Authors Francois Lombard[1], Marie-Claude Blatter [2]
Geneva University [1]TECFA, LDES, IUFE, [2] SIB Swiss Institute of Bioinformatics

Title : Adapting teacher training to new evolution research approaches.

Abstract :

As evolution research methods have evolved to include new genomic approaches, based on freely available data and tools, an opportunity for proving and teaching evolution has been translated into teacher training programs in Geneva.
The data from countless entire genomes (DNA and protein sequences) and tools for comparing and extracting evolution evidence in conserved patterns, (BLAST, etc.) or building phylogenetic trees (PhyML,…) can be easily and freely accessed via Internet. Ever more research in evolution is based on sequence analysis, providing new and very strong evidence. Any student or teacher can freely use these authentic data and tools, opening new educational opportunities to explore, test and validate hypotheses. Possibly the strongest evidence ever is directly available to all schools.
However new knowledge and competencies need to be developed to allow teachers to integrate these approaches into their classes. Indeed, these new information processing approaches in biology might be unfamiliar to biologists trained only a few years ago.
As part of a comprehensive teacher training program in Geneva, evolution teaching and inquiry modules were developed within Geneva university in a collaboration of researchers in educational science LDES, TECFA and bioinformatics (Swiss-Prot group at SIB). The teaching was deployed in teacher training programs since 5 years with scenario-based modules freely available online.

How to include this new approach of evolution teaching in various chapters of biology, opportunities for new inquiry tracks for students will be discussed. Conditions and reasons for uneven acceptance by institutions or teachers, and possible solutions will be discussedEvolution teaching is difficult

 "Nothing in biology makes sense except in the light of evolution » [1], it is, however, a tricky topic for teaching as most learners come to it with previous knowledge and it is fraught with misconceptions [2]. And of course evolution teaching is a contentious issue [3].
Evolution is the chapter by which biology – up to then mainly ontological and descriptive - became explanatory. The questions, that were "What is this species, this structure ?" moved towards conceptual questions "How did this species appear ? Why did this species acquire this particularity ? What are the forces that cause species to evolve in certain ways? " [4]. The main questions in molecular biology research nowadays are of the type "What are the underlying mechanisms ?".

Biology changes
However, much literature [4, 5] and our research shows we are now seeing another paradigm change [6] in biology : towards information processing IT-Rich Biology (IT= information Technology), as Butler put it in a nutshell [7] "Are you ready for the revolution ?".
Our research has identified 4 aspects of IT-enhanced Biology that seem relevant to education:
- Bioinformatics, the application of computers in biological sciences and especially storage and analysis of biological sequence data (DNA and proteins), and other experimental data such as 3D structure or microarrays : all the range of 'omics: genomics, transcriptomics, proteomics, etc.
- Other biological databases such as botanical zoological or georeferenced data (biological data on GoogleEarth).
- Systems biology, synthetic biology and simulations.

- Knowledge building in an infodense world: the ability to locate, use, and evaluate information [20]

"For life sciences ranging from ecology, botany, zoology, and developmental biology to cellular and molecular biology […], IT is essential to collect key information and organize biological data in methodical ways in order to draw meaningful observations. Massive computing power, novel modelling approaches, new algorithms and mathematical or statistical techniques, and systematic engineering approaches will provide biologists with vital and essential tools for managing the heterogeneity and volume of the data and for extracting meaning from those data"[4]. We would like to stress that this will never replace the "wet lab" or field observations.

This new expansion of biology offers new way of experimenting, of building knowledge and of publishing science [8]. In fact informal surveys have shown biologists spend more than half their time practising this IT-Rich biology. Most research published in high impact magazines relies crucially of even only on this sort of experimenting [9-11].

Massive new data and new tools offer opportunities to explore, test and validate hypotheses, which define experimental biology. We shall therefore speak of experimenting for searching, comparing sequences, and other explorations of the massive amounts of authentic data accessible in classrooms. Some may recoil at this, but we would like to argue that in terms of learning potential, these "experimental approaches" are best thought of as we do for experimental, hands-on laboratory work.

Should evolution teaching change ?

The field of research in evolution is also evolving with IT, but let's just make it clear: this article is not about new teaching tools using IT (e.g. [12]). In contrast we suggest integrating IT-rich biology in most chapters of biology education with some of the data, the tools and methods used by today's evolution researchers. Moore [13] wrote "Science teaching must evolve". He argues that "Many teachers are not scientifically capable of teaching evolution using modern approaches".

