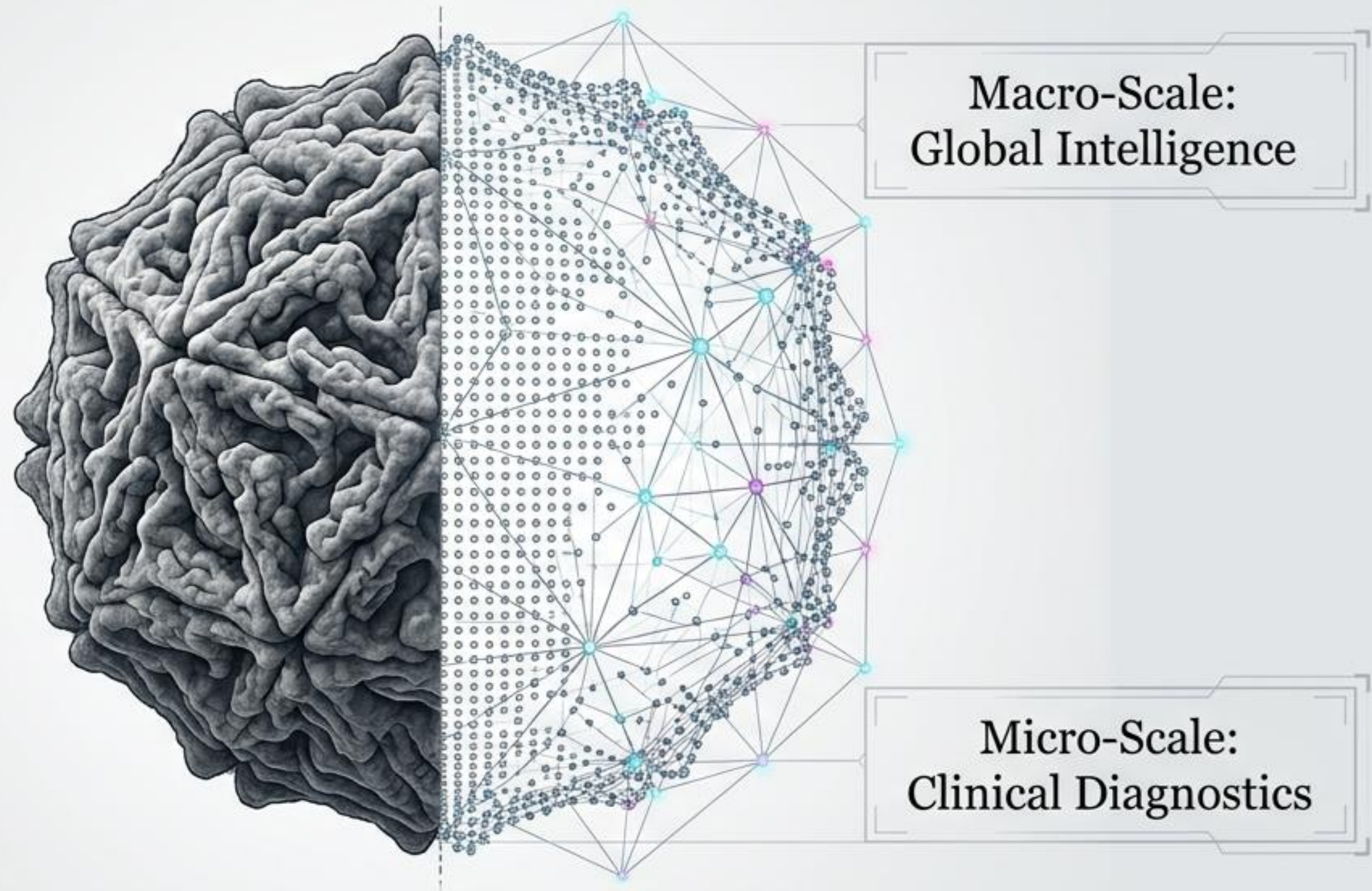


Applications of Artificial Intelligence in Microbiology and Virology

