EMBL-EBI’s Train online e-learning portal

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Scientific Training Officer (e-learning)

Wednesday 16th September 2015
www.ebi.ac.uk/training/online
Overview

• Why and how we train at EMBL-EBI
• Choosing the right e-learning platform
• What is Train online? How do we train our users?
• Impact of Train online
Why and how we train at EMBL-EBI
Training at EMBL-EBI

Lots of resources and databases!

Need to train users
How we train our users

www.ebi.ac.uk/training

TRAINING
On-site

Delivering courses to develop practical skills and knowledge; led by EMBL-EBI experts and hosted in our purpose-built training suite.

TRAINING
Off-site

Sending our dedicated trainers to host organisations to provide hands-on training on EMBL-EBI data, tools and resources.

TRAINING
Online

Providing free access to EMBL-EBI courses, allowing individuals to choose when, where and how they learn.
Choosing the right e-learning platform
How we chose

**Key requirements**
- Open source
- Interactive
- Easy to use
- Easy to update
- Internally developed
- Self-paced learning

**Key stakeholders**
- Users
- Subject matter experts
- Web developers / system administrators

3 LCMSs

Tested by stakeholders

Drupal

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E-learning with Drupal

- Built using bespoke e-learning module in Drupal 6 (upgrading to Drupal 7 – end of 2015)
- Drupal is a CMS used across EMBL-EBI websites – trainers are familiar with it
- Self-paced learning
## Costs

<table>
<thead>
<tr>
<th>Position</th>
<th>Set-up (1 ½ year period)</th>
<th>Maintenance (ongoing)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Web developer</td>
<td>1 person year (~65%)</td>
<td>½ month (5%) – ideally would like 10-15%</td>
</tr>
<tr>
<td>Scientific training officer (STO)</td>
<td>1 ½ person years (100%)</td>
<td>1 person year (100%)</td>
</tr>
<tr>
<td>Managerial</td>
<td>4 months (20%)</td>
<td>½ month (5%)</td>
</tr>
<tr>
<td>Subject matter experts</td>
<td>Varies – goodwill</td>
<td>Varies – goodwill</td>
</tr>
</tbody>
</table>
Key tasks

- Strategic review
  - STO, managerial, web developer
- Write
  - Subject matter expert(s), STO
  - Review
  - STO, managerial
- Review & publish
  - Subject matter expert(s), STO
- Update courses / development updates
  - Subject matter expert STO, web developer

Engage subject matter expert(s) & set-up course template

Subject matter expert(s), STO
## Drupal as an e-learning platform

<table>
<thead>
<tr>
<th>Advantages</th>
<th>Limitations</th>
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<tbody>
<tr>
<td>Flexible learning</td>
<td>Trainees need to be motivated, no live trainer support</td>
</tr>
<tr>
<td>Good accessibility</td>
<td>Not optimised for tablet / mobile</td>
</tr>
<tr>
<td>No need to register</td>
<td>Can’t track trainee progress</td>
</tr>
<tr>
<td>Used throughout EMBL-EBI</td>
<td>Interactivity is limited</td>
</tr>
<tr>
<td>Community driven</td>
<td></td>
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</table>
What is Train online?
Train online (www.ebi.ac.uk/training/online)

- Launched in September 2011
- 71 courses covering functional genomics through to chemical biology and literature. All free!
- Creative Commons ShareAlike

Aims

- Act as a gateway to our resources
- To make our users more confident users of these tools and resources
- To be accessible to different audiences, their needs and different learning styles. Depth and variety!
- To develop standalone tutorials
Target audiences

Bench-based life scientists

- What resource should I use to do....?
- How do I use it?

Bioinformaticians / developers

- What other resources are available?
- Recap on how to use resource x
- Programmatic access

Tutors

- What courses and resources can I direct my students to?
- Do you have exercises?

Credits:
[1] Jenny Cham’s blog
[2] Cliparts.co
Structure of courses

Key features:

- No need to register
- Dip in and out
- Take entire course or just relevant sections
- Repeat courses multiple times
Types of courses

Conceptual

What is metabolomics?

Metabolomics is the large-scale study of small molecules, commonly known as metabolites, within cells, biofluids, tissues or organisms. Collectively, these small molecules and their interactions within a biological system are known as the metabolome.

Figure 1 An overview of the four major “omics” fields, from genomics to metabolomics.

Quick tours

What is Ensembl?

Ensembl provides a genome browser that acts as a single point of access to annotated genomes, primarily for vertebrate species (Figure 1).

