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Multi-omics: A Holistic View Towards Animal Health

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Abstract:

The rising global prevalence of both infectious and non-infectious diseases underscores the need for a comprehensive approach to understanding and managing animal health issues. Today's animal healthcare system largely emphasizes treating diseases after they emerge, rather than focusing on prevention, which leads to the high costs associated with managing advanced conditions. Additionally, conventional healthcare strategies often overlook individual variations in genetics, environmental factors, and managemental, thereby limiting the effectiveness of treatments. Omics technologies, which include genomics, epigenomics, transcriptomics, proteomics, and metabolomics, provide in-depth insights into the molecular dynamics of health and disease. Genomics, bolstered by the advancements and affordability of Next-Generation Sequencing (NGS), examines genetic data, while epigenomics studies DNA and histone modifications. Transcriptomics reveals gene expression profiles, proteomics identifies and quantifies proteins for biomarker discovery, and metabolomics investigates small molecules to give a broad perspective on gene-environment interactions. The integration of multi-omics data broadens our understanding of complex diseases, facilitating personalized precision health strategies. Nevertheless, clinical implementation faces hurdles, such as data management challenges, complex analytics, and the need for interdisciplinary cooperation, which calls for standard protocols, sophisticated tools, and specialized training. However, with decreasing costs and advancements in informatics, multi-omics precision medicine is expected to revolutionize healthcare by 2030. Routine integration of multi-omics data, microbiome analysis, real-time health monitoring, and wearable technologies are anticipated to significantly improve healthcare quality and management.

Keywords: Disease, epigenomics, genomics, metabolomics, proteomics, transcriptomics

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Introduction:

Current animal healthcare usually treats illnesses after they appear rather than focusing on preventing them, which leads to high costs, especially for long-term diseases. Traditional treatments often don't consider individual genetic differences, physiology, and environmental factors, so many animals don't benefit from treatment. New "omics" technologies that study molecules like DNA, RNA and metabolites have improved our understanding of health and disease by uncovering complex biological processes. The global livestock industry suffers heavy financial losses from disease, estimated at 20% of production, or around USD 358.4 billion every year. For instance, Foot and Mouth Disease costs USD 21 billion yearly, while the 2019 African Swine Fever outbreak caused losses of USD 112.5 billion. The poultry industry loses USD 5.6 billion annually due to disease, and zoonotic diseases, which can spread to humans, cause about 2.2 million human deaths every year. In India, FMD costs USD 3.2 billion, Brucellosis USD 3.4 billion, and Avian Influenza USD 3.3 million every year. These numbers highlight the urgent need for stronger disease prevention and management strategies.

Traditional single-omics approaches studying one type of biological data at a time, such as genetic information often only show associations rather than revealing true causes. For instance, genome-wide association studies (GWAS) can identify risk areas in the genome linked to diseases but rarely pinpoint the exact genes causing them. Integrating multiple types of omics data, like transcriptomics, proteomics, and metabolomics, adds important layers of insight by helping researchers understand the interactions among molecules and their roles in diseases. By analysing multi-omics data over time, scientists can better understand disease development and progression, leading to earlier and more precise treatments. This shift to precision health, which integrates genetics, environment, and lifestyle, surpasses traditional symptom-based care by emphasizing prediction, prevention, and personalized treatment. It enhances care for specific populations and overall healthcare quality and efficiency. In areas like cardiometabolic diseases and cancer, multi-omics approaches provide a comprehensive view of complex molecular interactions, showcasing the transformative potential of these technologies for future healthcare.

The Omics Exploration:

Advances in DNA sequencing, mass spectrometry, wearable technology, and data management tools have pushed omics sciences forward, reshaping biology and medicine. Major areas within omics are genomics, epigenomics, transcriptomics, proteomics, and metabolomics which are developing quickly, helping us better understand complex biological systems.

Genomics, the most established field, studies entire genomes and genetic variations, like single nucleotide polymorphisms (SNPs) and structural changes in DNA. Since the first sequencing technology was introduced in 1977, the field has, the field has progressed dramatically, with costs dropping from

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billions to as low as $100 per genome. Today's next-generation sequencing (NGS) allows for fast, large-scale genome analysis, transforming genetic disease diagnosis and enabling targeted treatments. Long-read sequencing further speeds up genome analysis, helping us quickly understand trait differences and disorders. Since the discovery of DNA methylation in 1948, epigenomics has been used to describe the chemical changes that occur to DNA and histones. With next-generation sequencing tools like bisulfite sequencing and ChIP-seq, scientists can now closely analyse these modifications. ChIP-seq, for example, provides high-resolution mapping of chromatin changes.

