Quantitative methods to predict the effect of climate change on microbial food safety: a needs analysis

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Abstract

Background

Food systems are both affecting and being affected by climate change. Anticipated effects of climate change on microbial food safety are both direct (e.g., on microbial prevalence) and indirect (e.g., increased risk of floods on water microbial contamination).

Scope and Approach

This paper highlights the necessity to build a quantitative framework to evaluate the effects of climate change on microbial food safety. The tools available from the fields of climate modelling and predictive microbiology are analysed, knowledge gaps and data needs are identified. Moreover, key sources of uncertainty are underlined by emphasising on the importance of an integrated study of the uncertainties involved.

Key Findings and Conclusions

Due to the high complexity of both climate change and microbial dynamics, a multidisciplinary research approach is essential. After selecting one food product and location to focus on, the appropriate climate change projections relative to microbial dynamics need to be determined and generated. The development of the impact model is based on the relationship between environmental pathogen preva-

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lence and dispersal and climatic factors. This is linked with the impact of climatic factors on microbial dynamics. These mechanisms remain poorly understood. The knowledge gap of the mechanisms regarding food microbial contamination and the role of climatic variables remains unexplored. Since controlled experiments on the climate system are challenging, international collaboration is imperative to gather the appropriate observational datasets. Moreover, identifying and evaluating the sources of uncertainty is critical to build reliable models.

Keywords: Climate change, Food safety, Predictive microbiology, Impact modelling

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1. Introduction

Climate change is considered the defining issue of our time, ranking as one of the biggest risks for both humans and the planet. Global warming is indisputable with unprecedented evidence. The rise in the atmospheric and oceanic temperatures, the decreased amounts of snow and ice, and the rise of the sea level are evidence of this phenomenon (IPCC, 2014). In 1896, the Swedish scientist Svante Arrhenius stated for the first time that the amounts of carbon dioxide released to the atmosphere by human activity could lead to warming of the earth (Arrhenius, 1896). Since then, a significant amount of research has been conducted and the underlying phenomenon, known as the greenhouse effect, has been explored.

Current knowledge suggests that from the short-wave radiation (ultraviolet and visible light) from the sun that reaches the earth, an amount is reflected back and the remainder is absorbed by the planet. This radiation leads to the planet's warmth and is called radiative forcing. In turn, water bodies and land radiate their warmth as long-wave infrared radiation. Atmospheric gases like water vapour, carbon dioxide, and methane (known as greenhouse gases, GHG), absorb part of this long-wave radiation and are warmed by it (Lean, 2009). This results in an increase of the atmospheric temperature. Without the greenhouse effect, the earth would be about 35 °C colder (AAS, 2015). Thus, it is an essential element for life on the planet.

The industrial revolution accompanied by the combustion of fossil fuels started and accelerated the release of the stored carbon. This leads to the increase in the concentration of GHG in the atmosphere, resulting in an amplified greenhouse effect. Consequently, temperatures have been increasing, reaching nowadays an unprecedented rate of global warming along with numerous implications. The current rate of warming is estimated to be 0.2 °C (±0.1 °C) per decade, which means that global warming reached 1° C above pre-industrial levels around the year 2017, and would reach 1.5 °C around the year 2040 (IPCC, 2018). Generally, a change in the climate may have many origins; it may be attributed to natural processes occurring internally, changes in the incoming amount of radiation in the planet, to anthropogenic shifts in the composition of the atmosphere or in the arrangement of land use.

The World Economic Forum's "Global Risks Report" of 2021 places climate action failure as the most impactful and second most likely long term risk (World Economic Forum, 2021). Apart from being an environmental issue, climate change is also a health issue with numerous associated health risks, such as infectious disease (Costello et al., 2009; Semenza, 2014; Lake & Barker, 2018). The food system is associated with one class of infectious diseases; foodborne diseases. Climate change and the food system are at the heart of the 17 Sustainable Development Goals (SDGs) as set by the United Nations (Schmidt-Traub et al., 2017). They are associated with the majority of the goals, e.g., zero hunger, climate action, good health and well-being, clean water and sanitation, life below water, etc.

Since the early stages of our society, the food system has altered drastically. Food production, processing, and consumption have become commercial and specialised activities that serve as sources of added value, jobs and incomes in both rural and urban areas. Food is reported to be the world's largest economic sector in terms of employment (FAO, 2019). According to the Food and Agriculture Organisation, FAO, (FAO, 2018), the term food system "encompasses the entire range of actors and their interlinked value-adding activities involved in the production, aggregation, processing, distribution, consumption and disposal of food products that originate from agriculture, forestry or fisheries, and parts from the broader economic, societal and natural environments in which they are embedded". Based on this definition, the food system is beyond the food itself; it is more about the activities involving food production. Several sub-systems are defined, e.g., the farming system, processing system, waste management system. The development of models to describe food systems should follow such a holistic approach. This leads to a higher model complexity, but offers certain key benefits. Including the relationships between the several sub-systems yields more realistic models. These are appropriate for climate change action, mitigation, and adaptation planning, leading to resilient food systems.

The Intergovernmental Panel on Climate Change, IPCC, is the United Nations body that serves as the link between the scientific community and the policy makers. The IPCC releases regular scientific Assessment Reports about state-of-the-art knowledge on climate change: its causes, potential impacts, and response options. The Paris Climate Agreement of 2016 was initiated based on the scientific input of the IPCC's Fifth Assessment Report. As a part of the Sixth Assessment Cycle, in 2019 IPCC published the "Special Report on Climate Change, Desertification, Land Degradation, Sustainable Land Management, Food Security, and Greenhouse Gas Fluxes in Terrestrial Ecosystems", also known as the "Special Report on Climate Change and Land" (IPCC, 2019), including a chapter dedicated to food security. The food system is of particular significance since it is both affecting and being affected by climate change (Vermeulen et al., 2012). Food production has been in the spotlight since previous IPCC reports, however, little attention has been given in them to food safety. In general, climate change is expected to affect all four pillars of food security: (1) food availability, (2) access, (3) utilisation, (4) stability, and their interactions (Godfray et al., 2010). Food safety falls under food utilisation, which involves the nutrient composition of food, its preparation, and the overall state of the consumer's health. According to the EU General Food Law Regulation (Regulation (EC) No 178/2002), food is deemed unsafe if it is considered to be: injurious to health or unfit for human consumption. While anticipated effects of climate change on food security are being thoroughly explored (Dawson et al., 2014; Myers et al., 2017), the understanding of how climate change may affect food safety remains unexplored (Vermeulen et al., 2012; King et al., 2017; FAO, 2020).

Due to its high complexity, climate change is expected to have a variety of impacts on food safety, both directly (e.g., increased prevalence of pathogens and toxins) and indirectly (e.g., higher risk of flooding, increasing the environmental dispersal of pathogens)(Herrera et al., 2016). Higher atmospheric and sea temperatures, changes in the precipitation patterns, increased frequency of extreme weather events, ocean acidification and sea level rise are some of the climate drivers expected to contribute to the vulnerability of the food system both in terms of food security and safety (FAO, 2020; IPCC, 2019; Miraglia et al., 2009; Tirado et al., 2010). For example, increasing atmospheric temperatures may impact dairy cattle by increasing animal diseases (Bett et al., 2017), and increasing animal heat stress (Polsky & von Keyserlingk, 2017), and consequently affecting milk production, safety, and quality (Rojas-Downing et al., 2017; Bett et al., 2017). On the other hand, extreme weather events (e.g., droughts or floods) may have an impact on feed and water quality, and availability, indirectly influencing milk production, safety and quality. Furthermore, there is an established relationship between mycotoxin presence on maize and wheat and climate change (Paterson & Lima, 2010; Battilani et al., 2016; Van der Fels-Klerx et al., 2016). This specific hazard can also propagate to other food products, e.g., contaminated milk that originates from bovine farms using contaminated feed (Van der Fels-Klerx et al., 2019). Since most published research has a qualitative character, quantitative research on the climate change effects on food safety is limited (Uyttendaele et al., 2015; FAO, 2020). One example of such quantitative effort is the EU FP7 "Veg-i-trade" project that was launched in 2010. It was aiming to study the impact of international trade and climate change on fresh produce safety by combining field studies, statistical analyses, scenario analyses and risk assessments (Jacxsens et al., 2010).

