

White paper

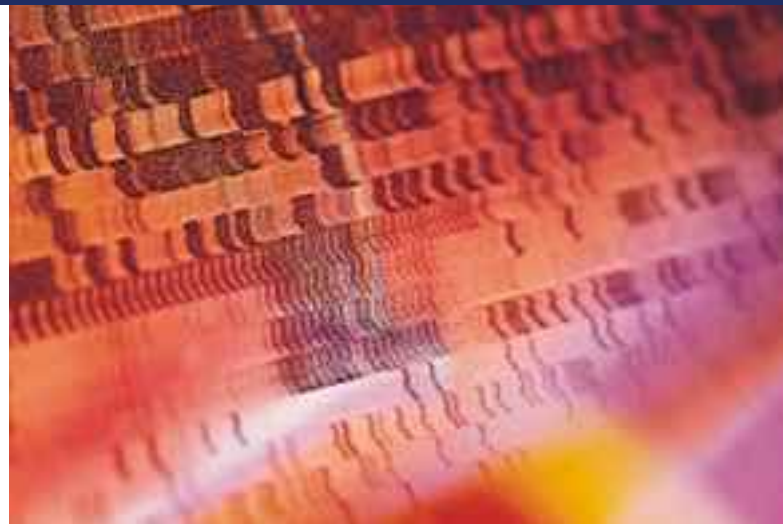
# The mapping of the human genome: where next?

An analysis and point of view

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Pharmaceuticals & Medical Products

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On 26 June, 2000, scientists announced to the world that they had completed a first draft of the human genome. This simple announcement heralded the start of a new era in which the availability of genomic information will change the face of many of our traditional industries. Like most of the revolutionary technologies in the past, this is a global result; it impacts individuals' lives; it touches multiple aspects of business operations and it is highly dependent on our ability to manage significant quantities of information.

Genomics offers a new set of opportunities and challenges for pharmaceutical companies to achieve the long held goals of finding the **right target** leading to **right drug candidate** for the right patient treating the **right disease**. Achieving these goals will require fundamental changes in the way discovery and development is undertaken and decisions are made today. Various technologies within genomics, proteomics, pharmacogenomics and bioinformatics hold the keys to finding new and better medicines.

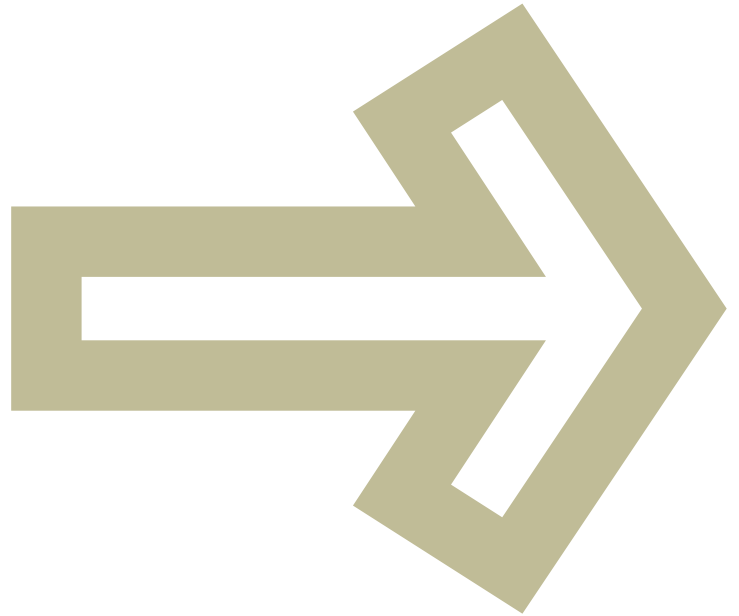
The impact of genomics on the pharmaceutical and biotechnology industry is likely to approach in three waves: drug discovery, drug development, and a shift in medical/commercial practice. As a disruptive technology, genomics will have a profound impact on every aspect of the value chain in the drug discovery, development and commercial areas.  
(Figure 01, page 02)  
(Figure 02, page 03)

#### About Accenture

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With more than 75,000 people in 47 countries, Accenture can quickly mobilize its broad and deep global resources to accelerate results for clients. The company has extensive experience in 18 industry groups in key business areas, including customer relationship management, supply chain management, business strategy, technology and outsourcing. Accenture also leverages its affiliates and alliances to help drive innovative solutions. Strong relationships within this network of businesses extend Accenture's knowledge of emerging business models and products, enabling the company to provide its clients with the best possible tools, technologies and capabilities. Accenture uses these resources to serve as a catalyst, helping clients anticipate and gain value from business and technology change.

