and WHO. The Initiative aims to 'reduce risk of childhood death and disability through sustained use of Hib vaccine'. (www.hibaction.org. 25.3.2009)

produce qualitative, anticipatory predictions of the potential vaccination effects on the population level. The translation process meant that the modellers needed to study particular mechanisms that were responsible for the behaviour of the bacteria. In order to address these mechanisms in the integrated model, they studied them separately.

The global concern over whether to implement conjugate vaccines is based on data from the UK and Finland. Both countries tell their own 'success stories' that support the initiative to include Hib conjugate vaccines in the vaccination programmes.

Figure 1: Hib cases in England and Wales 1990-2003. (Source: Health Protection Agency). The arrow points to the year (1983) when Hib vaccines were introduced to the national vaccination scheme.

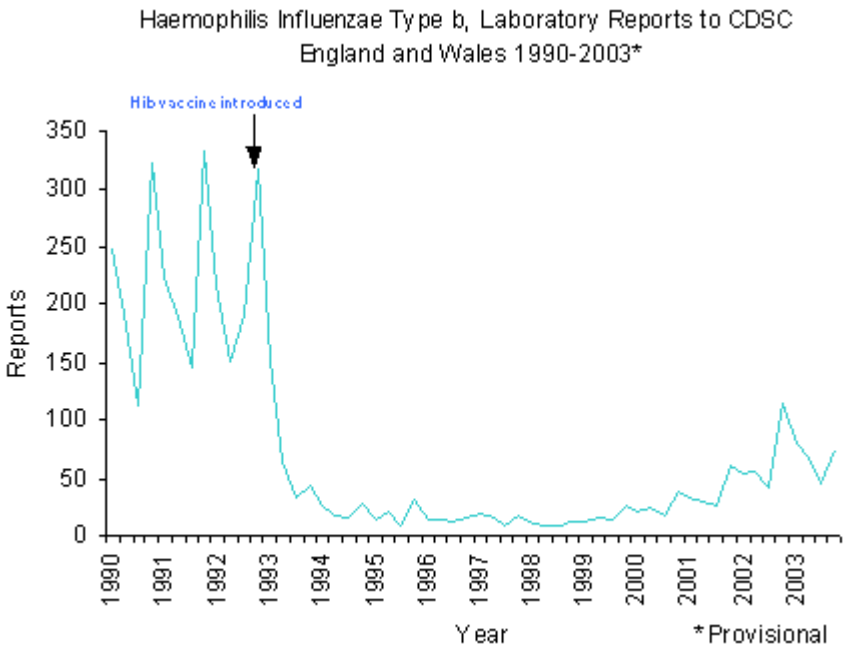
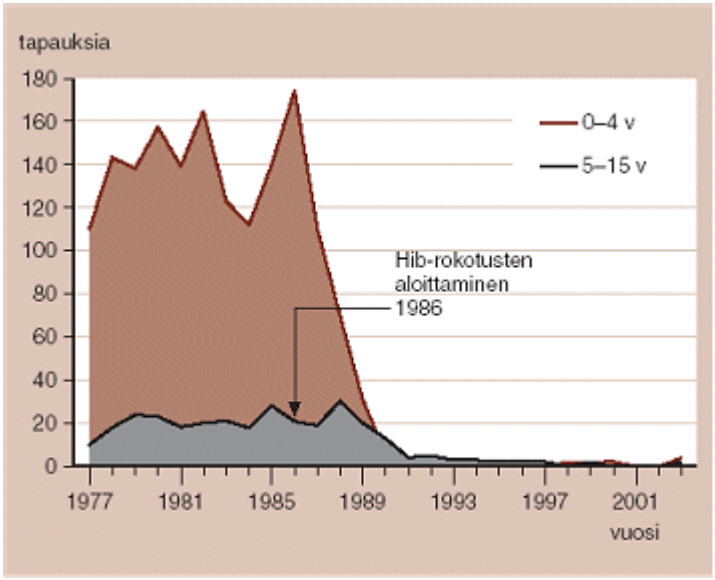


Figure 2: Hib cases in Finland 1977-2001. (Source: The National Institute of Health and Welfare). The arrow points to the year (1986) when Hib vaccines were introduced to the national vaccination strategy.



