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How is Information Used? Applying task analysis to understanding information use

Abstract: Understanding information use is critical in the context of a goal-oriented information problem. We applied task analysis to examining information behaviour in the context of a work task, to understand how information was used to accomplish the task. We also propose a model for considering information use.

Résumé : Comprendre l'utilisation de l'information est indispensable dans le contexte d'un problème informationnel orienté vers un but. Nous avons appliqué l'analyse des tâches pour examiner le comportement informationnel dans le contexte des tâches de travail, afin de comprendre comment l'information était utilisée pour accomplir la tâche. Nous proposons également un modèle pour comprendre l'utilisation de l'information.

1. Introduction

People use information to create knowledge, “but not just in the sense of data and facts but in the form of representations that provide meaning and context for purposive action” (Choo 2002, 45). Surprisingly, information science often stops short of examining what people do with the information once it has been received. Information use is one of three core elements of information behaviour, along with information needs and information seeking (Wilson 1999). Information needs and information seeking have been well studied and characterized (e.g., Dervin 1983; Ellis 1993; Marchionini 1995). Information use, however, has received less attention in the research literature. It is often linked to information need, in that information is needed so that it can be used. Another perspective is to consider what happens with the information once it has been obtained, and how it is applied to accomplishing a specific task or goal. In the case of a goal-oriented information problem, it is essential to explicitly understand how information is used to address the problem. Otherwise we do not know if the actions, the help provided or the systems implemented produce relevant (to the user) results. If the information sought and returned is inadequate for the work task then such a system cannot claim to support the user.

In this paper, we focus on information use. Because use is the final step in an information seeking process, we approached the problem by examining information behaviour in a workplace setting to understand the full cycle from emergence of a need through to locating the information to solve that need through to the information's ultimate use. Rather than examine a single episode, we explore use within a complex work task – a specific scientific problem – so that we can observe multiple iterations of that cycle.

2. Research Objective

This analysis is part of a larger study to understand, within a framework of information behaviour and task analysis, the application of bioinformatics analysis to a specific scientific problem – that of predicting gene function from sequence data (Bartlett 2004). The work reported here isolates how information was used within that context, and proposes a model of information use.

3. Background

For this examination of information use, we drew on the literature and research traditions of information behaviour and task analysis. Alone, neither would have given the depth of analysis obtained by their combination. Information behaviour provides a rich portrait of a group of information users, but does not provide for the level of detail required to adequately describe the work process. Task analysis, while providing for a very detailed description of the means by which a task is accomplished, does not describe the broader context in which that task occurs. When combined, the dual approach of information behaviour and task analysis provides a finely-grained analysis of the bioinformatics analysis process, set within the broader understanding of the information behaviour of bioinformatics researchers.

3.1 Information Use

There is a long history of research into information behaviour and its constituent elements of information need, information seeking and information use. However, the three elements have been studied at varying degrees of detail. Information needs and information seeking (and the narrower concept of information search) have been well modelled and studied (e.g., Belkin 1980; Ellis 1989; 1993; Kuhlthau 1991; Marchionini 1995; Wilson 1999). In contrast, information use has received less attention, and remains a poorly defined concept (Case 2002; Taylor 1986; Wilson 1999). It is often linked to the concept of information need, in that information is needed so that it can be used. When discussed, use is often addressed at an abstract level, with reference to the broad, general goal that the use of information will help to achieve.

Early studies of information needs and uses (e.g., Menzel 1966; Paisley 1968) focussed on information systems, at the time consisting primarily of paper-based library collections of books and journals. In these studies, information use referred to the information packages (e.g., books, journals, indices, etc.). The concept of information use is therefore historically associated with the resource itself, rather than the information contained within. The emergence of self-serve searching and the web has changed the way we now view the object of use from those physical items to the information chunks.

Dervin's (1983; 1992) Sense-Making Theory views information behaviour in terms of a situation, a gap and an outcome, with information being used to bridge the gap and achieve the outcome. This framework, with its recognition of the importance of understanding how the information helps the user "make sense" of a situation, highlights the role of information use. However, in subsequent discussions of Dervin's work (e.g., Choo 1993; Wilson 1999), it is often the classification and articulation of information needs (i.e., the nature of the gap) that is emphasized. While need and use are clearly linked since information is needed to fulfill a use,

there is a shift in perspective and emphasis depending on whether the focus is on needs or uses. Discussion of need tends to highlight the purpose for which the information is sought – the goal or objective – but does not usually extend to including how exactly the information is applied to achieving the goal. Shifting the focus to use can highlight the latter.

