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Chapter 16

Interdisciplinary approach to biomedical research: a panacea to efficient research output during the global pandemic

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Chapter outline

16.1 Introduction

Biomedical research is a field of general study that involves both life science and physical science. By researching life, illness, and causes of death, the clinical study tries to investigate physical, chemical, and functional knowledge of life. Biomedical research is growing rapidly as modern methods and the study of life science improve human body understanding. Pathogenic

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microbial studies, more understanding on the link among the biochemical processes of the human body, DNA-based research, and rapid improvements in biotechnology have enhanced progress in biomedical research. Biomedical science begins with finding the basics of life tracing in function challenges, finding the causes of illness, finding medicines for the particular illness, testing the medicine in model organisms, finding response and side effects, and finally diagnosing it in humans. Such experiments enable researchers to test their medications first on animals and then on humans. There are mainly two kinds of studies engaged in biomedical research such as fundamental and applied research that includes clinical studies. When basic research provides knowledge of life and disease mechanisms, applied study deals with drug findings and therapeutic discoveries where basic research information can be used.

Interdisciplinary research implies the joint effort of various researchers in a sector where there is no distinction between individual efforts. Convergence is a fresh word used by Sharp et al. [1] to combine distinct disciplines, devices, and technologies. This type of effort requires the participation of quite a large group of people such as physicians, researchers, scientists, laboratory technicians, engineers, computer professionals, etc. Different knowledge is used in each phase of the study to obtain a precise outcome. New illnesses including various cancers and medications with lethal side effects are significant issues nowadays. To recognize and solve these issues, there should be an interdisciplinary approach. An interdisciplinary team of 180 researchers from different nations investigated various methods to treat cancer with lesser side effects [2]. Global pandemic is the most serious threat we are facing nowadays. Coronavirus shook the entire economic, social, mental, and physical well-being of the human race all over the world. Decreased immunity in aged people causes higher risk in that category. The rapid rate of evolution of the viral genome and varied susceptibility of viruses within different human races caused drastic changes in the intensity of infection in different countries. Interdisciplinary management systems should be intensified globally to decrease the spread and eradicate the disease.

The Human Genome Project completed in 2013 was a wonderful interdisciplinary biomedical research initiative that brought together engineers and researchers from 20 study centers across six nations. The research resulted in groundbreaking research in the field of human genetic−related illnesses. Human genome sequenced information is now the basis for genetic disease research and contemporary techniques like gene editing by CRISPR (clustered regulatory interspaced short palindromic repeats). Sequencing of separate human DNA samples has revealed the genotypic modifications in people and thus the conclusions about distinct phenotypes were drawn. Fifteen million single-nucleotide polymorphisms, one million brief insertions and deletions, and 20000 structural variations are recognized through three major initiatives involving the sequencing of 179 people from four populations [3]. The enhanced DNA sequencing techniques and knowledge supplied the previously

unknown data about the cause of various genetic diseases. The same kind of approach is going on in finding the cause of varying intensities of COVID-19 on a genomic perspective in various races and communities throughout the world. Tracing of variations and associated risk factors in different strains of SARS-CoV-2 in various countries also needs an interdisciplinary approach. Regenerative medicine is one of the most sophisticated areas of medical science that makes excellent use of interdisciplinary fields using various techniques like stem cell technology. Stem cells are undifferentiated cells that can evolve into distinct kinds of cells. The stem cells can be modeled by novel techniques to generate a specific cell line that can replace a nonfunctional cell line in a person.

Biomedical research is going through several issues particularly that arises from the increased attention on expertise in individual sector. The problem is evidently obvious in the field of medical practice where there is no greater appreciation for general medicinal practices today. As a result, the doctors visualize the human body as a group of specialized organs, not as a structure. The smooth functioning of the human body system can be damaged by inappropriate medication for a specific issue. In a research conducted in the United States, the use of four distinct drugs for type-II diabetes has found to have boosted the incident fall in aged patients with adult diabetes [4].

