Bioinformatics and Computational Biology Service

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Introduction

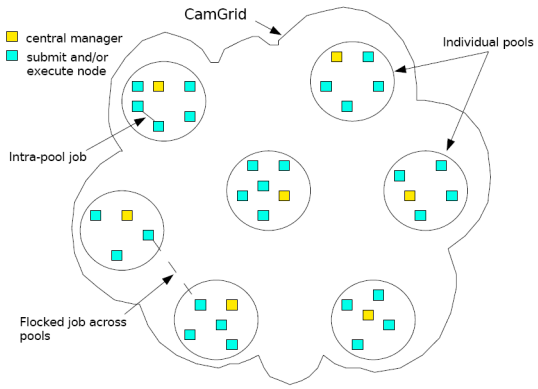
The Department of Biochemistry has a bioinformatics and computational biology service used by people in several Schools in the University. You can apply for an account to use the resources it provides. There are servers with many cores and very large memory (RAM) in a cluster where you can run computing jobs that require more resources than your desktop computer can provide. You can get help with using software and also use the service to reach CamGrid, the University's campus grid. We hold a number of DNA sequence and other databases and can set up your own databases eg for BLAST.

What can I use it for?

You can carry out a wide range of tasks. Typical computing-intensive tasks include: running many thousands of BLASTs, structural modelling, phylogenetic analyses, population genetic analyses and genome assembly and annotation. There are also lots of smaller tasks you can carry out, such as restriction mapping and short sequence comparisons. People may use the large servers to run parallel computer jobs. Some high-throughput work is sent to CamGrid. You can get advice on which resource is most appropriate. This may include suggesting you need the High Performance Computing Service (HPCS), for which you need to open a separate account. Factors include how much memory is needed and overall running time.

How does CamGrid work?

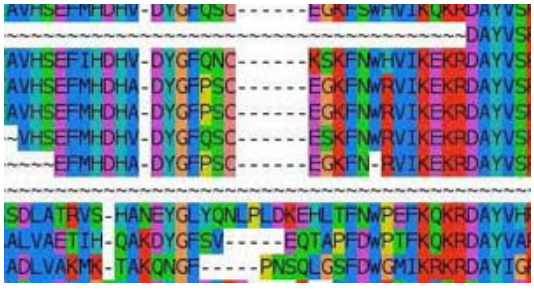
CamGrid is a federation of computers looked after by different people. Most of the clusters are in other departments eg Chemistry, Earth Sciences, Physics. Their owners have agreed to share resources so that students or staff with a lot of jobs they need to run can get this done far more quickly. It is now coordinated by the University Computing Service. In the figure, a cluster is called a pool and a flocked job means your computing work is being sent to other departments. Usually where jobs run is not something you need to worry about.



How do I get started?

Once you have opened your new account you can come and get help in person or via email.

If you need more extensive training in bioinformatics or programming you can choose from a wide range of courses held nearby. Links to all the information you need are on our web site. If you want to try something simple first there are web interfaces to some software, eg the EMBOSS package.



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Reference See http://computing.bio.cam.ac.uk