TOOLS, TECHNIQUES & ADVANCEMENTS IN OMICS TECHNOLOGY

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ABSTRACT:
Big data from different sources are the base of medicinal, clinical research & development in current scenario one of the technologies which used is omics technology including genomics, proteomics, metabolomics, transcriptomics, lipidomics & microbolomics etc. All these techniques now become one of the fastest growing tools & technique. The acceleration of covid- 19 research in area of omics is upgraded & changed due to the technologies & its advancements. In bio-manufacturing new drug research can be elicited by using omics technology. Moreover the new lead discovery are also undergoing through the omics. Bioinformatics tools are also useful in development of clinical trials. As we are currently faces one of the biggest pandemic of the century. This covid-19 revealed that how quickly the information can be formed & analyzed by using omics approaches but also have some limitations. Omics study provides a platform of using big data with precision. There were more than 600 structures of proteins of SARs CoV-2 virus can be available in protein data bank(PDB) with various confirmations & binding with different ligands one of the technologies that is known as proteomics is useful in study & development of covid vaccine as a result many of the countries in the world can strongly fight against pandemic. However transcriptomics technology initiates the study of various cancer cells also known as cancernomics one of the resent trends in transcriptomics based cancer studies of breast. In this present review it was target that to provide a brief information regarding system biology, advantages disadvantages, tool techniques & information of omics technology.

Key words: - *Omics, Etiopathogensis, Transfections, Toxicogenomics, Transcriptomics.*

INTRODUCTION

In last few years we see that there is a huge change in bio-medical science and medical technology like how the human genome can be involved in drug discovery & development. The human genome sequence has showed that differences in sequence are ubiquitous. Earlier genetics have the large amount of genetic variants with human disease and adverse reaction due to vulnerability of drug or toxic substances which suggested that genome perform a major role in sensitivity of drug & other environmental agents, diseases vulnerability & therapeutics activity. When these facilities are changes into real things the regulatory toxicology practices is probably developed subsequently by conjunction of typical pathology, toxicology, molecular genetics, biochemistry, cytology & computational bioinformatics shows a great result to monitor functional disturbance of the molecule.[1]

The whole human genome has been sequenced & a growing amount of biological data is not accessible in many sources enabling a detailed analysis of all biological domains. The development of medical technologies like the microarray, liquid handler, lab on chip & fluorimeter that can assimilate & imbrute the analysis of biological molecule & their interactions as well as development of bioinformatics approaches to find out huge amount of information generated by high throughput analysis has led to the joining of biological engineering & bioinformatics in vitrous synergy. [2]

Omics is a new technology that allows as to continuous observation of centuries or thousands of large & micro fragments assured permitting effective observations of multiples of key cellular pathways continuously. Omics is one of the current techniques of determining brood of cellular fragments such as DNA, RNA, proteins & its metabolites. These omics have ability to identify all or most members of family of molecule by one analysis by this new tool we can find out evaluation of functional activities by biochemical pathway & structural genetics difference between different individual and species. Omics is one of the exciting words in life science & medical technology. Omics is used to define something huge & referred in the area of study of medical technology & life sciences. It is mainly focused on very large scale data or type of information to understand the living things or life. All the study related lives are summed up in omics.

To put it another way, the omics are derived from the "Om" (pronounced "Aum"), an ancient Sanskrit holy spiritual symbol in Indian religion, which is like a musical eclipse and a barrier of age, race, culture, and species. The Sanskrit letters aa, au, and ma were combined to create the term "Om," which alludes to the completeness of Atman (one's self) and Brahman (Supreme spirit). Om is a mantra that, if shouted regularly with real inflection, may resonate throughout the entire body and serve as the focal point of the ones who have the atman and soul. It has been said that the fundamental sound of the world comprises all other sounds. This is a straightforward yet profoundly philosophical sound: harmony, serenity, and blessings. The scientist who studies the omics is called Omicist. Omics are categorized into various subfields like genomics, proteomics, metabolomics, metallomics, interactomics, lipidomics, transcriptomics, spliceomics, neuromics, physiomics, predictomics etc.[3-4] The steps for data analysis in omics technology is shown in figure 1.

