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Editorial

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Mini review section – Infectious diseases remain a major global health concern, with a growing burden of antimicrobial resistance and consequent higher mortality in the human population. Accurate bacterial identification is fundamental across clinical, veterinary, agricultural, and research settings, supporting effective diagnosis, antimicrobial stewardship, infection control, food safety, and environmental monitoring; however, conventional approaches are limited by time constraints, reduced sensitivity, and challenges in detecting fastidious or uncultivable organisms.

Current Trends section – The integration of AI in microbiology is not limited to a single domain but spans virology, parasitology, mycology and bacteriology. The synergy of AI with advanced data collection devices, enhanced computing power and global networks, epitomized by Big Data, Moore's Law, and the Internet has catalysed the effective application of AI in microbiology. This fusion is particularly evident in the field of drug design, where AI-driven approaches are pioneering the development of novel antibiotics to combat multidrug-resistant organisms, a looming threat to global health. AI's role in clinical microbiology is equally transformative, optimizing data processing and enhancing diagnostic accuracy

In Profile Scientist – Dr. Maurice Ralph Hilleman (1919–2005) was one of the most influential vaccinologists of the 20th century. Although his name is not as widely recognized as those of Louis Pasteur, Edward Jenner, Jonas Salk, or Albert Sabin, his contribution to human health was extraordinary. Hilleman was involved in the development of more than 40 experimental and licensed vaccines, many of which protected people against serious diseases such as measles, mumps, rubella, hepatitis A, hepatitis B, chickenpox, meningitis, pneumonia, and influenza. His work fundamentally changed modern vaccinology and helped protect millions of people from infectious diseases.

Bug of the month – *Morbillivirus* is a genus of viruses belonging to the family **Paramyxoviridae**. These viruses are important pathogens because they can cause highly contagious diseases in humans and animals. The best-known member of this genus is **measles virus**, which causes measles in humans. Other members include **canine morbillivirus**, which causes canine distemper, and viruses that infect marine mammals such as seals, dolphins, and porpoises. Morbilliviruses are particularly significant in medicine and veterinary science because they can spread efficiently among susceptible populations and, in some cases, cause severe disease involving multiple organs.

Did You Know? -- Caffeine is the most widely used stimulant and psychoactive substance in the world, and coffee is how most people consume it. According to a new scientific statement from the American Heart Association, most adults can safely consume up to 400 mg of caffeine/day (or up to five 8-ounce cups of caffeinated coffee per day). For some people, moderate coffee consumption may also be associated with a lower risk of cardiovascular disease.

Best Practices – In today's office environment we put in 6, 8 or more hours at our desks with laptops, desktop monitors, smartphones and in video meetings. We spend long times up close to screens which can leave the eyes dry, tired, irritated, or with temporary blurriness. In recent years, many people would probably say the time they spend looking at displays has increased. In addition to televisions and PCs, smartphones and tablets have quickly become popular, and displays have penetrated every aspect of our lives. Information technology has made our lives more convenient, but at the same time, eye fatigue caused by continuous viewing of displays has increasingly become a social problem.

Tickle yourself to enjoy the jokes in our **Relax Mood section**.

Our JHS team is thankful to all our readers for their ever-increasing appreciation that has served as a reward & motivation for us. Looking forward to your continuous support.

Evolving Approaches to Bacterial Identification: A Review of Classical and Modern Techniques

Infectious diseases remain a major global health concern, with a growing burden of antimicrobial resistance and consequent higher mortality in the human population. Accurate bacterial identification is fundamental across clinical, veterinary, agricultural, and research settings, supporting effective diagnosis, antimicrobial stewardship, infection control, food safety, and environmental monitoring; however, conventional approaches are limited by time constraints, reduced sensitivity, and challenges in detecting fastidious or uncultivable organisms. Global analysis indicates that more than 39 million people around the world could die from antibiotic-resistant infections between 2024 and 2050. Therefore, early and effective management of bacterial infectious diseases is a priority area that necessitates a multifaceted approach, including accurate microbiological diagnosis.

Current Methods for Bacterial Identification

Methods for bacterial detection and identification are commonly classified as phenotypic or genotypic, and as culture-based or culture-independent. Classical methods, often referred to as traditional approaches, rely mainly on phenotypic, culture-based techniques, including microscopic examination, assessment of colony morphology, and biochemical tests evaluating metabolic and enzymatic activities.

1) Microscopic Examination of Bacteria

Although bacterial identification methods have advanced significantly, microscopic assessment remains important in microbiological diagnostics.

The **Gram stain** remains the most widely used staining technique and cornerstone of bacterial microscopy, distinguishing Gram-positive from Gram-negative bacteria based on cell wall composition, providing information on morphology (cocci, bacilli, and coccobacilli) and arrangements (chains, clusters, palisades, “Chinese letter,” or seagull-wing patterns).

Acid-fast (Ziehl–Neelsen) staining is a cost-effective primary tool for tuberculosis diagnosis and guides further analyses. Besides *Mycobacterium* species, other acid-alcohol resistant bacilli (ARB) include *Nocardia* and *Rhodococcus*.

Special stains are highly specific techniques designed to highlight unique, specialized structures, such as capsules, flagella, or spores that are not present in all bacteria.

Microscopic examination of colonized sites (e.g., wound samples) helps distinguish true infection from colonization, as the presence of polymorphonuclear leukocytes indicates active infection. Gram-stained smears also differentiate true sputum from saliva: 10–25 squamous epithelial cells per low-power field indicate contamination, while leukocyte-rich, low-epithelial samples should be considered lower respiratory tract specimens and are suitable for culture.

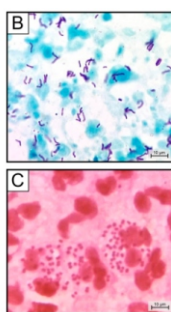
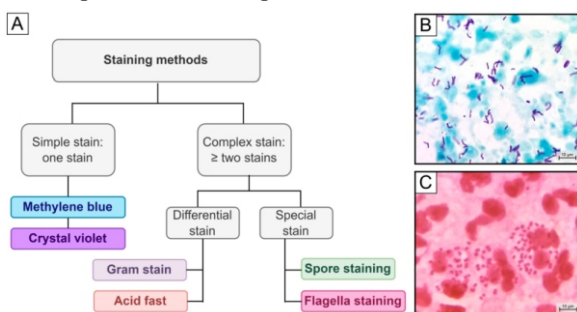
Microscopy alone can provide a final diagnosis in selected cases: in bacterial vaginosis, vaginal Gram stain, the reference method, quantifies lactobacilli, small Gram negative and Gram-variable rods (i.e., *Gardnerella vaginalis* or *Bacteroides*), and curved Gram-negative rods (i.e., *Mobiluncus*). In men, urethral discharge microscopy can confirm symptomatic gonorrhoea, as Gram-stained smears showing polymorphonuclear leukocytes with intracellular Gram-negative diplococci are highly specific and sensitive and can be considered diagnostic for *Neisseria gonorrhoeae* infection in symptomatic cases.

However, detection thresholds in microscopy vary: Ziehl–Neelsen staining for *M. tuberculosis* requires $\sim 10^4$ bacilli/mL, Gram staining 10^5 – 10^6 bacteria/mL, and urethral smears for gonorrhoea > 10 – 10^2 intracellular diplococci per oil-immersion field. While rapid and inexpensive, microscopy is less sensitive than culture or molecular methods and is operator-dependent, though automation improves reproducibility and turnaround time.