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# The opportunity

To be successful, companies need to have a portfolio of technologies in their arsenal and must have the ability to integrate them to achieve the results of finding new, validated targets – hence the evolution of proteomics and functional genomics.

Impact on pharma industry			
	Drug discovery	Drug development	Commercial
Scope	<ul style="list-style-type: none"> <li>Pharma companies</li> </ul>	<ul style="list-style-type: none"> <li>Pharma companies</li> <li>Regulatory agencies</li> <li>Patients</li> </ul>	<ul style="list-style-type: none"> <li>Pharma companies</li> <li>Regulatory agencies</li> <li>Providers</li> </ul>
Impact	<ul style="list-style-type: none"> <li>Integrate genomics into the discovery process &gt; shorter time; more drug targets</li> <li>Expect more large molecule entities (LME) as drugs: peptides, proteins, antibodies, antisense, ribozymes, gene therapy</li> </ul>	<ul style="list-style-type: none"> <li>Enable the development of customized drugs, i.e. pharmacogenomics</li> <li>Change the definition of blockbuster drugs</li> <li>Create a new set of economics for drug development</li> </ul>	<ul style="list-style-type: none"> <li>Strain resources because of more product launches</li> <li>Need more effective marketing messages</li> <li>Educate physicians on genomics and drugs based on genomics</li> </ul>

Figure 01 The impact of genomics on the pharmaceutical and biotechnology industry.

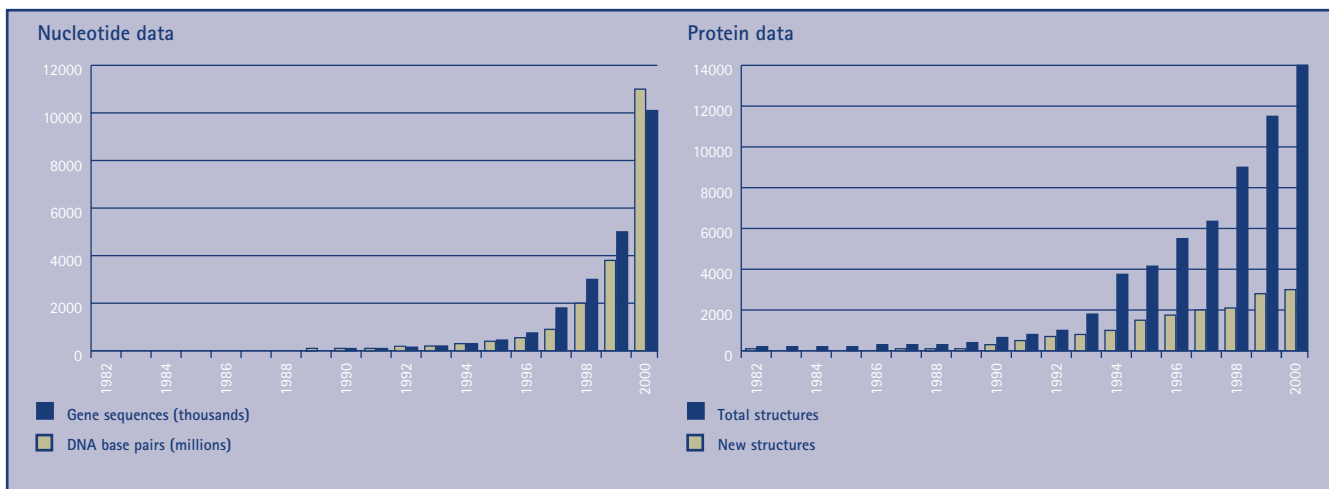


Figure 02 The impact of genomics on the pharmaceutical and biotechnology industry.

Source: DNA data from Genebank, protein data from PDB

### Targets

With the full sequence of the human genome available, and public Expressed Sequence Tags (EST) databases growing continually, any competitive advantage derived from competence in gene discovery will quickly disappear. In the short term, however, access to EST data; from computational tools for mining, finishing, organizing, and filing patents on sequence data and by assembling a complete set of verified full-length sequences and physical clones will be of primary importance for at least high-priority genes for drug, diagnostic and pharmacogenomic markers.

