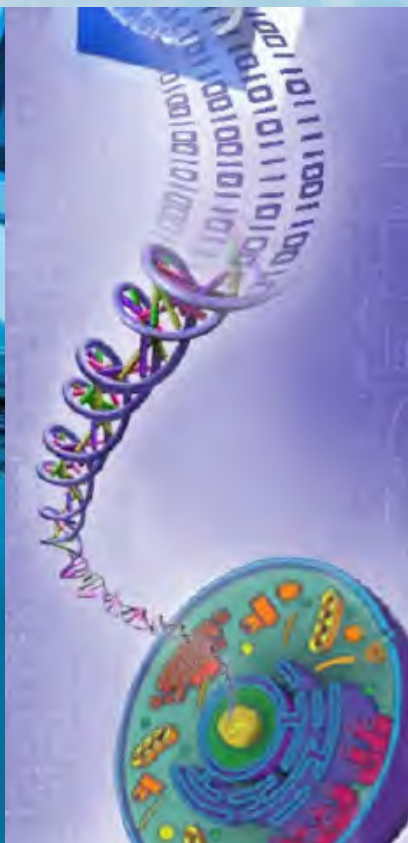


miet

Biotaction

Reaching new Horizons...

**Industrial Biotechnology
&
Bioinformatics**



MIET BIOTECHNOLOGY SOCIETY, MEERUT

2022-23

Biotaction

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Departmental Vision

To be a leading department in the country imparting biotechnological education and problem solving skills to the budding biotechnocrats capable of meeting emerging challenges in the area of inter-disciplinary education and industries.

Departmental Mission

1. Educating young aspirants in the field of biotechnology and allied fields to fulfill national and global requirements of human resource.
2. Generating trained man-power with advanced techniques in order to meet the professional responsibilities.
3. Imparting social and ethical values in graduates for progressive attainment at social level.

Program Educational Objectives (PEOs)

The Biotechnology Department of Meerut Institute of Engineering & Technology, Meerut produces graduates with a strong foundation of scientific and technical knowledge and who are equipped with problem solving, teamwork, and communication skills that will serve them throughout their career. The specific program educational objectives are:

PEO1: Pursue career as biotechnocrats in core and allied biotechnological fields all over the world.

PEO2: Undertake advanced domain research and development in the field of translational research, in a sustainable, environment-friendly, and inventive manner.

PEO3: Become an entrepreneur to meet the expectations and demand of modern industrial technologies and health care system.

PEO4: Carry out professional leadership roles in industries as well as academics with a commitment to continuous learning.

PEO5: Serve the society as a bonafide global citizen with strong sense of professional responsibility and ethics.

Program Specific Outcomes (PSOs)

1. An ability to apply biotechnology skills (including molecular & micro biology, immunology & genetic engineering, bioprocess & fermentation, enzyme & food technology and bioinformatics) and its applications in core and allied fields.
2. An ability to integrate technologies and develop solutions based on interdisciplinary skills.

Message from
Chairman



Shri Vishnu Saran
B.E. (Mechanical)

To burn always with this hard gem like flame, to maintain this ecstasy, is success in life.

It's a feeling of pride for me that the MIET Biotechnology Society is coming up with the new edition of magazine **BIOTACTION**, which is going to explore the technical and creative talent of our students. We in MIET have always supported intellectual and technical growth in all the distinct spheres of life. The publication of this magazine is a example of the same, and for sure it showcases talent, innovation and dedication of our students who deserve to excel and achieve the zenith. I wish my students good luck in their current academic endeavors and their future and professional careers. I congratulate the entire Biotechnology Society for the excellent effort of brining out **BIOTACTION**.

There is no limit to the goals you can attain or success you can achieve, your possibilities are as endless, as your dreams

MIET stands for a healthy, intellectual and creative environment so that the young minds are transformed into responsible and progressive citizens of the nation. It is a great feeling ahead to the numerous positions. It is a matter of immense pleasure and pride that the MIET Biotechnology Society is coming up with its new edition of the Biotech magazine **BIOTACTION**. I sincerely appreciate the initiative of the students of Biotechnology in bringing up this magazine. I wish this opens up new vistas of knowledge and the good work continues in time to come.

Message from
Director



Dr. Brijesh Singh
B.Sc. Engg., M.E., Ph.D.

Message from
HoD



Dr. Avinash Singh
M. Tech., Ph.D.

Dear Students,

I am elated to present the new issue of the MIET Biotechnology Society's official magazine: **BIOTACTION**.

In today's world, it is extremely important, especially for students, teachers as well as entrepreneurs in the field of biotechnology to be fully aware of the recent developments in the biotechnological arena.

Biotechnology offers the widest range opportunities in the present global scenario. Therefore, **BIOTACTION** is an effort from the MIET Biotechnology Society towards increasing the knowledge-base of its readers.

I hope the exposure that **BIOTACTION** provides is helpful in generating interest, increasing awareness and spreading the message to the Society.

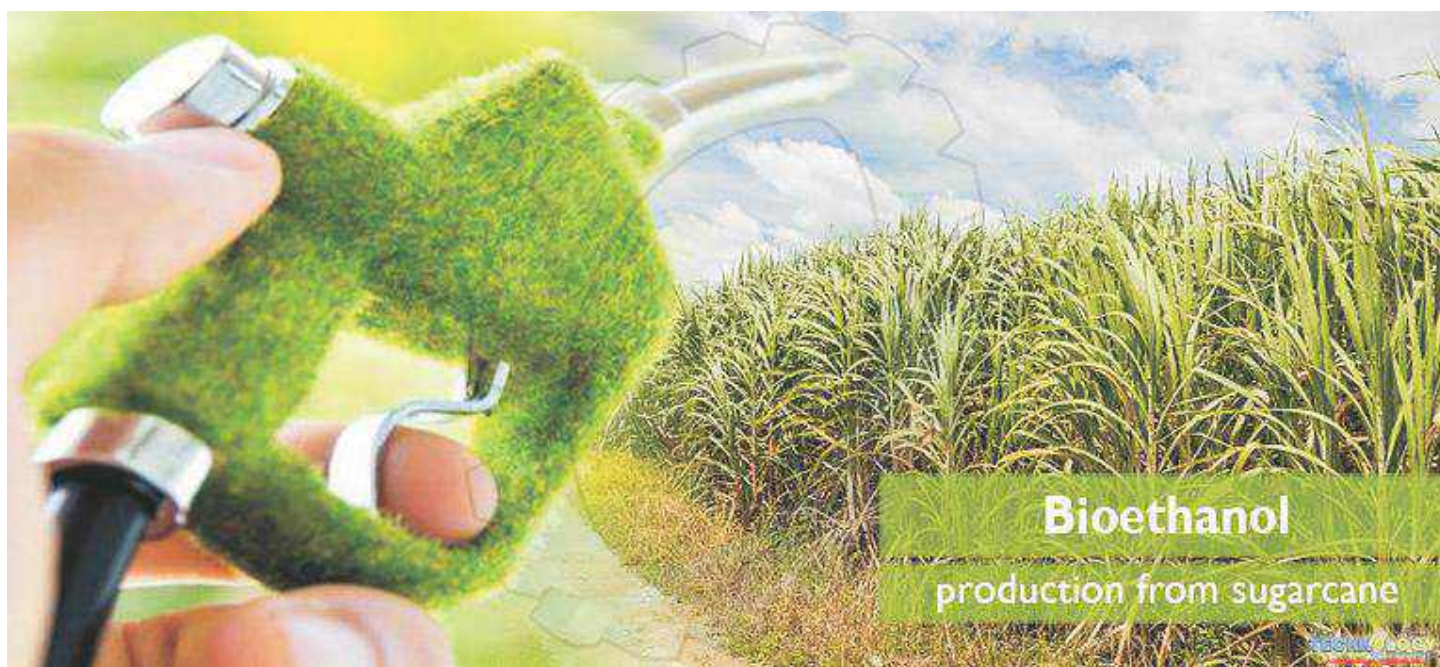
My sincere best wishes to all.

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Ethanol Production from Sugarcane

Sugarcane feedstock consists of sugar in the form of disaccharides which can be fermented into ethanol. The process of making ethanol from sugarcane starts when sugarcane is crushed to extract sugarcane juice is collected and delivered to the fermentation tank where the yeast fermentation reaction occurs to generate ethanol. The leftover material which is fibrous residue called bagasse, after juice extraction process is commonly combusted to generate heat and electricity. After fermentation, the broth (which is formed during fermentation) containing approx 5.12% ethanol by weight which is now called beer the beer is delivered to distillation column where the ethanol is recovered and the liquid residue known as vinasses, it is co-generated at the bottom of



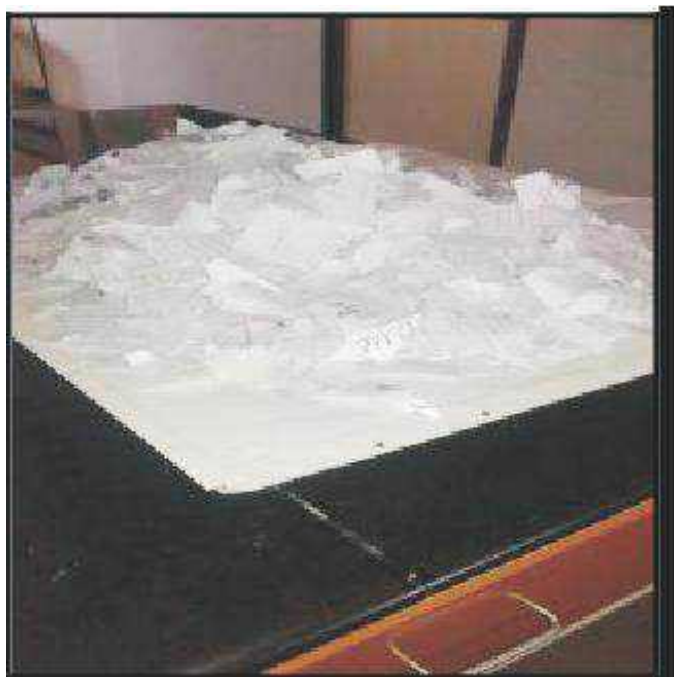
distillation column. In this process the purity of ethanol can be upto 90% to 95% therefore further water separation process required, commonly dehydration of the residual water is carried out using molecular sieve resulting in the final product, a fuel grade anhydrous ethanol (200 proof or 100% ethanol).

