| SCIENCE |

How a cloud-based database can help diagnose illnesses

ZYMA ISLAM

During the chikungunya outbreak of 2017, children kept turning up at the Dhaka Shishu Hospital—with meningitis.

At first glance, there is no reason to think that the two might be related.

Meningitis is a disease in which the membrane that envelops the brain and spinal cord, protecting them, becomes inflamed. In this country, it is caused by a number of bacteria including *meningococcus* and *pneumococcus* and on the rare occasion, *Haemophilus influenzae* or Hib for short. A regimen of antibiotics at the right time is usually enough to treat these symptoms, and meningitis is no longer a main cause of fatality in children.

But the children who showed up all tested negative for the above-mentioned bacteria, meaning they were not responding to the treatment either—and meningitis, left untreated, can cause brain damage, or even prove fatal.

"I needed to do metagenomic sequencing to find out what exactly was causing the meningitis," says Dr Senjuti Saha, a microbiologist at the hospital and also a postdoctoral fellow shared between Stanford University, and a domestic research outfit called the Child Health Research Foundation.

Metagenomic sequencing is a process where Dr Saha would take the cerebrospinal fluid found in the patient's brain and spinal cord and separate out all the genetic material. By deconstructing the fluid to its smallest most basic components (the RNA or DNA), she would be able to detect what is causing the meningitis.

There were several major barriers to doing this. "One problem is that no hospital in this country does metagenomic sequencing as a routine part of their diagnosis so a sequencer is hard to find," she says.

The other problem was perhaps the bigger one—even if she did manage to

sequence it, how would she recognise the microbe just by looking at its genetic material? She would need to compare the sequence to a database containing sequences of all microbes to find a match, and currently no such database exists in a data-desert like Bangladesh.

It was then that a cloud-based online database called "IDseq" came into the picture.

IDseq is a platform containing sequence databases created by two research foundations owned by Facebook founder Mark Zuckerberg and his wife, philanthropist Priscilla Chan.

"The database contains a vast collection of sequences of pathogens. Doctors can upload their own sequences and then compare them against the existing ones in the database to find out matches," explains Dr Saha.

That is exactly what she did with the meningitis samples. She sequenced all the

A cloud-based database of metagenomic sequences can help doctors like Senjuti Saha identify unknown diseases
PHOTO: **KAZI TAHSIN AGAZ APURBO**
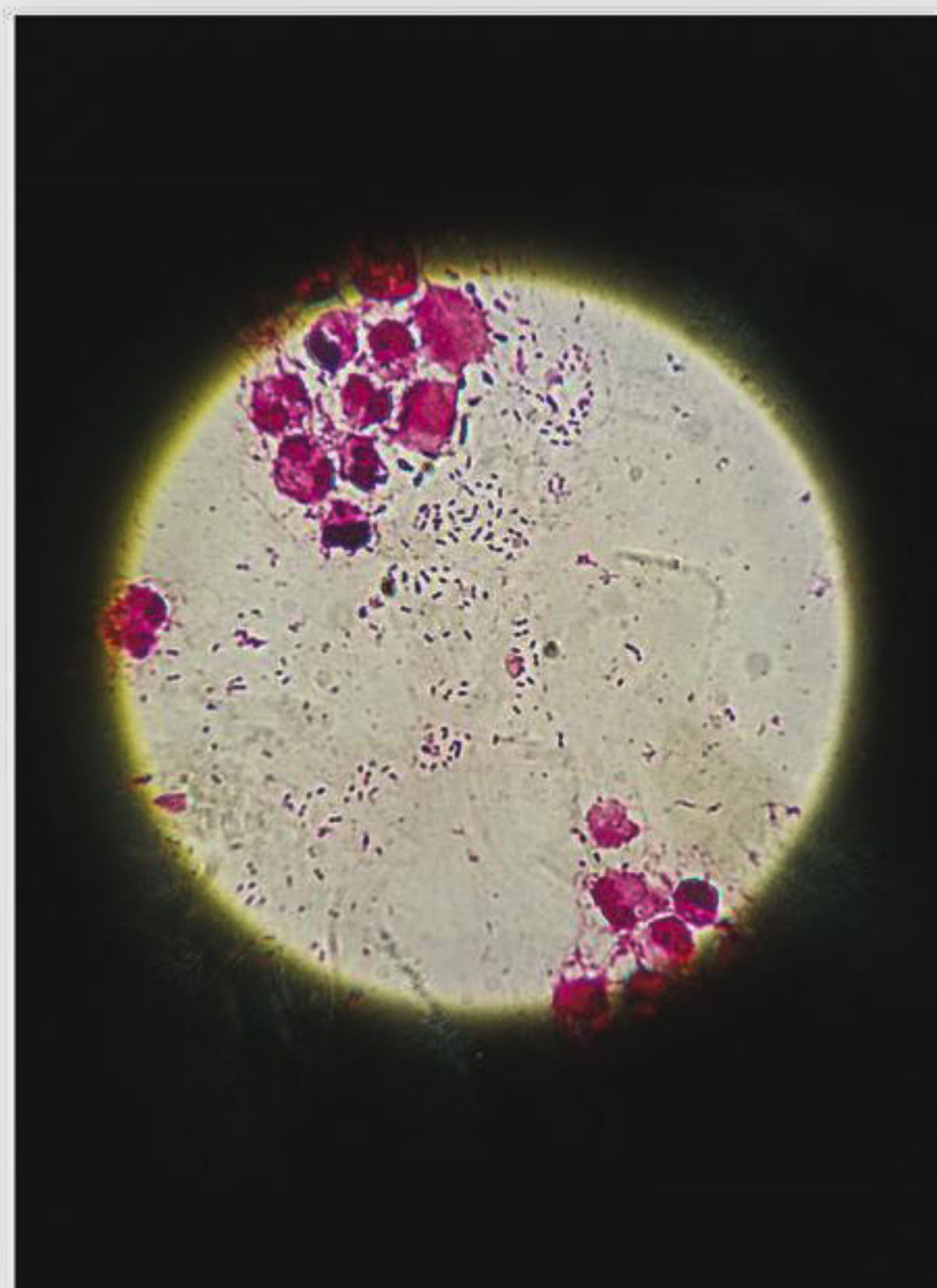
A slide showing a common form of meningitis caused by pneumococcus