As DNA sequence information becomes a level playing field, the race will intensify to identify and exploit the small subset of genes that are useful for developing therapeutics or diagnostics. To be successful,

companies need to have a portfolio of technologies in their arsenal and must have the ability to integrate them to achieve the results of finding new, validated targets – hence the evolution of proteomics and functional genomics.

An explosion of valuable information has resulted from these areas of discovery.

### Genomics

The emergence of the field of genomics has forced a paradigm shift in the manner with which the pharmaceutical industry approaches the discovery and development of new drug compounds. Traditional pharmaceutical research involved individual target identification coupled with screening for inhibitory chemical compounds. Our understanding of the molecular basis of disease is expected to expand immensely as the data encoded by the human genome is transformed into knowledge. This includes diseases caused by external pathogens as well as those that arise out of variations within the human genome.

Through the work of Celera Genomics<sup>1</sup> and Human Genome Project, the human genome has been sequenced. Based on the initial sequence analysis of the human genome, it is estimated that the pharmaceutical industry will have ten times as many therapeutic targets than were previously known. All existing therapeutic drugs currently focus on only 500 targets; estimates of 3,000 to 5,000 new potential targets, unveiled by genomic research hold immense promise and raise new and different challenges for pharmaceutical and biotech companies. With many new complementary areas of research, companies are flooded with information overload from the genome, Single Nucleotide Polymorphs (SNPs), and the proteome that are all growing rapidly. The need to filter through potential targets to select only those that are both relevant to disease and are chemically tractable has led to an industrial approach to traditional biology and chemistry.

1 Source: www.celera.com

## Any competitive advantage derived from competence in gene discovery will quickly disappear.

### Proteomics

Proteomics is a new enabling technology that is being integrated into the drug discovery process. Proteomics seeks to provide functional information for all proteins. Proteomics is highly complementary to genomic approaches in the drug discovery process and offers scientists the ability to integrate information from the genome, expressed mRNAs, their respective proteins and subcellular localization. Much like genomics, proteomics is more of a concept than a defined technology, and refers to any protein-based approach that has the capacity to provide new information about proteins on a genome-wide scale. Due to the greater technical challenges, high-throughput analysis of protein sequences and structures has lagged behind that of gene sequences. Given that proteins are the targets of most drugs, it is critical that this information be revealed. There has been substantial effort and progress in this area, specifically the development of structural genomics, protein modelling and specialized, high throughput mass spectrometry techniques.

Companies, such as Myriad Genetics<sup>2</sup> are developing proteomics technologies and using them to map the human proteome. Generating a map of the human proteome provides a blueprint for the accelerated identification of drug targets. Given that more than 75% of the predicted proteins in multi-cellular organisms have no known cellular function yet, proteomics faces an enormous challenge. However, proteomics is poised to yield remarkable discoveries since this set of proteins is likely to include new enzymes, signalling molecules and pathways that may be excellent and present previously untapped therapeutic targets. Proteomics can be used to evaluate the role of a chosen target protein in signal transduction cascades directly relevant to the disease.

Proteomics can also be used to create a new type of analysis to the study of toxicity at the protein level, a concept that may best be named 'Pharmacoproteomics'. Animals can be dosed with increasing levels of an experimental drug over time, and serum samples can be drawn for consecutive proteome analyses. Using this procedure, it should be possible to identify individual markers or clusters of markers that are dose related and correlate with the emergence and severity of toxicity. This application can extend to tracking toxicity of drugs in clinical trials where serum can be readily drawn and analyzed. Therefore, technologies to predict pathway analysis, *in vivo* response, chemoinformatics and even Absorption, Distribution, Metabolism, Elimination and Toxicology (ADMET) response are being integrated to create a comprehensive profile of potential target success in early discovery, pre-clinical and clinical phases of drug product development.

## Efforts in the structural biology community aim to allow scientists to obtain macromolecular structures in a fraction of the time required today.