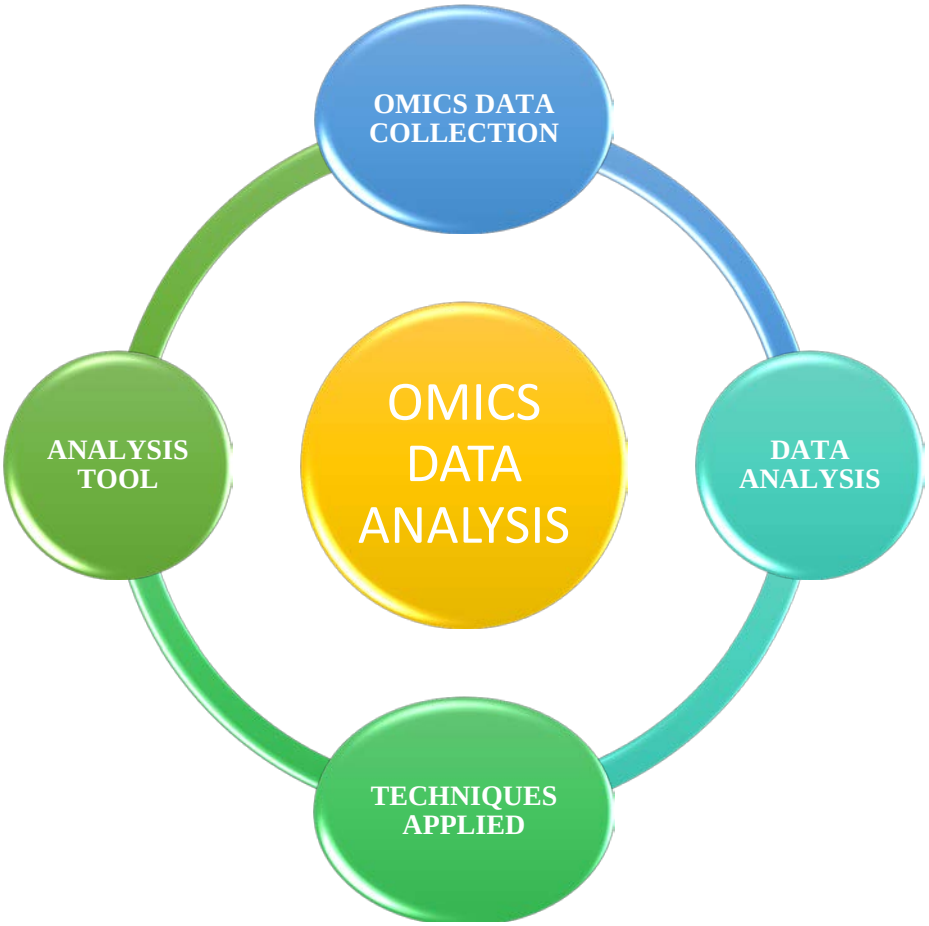

Figure 1. Process of analysis in omics based technology

History of omics: As per the definition of omics it occur from an ancient Sanskrit word Om with the origin of universe but the use of word omics as technology mainly as suffix omw which meant for any object like genome, proteome or metabolome etc. In year 1920 Hans Winkle (1877-1945) was a German botanist who joined the two words gene & chromosomes to define the body of gene which is called as genome so the genome and genomic are the parent of all the omics technologies.[5]

Statistics in omics technology

Omics technology is broadly classified into five types for its applications in various fields of statistics. The diagrammatic representation is shown in figure 2.

1. Exploratory Method
2. Clustering Method
3. Network Learning Method
4. Regression Based Method
5. Biological Knowledge Enriched Learning

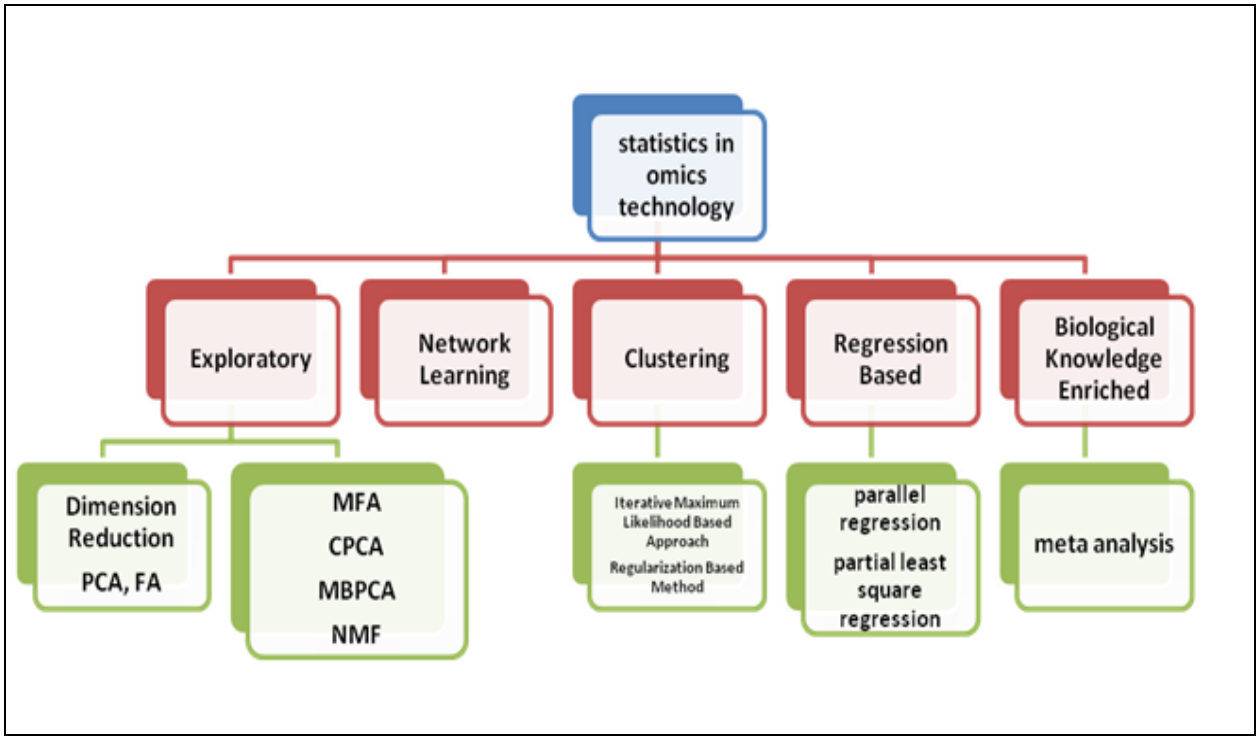

Figure 2. Types of omics technology in statistics

1. **Exploratory Method**

Dimension Reduction: - Dimension reduction method is one of the most important multivariate analytical techniques. Which can be used to identify existing structure which is not seen but presented in observation that are the result of the observable structures. Existing structure is described as having a minimum amount of proportions or components compared to the total number of variables in the statics group.
Primary Component Analysis (PCA) & Factor Analysis are two basic statical approaches for dimension reduction .In various literatures of combinatorial omics dimensions reduction method have various kinds of alternative from principal component analysis & factor analysis.[6] These are -

