Increase of Potential Intellectual Bandwidth in a Scientific Community through Implementation of an End-User Information System

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Abstract

Qureshi, et al. (2002) [1] *presented a case study where they used a framework, the Intellectual Bandwidth Model to measure an organization's ability to create value. The model consists of two dimensions, information assimilation and collaboration. The IB model is a useful tool for managers because it enables them to plan solutions to complex business problems and to easily communicate these plans to key individuals. The model can also serve as a guide when making investment decisions. While it is important to increase an organization's intellectual bandwidth, it is equally important to assure that the resulting increase is employed to improve the organization's ability to innovate since, as it has been shown, innovation is the number one creator of organizational wealth* [2]. *In this paper we discuss how intellectual bandwidth as proposed by Nunamaker et al. (2001)* [3] *can be extended beyond the highest level of information assimilation identified in the model, automated sense-making, to ensure implementation of product innovations. To do this we propose adding two new information assimilation features, automated utilization and automated implementation.*

A real business example from the bioscience industry is presented in order to demonstrate how the IB model with extensions can be used. The study discusses an end-user information system, its current use and its potential to enhance an organization's value-creating capability.

1. Introduction

The knowledge base of the biosciences industry that includes, biotechnology, pharmaceuticals, health care, and diagnostics is both complex and expanding, and the sources of expertise are widely dispersed. The sequencing of HIV, a highly mutable virus, requires different expertise and different data depending upon the resulting mutation. In order to properly diagnose and hopefully treat the next mutation, data from different patients from different countries, involving different laboratories and physicians with different expertise will be required. In such situations, the locus of knowledge needed for innovation is found in global networked organizational environments with access to dispersed data, information and knowledge [4].

In this paper we will discuss an "end user information system" (EUIS) that can be employed to facilitate what is described in the intellectual bandwidth model (IBM) as automated sense making. Then we will discuss how the model can be extended to ensure even greater potential intellectual bandwidth by adding information assimilation features that we have termed "automated utilization" and "automated implementation". Such capabilities require an appropriate infrastructure that goes beyond technology in order to ensure unprecedented coordination and collaboration.

First we describe the situation in small laboratories that are not automated and do not employ sophisticated support of information technologies. We compare the smaller laboratories with larger ones with IT support, high levels of automated lab devices and better organizational efficiency. After that we discuss how the potential intellectual bandwidth (PIB) can be increased through the use of a web-based end user information system (EUIS) and how this can be operationalized in the IB model. The EUIS has the potential to help organizations and communities in the bioscience industry establish a global network over the Internet where laboratories worldwide can be interconnected. With the Internet as backbone of the network those who wish to participate in the network need almost no IT investment, other than an Internet connection. This enables participation of even of the smallest laboratories and ensures a robust network, and hence a greater potential for information assimilation. Next, we discuss how the system can be augmented to automatically identify mutations and make sense of as well as make use of mutations that are known to cause drug resistance. To achieve automation, sense-making-

software termed SMS-1 is added to the network. SMS-1 identifies and extracts from a patient sequence all mutations with known drug resistant properties. The result is a list of all mutations that are present in a patient sequence and a list of drugs that can or cannot be used in therapy. These results can then be communicated through the existing EUIS to the physician. Participation of physicians in a worldwide network can significantly increase PIB by enhancing potential information assimilation capabilities and ensuring the collaboration needed to ensure value creation. Finally, we discuss how the system can automatically make sense of and use knowledge about new mutations with unknown drug resistant properties. This information can be utilized in numerous ways: patients can obtain proper drugs, insurance companies will be able to avoid paying for useless treatments, and society can become healthier as a result of a better health care system. In future versions new findings such as these can be automatically employed in the production of diagnostic tests and in drug development.

2. The Intellectual Bandwidth Model

To begin our discussion of the extensions to the Intellectual Bandwidth Model (IBM), we believe, it is necessary to briefly present the original intellectual bandwidth model. The following figure shows the two dimensions that make up the model and the key ideas associated with each dimension.

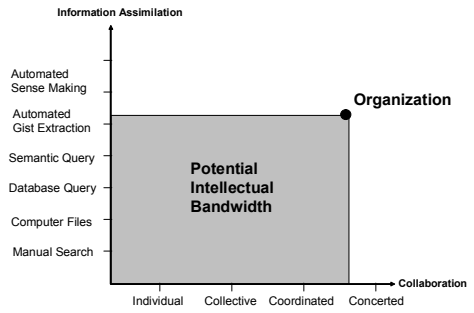


Figure 1: Standard IBM. PIB is the product of information assimilation and collaboration to create value [3].

The potential intellectual bandwidth (PIB) of an organization can be defined as the product of the ability to assimilate available information and the ability and willingness of people to collaborate. PIB can be increased either by increasing a team's ability to assimilate information or by increasing the ability of its members to collaborate; when both are increased, the resulting gain in intellectual bandwidth is greatly increased [3, p. 114].

