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Identifying vulnerable populations and transmission pathways by geographic correlation of the environment to human health

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HIGHLIGHTS
• A spatial framework for tying environmental features and change over time to health.
• The framework helps to identify transmission pathways and vulnerable populations.
• Framework for relating environmental features to the health of a population.
• Data creation useful for the management of emerging infectious diseases.

GRAPHICAL ABSTRACT

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ABSTRACT

The social determinants of individuals’ health (e.g., socio-economic, demographic, and genetic conditions) play a major role in the health of an entire population. However, in comparison to environmental data, global data on the social determinants of health is spatially coarse, infrequently updated, and costly to measure. From global mapping efforts of the recent COVID-19 pandemic it is clear that social data is not meeting the fine spatial quality needed for mapping vulnerable populations and transmission pathways. Most maps produced generalized to larger administrative units (such as counties, states), and have not identified distinct areas of vulnerable populations apart from the surrounding environment where no population resides. We present a framework that uses environmental determinants of health, instead of social ones. Other studies that link the environment to human health have done so by analyzing one ecosystem service (such as clean air) to the health of the population. Instead of relating one ecosystem service to the health of the population, this framework breaks the environmental features that produce the ecosystem service into parts (forest, temperature, precipitation). Each feature is then related to human health. With the amount of data available it is feasible to include change in monitored features over time, and create predictors for the impact of the change of monitored features on the health of populations. This framework generalizes ecosystem services and disservices into one value that an environmental feature provides. This helps to manage uncertainty of how an individual ecosystem service affects health. Application of this framework will allow for fine scale monitoring of vulnerable populations and transmission pathways of various infectious diseases. This framework is particularly relevant to newly emerging infectious diseases, such as COVID19, whose socially determinant risk factors are unknown (or data scarce) and to which we have to respond in a rapid manner.

1. Introduction

85 of the 102 major diseases are recognized, by the World Health Organization, to be associated with environmental risk factors (Prüss-Üstün et al., 2016). Environmental data is available globally on
2. Methods

2.1. Mathematical model

The three core environmental components to measuring resistance of a population to diseases are: the environmental features present, the distance that a population is from these features and the change (rate and quantity) over time of both the environment and population. In order to measure how vulnerable a population is to a disease these factors need to be compared to the outbreak of the disease. The following equation (Eq. (1)) was developed for this study to show the steps needed to find a resistance score for an area. All parts of the equation will be discussed in further detail in the following section.

\[ v \approx \left( \frac{e + m}{d} \right)^r \times or \div (q \times r) \div (p \times w) \times \frac{d}{r} \times or \div (p \times w) \times \frac{d}{r} \]

where \( v \) is the total vulnerability or resistance score, \( e \) is the amount of an environmental feature, \( m \) is the distance of a population from an environmental feature \( d \) is density of a population in the area, \( a \) is the amount of change of the environmental feature, \( z \) is the rate of change of the environmental feature, \( p \) is the population change, \( w \) is the rate of change of the population, and \( r \) is the regression to compare the environmental components experienced by the population to the disease (it is different for each value regressed). As there are variations of how a population experiences a disease at any scale (based on genetics, socio-economic status, availability and other variables not measured), it is advised to use a regression technique that can better account for these variations (such as geographic weighted regression instead of linear regression). The relationship of the different components to each other can take any of the four signs: addition (+), subtraction (−), multiplication (×) and division (÷). This relationship changes based upon if the component experienced is positive (e.g., increased forest or decreased population, multiplication or addition) or negative (e.g., decreased forest or increased population, division or subtraction). If the exact relationship between the three components of the equation is known, then multiplication or division is able to be done. However, if the relationship is not known it is advisable to use addition or subtraction. This is due to the large change in overall resistance levels when using multiplication or division. Measurements of each variable can change based upon the resources available to a study.