16.2 Interdisciplinary biomedical research and COVID-19

In the field of biomedical research, the interdisciplinary strategy is not completely a new concept. Youmans recognized the significance of cooperation in the field of medical education and patient care in 1953 [5]. The constriction of information in a specific sector can decrease the scientist's thinking process in a manner that can negatively affect the outcome. As basic knowledge on various subjects acquired in public education is used by common man in everyday life, researchers should also attempt to correlate topics with different recognized related areas and methods in a manner that produces maximum outcome. Biomedical research requires more cooperation especially in emergencies like COVID-19. Research should be at a good pace with inventive technologies and diagnostic methods in an inclusive manner (Fig. 16.1).

COVID-19 is spreading throughout the world in quick time and only supportive and preventive modes of efforts are being taken for combating the infection as of now. Governments are yet to come up with innovative plans in biomedical fields to find the cure and eradicate the pathogen. In the case of COVID-19, disease diagnosis is the critical field that needs convergence of different group of people, right from ambulance driver and nurses to the virologist who tests the presence of the virus in the swab by molecular and antibody tests. In general, molecular testing needs RT-PCR technique and huge demands of facilities in short notice caused the scarcity of employees and labs

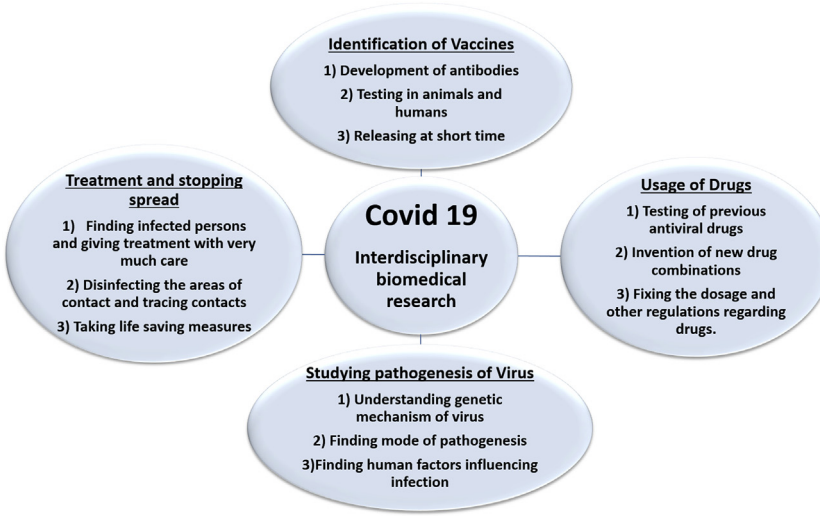

FIGURE 16.1 Interdisciplinary biomedical research in COVID-19 pandemic.

in public sector with such facilities. In such situation, the governments are forced to seek the support of other related persons in various fields to do the testing as an interdisciplinary approach.

From different experiences, it is found that the varied intensity of infection is related to factors like age, lifestyle diseases, immunity, etc. Coronavirus generally destabilizes the innate immunity system and causes severity for those who suffer from other diseases. It is estimated that 81% of the patients are asymptomatic or with mild pneumonia, 14% have severe disease and respiratory problems like dyspnea, and 5% have critical respiratory problems, multiple organ dysfunction, and septic shock [6]. Patients with existing respiratory problems are badly affected by the virus and a large number of ventilators are needed for treating them. The virus is spreading in different parts of the world with emergent multiple strains under three different types, A, B, and C (Table 16.1). Each type has varied intensity of infection and hence tracking the disease history of patients should enable the physician to provide suitable supportive treatment.

16.3 Interdisciplinary approach in biomedical education

Though general medicine education is widely regarded as a good method, the biomedical education has become more specialized. The physicians and nurses who are specialists in their fields are inexperienced in other fields related to their profession. This narrowing of expertise causes diagnostic issues and problems in provision of adequate therapy. In a research carried out in Australian hospitals, the employees' ignorance of identifying the disease is

TABLE 16.1 Types of SARS-CoV-2 virus.

S/No.	Type	Origin of the type	Countries severely affected
1	Type A	Original virus that infected humans from bats and pangolins in China. It mutated to give type B	Australia, USA, Chile, India
2	Type B	Developed in China, most spreaded type in China in December	Europe—Netherlands, Germany, France, Belgium, Brazil, Canada, China
3	Type C	Developed in China from type B	Singapore, Italy, Hong Kong

reported to have caused diagnostic mistakes [7]. Diagnostic mistakes while doing testing and treatment will be counterproductive for COVID-19 since they will enhance the spreading of the disease to doctors and other staff and in turn spread to the patients treated by them. A similar situation is present in many countries having average health infrastructure. However, it is appreciable that governments of different countries have created COVID hospitals equipped with task forces.