The model is based upon a number of premises three of the most important of which are:
1: "One person can assimilate only so much information, perform only so much reasoning, do so much, and take only so many actions in a day."
2: "An organization's ability to create value is bounded by its potential intellectual bandwidth, which is a measure of its potential to acquire information, make sense of it and take action with respect to a goal."
3: "The potential intellectual bandwidth of a team or an organization represents its potential to do meaningful work [3]."

Information assimilation is described as the amount of mental effort required for organizational members to find and understand *needles of information buried in haystacks of vast data stores*. The IB model consists of six levels of information assimilation ranging from the lowest level, manual search procedures to the highest level, or what has been described as the Holy Grail of information assimilation--automated sense making [3].

Manual search at the lowest level represents the most basic means by which information can be accessed. Think of offices filled with clerks processing untold numbers of paper documents who search them one by one in order to find one document that fulfills their needs. Finding, for example an individual with a specific characteristic or trait is difficult even with data that have been organized according to some schema. **Computer data files** offer a means to efficiently store, process, and access information. Miller [5] demonstrated the need for cognitive aids such as computers in his classic paper entitled *The Magic Number Seven Plus or Minus Two*. The first computer programs were written to help organizations such as banks do exact matching in order to find, for example, all customers with both mortgages and checking accounts. **Database Queries** arose **w**ith the advent of more powerful computers. With more interactive capabilities it became possible for individuals to store data and information in databases and then through standard query language (SQL) routines access these data quickly. Both fixed and ad-hoc queries are possible. By creating queries it is possible to request data from specific fields, merge or join these data with data found in other databases and have them displayed in meaningful ways. **Semantic Queries** are generally ignored in traditional query languages because they are mainly designed to operate over a known schema on the basis of well-established algebra. By combining neural networks and standard query techniques queries can result in searches where none of the terms used in the original query appear in the final result. Nunamaker et al

[3] state that these queries operate on the principle "Go find what I mean, not what I say." The authors provide an excellent example of such a query where someone who asks about international transportation of products in Europe receives information about commercial trucking in the EU. As they note, "none of the words that form the original query appear in the response". Similar results can be achieved with search engines such as WordNet that employ linguistics to achieve more efficient and effective searches. In neither the article mentioned above [3] nor the book chapter entitled Value Creating Technology [6] do the authors provide a good example of **automated gist extraction**. To explain the notion of gist extraction, consider the following classroom setting. Suppose Professor Smith tells his students that the quiz for next class will cover the chapters that describe the strategic assumption surfacing technique and business systems planning. A gist extraction process might leave a student with the memory that they had to read the sections about information systems planning techniques. Automated gist extraction is used to skim the main content of a text to assess if a subject of interest is present and to extract and list of patterns and links. Nunamaker (2001) calls **automated sense making** the "The Holy Grail" of information assimilation. With automated sense making a person might describe to the system what he or she knows about a problem. The system would interview the user further to collect relevant information, organize it and suggest possible root causes for the problem as well as possible courses of action for solving the problem.

In subsequent sections we discuss two additions to the information assimilation dimension of the IB model -- automated utilization and automated implementation. **Automated utilization** goes beyond automated sense making to determine the usefulness and value of information obtained from the automated sense making step. The utilization feature helps determine how information can be used, for example, by R&D or by manufacturing to improve the quality of products and processes.

Once information is assessed as to its value, usefulness, and potential application it then becomes an input to the next level -- **automated implementation**. This feature will automatically incorporate new information and knowledge obtained from the previous steps into existing production processes.

The following is a discussion of a complex real-world problem in the diagnostics/pharmaceutical industry that will be used to discuss how the original IB model along with the two extensions can be employed.

Suppose that in the domain of HIV testing and diagnosis a researcher has 100,000 patient sequences. In position 151 there is a mutation (see figure 2) that we find in 10,000 patients. In order to determine whether mutation 151 is resistant to certain drugs, the system has to "interview" patient records to collect relevant information such as drugs used in therapy. The resulting information can be organized according to whether a therapy is successful or unsuccessful, and suggest possible causes of therapy failure. Since the new mutation 151 does not exist in a diagnostic test, we have to update existing tests or develop new diagnostic tests and drugs. We will focus on these last two ideas in our effort to show how to extend the IB model to include automated utilization and implementation into a production process.

