Technosciences in Academia: Rethinking a Conceptual Framework for Bioinformatics Undergraduate Curricula

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ABSTRACT

Technosciences in Academia: Rethinking a Conceptual Framework for Bioinformatics Undergraduate Curricula

Iphigenia Sofia Symeonidis

This paper aims to elucidate guiding concepts for the design of powerful undergraduate bioinformatics degrees which will lead to a conceptual framework for the curriculum. “Powerful” here should be understood as having truly bioinformatics objectives rather than enrichment of existing computer science or life science degrees on which bioinformatics degrees are often based. As such, the conceptual framework will be one which aims to demonstrate intellectual honesty in regards to the field of bioinformatics. A synthesis/conceptual analysis approach was followed as elaborated by Hurd (1983). The approach takes into account the following: bioinformatics educational needs and goals as expressed by different authorities, five undergraduate bioinformatics degrees case-studies, educational implications of bioinformatics as a technoscience and approaches to curriculum design promoting interdisciplinarity and integration. Given these considerations, guiding concepts emerged and a conceptual framework was elaborated. The practice of bioinformatics was given a closer look, which led to defining *tool-integration* skills and *tool-thinking* capacity as crucial areas of the bioinformatics activities spectrum. It was argued, finally, that a process-based curriculum as a variation of a concept-based curriculum (where the concepts are processes) might be more conducive to the teaching of bioinformatics given a foundational first year of integrated science education as envisioned by Bialek and Botstein (2004). Furthermore, the curriculum design needs to define new avenues of communication and learning which bypass the traditional disciplinary barriers of academic settings as undertaken by Tador and Tidmor (2005) for graduate studies.

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DEDICATION

To my parents.

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A Bioinformatics Primer

When presenting his "gentle overview" to bioinformatics, Nair starts by asking the question: what would Louis Pasteur, (considered as the forefather of biotechnology) and Babbage, (considered as the forefather of computer science), have talked about had they ever met? Although, as he explains, historically it is not known whether or not they actually did meet, the answer to this question today has become rather straightforward: bioinformatics. (Nair, 2007)

Bioinformatics can be understood as the utilization of the computational capacity of computers for the elucidation of biological questions. Traditionally, biology has had two means of experimentation, either within living organisms, referred to as *in vivo* experiments, or in artificial test-tube environments referred to as *in vitro* experiments. The data-mining and simulation potential of computers has led to a third way of conducting biological experiments: *in silico* experimentation (named so after the silicon chips of microprocessors) (Claverie & Notredame, 2003, p. 10). The *in silico* experiments need not necessarily be separated from the more traditional forms of experimentation but rather become a significant part of the molecular biology experimental cycle, as illustrated in figure 1 (Macmullen & Denn, 2005), by providing valuable insight for the design of the *in vitro* experiments.

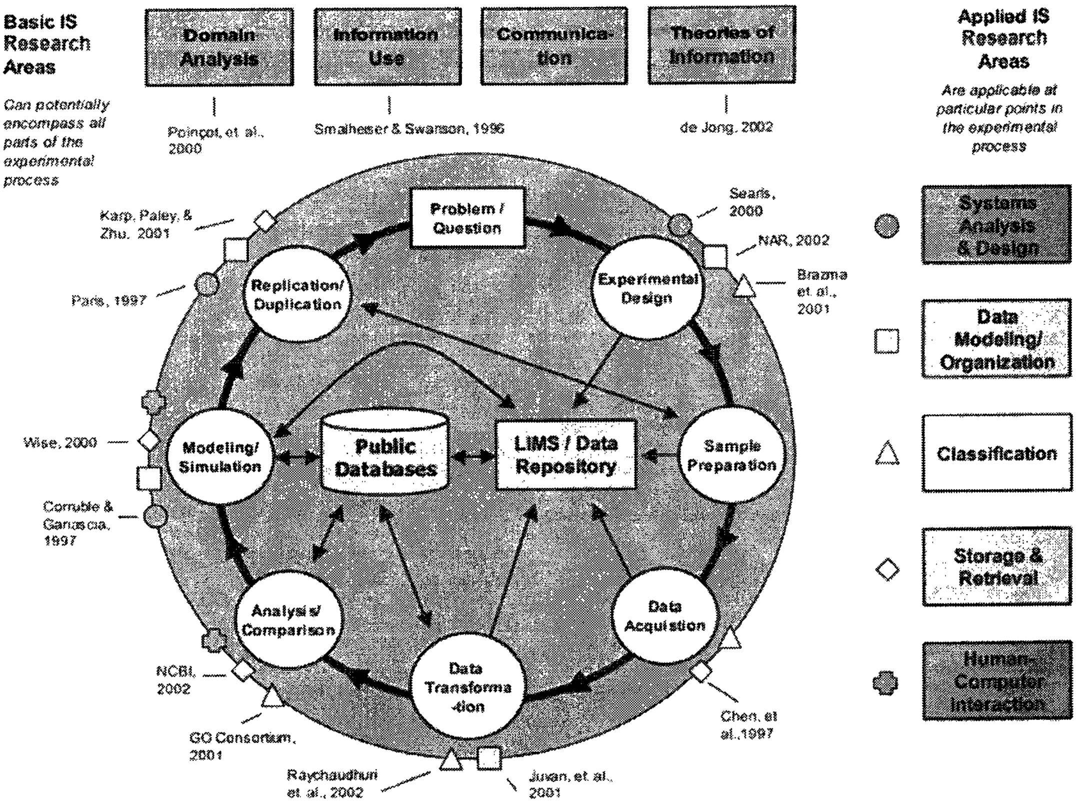


Figure 1. Molecular biology experimental cycle. The cycle depicts the type of information processing taking place along the cycle. The in silico experimentation need not be separate from the traditional molecular biology experimental cycle. (Macmullen & Denn, 2005)

Despite the immense attention given to Bioinformatics in the last decade it has, in a way, existed since the 1970's:

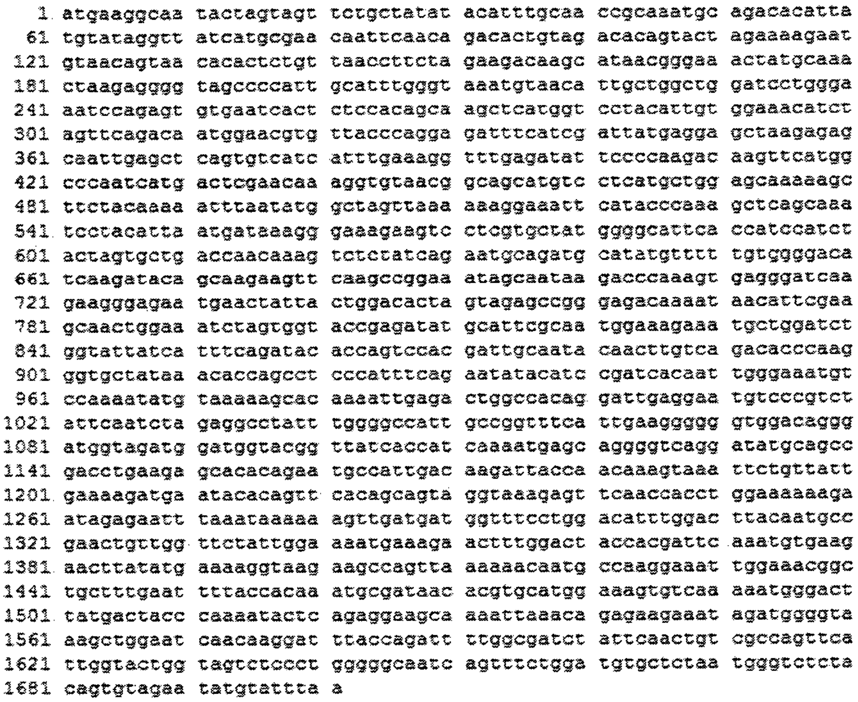
> … sequences were assembled analyzed, and compared by (manually) writing them on pieces of paper, taping them side by side on laboratory walls, and/or moving them around for optimal alignment (now called *pattern matching*). As soon as the early computers became available (as big as locomotives and just as fast, and with 8K of RAM!), the first computational biologists started to enter

these manual algorithms into the memory banks (Claverie & Notredame, 2003, p. 12).

But, it wasn't the processing capacity alone of computers which produced this shift in methodology; other technologies appeared which generated quantifiable biological results:

> Only when measurable biological quantities started appearing in the form of sets of three-dimensional co-ordinates, or later, as strings of characters, then computation in biology boomed … When in the 1970's, the first algorithms, and most importantly, their computer implementations became available, biological computation and theoretical research in biology started being shaped towards its present state. (C. Ouzounis, 2000, p. 188).

In the recent history of life sciences one such technology which changed how data are collected was high-throughput DNA sequencing technology. This technology, along with the continuous improvement of the processing capacity of computers, is what firmly established bioinformatics as a field of study. Further, this technology is constantly evolving and it is common to hear of next-generation sequencing technology. Without getting into the details of the mechanisms of the DNA sequencing technology, we can simply metaphorically say that given a DNA sample, it 'reads' and outputs a sequence made up of four distinct characters, generally visualized as A, T,C, G, representing the four nucleotides which make up DNA (adenine, thymine, cytosine and guanine abbreviated A,T,C,G). For example, figure 2 represents the sequence of the Influenza A H1N1 virus which has been sequenced.



```
   1 atgaaggcaa tactagtagt tctgctatat acatttgcaa ccgcaaatgc agacacatta
  61 tgtataggtt atcatgcgaa caattcaaca gacactgtag acacagtact agaaaagaat
 121 gtaacagtaa cacactctgt taaccttcta gaagacaagc ataacgggaa actatgcaaa
 181 ctaagagggg tagccccatt gcatttgggt aaatgtaaca ttgctggctg gatcctggga
 241 aatccagagt gtgaatcact ctccacagca agctcatggt cctacattgt ggaaacatct
 301 agttcagaca atggaacgtg ttacccagga gatttcatcg attatgagga gctaagagag
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 421 cccaatcatg actcgaacaa aggtgtaacg gcagcatgtc ctcatgctgg agcaaaaagc
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1441 tgctttgaat tttaccacaa atgcgataac acgtgcatgg aaagtgtcaa aaatgggact
1501 tatgactacc caaaatactc agaggaagca aaattaaaca gagaagaaat agatggggta
1561 aagctggaat caacaaggat ttaccagatt ttggcgatct attcaactgt cgccagttca
1621 ttggtactgg tagtctccct gggggcaatc agtttctgga tgtgctctaa tgggtctcta
1681 cagtgtagaa tatgtattta a
```

Figure 2. Influenza A H1N1 sequence. Example DNA sequence depicting how the output format of the sequencing process is visualized. (Sequence from http://www.ncbi.nlm.nih.gov/nuccore/GU968907)

Advancements in this technology have made possible the generation of large amounts of data within reasonable time spans and at sensible costs. Figure 3, which represents the total number of sequences stored in the GenBank Database, demonstrates the exponential growth of available data. Thus the need for bioinformatics expertise to analyze this promising and ever-growing information is paramount.

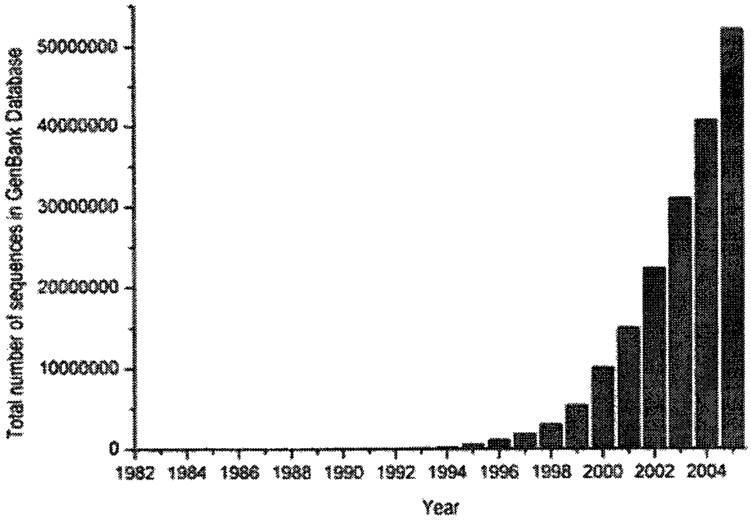


Figure 3. Exponential growth of sequence data in the GenBank Database. Depiction of the mid 90's biological data explosion. (From NCBI http://www.ncbi.nlm.nih.gov/bookshelf/br.fcgi?book=bioinfo&part=A135&rendertype=figure&id=A142)

Dupré's Visit to the Sanger Center

In order to gain a better grasp of the field of Bioinformatics, Dupré's anecdotal account of his visit to the Sanger Center, where a substantial part of the sequencing of Human DNA was realized, is highly useful and insightful; through his narrative a number of key aspects of bioinformatics are exposed:

> Over the reception desk an electronic display flashes a stream of Cs Gs As and Ts which, we are informed, constitute a real time read out of some DNA that is being sequenced somewhere on the premises. Touring the building where the sequencing actually takes place, the first stop is a room in which large robots stick tiny probes into Petri dishes and then into rectangular arrays of test tubes. Spots on the nutrient gel in the Petri dishes, we are told, contain bacteria infected by

> viruses with pieces of human DNA. We next peer through a window in the door of a room containing small but expensive machines that perform the polymerase chain reaction, the process that multiplies the quantities of DNA generated in the first process to the quantities required for the sequencing machines. These latter, finally, occupy a warehouse-sized space in which conversation is rendered difficult by the hum of the powerful cooling systems. There are perhaps a hundred of these machines, each connected to a familiar looking desktop computer, all busily sequencing genomes. The room is largely devoid of human activity, except for the occasional lab assistant carrying trays of material to be fed into the machines. A separate building, which I did not see inside, houses the bioinformatics operation, in which the output of all these machines, and others like them around the world, are chewed over by powerful computers.

He then continues by commenting on the division of labour in modern science often referred to as ‘team’ science or ‘big’ science:

> Perhaps the most interesting moral of this comparison is the way in which it points to the division of labour in much of modern science. Though there are of course plenty of biologists who understand the basic biological principles underlying the various bits of machinery in the sequencing lab, it's a fair bet that few or none of them know in any detail how all of these machines work. Moreover, even those who know how they work in some detail surely don't normally have the expertise in operating them possessed by experienced technicians familiar with their quirks and occasional malfunctions. And even those technicians surely

> don't have the expertise of the engineers who design and construct the machines or who repair them when they malfunction in serious ways. To cut a long story short, a project such as the sequencing of the human genome involves the collaboration of thousands of people with hundreds or thousands of different forms of expertise, not to mention requiring many years of work by this large and diverse group of people. Clearly no one could offer a demonstration that the human genome was. . . . One is reminded of Descartes' concern that a proof should be compact enough to be held in the mind at the same time, though presumably Descartes never dreamed of anything quite this far from meeting this optimistic ideal. If one has confidence that the published drafts of the human genome bear some close relation to something in reality this is based not on proof or demonstration, but on trust.

Dupré's account easily conveys to the reader that Bioinformatics is yet another example of what is often referred to as Big Science. The enterprise involves thousand of people and it is impossible for any one person to completely understand the whole process. So how does one approach the problem for designing curricula for such an enterprise? Before further refining this question let us first review some definitions of bioinformatics.

Definitions of Bioinformatics

When considering bioinformatics education it would seem at first glance paramount to establish a definition of bioinformatics. This can be a standardized and agreed upon definition or at least a clearly stated static definition given a particular context. Let us first consider some definitions of bioinformatics. We shall than contemplate whether a stable and solid definition of the field is actually desirable for the carrying out of this analysis pertaining to the design of a conceptual framework.

The National Centre for Biotechnological Information (NCBI) states that "Bioinformatics brings together the fields of biology, computer science (CS), and information technology (IT) to analyze biological data that have been collected over the past fifteen or more years and continue to be generated today"(Burhans & Skuse, 2004, p. 417).

The National Institutes of Health (NIH) Biomedical Information Science Technology Initiative documentation defines bioinformatics as follows: "Research, development or application of computational tools and approaches for expanding the use of biological, medical, behavioural or health data, including those to acquire, store, organize, archive, analyze or visualize such data" (as cited in Heidorn PB, Palmer CL, & Wright D, 2007).

The first definition emphasized analysis. The second emphasizes data expansion (which of course will inevitably involve, as stated in the definition, acquisition, storage, organization, archiving, analysis and visualization of the data) Analysis and expansion both imply the creation of new knowledge. This new knowledge can be more data, more tools and approaches, or the elucidation of biomedical questions based on the data. Like all knowledge activities, the data will hopefully then become information (understanding relations) which will lead to knowledge (understanding patterns) and ultimately become wisdom (understanding principles) (Bellinger, 2004). Bioinformatics is therefore involved at each level of understanding.

This is not always the viewpoint which is followed. Depending on where the line is drawn with the involvement of bioinformatics in the knowledge creation enterprise different facets of doing bioinformatics are emphasized while others are left in obscurity. Often, what results is perhaps an over-simplification of bioinformatics: “Bioinformatics is often defined as 'applications of computers to biology'. In recent decades, biology has raised fascinating mathematical problems and reducing bioinformatics to 'applications of computers in biology' diminishes the rich intellectual content of bioinformatics” (Pevzner, 2004, p. 2160).

Like many emerging fields of study, the borders with neighbouring fields are often blurry. This seems to be the case between bioinformatics and computational biology: “Although some interpret it narrowly as the information science techniques needed to support genome analysis, many have begun to use it synonymously with 'computational molecular biology' or even all of 'computational biology'”(Altman, 1998, p. 549).

One author specifies that “The omission of physics differentiates bioinformatics from typical computational biology programs” (Burhans & Skuse, 2004, p. 420). The NIH defines computational biology as follows: “The development and application of data -- analytical and theoretical methods, mathematical modeling and computational simulation techniques to the study of biological, behavioural and social systems.” (as cited in Zatz, 2002, p. 353)

What the review of bioinformatics definitions along with computational biology definitions demonstrates is that appropriating a very rigid definition of bioinformatics, in the context of this thesis dealing with curriculum development which touches the root of such epistemological concerns, is perhaps not desirable.

Thus when reviewing undergraduate bioinformatics curricula in Chapter 4, we will not contrast them to a rigid definition of bioinformatics to see how they respond to it but rather examine the curricula through the definitions *they* give rise to. Similarly to the dictum spoken in Alice in Wonderland by Humpty Dumpty, “When *I* use a word [...] it means just what I choose it to mean - neither more nor less.” (Carroll, Lin, & Carroll, 2004, p. 219), bioinformatics will “mean” what a particular curriculum “chooses” for it to mean.

So what does Bioinformatics mean according to the curricular voice expressing a bioinformatics degree? We shall now proceed to more thoroughly stating the curricular problem pertaining to bioinformatics education and the research question explored throughout this thesis.

Problem Statement and Research Question

The advent of the human genome project constituted the final push to the paradigm shift in the life sciences for a quantitative biology. With a tremendous amount of biological data regarding gene sequence becoming available, molecular biologists are turning towards *in silico* methodologies for conducting their research. In response, the field of bioinformatics, which can be defined as the computational handling and processing of genetic information (C. A. Ouzounis & Valencia, 2003), is finding its place among university programs. Indeed, The BIO 2010 report, commissioned by the NIH and the Howard Hughes Medical Institute, mandates the use of computers at the undergraduate level and the American Society for Biochemistry and Molecular Biology (ASBMB) stresses the inclusion of bioinformatics as core content in biochemistry and molecular biology as well as the use of computer databases for problem-solving (as cited in Voet et al., 2003). In the United Kingdom, the Biotechnology and Biology Science Research Council had stressed the demand for trained bioinformaticians and all the main funding agencies recognize this as a high priority (Brass, 2000).