Sugarcane Ethanol Residues

There are two principal from sugarcane to ethanol production including bagasse (solid residue) and vinasses (liquid residue). Normally bagasse is used to provide heat/steam/ electricity for the ethanol plant. However, vinasses could not be used as an energy source and has to be treated before disposal. Therefore vinasses is still a major burden for sugarcane ethanol production.

Production of Biofuel from Waste Paper

Raw waste paper collected is finely grinded into small pieces to increase the surface area and then soaked into water for one day. Soaking help in separating cellulose from wastepaper. After one day wastepaper is filtered out and mechanically crusty and converted into pulp. Dried pulp is mixed with the 15% of H_2SO_4 for one day for the purpose of removing ink from wastepaper as it effects the final yield of ethanol. After this process the mixture is washed with water and dried. After linking of wastepaper the amount of cellulose is determined using carboxyl methyl cellulose was used as a standard component. Acetolysis is performed in which cellulose get dissolved to form celludoxtrin which get the dissolved and hydrolyzed to form glucose molecule when treated with 57% H_2SO_4 with final glucose molecule is dehydrated to form hydroxyl methyl furfural which forms green color product with anthrone method and the color intensity is measured at 630 nm. After this cellulose molecules are hydrolyzed to broken into small particles. After fermentation of severing is carried out with the help of *Saccharomyces cerevisiae* anaerobically for three days at pH 4. At the end of fermentation ethanol and other constituents are filtered. The fermented liquor is than distilled at the temperature 85-89% and the pure ethanol is derived with the water vapour which can be separated by reflux method. By using the method blending with H_2SO_4 . 68% pure ethanol can be obtained. For every 100 ml of fermentation 40 ml of ethanol is obtained.

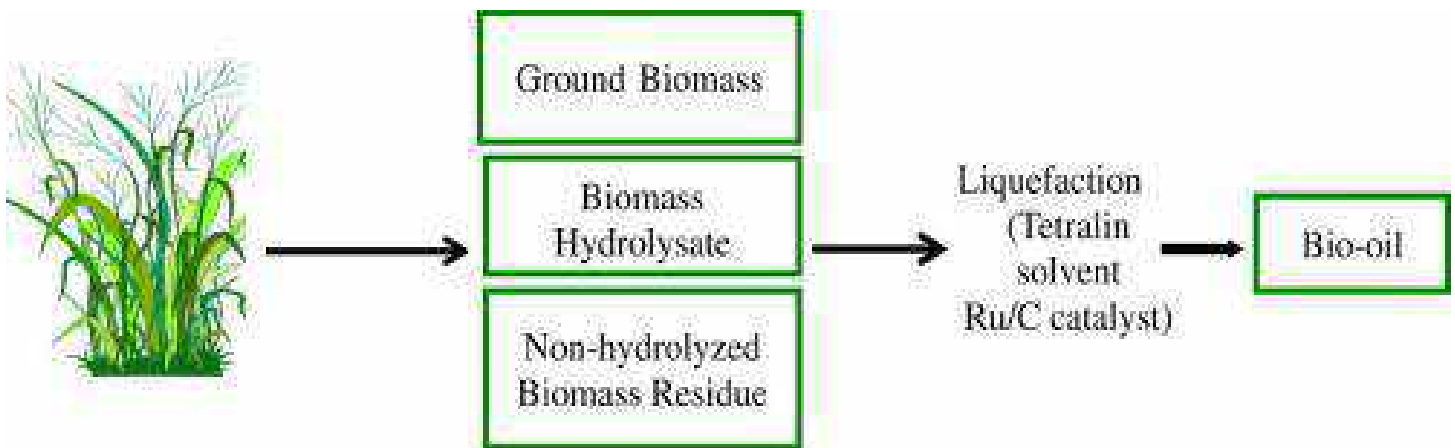


Conclusion

Waste paper are rich in cellulose content which can be effectively used for the production of bioethanol upto certain level of purity. Studies on production of biofuel from wastepaper shows that *Pseudomonas aeruginosa* and *Saccharomyces cerevisiae* are effective for producing best quality ethanol which is one of the first generation biofuel used with conventional petroleum fuels.

Biofuel Production by using Hibiscus Plant

Fast depletion of fossil fuels, rapid increase in the prices of petroleum products and harmful exhaust emissions from the engine jointly renewed interest among researchers to find the suitable alternative fuels. The properties of the crop and its oil have persuaded investors and policy makers consider these two plants as substitute for fossil fuels to reduce greenhouse gas emission. Hibiscus species plants are widely growing hardy species in arid and semi arid regions of the country on degraded soil having low fertility and moisture. The seeds of these plants contain 21.25% oil. It is found that physical and chemical properties of *Hibiscus cannabinus* and *Hibiscus sabdariffa* oil and biodiesel are very close to fossil diesel.



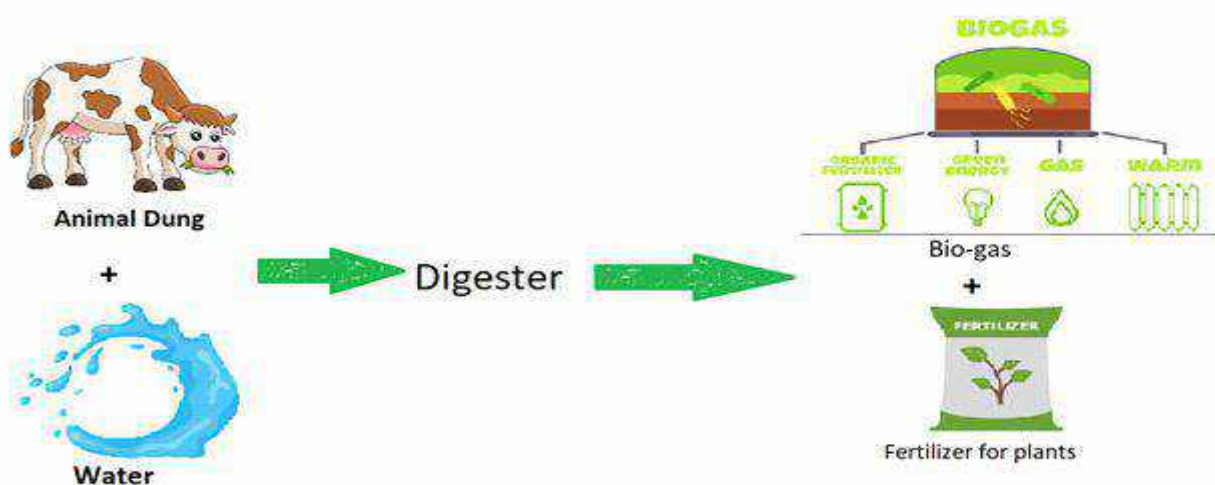
In this study, the oil has been converted to biodiesel by the well-known transesterification process and used it to diesel engine for performance evaluation. Performance tests was conducted on a single cylinder four-stroke water-cooled compression ignition engine connected to an eddy current dynamometer with different percentage of *Hibiscus cannabinus* and *Hibiscus sabdariffa* biodiesel blended with diesel. The performance and combustion characteristics of blends were evaluated at variable loads at constant rate speed and results were finally compared with the diesel.

Finally, conclude that *Hibiscus cannabinus* and *Hibiscus sabdariffa* oil biodiesel can be used as an alternative fuel in the blending form.

Bio-Gas: The Game Changer

The need for sustainable energy sources has never been more urgent, and biogas has the potential to be a game-changer in the fight against climate change. The increase in the use of CNG for transport has shown an increase in awareness of the decrease in availability and various other disadvantages of non-renewable resources. Due to the increase in demand for Natural and eco-friendly resources, these types of renewable resources have begun to overtake the market.

CNG primarily contains methane gas, a natural gas found in the earth's crust. It may also contain small amounts of other gases, such as ethane and propane. Likewise, Biogas is a type of gas that is produced by the breakdown of organic matter, such as animal waste, food scraps, and sewage. It contains primarily 35-75% methane gas, but may also contain small amounts of other gases, such as 25-65% carbon dioxide, 1-5% Hydrogen, and 0.3-3% Nitrogen.



Production of Bio-Gas through Animal Waste

Cow dung and water produce biogas through a process called anaerobic digestion. Anaerobic digestion is a natural process where microorganisms break down organic matter in the absence of oxygen. In a biogas digester, cow dung and water are mixed in an airtight container called a digester. The microorganisms in the digester break down the organic matter in the cow dung, producing biogas as a by-product. The biogas can then be collected and used as fuel for cooking or generating electricity. The leftover material from the digester, called digestate, can be used as a fertilizer.