In biomedical education, there is a concerted effort to bring different scientific disciplines together to optimize the individual field of studies, and this integration enables work to be carried out more efficiently. For example, a programmer may create a computer algorithm to search for the pattern of DNA sequence, while a geneticist is required to study its comparative role in biology. In an experimental study conducted by King et al. [8], interprofessional simulation education of learners from various disciplines such as nursing, respiratory therapy, and medical students were found to have allowed them to comprehend distinct areas other than their discipline. For achievement, interdisciplinary biomedical education requires some measures including selecting suitable teams for interdisciplinary education [9].

Modern-day projects involve several scholars and other institutions that concentrate mainly on bringing together many disciplines so that through an interdisciplinary strategy they can concentrate on an individual objective. The Deutsche for Schungsgemeinschaft is funding collaborative research centers (SFBs), bringing together university scientists within 50 km. For example, an SFB focused at Frankfurt University in RNA science studies involves organic chemists, theoreticians, computer researchers, X-ray crystallographers, geneticists, microbiologists, and physicists. Other institutions involved in such studies include the following: (1) Joint Institute for Laboratory Astrophysics (JILA) at the University of Colorado bringing together physicists, chemists,

and instrument technicians and manufacturers who have won two latest Nobel Prizes, (2) BIO-X at Stanford University has equal doses of biology, physics, and engineering, and (3) the Center for Integrative Genomes at Princeton University combines areas of molecular biology [10].

Evans Center for Interdisciplinary Biomedical Research (the Evans Center) at Boston University established in early 2009 [11] involved interdisciplinary research groups—*affinity research collaboratives* (ARCs)—from several academic departments with at least two research disciplines related to studies involved in human diseases. From the day of its establishment, the Center had achievements at discovery/publication, grant awards, and educational levels. The brought about of Evans Center was based on the principle that a combination of organization, investigator-driven development of research goals, early and rigorous peer review of collaborative visions, and financial and structural support would develop interdisciplinary research. Many projects and activities include trainees at the graduate and postgraduate levels, leading or co-leading cross-departmental interdisciplinary seminars, and developing interdisciplinary courses and workshops. It provides a "bottom-up" approach to develop own areas of research. The Center does not focus on a general area of research or disease, but provides infrastructure including rigorous peer review. Multiple ARCs, each with investigators from different backgrounds and expertise, involved in studying a biomedical problem or a disease of their choice. The aim is to develop diagnostics and tools rather than focusing on a particular field and to communicate with the external community that would help in information gathering and sharing. They provide a "virtual center" where the collaborating investigators remain in their existing research spaces. ARCs are formed by a faculty/founding director on general areas of research. The members include about five colleagues and each ARC has at least two disciplines related to the investigation. Monthly or bimonthly meetings are held to discuss research and translational potential with the director. The ARCs at Evans Center research in the fields of protein trafficking and neurodegenerative diseases, mitochondrial dynamics in health and disease, regenerative medicine, obesity, cancer, and inflammation, etc. An ARC may collaborate with other ARCs to carry out extensive research works. About 93 co-authored publications, 33 grants funded, and 15 grants pending have been done along with 97 presentations at meetings; 57 predoctoral and 27 postdoctoral trainees affiliated with ARC activities show the overall success. Similar collaboration is seen in COVID-19 vaccine development in Britain by campaigning research groups including Cambridge University viral research group.