'What would happen if'-questions as a key to explanation-based predictions

Seeking answers to 'why'-questions means *explaining* a particular phenomenon, say the cause of an infection. When 'why'-questions are addressed in models, they search for a particular mechanism that is responsible for the phenomenon. In other words, models capture epidemiological mechanisms and extrapolate explanations on the basis of that. But what are mechanisms and how are they addressed in models?

In order to develop the notion of explanation-based predictions as anticipatory techniques for addressing public health risks, I will discuss how the mechanism of natural immunity was expressed in a population-simulation model in order to gain short-term predictions for assessing the efficacy of Hib-vaccines. So, the short-term predictions that answer 'what would happen if'-questions, even though studied in the Finnish context, provide a potentially broader application context when extended or applied to addressing the benefits of implementing Hib vaccines in developing countries.

In general terms, *explanation-based* predictions are predictions that explain the causal mechanism(s) responsible for a particular phenomenon and extrapolate short-term predictions on that basis i.e. answers to 'what would happen if'-type questions. In order to unpack this, I will briefly discuss what mechanisms are, and how they are addressed, in predictive epidemiological models. The main importance of elaborating on the role of mechanisms and their relation to explanation-based predictions is that *mechanisms* form the basis, or *anchor* the explanations to the available datasets, of the epidemiological ground of the phenomena. Bechtel and Abrahamsen (2005, 423) define a mechanism as follows:

> A mechanism is a structure performing a function in virtue of its component parts, component operations, and their organization. The orchestrated

functioning of the mechanism is responsible for one or more phenomena.

This definition clearly underlines that a mechanism is involved in orchestrated functioning, which I interpret as having the capability to bring together specific properties, parts or operations of the phenomena. Mechanisms are responsible for a phenomenon: orchestrating its cause, occurrence or development. In this sense, mechanisms contain the generalizable properties of the phenomena.

Disease transmission is a multiplex phenomenon, which is dependent, for example, on the frequency of contacts within a population group, infectivity of the pathogen, and the existing immunity within the population. These aspects of the transmission were taken into account when a mechanism was explained in a model. In other words, studying research questions in the family of Hib-models[15] helped clarify the disease transmission mechanism and uncovered the connection between a mechanism and the research questions addressed in modelling. Let us study more closely the way in which *explanation-based* predictions were established in a population-simulation model.

The leading question motivating the building of the population-simulation model was: What would happen if a five-year-old child x acquires a Hib infection and how likely is she to infect the members of her family? This question is by its nature a 'what would happen if'-question that has a predictive emphasis. To see how this question was manipulated in the model, we need to unpack the structure of the model itself. The population-simulation model, published in 2004, has a three-part structure: a demographic model (covering the age-structure of a Finnish population), a Hib-transmission model (including the contact-site structure) and an immunity model (including the immunisation programme and its effects). Yet, this simulation model was formed after a ten-year period of modelling work, which was dominated by integrating practices that brought together the three parts built earlier in the project[16]. So all three parts, especially the transmission model and immunity model, were partially studied prior to the completion of the population-simulation model (2004) in terms of the following questions (the year in brackets refers to the published model):

- How long does the immunity [against Hib] persist? (1999)
- How do we estimate the interaction between the force of infection and the duration of immunity? (2000)
- What is the effect of vaccinations? (2001)

These questions address particular aspects that affect the transmission dynamics in a population: length of immunity, estimate related to the force of infection and the effect of vaccinations. In particular, two mechanisms were detected in these models: the mechanism of immunity and the mechanism of transmission. The mechanism of immunity was defined as:

> Natural immunity is believed to depend on repeated exposure to Hib bacteria resulting in the production of functional antibody (Leino et. al., 2000).

[15] This set of models was built during 1994-2003 within the research collaboration between the National Public Health Institute and the University of Helsinki.
[16] Analysis of the efforts and practices leading to this model is published in Mattila (2006c).