Different Sources of Bio-gas Production:

There are several sources of organic matter that can be used to produce biogas, including:

1. Animal manure: Manure from cows, pigs, and other livestock is a common source of organic matter for biogas production.
2. Food waste: Food scraps from homes, restaurants, and grocery stores can be used to produce biogas.
3. Agricultural waste: Crop residues, such as corn stalks and wheat straw, can be used to produce biogas.
4. Sewage: Sewage treatment plants can capture biogas from the breakdown of organic matter in wastewater.
5. Landfills: Landfills produce biogas as organic waste decomposes, and this biogas can be captured and used as a fuel source.

6. Energy crops: Crops such as corn, sugarcane, and switchgrass can be grown specifically for biogas production.
7. Industrial waste: Organic waste from industrial processes, such as food processing and paper production, can be used to produce biogas.

The choice of feedstock for biogas production will depend on factors such as availability, cost, and local regulations.

Overall Advantages over other Energy Sources:

1. The technology is cheaper and much similar to those for other biofuels, and it is ideal for small-scale applications.
2. Recovery of the product (methane) is spontaneous as the gas automatically separates from the substrates.
3. Dilute waste materials (2-10% solids) can be used as substrate.
4. Organic pollutants are removed from the environment and used to generate useful biogas; this helps clean up the environment.
5. Aseptic conditions are not needed for operation.
6. Any biodegradable matter can be used as a substrate.
7. Biogas is suitable for heating boilers, firing brick and cement kilns, and for running suitably modified internal combustion engines(to generate electricity).
8. There is a much-reduced risk of explosion as compared to pure Methane.
9. Anaerobic digestion inactivates pathogens and parasites and is quite effective in reducing the incidence of water-borne diseases.

In conclusion, biogas has the potential to revolutionize the renewable energy industry and contribute significantly to the fight against climate change. With a range of sources for organic matter and various methods for purification and upgrading. Biogas is a versatile and sustainable energy source that can be used in a variety of applications. As the world continues to prioritize sustainability and eco-friendliness, biogas is poised to become an increasingly important player in the energy market. The use of biogas can reduce greenhouse gas emissions and provide a reliable source of energy, especially in rural areas. By utilizing various sources of organic matter for biogas production, we can reduce waste and create a circular economy. It is time for us to recognize the potential of biogas and invest in its development to create a cleaner and more sustainable future.

Butanol Production through Acetone–Butanol–Ethanol (Abe) Fermentation

Butanol has superior fuel properties, such as high calorific value, high hydrophobicity, low flammability and corrosiveness, ability to be mixed with gasoline and diesel in high proportions, ability to be transported by pipes, and can be produced from both glucose and xylose sugars. While biobutanol production from lignocelluloses on a commercial scale is currently not occurring, the US, Brazil and China all plan to develop large-scale butanol production plants.

Industrial biobutanol production also has support from government mandates, such as the Energy Independence and Security Act of 2007, which require 36 billion gallons of renewable fuels be produced by 2022, including 16 billion gallons derived from cellulosic biomass. Converting cellulosic biomass to butanol will significantly help fulfill federal biofuels production mandates; however, improvements to the cellulosic fermentation process are needed to improve the production efficiency before commercialization is possible.

It is divided into four major aspects of ABE fermentation:

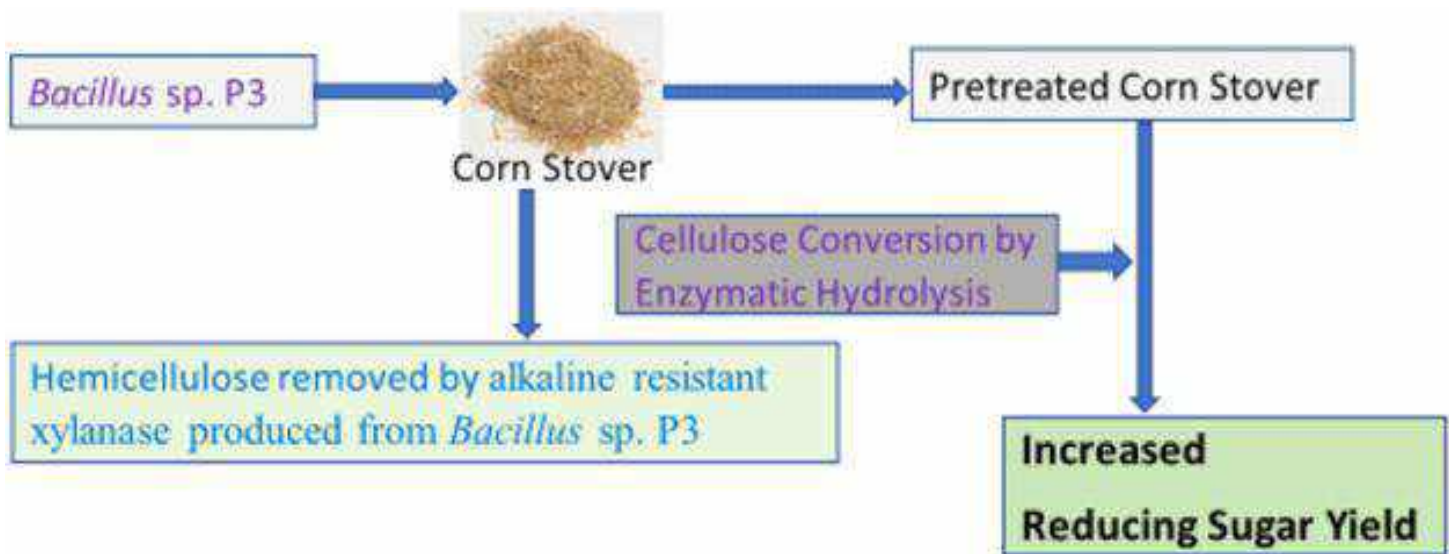
- (i) feedstock for ABE fermentation,
- (ii) pretreatment and enzymatic hydrolysis of lignocellulose,
- (iii) ABE fermentation and recovery
- (iv) economic viability and potential commercialization.

Feedstock for ABE Fermentation

Butanol can be produced from different types of biomass, such as forest residues, agricultural residues, energy crops and municipal solid wastes. Agricultural residues have great potential as reliable feedstocks due to widespread availability. Corn stover dominates the other agricultural residues in terms of yield per hectare, availability and price, but also has by far the greatest price variability.



It is divided into four major aspects of ABE fermentation:



Conclusions

Biobutanol has the potential to be a viable liquid fuel for the transportation industry. Corn stover appears to be an ideal fermentation substrate for biobutanol production due to its sugar content and widespread availability. Although much progress on the use of nonfood substrates for the production of fuels and chemicals has been made, substantial research efforts are still being expended on the development of technologies that improve sugar yields from corn stover and similar lignocellulosic biomass without generating significant levels of LDMICs.

In-silico Study of Phytoconstituents for Anti-Cervical Cancer Drug

"In Silico Study of Phytoconstituents as an Alternative for Anti-Cervical Cancer Drug" aimed to explore the potential of natural compounds as alternative therapies for cervical cancer. Using computational methods, researchers conducted molecular docking to identify phytoconstituents that interact with target proteins involved in cervical cancer. Additionally, ADME analysis was performed to assess the pharmacokinetic properties of these compounds. The project provided valuable insights into the potential efficacy of phytoconstituents, their molecular interactions, and drug-like characteristics, highlighting their promising role in the development of personalized medicine approaches for cervical cancer treatment.

Cervical Cancer: Cervical cancer is a malignancy that affects the cervix, typically caused by persistent infection with high-risk strains of human papillomavirus (HPV) and characterized by abnormal cell growth in the cervical tissues. Early detection through screening and vaccination against HPV are important preventive measures.

Phytoconstituents: Phytoconstituents are bioactive compounds derived from plants, and have long been recognized for their medicinal properties. They exhibit diverse chemical structures and have shown promising anti-cancer activities in various preclinical and clinical studies. Harnessing the potential of phytoconstituents as alternatives for anti-cervical cancer drugs through in silico studies holds immense promise.

Molecular Docking: Molecular docking is a computational technique used to predict and study the interaction between a small molecule (ligand) and a target protein. It helps in understanding how the ligand binds to the active site of the protein and predicts the binding affinity. Docking plays a crucial role in drug discovery, aiding in the identification of potential drug candidates, optimizing their structures, and assessing their binding strength, which can guide further experimental validation and development of new therapies.

Human Papillomavirus type (HPV-18 E1) protein (PDB ID: 1R9W) was selected for molecular docking with major bioactive phytoconstituents from the selected medicinal plants to identify its potential inhibitor. The 3- dimensional monomeric structure of HPV-18 E1 (4R9W) was downloaded from the protein databank (<http://www.rcsb.org/pdb>).

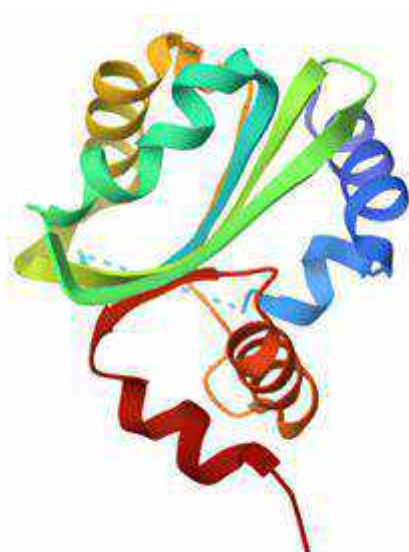


Fig. PDB predicted 3D structure of HPV-18 E1 (PDB ID: 1R9W)

ADME Screening: ADME analysis stands for Absorption, Distribution, Metabolism, and Excretion analysis. It is a process used in drug development to assess the pharmacokinetic properties of a compound. ADME analysis evaluates how a drug is absorbed into the body, distributed within tissues, metabolized by enzymes, and eliminated from the body. This analysis helps determine the drug's bioavailability, potential toxicity, and overall suitability as a therapeutic agent, providing valuable insights for optimizing drug design and predicting its behavior in vivo.