Information such as gene sequence, splice variants and further can be retrieved at the genome, gene and protein level. This includes information on protein domains, genetic variation, homology, synteny, genomic regions and regulatory elements. Coupled with analyses such as whole genome alignments and the effects of sequence variation on proteins, this powerful tool aims to describe a gene or genomic region in detail.

Ensembl imports genome sequences from consortia, which is consistent with many other bioinformatics projects. Each species in Ensembl has its own homepage, where you can find out who provided the genome sequence and which version of the genome assembly is represented. To see an example, visit the Ensembl home page for human.

Tutorials

Exploring the UniProtKB results page

When you do a search within UniProtKB, you will see a page showing all your results (Figure 16).

Figure 16. The UniProtKB results page for insulin.

Videos

Webinars
Engaging and accessible content

Guided examples

Searching for the OSM gene

1. Search for the human OSM gene as in the figure. (Alternatively use the search box at the top right of every Ensembl page).
2. Click 'Go'.
3. Click through to the gene tab. For a reminder of how to do this see the "How to search Ensembl" section.

Annotated screenshots

Phenotype: abnormal glucose homeostasis

Exercises

Finding entries with 3D structures

Scenario

You were flipping through a past issue of Science and came across the following article:

The Protein Kinase Complement of the Human Genome

Exercise

You want to find all human protein kinases in UniProt that have a 3D structure associated with them. How would you do this?

Short videos

Exploring sources of biological data

What are the types of nodes indicated with coloured spots in the tree below?

Quizzes
How we measure impact
What we capture

- Feedback forms at the end of each course - did you find the course useful? Why? How will you apply what you have learnt?
- Suggest a course feature
- Video analytics data from EMBL media site and Youtube
- Google analytics
- Broader reach - e.g. through social media
Analytics data

- Over 324,000 unique users since July 2012
- From 217 countries
- Currently averaging around 16,000–17,000 unique users per month
- 40% returning users
Most popular courses in 2015

Unique Pageviews in 2015

- Next generation sequencing: 186,544
- Ensembl Genomes tutorial: 32,654
- EMBO high-throughput sequencing: 19,571
- Biomacromolecular structures: 12,080
- Introduction to metabolomics: 11,199
- Interpro tutorial: 8,066
- Introduction to phylogenetics: 5,541
- Introduction to functional genomics: 5,126
- Protein interactions and their: 4,388
- Other: 3,680
How we use this feedback

- Areas to improve on both for courses and functionality / usability
- What new courses to develop
- As a motivator for both existing and new trainers – monthly reports
- To develop a core community of Train online users – e.g. through our newsletter (over 6,900 registered users)
Acknowledgements
Thank you! Any questions?

www.ebi.ac.uk/training/online

Twitter: @EBItraining
Top 10 countries accessing Train online

<table>
<thead>
<tr>
<th>Country</th>
<th>Sessions</th>
<th>% New Sessions</th>
<th>New Users</th>
</tr>
</thead>
<tbody>
<tr>
<td>United States</td>
<td>125,916</td>
<td>68.40%</td>
<td>86,124</td>
</tr>
<tr>
<td>United Kingdom</td>
<td>79,793</td>
<td>49.23%</td>
<td>39,285</td>
</tr>
<tr>
<td>India</td>
<td>54,970</td>
<td>66.37%</td>
<td>36,481</td>
</tr>
<tr>
<td>Germany</td>
<td>22,402</td>
<td>51.01%</td>
<td>11,427</td>
</tr>
<tr>
<td>Canada</td>
<td>15,583</td>
<td>67.14%</td>
<td>10,463</td>
</tr>
<tr>
<td>Australia</td>
<td>13,604</td>
<td>66.72%</td>
<td>9,076</td>
</tr>
<tr>
<td>Spain</td>
<td>12,462</td>
<td>52.49%</td>
<td>6,541</td>
</tr>
<tr>
<td>China</td>
<td>12,012</td>
<td>58.08%</td>
<td>6,976</td>
</tr>
<tr>
<td>Italy</td>
<td>10,774</td>
<td>55.65%</td>
<td>5,996</td>
</tr>
<tr>
<td>France</td>
<td>10,362</td>
<td>57.94%</td>
<td>6,004</td>
</tr>
</tbody>
</table>
Some comments

As someone just getting into bioinformatics, this was a painless introduction to an otherwise overwhelming program. I will use this protocol for experimental design.

It's important for me as a researcher to know structures of molecules and their biological function. Now I can research relevant molecules and identify more structures or genes for the genetic manipulation.

It's thorough and easy to follow. I'm taking this tutorial as a part of my bioinformatics course at my university and I will definitely turn to it if I'm stuck in future assignment and/or future research.

I'm studying metabolomics at university, and I didn't have such clear and precise notes like these ones I think I'll have a better mark in my subject.