This mechanism is primarily about how to sustain natural immunity in a population. In the simulation model, it was used for explaining what would happen to the natural immunity when vaccinations were introduced on a population level. This was an important aspect, since the epidemiological studies of the chosen vaccine confirmed that the vaccine itself is capable of reducing carriage. The reduction of carriage in a population could potentially lead to the waning of the natural immunity that had a protective impact on a population level. In other words, *herd immunity*[17], which is the population level's protection against an infection, could be affected. This indirect effect was documented in the model studying the dynamics of natural immunity. This mechanism and its numerical estimates, which were defined in terms of Hib antibody dynamics, show the descending trend in serum antibody concentration. Later, this mechanism was integrated into the population-simulation model, in particular into its immunity model part. Hence, the mechanism of natural immunity, when manipulated within the simulation model, showed that if the bacterial circulation is diminished, the natural immunity is likely to weaken and a potential increase in serious infections may affect those who are not vaccinated.

Explanation-based predictions thus allow us to both explain the phenomenon of interest and predict, in the short-term, its development i.e. the course of Hib transmission in a population and the underlying epidemiological mechanisms that maintain circulation of the bacteria. An interesting parallel can be drawn with the work of Butter and Morgan (2000, 296):

> More general empirical models provide a consistent and quantitative indication of the net outcome of the various principle mechanisms thought to be at work based on the particular case (not stylised facts) and which might be affected by the policies proposed.

As they show, empirical economic models are linked to mechanisms as well. These models provide a foundation upon which to work for a particular case; allowing for an examination of the kinds of effects that suggested policies have. In a similar way, explanation-based predictions in public health policies allow estimations of risks by showing the short-term development of the infections, explicating the optimal immunity levels within the community, and sometimes even providing unexpected results for the optimal vaccination coverage.[18]

Reliable encounters with model-based predictions

When models function as measuring instruments used for predicting disease outbreaks, we are eager to know on what grounds we can rely on them. Oreskes et al. (1994) assume that numerical models are complex open systems because they require input parameters that are incompletely known. As we noticed, Habbema et. al. point to the step of validation[19] of models, by which models are assessed using available

[17] Analysis of the history of the concept in Fine (1993).
[18] As discussed in a lecture by Auranen and Leino (30.3.2008), Hib conjugate vaccine minimises the carriage of the bacteria and allows optimisation of vaccine coverage to be as low as 10%.
[19] Verification of a model denotes a propositional value to the model. Validation implies that models tell us 'how the world really is by comparing the measured response from *in situ* testing with the results of models.' (Oreskes et. al. 1994)

data. On the contrary, Oreskes et al. argue that verification is not possible in open systems, and can take place only in systems in which 'all the components of the system are established independently and are known to be correct'. Our examples from infectious disease modelling are open systems, in this sense. Even though our Hib model was based on explanatory mechanisms, not all of the model parameters were established independently; part of them were model estimates or approximations from data. Therefore, I will follow Oreskes' terminology and discuss reliability of models.

Boumans (2004) develops *instrumental reliability* in order to understand the formation of reliability in models. 'The inner workings of the instrument' reveal the facts about the phenomena under study. In his case, the instrument was a filter used for making unobserved components of data visible. He listed five points that defined the filter as a reliable instrument: i) it was a mechanical procedure; ii) it carried the reputation of the instrument maker; iii) it was calibrated; iv) it was a precise instrument; and v) on the outside it looked like new technology, but inside there was a reliable old mechanism. These five points aptly incorporate the role of experts, the practice of calibration and the procedures executed with the instrument. It could be read as a continuation of reliability, uniting the social and epistemic sides required to accomplish the model.