### Structural Biology

The overwhelming success of the genomic sequencing efforts has spawned comparable efforts in the structural biology community. These efforts aim to create and execute high throughput structure determination that would allow scientists to obtain macromolecular structures in a fraction of the time required today. Companies such as Structural Bioinformatics Inc. (SBI)<sup>3</sup> and Inpharmatica<sup>4</sup> are working towards database products that provide structure-function relationship data covering the entire human proteome. The expectation is to directly identify potential leads *in silico* by exploiting the 3D structures of proteins and advances in computer-aided drug design. Such information will work to facilitate structure based drug design/discovery. SBI utilizes a variety of methods, including augmented homology modelling techniques, local tertiary-structure prediction and loop generation algorithms to build structural models of proteins. A structural genomics consortium (SGC) was held by the

major pharmaceutical companies in late 2001. An important aspect of structural genomics is connecting coordinate data with whole genome information related to phylogenic occurrence, protein function, gene expression and protein-protein interactions. This works to increase the value of database integration, by allowing more specific search techniques to be implemented.

*In silico* cellular modelling constructs models of intracellular signal transduction pathways where drugs may interfere, and converts it to a software algorithm process. With signal pathway models, scientists can design experiments to test the effects of drugs, transgenic over expression or genetic knockouts. Physiome Sciences<sup>5</sup> tools identify which steps of the process are chemically relevant to a given molecule, which are committed (cannot be evaded through a workaround reaction) and displays kinetic profiles when available. Current applications include immune cell signalling and apoptosis pathways.

<sup>3</sup> Source: [www.strubix.com](http://www.strubix.com)

<sup>4</sup> Source: [www.inpharmatica.com](http://www.inpharmatica.com)

<sup>5</sup> Source: [www.physiome.com](http://www.physiome.com)

# Finding the right **compound**

Predictive ADMET and informatics-enabled chemistry are helping the industry to improve discovery and development processes.

High-throughput screening and combinatorial and medicinal chemistry are clearly major strengths of the pharmaceutical industry. Lead optimization remains a key bottleneck in the discovery and development processes with more than 50% of drug candidates failing in clinical trials due to unacceptable side effects and toxicities. Predictive ADMET and informatics-enabled chemistry offers ways to address these problems.

## Predictive ADMET

Predictive ADMET technologies will have a major impact on the productivity of drug development, with the potential to eliminate about 50% of all failures in this process, by prospectively identifying compounds destined to fail because of poor ADMET properties. Few technologies with this

## Lead optimization remains a key bottleneck in the discovery and development processes.

capability currently exist. Those that do are often unreliable and/or clumsy to apply to significant numbers of compounds. These will include automation and miniaturization of current absorption and metabolism assays; improved cellular models of intestinal membranes; novel *in vitro* methodologies, such as liposomes immobilized on Spatial Proximity Resonance (SPR) arrays and artificial membranes immobilized on chromatographic columns; transcriptional profiling to identify 'toxic' fingerprints; and computational algorithms for structure ADMET relationships.

### Information enabled chemistry

Information enabled chemistry takes advantage of advances in computational capabilities and/or knowledge of the target to reduce the number and duration of the synthetic cycles required to generate a lead compound. This involves, for example, libraries that can be expanded and screened *in silico* for compounds that dock most effectively with the known or projected 3-dimensional structure of the target's active site; or self-evolving libraries that participate in target-directed synthesis of highly specific compounds.

### Simulation and Predictive Modelling (*in silico*)

Virtual (*in silico*) screening is emerging as a potentially very powerful technology in drug discovery that has the real prospect of exploiting protein structural information on a genome scale for discovering better drug leads faster. The aim is to use *in silico* screening as a complementary technology to High Throughput Screening (HTS) using virtual compounds rather than in-house collections. The technique requires a 3D molecular structure of the target molecule, either determined using X-ray crystallography and/or NMR, or by homology modelling. The molecular structures to be screened exist as a virtual collection of molecular structures obtained from a preferred set of combinatorial chemistries.

There is also great effort towards developing computational models for the prediction of the ADMET properties of pharmaceutical drug candidates. *In silico* ADMET screening capabilities use ADMET profiling data collected in-house as well as literature data where appropriate. The goal is the early selection of compounds that have optimal ADMET properties. These predictive models permit the high-throughput analysis of virtual compounds or libraries before synthesis at very early stages in the drug

discovery process, thereby reducing the need for and complementing the interpretation of iterative compound synthesis and experimentation cycles.

In addition to these three key areas, there are several other new techniques/technologies that offer promise for speed, quality and success rates in drug discovery and development. Notable among these are cell-based high-throughput 'phenotypic screening' using (for example) transcriptional profiling as a readout; function-blind screening using Spatial Proximity Resonance (SPR) arrays or microfluidic thermal stability assays; and microfluidics-based high-throughput screening in general.