Climate change poses major risks to the food system in the future. Risk analysis has proven to be one of the most valuable tools in decision making. The principles of risk analysis encourage the systematic assessment of risks. The risks can be quantified by utilising mathematical models that describe the system under study. Developing such a quantitative risk analysis framework is imperative to quantify the safety risks that the food system is expected to face due to climate change. This can be implemented by using models of the anticipated climatic state and models linking climatic factors with food safety aspects. Climate models provide future trajectories of climate variables (climate projections), which are in turn used by the climate-specific food safety models to predict future food safety risks due to climate change. Such a framework can serve as a potential tool for policy making in order to mitigate risks, shifting from the reactive to the proactive approach, and eventually contributing to the resilience of the food system. As both the climate and the food system are highly diverse and complex, it is critical for decision making purposes to account for the uncertainties involved. When studying the impacts of climate change, the uncertainty grows at each step of the process, i.e., from GHG emission scenarios to the climate projections and to the impacts on the system under study (Seneviratne et al., 2018). Overall, uncertainty analysis is closely related to the model development process and is a key necessity in building reliable models.

This paper focuses on presenting the necessary steps for building a quantitative framework to study the impacts of climate change on microbial food safety. Several considerations that need to be accounted for are presented. Primary needs are identified, existing quantitative tools that serve towards that goal are reviewed, and the main challenges that are involved in developing such a framework with respect to uncertainty analysis are presented. The paper is divided in three sections. The first section describes the quantitative methods to obtain future climate projections. The second section reviews the available quantitative tools to assess microbial food safety, and the third section deals with the main challenges in the uncertainty analysis techniques that are required to quantify the food safety risks.

2. Numerical modelling of the climate system

The climate system consists of the atmosphere, hydrosphere, cryosphere, lithosphere, biosphere, and the interactions among them (Figure 1) (IPCC, 2014). Climate's definition is formed by the statistical description of the variability in the climate factors over a long period. The World Meteorological Organisation has defined this period as 30 years (WMO, 2018). These factors are related to the Earth's surface, such as temperature, precipitation, and wind. Due to the statistical nature given to climate's definition, climate change is considered in statistical terms as well. In the rest of this paper, climate change is considered as, "a change of climate which is attributed directly or indirectly to human activity that alters the composition of the global atmosphere and which is in addition to natural climate variability observed over comparable time periods" (IPCC, 2019). The distinction between climate variability and climate change lies in the analysis of anomalous conditions. One example of a shift belonging to climate change is when the occurrence of events that are considered rare is becoming persistent, e.g., higher incidence of heat waves during the summer period. These shifts are reflected in the probability distribution (either in its shape, center or both) of the occurrence of such events (Collins et al., 2018). This means that a sole event, such as a severe flood, cannot be considered as a result of climate change, and is attributed to climate variability. However, such sole extreme events can be valuable for evaluating their effects on the food system.

In general, a mathematical model is the description of a system given in term of a set of mathematical equations. The model aims to produce an accurate representation (or simulation) of the system under study with the minimum complexity to avoid overfitting. Climate models are mathematical descriptions of the earth's atmosphere taking into account its interactions with the other compartments of the climate system (e.g., hydrosphere, cryosphere, etc.) and the incoming solar radiation. Weather is a short term condition of the atmosphere for a period of a day, a week, a month or even a year. Climate is the long term summary of the weather for a particular location over a timespan of several decades. Thus, in climate modelling terms, weather is the solution of the climate model (or the state of the climate system) at a given time, whereas climate would be represented as the simulation of the climate model for a timespan of decades.

Climate models aim to describe the fundamental physical laws governing the system, like conservation of momentum, mass, and energy. These describe phenomena from sea ice forming to the moisture exchange between soil and the air above it. Amongst the most important are the Navier-Stokes equations, which describe fluid motion in terms of velocity, pressure, temperature, and density. This set of partial differential equations (PDEs) can be applied to both the atmosphere and the ocean. The flows are computed spatio-temporally (the three spatial dimensions are latitude, longitude, and height) and the effect of the Earth considered as a rotating sphere is accounted for. Numerical methods are exploited to solve the discretised mathematical expressions. The Earth is split in the three spatial dimensions in boxes, referred to as grids. Each of these grids is considered homogeneous. The higher the resolution, the smaller the grid size of the climate model. Based on their resolution, climate models can be classified into Global and Regional Climate Models (GCMs and RCMs, respectively). The implementation of processes taking place in smaller scales than the grid size of the GCM (sub-GCMgrid scale) is called parameterisation (McFarlane, 2011). It is important to note that certain climate features, such as droughts, storms, etc., are generated in the simulation of the climate model as a result of all the individual processes implemented in the mathematical description of the climate system.

In general, climate modelling serves two purposes: gaining insight into the climate system and producing future climate projections. The focus of this work is on obtaining climate projections. These are generated by considering several different alternative scenarios for future climate change mitigation. In the rest of this paper these scenarios are referred to as Climate Mitigation Scenarios (CMS). The development of the CMSs takes into account several alternatives for demographic, economic and technological advances, and patterns of governance (Cubasch et al., 2013). Each CMS describes a different socio-economic narrative of the future (e.g., strong or weak global corporation for climate action), which is translated into a trajectory of GHGs and aerosols concentrations. In turn, the trajectory is linked to a radiative forcing. These forcings act as input for GCMs and initialise them. Radiative forcings describe the residual energy absorbed by Earth after the reflection of the solar radiation. When finer resolution is required (smaller grid size), the output of the GCMs is downscaled (Figure 2). The downscaling process transforms climate projections from the global scale to a local region scale and is analysed later in this section.

Common practice in climate science is the development of impact models (IMs). When initialised with the output of climate models, they assess and quantify the risks associated with climate change (Figure 3). They can refer to both natural and human systems; in this case the IM describes the food system focusing on microbial food safety. The suggested approach for the development of the IMs is described in the second section by utilising predictive microbiology models.

2.1. Global Climate Models

GCMs serve as essential tools to delve into the mechanisms governing the climate system. Different radiative forcings, especially those related to human activity contributing to higher GHG concentrations in the atmosphere, are the inputs of the GCMs. Radiative forcings represent the amount of solar radiation that the Earth absorbs. GCMs are sophisticated models that represent the internal processes of the climate system elements, interactions, and feedbacks among them (Touzé-Peiffer et al., 2020; Adcroft et al., 2019). The start of what is called today climate modelling can be considered as the work of Manabe & Wetherald (1967). They published the first computer model that simulated the entire planet's climate, by coupling atmospheric and oceanic models. Currently, the GCMs (also referred to as *Earth System Models*, ESMs) also include biogeochemical processes among the compartments of the climate system (Figure 1). Among others, they are able to reproduce the fluids circulation in the oceans and atmosphere, the annual seasonality cycle, heat transfer between soil and the air above it, the carbon and nitrogen cycle, ocean ecology, etc. Moreover, they account for land use changes by mathematically describing the effect of changes in vegetation on the climate system. This is achieved by including plant physiology models, which express light and moisture absorption from different vegetation types.