Boumans argues that calibration assesses 'whether outcomes of models are facts or artefacts' (2005, 268). What, then, is calibration? Within economic methodology, it is considered a method of estimation, or tuning (Boumans 2001, 442). More precisely, it is 'the use of a surrogate signal to standardise an instrument' (p.443). In practice, calibration, which could also be understood as 'debugging' the simulation program to minimise 'noise', is a demanding task. It is not always easy to find the bugs, the wrong parameter values, or the technical instabilities that cause the noise. In some cases too, the bug may not have a significant effect on the simulated results, as was the case with the so-called 'Jesus child[20]' in the integrated simulation-model on Hib. All these characteristics of simulation models show that they are a promising but demanding experimental tool. Why is that? Consider the simulation-model, which generates the data for predicting bacterial behaviour. Add vaccination interventions to the scheme and mix in the heterogeneous antibody levels due to the individual alternation of population members. It is not that simple to identify a novel, stable idiosyncratic pattern: the criteria for distinguishing between data, phenomena and noise may be blurred in the process.

Why do we then rely on model-based predictions? Or what does this step of 'validation' tell us about the *modelled encounters* with public health risks? The main 'message' is that 'validity' is not a comprehensive way of looking at the question. As we learned through the case of *explanation-based* predictions, when predictions are addressing mechanisms embedded in the data, they are bound with explanatory capacities and that increases their reliability. Sometimes, the predictive capacity of models is not used for re-examining something that has been grounded on data. The forward-looking predictions, limited by the scarcity of data, are key to the modelled encounters with public health risks. In that case, the quality of models, and the

[20] The simulation-model generated a child who was 2000 years old and the modellers named the artefact/bug a 'Jesus child' (Mattila, 2006b).

expertise of the modellers, form the reliability of models. These are important factors when we come to explore *scenario-based* predictions.

Building pandemic scenarios

Predictive capacities of models encompass the ambition to 'access the inaccessible', as Oreskes (2007) shows in her analysis of scale models in geology. She refers to models 'whose predictions are temporally or physically inaccessible'. But this ambition is not merely epistemic. Models, either physical or numerical, seem not to adjust to the changes in epistemic values shared in scientific communities but also reflect aspirations of scientific patrons, as Oreskes discusses. Models seem to do more than epistemological work: in the attempts to predict the future, models generate predictions that inform policy decisions. This is what Oreskes argues to be the primarily social role of predictions. In a way, *scenario-building* capacities of models express the social role by providing 'access to the inaccessible', even though scenarios may not satisfy the epistemic quest of explaining the viral mechanisms of a pandemic.

Explanation-based predictions, as discussed above, provide the ideal ground for short-term anticipation of public health risks, or low-impact, high-frequency events, as referred to in risk literature (Hutter & Power, 2005). However, most of the media attention is given to high-impact, low-frequency events, which in the public health context are pandemics. How do we respond to these events? Following International Health Regulations (IHR, 2005), each country is responsible for notifying WHO of 'any events that may constitute a public health emergency of international concern'. In a way, these internationally coordinated activities are an early warning, but they may not be able to anticipate or predict the occurrence of a pandemic. According to WHO, we are currently living in a pandemic period, which means that preparedness plans are in use on national and international levels and predictive models influence new daily estimates of the course of the pandemic.

How do *scenario-building* predictions form a part of the scientific evidence-base for decision-making? *Scenario-building* predictions are predictions that 'sketch, outline or describe an imagined situation or sequence of events, and outline any possible sequence of future events' (OED). In other words, *scenario-building* predictions are primarily tools that *produce qualitative scenarios* based on the available, past data, and as such they provide model-based encounters with future risks. These scenarios are not necessarily grounded directly on data about the future event (which does not exist), but build upon available sources of past data in order to anticipate the 'unknown'.

Predicting the pandemic

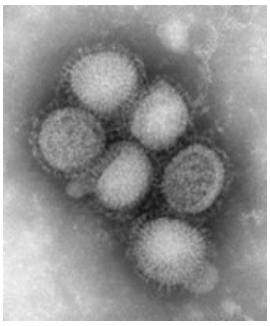
Humankind has faced cycles of pandemics, one of the most famous being the 1918 Spanish flu that killed, according to older estimates, approximately 50 million people worldwide. The pandemic spread all around the world and lasted about two years (1918-1920). Its oddities were that it infected and killed the young and healthy, and it spread during the spring months. In 2005 scientists resurrected the virus by modifying

it genetically at the Centre for Disease Control, Atlanta in order to study the infectiveness and symptoms related to the strain. As is documented with the Spanish flu, the close contact between poultry and human populations is thought to be the cause of the potential pandemic strain. The fear is that the virus is capable of jumping from birds to humans and mutating in humans so that human-to-human transmission is possible. We know that 70% of infections come from the animal kingdom and every year 2 new infections emerge. In order to detect the strain, laboratory analyses are of course the core practices. If the samples turn out to be of a dangerous strain, cleaning and disinfection will take place.