# Selecting the right patients

Genomics based diagnostics will provide a clear understanding of the true underlying cause of a patient's condition.

'Selecting the right patient' using genome based diagnostics and matching with disease phenotype is now possible and can streamline the drug development process. For personalized medicine, genomics based diagnostics will provide a clear understanding of the true underlying cause of a patient's condition, and pharmacogenomics the ability to determine whether (s)he will respond to and tolerate a particular drug. Through this same ability, pharmacogenomics will also play a major role in increasing the productivity of clinical development, by helping reduce the size, duration and failure rates of clinical trials.

Genome-based diagnostics currently rely on the expression profiling/biology to identify gene expression markers that correlate with specific diseases. To achieve universal use, this technique must improve so that it can reliably profile the entire genome.

## Pharmacogenomics

Pharmacogenomics can be considered the marriage of functional genomics and molecular pharmacology. Pharmacogenomics is the area that works to characterize the genetic component of disease in an effort towards creating gene-based personalized medicine and gene

therapies targeted to specific areas of the genome with disease. Attached to this are the concepts of predictive medicine and disease prevention. The potential for writing prescriptions that are customized to a specific patient population is a concept only beginning to be considered by the pharmaceutical industry. Such studies require advanced bioinformatics capabilities to analyze vast amounts of data from various sources. The greatest challenge for pharmacogenomics today is to prove definitively the universal correlation between normal versus disease patterns of gene expressions.

# Advances in drug **discovery** approaches

Integration of genomics and the associated technologies with the drug discovery process is the key to improving overall productivities.

The goal of drug discovery in this information rich environment is to rapidly and accurately evaluate therapeutic potential based on genome sequence or protein structure information. The inability to identify valid drug targets by examining gene sequence information has created a gap between genomics and drug discovery. The problem resides in the fact that gene sequence reveals little about protein function or disease relevance. Accordingly, the true value of the genome sequence information will only be realized after a function has been assigned to all of the encoded proteins.

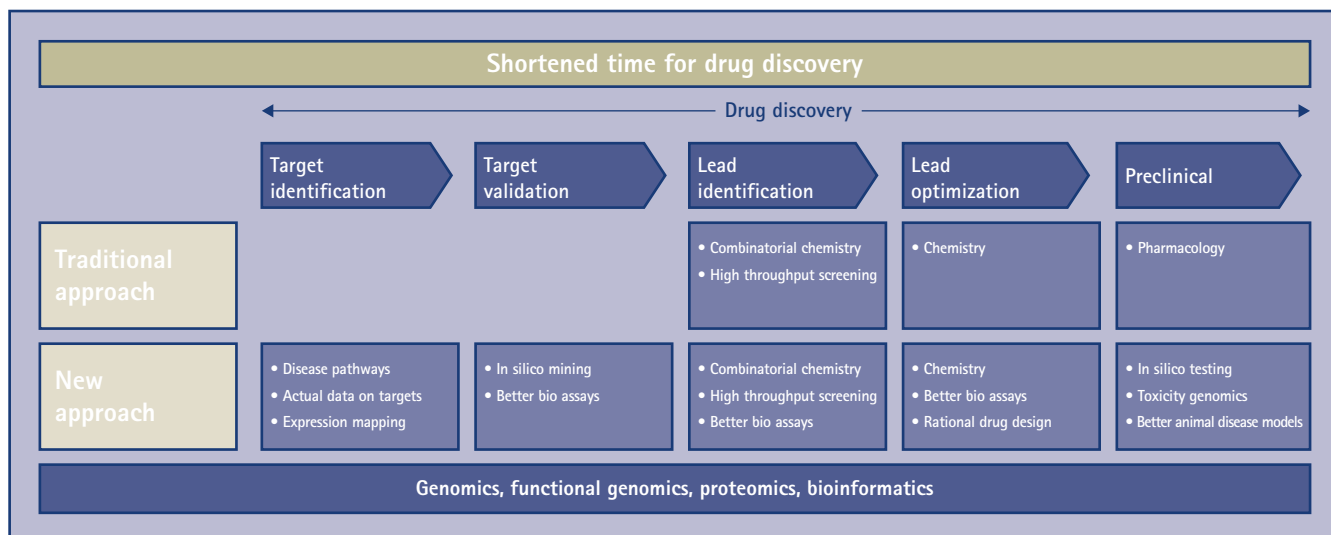


Figure 03 Shortened time for drug discovery.