The In silico study of phytoconstituents as an alternative for anti-cervical cancer drugs project provides valuable insights into the potential use of natural compounds in the treatment of cervical cancer. By employing computational methods and tools, researchers can explore the interaction of phytoconstituents with protein targets, predict their pharmacokinetic properties, and investigate their mechanisms of action. This project highlights the following key learning points:

1. In Silico Screening: In silico screening techniques, such as molecular docking, can efficiently identify potential phytoconstituents that interact with target proteins involved in cervical cancer. This approach enables researchers to narrow down the pool of compounds for further investigation, saving time and resources compared to traditional screening methods.

2. Molecular Interactions: Through molecular docking studies, researchers can analyze the binding affinity and interaction patterns between phytoconstituents and target proteins. This information helps understand the molecular basis of their anti-cancer effects and provides insights into the structural requirements for their activity.

3. Pharmacokinetic Evaluation: In silico tools for predicting the pharmacokinetic properties of phytoconstituents offer valuable information regarding their absorption, distribution, metabolism, excretion, and toxicity. Assessing these properties aid in selecting compounds with favorable drug-like characteristics for further development.

4. Mechanisms of Action: Molecular dynamics simulations and pathway analysis can elucidate the molecular mechanisms underlying the anti-cancer effects of phytoconstituents. Understanding these mechanisms is crucial for developing targeted therapies and optimizing the efficacy of phytoconstituent-based drugs.

5. Rational Drug Design: The in silico study provides a foundation for rational drug design and optimization of phytoconstituent-based drug candidates. By identifying key structural features and interactions, researchers can modify the chemical structures of phytoconstituents to enhance their potency, selectivity, and pharmacokinetic profiles.

Conclusion:

Overall, this work highlights the potential of in silico approaches in accelerating the discovery and development of phytoconstituent-based anti-cervical cancer drugs. The computational tools and methodologies employed provide valuable insights into the interaction of phytoconstituents with target proteins, offering a promising avenue for future research and the advancement of personalized medicine approaches in cervical cancer treatment.

PhyloFacts: An Online Structural Phylogenomic Encyclopedia for Protein Functional and Structural Classification

The Berkeley Phylogenomics Group presents PhyloFacts, a structural phylogenomic encyclopedia containing almost 10,000 'books' for protein families and domains, with pre-calculated structural, functional and evolutionary analyses. PhyloFacts enables biologists to avoid the systematic errors associated with function prediction by homology through the integration of a variety of experimental data and bioinformatics methods in an evolutionary framework. Users can submit sequences for classification to families and functional subfamilies.

Computational methods for protein function prediction have been critical in the post-genome era in the functional annotation of literally millions of novel sequences. The standard protocol for sequence functional annotation - transferring the annotation of a database hit to a sequence 'query' based on predicted homology - has been shown to be prone to systematic error. The top hit in a sequence database may have a different function to the query due to neofunctionalization stemming from gene duplication, differences in domain structure, mutations at key functional positions, or speciation. Annotation errors have been shown to propagate through databases by the application of homology-based annotation transfer. While the exact frequency of annotation error is unknown (one published estimate is 8% or higher), the importance of detecting and correcting existing errors and preventing future errors is undisputed.

An additional complicating factor in annotation transfer by homology is the complete failure of this approach for an average of 30% of the genes in most genomes sequenced: in some cases no homologs can be detected within a particular significance threshold, for instance, a BLAST expectation (E) value (that is, the number of hits receiving a given score expected by chance alone in the database searched) of 0.001 or less, while in other cases database hits may be labeled as 'hypothetical' or 'unknown'.

With the huge array of bioinformatics software tools and resources available, it might seem unthinkable that functional annotation accuracy would be so difficult to ensure. Rather like the parable of the blind men and the elephant, each tool used separately provides a partial and imperfect picture; taken as a whole, the probable molecular function of the protein, biological process, cellular component, interacting partners, and other aspects of a protein's function can often come into better focus. For instance, annotation transfer from the top BLAST hit may suggest a protein is a receptor-like protein kinase, while domain structure prediction reveals that no kinase domain is present; the two orthogonal analyses prevent mis-annotation of the unknown protein.

In this paper we present PhyloFacts, an online structural phylogenomic encyclopedia containing almost 10,000 'books' for protein families and domains, designed to improve the accuracy and specificity of protein function prediction. PhyloFacts integrates a wide array of biological data and informatics methods for protein families, organized on the basis of structural similarity and by evolutionary relationships. This enables a biologist to examine a rich array of experimental data and bioinformatics predictions for a protein family, and to quickly and accurately infer the function of a protein in an evolutionary context.

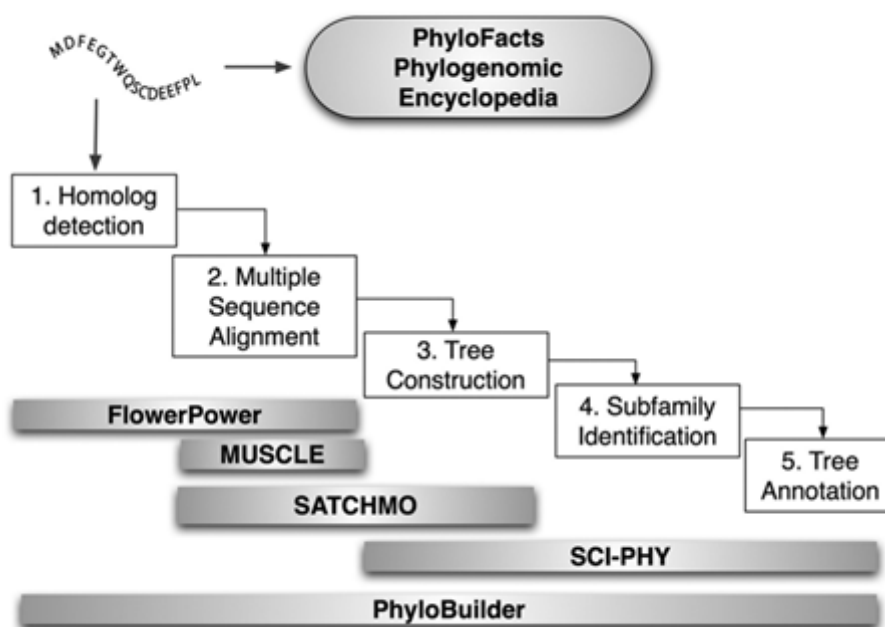
Annotation Accuracy Requires Data and Method Integration

PhyloFacts is motivated by two of the biggest lessons of the post-genome era - the power of integrating data and inference tools from different sources, and improved prediction accuracy using consensus approaches in

bioinformatics. For instance, protein structure prediction 'meta-servers' making predictions based on a consensus over results retrieved from several independent servers typically have lower error rates than any one server used separately. In the case of protein structure prediction, we can also take advantage of the fact that members of a large diverse protein family tend to share the same three-dimensional structure even when their primary sequence similarity becomes undetectable. This enables us to use another type of consensus approach involving the application of the same method to several different members of the family to boost prediction accuracy.

We employ the same basic principles in this resource, by integrating many different prediction methods and sources of experimental data over an evolutionary tree. In cases where attributes are known to persist over long evolutionary distances (such as protein three-dimensional structure), we can integrate predictions over the entire tree to derive a consensus prediction for the family as a whole. In cases where attributes are more restricted in their distribution in the family (for example, ligand recognition among G-protein coupled receptors), inferences will be more circumspect, potentially restricted to strict orthologs. Evolutionary and structural clustering of proteins enables us to integrate these disparate types of data and inference methods effectively, to identify potential errors in database annotations and provide a platform to improve the accuracy of functional annotation overall.

In addition to new methods developed by us for phylogenomic inference, PhyloFacts includes a number of standard bioinformatics methods available publicly. To motivate the need for protein functional classification integrating diverse methods and data in an evolutionary framework, we examine the major classes of bioinformatics methods in turn, and discuss their different pros and cons. Methods designed for predicting the biological process(es) in which a protein participates (for example, bioinformatics approaches such as Phylogenetic Profiles and Rosetta Stone, analysis of DNA chip array data, and proteomics experiments such as pull-down experiments, yeast two-hybrid data, and so on) are clearly complementary, and will be included in future releases of the PhyloFacts resource.



Ritika Gupta
 Batch: 2021-2025

Understanding the Microbial Components of the Human Genetic and Metabolic Landscape

Before the Human Genome Project was completed, some researchers predicted that ~100,000 genes would be found. So, many were surprised and perhaps humbled by the announcement that the human genome contains only ~20,000 protein-coding genes, not much different from the fruitfly genome. However, if the view of what constitutes a human is extended, then it is clear that 100,000 genes is probably an underestimate. The microorganisms that live inside and on humans (known as the microbiota) are estimated to outnumber human somatic and germ cells by a factor of ten. Together, the genomes of these microbial symbionts (collectively defined as the microbiome) provide traits that humans did not need to evolve on their own¹. If humans are thought of as a composite of microbial and human cells, the human genetic landscape as an aggregate of the genes in the human genome and the microbiome, and human metabolic features as a blend of human and microbial traits, then the picture that emerges is one of a human 'supra-organism'.

