Earthquakes and Floods have been the Most Damaging Natural Disasters in the Past

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Editorial

We really wanted to make sure that we represented the diversity of work on planning and forecasting for large-scale emergencies when soliciting and choosing articles for this issue. Disasters threaten all societies, anywhere in the world, but disaster management is organised differently in different countries and even different areas of the same country. As a result, we wanted to make sure that our work covered a wide range of countries, which we do, including Australia, Cyprus, Finland, Israel, Italy, Malaysia, Romania, Spain, and the United Kingdom, as well as the United States. Second, rather than merely academics, we wanted to include the opinions of actual managers and practitioners; two of the articles chosen are case studies by practitioners. Finally, we wanted ssto include a wide range of research approaches, so we have papers based on case studies, unstructured interviews, coding and statistical analysis of literature review results, surveys, and modelling. We can understand why failures and errors occurred, as well as what we can do to enhance all phases of emergency response.

The theories of behaviour for High Reliability Organizations, as well as the associated suggested "Science of Muddling Through," emphasise the importance of those organisations seeking out and exposing any errors or harm they cause so that they can be corrected in order to better handle future emergencies. Unfortunately, most firms do not see the need to assess and improve past catastrophe preparation and response performance. There is increasing concern about public perceptions, liability issues, and political ramifications. We have the potential to learn from tragedies that showed clear shortcomings in response by studying them and are needed to improve planning and response. Turner's framework is used in both of these case studies. Turner looked at 84 official accidents. Related reports issued over an eleven-year period by the government of the United Kingdom In the intervals; he shows out that there is a degradation of time between significant similar tragedies. The main cause of death is a lack of knowledge and preparation.

The next time a similar event occurs, there will be a weak response. His the six-stage disaster paradigm is really useful. for leading an investigation into the root causes of ill health a lack of planning and vision, as well as the ensuing bad performance a reaction. It is simple to see how these two situations are related when one reads them. to demonstrate how four significant disaster response failures in recent years can be linked can be readily included into the same framework. The Turner framework helps to reveal many of the root reasons of "foresight failures". In the average "official report," this is rarely stated explicitly. Either in the past or in the present two summary tables are provided. From the Turner paper, which provides a brief review of the subject framework, which is applicable to a large range of different topics In this collection, there are writings that are consistent with particular points was created. The absence

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of one important trait throughout the incubation stage is the incompatibility of goals and objectives. For a large number of recent disasters The reduction in maintenance can be identified. Costs, limiting infrastructure investment, and other measures that can save money or increase profits in the short term but this decreases safety and raise risk.

Methods for determining a gene's locus and the distances between genes are referred to as gene mapping. The distances between distinct places inside a gene can also be described via gene mapping. The goal of all genome mapping is to place a collection of molecular markers on the genome in their proper locations. Molecular markers come in a variety of shapes and sizes. Genes can be thought of as a special form of genetic marker that can be mapped in the same way as any other marker in the development of genome maps. In the field of genome mapping, there are two sorts of "Maps": genetic maps and physical maps. While both maps are made up of genetic markers and gene loci, genetic maps employ genetic linkage information to calculate distances, whereas physical maps use real physical distances, which are commonly measured in base pairs. While the physical map may be a more "accurate" representation of the genome, genetic maps can reveal a lot about the nature of different chromosome regions. For example, the genetic distance to physical distance ratio varies a lot at different genomic regions, reflecting different recombination rates, which is often indicative of euchromatic (usually gene-rich) vs heterochromatic (usually gene-poor) regions of the genome.

Researchers start a genetic map by taking blood, saliva, or tissue samples from family members who have a conspicuous disease or trait and those who don't. Saliva is the most commonly utilised sample in gene mapping, particularly in personal genomic studies. Scientists then isolate DNA from the samples and examine it closely, seeking for patterns in the DNA of family members who do carry the disease that aren't present in the DNA of those who don't. Polymorphisms, or markers, are the names given to these distinct molecular patterns in DNA. The development of genetic markers and a mapping population are the first steps in creating a genetic map. The closer two markers are on the chromosome, the more probable they will be passed down in the same generation. As a result, all markers' "co-segregation" patterns can be used to rebuild their order. Keeping this in mind, the genotypes of each genetic marker are recorded for both parents and subsequent generations of individuals.

The number of genetic markers on the map and the size of the mapping population are two parameters that influence the quality of genetic maps. The two aspects are connected, as a greater mapping population might boost the map's "resolution" and keep it from being "saturated." Any sequence feature that can be reliably identified from the two parents can be utilised as a genetic marker in gene mapping. In this case, genes are represented as "traits" that can be accurately differentiated between two parents. The actual gene loci are then bracketed in a region between the two nearest nearby markers, as if they were common markers. The approach is then repeated by looking at other markers that target that region in order to map the gene neighbourhood to a higher precision and eventually identify a single causal locus. This technique is known as "positional cloning," and it is widely utilised in the study of plant species. Maize is one plant species in which positional cloning is used extensively. Genetic mapping has the advantage of being able to determine the relative position of genes merely based on their phenotypic effect [1-5].

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Conflict of Interest

The Author declares there is no conflict of interest associated with this manuscript.

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