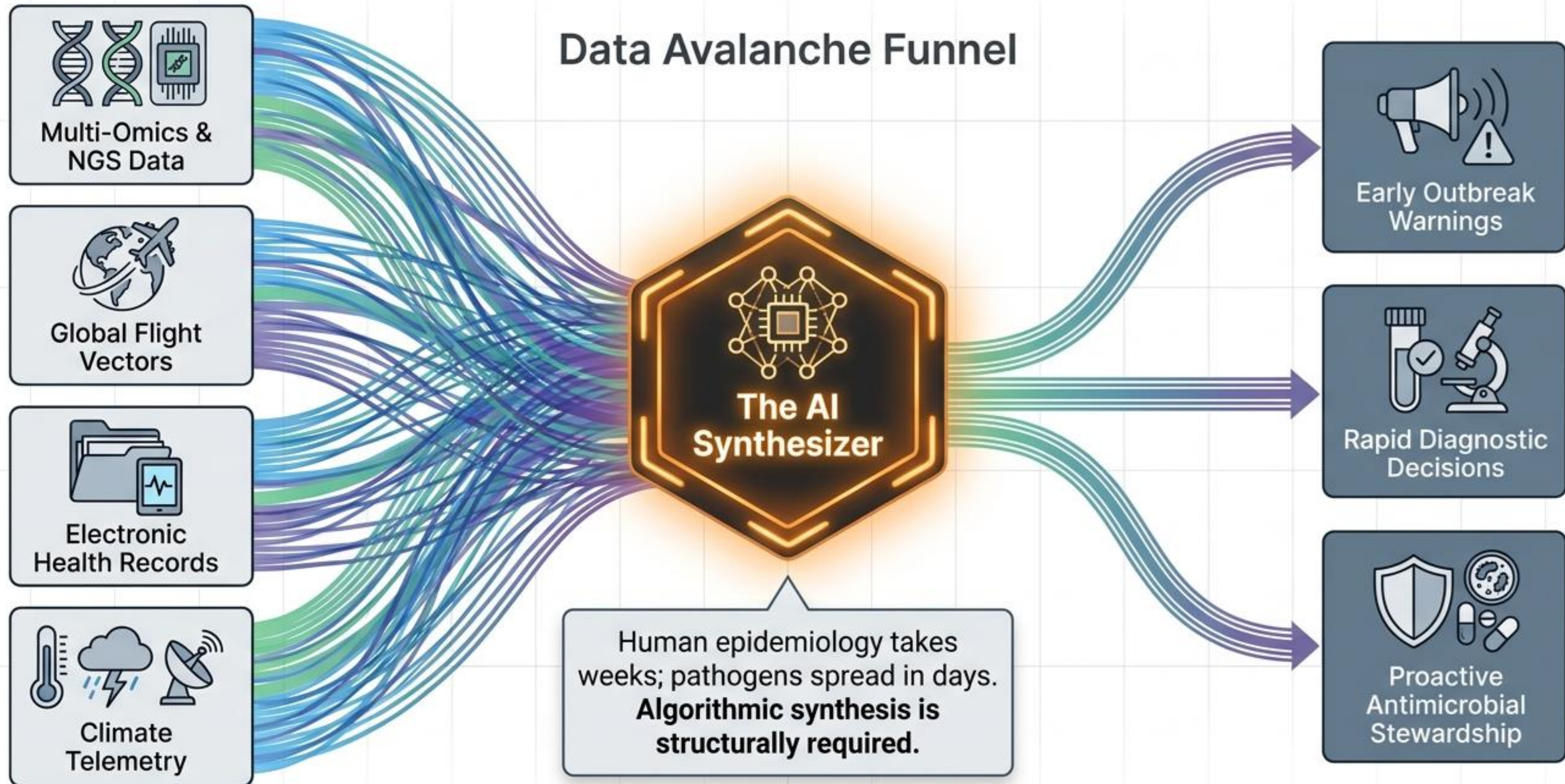
From Global Epidemiological Surveillance to Single-Cell Antimicrobial Resistance