GCMs act as a tool to gain knowledge on the causes of previous climate changes and to produce future climate change projections. These models are driven by the radiative forcings corresponding to the different socio-economic narratives considered in the CMSs (Taylor et al., 2012). Thus, GCMs are suitable for assessing the impact of various different policies on stabilising the GHG emissions to a specific target, e.g., 1.5 °C global temperature increase. As a single model has not been identified as the best performing when simulating the climate system, a group of simulations, a model ensemble, should be considered. The climate change projections needed to study the microbial food safety risks due to climate change should originate from a multi model ensemble. This comprises of a set of several different climate models that are considering the same CMS. Currently there are more than thirty modelling groups worldwide focusing on the development of climate models and the list is growing. Both the development and the assessment of climate models are time and resource intensive processes. Thus, international collaboration is imperative. The Coupled Model Intercomparison Project (CMIP) of the World Climate Research Programme is a global effort of climate scientists to share, compare and analyse developed climate models by the different modelling groups around the world. CMIP is considered the state-of-the-art concerning climate modelling and is currently going through its sixth phase (CMIP6) (Eyring et al., 2016).

In general, the grid size of each homogeneous box of a GCM lies between 100 km and 500 km. The finer scales, which encompass the sub-GCMgrid heterogeneity of the climate system are ignored (Figure 4). Due to their coarse resolution, the estimates originating from GCMs are valid only for large timescales and on a global spatial scale. However, primary food production takes place in finer scales, making the resolution of a GCM inadequate. Increasing the resolution of a GCM comes with extremely high computational costs. Modelling the impacts of a changing climate on microbial food safety and the adaptation strategies required to deal with the emerging risks demands smaller, regional and national scales (Barsugli et al., 2013). Numerous techniques have been developed to downscale to the regional scale (Rummukainen, 2009; Tapiador et al., 2020). The downscaled models, called RCMs, provide climate projections for regional levels. Quantitative tools to obtain climate model projections adequate for regional scales, i.e., regional climate projections, are analysed in the following subsections.

2.2. Regional Climate Models

As the effect of climate change is unique for each region, it is necessary to also evaluate the potential impact of climate change for the location under study. Thus, the first step to assess the effects of climate change on microbial food safety is to define the region under study. Since each region is characterised by one or more primary production food categories, a number of them needs to be selected. Another approach is to determine one food category to focus on and select those regions that are associated with it. For example, there are specific regions around the world associated with primary coffee production. Once the regions and food categories have been defined, regional climate projections for the associated regions need to be obtained.

The downscaling process incorporates sub-GCMgrid scale processes and heterogeneities to the GCMs output, yielding to an enriched and more realistic simulation of the climate system (Gaur & Simonovic, 2019). Each RCM is explicitly developed for one region. Downscaling methods derive fine scale climate projections on both spatial (e.g., from a 500 km grid cell GCM output to a 20 km grid cell) and temporal (e.g., from monthly to daily timespans) aspects. One critical assumption under this framework is that the climate of the region is governed by the processes involved between the atmosphere (circulation, temperature, moisture, etc.) and the features (water bodies, mountains, etc.) of the region. Overall, the downscaling process is valuable for detailing the internal processes of the climate system and for evaluating the impact of climate change on smaller scale systems. The development of RCMs comes with a significant challenge: the accurate reproduction of the variance of climatic variables as well as the reproduction of extreme events, not only in frequency but also in amplitude (IPCC, 2018). RCMs come with technical and scientific limitations, which need to be addressed carefully (Rummukainen, 2009; Giorgi, 2019). In terms of the CMIP6, RCMs fall under the Coordinated Regional Downscaling Experiment (CORDEX) (Gutowski et al., 2016).

To quantify the effects of climate change on microbial food safety, the scale of the system, i.e., microbial dynamics throughout the food system, imposes the necessity to downscale. Critical considerations in this process include defining the appropriate temporal and spatial resolution required to study microbial dynamics, and screening the most influential climate variables. Simplifications can be made, such as selecting a limited number out of all the available CMSs. The set of GCMs that are going to be included in the model ensemble is a trade-off. More than one GCMs should be considered to get an accurate climate simulation. However, the more GCMs are included, the higher the computational costs. Additionally, the downscaling method used to develop the RCM has to be selected. These methods are explained in the next subsection.

2.3. Downscaling Methods

Overall, there are two broad downscaling approaches: dynamical and statistical (Barsugli et al., 2013). In dynamical downscaling, the RCM is considered as a high resolution GCM. It is based on the same principles, but to reduce the computational costs, is limited to the studied region. These RCMs encompass (for the studied region, or period) detailed information about the climate system components, including the associated heterogeneities, that a GCM lacks. The output of the neighbouring grid cells of the GCM serves as an input for the defined RCM's boundaries of the area or period under study (Knutson et al., 2007). Since such a RCM is embedded in a GCM, its performance is connected to the chosen GCM and its accuracy (Bender et al., 2010; Knutson et al., 2013). Both the developed RCMs and GCMs are vulnerable to systematic errors (Rummukainen, 2009). To eliminate these errors, climate model projections need to be adjusted to mimic observed climate statistics. This process is called bias correction (Maraun, 2016; Maraun et al., 2017). Hawkins et al. (2013) assessed methods for obtaining climate projections data for crop modelling, concluding that exploiting a variety of methods is essential to ensure robustness and reliability. When conducting an impact study, it is crucial to avoid modifications in the output of the IM that originate from the bias correction process (IPCC, 2018).

Statistical downscaling sets up empirical models relating past and/or current large-scale and small-scale climatic variables. The output of the GCM serves as input, and the climate variables are determined for the smaller scale in a black-box modelling approach (Dixon et al., 2016; Lau & Nath, 2012). This methodology imposes a critical assumption: the several different radiative forcings associated with future emission scenarios do not affect the relationship between large-scale and the small-scale characteristics (Lanzante et al., 2018). The bias correction of the output of a GCM is included in the statistical downscaling process. Madsen et al. (2012) presented a statistical downscaling methodology to obtain climate change projections. These were associated with impact models to evaluate the effect of climate change on mycotoxin presence in crops. Liu et al. (2015) applied the *Delta method*, a statistical downscaling method, to downscale climate projection data from two GCMs for four CMS to study the effect of climate change on the microbial safety of leafy green vegetables. They concluded that more GCMs are needed to obtain an accurate climate simulation.

The choice of the downscaling method relies on the scientific expertise in climate modelling. Developing a dynamical RCM is similar to developing a GCM, needs collaboration, high level of technical expertise in climate science, and is computationally expensive. Conversely, statistical downscaling approaches do not require high level of expertise, are computationally efficient, but are based on many assumptions, and should be applied with caution.

3. The food system and predictive microbiology

Each primary food sector faces its own microbial risks and involves different levels of microflora richness. Addressing the effect of climate change should account for these unique characteristics. Thus, each IM should refer to one food sector. The modelling approach may differ based on the complexity and the origin of the microbial risks involved in the food class. For example, given that milk forms a suitable environment for the growth of many microbial species, studying the effect of climate change on these microbial communities is essential. For any food sector chosen, the IM should have as input future climate projections and as output the food safety risks associated with the food sector under study. The output of the downscaling process, i.e., regional climate projections, should be in the appropriate form to study the impacts of climate change on microbial food safety. Moreover, extreme weather events are expected to be more frequent due to climate change and the impact of these events on the microbial dispersal in the environment, and consequently on raw materials, is poorly understood. Before studying the impact of extreme weather events on the food category under study, which extreme weather events are expected to be more frequent for the region under study have to be determined. Overall, the knowledge of the future climate conditions for the region under study is essential. Based on this knowledge, food safety hazards need to be identified and evaluated, similarly to the risk analysis approach. In this section, predictive microbiology is introduced and evaluated as a tool for the quantification of the microbial food safety risks associated with climate change.