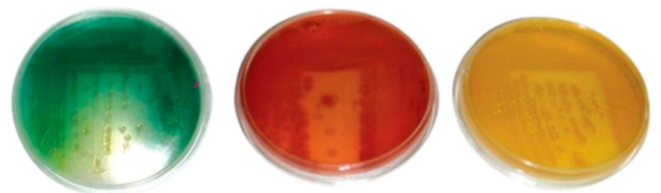
2) Bacterial Cultures

Clinical microbiology laboratories use culture-based methods to grow bacteria, enabling isolation and preliminary identification based on metabolic and nutritional characteristics. Culture media may be liquid (broth), solid, or biphasic (e.g., blood culture bottles) and are generally classified as basal, enriched, selective, differential, or chromogenic, with some media combining multiple properties.

Colony features, morphology, color, and sometimes odor aid identification. For instance, *Pseudomonas* spp. produce pigments, *Serratia marcescens* develops red colonies at room temperature, *Proteus* spp. show swarming growth with a putrid odor, and *Bacillus anthracis* forms non-hemolytic “medusa-head” colonies. Bacterial growth depends on O_2 , CO_2 levels, and temperature; typical requirements and incubation times.



(A): Classification; examples of differential stains: Gram stain; (B): Positive Ziehl–Neelsen stain, with acid-alcohol-resistant bacilli (ARB); (C): Intracellular Gram-negative *N. gonorrhoeae* diplococci.



Pure bacterial cultures of *Pseudomonas* spp. (different pigments production on Mueller–Hinton agar, 37 °C, aerobic conditions, 24 h incubation).

While culture-based methods remain central to bacterial identification, primarily because they enable AST on isolated

strains, certain organisms cannot be cultivated using bacterial culture media, including *Mycobacterium leprae*, *Treponema pallidum*, and obligate intracellular bacteria like *Chlamydia* spp. and *Rickettsia* spp. Some pathogens are slow growing, such as *Mycobacterium tuberculosis* and *Legionella pneumophila*. Such limitations underscore the importance of complementary approaches, including microscopy, antigen detection, and molecular assays, to ensure timely and accurate diagnosis.

3) Biochemical Tests

Bacteria produce characteristic sets of enzymes and metabolites that biochemical tests exploit for identification and preliminary differentiation. These assays detect enzyme– substrate reactions, often via colour change, using minimal culture and yielding results within minutes to 24 h.

The **catalase test** detects the enzyme catalase and is commonly used to differentiate catalase-positive *Micrococcaceae* from catalase-negative *Streptococcaceae*.

The **oxidase test** detects cytochrome oxidase, primarily used to distinguish oxidase positive *Pseudomonaceae* from oxidase-negative *Enterobacteriaceae*.

The **urease test** detects urease activity, enabling rapid identification of urease-positive organisms, including *Helicobacter pylori* in gastric biopsies, and supporting differentiation of certain Gram-negative coccobacilli.

Some bacteria (e.g., *E. coli*) produce indole from tryptophan via tryptophanase.

BIOCHEMICAL TESTS

FOR IDENTIFICATION OF PATHOGENS AND ANTIBIOTIC-RESISTANT BACTERIA



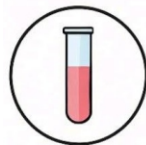
Catalase Test

DETECTS:
Enzyme catalase



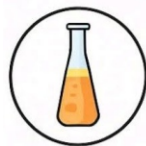
Oxidase Test

DETECTS:
Cytochrome c oxidase



Indole Test

DETECTS:
Tryptophanase enzyme



Methyl Red & Voges-Proskauer (MR-VP) Tests

DETECTS:
Acid/gas
Fermentation between mixers & butylene glycol producers



Urease Test

DETECTS:
Urease enzyme

Methyl Red & Voges-Proskauer (MR-VP) Tests



DETECTS:
Acid/gas production pathways

PURPOSE

Differentiate between mixed acid fermenters & butylene glycol producers

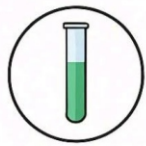
Triple Sugar Iron (TSI) Agar Test



DETECTS:
Urease enzyme

identifies
Proteus, *Klebsiella*

Citrate Utilization Test



DETECTS:
Ability to use citrate as sole carbon source

Differentiates between *Enterobacteriaceae*

4) Immunological Methods, Including Serology, in Bacterial Detection

Immunological methods detect bacteria via antigen–antibody reactions. Serology, in the narrow sense, refers specifically to antibody detection. Together, they enable rapid and specific identification of bacteria and their differentiation at the species or strain level.

i) Agglutination Tests

Agglutination methods identify conserved bacterial antigens or antibodies and can be divided into direct, such as slide agglutination, and indirect or passive, including latex agglutination, biosensor-based assays, and passive haemagglutination. **Slide agglutination** identifies bacteria by directly mixing colonies with specific antisera on a slide. **Latex agglutination** detects bacterial antigens through visible clumping between antibody-coated beads and bacterial cells. **Coagglutination** employs antibodies bound to carrier particles, such as protein A-coated cells, to detect bacterial antigens, and passive haemagglutination, such as TPHA, detects antibodies against pathogens like *T. pallidum*. Agglutination tests require fresh reagents and optimal colonies. Results may be compromised by low antigen levels, degraded antibodies, or improper colony selection.

ii) Enzyme-Linked Immunosorbent Assay

Enzyme-linked immunosorbent assay (ELISA) is widely used to detect antibodies in sera (indirect or competitive ELISA) or to identify bacteria directly (direct and sandwich ELISA).

In **direct ELISA**, immobilized antibodies bind the target antigen, and a chromogenic substrate produces a colour change for detection.

“**Sandwich**” ELISA is a highly sensitive and specific method for detecting bacteria in liquid samples, using a capture antibody immobilized on a microtiter plate and a secondary enzyme-labelled antibody to form an antibody–antigen “sandwich,” with signal intensity proportional to bacterial concentration. Its main limitation is its relatively high detection threshold, often requiring high bacterial loads (e.g., 10^5 – 10^7 CFU/mL for *E. coli* O157:H7).

ELISA is often preferred over traditional techniques due to its rapid turnaround time and suitability for high-throughput automation, but manual performance requires expertise and may affect reproducibility. An additional advantage of ELISA is that it provides quantitative results, enabling direct comparison between samples.

iii) Western Blot

Western blot (immunoblotting) is a confirmatory serologic technique detecting pathogen-specific antibodies or, less commonly, antigens after SDS–PAGE separation and membrane transfer. In *Borrelia burgdorferi* infection, it confirms positive or equivocal screening results by assessing reactivity to defined bands (e.g., OspC, p41, VlsE), with IgM indicating early and IgG multiple-band reactivity supporting later disease.

iv) Flow Cytometry

Flow cytometry (FCM) detects fluorescence from labelled probes to analyse cellular properties and identify specific populations. In microbiology, it enables rapid characterization of microorganisms, assessment of viability, pathogen detection, and monitoring of immune responses, thereby improving infection management. Alongside Gram staining and culture, FCM

complements routine diagnostics by providing rapid bacterial quantification. It has also been applied to detect and differentiate carbapenemase types in enterobacteria. For high-throughput single-cell detection and characterization of microorganisms, FCM can be combined with fluorescence in situ hybridization (Flow-FISH), which uses highly specific DNA or (m)RNA probes targeting the microorganism or transcript of interest.

v) Urinary Antigen Detection in Pathogen Identification

Immunological assays based on urinary antigen testing (UAT) are widely used for rapid detection of soluble bacterial antigens excreted in urine. Urine passes along a membrane containing antibodies against target bacterial antigens, and antigen binding generates a visible signal.