The above facts give rise to educational questions pertaining to the design of undergraduate degrees in bioinformatics. According to Altman, the nature of bioinformatics readily tends itself to two career path teaching models: "computer scientists who will specialize in biology" and "biologists who will specialize in computer science" (Altman, 1998, p. 549). This dichotomy is not without prejudice as biologists advocate for tool-driven bioinformatics and computer scientists advocate for algorithm-driven bioinformatics. This translates itself to the central question posed by Pearson (2001, p. 761) as: "Are Computational Biology and Bioinformatics tool-building engineering disciplines? Or are they disciplines that address fundamental scientific questions and provide insights into biological processes?" - Or both? The answers given to these questions will be of great consequence to the kind of curriculum which will be conceived for the teaching of bioinformatics at the undergraduate level.

Indeed perceiving a need is just the start of potentially finding a solution and bioinformatics, as a field, is dealing with a number of growing pains. Hasty decisions have often led to the establishment of a course or two in life science and computer science departments that mostly teach how to utilize bioinformatic tools but do not actually teach the bioinformatics way of thinking. Altman criticizes this and comments on his own approach to curriculum design:

> I approach the problem of defining curriculum with a bias that bioinformatics is not simply a subset of biology or computer science, but has a growing and independent base of scientific tenets that require specific training not appropriate for either biology or computer science alone. (1998, p. 549)

Ouzounis (2000, p. 189) also reflects upon this unfortunate misinterpretation of the field:

> There is serious intellectual content in the field, with a range of challenging scientific questions to be answered. ... By approaching bioinformatics (or computational biology) as a science, the field will not be misapprehended as a technology platform. ... Instead, it should be viewed as a genuine scientific discipline where vivid imagination and fleeting serendipity take equal stance along careful planning and precision engineering.

Therefore, when researching curricular design in bioinformatics it is important to grasp what is this seemingly elusive bioinformatics way of thinking and to pay close attention to how this can be honestly expressed in the curricular design. There is an assumption made here that the curricular design for the teaching of a field of study will reflect the epistemological interpretation given to that field of study.

The complexity of the field and its varied interacting (or not) subparts makes delimitating a clear-cut definition for bioinformatics complicated. Thus computational biology, systems biology, genomics, proteomics, biomedical engineering, and bioinformatics often overlap and are used interchangeably by the non specialists, and understandably so. It may well be that this complexity leads to a simplistic categorization of bioinformatics as the application of computers to biology.

Similar science-technology troubled regions exist between pure computer science and software engineering as well as in mechanics as taught from a physics standpoint and the more problem-centric mechanical engineering (Jakobsen & Bucciarelli, 2007).

To date, much research on bioinformatics education is mostly focused on course level design or selection of subject-matter for the curriculum. Articles that take a conceptual approach to the problem of curriculum design often are perspectives or viewpoints of bioinformatics experts. Although quite insightful, a methodical approach and analysis is not outlined in such articles and thus attempts to sketch a conceptual model or framework are inconclusive.

The purpose of this analysis is to identify useful guiding concepts which surpass the over-simplification or one-dimensional understanding of the field and which will lead to imagining powerful bioinformatics undergraduate curricula. Powerful here should be understood as having truly bioinformatics objectives rather than the enrichment of computer science degrees or life science degrees.

Thus my research question may be stated as: what are useful guiding concepts for the design of a bioinformatics undergraduate curriculum? Concept may mean guidelines, realizations, ideas etc.

The goal of this thesis is to propose a set of such concepts which could be used in the design of a bioinformatics undergraduate degree, or revision of an already implemented degree. The concepts will not be presented as mere guidelines but will be considered in the context of the higher education undergraduate learning environment. This will allow identifying beneficial interactions with the learning environment as well as the obstacles which could disable the enactment of such concepts as expressed in the ideal curricular design.

Indeed, it is not ideals which govern curriculum implementation but constraints, namely, funding and time. This is beyond the scope of the paper, which will not deal with the management of curriculum implementation. Nonetheless, we will comment on the potential of the conceptual framework for being translated into reality given the learning environment of interest, that of undergraduate university education.

Thus the output product of this work will be a set of guiding concepts which will constitute a conceptual framework for powerful undergraduate curriculum design. Methods of synthesis and conceptual analysis, thoroughly presented in the next chapter will be utilized as to undertake a qualitative analysis of undergraduate bioinformatics curricula.

Who can benefit from such an analysis? This analysis will be of interest to individuals involved in the design or rethinking of bioinformatics undergraduate degrees as well as to those individuals involved in the design of curricula for emerging new techno-scientific fields. It may serve as a cautionary tale of against rapid responses in curriculum design in regard to new ‘hot’ fields as well as a road map for these new interdisciplinary fields to settle within the disciplinary constraints of most universities.

Finally, this research may also serve as case-study in regards to interdisciplinarity and integration in undergraduate modern science curriculum design.

Chapter 2: The Approach

In order to discover guiding concepts for bioinformatics curricula, I shall follow an integrative form of curriculum inquiry, specifically a conceptual synthesis approach falling in the more general category of integrative inquiry. Thus, in this chapter, I shall present why such an approach was chosen, what it consists in and how it will apply to the case study of undergraduate bioinformatics education.

In the book entitled "Forms of Curriculum Inquiry", a variety of ways of thinking of curriculum issues, specifically 17 different approaches, are identified and presented (Short, 1991). Depending on the question one seeks to answer, one form of inquiry will be more appropriate than another -- although the complexity of the questions addressed in curriculum inquiry will generally require using several forms of inquiry (p. 16).

Given the purpose of this thesis, which is to identify guiding concepts for the design of powerful undergraduate bioinformatics curricula, the integrative form of inquiry seems of particular interest.

I shall therefore start by presenting what is the premise of such a form of inquiry and in what it consists. Particular attention will then be given to Hurd's (1983) conceptual analysis/synthesis methodology (1983) which is a form of integrative inquiry and represents the only published guidelines for the elaboration of a conceptual curricular framework (Marsh, 1991). This analysis/synthesis methodology yields the construct of the conceptual curriculum framework, a powerful tool for curriculum deliberation. Following this approach, I shall begin by uncovering guiding concepts for undergraduate bioinformatics education which will be part of the conceptual curriculum model. A more thorough understanding of the construct of guiding concepts as an outcome of this thesis will be reached by the reader after reading this chapter. Finally, I will conclude this chapter by presenting a road map of the synthesis/conceptual analysis conducted in the next chapters. This roadmap will present to the reader a preliminary introduction to the type of information and knowledge selected to be added to the data set of this synthesis/analysis.

The Integrative Form of Inquiry

What is inquiry synthesis? Curriculum deliberation involves decision-making. In order to make such decisions, knowledge is obviously necessary. The challenge lies in identifying the different sources of information which should be studied in order to build sophisticated knowledge which will address the complexities of reality: "Here is the place for a form of inquiry that yields integrative knowledge, that is, the type of knowledge that brings together what is known from various, perhaps disparate, studies that may be relevant to the particular needs of practice" (Marsh, 1991, p. 271).

This is not a summarizing activity but a truly synthesizing activity as the knowledge brought together must actually generate new knowledge better fit to address the research question:

> Knowledge that already exists in individual studies or reports is not usually in an appropriate form for direct use in decision-making. This knowledge needs to be related to other knowledge generated in other relevant studies, and the whole body of knowledge needs to be assessed, reorganized and interpreted in terms dictated by the existing need for knowledge. In other words, it must be transformed into synthesized knowledge if it is to be

> useful and appropriate for dealing with practical educational decisions. Thus, integrative inquiry is one of the most important and complex forms of practical inquiry that can be undertaken. Its value lies in matching knowledge to need and in the skillfulness with which the process of synthesis is accomplished. … It is more than just assembling sets of information. The emphasis is upon integrating diverse material into a particular conceptual framework so that some new perspective or relationships are introduced. (Marsh, p. 272)

Thus the notion of emergence of new knowledge in the form of perspectives or relationships is introduced. Ultimately these will define a conceptual framework. The phenomenon of emergence which takes place in effective synthesis is also stressed by Coates (as cited in Hurd, 1983), as it "implies creating a more holistic view and a new perspective since the interpreted whole is greater than the sum of its parts".

Thus we can summarize by saying that integrative inquiry is a form of inquiry in which some possibly very diverse knowledge is considered simultaneously as a means of creating/discovering or becoming aware of new different knowledge which will be paramount to the alternative design of a conceptual curriculum framework.

Why was this approach chosen? Curriculum inquiry is a field of study which is practical in nature. An integrative form of inquiry which focuses on acts and events can respond more truthfully to the messiness of curriculum reality then an analytical approach:

> In many of the disciplines, at least some of the time, it is possible to ask and answer questions that relate solely to ideas and not acts or events. In some cases,

> whole domains have arisen that have been distinguished from each other by analytic distinctions rather than actual ones. The domains of mathematical inquiry provide the best examples of this. (Short, 1991, p.7)

Obviously this is not the case with curriculum inquiry. In such inquiry it is necessary that the acts and events which occur in these forms of inquiry remain whole and are not reduced to a single idea. Research surrounding a sterilized idea may be accurate given the defined variables but ultimately useless:

> The acts and events of curriculum practice occur as entities, as wholes. They cannot be divided arbitrarily into parts which correspond to some analytic scheme which may be possible to create mentally. To attempt to do so would distort the reality of these acts and events and substitute mental constructs for real ones. These acts and events come whole and must remain so if we are to deal with the reality as it presents itself to us and not deal merely with a thought or idea with which there is no corresponding reality. Domains of inquiry in practical fields such as curriculum must, therefore, be distinguished in ways that respect existing acts and events as entities or wholes rather than using analytic categories to distinguish them. If they are not distinguished in this way, inquiry may proceed on matters that exist in name only and do not relate to actual curriculum acts or events (Short, 1991, p. 6-7).

Thus when I shall proceed in my synthesis/conceptual analysis process, despite that its essence lies in a conceptual dimension is should nonetheless be firmly grounded in context. In this thesis context is understood as the learning environment situated in the more general modern scientific knowledge landscape.

Further, integrative inquiry will often imply a multidisciplinary and transdisciplinary direction. By adding a prescriptive orientation to the research, the ideas or concepts become inevitably grounded in reality: multidisciplinary or transdisciplinary knowledge will be knowledge pertaining to actions or events *a priori* (Jantsch, 1972). As Short explains:

> The most common types of questions asked in curriculum inquiry, however, are those which require multidisciplinary or transdisciplinary forms of inquiry, such as the theoretical, the normative, the critical, the evaluative, the integrative, the deliberative, and the actions forms of inquiry. This is the case because of the nature of curriculum activity itself, the kind of knowledge required in the course of doing curriculum activity, and the type of inquiry questions formulated to obtain this kind of knowledge (1991, p. 16).

The type of qualitative integrative analysis we shall be undertaking here also presents some benefits over an integrative quantitative analysis such as meta-analysis:

> The synthesis process may proceed along qualitative lines such as in meta-analysis. [...] Synthesis processes may also be used with qualitative data. Qualitative processes are especially useful for identifying issues, themes, movements, concerns, and trends and for generating intellectual maps and frameworks. The results of qualitative synthesis tend to be conceptual, philosophical, or propositional – representing a point of view, a normative position, or new perspective (Hurd, 1983, p. 648)

Indeed this is much better suited to our research questions of identifying guiding concepts than a quantitative approach. Further a synthesis approach is also better suited than an empirical approach:

> In both synthesis and empirical research, there are procedures (such as the processing of information) which are similar. However, each form of research provides insights and interpretations excluded from the investigative procedures of the other. Conceptual research for example seems to be responsive to a total situation and to incorporate a wider realm of human experience than is found in the sampling techniques of empirical studies. (Hurd, 1983, p. 647)

Further, the integration process allows freedom from personal beliefs or ideology, and traditionalism and cliché. Curricula tend to be assembled by committees that have active administrative and teaching positions in a particular field. Although this brings very high subject-matter knowledge expertise to activities of curriculum deliberation, such expertise is field specific and does not necessarily consider education research, or the changing faces of society, knowledge and technology:

> Typically, curriculum frameworks are a product resulting from arbitration between conflicts of interest a negotiation of competing value judgments argued amongst members of the framework committee. In contrast, the synthesis procedure uses information, derived from relevant and scholarly sources, which is treated to minimize bias, and to make practical good sense (Hurd, 1983, p. 658).

About the Process

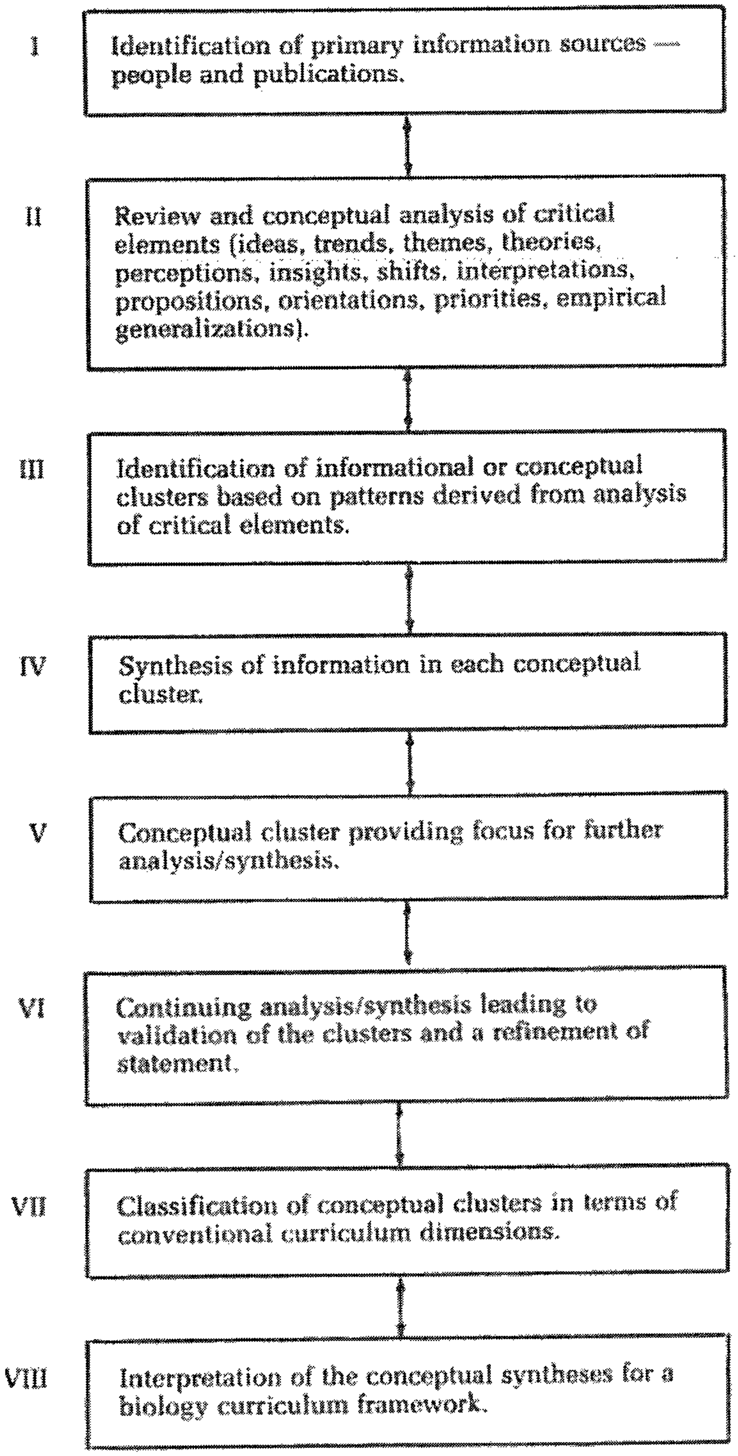
Conceptual analysis/synthesis process. According to Marsh, "Hurd (1983) has written the only published guidelines for doing synthesis in curriculum inquiry".

Specifically, Hurd synthesizes and proposes a conceptual framework for the school biology curriculum. I shall now present the characteristics of his approach while paralleling them to my efforts of identifying guiding concepts in undergraduate bioinformatics curricula. Hurd explains the following for conceptual analysis:

> In conceptual analysis, the search is for ideas, themes, insights, pressures, trends, and changes – whatever makes a difference in the design of a curriculum framework. Categories for coding data are not set in advance; they emerge from ways in which the data collected clusters as the research progresses.(Hurd, 1983, p. 657)

Such categories not only emerge but point towards new types of data to collect. As Hurd demonstrates in figure 4, it is a back and forth process represented by repetitions between steps IV "Synthesis of information in each conceptual cluster" and V "Conceptual cluster providing focus for further analysis/synthesis".

Indeed, this process has begun with I, "Identification of primary information sources – people and publications" and II, "Review and conceptual analysis of critical elements (ideas, trends, themes, theories, perceptions, insights, shifts, interpretations, propositions, orientations, priorities, empirical generalizations.)" The synthesizer collects qualitative data from which themes and patterns will start to emerge through the exercise of conceptual analysis:



I Identification of primary information sources — people and publications.

II Review and conceptual analysis of critical elements (ideas, trends, themes, theories, perceptions, insights, shifts, interpretations, propositions, orientations, priorities, empirical generalizations).

III Identification of informational or conceptual clusters based on patterns derived from analysis of critical elements.

IV Synthesis of information in each conceptual cluster.

V Conceptual cluster providing focus for further analysis/synthesis.

VI Continuing analysis/synthesis leading to validation of the clusters and a refinement of statement.

VII Classification of conceptual clusters in terms of conventional curriculum dimensions.

VIII Interpretation of the conceptual syntheses for a biology curriculum framework.

Figure 4. The steps of the analysis/synthesis process as described by Hurd (1983). (Modified from source to fit in one page.)

Outputs will be generated through the emergence phenomenon and take some pre-specified shapes such as rationale, goals, context, practice, and criteria for subject-matter selection but also shapes which may be of concern to the particular case-study:

> As the synthesis information increases in amount and the messages become clearer, categories or descriptors are established that encompass the various dimensions of the science curriculum, such as rationale, goals, contexts, and practices. Categories are also made from themes or concerns that are emerging, for example, criteria for the selection of subject matter, interdisciplinary courses, and science and social policy. (Hurd, 1983,p. 658)

Applying Hurd's approach to this thesis. In step VII Hurd dictates the "Classification of conceptual clusters in terms of conventional curriculum dimensions." Thus the conceptual clusters or guiding concepts will be organized according to whether they inform educational goals, the curriculum framework or context. The last step involves the interpretation of the conceptual synthesis for, in this case, a bioinformatics curriculum framework. In the context of this thesis we shall stop at this step. A curriculum committee is better positioned once informed of these guiding concepts to interpret and incorporate them into a curriculum given their subject-matter expertise and experience. My intent as the synthesizer is to utilize the skills I have acquired during my Master's pertaining to educational analysis along with my familiarity with bioinformatics in the form of an undergraduate degree in order to identify guiding concepts with a particular ability. The interest of my contribution from such an angle is the enrichment of the analysis by my personal experience as a bioinformatics student as this might lead to greater insight.

Thus, in this thesis I have followed steps I to VII. The last step (VIII) is commented upon in the conclusion where the pre-sketch of bioinformatics undergraduate degree is presented and serves more as an overture for future work rather than the ultimate purpose of this thesis.

How the different steps of Hurd's synthesis process were followed, as well as how the emergence of new conceptual clusters which further inform synthesis took place, is explained in more detail in the last part of this chapter entitled Thesis Roadmap

Selecting the data to be used in the synthesis. The data set for the job of synthesis must *a priori* be diverse and informed by several disciplines. This because, according to Hurd, it is change in society and science which creates a need for curriculum reformulation and change is studied through different disciplinary lenses:

> Changing conditions in science and society are studied by a variety of scholars, such as sociologists, economists, sociologists and philosophers of science, futurists, specialists in knowledge processing, and educators. These scholars generate interpretations and insights that have potential meaning for curriculum development. A constraint on the use of this knowledge for curriculum reformulation is that the knowledge is scattered over several disciplines. To be useful it must be brought together in some coherent and rationale way (Hurd, 1983, p. 649).