The HMP is a logical conceptual and experimental extension of the Human Genome Project. The HMP is not a single project. It is an interdisciplinary effort consisting of multiple projects, which are now being launched concurrently worldwide, including in the United States (as part of the next phase of the National Institutes of Health's Roadmap for Medical Research), Europe and Asia. The advent of highly parallel DNA sequencers and high-throughput mass spectrometers with remarkable mass accuracy and sensitivity is propelling microbiology into a new era, extending its focus from the properties of single organism types in isolation to operations of whole communities. The new field of metagenomics involves the characterization of the genomes in these communities, as well as their corresponding messenger RNA, protein and metabolic products.

Ecology and Considerations of Scale

Questions about the human microbiome are new only in terms of the system to which they apply. Similar questions have inspired and confounded ecologists working on macroscale ecosystems for decades. It is expected that the HMP will uncover whether the principles of ecology, gleaned from studies of the macroscopic world, apply to the microscopic world that humans harbour. In particular, the following questions might be answered by the HMP. How stable and resilient is an individual's microbiota throughout one day and during his or her lifespan? How similar are the microbiomes between members of a family or members of a community or across communities in different environments? Do all humans have an identifiable 'core' microbiome, and if so, how is it acquired and transmitted? What affects the genetic diversity of the microbiome and how does this diversity affect adaptation by the microorganisms and the host to markedly different lifestyles and to various physiological or pathophysiological states?

Large Variation in Bacterial Lineages between People

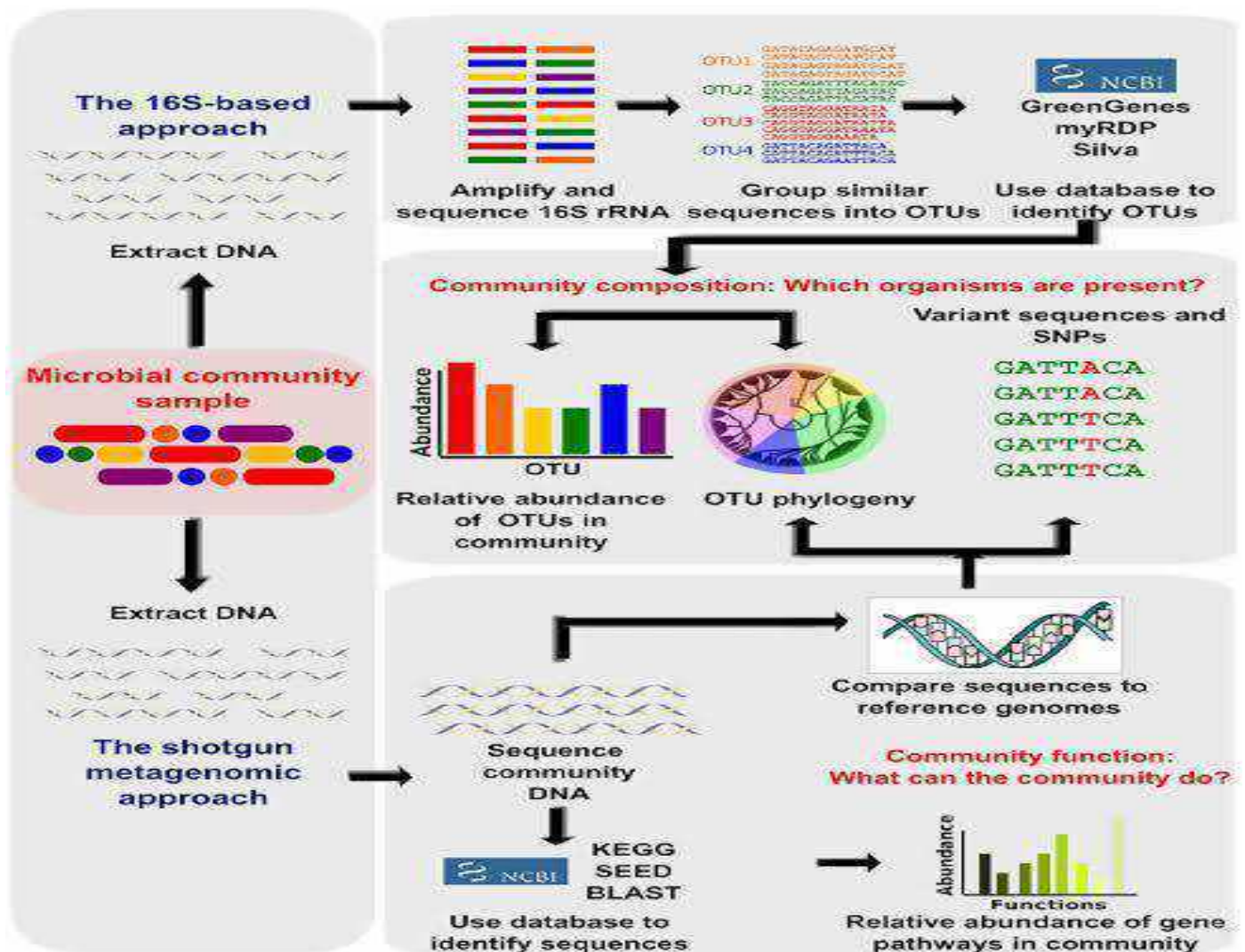
The decreasing cost and increasing speed of DNA sequencing, coupled with advances in the computational approaches used to analyse complex data sets^{7,8,9,10,11}, have prompted several research groups to embark on

small-subunit (16S) ribosomal RNA gene-sequence-based surveys of bacterial communities that reside on or in the human body, including on the skin and in the mouth, oesophagus, stomach, colon and vagina.

Ecosystem-Level Functions

Comparative metagenomics has uncovered functional attributes of the microbiome. The first reported application of metagenomic techniques to a human microbiome involved two unrelated, healthy adults. Compared with all previously sequenced microbial genomes and the human genome, metabolic reconstructions of the gut (faecal) microbiomes of these adults showed significant enrichment for genes involved in several metabolic pathways: the metabolism of xenobiotics (that is, foreign substances), glycans and amino acids; the production of methane; and the biosynthesis of vitamins and isoprenoids through the 2-methyl-D-erythritol 4-phosphate pathway.

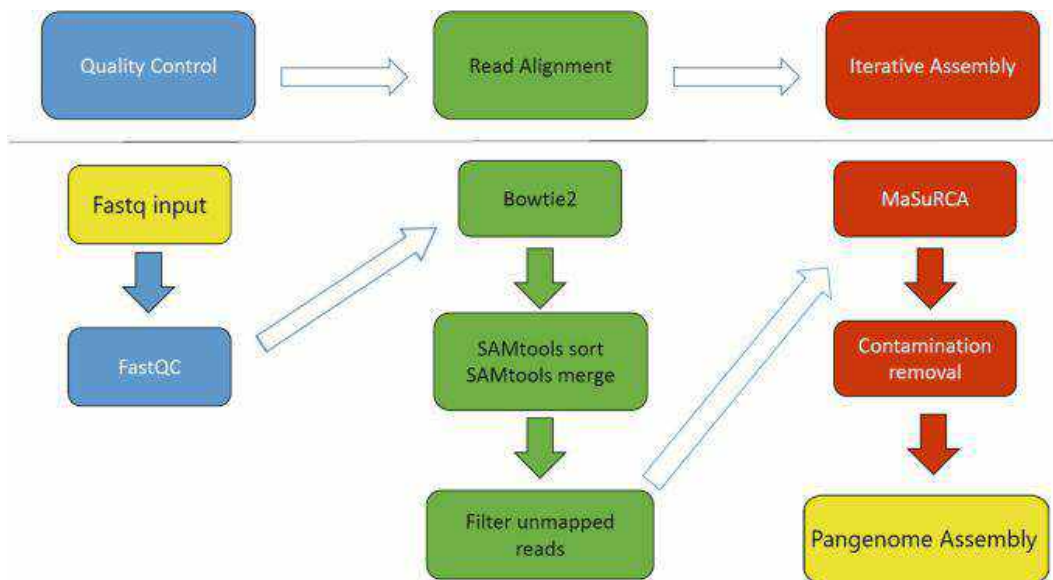
Metagenomics Technique



From One Genome to Many Genomes: The Evolution of Computational Approaches for Pangenomics and Metagenomics Analysis