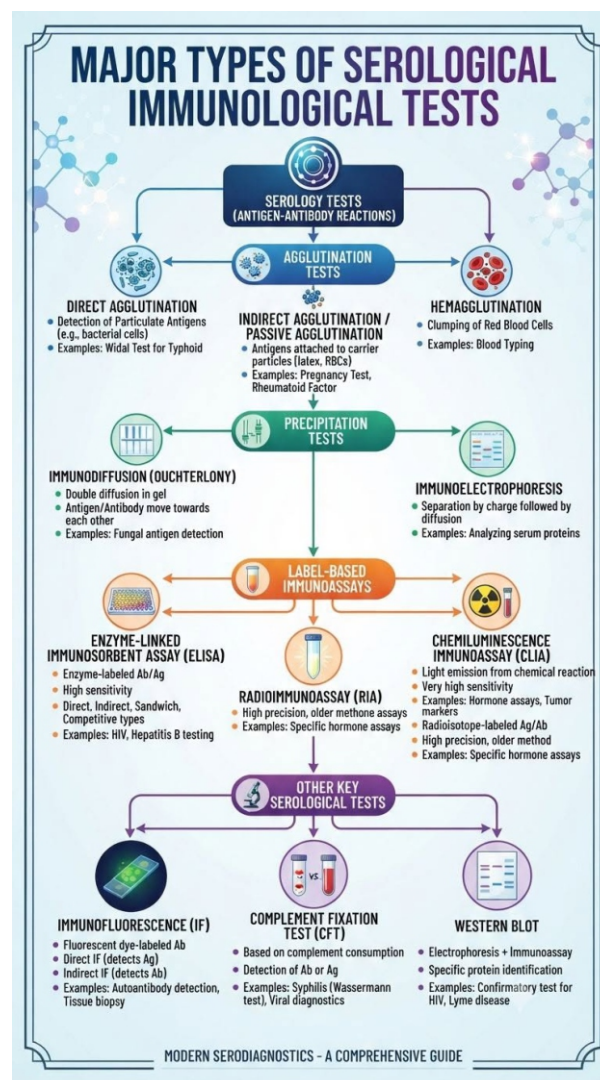
Compared with conventional microbiological methods, which often fail to identify the causative pathogen and therefore necessitate empiric therapy, UAT offers several advantages, including rapid turnaround time, non-invasiveness, high specificity (>95%), and moderate sensitivity (approximately 75–85%). These characteristics enable timely pathogen-directed therapy and may reduce complications associated with empiric antimicrobial treatment, including antimicrobial resistance and *Clostridioides difficile* infection.

vi) Lateral Flow Immunoassay

Lateral flow immunoassay (LFIA) is a chromatography-based technique that uses capillary flow of a liquid sample through device components, including the sample pad, conjugate pad, nitrocellulose membrane, absorbent pad, and backing layer. This platform is a rapid (5–20 min), point-of-care tool for on-site pathogen detection. The assay relies on antibodies or alternative bioreceptors targeting specific microbial epitopes. Antigen–bioreceptor binding is visualized as a test line, while a control line confirms proper sample migration and conjugate release.

Recent advancements include nanozyme-based labelling, improving signal amplification, stability, diagnostic accuracy, and usability. Thus, LFIA systems are increasingly incorporating nanoparticles instead of conventional antibodies. For instance, silver nanoparticle-enhanced LFIA enables detection of *Salmonella enterica* and *E. coli* O157:H7 in meat samples at

levels as low as 1–10 CFU/g [3]. Aptamers, synthetic DNA/RNA “chemical antibodies”, are emerging as stable, cost-effective alternatives to conventional antibodies.



Microbiology in the era of artificial intelligence: transforming medical and pharmaceutical microbiology

The integration of AI in microbiology is not limited to a single domain but spans virology, parasitology, mycology and bacteriology. The synergy of AI with advanced data collection devices, enhanced computing power and global networks, epitomized by Big Data, Moore's Law, and the Internet has catalysed the effective application of AI in microbiology. This fusion is particularly evident in the field of drug design, where AI-driven approaches are pioneering the development of novel antibiotics to combat multidrug-resistant organisms, a looming threat to global health.



AI's role in clinical microbiology is equally transformative, optimizing data processing and enhancing diagnostic accuracy. Techniques like matrix-assisted laser desorption/ionization time-of-flight mass spectrometry-(MALDI-TOF MS), coupled with AI, are revolutionizing microbial identification and antimicrobial resistance profiling, offering rapid, reliable and cost-effective solutions. Moreover, AI's capability to handle 'big data' such as genomic data and digital images from advanced diagnostic technologies is instrumental in refining laboratory reports and accelerating diagnostic processes.

The potential of AI in microbiology extends to addressing public health challenges, such as the management of infectious diseases and sepsis, where AI aids in diagnosis, prognosis and personalized treatment strategies. Furthermore, AI's application in infection prevention and control is notable, with its ability to analyse large health datasets, aiding in outbreak detection and infection control strategies.

Fundamentals of AI in microbiology

Machine learning (ML)

Machine learning, a vital component of artificial intelligence (AI), is reshaping microbiology. This technology offers robust methods for data analysis with applications ranging from microbial identification to predicting antibiotic resistance. The support vector machine (SVM) algorithm has been used to identify known and novel antimicrobial resistance genes in *Mycobacterium tuberculosis* using a dataset of over 1500 genomes.

Basics of machine learning

Machine learning enables computers to learn from data, making decisions autonomously. This is particularly beneficial in microbiology, allowing for new perspectives in microbial analysis, and significantly enhancing our understanding of microbial behaviour and disease outcomes.

Supervised learning

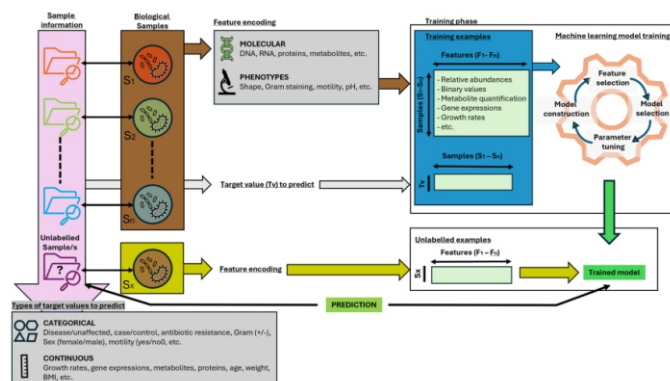
Supervised learning involves training algorithms with labelled datasets. In microbiology, this method is effective for tasks like predicting microbial behaviour or disease outcomes. Adaptive boosting classifiers are developed for identifying antimicrobial resistance in various bacterial species.

Unsupervised learning

Unsupervised learning involves analysing unlabelled data to uncover hidden patterns in complex microbial datasets. This method is invaluable for enhancing our understanding of diverse microbial communities and their relationships.

The role of deep learning

Deep learning, an advanced subset of machine learning, uses neural networks to process extensive datasets. In microbiology, deep learning models like deep antibiotic resistance genes (ARG) are used for predicting antibiotic resistance genes, aiding in environmental monitoring.