Other useful elements that can inform the necessary synthesis are the writings of scholars which need to be recast by the synthesizer within a curricular framework:

> Scholars who are concerned with the evolution of their specialty, its current status, and emerging techniques and perspectives can be found in nearly every discipline. Although the writings of these people are in themselves a synthesis, we are not likely to find them in the context of a science curriculum framework. (Hurd, 1983, p. 656)

Finally, Hurd stresses the necessity to start the thinking process anew without relying on previous frameworks:

> The reason for starting anew is to escape traditional practices, bandwagon rhetoric, questionable historical continuities, stereotypes and the educational slogans of the day. The focus of the researcher is that of isolating new conceptual shifts, movements and developments, and the context in which they occur. The shift in biology from a molecular to an ecological view, as expressed in the environmental movement is an example. It is from this position that a judicious synthesis is created which may or may not project a curriculum framework different from that which now dominates. (Hurd, 1983, p. 647)

Starting anew, though, does not imply dismissing previous frameworks as part of the analysis. Hurd himself gives the example of a curricular framework built from both retrospective and prospective syntheses -- a before and after comparison. Bioinformatics represents a shift in biology as brought about by sequencing technology. Thus, this shift should put in the foreground during bioinformatics curriculum inquiry; however, the synthesizer should exercise caution in interpreting the educational implications of such a shift.

Outcomes of Conceptual Synthesis and Limitations

What shape do the results of a conceptual analysis of curriculum take? That of concepts: some can be specific to the curriculum and express key dimensions of the curriculum design and the instructional practice which will take place within it: these dimensions are a rationale (a conceptual framework), goals and context. Others might be particular to a given case study and may take any of the following forms: "such as policies, inferences, trends, generalizations, points of view, perspectives, shifts, new alignments, transformations, frames of reference, models, or hypotheses." Once again, these concepts or results of the analysis bear the characteristic of emergence: "[They] are more than the totality of the combined information of which they are a product (Hurd, 1983, p. 658).

Guiding concepts are a construct embodying the format of my results. Guiding concepts in the forms of rationales, goals, contexts, practices, policies, inferences, trends, generalizations, points of views etc., are what make up the curriculum framework. This thesis does not represent an extensive discovery of all such guiding concepts. Rather the curriculum framework will consist of whatever concepts emerge given the data set available in this study. Future research can be build around these concepts and enrich them so as to lead to a highly detailed curriculum framework. Thus, when attempting to identify guiding concepts, a curriculum certainly is not viewed as a list of ideal and desirable subject-matter, but rather as a framework made up of those guiding concepts.

Thus, for the time being, we can imagine that the curriculum we are trying to deliberate upon in this thesis can be construed as a set of guide-lines or best-practices as synthesized from an advanced review of the literature. As relationships between the desired elements of that curriculum begin to emerge, we are hoping to provide a more comprehensive conceptual framework or model for thinking about undergraduate bioinformatics curriculum design. Indeed, "The curriculum developer, policy and decision makers, educational researchers, and teachers use the conceptual framework as a point of departure for curriculum deliberations or argument."(Hurd, p. 661)

The above description provides us with the purpose our curriculum model or results should fulfill and thus provides the first glimpses into the shape this model should have. Most importantly, the dimension of time should be part of the model allowing the reader to readily make an analogy with what seems to be the present *status quo* of some facet of the curriculum and what future desirable improvements or alternatives of this facet may be.

Finally, the last characteristic of a conceptual model is that of portability in space but obviously not in time; the exercise of curriculum synthesis is one whose results are ephemeral: "The conceptual framework and context provide a flexible pattern for curriculum reformulations adaptable to local conditions but within the context of shifts and movements in society and science" (p. 667).

A main issue of concern or limitation of this study is time. Hurd's portrayal of curriculum synthesis was a product of ten years of work which obviously does not compare with the time span dedicated to this Master's thesis. Thus, some limitations or shortcomings of this synthesis will have to be addressed in future, complementary research work. For example, I do not deal at all with transdisciplinary concerns of bioinformatics undergraduate education.

Thesis Roadmap

In the next chapter, Bioinformatics Educational Goals, we will start our conceptual exercise by comparing bioinformatics educational goals as they are presented by the departments offering bioinformatics degrees with the more idealized educational goals of researchers and scholars of the bioinformatics field. Do these goals fall into harmony or do they represent educational challenges requiring subsequent attention? We will also compare these departmental goals and ideal goals with the learning objectives framed by the practice of bioinformatics. In other word, we will explore what "doing bioinformatics" means and how this affects defining educational goals for a powerful curriculum design. Thus in this third chapter we will consider guiding concepts in terms of educational goals, a subcomponent of the conceptual curriculum framework as advanced by Hurd.

Chapter 4 considers five undergraduate bioinformatics curriculum case-studies as a basis to extrapolate different curriculum models for teaching bioinformatics, their benefits and weakness. Particular attention is given to the degree of interdisciplinary education they exhibit as this emerged as an important educational goal in chapter 3. Considering these curriculum models also allows us to take a closer look to instructional practices utilized in the teaching of undergraduate bioinformatics which may be incorporated into our conceptual curriculum framework.

Chapter 5 revisits the practice of bioinformatics but recasts our understanding of it by considering bioinformatics as a technoscience and the educational consequences of this. This is done because chapter 3 as well as chapter 4 demonstrated the challenges of uniting the different facets (science versus technology) of the practice of bioinformatics. Technoscience serves as a unifying concept for the design of bioinformatics education.

Chapter 6 considers two curriculum design approaches which promote interdisciplinarity and integration and also remedy the technology/science divide: concept-based curriculum design and process-based curriculum design. The pertinence of each to bioinformatics education is explored.

Finally, in chapter 7, we discuss what we learned from this synthesis/analysis exercise, namely what guiding concepts for the design of undergraduate bioinformatics curricula emerged. Finally, a pre-sketch or interpretation of an undergraduate bioinformatics curriculum is proposed taking into account the emergent guiding concepts of this synthesis.

Chapter 3: Educational Goals in Bioinformatics

The advent of new genome sequencing technologies generated large amounts of data the analysis of which was perceived as highly promising by both the scientific community as well as the pharmaceutical industry. In consequence, bioinformatics education became an issue of high interest in universities. As we shall see in the next chapter, when we will take a look at different existing undergraduate bioinformatics degrees, we will see that they are rarely built from scratch. Rather, they are generally built upon existing life science degrees or computer science degrees.

There is an important fact to take into account when considering bioinformatics degrees whose foundational design is that of a life science degree or computer science degree: the anticipated shift in the purpose of bioinformatics education in respect to each housing department. The respective life science or computer science departments will have their own educational needs to satisfy to which the teaching of bioinformatics will be of service. That is, rather than a hypothesised "ideal" bioinformatics education towards its own ends, bioinformatics education becomes instrumental to either life science or computer science education. Furthermore, it is sensible to anticipate that even "ideal" bioinformatics education goals have the potential of being distorted when placed within the framework of such foundational designs.

Thus, in the first part of this chapter we will consider the educational needs of the two main housing departments of bioinformatics undergraduate degrees, computer science departments and life sciences departments, and how these needs relate to the teaching of bioinformatics.

In the second part of this chapter will consider the bioinformatics educational goals *de novo* and in an uncompromised fashion as expressed through the viewpoints and opinions of leading bioinformatics scientists and researchers. This will allow us to contrast these "ideal" educational goals with those expressed by the need for bioinformatics education in computer science and life science departments.

In the third part of this chapter we will look at bioinformatics as practice. What does "doing bioinformatics" mean? We will explore the different degrees of sophistication when practicing bioinformatics and consequently how this frames educational goals.

Educational Goals within Housing Departments

Bioinformatics education in the life sciences. A series of reports have been stressing the need for change in life science education. Let us proceed to an overview.

In 2002, The Quality Assurance Agency for Higher Education in the United Kingdom published the skills set related to numeracy and information technology that bioscience graduates should achieve (as cited in Hack & Kendall, 2005). They are summarized by Hack and Kendall as:

> - Preparing, processing, interpreting and presenting data, using appropriate qualitative and quantitative techniques, statistical programs, spreadsheets, and programs for presenting data visually.

- Solving problems by a variety of methods including the use of computers.
- Using the internet and other electronic sources critically as a means of communication and a source of information (Hack & Kendall, 2005).

Thus, graduates from biological science degrees should be able to conduct computer-aided statistical analysis of biological data.

In 2003, the American society for Biochemistry and Molecular Biology (ASBMB) stated that the ability to use computers effectively as information and research tools should be amongst the skills that biochemistry and molecular biology students should obtain (as cited in Voet et al., 2003). Despite this fact, biochemistry and molecular biology degrees seem to only offer two “hard” science courses, a mathematics calculus course as well as a physics course amidst a plethora of “soft” courses. (Voet et al., 2003).

A report issued by the National Research Council in 2003 entitled “BIO 2010: transforming Undergraduate Education for Future Research Biologists” expresses the need for change in life science education. This time though, the need for change is not only expressed in terms of statistical analysis competencies amongst graduates but the foundational issue of interdisciplinary education and integration is also addressed. The report expresses the need for an interdisciplinary undergraduate education which would “seamlessly integrated biology with mathematics, statistics, computer science, physics and chemistry” (as cited in Chapman, Christmann, & Thatcher, 2006).

Indeed, a paradigm shift is taking place in the life sciences towards a quantitative biology (Hack & Kendall, 2005). Thus the ability to use computers as research tools as stated by the ASBMB becomes paramount. One is brought to question how the described subject matter of typical life science degrees, characteristically containing one calculus and one physics course amidst a bulk of chemistry and biology courses, can respond to this paradigm shift. Further transforming traditional life science education into interdisciplinary education is no small feat. Even departmental divisions at the biology and chemistry level have proven challenging, let alone combining mathematics or computer science that have a quite different epistemological premise than the life sciences (Voet et al., 2003).

Bioinformatics seems to be the logical continuation of the life sciences by concretely representing the quantification of biological problems:

> The relatively new discipline known as bioinformatics already provides a bridge from molecular biology to computer science, statistics, and information theory. Adding a bioinformatics course to the undergraduate biology curriculum thus represents an easy, natural step toward the goal of providing quantitative, interdisciplinary coursework for all bioscience students (Chapman et al., 2006)

When designing such a course learning outcomes were specified in regards to informatics. Thus when completing such a course a student will exhibit the following knowledge:

> 1) understands the design principles of biological databases, 2) has a basic understanding of information theory, 3) has a working knowledge of

> statistics and probability, 4) understands principles of sequence search and alignment, 5) is familiar with common bioinformatics algorithms"
> (Chapman et al., 2006)

We may summarize that the goal of bioinformatics education within life science degrees is to inspire interdisciplinary teaching by notably incorporating more physical science courses into traditional curricula. Thus the teaching of bioinformatics becomes instrumental to serving the needs of a quantified biology.

Bioinformatics education in computer science. Let us now explore how bioinformatics educational goals are expressed within Computer Science departments. Whereas in the previous part we saw how bioinformatics helped in satisfying the need for a quantitative biology, it would seem that in the case of Computer Science arguments are raised as to how Computer science may serve bioinformatics education and not the other way around. Nonetheless, let us first take a look at what bioinformatics education has offer to computer science education.

If bioinformatics can show the way for a quantitative biology, in the case of computer science it presents an opportunity for modernising curricular content:

> Classically computer science has focused on the study of computer hardware and software. A more contemporary view of information technology however must recognize that storage, transmission, and distribution of data make up a significant portion of the future demand on the discipline and on future computer professionals.(Doom, Raymer, Krane, & Garcia, 2003)

Thus, some hardware courses become obsolete when considering the bioinformatics enterprise and should be replaced by advanced information processing classes.

Computer science departments, unlike the life science department, do not necessarily speak of radically transforming their own discipline like is the case for a quantitative biology, but aim at achieving interdisciplinarity through the enhancement of collaboration and communication skills of their graduates:

> Many of today's and tomorrow's careers demand not only depth of knowledge in a specific area, but also a general sense of vocabulary, tools, and concepts across other disciplines as well. ... Turning the vast quantities of information generated by the genome and proteome projects into useful science, biomedical tools and cures is requiring collaborations between computer scientists, information specialists and biomedical researchers. We are failing our students if we do not involve them in collaborative learning and research. (Fetrow & John, 2006)

Therefore, incorporating bioinformatics teaching in computer science undergraduate degrees can help modernize those degrees specifically by enhancing the interdisciplinary quality of learning. But that is not all that incorporating bioinformatics may offer; it may also help assure clientele for universities both at the undergraduate and graduate level.

Beck, Buckner and Nikolava (2007) argue how a bioinformatics degree may serve as a means for recruiting and retaining computer science students. Indeed, computer science as part of the engineering disciplines has witnessed a decline in interest. An explanation for this is that students fail to see the reason for studying computers as a means in themselves; they are generally interested in the application of computers to other problems often of societal nature. This seems to be especially true in the case of female applicants:

> Specifically, women link their interest in computer science to other arenas. In our experience, biological investigations are viewed as particularly socially relevant by female students, as they so often have applications that benefit society in areas such as medicine, nutrition, and public health. (Beck, Buckner, Nikolova, & Janick-Buckner, 2007)

Further, undergraduate bioinformatics education in computer science will help overcome the high entrance barriers for graduate bioinformatics programs given the high amount of prerequisite knowledge required (Doom, Raymer, Krane, & Garcia, 2002). As such, undergraduate bioinformatics degrees in computer science settings promote continuing to bioinformatics graduate studies. Dressel (1963) has in fact identified this as one of the main educational goals of most curricular models in higher education. Thus, bioinformatics education enables bioinformatics departments to both modernize and regenerate themselves. Let us now explore what computer science as a discipline can specifically offer to bioinformatics.

The Computing Curricula 2001 Report from the Association for Computing Machinery (ACM) discusses the role of computer science in interdisciplinary areas and mentions bioinformatics as one such area:

> The Computing Curricula 2001 Report from the ACM lists bioinformatics and computational biology as two of the scientific computing areas that are a "vital part of the discipline," whereas the 1991 document of the same body contains no reference to them (as cited in Beck et al., 2007).

Leblanc and Dyer (2004) make a case as to why computer science departments have a significant role to play in regards to bioinformatics education based on the fact that 10 out of the 14 knowledge focus groups in the 2001 computing curricula significantly overlap and may help tackle bioinformatics issues.

We see that while life science departments are trying to teach numerical skills to their students, computer science departments seem to be already taking bioinformatics education within their own hands and defining the role of computer science in regards to bioinformatics.

Conspicuous by its absence is the description of any life science subject matter which may be of interest to bioinformatics. For now, the natural question that arises is which of these two avenues is more desirable for bioinformatics education? The question which follows is: is building a bioinformatics degree over an existing life science or computer science degree a sensible educational enterprise?

This will of course depend on the level of interdisciplinarity and integration such a degree will be able to demonstrate. Nonetheless, let us cautiously remark that adapting either degree to bioinformatics education is representative of the kind of reverse engineering in curricula design which can highlight the points of compliance of bioinformatics within each of the two disciplines while leaving in the shadows the potentially crucial but consequently unaddressed areas of bioinformatics. In order to understand where the grey zone lies for bioinformatics it would be informative to consider what leading bioinformaticians identify as crucial educational goals of bioinformatics.

Educational Goals According to Bioinformatics Scientists/Researchers

When considering the writings of scholars on issues concerning bioinformatics education, training or curriculum, certain useful insights are obtained. A common concern among scholars seems to be educating in depth when it comes to bioinformatics. But what does 'depth' mean exactly in the given context and how is it translated in terms of educational purposes or goals?

A first notion which appears is the "Scientist rather than technician" ideal. For Pearson, depth education is one which will enable bioinformaticians to conduct research rather than "to produce solely technicians who are not primary contributors to research question selection and experimentation" (2001, p. 761). Pearson foresees a type of training which will prepare for graduate studies and lead to post-doctoral fellows who will be capable of conducting independent new research. We shall see in the next part of this chapter that this dichotomy is important and will be the metric by which different levels of doing bioinformatics will be assessed (Pearson, 2001).

Another important notion is the centrality of biological research understanding leading to experiment design. Depth in education for Pearson means depth in the life sciences rather than depth in computer science: "An alternative perspective, to which I subscribe, argues that Genomics, Computational Biology, and Bioinformatics offer fundamentally new opportunities for insight into Biological processes, which are difficult to identify and exploit without in-depth training in biological research" (2001, p. 762). This can also be argued upon in regards to the inherent variability of biological results with which life science students are accustomed and thus better trained in designing experiments and stating hypothesis which can control that variability. Life Science students are better trained in identifying biological problems. This is why biologists should be trained in the development of "computational strategies for large-scale analysis" (p. 762).

Finally, a third important notion is emphasizing statistical and algorithmic understanding: "Many of the fundamental advances in sequence analysis, particularly at the genome scale, are based on statistical insights, yet neither Computer Science nor traditional biochemistry Molecular Genetics, Pharmacology, or Physiology curricula typically include statistics courses" (Pearson, 2001, p. 762). Pevzner (2004) also supports this claim and adds that depth of understanding of the statistical underpinnings of algorithms is necessary for correct interpretation of results. This implies familiarity with the statistical formulae utilized, but also an understanding of the overall algorithm as well as being able to communicate using that language. Pevzner adds that attempting to bypass this by offering undergraduate students what he calls recipe-based bioinformatics, which do not teach the computational ideas behind them, leads to the development of technicians rather than scientists. This is a futile educational effort since "protocols change quickly but the computational ideas do not seem to" (2004, p. 2160).

Both Pevzner and Pearson direct us towards depth learning in the life sciences as well as algorithmic/statistical understanding as these two elements will differentiate scientists from technicians.

Finally another educational goal is expressed in terms of understanding bioinformatics as "discipline" or the culture of bioinformatics. If statistical know-how and experimental design capacity can be excavated from computer science and life science departments respectively, can this alone define the field of study that is bioinformatics? Altman (1998) responds to this question by stating: "The final and most critical portion of the curriculum would be a set of core bioinformatics courses that build upon the contributing disciplines to present the basic intellectual structure of the field."

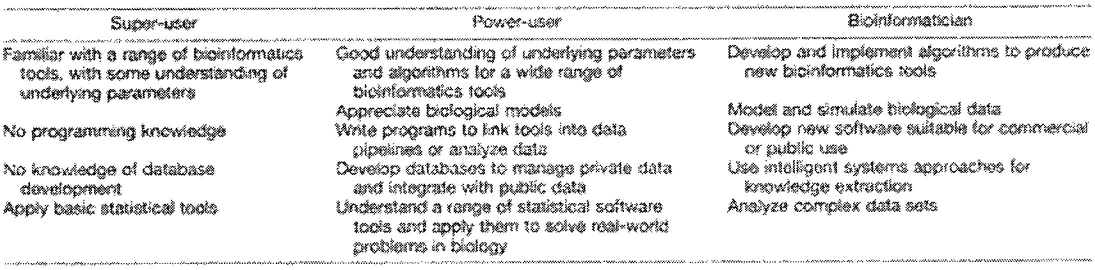
Ouzounis (2000) uses the term discipline to characterize the field. If bioinformatics is to be considered a discipline and not a field, (assuming the validity of such a statement and not dismissing it as a play of words), this makes it clear that housing such an education in either department is evermore undesirable: "The subject does not naturally 'belong' to any one research council" (Brass, 2000). Thus departmental collaborations are paramount. This requires funding schemes which bypass departmental barriers which will lead to the established of an appropriate learning environment for bioinformatics education.

Such a learning environment would lead to a crucial conceptual shift when thinking about bioinformatics curriculum design. The demands of such a design in terms of capacity both in funds as well as knowledge are much higher than the previously commented upon reverse engineering of curricula. For this reason, most examples of bioinformatics curricula found in the literature are not standalone programs but belong to computer science departments or life science departments. A notable exception to this is the University of California Santa Cruz which has a department of Biomolecular Engineering (Hughey & Karplus, 2001). In the next chapter we will explore different structures of curriculum in both departments and see what can be learned and possibly reapplied or modified in regards to the conceptual framework we are attempting to devise. For now, let us continue our exploration of bioinformatics educational goals by looking at the practice of bioinformatics.

Educational Goals in Regards to Bioinformatics as Practice

Several authors seem to be proceeding to a conceptual division of the practice of bioinformatics into two or three parts. Let us explore the characteristics that set the boundaries between these parts.