The larger the study area the more likely it is that errors are introduced. Depending on computing capability and the available data, the equation can be run on smaller subregions, then pieced together instead of analyzing the entirety of the area at once. Dividing the analysis can increase the accuracy of the results.

2.2. Explanation of mathematical model

2.2.1. First part – environmental feature, distance, and population density

The following section will explain the first part of the mathematical model presented above (Eq. (1)):

\[ \left( \frac{e + m}{d} \right)^r \]

The amount of an environmental feature present in an area can be quantified \( e \). Proximity to the environmental feature affects the amount that the population experiences it, the closer that a population is to the feature the more they experience it \( m \). The total of the environmental feature experienced by a population is then divided by the entire population \( d \), to give an estimated amount of the environmental feature experienced by each individual of that population. The amount of an environmental feature that an individual experiences affects their health. When a disease enters the area, relating the amount of an environmental feature that an individual experiences to the number of
reported incidents or deaths $r$ can show how the health of each member of the population is likely being affected by the environmental feature. This part of the equation shows the resistance of the population to a disease based on amount of environmental feature, measured distance, amount of population and relating this to reported incidents or deaths. This is run for each environmental feature monitored.

2.2.2. Second and third parts - change in population and environmental feature

This section will explain the second and third parts of the mathematical model (Eq. (1)) which incorporate change over time:

\[(a \times z \times w) \pm x \times or \div (p \times w) / r\]

Environmental features change naturally (natural caused fires) or due to external causes (human caused deforestation). The change experienced $a$ is able to be quantified. The effect of this change on the population is strengthened or weakened by the rate at which it occurs. The rate of change $z$ is also able to be quantified. When a disease enters the area, the response of the population to the disease $r$ can show how each member of the population is being affected by the change in environmental feature. This equation is run for each environmental feature monitored.

Changes in population also occurs naturally (births) or due to external causes (forced migration). The change in population level $p$ that an area experiences is able to quantified. The effect on health from change in population is strengthened or weakened by the rate $w$ at which the change in population occurs. When a disease enters the area, the response of the population to the disease $r$ can show how each organism is being affected by the change in population.

Change in environmental feature and population can either be positive (reforestation, decrease in population) or negative (deforestation, increase in population) to the overall impact on health.

2.3. Numerical illustration and data

We illustrate the framework with a numerical example from three landscapes. In this example all relevant environmental features are compiled into one value, hereby called ecosystem services. Two of these landscapes have four different ecosystem groupings (Figs. 1 and 2) and one has twelve groupings (Figs. 3 and 4). The data used in the numerical example is theoretical, but reflects the current scientific understanding of what ecosystem service levels might be for certain ecosystem (land use land cover) groupings (Burkhard et al., 2009; Dallimer et al., 2015; Toeless et al., 2017; Wu et al., 2013). Generally higher amounts of living biomass are able to provide more ecosystem services (clean air, clean water, shelter from extreme temperatures). Both the decrease of ecosystem services supplied through space and distance traveled are arbitrary. The numbers assigned to population density, change over time of population, change of environmental feature, regressions and starting point of disease were randomly assigned using a computer generator. The timeframe for change of environmental feature was set to be the same so as to portray that the change measured can occur over the same timeframe or different based on the data available.

3. Results

The theoretical application of the framework gives us four key results demonstrating, (i) distribution scheme of ecosystem services (Fig. 1), (ii) transmission pathways of a disease (Fig. 2), (iii) change of resistance levels from incorporating change in environmental feature (Fig. 3), and (iv) change of resistance levels of existing populations from an increase in population (Fig. 4). The results are explained below.