General workflow and example for machine learning applications in microbiology

Applications of AI in microbiology and current advances

Advancements in clinical diagnostics and disease identification

Artificial intelligence (AI) and machine learning (ML) are revolutionizing medical microbiology, offering rapid and precise diagnostics and treatments for infectious diseases. In malaria diagnosis, for example, ML techniques such as convolutional neural networks (CNNs) applied in computer-aided diagnosis (CADx) software significantly enhance the accuracy of identifying malaria-infected cells. Similar methodologies have advanced parasite detection in faecal samples, surpassing traditional human slide examination in sensitivity.

Automated systems are now capable of analysing laboratory samples represented as images, transforming the recognition of

bacterial genera and species. These systems identify bacteria based on shape, colour, and colony patterns, crucial in various sectors including medical, veterinary and food industries.

Epidemiology and disease prognosis

ML models like logistic regression (LR) and artificial neural networks (ANN) are used in epidemiology to predict patient outcomes for diseases such as Ebola virus disease (EVD).

Point-of-care (POC) diagnostics

The impact of ML on point-of-care (POC) diagnostics is transformative. In diagnosing sexually transmitted infections like trichomoniasis, ML algorithms distinguish between positive and negative cases using routine test results, such as urinalysis. This approach is particularly beneficial in resource-limited settings. Advances in smartphone technology have also enabled the development of mobile microbiological laboratories, making diagnostics more accessible.

Drug and vaccine discovery

ML is invaluable in identifying new compounds and vaccine candidates. It has been used to analyse data from public databases like opportunistic infection and tuberculosis therapeutics database (ChemDB) for potential antiviral compounds against human immunodeficiency virus (HIV), demonstrating its potential to accelerate drug discovery.

Antimicrobial resistance and outbreak prediction

ML plays a crucial role in understanding and combating antimicrobial resistance (AMR). It has been instrumental in identifying drug resistance in pathogens like tuberculosis (TB) and HIV, opening new avenues for resistance prediction and management. Additionally, ML has been used to predict disease outbreaks using data from non-traditional sources like social media and search engines, indicating its potential in real-time infectious disease tracking.

Microbial ecology and forensics

In microbial ecology, ML aids in understanding the interactions and dynamics of microbial communities. algorithms like random

forest (RF) have been used to predict interactions within ecosystems. Forensic microbiology benefits from ML in analysing post-mortem microbiomes, significantly contributing to forensic science and public health diagnostics.

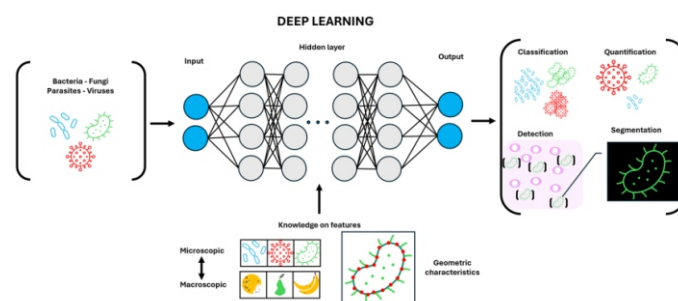
Dimensionality reduction and microbiome analysis

ML is crucial in microbiome analysis, especially in dimensionality reduction methods like the generalized linear model-based ordination method for microbiome samples (GOMMS). These techniques address challenges in microbiome dataset analysis, enhancing our understanding of microbial communities.

Enhancing productivity and precision in medical microbiology

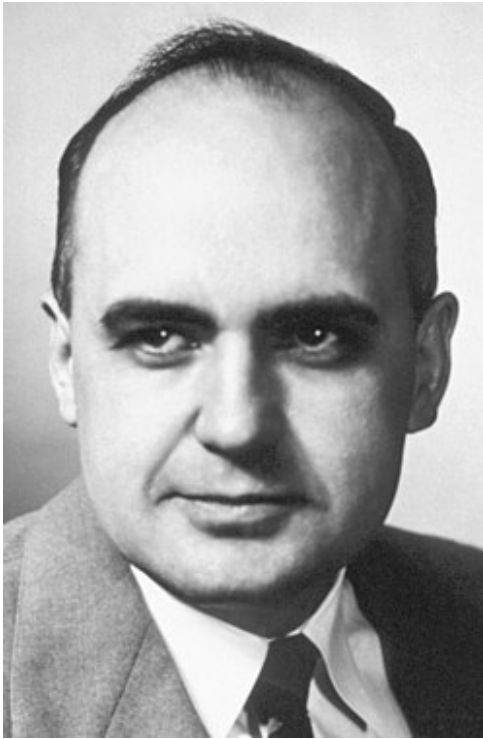
AI applications in microbiology are diverse:

- Automated interpretation of blood culture Gram stains using convolutional neural networks (CNNs).
- Automation in culture plate image analysis, improving sensitivity and time efficiency.
- Advancements in MALDI-TOF MS for direct sample identification and AMR detection.
- Using WGS and ML to predict AMR by analysing DNA sequences.



A schematic diagram illustrating the process of analysing microscopic images of microorganisms using deep learning techniques, focusing on the assessment of their geometric properties and macroscopic resemblance.

Dr. Maurice Ralph Hilleman



Dr. Maurice Ralph Hilleman (1919–2005) was one of the most influential vaccinologists of the 20th century. Although his name is not as widely recognized as those of Louis Pasteur, Edward Jenner, Jonas Salk, or Albert Sabin, his contribution to human health was extraordinary. Hilleman was involved in the development of more than 40 experimental and licensed vaccines, many of which protected people against serious diseases such as measles, mumps, rubella, hepatitis A, hepatitis B, chickenpox, meningitis, pneumonia, and influenza. His work fundamentally changed modern vaccinology and helped protect millions of people from infectious diseases. He was a scientist who combined strong laboratory research with an exceptional ability to recognize emerging health threats and turn scientific discoveries into practical vaccines.

Maurice Hilleman was born on September 30, 1919, on a farm near Miles City, Montana, in the United States. His early childhood was difficult. His twin sister died at birth, and his mother died shortly afterward. He was subsequently raised by relatives on a farm. Growing up in a rural environment exposed him to agriculture, animals, and practical farm life. Interestingly, his experience with chickens later became relevant to his scientific career because fertilized chicken eggs were widely used for growing viruses and producing vaccines. Hilleman developed a strong interest in science while he was young. He attended Montana State University, where he studied microbiology and chemistry. He later received a fellowship to study at the University of Chicago, where he earned his doctorate in microbiology and chemistry in 1944. His doctoral research focused on *Chlamydia trachomatis*, an organism that was then incorrectly considered to be a virus. His research helped establish that it was actually a bacterium that could reproduce only inside living cells.

After completing his doctorate, Hilleman began his professional scientific career at E. R. Squibb & Sons. There he worked on infectious diseases and vaccine-related research. During this period, he contributed to studies of Japanese encephalitis, a serious viral disease that was of particular concern to military personnel during World War II. In 1948, Hilleman moved to the Walter Reed Army Institute of Research, where he became deeply involved in the study of respiratory infections, particularly influenza. His work on influenza became one of the most important achievements of his early career. Hilleman understood that influenza viruses were capable of changing over time. Small genetic and antigenic changes, known as antigenic drift, can allow influenza viruses to evade existing immunity, while larger changes, known as antigenic shift, can produce significantly different viruses with pandemic potential. His understanding of influenza virus variation became extremely important for vaccine development and helped establish principles that continue to influence influenza surveillance and vaccination strategies today.

