# Correspondence

#### Earth-observation data must stay free

US President Donald Trump's administration is considering whether to charge for access to Earth-observation data (*Nature* **556**, 417–418; 2018). As former director of the Group on Earth Observations (GEO), I urge the US government not to falter in its global leadership in opendata policies or to dismiss the importance of their worldwide benefits, particularly for the United States.

As you point out, this would not be the first time that the United States has charged for Landsat satellite data. Until 2008, it used a cost-of-fulfilling-userrequests model, bringing in about US\$4.5 million annually. The largest purchaser of data was the federal government itself, so its net profit was negligible. Meanwhile, external research and innovation withered.

Once replaced by an openaccess policy, economic returns followed: in 2011, for example, these were \$1.7 billion for the United States and \$400 million for other countries, bringing the global total to \$2.1 billion. Today, there are more than 400 million international open Earth-observation data and information resources (see www. geoportal.org).

We must remain committed to keeping Earth-observation data — collected at taxpayers' expense — freely and readily available to inform policy decisions, including those called for in the Sendai Framework for Disaster Risk Reduction, the United Nations 2030 Agenda for Sustainable Development and the Paris climate agreement. **Barbara J. Ryan** Bonita Springs, Florida, USA. bjrgeneva@gmail.com

### Predict trajectory, not emergence

It is important to distinguish between predicting the emergence of infectious diseases and their trajectory (see E. C. Holmes *et al. Nature* **558**, 180–182; 2018). It is currently impossible to predict emergence, but feasible and effective to predict the trajectory.

For example, modelling of established outbreaks was important for responding to those caused by the Ebola, Zika, H1N1 influenza and severe acute respiratory syndrome (SARS) viruses. It helped decisionmakers to plan bed capacity (M. I. Meltzer *et al.* MMWR Morb. Mortal. Wkly Rep. **65**, 85–89; 2016), anticipate travel-related spread (I. I. Bogoch *et al.* Lancet **385**, 29–35; 2015) and plan vaccine trials (A. Camacho *et al.* Vaccine **35**, 544–551; 2017).

Several US government agencies maintain such capabilities, including the Centers for Disease Control and Prevention, and the **Biomedical Advanced Research** and Development Authority. And the White House Office of Science and Technology Policy published a report in 2016 that identified epidemic prediction and forecasting as a crucial tool in outbreak preparedness and response (see go.nature. com/2ubIwjt). Caitlin M. Rivers Johns Hopkins Center for Health Security, Baltimore, Maryland, USA. Samuel V. Scarpino Network Science Institute, Northeastern University, Boston, Massachusetts, USA. crivers6@jhu.edu

# Biomedical success on the cheap

A handful of science students at Bellevue College, a small community institution in the United States, have pioneered their own training in biomedical research methods — with no wet lab facilities and on a minimal budget.

Our group identified a promising project by tapping into advances in computational analysis and the vast, readily accessible amounts of genomics data. We decided to search for viral protein sequences that could be important for tissue tropism.

Human pathogenic viruses were classified according to the tissue they infect (pulmonary, gastrointestinal, and so on) — irrespective of whether they were enveloped or non-enveloped RNA or DNA viruses. The students majoring in computer science developed programs to speed up proteinsequence comparisons and alignments in each category. The biologists identified consensus protein domains.

Within a month, the students had localized a consensus amino-acid sequence on the adherence spikes of the chikungunya virus (CHIKV). A literature search revealed that this sequence is responsible for binding to a receptor on human cells and infecting them (R. Zhang et al. Nature 557, 570-574; 2018). They then came up with the idea that this domain could be used as an antigen for producing a vaccine against CHIKV. Clinical trials of virus-like particles are ongoing (see go.nature. com/2nzgvpw and go.nature. com/2lhwjrh).

It is heartening that a group of young scientists in a community institution, who had never before heard of CHIKV, achieved so much as a result of their curiosity and motivation.

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## Health-care impacts of web shutdowns

Governments in Africa, Asia and the Middle East are increasingly shutting down the Internet as a blunt response to threatening situations such as political unrest (see go.nature. com/2msruv2). We call on inter- and non-governmental organizations to put pressure on governments to evaluate the potentially devastating effects of this tactic on health care.

In Cameroon, for example, the government cut off the Internet for three months last year. This disrupted crucial services such as the GiftedMom smartphone app, which connects rural mothers with physicians and guides them through infant vaccinations, in a country where children are almost twice as likely as the global average to die before their fifth birthday.

Furthermore, Cameroon was unable to submit 85% of its health-performance data to the District Health Information System data set DHIS2, which is used to guide funding decisions. Health workers received only partial pay because they could not report their progress to the World Bank's performance-based financing system.

Yet no empirical research exists for the health impacts of such shutdowns. We need to know, for example, the risks they pose to emergency services and to funding for Internet-enabled medicine. Policymakers must have comprehensive data on interruptions to online services if health outcomes in the developing world are to be improved.

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#### **CONTRIBUTIONS**

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