- Multiple Factor Analysis (MFA)[7]
- Consensus Principal Component Analysis (CPCA)
- Multiple Blocks Principal Component Analysis (MBPCA)[8]
- Non-negative Matrix Factorization (NMF).[9]

Hassani and his collaborators presented consensus main component analysis in 2010 as a "Blocks" technique for various omics data sets with three validation tools. In this CPCA approach, numerous blocks are gathered from the same biological samples using genetic fingerprinting data to show one sort of omics measurement. Consensus PCA is used to extract the bilinear structure from the combined measurement data using the nonlinear iterative partial least squares (NIPALS) technique. NIPALS can determine several block parameters from the

latent structure, such as the global loading score, block score, and global score. There are three ways to choose components: stability plot, uncertainty t test, and root mean square error.[10-11]
Factor Analysis & Its Variations: Unlike PCA, this places the examination in the contemporary quiet structuralized space. The latent structure that may explain the given data is found through factor analysis. By Sanchez and colleagues, multiple factor analysis may be used to reduce proportion and bring more data about the original omics data set together in a single location. Multifunctional analysis begins with a PCA on each data block, then uses a global PCA to jointly analyse the single value normalised data.
Non-negative Matrix Factorization (NMF): As likewise of dimension reduction analysis conventional non-negative matrix factorization method spoils the data model using a dormant factor model W & basic component data modal. NMF is more analyzable for non-negative omics measurement like micro RNA (miRNA) & gene expression because it is similar like PCA.[12]

2. **Clustering Method**

Clustering method is one of the commonly used approaches in unified omics technology for subject & features partitioning. Exploratory views of underlying cluster pattern are analyzed by using this tool. The diverse omics technologies have composite data topology. For the purpose of identifying the sub-divisible structure of unified information, a fresh innovative idea and action plan are required. In addition to the more traditional clustering perspective employing different interspaces measurements. Self organizing maps (SOM), a modified version of the clustering approach created by Newman & Cooper, are utilized in geography cartography. [13-14]

Iterative Maximum Likelihood Based Approach: - Newman and Cooper introduced an unsupervised clustering strategy based on self organizing map (SOM), a speculative clustering method, to reduce the percentage and preserve the local topology of gene expression. SOM determines the dissimilarity surface by first determining the similarities of nearby nodes (error matrix). The borders of cluster & group similar data are identified by using error matrix. The AutoSOME method is used for density homogenization which is technique for cartography SOM is also used in transcriptomics sample of 3 different data set myelodysplastics syndrome, Alzheimer & colorectal cancer to categorized patient from diverse disease stages.

Regularization Based Method:-One of the common techniques in statical analysis to control difficulties & achieve precision is regularization or penalty constraints. When true consortiums between molecular characteristics are known to be condensed than all feasible consortium, or when the amount of observation or observed data should be significantly beyond the number of attributes, this approach is applied. To determine the number of clusters and the integration of clusters for integrated genetic or genomic data like copy number variation (CNV) and DNA methylation, Shen and his colleagues proposed a penalty-based clustering approach (i-cluster).

3. **Network Learning Method**

Network composing fork & arch provides an advanced tool for demonstration & interaction between large numbers of constants in unified omics. In theories of network learning the variables are introduced & fork informal relation or association are introduced as arch or edge between forks. The network learning method for informal & conditional dependent network can

be used for investigation of multilayer association & causal relation omics features in unified omics technique. Determining Consortium Inside Metabolite & COPE with Lying Sample: Kayano et al. described ranking-based MF-PCcor to ascertain the consortium inside the metabolite & COPE with lying sample. [15]

4. **Regression Based Methods**

The Regression equation are set for illustrate inter & intra system relation & interaction in unified omics. Parallel & sequential regression strategies occasionally used with constraints parallel regression is chosen to model informal relation in conjunction with numerous molecular responses (i.e. metabolites & genes) on persistent or categorical scale & their interconnecting effect as well as factor of interest i.e. pathway membership inter-response relation in the explanatory factor for this reason multivariate response technique is not suitable. E.g. same pathway involves in active pathway membership of gene affected metabolites.

Parallel Regression: -The parallel regression approach is used to describe intersystem response concurrently in various omics responses. The model is one example of integrating transcriptomics & metabolomics data to generate an illuminating route level resolution, according to Jauhiainen et al. Jauhiainen can suggest two linear models to represent how a gene's and a metabolite's presence affect a pathway's membership. The model was chosen at two levels, first at the global pathway level to identify the active route and then at the level of distantly expressed genes that may demonstrate their influence on metabolite expression. Poisson et al. provide two combined tests for gene expression and metabolite information using two parallel logistic regressions in (A). This approach fills up separate logistic regressions with information about gene expression and metabolite levels. Both of these probabilities predict that the added gene or metabolite set will exist. In the first test, the obtained regression coefficient is subjected to a two-degree-of-freedom Wald test. Using sum of square statistics for genes and metabolites, the second test is an enrichment test.