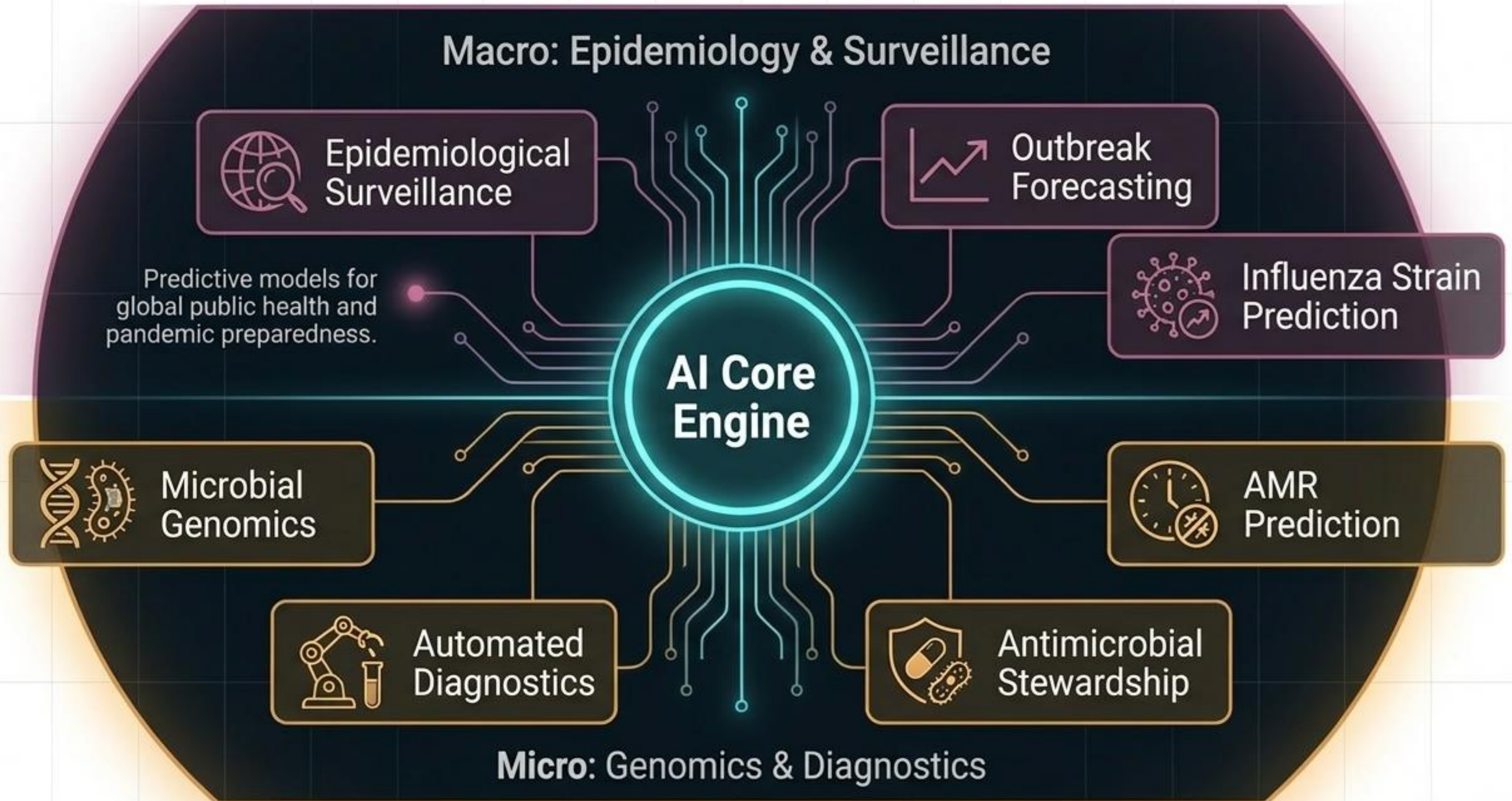
Greta Romano, PhD

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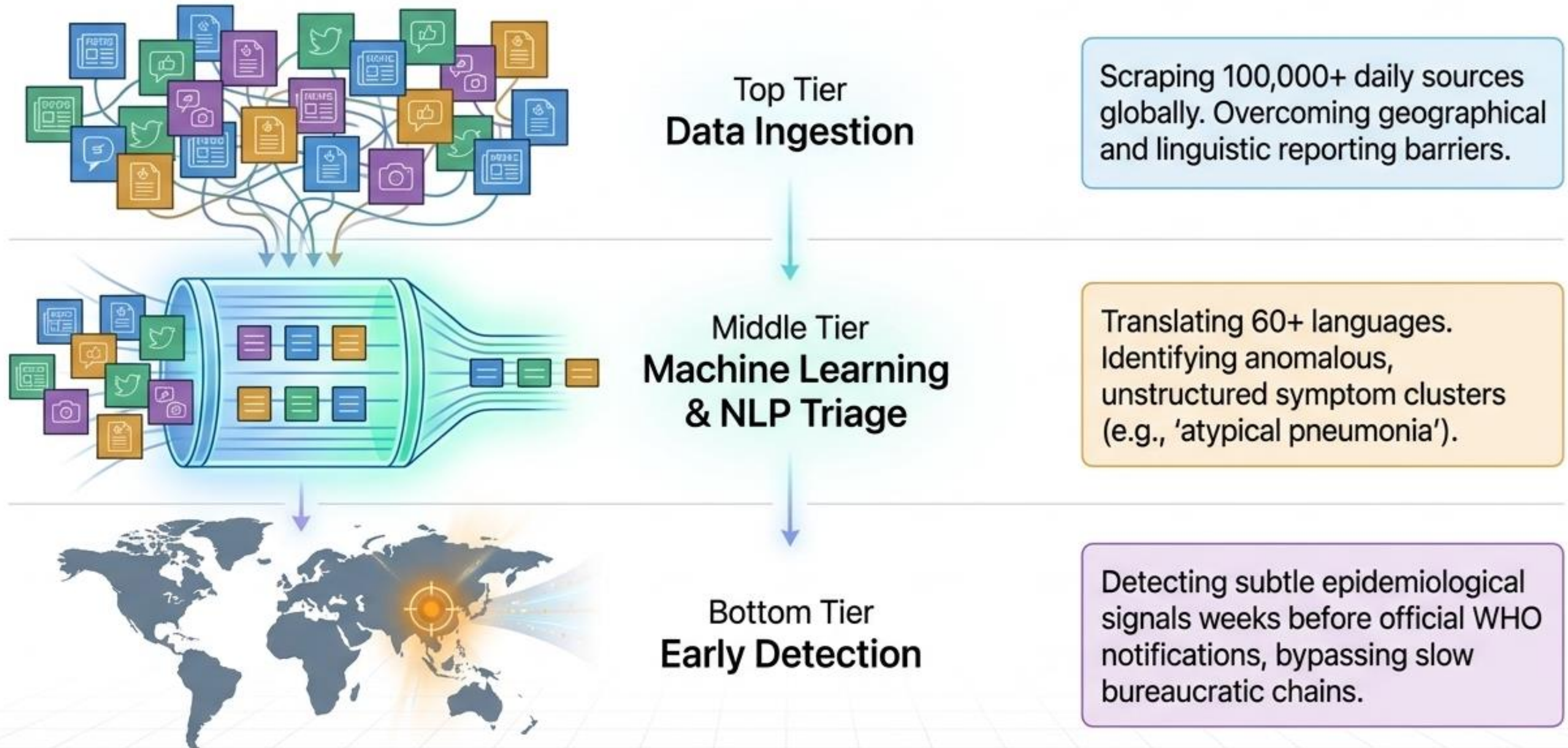
The Data Avalanche: Why Microbiology Needs AI



The AI Application Ecosystem: A Multi-Scale Roadmap



AI and Epidemiological Surveillance: The NLP Pipeline



Case Study: Commercial Epidemic Intelligence



The Platform: BlueDot

A proprietary, commercial epidemic intelligence system based in Canada.

The Engine

Fuses NLP (global media scraping) with commercial airline ticketing data and machine learning spatiotemporal models.

Impact & Limitations

Flagged the anomalous Wuhan cluster on Dec 31, 2019. Accurately predicted the top 11 dissemination cities via flight volumes.

Limit: High operational cost and reliance on regions with high digital footprints.

Case Study: Open-Source Academic Surveillance



The Platform: HealthMap

An open-access, academic surveillance tool run by Boston Children's Hospital and Harvard University.

The Engine

Aggregates ProMED, official WHO alerts, and crowdsourced public data via automated ML classifiers.

Impact & Limitations

Crucial in mapping the 2014 Ebola, Zika, and Dengue outbreaks. Provides democratic, open global situational awareness.

Limit: Focuses on aggregation and visualization rather than complex, proprietary travel forecasting.

Case Study: WHO Epidemic Intelligence from Open Sources (EIOS)

Objective: A unified global platform driving international One Health data sharing.