The establishment of Janelia Farm Research Campus at Howard Hughes Medical Institute (HHMI) brings together biomedical scientists along with computational scientists and instrument builders [9]. Two such organizations in biomedical collaboration are the Medical Research Council Laboratory of Molecular Biology (MRCLMB) and the ATandT Bell Laboratories, the former extensively involved in biological research and the latter a private-sector

electronics enterprise. This collaboration promotes individual small groups in developing interinstitutional communication. As a result, larger projects are conducted by self-assemblies of smaller groups. Excellent support facilities, infrastructure, internal sources for funding, and presence of experienced scientists allow research to be carried out effectively. Janelia Farm Research Campus aims to provide technological advancements and to produce an integrated team of biologists and tool builders that would eventually address biomedical problems. Group leaders are recruited through an open international competition. Research groups have about six people including postdocs and technicians and are given core facilities. Single laboratories with 400 individuals from different disciplines are involved and the works are funded by HHMI. Apart from biotech companies, academic institutions have a supply of graduate, undergraduate, and postdoc fellows and are given effective exposure to such collaborative research. Programs like Visiting Scientist enable them to partake in projects. They also give opportunities for women to be involved in biomedical research. These establishments are focused mainly on research which is difficult to conduct and time-consuming than general fields. Centers for Mendelian Genetics (CMGs) established by NIH (National Institute of Health) is involved in large-scale whole exome sequence (WES) analysis in affected individuals and their relatives for the discovery of genetic basis of "unresolved" Mendelian traits [12]. Key factors for the success of CMGs are due to diverse partnerships between clinicians, physicians, and biomedical research scientists across the world.

Biomedical engineering is another important field where the technicians should be aware of the mechanical aspects of diagnosis. The biomedical engineering students get interdisciplinary training to handle any situation pertaining to clinical equipment. Courses that offer basic knowledge about particular disease diagnosis with practical exposure to problems in different clinical setups will produce good technicians. Engineering courses like BME465 and BME448 are developed to collaborate biomedical engineers with mechanical engineers and nurses [13]. Students of these kind of courses are offered training with other engineers, businessman, and clinical staff to make their foundation strong in biomedical engineering and experience teamwork with other research laboratory staff [14]. Persons who have undergone such courses can be utilized in carrying out testing and treating patients when adequate professional staff is not available during a pandemic like COVID-19.

16.4 Use of model organisms and advancements in drug development and treatment

Model organisms serve as a useful tool in fundamental biological and clinical research. Organisms having genetic similarity with man are good candidates for testing of drugs and vaccines and their probable side effects. The usage of model organism—based drug validation needs multidisciplinary research

including drug discovery and manufacturing, application of drugs in model organisms, scanning of organisms for probable side effects, etc. Nowadays model organisms help scientists to address several problems related to biomedical research. Common model organisms used to understand different aspects of molecular mechanisms include *Caenorhabditis elegans*, *Drosophila melanogaster*, *Arabidopsis thaliana*, zebrafish, and rodents. Though cultured human cells and organoids (multidimensional culture systems) used in drug development show a high degree of target validity, they do not provide physiological interaction among organs since they are isolated from their current environment [11]. Therefore, the uses of animal models become important in the field of biological research. With the advancement of gene editing systems like CRISPR/Cas system, precise mutations can be induced in these models to study the pathophysiology of various disorders like Duchenne muscular dystrophy in rabbits [11].

The use of models to study a particular disease is dependent on several factors which must be followed up to improve the success rate in clinical trials [15]. They are

- The similarity in biology, symptoms, and clinical effects between the model and diseased system.
- Target under study should have a similar role in a disease model.
- The closeness of model organism to the system at various levels of biological hierarchy.
- Complexity—higher complexity means more relevant mechanisms will be involved.
- Time course for treatment.
- Strain, age, gender, and health status of model and system.
- Reproducibility of the experiment.

Even though animal models are used widely, with the emergence of new approaches like in silico techniques and stem cell–based technologies that attained recent acknowledgment, the future of animal models in biomedical research looks dim. Also, clinical trials of drugs in humans yielded defective results that have shown adequate results in a model organisms (TGN1412) [16]. However, these are extremely useful in identifying genes and molecular pathways underlying several disorders. Several discoveries like Hedgehog pathway in growth and development were discovered in *Drosophila*; excessive iron uptake due to gene mutation in zebrafish that shows gene orthology to humans; and also the study of blood development in early embryos due to exogenous fertilization in the embryo of zebrafish. *Drosophila* has been used to study molecular mechanisms underlying learning and memory formation. Hence, at certain prospects, we cannot completely ignore the importance of model organisms [16].