Partial Least Square: -It is a technique that is frequently used in unified omics studies. By enhancing the covariance between the variables, this multivariate approach may be utilised to detect the latent structure of both predictors and reactions. Since Wold first developed the NIPALS method for PCA and PLS in chemo metrics in the 1980s, NIPALS has grown to be one of the most widely used computer algorithms for partial least squares (PLS). For unified omics, Le Cao et al. developed a sparse PLS (SPLS) that employs lasso penalization. Using a penalty term of loading vector of responses matrix Y and predictor matrix X, Sparse PLS corrects square error terms.

5. **Biological Knowledge Enriched Learning: -**
Enriching learning for biological knowledge is described as using response variables in device-based instruction. In statistical learning, prior knowledge may be utilized to either determine the Bayesian prior or to guide the model choice.

Meta Analysis: - Condensed statistic level data integration is accomplished using this technique. Also, it is utilized to combine information from disparate research on the level of discrete

observation, known as a diversified method. Meta analysis is utilized to provide knowledge to clarify the analysis of fresh research in the final application.[16]

Table 1 - Merits & demerits of omics technology

S.N.	TYPES OMICS TECHNOLOGY	TOOL OMICS TECHNOLOGY	MERITS	DEMERITS
1.	**Genomics**	**(RFLP, ASO, AFLP PCR, RAPD, DNA microarrays etc.)**	❖ Reorganization of SNPs gives beneficial particulars for initial diagnosis, prevention and treatment of ordinary diseases. ❖ Examination of gene polymorphisms, principally on metabolizing enzymes, distinctly indicates the independent susceptibility to some drugs and different responses in between different individuals. For example:- Affymetrix SNP GeneChip and IIIumina Golden Gate Bead Chips assays: - best technique for high number of SNP and a small sample size in genome broad study group. TaqMan assay: - best method for a small number of SNP and a huge sample size.	❖ It is very strenuous to anticipate the final biological effect of DNA by at most genome analysis because of post-transcriptional and post-translational changes and epigenetic NGS, PCR, RFLP-PCR approach for progression of DNA fragments; although data should be confirmed with Sanger Sequence tool
2.	**Transcriptomics**	**Sequence –based, Taq base- methods (SAGE; CAGE, MPSS etc.)**	❖ High throughput and give accuarte “digital” gene expression level	❖ Proportionally moderate throughput, not economical and subjective. ❖ Costly and separation of isoforms is tough

		RNA-seq, Whole Transcriptome Shotgun Sequencing; WTS	❖ Gives modern transcriptomic perspective. ❖ Perfection on transcription level. ❖ High throughput	throughout the analysis.
		EST	❖ Forecast of complete mRNA abundance. ❖ Convenient for gene discovery.	
		SAGE	❖ More systematic than large-scale EST sequencing. ❖ Complete forecast of transcript abundance.	❖ Tough to plan tags to genes. ❖ For distinct conditions such as tissue, gender, it should be replicated.
3.	**Proteomics and Metabolomics**	**(MS-based Proteomics, MS, NMR, LC-MS, GCMS, EC, HPLC, TOF etc.)**		❖ Costly, justly insensitive to moderate copy proteins not use for whole proteome. ❖ Precipitation at isoelectric point (pI) ❖ Individual outcomes because of post-translational changes.
		Gel based proteomics 2DGE	❖ Allows the investigation of proteins with low abundance in multiplex samples.	
		Gel free proteomics 2D-DIGE	❖ Gives the quantitative relative investigation using a single gel. ❖ Eliminate post-electrophoretic processing steps such as attachment and	

			withdrowing. ❖ Elevation of reliability by directly differentiation of samples under alike electrophoretic situations.	
		Metabolomics technologies	❖ Metabolomics has extra advantages as compared to genomics and proteomics. Innermost metabolites are less than genes, transcripts and proteins, so fewer data is accessible for interpretation. ❖ Determination of biomarkers of diseases such as cancer.	
		TOF	❖ Highly responsive, no upper mass limit.	❖ Low mass resolution.
		MS, NMR spectroscopy	❖ Satisfactory responsiveness (femtomolar to attomolar)	
		MS-based Proteomics		❖ A bit of details about protein because the peptides might not have all come from a single protein species.
		LC-MS,GC-MS, CE	❖ High-throughput (examination more than hundreds of seprate species within a single sample).	❖ The MS signal potency is overwhelmed by sample preparation technique used and its molecular surroundings, for that reason analysis

		MS	❖ Putting familiar quantity of internal isotope-labeled standards gives rightness for particular molecules. ❖ Although coupling MS with LC or GC, good responsiveness and selectivity.	problem arise. ❖ It utilized the internal isotope-labeled standards which is not empirical for purely discovery-driven metabolomics research. ❖ Microarrays gives for the plenty of quantification for a limited set of target transcripts, however typical MS analysis does not

There are numerous advantages & disadvantages in omics & its technologies therefore to control provocations appears from various omics. To improve the efficacy of technique one or two omics are jointly performed one of the important point is to select a method which remove the disadvantages of another method additionally data unification & explication should be meticulously.[17] The advantages and disadvantages of respective omics technology is listed in table 1.

