DISTANCE EDUCATION THROUGH THE INTERNET: THE GNA-VSNS BIOCOMPUTING COURSE

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A prototype course on biocomputing was delivered via international computer networks in early summer 1995. The course lasted 11 weeks, and was offered free of charge. It was organized by the BioComputing Division of the Virtual School of Natural Sciences, which is a member school of the Globewide Network Academy. It brought together 34 students and 7 instructors from all over the world, and covered the basics of sequence analysis. Five authors from Germany and USA prepared a hypertext book which was discussed in weekly study sessions that took place in a virtual classroom at the BioMOO electronic conferencing system. The course aimed at students with backgrounds in molecular biology, biomedicine or computer science, complementing and extending their skills with an interdisciplinary curriculum. Special emphasis was placed on the use of Internet resources, and the development of new teaching tools. The hypertext book includes direct links to sequence analysis and databank search services on the Internet. A tool for the interactive visualization of unit-cost pairwise sequence alignment was developed for the course. All course material will stay accessible at the World Wide Web address (Uniform Resource Locator) http://www.techfak.uni-bielefeld.de/bcd/welcome.html. This paper describes the aims and organization of the course, and gives a preliminary account of this novel experience in distance education.

1 Introduction

1.1 The Need for Biocomputing Education

Biocomputing has become a field of particular importance in many areas of biological research, but it has acquired particular prominence in molecular biology. Due to the great accumulation of molecular sequence data in the public nucleic acid and amino acid databanks, product of individual and collaborative sequencing efforts, the analysis of sequence data by biocomputing methodology has become a research field of its own. Some experimental molecular biology research projects include a significant amount of nucleotide sequence determination. Thus, there exists a strong demand for learning the basics of computer

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assisted sequence analysis on the part of the molecular biology experimentalists.

It is unsatisfactory for practicing scientists to simply apply available software tools to their sequences at hand without the necessary knowledge of their "inner workings". Many wrong and misleading interpretations of sequence data can still be seen printed in major scientific journals, and lots of sequences are deposited in the databanks without comprehensive analysis. This problem has been addressed by the scientific community in several ways (see also [1]). (1) Introductory books and literature with a mainly practical approach to the subject have become available. (2) Introductory courses in biocomputing have been included in the graduate and postgraduate curricula. (3) Workshops on the subject have been organized. (4) Specific curricula to train biocomputing professionals have been developed at some universities.

It is well known that the scarcity of biocomputing professionals is mainly due to a lack of specific biocomputing curricula at the major academic centers. Most of the current specialists in the field have arisen by the self education of biologists interested in computer approaches, or by computer scientists and physicists interested in biological problems. The training of biocomputing professionals can undoubtedly increase the assistance available to research groups dealing with sequence data, and it may help to develop a critical mass of biocomputing scientists to tackle more effectively the current problems of the field. Even if the number of biocomputing professionals increases, it is clear that every practicing molecular biologist will benefit greatly from gaining basic computer skills and knowledge on sequence analysis. The researchers that are already working in the field must be offered ways to complement their education.

1.2 Biocomputing Education via Computer Networks

An alternative way to satisfy the increased demand in biocomputing education is to use the now widely available global networking infrastructure to design and implement educational services. Nowadays a large number of services related to molecular biology can be accessed through the Internet, notably molecular sequence databanks. Thus, it is now quite common for molecular biology groups to have Internet access, pointing to this medium as an ideal delivery system for biocomputing distance education to a wide audience. This kind of delivery is different from the kind that involves dedicated teleconferencing systems, which require costly equipment and telecommunications facilities; the use of the Internet requires only a low entry cost. Most Internet services are currently implemented using the World-Wide-Web (WWW) hypertext protocol, which makes it possible to serve documents that may contain clickable links to other services, images, forms, and more.

2 Organization of the GNA-VSNS Biocomputing Course

2.1 Background and Parallel Courses

On the Internet, a couple of organizations help teachers who wish to offer educational services.

The Globewide Network Academy (GNA) is a federation of educational and research institutions whose purpose is to provide a central location at which students and teachers connected to the Internet can find each other, and to provide administrative support services to aid teachers [2]. GNA consists of independent members, each having their own internal finances, and course and curriculum policies.

The Virtual School of Natural Sciences (VSNS) is a GNA school focusing on collaboration between real colleges and educational institutions for natural sciences [3]. The first course offered by the VSNS was the "Principles of Protein Structure" course [4].