Our own research[14] suggests that education is slow in recognizing this new IT-Rich biology, and that new stimulating opportunities for authentic learning have arisen. Indeed Thomas Kuhn[6] predicts that when a paradigm changes, as it changes the fundamentals on which our professional identity relies, most practitioners will resist the change. Many of us will remember how strongly the expansion of biology to include molecular approaches was resisted in schools and universities some 30-40 years ago.

We will attempt to address in this article how to integrate new approaches to evolution in curricula and classroom practices.

Evolution teaching: new opportunities

As our research suggests [8] that the change of biology is widespread, and affects most if not all aspects of evolution. It follows that there is no need to add a new chapter to biology or evolution, but that knowledge related to these new approaches (fundamentals such as sequence coding, database organisation, concepts such as alignment, underlying concepts such as parsimony principle for cladograms, etc.) and competencies to manage this knowledge (how to extract a sequence, and similar sequences, how to compare them,…) are needed. Moore mentions that "there is a big difference between mere information and a teaching unit: teachers generally have no time or guidance to elaborate new course units from raw materials." Rather than producing teaching units, we would argue for training teachers to use real authentic tools available everywhere via internet for free.

Much research [15, 16] point to the importance of authenticity "engagement in inquiry activities similar to those of scientists" [15]. Authenticity goes three levels [16]: A first level involves the facts: true research data is more authentic than carefully selected, educationally polished data. A second level involves the tools and methods: involving students in similar tasks, with the same tools and methods as professional. A third level would involve students in "doing real research", creating new knowledge.

Research and standards [17] encourages empowering learners to face real, complex problems rather than oversimplify in an attempt to make learning easier [18] : "The greatest intellectual sin that we educators commit is to oversimplify most ideas that we teach in order to make them more easily transmissible to

learners. In addition to removing ideas from their natural contexts for teaching, we also strip ideas of their contextual cues and information and distill the idea to their "simplest" form so that students will more readily learn them. But what are they learning? That knowledge is divorced from reality, and that the world is a reliable and simple place. But the world is not a reliable and simple place, and ideas rely on the contexts they occur in for meaning "[18].

Consequently rather than developing new educational resources about this new IT-Rich biology, we set off to develop around existing authentic tools and data new teaching designs that might allow engaging student in authentic activities at level 1 and 2. This is possible because of the wide availability of authentic biological data, through the web (all the range of "'omics", but also systematic (e.g. UniProt Taxonomy), zoological and botanical (GBIF), biogeographic, ecological etc.) and freely available tools such as BLAST, alignment (e.g. ClustalW), phylogenetic tree building tools (Phylodendron, PhyML), etc.

Our examples have been developed to integrate modern IT-Rich biology's authentic tools into most chapters of biology. Indeed paralleling the evolution of our science, we see, in accord with Moore[13] but for the rest of biology too, an opportunity for science education to move closer to science.

Opportunities for new inquiry tracks and strong evidence for Evolution

The push to change of education towards more experimenting and inquiry strategies [19-21] is strong worldwide. And has translated into lab and field opportunities for learners to observe and experiment. One of the problems of evolution teaching is that typical courses offer limited opportunities for experimenting.

It is ironical that the field of evolution that brought biology out of a purely descriptive science into explanation of causes [4] has been so resistant to experimental approaches in education. Indeed, evolution changes often happen in a time frame incompatible with schools : over the course of millions of years - or within tiny invisible species such as bacteria. In both cases, they remain rather abstract to most students. Availability of authentic data and tools that can be freely used by any student or teacher, opens new educational opportunities to explore, test and validate hypotheses.

There are indeed simulations (e.g. MacEvolut one of us developed for simulating giraffe evolution) and typically a few fossils or semi-authentic data such as plastic models of skulls are typically available in class. Possibly the strongest evidence and experimental exploration ever for evolution - based on authentic research data - is now directly available to all schools. Evolution, or as Darwin put it "Descent with Modification" [22], refers to common origin and evidence of gradual change, that can be related to environment. Vast amounts of sequences easily available offer strong opportunities to test common origin by exploring and showing the universality of DNA, and 'quasi-universality' of the genetic code. Numerous proteins with similar function in different species (orthologs) are easy to find and constitute strong evidence of common origin. Aligning their sequences reveals similarities and graduated differences, which constitute evidence of progressive change.