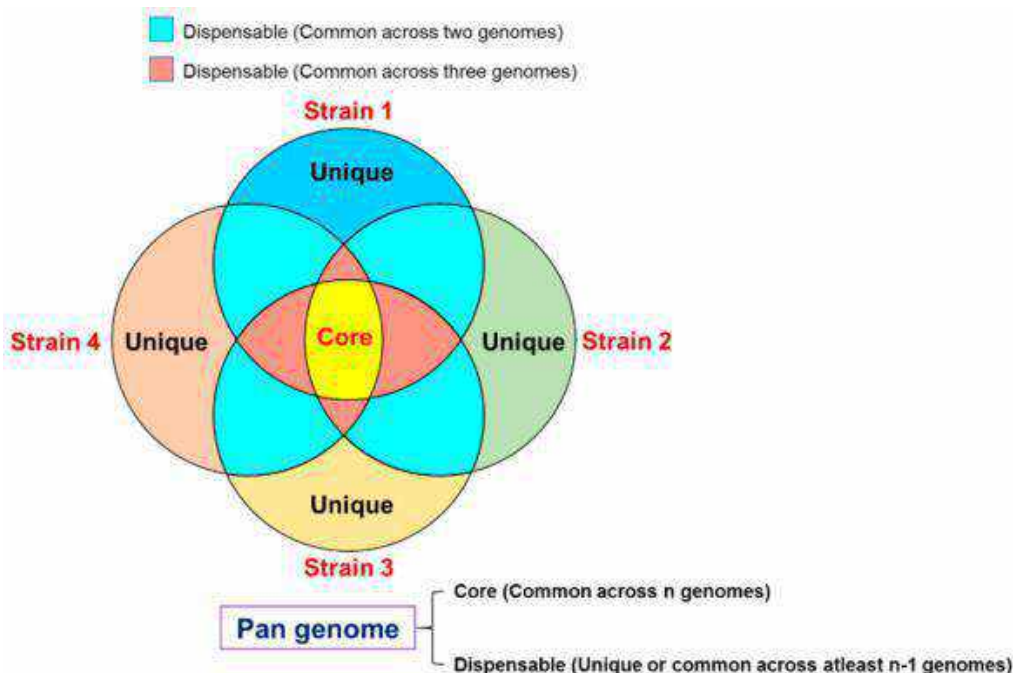
In the last few decades, the evolution of sequencing technologies has revolutionized genome analysis, pushing towards the design of scalable computational approaches for the analysis of massive datasets produced by both popular short read sequencers, and more recent long read technologies. Besides scalability, the third-revolution in sequencing technologies calls for the methodological re-thinking of many classic sequencing-related problems (e.g. mapping, assembly, and error correction) due to the different nature of sequencing errors on longer reads. But even more computational challenges are brought into play by the “conceptual shift” from the single-genome analysis paradigm to the many-genomes paradigm that the huge amount of available sequencing projects now allows. Moreover, depending on what we mean by “many”, we can intercept different biological contexts, together with their associated computational problems: pangenomics, where several genomes from the same species are considered in the analysis; and metagenomics, where the genomes of several different species are present in the same sample. The algorithmic answer to these challenges has just begun, starting with the proposal of graph-based representations and the exploitation of compressed indexes and learning algorithms. However, there are still many open computational challenges to be addressed to enhance the many-genomes paradigm with tailored processing capabilities to tackle specific biological questions. The goal of this Research Topic is to generate a collection of high-quality papers describing a next-generation of practical and scalable bioinformatics tools that are specifically designed to index and process several genomes at once, exploiting state-of-the-art research on compressed data structures, graph representations of genomes, combinatorial pattern matching, sketching techniques, artificial intelligence and machine learning. The advantages of designing and exploiting efficient data representations, together with tailored algorithms for multiple genome analysis, will bring together not only a more rational use of computational resources (and associated running costs), but will also allow researchers to infer more information from the comparative analysis of larger datasets, thus leading to higher quality results on associated biological analyses. We are interested in submissions describing novel algorithms, data structures, and tools for processing genomic datasets that represent more than one genome, with application to pangenome or metagenome analysis. Techniques developed for either short or long reads (or combination of both) are welcome. Besides the description of the methodological aspects, submissions should include experiments showing the practical applicability of the proposed methods. A limited number of papers presenting a perspective or reviews including comparative analysis of state-of-the-art tools are also welcome.

Pangenomes representations- A pangenome models the full set of genomic elements in a given species or clade. Pangenomics thus stands in contrast to reference-based genomic approaches which relate sequences to a particular consensus model of the genome. Genomes that are reconstructed with the aid of a reference genome can appear more similar to the reference than they actually are. Pangenomic reference systems can reduce this bias by enabling the direct relationship of new genome to all those represented in the pangenome.



Metagenomics Samples Comparison-

Sequence signatures, as defined by the frequencies of k-tuples (or k-mers, k-grams), have been used extensively to compare genomic sequences of individual organisms, to identify cis-regulatory modules, and to study the evolution of regulatory sequences. Recently many next-generation sequencing (NGS) read data sets of metagenomic samples from a variety of different environments have been generated. The assembly of these reads can be difficult and analysis methods based on mapping reads to genes or pathways are also restricted by the availability and completeness of existing databases. Sequence-signature-based methods, however, do not need the complete genomes or existing databases and thus, can potentially be very useful for the comparison of metagenomic samples using NGS read data. Still, the applications of sequence signature methods for the comparison of metagenomic samples have not been well studied.



Bioinformatics and Computational Biology for Investigating the Impact of Food Metabolites on Human Health

It is widely known that bioactive food compounds affect the overall health of an individual, both physically and mentally, resulting in the prevention or reduction, but also in some cases on the contrary in the initiation of metabolic abnormalities and various diseases. However, due to the complex nature of food-bioactive compounds and the different mechanisms of absorption, metabolism, and excretion, the comprehension of the bioavailability and bioefficacy of the resulting primary and secondary metabolites, along with their possible synergistic or antagonistic effects or possible interaction targets still needs extensive research.



Moreover, due to this lack of standardized knowledge, there is lack in the regulatory measures for natural products and extracts that may be commercially available as therapeutic agents. Nowadays, bioinformatics is used in drug target identification and validation and in the screening of compounds' toxicological and pharmacological properties to maximize their therapeutic benefit, while minimizing their toxicological effect.

The main goal of this research topic is to address recent advances in the bioinformatics tools and the methodological in-silico approaches that could be used in the exploration of natural metabolites' bioactivity screening; giving also details and suggestions about workflow and protocols used by means of examples of case studies. Metabolomic

data already available from suitable database(s) or newly produced data, as long as the bioinformatics procedures of data analysis/production represent the main study approach, are accepted.

Data could derive from experiments on human cell lines, edible plants, farm animals, or other experimental setup/model providing direct correlation with human nutrition/health (murine models and similar are excluded). Discussion about the role of primary and secondary metabolites as markers for safety and quality of unprocessed/processed/ultra-processed foods is also encouraged, as well as "omic" approaches oriented to the investigation of the impact that genetic and environmental factors may have on the abundance of certain metabolites. We endorse the submission of purely in-silico studies as well as computational studies supported by biological assays or exploiting bioassay data as starting point of their research.



Phytoconstituents: An Alternative for Cancer Drug

Cervical cancer is a type of cancer that develops in the cells of the cervix, the lower part of the uterus that connects to the vagina. It is a leading cause of cancer deaths in women worldwide. It is primarily caused by persistent infection with certain types of human papillomavirus (HPV), a sexually transmitted infection. The current treatments for cervical cancer, such as chemotherapy and radiotherapy, have many side effects, and drug resistance is a significant challenge. Therefore, there is a need for alternative treatments for cervical cancer. Phytoconstituents have emerged as potential alternative treatments for various diseases, including cancer. Phytoconstituents are the natural chemical compounds present in plants. They can include a wide range of compounds, such as alkaloids, flavonoids, terpenoids, phenolics, glycosides, tannins, saponins, and many others. These compounds are not only responsible for the medicinal properties of plants but also contribute to their color, flavor, and aroma. These compounds are extracted from plants and used in various industries, including pharmaceuticals, herbal medicine, cosmetics, and food and beverage production. In this study, an in-silico analysis of phytoconstituents as a potential alternative for anti-cervical cancer drug therapy was performed. The research aimed to identify the natural inhibitors of HPV-16 E6 protein (4XR8) from various medicinal plants with lesser toxicity and higher potency.



Fig. PDB predicted 3Dstructure of HPV E6

In this study, phytoconstituents of various important traditional medicinal plants were selected for molecular docking with the target protein 4XR8 of HPV-16 E6. Molecular docking was performed by AutoDock software. Molecular Docking is a computational technique used in drug discovery and molecular biology. It involves the prediction of how small molecules, such as drug candidates, bind to a target protein or receptor. By simulating the interaction between the ligand (small molecule) and the receptor, molecular docking helps identify potential binding sites, evaluate binding affinities, and optimize drug design. This powerful tool plays a vital role in understanding molecular interactions and aiding the development of new therapeutics. After that ADME/T screening of the bioactive phytoconstituents was done by SwissADME. ADME is an acronym that stands for Absorption, Distribution, Metabolism, and Excretion. It refers to a set of pharmacokinetic parameters that play a crucial role in determining the fate and effectiveness of a drug in the body.

Absorption: Absorption is the process by which a drug enters the bloodstream from its site of administration. Factors such as the route of administration, solubility, and drug formulation influence the absorption of a drug.

Distribution: Distribution refers to the movement of a drug within the body after it has been absorbed into the bloodstream. Factors like protein binding, blood flow, and tissue permeability influence the distribution of a drug.

Metabolism: Metabolism involves the biochemical transformation of a drug into metabolites by enzymes in the body. The primary site of drug metabolism is the liver. The metabolites produced can have different pharmacological properties compared to the parent drug.

Excretion: Excretion refers to the elimination of drugs and their metabolites from the body. The main routes of excretion are through urine, faeces, bile, sweat, and breath. The kidneys and liver play critical roles in drug excretion. The docking results showed that some phytoconstituents had good binding affinity with the target protein, suggesting that these compounds could potentially be used as anti-cervical cancer drugs. Among all the selected phytoconstituents eriodictyol-7-glucuronide, stigmasterol, rutin, pikuroside, thalirugidine, and curcumin showed the best interactions with a docking score of - 9.27, -9.43, -8.83, -8.6,-8.43, and -8.21 kJ/mol. Based on the ADME screening, only three phytoconstituents namely stigmasterol, thalirugidine and curcumin were selected as the best inhibitor of HPV E6 protein.