Often the more significant work is found in studies of browsing, as browsers meander down a path of seeking, finding and extracting, before moving on to the next episode. Marchionini (1995, 57-58) in his model of information seeking argues that use includes instances of information extraction that include reading, scanning, listening, classifying, copying and storing information. Notably these are higher level conceptual skills that indicate how the information is *handled*.

Taylor (1991, 230) proposed a taxonomy of eight classes of information uses, generated from the information need(s) perceived by users:

- Enlightenment: context information
- Problem Understanding: better comprehension of a specific problem
- Instrumental: what to do and how to do something
- Factual: precise data
- Confirmation: verify a piece of information
- Projective: future oriented
- Motivational: relates to personal involvement
- Personal or Political: relationships, status, reputation, personal fulfillment

These classes of information use were developed from expressions of perceived needs, rather than of observation, report or discussion of actual information use. As such they represent the objectives of the information seeking episode (e.g., precise data) rather than a set of uses of that information.

In examining the value of library and information services, a concept with clear links to information use, Saracevic and Kantor (1997, 533-4) described a three-step model of information use, with the following components:

- Acquisition: getting information or objects potentially conveying information, as related to some intentions
- Cognition: absorbing, understanding, integrating the information
- Application: use of this newly understood and cognitively processed information

This model clearly links the seeking and acquisition of information to its use; however, the discussion of use remains at a broad, conceptual level.

Choo (2002) views information use as “a dynamic, interactive social process of inquiry that may result in the making of meaning or the making of decisions.” The first type of use is intrinsic to the user, involved with human understanding and integration with the user’s knowledge base. This is a process of interpretation that may evolve into a process of inquiry and debate that ultimately results in knowledge creation. This type of information use has no visible indicators except in the depth and breadth of one’s personal knowledge base. The second form of information use concerns decision-making. While Choo discusses this form in the context of organizational decision-making, some aspects are equally applicable to individual decision making. Interestingly, his approach is also at a conceptual high-level matching of potential uses with stages of the decision-making process: identification, development, and selection.

Information use is the factor that drives all other information behaviours, since it represents the

ultimate purpose for which information is needed and sought. Without consideration of information use, consideration of activities such as information seeking or information retrieval is incomplete. It is the use of the information that informs and drives the information seeking. It is not surprising that one of the common questions to arise during a reference interview is to ask how the information will be used, or for what purpose it is sought. In the same way that the answer can inform the subsequent reference interaction, understanding information use can also inform how an information system is designed and implemented. How then, is an understanding of information use to be achieved? Discussions of use in isolation from need do not lend themselves to a comprehensive understanding of the process. Was the information that was needed and sought actually used to meet a goal or even possible to solve that goal? To make those connections we used a technique developed in business and industrial engineering which has examined many types of work processes – task analysis.

3.2 Task Analysis

Task analysis has been defined as “the study of what an operator (or team of operators) is required to do, in terms of actions and/or cognitive processes, to achieve a system goal” (Kirwan and Ainsworth 1992, 1). Approaches to task analysis have been classified into three complementary categories: normative, descriptive and formative. According to Vicente (1999, 61-62), normative approaches “prescribe how a system should behave,” descriptive approaches “describe how a system actually works in practice,” and formative (also called predictive) approaches “specify the requirements that must be satisfied so that the system could behave in a new, desired way.” The nature of the work domain and the task influence the type of analysis that is appropriate. Both the normative and descriptive approaches are applicable to analysing existing systems, while the formative approach can be applied to developing a new system that will support work that has not previously been done, or to allow the work to be done in a new way. The normative approach, is appropriate for a very mechanical and predictable work environment; as the work becomes more complex and unpredictable, requiring more judgement and discretion from the work, then the formative approach becomes applicable.