Differences in function of similar/homologous genes within a given species (paralogs) reveal common origin (gene duplication). How random changes can produce slightly different proteins can be explored. Convergence of gene-function can be discovered.

A comprehensive teacher training program in Geneva

All too often interactions between universities and in-service teachers amount to a conference given by a specialist to very impressed teachers, who then go back to school and teach as ever before. Although these courses involved high profile researchers of the Geneva university, the course was designed so as to spend most of the time in interactions around how to integrate this new knowledge into classrooms, as this is known to be a key difficulty. Indeed the obstacles to information transfer [23] effectively to teachers are known: differing values, immediate usability, close availability, etc.

Building teaching knowledge by confronting scientific specialist and education specialist with teachers

In a collaborative scheme involving the Geneva University (Swiss Institute of Bioinformatics (Swiss-Prot group), LDES and TECFA) and Geneva High School teacher training, we developed many scenarios and

trained teachers to integrate in their teaching many of the new approaches that IT-rich Biology offers. We took time to build a common language, and identified the implicit differences between meanings of same terms, data representation, knowledge structure and priorities that are embodied in the databases etc. Indeed tools such as BLAST, alignments, phylogenetic tree building are not "just tools": they are neither transparent nor free of assumptions which influence the manner in which they can be used [24] and the changes they induce change in the strategies and their affordances need to be learned.

With successive iterations of this course, this interaction of researchers and teachers meeting halfway from the lab to classrooms was pushed one step further : an expert presented how his field of biology is expanded by IT, what changes he imagined this could imply in education, and then discussed with teachers how classroom and curriculum realities could accommodate this.

Acknowledging the need to articulate the three forms of knowledge involved [25] was key to structuring the design: disciplinary scientific knowledge was brought by a bioinformatics specialist (M.-C. Blatter), an educational research specialist (F. Lombard) playing the role of a naive journalist asking questions to highlight crucial differences or possible misunderstandings. This was geared towards helping participant teachers build the third form of knowledge: teaching knowledge. So a lot of the training time was organized around interactions focussed on how scenarios can be implemented in schools, between specialists of content and of education research with teachers seen as specialists of teaching .

Focussed on scenarios

Since teacher's activity is mainly organized around what happens in class, the design was built around the teaching knowledge discussed on the basis of nearly class-ready scenarios. The scenarios were designed to empower the participants to use authentic research data and tools.

As it has often been observed that teachers need to modify, adapt and personalize whatever teaching material they use, the scenarios are open to customization. In fact it has been shown that reusability is great for the technical part of scenarios, but minor for the pedagogical part [26].

Each step of the scenarios is guided with detailed instruction and comments. Links allow picking up the scenario at any point.

All these scenarios are online and freely available on our web page http://tecfa.unige.ch/perso/lombardf/bist/. Explicit place of insertion in the curriculum was discussed. Most of the time, one key use of data and tools could be implemented in different chapters. E.g. finding the sequence of Insulin could be used while discussing the physiology of glucose regulation or as an example for biosynthesis of proteins or in evolution to establish the existence and similarities of such proteins in various species, and align them to form a phylogenetic tree. Cross-opportunities to establish the evolutionary evidence within physiology, molecular biology or ecology were highlighted. E.g. when searching for human Cytochromes in the context of cellular respiration the fact that other similar Cytochromes from other species than ours turned up could be incidentally highlighted.

Each scenario was explored by teachers during a course lasting 1-2 days offered to in-service secondary biology teachers. The training involved a guided exploration of the experimentation scenarios and the participants had time to explore and get familiar with using the scenario and trying to customize them, e.g. by using their favourite protein, or adapting them to their specific teaching context with the help of the trainers. The scenarios being available on-line remain available for use in any school.