According to the Regulation (EC) No 852/2004 on the hygiene of foodstuffs, food safety should be guaranteed throughout the food supply chain. The development of an IM should follow this concept and integrate the entire food chain, starting with primary production. The effect of climate change on microbial food safety at the time of consumption is influenced by the whole production process (e.g., level of contamination at the production and processing sites, effect on growth rate during storage etc.). Depending on the conditions that are met throughout the food chain, different types of model structures should be introduced, i.e., growth, growth/no growth, survival or inactivation models. The most commonly used method to assess and manage microbial food safety is the implementation of the risk analysis approach, resulting in what is called Microbial Risk Assessment (MRA). According to the Codex Alimentarius (FAO/WHO, 1999), MRA is a scientifically based process consisting of: hazard identification, characterisation, exposure assessment, and risk characterisation. Predictive microbiology forms an essential element in Quantitative Microbial Risk Assessment (QMRA). QMRA quantifies the exposure of a certain microbial hazard by building a model to describe its level throughout the life span of a food product (Membré & Boué, 2018). The relationship of climatic variables with the contamination levels and the prevalence of pathogens in raw food material is the linkage needed to build IMs in a risk analysis approach. Eventually, the developed IMs are climate oriented predictive microbiology models. These intend to have as input regional climate projections. The opted output of the IMs is a trajectory of quantified food microbial risks, linking climate change with microbial food safety.

3.1. Modelling microbial dynamics in food

A fundamental tool in quantifying microbial food safety is predictive microbiology, a sub-field of food microbiology. Predictive microbiology involves the use of mathematical models, that are intended for the description of microbial dynamics in food products. In terms of predictive microbiology, the system to be modelled is the microbial behaviour (e.g., growth, survival and inactivation) in food under the influence of intrinsic and extrinsic factors. Intrinsic factors comprise the physico-chemical properties of the food itself, e.g., pH, water activity, and redox potential, whereas extrinsic factors are the environmental factors not related to the food itself (e.g., temperature and relative humidity) (McKellar, 2004). Several of these factors are directly (e.g., temperature) or indirectly (e.g., ocean acidification resulting in lower pH) linked with climatic factors, establishing a primary applicability towards the scope of this research. The onset of the field of predictive microbiology is considered to be the works of Bigelow & Esty (1920), Bigelow (1921) and Esty & Meyer (1922) involving the development of a model to predict the inactivation of spores of *Clostridium botulinum* during thermal processing. Since then, the domain gained more attraction, in particular during the 1980s and 1990s, leading to intensive research in the field (McMeekin et al., 2002).

Models are traditionally classified into two types based on the nature of the information used to develop the model: mechanistic and empirical. Mechanistic (also referred to as deductive or white box) models are developed based on general laws of physics and the understanding of the underlying phenomena governing the system. Nonetheless, mechanistic models, are rarely used in predictive microbiology. In contrast, empirical models (also mentioned as inductive or black box) are strongly dependent on available data and solely aim to describe the observed system response. Thus, black box models are valid only for the range of conditions associated with the dataset used to construct them. Therefore, they are preferred in cases where *a priori* knowledge is limited, but obtaining experimental data does not require significant efforts. A common practice in this field is to couple mechanistic and empirical approaches leading to the so-called grey box model or semi-mechanistic models.

Microbial dynamics are studied at three scales: macroscopic, mesoscopic, and microscopic level (Figure 5). In the macroscopic approach, the population is considered homogeneous and is modelled as a whole. The mesoscopic approach takes into consideration the heterogeneity among populations, whereas in the microscopic approach microbial cells are modelled individually. Multi-scale models serve as a linkage between the different spatial levels (Van Impe et al., 2013).

3.2. Macroscopic microbial modelling

At the macroscopic level, the information gained refers to the characteristics of the overall microbial population and its behaviour. Macroscopic models provide accurate predictions of microbial population dynamics under close to optimal conditions. Thus, they are the basic tool to quantify microbial dynamics in food. The four phases of a typical microbial population are (1) the lag phase, defined as an adjustment period during which the cells adapt to the new environment, followed by (2) the exponential growth phase, in the end of which the population reaches (3) the maximum population density (stationary phase), and finally (4) the decline phase due to, e.g., nutrient unavailability (Figure 6). Insights obtained from macroscopic models may form the *a priori* knowledge to quantify the effect of climate change on microbial dynamics. The scientific understanding of microbial dynamics assumes that the increase of the population is proportional to the population size (Van Impe et al., 2005), expressed as:

$$\frac{dN(t)}{dt} = \mu(\cdot)\ N(t) \tag{1}$$

$N(t)$ [CFU/mL] represents the concentration of microorganisms at time t [h] and $\mu(\cdot)$ [1/h] the specific growth rate. $\mu(\cdot)$ depends on process conditions (e.g., temperature), atmospheric conditions (e.g., relative humidity), food properties (e.g., pH) and components governing microbial interactions. $\mu(\cdot)$ is positive in the case of microbial growth and negative in the case of population decrease. According to Bernaerts et al. (2004), microbial behaviour in time can be expressed as:

$$\frac{dN_i(t)}{dt} = \mu(N_i(t), < env(t) >, < phys(t) >, < P(t) >, < S(t) >, < N_j(t) >, ...)N_i(t) \tag{2}$$

$N_i(t)$ [CFU/mL] represents the microbial population of the species i at time t [h]. μ [1/h], the specific growth rate, which is determined by the physicochemical environmental conditions $< env(t) >$, the physiological state of the cells $< phys(t) >$, concentration of the metabolic products $< P(t) >$, availability of the substrate $< S(t) >$, and the interactions with other species $< N_j(t) >$. Each of these factors can be represented as an additional building block in models describing microbial dynamics (Van Impe et al., 2005). Expanding our knowledge on the influence of climatic factors, such as relative humidity and atmospheric carbon dioxide, on microbial dynamics means, in practise, establishing a relationship between them and $\mu(\cdot)$ by adding the associated building blocks.

Macroscopic microbial models can be classified into: (1) primary models describing microbial responses, such as population growth, in relation to time; (2) secondary models, which describe the kinetic parameters of the primary models in relation to the changes of intrinsic and extrinsic factors; (3) tertiary models, which include the primary and secondary models in the form of software tools. One approach to exploit predictive microbiology models to assess the effect of climate change on microbial behaviour is to modify the secondary models to describe the effect of climatic factors on microbial dynamics. Coupling them with primary models will be valuable to determine the effect of climate change on microbial prevalence both in the environment and in raw materials.