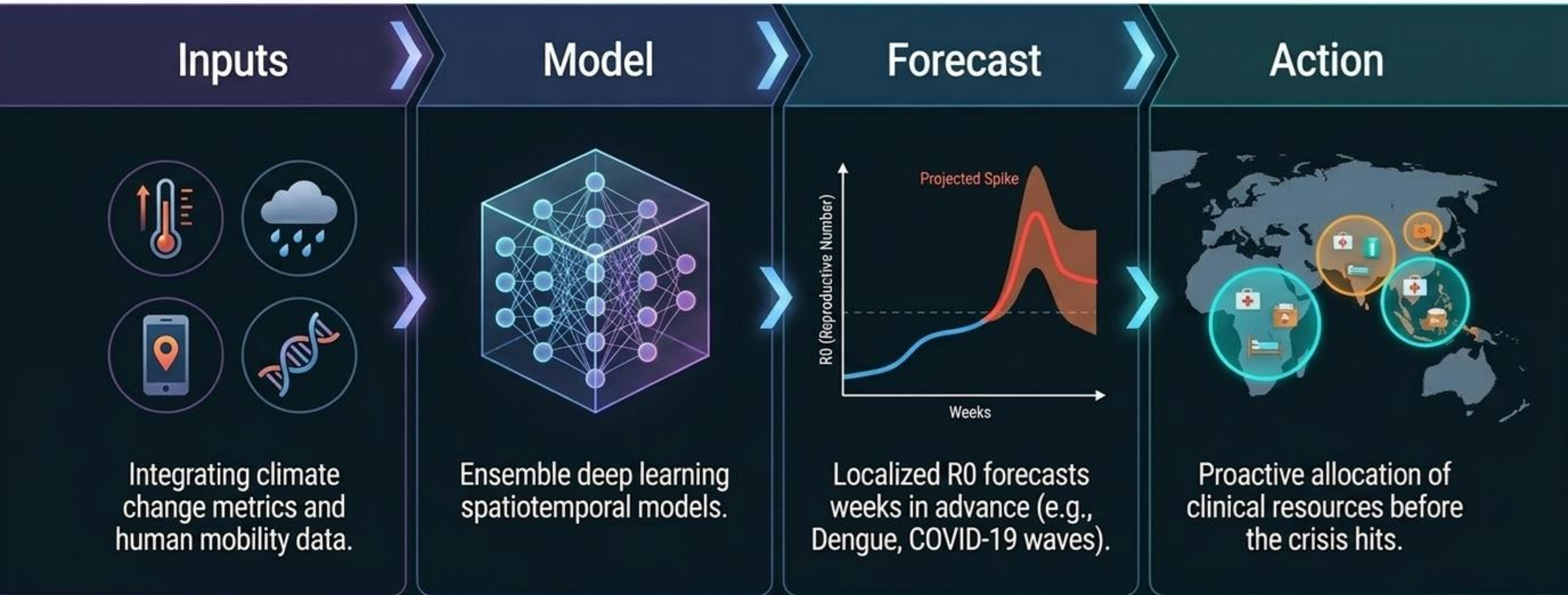
Data Integration:
Merges official Member State reporting with continuous open-source AI scraping.



Actionability:
Early warning matrix prioritizes threats by algorithmic confidence for policymakers.

AI is institutionalized in global health: algorithms filter the noise, human experts verify the signal.