Integration of genomics and the associated technologies with the drug discovery process is the key to improving overall productivities. Genomics/proteomics/new technologies and process if properly used and integrated with the discovery and development processes can:

- Shorten the time to identify and validate targets and leads.
- Increase the number of drug targets and lead compounds coming into the pipeline.
- Develop assays to screen out toxic or less promising compounds at earlier stages.

**The inability to identify valid drug targets by examining gene sequence information has created a gap between genomics and drug discovery.**

# Challenges

Deciding which technologies to invest in, staying current on data, collaborating with other researchers and setting up the right infrastructure and support systems are key challenges for researchers.

- Key challenges faced by the researchers in this complex, information rich environment are
- How to choose/decide in which technologies to invest?
    - Companies need to have a set of core technologies that constitute the foundation and then build specific technologies to suit their specific research strategies.
  - How to stay current on both external and internal data/information?  
How to collaborate with other researchers within the company and with partners?
  - How to set up the right infrastructure and support systems?

## Foundation technologies

### Microarrays/Gene chips

Microarrays/Gene chips are used for detecting mutations in specific genes related to a disease condition or resulting from drug treatment. These are also used to detect the differences in gene expression levels in diseased cells versus normal cells. New technology in this area is in the area of protein biochip leading rapid detection of protein-protein interactions.

### Microfluidics

The ability to perform genomics and drug discovery assays in nanoliter (10<sup>-9</sup> liter) volumes, a field termed microfluidics, is transforming the process of drug discovery proteomic analyses on one or a few cells.

### Biosensors

Optical biosensors are quickly becoming a valuable tool in a broad range of pharmaceutical research applications. Biosensors have the ability to detect not only protein/protein interactions, but also small molecule/protein interactions that play a role in preclinical evaluation of drug candidates.

### Imaging

Generally speaking, imaging refers to the acquisition (and subsequent analysis and display) of data where the preservation of spatial relationships between individual data points is of importance. These spatial relationships contain information in addition to that provided by the individual points, and constitute a highly efficient, multiplexed method for obtaining and organizing data. Image management technologies are beginning to play critical roles in the analysis of genomics and proteomics data.

### High-Throughput DNA Sequencing

High-throughput sequencing is essential to the process of identifying and cataloguing specific genes and gene variants. While frequently incomplete, they allow scientists to tag genes that are likely to be expressed as protein (mRNA), hence the name Expressed Sequence Tags, or ESTs.

### Clustering

Clustering is the process of grouping all sequences together that overlap. This technique creates a single consensus sequence derived from multiple input sequences, e.g. ESTs for each potential gene, and provides the templates for target identification.

### Database Mining

Database mining is a highly automated process using proprietary software tools whereby the consensus sequence for each identified gene is computationally compared to all known genes and motifs for the best match, and the results are stored in a database with an annotation to reflect this match. Scientists review all novel proteins matching high priority protein target classes and select the most promising for further sequencing and expression studies.

### Genome Assembly and Target Identification

Stretches of genome sequence, downloaded from the public databases daily, are scanned for protein encoding regions called exons; these exons are then linked together to form putative genes. Once formed these 'genes' are compared to ESTs in the database to help refine the boundaries of the exons and the resulting 'best' gene is mined computationally as described above for similarity to known genes and motifs.

**There is now an enormous amount of high quality, publicly available data provided by several collaborative websites.**

#### **Expression Profiling**

Genetic messages and their encoded proteins respond to the cellular environment to modulate development, growth, disease and death. Expression patterns can be determined using a variety of approaches directed toward either the transcription (process of generating mRNA from a DNA template) or the translation (synthesis of a protein molecule from mRNA) stages of gene expression. Microarray-based transcriptional profiling technology allows our scientists to simultaneously monitor the expression of tens of thousands of genes in a single experiment, providing a detailed conceptual view of the cellular circuitry by expression monitoring at the level of the whole genome. The power of this technique is in its scope: scientists can investigate differences between normal and malignant tissue, identify novel drug targets and genetic markers, elucidate specific genetic pathways regulated by a given drug and determine the function of novel genes.