3.1. Distribution scheme of ecosystem services

In the first key result there are four different ecosystem groups (one forest, two different agriculture, and one urban) organized as two different landscapes. The four ecosystem groups generate an amount of ecosystem services (central number in each ecosystem diagram in Fig. 1), in each organization pattern these amounts are the same. The ecosystem services generated are shared with the neighboring ecosystems. The rates at which these ecosystem services decrease through space are the same for all four ecosystem groups. The total of the ecosystem services available (underlined number on top right of each ecosystem diagram in Fig. 1) is the sum of the original amount that the ecosystem generates (central number in each ecosystem diagram), and the amount of ecosystem services that are shared with it (total of all numbers on arrows pointing towards ecosystem diagram). Based upon the spatial organization of the four different ecosystems there are different levels of ecosystem services available. In this example on the left of four ecosystem groups the forest has more ecosystem services than the forest in the example on the right. However, the agriculture group on the right provides

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Fig. 1. Distribution Scheme of Ecosystem Services for Two Example Landscapes (Numbers- central: starting ecosystem services $e$, on lines: shared ecosystem services $s$, top left: sum of ecosystem services shared and starting).
more ecosystem services than the agriculture on the left (Fig. 1). This is primarily due to the proximity of the urban area to either agriculture or forest. The more ecosystem services that a population is able to experience the healthier the population is likely to be, for the purposes of this framework we call the sum of the equation the resistance score. The resistance score for each ecosystem group makes the population living in that ecosystem more or less resistant to a disease from the neighboring population, the lower the sum the less resistant a population is.

3.2. Transmission pathways of a disease

All four ecosystem groups had the same amount of population living within them (second number in equation on each diagram in Fig. 2). However, the population did not respond the same to the introduction of a disease (i.e., sneezing face). The reasons their responses were different was due to the amount of ecosystem services available to each population (first number in equation on each diagram) and their ability to

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Fig. 2. Transmission pathways of an illness in two example landscapes with different resistance levels (Numbers- Sum of ecosystem services e + m / population count d * regression of environmental features to disease r = resistance score).

Fig. 3. Resistance scores of different landscapes including change of environmental feature (Numbers- Resistance score from ecosystem services ((amount of change of environmental feature a * rate of change of environmental feature z) * regression of change of environmental features to disease r) = resistance score incorporating change in environmental feature).
respond to the disease (through technology, social coordination etc.) (third number in equation on each diagram).

In the four ecosystem groups on the left the disease starts in the forest and travels to the urban area then to agriculture. On the right the disease starts in the urban area then travels to forest and then agriculture. In both the left and the right, the disease travels from the point of origin to the next area with the least resistance, this is expected to be the standard travel path for the spread of a disease (Fig. 2).

3.3. Change in resistance levels from incorporating change in environmental feature

The first two key results did not incorporate change over time of either population or environmental feature. As the world is ever changing, change in environmental feature is necessary to incorporate (second number in equation on diagram in Fig. 3). For the third key result, all of the ecosystem groupings experienced different levels of change over the same timeframe (third number on diagram in Fig. 3). All ecosystem groupings underwent a positive change (reforestation for forests, planting of trees for agriculture, and green roofs for urban areas for example). The positive change did not affect all populations equally. Some were able to experience far greater change in resistance from the change while others experienced little (fourth number in equation). For all ecosystem groupings the positive change that the ecosystem groupings went through improved their overall resistance score (original resistance score first number, sum of equation is new resistance score) (Fig. 3).

In the third key result, the disease travels from the point of origin to the next area with the least resistance for most ecosystem groupings. However, based upon the time passed since a neighboring population was introduced to the disease and how far the disease has spread, divergence from the norm of trajectory is encountered (grey arrows). Based upon the resistance score of both areas the disease may be temporarily wavered from entering the ecosystem grouping, however over time the disease is likely to enter. The amount of time that the ecosystem grouping is able to ward off the disease depends on the overall resistance score, the adaptability of the disease, among other factors. It is more likely that the disease comes from a neighboring community that was affected first rather than one that was affected later. This means, for example, agriculture is transmitting the disease to both the forest and agriculture in both examples instead of the urban area. If the disease does not enter either of the ecosystem groupings over time an environmental boundary for the disease is able to be determined. An example of an environmental boundary would be a disease from a temperate area not being able to enter a tropical forest. These boundaries are able to be determined through reports of cases of a disease and distribution patterns (Howard and Fletcher, 2012; Peterson, 2008; Seabloom et al., 2013; Usme-Ciro et al., 2012) (Fig. 3).