The BioComputing Division (BCD) of the VSNS can at present be identified with the organizers of the biocomputing course discussed in this paper. In the long term, it shall offer a wide array of courses and related services in biocomputing.

The computer science department at Bielefeld University is running a biocomputing program that started in 1989.[b] R. Giegerich has been the chief responsible for this curriculum, where students are passed back and forth between classes offered by computer science and biology departments. A lecture on "Algorithms on Sequences" is regularly offered (with about 30% overlap with the GNA-VSNS Biocomputing Course content). Furthermore, the Bielefeld Research Center for Studies in Structure Formation hosts quite a bit of interdisciplinary research in mathematics, science and informatics, and runs a small PhD program. This background allowed us to have three chapter authors and two instructors locally available and helped in the intensive course preparation phase.

During the GNA-VSNS Biocomputing Course, three courses were given in a traditional way: At Bielefeld, a group of 5 students (3 in biocomputing, 2 in biology) was instructed by G. Fuellen based on the course material. At Jülich, W. Altenhofen instructed a group of four students, also in parallel to

[b]In the German system, academic education starts at the junior level and leads to a diploma degree roughly equivalent to a Masters including two years of graduate study.

his "virtual" group. At Mexico City, F. de la Vega coordinated a course on Sequence Analysis for 10 postgraduate students using some material from the course. Currently a course on "Sequence Analysis with Distributed Resources" is jointly offered by the biology and computer science departments at Bielefeld. It also draws on the GNA-VSNS Biocomputing Course experience, but is organized in a project-oriented fashion.

2.2 Overall Course Design

The design of the GNA-VSNS Biocomputing Course was based on three ideas:

1. The course was aimed at a mixed group of students with backgrounds in molecular biology, biomedicine or computer science. The goal was to complement and extend these skills by giving the students a piece of true biocomputing education. All students needed to have at least late undergraduate (senior) level experience in either the biology or the computer science subject area.

2. The course was designed to exploit the coincidence of form and content. Being an Internet course dealing with biocomputing resources on the Internet, the course text should link to all these resources, and other hypermedia should be used wherever appropriate.

3. In contrast to the Principles of Protein Structure course, we decided to take a rather conservative approach to teaching. The textbook covered the complete course contents, fixed groups of students were assigned to instructors, and online exercises and homework assignments were an integral part of the course.

2.3 Course Syllabus

Aiming at a profound introduction rather that a cursory overview, we decided to concentrate on the fundamental aspects of sequence analysis (in spite of the much wider title of the course). After a short introduction, the course content was arranged in 5 chapters [5].

1. *Pairwise Alignment* treats the formal notions of sequence distance and similarity, the famous dynamic programming scheme for pairwise alignment [6] plus some of its vacations, and sketches the heuristics behind FastA [7] and BLAST [8]. We also imported a section on the determination of scoring functions.

2. *Networking* gives a general introduction to networking concepts like FTP, Telnet, WWW, WAIS, and the biomolecular data banks. It then directs the student to a careful selection of biocomputing resources on the Internet. Entrez [9], SRS [10], and the BCM search launcher [11] are covered in some detail. Links to various resource lists are also included.

3. *Multiple Alignment* discusses the complexity of the global alignment problem for many sequences, explains the Carrillo-Lipman technique [13] as well as alignment methods that proceed along a tree, e.g. Clustal [12]. It also contains a detailed case study of aligning a family of immunoglobulins, using tools on the WWW to illustrate and recapitulate the results of an original paper.

4. *Mathematical Basis of Molecular Phylogenetics* introduces phylogenetic trees and linkage algorithms. It covers various clustering methods including the split-decomposition technique of Bandelt and Dress [14].

5. *Genetic Algorithms and Protein Folding* was designed as a final chapter giving an outlook into those two areas, which could not be covered in the course text more deeply.

The ordering of Chapters 1 and 2 was actually an intensely debated decision. The final outcome - fundamentals before tools - was chosen for its better expression of the overall intent of the course. Aside from the fact that all chapters rely on the basic notions of Chapter 1, the chapters are actually rather independent.

2.4 Study Groups

Seven small study groups were formed to allow discussion of the course material by email and weekly sessions in the electronic classroom [15]. Each group was led by one of the instructors, and the average size was 4-6 participants. The student-instructor matching was based mainly on two factors: (1) The students' interest in the instructor's specialty as advertised on the application form, and (2) common geographic time zones so that scheduling weekly electronic meetings was not too difficult. Due to the significant amount of experienced researchers among the students, the distinction between instructors and students was rather fuzzy at times, resembling a common learning experience more than lecture style education.