A model is a simple representation of a complex system and can be used to study certain aspects, but cannot reproduce all the traits concerning the whole

complexity of an organism. Animal models have filled the gap that prevents the chemical substance to pass as an effective drug. In relation to computer-aided drug design, the model systems provide an effective path to carry out clinical trials and to determine the effectiveness of that compound. Even though worms and flies are used to understand mechanisms, their evolutionary divergence from humans makes them ineffective candidates in clinical research to study human disorders. Mouse models provide an effective tool in studying the corresponding pathophysiology because of their similar mammalian characteristics, gene conservation, and their ability to engineer nearly any human mutation [11].

Humanized mouse models in which immunodeficient mice are engrafted with human cells or tissues are considered for in vivo studies. The most commonly used ones in biomedical research include human tumor xenograft model for cancer study and those that mimic the human immune system [15].

Human tumor models: The patient-derived xenograft models are surgically rejected from primary tumor samples and engrafted to immunodeficient mice. Clinical trials of various chemical substituents are carried out on such models to understand the drug activity, combination, biomarker discovery, cytotoxicity, dosage, etc. But these models lack the intact human immune component and microenvironment for tumor growth and therefore complication in implantations and poor production values can emerge.

Mice with the humanized immune system: The first immunodeficient strain of mice includes nude and SCID (severe combined immunodeficient) mice. Introduction of mutated IL-2 receptor (IL-2 Rγ) into parent NOD/SCID and RAG 1/2 immunodeficient mouse strains shows multiple deficiencies including defects in T-, B-, and natural killer cells, reduced macrophage, and dendritic cell function. Implantation of human hematopoietic stem cells to these immunodeficient mice helps to understand multilineage hematopoietic cell development and differentiation. These are mostly used in cancer immunotherapy, regenerative medicine, human stem cell transplantation, and vaccines.

In order to improve and extend rare disease investigations, a need for developing new programs required for models to study pathogenicity and clinical testing emerged. Examples of such programs include rare disease models and mechanism network, Model Organisms Screening Center, etc. [11].

Novel coronavirus causing COVID-19 pandemic is reported to be transferred to humans from bats and pangolins. This information can be used as the basis for all investigations related to vaccine development. Experiments in different animals will provide adequate information regarding pathogenesis and treatment. The scientists have to change their laboratory settings from microbes like yeast in the Petri plates to various groups of animals related to human. The virus uses certain kind of receptors in the human body for infection and the animals which don't have these receptors are not infected.

Some animals get severely infected and die without any response like antibody production. Studies are going on for artificially fixing the receptors in experimental mice and finding response. There are also cases in which experimental animals have shown drastic difference in symptoms compared to humans. Studies of these kind are not continued due to lack of result. In this condition, scientists require animals that get infected and show mild symptoms or become asymptomatic. Some laboratories concentrate on SARS susceptible rats whereas some others try to find solution in most related species like macaques, African green monkeys, etc. Recently it is found that golden Syrian hamster is a good small animal model in COVID-19 research. This species of rats shows similar symptoms like rapid clearance of viral particles and tissue repairing which are seen in mild infected patients [17].

16.5 Gene editing and stem cell technologies—an interdisciplinary look

Genetic diseases are incurable with fundamental diagnostic methods. Gene editing or genome editing is the editing of a specific part of the DNA using techniques such as CRISPR, protein-based and chemical-based nuclease systems, adeno-associated virus system, and protein RNA-based system [18]. Application of these systems in human beings needs proper testing and validation, where different disciplines need to be collaborated. For instance, in studies where zinc finger nuclease used to induce HIV-1 resistance in CD4+ T immune cells in humans need the collaboration of different disciplines like designing of zinc finger nucleases, cell culturing, in vitro and in vivo HIV-1 infection challenges, microscopy, and sequencing [19].

CRISPR is a self-protection system seen in archaea and bacteria. Cas9 is an enzyme that utilizes the CRISPR sequence to edit the gene within an organism. The application of CRISPR/Cas9 system will be revolutionary in the field of genetics-based biomedical research. Several close interdisciplinary fields enable CRISPR to develop as one of the most important fields in the medical field [20]. To develop proper understanding and knowledge related to several disciplines like omics, genetics, bioinformatics, biochemistry, changes in molecular when CRISPR is introduced. There was a rapid development in the last few decades in genome editing technologies, especially CRISPR. This has revolutionized some particular disciplines like the human disease models. Various animals and cell lines are prepared to study the efficiency of the mechanism [21]. Bioinformatics is another field that developed and produced new tools to understand the mechanism of the CRISPR/Cas9 system [22].