Human deaths caused by the highly pathogenic strain of H5N1 avian influenza virus caused concerns about the emergence of a potential pandemic. However, instead of *avian flu*, originating from South-East Asia, the world is currently witnessing a pandemic of 'swine flu', human A(H1N1)v, that originated from Mexico in April 2009 and spread around the world in couple of months. Let us summarise the course of the pandemic[21].

At the end of April, human cases of a novel influenza type A virus were confirmed. These cases were identified in the US and in Mexico. The virus, according to epidemiological evidence, had been circulating in Mexico since February and may have already emerged earlier this year. It was also confirmed that the new human strain was identical to a strain[22] of virus that had been circulating in pigs in North America.

Figure 3: The H1N1 influenza virus (Source: Centers for Disease Control and Prevention, USA, Influenza Laboratory)

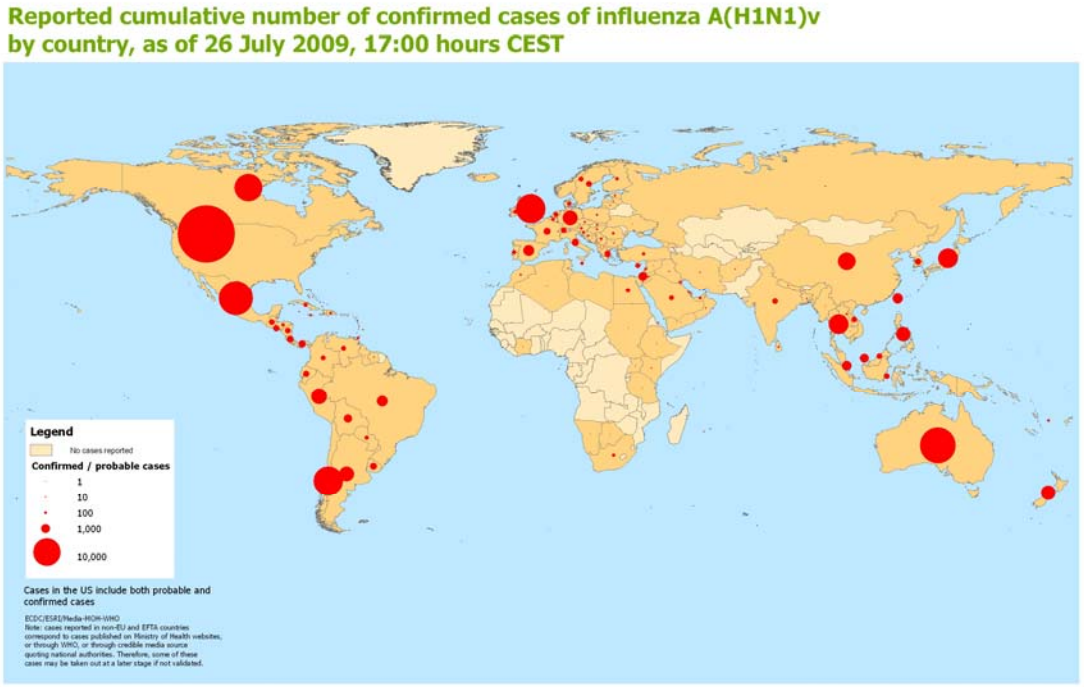


The strain spread rapidly, the first infections happened through contact with those who had travelled or were travelling from Mexico. WHO reacted to the public health emergency by raising the Pandemic Alert Level from 4 to 5 (sustained community outbreaks in a limited number of countries) at the end of April. On the 11th of June 2009, WHO declared a pandemic and raised the Alert Level to phase 6, which means wide geographical spread, but does not indicate the severity of the infection.