Another perspective to task analysis is to consider the distinction between instruction-based and constraint-based analysis. Instruction-based, which traditionally has been more common, specifies the task in terms of what *should* or *must* be done (Vicente 2000). As such, the instruction-based approach provides a great deal of direction to the worker, and leaves little or no room for flexibility or discretion. This approach is typically also *device-dependent*, since it is strongly linked to the specific system used to accomplish the work (Benyon 1992). In contrast, the constraint-based approach specifically provides for the incorporation of the worker’s judgement and discretion into the work process, by specifying the parameters (constraints) within which the work will take place (Vicente 2000). Since the task analysis is not necessarily linked to a specific system, this approach can be considered to be *device-independent* (Benyon 1992).

Task analysis has little history in information science research, although interest and use has been growing in recent years. An early example of its application is in the work of Rasmussen, Pejtersen and Goodstein (1994), in which task analysis was applied to the development of a library catalogue information retrieval system. Hersh and Pentecost (1996) advocated a task oriented approach to the evaluation of information retrieval, in place of the traditional measures of precision and recall. Vakkari (2003) concluded that few studies consider information searching from the perspective of the task, in spite of the link between them. He called for a

research approach to consider information searching in the context of task performance. Likewise, Järvalin and Ingwersen (2004) argued that information seeking research must expand to encompass consideration of task. Most recently, Fidel and Pejtersen (2004) put forward a strong argument in support of using Cognitive Work Analysis (CWA – a form of task analysis) to inform the design of information systems.

In this study, task analysis is applied to understanding the details of a goal-oriented information task, set within the broader context provided by an understanding of information behaviour.

4. Methods

4.1 Overview

In this research, we investigated the use of information within a complex work task, that of bioinformatics analysis. To do so, we interviewed bioinformatics analysts about how they would accomplish an information-based work task.

4.2 Scientific Scenario

Given the complexity of bioinformatics analysis, and the range of tasks to which it can be applied (such as gene prediction or protein modelling), we undertook our research using a specific type of problem. The research was therefore grounded in the task of conducting a functional analysis of a gene sequence, that is, predicting the possible or likely function of a gene product, based on its sequence data. This is a very timely problem, given the fact that the Human Genome Project and other large sequencing projects have generated vast quantities of sequence data, for which little or nothing is known about the biological significance or function. Determining the function of these genes is one of the major challenges for biomedical research. From a practical standpoint, laboratory determination of gene function could take weeks, months or even years. In contrast, using bioinformatics analysis to predict the function could take as little as a few hours. While the bioinformatics analysis does not provide a conclusive answer – the findings must ultimately be empirically verified in the laboratory – it is extremely valuable in guiding and directing the laboratory investigation in the most promising direction, ultimately leading to savings of both time and resources. Thus, this was a complex problem which had multiple sub-tasks involving many forms of data and information. It was an ideal situation for studying information use.

4.2 Procedures

Twenty bioinformatics experts were the participants for this study. These individuals were proficient in the use of bioinformatics resources, and experienced with the application of bioinformatics analysis to the functional analysis of a gene sequence. Most held graduate degrees in a biological science; several had additional education in computer science. They were selected from eight different research groups in Canada and the United States (six academic, one government and one private sector).

Data were collected through semi-structured interviews, revolving around the question of how bioinformatics analysis would be applied to address the problem of predicting gene function from sequence data (functional analysis of a gene sequence). The primary goal of the research

was to understand and model the bioinformatics analysis process followed by the participants. The interviews followed a flexible script, based on a task analysis approach. Each interview began with asking the participant to describe his or her approach to the problem of functionally analysing a gene sequence. Probe questions ensured that essential points were covered. These included:

- What triggers this process?
- What information do you have at the start of the process?
- What information comes out of the process at each step and at the end?
- What happens next?

An integral component of the interview, and the focus of this paper, was the need to understand what was done with the information obtained through bioinformatics analysis. That is, how was the information used? Given the importance of this point, some of the most critical questions were those that asked participants to comment on what information was taken from the bioinformatics analysis process, and how that information was used, applied or integrated both as part of the bioinformatics analysis, and as part of the broader research agenda.

