

MicroMart Folding Article, By Tom Morton

Regulars of the MicroMart forum may have noticed a new phenomenon affecting it recently, strange words such as 'folding' and 'work units' are being used. So is this a new form of virtual origami or something else? In fact we are talking about Folding@Home a distributed computing initiative from Stanford University in San Francisco. Confused? allow me to explain.

A lot of you will probably have heard of the SETI project. The search for extra terrestrial life includes the processing of millions of radio signals from outer space, a job that would take years on just one computer. The solution was distributed computing. Users all over the globe download a small program which processes small chunks of the data before sending the results back. Millions of GHZ of free processing power gets donated to the search for extra terrestrial life.

Folding at home employs the same principal but, instead of aliens, Stanford's application researches the folding of proteins. What is folding? Well proteins (constructed from amino acids) are found inside every living cell and determine the cells structure, detect and destroy viral infections and cause biochemical reactions (for example as enzymes in the stomach). Put simply they tell the individual cell how to work, if this sounds remarkable you haven't heard the half of it yet. The most amazing thing about proteins is that they are able to build themselves, a process known as folding. Because this happens so quickly on such a small scale very little is known about how proteins actually fold. Stanford decided to address this problem and so wrote a program to simulate the folding process. Almost immediately they ran into a massive problem. It takes about one day to simulate one nanosecond (one thousand millionth of a second). As proteins take around 10,000 nanoseconds to fold it would have taken months just to simulate each one. Once again the solution was distributed computing.

The university developed a way of breaking up the simulations into smaller chunks, called 'work units' which can then be distributed to millions of computers via a small program called a client. To make things more interesting all of the work units are worth points if completed on time, with larger units worth more than smaller ones. Folding@Home (the name of the initiative) users can also join teams where their points go towards the team's total. At the time of writing there was around 41562 teams and 513083 registered users but these figures go up all the time.

The MicroMart folding team was started way back in September by Dr-Jon a forum regular. Currently the team has 34 members and are placed around the 2300 mark, but there is always room for more.

So why is this research so important? Well when proteins fail to 'fold' correctly it can cause diseases like Alzheimers, BSE (Mad cow disease) , Parkinson's, Cancer. By learning how these mutations happen scientists hope to find cures. As well as this the research is helping in the development of protein 'nano-machines' small devices that will help in medical treatments (for example by removing a blood clot).

Strong stuff! So how can you get involved? Well, simply point your browser at <http://folding.stanford.edu/download.html> where you will find a selection of

Folding@Home clients to download. There are 2 options the GUI version and the console version. The GUI client is a graphical program which includes all of the distributed computing / folding software and a graphical interface. The interface lets you view the current progress of your work units, time remaining, the number of completed units and a fancy graphical display of the currently folding protein. The program installs like any other windows program and runs quietly in the system tray, from where you can also change the advanced options. There are some known problems, however, with the GUI client on some systems, especially as the graphical display can eat up a whole chunk of processing power and memory, slowing down the folding process.

Those of you with a problem or who just want something a bit simpler might like to try the console client. The download is a .zip file which contains only core folding files and a DOS-like console. When the console is first run you can set all of the configuration options, set the program to be installed as a service and then forget about it. It runs invisibly when your system starts meaning there are less overheads than the GUI client which tends to cut out the compatibility problems and increases the speed of your folding. The disadvantage to this version is that there is no way to see the progress of the current work unit without a 3rd party program.

Once you have a Folding@Home client installed it is a simple matter of choosing a username and adding yourself to a team, obviously I'd recommend the MicroMart team (number 46590) and away you go! The programs work 'out of the box' but for those who like to meddle there are certain options you can tweak to get the best performance. For example you can choose the amount of processing power (from 5 to 100%) or the amount of memory Folding@Home can use, the size of work units to download or the checkpoint (where the client saves its current work data) interval. As well as this there are options to for those with odd Internet connections or who use a proxy or those with dodgy system clocks. Settings can be accessed easily by right clicking the Folding@Home icon in the system tray (for the GUI client) or can be set when you first run the console version.

Earlier I mentioned third party monitoring programs, the GUI client display is all very well and good but there are many other options out there that are much better. A good example is Fahmon (<http://fahmon.silentblade.org>), a small program that will monitor the progress of a work unit and shows it's percentage completion. It also tells you (among other things) how many points the unit is worth. Another option is FAH logstats (<http://sourceforge.net/projects/fahstats>) which gives more detail than Fahmon and also provides information about other work units that are currently being researched. On-line there is www.fahstats.com which gives loads of information about individual users and teams. There are work unit history and graphs to show predict your rise through the producer charts. If you are looking for information about a specific work unit then visit jmol.sourceforge.net/fah where you will find a handy Java applet that will tell you all sorts of useful info about different work projects and includes a link which will explain exactly what each work unit is researching, well worth a read!

Before I go just a few last points for those of you who want to start folding. Make sure you disable your screensaver if you plan to leave Folding@Home running for long periods because it can eat up valuable system resources, instead set your monitor to power down after a period of time (in control panel – power options). Some of you

may be wavering as to whether or not to fold because your worried about the system requirements. Don't worry! Folding@Home will work on just about any PC and you can set the amount of system resources it uses (i.e. The CPU percentage) to a value that doesn't impact too greatly on the computer performance.

Finally remember if you join team MicroMart (no: 46590) please come to the forum (forum.micromart.co.uk) and let us know you've joined! We look forward to hearing from you.