

E-Learning Approaches to Bioinformatics Education at UCL

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HTMLW – the HTML Wrapper

The HTMLW system was developed by Andrew Martin as a simple tool for creating consistent, attractive web-based practical materials with a minimal investment of time. Practical materials developed using HTMLW have been used by hundreds of students on courses in the Biochemistry department including bioinformatics courses such as C40 and large molecular biology courses such as B200.

Features

- Free software, fully open-source
- Simple and quick to set up and deploy
- Requires no maintenance
- Content and questions can be mixed (unlike WebCT or Moodle)
- Consistent look-and-feel using a few simple commands
- Automatic marking system
- Ideal for distance-learning and traditional teaching environments

Applications

- Used by lecturers at Reading and UCL for more than 6 years
- Successful course materials developed using HTMLW include undergraduate, postgraduate and professional training materials
- A core part of the popular and successful BCB Introduction to Bioinformatics course.

Title Bar: HTMLW Demo: Page 1 of 1

Subtitle Bar: HTMLW

“Home” Logo: UCL logo

“Top” Logo: Upward arrow icon

Multiple Choice Question: How many Eukaryote genomes are “complete” as of 1st March 2006?
 26
 34
 41
 53

Question with Free Text Answer: Which species’ genome was the first to be sequenced?
 Baccheromyces cerevisiae

Image: 3D protein structure

Body Text: The HTMLW system is ideal for rapid deployment of web-based practical materials. Creating attractive, consistent practicals is simply a matter of producing a short text document marked up with HTMLW tags specifying the organisation of content into separate pages as well as overall features such as background and text colours.

Figure 1: Example HTMLW page.

The page above demonstrates the key features of HTMLW. Many of the features identified are added automatically by the software simply by specifying the requisite HTMLW tag. For example, the Subtitle Bar identified above is simply specified by the code at the top of the box to the right. Questions are similarly simple, as shown at the bottom of the box to the right.

```
<<subtitle>>
HTMLW
<</subtitle>>

<<question>>
Which species’ genome was the first to be sequenced?
<</question>>
```

Introduction

Bioinformatics exists to provide life-science researchers with simple yet powerful tools to access the wealth of biological data now available.

Bioinformatics software tools have a large user base with a broad range of computer literacy. High quality documentation and training materials are essential if the tools are to be adopted by the wider community.

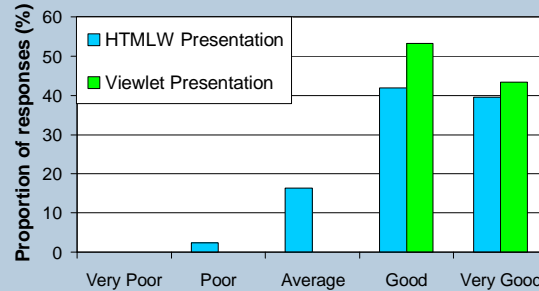
HTMLW and Qarbon ViewletBuilder are two applications for rapid creation of high-quality, user-friendly tutorials and practical materials.

This poster demonstrates these simple, powerful tools in the context of the biannual BCB Introduction to Bioinformatics course.

User Feedback

The HTMLW-based practicals, with embedded Viewlets, were evaluated in two of the five days of the BCB Introduction to Bioinformatics course.

43 responses were obtained from a total of 56 students. These are summarised in the graph below.



66% of students further indicated that they would welcome more Viewlets, with 96% stating that they would refer to an online Viewlet Cache with tutorial information on the most widely used bioinformatics tools and websites.

HTMLW is available free from Andrew Martin’s website:

<http://www.bioinf.org.uk/htmlw/>

BCB practical materials and Viewlets can be accessed from UCL at:

<http://www.bcb.lon.ac.uk/l2B/practicals>

HTMLW was developed by Andrew Martin, Ian Sillitoe & Michael Sadowski.

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The BCB Introduction to Bioinformatics Course is sponsored by the UCL Graduate School



Qarbon Viewlets for Real-Time Software Demonstrations

Development of high quality documentation and tutorial materials is essential if software is to appeal to a wide user base but academic software developers rarely have the time to invest in it. Qarbon viewlets provide a simple, easy-to-use way to develop short Flash movies for simple, accessible tutorial materials and user-friendly documentation.

Features

- Commercial software developed by Qarbon (www.qarbon.com)
- Simple point-and-click graphical user interface.
- Access to a subset of FLASH functionality, balancing power with ease-of-use
- Interactive hyperlink style feature allows sophisticated user interaction
- Add sounds, images, vector graphics for a full multimedia tutorial
- Additional interactive features turn demonstrations into simulations

Applications

- BCB training course materials - tutorials for key software packages in protein structure analysis: RasMol molecular viewer and Swiss-PDB Viewer molecular modelling software
- Applied to bioinformatics software training by Affymetrix for their GeneSpring software package
- Used for training in a variety of settings by companies such as Oracle and ADP

Highlighting Box: Points to a menu in the software interface.

Mouse Pointer: Points to a mouse cursor over the protein structure.

Application Screenshots: Points to a screenshot of the software interface.

FLASH Player Controls: Points to the video player interface.

Text Box: Points to a text annotation: "Ribbons is a good way to display secondary structure of the backbones."

Figure 2: Anatomy of a Qarbon Viewlet

This screenshot, taken from the RasMol tutorial developed by Dan Frampton (BCB), demonstrates the basic features of a Qarbon Viewlet. Application screenshots are taken using the ViewletBuilder software’s own screen capture facility or imported from any image source. The framework is then completed with text annotations, highlighting and other imported images. An animated mouse pointer represents the user’s interaction with the viewlet and is used to guide attention. The final viewlet is a FLASH movie object that can be embedded into a website or downloaded for viewing as a standalone object.