

## Not so sunny weather: When currents go bad

On Aug. 4, 1972, a surge of electricity raced down a telephone cable in the midwestern United States, temporarily snarling long-distance phone service. Nearly 3 decades later, two Canadian scientists report that they have nabbed the culprit in that case and, in the process, have illuminated a dark side of the sun's influence on Earth.

Space physicists have long suspected that solar disturbances played a role in the phone crisis, but they thought that the problem lay 30,000 kilometers above Earth's surface, where the solar wind plows into Earth's protective magnetic shield. The new study indicates the trouble resided much closer to the planet, only 100 km above northern Canada, in a region of the sky called the ionosphere.

As the sun gears up for a new round of turmoil over the next 2 years, the Canadian study can help scientists and engineers plan for emergencies. "This gives us a better understanding of the type of event that causes problems on the ground," says David H. Boteler of the Geological Survey of Canada in Ottawa, Ontario. He and his colleague G. Jansen van Beek describe their work in the March 1 *GEOPHYSICAL RESEARCH LETTERS*.

Every second, on average, the sun spits out 1 million tons of electrons, protons, and denser matter. As that solar wind approaches Earth, it gets deflected by the planet's geomagnetic field and wraps around the backside of Earth, much like air streaming around a car. The boundary separating Earth's magnetic sphere of influence from the solar wind is called the magnetopause.

During so-called solar storms, the sun jettisons blobs of matter and magnetic energy that are faster and denser than usual. When these crash into Earth's magnetosphere, they push the magnetopause inward, sometimes quite dramatically (SN: 2/1/97, p. 68).

The 1972 phone-cable problem occurred at about the same time that a solar storm dented the magnetopause, leading investigators then to link the two events. Researchers concluded that electrical currents in the magnetopause induced harmful currents in the long-distance phone line.

Boteler and van Beek revisited that event after studying problems caused by solar storms in 1989, which caused power outages in Quebec and electrical malfunctions along the U.S. East Coast. They realized that some of the 1989 disturbances resulted when the storms caused a sudden intensification of electric currents that run eastward in Earth's ionosphere. In the past, researchers have thought these currents incapable of building so abruptly.

To resolve what happened in 1972, Boteler and van Beek calculated the ex-

pected effects of currents in the magnetopause and the ionosphere. Magnetopause currents, because they are so high, should have caused disturbances across the entire Earth—a pattern that does not match the data, the researchers report. Currents in the ionosphere, however, should disrupt a smaller region, which matches the observations.

The new interpretation has won over Louis J. Lanzerotti of Lucent Technologies' Bell Labs in Murray Hill, N.J., one of the authors of the original study implicating the magnetopause. "It says something about how much we've learned

about Earth and space characteristics," he says.

Solar storms are most frequent when the sun reaches the most active part of its 11-year-long cycle. Such a peak is expected next year. When they hit, these storms can damage satellites, hinder radio communications, and set up currents in power lines, telephone cables, and pipelines. Engineers are developing ways to lessen solar-storm damage.

"Trying to figure out what caused that particular outage in 1972 is important for making sure it doesn't happen again," says JoAnn C. Joselyn of the National Oceanic and Atmospheric Administration's Space Environment Center in Boulder, Colo. —R. Monastersky

## Simulations nab protein-folding mistakes

The human body manufactures thousands of different proteins, which act as enzymes, structural elements, or carriers. Each protein starts out as a long strand that must fold itself into the proper shape to perform its specific function.

To gain insights into the folding process, researchers have developed mathematical models that attempt to capture how a single strand rapidly collapses into its correct configuration (SN: 5/9/98, p. 296). New computer simulations now reveal how one protein strand can interfere with the folding of another.

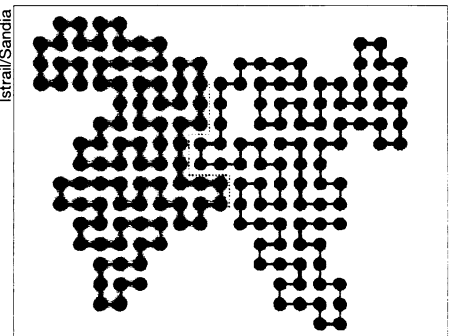
"This is a step toward successful protein engineering," says computer scientist Sorin Istrail of the Sandia National Laboratories in Albuquerque. "It provides our first clue in how to design sequences of laboratory proteins that can survive the essential but complicated folding process."

The results could also help laboratory scientists understand the mechanisms underlying protein-folding mistakes, which are implicated in Alzheimer's disease (SN: 7/4/98, p. 4) and other maladies.

Istrail and his collaborators, biologist Jonathan A. King and computer scientist Russell Schwartz of the Massachusetts Institute of Technology, report their findings in an upcoming *JOURNAL OF COMPUTATIONAL BIOLOGY*.

Each protein is a string of amino acids spelling out a characteristic sequence. Scientists divide the 20 distinct amino acids into two groups according to whether they attract or repel water molecules, the main constituent of cells. Those interactions drive protein folding, creating globular structures in which water-repelling amino acids end up on the inside and water-attracting ones on the outside.

A simple model portrays a protein as a stiff but jointed structure, made of two types of beads, that can snap into a few positions at each joint. Because of the huge number of different folding possibilities for even a short strand, however, simulating the process on a computer



In this computer simulation, two protein strands have linked (along dashed line) to create a misconfigured lump. The blue beads are water-attracting amino acids, and the red beads are water-repelling.

has proved difficult.

Moreover, protein strands in cells have many jostling neighbors, King notes. Two partially folded protein molecules may end up sticking together.

To capture that additional complication, Istrail and his coworkers started with a well-studied, jointed-structure model originally developed by Ken Dill of the University of California, San Francisco. Taking advantage of Sandia's powerful computers (SN: 7/5/97, p. 5), the researchers examined what happens when strands move about and bump into each other.

Although the specific amino acid sequence determines the protein's function, the location of water-attracting components appears to be random. By tracking two highly simplified protein chains interacting on a grid, Istrail and his coworkers showed that this irregular arrangement plays an important role in preventing water-repelling units from binding to those of another strand.

A protein with an ordered distribution of water-attracting units tends to aggregate with other proteins to form an inert lump, Istrail says. Random positioning appears necessary to keep different strands apart, allowing the formation of the correct folds. —I. Peterson