Bioinformatics We

EBI - NCBI
UCSC - Stanford

June 12-16,

Course Descriptions

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EBI Overview

Description
The European Bioinformatics Institute (EMBL-EBI) in Hinxton, UK, grew out o
work by the European Molecular Biology Laboratory (EMBL) to provide biolog
the research community. Today EBI is a centre for research and services in b
housing a wide variety of databases of biological data, including genomic, pro
biochemical, structural, interaction, and expression data, amongst others. In
provides a toolbox of bioinformatics software and search engines with which
collate the wealth of biological data. The EBI training workshop will provide a
grounding in a selection of fundamental EBI genomic and proteomic database
appropriate analysis software.

EBI - ArrayExpress

Description
The Microarray team at the EBI provides public resources for storing, managi
microarray data, and is a public, online repository for microarray data that co

Microarray Minimum Information for Microarray Experiment (MIAME) standar
stores both normalized and well-annotated raw data from 40,000 hybridizatio
than 70 species. Data can be submitted on-line, and password protection to
data is provided for authors and reviewers. This course will examine how to
ArrayExpress, deposit data, and give yourself and other microarray communi
access to your data at the level of the experiment or the gene. ExpressionPro
written to conduct online microarray data analysis, will also be introduced.

Audience
No prior experience is required.

Format
The course consists of a 1-hour lecture OR a 2-hour hands-on workshop whic
content of the lecture (see below). Lecture attendees may bring their wireles
computer laptops and follow the lecturer, as conditions permit.

- **Lecture**
  Registration for the lecture is unrestricted and open to all Stanford Univ
  staff, (including visiting faculty and staff) and graduate students. An op
  period with EBI instructors for lecture participants will be available.
- **Hands-on Workshop**
  The workshop duplicates the content of the lecture, but differs in that it
  on practice of the lecture demonstration examples. Individual consultat
  instructor will be available to workshop participants immediately followi
  **Workshop computer space is limited to a single session due to i
  availability! Register early. Registration will be "first come - firs**
  waiting list will be maintained if necessary.

Registration
Registration is required for either the ArrayExpress lecture or workshop.

Instructors
Helen Parkinson

Times
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EBI - Macromolecular Structure Database

of macromolecular structure data. Since its inception in 1996, the MSD group
partners around the world to improve the quality of PDB data, through a clea
that addresses inconsistencies and inaccuracies in the legacy archive. The im
data quality in the legacy archive have been achieved largely through the cre
data archive, in the form of a relational database that stores all of the data in
implementation of the MSD database, together with the parallel development
and methodologies for data harvesting, validation and archival, has lead to si
improvements in the quality of data that enters the archive. The MSD has de
query systems in order to allow users to interact with the database and retrie
consistent data for their own use. In addition, the MSD has also developed ne
visualization methods to help analysis of structures and improved the deposit
the latest release of AutoDep4.0 (http://www.ebi.ac.uk/msd-srv/autodep4/),
archival and web-based structure deposition tool. This workshop will introduc
various services offered by the MSD that can help in soling research problems

Audience
No prior experience is required.

Format
The course consists of a 1-hour lecture OR a 2-hour hands-on workshop whic
content of the lecture (see below). Lecture attendees may bring their wireles
computer laptops and follow the lecturer, as conditions permit.

- **Lecture**
  Registration for the lecture is unrestricted and open to all Stanford Univ
  staff, (including visiting faculty and staff) and graduate students. An op
  period with EBI instructors for lecture participants will be available.
- **Hands-on Workshop**
  The workshop duplicates the content of the lecture, but differs in that it
  on practice of the lecture demonstration examples. Individual consultat
  instructor will be available to workshop participants immediately followi
  **Workshop computer space is limited to a single session due to i
  availability! Register early. Registration will be "first come - firs
  waiting list will be maintained if necessary.

Registration
Registration is required for either the ArrayExpress lecture or workshop.

Instructors
Sameer Velankar

Times

EBI - Reactome

Description
Reactome is a collaborative project between the EBI and the Cold Spring Harb
USA, consisting of a curated knowledgebase of biological processes described
reactions, pathways, macromolecules, small molecules, complexes and cataly
These processes include both well-defined metabolic pathways, such as glycol
diverse range of other pathways, such as signalling pathways and cell cycle re
Reactome web interface provides a textbook-like view of cellular processes, p
keyword searching, integrating expression data and generating protein-protei
This course describes the underlying concepts behind Reactome, and explores
features of the web interface using hands-on exercises. In addition, participar
through the process of setting up their own Reactome site, and shown how to
tools available.

Audience
No prior experience is required. Anyone with an interest in using and/or discu
forum how to enhance and/or improve bioinformatic services at Stanford is er
attend.

Format
The course consists of a 1 hour lecture followed by a 30 minute open consulta

Registration
None.

Instructors

Times
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EBI - Web Services

EBI Web Services, such as SOAP (Simple Object Access Protocol), is an integ
that provides information retrieval and data analysis tools for use with multip
without the need for manual searching through a web browser or for installin
databases in-house. Moreover, information retrieval and analysis are linked,
combination and manipulation of search results. Using these technologies, pr
build complex applications in their language of choice (such as Java, Perl, VB
Python, Ruby, R and PHP), with data access directly from and to your code. A
can submit large and complex jobs straight from your data pipeline with all o
returned directly to your software for processing at the next stage. The numl
databases at the EBI that have Web Services access is now in double figures,
adoption of this technology very advantageous for any laboratory involved in
research. You can retrieve data from multiple EBI databases using the WSDb
and you can make use of sequence similarity tools such as Blast, Fasta and M
perform multiple sequence alignments using ClustalW, T-Coffee or MUSCLE. Y
explore the InterPro protein families and domains database using InterProSca
powerful queries over 40 different biological ontologies via the ontology looku
lecture, the EBI Web Services will be demonstrated, providing an overview of
individual Web Services can offer.