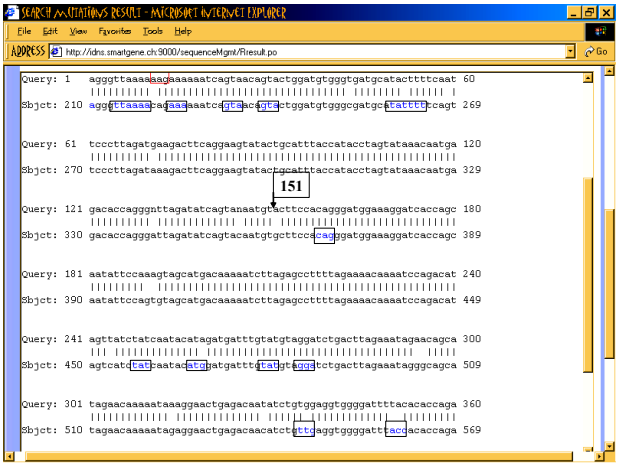


Figure 2: The patient sequence (starting next to "Query:") is compared to the consensus HIV sequence NL43. Mutations of nucleotides in rectangular boxes are known to have drug resistant properties. The mutation in position 151 is an example of a mutation that is not known for having drug resistant properties. The goal is to determine whether such a new mutation could have drug resistant properties by identifying all patients with this mutation and analyzing the success of their therapies.

The following sections describe the HIV domain and the means by which we believe that these new additions to the IB model can be achieved.

3. Extending the Intellectual Bandwidth Model: A Case Study

In the following sections we discuss how the process of finding mutations has progressed from small laboratories equipped with nothing more than basic equipment to the most advanced diagnostic laboratories. In so doing we hope to show how the process relates to a number of the various information assimilation stages identified in the IB model, and what the possibilities are for extending it. Finding mutations and drugs that block the replication of the virus is a complex task that requires not only the

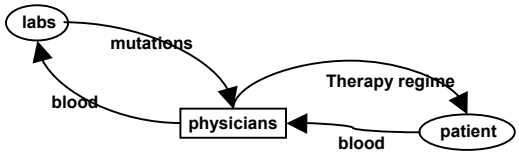
identification of mutations with known drug resistance, but also the identification of new mutations with unknown drug resistant properties. The crucial point is that the active chemical compound of a drug must (e.g., block the catalytic center of a virus protein) disable a vital protein in the reproduction cycle of the virus. The potency of the drug is lost when the virus protein changes its three-dimensional structure so that the drug can no longer disable it. The change in the three-dimensional structure is induced by a mutation of the virus-gene, which could be, for example, the mutation in position 151 shown in figure 2. It changes the protein in a way so that the drug can no longer influence the activity of the protein. In order to achieve the most effective therapy a physician typically prescribes three or more drugs which attack and disable different virus proteins (protease inhibitor, transcriptase inhibitor, and fusion inhibitor). The therapy is effective, if the virus-replication is suppressed and the viral load (virus particles/ml blood) falls below detection level.

3.1 HIV Mutations Assessed by Small Laboratories with only Basic Information Assimilation Capabilities and High End Laboratories: From Manual Search to Database Queries

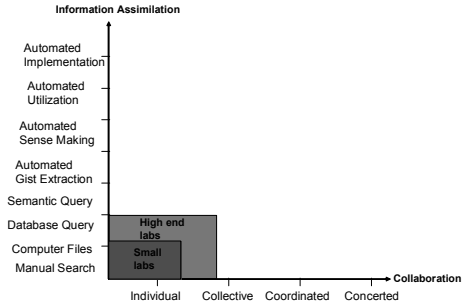
In order to gain an appreciation for the value of information technology and collaboration in helping to address the problem of diagnosing HIV mutations and finding the proper therapy, we begin with a description of what a small laboratory with manual equipment and limited collaboration capabilities has to do to solve the riddle of identifying mutations in the HIV sequence of a patient sample so that it can suggest possible therapies.

The process begins when blood is sent from a physician (who has drawn it from a patient) to a small laboratory. The laboratory must spend several hours separating the plasma from the whole blood, extracting the virus, and preparing the RNA for sequencing with radioactive labeling. The prepared sample is manually loaded on a gel, the DNA fragments are then electrophoretically separated, and then the gel is detached, dried and exposed to a film. After the film has been exposed it is manually examined and mutations are observed and recorded. An expert does this by comparing it to a consensus HIV sequence (e.g., NL43) and determining whether the mutations are relevant (indicate drug resistant properties). In large laboratories, most of these steps are automated through the use of information technology. Here systems automatically determine whether a mutation has known drug resistant properties or whether it is a new mutation with unknown drug resistant properties.

The following figure 3.1 shows how non-networked laboratories whether small or large communicate with the physician. Figure 3.2 shows how IT in larger laboratories can increase PIB.



Figures 3.1



Figures 3.1 and 3.2: The potential increase in intellectual bandwidth between small and large laboratories can be achieved through better IT support. Sequencing, identification of mutations and identification of drug resistance is highly automated in large high end laboratories, which significantly decreases "hands-on" time (practical work) and increases information assimilation. Subsequently, lab personnel can allocate their time to other value creating activities. Value creation is achieved through shorter response time (the time a patient sample arrives at the lab till the time the physician gets the results), higher accuracy and precision of results, and potential collaboration between personnel.

If these laboratories were connected to one another via the Internet, a networked community would result that could significantly increase the potential for information assimilation.