Hilleman's ability to recognize emerging infectious threats became particularly important during the Asian influenza pandemic of 1957. A new strain of influenza appeared in Hong Kong, and Hilleman quickly recognized that it could cause a major international outbreak. He obtained samples of the new virus and immediately began working on a vaccine. His team developed an influenza vaccine in an extraordinarily short period of time and produced millions of doses for use in the United States. This rapid response demonstrated the importance of early identification of dangerous pathogens and the ability to move quickly from laboratory research to vaccine production. Hilleman's response to the 1957 influenza pandemic established his reputation as a scientist who could not only conduct research but also respond effectively to real-world public health emergencies.

In 1957, Hilleman joined Merck & Co., where he became director of virus and cell biology research. He spent the majority of his career at Merck and led research programs that resulted in an extraordinary number of vaccines. His work covered many different viruses and bacteria, and he contributed directly or indirectly to vaccines against measles, mumps, rubella, hepatitis A, hepatitis B, chickenpox, pneumococcal disease, *Haemophilus influenzae* type b, and influenza. His scientific contributions were remarkable because they covered a wide range of infectious diseases rather than focusing on a single pathogen. He helped develop technologies and research approaches that allowed vaccines to be produced safely, consistently, and on a large scale.

One of the most memorable stories associated with Hilleman's career involves his daughter, Jeryl Lynn. In 1963, when his young daughter developed mumps, Hilleman collected a sample from her throat. He recognized that the virus could potentially be useful for vaccine development. The virus was isolated and subsequently weakened through laboratory methods so that it could stimulate immunity without causing the full disease. This strain became known as the Jeryl Lynn strain and formed the basis of the mumps component used in the combined measles, mumps, and rubella vaccine in many countries. The story is a remarkable example of how Hilleman's scientific curiosity and practical

thinking could turn an everyday observation into a major medical advancement.

Hilleman and his colleagues also played a major role in the development of the combined MMR vaccine. Combining vaccines against measles, mumps, and rubella into a single preparation simplified immunization programs and reduced the number of injections required. The measles vaccine component was also improved through Hilleman's research. These vaccines became important tools in reducing childhood illness and deaths caused by highly contagious viral infections. The success of the MMR vaccine demonstrates the broader importance of Hilleman's work: he was not simply interested in discovering viruses or understanding disease mechanisms; he wanted to develop effective preventive tools that could be used by healthcare systems and protect large populations.

Hilleman's work extended well beyond childhood vaccines. He contributed significantly to the development of vaccines against hepatitis A and hepatitis B, two viruses that can cause serious liver disease. He also worked on vaccines against chickenpox, pneumococcal infections, and *Haemophilus influenzae* type b. These diseases once caused substantial illness, disability, and death, particularly among children. The development and widespread use of effective vaccines dramatically changed their impact on communities. Hilleman's career therefore represents an important period in medical history when advances in virology, immunology, cell culture, and biotechnology were increasingly being transformed into practical vaccines.

Hilleman was known for his direct personality, demanding standards, and intense dedication to scientific work. He expected his research teams to maintain high standards and was strongly focused on results. His philosophy was practical: scientific discoveries should ultimately be translated into products that improve human health. Vaccine development requires much more than discovering a virus or identifying an immune response. A vaccine must be tested for safety and effectiveness, manufactured consistently, subjected to quality control, and

distributed to the population. Hilleman's career demonstrated the importance of connecting basic science with applied research, manufacturing, and public health.

Despite his enormous contribution to medicine, Hilleman remained relatively unknown to the general public. He received many important scientific honors during his lifetime, including the National Medal of Science in 1988 and the Albert B. Sabin Gold Medal Award in 1997. He retired from Merck in 1984 but continued to contribute to vaccine science and advise researchers. Hilleman died on April 11, 2005, at the age of 85. By the time of his death, his work had already become an important part of the history of modern medicine.

Maurice Hilleman's legacy can be seen in vaccination programs used around the world. His contributions to vaccines against measles, mumps, rubella, hepatitis A, hepatitis B, chickenpox, influenza, pneumococcal disease, and other infections have had an enormous impact on public health. His achievements are particularly remarkable because they were not limited to one major discovery. Instead, his career was characterized by continuous innovation, rapid response to emerging diseases, and a determination to transform scientific knowledge into effective vaccines. He demonstrated that successful vaccinology requires a combination of laboratory science, clinical understanding, epidemiology, manufacturing expertise, and public health awareness.

Maurice Hilleman is therefore remembered as one of the great pioneers of modern vaccinology. His journey from a farm in Montana to the forefront of vaccine research is an inspiring example of how education, scientific curiosity, persistence, and practical thinking can change the world. The diseases against which he helped develop vaccines once caused widespread illness and death, but vaccination has dramatically reduced their impact. His work continues to influence vaccine research and infectious disease prevention, making his legacy an enduring contribution to science and human health.



Jokes



A teacher asked, "Why are you late to school?"
The student replied, "Because of the sign on the road, ma'am."
The teacher asked, "What sign?"
The student said, "School Ahead, Go Slow!"

A patient asked the doctor, "Doctor, how can I live longer?"
The doctor replied, "Get married."
The patient asked, "Will that help me live longer?"
The doctor smiled and said, "No, but it will make you wish you hadn't!"

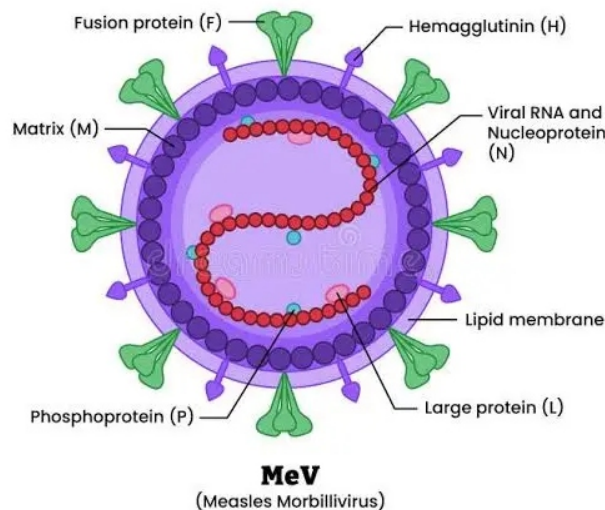
A man told his computer, "You are so intelligent!"
The computer replied, "Thank you!"
The man asked, "How do you know so much?"
The computer said, "Because I have a lot of memory!"
The man laughed, "Then why do you keep forgetting what I told you?"
The computer replied, "That's because I'm running out of space!"

The teacher asked, "What is the chemical formula for water?"
A student replied, "H-I-J-K-L-M-N-O!"
The teacher looked confused and asked, "What?"
The student explained, "You said it was H to O, ma'am!"

The manager asked an employee, "Why are you always taking breaks?"
The employee replied, "Because I work better under pressure."
The manager asked, "What pressure?"
The employee smiled and said, "The pressure of finishing everything before you notice!"

A man bought a parrot that could speak.
One day, he asked, "What is the secret to happiness?"
The parrot replied, "A good owner, good food, and a comfortable cage!"
The man laughed and said, "That sounds like a wonderful life!"
The parrot replied, "Yes, especially when you stop asking so many questions!"

