individual! Let me emphasize at this point that no 'academic' scientist should consider it beneath his/her dignity to get deeply involved with such issues. After all, it was Barry Trost who coined the term 'atom economy' in synthesis. And it is Noyori who has come up with a novel way of oxidizing cyclohexanone to adipic acid using only aqueous hydrogen peroxide (the existing process using nitric acid results in the emission of the oxides of nitrogen – the cause of ozone depletion, smog and acid rain). Noyori's process employs a biphasic system with two catalysts – tungsten oxide along with a phase transfer catalyst (Bolm, C., Beckmann, O. and Dabard, O. A. G., *Angew. Chem.*, 1999, **38**, 907).

And yet, the future is not altogether bleak. Several leaders of the chemical industry are fully aware of the urgent need to take remedial action, including change of reagents, solvents and even of the whole process if alternatives are available. There has also been some significant progress in replacing traditional polluting technologies with new non-polluting ones in the Indian industry. One such example is the replacement of hydrogen fluoride by a zeolite in the synthesis of linear alkyl benzenes. However, such instances are too few; the whole movement will gain momentum only if the academicians and science establishments undergo a change of attitude.

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The multitude of 'omics' and 'omes': Evolution of scientific terms in molecular biology in the new millennium

The era of large-scale molecular biology has started. Information generated by the application of automation in molecular biology has been extensive and intensive. The complete sequences of 22 genomes[1] are now available; many others are close to being completed.

The term genomics meant to cover all facets of genetic studies and even a new journal called *Genomics*[2] was initiated recently. In close succession, a term called 'functional genomics' emerged (see for example Rastan and Beeley[3]). Next came the term transcriptome[4] that denotes the messenger RNA transcripts from a genome. The proteome is the expressed protein complement of a genome and proteomics is functional genomics *at* the protein level[5].

The excitement over embarking upon genome-scale investigations is in the log phase. The emerging metabolic genotypes and the accompanying proteomics has stimulated some authors to investigate the genotype–phenotype relationship using the methods of systems science leading to a new field called phenomics[6]. Similarly, the *cis* acting transcriptional regulators in genome can be termed catrome. These are functional sites (as shown by experiments[7,8]) and therefore the term catrome has similar basis as transcriptome and proteome that represent real molecules. Similarly, the *trans* acting factors in a cell may be called tafome. The terms for the analyses of the relationships between the *cis* acting sites and gene expression at the genome level may evolve as catromics. Similarly, the analyses of the relationships between *trans* acting factors and gene expression may evolve as tafomics.

Binomial terms are also evolving at a great speed. After several genomes have been completely sequenced, 'comparative genomics' has emerged. Similarly, 'structural genomics' although referred to earlier[9] in the context of gene identification through computational analysis, has emerged again at the protein level[10] now, and may grow to cover other topics as well. Comparative genomics and structural genomics and related work carried out *in silico* can be grouped as 'genome-informatics'. Genome-informatics which comprises analysis at the genome level, is an offshoot of bio-informatics.

Thus, at the beginning of this era, we are exposed to a shower of several new terms. This development is very attractive but also young. Some terms represent relatively straightforward issues but others are somewhat less clearly defined. The term genomics meant to cover all facets of genetic studies but most of the papers published by the journal *Genomics* focus on gene mapping.

Generally, after a genome is sequenced, most of the encoded proteins are predicted computationally either using the first generation set of programs such as BLAST and FASTA, or the second generation set of programs such as GeneMark[11], GeneScan[12,13] and TB-parse[14]. The expression status of these protein products may be known after a detailed analysis of the different proteomes through the analyses of 2D gels, advanced imaging software and staining techniques[15]. Present work on proteomes indicates that the term represents expressed molecules. It is ambiguous whether many of the computationally predicted proteins, whose expression status in a given organism is not known, can be included in the proteome.