The scenarios aimed at allowing teachers to :

- Develop a global view of the main databases and basic understanding of their specificities, so as to be able to find nucleotide (Genbank, EntrezGene, etc) and protein (UniProtKB/SwissProt, etc) sequences from the names of genes and proteins, to be able to get research up-to-date information about genetic illnesses (Genes&Diseases), genes, proteins. To find and visualize 3D structure of the proteins, or to find articles in PubMed.
- Have a basic familiarity with the crosslinks and context indices so as to keep track and know enough to understand what is being viewed.
- Develop a minimal familiarity with the basic tools, such as:

- BLAST allowing to find genes and proteins from their sequence (such as read from a gel), or to find similar sequences.
  - ClustalW (e.g) for aligning sequences to show conserved regions or prepare for tree building.
  - PhyML, Phylodendron (e.g) for producing phylogenetic trees.
- Develop a basic knowledge of the concepts and terms.
- Understand the logic of theses databases, which is research – oriented and often differs from the way teachers might expect the information to be structured: e.g. that RNAs are recorded as their cDNA sequences, or that there are as many sequence redundancy for a protein as there have been researchers publishing about that sequence.
- More generic information high-level literacy competencies appeared as critical: being capable of teaching and learning efficiently without understanding all the information available. Capacity to synthesize from very different, fluctuating information sources, etc.

An example of scenario

One group of scenarios searches differences in equivalent proteins (orthologs) and builds phylogenetic trees, which can be compared with those built with other types of data: morphological and physiological characters for example.
As an example we will develop in some detail a representative scenario: building a phylogenetic tree from sequences of a given protein (insulin for example) in different species
Like most other scenarios, we proposed 3 different levels in terms of authenticity:
1) Basic level : Relies on a piece of on-line software (PhiloPhylo) developed by the Swiss-Prot group specifically for educational purposes : It guides the learner along the key steps of a phylogenetic sequence analysis : choice of the sequences from proteins for which sequences are available from many species, comparison of these sequences (multiple alignment), building and visualization of the tree. Results are then discussed.
By limiting the steps and offering a minimum of options this scenario reduces the risk of getting lost, and could helps focus on the main concepts. Doing so trades authenticity for simplicity of use and offers teachers a reassuring linear route by which students are guided. However, this might give the idea that the biological concepts explored are simple and straightforward.

2) Medium level : This scenario uses authentic databases (UniProKB) for selecting proteins from their name, the on-line tools for aligning sequences and formatting the alignement (ClustalW), then uses a simplified research tool (Phylodendron) for producing and visualizing the tree. As such this scenario is more complex but more authentic, giving students a glimpse into the richness of data available but guiding them enough to produce meaningful results. As for any hands-on lab activity, the guidance and perspective the teacher gives is crucial to help students build real knowledge and not only go through the motions, in what Bereiter calls "reduction to activity" [27](Scenario 5)
3) Advanced level: this scenario uses the tools available on the web as researchers in their lab (Scenario 5pro). This scenario differs mainly in that it explores into more depth the options of how the same alignment can often lead to slightly different trees depending on the assumptions made. And allows students to develop perspective on the assumptions implicit in building trees.
These scenarios have been integrated to some degree or other in many secondary and high schools in Geneva.

Conclusion
We believe the time is ripe for integrating IT-rich evolution into classrooms, and that this needs proper teacher training. We suggest explicitly addressing the fact that biology is changing, in particular by having recognized biology researches describe how IT plays into their work. We suggest that a design needs inputs

from disciplinary biology experts, education experts and should be described in terms of teaching knowledge (possibly framed as scenarios).

We suggest this includes helping teachers develop information literacy strategies to avoid information overload, which should be thought of as a long-term training effort, and could be supported by adequate frequent updating media such as blogs or newsletters bridging research literature and educational practitioners.

We propose the following design rules: approach IT-rich biology as experimental lab work, empower students to use authentic data and tools whenever possible, design very precisely the technical part and loosely suggest the pedagogical part of scenarios.