Application of omics in pharmaceutical research

Role of omics in Drug development & Pharmaceutical Research: -

The analysis of omics data occasionally yields outcomes that are both falsely positive and falsely negative. There are still restrictions on the use of omics since certain crucial molecular characteristics cannot be seen in the face of such massive and complicated data sets owing to inadequate sensitivity or subpar processing techniques. Although while omics research sometimes goes unnoticed, interest in it is expanding on a global scale. Currently, building large-scale omics datasets has become commonplace, ushering in a new omics age for drug development. Genomic, transcriptomic, proteomic, metabolomic, and even a mix of several omics technologies are being used in drug research. Omics technology may be employed as a potent systematization tool in all areas of pharmaceutical science and research associated with drug development, including target identification, safety evaluation, assurance, understanding mechanisms research, customized medicine, etc. One of the most crucial areas of omics research is systems biology and network biology. It shows the primary pathways and potential processes of drug therapy and drug research and aids in properly comprehending the etiology of illnesses. Moreover, omics research can identify prospective targets for the creation of novel drugs, facilitating the development of customized medicine and a methodical safety evaluation. Omics

are now acknowledged as a potent method for drug discovery, with applications primarily in target discovery, personalized medicine, toxicology, and traditional Chinese medicine.

Target Discovery: - Target discovery: - Target discovery plays a very important role in drug development. Previously, drug development mainly relied on only 500 known drug targets, and there were no longer any sources of drug target information. Human genomics studies provide insight that humans have 30,000-40,000 genes and many more proteins that are potential targets for drugs for human diseases. Therefore, studies have shown that at least 90% of the isolated proteins are still unknown to researchers. To discover & validate new drug target is first footstep in new drug development & it also have great importance for explanation of mechanism of etiopathogensis & the effects of drugs. Previously the drug development was based on single target which have low efficacy. Now in modern day's omics & other system biology technologies & tools are broadly applied and give new imagination for new drug development & target identification of. Several omics-based approaches, including microbial genomics, differential proteomics, gene transfection, and gene knockout models, are now used for target finding. These high throughput approaches generate a significant quantity of data, leading to the establishment of several databases, including TTD (Therapeutic Target Database), OMIM (Online Mendelian Inheritance in Men), and Cancer Gene Census. The effectiveness of target identification will be improved through omics research and associated databases. [18]

Internet database for target discovery: -Genome databases provide the foundation for finding therapeutic targets. During the late 1990s, novel genes like cathepsin K and orexin receptors have been discovered using the expressed sequence tag (EST) databases. Many more related databases have been confirmed, and the human genome project (HGP) and subsequent genomic research have produced enormous amounts of information on genes and expressed sequence data. Some of these databases store information associated with disease-related genes and may be used for target discovery. NOMIM (Online Mendelian Inheritance In Men, http://www.ncbi.nlm.nih.gov/omim) and GEO (Gene Expression Omnbus), two key databases with a lot of cancer-related microarray data, both provide information on human disease-related genes. Prospective Drug Target Databases (PDTD) are dual-purpose databases that link structured databases of known potential drug targets with informatics databases. PDTD is a large database of drug targets that is accessible online and concentrates on those targets that have known 3D structures. The Protein Data Bank's 1207 entries in the PDTD encompass 841 known potential pharmacological targets (PDB).[19-20]

Omics based target drug discovery: - Genomics & transcriptomics have supplied the earliest application for target discovery. Microarray analysis can concurrently screen & identify drug & disease related gene by differentiating chip data between disease group & control group which perhaps used to forecast relevant bio-markers or potential drug targets but it requires a complex procedure of data processing & to a great extent of validation activities & it throw back the level of m-RNA expression which may not be accordant with protein expression & function. This may be restrictions for extensive application of microarray in field of drug target discovery & validation. However there are various successful examples especially in drug target study of Alzheimer's disease. Proteomics can also simply determine disease related protein by comparative analysis of the proteome from normal & diseased cells & these proteins may be

have capable target for drug development.[21-23] The step of conventional drug discovery process is shown in figure 3.

