

WMLUG Meeting Notes October 2008 - Folding@home

Install and Set Up [Folding@home](#)

What is Folding@home?

Folding@Home is a distributed computing project that studies protein folding, protein misfolding, and related diseases. The website is <http://folding.stanford.edu/>. If you have some spare computing power, it is an altruistic use for it.

Downloading the client

<http://folding.stanford.edu/English/Download>

Install and configure

Make a folder for it and change to that folder:

```
mkdir ~/folding
cd ~/folding
```

Extract the tar file to the folding directory:

```
tar xzvf /download_location/FAH6.02-Linux.tar.gz -C ~/folding
```

Configure the client:

```
./fah6 -configonly
```

You will be asked for a user name and a team name (optional); keep the rest of the options at the defaults. If you don't enter a user name you can just use anonymous. You can check for a name on the website. Optionally, you can create a team or enter the number of an existing team.

Running Folding@home

To run it manually:

```
~/folding/fah6 -verbosity 9
```

You can also create a script by creating a file named fah with the following contents:

```
./fah6 -verbosity 9
```

and make it executable with

```
chmod +x fah
```

Start it with:

```
~/folding/fah
```

You can run FAH as a service too. Reference the instructions on the website.

If you find that FAH uses too much CPU (it will run at 100% if it can), you can limit it by installing the fahlimit program available at <http://calxalot.net/downloads/>.