Morbillivirus



Morbillivirus is a genus of viruses belonging to the family **Paramyxoviridae**. These viruses are important pathogens because they can cause highly contagious diseases in humans and animals. The best-known member of this genus is **measles virus**, which causes measles in humans. Other members include **canine morbillivirus**, which causes canine distemper, and viruses that infect marine mammals such as seals, dolphins, and porpoises. Morbilliviruses are particularly significant in medicine and veterinary science because they can spread efficiently among susceptible populations and, in some cases, cause severe disease involving multiple organs.

Morbilliviruses are **enveloped, single-stranded, negative-sense RNA viruses**. Their genetic material consists of a single RNA molecule that carries instructions for producing viral proteins. Because the RNA genome is negative-sense, it cannot be directly used by the host cell to produce proteins. The virus therefore carries an RNA-dependent RNA polymerase within the viral particle. Once the virus enters a susceptible cell, this enzyme produces messenger RNA from the viral genome, allowing the infected cell to manufacture viral proteins.

The structure of morbilliviruses is relatively simple but highly specialized. The viral envelope is derived from the membrane of the infected host cell and contains important viral glycoproteins. Two particularly important surface proteins are the **hemagglutinin (H) protein** and the **fusion (F) protein**. The H protein helps the virus recognize and attach to receptors on susceptible host cells. The F protein then facilitates fusion between the viral envelope and the host-cell membrane, allowing the viral genetic material to enter the cell. These proteins are therefore essential for infection and are also important targets of the immune response.

The **measles virus** is the most medically important morbillivirus. Measles is an extremely contagious viral disease that primarily affects children but can occur in people of any age who lack immunity. The virus spreads mainly through respiratory droplets and fine airborne particles released when an infected person

coughs, sneezes, breathes, or talks. Because measles virus can spread rapidly in communities where vaccination coverage is low, outbreaks can occur when susceptible individuals come into contact with an infected person.

After entering the body, measles virus initially infects cells of the respiratory system and then spreads to immune cells. It can subsequently disseminate throughout the body. The incubation period is usually around **10–14 days**, although the exact interval can vary. Early symptoms commonly include fever, cough, runny nose, and conjunctivitis. A characteristic feature of measles is the development of **Koplik spots**, small lesions that may appear inside the mouth before the skin rash. A widespread maculopapular rash typically develops several days after the initial symptoms and often begins on the face before spreading downward to the trunk and limbs.

Although many people recover from measles without permanent complications, the disease can sometimes become severe. Complications include **pneumonia, ear infections, diarrhea, dehydration, and inflammation of the brain (encephalitis)**. Young children, pregnant women, and people with weakened immune systems may be at greater risk of severe disease. A rare but serious late complication called **subacute sclerosing panencephalitis (SSPE)** can develop years after measles infection. SSPE causes progressive neurological deterioration and is usually fatal.

One of the remarkable characteristics of measles virus is its ability to affect the immune system. Infection can temporarily alter immune memory, reducing the body's ability to respond effectively to some pathogens that it had previously encountered. This phenomenon is sometimes described as **immune amnesia**. Consequently, the effects of measles infection may extend beyond the immediate illness because susceptibility to other infections can increase for a period following recovery.

The immune response to morbilliviruses involves both **innate and adaptive immunity**. The innate immune system provides an

early response through mechanisms such as interferons and other antiviral defenses. Later, the adaptive immune system produces antibodies and activates virus-specific T cells. Antibodies directed against viral surface proteins can prevent the virus from entering cells, while T cells help eliminate infected cells. Following measles infection or successful vaccination, long-lasting immune memory generally develops.

Vaccination is therefore one of the most important tools for controlling measles. The measles component of the **measles, mumps, and rubella (MMR) vaccine** uses a live attenuated virus that stimulates protective immunity without causing typical measles disease in healthy individuals. High vaccination coverage reduces the number of susceptible people in a population and interrupts transmission. This population-level protection is particularly important because measles spreads so efficiently.

Morbilliviruses are not limited to humans. Several species infect animals and can cause serious diseases. **Canine morbillivirus**, commonly known as canine distemper virus, affects dogs and several other carnivorous mammals. Canine distemper can cause respiratory, gastrointestinal, and neurological disease. Animals may develop fever, nasal and ocular discharge, coughing, vomiting, diarrhea, and neurological abnormalities. Vaccination is an important method of protecting domestic dogs against canine distemper.

Marine mammals can also be affected by morbilliviruses. **Phocine distemper virus**, for example, has caused significant disease and mortality in seals. Other morbilliviruses have been identified in dolphins and other cetaceans. These infections demonstrate the ecological importance of the genus and show that morbilliviruses have adapted to a variety of mammalian hosts.

From a laboratory and diagnostic perspective, morbillivirus infections can be investigated using several approaches. **Molecular methods such as reverse-transcription polymerase chain reaction (RT-PCR)** can detect viral RNA in appropriate clinical specimens. Serological tests can detect antibodies

produced by the host in response to infection or vaccination. Antigen-detection methods may also be used in certain diagnostic settings. Laboratory diagnosis is especially useful for confirming suspected cases, investigating outbreaks, and conducting epidemiological surveillance.

The study of morbilliviruses is also important from an evolutionary and public-health perspective. Their ability to infect different mammalian species demonstrates how viruses can evolve alongside their hosts. Understanding viral receptors, host susceptibility, transmission pathways, and immune responses helps researchers develop improved vaccines, diagnostic methods, and control strategies. Surveillance of animal morbilliviruses is particularly valuable because changes in viral distribution or host range can have consequences for wildlife health and conservation.

An interesting feature of morbilliviruses is their ability to produce **cell-to-cell fusion**. Infected cells can fuse with neighboring cells, producing large multinucleated cells called **syncytia**. This characteristic is associated with the activity of the viral fusion protein and can contribute to viral spread within tissues. The formation of syncytia is also a useful feature for understanding viral pathogenesis and studying morbillivirus biology in laboratory systems.

Overall, *Morbillivirus* represents an important genus of viruses with major significance in human health, veterinary medicine, wildlife biology, and infectious-disease research. Measles virus demonstrates how a highly contagious virus can affect entire populations, while animal morbilliviruses illustrate the broader ecological impact of this viral group. Their enveloped structure, negative-sense RNA genome, specialized attachment and fusion proteins, efficient transmission, and interaction with the immune system make morbilliviruses fascinating subjects of scientific study. Continued vaccination, laboratory diagnosis, epidemiological surveillance, and research remain essential for reducing the burden of morbillivirus diseases and protecting both human and animal populations.

Coffee may protect your heart but energy drinks could harm it.....

Caffeine is the most widely used stimulant and psychoactive substance in the world, and coffee is how most people consume it. According to a new scientific statement from the American Heart Association, most adults can safely consume up to 400 mg of caffeine/day (or up to five 8-ounce cups of caffeinated coffee per day). For some people, moderate coffee consumption may also be associated with a lower risk of cardiovascular disease.

The picture changes at higher doses. Concentrated sources of caffeine, especially energy drinks including energy shots, may raise the risk of cardiovascular problems. The findings were published in the American Heart Association's flagship peer-reviewed journal *Circulation* in the scientific statement "Caffeine and Cardiovascular Disease."

"Caffeine consumed in coffee is a key part of daily life for millions of people, and in our review of the most recent research, for most adults, intake of up to 400 mg of caffeine/day, the equivalent of up to 5 cups of caffeinated coffee per day without added sugars or fillers, is safe and does not increase cardiovascular risk," said Chair of the scientific statement volunteer writing group Gregory M. Marcus, M.D., M.A.S., FAHA, a professor of medicine at the University of California, San Francisco School of Medicine and the associate chief of Cardiology for Research at the University of California, San Francisco Health. "However, high doses of caffeine, such as those found in energy drinks including energy shots, may have harmful effects on the heart and should be avoided."