2.5 WWW: The Hypertext Book and Other Resources

The subject matter of the course was studied by reading a chapter of the hypertext book, solving the exercises proposed therein, and discussion during the weekly electronic session. The hypertext book was assembled from chapters translated from different formats, and made available by a World-Wide-Web (WWW) server at Bielefeld[5]. Two mirror sites were set up at Baylor College of Medicine (USA)[17] and at the Manchester and North High Performance Computing Training and Education Centre (UK)[18]. They served as a backup, and to reduce transatlantic Internet traffic. Some chapters were translated from TEX format to hypertext format, taking advantage of WWW links to several biocomputing facilities, online tools, and resources. Due to the widespread availability of biocomputing tools and databases on the WWW, essential skills taught to students was to navigate the Internet looking for specific information, and to deal with WWW browsers.

Additionally, the GNA-VSNS Biocomputing Course Home-Page[16] includes pointers to homework, archives of the mailing lists, transcripts of the faculty meetings, old newsletters, and other information. Each study group set up a WWW page pointing to the students' personal home pages, when available, and group-specific announcements[15]. Homework problems were assigned each week and posted. Many students posted their answers on the WWW. Thus, WWW was a very important resource used in the course for asynchronous communication. Finally, a hypertext glossary of biocomputing terms was implemented as a collaboration between authors, instructors and some students[19].

It should be pointed out that the whole hypertext book and the course archives were available at all times to anyone with Internet access, and they will be kept accessible. After further editing, we hope this book will become a valuable source for training in biocomputing, usable by other courses and/or as a source of reference material.

2.6 The Virtual Classroom and BioComputing Division Complex at BioMOO

A virtual BioComputing Division (BCD) complex including classrooms and instructors' offices was created at BioMOO, the text-based electronic conferencing system for Biologists founded and maintained at the Weizmann Institute by Gustavo Glusman[20, 21]. Its purpose was to provide appropriate "virtual" rooms for the groups' weekly interactive sessions and lectures, and for contacting the instructors during their office hours.

The most notable tool created for the course, and accessible via BioMOO, is a visualization tool for pairwise sequence alignment, implemented by Gustavo Glusman[22]. It allows the unit-cost alignment of short sequences using the dynamic programming algorithm. Per default, all the steps performed by one student are "heard" by his/her instructor and peers as long as they are in the same virtual room. In this way, each student can operate his/her own "sequence aligner", and the instructor and fellow students can check results. Moreover, WWW pages are being generated and updated that allow easy examination of the dynamic programming matrix as the alignment proceeds, employing "BioWeb" [23], BioMOO's MOO/WWW interface.

A guest lecture by an invited expert on fast database searches, Dr. Bill Pearson of the University of Virginia, was carried out as part of one of the study groups' weekly sessions. Pearson and the instructor (F. De La Vega) connected from a meeting ("Patterns in Biological Sequences" Workshop) held at the Aspen Center for Physics. Students were able to ask questions regarding fast database searches to one of the most prominent workers in the field. A second invited lecture was given on the subject of optimal Multiple Alignment, by Dr. John Kececioglu of the University of Georgia, Athens. Dr. Kececioglu explained his recent analysis and improvements to the MSA software, currently the most powerful tool for optimal multiple sequence alignment. Both recordings are kept archived and are accessible from the course WWW server [24].

3 General Discussion

3.1 Overall Evaluation

In the collective judgment of organizers, instructors and students, as solicited at the end of the course, this has been a successful enterprise. In spite of the numerous problems that had to be solved or circumvented (the rest of this chapter is devoted to their discussion), all 7 study groups covered the text in considerable depth, and sustained lively discussions until the last week of classes. Some student answers to homework exercises were so excellent that they will be integrated as additional course material in the future. An exchange of ideas, experience and research perspectives was fostered between partners that may never meet in real life. A final instructors' meeting brought about a bunch of new ideas on distance education, yet to be evaluated and implemented in future courses.

3.2 Technical Problems, Attendance and Dedication Problems

As in all distance education efforts using computer-mediated communication, many problems were related to the technology used. Some students had problems finding appropriate Internet access or configuring software. Common problems included: network delay and down-times, SLIP/PPP configuration and unfamiliarity with the commands and clients used for electronic conferencing.