Secondary models may have a major contribution to the scope of this research, i.e., quantifying the effect of climate change on microbial behaviour. Concerning predictive microbiology secondary models, there are two different modelling approaches. In the first approach, the developed models describe the effect of intrinsic and/or extrinsic factors simultaneously using a polynomial equation, leading to the response surface models. In the second approach, each factor is individually described and a general model can be used for the combined effects of the factors. This approach involves the use of the gamma hypothesis introduced by Zwietering et al. (1992), describing the growth rate in relation to its maximum value at the optimal influencing conditions for growth. This can be expressed as:

$$\mu_{max}(e) = \mu_{opt} \prod_{k=1}^{E} \gamma_{e_k}(e_k) \tag{3}$$

E is the number of the influencing conditions e, $\gamma_{e_k}(e_k)$ is the reduction of the growth rate due to a non-optimal value of one of the influencing conditions e, and μ_{opt} is the optimal growth rate, which is reached if all influencing conditions e are at their optimal values. Akkermans et al. (2018a) propose a novel gamma-interaction model for describing the effect of temperature, pH and water activity on the microbial growth rate. Akkermans & Van Impe (2018) developed a model of the inhibitory effect of pH on microbial growth by including the effects of the lag and stationary growth phases on microbial growth rate as independent gamma factors. Dolan et al. (2019) developed a secondary model, following the gamma hypothesis, for the effect of diffused carbon dioxide in the context of modified atmosphere packaging. Similarly, the gamma factors associated with climatic variables, such as relative humidity and atmospheric carbon dioxide, can be introduced to describe their impact on microbial dynamics.

Secondary models may be valuable tools in the effort to quantify the effect of climate change on microbial dynamics. Liu et al. (2015) present an illustrative application of downscaled climate projections on secondary models. As presented in Figure 7, expressing the effect of temperature on the growth rate of different microorganisms (in this case $Bacterium_1$ and $Bacterium_2$) with secondary models can be useful to compare differences in microbial growth dynamics. In this illustrative example, for a given temperature T_1, $Bacterium_1$ appears do be dominant with a higher growth rate compared to $Bacterium_2$. However, at a higher temperature, T_2, $Bacterium_2$ has a higher growth rate. Thus, from the microbial food safety perspective, with an increase in temperature experts are able to quantify and eventually identify the emergence of pathogen species.

Another approach focuses on evaluating the growth boundary conditions. The reasoning behind this approach states that the range of each factor affecting microbial growth are finite, indicating that growth can decline abruptly with a small increase or decrease in one of the factors (McKellar, 2004). Models under this category are known as probabilistic models or logistic type models and include growth/no growth models, survival/death models, recovery/no recovery models, and spoilage/no spoilage models. These models can be modified to characterise the boundaries by quantifying the probability of growth, survival, recovery or spoilage as a function of a set of the influencing factors (Ratkowsky & Ross, 1995). In mathematical terms this can be expressed as:

$$logit(P) = ln\left(\frac{P}{1-P}\right) \tag{4}$$

P is the probability of the studied phenomenon for a given set of values of the influencing factors. This can be related to macroscopic secondary models, such as response surface models. Such a response surface model with two influencing factors can be described as:

$$logit(P) = b_0 + b_1X_1 + b_2X_2 + b_3X_1^2 + b_4X_2^2 + b_5X_1X_2 \tag{5}$$

X_1, X_2 are the influencing factors and b_0-b_5 are the regression coefficients to be estimated. This approach can be utilised to evaluate the effect of multiple climatic factors (temperature, relative humidity, carbon dioxide etc.) on the growth limits of microorganisms in complex microbial niches such as soil etc.

3.3. Beyond the macroscopic modelling approach

The above mentioned models fall short of describing more realistic conditions, e.g., under stress environments. These models are developed based on experiments with liquid systems, mainly considering factors such as temperature, pH, etc. Extreme weather events, e.g., droughts, could be integrated into the predictive microbiology framework as stress environments. Furthermore, climate change is expected to play a role in population heterogeneity (Cavicchioli et al., 2019) and is a key driver for stress adaptation. Integrating complex features, such as background flora, stress adaptation etc., is challenging but essential to study the effect of climate change. In this subsection we describe predictive microbiology modelling approaches that aim to integrate such complex features: mesoscopic, macroscopic, and multi-scale. IMs that are developed based on these modelling approaches aim to link climatic variables and these complex features.

The mesoscopic modelling approach falls under the category of the top-down approaches. The macroscopic models are expanded by including information associated with differences in cell behaviour from the microscopic level. Mesoscopic modelling focuses on parts of the microbial population like sub-populations or colonies. The resulting models are also referred to as population balance models, since environmental or population heterogeneity is considered. Observed differences in the microbial responses are described, when following such a modelling approach. Since the population is no longer considered homogeneous, the behaviour of the microbial cells is classified accordingly, e.g., the population can be subdivided into growing and nongrowing groups (McKellar, 1997) or into heat-sensitive and heat-resistant subpopulations (Van Derlinden et al., 2009).

In the case of the microscopic modelling approach, biomass units or microbial cells are considered individual units and spatial aspects among them are integrated. In this bottom-up approach, the microbial dynamics materialise from the behaviour and interactions among them. These intercellular interactions can be integrated when the microbial cells are represented in the form of discrete entities in individual- or agent-based models (IbM/AbM). IbMs describe the global dynamics of a system in terms of its composing individuals or agents (Tack et al., 2017). In this case, the key advantage is that the population dynamics originating from the model are not implemented explicitly but arise from the modelled processes at the microscopic level. A high level of detail is included; spatial and microbial differences, randomness, interactions etc. (Tack et al., 2015). This approach is valuable to study population heterogeneities and describe microbial behaviour in complex environments, such as soil etc. Another potential application of IbMs is environmental stress adaptation. IbMs can contribute significantly to two research directions. Firstly, exploring the climate change potential as a key stress adaptation driver. Secondly, unravelling the cross-protection mechanisms that take place when adaptation to one environmental factor, e.g., extreme temperature, induces adaptation to several other factors related to food products and processes, e.g., pH (Cavicchioli et al., 2019; FAO, 2020). Furthermore, IbMs can be utilised to assess spatial differences in environmental microbial dispersal and prevalence.

Cavicchioli et al. (2019) suggest that elevated temperatures due to climate change may lead to shifts in carbon intake from microorganisms. In the context of microbial food safety, the use of metabolic network models (Van Impe et al., 2013) may be useful. These models study the behaviour of microorganisms in relation to their metabolism, i.e., biochemical reactions taking place inside the cell. The depth of detail of these metabolic networks may vary from describing only the most important reactions of the metabolism to a more involved network. This modelling approach integrates knowledge originating from the microscopic level, as expressed through the metabolic network, with macroscopic level models, composing what is called multi-scale modelling.

3.4. Towards modelling the impact of climate change on microbial dynamics

Even though the above mentioned models can be exploited and serve as valuable tools to evaluate the effect of a number of climatic factors on microbial food safety, the knowledge gap is apparent. Before quantifying the effect of climate change on microbial behaviour, the effect of climate has to be studied in detail. It is important to broaden the understanding of the effect of climate variables (or climatic factors) besides temperature, such as relative humidity, precipitation, carbon dioxide etc., on microbial population dynamics. This knowledge will aid in determining which climatic variables are the most influencing, and thus should be included in the study, for each food category. In principle, an IM should describe the relationship between those climatic variables and microbial responses throughout the life span of the food product.

Liu et al. (2016) in their attempt to determine the climatic factors that play a role in the *Escherichia coli* contamination of leafy greens concluded that temperature ranks first. Medina-Martínez et al. (2015) describe *Pseudomonas* spp. growth on baby lettuce as a function of several climatic variables, such as variations in temperature, relative humidity, rainfall spells, and wind. López-Gálvez et al. (2018) revealed a positive effect of increased relative humidity levels on the survival of *Salmonella* spp. on plants. In another study relative humidity and solar radiation demonstrated a positive relationship with *Pseudomonas* spp. presence (Truchado et al., 2019). Pang et al. (2017) studied the influence of climatic factors on the prevalence of *Listeria* spp. A black-box modelling approach was applied to develop models predicting the risk of contamination for the pathogen.