The data were analyzed in two rounds. The first involved a narrative summary of the individual approach taken by each participant. In addition to identifying the types of bioinformatics analysis and the resources used, the first round of analysis also identified the ultimate goal of the bioinformatics analysis. This understanding of what the bioinformatics analysis was intended to accomplish, and how the information would be applied was critical. The second round of analysis took a task analysis approach. Data was coded to identify *what* was done, and also *why* it was done. Again, a critical element at this stage was identifying and understanding the purpose for which each piece of information was obtained, and how it would be used. The twenty individual approaches were iteratively (through six rounds of analysis) merged into a single protocol describing the approach to functionally analysing a gene sequence. Findings from the second round of analysis were used to inform the development of the protocol, as well as to flesh out the series of steps with a more detailed analysis and description of each step in the protocol. As a result, each step of the protocol not only describes a type of bioinformatics analysis and the tools used, but also the reasons why that particular analysis should be done and how the results can be applied to solving the scientific problem.

5. Results and Discussion

The final version of the bioinformatics analysis protocol contains a series of twelve steps, grouped in three parallel pathways as illustrated in Figure 1. Each step represents one specific type of bioinformatics analysis, and one sub-task within the larger work task of conducting a functional analysis of a gene. Each step also represents an instance of information need, seeking and use. Each step adds one more piece of information to the overall analysis of the gene sequence, and in turn ‘causes’ a new information need to arise until the entire set of steps are complete.

The secondary analysis of the interview data focussed on understanding the reasons behind each step of the process, which types of decisions are being made, and how those decisions are made. This illuminated how the information was used within each step. The analysis led to a seven point detailed description of each step, including:

- The rationale for each type of analysis
- Which tools are used

- Which datum/data is input and output
- How the results of the analysis are interpreted and applied to the broader scientific problem
- Which step(s) to follow next
- Any caveats to consider

For some steps, the analysis was highly regular, predictable and mechanical; in others, there was the need for considerable judgement, interpretation and decision-making on the part of the scientist. An example of the detail for one step, Step 4 – Homology Search, is shown in Figure 2. This particular step is one requiring considerable human interpretation. Note that the information provided at this step, a listing of similar sequences, is used to suggest possible functions of the index sequence. The scientist must then decide which possibilities are most likely or merit further investigation. This is an instance of information being used to aid interpretation; it suggests possibilities to consider.