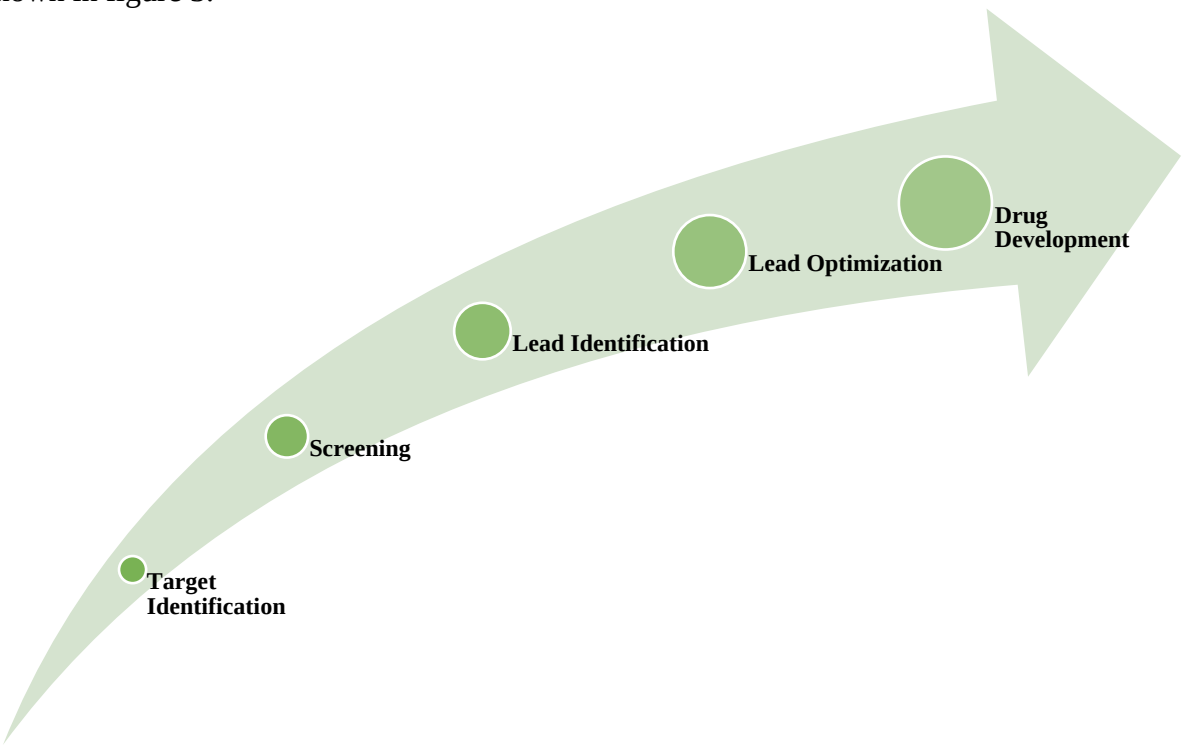

Figure 3. Steps of Conventional Discovery

Toxicity: - Application of drug toxicity plays very important role in new drug development & Pharmaceutical research. In fact drug development process should be stopped due to drug toxicity. Study of drug toxicology can advice as for clinical medication which helps to reduce the adverse drug reaction. From last two decades there are various types of omics technologies has been developed & applied in toxicology to ensure the development of kind of research in the area of toxicology.

Toxicogenomics: - The word toxicogenomics is came from the two words toxic+ genomics it mean using the applications of genomics in the area of toxicology. The study of toxicogenomics is used to illuminate the correlation between toxicity & change in gene expression & further to pick out probable genetic toxicants & to know their mechanism of action. In toxicogenomics microarray is usually used as per the studies we know that toxic reactions occur due to changes in gene expression. In the comparison with older toxicity studies toxicogenomics gives as more potent stage for drug safety analysis.[24-25]

Toxicoproteomics: - Toxicoproteomics is used to determine complex protein & pathway in any biological system that can be influenced by & produce responses to adverse chemical & environment exposure using global protein expression technologies. In simple word toxicogenomics is a part of genomics that deal with study of proteins that are responsible to produce toxicity. Now toxicoproteomics is used to understand toxicant reduced protein expression & post translational modification & interaction between two different proteins.[26]

Toxicometabolomics: - In toxicology the use of metabolome is known as toxicometabolomics. It is one of the fastest growing technique mainly in advance mass spectroscopy. Toxicometabolomics is mainly used in life science for phenotyping diseases condition. Toxicometabolomics generally find out the biomarkers which are related to toxicity can be analyzed. There is an uncertain change in the amount of endogenous metabolites of biological fluid which can relate with the toxicity related markers. Genomics, transcriptomics & proteomics are directly & indirectly involves disclosure of effects of toxic substances however they may show the possibilities of toxicity but in metabolomics study metabolites directly indicates certain biological reactions which are already happened in biological system because metabolites are the end products of all biological processes. As per the studies we can say that metabolomics gives more definitive scientific bases for toxicity studies. [27-28]

Personalized medicine: - The temperament of a drug to the organism can be affected by the various factors like genetics, environmental & lifestyle of the person which shows difference of responses of the drug to different individuals however the physician & clinicians can use same drug & same dose to the patients which may produce serious side effects. Almost in all countries whole over the world prescriptions of the drug is based on local ethnic group which may be not suitable for population of other countries which causes poor efficacy & various serious adverse reactions for that reason there is a requirement for enlarging research area in personalized medicine. Personalized medicine is one of the most crucial challenges in health care system in 21^{th} century. [29-30]

Types of omics technology

Omics as advanced technique is classified into five types (shown in figure 4) namely Genomics, Proteomics, Transcriptomics, Metabolomics and Lipidomics depending upon their applications. Each type is further discussed below.