It is essential to expand current knowledge on the relationship between climate factors and microbial prevalence and dispersal in the environment. Thus, the implementation of secondary models describing the effect of intrinsic and extrinsic factors on microbial dynamics needs to be further studied. One approach would require the re-estimation of the model parameters of already developed and validated models, given that the studied environment will be different, i.e., the food matrix. One example of such change in the food matrix is climate change affecting raw milk composition characteristics. However, the existing model structures will most likely still be applicable for this new application. Another approach could be to focus on the proliferation of microorganisms in the environment, i.e., air, soil, and water by incorporating the spatial dimension. Predictive microbiology adopts an additional dimension, yielding predictive environmental microbiology. Another approach could integrate climate change information by focusing not only on the factors that are considered most relevant with regard to microbial dynamics but also with regard to the likelihood and magnitude of change they are expected to have due to climate change.

Furthermore, studying the effects of extreme events, such as floods, on microbial food safety is essential, since these events are expected to be more frequent and severe due to climate change. Castro-Ibáñez et al. (2015) in their work concluded that flooding comprises a risk factor for microbial contamination of leafy greens. Shiraz et al. (2020) conducted flooding experiments in strawberries production, detecting generic *E. coli* in soil samples up to 48 hours after flooding.

4. Handling Uncertainty

Whether dealing with the climate system or microbial dynamics, confidence in projections (when it comes to climate models) or predictions (when it comes to predictive microbiology models) is of utter importance. At its core, modelling is an approximation of reality. Thus, uncertainty is an ever-present phenomenon. Furthermore, the model parameters are estimated from experimental data, i.e., a process where uncertainty is an inherent property, and in some cases, exogenous disturbances are not accounted for. Uncertainty derives from the lack of knowledge and is often classified into aleatory and epistemic (Oberkampf et al., 2002).

Aleatory uncertainty or stochastic uncertainty (or variability) is present due to inherent variation or randomness of the studied system, often referred to as noise. For microbial behaviour, the term variability refers to the heterogeneity of the microbial cells. One of the major sources of variability is related to biological variability (Akkermans et al., 2018b). According to Membre et al. (2005), variations in growth rates have been reported for different strains of several pathogens, such as *Listeria monocytogenes*, *Salmonella* spp., *E. coli*, *Clostridium perfringens* and *Bacillus cereus*. Epistemic uncertainty originates in the lack of knowledge (Oberkampf et al., 2002).

The approach followed to handle uncertainties differs depending on the definition of probability. The two main approaches are the frequentist and the Bayesian. The latter is based on the definition of probability being related to the degrees of belief. The Baye's theorem is the tool used to update probability distributions by taking into account new knowledge. In this way, the probability distributions of the parameters and model outputs become more reliable. In contrary, according to the frequentist approach, probability is associated with the frequency of the occurrence of an event. Following this approach means that point estimates of the parameters are used, and uncertainty is quantified with confidence intervals.

If possible, it is advised to characterize biological variability separately from uncertainty, especially in the framework of conducting a QMRA (Busschaert et al., 2011). The key difference is that biological variability can always be quantified, but never eliminated, whereas experimental uncertainty can often be reduced significantly. The framework proposed by Garre et al. (2020) is tackling this issue by introducing multi-level models that account for the different sources of uncertainty. In their work, microbial dynamics are described with probabilistic predictive microbiology models and uncertainties are handled using the Bayesian approach. The main objection to the Bayesian approach is that when using prior distributions, which is part of the Baye's rule, the subjective element is introduced in the process of assigning the prior. This means that ending up with reliable models comes with a great cost linked to the prior knowledge. In the case of biological applications, such as this, adequate prior knowledge, in terms of data requirements, is not always necessarily available or accessible.

In general, sources of uncertainty in model outputs vary. They may be related to: (1) the model inputs (e.g., parameters, initial conditions, boundary conditions, forcings), (2) the model structure either due to unmodelled system phenomena or due to impossible discrimination between competing model structures, (3) to computational costs that are limiting the number of model iterations, and (4) to computational errors (Ghanem et al., 2016). Hence, uncertainty propagation is an important step in building reliable models. Uncertainty propagation can be performed in two directions; forward and backward. Forward uncertainty propagation techniques propagate the uncertainty from model inputs through the mathematical model to the model outputs (or responses) to quantify the uncertainty on the model responses, while backward uncertainty propagation techniques start from the experimental data and model simulation results estimating parameter uncertainty. Akkermans et al. (2018c) studied the influence of both parameter estimation and several uncertainty propagation methods on the calculation of model prediction uncertainty in the context of predictive microbiology. Uncertainty propagation is typically performed with Monte Carlo simulations, while other techniques include the linear approximation method, polynomial chaos expansion method, and the sigma point method (Bhonsale et al., 2018). In the case of probabilistic models, uncertainty propagation can be also performed by Bayesian approaches. Van Boekel

(2020) compares the application of Bayesian methods for uncertainty propagation and parameter estimation with the frequentist approach. Some of the key conclusions are that Bayesian methods offer better interpretation of model parameters, direct estimation of the confidence intervals in model predictions, and, in general, more intuitive results. However, the authors point out at the prerequisite of background in probability theory, as well as at the requirement for well-established prior knowledge. Thus, the choice of the method depends on the model's computational efficiency, the modeler's expertise in probability theory, and the needed data availability.

4.1. Climate models and uncertainty

Typically, the uncertainties involved in climate projections are quantified with the use of ensembles of climate model simulations, however, the sources of uncertainty should always be noted (Moss et al., 2010). There are multiple key sources of uncertainty in climate modelling. Firstly, uncertainty related to input data referring to the lack of knowledge of the boundaries and the inherent noise of the data used in climate simulations. Secondly, parametric and structural uncertainties, originating from the lack of knowledge about processes leading to different parameterisations and model structures. Moreover, errors in observational data, which include noise and the lack of knowledge of the covariance structure of the data. Uncertainty related to the downscaling process and the uncertainty introduced by the off-line coupling of climate models and impact models, due to the fact that it permits only a certain number of linkage variables, thus key feedbacks may be eliminated. Furthermore, uncertainty related to the tuning process, i.e., forcings used for climate projections are very different to those used for tuning, and uncertainty related to the bias correction process of the output of the GCM. Recent advances in addressing uncertainty in climate models include the work of Sherwood et al. (2020), which narrows down uncertainty associated with climate sensitivity. Uncertainty is compounded with the downscaling process. Thus, quantifying uncertainty is considered as a trade off in finer-resolution projections. Furthermore, a major challenge in producing reliable climate projections is related to proper uncertainty propagation analysis at each phase, e.g., from radiative forcings to global climate models, from global to regional climate models, from regional climate models to impacts at the ecosystem level, etc (IPCC, 2018).