Similarly, comparative genomics could be interpreted to address the issues related to the analysis of information in the genetic material. These include synteny (order of genes on the chromosomes of different species), absence or presence of genes[16], strand compositional asymmetry[17], comparative hybridizations by whole-genome DNA microarray[18] and so on. A recently published work, however, deals with proteins[19], and so it can be debated whether 'comparative proteomics' could have been used instead of comparative genomics.

Our perception of functional genomics is graphically displayed in Figure 1. Although computational comparative genomics was referred to as functional genomics by pharmaceutical companies, a bioinformaticist from the National Centre for Biotechnology and Information has re-described the term[9] in line with the scheme in Figure 1. Functional genomics integrates the information and emerging concepts from genome-informatics, experimental comparative

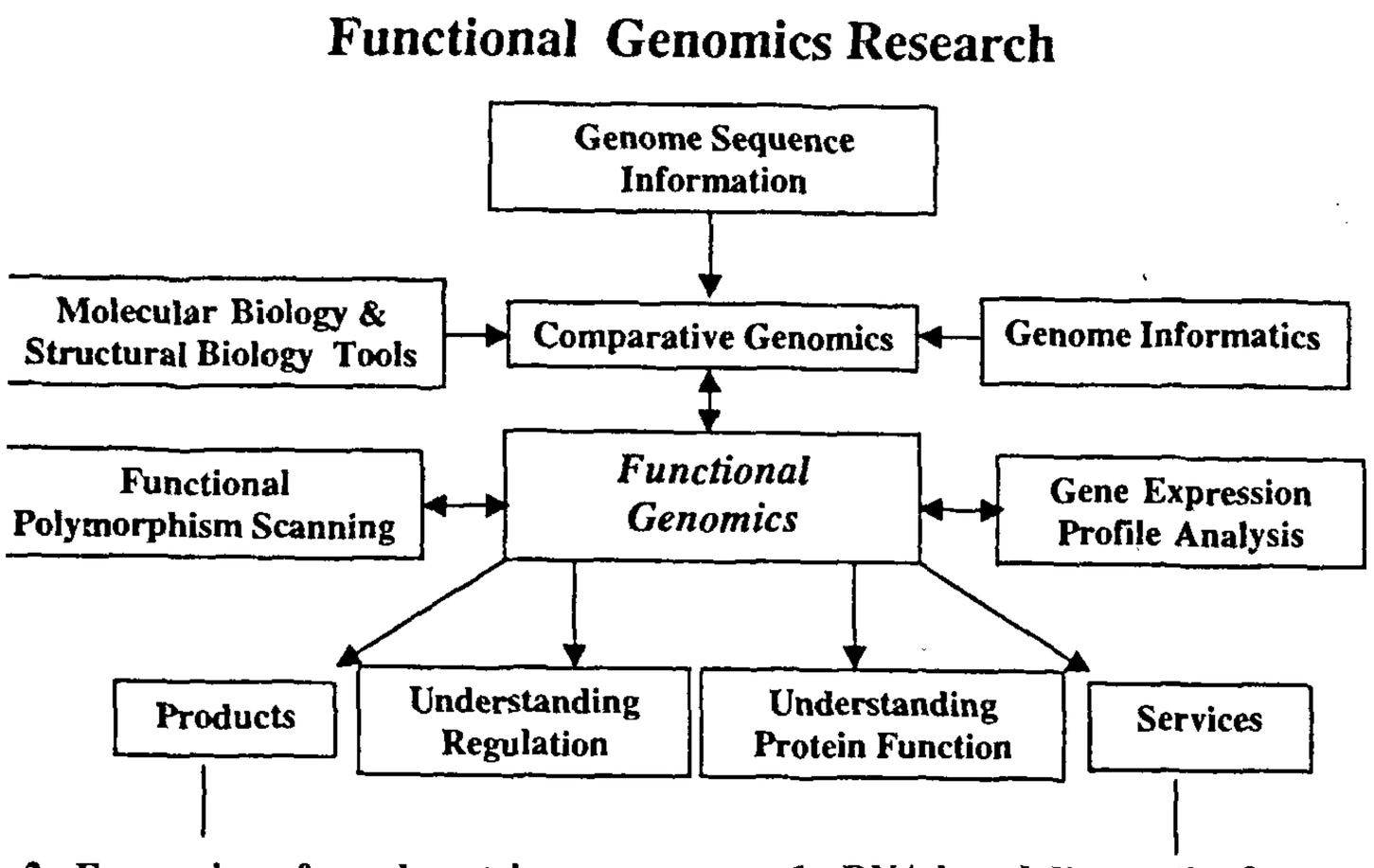
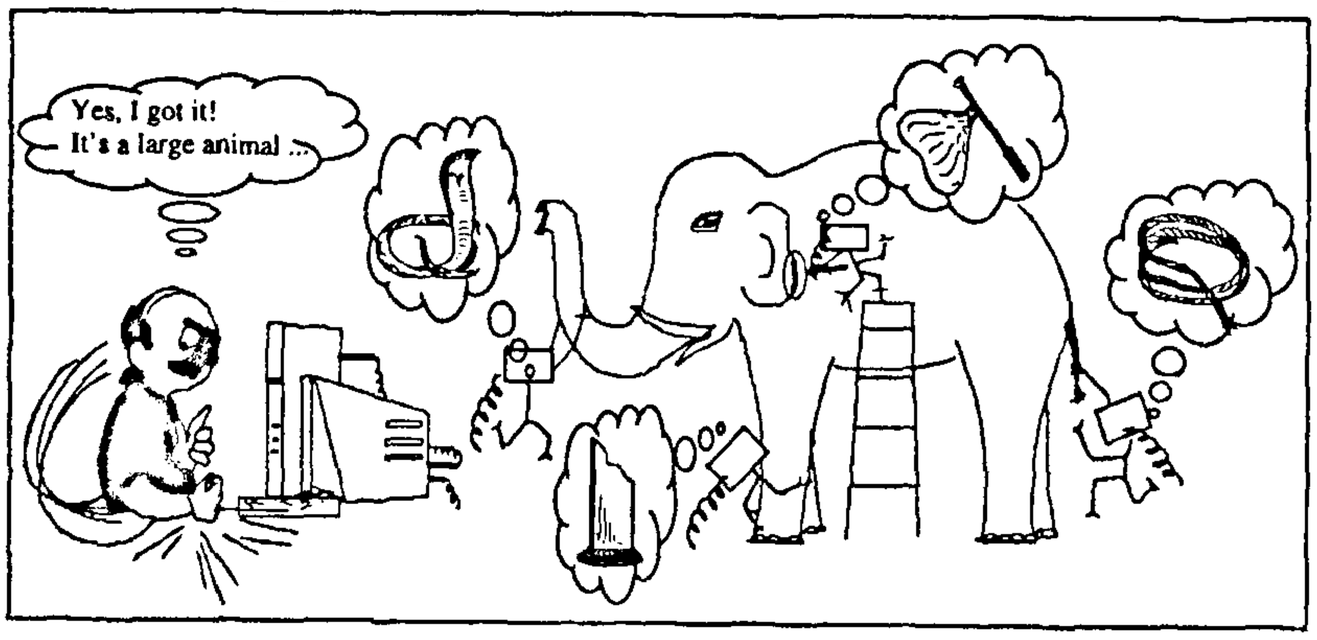


Figure 1. Graphical representation of the concept of functional genomics.

Functional genomics: A holistic view



enomics, gene expression profiles ncluding interactions between them) id functional polymorphism scanning. unctional polymorphism scanning rep- sents the determination of sequence ariations (mutations) in both regulatory id coding region of genes and its atistical correlation with functional henotypes. Thus, functional genomics ill lead to a better understanding of the iology of the system and the origin of ew technologies. Indeed, a functional enomics institute has been initiated[20]. Perhaps, it is a matter of time before these terms get shaped and polished further through extensive research to represent more clearly the exact issues of the respective studies.

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