3.2 Establishment of Global Network to Gather HIV Mutations via Internet and End User Information System (EUIS) Over the Internet to a Central Location: Enabling Improved Collaboration and Information Assimilation

Instead of having patient sequences stored locally in manual paper files, computer files or small databases the laboratories now are connected via the Internet to a central location where all data are stored. This will enable user-defined networks where all laboratories can be interconnected. For example if five laboratories want to do a study together all five laboratories will be able to enter their data into a mutual study-database to which all of them will have equal access. Data can be entered into the EUIS using web-pages similar to those shown below

(see Figures 5-7). Here laboratory personnel can copy/paste sequences, which are automatically stored in a single or mutual database in the central location. Each laboratory retains ownership of the data and all data inflows and outflows are tracked and recorded.

The potential intellectual bandwidth can be increased when the system automatically records and evaluates HIV sequences without the intervention of experienced professionals. The improvement of the potential intellectual bandwidth can be seen in figure 4.2:

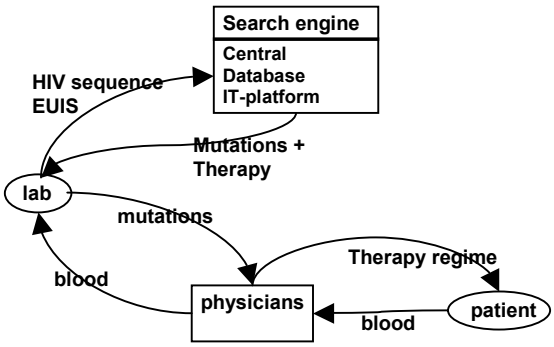


Figure 4.1

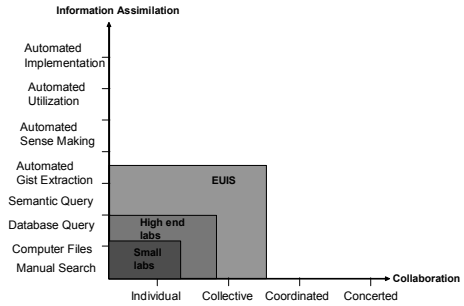


Figure 4.1 and 4.2: The potential increase of the intellectual bandwidth can be accomplished through networking of laboratories, which can significantly improve information assimilation and enable collaboration. Laboratories can potentially collaborate over the Internet, by using the same IT platform, e.g., the IDNS platform (see Figures 5-7). Whether collaboration takes place, however, is more dependent on the level of trust and shared values that exist among participating members. Value will be created if laboratories agree to share and exchange their data, information, and the knowledge of their key personnel.

The end user information system (EUIS) is the first step in the development of an integrated collaborative network [7] to achieve the goal of automated sense making, utilization and implementation. These will be discussed in the following three sections. To the basic EUIS, here of the integrated database network system (IDNS) of SmartGene, two features (SMS-1 and SMS-2) are added, one to advice physicians on mutations with known drug resistant properties, and a second even more exciting feature, which benefits not only patients, but insurance companies, health care systems, and society in general.

Example for end-user information system:

Figure 5: Shows how lab personnel can directly access their own database. The unique password ensures that the laboratory can only access their database (optionally it can allow others on a user-defined network to access this information). It also allows definition of levels of access of expertise (laboratories, physicians, study coordinators, etc.) and login of authorized researchers from any computer connected to the Internet.

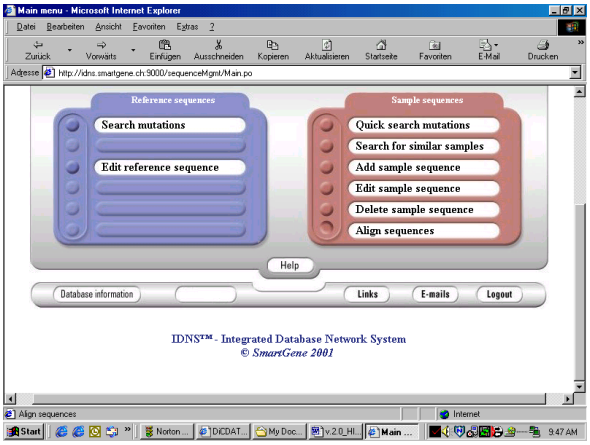


Figure 6: Is an example of an end-user information system for data management. Web-pages are customized for each laboratory and personalized for each individual (traceable password). Data-entry is made through the feature "***Add sample sequence***", which leads to the web-page shown in Figure 7. It facilitates input and storage of new samples sequences into the IDNS system. New Samples are furnished with a patient number, a laboratory number, and a sample date and sequence date. These parameters can be individually customized and adapted to the laboratory condition. New sequences are copied directly out of the respective sequencing program as text file and are inserted into the respective window. A further important option is the comparisons of samples in particular studies, which are user-defined and implemented on request. Studies create data sub-groups, which can be shared with other laboratories or can be separately managed. This function facilitates the compilation of research programs or multi-center studies, without the need for the user to manage data twice. Samples or sequences that are assigned

to certain studies will be adapted automatically for all users if the first user who inputted the sequence changes it later.

