

Folding@Home Distributed Computing

Executive summary

Our goal: to understand protein folding, protein aggregation, and related diseases

What are proteins and why do they "fold"? **Proteins** are biology's workhorses -- its "**nanomachines**." Before proteins can carry out their biochemical function, they remarkably assemble themselves, or "**fold**." The process of protein folding, while critical and fundamental to virtually all of biology, remains a mystery. Moreover, perhaps not surprisingly, when proteins do not fold correctly (i.e. "misfold"), there can be serious effects, including many well known **diseases**, such as Alzheimer's, Mad Cow (BSE), CJD, ALS, and Parkinson's disease.

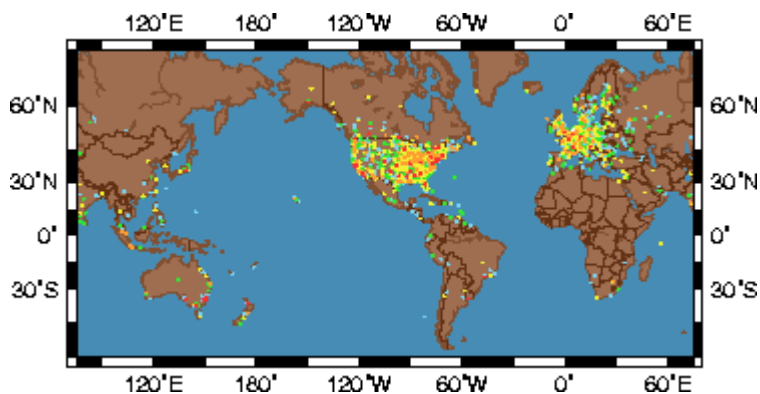


What does Folding@Home do? Folding@Home is a distributed computing project which studies **protein folding**, misfolding, aggregation, and **related diseases**. We use novel computational methods and large scale distributed computing, to simulate timescales thousands to millions of times longer than previously achieved. This has allowed us to simulate folding for the first time, and to now direct our approach to examine folding related disease.

Folding@Home is based at Stanford University and Stanford University Medical School and is funded by the National Institutes of Health and the National Science Foundation

How can you help? You can help our project by **downloading** and running our client software. Our algorithms are designed such that for every computer that joins the project, we get a commensurate increase in simulation speed.

What have we done so far? We have had several successes. You can read about them on our **Science page**, **Results section**, or go directly to our **press and papers page**.



*Since October 1, 2000, over 400,000 CPUs **throughout the world** have participated in Folding@Home*

Want to learn more? Visit <http://folding.stanford.edu>

More detailed questions

What is protein folding and how is it related to disease?

Proteins are necklaces of amino acids --- long chain molecules. Proteins are the basis of how biology gets things done. As enzymes, they are the driving force behind all of the biochemical reactions which make biology work. As structural elements, they are the main constituent of our bones, muscles, hair, skin and blood vessels. As antibodies, they recognize invading elements and allow the immune system to get rid of the unwanted invaders. For these reasons, scientists have sequenced the human genome -- the blueprint for all of the proteins in biology -- but how can we understand what these proteins do and how they work?

However, only knowing this sequence tells us little about what the protein does and how it does it. In order to carry out their function (eg as enzymes or antibodies), they must take on a particular shape, also known as a "fold." Thus, proteins are truly amazing machines: before they do their work, they assemble themselves! This self-assembly is called "folding."

What happens if proteins don't fold correctly? Diseases such as Alzheimer's disease, cystic fibrosis, BSE (Mad Cow disease), an inherited form of emphysema, and even many cancers are believed to result from protein misfolding. When proteins misfold, they can clump together ("aggregate"). These clumps can often gather in the brain, where they are believed to cause the symptoms of Mad Cow or Alzheimer's disease.

Who "owns" the results? What will happen to them?

Unlike other distributed computing projects, Folding@home is run by an academic institution (specifically the [Pande Group](#), at [Stanford University's Chemistry Department](#)), which is a *nonprofit* institution dedicated to science research and education. We will not sell the data or make any money off of it. Moreover, we will make the data available for others to use. In particular, the results from Folding@home will be made available on several levels. Most importantly, analysis of the simulations will be submitted to scientific journals for publication, and these journal articles will be posted on the web page after publication. Next, after publication of these scientific articles which analyze the data, the raw data of the folding runs will be available for everyone, including other researchers, here on this web site.

Why not just use a supercomputer?

Modern supercomputers are essentially clusters of hundreds of processors linked by fast networking. The speed of these processors is comparable to (and often slower than) those found in PCs! Thus, if an algorithm (like ours) does not need the fast networking, it will run just as fast on a supercluster as a supercomputer. However, our application needs not the hundreds of processors found in modern supercomputers, but hundreds of thousands of processors. Hence, the calculations performed on Folding@Home would not be possible by any other means! Moreover, even if we were given exclusive access to all of the supercomputers in the world, we would still have fewer cycles than we do with the Folding@Home cluster! This is possible since PC processors are now very fast and there are hundreds of millions of PCs sitting idle in the world.

Can I run Folding@Home on a machine I don't own?

Please only run Folding@Home on machines you either own or on which you have the permission of the owner to run our software. Any other use of Folding@Home violates our license agreement (and just isn't a good idea in general).

How do the results get back to you?

Your computer will automatically upload the results to our server each time it finishes a work unit, and download a new job at that time. At this time, there may be problems if your computer is only connected to the Internet sporadically. We are working on better support for these cases. Only the console version currently works at all over a modem connection, and there still may occasionally be a few bugs with that.

How much power/money is used by keeping a F@H running 24/7 on a computer?

Roughly, a CPU uses about as much power as a 60 watt light bulb. Here's a report on [computer power management](#) from Lawrence Berkeley government labs, and there are other references on the web you can find. Although power supplies on most computers are rated at 250 watts, average usage is much lower. On average, a Pentium-type computer uses between 45-70 watts (I've read various different sources on this) while it is on. If the computer has no idle mode, it will use the same amount of energy whether it is running a program or not. If it is on idle, it will consume around 25 watts. So, the daily difference between off and running F@H is about $24 \times (45 \text{ to } 70) = 1.1 \text{ to } 1.7 \text{ kWh}$. At \$0.14 per kWh (from PG&E here in California), this works out to about \$0.15 to \$0.24 per day, or perhaps \$6 a month. The difference between an idled computer and one running F@H would be closer to \$4 a month - and if the computer was already being used 8 hours a day, it would be closer to \$3 a month. In general, lighting and climate control use a much larger share of household power than computers do. So the best bet for cutting costs and conserving energy would be to turn off lights, turn off your computer monitors (which use more power than a CPU), and turn down the heat. And keep folding :)

What about security issues?

We have worked very hard to maintain the best security possible with modern computer science methodology. Our software will upload and download data only from our data server here at Stanford. The data server doesn't download any executable code to your computer. *Actually, our software is considerably safer than the browser you're using to read this!*

How is this possible? We take extensive measures to check all of the data entering your computer and the results we send back to Stanford with 2048 bit digital signatures. If the signatures don't match (on either the input or the output) the client will throw away the data and start again. This ensures, using the best software security measures developed to date (digital signatures and PKI in version 3.0), that we are keeping the tightest possible security. Finally, the client/screen saver are available for download only from this web site, so that we can guarantee the integrity of the software. We do not support Folding@home software obtained elsewhere and prohibit others to distribute the software.