[21] This summary is based on Flusurvey.org.uk site (situation on 27.7.2009), which is an internet based monitoring system for Influenzae Surveillance, in collaboration with the Health Protection Agency, London School for Hygiene and Tropical Medicine, EU FP7 and Epiwork.

[22] Flusurvey reports that the current strain has a complicated history: 'some of its genes moved to birds to pigs in 1918, other genes from birds to pigs at the end of the 20th century, some got into pigs in the 1960s having first passed through humans'.

Figure 4: Map of the spread of A(H1N1) cases. (Source: European Centre for Disease Prevention and Control, Situation report, 27.7.2009)



According to ECDC Situation Report (27.7.2009), within the EU/EFTA countries there are 20,512 confirmed[23] cases and 35 deaths among those cases. Outside EU/EFTA countries the corresponding numbers are 139,526 confirmed cases and 956 deaths. So far, critical voices have questioned the rationale of the pandemic alertness, since the cases seem to be somewhat mild and respond to the antiviral treatments. The major concern, however, is that there is very little natural prior immunity to the new strain and the infection it causes. This is already seen in the fact that the main group of the infected are children. Due to the uncertainty of how serious the new type of virus is, the information campaigns call for increased hygiene, and advice for general audiences and risk groups is available. Currently, vaccine production is underway: the first vaccines should be available for risk groups in September 2009, and the UK, for example, has bought 90 million doses of vaccine in order to vaccinate the whole of the population.

These uncertainties raise questions about how to develop mitigation strategies to protect populations. Simulation models provide a way to predict the possible future course of the pandemic flu and hence function as a tool for planning and testing intervention strategies. When the simulation techniques are used in the preparedness planning, the data is grounded on observations from the past pandemics (1918 and 1957). These predictive simulation models allow for the study of various mitigation strategies.

[23] The confirmation policies depend on national laboratory testing policies.

What kinds of models are used as a scientific evidence-base for preparedness planning?

One of the major public health concerns in infectious disease studies is our limited capability to predict the emergence of outbreaks and peoples' behaviour in such an event. To mitigate this problem, several studies have developed large-scale simulation models that utilise data on travel patterns and population density from past pandemics. In the following, I will focus on one rather recent pandemic flu model and discuss its predictive capabilities. The model in question is an individual-based simulation model of pandemic influenza transmission for Great Britain and the United States[24]. It represents transmission in households, schools and workplaces, and the wider community. The main aim of the model is to study strategies for mitigation[25] of an influenza pandemic. I will focus on two model-based assumptions that affect the transmission: the estimate for the reproductive rate, and the behaviour. On the basis of a closer analysis of these assumptions, I will discuss the nature of *scenario-building* predictions and especially reflect on the suggested policy outcomes of this model.

Fingerprint of the pathogen – and of the population

Transmission is quantified in epidemiological models as a basic reproductive rate, which is the rate that is used for estimating the spread of infection in a susceptible population. It is defined as R_0, which is the average number of individuals directly infected by an infectious case, during her entire infectious period, when she enters a totally susceptible population. In infections that are transmitted from person-to-person, the potential of the spread is called the reproductive rate that depends on the risk of transmission in a contact and also on how common the contacts are. The reproductive rate is determined by the following four factors (Giesecke, 2002):

i) the probability of transmission in a contact between an infected individual and a susceptible one
ii) the frequency of contacts in the population
iii) how long an infected person is infectious
iv) the proportion of the population that is already immune

All these characteristics can be expressed by mathematical equations to provide numerical estimates of the transmission dynamics in a population. This rate is usually determined by empirical data, i.e. by deriving the estimate from previous epidemiological studies. However, it is a rate that carries a 'fingerprint' of the pathogen. By this I mean that the reproductive rate is sensitive to a particular strain of the pathogen in question. This sensitivity brings in a question of uncertainty in the model-based predictions. What if the strain is not so virulent? Alternatives are taken into account by modelling different possible scenarios based on different approximates of the reproductive rate. But what do the models do to the reproductive rate? In pandemic flu modelling, a future strain is unknown and therefore the models actually use data from the past strains. This relies, of course, on the assumption that the future pandemic is as virulent and contagious as the past one. If we look more closely at the reproductive rate and its variation, we can see how it manifests itself as