Additional customer defined features are: (1) "***Quick search mutation***". With this automated function, mutations of the patient sample can be obtained quickly by comparing the patient sequence to NL43; (2) "***Search for similar mutations***". It serves to query certain sequence patterns. It also can search new mutations in the sample databank and compare discovered sequences. The combination of "Search for similar samples" and the direct "Multi-alignments" function permits a fast and certain comparison of several sample-sequences. Interesting mutation patterns become recognizable and obvious, for example, for epidemiologic aspects or the recognition of newer mutating sites under therapy-influence; (3) "***Edit sample sequence***". This function permits the user to sort samples and sequences according to certain criteria or to summarize them in groups. At the same time, samples can be organized into lists along different criteria, printed out and single samples if necessary can be edited and modified. It also permits the specific administration of studies as a sub-group of the sample databank; (4) "***Delete sample sequence***". The function is used to delete samples-entries and also the associated sequences. This function can be blocked for unauthorized users to prevent unintentional manipulation and deletion of entries; (5) "***Align sequences***". This function is used for the specific comparison of single sequences that are single itemized through the "Align Sequences" - function or in list and then selected through a mouse-click and therewith ready for alignment. The alignment-sequence list can include several lists/pages and single sequences can be deleted. With this function, for example, all sequences of a patient or a patient group can be compared together. Therefore, the development of resistances under therapy can be observed. This function is especially important for physicians and drug development because the mutation frequency under therapy and the probability of the development of drug resistance can be detected.

The feature "***Search mutations***" (see figure 6) allows users to detect and identify the mutations of a sample sequence by comparing it with the designated consensus sequence. Any sequence entered into the "*Search mutations*" function is compared to the respectively valid reference sequence, which is already stored in the database. This comparison is represented through pair-wise alignment marked by vertical bars indicating identical positions. Mutations of the entered sequence can easily be recognized, identified and (through a mouse click) automatically translated and stored into the corresponding amino acid including the amino acid position. This function also recognizes deletions and insertions. Note: these do not lead to a change of the reading-frame and therewith to incorrect positioning in later comparisons.

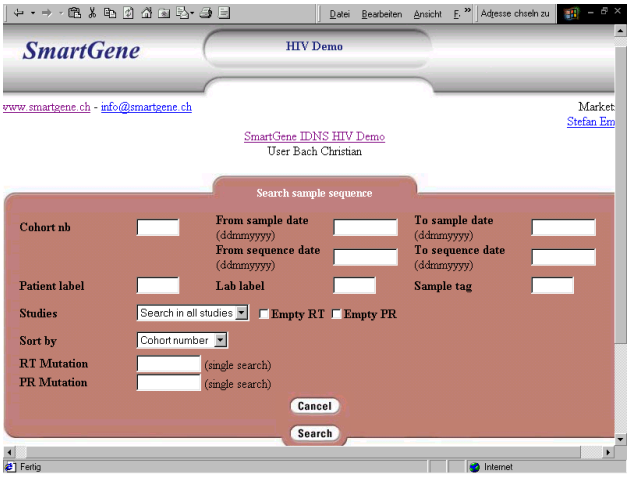


Figure 7: Example of end-user information system where the lab personnel can add patient samples (HIV sequence), manage, search, sort, compare, assign to database and manipulate it. The application is specific (HIV, HCV), sequences are entered by copy/paste as text or automated, and it is compatible to all computer operation systems (PC, Mac, Sun). The following function can be executed through this web-page: (1) "***Cohort nb***": The "Cohort nb" represents the label or name of the laboratory. It also can be used as "Patient ID number"; (2) "***Patient label***": Another patient ID, can also be named laboratory label or study label. All labels can be named and defined (number of positions) according to the customer's custom requirement. With the "Patient Label", the lab personnel can type in the patient number or unique identifier without revealing patient name and other private data; (3) "***Lab label***" / "***Sample tag***": This is to be used as the lab designation of the sample (e.g. tube #12345); (4) "***From sample date***"/"***To sample date***" Defines a period of time for the edition of samples: e.g. all samples from April 1st to June 30th for surveillance studies and lab management (e.g. accuracy testing of the sequencer, work load determination…); (5) "***Studies***": Lab personnel can select in which research program the entry should participate. Sequences can be stored in multiple study databases without duplicating entry procedures. Study subsets can be managed separately and disclosed to other labs in a collaborative network; (6) "***Emty RT***", "***Emty PR***": Selects sample entries where RT or PR sequences have not yet been entered – this tool enables lab personnel to check easily on work that currently is incomplete; (7) "***Sort by***": Patient samples can be sorted by cohort number/sequence date/sample data and also for a certain time period (see above sample date from – to). This enables retrieval of specific sample and the setting of samples in relation, e.g. all samples from 1 patient sorted by date; (8) "***RT Mutation***" / "***PR Mutation***": Here, specific mutations can be searched for and displayed (one at a time), e.g. 215Y in RT sequences.