Transcriptomics, on the other hand, examines RNA transcripts and their levels to understand cellular functions. Early techniques, like microarrays, had limitations, especially for finding new transcripts. The introduction of RNA sequencing (RNA-Seq) in 2008 was a breakthrough, allowing large-scale transcriptome analysis, discovery of new transcribed regions, and measurement of rare RNAs. Improvements in RNA-Seq have advanced disease diagnosis, prediction, and the detailed tracking of gene interactions over time. Proteomics is the large-scale study of proteins, focusing on understanding their structure and function. In its early days, detecting a wide range of proteins was difficult, but advances in mass spectrometry, like electrospray ionization (ESI) and matrix-assisted laser desorption ionization (MALDI), have made this easier. Technologies such as multidimensional protein identification and liquid chromatography-mass spectrometry (LC-MS/MS) now allow faster, more sensitive, and affordable protein analysis. New techniques, like tandem mass tags, have improved detection sensitivity and reduced costs, making proteomics essential in clinical diagnostics and identifying biomarkers for diseases.

Metabolomics, on the other hand, studies small molecules in biological systems, usually under 1500 Da. It includes targeted metabolomics, which focuses on measuring specific molecules, and untargeted metabolomics, which can analyse over 10,000 different molecules. Fluxomics tracks labelled molecules to understand reaction rates, while metabolite imaging helps visualize molecules in specific tissues. Metabolomics links genes, environment, and gut bacteria, aiding in discovering biomarkers, diagnosing diseases, and predicting health outcomes. Lipidomics, a fast-growing area within metabolomics, benefits from advancements in mass spectrometry to improve understanding of disease-related biomarkers. Each omics field has contributed to precision medicine, helping to improve diagnostics, predict treatment responses, and develop personalized therapies. Combining genomics, epigenomics, transcriptomics, proteomics, and metabolomics gives a complete picture of biological processes, moving biomedical research and clinical care forward.

Data Integration:

Omics technologies produce large datasets, called Big Data, that need advanced tools for managing and analysing them. These datasets include information from genomics, proteomics, transcriptomics, and metabolomics. Their complexity depends on factors like the animal's health, age, sex, and diet. To understand these data accurately and avoid errors, we need specialized bioinformatics, statistical, and computational tools.

To tackle these challenges, several software tools help combine different types of biological data (like genomics, transcriptomics, and proteomics). For example, MixOmics is an R package that uses a method called Sparse Partial Least Squares (sPLS) to connect these data types, making it easier to find meaningful patterns with tools like heatmaps and scatter plots. MOFA+ (Multi-Omics Factor Analysis) uses a Bayesian approach to break down complex data into shared and unique patterns, providing visualization options to explore interactions and generate research ideas. Another tool, iClusterPlus, available in Bioconductor, clusters different data types along with clinical information to find links between molecular features and health outcomes. MiBiOmics, a web-based tool, simplifies multiomics analysis with interactive features like clustering and pathway enrichment, helping users explore relationships within each data layer.

Multiomics data integration uses various statistical methods to study complex biological relationships. Regression models help identify important factors, while machine learning techniques, like clustering, group data to uncover hidden patterns. Bayesian methods allow researchers to include previous knowledge and measure uncertainty in their analyses. Additionally, network-based integration utilizes biological networks, such as protein-protein interaction networks, to connect multiomics data across different levels. This approach helps identify key regulators and pathways that play a role in biological processes and diseases. Dimensionality reduction methods are important for managing high-dimensional omics data. Techniques like Principal Component Analysis (PCA), t-Distributed Stochastic Neighbor Embedding (t-SNE), and Uniform Manifold Approximation and Projection (UMAP) help simplify the data while keeping key patterns intact. PCA reduces complexity by focusing on the most important components that explain the data's variation. t-SNE groups similar data points together in a lower-dimensional space, making it easier to see clusters. UMAP maintains the overall structure of the data for a more accurate view. These methods enhance the understanding of data, making it easier to draw biological conclusions.

Deep learning uses tools like DeepOmix and MiNet to help integrate various omics data types (such as proteomics and genomics). These tools use deep neural networks (DNNs) to find patterns in the data and often include networks like feedforward neural networks (FNNs) and attention mechanisms. This approach allows researchers to model diseases, predict traits, and identify biomarkers by organizing omics data in ways that relate to genes and biological pathways. Network and pathway analyses help bring together data by showing how different biological processes and functions are connected. This helps researchers understand complex biological systems better and find new targets for treatments.

By integrating different types of data, scientists can see how molecular components affect variations in traits, which can lead to new approaches in precision medicine.

Applications in Precision Health:

Integrated multi-omics methods are revolutionizing our understanding and management of health problems. By combining information from genetics, transcription, proteins, metabolites, and microbiomes, these methods help us learn more about how diseases develop and how to identify them. This results in better ways to find biomarkers and personalize treatments for individuals, improving prediction and care.