References

1. Dobzhansky, T., *Nothing in biology makes sense except in the light of evolution.* American Biology Teacher, 1973. **35**(3): p. 125-129.
2. Bishop, B.A. and C.W. Anderson, *Student conceptions of natural selection and its role in evolution.* Journal of Research in Science Teaching, 1990. **27**(5): p. 415-427.
3. Skoog, G., *The Coverage of Human Evolution in High School Biology Textbooks in the 20th Century and in Current State Science Standards.* Science & Education, 2005. **14**(3 - 5): p. 395-422.
4. Wooley, J.C. and H.S. Lin, *Catalyzing Inquiry at the Interface of Computing and Biology. Committee on Frontiers at the Interface of Computing and Biology, National Research Council*, in *Committee on Frontiers at the Interface of Computing and Biology, National Research Council*, J.C. Wooley and H.S. Lin, Editors. 2005, National Academies Press.
5. NRC Committee on Undergraduate Biology Education to Prepare Research Scientists for the 21st Century, *BIO2010: Transforming Undergraduate Education for Future Research Biologists* 2003, National Research Council.
6. Kuhn, T., S., *La structure des révolutions scientifiques.* 1972, Paris: Flammarion.
7. Butler, D., *Are you ready for the revolution?* Nature, 2001. **409**: p. 758-760.
8. Lombard, F. *L'actualité de la biologie : vulgariser ou autonomiser ?* in *JIES : XVIIIes Journées internationales sur la communication, l'éducation , la culture scientifiques techniques, et industrielles.* 2007. Chamonix.
9. Pollard, K.S., et al., *An RNA gene expressed during cortical development evolved rapidly in humans.* Nature, 2006. **443**(7108): p. 167-172.
10. Bakewell, M.A., P. Shi, and J. Zhang, *More genes underwent positive selection in chimpanzee evolution than in human evolution.* PNAS, 2007. **104**(18): p. 7489-7494.
11. Gibbons, A., *Human Evolution Is Speeding Up.* Science, 2007. **ScienceNOW Daily News**(10december 2007).
12. Sandoval, W.A. and B.J. Reiser, *Explanation-Driven Inquiry: Integrating Conceptual and Epistemic Scaffolds for Scientific Inquiry* Science Education, 2003. **88**(3): p. 345-372.
13. Moore, A., *Science teaching must evolve.* Nature, 2008. **453**(7191): p. 31-32.
14. Lombard, F. *Information Technology (IT) to change biology teaching, or teaching IT-changed biology ?* in *BioEd 2008, Biological Sciences Ethics and Education The Challenges of Sustainable Development.* 2008. Dijon.
15. Schwartz, R.S., N.G. Lederman, and B.A. Crawford, *Developing views of nature of science in an authentic context: An explicit approach to bridging the gap between nature of science and scientific inquiry.* Science Education, 2004. **88**(4): p. 610-645.
16. The Cognition and Technology Group at Vanderbilt, *Anchored Instruction and Its Relationship to Situated Cognition.* Educational Researcher, 1990. **19**(6): p. 2-10.
17. AAAS, *Project 2061, Benchmarks for Science.* 1993, American Association for the Advancement of Science: Washington.
18. Jonassen, D.H., *Learning to Solve Problems with Technology: A Constructivist Perspective.* 2003, Upper Saddle River NJ USA: Merrill Prentice Hall.
19. Rocard, M., et al., *Science education Now : a renewed pedagoy for the future of Europe*, in *Directorate-General for Research* M. Rocard, Editor. 2006, OECD EUROPEAN COMMISSION Bruxelles.
20. NRC National Research Council, *Inquiry and the National Science Education Standards. A Guide for Teaching and Learning.* Centre for Science, Mathematics, and Engineering Education, ed. C.o.D.o.a.A.t.t.N.S.E.S.o.S. Inquiry. 2000: National Acadmies Press.
21. NRC, N.R.C., *National science education standards.* 1996, Washington, DC: National Academy Press.
22. Darwin, C. and J. Carroll, *On the Origin of Species.* 2003: Broadview Press.
23. Huberman, M., *Répertoires, recettes et vie de classe : comment les enseignants utilisent les informations.*, in *L'art et la science de l'enseignement.*, M. Crahay and L. D., Editors. 1986, De Boeck: Bruxelles. p. 151- 185.
24. Rabardel, P., *Les hommes et les technologies, approche cognitive des instruments contemporains.* 1995, Paris: Armand Colin. .
25. Tardif, M., C. Lessard, and L. Lahaye, *Les enseignants des ordres d'enseignement primaire et secondaire face aux savoirs: Esquisse d'une problématique du savoir enseignant.* Sociologie et sociétés, 1991. **23**(1): p. 55-69.
26. Pernin, J.-P. and A. Lejeune, *Dispositifs d'apprentissage instrumentés par les technologies : vers une ingénierie centrée sur les scénarios.* Technologies de l'Information et de la Connaissance dans l'Enseignement Supérieur et de l'Industrie. 2004, Compiègne: Université de Technologie de Compiègne. 407-414.
27. Bereiter, C., *Education and Mind in the Knowledge Age.* Second ed. 2002: Lawrence Erlbaum Associates.