3.3 Adding Sense Making Software for Mutations (SMS-1): A Decision Support System for Physicians

To improve the EUIS, sense-making-software (SMS-1) we propose adding. Embedded in this software is an integrated database of HIV mutations with known drug resistance and all existing drugs. The software knows which mutation has drug resistance properties and to which drugs it is resistant. No link to patient records is yet established. If the SMS-1 can be enhanced to cover all mutations with known drug resistance the system can, together with automated quality control and feedback control features, release the results directly to the physician as well as a list of all combinations of HIV drug cocktails possible for a particular patient therapy. In the future this system could automatically monitor patients so as to inform physicians of any changes in the virus load and hereby help control the disease by automatically administering appropriate doses of drugs.

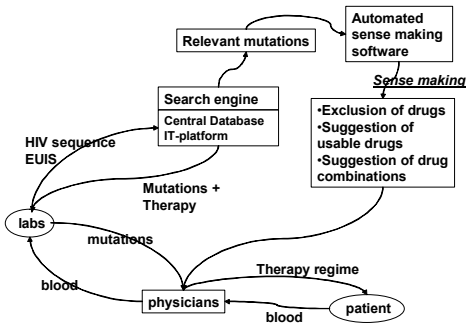


Figure 8.1

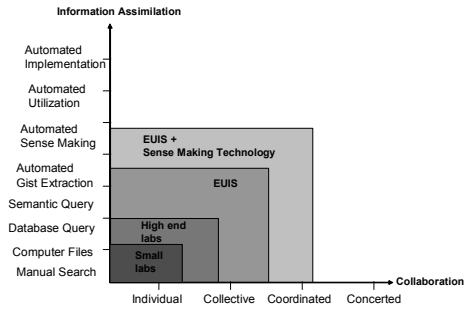


Figure 8.1 and 8.2: The potential increase of the intellectual bandwidth can be accomplished through networking with physicians. The possibility that physicians can participate in the network enormously enhances the potential of the intellectual bandwidth. The first sense-making-software (SMS-1) is used to automatically extract mutations. The software automatically identifies the mutations that are known to be resistant to certain, but not all, drugs. The identified relevant mutations are automatically sent to another sense-making-software, for example Retrogram [8], which automatically provides advice or suggestions for therapy regimes to physicians. Which therapy is appropriate for a particular patient is up to the physician and the patient. It could be that the patient does not tolerate certain drugs, whereas other drugs are better digested. Appetite, physical condition and many other factors must be considered in developing, monitoring, finding and adjusting a therapy.

3.4 Automated Identification and Utilization of new HIV Mutations

In the previous sections we discussed how a sense-making-software (SMS-1) for mutations with known drug resistance can act as a decision supports system (DSS) for physicians. In this section we add a second sense-making-software (SMS-2) package that will enable researchers/physicians to find heretofore-unknown new mutations and determine whether they have drug resistant properties. This software package can compare HIV mutations with patient records.

The SMS-2 software compares new mutations with therapy successes in patient records. It identifies all patients that are infected by a HIV strain with the same mutation and also identifies with which drug(s) the patients were or are being treated with. The software then compares the success of the therapies (negative or positive) and looks for correlations, for example, whether a new mutation correlates with the negative response (no decrease in viral load) of a patient therapy. For example, if 80% of patients with the same mutation and drug treatment have negative therapy success, it could be due to drug resistance of the mutation. Such a finding must be verified with more diagnostic and clinical data involving more patient cases. For this it would be helpful to have the new mutation on existing diagnostic tests to identify more patients and drug cases, which can significantly enhance drug development processes. The potential intellectual bandwidth would be dramatically improved with unprecedented potential for information assimilation and collaboration.

The HIV-EUIS and the IDNS platform shown in figures 5-7 can be used to accomplish the discussed tasks and have already been used in several HIV clinical studies in the late 90s by a major pharmaceutical company and by the national HIV Swiss cohort study.