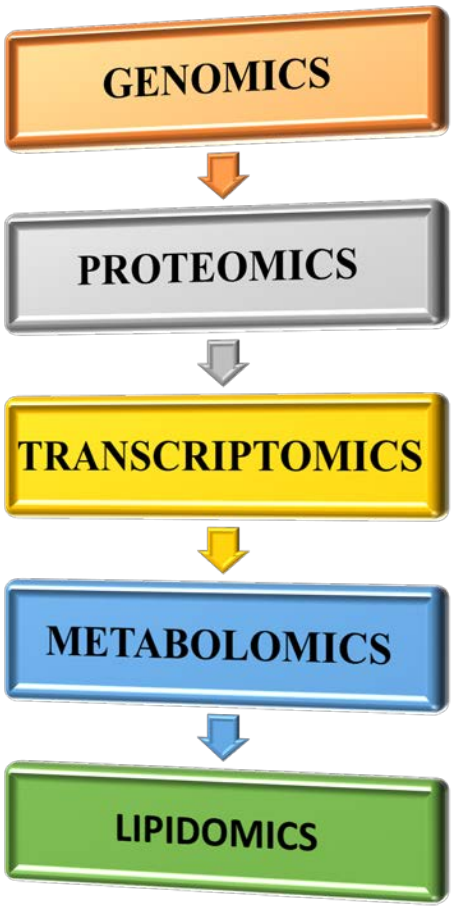

Figure 4. Different types of omics technology

GENOMIICS: - The term genomic comes from the term genome in biology, which is all of an organism's innate information, encoded in DNA (or RNA in some viruses). It contains genes and non-coding DNA sequences. More specifically, the genome of an organism is the complete DNA sequence of a set of chromosomes. Genomics is one of the most advanced omics technologies because the properties of nucleic acids are considered by the sequence of nucleotides that compose them, rather than by highly variable chemical and physical properties, which simplifies the development of analytical techniques. Almost all nucleic acid analysis techniques are based on A-T and G-C base pairing, which allows for the formation of double strands with complementary sequences, one of which may be a probe generated for analysis with l other strand of the sample being analyzed. Nucleic acid-based omics are used to analyze DNA and RNA, genotypes and their expression in different types of protein-coding mRNAs or regulatory non-coding RNAs (ncRNAs). [30]

Sub classes of genomics technology includes:-

Metagenomics: - Metagenomics enriched techniques is an appealing option which helps to get impartial clearity of grouped structure of microbial genome within the place. Marine

metabolomics study based on DNA based shotgun sequencing technologies using random sharing of DNA.

Nutri-genomics: - Nutri-genomics is science that is applicable for studying of high throughput genomics tools in field of nutritional technology. Now in this era due to development there is changes in ways of living, dietary patterns people becomes better liable to diseases gradually. The nutri-genomics technology plays very important role to open out nutrition on gene expression by using multidisciplinary approaches like bioinformatics, molecular biology nutritional genomics. We know that the nutritional value of the food is obtained after the enzymatic reactions the food obtained from the marine sources are very high nutritional values that's why in marine genomics & other food industries there is a vital role of nutri-genomics studies.

Sponge genomics: - With the origin of life in earth there is an existence of sponges it is a primordial form of life. The development of sponges started 600 million year ago which have distinct genomics that can make a revolution for evolution of composition of animal genomes. A synergistic relationship between various multi-cellular form of organism setup by sponges which may be a model for evolution & ecological basis of animal-microbial synergy. Sponge genomics is also applicable for large scale production of metabolites for new drug investigation because in contrast of other marine life form sponges are more productive in bioactive metabolites (like alkaloid, terpenoids, peptides etc.) [31]

Pharmacogenomics: - The pharmacogenomics is one of the considerable techniques in the fields of cancers studies. By these we are using computational biology tools as a propensity of ubiquity were illuminate in different contest. With the development of epigenetic research has used pharmacogenomics tool for determination of biomarkers of cancers. Epigenetic markers data. bases provide as information of molecular mechanism of disease in early stages or which are unknown[32]

Proteomics

In biological system proteins are responsible for regulation of responses & to maintain the metabolic activities needed for survival of life. Anciently molecular biologist generally examines biological mechanism by understanding the role of single protein or interconnection between two different molecules in place of all the proteins in cell. These reductionist approach used by biologist are very successful but it can't gives the information which are needed to be recognized how the cellular system works as unit & in which organ of the cellular system interactions are taking place within thousands of different component. Data from genomic revolt are being arranged & make it approachable in variety of database & libraries. These databases have ability to describe & for recognition of genes, RNAs & proteins revealed by a tissue or additionally their structure, function & macromolecular interactions but all of these computation done in static manner. As per the studies oppositely many biological processes are dynamic responses of external factors(like drugs, diseases & environment) so to determine the quantity of changes included by external factors accurately is one of the most important part of studies of dynamics biological processes. Proteomics determine all ranges of protein in any part of organism (known as proteome) at a particular time mainly by using mass spectroscopy. These techniques allow as to analyzing post-transcriptional changes & interaction between proteins. Proteomics is now a

very important tool which involves in rapidly acting drug discovery process, sensitive processes & to define the changes in protein expression & alteration of protein in high throughput technique. Previously the proteins are investigated by targeting approaches such as antibodies, immune-blotting, microscopy & fluorescence activated cell sorting. Now the proteomics is based on latest generation of mass spectroscopy technique which gives accuracy, precision & speed. Advancement of chromatography of mass spectroscopy makes the process rapid & deep proteomic profiling. [33-34]

