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Climate science

Marine heatwaves reliably forecast by climate models

Markus G. Donat

Climate models can provide accurate seasonal forecasts of unusually warm ocean temperatures, enabling the models' predictions to guide decisions made by stakeholders in the marine industries and conservation. **See p.486**

Prolonged periods of anomalously warm ocean temperatures, known as marine heatwaves, can severely affect marine ecosystems, as well as industries such as fisheries and tourism. On page 486, Jacox *et al.*[1] report that these extreme events can be predicted several months into the future, offering valuable information for marine stakeholders seeking to mitigate such effects – or to benefit from them.

The frequency and duration of marine heatwaves have increased globally over the past century[2], and further increases are expected as Earth's climate continues to warm[3]. Such long-term changes will require suitable adaptation and mitigation measures, but marine heatwaves are also affected by climatic variations between one season or year and the next. Predicting these short-term effects could aid operational decisions to manage their impact. For fisheries, for example, this could mean protecting populations from being overfished when heatwaves reduce productivity, or preparing to harvest more when productivity is enhanced.

Seasonal climate predictions are made using numerical models that represent our understanding of the physical climate system consisting of the atmosphere, ocean, sea ice and land surface, and the interactions between those components. Simulations of such models typically start from our best estimate of the present climate state and forecast plausible climate trajectories for the coming months[4]. These simulations can be used to compute the probability that a marine heatwave will occur.

Such seasonal predictions are now provided on a regular basis by a number of forecasting centres around the world. These centres also produce large sets of retrospective forecasts, which are initialized from conditions in the past. By comparing retrospective forecasts with past observations, researchers can assess the quality of the predictions, and determine to what extent they provide trustworthy information.

Jacox *et al.* used a collection of retrospective seasonal climate predictions (made with multiple models)[5] to analyse the occurrence of anomalously warm ocean surface temperatures, and to calculate the accuracy with which they can be predicted. They defined marine heatwaves as events in which monthly average sea surface temperatures were in the warmest 10% of those recorded between 1991 to 2020, taking into account seasonality and location.

Their analysis shows that the occurrence of marine heatwaves can be predicted up to four months in advance with high forecasting 'skill' (a metric that quantifies the quality of a forecast, including its accuracy and reliability) for large areas of the global ocean (Fig. 1). The predicted duration of these heatwaves is also closely correlated with their observed duration. In some regions affected by large-scale climate modes, such as the El Niño–Southern Oscillation, in which the surface waters of the tropical Pacific Ocean periodically warm and cool[6], marine heatwaves can be predicted with even longer lead times, of up to 12 months.

The ability to make skilful forecasts of marine heatwaves on the basis of existing prediction systems is good news for climate scientists and model developers, because it provides evidence that such systems are accurate to some extent. But can the predictions be used to guide decisions in other areas of research and industry? The answer depends on the relative needs of the user – including their tolerance to the risk of marine heatwaves and the cost and probable impact of evasive action.

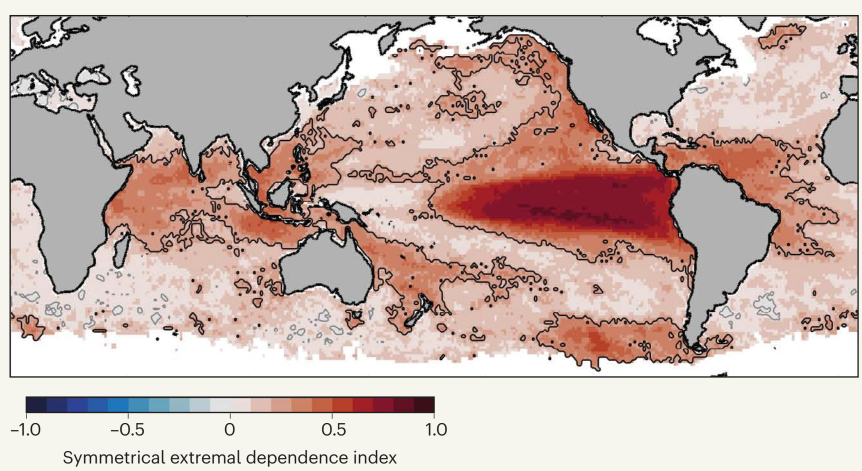

Figure 1 | Predicting marine heatwaves using seasonal climate forecasts. Jacox *et al.*[1] made predictions for prolonged periods of unusually warm ocean temperatures (marine heatwaves) using seasonal prediction models that simulate the climate several months into the future. The authors' predictions were accurate for large areas of the global ocean, as shown by a measure known as the symmetrical extremal dependence index, which varies between −1 for poor forecasts and 1 for perfectly accurate forecasts, with a positive index indicating that the prediction is better than one made by chance. The predictions evaluated here are for forecast times 3.5 months into the future. (Adapted from Fig. 1b of ref. 1.)