[24] This model is built by Ferguson et. al. (2006).
[25] Mitigation in the context of pandemic preparedness work is a collective term for all actions that aim at reducing the impact of a pandemic (Nicoll & Coulombier, 2009).

a fingerprint of the pathogen[26]. Nicoll and Coulombier (2009, table 4) provide following estimates for R_0:

- in seasonal influenza: R around 1.1-1.2
- in pandemic influenzas: R=1.5-2.5
- in current pandemic (H1N1): R=1.5-2
- in measles: R0>10

The variance in R_0 leaves an element of uncertainty in the predictions. This uncertainty is decreased once the pandemic begins to spread, and the pathogen is isolated and its virulence within a population (e.g. those who are encountering the infection) is known.

Behavioural assumptions and their alternatives

The simulation model that studies strategies for mitigating an influenza pandemic makes assumptions concerning the effectiveness of behavioural interventions. These are movement restrictions, travel restrictions, quarantine, and school closure. The question is: What kinds of behavioural assumptions are made in order to predict the spread and transmission of the outbreak?

In Ferguson et. al. (2006) a rather clear behavioural assumption is claimed when reporting on the model design:

> We do not assume any spontaneous change in behaviour of uninfected individuals as the pandemic progresses, but note that behavioural changes that increased social distance together with some school and workplace closure occurred in past pandemics.

Furthermore, the underlying assumption is to consider that individuals will behave according to the guidelines, rules and restrictions given by the health authorities. In a way, the effectiveness of behavioural restrictions is based on the assumption of rational agents. But how reliable is this assumption? In a recent discussion on the novel ways to study real world epidemics, Eric Lofgren and Nina Fefferman (2007) suggest that virtual game worlds might provide a different perspective. According to their analysis of an outbreak in an Internet playground, World of Warcraft, they observed that individuals did not follow the rules of movement restrictions and some voluntarily spread the disease. The question is: if the scientific simulation models are used for preparedness planning, how do we find reliable assumptions concerning the behaviour, which is, after all, key to preventing the spread of pandemics?

Scenario-building predictions

What is, then, the policy outcome of the model? What kind of scenario does the model imply? Both epidemiological and behavioural assumptions have their limitations. On the epidemiological level, the assumptions represent the *fingerprint* of the pathogen, hence leaving some level of uncertainty when applied to predictive scenarios. On the behavioural level, the assumption that individuals' behaviour

[26] Population density affects the estimate, since R_0 tends to be higher in crowded populations.

remains unchanged during the pandemic period opens up questions of credibility over these scenarios. Yet it was clearly stated that the models allowed for the exploration of a 'number of scenarios' regarding the transmissibility of the pathogen, its movement and travel restrictions. One could easily think that if *scenario-building* predictions are relying on particularly uncertain assumptions, they are mere fantasies, no better than 'fortune-telling'. However, this is not the case. As documented already with the Helsinki models on Hib, models provide a useful playground, a platform[27] to examine and explore particular features of the infection and its transmission (Mattila, 2006c).

Scenarios, which allow us to 'access the inaccessible', provide qualitative tools for producing evidence of the unpredicted for decision-making. The challenge of how to communicate this particular mode of evidence – its changing and mutable nature - remains.[28] As Ferguson et. al. (2006, 451) state: 'The transmissibility of a future pandemic virus is uncertain[29], so we explored a number of *scenarios* here.' They argue that these scenarios depend on 'model validation and parameter estimation', which should be given priority in future research. Transmissibility, which is based on the estimate of the reproductive rate, is considered to be on the level of 1918: if it actually follows the levels seen in the 1968 or 1957 pandemics then 'global spread will be slower and all the non-travel-related control policies examined here will have substantially greater impact'. Ferguson et. al. emphasise the importance of collecting the 'most detailed data on the clinical and epidemiological characteristics of a new virus'. In other words, he is calling for research that allows us to base the scenario-building on a detailed understanding of the explanatory mechanisms of phenomena. The 'fingerprint' of the pathogen is important, as we learned in the case of Hib modelling.