3.4. Change in resistance levels from incorporating population change

For deriving the fourth key result, we assume that all ecosystem groupings underwent a change in population that affected them negatively (urbanization, increased influx of people, etc.). The rates of change in the areas analyzed as well as the timeframe by which the change happened were different. Again, not all areas experienced this change the same way. Each part of the equation contributes to our perspective of the vulnerability of the population and the possible transmission route. The past example two possible areas where the disease was potentially warded off can be identified. By incorporating the population change it is now clear that both areas are likely to be affected through a standard transmission route (travels to the next least resistant). The transmission route and thus the timing from which various ecosystem groups might be affected by the disease is now different as well. For example, in the past figure the agriculture, second to the left on the top, was the third ecosystem group affected (following the transmission line) in this example it is the 8th (Fig. 4).
4. Discussion

The way in which an environmental feature affects health varies based upon location and the rest of the environmental variables experienced. Take a population living in a forest (i.e., the environmental feature) as an example. If the forest also had high levels of precipitation and tropical temperature the population living in this area would depend differently on that forest for their health as compared to a forest with low levels of precipitation and temperature. It is known that these two ecosystems provide different levels of ecosystem services, which affects health (Del Grosso et al., 2008).

The farther away a population is from a large amount of biomass (say a forest) the less resources (ecosystem services) they are able to experience and use (Bagstad et al., 2013). However, the migration to urban centers of rural populations is present throughout the world. By migrating to these areas populations gain better access to life supporting infrastructure such as hospitals. So even though the health supporting resources (ecosystem services) are higher in rural areas (forests), the life support infrastructure is greater when living in urban areas. Both of these components affect the health of a population. There are many ways to enhance the health of urban populations, one of the ways is by increasing the amount of biomass present in cities (green roofs, sidewalks lined with trees, urban gardens, etc.) and thus the levels of resources (ecosystem services) provided (Hunter et al., 2019).

Our world is ever changing, and the change that we experience affects our health. Seasonality has long been noted as one such change that affects our health, i.e., flu season (Buonomo et al., 2018). For population levels, if a population were to grow by a large amount in size over a short time frame the shock to the preexisting population from losing resources (ecosystem services) to newcomers will be greater than that if a population were to grow by a large amount over a long-time frame (Raskin, 1995). The rate and quantity of change in environmental features and populations are harder to monitor but are a data source that should be included in a monitoring system in order to see a more complete picture. This was exemplified in the mathematical framework we presented in this paper with how incorporating changes in environmental features and population levels changed the likely transmission route of a threat to human health.

Using environmental features to identify vulnerable populations we can start to see on a large landscape level where the vulnerable populations are. When we have established where vulnerable populations are, we can start to predict the likely travel trajectory for a threat to human health when it spreads across a community. As we monitor different threats to health it is likely that we will find barriers that these threats are not able to transfer across, or are only able to transfer across through mutation (Ma et al., 2016). One example of such a barrier, is for many tropical diseases not being able to transfer to temperate areas with colder temperatures, however climate change is making this easier. When these barriers are found in a transmission route we can start to define where likely environmental niches are for these threats. If an environmental niche is able to be established it will help to determine where effective areas to implement intervention techniques are. At the same time as the threat to health spreads, areas to implement intervention strategies (for example closing of the transportation route) will become clear (Mandal et al., 2020).