As the authors point out, users with a high tolerance to the risks involved might wish to avoid action, taking into account the possibility that a predicted marine heatwave might not occur. Those with lower risk tolerance might prefer to take action even when the probability of a marine heatwave occurring is low. The most suitable decision threshold will be user specific and will depend on balancing the cost of action with the cost of potential loss or damage in the case of inaction.

Aside from minimizing the effect of false positives and false negatives depending on a user's risk profile, there are other factors to consider when using such forecasts. Climate predictions are not perfect, and even if they are deemed to be skilful, they will sometimes be wrong. Consequently, users who strictly follow these predictions will make a wrong decision in some cases, but they should benefit in the longer term from receiving correct information more often than incorrect information. Users must therefore understand how accurate the predictions need to be to make them trustworthy enough to underpin decisions — as well as considering the critical forecast probability that should trigger action, on the basis of users' risk profiles. Both thresholds will probably differ between users.

Information from such predictions can be further optimized by identifying time periods or conditions (sometimes referred to as windows of opportunity) in which a prediction is regarded as more accurate than it is under other conditions[7]. Strategically targeting such periods when incorporating predictions into the decision-making process could further increase the predictions' usefulness. Jacox and colleagues' results suggest that the El Niño–Southern Oscillation modulates the forecasting skill of predictions, with marine heatwaves being more accurately predicted in large areas of the globe during the warm (El Niño) and cool (La Niña) phases of the oscillation, as opposed to during neutral phases.

There are also prospects for skilful predictions of marine heatwaves on longer timescales: previous studies have shown that climate forecasts for multiple years or even a decade can predict slowly varying ocean surface temperatures[8,9]. Marine-heatwave predictions could be further refined by taking the severity of events into account[10], because different heatwave intensities might have varied effects on users of the prediction, or require different actions to be taken.

In addition to improving the prediction systems further, future research should understand the specific needs of stakeholders in order to develop tailored forecast products that address these needs. This will further enhance the ability of predictions to aid decision-making — thereby increasing the resilience of communities that depend on marine resources.

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Psychiatric genetics

Origins of schizophrenia find common ground

Conrad O. Iyegbe & Paul F. O'Reilly

Two differing approaches that are used to study common and rare genetic causes of schizophrenia reveal convergent clues about the biology underlying this complex disorder. **See p.502 & p.509**

There has long been debate about whether the genetic component of complex disorders, such as schizophrenia, is attributable mainly to rare or common DNA variants[1]. Two studies in *Nature* now provide evidence for key roles of both types of variant. In the first study, Trubetskoy *et al.*[2] (page 502) identified hundreds of common genetic variants that each have a tiny influence on schizophrenia risk. By contrast, in the second, Singh *et al.*[3] (page 509) discovered a handful of rare variants, each of which have a large effect. Together, these studies show that common and rare genetic causes of illness might often disrupt the same biological processes that lead to disease.

Genome-wide association studies (GWASs), which analyse the differences in people's DNA to identify common variants linked to a disease or trait, are now so commonplace that practitioners don't flinch at studies of hundreds of thousands of people in which hundreds of genetic variants are associated with a disease. They know the drill: increase the sample size and the genetic hits will pour in. Even so, few scientific teams have such a finely tuned pipeline as the Psychiatric Genomics Consortium (whose members co-authored the first of the current papers), one that has produced a bounty of hits for 13 neuropsychiatric disorders[4–6].

Critics of GWASs — and there are plenty — point out that common genetic variants typically have minuscule effects on disease risk, and highlight the difficulty of deciphering biological effects from hundreds of risk variants of disparate function, scattered across the genome. But then, life probably didn't evolve for millions of years only to be decoded in the course of a five-year research grant. Judging from Trubetskoy and colleagues' current study, the patient, meticulous work of GWAS researchers is starting to reap rewards.

Trubetskoy *et al.* studied the genomes of 76,755 people with schizophrenia and 243,649 healthy control participants. Their analysis revealed 342 common genetic variants that can increase the risk of schizophrenia. Although each variant increases the risk by only a small amount (less than 5%), the many risk variants identified allowed the authors to gain insights into the biological processes that these variants modify.

In one key analysis, Trubetskoy *et al.* established the tissues and cell types in which the newly identified risk variants are most biologically active. Reassuringly, the genes are most highly expressed in brain tissue. Although this might seem obvious for schizophrenia, the consortium demonstrated that it is the increased size of its GWAS data sets — from big studies published in 2011 (ref. 7) and 2014 (ref. 8), to its massive one today — that has allowed these biological signatures to emerge from the tiny genetic effects involved. The consortium then further leveraged this power gain by zooming in to the cellular level, revealing the three neuronal-cell subtypes (pyramidal, medium spiny and granule) that are most closely associated with schizophrenia risk.

GWASs highlight regions of the genome that