Editorial

From Biomedical Data to Clinical Impact: Advancing Precision Medicine in Indonesia

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Medicine is entering an era in which the ability to generate, integrate, and interpret biomedical data increasingly determines the pace of scientific and clinical innovation. Genomics, epigenomics, transcriptomics, proteomics, metabolomics, and metagenomics provide complementary views of human biology, while bioinformatics and artificial intelligence (AI) enable these complex datasets to be transformed into biological knowledge. This convergence is shifting biomedical research from a reductionist view of disease toward a more integrated understanding of molecular mechanisms.[1,2]

Precision medicine has consequently expanded beyond genomics to include molecular phenotypes, the microbiome, environmental exposure, lifestyle, and clinical characteristics.[1,3] This transition is particularly relevant to Indonesia, a country characterized by substantial genetic, geographic, environmental, dietary, and microbial diversity. Yet Indonesian populations remain relatively underrepresented in many global biomedical datasets. Developing population-relevant biomedical resources should therefore be regarded not only as a research priority but also as a critical component of national health-system development.

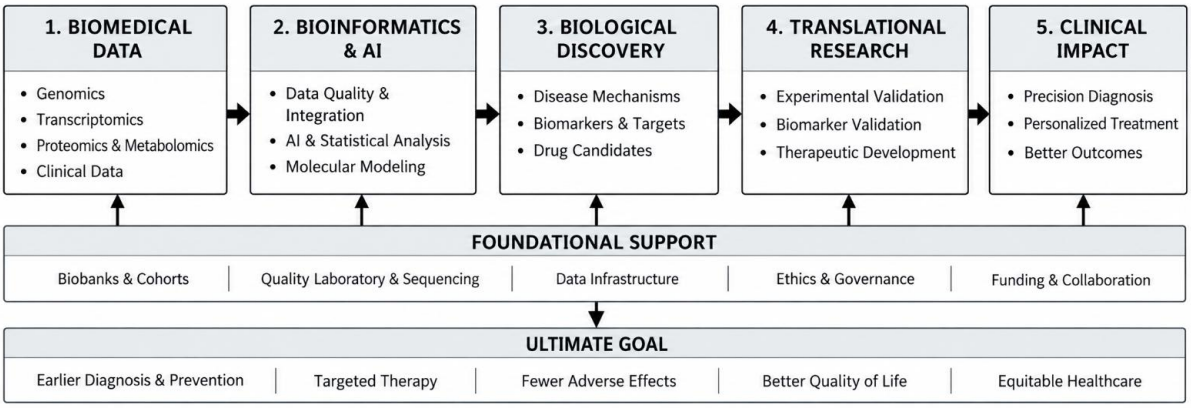


Figure 1. Proposed Continuum from Biomedical Data to Clinical Impact

Figure 1 illustrates the proposed continuum from biomedical data to clinical impact: multi-omics data are integrated through bioinformatics and AI, translated into biological discoveries and candidate biomarkers or therapeutic targets, experimentally validated, and ultimately directed toward precision diagnosis, risk prediction, and personalized treatment.

Building Population-Relevant Biomedical Data

Genomic research conducted through the Faculty of Medicine, Universitas Indonesia (FMUI), and the Indonesian Medical Education and Research Institute (IMERI) demonstrates the feasibility and value of generating locally relevant genomic resources. Whole-genome sequencing of *Escherichia coli* isolated from bloodstream

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infections at Cipto Mangunkusumo National Hospital revealed substantial diversity in sequence types, virulence genes, and antimicrobial-resistance determinants.[4,5] These findings demonstrate the potential of genomic surveillance to provide an early-warning system for emerging pathogens and resistance mechanisms.

Similar efforts have been extended to fungal pathogens. Whole-genome sequencing of *Candida krusei* isolates from clinical samples in Jakarta generated genomic data that could be associated with fluconazole resistance and resistance-associated mutations.[6] Such datasets are particularly valuable because pathogen genomic characteristics may differ between geographic settings and healthcare systems.

Cancer genomics provides another important example. Targeted sequencing of germline breast-cancer susceptibility genes in the Jakarta population identified pathogenic and likely pathogenic variants and highlighted the importance of examining susceptibility genes beyond BRCA1 and BRCA2.[7] In parallel, genomic datasets derived from fresh-frozen breast carcinoma tissues collected through the IMERI-FMUI biobank provide a resource for investigating cancer-associated genomic alterations and developing future biomarkers.[8]

These studies demonstrate an important principle for precision medicine: clinical interpretation requires population-relevant data. Indonesian genomic resources can contribute to more accurate variant interpretation, disease-risk assessment, molecular diagnosis, and future treatment selection.

Integrating Microbiome and Metabolome

The genome alone cannot fully explain human health and disease. Microbial ecosystems, metabolic activity, immune responses, and environmental factors contribute substantially to clinical phenotypes. The human microbiome is increasingly recognized as an active component of host physiology, influencing metabolism, immunity, inflammation, and susceptibility to disease.[9,10]

Research in Indonesia has begun to investigate microbiome variation in conditions including childhood growth disorders and gastrointestinal diseases. Such studies suggest that microbial community composition may provide candidate disease-associated signatures. However, the greater opportunity lies in connecting microbial composition with host molecular phenotypes.