Stem cells are totipotent cells that are not differentiated and can develop into different cell types, which can be used to treat different diseases [23]. Stem cell technology needs the collaboration of different disciplines. Scientists from different disciplines like bioinformatics, virology, mathematics, medicine, cell biology, etc., joined in a workshop named stem cell MATLAB to

understand the utilization aspects of each discipline in the establishment of stem cell research [24].

16.6 Genetic engineering and improvements in microscopic techniques

The synergistic combination of four major "NBIC" provinces of science and technology is being considered, each of which is currently progressing at a rapid rate: (1) nanoscience and nanotechnology, (2) biotechnology and biomedicine including genetic engineering, (3) information technology, including advanced computing and communication, and (4) cognitive science, including cognitive neuroscience [25].

Engineering natural processes to harness new materials, biological products, and machines from the nanoscale up to the scale of meters can be improved by closely related multidiscipline researches. Various developments in genetic engineering have given a major insight into the frontier beyond biomedical research. Transhumanism promotes an interdisciplinary approach to understand and evaluate opportunities enhancing human conditions, giving attention to present technologies like genetic engineering and anticipated future ones, such as molecular nanotechnology and artificial intelligence [26]. CRISPR/Cas9 enables the introduction of changes in DNA sequence that correct genetic disease in the mouse model, changes in pluripotent embryonic stem cells, replicate genetic basis for human disease in model organisms, etc. [27]. The practice of germline enhancements via genetic engineering could reduce the risk of congenitally acquired disorders and help to alleviate human suffering [26]. Antibiotic production has been a major field in therapeutic research. Bacterial resistance toward several antibiotics has made a concern to make a move toward genetically engineering antibiotic biosynthetic pathways in several microorganisms and to speed up the process of evolution by many orders of magnitude to compete with the natural evolution of microbial pathogens. One such engineered antibiotic is "oritavanacin," a synthetic derivative of chloroeremomycin used against vancomycin-resistant enterococci [28]. *Escherichia coli* is an important microorganism as it is one of the most widely used microbes to produce recombinant drugs. Several changes in *E. coli* have been made in recent years that enabled to extend it to further application. High-density fermentation and full-length glycosylated antibody can be expressed with high yield and the production of different fab fragments can also be achieved in high titers in protease-deficient *E. coli* mutants. Cell-free systems to generate therapeutics also look promising [29].

Biomedical imaging is an interdisciplinary field that requires collaboration among biologists, chemists, medical physicists, pharmacologists, computer scientists, biomedical engineers, and clinicians of all specialties and is essentially a basic clinical investigational tool [30]. Systems biology elucidates the relationship between molecular system states and higher-order

phenotypic states [31]. Recent advancements in light microscopy allow unprecedented insights into nanostructures as well as unprecedented experimental throughput. Optical imaging can be used as a powerful tool for studying the temporal and spatial dynamics of biomolecules and their interactions. Light-sheet microscopy used to probe the internal architecture of large embryos and tissues provides isotropic and near diffraction-limited resolution in mm-sized samples [32]. Single-molecule imaging in living matter provides the ability to study molecular organization in cells and tissues by localizing specific molecules such as RNA and proteins in a native cellular context. Cell-based screening for biological or chemical compounds with biological effects is at the core of modern translational systems biology [31]. A combination of microscopy and endoscopy (microendoscopy) gives access to subcellular resolution within the context of living tissues [32]. These kinds of technologies are employed to find out the mode of pathogenesis of novel coronavirus in different tissues.