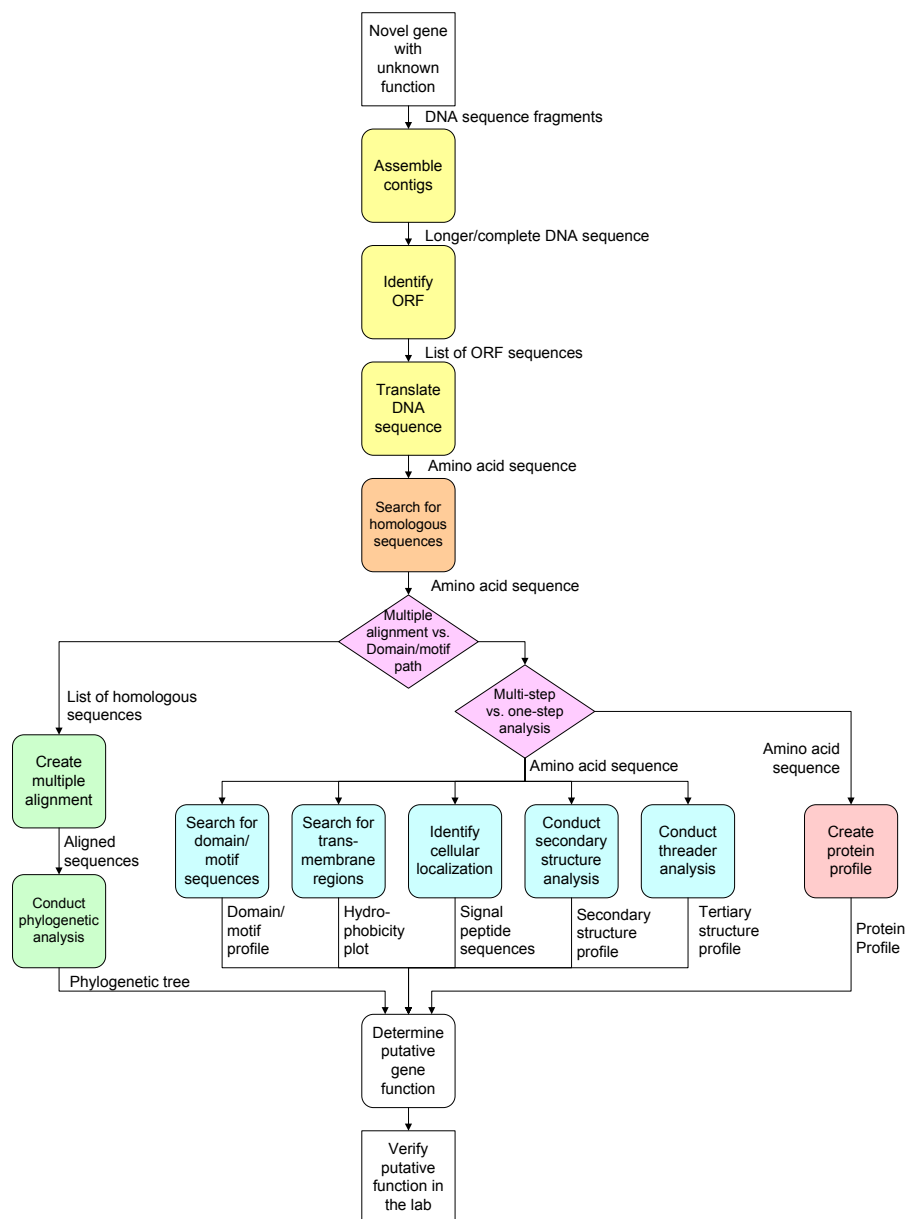


Figure 1. Bioinformatics Analysis Protocol (High level representation)

Step 4 - Homology searching

- looks for similar sequences

Why?

- considers the sequence as a whole, or in smaller portions, and looks for similar sequences in the same or other organisms
- useful for making cross-species comparisons, evolutionary analysis, or finding families of proteins
- can be used to compare a sequence against itself, to identify repeating units

Tools

- BLAST (phi-BLAST, psi-BLAST)
- ScanPS
- Locus Link
- COG
- GoldenPath
- MGD
- OMIM
- S Search
- UniGene

Input

- amino acid sequence
- DNA sequence

Output

- list of similar protein sequences
- list of similar DNA sequences

Interpretation

- “if it looks like a duck, and walks like a duck, then it almost always is a duck”
- if two or more proteins look similar at a sequence level, then the function is likely conserved
- DNA homology - look for longer stretches of sequence (50bp, >80% identity)
- homology is usually only seen across functional domains, so it's not reasonable to expect high homology across the full sequence
- instead, look for high homology across short (≥ 5 aa) stretches of sequence
- conservation decreases with evolutionary distance, therefore stringency should also decrease
- consider chromosome location in the interpretation - are the chromosome locations related to similar function
- may find protein families - related proteins within one organism
- repeating units likely to be functionally significant
- if a particular function is suspected or of interest, look for homology to proteins with similar function
- may find similar proteins in other organisms (e.g., mouse)

Next steps

- Multiple alignment path
- Domain/motif path
- laboratory verification of putative function

Caveats

- similar sequence does not always confer similar function
- function of interest may be a secondary feature of one protein, but only the primary function may be conserved
- some proteins have two distinct functions - so sequence alone is not necessarily a predictor of function

Figure 2. Detail for Step 4 – Homology Search

The various elements of each step or sub-task in the bioinformatics analysis protocol can be linked to one or more aspects of information behaviour. These connections are illustrated in Figure 3. The three core elements of information need, information seeking and information use are present in a cyclical relationship; information is needed, sought, and then used to satisfy the need, and potentially generate a new information need. However, information is also used outside of the bioinformatics information environment; information is used in laboratory analysis in the scientific research environment. As indicated by the darker arrows, the bioinformatics analysis process may follow several iterations of information need, seeking and use before involving the step of laboratory analysis, a cyclical effect that is present within each step in Figure 1.

Each sub-task contains the three elements of information behaviour. The rationale for each analytical step dictates the information need; there are twelve specific information needs, one for each step. Information seeking relates to the bioinformatics tools used for each step; analogically the data input may be equated to the traditional query (or queries) in standard text systems while data output is the result. The interpretation of results and caveats to consider are instances of information use. Input data is also a type of information use; like the text world, the creation and submission of a query is a form of information use. In the task represented here, input data is an integral part of information seeking. However, input data can also be an instance of information use, as in the case of *Step 3 – Translation*; the information from this step is used as input data for subsequent steps.