Predicting Disease Risk:

Multi-omics is a method that helps predict the risk of diseases by finding specific markers in genes, proteins, and metabolism that are linked to how likely animals are to get sick or how well they can recover. For example, research on bovine respiratory disease (BRD) has shown that cattle that are more likely to get sick have different metabolic patterns, especially in proteins related to inflammation. Similarly, studies on poultry have found that some birds are more susceptible to heat stress due to variations in proteins and gene activity related to heat. By identifying important genetic and metabolic pathways involved in immune responses and how hosts interact with pathogens can help in prediction of the disease risk. Multi-omics can help improve breeding and health management strategies for better animal welfare.

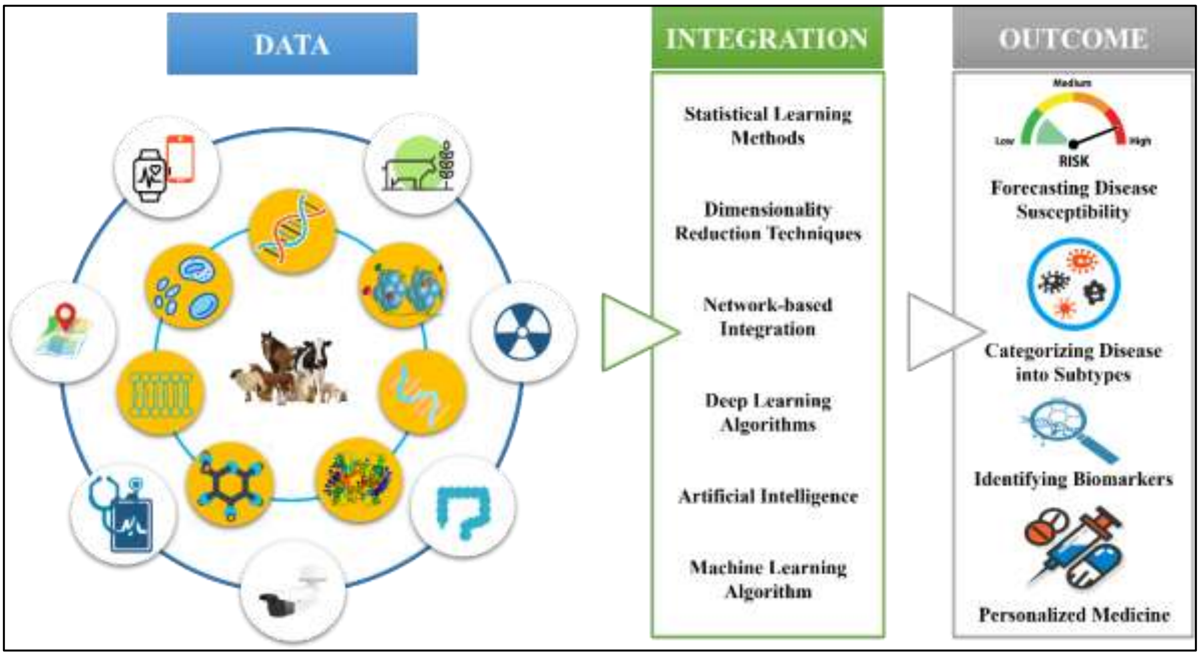

Figure 1. Integrating Wearable Data and Multi-Omics to Unlock Precision Health Insights.

Classifying Diseases into Subtypes:

Multi-omics is also useful for grouping diseases into different types at the molecular level, which allows for more targeted treatment in veterinary medicine. For instance, glucotypes and ageotypes, where “glucotypes” categorize diseases based on how the body manages glucose, which can help with conditions like insulin resistance and obesity in pets. Similarly, "ageotypes" focus on diseases that affect older animals, such as osteoarthritis. By using multi-omics data can help classify diseases in a way that leads to more personalized treatments. Advanced tools like deep learning models (such as DeepMO) further improve this classification by analysing various omics datasets, which has helped identify different cancer types. These methods support tailored management by pinpointing specific gene variations and expression patterns linked to diseases.

Identifying Biomarkers:

Multi-omics helps find early signs of diseases and track them more accurately. For instance, research has shown that it can identify specific circulating microRNAs and proteins, like S100A8, which can help detect muscular dystrophy. In poultry, studies on immune responses have found biomarkers that differentiate laying strains based on their immune cell profiles, metabolites, and gene expression. In cases of subclinical mastitis, multi-omics has detected changes at the genomic and epigenomic levels that can act as biomarkers for immune defence and mammary gland health. These markers allow for earlier disease detection and help create personalized treatment plans.