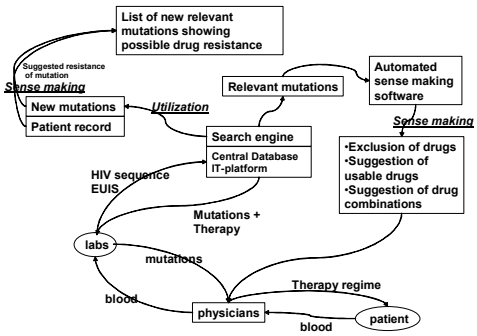


Figure 9.1

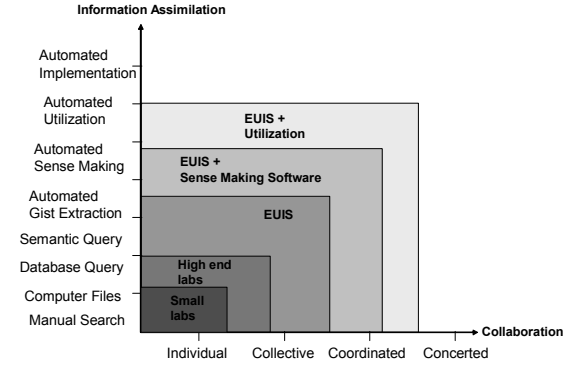


Figure 9.1 and 9.2: Increasing potential intellectual bandwidth through the addition of automated utilization. After establishing a global network of laboratories to feed the central database with HIV sequences on a continuous basis, sense-making-software (SMS-2) can be added to identify and utilize new mutations that occur because of the high mutability of HIV new mutations constantly emerge and must be monitored.

Through a combination of information from therapy success and new mutations, SMS-2 evaluates and identifies correlations. As shown in figure 10 the mutation "151" (remember figure 2) is compared by SMS-2 to the therapy success of six patients (P1-P6) with the mutation "151" (see figure 10). For patients who are taking the anti-HIV drugs W, X, Y, and Z in different combinations, the therapy success is negative for patients 1-5. Only in patient 6 is there a positive response to the treatment with drug Z. This suggests that mutation "151" causes drug resistance to drugs W, X, Y and is sensitive to drug Z. The first utilization of these findings is to stop treating patients 1-5 with drug W, X, Y and treat them with drug Z.

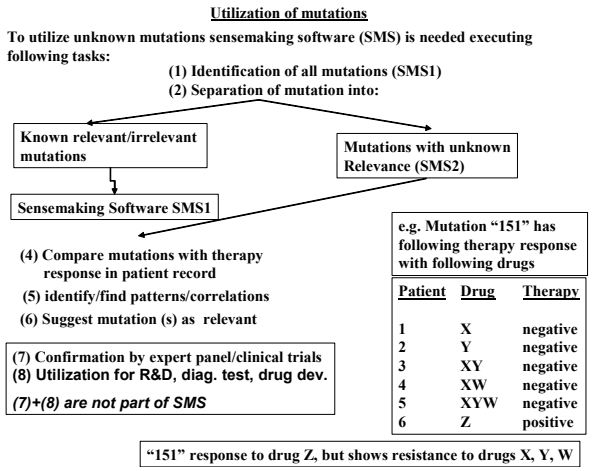


Figure 10: Identifying new mutations and assessing whether they have drug resistant properties.

Such an integrated system enormously improves the IB model of the health care system, creates immediate value for patient (personal benefit), insurer (lower costs) and society in general.

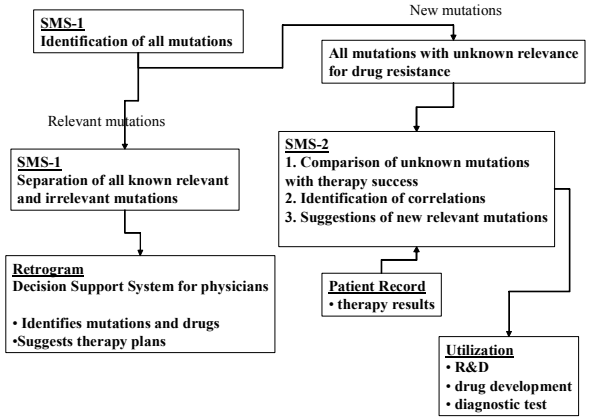


Figure 11: A map of the current sense making capabilities available via IDNS (integrated database network system), which is the potential to enhance the intellectual bandwidth. After the identification of all mutations is done by SMS1 only relevant mutations are used in the sense-making-software, for example Retrogram [8], which is a decision support software for physicians. New mutations with unknown drug resistance are sent from SMS-1 to SMS-2, which is linked to the patient record system.

In this example, SMS-2, automatically utilizes information obtained from the HIV sequence database and the patient record database to identify the drug resistance of new mutations. Further automated utilization achieved through employment of information technology of these results could be (1) in the drug

discovery process, (2) in the R&D process to support basic research, and (3) in redesigning or updating existing diagnostic tests or in the design of new diagnostic test. The two SMSs are separated because of the complex subject matter that needs constant monitoring and updating and also because of legal issues that could arise in case the system makes mistakes.

3.5 Automated Implementation of new HIV Mutations into Existing Diagnostic Tests

The following figure shows the possibility of automated implementation of new mutations into a microarray (gene-chip) or other diagnostic test used in laboratories.