Transcriptomics

Transcritomics technology deals with protein & gene expression it is mainly applicable to describe the changes on protein levels & activities. The transcriptome is a complete set of transcripts including mRNA in a cell & amount of transcripts. The possibilities of making relation between genotype & an expression phenotype are done because mRNA matches with particular gene of genome. RNA summarization gives indication to physiological difference between tissues & cell type and interaction between genes, expressed sequence & gene of genome, gene regulation and regulatory sequence & recognition of candidate gene for any disease condition. Majorly DNA microarray technology is used for the study of transcriptomics or expression profiling which scrutinized mRNA expression level. There are various methods available in transcriptomics technology like gene expression array(evaluation of transcripts in plenty, single/multiple 3' probe), genome tiling array(to find out transcribed sequence, multiple probe along with genome), alternative splicing array(determination of various RNA iso-forms & probe in axon & axon-axon junction), RNA tag sequencing(determination of transcript abundance & single end of each RNA species) & whole RNA sequencing(identification of transcribed sequences & multiple read along with each RNA species. Transcriptomics has much benefit it is used to investigate gene expression responses to xenobiotics exposure & drug therapy & the analysis of functional relationship between modulated genes. Various new technologies have been development for transcriptomes analysis including hybridization. Transcriptomics have been applied in various fields like in pharmaceutical industry, diagnosis & therapeutics, gene therapy application, pharmacogenomics & disease prevention for development of biology. [35-37]

Metabolomics

Metabolomics is the branch of science where we can study of metabolites which are formed in an organism & it is act as reflection of enzymatic activities & network encrypted in genome. The metabolomics studies are still in their beginning stage because of less numbers of references databases & sample preparation is very tedious process. One of the advantages of metabolomics is that it can guide us for the development of hypothesis due to the finding of unexpected relationships & metabolite responses to know more about different organisms interactions between organisms & niches for understanding formation of primary metabolites, secondary metabolites, genetic expressions & cellular anatomy this provide guarantees of welfare and survival of life's.[40] As per the biochemical studies on metabolism. Metabolomis allows as for the determination of molecular processes involved in the regulation of different types of biological activities in a biological system. Previously the metabolic studies mainly deal with single or specific classes of metabolites, macromolecule or metabolic pathway that were understandable separately. These metabolomics types of studies gives some limit in generalization of result to reorganization of actual physiology of the biological system in an

organism. One of the most important analytical techniques which are used under metabolomics studies is spectrometric techniques like (IR, NIR, UV, NMR & Mass spectroscopy). All of these spectroscopy techniques generally needed complex sample manipulations & long analysis time & have only low sensitivity so that not all the metabolites can be quantified. Metabolites are the end products of complex biochemical pathways that can be linked with genomes, proteomes & transcriptome which give important key tools for detection of genetic bases of metabolic changes. Metabolomic can be applicable for determination of relative & absolute amount of sugar, lipid, amino acids, organic acids, nucleotides, steroids, drugs & environmental constituents from the different sources of sample types like primary cell, cell-line, tissue, biological fluids, whole organism & diverse geo climatic environment. The main steps for metabolomic studies involves experimental design, suitable sample collection, quenching of metabolism, optimized metabolite extraction & reformation fro sample, optional sample derivatisation, data analysis including data alignment, filtering imputation, statistical analysis each of all these steps are highly changeable depending upon the platform we used for sample analysis under metabolomics. [39-41]

Lipidomics

Lipids are the one of the major constituents of organization structure of human body there are two types of lipids are present highly abundance structural or molecular lipid(e.g. phospholipids) & low abundance singling lipids(e.g. eicosanoids). Lipids have mainly primary role in our body in which if there is any changes in composition, biosynthesis or downstream metabolism influenced directly on worsening of disease severity. On other hands we can say that constitutions of lipid may changes as the results of disease processes which suggested that as biomarkers of condition to maintain the effect of drug or to understand the like hood of worsening. As we know that lipid is structural components of cell membrane & it acts as energy storage source & also involves in various types of important biological functions. Previous studies proved that critical disease occurs due to the lipid metabolism like Alzheimer disease, diabetes & some other infectious disease. The lipidomics is study of complete profile about the lipid within the cell, tissue & organism & it is a subset of metabolome. Lipidomics is large scale studies of pathways & networks of cellular lipid in biological system. Lipidomics technology is mainly based on multidimensional liquid chromatography/mass spectroscopy technique which having following steps; lipid extraction, lipid separation, lipid detection, lipid identification, quantification & data processing. Lipidomics mainly applies to understand key lipids & enzymes which can gives an idea about potential abnormal pathway or pathogenic mechanism, which helps effectively in diagnosis & treatment of disease condition. Now a day the studies of lipidomics have been increases as area of interest in diagnosis, drug target determination & to understand pharmacological mechanisms.[41]

CONCLUSION

Omics is a latest and advanced technology which allows estimation of micro and macro fragments assured to permit effective observations of multiples of key cellular pathways continuously. It is currently utilized in almost every field of allied science with special emphasis on robotics and genomics. The scientist who studies the omics is called Omicist. Omics as advanced technique is classified into five types namely Genomics, Proteomics, Transcriptomics,

Metabolomics and Lipidomics depending upon their applications. It is categorized into various subfields like genomics, proteomics, metabolomics, metallomics, interactomics, lipidomics, transcriptomics, spliceomics, neuromics, physiomics, predictomics etc. One of the most crucial areas of omics research is systems biology and network biology. It shows the primary pathways and potential processes of drug therapy and drug research and aids in properly comprehending the etiology of illnesses. Moreover, omics research can identify prospective targets for the creation of novel drugs, facilitating the development of customized medicine and a methodical safety evaluation. Omics are now acknowledged as a potent method for drug discovery, with applications primarily in target discovery, personalized medicine, toxicology, and traditional Chinese medicine. In future; this omics will occupy the market in field of research and health sector to attain maximum benefits with minimum cost.

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CONFLICT OF INTEREST

The authors declare that they have no competing interests.

ETHICS STATEMENT

N/A

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