Why Caffeine Research Is Complicated

Understanding exactly how caffeine affects the cardiovascular system is difficult. Coffee is the main source of caffeine in most studies, but coffee contains many other substances that could influence health. Experimental research suggests that some bioactive compounds in coffee have antioxidant and anti-inflammatory properties, which may contribute to its possible benefits.

It is also hard to distinguish the effects of caffeine from those of ingredients commonly added to coffee, including milk, cream, flavored syrups and/or sugar. Most caffeine research is observational as well, which means it can identify associations but cannot establish cause and effect.

Coffee is not the only source of caffeine. Tea, chocolate, soda and energy drinks, as well as over-the-counter and prescription medications, can all add to a person's daily intake. Researchers say more studies are needed to clarify the caffeine content and cardiovascular effects of these other products.

The new statement reviews recent evidence about caffeinated coffee and its possible relationships with high blood pressure, cholesterol, Type 2 diabetes, coronary heart disease, stroke, heart failure, atrial fibrillation, other arrhythmias and other cardiovascular conditions.

How Much Caffeine Is Considered Safe?

Based on the latest studies included in the review, up to 400 mg of caffeine per day is considered safe for most adults. That amount is

roughly equal to no more than 3 to 5, 8-ounce cups of regular black caffeinated coffee per day (without sugars, sweeteners, flavors or added fillers). Regular brewed, non-specialty, caffeinated coffee usually contains 9.4-20.6 mg of caffeine per fluid ounce.

Drinking caffeinated coffee without added sugars, flavors, or cream was associated with lower risks of Type 2 diabetes, heart disease, stroke, heart failure, and some irregular heart rhythms.

Randomized trials, which are considered the most rigorous and reliable study design, have linked caffeine from coffee to a lower risk of atrial fibrillation. However, the same research also connected it with a higher risk of premature ventricular contractions.

Adding sugar, flavored syrups, milk and/or cream may weaken coffee's potential health benefits. Researchers say more work is needed to determine exactly how these additions affect health outcomes.

High caffeine intake may pose greater risks. Levels commonly found in energy drinks, including energy shots, were associated with high blood pressure and irregular heart rhythm. Energy drink shots may contain 40-69 mg of caffeine per fluid ounce, 3-4 times more caffeine than regular caffeinated coffee.

What Caffeine Does Inside the Body

After caffeine from coffee enters the body, it is processed by the liver and usually reaches its highest concentration within about an hour. The speed at which this happens varies according to genetics, metabolism, age, and previous caffeine use.

People who regularly consume larger amounts of caffeinated coffee may gradually develop a tolerance. Others can experience strong effects from much smaller amounts. In the short term, caffeine may temporarily increase blood pressure, heart rate, blood sugar and alertness. It can also cause heart palpitations and/or sleep disruption in some people.

Caffeine and Blood Pressure

Coffee may affect blood pressure differently depending on how much a person drinks. Among people with optimal blood pressure, consuming 1-3 cups a day was associated with a greater risk of developing high blood pressure. Surprisingly, drinking more than 3 cups per day was associated with a lower risk.

High doses of caffeine (such as those from energy drinks or energy shots) can cause significant increases in blood pressure. This effect may be especially concerning for people who already have high blood pressure.

Possible Effects on Type 2 Diabetes

Research indicates that caffeinated coffee may temporarily reduce insulin sensitivity. At the same time, regularly drinking black, caffeinated coffee (no additives, flavors, or sweeteners) was associated with a lower risk of developing Type 2 diabetes.

Scientists do not yet know whether caffeine is responsible for that association. Other compounds in coffee may provide some or all of the benefit. Additional research is needed to separate the effects of caffeinated coffee vs. various compounds in coffee.

Coffee Preparation May Affect Cholesterol

Randomized clinical trials have found that cafestol, a substance present in both caffeinated and decaffeinated coffee, was associated with higher levels of low-density lipoprotein (also known as "bad" cholesterol).

Cafestol is found in unfiltered coffee (such as espresso, French press, Turkish coffee or boiled coffee) but is not found in coffee prepared with paper filters or in instant coffee. Researchers still need to determine which products contain the highest levels of cafestol and how it affects cholesterol.

Coffee, Caffeine and Heart Rhythm

Recent analyses based on participant-reported health information found that consuming 1-3 cups of caffeinated coffee per day was not associated with a higher risk of atrial fibrillation or abnormal heart rhythm.

However, that same amount may be linked to more premature ventricular contractions (or PVCs). These are early beats that begin in the lower chamber of the heart.

Very high caffeine doses (such as those in caffeinated energy drinks or energy shots) have been associated with abnormal heart rhythms even in people who are normally considered at low risk for cardiovascular disease, including healthy adults younger than age 30.

Heart Disease, Heart Failure and Stroke

Drinking 2-4 cups of caffeinated coffee per day was associated with lower risks of heart disease, heart failure and stroke.

However, the relationship may change at higher levels. Consuming more than 4 cups of caffeinated coffee a day may increase the risk of heart failure.

Not All Caffeine Sources Are Equal

Researchers emphasize that caffeine products should not all be treated as interchangeable. More studies are needed to compare different kinds of caffeinated coffee with tea, soda, energy drinks and energy shots, and foods.

Tea has received less research attention than coffee. Even so, tea consumption has been associated with reduced risks of atrial fibrillation, heart failure and stroke, similar to caffeinated coffee. Energy drinks, bars, gels and caffeine-based supplements may contain additional ingredients that help the body absorb caffeine more rapidly. These additives may speed up caffeine's effects, increase blood pressure and raise the risk of cardiovascular harm.

More Rigorous Studies Are Needed

The writing group called for more randomized controlled trials examining caffeine in coffee and other caffeinated products. Scientists need a clearer understanding of why people respond differently and how each caffeine source affects cardiovascular health.

The researchers also highlighted the limited evidence available for caffeinated energy drinks and other increasingly popular caffeine products. Because there is not yet enough rigorous evidence to establish formal intake recommendations, caffeine was not included in the Association's 2026 Dietary Guidance to Improve Cardiovascular Health.

"Although research suggests that caffeine consumption may be associated with certain cardiovascular benefits for some people, it's important to remember that there is no 'one-size-fits-all' strategy for safe caffeine consumption. People can respond very differently to caffeine based on various factors, such as age, medications, underlying health conditions, genetics and how quickly their bodies metabolize it. What may be a reasonable amount for one person could cause unwanted effects, such as heart palpitations, anxiety or sleep disruption, in another. That's why it's important to pay attention to how your body responds to caffeine and talk with your healthcare team about what is right for you," Marcus said.

10 ways to address eye fatigue caused by displays at workplace

In today's office environment we put in 6, 8 or more hours at our desks with laptops, desktop monitors, smartphones and in video meetings. We spend long times up close to screens which can leave the eyes dry, tired, irritated, or with temporary blurriness. In recent years, many people would probably say the time they spend looking at displays has increased. In addition to televisions and PCs, smartphones and tablets have quickly become popular, and displays have penetrated every aspect of our lives. Information technology has made our lives more convenient, but at the same time, eye fatigue caused by continuous viewing of displays has increasingly become a social problem.