Metabolomics provides an important complementary layer because metabolites represent dynamic biochemical states. Unlike genomic data, which primarily describe biological potential, metabolomic profiles reflect downstream physiological and pathological processes.[11]The integration of microbiome and metabolomic data can therefore reveal relationships between microbial dysbiosis, host metabolism, inflammation, and clinical phenotypes.

This approach may be particularly relevant to metabolic diseases, cancer, infection, and nutritional disorders. Rather than focusing on a single microorganism or metabolite, future research should increasingly identify integrated molecular signatures that can be validated as diagnostic, prognostic, or treatment-response biomarkers.

Bioinformatics as the Integration Engine

The rapid expansion of biomedical data has created a fundamental challenge: data generation is increasing faster than the capacity to interpret and translate these data into actionable knowledge. Bioinformatics is therefore becoming a core component of modern biomedical research rather than merely a supporting discipline.

Bioinformatics enables sequence analysis, variant annotation, pathway and network analysis, microbiome profiling, molecular modeling, molecular dynamics, and multi-omics integration. Research at FMUI has demonstrated how computational network analysis can be used to identify potential breast-cancer stem-cell biomarkers from secretome data.[12] Such approaches can connect molecular datasets with disease pathways and generate experimentally testable hypotheses.

Machine learning provides another layer of analytical capability. Metabolomic data, for example, can be combined with machine-learning approaches to identify candidate biomarkers for cancer. Research involving FMUI has explored metabolite biomarker discovery for lung cancer using machine learning, illustrating a pathway from metabolic phenotype to computational biomarker prioritization.[13]

However, AI performance should not automatically be interpreted as clinical utility. Models require appropriate training populations, external validation, reproducibility, interpretability, and assessment of potential bias. For Indonesia, population-specific datasets are particularly important because algorithms developed using predominantly non-Indonesian populations may not necessarily perform optimally in Indonesian patients.

From Molecular Discovery to Therapeutic Candidates

The integration of bioinformatics with medicinal chemistry provides a further pathway from biomedical data to clinical impact. Molecular profiling can identify disease-associated pathways and potential therapeutic targets, while molecular modeling and computational chemistry can prioritize compounds for experimental evaluation.

This approach is particularly relevant to Indonesia because of its extensive biodiversity and traditional medicinal resources. However, natural products should not be translated into therapeutic candidates solely on the basis of traditional use or computational prediction. Chemical characterization, target validation, pharmacological testing, and safety assessment remain essential.

Research involving FMUI illustrates this integrated strategy. Molecular simulation combined with *in vitro* SH-SY5Y validation identified potential neuroprotective flavonoids for Alzheimer's disease research.[14] Network pharmacology integrated with molecular dynamics has also been used to investigate bioactive compounds and potential targets of *Tinospora crispa* as an insulin-sensitizing agent.[15] These studies illustrate how computational approaches can reduce the chemical search space and generate mechanistic hypotheses for subsequent experimental validation.

A translational framework can therefore be conceptualized as: clinical phenotype → multi-omics profiling → pathway and target identification → computational prioritization → experimental validation → therapeutic candidate development → clinical evaluation.

The value of computational approaches lies not in replacing experimental science, but in making the discovery process more rational and efficient. The strategic challenge for Indonesia is now to move from individual datasets toward an integrated biomedical data ecosystem. Such an ecosystem should connect population cohorts and biobanks, genomic and microbiome resources, metabolomics platforms, bioinformatics infrastructure, clinical information, and translational research.

Four Priorities are Particularly Important

First, population-representative biomedical databases should be developed using standardized protocols and appropriate ethical and data-governance frameworks. Second, bioinformatics infrastructure and human resources must be strengthened in parallel with sequencing, mass spectrometry, and other high-throughput technologies. Third, biomarker discovery should be connected to independent clinical validation, because statistical association alone is insufficient for clinical implementation. Finally, interdisciplinary collaboration among clinicians, molecular scientists, chemists, pharmacists, bioinformaticians, statisticians, and data scientists should become a central feature of precision-medicine research.

Indonesia also has an opportunity to establish a distinctive research strength by connecting population genomics, microbiome research, metabolomics, computational biology, and natural-product discovery. This combination could transform the country's biological diversity into a scientifically rigorous source of biomarkers and therapeutic candidates. The objective, however, should remain patient-centered. Precision medicine should ultimately improve

diagnosis, risk stratification, treatment selection, monitoring, and health outcomes. Sophisticated molecular technologies will have limited impact if they cannot be translated into clinically accessible and cost-effective solutions.

Conclusion

The future of precision medicine in Indonesia depends on the ability to transform biomedical data into clinically meaningful knowledge. Genomics and epigenomics describe genetic and regulatory variation; microbiomics captures host–microbe interactions; metabolomics reflects dynamic biochemical phenotypes; bioinformatics and AI integrate these complex layers; and medicinal chemistry provides a pathway toward therapeutic discovery. Research from FMUI–IMERI demonstrates that important components of this ecosystem are already emerging, including pathogen genomics, cancer genomics and biobanking, computational biomarker discovery, metabolomics–assisted machine learning, and molecular simulation. The next step is to connect these efforts through interoperable datasets, standardized analytical pipelines, interdisciplinary training, rigorous validation, and clinically oriented research.

The biomedical data revolution should therefore be measured not by the amount of data generated, but by its capacity to improve diagnosis, prediction, treatment, and health outcomes. For Indonesia, the pathway from biomedical data to clinical impact offers an opportunity to strengthen scientific sovereignty while contributing population-relevant knowledge to the global precision-medicine community.

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