Hack and Kendall (2005) divide the practice into three parts as demonstrated in Table 1. They use the terms "Super-user", "Power-user" and "Bioinformatician". Although the terms are not the best for clarity (given the similarity in meaning of super-user and power-use, as well as the redundancy of the term Bioinformatician) the authors have successfully generated lists of tasks each of the groups should be able to accomplish.



Super-user	Power-user	Bioinformatician
Familiar with a range of bioinformatics tools, with some understanding of underlying parameters	Good understanding of underlying parameters and algorithms for a wide range of bioinformatics tools	Develop and implement algorithms to produce new bioinformatics tools
	Appreciate biological models	Model and simulate biological data
No programming knowledge	Write programs to link tools into data pipelines or analyze data	Develop new software suitable for commercial or public use
No knowledge of database development	Develop databases to manage private data and integrate with public data	Use intelligent systems approaches for knowledge extraction
Apply basic statistical tools	Understand a range of statistical software tools and apply them to solve real-world problems in biology	Analyze complex data sets

Table 1. Description of skill-sets of super-users, power-users and Bioinformaticians according to Hack and Kendall .

When considering the table, the Super-user category seems to refer to tool-users. The Power-user category encompasses programming skills and statistical analysis as well as an "appreciation of biological models" and linking tools with one another and databases. The notion of linking between different data sets is pervasive within this category. Thus we may rename this category "tool-integrator". The last category, Bioinformatician, can be given the title of "tool-conceiver". Indeed, it is the category which is at the highest theoretical level in regards to the computer science discipline, where conception and development take place, as well as modelling and analysis.

Kamenskaya (2005) describes three groups as well; bioinformatics may be practiced on three levels: 1) use of program facilities, 2) creating computer programs, 3) devising algorithms and theoretical principles. He stresses the importance of training researchers as there seems to be in Western Europe "an overproduction of middle-level experts but not directors of projects."

Let us remark that research in bioinformatics can indeed concern tool conception and development through the implementation of novel algorithms, as conducted in computer science, but also advanced research designs with heavy pipelining which integrate several of these new tools as to generate meaning. Thus, the tool-user category can be a bit deceitful as it is more readily associated with a low, almost technical, level of practice when in fact it can be incorporated into complex life science research. The same is true and perhaps more so for the tool-integrator level. The sophistication of each level and its worth as an educational goal must not be assessed according to a technical-scientific dimension but must be reassessed according to how each task fits in and is an integral part of a particular experimental design. Thus the most technical or simple tasks of the practice do not consist in less important or valued knowledge then the high end algorithmic conception. Experimental designs may encompass any or all of these three levels; therefore each level must ideally be expressed as an educational goal when designing an undergraduate bioinformatics degree. If this is not the case, the curriculum model will run the risk of being what Hurd characterized as intellectually dishonest.

Another way of interpreting the three levels of doing bioinformatics is along the lines of the dichotomy between scientists and engineers:

> A key difference between scientific processes and engineering processes is that scientific processes are concerned with the analysis, generalization, and synthesis of hypothesis, while engineering processes are involved with the analysis and synthesis of designs, where one reaches decisions on incomplete data and approximate models. (Donald, 2002, p. 63)

Are bioinformatics problems bound (like physics) or unbound (like engineering)? It would appear we can distinguish between the life science researcher utilizing bioinformatics tools and pipelining process versus the bioinformatics engineer. Karplus and Hughey (2001) further enhance this dichotomy and write about their curriculum design: “we plan to offer tool-user courses for biology students, but the bioinformatics students will concentrate on the design and construction of tools." What is becoming apparent is that the term Bioinformatician seems to be reserved to the practice of tool-building and conceiving and therefore is more reminiscent of engineering than a life science researcher who conducts experiments with advanced software tools.

In 2000 Gen Myers, then Vice President of Informatics Research of Celera Genomics, described bioinformatics tools users and bioinformatics developers respectively as "miners" and "developers" separating researchers from engineers (as cited in Counsell, 2003). But, it is through the tools-users that life science research takes place. This is also illustrated in Denn's and Macmullen's (2005) experimental cycle model, presented in chapter 1, which clearly delineates the position of such tools within the cycle.

The issue therefore becomes a problem of using precise wording which would surpass the inherent ambiguity of the field. For example, does "conducting bioinformatics research" mean researching life science problems with means of bioinformatics or engineering/building tools? Or both? There is a clash between the technical aspect of basic information extraction, the engineering aspect and the research design aspect.

Veblen (as cited in Barnes, 2005, p. 158) argues that "men have learned to think in the terms in which the technological processes act." This seems to be particularly relative to bioinformatics. I believe that this issue can be dissolved by considering bioinformatics as a technoscience and seeing how this re-shapes educational goals. There is a clash between the technical aspect, the engineering aspect and the research design aspect which are all part of the practice of bioinformatics. Such a clash is anti-educational and treating bioinformatics as a technoscience can help overcome this (this will be further explored in Chapter 5). Both the structure and ideology of university settings are not particularly inviting to this but there are means of overcoming this obstacle (as detailed in Chapter 6).

Let us briefly comment upon the role of industry in shaping the practice of bioinformatics and in consequence educational goals for bioinformatics. Despite predictions of a two billion dollar industry in bioinformatics (as cited in Doom et al., 2002), it would appear that the industry is in fact not taking the shape which was expected. “Bioinformatics training programs are hot but the job market is not” entitle their article Black and Stephan (2005) who have been following the phenomenon and the actual job opportunities offered. In consequence, educational goals seem to be geared more towards graduate studies rather than to being responsive to a market demand. It is interesting to note that some researchers have proceeded to the describing a taxonomy for bioinformatics educational goals for master and doctoral students (Dubay, Brundege, Hersh, & Spackman, 2002). The subject-matter of the degree varies according to whether the student is interested in working in the industry or in an academic setting. Such considerations need to be undertaken for undergraduate bioinformatics studies as well.

As we shall see in the next chapter, these different interpretations of bioinformatics will give rise to different types of curricular models. It is to be expected that those curricula which are housed within computer science departments will have educational goals more aligned with engineering educational goals whereas those housed within life science departments will follow tool-user educational goals and perhaps tool-integrator educational goals. For now, let us summarize our findings in regards to bioinformatics educational goals.

Summary of Bioinformatics Educational Goals

Let us now conclude the chapter by summarizing the different educational goals gleaned from the literature and contrast them in relation to those advanced by the computer science and life science departments. We will also compare the educational goals expressed by the bioinformatics researchers and compare them to those expressed by bioinformatics as practice. Table 2 below presents the different educational goals.

Life science departments wish to shift towards a quantified biology paradigm. Foundational to this is interdisciplinary teaching and bringing in new courses such as advanced statistics and programming to the more traditional life science curricula. The interdisciplinary nature of bioinformatics presents an ideal opportunity for achieving these educational goals. It is sensible to remark that the educational goals are life science goals to which bioinformatics are instrumental. Pevzner recentralized the interest on bioinformatics, by stating as an educational goal the design of *in silico* life science experiments utilizing bioinformatics tools. Thus, in order to design such experiments, students must be versed in statistical analysis as well as algorithmic understanding which become secondary educational goals. Algorithmic understanding will imply that the students develop rudimentary programming skills. Pevzner's motives are slightly different to those of life science departments in that he redefines the practice of life science research. One such redefinition is bioinformatics. In this way a culture of bioinformatics can be achieved rather then bringing bioinformatics into the curriculum as a foreign element which will only serve the interdisciplinary mandate.

Computer science departments are gaining leverage on the fact that they are indeed well-positioned in relation to subject-matter as to deliver bioinformatics education. But subject-matter alone does not account for a successful curriculum, and the research problems do originate in life science departments. Indeed, life science research can help in framing interesting new algorithmic problems. Therefore, computer science departments serve the educational goals of the practice of bioinformatics defined as engineers or tool-conceivers/tool developers. Bioinformatics degrees within such departments will resemble engineering degrees more so than research degrees. This is not satisfactory in relation to the educational ideals expressed by bioinformaticians. Bioinformatics authorities point towards the construct of depth bioinformatics as an educational goal. Depth represents placing emphasis on holistic experimental design rather than completion of bioinformatics tasks. This requires both knowledge of statistics and algorithms in order to correctly interpret results as well as knowledge on how to appropriately design experiments which overcome the messiness of data. The intellectual structure of bioinformatics must be promoted rather than promoting belongingness of bioinformatics to a particular discipline. In other words, bioinformatics must be approached as a form of inquiry rather than a sub-category of biology or computer-science. Finally, when considering the practice of doing bioinformatics three levels of sophistication seem to emerge. The technical dimension separating the three levels disappears when the different experimental tasks described cease to be viewed as self-serving but rather as part of an experimental design.

Source	Educational goal
Life science departments teaching bioinformatics	• Interdisciplinary science education for a quantified biology. • Computer aided statistical analysis of biological data • Familiarity with biological databases, information theory, probability and statistic, algorithms.
Computer science departments teaching bioinformatics	• Information processing understanding (storage, transmission and distribution of data) • Capacity of interdisciplinary communication and collaboration. • Emphasis on social relevance (purposive interdisciplinary goal) • Promote continuation to graduate studies • Bioinformatics positioned as vital part of computer science; computer science as backbone to bioinformatics • (Life science subject matter not very commented upon)
Bioinformatics authorities (scientists, researchers)	Depth bioinformatics: • Scientist rather than technician • Holistic experiment design rather than completion of specific bioinformatics tasks • Understanding and managing inherent variability of "dirty" biological data through the experimental design • Statistical and algorithmic understanding of correct result interpretation Culture of bioinformatics: • Students understand that bioinformatics does not belong to any one department • Students are familiar with intellectual structure of field
Bioinformatics as practice:	Three levels of doing bioinformatics: • Tool-usage: capacity to effectively use software dealing with biological data • Tool-integration: write computer programs which may possible link several software tools to one another and to several databases; implement pipelines. • Tool-conception: devising algorithms and theoretical principles
Industry:	Mild influence on educational goals; academic skills and graduate studies promoted through educational goals rather than professional skills.

Table 2. Bioinformatics Educational Goals. This table summarizes the educational goals in bioinformatics according to the source/defining authority as emerged from the synthesis/analysis.

Three themes are important when defining educational goals:

1. Interdisciplinary education possibly facilitated or rendered less demanding through effective communication and collaboration skills is essential.
2. Centrality of the experimental design in the bioinformatics enterprise requiring statistical understanding, algorithmic understanding, life science understanding and information processing which needs to be reflected in the educational goals
3. Certain experimental designs are only possible when certain engineering problems are solved: engineering activities are part of the bioinformatics enterprise. This is also reflected through the different levels of doing bioinformatics or the different facets of the bioinformatics field. This must be reflected in educational goals.

Let us now proceed to considering five bioinformatics curricula case-studies and how they incorporate some of these goals, while omitting others. This will give us a chance to see how the intent of incorporating certain goals may actually be enabled or destroyed depending on the model of the curriculum design. This will also allow us to explore how these conceptual goals can possibly be expressed through a variety of curriculum designs. Particular attention will be paid to the educational goal of interdisciplinary education as the other two themes are directly reliant upon it.

Chapter 4: Undergraduate Bioinformatics Case-studies and Interdisciplinarity

Accomplishing the bioinformatics educational goals discussed in the previous chapter requires mastery of several different disciplines. This is true when considering the educational goal of teaching a quantitative biology, the educational goal of imagining and creating new tools, and the educational goal of teaching 'depth' in bioinformatics. All these goals require that the students be able to integrate the knowledge of different disciplines. An interdisciplinary design in bioinformatics curricula seems to be paramount. Interestingly, some articles dealing with bioinformatics curricula tend to use the term interdisciplinary without providing a clear definition for it or what is wished to be accomplished. Jantsch writes about this phenomenon (1972, p. 17):

> … With the introduction of interdisciplinary links between organizational levels the scientific disciplines defined at these levels change in their concepts, structures aims. This is usually overlooked in superficial attempts to bring together specialized knowledge and methods in research and education –most of the approaches called interdisciplinary today are at best pluri-disciplinary of cross-disciplinary.

The natural next step therefore is to consider existing bioinformatics undergraduate curricula and the level of interdisciplinarity they may demonstrate. For this we will consider the definitions of pluridisciplinarity, crossdisciplinarity, multidisciplinarity, interdisciplinarity and transdisciplinarity formulated by Jantsch (1972) as presented in the next part of this chapter.

This will be interesting as Cattley (2004) commented on this issue in her review of bioinformatics education in Australia: many degrees baring the name bioinformatics teach very different things. By drawing pie-charts representing the subject matter content of each degree, she illustrated that a variety of degrees entitled bioinformatics can vary greatly with regards to what the graduates of those degrees will have learned.

Here, we will follow a similar approach but we will pay a particular intention to the level of integration. We will follow the premise that the more integrated the learning is, the more desirable it will be in regards to the educational goals stated in the previous chapter. In order to assess or describe the level of integration qualitatively, we cannot only look at the structures of curricula but must address how the different parts of those structures interact. This interaction can sometimes be depicted at the instructional design level. Thus, in this chapter we adhere to Petrina's views (2004) on the co-influence and dependency of curriculum theory and instructional design.

When we will consider the different examples of bioinformatics undergraduate curricula we will also attempt to characterize bioinformatics curricular models. We will then explore if there is a direct link between a certain type of model and the level of disciplinarity which can be accomplished (or not) by following a particular model. Can more them one model lead to the same level of disciplinarity? Can certain models be limiting to disciplinarity? Do certain departments (life science versus computer science) give rise to certain specific models? Which model is most suitable for the highest level of integration? And, finally, how much integration can be accomplished at the undergraduate level?

Only curricula which were featured in a publication or mentioned in an article are considered here. Although it would have been possible to consider the curriculum of undergraduate bioinformatics degrees as featured on university websites in the form of a list of courses, this was decided against as this does not offer much information concerning design choices and constraints. Instead curricula presented in published articles were considered since a variety of information and knowledge regarding their design is available.

Thus we will consider five bioinformatics undergraduate curriculum case studies spanning a variety of learning environments: a technical college, a university computer science department, a university life science department and a university school of engineering. How do the environments, within which the degrees are enacted, influence the enactment of those degrees? As we saw in the previous chapter, sometimes even the educational goals (despite the fact that at the conceptual level they need not be) are stated according to the institutions which contain them.

The five curricula examples are grouped according to the departments which house them. Thus three degrees belonging to life science departments and two degrees offered by computer science departments are presented. We explored in the previous chapter the fact that bioinformatics educational goals are readapted to better fit the departments they are in as well as to better match the strengths of each department. Therefore, it is sensible to assume that their might be a relationship between educational goals, housing departments and curricular model-type followed. Although we are not considering enough case-studies to draw solid conclusions we can nonetheless attempt to state some kind of hypothesis or impression.

As to facilitate comparison of the subject-matter content of the five curriculum case-studies, we will utilize pie-chart representations depicting seven subject-matter content-areas: Computer Science, Mathematics, Statistics, Chemistry/Biochemistry, Biology, Bioinformatics and Physics. Credits from a particular course were placed in a content-area according to the subject-matter it represented and not according to the department which received credit for the course. For example a course entitled Programming for Bioinformatics is placed in the Bioinformatics content-area despite being allocated Biology credits. Only required courses are represented in the pie-charts as well as restricted science electives whose content-area is clearly specified. General electives are not represented. Proceeding in this manner, which is looking at the core curricula along with science electives, will be more representative of design choices. As stated before, we are also interested in how the different subject-matter blocks interact. Therefore, along with the pie-charts we will also note specific instructional design efforts with particular attention to integration efforts realized by the designers of the considered curricula.

Definitions of the Different Types of Disciplinarity

In order to discuss the design of an interdisciplinary or multidisciplinary program, it is necessary to clearly specify what is meant by those terms. In order to propose a framework for the definition of such terms, as well as others like cross-disciplinary, pluridisciplinary and transdisciplinary, one can follow Jantsch's proposition of an anthropomorphic view of an education/innovation system. From such a viewpoint it follows that the system will not be a mechanistic model but a human action model and will therefore not be objective; it will be led by a purpose. This model surpasses the scope of this thesis as we will not be dealing with transdisciplinarity here. Regardless of this, the definitions provided within Jantsch's framework are useful for characterizing the level of disciplinarity each degree may represent (Jantsch, 1972).

When imagining such a purposive system, it is understood that it must overcome the disciplinary barriers artificially created in universities through the organization of knowledge into departments. "Disciplinarity in science is essentially a static principle which becomes meaningless if considered in the framework of a purposive system" (Jantsch, 1972, p.13). Jantsch argues that interdisciplinarity must be viewed both as a normative and teleological concept. He proposes following education/innovation systems as depicted by figure 5. According to at which level(s) of the system one chooses to act (or to design curriculum in our case), the nature of his educative/innovative action will follow.

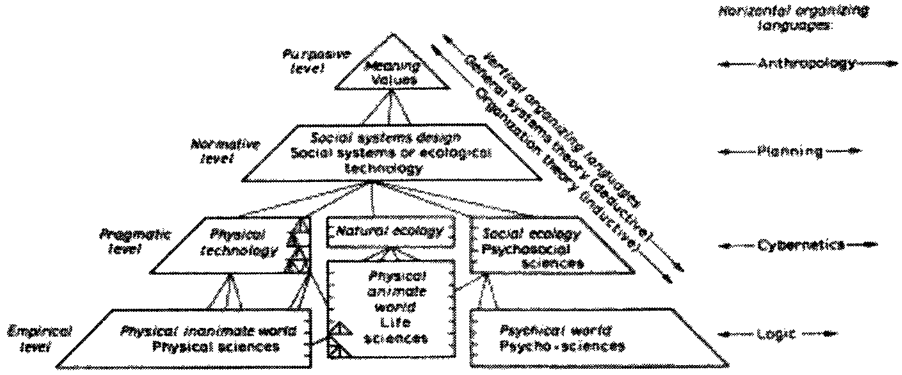


Figure 5. The education/innovation system as depicted by Jantsch (1972). The interactions between different levels depict varying degrees of disciplinarity.

This model provides the conceptual framework on which the different definitions of disciplinarity may be based. The definitions as proposed by Jantsch are as follows (1972) and are illustrated in Figure 6:

- *Multidisciplinarity*: A variety of disciplines, offered simultaneously, but without making explicit possible relationships between them.

- *Pluridisciplinarity*: The juxtaposition of various disciplines, usually at the same hierarchical level (i.e., empirical or pragmatic), grouped in such a way as to enhance the relationships between them

- *Crossdisciplinarity*: The axiomatics of one discipline are imposed upon other disciplines at the same hierarchical level, thereby creating a rigid polarization across disciplines towards a disciplinary axiomatics.

- Interdisciplinarity: A common axiomatics for a group of related disciplines is defined at the next hierarchical level, thereby introducing a sense of purpose;

more specifically, we may distinguish between *teleological interdisciplinarity* at and between the empirical and pragmatic levels and sublevels, *normative interdisciplinarity*, signifying the important step from the pragmatic to the normative levels (where the question of "good" and "bad" is raised), and *purposive interdisciplinarity*, bridging from the normative to the purposive level.

- *Transdiciplinarity*: The coordination of all disciplines and interdisciplines in the education/innovation system on the basis of a generalized axiomatics (introduced from the purposive level) and an emerging epistemological pattern

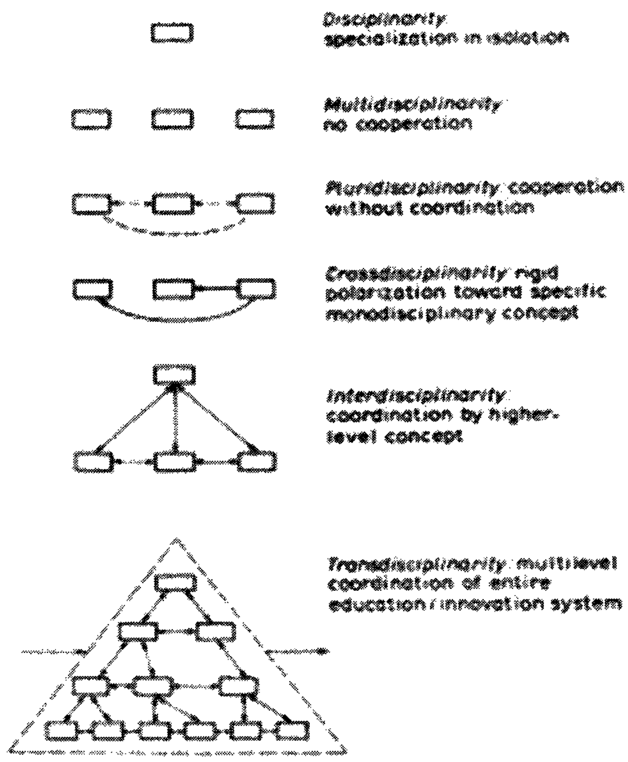


Figure 6. Representations of varying degrees of disciplinarity as advanced by Jantsch (1972). Definitions of the different types of interactions between disciplines.