Environmental data is readily available for the public at fine scales. Two data sources that could have been used for the theoretical landscapes presented in this paper are land cover data and population count (Gong et al., 2019; Leyk et al., 2019). In order to relate some environmental feature data to health responses the environmental data might need to be transformed, through logarithmic or other transformation. When this framework is applied, we will come to a closer understanding of how population health is dependent on various environmental features. The application of this framework could help to create a monitoring system with easily understood imagery, heatmaps, of where vulnerable populations are (Fig. 5). The total amount of vulnerable population estimated for an area can be useful for determining vaccine distribution. It is crucial that we start to use the data that is already available to us to better understand threats to population health. When we better understand the relationship of health to the environment, perhaps, we will start treating the environment in a more just and sustainable manner.

Environmental features are a great starting point for this monitoring system but it is not the end for the data that should be incorporated into a monitoring system. As available and able, other data should be included including social indicators of health, travel routes of populations (including migration corridors and roads), among others. Contact tracing of social networks was useful in the COVID-19 pandemic and is one such data source that should be included into a monitoring system (Ahmed et al., 2020).

Although the framework presented could be carried out for the entire world in one run through, when splitting up the analysis into smaller distinct regions more accurate results are able to be produced. These smaller distinct regions help us to realize the variation of dependency for these different environmental features on health.

Over time as we use environmental data to monitor population health, we will increase our understanding of how distinct environmental features affect health across different ecosystems. The more we are able to understand about the influence of environmental features on health, the more accurate the identification of vulnerable communities will become for a specific threat to our health. When an emerging infectious disease arises, we can use what we already know from monitoring the relationship of environmental features to health and develop a monitoring system specified to that emerging infectious disease. By constantly monitoring population health we can start to implement and quantify the effectiveness of intervention techniques that may increase the resistance of a population to threats to their health. These techniques could include sustainable management of an area (reforestation, wetland restoration), preemptive healthcare (vaccination, preemptive drug placement, etc.) or educating the population as to potential health hazards (vectors, high risk areas, etc.).

5. Conclusion

Ever since humans changed from hunter gatherers to agriculturalists, around 12,000 years ago, we have been decreasing ecosystem services globally. This change also brought with it a change of forests being our natural habitat to human modified environments. Though there have been many advantages to this lifestyle switch, the threats made to our life by new illnesses arising from our treatment of the environment is not one. We have changed the environment so much that the emergence of previously unknown infectious diseases is now almost inevitable (Morens and Fauci, 2020). Our continued alterations of the environment come with more and more extreme repercussions; science and technology (medications, infrastructure, etc.) may remedy some of these repercussions but it will not be able to resolve all of them. By properly understanding and valuing our ecosystems we can start an effective strategy for the control and mitigation of infectious disease (Daily and Ehrlich, 1996).

The mathematical framework presented in this paper is a robust approach to assessing ecosystems effects on human health. This framework has few data needs, is applicable in a global context, and has a faster processing time than running production functions for every ecosystem service individually.

As this framework is able to use as little as one environmental feature and population data to determine vulnerable populations, it is suitable for even the most data sparse areas. In countries where socioeconomic, demographic and other information usually used to measure vulnerability of populations in nonexistent or unreliable, using environmental information will strengthen healthcare responses greater than previously possible. In developed countries where traditional sources of vulnerability information are readily available, incorporating environmental
information will strengthen our understanding of how the environment affects our health. This is especially useful for emerging infectious diseases that have little information about what ecosystem service could be affecting the resistance of the populations and outbreak levels as well as what social determinants of health impact the resistance of the population.

By having little data needs, change over time is easily incorporated. This is especially important in the analysis of future health affects where there is great uncertainty and little available information of how environmental features or the ecosystem services provided by them might change.

The application of this framework is useful for the identification of transmission pathways and measuring vulnerability of populations to various diseases. Enhanced understanding of how the environment affects human health will be established after each application of this framework for a disease. As emerging infectious diseases are unlikely to cease in the future, this framework will help everyone to prepare for what is ahead.

CRediT authorship contribution statement

Thomas Ryan Vernon Price: Conceptualization, Methodology, Investigation, Writing – original draft, Visualization. Sepul Kanti Barua: Writing – review & editing, Supervision.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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