High-content screening combines high-throughput microscopy with automated extraction of a multitude of single-cell physiological features. Automated microscopes equipped with an autofocus system can perform high-throughput experiments. It is used to study the effects of compounds or to study genetic perturbations [31]. Other optical imaging techniques include optical coherence tomography, multiphoton microscopy, total internal reflection fluorescence, and speckle microscopy [30]. Quantitative fluorescent speckle microscopy in which polymers are labeled sparsely with single molecules can be used to study their dynamics, images of their sites, and their positions [32]. Live-cell imaging is used to assess the dynamics of cellular events, their cellular heterogeneity, and synchrony. *Fluorescence resonance energy transfer* and fluorescence lifetime imaging microscopy determine the dynamics of fast spatiotemporal protein−protein interactions at molecular resolution [31]. Electron microscopy revolutionized the biomedical research in which different cells can be imaged with high magnification and clarity. Scanning electron microscopy (SEM) and transmission electron microscopy are widely used to image drug interaction, cellular changes, extend of pathogenesis, etc. Different features of SARS-CoV-2 virus pathogenesis is identified by SEM.

16.7 Omics in biomedical research

Interpretation of high-throughput results, translation of biological data to clinical application, data handling, storage, and sharing issues as well as reproducibility is one of the facing challenges in biomedical research. Overwhelming biomedical articles from omics research have accumulated an abundance of information and require advanced event extraction systems to support the complexity of available information and coverage of varieties of biomedical subdomains [33]. Omics studies is a part of interdisciplinary field

which incorporates genomics, transcriptomics, proteomics, bioinformatics, and biostatistics along with metabolomics, epigenomics, and pharmacogenomics in order to evaluate data collected and shared in biomedical research. Implementation of data generation, analysis, and sharing needs multidisciplinary teams correlated with bioinformaticians and biostatisticians [34].

The genetic constitution of the human genome contains about 3 billion DNA base pairs and approximately 20,000 genes, among which 1%−2% are coding and 98%−99% are noncoding in nature. Understanding variants for several disease studies and to find out whether they affect the normal phenotypic expression and promotion to pathogenic phenotype are important in omics studies. There are mainly two types of variations: single-nucleotide polymorphisms (SNPs) and structural variants. These variants can be sequenced using traditional methods like Sanger sequencing to modern techniques like next-generation sequencing. One of the most influential advancements in interdisciplinary research arose with the completion of Human Genome Project (HGP) which provided more insight into human biology and also paved the way to develop new techniques as well as other collaborations [34].

There has always been an increasing demand for incorporating omics data with other fields of study. Recent developments have mostly focused to address this problem. Systems that help to meet the demand for working with omics data include Gene Expression Omnibus (GEO), Array Express, and Proteomics Identification Database (PRIDE). The integration of clinical data with omics introduced the use of Clinical Data Warehouses. Several other translational platforms include BRISK (Biology-Related Information Storage Kit), caTRIP, and cBio Cancer Genomics Portal, etc. [35].

International HapMap projects identified common variants across genomes of different populations—mapping of up to 10 million SNPs. The 1000 Genomes Project in 2015, with 2504 genomes from 26 populations, was established to study variations at the genome level and to understand their importance. Some recent ones include UK10K, 100,000 Genomes Project, and Precision Medicine Initiative. GWAS (genome-wide association studies) catalog, curated by the National Human Genome Research Institute (NHGRI), EMBL (European Molecular Biology Laboratory), and NCBI (National Center for Biotechnology Information), is involved in exploring genetic associations within a variety of traits. Exome Aggregation Consortium is an online tool used to evaluate WES results like exploring genes, variant types, and frequencies and predicted effects. Other databases include NCBI, Ensembl, and University of California Santa Cruz (UCSC) portals which are involved in genome analysis studies. General disease databases that correlate to the pathogenic effects of variations and the diseases associated with them can be studied using Online Mendelian Inheritance in Man (OMIM), ClinVar, etc. [34].

Transcriptome refers to the total complement of RNA transcripts in a cell (coding RNAs, noncoding RNAs, nuclear, snRNA, miRNA, and lncRNAs) and the study of the whole transcriptome is called as transcriptomics. The field helps to understand the dynamics of cellular and tissue metabolism and how changes in transcriptome profile affect health and disease. RNA sequencing and RNA microarrays have been used extensively in the field of transcriptomics. Expression quantitative trait loci is used to identify gene variants that influence mRNA expression. Not only coding variants affect mRNA expression, but also variants in noncoding regions affect it. MiRNA is extensively studied to understand its relation to diseases and mRNA expression. This principle led to the introduction of tools like MiRNA and genes integrated analysis webtool (MAGIA), GenMiR++, and mirConnX [34].

