Folding@home's fight against COVID-19 enlists big tech, gamers, and pro soccer

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The crowdsourced supercomputing project Folding@home harnesses the combined processing power of computers whose owners download the project's software and run simulations to model protein motion. In

response to COVID-19, individuals, universities and companies have joined the effort. In the video, new simulations already have modeled how the coronavirus' spike protein opens up to bind to the ACE2 receptor—found on the surface of many human cells—and causes infection.

When the crowdsourced supercomputing project Folding@home first announced a shift to coronavirus research and asked for new volunteers to run its software and expand its computing capacity, organizations and citizen scientists from all walks of life heeded the call. Now, about four months later, the number of volunteers has increased a hundredfold.

Based at Washington University School of Medicine in St. Louis, the computing project simulates the movements—or folding—of proteins involved in disease. Researchers leading the effort pivoted quickly to COVID-19 and found a wealth of people eager to help. Before the switch to the novel coronavirus, about 30,000 devices were running Folding@home software. With the prospect of contributing to coronavirus research, new volunteer "folders" have boosted that number to over 4 million to date, with major companies and organizations eager to donate their own computing resources to the cause.

Organizations and technology companies such as Microsoft, Avast, Amazon Web Services, Pure Storage, AMD (Advanced Micro Devices), VMware, Cisco and Oracle are all supporting the project. Microsoft's AI (artificial intelligence) for Health initiative has donated computing space in Microsoft Azure, the company's cloud computing system. Other contributors include CERN, the European Organization for Nuclear Research, which runs the Large Hadron Collider, the world's most powerful particle accelerator.

Many of the companies lending support are involved with computer technology, including those that make graphics cards for video gaming,

antivirus software and cloud computing systems. But even pro sports have jumped in to help. La Liga, the Spanish professional soccer league, shifted the use of its supercomputer from a focus on catching illegal broadcasts of games—the league's soccer matches were halted during the peak of the pandemic—to a focus on protein folding.

"We've got an incredible community—here and out in the world—contributing to the scientific process of understanding this virus," said Greg Bowman, of Washington University School of Medicine, who leads Folding@home. "The outpouring of support has been extraordinary."

Among those heavily involved in the project is Washington University's Office of Information Technology, which is helping manage the Folding@home servers and has deployed the software on many desktops across campus that have been sidelined while faculty, staff and students telecommute to help stop the spread of the virus.

The project relies on the combined processing power of volunteers' home computers to perform the billions of calculations required to simulate how proteins move. Understanding how they move—or fold into their characteristic shapes—can reveal how they work. It also can uncover ways to interfere with harmful proteins.

With the focus on COVID-19, Bowman and his collaborators are working to understand the proteins that allow the novel coronavirus to invade cells, multiply and spread. That knowledge could lead to new treatments.

"We're basically building maps of what these viral proteins can do," said Bowman, also an associate professor of biochemistry and molecular biophysics at the School of Medicine. "If we compare this to maps of cities and towns, this map would show protein structures."

Scientists don't have a way to take a satellite image of the area they would like to map, he said. "Instead, we're trying to build this map by having lots of people run simulations on their separate computers and send us back the data. In the map analogy, this is like having people around the globe jump in their cars and drive around their local neighborhoods and send us back their GPS coordinates at regular intervals. If we can develop detailed maps of these important viral proteins, we can identify the best drug compounds or antibodies to interfere with the virus and its ability to infect and spread."

Calculations on this scale require tremendous computing power. With the surge of new participants, Folding@home's distributed computing network now has more raw computing power than the world's largest 500 traditional supercomputers combined.

Folding@home also recently received a grant from the National Science Foundation (NSF) called a RAPID award, which provides funding quickly to researchers studying SARS-CoV-2, the virus that causes COVID-19. Past RAPID awards have focused on Ebola and Zika viruses and improving responses to disasters such as major hurricanes and oil spills.

In the spirit of open science and the quick dissemination of crowdsourced research about COVID-19, the Folding@home team will share their data in public databases and publish their findings on free and open-access preprint sites, such as bioRxiv.

More information: To download the Folding@home software and start contributing to COVID-19 research,
visit foldingathome.org/start-folding/