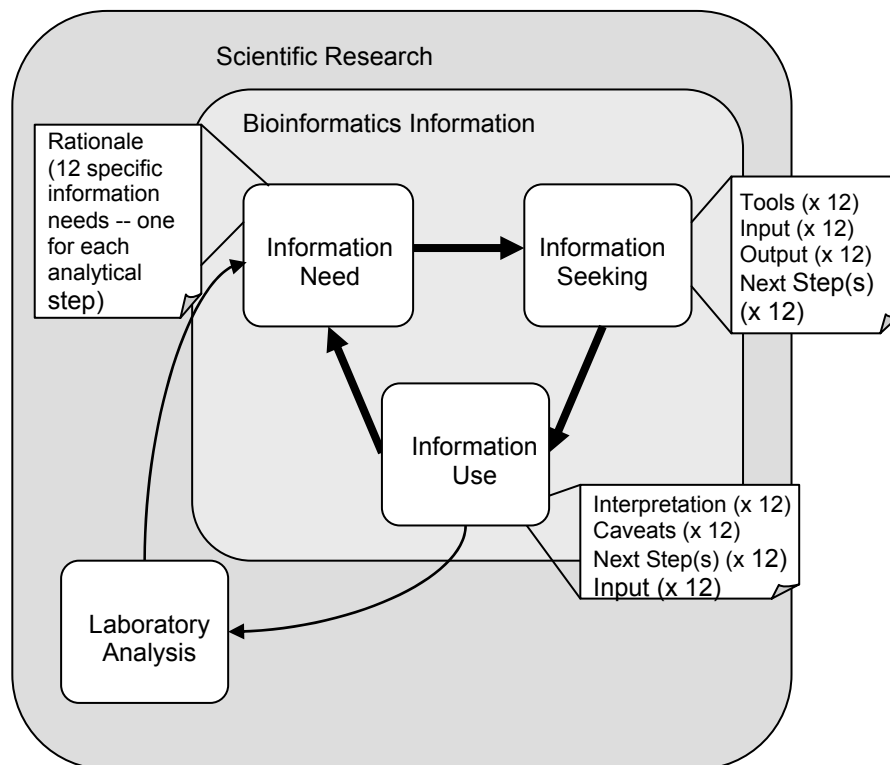


Figure 3. Link between elements of bioinformatics analysis and aspects of information behaviour

The bioinformatics analysis protocol also highlights the link between information behaviour, especially information use, and the scientific task by making explicit connections between the

two. We identified what the scientists did with the information obtained at each stage, how that information influenced their understanding of the problem, and how the knowledge gained from the information affected the direction of the research.

The type of analysis conducted at each step was different, as was the use of the information obtained. Some analyses (e.g., *Step 3 - Translation*) transformed information, with the resulting output used as the input for further analysis. This step was very mechanical. It was needed to transform or convert the initial data (nucleic acid sequence) into the required format (amino acid sequence) for subsequent analysis. Following the standard genetic code, the sequence data is translated from one format to another. This step requires no interpretation or analysis of results. Rather, the information in this case is serving purely as data – there is no transformation of knowledge occurring. The information obtained at this step is simply used as the input data for subsequent steps, as it is at those steps that the information becomes meaningful.

In some steps, information was used to suggest possibilities (e.g., *Step 4 - Homology Analysis*), expanding the number of options that could be studied further. This step identifies protein sequences that are similar to the index sequence under study – this is useful in that if proteins are similar at the sequence level, they may also share similar biological function. In this case, the information provided by the analysis is listing of similar sequences. Each one suggests a possible function of the index sequence, indicating a potential direction for future research. This information is used both as input for the subsequent step, and also to suggest possibilities, expanding the list of potential functions. If a point of difference is found in an otherwise similar sequence, then this information suggests that the difference may be functionally significant. This again suggests a direction for the research to follow.

So we work on genes that are conserved right down to the fruit fly. So one of the mutations that we found for a certain disease . . . it's always an arginine . . . in our patient there was a histidine. That really gave us an idea that could be a mutation.
(Interview 12)

By contrast, other steps led to data reduction (e.g., *Step 6 - Multiple Alignment*), narrowing down the possible options that merited further study. Multiple alignment follows homology searching, with the list of similar sequences output from homology searching being the input data for multiple alignment. This analysis compares the similar sequences, and identifies and aligns the specific regions of similarity or identity. The information provided is typically a graphic representation of the aligned sequences, identifying the regions of sequence that are conserved (similar or identical) among the sequences – regions that are most likely to be of functional significance. This is used by the scientist to narrow down the possible functions of the index sequence, by focussing on the known function of the conserved portion of the sequence. Again, the knowledge of this information then guides the direction of the research.