What kind of scenario was built around the behavioural assumption? Interestingly, the outcome of the simulation-model suggests that travel restrictions, which include both border controls and internal country restrictions, 'achieve little' in delaying the peak of the epidemic. This was taken into account when WHO gave recommendations and guidance on travelling during the current A(H1N1)v pandemic: 'Scientific research based on mathematical modelling shows that restricting travel would be of limited or no benefit in stopping the spread of disease.' (7.5.2009, WHO, GAR, Travel: Is it safe to travel?)

The social function simulation models are also worth emphasising. Scenario-building helps allocate resources; agree on, for example, pre-ordering and manufacturing the vaccines, and stocking the antivirals. As we observed in the two examples, the scientific models have 'uncertainty' built-in: the assumptions made on the basis of past facts may not provide accurate predictions of the scale of the outbreak. Nor are they capable of capturing the changing behavioural patterns of individuals. Testing out both assumptions and exploring them as part of various scenarios was 'doable' only by modelling. This is an indication of the usefulness of *scenario-building* predictions; they are qualitative tools that 'fill the gaps' in existing knowledge,

[27] Keating and Cambrosio (2000, 2003) introduce the concept of platform through their analysis of the development of biomedical science.
[28] Cf. Mansnerus, 2008.
[29] Notice please that Ferguson et. al. stated the uncertainty of transmissibility in 2006, currently, as Nicoll and Coulombier (2009) claim we can estimate transmission rate for the current pandemic.

allowing the reasoning process to touch upon the 'known unknowns' and perhaps 'unknown unknowns[30]'.

Conclusion

This paper shows how explanation-based and scenario-building predictions form modelled encounters with public health risks. Explanation-based predictions, in the case of modelling *Haemophilus influenzae* type b bacterial circulation and vaccine efficacy, are predictions that primarily address short-term development. They explain the causal mechanisms responsible for the course of a Hib infection and extrapolate its course within a limited time range. Explanation-based predictions, as analysed, are anticipatory techniques to encounter public health risks. Scenario-building predictions produce qualitative scenarios for the potential development of a pandemic outbreak. Their explanatory capacities are limited by the lack of data, but they are useful, for example, in assessing mitigation strategies.

Following Espeland and Stevens' account of quantification practices, modelling as a measuring practice aims at controlling[31] through quantification. The modelled encounters with risk, after all, are encounters aimed at minimising the risk; they allow us to predict and to be prepared in the face of the uncertain course of events. In broader terms, both types of prediction, explanation-based and scenario-building, are *technologies of governance* that allow different interest groups to act at a distance (cf. Miller & Rose, 2008). In explanation-based predictions, the underlying uncertainties are smaller, perhaps more manageable, whereas in scenario-building predictions the distance between what is known and what remains unknown is greater. Scenario-building predictions share some similarities with audit processes, as discussed by Power (1997, 40):

> The audit process shrouds itself in a network of procedural routines and chains of unverified assurance, which express certain rituals of evidence gathering, but which leave the basic epistemic problem intact.

In scenario-building, the epistemic - for example, the precise rate of transmissibility - plays a secondary role. The main importance is to explore and evaluate various outcomes. On the contrary, explanation-based predictions, when they successfully encompass epidemiological mechanisms, accommodate both the epistemic and social functions.

What kinds of modelled encounters with public health risks do the two types of predictions provide? How reliable are they? The analysis supports Boumans' (2004) notion of instrumental reliability, which incorporates both the 'instrument' and expertise required. In other words, reliable predictions, in both cases, result from the quality of the model and the expertise of the modellers. Both types of predictions show that modelled encounters with public health risks depend on the complex chain

[30] A good example of 'unknown unknowns' was the origin of the current pandemic. The main focus was on avian (H5N1) influenza that is currently circulating in South-East Asia. However, the pandemic emerged from the pig farming industry in Mexico.
[31] Auditing (in Power, 1997) could be seen as a practice of controlling through quantification.

of interaction between experts and technologies, between users and producers of these predictions.

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