Staring at a computer or laptop at work for several hours a day can take a toll on your eyes and lead to several vision problems. This includes eye strain, dryness, redness, irritation or burning sensation, increased light sensitivity, headaches, and blurred or double vision. These symptoms are collectively known as Computer Vision Syndrome (CVS) or Digital Eye Strain, a serious type of repetitive strain injury that affects the eyes and vision because of prolonged digital screen use. Studies indicate that more than 40 million people use a computer every day in India, and 80% of them suffer from some form of CVS. Thus, Office Eye Care is a key component of health and wellbeing. The multitude of visual problems associated with Computer Vision Syndrome can be prevented or reduced by following certain precautions.

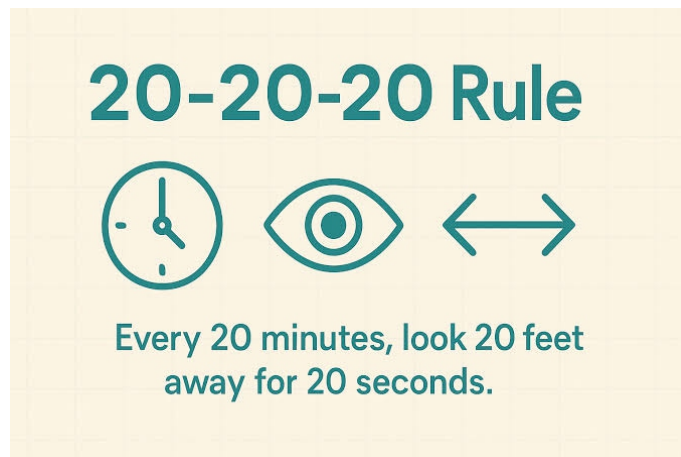
1. Take regular breaks from the computer screen

Reduce eye fatigue by taking a 15-minute break after 2 hours of continuous screen use or a 5-minute break for every 30 minutes of work.



2. Follow the 20-20-20 rule to prevent eye fatigue

After 20 minutes of computer viewing, look 20 feet into the distance, for 20 seconds. This practice of looking away reminds to blink which in turn makes for a more comfortable 8-hour shift.

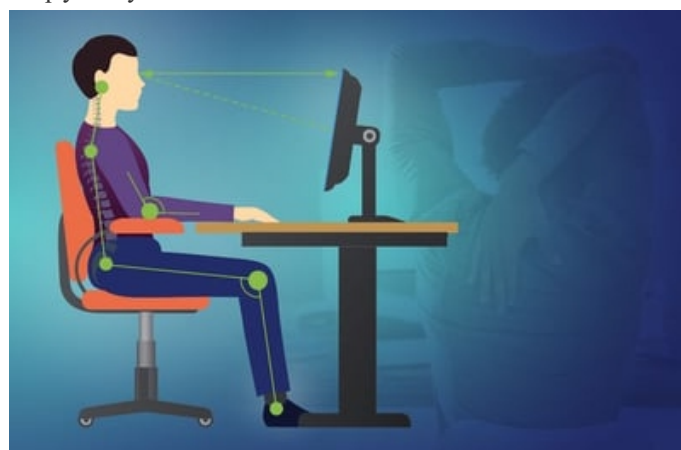


3. Remember to blink your eyes more often

Blinking is what spreads the tear film over the eye surface. This can prevent dryness and irritation. Consult an eye specialist about artificial tear drops that can be used to keep your eyes comfortable and moist during the workday. Do not ignore repeated dryness.

4. Adjust your workstation (desk and chair)

so that your eyes are at the recommended viewing distance (an arm's length) from the computer monitor and your gaze is at eye level, or slightly below the top of the computer screen. This will keep your eyes comfortable.



5. Blue light protection

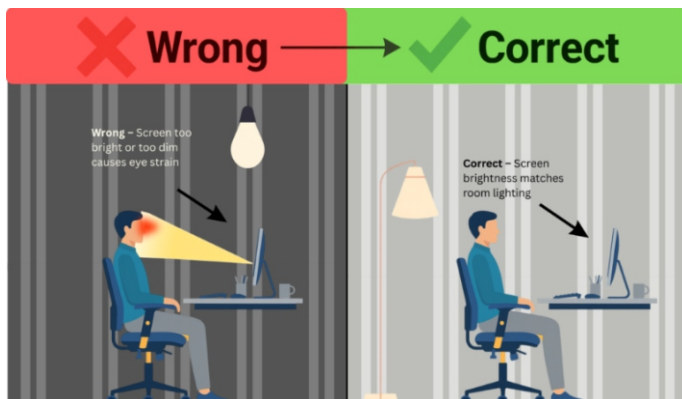
Use prescription glasses or computer glasses with UV filters and anti-glare coating to block UV rays produced by computer monitors and glare produced by fluorescent lighting. You could also use anti-glare screen filters or reduce the colour temperature of your display to cut down on the amount of blue light emitted by the monitor.

6. Computer display settings

Minimise eye strain and fatigue by modifying the display setting of your computer monitor. Adjust the brightness, backlight, contrast, and resolution of the computer screen to a level that's comfortable for you. Upgrade to a high-resolution LCD monitor that does not flicker and is gentler on the eyes and enlarge the font size so that you can read text comfortably.

7. Proper lighting can reduce eye strain

Too much natural or artificial light can increase glare on your computer screen. For comfortable viewing, ensure that windows and other light sources are not directly behind or in front of you, or use drapes /blinds on windows. Use floor lamps to provide indirect lighting instead of harsh overhead lighting.



8. Increase indoor air humidity

Air conditioners or fans at the workplace can make the air drier and this can lead to dry eyes. To prevent your eyes from drying up, use an air humidifier, keep some real plants around your work area, and avoid sitting in front of an air conditioner or under a fan while working on a computer.



9. Regular eye exams

If you have a visually demanding job with extended computer use, even minor vision problems such as under-corrected refractive errors or eye muscle imbalance can significantly increase the severity of computer-related eye stress. Regular eye exams can identify potential eye health issues which can be rectified to prevent further vision complications.

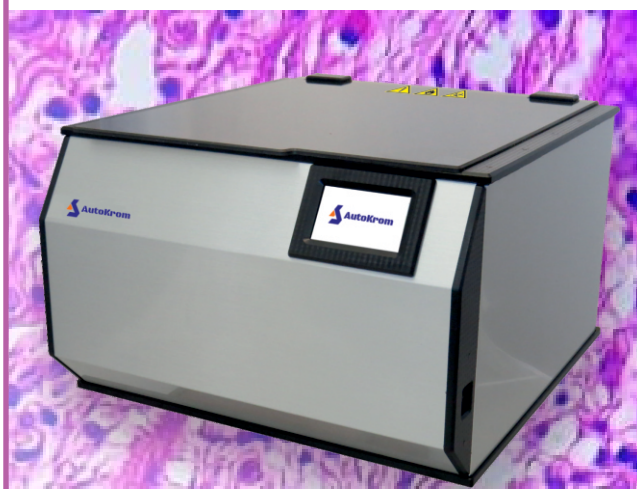
10. Give your eyes a break from contacts

Using contact lenses every day can exacerbate dry eye and other symptoms of computer vision syndrome. Switch to spectacles once or twice a week to reduce the strain on your eyes.

When It's Time to See a Specialist

If symptoms like blurred vision, dry eyes, or discomfort may persist of computer vision syndrome do not reduce or become worse in spite of following these precautions, get your vision checked by an ophthalmologist who can evaluate your vision and advise you about how to protect your eyes from digital eye strain.





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