Other problems encountered during the development of the course were related to electronic meeting attendance. In two cases, scheduling problems were solved by assigning the students to another study group. Most of the attendance problems and drop-outs were caused by participants underestimating the time needed for the course. It was clear that it was not possible to keep up with the course unless at least 5 hours per week were devoted to it. A few students were discouraged by technical problems.

However, two-thirds of our students (i.e. 22 out of 34) were still actively participating in the electronic meetings during the last weeks of the course. Only four official resignations were received and the causes argued were related to excessive workload (apart from the course). The overall drop-out was considerably lower than in previous GNA courses, also due to stringent application and self-selection policies that had been applied for registration.

3.3 Group Heterogeneity Issues

Some problems have arisen due to the heterogeneity of the participants. Practicing biologists found the mathematical approach of the subject difficult, and were looking for more practical approaches. Others were computer scientists who found it very easy to understand some of the concepts, going far ahead of their peers. These two populations of students coexisted in our course although they had rather different goals with respect to biocomputing, and this caused some problems, disappointing some of the practicing biologists.

A similar problem of group heterogeneity was also encountered during the GNA C++ course, one of the antecedents of our course [25]. They concluded that in future editions of the course the two main groups of attendants had to be separated. In the next section, we discuss the pros and cons of such a separation in our case.

4 Conclusions

4.1 Further Development of the Course

At the writing of this manuscript the course has just finished, and although some of the information is still fresh in our minds, a period of meditation and analysis would be required to fully appreciate the accomplishments and correctable deficiencies of the course. A second edition of the course is planned for the Spring of 1996 [26]. This time the course syllabus shall offer further material on the applications of the various methods and algorithms used in sequence analysis, while retaining the emphasis on understanding the fundamental mathematical and algorithmic concepts in biocomputing.

It is conceivable to separate future applicants in two main groups: computer scientists, and molecular biologists. Since these groups have quite different goals in approaching biocomputing, they can form separate study groups that may cover the practical and theoretical material with different emphasis. However, although this separation looks like a good pragmatic decision at first glance, it may actually be a step backward ! If biocomputing is going to mature from an interdisciplinary field to an integral discipline, the separation between both sides must eventually be overcome.

Many further improvements are possible: better use of hypertext and multimedia in the book chapters; inclusion of a set of additional readings centered on a few remarkable reviews; and an encouragement to organize guest lectures with widely recognized experts. To solve some of the technical problems, a more extensive set of manuals and tutorials is needed. An archive containing several pieces of pre-configured software and tutorials would be desirable. Perhaps an "Internet-in-a-box" approach along the lines of the public domain "DOS Internet Kit" would be helpful to participants with little previous computer and network experience.

As a long-term goal, the depth and breadth of the hypertext book and course offerings shall be expanded considerably, involving contributions from many more researchers and teachers. However, such an expansion could only take place if the project is managed by full-time staff, and/or run as a commercial enterprise, because the organizational load is considerable and the 1995 course has already stretched the time limits of the organizers. If there were not the bottleneck of this purely volunteer-based coordination, more contributions could be called for, including a shared hypertextified bibliography, maths tutorials, and further plenary discussions. More interactive learning tools should be developed in the spirit of the visualization tool for pairwise alignment implemented at BioMOO, even a 3-dimensional visualization of the calculation of a multiple alignment using VRML (Virtual Reality Modelling Language). Such efforts may eventually yield an online interactive laboratory for biocomputing teaching and research.

4.2 Perspectives on Distance Education via Computer Networks

We expect that biocomputing will continue to serve as a major field of research on distance education via the Internet. While the necessary technology is still emerging, it is too early to make reliable conjectures about its future. Our current experience can be summarized as follows. Computer-mediated distance education is both cheap and expensive. It is cheap as long as it is based on volunteer work by people who are paid by other sources. As long as it is new and exciting, there should be no problems recruiting volunteers. However, if our course had been run by paid instructors, it would have been very expensive even if we neglect the organizational extra work. The amount of work spent by each instructor was in the order of teaching a real-life lecture to all 34 students. Allocating a teaching assistant for grading homework, we may estimate an overhead of 7:2 for distance education. Much of this overhead is certainly due to the experimental nature of computer-mediated distance education, and will be diminished by more reliable and more powerful technology. The remaining overhead must be justified by intrinsic benefits of computer-mediated communication.

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