. . . using multiple alignment I identified all the conserved amino acids . . . to provide strong evidence that my protein was in fact a histidine kinase . . .
(Interview 7)

. . . we would line them all up. In that case what you're looking for is conserved regions . . . with the idea that conservation is somehow important in function . . . so a protein which has very highly conserved regions, those regions tend to be maybe the business components of the molecule (Interview 12)

It is interesting to note the use of words such as “maybe” and “evidence” in the discourse of the scientists. The information at this point did not provide absolute proof or definitive answers, but instead suggested or indicated possibilities that still required further investigation.

Another use of information was to guide decision-making – the information obtained from some analyses (e.g., *Step 14 - Protein Profile Analysis*) served as the basis for deciding which approaches to pursue. Specific parameters and constraints were considered as part of the decision-making process. Protein profile analysis identifies chemical characteristics of the protein, as well as possible structural and functional regions (domains) of the protein. It is a one-step approach to obtaining a “big picture” profile of the protein. One use of the information obtained at this step is to guide decision-making. There are specialized tools that search for specific types of domain, allowing much more refinement of the analysis than with the one step protein profile. The information obtained from protein profile analysis, an indication of the types of domains present, can then be applied to deciding which domain specific analyses to pursue.

You go to the site that has the most kind of things linked like that Smart site because there, all of a sudden, you know there's a DTT domain, there's two PHD finger domains, there's a bromo domain, and there's also several regions of coiled coils, so now what I might do is go to the coiled coil program and run that through and see if these coiled coils match up. (Interview 11)

By identifying ways in which information is used, this research provides a preliminary framework for considering information use, as summarized in Table 1.

Table 1
Types of Information Use

Category	Description
Input	Information is entered into another process (e.g., <i>Step 3 - Translation</i>)
Interpretation	Information is used to aid understanding of a phenomenon (e.g., <i>Step 6 - Multiple Alignment</i> , data reduction; <i>Step 4 - Homology Analysis</i> , suggests possibilities)
Direction	Information guides decision-making (e.g., <i>Step 14 - Protein Profile Analysis</i>)

These types of uses fit within the scheme proposed by Choo (2002). Like Choo we found *interpretation* and *decision-making* (direction). It is interesting that strong overlap was found, given that Choo’s scheme was developed around the context of organizational information management, while ours came from empirical studies of the work practices of scientists. This suggests the presence of common facets of information use that span different information environments. In addition, we noted a type of use called *input* which reflects the manipulation of data and/or information. This is neither interpretative, nor direction. Instead, the information obtained from one information seeking event is intended for use as the entry point to another event.

Parallels are also found with Marchionini’s discussion of information extraction. The use of information as input involves *copying* and *manipulation*, as the information is taken from one

source and copied as it is input into another process. Many of Marchionini's categories are inherent in categories of *interpretation* and *direction*. Information is *read*, *scanned*, *classified*, *stored* and *integrated*. These categories relate to the management of the information "chunks", which is necessary for the information contained within them to be used or applied.

In addition, our categories of information use are somewhat related to Taylor's taxonomy. He described one type of information use as *factual*, involving precise data. This is similar to the *input* category of information use. Our *interpretation* category relates to two of Taylor's, *enlightenment*, involving context information, and *problem understanding*, relating to comprehension of a problem. The third category of *direction* is similar to Taylor's *projective*, as they are future oriented. Our categories present a different perspective from Taylor's, as they are based on empirical descriptions of information use, rather than expressions of information need.

6. Conclusions

In spite of its significance, information use remains an understudied aspect of information behaviour. Yet, in the context of goal-oriented information problems, an understanding of how information is used to accomplish the goal is critical. In our research, we have shown how integrating task analysis with information behaviour research can provide a means for explicitly studying information use, in addition to information needs and information seeking. From our findings, we have also developed a preliminary framework for considering different categories of information use, which are related to those developed by Choo, Marchionini and Taylor. All provide slightly different perspectives to information use; there still remain many other dimensions of information use to explore.

7. Acknowledgements

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