For the purpose of this chapter we will only make use of the definitions of disciplinarity, multidisciplinarity, pluridisciplinarity, crossdisciplinarity, and finally teleological interdisciplinarity (which falls between the empirical and pragmatic levels of figure 5). According to this model, we can readily see how multidisciplinarity, pluridiscipliniarity and crossdisciplinarity, within this framework are not desirable as they do not depict integration or "coordination by a higher level concept" which would position bioinformatics as a discipline in its own right.

Jantsch goes on to present a restructuring of the university which would enable the different kinds of described interdisciplinarity, notably the normative and purposive varieties. This is beyond the scope of this thesis and these shortcomings are discussed in chapter 7. What needs to be established here is the highest level of disciplinarity which can be accomplished for the design of bioinformatics undergraduate curricula given these architectural/structural/departmental constraints.

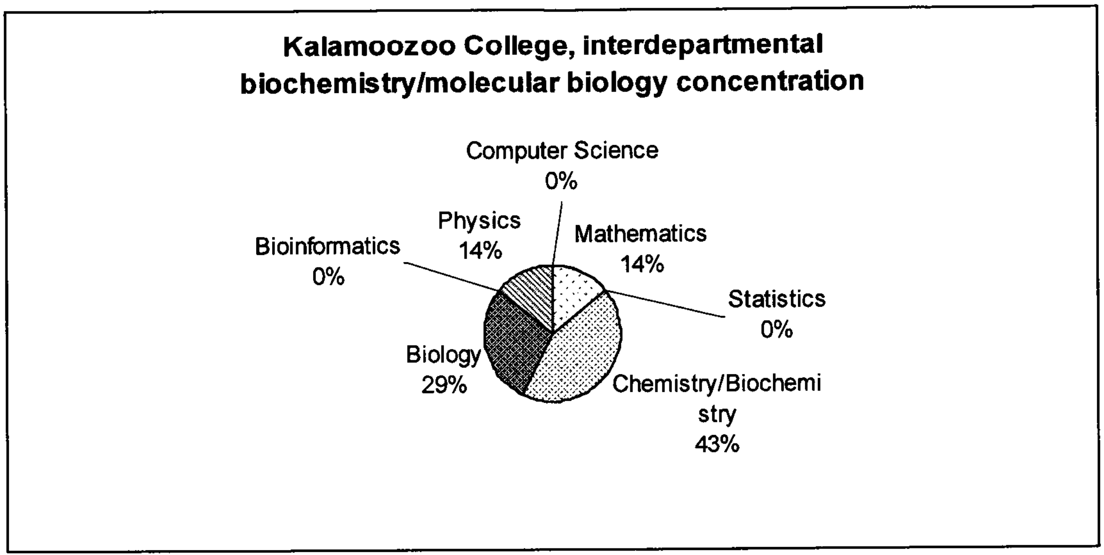
So having specified these definitions let us now consider the five bioinformatics curricula case-studies with a view to elucidating what level of disciplinarity was entailed in the development of the degrees. Particular attention will be given to how the different disciplines within the degree actually interact.

Undergraduate Bioinformatics Curricula Overview

Life science curriculum foundation.

Case-study 1: Kalamazoo College, a bioinformatics modules infusion model.

Let us consider the case-study of Kalamazoo College in Michigan. (Furge, Stevens-Truss, Moore, & Langeland, 2009) They opted for the incorporation of bioinformatics modules into existing courses required for the biochemistry/molecular biology concentration. Thus, although bioinformatics subject matter is taught it is not represented in the pie-chart of figure 7 as it does not represent a course. This infusion of degrees with bioinformatics through modules is common in cases where there are budget limitations as well as expertise limitations. This is often characterized as vertical integration (Boyle, 2004).



Notable design initiatives:

- Incorporation of bioinformatics modules in order to accomplish interdisciplinarity
- Modules not limited to life science departments but also added to computer science, mathematics and physics courses (despite the fact that biology concentration students do not take this courses)
- Two capstone courses which are life science courses and not a bioinformatics capstone but which incorporate bioinformatics tools.

Figure 7. Profile of the interdepartmental biochemistry/molecular biology concentration at Kalamoozoo College

Their educational goal was expressed in regards to interdisciplinarity: "we believe that a true interdisciplinary experience is best served by introduction of bioinformatics modules within existing courses..." (Furge et al., 2009). Over a dozen such modules have been incorporated into five required courses of that program. Aside from the standard biology and chemistry courses, two calculus courses and two introductory physics courses are undertaken.

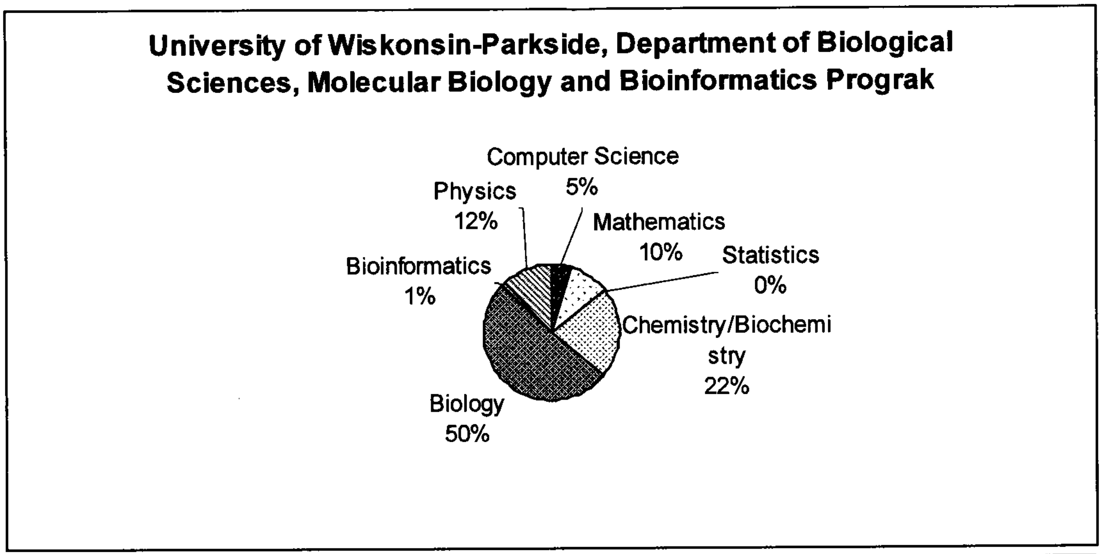
From the description of the bioinformatics modules in the article, we can summarize that the content consists in familiarizing the students with on-line bioinformatics tools and databases. Given the module structure, the bioinformatics content enhances or reiterates the course content, scaffolding students understanding.

The University of Wiskonsin-Lacrosses describes a similar instructional design initiative. It launched the Bioinformatics across the Life Sciences curriculum strategy. It consists in the addition of 10 courses spanning three departments (biology, chemistry, microbiology). Bioinformatics is incorporated into first year courses so that all life science students, regardless of their major, are exposed to the field. The design process is such that bioinformatics is not taught for its own sake but for the simulation and probing capacities bioinformatics tools offer which help students better understand key molecular biology concepts. Thus, an interesting synergy is taken created (Miskowski, Howard, Abler, & Grunwald, 2007). Such synergetic effects should definitely be taken note of by all persons involved in the design of Bioinformatics curricula.

Returning to our case-study, Kalamazoo College, the subject-matter of the modules belonging to the biochemistry/molecular biology concentration consists in: use of tools for virtual translation of nucleotide sequence, local alignment search tools, use of tools for building phylogenetic trees and tools for molecular structure visualization. Also offered are an advanced molecular biology capstone course and biochemistry capstone course which incorporates online bioinformatics tool.

Case-study 2: University of Wiskonsin-parkside, bioinformatics module infusion module along with one specialized bioinformatics course. The University of Wisconsin-Parkside developed a multidisciplinary undergraduate curriculum in

Molecular Biology and Bioinformatics (MBB) within the Biological Sciences department.(Pham, Higgs, Statham, & Schleiter, 2008). Its characteristics are summarized in figure 8. It goes a step further than creating capable users of computational tools related to bioinformatics by stating as a learning outcome gaining understanding of mathematical and physical concepts related to biology. This is also reflected in the curriculum: 22 credits out of the 85 core credits are dedicated to mathematics, physics and computer science. This physical science subpart of the curriculum represents a turning point from other life science curricula housed in life science departments. The undergraduates also complete a year long independent research capstone class. It is unclear how much emphasis is on molecular biology and how much on bioinformatics within the context of that class. The bioinformatics programming course familiarizes students with bioinformatics tools as well as the scripting Perl and Php languages with which the students develop web applications.



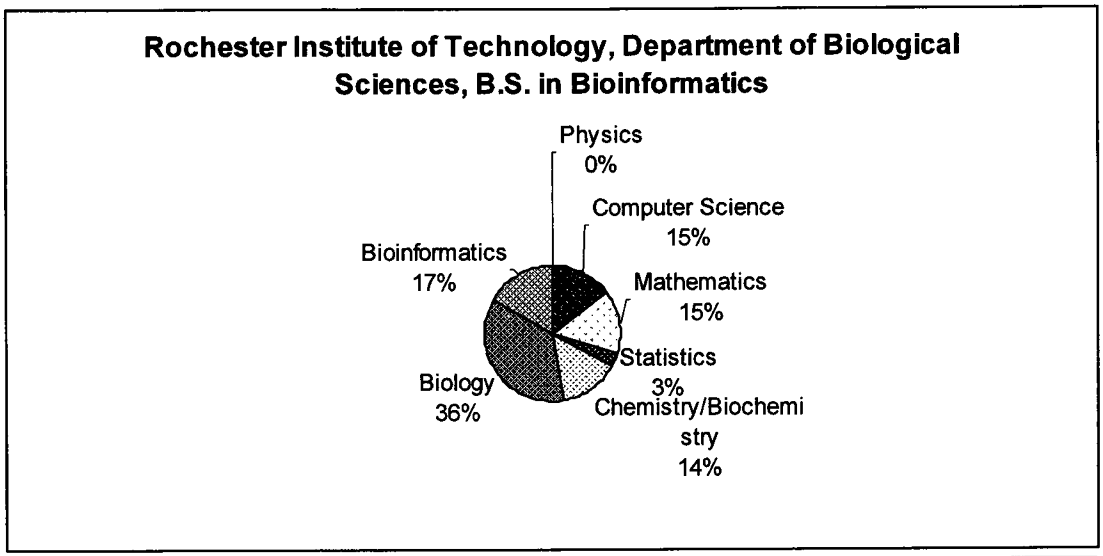
Notable design initiatives:

- 1 year research capstone class: molecular biology and bioinformatics senior thesis
- Studio approach to course, in-vivo/benchwork and in-silico/computer-aided predictions taught side by side
- The 1% representing Bioinformatics course is a bioinformatics programming course. It is co-taught by a biochemist and computer scientist.

Figure 8. Profile of the molecular biology and bioinformatics program at the University of Wiskonsin-Parkside offered by the department of Biological Sciences.

An interesting instructional design notion or strategy to take away from this example is the studio approach to coursework. The studio approach enables both physical and conceptual movement of the classroom between lecture, discussion, and computer terminal and laboratory bench. This is interesting as it overcomes the traditional and, at times, even architectural limitations to interdisciplinarity. The authors comment: "This approach reflects the actual research environment in that it provides the flexibility to address the complex topics using multiple methodologies and creates a more effective learning process by using inquiry or problem-based learning" (Pham et al., 2008, p.107).

Case-study 3: Rochester Institute of Technology, mosaic structure model with high number of specialized bioinformatics courses. The next case-study is that of a technical college, the Rochester Institute of Technology (RIT). Comparing the pie-chart depicting the curriculum (see figure 9) with the pie-charts of the two previous case-studies, we can see that the biology and chemistry/biochemistry content areas which taken together represented in the previous case-studies about three-quarters of the pie-charts are now reduced to representing half. This makes room for more computer science and statistics courses and in particular a "statistics for bioinformatics" course (Burhans & Skuse, 2004). Bringing to mind the importance attributed to statistics when describing "depth" bioinformatics, it is worth noting that this is the only instance within the case-studies considered in this chapter in which a statistics course tailored to bioinformatic needs is offered. Furthermore, six courses were developed which specialize in bioinformatics, representing the highest count within all case-studies considered as well as a significant percentage of computer science courses, despite being in a Biological Science Department. This degree was built over an already successful biotechnology degree.



Notable design initiatives:

- Statistics course is present and adapted to bioinformatics ("Statistical Analysis for Bioinformatics")
- Designed over already existing biotechnology undergraduate curriculum
- Aimed towards skill-set attractive for employers
- high percentage of bioinformatics courses

Figure 9. Profile of the B.S. in Bioinformatics at the Rochester Institute of Technology offered by the department of Biological Sciences.

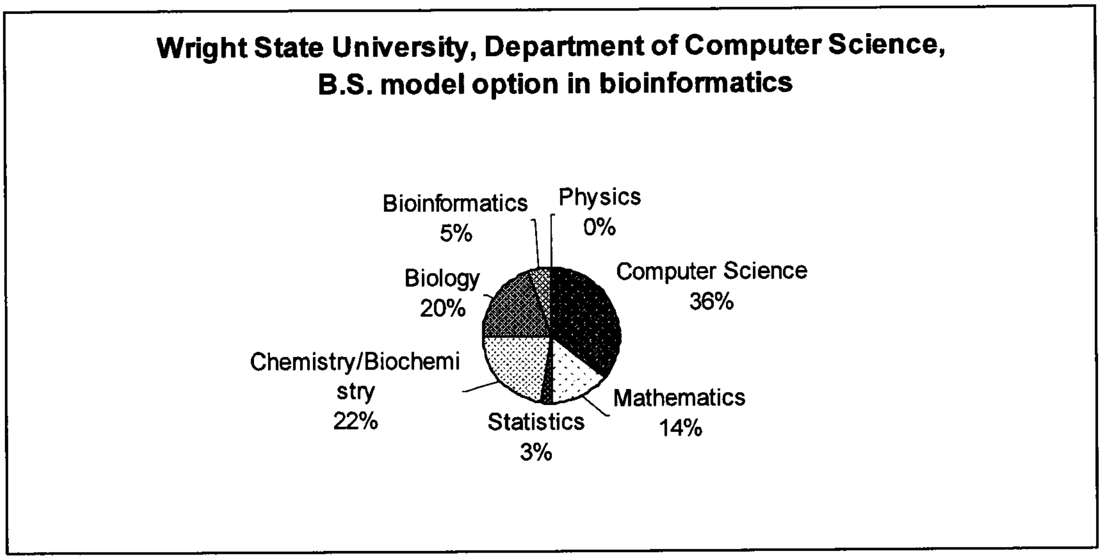
The article does not give a lot of details concerning the subject-matter. The bioinformatics course titles are: introduction to bioinformatics, introduction to bioinformatics computing, molecular modeling and proteomics, advance bioinformatics computing, high performance computing. The authors of the article comment on the fact that graduates of this degree have a skill set attractive to employers.

Complementing the information available in the article with the information regarding the bioinformatics' courses content available on the website of the institute, we see that the students will engage in knowledge extraction or data mining on dna/protein sequences, they will familiarize themselves with parallel computing, and of course will learn about relevant algorithms and issues concerning performance and correctness of the generated results (Rochester Institute of Technology, 2010).

It is also interesting to keep in mind that this degree does not exist in a university or college setting but rather in an institute of technology within the Biological Science Department. The content areas are more balanced and resemble in shape more the bioinformatics degrees housed in Computer Science departments, as we shall see in the next set of case studies, than the ones housed in life science departments.

Computer science curriculum foundation

Case-study 4: Wright State University, mosaic structure model with two bioinformatics courses. Wright State University instituted a baccalaureate computer science option in bioinformatics (Doom et al., 2003). Its characteristics are represented by figure 10. The program is composed of existing coursework in computer science and biological science with two new bioinformatics courses. Without considering the general education requirements, 52 credits are dedicated to computer science, 29 to biology, 33 to chemistry and 25 to mathematics, four of which are a statistics course. Eight credits are dedicated to two bioinformatics courses: an introductory class to be followed at the beginning of the degree and a capstone class, "Algorithms for bioinformatics", to be followed at the end of the degree.



Notable design initiatives:

- Interdisciplinary student teams in bioinformatics courses, active-cooperative learning approach
- co-taught bioinformatics classes by computer scientists and biologists as to provide the "appropriate interdisciplinary mix"
- capstone bioinformatics class

Figure 10. Profile of the Bachelor of Science model option in bioinformatics at Wright State University offered by the Department of Computer Science.

The goal of the program is to expose students to the fundamental concepts required for the education of engineers and scientists:

> The goal in the development of this model is to provide exposure to the fundamental concepts required to produce engineers and scientists well prepared for postgraduate bioinformatics education capable of carrying out research and development into new bioinformatics techniques and tools. Students will learn the algorithms, data representations and ontologies at the core of current bioinformatics analyses. They will also learn how to implement these algorithms at the same time as they are exposed to the

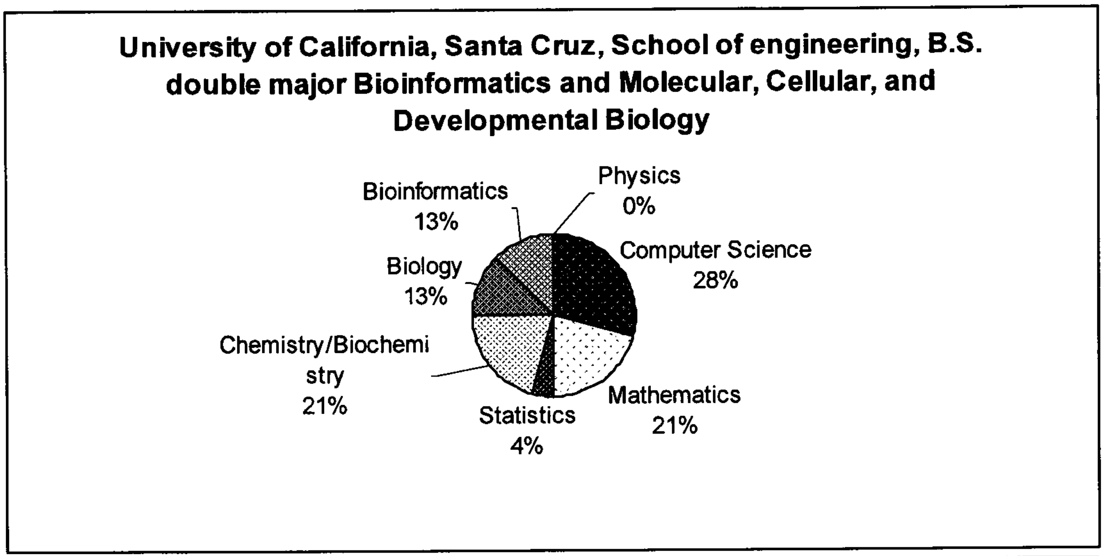
> experimental techniques used by molecular biologists to gather data. By the end of their course of study, students will be ready to enter the bioinformatics job market or participate in on-going research projects involving analysis of molecular data."(Doom et al., 2003, p. 388)

The educational goals are geared towards bioinformatics techniques and tools, algorithm implementation, and exposure to experimental techniques. The predominance of engineering goals is noticeable but the students seem to receive a well-rounded exposure to biological issues. Indeed, in the pie-chart we can see how a bit more than half of the degree is dedicated to physical sciences and a bit less than half to biological sciences.