Proteomics studies involve a combination of various approaches such as proteomes, structural proteomics, and protein−protein interaction analysis. The 3D structural information of proteins can be elucidated by X-ray crystallography, NMR, and cryo-electron microscopy. They also help to investigate structural changes in mutation studies, drug discovery, the study of domain, etc. Human Proteome Organization Proteomics Standards Initiative (HUPO−PSI) provides the communal format and unique vocabulary to handle protein information. X-change consortium collects proteome experimental data, and protein data bank gives the 3D information obtained from various resources. Epigenomics deals with the study of macromolecules that bind and affect DNA metabolism. ENCODE (Encyclopedia of DNA Elements) collects data on epigenetic studies like DNA methylation, histone modifications, transcription factors, suppressors, and polymerases. Drug2Gene and Drug Bank are curated databases associated with drug omics study. Human Metabolome Database and METLIN are similarly involved in metabolomics study [34].

Even though several advancements have been made, there still exist several flaws in integrating and analyzing data. With lower costs of high-throughput technologies, a large amount of omics data is being introduced. Therefore, curating this information is important. The inability of researchers to gather data and analyze bioinformatics tools possesses a problem. Therefore, adequate training in these fields should be considered. It is to be made clear to researchers how the bioinformatics approach is advantageous in biomedical research. Other main factors involve a lack of communication among scientists. Therefore, they need be brought together by meetings, seminars, etc., to make proper amendments [36].

16.8 Conclusion and future perspectives

A multidisciplinary approach is needed in biomedical research, medication, and overall management of this COVID-19 pandemic. The governments have to combine different fields like virology, hospitals, drug discovery, employment,

economics, police force, foreign affairs, local bodies, etc., to implement accurate plans in order to decrease the spread, thereby maintaining the prosperity of the society. Clubbing and decompartmentation of different fields of science is very important in this period for different purposes like finding the mode of pathogenesis, tracking the evolution of virus, invention of vaccines, proper treatment of individuals with new and existing drugs, and understanding different effects of virus in various categories of people having different lifestyle diseases like those caused from smoking and alcoholism, etc. Different scientists, doctors, virologists, pathologists, and physicians need to work together to develop the best treatment method for COVID-19. The developments in computer-based drug designing, testing by model organisms, microscopic techniques, and genome-based studies have to be utilized in treatment and finding vaccines.

List of abbreviations

ARCs Affinity research collaborative
BRISK Biology-Related Information Storage Kit
CDWs Clinical Data Warehouses
CMGs Centers for Mendelian Genetics
COVID-19 Coronavirus disease-19
CRISPR Clustered regularly interspaced short palindromic repeats
EMBL European Molecular Biology Laboratory
ENCODE Encyclopedia of DNA Elements
eQTL Expression quantitative trait loci
FRET *Fluorescence resonance energy transfer*
GEO Gene Expression Omnibus
GWAS Genome-wide association studies
HCS High-content screening
HHMI Howard Hughes Medical Institute
HSCs Human hematopoietic stem cells
HUPO-PSI Human Proteome Organization Proteomics Standards Initiative
JILA Joint Institute for Laboratory Astrophysics
MAGIA MiRNA and genes integrated analysis
MOSC Model Organisms Screening Center
MRCLMB Medical Research Council Laboratory of Molecular Biology
NCBI National Center for Biotechnology Information
NHGRI National Human Genome Research Institute
NIH National Institute of Health
OMIM Online Mendelian Inheritance in Man
PDX Patient-derived xenograft
PRIDE Proteomics Identification Database
qFSM Quantitative fluorescent speckle microscopy
RDMM Rare Disease Models and Mechanism
RT-PCR *Reverse transcription polymerase chain reaction*
SARS-CoV-2 Severe acute respiratory syndrome coronavirus 2
SCID Severe combined immunodeficient
SEM Scanning electron microscopy

SNPs Single-nucleotide polymorphisms
TEM Transmission electron microscopy
UCSC University of California Santa Cruz
WES Whole exome sequence

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