4.2. QMRA and uncertainty

Biological variability includes both the heterogeneity in individual cell behaviour, known as cell variability, as well as the inherent diversity in microbial behaviour of strains of the same species undergoing the same conditions, known as strain variability (Koutsoumanis & Lianou, 2013). Traditionally, the effect of extrinsic factors on biological variability can be addressed by using probability distributions for the model parameters. The resulting models are also known as stochastic predictive microbiology models (Koutsoumanis et al., 2016). Codex Alimentarius guidelines underline the importance of taking uncertainty into consideration and performing sensitivity analysis when conducting a MRA, especially for a QMRA (Thompson, 2002). Sensitivity analysis aims to characterise the different sources of uncertainty by assessing how each one contributes to the uncertainty of the output of the model. Uncertainty and sensitivity analyses should be conducted together (Saltelli et al., 2007). Traditionally, when conducting a QMRA two approaches can be followed to address uncertainty; either applying robust or stochastic methods. Robust methods are based on formulating a worst-case scenario, while stochastic methods characterise uncertainty with probability distributions that formulate expected outcomes and chance constraints. Once the mathematical model is developed and the variability of the input factors and the model parameters is estimated through a distribution, forward uncertainty propagation methods can be implemented to consider the distribution of possible outcomes for different values of the input factors. Bayesian methods have also been exploited for performing a QMRA (Ancelet et al., 2012). Beaudequin et al. (2015) reviewed several such applications and underline the benefits and the needs of developing Bayesian networks for risk assessments.

Both the climate system and microbial behaviour are highly complex and involve multiple uncertainties, which need to be addressed properly to produce reliable knowledge. Ongoing climate research investigating the highly complex interactions and feedbacks of the climate system aims to cover knowledge gaps pertaining to GCM outputs and the downscaling process. The uncertainty analysis becomes further involved due to uncertainties that are introduced from microbial dynamics. The inherent biological variability of microbial behaviour should be characterised and be separated from other sources of uncertainty. At each step, starting from the future scenarios to the GCMs, then further to the downscaled projections, and to the system described by IMs that includes microbial responses, new sources of uncertainty are introduced. This, in combination with the fact that multiple likely future scenarios are considered, indicates the necessity to implement an integrated study of the uncertainties involved.

5. Conclusion

The IPCC identifies the following as key challenges in coupling climate projections with impact models: (1) the result of the impact model of the system under study, driven by the output of the climate model, should not be affected by the bias correction of the climate model, (2) conducting the downscaling process having regard to physical consistency of the downscaled information, and (3) the development of an integrating framework to perform uncertainty analysis. Moreover, the model ensemble approach is necessary to assess the stochastic nature of climate models. Thus model intercomparison projects, such as the CMIP, are invaluable. The paramount need, in terms of climate modelling, is the increase of resolution of GCMs, so that the downscaling process, which introduces uncertainty, is omitted. Equally important is to pursue efforts to narrow down uncertainty in climate projections data following the example of Sherwood et al. (2020). Focusing on tackling these challenges, the involvement of climate specialists is essential.

Furthermore, there is a clear knowledge gap of the impact of climate factors, such as precipitation, wind speed, and carbon dioxide, both on microbial behaviour and contamination levels of raw food. Another important aspect remained to be studied is the impact of extreme weather events, such as floods. A characteristic of Earth sciences, also applied to this research, is that performing experiments under controlled conditions is extremely demanding. An observational dataset is much more easily accessible. Therefore, to study the influence of climatic factors on microbial dynamics and microbial environmental dispersal and prevalence, international initiatives on gathering microbial prevalence-specific observations is imperative. One example of these observations is a dataset containing soil microbial population levels of selected pathogenic bacteria (e.g., *Listeria monocytogenes*) for decadal time spans. The soil samples should originate from different regions (e.g. countries of Sweden, Belgium, and Greece), which are expected to experience differently the climate change effects. Analysing such datasets in relation with the associated climate observations referring to the same timespan will make the onset on the establishment of the intended relationship.

Identifying the most climate change relevant microbial food safety risks for specific food products or processes and assessing the emergence of pathogens is crucial. Remote sensing data from different regions can be utilised. This will lead to a spatio-temporal modelling approach that will ultimately link microbial responses with geoinformatics. This can be the onset of a brand new multi-scale modelling aspect and will yield to the modelling of the distribution and spread of pathogenic bacteria as a function of climate change factors. The selection of appropriate model structures for the current application is a data-driven process; i.e., its efficiency and accuracy are determined by the quality and quantity of the data available. Nonetheless, acquiring such a specific, both microbial responses and climate oriented dataset is challenging and requires international efforts. *In silico* studies exploiting the limited observational data that are currently available will prove a valuable tool. Due to the complexity of both the climate system and microbial dynamics a multidisciplinary research approach is the most suitable.

Nevertheless, in developing computational tools, identifying sources of uncertainty is a key element in the process. Especially when the studied system is of biological nature, separating uncertainty from biological variability is imperative. Uncertainty propagation may be computationally expensive when dealing with such complex systems and large scale nonlinear models. To cope with such issues, different uncertainty propagation methods (e.g., sigma point method instead of Monte Carlo simulations) have to be implemented. Uncertainty is introduced at each step of the process. Additionally, several different scenarios, each one accompanied with its associated uncertainty levels, are considered. Therefore, developing tools to conduct an integrated study of the uncertainties involved is crucial.

Finally, taking a food systems approach is an essential strategy, which considers the high complexities of the systems under study. Overall, quantification of the food safety risks associated with climate change by implementing such a holistic approach is the adequate tool for policy making to mitigate these risks. Nevertheless, food safety is only one aspect of the food system. Climate change is expected to affect food security and food quality as well. Adapting the quantitative framework presented in this paper to consider the link between climate and food quality traits, e.g., raw cow milk fat content, and food security characteristics, e.g., raw cow milk yield, will give a multifaceted view of the anticipated changes to come. This approach will contribute to the shift from the reactive to the proactive approach. Eventually, the international effort to achieve the goal of shaping resilient food systems will be benefited.

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Figures

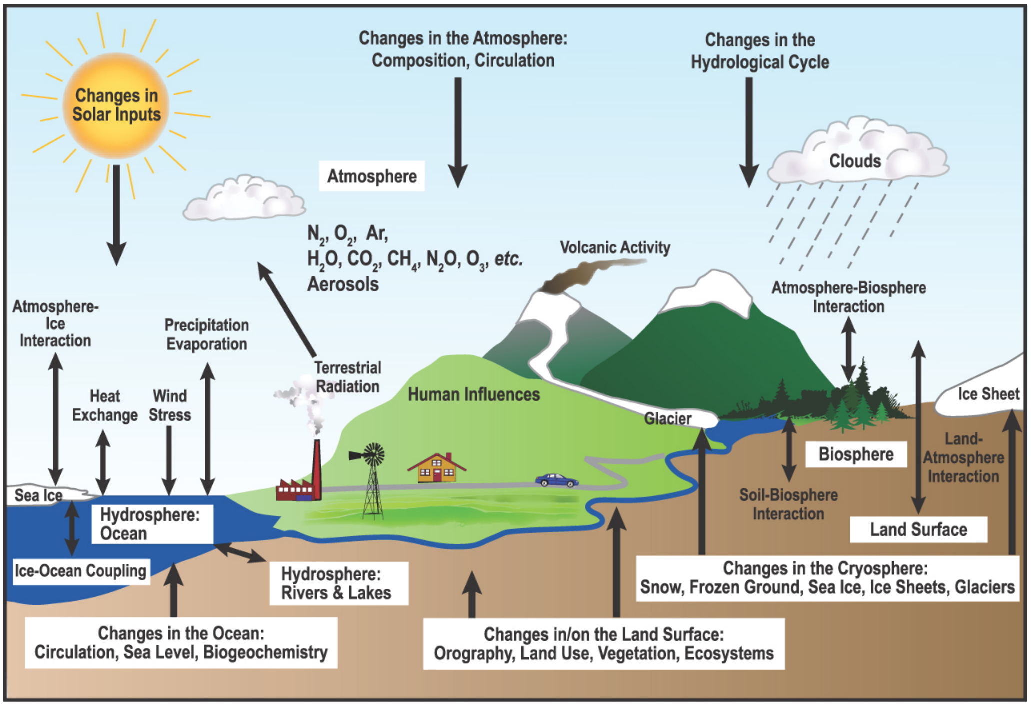

Figure 1: Schematic view of the components of the climate system, their processes and interactions. Source: Le Treut et al. (2007).