#### **Pathway Profiling**

Any given property of an organism usually reflects the coordinated activity of a set of genes and/or a set of proteins acting in concert, rather than the isolated activity of an individual gene or protein. Accordingly, each gene emerging from a discovery effort has a two-fold significance. First, it may prove useful as a drug target or, in biotherapeutics, as a drug itself. Second, it represents an entry point into a pathway composed of additional, possibly superior, potential drug targets. The process of mapping and identifying additional proteins along a pathway is known as pathway profiling. Signal transduction profiling has become one of the key areas for drug discovery.

#### **Knockouts, Transgenics, and Cellular Regulation**

Mouse and various insect genomes e.g. *Drosophilla* have also been mapped along with the human genome. These are proving to be highly important tools in the understanding of functions of various human genes. Transgenic animal model allows the establishment of validation of functions of certain genes.

#### **Knowledge management and collaboration**

##### **Knowledge Management**

Internet technology has led to significant growth of the amounts of data available to researchers, since there is now an enormous amount of high quality, publicly available data provided by several collaborative websites. This wealth of information together with internal proprietary databases, contains critical facts that need to be properly organized, integrated and displayed in order to maximize effectiveness.

The flood of data means that researchers are challenged to make use of the volumes of data that are available. With the volume of data doubling every 18 months, researchers need new techniques for keeping up-to-date with scientific discoveries. To this end, multiple knowledge management solutions are being developed to aid in the dissemination of information and encourage collaboration.

Such solutions range from applications that monitor changes in available information to those that disseminate information enterprise-wide. Researchers can annotate their discoveries on relevant data objects and are able to choose whether or not to share those annotations with their colleagues.

### Collaborative Environment

Both structured and unstructured information needs to be analyzed and categorized in order to automatically generate a Knowledge Map so that the displayed relevant content categories can be easily searched.

Enterprise-level scientific collaboration systems assist in sharing information and reducing the discovery life cycle. Collaboration tools allow a virtual laboratory and library to be utilized by all research team members. Collaboration does not end with the discovery of drug targets, but continues through the arduous process of gaining approval for a new drug.

### Standards Development

With the influx of such large volumes of data from a number of disparate sources, there is a large gap in the data management and integration practices. A significant amount of time and money is spent on systems integration and data quality assessment. The need for a platform to integrate applications and data used in the drug discovery area is paramount as there are over 1,000 of such applications with more than 100 publicly accessible databases.

A consortium of around 50 organizations, Interoperable Informatics Infrastructure Consortium (I3C), has been recently created to address this issue. It is charged with a mission to facilitate and enable data exchange, data management, and knowledge management across the entire life science community by promoting common protocols that ensure interoperability in an open, consistent and robust manner. Its membership includes hardware and software vendors, content providers, pharmaceutical and biotech companies as well as various government agencies. This group has just begun to develop methodologies, and approaches. It will be some time before these are accepted and put into practice. Once these practices have been implemented, there will be a significantly higher level of data integration between the various discovery-computing environments. With such standards in place, the potential for a far more seamless information flow exists, one that can reduce systems integration timeframes.

### Infrastructure and support systems

#### Data Visualization

New data visualization tools allow researchers to extend their intuitive abilities to visually interpret experimental results by providing a user interface that exploits our natural abilities in visual perception.

New visual interfaces are required for the new discovery techniques. Traditionally, the data is returned in varying formats. The ability to quickly and accurately interpret this information is currently non-trivial. There is a new breed of software vendors that specialize in the on-screen and 3-D visualization of these numbers. This visualization lends itself to quick data interpretation. These tools include visualization of data from microarrays, pre-clinical evaluations or genomic analyses.

**Once most major organisms and infectious agents are sequenced, all pharmaceuticals and biotechnology companies will have the same data.**

## Pharmaceutical and biotechnology companies are increasing their collaboration with one another, requiring measures to protect intellectual property rights.

Current leaders OmniViz<sup>6</sup> and Spotfire<sup>7</sup> also offer further insight into the data by demonstrating relationships that occur through secondary properties and statistical patterns. These 'novel discoveries' are key for competitive advantage. Once most major organisms and infectious agents are sequenced, all pharmaceuticals and biotechnology companies will have the same data. Gaining insight into that data depends on the characteristics and quality of the analysis – a major goal of bioinformatics and chemoinformatics.