The two bioinformatics courses are conceptually organized in three sub-parts, each broken down in the following manner: prerequisite knowledge from biology, knowledge from computer science, lab activity. The introductory class presents a tools-oriented approach to bioinformatics and helps students develop Perl programming skills. The capstone class represents a theory-oriented approach to the application of contemporary algorithms to bioinformatics. Its completion requires that the students undertake a formative research project (Doom et al., 2003, p. 391).

It is crucial, in the opinion of the authors, that the classes are co-taught so as to provide the "appropriate interdisciplinary mix". Thus they are co-listed as CS/BIO and therefore also open to biology students. The authors remark on the effect of co-listed courses which attract a variety of students from majors other than the bioinformatics option. Interdisciplinary student project teams are purposely created for the student assignments and activities, as this will have a beneficial integrating effect: "... students with a stronger biology background take the lead in experimental design and data interpretation, while students with a stronger computer science background take the lead in the development and implementation of representation methodologies and optimized solution-finding algorithms"(Doom et al., 2003). This strategy promotes students' communication skills and in particular the ability to effectively express ideas within disciplinary frameworks that are not necessarily their own.

Case-study 5: University of California Santa Cruz, mosaic structure model with three bioinformatics courses. The University of California Santa Cruz, School of Engineering has established an undergraduate program in bioinformatics. Its characteristics are represented by figure 11. It also follows a mosaic structure containing three bioinformatics courses of which the third is an elective (Hughey & Karplus, 2001). The educational goal is stated as follows and is aligned with traditional engineering degree goals: "Our goal at all levels is to hone the engineering design skills and scientific understanding required to develop new bioinformatics tools and methods to solve real problems" (p. 101).



Notable design initiatives:
- capstone bioinformatics class in the last year.

Figure 11. Profile of the Bachelor of Science double major in bioinformatics and molecular, cellular, and developmental biology at the University of California, Santa Cruz offered by the School of Engineering.

The first-year introduction to bioinformatics course contains the following content: statistics and stochastic models, sequence comparison methods and algorithms, Perl scripting and its use in pipelines, internet and command line tools. The remaining time involves discussions on genomics, microarrays, remote homology detection, protein structure prediction, and phylogeny. The last-year bioinformatics course focuses on core statistical methods regarding their understanding and application to new problems. Also, students do a quarter long project in bioinformatics which serves as the “capstone” experience during which they design and implement a solution to a real problem. The preparation of the degree towards graduate studies is clearly stated and the authors identify five key areas of the mosaic-type curricular design: biochemistry, bioethics, programming, statistics, and introductory bioinformatics.

Analysis of Case Studies in Regards to Levels of Disciplinarity

Models of curricular types. Burhans and Skuse classify bioinformatics degrees into three categories (2004):

> (1) those programs that include a significant number of newly-developed courses (e.g. RIT), (2) broad, interdisciplinary programs that are not based on a traditional major and include a few newly developed specialized courses [...], (3) programs that require a full traditional major in a supporting area such as Math, Computer Science or Biology along with an appropriate selection of biology, chemistry, and computer science courses [...]. Such programs may include one or two new course specifically devoted to bioinformatics, typically at the senior level.(p. 420)

According to this categorization, the Rochester Institute of Technology would fall in group one, the University of California Santa Cruz and Wright State University in group two, and Wisconsin-Parkside in group three. Kalamazoo does not readily fall into any of these categories but would better fit what Leblanc and Dyer (2004) characterized as an infusion model. It could potentially fit in group three as it requires a traditional life science major though no appropriate selection of computer science courses is present.

Thus, given the case-studies considered in this chapter we may identify the following categories:

- Infusion model with or without the addition of specialized course(s) such as Kalamazoo College, Wisconsin-Parkside University.
- Highly specialized, mosaic structure such as the Rochester Institute of Technology.
- Capstone bioinformatics course, mosaic structure such as Write State University, University of California Santa Cruz.

We shall refer to a mosaic structure when neither traditional life science nor physical science subject matter encompasses significantly more than half of a degree. Thus the different content areas are relatively balanced. Indeed, the degrees we explored in computer science departments seemed more balanced in their subject matter than the life science degrees of which about three quarters of subject-matter was life science subject-matter. This is also reflected, and expectedly so, in the fact that degrees housed by computer science departments were mostly aimed towards tool-building and those housed in life science departments towards tool-using.

From the case studies we explored, we saw that bioinformatics content may be incorporated via an infusion model or by adding specialized courses to a traditional major. Often, these specialized courses were an introductory and capstone course.

Leblanc and Dyer ask: “Can bioinformatics be presented via an infusion model? Or is a separate “Bioinformatics major” essential?” (2004). They concluded in their article that any approach can be effective. But what does each model imply in terms of integration? Exploring Leblanc’s and Dyer’s question from this perspective will allow us to enrich our understanding of curriculum design in undergraduate bioinformatics. Let us revisit the question with our five case-studies, paying particular attention to the level of integration each model can support.

Integration within and without bioinformatics courses and levels of disciplinarity. Considering the content breakdown of the subject-matter of each degree alone is not informative enough to permit comment on whether the educational goal of integration is achieved. Even more so in the case of bioinformatics modules which are not represented in the pie charts as there is no way of quantifying them in terms of credits given the information present in the articles. We must therefore consider what is taught in the bioinformatics module or courses and whether it interrelates explicitly, with the rest of the subject matter. That is, does the knowledge acquired by the students fragment or integrate? Do the mosaic structures of the computer science degrees lead to integration or is a modular approach more effective for integration?

Mosaic type degrees housed in computer science departments seem to rely on capstone courses to bring everything together. The capstone class focuses on statistical methods and algorithmic applications. If a capstone course is not successful such mosaic structure degrees run the risk of being multidisciplinary; there is no cooperation between the different disciplines. Indeed, considering the mosaic structure degrees of University of California Santa Cruz and Wright State University, the disciplines of mathematics, chemistry/biochemistry, and biology and computer science don't exhibit any explicit interaction outside of the capstone classes (and possibly the introduction to bioinformatics classes). Thus the question that rises is: can one or two capstone classes differentiate an interdisciplinary bioinformatics degree from a multidisciplinary degree?

If the capstone class is successful, the best that may be achieved is crossdisciplinarity; capstone classes housed in computer science degrees tend to focus their educational goals on tool-building. This carries strong connotations of engineering educational goals. Thus, there is a rigid polarization towards the mono-disciplinary concept of tool-building.

In that sense, infusion through a modules approach seems promising as it may possibly help in overcoming the shortcomings of relying too strongly on capstone courses. Indeed, with modules, a possibility for integration offers itself within every course a module is incorporated. But, when considering our two case studies of infusion models, the depth of bioinformatics education attained is questionable. The modules approach as seen in our two case-studies tends to incorporate tool-using bioinformatics along with familiarization with database searches.

The addition of a programming for bioinformatics course in the case of Wright State University enabled for the programming of bioinformatics scripts. We also saw how bioinformatics software was used to further enhance the understanding of certain key biological concepts. Thus, given our case studies we can only conclude that the modules approach led to tool-using bioinformatics. The degrees may be characterized as cross-disciplinary as there is rigid polarization towards life science concepts.

Many specialized bioinformatics courses seem to be desirable as in the case of the Rochester Institute of Technology. Indeed this specialization allows for learning new skills highly relevant to bioinformatics such as parallel computing and data-mining techniques. The information technology aspect is more stressed in this degree and the knowledge disclosed is more unique in relation to the other case-studies explored in this chapter. Considering the subject-matter of the RIT degree, we saw that the tool-usage concerned much more sophisticated tools in relation to those used in life science departments. Further, using the tools appropriately for their own sake is the educational goal rather than scaffolding the understanding of life science concepts.

This degree gives rise to what Hack and Kendall (2005) described as Power-users of bioinformatics whereas the life science degrees seem to give rise to Super-users. Computer science or engineering degrees with bioinformatics options describe what Hack and Kendall described as Bioinformaticians. It is interesting to note that the in-between Power-users placed at the middle of the spectrum of bioinformatics practice (where Super-users and Bioinformaticians are placed at each end), is only found in the setting of a technical college. Could it be, therefore, that the unifying interdisciplinary concept is in fact the bioinformatics tools? That is, is the understanding of *complex* and *sophisticated* bioinformatics tools the higher level concept which coordinates the curriculum giving rise to interdisciplinarity in the case of bioinformatics? Tool-usage as a higher-level concept is often dismissed as it does not necessarily fit with the scientific culture of academia.

In the next chapter, I will explore the educational implications and gains in regards to curriculum design when bioinformatics is considered as a technoscience, rather than being denied this identity in order to better fit in university settings. Nonetheless, for now we may conclude that most examples in life science with the exception of Rochester Institute of Technology seem to be cross-disciplinary. Bioinformatics tools are used to better teach life science concepts. Capstone courses start to allow bordering from crossdisciplinarity to teleological interdisciplinarity provided the students go through the capstone by coordination from a higher level concept. If the capstone course is not successful in this it becomes multidisciplinary rather than interdisciplinary.

This does not mean that the modules approach should be dismissed but rather that the content of the modules be revised and possibly have courses from supporting disciplines strategically added. For example, in the case of Kalamazoo College bioinformatics modules were added in supporting disciplines such as computer science but the computer science course was not offered to students in the life science degree.

Chapter 5: Integration through Technoscientific Awareness

In the previous chapter, we saw how the Rochester Institute of Technology, which based its bioinformatics degree on a previously established successful biotechnology degree, offered the highest number of specialized courses. It is interesting to note that this institute, which is by nature a technical college, offered this high number. Could it be that the educational goals as expressed through a technical college are conceptually more congruent with the educational goals of bioinformatics? Could it be that departments in such settings are more flexible and adaptive in regards to their educational goals? Indeed implementing changes takes place at a faster pace than university settings where changes require a series of exterior approvals. Nonetheless, the consequences in the curriculum design of this adaptivity and flexibility, as evolved from a biotechnological foundation, are worth giving further attention.

In this regard, we shall consider the concept of technoscience, whether bioinformatics should be considered as a technoscience and the consequences of considering bioinformatics as technoscience in respect to curriculum design. When bioinformatics is taught in university setting it must adhere to certain ideological educational goals of those settings. The tendency is for bioinformatics to be emphasized as a science rather than a technology. Further, certain curricular design models (for example, vertical integration in the life sciences) can stress more its technological nature rather than its scientific nature. We will argue that understanding or interpreting bioinformatics as a technoscience can be enlightening in curricular decision making.

Challenges of Describing a Practice

When asking the question "what is an ideal curriculum for teaching bioinformatics?" the answer is dependent upon another question "what is bioinformatics?" This poses the problem of describing a practice which was also considered in chapter three where we overviewed educational goals in accordance with the different levels of "doing" bioinformatics.

Fischer demonstrated how the relationship between practices isn't necessarily coherent with the description of those practices. Barnes explains of his work that "the question was raised of how far accounts of what we do relate to intrinsic features of the doing, and how far to the context and the goals of the doing" (Barnes, 2005, p. 143).

This is a particularly interesting question to consider in regards to techno-sciences. Let us recall a previously considered statement by Ouzounis: "By approaching bioinformatics (or computational biology) as a science, the field will not be misapprehended as a technology platform, where people know the problems whose solutions are only a matter of time and resources" (2000, p. 189). This claim demonstrates fairly clearly the clash between science and technology. But, what is the difference between science and technology?

Barnes (2005) turns our attention to the Latin terms of *ars, scientia, techne* and *episteme* and the difficulty in making firm distinctions among them. He brings to our attention the examples of hunting and pugilism and how they were regarded at some point in time as sciences. By today's interpretation, we would be more inclined to call them *ars* or *techne*. What this point demonstrates is that the value we attribute to something is what will classify it as a science or not. In either way, this will lead to error for *scientia* cannot be separated from *techne*, they are one and the same in such that one cannot exist without the other. This subscribes to the *interactionist* view of the science-technology relationship which: "considers scientists and technologists as groups of people who learn from each other in mutually beneficial ways" (Gardner, 1994, p. 5). Other views do not adhere to this synergy effect. A popular view is the *technology as applied science,* reminiscent of the leitmotiv of university science settings, in which scientific knowledge is predecessor to technology. The *demarcationist* view considers science and technology as independent, whereas the *materialist* view "asserts that technology is historically and ontologically prior to science, that experience with tools, instruments and other artefacts is necessary for conceptual development" (Gardner, 1994, p. 3-4).

Recalling how bioinformatics established itself as a field, thanks to advancements in sequencing technology which led to an explosion of data, one is quite inclined to follow this materialist view. On the other hand it can be argued that the processing of data relied on already established algorithms and the processing is in fact technology as applied science. Nonetheless, many authorities in the field of bioinformatics have stated that new scientific problems are framed which would not have been considered if not for the technology. The technology contributed to conceptual development and we are brought back to reconsidering the materialist view and, after this series of realizations, the interactionist view. It is my opinion that such an interactionist view is necessary for designing intellectually honest bioinformatics curricula. Indeed, in the case of bioinformatics it is particularly true that science and technology should be viewed as one and the same, since without the appropriate technology their would not exist the science of bioinformatics and without the science of bioinformatics much of that technology would not have been conceived and created.

If the practice of bioinformatics is chosen to be characterized as a science rather than a technology or vice-versa, the implications for curriculum design will be severe and damaging, as an important aspect of what doing bioinformatics is will not be taken into account. This was indeed seen in the case-studies of the previous chapter where different curricular models explored different levels of doing bioinformatics. They were mostly positioned at the tool-using or the tool-engineering ends of the spectrum of the practice of bioinformatics. Only the technical college case-study dealt with more complex and sophisticated tool-usage.

This notion of the dependency of science in regards to technology is well illustrated by the following realization by Veblen (as cited in Barnes, 2005, p. 158) "men have learned to think in the terms in which the technological processes act." Thus separating tool-usage from tool-building in the case of bioinformatics, or separating theoretical scientific principles from technological realities will not lead to depth in bioinformatics. This is particularly accurate in regards to pipelining, a process by which different software tools are interfaced in order to mine data and generate results.

Doom *et al.* state: "There exists a clear demarcation between research problems that utilize developed bioinformatics algorithms and the development of new algorithms. The demarcation facilitates a multidisciplinary approach to the understanding of bioinformatics methods."(2003, p. 389) The problem with such a statement is that there is a grey zone of the practice of bioinformatics which is not accounted for. Specifically, this grey zone involves tool-integration (Hack's and Kendall's Power-users) through the process of pipelining which is ultimately technologically dependant. It would be possible to imagine processing data a certain way but would not be possible to actually do it if not for the technology. The technology unites the conceptual with the practical, thus facilitating the interdisciplinary unification of what Doom *& al.* are forced to reductionally reductively characterize as a multidisciplinary approach to understanding.

The existence of this grey zone can be very concretely demonstrated by the work of Toms and Bartlett (2005). After interviewing 20 researchers conducting bioinformatics analysis, they extracted a model flowchart describing a process containing 15 steps and utilizing numerous software tools and databases. Therefore, the model contains 15 decision points. Some of the decision-making is quite complex and cannot be automated: it requires human intervention. This fact led the interviewees to describe their decision making as an "art rather than a science" (p. 478). This is of particular interest as it is reminiscent of tacit knowledge. Davenport and Prusak explain:

> Tacit knowledge developed and internalized by the knower over a long period of time is almost impossible to reproduce in a document or database. Such knowledge incorporates so much accrued and embedded learning that its rules may be impossible to separate from how an individual acts. ... The knowledge a creative research scientist uses to decide which line of inquiry to follow likewise cannot be turned into a step by step list or report. If it were possible to extract knowledge form the knower in this way, it would radically change our compensation and education policies. (2000, p. 70-71)

In silico analysis is crucial to bioinformatics. Finding ways to transfer that tacit knowledge (or to the least generate the learning environments in which it can develop) and taking it out of the grey zone of bioinformatics subject-matter is fundamental to any bioinformatics curriculum design. There is more to be learned from protocols than just the protocol or what Pevzner characterized as recipe-based bioinformatics. As Davenport and Prusak explain, there is knowledge which cannot be separated from the doing and in the case of bioinformatics it cannot be separated from the technology.

Let us take now take a closer look at the philosophy of technoscience and explore how it may inform bioinformatics curricula.

Legitimizing Technology as Science:

It is believed that the term technoscience was first used by Bruno Latour, according to Idhe (as cited in Sullins, 1998):

> [Technoscience] is used to refer to his belief that modern science is embodied in its instruments. What this means is that no longer is science practiced purely as an observation of natural events but that the entire experimental process is influenced entirely by the apparatus used to conduct the experiment, the scientist experiences the phenomena he or she studies through scientific instruments and without those instruments modern science is impossible, science and technology are now inseparable.

To further argue our point of the place that technology may hold in science let us consider a more radical example: that of synthetic biology or artificial life (AL). This field has been criticized within the scientific community because of its strong reliance on computer simulations. Sullins (1998) summarizes the problem in the following paragraph:

> Through the skills of programming the AL researcher, in a very real way, crafts the world that he or she plans to study. This fact has put some theoretical biologists off from seeing AL as truly contributing to the knowledge of living systems and biology (Emmeche). The awkward situation of having a technology color a field of study so thoroughly places the science of AL squarely in the middle of the debate that been going on for some time in the philosophy of technology. And that debate is over the question regarding what is the relationship between science and technology.

This seems to be particularly salient in the case of bioinformatics and the instruments Sullin (1998) speaks of are the software and hardware tools. Indeed, as he explains: "…today each new scientific discovery quickly suggests new technological applications and each new technology creates new tools to be used in scientific endeavors, high technology and science have become almost indistinguishable."

Indeed, this can be paralleled with the appearance of sequencing technologies and next generation sequencing technologies are redefining how life science research is conducted and what is bioinformatics research. Such a phenomenon is nothing new: cloning technology gave rise to molecular biology techniques and so molecular biology degrees started to appear along side the more traditional biochemistry degrees. At some point, though, molecular biology became so pervasive that the two branches more or less merged into one.

Another example may be drawn from the science of chemistry in the 18th century. Indeed, technoscience is not a recent phenomenon in science. Its elusiveness can be explained perhaps by the beliefs which model our world views:

> The interconnection of chemical science and technology … was firmly established on the communal and institutional level of eighteenth-century chemistry. It was entrenched in a shared material culture that was extended from the academic laboratory to the chemical workshop, comprising material objects of inquiry, instruments, reagents, types of manipulation and sites of experimentation. … Unlike the later technoscientific alliances, however, this early form of technoscience was not the results of a convergence of previously separated scientific and technological cultures and practices, but rather a hybrid scientific-technological endeavour from the very beginning of its institutionalization in the late seventeenth-century Europe (Klein, 2005, p. 227).

This is why bioinformatics should not be seen as the combination of computer science and life sciences for it is not the combination of two areas but rather a new form of inquiry reliant on technology. Klein (2005, p. 228) goes on explaining of the science-practice of chemistry:

> Eighteenth century chemists working at medical faculties, professional schools and other medical institutions instructed their students about pharmaceutical techniques and various areas of "applied chemistry". They repeated artisanal operations and analyzed materials produced and applied in the chemical arts and crafts, in the first half of the eighteenth century using almost exclusively instruments shared with assayers, apothecaries and other artisans.

It is interesting to note that the discipline of chemistry or the inauguration of chemistry departments appears natural and chemistry as scientific discipline is not second-guessed. Perhaps this is because we are more used to the technologies pertaining to the practice of chemistry which have more familiar manual and physical actions as part of their epistemic mythology than the newer, more "high-tech", robotic and silicon chip technologies pertaining to bioinformatics.

Harwood gives an interesting account of how this distinction between science and technology is made for strategic reasons without having a philosophical basis. In his case study of German agricultural education in the nineteenth century, he shows how the separation between science and technology is used as a strategy for either gaining prestige (promoting science and neglecting technical skills) or establishing partnerships with industry and community (promoting the technological aspect) (Harwood, 2005).