genetic material of the cerebrospinal fluid samples, then loaded them on a hard disk and sent it to the database's headquarters in USA.
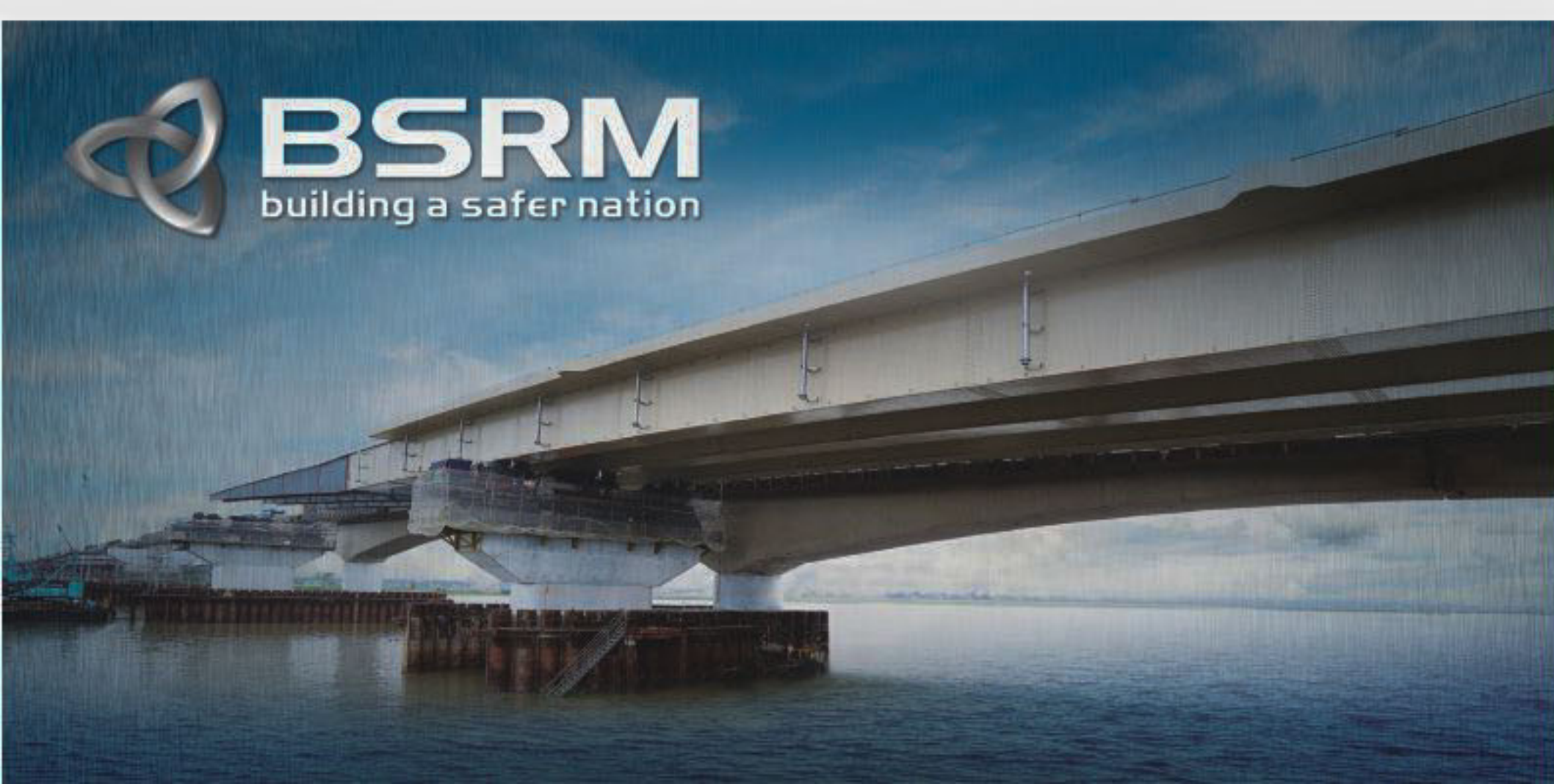
"Their database subtracted human genetic material (like the fluid's own) from the samples and isolated the pathogen. Then it ran the sequence of the pathogen against the many in its database to identify what it is," describes Dr Saha.

And the result? Chikungunya virus.

"The database found that the chikungunya virus was causing a large proportion of the meningitis—and this also made sense since the patients came in at the same time as when the chikungunya outbreak was happening," she says.

This revelation adds more knowledge to the baffling illness that has swept over towns and cities during