The current data visualization market offers client/server or desktop tools. There are efforts within pharmaceutical companies to merge these tools with customizable web-based searching applications to complement data analysis with real-time updating when new genes are discovered and data mining warehouses are modified. A leading global pharmaceutical company is pioneering the coupling of portals for scientists with data analysis tools in a highly usable format.

### Affordable Super Computing

Linux has emerged as a favoured enterprise operating platform for affordable, scalable, calculation-intensive computing. Traditional high-performance computing vendors, including Sun Microsystems<sup>8</sup>, IBM<sup>9</sup>, Compaq<sup>10</sup> and Silicon Graphics<sup>11</sup> now all offer Linux-based solutions. Pharmaceutical companies that are faced with increasing data requirements are embracing these flexible systems rapidly. Linux, running on a battery of Intel servers, mostly dual-processor machines, has been shown to be an efficient way for processing human genome information for use by pharmaceutical companies and drug research.

### Infrastructure

Technology infrastructure requirements for the genomics market in the past have required three core capabilities: speed, extendibility, and scalability. For example, in order to participate in the human genome project (HGP), every sequence was required be reported within 24 hours with no ownership strings attached. This meant high-speed processes and technology were a must. The ability to share and access data within and between companies is also essential during the market trend toward mergers, this makes extendible systems a must. The core of the HGP and Proteome initiatives focus on making every bit of raw and curated data available for mining, requiring open and extendable systems to support this effort. As new groups enter the R&D organization and market constantly, systems need to be able to adequately scale to support the volumes of users. For example, the HGP involved countries which joined from the inception with others on board just months before the completion. Companies have other emerging infrastructure requirements, specifically in the areas of information security and system and systems and network throughput. Since companies require assurance that data is being exchanged without being compromised, information security is coming to the forefront. Similarly, pharmaceutical and biotechnology companies are increasing their collaboration with one another, requiring measures to protect

6 Source: [www.strubix.com](http://www.strubix.com)

7 Source: [www.inpharmatica.com](http://www.inpharmatica.com)

8 Source: [www.physiome.com](http://www.physiome.com)

9 Source: [www](http://www)

10 Source: [www.inpharmatica.com](http://www.inpharmatica.com)

11 Source: [www.inpharmatica.com](http://www.inpharmatica.com)

the intellectual property rights that are essential to these firms' bottom lines. As these data exchanges grow, increasing throughput and data complexity should not compromise performance or integrity of the data. With relevant data doubling every 18 months, infrastructure must be capable of scaling accordingly.

Genomics promises to bring about new medicines to treat and/or prevent currently diseases which are unable to be treated and would allow early diagnosis and prevention. However, the benefits are by no means guaranteed. Major technical and social issues need to be resolved before the promise is fully realized. The impact of genomics

on the pharmaceutical industry is expected to be significant, yet the full impact is unlikely to be fully realized several years hence. Genomics-driven changes in discovery and development will be significant over the next two to five years. But as we have seen here, due to the timeline for drug development and the uncertainties surrounding science and technologies, a major shift in medical practice and patient care is in all probability at least 5-10 years away. At Accenture, we believe that pharmaceutical and healthcare companies need to act now to integrate these technologies into discovery and development processes, develop diagnostic methods to allow pharmacogenomics-based clinical investigation and permit smaller clinical trials. Education amongst

physicians, patients and healthcare communities is a critical path if the bioeconomy is to bring about the promised profound change in healthcare and significantly improve the quality of life. Above all, as companies strive to influence their commercial environments with these powerful technologies, the real challenge has to be how to best integrate science and technology to create shareholder value whilst bringing maximum benefit to the way in which the world works and lives.

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Dr. Banerjee is the Partner-in-Charge of the pharmaceutical Research & Development practice at Accenture plc. He has extensive experience in the pharmaceutical industry and management consulting in general management, business development, strategic and technology/market planning, and managing pharmaceutical R&D. He has authored several reports on R&D productivity and management issues. He is currently involved in various strategic and operational R&D management consulting in genomics, bioinformatics, discovery, pre-clinical and clinical development activities for a number of major pharmaceutical companies.

Previously he has served as President of a biotechnology company, President of a generic drug company and Head of Worldwide project management and new opportunity development at Kodak. He had also held R&D management positions at SmithKline and Abbott. He holds a PhD in Pharmacy from University of Wisconsin and an MBA from the Wharton School of Business.



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