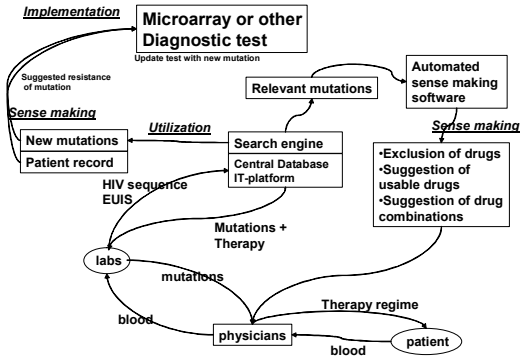


Figure 12.1

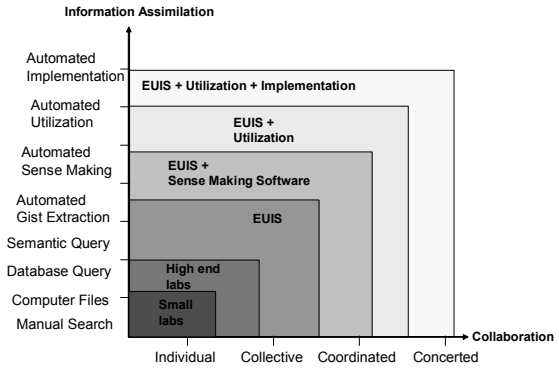


Figure 12.1 and 12.2: An example of practical utilization is the implementation of new mutations into an existing diagnostic test to identify and generate more data, which increases the potential intellectual bandwidth of the scientific community as well as business organizations.

Figure 12.1 illustrates the means by which newly identified relevant mutations can be automated to implement the new information and knowledge into existing production processes. To confirm the relevance of new mutations more data from more patients are needed. For this reason it is useful to add the new mutations into existing diagnostic tests to identify new patients and gather more data for drug discovery and for later use in the FDA approval process. It can also be used for epidemiological studies that could help to better track and handle an outbreak and to allocate needed resources accurately. The implementation process automatically can make changes in the production process. As soon as SMS-2 has identified potentially new relevant mutations new mutations can be added in the next batch of gene-chips or other diagnostic test devices. As noted earlier the ability to extend the IB model is highly contingent upon the degree of collaboration that we are able to ensure.

3.6 Collaboration

The second component of value creation is collaboration, which is the degree to which people in an organization or network can combine their mental efforts so as to achieve common goals. Nunamaker et al. describes four level of collaboration ranging from the lowest – individual effort to the highest – concerted effort.

Think of ***individual effort*** as a starting point, the part at which there is no collaboration. Here, each individual does his or her own thing without concern of others. With no collaboration, no matter what information assimilation techniques are employed, the organization's intellectual bandwidth will be severely limited. The simplest form of teamwork is ***collective effort***, where each person makes an individual effort, but the efforts are only organized to the point where the individual efforts add to productivity by the whole group. The productivity of a group is simply the sum of the productivity of the individuals. Nonetheless, the value creation is greater than in the case of non-collaborative individual effort because the many minds are at least non-duplicating or accidentally thwarting one another's efforts. In ***coordinated effort*** tasks are differentiated. People become specialists at doing pieces of the whole task. Each member of the organization works independently of the others, but each must carefully coordinate handoffs of deliverables because the work of each depends to some extent on the productivity of the others. Total Quality Management (TQM) would be impossible without this level of collaboration. Team productivity is a function not only of individual effort but also of the degree of coordination among those efforts. In a ***concerted effort***, all team members must be making the right effort at the right time toward a mutually agreed upon goal. The efforts of each member directly affect the efforts of others. Any local disruption creates global impact. Weick and Roberts [9] introduced the term heedfulness to describe this type of collaboration. It is the level of coordination and collaboration among 19 year old sailors that ensures that

$40 million aircraft take off and land on aircraft carriers each day without incident.

In the case of HIV diagnosis and treatment there needs to be unprecedented concerted effort. Physicians and scientists in laboratories and institutions must be willing to share knowledge with one another. They must be heedful of the tasks performed by their colleagues and the support they need to properly carry out their tasks. One thing that is fundamental to establishing the cooperation and collaboration necessary to make a scientific community successful is trust. In the HIV case presented in this paper, physicians, laboratories, hospitals, and patients from throughout the world must work together in a seamless, and selfless sharing of knowledge. The only way to ensure the level of collaboration needed in such an arrangement is to create an incredible high level of trust among all stakeholders.

4. Conclusion

The IB model is a good visualization tool as well as a good communication tool that can be used in many business situations to not only call attention to what can be achieved, but also to what needs to be addressed if an organization is to achieve its maximum potential to create value.

The discussion of the IB model in the context of the HIV example discussed above demonstrates the value of the model in a complex scientific and business situation. While the IB model was only theoretically employed in the HIV example discussed in this paper, it nevertheless mapped nicely onto this very real bioscience problem providing ample evidence of the validity and value of the original IB model and of the proposed extensions to the information assimilation dimension.

The usefulness of the IB model derives from the integration of technological and human dimensions into one model. Too often decision makers focus on technology while ignoring the human dimension. By juxtaposing these two dimensions it becomes clear that both must be addressed. No matter how much technology is employed, an organization's true potential cannot be realized unless the human factor is addressed. Here the model is less than informative. More discussion concerning the collaboration dimension of the IB model is needed.

5. Reference

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