

## Ensembl at your institute



Ensembl is a joint project of the European Bioinformatics Institute and the Wellcome Trust Sanger Institute, funded mainly by the Wellcome Trust, with additional funding from EMBL and NIH-NIAID.

These courses are coordinated by Xosé M Fernández ([xose@ebi.ac.uk](mailto:xose@ebi.ac.uk)), member of the Ensembl team involved with user queries and workshops. Throughout the year we run a number of workshops, thus have developed a quite extensive 1-day course suitable for up to 30 people with a hands-on training aspect in Ensembl that should help the attendees get the most out of the system and apply it to their own projects. We are aiming to give this course once a month, and we are considering requests for this coming year (2005).

### **Workshop:**

“**Access to genes and genomes with Ensembl**” we will introduce the latest developments on the website, emphasising tools for data mining. Practical exercises will assist the researcher in learning to get the best out of the data available, and some time will be allocated for participants to query the Ensembl team about issues derived from their own research. Short presentations followed by case studies.

Topics covered will be:

- Overview of the Ensembl system and the latest developments (*e.g.* new species, outlook).
- Introduction to the Ensembl system
- Hands-on examples to introduce the system
- Evaluating genes and transcripts
- Data mining with EnsMart
- Comparative genomics and proteomics in Ensembl
- Variation (SNPs, haplotypes)
- Data mining is provided through EnsMart. Attendees will be introduced to several user interfaces designed to work with the system: (i) MartView - the web interface (ii) MartShell - a command-line tool, and (iii) MartExplorer - a java graphical user interface. These clients provide the user with the ability to create complex queries of data, and integrate data from BioMart datasets across the network.

Pre-Requisites: Course participants should have some biology background to understand different kinds of genomic annotation presented within Ensembl.

The deal is that you pay for travel and accommodation for someone. For European travel this works out to be pretty cheap, especially as we are close to Stansted. For US locations we would suggest both for your cost and the sanity of the helpdesk people that two or three *nearish* (in US terms...) institutes organise a potential road-show.

The course requires an IT room of (*say*) 20 PC's with internet connection and a way for one of the machines to be projected. The course lasts one day and can be somewhat customised to the location. Usually one can have up to 2 people per machine.