Personalized Medicine:

By combining various types of omics data, personalized medicine tailor's treatments to an individual's genetic makeup, environment, and lifestyle. For example, using predictive models in melanoma treatment has been shown to optimize strategies by identifying specific molecular traits in different patient groups. AI-driven models, like AIGS for bladder cancer in canines, can predict how well patients will treatment, improving outcomes by targeting therapies more effectively. Furthermore, integrating machine learning and multi-omics improves targeted treatments for a range of cancers, such as breast and colorectal cancer.

Multi-omics is improving precision health by allowing for accurate disease prediction, better disease classification, the discovery of biomarkers, and personalized treatments. By combining different omics fields, we gain a comprehensive understanding of how diseases progress and build resilience. This approach helps develop specific care strategies that lead to better health outcomes for animals.

Challenges And Future Prospects:

Technologies like Whole-Genome Sequencing (WGS) and Whole-Exome Sequencing (WES) are becoming essential in clinical settings, facilitating genetic screening, treatment evaluation, and the identification of disease markers. However, integrating various omics approaches presents challenges, such as high costs, the need for specialized infrastructure, and a requirement for skilled personnel. While costs are gradually coming down, managing the data remains a significant challenge. Multi-omics data includes various biological types like genomics, transcriptomics, proteomics, and metabolomics are leading to issues with big data. The "curse of dimensionality" complicates clustering analysis because of high sample variance and sparse data, making it hard to interpret results. Additional factors like incomplete data, small sample sizes, class imbalances, and inconsistencies further diminish reliability. Moreover, batch effects from different experimental setups, inaccessible data formats, and a lack of standardized protocols increase complexity, limiting the integration of data from various sources.

To address these challenges, strong statistical and AI methods are essential. Advanced techniques like deep learning, data mining, and AI are needed to combine complex multi-modal data from sources such as wearable devices and Electronic Health Records (EHR). The growing volume of data, often exceeding terabytes, requires sophisticated management systems that ensure both capacity and security while maintaining privacy. These approaches are critical for transforming raw data into actionable insights and pushing forward advancements in fields like healthcare. Innovative multi-omics platforms, such as the Personal Health Dashboard (PHD), are designed to manage and analyse large-scale biomedical data. By integrating information from wearables, clinical records, and omics sources, these platforms enhance research and health management. Recent studies show their effectiveness in areas like insulin resistance and pre-symptomatic mastitis detection, emphasizing their potential for early diagnosis and treatment optimization. Additionally, emerging tools are combining imaging data with omics information, providing even deeper insights.

Scalability is crucial as multi-omics studies move from small groups to larger populations, which improves reliability. To effectively interpret data, clinician training is necessary, and scientists need to develop interdisciplinary skills to manage diverse datasets. Data security is also vital for cloud-based healthcare platforms, which must adhere to regulations like HIPAA and GDPR. Providers such as AWS, Google Cloud, and Microsoft Genomics offer certified solutions for securely managing multi-omics data, ensuring patient information remains protected while facilitating the use of big data in healthcare. Looking ahead, precision medicine is expected to undergo significant transformation by 2030, largely driven by advancements in multi-omics. With decreasing analysis costs and more sophisticated computational tools, integrating various omics data into clinical practice is becoming more achievable. This integration, supported by real-time health monitoring through wearable devices, will enable personalized treatment plans tailored to individual lifestyles and environmental factors. Ultimately, multi-omics technology will improve health management, disease prevention, and clinical outcomes overall.

Conclusion:

The integration of omics data represents a significant jump in precision health, shifting from a reactive to a proactive and personalized healthcare approach. This transformation is propelled by advancements in genomics, epigenomics, transcriptomics, proteomics, and metabolomics, which provide a comprehensive understanding of the molecular complexities related to health and disease. These technologies have enabled the identification of disease markers, predictions of disease susceptibility, classifications of disease subtypes, and the customization of treatments based on an individual's genetic makeup, environmental factors, and lifestyle. However, this omics revolution comes with challenges. The complexity of multi-omics data requires specialized expertise, advanced computational resources, and substantial investments in data collection, storage, and analysis. Additionally, issues of data privacy, security, and standardization must be addressed to ensure ethical management of patient information. Integrating multi-omics findings into clinical practice will also require a fundamental shift in healthcare systems and policies, along with adequate training for healthcare professionals and researchers. Despite these challenges, the potential of multi-omics in precision health is immense. As technology continues to evolve and costs decrease, multi-omics-driven precision medicine is expected to become standard practice in clinical settings. This evolution promises earlier disease detection, more effective interventions, and improved healthcare outcomes. By harnessing the power of omics data, we stand on the threshold of a transformative era in veterinary medicine, where personalized care takes precedence, paving the way for a healthier and more prosperous future.

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