Audience:

Format: The course consists of a 1-hour lecture/demonstration. The worksho
participants or less to maximize interactions between instructor and student.
waiting list will be maintained with one additional session added, if necessary
Bioinformatics Week.

Registration:

Instructor

Times
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EBI - Ensembl / BioMart

macaque, mouse, rat, dog, cow, opossum, chicken, zebrafish, among others)
imports the manually curated data from other model organisms to use as cor
Drosophila from FlyBase, C. elegans from WormBase and yeast from SGC). E
unique gene analysis pipeline with each piece of genomic information predict
supported by biological evidence. Additionally, ESTs, mRNAs, SNPs, proteins
biological information are mapped to the genomes.

This course is designed to present different data types available in the brows
"Views", how to compare and contrast various information from several sourc
the most out of the Ensembl database with the unique data-mining tool, BioM
builder" interface which allows users to specify genomic regions and refine re
simple, distributed data integration system with powerful genomic-based que
BioMart can generate a number of different types of output, including sequen
list data. This course will also introduce BioMart, focusing on how it can be us
based, non-programming, researchers.

Audience
No prior experience is required. Basic familiarity with the steps and processes
BLAST sequence searching is helpful, but not necessary.

Format
The course consists of a 2-hour lecture OR a 4-hour hands-on workshop whic
content of the lecture (see below). Lecture attendees may bring their wireles
computer laptops and follow the lecturer, as conditions permit.

- **Lecture**
  Registration for the lecture is unrestricted and open to all Stanford Univ
  staff, (including visiting faculty and staff) and graduate students. An op
  period with EBI instructors for lecture participants will be available Frid
  immediately following the lecture.
- **Hands-on Workshop**
  The workshop duplicates the content of the lecture, but differs in that it
  on practice of the lecture demonstration examples. Individual consultat
  instructor will be available to workshop participants immediately followi
  Workshop computer space is limited to a single session due to i
  availability! Register early. Registration will be "first come - firs
  waiting list will be maintained if necessary.

Registration
Registration is required for either the Ensembl lecture or workshop.

Instructors

[Xose Fernandez](#)

Times
[View Schedule](#)

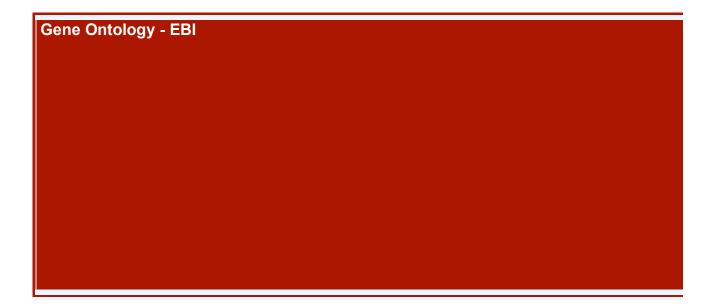## A Field Guide to NCBI GenBank and NCBI Molecular Biology Resources

Registration is required for both the Field Guide lecture and workshop.

Instructors
Peter Cooper, Eric Sayers

Times
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Gene Ontology - EBI

own GO subsets. Individual consultation with the EBI instructor will be
workshop participants immediately following the workshop. **Workshop
is limited to a single session due to instructor availability! Regis
Registration will be "first come - first serve."** A waiting list will be
necessary.

Registration
Registration is required for both the Gene Ontology lecture and workshop.

Instructors
Emily Dimmer

Times
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Proteomics Workshop - UniProt, InterPro, IntAct

Description
This workshop will introduce participants to three major EBI proteomic databa
InterPro, IntAct and PRIDE – and explore the wealth of information they conta
enhance your research. UniProt is a central repository of protein sequence and
by combining the information in Swiss-Prot, TrEMBL and PIR, while InterPro ar
free open source data and resources aimed at analysing proteomes and intera
provides information on the function, annotation and classification of proteins
major signature databases from Gene3D, Pfam, PIRSF, Prints, ProDom, Prosite
SuperFamily, Tigrfams, and PANTHER into a unified protein resource. InterPro
structural annotation by mapping individual proteins to PDB, MSD, CATH, SCO
SwissModel, as well as functional annotation through GO mapping, literature s
references, and links to several external databases (Pandit, CAZy, Merops, IUI
Cluster, Blocks, and Prosite doc). IntAct provides a comprehensive, annotated
protein interactions derived from literature curation and through direct submis
interactions can be viewed individually, or as part of an interaction network, u
to help define the proteins involved in such networks.

Audience
No prior experience is required. Basic familiarity with the steps and processes
sequence searching is helpful, but not necessary.

Format
The course consists of a 2-hour hands-on workshop. Lecture attendees may br
registered wireless-access enabled computer laptops and follow the lecturer, a
permit.

Hands-on Workshop
The workshop considerably duplicates the content of the lecture, but differs in
hands-on practice of the lecture demonstration examples. Both workshops are
the one that best fits your schedule. Individual consultation with the EBI instru
available to workshop participants immediately following the workshop. **Work:
space is limited to a single session due to instructor availability! Regis
Registration will be "first come - first serve."** A waiting list will be maint

Registration
Registration is required for either the Ensembl lecture or workshop.

Instructors
Sandra Orchard
Jennifer McDowall

Times

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