Effect of E-science on Curriculum Design

E-science is perhaps the clearest demonstration of how all modern science is inescapably technoscience. In this part we will explore what e-science is and how it may be of consequence to the teaching of bioinformatics.

If bioinformatics is viewed as multidisciplinary and the grey zone of thinking in terms of software tools is not explored in curriculum design this becomes even more problematic given the changing face of science -- once again, due to technological innovation. As science is moving towards e-science and cyberinfrastructures, bioinformatics is giving way to systems biology:

> To integrate biologic data, one would want to move seamlessly between biology and chemical process, organelle, cell, organ, organ system,

> individual, family, community and population. The diversity of data types explored in biomedicine is somewhat orthogonal. Technology permits the characterization of genomic, proteomic, metabolic, and other large scale characterizations. All of the above is further confounded by the organization of biomedicine into research fields and disciplines. Such disciplines focus generates an insidious challenge to information integration. Each community speaks its own scientific dialect. This community "speciation" results in reduced flow of information between disciplines, slowing the diffusion of knowledge and critical progress … New paradigms are required to support these investigations. The need for teem science also recognizes that many problems cross traditional discipline boundaries. (Buetow, 2005, p. 822)

Indeed, today's scientific endeavours are conducted at a much larger information scale than when Mendel was cross-fertilizing plant species as to demonstrate the existence of dominant and recessive genes.

Thus refusing students access to familiarization of software tools in bioinformatics is also refusing them familiarization with cyberinfrastructure research methodologies and paradigms for science:

> It is clear that big science and team science will be necessary to achieve the goals of biology and medicine. However, the small independent investigator is still the engine of innovative research. Widespread adoption of cyber infrastructure represents an alternative in which the two approaches can be blended to create virtual team science.

Bioinformatics students, just like independent researcher must be involved in big science facilitated through e-science infrastructures.

This changing face of science must also be considered during the curriculum design. "In bioinformatics, researchers and pharmaceutical companies are attempting to use e-Science technologies to reduce data to information and information knowledge." (Hey & Trefethen, 2005, p. 819) So what is e-science all about? Let us consider the descriptions of capabilities offered by the MyGrid project:

> The myGrid e-Science project is researching high-level middleware to support personalized in silico experiments in biology. These in silico experiments use databases and computational analysis rather than laboratory investigations to test hypothesis. In myGrid, the emphasis is on data-intensive experiments that combine the use of applications and database queries. These bioinformatics experiments often involve many processes or services that need to be orchestrated. Workflow tools enable this orchestration and help the biologist to design, describe, and record complex experiments in terms with which they can interact and that can also interact with the workflow of other researchers. Intermediate workflows and data are kept, notes and thoughts are recorded, and different experiments linked together to form a network of evidence, as is currently done in bench laboratory notebooks.(Hey & Trefethen, 2005, p.819)

Another e-science project is Comb*e*Chem whose infrastructure design encompasses the conceptual construct of a scholarly cycle:

> [It] has the ambitious goal of creating a Smart Laboratory for chemistry, using technologies for automation, semantics, and Grid Computing. ... One of the key

> concepts of the Comb*e*Chem project is Publication@Source, through which there is a complete end-to-end connection between the results obtained at the laboratory bench and the final published analysis. … The project has a vision for what they call a scholarly cycle, encompassing experimentation, analysis, publication, research and learning.(Hey & Trefethen, 2005, p. 819)

This scholarly cycle is demonstrated in figure 12 below. What is important in this cycle, in regards to the educational concerns of this chapter and namely the changing face of science, is how the virtual learning environment is embedded within the scholarly cycle. Learning no longer takes place in a conventional classroom setting, nor within a more modern e-learning virtual classroom. Learning is holistically embedded within the infrastructure which is creating new avenues of communication amongst scholars as well as new learning environments for students. Students therefore must have the appropriate degree of literacy in regards to this new infrastructure; students must learn how to use the infrastructure.

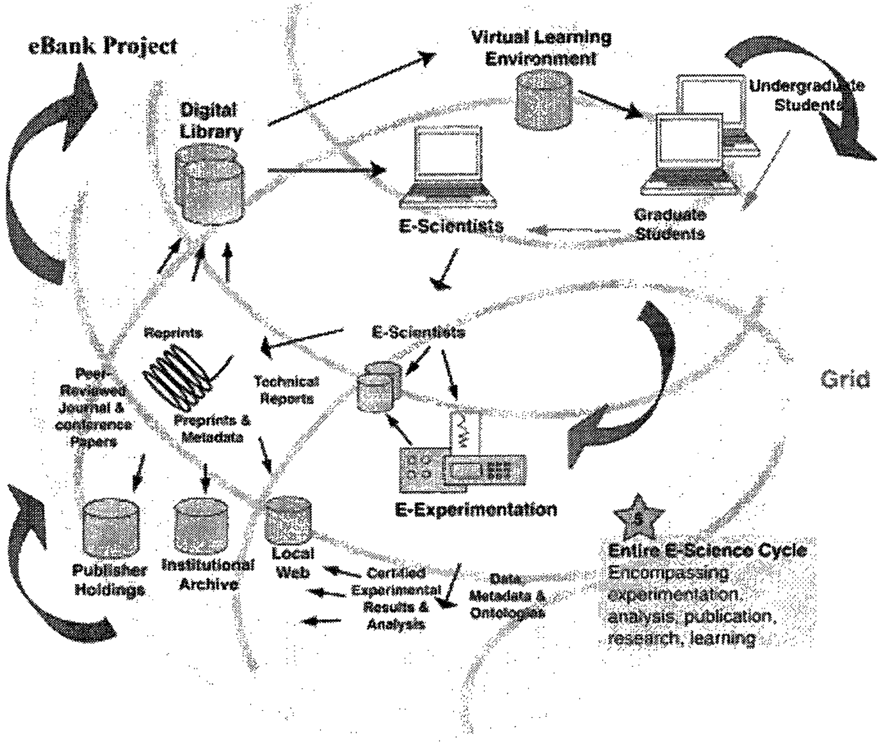


Figure 12. Representation of the scholarly knowledge cycle in e-Science. (Modifed to greyscale and reproduced from Hey & Trefethen, 2005) Experimentation, analysis, publication, research and learning are part of the cycle showing that the communication avenues in science are being transformed by technology.

So how does e-science affect the design of a bioinformatics curriculum? Firstly, utilizing such infrastructures needs to be part of the curriculum as bioinformatics evolves into systems biology. Secondly, the environment in which the curriculum is enacted is very important as it may facilitate an adequate translation of the curriculum to reality, or distort the intents of that curriculum. This is true in the case of the architectural environment but also with technological environments. Following the McLuhan precept of the 'medium is the message' we may advance that, to a certain extent, the environment is the curriculum. Considering the case of bioinformatics where a lot of the grey zone work takes place via interfaces, pipelines and software tools, in a virtual laboratory of sort, a cyberinfrastructure seems like an ideal environment for the enactment of such a curriculum pertaining to those grey zone skills.

So as science becomes e-science and enters the cyberinfrastructure, does curriculum design statically remain within the departmental organization of university? Modern day curricula need to respond/answer to cyberinfrastructures and, further, such infrastructures may hold the potential for bypassing disciplinary barriers. This has another important implication: when designing bioinformatics undergraduate curricula the potential offered by e-learning must be seriously considered. The goal is not to replace a physical course by a virtual one but rather to follow a blended learning approach where the physical classroom learning and virtual learning complement one another.

Summary of Implications

Let as now conclude this chapter by reviewing the role of technoscience as integrating concept in curriculum design.

We have identified two notions of technoscience which relate to bioinformatics. The first notion of the technoscientific nature of bioinformatics may be captured in the centrality of tool-usage. Following Veblen, we have characterized this complex and central tool-usage as tool-thinking, thereby placing it between the tool-using and tool-conceiving spectrum ends of bioinformatics practice. In chapter three, we identified tool-integration as the second level of Hack's and Kendall's model, that of a Power-user. When tool-integration is dictated by the higher level system of the experimental design, and the integration is realized according to the specific experimental design and does not simply follow pre-existing protocols, we notice that the actions of tool-integration start to border with the actions of tool-conception where tool-conception responds to a need identified by experimental designs. When this starts to happen, tools are not simply being linked to one another but experimental thinking is truly taking place and the language of that thinking are the tools. Tool-thinking may take place independently of the engineering know-how required to author such tools. For instance, a life scientist who has engaged in a tool-thinking activity may seek the expertise of engineers to implement the tools he imagined. I do not see why this would require a specialized bioinformatics education different than that of a software engineer. But for the actions of tool-integration and tool-thinking a specialized bioinformatics education becomes quite salient: thinking in terms of tools and protocols should be a central goal of bioinformatics curricula. Pipelining as an introduction to data-mining methodologies must also be introduced into the curricula.

Considering bioinformatics as a technoscience led to the specification of new or more precise educational goals: thus in the next chapter we consider curriculum designs which may successfully promote the educational goals of tool-integration and tool-thinking in bioinformatics. A challenge to this is that since trends come and go, how do we design enduring technoscience curricula? Indeed enduring technoscience is a bit of an oxymoron at a first look. As stated by Pevzner, we don't want to teach cookbook style bioinformatics. Technology is quickly surpassed so learning is not enduring. But this by no means lead to dismiss the centrality of tool-using/thinking in the curriculum; if we accept that technology changes how we think, familiarity with some ephemeral technological platform is necessary. It will allow familiarization with the next platform but also serve metaphorically as a platform for certain cognitive processes to take place and perhaps some of those processes will lead to the acquisition of tacit knowledge. Exploring theory alone will leave students in obscurity in regards to the nature of bioinformatics. Pevzner condemns a protocol-centric approach to bioinformatics which focuses on "parameter settings, application specific features and other details without revealing the *computational ideas* behind the algorithms" (p. 2160). Although this is valid point, a protocol-centric approach cannot be dismissed altogether: how can the computational ideas properly transfer and be utilized by the students if they are not embedded within the protocols or more specifically within the tools?

The second notion may refer to the new research paradigm of e-science which is information heavy and introduces new methodologies for research but also for learning. The information-heavy nature of these methodologies starts to interact with the learning enterprises which are transformed as a consequence of this. Learning is part of the research cycle and technology is perhaps removing it from the physical departments and putting it in the virtual infrastructures. Thus, students must be well versed in using e-science cyberinfrastructures but also these infrastructures might in fact be the ideal environments for learning the grey zone skills of bioinformatics. So how will the design of an undergraduate bioinformatics curriculum take this into account? Let us proceed to the next chapter in which curriculum design approaches that perhaps respond more adequately to these changes are considered.

Chapter 6: Curriculum designs which respond to interdisciplinarity

> In 1964, Price began work on a revitalization plan for the North Staffordshire Potteries, which he called the "Potteries Thinkbelt." The Thinkbelt was to be a "higher education facility" devoted to science and technology. Covering a 108 square mile "campus," Price's Thinkbelt would provide scientific education for 22,000 students and reestablish the North Staffordshire Potteries as a center of science and technology in the English Midland... The "PtB," as it became known, was not a "building" and perhaps not even "architecture" as it was understood at the time. Price proposed utilizing the derelict railway network of the vast Potteries district as the basic infrastructure for a new technical "school."... Mobile classroom, laboratory and residential modules would be placed on the disused railway lines and shunted around the region, to be grouped and assembled as required by current needs, and then moved and regrouped as those needs changed. Modular housing and administrative units would be assembled at various fixed points along the rail lines. (Mathews, 2008)

Integration is about linking different pieces of knowledge which have been artificially separate by the organization of this knowledge into disciplines. In chapter 4, we saw that interdisciplinary student teams and courses co-taught by a computer scientist and biochemist were utilized as a means of reconstructing those broken links (Pham et al., 2008; Doom *et al.*, 2003). Other authors in the literature concerned with bioinformatics education have also realized that artificially re-linking what was artificial separated by university or departmental structures would also be beneficial to their designs; Fetrow and John (2006), for example, focus on interdisciplinary student collaboration for completion of the class project as well as having the course team taught. Meanwhile, Leblanc and Dyer (2004) propose a linked courses approach which brings together interdisciplinary student teams in one course by bringing together two independently run courses which:

> share genomics/bioinformatics as a common thread in their respective syllabi and that share time in the form of guest lectures, some common lab sessions (e.g., four out of 12 labs over the semester), collaborative programming assignments outside of lab time, and final interdisciplinary team projects and presentations.(p. 66)

Further, sometimes architectural design must be revised as to allow for a particular learning environment which will host a certain type of learning. We saw an example of this in chapter four where, at Wiskonsin-Parkside, the in-vivo laboratory had to be modified as to accommodate the hardware necessary for in-silico research. Placing these "two ways of seeking knowledge" side by side enhances integration of that knowledge both practically and to the student's perceptions (Pham et al., 2008).

What is clear is that avenues are being sought to undo departmental separations. What are these avenues? What other types may exist? How can we reenact the pottery think belt in terms of curricular design? How can we modify the learning environment so as to facilitate interdisciplinary integration without changing the university structure?

In this chapter we explore how this re-linking can be accomplished at the curriculum design level. Two approaches or possible solutions are presented: the first looks at concept-based curricula and how they promote interdisciplinary learning, the second could be called process-based curricula (where the processes serve in fact as central concepts) and it is suspected that they be more appropriate to technoscience education.

Thus, in this part, we consider two viewpoints concerning integrated science curricula. The question we will answer is: what are necessary characteristics of integrated learning bioinformatics education and how are they reflected in curricular terms? I suspect that what makes integrated curriculum hard to express is that a lot of the integration action resides in an instructional design level rather than a curriculum theory level. In the world of ideals we would desire a concept-based curriculum but because university is not structured this way we have to bypass this by relying on instructional design or somehow creating a different learning environment. We will then complement our understanding of the questions by considering both the conceptual as well as architectural boundaries of departments and the influence this holds in regards to the development of integrated curricula along with some suggestions for overcoming such barriers.

Pre-sketches of a Biology Centered Concept-Based Curriculum

Let us first consider the thoughts of Bialek and Botstein (2004) for an integrated science curriculum. The authors share their viewpoints on the problem which is contextualized in regards to the quantitative education (or lack of) received by biology students.

The authors have identified a number of obstacles faced when attempting the teaching of an integrated quantitative science which we shall now summarize.

Mathematics, physics and or chemistry courses, which are part of life science degrees, are generally offered to life science students by each respective department. Thus, faculty who teach these courses are by no means properly prepared to make connections of this supporting subject-matter with the life science problems. Consequently, students will fail to see how this relates to their degree of interest and view these prerequisite mathematics, physics and chemistry courses as an obstacle to be overcome rather than an end in themselves.

Despite the fact that mathematics, physics and chemistry departments offer these courses, often the life science students are taught separately from the students majoring in each of these departments -- especially in large universities. Although this might present itself as an opportunity to give specialized courses to life science students which make the connection to life science subject-matter, what ends up happening is that rather than a well-thought up specialization of the courses, there is in fact a loss of sophistication in regards to content. The courses end-up being simplified versions (Bialek & Botstein, 2004).

Another important issue concerns the use of complex software tools: "yet distressingly few academic biologists feel comfortable teaching the underlying principles to their students, and fewer are even able to program a rudimentary software implementation of such an algorithm themselves" (Bialek & Botstein, 2004, p. 788). What is clear from the above two problem-statements is the key role the teacher has to play as an integrating agent.

There is also a discrepancy between the type of learning required from students in life science fields, which is strongly memory-based ("mastering huge arrays of facts"), whereas physical science fields are predominantly problem-solving-based ("focused on principles and reasoning as the goal of their education"). The authors comment on the fact that this is a stereotype but that nonetheless the psyche of the students if affected by it and ultimately their learning actions will be influenced by it (Bialek & Botstein, 2004, p. 788). We are starting to perceive the role students have to play as integrating agents. Indeed, the authors are recognizing that this is not easy: "There is an enormous challenge in raising a generation of scientists who are equally at home with this quantitative mode of thought and with the complexities of real organisms."

Let us now consider the characteristic of the proposed curriculum, which the authors refer to as an "Integrated Introductory Quantitative Science Curriculum", which is specifically suited to biologists. Their first recommendation is that the notion of a mathematics, physics, chemistry or biology course be abolished during the first year of study. Instead, they opt for a concept-based design: "the fundamental ideas of each of these disciplines should be introduced at a high level of sophistication in context with relevant biological problems." This, in turn, will not only affect the subject-matter but will also aim at affecting the student psyche. It will show students how arbitrary the boundaries between disciplines are when it comes to understanding the phenomena of life. Finally, a third consequence of this is ease of communication: "scientists trained in this way, regardless of their ultimate professional specialty, would share a common scientific language, facilitating both cross-disciplinary understanding and collaboration.

Finally, the importance of a broad but concept-specific education and the importance of the ability to partake and communicate are highlighted in this conceptual curriculum design. The challenge lays in identifying "each of the individual intellectual concepts, methods and facts which are fundamental and generalizable". Discipline specific research in identifying these has been carried extensively out by Donald (2002). Looking for overlap between her results in regards to each discipline contributing to the field of bioinformatics could be an interesting next step to take for future study.

A last point, as noted in the Kalamoozoo case-study, is that such concept-based teaching often creates synergy when it comes to learning. Therefore, once these concepts are identified opportunity for synergy should also be exploited by the designers.

What we learned and should retain from this conceptual design is the important role of teacher as integrating agent which will also enable students to act as an integrating agent. The role that communication has in bypassing disciplinary barriers and the learning benefits of a concept-based curriculum in terms of synergy which ultimately will enhance transfer should be clearly implemented in the curriculum design. Let us now pass from this conceptual curriculum design example to one which is actually implemented in a high school setting. It should help us again further understanding of conceptualizing as an approach to curriculum design.

Conditions for Interdisciplinary Education through Conceptualizing

Nikitina (2006) presents three basic approaches to interdisciplinary curricula: contextualizing, conceptualizing and problem-centering. Each describes a type of interdisciplinarity according to the nature of the inquiry taking place. Conceptualizing is of particular interested to the interdisciplinary educational goals expressed in bioinformatics: "Conceptualizing is an integrative strategy designed to take scientific and mathematical thinking beyond the facts and singular theories to the level of underlying concepts" (p. 261).

The example of the pre-university high school program of the Illinois Mathematics and Science Academy (IMSA) is presented by the author. Specifically the Mathematics Investigations program which is offered is organized in content/concept units more reminiscent of the modular approach to curriculum: "each unit addresses different content ideas centered on a single mathematical concept" (Nikitina, 2006, p. 261). Despite our interest in undergraduate level education, notions from this high school example may be of interest to our undergraduate bioinformatics case-study.

The following account of an interesting example of the type of learning taking place in the Scientific Inquiry (SI) program:

> In the SI program, students are asked to draw connections among scientific concepts that are quantifiable and generalizable. For example, to answer the question of how the atmosphere act as a radiation filter, students bring together chemistry (how bonds between the oxygen molecules in the ozone can be broken), physics (how ray energy makes molecules vibrate similar to string action), and mathematics (to calculate the frequency of these vibrations or oscillations per second) in order, as one student explains in her paper, 'to find the wavelength necessary to break the bond between two atoms'. The figure is then translated back into chemical terms helping to conclude that the 'free oxygen atom (the result of the atom split)' could potentially bind with oxygen molecule in ClO and release into the atmosphere as an instable and polluting gaz Cl_2. The implication of this chemical reaction is deduced from that: 'Since the chlorine end up unbonded at the end, it continues to destroy ozone'. It is not just a collection of

> chemical, physical and biological ideas that she brings together, but a tight mathematical matrix of relationships that the student constructs using the tools of different scientific disciplines (p. 261-262).

It is useful to parallel this example to the process of pipelining where different software tools and databases are linked together. Giving meaning to both the experimental design and interpreting the results does seem to also require a "tight matrix of relationships". So could particular pipelines or approaches be the central concepts for a bioinformatics integrated education? This is further explored in the next part of the chapter, the process-based curricula.

Similarly to Bialek and Boltstein (2004), the necessity of drawing explicit connections between subject-matter for the students rather than implicitly making the assumption that these connection will be made is also stressed. Thus, thinking back to the mosaic model of curriculum design in bioinformatics one wonders to what extent these connections are made at the appropriate level of depth which will enable effective problem-solving in the students' future bioinformatics endeavors. The role of the teacher in this is paramount and it may be described as that of a disciplinary translator.