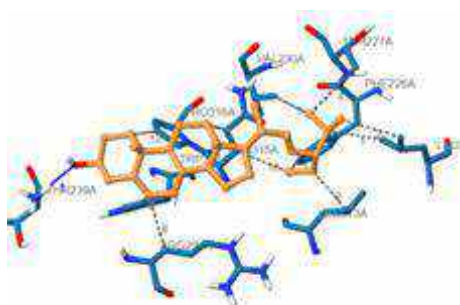


Fig. 2

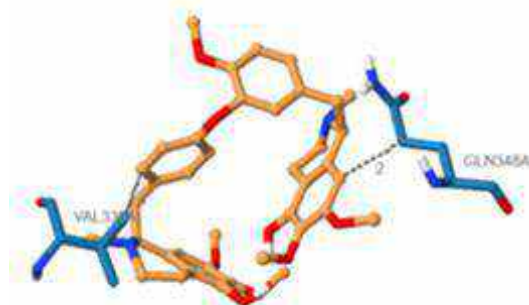


Fig. 3

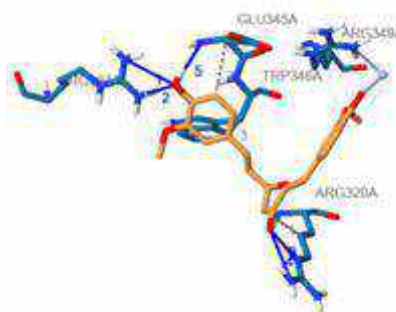


Fig. 4

Protein-ligand interaction diagram in 3D of: - 2.) Stigmasterol 3.) Thalirugidine 4.) Curcumin with E6 protein.

Internships, Summer Trainings & Industrial Visits

Sponsored Internship

Mission Amrit Sarovar “Jal Dharohar Sanrakshan Internship”

An internship in formulating a rejuvenation and reimagination strategy for Naukuchia Taal, Ranikhet, Uttarakhand, offered by Ministry of Housing & Urban Affairs, Government of India and implemented by AICTE from 1st July 2022 to 5th August 2022. The following students of B. Tech final year (Batch; 2019-2023) participated in the above mentioned internship under the mentorship of Dr. Sachin Kumar Tomar, Assistant Professor, Department of Biotechnology, MIET, Meerut. The students received “AICTE Grant-Mission Amrit Sarover-N”

Abhishek Kumar Singh
Ashutosh Singh

Kapil Kumar
Sagar Verma

Shubham
Suryansh Mishra



Summer Training Report (Batch 2019-23)

S. No.	Roll No.	Name of Student	Topic	Organization
1	1900680540001	Abhishek Kumar Singh	Formulating a Rejuvenation and Reimagination Strategy for Naukuchia Taal, Ranikhet, Uttarakhand	AICTE
2	1900680540002	Akanksha Singh	Training in Lab Medicine	Brahmanand Narayan Multispeciality Hospital
3	1900680540003	Akshita Panwar	Department of Pathology	Metro Multispeciality Hospital, Noida
4	1900680540004	Akshita Sharma	Bioinformatics	Edulife India, Bangalore, Karnataka
5	1900680540005	Amit Mani Tripathi	Antifungal testing of Essential Oils of Higher Plants	Department of Botany of Banaras Hindu University, Varanasi
6	1900680540006	Anjali Tanwar	Plant Extraction for Phytochemical Analysis	MIET, Meerut
7	1900680540008	Ansh Aggarwal	Basic Techniques on Plant Tissue Culture	Forest Research Institute, Dehradun, Uttarakhand
8	1900680540010	Anushka	Organic Manure	IIT BHU, Varanasi
9	1900680540011	Apoorva Suman	Diagnostic Lab Technician	Mangal Diagnostic Centre, Deoria
10	1900680540012	Archit Mohan Shukla	Principles of Drug Discovery and Development	Department of Biosciences and Bioengineering, IIT Indore
11	1900680540013	Arti Gupta	Study of Principles & Methods of Preparation of Platelet-Rich Plasma (PRP), Washed Platelet Isolation and Biochemical Techniques	Department of Biochemistry IMS, BHU, Varanasi
12	1900680540014	Ashutosh Singh	Formulating a Rejuvenation and Reimagination Strategy for Naukuchia Taal, Ranikhet, Uttarakhand	AICTE
13	1900680540015	Ayushi Chauhan	Microbiological Analysis of Pharmaceutical Products	AKUMS Drugs and Pharmaceutical Ltd. Sidcul, Haridwar
14	1900680540016	Chanda	Food Analysis	FICCI Research and Analysis Centre, New Delhi
15	1900680540017	Dukx Tyagi	Various Food Biotechnology Techniques	Helix BioGenesis
16	1900680540018	Hemant Rathore	Introduction to Forensic Science	Nanyang Technological University

17	1900680540019	Kapil Kumar	Formulating a Rejuvenation and Reimagination Strategy for Naukuchia Taal, Ranikhet, Uttarakhand	AICTE
18	1900680540020	Manjari Agrawal	Molecular Modeling and Docking Study of Essential Proteins from Marburg Virus	Bioinformatics Centre, Biotech Park, Lucknow
19	1900680540021	Neha Chaudhary	HR Generalist & Patroll Training Course	Tareeqa Global Solution Pvt. Ltd
20	1900680540022	Niti Choudhary	Various Food Biotechnology Techniques	Helix BioGenesis
21	1900680540023	Ritika	Industrial Training on Some Instruments such as Laminar Air Flow, Micropipette, Autoclave and Incubator	Weldon Biotech India Pvt. Ltd
22	1900680540024	Ritika Goswami	Production Department and Quality Analysis of Fast Foods	Fast Foods Pvt. Ltd.(Britannia) Ghaziabad
23	1900680540025	Riya	Food Analysis	FICCI Research and Analysis Centre, New Delhi
24	1900680540026	Roshni Bharti	Plant Extraction for Phytochemical Analysis	MIET, Meerut
25	1900680540027	Sagar Verma	Formulating a Rejuvenation and Reimagination Strategy for Naukuchia Taal, Ranikhet, Uttarakhand	AICTE
26	1900680540028	Saumya Singh	Training on Sterilization	Alexis Sterile Industries LLP, New Delhi
27	1900680540029	Shailja Bhardwaj	Laboratory and R & D Department	Nanglamal Sugar Complex, Meerut
28	1900680540030	Shikha Singh	Various Activities of Space Food Research and Product Development	Space Food Club
29	1900680540031	Shubham	Formulating a Rejuvenation and Reimagination Strategy for Naukuchia Taal, Ranikhet, Uttarakhand	AICTE
30	1900680540032	Simran Sharma	HR Generalist & Patroll Training Course	Tareeqa Global Solution Pvt. Ltd
31	1900680540033	Srishti Kapoor	Plant Extraction for Phytochemical Analysis	MIET, Meerut
32	1900680540034	Suryansh Mishra	Formulating a Rejuvenation and Reimagination Strategy for Naukuchia Taal, Ranikhet, Uttarakhand	AICTE
33	1900680540035	Umang Sharma	Food Production and Analysis	ITC Ltd. Kolkata
34	1900680540036	Vandana Vishwakarma	Develop a POC Detection Kit for Bilirubin Present Serum	IIT Guwahati
35	1900680540037	Vanshika Rana	Microbiological Analysis of Pharmaceutical Products	AKUMS Drugs and Pharmaceutical Ltd. Sidcul, Haridwar

**Industrial Visit to Patanjali, Haridwar (18-November, 2022)
Batch 2020-2024 & 2021-2025**

B. Tech Biotechnology students of batch 2020-2024 & 2021-2025 got an opportunity to visit **Patanjali, Haridwar** on 18-November, 2022 to know about the production and packaging of the many Patanjali products, such as toothpaste, soap, skin lotions, shampoos, etc. **Dr. Udai Pratap Singh, Ms. Nitika Vats, Dr. Sachin Kumar Tomar** and **Dr. Jayprakash Yadav** assisted the students for this visit.



A Visit to “MIET Sewage Treatment Plant”

The main purpose for this visit was to get the practical knowledge about water treatment plant process along with different units. Also in 7th semester subject like Environmental Biotechnology requires knowledge about how components of sewage plant are constructed, so it is very much convenient to see all the practical and components in real time work environment.

On 16th November, 2022, we reached at sewage treatment plant of MIET, Meerut. The visit started from the initial tank, where the waste water of MIET, Meerut was collected.

From this visit, the students of B. Tech VII Semester got the information and practical knowledge about the treatment of waste water and components used in treatment plant along with the detailed process of treatment.



MIET Sewage Treatment Plant



Wastewater collection tank



Step 1: Screening



**Step 3: Secondary treatment
(Aeration / Activated Sludge)**



**Step 2: Primary treatment
(Primary sedimentation tank)**




**Step 4: Secondary settling
(Secondary sedimentation tank)**



**Step 5: Sludge Digestion
(Anaerobic digester)**

National Seminar on “Unleashing the Power of Personal Branding for Students”

Dr. Bhumica Agarwal (Marketing Consultant and Personal Branding Expert) explained the importance of personal branding. How a person can make/develop his/her brand? was the main focus of the event. She also discussed the importance of LinkedIn, Twitter, Instagram and Facebook for personal branding.