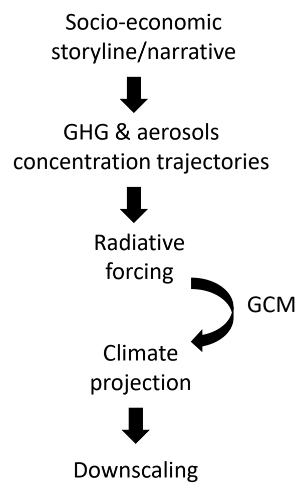

Figure 2: Work flow of climate models simulations based on IPCC (2018).

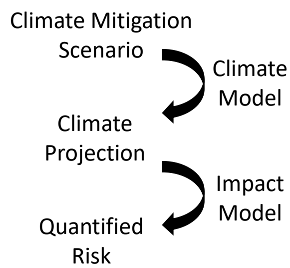

Figure 3: The impact modelling framework based on IPCC (2018).

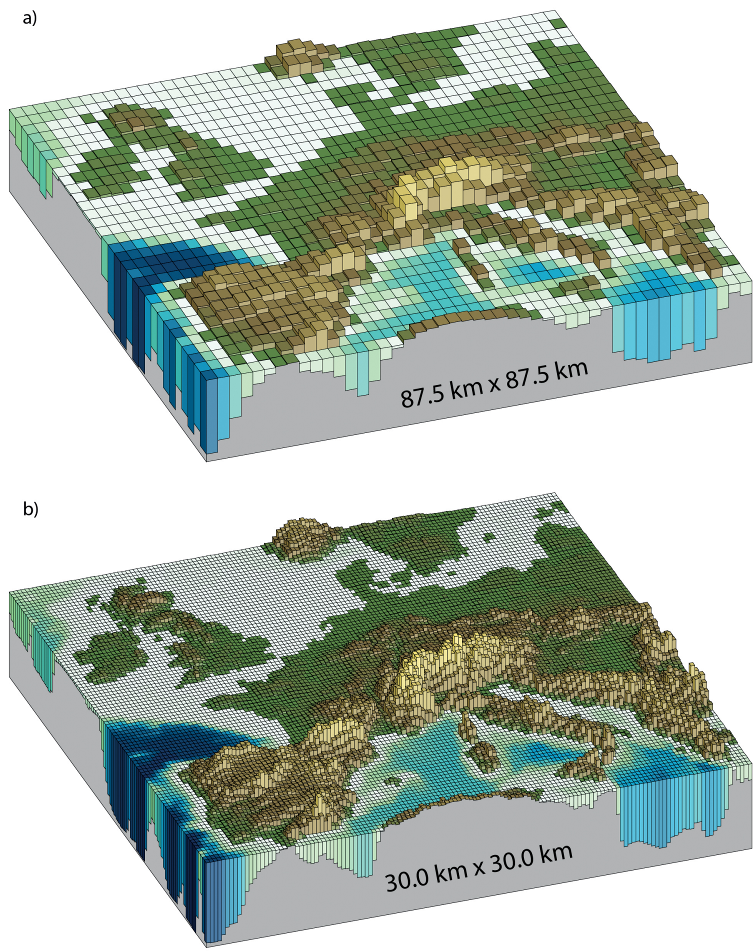

Figure 4: Illustration of the European topography at: (a) resolution of 87.5 × 87.5 km; (b) same as (a) but for a resolution of 30.0 × 30.0 km. Source: Cubasch et al. (2013).

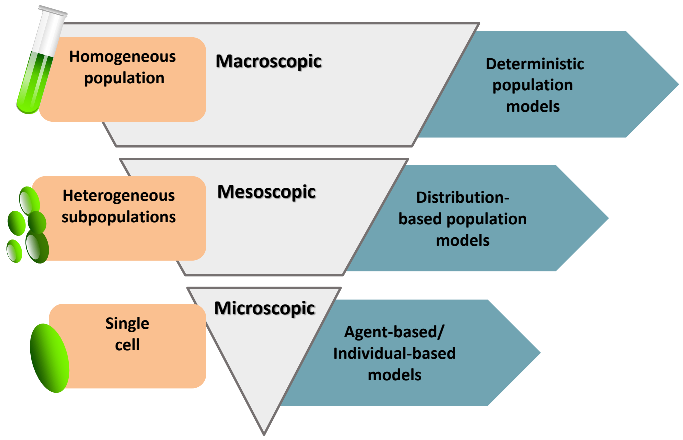

Figure 5: Description of the different scales in multi-scale microbial modelling based on Van Impe et al. (2013).

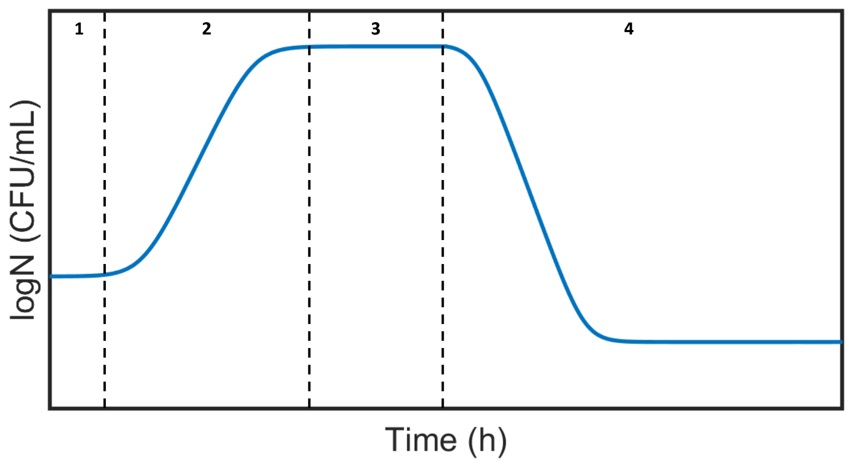

Figure 6: Illustration of the four phases of a typical microbial population. 1: lag phase, 2: exponential growth, 3: stationary phase, 4: decline phase.

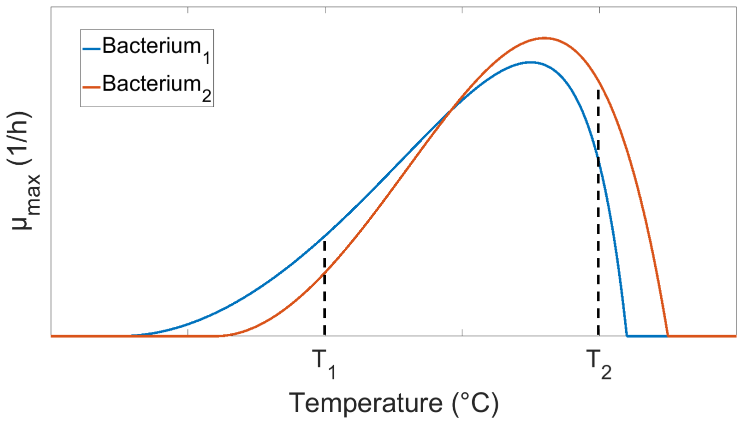

Figure 7: Effect of temperature on microbial growth dynamics: a toy example.