> The role of the teacher as a translator across different systems of disciplinary representation is crucial and needs to be emphasized. According to Suzan Yates, who teaches mathematics at the IMSA, 'Students on their own often don't se the connection between using different variables to describe the same underlying pattern. They don't see the pattern. They don't see the transfer.' (p. 262)

Not only is crossing disciplinary barriers difficult, but teachers don't perceive the role they have to play in helping students accomplish this: "Teachers in both disciplines [*referring to mathematics and chemistry*] often fail to stop and think through the connections with students" (p.262). The disciplinary structure of knowledge is so embedded in our society, due to the pervasiveness of this type of education, that surpassing it will require changing the professional psyche of the teacher.

Furthermore, this disciplinary translation can only take place by design and cannot rely on automatism: "Compared to more intuitive connections between ideas and their historical and cultural roots, conceptualizing connections in science are produced 'by design' and not by intuition alone" (Marshall, as cited in Nikitina, 2006, p. 262). Specifically, "It requires the co-ordination, re-sequencing, and re-structuring of the material around unifying concepts rather than disciplinary lines" (p. 263).

Two questions are raised in regards to applying the above information to bioinformatics undergraduate curricula. First of all, is a concept-based curriculum in bioinformatics desirable, i.e., will it enable the teaching of depth bioinformatics to a sufficient depth? Secondly, is such a redesign practically even possible? Designing concept-based curricula is a complicated task. Further, from a time and resource perspective it might not be feasible as it strongly requires rebuilding the organization of subject-matter within the curriculum from scratch.

Can this complicated effort of re-structuring be somehow bypassed with less foundational transformations of the curriculum which would require less effort and consequently less cost? Let us now consider the example of a systems biology curriculum in graduate school which isn't so concept-based but follows a process-based approach to curriculum.

An Alternative to Nikitina's Conceptualizing: Process-Based Curricula

We will now consider the curriculum design of the graduate Computational and Systems Biology degree offered at the Massachusetts Institute of technology (MIT). Once again, despite being primarily interested in undergraduate education, important notions or ideas which might be translated into guiding concepts for our bioinformatics undergraduate curricula conceptual framework might be learned from this example.

Perhaps it is not a coincidence that this curriculum example dealing with the subject-matter of systems biology manages to truly take a systems view on curriculum planning involving communities of practice, active and integrating agents, and horizontal integration through the inauguration of centers.

The first characteristic is the curriculum content is flexible and evolving. No compulsory core material is specified because "… a flexible and customized approach is consistent with the current status of systems biology as a field, as opposed to a discipline" (Tadmor & Tidor, 2005, p. 1186). In fact, it isn't the field which will define a curriculum, but the field will be defined through a curriculum:

> Together, the emerging student profiles are beginning to define niches in the educational, cultural and research landscape of modern systems biology; the coming years will further refine relationships among students, skills, classroom subjects and research areas that will further affect how learning communities in systems biology organize themselves. (Tadmor & Tidor, 2005, p. 1887)

Systems biology addresses a variety of questions which deal with different levels of abstraction of the data, ranging from molecules to whole eco-systems. Despite these differences in abstraction levels, and consequently the variety of questions which are addressed, commonality is found within the approach followed characterized as the 'four M's' standing for measure, mine, model and manipulate. It is an iterative process which assures a back and forth between computation and experimentation, enhancing the strength of results. (It is reminiscent of Denn and McMullen's experimental cycle presented in the introduction chapter.) The curriculum of the computational and systems biology graduate degrees is based on this process:

> The curriculum that is being built at MIT serves as an educational counterpart to the research paradigm of the four Ms – measure, mine, model and manipulate. Students in this curriculum are trained to do more than use current technologies; they are empowered to be the developers of the tools, algorithms, techniques and approaches of tomorrow. (Tadmor & Tidor, 2005, p. 1186)

The curriculum is based on what is in fact a protocol or process. This is in congruence with the argument we advanced in the previous chapter, namely, that tool-integration and tool-thinking may serve as unifying concept of interdisciplinary curricula dealing with technoscientific fields of study. Also, when considering the educational goal of such a curriculum the centrality of process is once again evident: "… matching the best available approach with a corresponding and well-articulated problem formulation is in important skill set for interdisciplinary researchers" (Tadmor & Tidor, 2005, p.1886).

So how is this curriculum model reflected at the course level? Several of the different phases of the four Ms iterative cycle are explored in the classes emphasizing problem-statement and possible approaches for finding solutions:

> Interdisciplinary graduate courses are being developed which integrate information from different areas (such as several of the four Ms, engineering

> and biology, or computation and biology) and that are accessible to students from diverse backgrounds. … Taken together these courses emphasize matchmaking between problems and solutions. (Tadmor & Tidor, 2005, p. 1186)

The centrality of process is perceivable in both the curricular and course level design.

Having explored this notion of a process centered curriculum which may serve as a guiding concept for the development of a conceptual framework for an undergraduate bioinformatics curriculum, let us now take a look at how the university structure is bypassed as to ensure a truthful enactment of this process-centered curriculum. In other words how can an architectural, conceptual and virtual potteries think belt be constructed as to promote interdisciplinary learning?

Tador and Tidmor first of all propose the institution of communities of practice. These structures will help in crossing disciplinary borders:

> To be truly effective, community structures must be built to facilitate the interaction of researchers, educators and students from multiple disciplines. This effort is aimed at integrating multiple interests into one community, a community of practice. In addition, educational programs must be re-cast to produce a new breed of researcher prepared and suited to working at the interface of multiple disciplines, thereby creating a second type of integration, a new learning community. (Tadmor & Tidor, 2005, p. 1883)

Tadmor and Tidor also propose surpassing the vertical departmental structure which provide "limited mechanisms to promote multidisciplinary research and education" by the inauguration of a horizontally integrating structure called the

Computational and Systems Biology initiative making possible new interactions both in research and education: "Joint activities in the field of systems biology promoted by CSBi include a seminar series, workshops, symposia, shared research facilities and large-scale research projects, as well as educational training and outreach activities" (Tadmor & Tidor, 2005, p. 1885). Let us remark that this desired integration also involves architecture in the form of shared facilities:

> At MIT, shared facilities are being developed in the areas of genomics, proteomics and structure, imaging, microfabrication, high-performance computing, and bioinformatics modeling. These capabilities provide not only crucial research resources for conducting experimental and computational studies but the shared facilities also serve as strong community integrators, where researchers with a common interest meet and learn together." (Tadmor & Tidor, 2005, p. 1185)

Finally, as stressed by the previous authors presented in this chapter, the crucial role of teachers and students as active and integrating agents as to promote this type of interdisciplinary research and education cannot be left to chance but must be defined in the curriculum as to hopefully be enacted in reality. Research staff members, also being part of this community of practice, have such an integrating role as well: "Their role is unlike that of traditional facility staff but rather it represents a new type of career path in an academic environment that requires integration of research and educational activities across multiple disciplines." (Tadmor & Tidor, 2005, p. 1185-1186)

The role of students as active integrating agents is enabled through joint mentorship in which the student becomes a communication bridge between the two research groups: “In addition they will be well positioned to act as integrating agents in the community by serving as communication bridges or translators between two distinct research groups and approaches.” (Tadmor & Tidor, 2005, p.1187)

So how can all these integration strategies perhaps be of service to undergraduate bioinformatics education? This will be explored in the last chapter where a summary of all the findings of this synthesis/analysis is given (always relative to the utilized data set) and where guiding concepts and a conceptual framework are described. For now, let us summarize the findings of this chapter and comment on the choice of a concept-based or process-based curriculum.

Summary of Findings

Is a concept-based curriculum more desirable than a process-based curriculum for bioinformatics education or the converse Given the different levels of doing bioinformatics proposed by Hack and Kendal, as well as the subdivisions of the middle level into tool-thinking and tool-integrating, it would be sensible to advance that perhaps curricula pertaining to technoscientific fields are best disclosed following a process-based model; conceptualizing may be good paradigm for old school interdisciplinary science which has a weaker technology dependence than the pervasive information processing requirements of much modern science. The educational goals for the transmission of knowledge and skills useful to modern science must therefore be responded to by a curriculum that expresses the pivotal position of process despite the disciplinary structure of academia. Nonetheless from a theoretical perspective, process-based curricula may be viewed as a sub-group of concept-based curricula where the concepts are in fact processes.

More importantly, an interdisciplinary process-centered curriculum for modern scientific enterprises also modernizes the definition of interdisciplinarity. It is no longer the older one which was valid in older school science, but a technoscientific interdisciplinarity more representative of 'big' science and team science.

Further, the curriculum alone cannot ensure its straightforward enactment. The learning environment in which it is enacted, as well as the people involved in it at any point in time, has the potential of either truthfully translating it to practice or distorting it. They act as integrating agents and new interpretations of teacher and student roles are necessary. These interpretations must be defined within the curriculum but as well within the personal psyche of the individuals within the curriculum.

Overcoming departmental barriers which are also visible in the form of building and facility architecture requires communication enabled through the formation of communities of practice. This may be seen as a more sophisticated implementation/variation of team taught courses and interdisciplinary student teams discussed in chapter four. Seeing that a total restructuring of the university isn't possible other structures which may remedy the drawbacks of traditional academic structures may be seminar series, workshops, symposia, shared research facilities and large scale research projects, as well as educational, training and outreach activities.

New communication avenues and communication agents are purposely and rigidly, or semi-hazardously and loosely, instituted as to override the departmental structures of academia. This is a virtual and/or conceptual "pottery think belt" made possible by rethinking the curriculum design through a systems view perspective.

Chapter 7: A Conceptual Curriculum Framework for Undergraduate Bioinformatics Education

Review of Guiding Concepts

We began this conceptual synthesis exercise with the intent of identifying guiding concepts for the design of undergraduate bioinformatics curricula. What follows is a summary of the findings and how they translate into guiding concepts. We will place these concepts within the model of a curriculum framework.

We started by considering bioinformatics educational goals. Seeing that most bioinformatics undergraduate degrees are housed within life science or computer science departments it was sensible to begin by considering the educational goals as expressed by each department. We saw how the teaching of bioinformatics becomes instrumental to the promotion of life science and computer science educational goals, respectively, rather than for its own sake. The intellectual structure of bioinformatics must be promoted rather than promoting belongingness of bioinformatics to a particular discipline; that is, bioinformatics must be viewed as novice form of inquiry rather than a sub-category of biology or computer science of which it is not. Thus, it is important to recentralize educational goals to the teaching of bioinformatics, a concern stressed by authorities in the field. Doing this will enable teaching depth bioinformatics. Depth bioinformatics therefore becomes a construct which may serve as a guiding concept during the design of curricula and may be defined in the following way: it represents placing emphasis on holistic experimental design rather than the completion of singular bioinformatics tasks. This requires both knowledge of statistics and algorithms required to correctly interpret results, as well as knowledge regarding how to design experiments that overcome the messiness of data appropriately. Key concepts or realizations when designing bioinformatics curricula are: 1) acknowledging the interdisciplinary nature of the field and clearly stating the definition attributed to interdisciplinarity in the given context, 2) facilitating interdisciplinary education by teaching students effective communication and collaboration skills, 3) acknowledging the centrality of the experimental design in the bioinformatics enterprise (this leads to educational goals pertaining to statistical, algorithmic, life science and information processing understanding), 4) acknowledging that tool-conceiving activities are part of the bioinformatics enterprise.

In Chapter 4, we studied five case-studies of bioinformatics undergraduate curricula as to see what could be learned from their design and how it could contribute to the conceptual framework. This led to identifying three models for curriculum design: the infusion through bioinformatics modules model, the mosaic type structure with reliance on one or two (bioinformatics) capstone courses and the mosaic structure with a higher number of specialized bioinformatics courses. Mosaic type structures were problematic due to their overreliance on the capstone course for the promotion of both bioinformatics educational goals and interdisciplinarity. In fact, the capstone classes represent the only opportunities for interdisciplinary teaching; no links were made among the other courses contributing to the degree. If the capstones are unsuccessful, the degree would in fact be a multidisciplinary degree rather then an interdisciplinary one. Nonetheless, depending on what kind of bioinformatics project took place as part of the capstone course, depth bioinformatics teaching may potentially be achieved. Infusion through bioinformatics modules is by definition alone very promising: the modules represent an ideal structure for linking course subject-matter to bioinformatics knowledge. Unfortunately the depth of bioinformatics education achieved in such a way, given the studied cases, is questionable. Such degrees are not so much interdisciplinary promoting depth bioinformatics but rather crossdisciplinary.

Finally, the third approach which consists in many specialized bioinformatics courses seem to be desirable as in the case of the Rochester Institute of Technology. Indeed this specialization allows for learning new skills highly relevant to bioinformatics such as parallel computing and data-mining techniques. The information technology aspect is more stressed in this degree and the knowledge disclosed is more unique. Considering the subject-matter of the RIT degree, we saw that the tool-usage concerned much more sophisticated tools in relation to those used in life science departments following infusion model approaches. Further, using the tools appropriately for their own sake is the educational goal rather than the clarification of life science concepts.

This realization led to stating the following question: Could it be that the unifying interdisciplinary concept is in fact the bioinformatics tools whose usage embeds the process, experimental approach and methodology? This led to adding a new type of data to our data set, namely, the writing of scholars pertaining to technoscience and technoscientific education. Tool-usage as a higher level concept is often dismissed as this does not always match the educational ideologies or sensibilities of academic settings. Considering bioinformatics as technoscience led to the specification of new, more precise educational goals pertaining to tool-integration and tool-thinking skills and understanding._These new educational goals may serve as guiding concepts for the future elaboration of learning objectives contextualized within subject-matter. Further, the actions of tool-integration and tool-thinking justify the existence of a specialized bioinformatics education; If bioinformatics pertained to simply tool-engineering, an engineering curriculum would suffice. Thinking in terms of tools and the protocols facilitated by those very tools are educational goals which should serve as guiding concepts during the design of undergraduate bioinformatics curricula.

We also considered the changing face of science and its shift towards e-science. This carries implication for curriculum design which must be responsive to this paradigm shift; furthermore, the cyberinfrastructure might be the ideal environment for learning the skills involved in grey zone bioinformatics (tool-integrating and tool-conceiving). Thus the conceptual curriculum must describe the incorporation of the cyberinfrastructure into the learning activities.

Thus, in the next chapter we considered curriculum designs which may successfully promote the educational goals of tool-integration and tool-thinking in bioinformatics while being responsive to the shift of modern science towards e-science with its strong information processing component. Process-centered curricula (viewed as a sub-group of concept-based curricula where the concepts are processes) will most likely prepare students for e-science. The roles of teachers and students within these curricula are redefined to that of active and integrating agents. Integration is further assured by the creation of communities of practice and different activities they engage in. A new type of interdisciplinarity, perhaps by the name of technoscientific interdisciplinarity, may be defined which is more appropriate to Big science and team science. In turn, these large scale projects also work as integrating activities. What this demonstrates is the systems approach to curriculum design is paramount as any factor (teachers, department architecture, instructional design at the course level…) pertaining to its enactment may enhance or distort it.

The findings of this synthesis in terms of guiding concepts which make up a conceptual framework are summarized in table 3.

Present state	Shifting towards	Chapter
Bioinformatics	Systems biology	-
Educational goals expressed as instrumental to the teaching of computer science or life sciences	Educational goals expressed in terms of achieving depth bioinformatics	3
Multidisciplinary and crossdisciplinary curricula	Interdisciplinary curricula which highlight the centrality of experimental design along with a tool-conception component	4
Curricula take the mosaic model or infusion model	Curricula follow a highly specialized model	4
Discipline-centered	Tool-centered	4
Three levels defined by Hack and Kendal	Emphasis placed on middle level which splits into tool-integration and tool thinking. Four levels defined.	5
Software engineering degrees seen as equivalent to bioinformatics	Tool-thinking and tool-integration justify specialized bioinformatics education	5
Sterile learning environments, classroom learning	New communication avenues creating more interdisciplinary learning environments (such as e-science infrastructures). Blended learning environments as an element of the curriculum design	5
Old definition of interdisciplinarity	New definition: technoscientific interdisciplinarity	6
Passive student, monodisciplinary teacher	Teacher and students as active integrating agents	6
Curriculum as subject-matter with notable instructional design initiatives specified	Systems view of curriculum is paramount encompassing physical, conceptual and virtual environments as well as people.	6

Table 3. Conceptual framework for undergraduate bioinformatics

Sketching an Undergraduate Curriculum and Future Research Directions

The bioinformatics educational goals expressed concern the whole spectrum of bioinformatics activity from experiment design to tool engineering. So how can all this be translated into subject-matter and more importantly fit within the time span of an undergraduate curriculum?

If Bialek's and Botstein's vision of a highly integrated first-year in university for all science students becomes a reality in university, it could also be beneficial to bioinformatics undergraduate education. This can be completed by a philosophy of science course which explicitly exposes students and helps them grasp the meaning of different frameworks of thought as well as expose them and help them fine-tune their own epistemological beliefs (Chapman et al., 2006, p.181).

The remaining curriculum should progressively take the students through the different levels of the practice of doing bioinformatics with particular focus towards tool-using and tool-integrating. Thus, appropriate programming skills and life science understanding should make up the subject-matter. Given a first year study of integrated science, as described by Bialek and Botstein, subsequent subject-matter from computer science, mathematics, and life sciences should be specialized to the bioinformatics enterprise.

As the students enter the last year of their degree, they must be able to think of solutions in terms of tools as well as define new research problems which may require the conception of new tools. I do not hold the opinion that they must have the expertise for implementing these tools, but they must have a thorough understanding of statistics and algorithms.

Whether this is realistically possible in the time span of undergraduate degree is still a topic which requires more research from an instructional design perspective. Nonetheless, e-learning technologies should be intelligently and strategically utilized. Reminiscent of the infusion model case-studies of chapter four, perhaps e-learning modules might be of service. They would offer an opportunity to present explicit interdisciplinary links to the students removing the responsibility from the monodisciplinarily trained teachers. Further, the e-modules would transport the classroom into the cyberinfrastructure, an appropriate environment for the teaching of grey zone bioinformatics.

In regards to the roles of teachers as integrating agents, information management technologies such as curriculum mapping could be embedded within the cyberinfrastructures. These would allow teachers to share with one another what they are teaching and opportunities for interdisciplinarity could be identified and exploited, as well as learning synergy. Further, curriculum mapping also represents an interesting data collection technique for future explorative/qualitative studies of bioinformatics curricula.

Finally, an aspect of curriculum design not at all considered within the scope of this paper is the issue of transdisciplinarity. Transdisciplinary perspectives in bioinformatics curriculum design should be considered. An interesting idea could be designing a curriculum which defines its enactment not in one university but in two. The goal would be to pair a university in a developed country with a university in an underdeveloped country. Developing countries often have a great biodiversity of flora and fauna which can serve as a rich data set for novice knowledge creation (Davila , Steindel, & Grisard, 2006). These countries also have their own set of pathogens which threaten both their livestock as well as their human population. Unfortunately this does not represent a profitable market, and therefore not much research is conducted on those pathogens. In a survey aiming to establish which biotechnologies would be the most likely to improve health in developing countries, bioinformatics was amongst the top ten (Daar et al., 2002). Thus, if developing countries do not acquire the resources which will aid them in developing bioinformatics expertise they will not benefit as Davila states “from what is arguably the most golden era of biology and medicine”. This is referred to as the genomic divide where 90% of health research dollars is spent on 10% of the world's population. Further, another obstacle faced by developing countries is one which pertains to bioinformatics knowledge and expertise. A joint curriculum could enable a sharing of expertise and research problems.

This can be one avenue to follow in exploring transdisciplinary bioinformatics curriculum design. Either way, when Price conceived the Pottery Thinkbelt, despite its capacity to assemble learning environments as seen fit, it also made education accessible to individuals at geographic locations further away from predominant knowledge centers. Hopefully, a transdisciplinary bioinformatics education could serve a similar purpose.

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