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**MEERUT INSTITUTE OF ENGINEERING & TECHNOLOGY
MEERUT (U.P.)**

DEPARTMENT OF BIOTECHNOLOGY


*National Seminar
on*

“Unleashing the Power of Personal Branding for Students”

Date: April 28, 2023; Time: 02:00 PM; Venue: Seminar Hall (Room No. 130)



Keynote Speaker
Dr. Bhumica Agarwal
(Marketing Consultant & Personal Branding Expert)



Moderator
Dr. Ashima Kathuria
(Professor-Biotechnology, MIET)

Event Co-ordinator: Ms. Kanchan Sharma (Assistant Professor), E-mail: kanchan.sharma@mi et.ac.in; +91-7838064094
MBS Co-ordinator: Dr. Gourav Mishra (Assistant Professor), E-mail: gourav.mishra@mi et.ac.in; +91-9408353322



Events Organized

IPR Awareness Programme (Under National Intellectual Property Awareness Mission)

Office of the Controller General of Patents, Designs & Trademarks, Ministry of Commerce and Industry, in collaboration with **Department of Biotechnology, MIET, Meerut**, organized an IPR awareness programme (under **National Intellectual Property Awareness Mission: NIPAM**) on **November 17, 2022**. An insightful knowledge about Patents, Designs & Trademarks were delivered by **Shri Lokesh Mohan Sharma** (NIPAM Officer). B. Tech Biotechnology students and faculties interacted with Shri Lokesh Mohan Sharma, resulting in awareness about IPR and career opportunities in IPR domain.

Intellectual Property India
NATIONAL INTELLECTUAL PROPERTY AWARENESS MISSION

MIET

Government of India
Ministry of Commerce and Industry
Department for Promotion of Industry and Internal Trade

Office of the Controller General of Patents, Designs & Trademarks
in collaboration with
Department of Biotechnology, Meerut Institute of Engineering & Technology, Meerut (U.P.)
organizes

IPR Awareness Programme
(Under National Intellectual Property Awareness Mission)

Invited Speaker



Shri Lokesh Mohan Sharma
(NIPAM Officer)
Examiner of Patents & Designs
IP Office, New Delhi

Date: November 17, 2022
Time: 11:00 AM onwards
Mode: Offline
Venue: Seminar Hall (Room No. 130),
Biotechnology Block, MIET, Meerut

Azadi Ka Amrit Mahotsav

Creative India; Innovative India

* Registered participants will receive Certificate from The Patent Office, Government of India *



Free Dental Checkup and Health Camp

A Free Dental Checkup and Health Camp was organized on 7th February, 2023, by Department of Pharmaceutical Technology and Department of Biotechnology in collaboration with Subharti Dental College, Meerut. The main aim of the event was to make students aware of the cleaning and maintenance of teeth and students were also advised about the proper ways of brushing their teeth.

निःशुल्क दंत चिकित्सा शिविर का आयोजन, सौ से अधिक विद्यार्थियों का हुआ इलाज



पब्लिक एशिया व्यूरो

मेरठ। ओरल मेडिसिन एंड रेडियोलॉजी विभाग, सुभारती विश्वविद्यालय और फार्मेसी विभाग, एमआईटी के तत्वावधान में निःशुल्क दंत चिकित्सा शिविर का आयोजन किया गया। शिविर का उद्घाटन एमआईटी के चाइस चैयरमैन पुनीत अग्रवाल द्वारा किया गया। पुनीत अग्रवाल ने बताया कि एमआईटी शिक्षा के साथ-साथ अपनी सामाजिक उत्तरदायित्व को पूरा करने के लिए विभिन्न तरह के कार्यक्रमों का आयोजन करते रहा है। इस तरह के आयोजन से विद्यार्थियों में जागरूकता के साथ उनका सर्वांगीण विकास भी होता है। इस शिविर के आयोजन का मुख्य उद्देश्य छात्र-छात्राओं में दांतों के साफ-सफाई और देखभाल को लेकर जागरूकता लाना था। शिविर में विशेषज्ञ दंत चिकित्सक डॉ नागराजु उपस्थित थे।

उन्होंने विद्यार्थियों के दांतों की जांच की साथ ही ब्रश करने के तरीका बताया। चिकित्सक ने विद्यार्थियों को दांतों की सुरक्षा और देखभाल से संबंधित आवश्यक जानकारी के शिविर में 100 से अधिक विद्यार्थियों ने अपने दांतों की जांच कराई। ओरल मेडिसिन एंड रेडियोलॉजी विभाग, सुभारती विश्वविद्यालय से असिस्टेंट प्रोफेसर डॉ अभिनव शर्मा, डॉ मर्याद डिपार्टमेंट ऑफ पीपचडी, डॉ उल्कर्ष, डॉ बिंदु, डॉ कृष्ण, शिवेंद्र, समृद्धि, सौम्या, अहमद रिजवी, अनन्या ने शिविर में छात्र छात्राओं के दांतों की जांच की। फार्मेसी विभाग से प्राचार्य डॉ गरिमा गर्ग और बायोटेक्नोलॉजी विभागाध्यक्ष डॉ उदय प्रताप सिंह ने दंत चिकित्सक डॉ नागराजु और उनकी टीम को शिविर के सफल आयोजन के लिए धन्यवाद दिया। इस अवसर पर मुख्य रूप से विशि खन्ने, डॉ नेहा सिंह, डॉ नाजिया सिद्दीकी मौजूद रहे।



World Health Day 2023

Department of Pharmaceutical Technology and Department of Biotechnology organized a National Seminar on "World Health Day 2023" on 7th April, 2023. Dr. Bhavna Gandhi reminded us the importance of healthy diet for maintaining good health.



Organize by:

Department of Pharmaceutical Technology and Department of Biotechnology

Student Achievements

Student Achievements

Area	Name	Roll No.	Course	Event	Recognition
Academic	Istuti Gupta	1806854027	B. Tech	Master of Science University Merit (Chemical Engineering Group)	University of Alberta, Canada 4th Rank
	Ansh Agarwal	1900680540008	B. Tech	International Conference	Best Paper Award
	Narayan Chaudhary	2000680545002	M. Tech	International Conference	Best Oral Presentation
	Akshita Sharma	1900680540004	B. Tech	Poster Making Competition	2nd Position
Cultural	Akshita Sharma	1900680540004	B. Tech	Group Discussion Event	2nd Position
	Akshita Sharma	1900680540004	B. Tech	Kai Poche Event	1st Position
	Anishka Khari	2100680540009	B. Tech	Duet Dancing	1st Prize
Sports	Anjali Tanwar	1900680540006	B. Tech	Sports Fest (Zonal Level)	Winner Position
	Vanshika Rana	1900680540037	B. Tech	Sports Fest (Zonal Level)	Gold Medal





69% Placement
(Till publication)

in
Department of Biotechnology
Our Major Recruiters in 2023



Batch 2019-23 Placement Record

S.No	Roll No.	Student Name	Organization
1	1900680540002	AKANKSHA SINGH	Cognizant
2	1900680540003	AKSHITA PANWAR	Saraca
3	1900680540004	AKSHITA SHARMA	Planet Spark
4	1900680540005	AMIT MANI TRIPATHI	Saraca
5	1900680540008	ANSH AGGARWAL	Saraca
6	1900680540011	APOORVA SUMAN	Saraca
7	1900680540012	ARCHIT MOHAN SHUKLA	Higher Studies (GATE Qualify)
8	1900680540013	ARTI GUPTA	Planet Spark
9	1900680540015	AYUSHI CHAUHAN	J. Mitra
10	1900680540016	CHANDA	Saraca
11	1900680540017	DUKX TYAGI	Hike education
12	1900680540019	KAPIL KUMAR	Swastik Agro food
13	1900680540020	MANJARI AGRAWAL	J. Mitra
14	1900680540021	NEHA CHAUDHARY	ShiftPurple
15	1900680540022	NITI CHOUDHARY	Hike Education
16	1900680540024	RITIKA GOSWAMI	G.G. Enterprises
17	1900680540025	RIYA	Higher Studies (Indraprastha Institute of Information Technology Delhi; IIIT-Delhi)
18	1900680540026	ROSHNI BHARTI	Higher Studies (GATE & GAT-B Qualify)
19	1900680540028	SAUMYA SINGH	Root Analysis
20	1900680540029	SHAILJA BHARDWAJ	Learning Shala/Verzeo/Saraca
21	1900680540030	SHIKHA SINGH	Verzeo
22	1900680540031	SHUBHAM	Swastik Agro food
23	1900680540035	UMANG SHARMA	Higher Studies (GATE Qualify)
24	1900680540037	VANSHIKA RANA	J. Mitra

About Department of Biotechnology

Courses Offered:

- B.Tech
- M.Tech

Approvals & Accreditations:

- Approved by AICTE
- Affiliated with AKTU
- NBA Accredited

Laboratory Facilities:

- DST-FIST Center
- Medical Translational Biotechnology Research Lab
- Nanotoxicity & *Drosophila* Research Lab
- Analytical Biochemistry Lab
- Cellular and Microbiology Lab
- Instrumentation Lab
- Bioinformatics Lab
- Bioprocess and Protein Engineering Lab
- Plant Tissue Culture Lab
- Genetics and Molecular Biology Lab

Extracurricular Activities:

- Sanskriti - The Tradition Goes On...
- Abhivyakti - The Literary Lore
- Odyssey, The Literati....
- Sports Committee
- The Land of Art
- RIM4.0
- AHIMSA- Quest for Peace and Change

Other Important Activities:

- Guest Lectures
- Personality Development Programs
- Alumni Connect Sessions
- Mentoring Classes
- Industrial Visits





Department Of Biotechnology

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