



EMBER — A EUROPEAN MULTIMEDIA BIOINFORMATICS EDUCATIONAL RESOURCE

FOLLOWING THE COMPLETION OF HUNDREDS OF genome projects, bioinformatics has grown in prominence. The data overload that has been witnessed in recent years has created a demand for people to build and maintain databases, to design more incisive analysis software, to use disparate databases and software tools, and to understand both the statistical and biological significance of results generated in silico. It is rare to find individuals with such a range of skills, yet such scientists are needed in sequencing centres, research/academic institutes, pharmaceutical/agrochemical companies, software houses and start-up companies. But the rate of growth of the field, and its cross-disciplinary nature, has created a problem: while there are many trained biologists and computer scientists, there are few computer-literate biologists or biology-literate computer scientists. Consequently, there has been a dearth of skilled staff in bioinformatics, and this has stimulated the development of several postgraduate and undergraduate bioinformatics courses.

For some years, the University of Manchester has run a bioinformatics MSc. In 1999, we introduced into its first module an interactive practical, BioActivity (<http://www.bioinf.man.ac.uk/dbbrowser/bioactivity>) (Attwood, 1999a, 1999b, 2000), which is supported by an introductory textbook (Attwood and Parry-Smith, 1999). Being freely available on the Web, BioActivity is also now used worldwide. But its regular in-house and external use meant that it had to be revised and updated constantly (embedded links change and the field moves on); its maintenance was therefore becoming burdensome.

To address these issues, in 2001 the European Commission funded a new educational project, EMBER, which aimed to develop a set of bioinformatics teaching materials suitable for use in conventional face-to-face classes, or in self-paced settings, such as the home or the workplace.

THE PROJECT

EMBER comprises a self-contained, interactive Web-tutorial in bioinformatics (with emphasis on protein sequence and structure analysis) and the equivalent stand-alone tutorial on

CD-ROM. The project, coordinated at the University of Manchester, involved several organisations, each with different roles: some of the partners helped to develop the new teaching materials; others tested them by conducting user trials. Collaboration with a professional multimedia publisher was also essential to ensure high-quality production of the materials.

In the first months of the project, a survey of bioinformatics skill requirements was conducted, by sending out a questionnaire to potential employers from academic and industrial organisations. Feedback was poor (only 16% of contacts replied), but the responses we did get were useful and allowed us to compile a tutorial outline (Mabey and Attwood, 2001).

The principal areas covered in the tutorial include basic and advanced aspects of bioinformatics, and supplementary topics (Table 1). The basic topics deal with translation of DNA sequences, searches of protein sequence and protein family databases, sequence alignment and protein structure classification; the advanced topics cover homology modelling and threading, and more challenging analyses with uncharacterised sequences; and the supplementary topics are introduced via specific case studies with particular biological themes, using tools from the basic chapters and new tools.

With this outline, we revised and expanded the existing Web practical. We also incorporated assessment tools, to evaluate the product (e.g. look-and-feel, ease of navigation, etc.) and to evaluate student performance. The results were sent to our electronic publisher to develop the 'new-look' Web- and CD-ROM-based tutorials, and these were then tested by conducting user trials; feedback from the trials allowed us to make important improvements.

Table 1 Main themes covered in the EMBER tutorial

Basic tutorial

- Translation and identification
- Sequence database searches
- Protein family analysis
- Sequence alignment
- Property profiles
- Fold classification

Advanced tutorial

- Homology modelling
- Threading
- Mystery sequences

Case studies

- Investigating the human genome
- Investigating the inositol phosphatase family
- Investigating phylogeny relationships of ABC transporter domains
- Investigating sickle cell haemoglobin

FORMAT OF THE TUTORIAL

Each chapter has a set of aims, step-by-step instructions, background information, references and a Multiple Choice Quiz (MCQ). A notepad is available for saving results between chapters, and a list of contents is always visible on the left-hand side of the page. Navigation may be effected either via the labelled page tabs or by means of the table of contents.

The instruction pages are broken down into convenient steps and navigation arrows are provided to allow progression to subsequent steps once all tasks have been completed. The information pages provide supporting theoretical information, broken down under suitable sub-headings and illustrated, where possible, with a variety of images, diagrams and so on. Again, navigation arrows allow progression to and from different sub-headings. A glossary is also provided, allowing information retrieval by glossary term, by definition, abbreviation and/or synonym.

As mentioned above, assessment tools have also been incorporated into the tutorial, commencing with an MCQ to gauge student knowledge before undertaking the tutorial, followed by self-assessment quizzes in each chapter, and a final MCQ to gauge student knowledge having completed the tutorial. For each MCQ, answers are computed and relayed to the student, with information to indicate how many correct answers were obtained and, if mistakes were made, what the errors were. The results of the final quiz are related to those of the initial quiz, so students may see how they have performed overall relative to when they commenced the tutorial.

CONCLUSION

EMBER is one step towards the provision of self-contained bioinformatics teaching materials suitable for face-to-face

delivery, or self-paced tuition at home or in the workplace. It has already replaced BioActivity in Manchester's Bioinformatics MSc and will be used in our Distance Learning MSc. The website is now open for wider testing (contact attwood@bioinf.man.ac.uk for details); we welcome your comments.

REFERENCES

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NEW GUIDES

LTSN BIOSCIENCE IS PRODUCING A SERIES OF guides intended to be an accessible introduction to good learning and teaching practice within the context of competing research and institutional pressures (see <http://www.bioscience.heacademy.ac.uk/TeachingGuides/>). The general title of the series is 'Teaching Bioscience — Enhancing Learning' and the first publication is *Self- and Peer-Assessment: Guidance on Practice in the Biosciences*. The aim of each publication is to provide a persuasive overview of the pedagogic reasons for adopting a particular practice, supporting these reasons with sufficient practical guidance and information to turn ideas into reality. The guides are structured around a common format; Chapter 1 provides a general introduction to the topic, Chapter 2 advice on how to implement the topic and Chapter 3 more in-depth information on the topic and the opportunity to investigate further.

In addition, each guide contains a collection of bioscience case studies highlighting how others have introduced the topic into their teaching practice. It is intended that the guide will be useful to academics in their first year of lecturing,

particularly those who are studying for a Postgraduate Certificate in Learning and Teaching in Higher Education, as well as to those with many years of teaching experience.