AI for Outbreak Prediction: Moving from Detection to Forecasting



AI and Influenza Strain Prediction: Viral Language Models



The Challenge

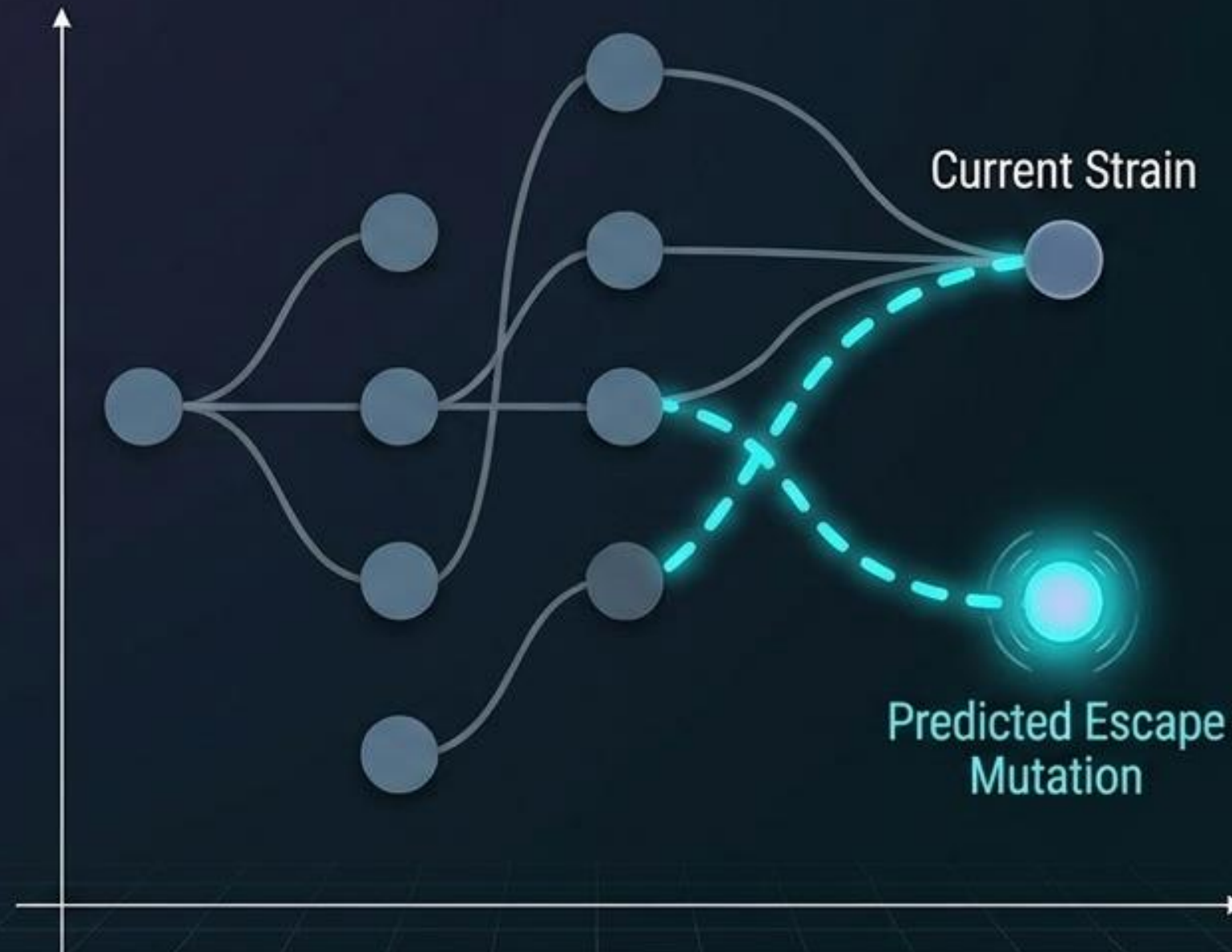
Rapid viral evolution and antigenic drift make strain selection notoriously complex.



The AI Upgrade

Deep learning algorithms (Viral Language Models) treat viral genomics like text, predicting the sequence mutations most likely to cause immune escape.

Antigenic Cartography



Clinical Benefit

Shifts the WHO vaccine composition process from retrospective analysis to proactive formulation, maximizing seasonal efficacy.

AI and Microbial Genomics: Automating the Bench

Raw Data



Next-Generation Sequencing (NGS) generates massive data volumes requiring weeks of manual bioinformatics.

The AI Bioinformatic Engine



Algorithms automate variant calling, assembly, and alignment instantly.

Automated Clinical Outputs



Rapid identification from highly mixed metagenomic samples.



Real-time phylogenetic clustering.



Tracking nosocomial transmission chains of multiresistant bacteria.

AI and Antimicrobial Resistance: Breaking the Time Bottleneck

The Silent Pandemic



AMR is projected to be a leading cause of global mortality by 2050. In severe infections like sepsis, the critical clinical variable is time. Broad-spectrum empiric use drives further resistance.

Bypassing the Culture



Traditional Antimicrobial Susceptibility Testing (AST) takes 48-72 hours. AI predicts phenotypic resistance directly from raw genomics or imaging in hours, enabling immediate precision medicine.

Study Profile: Genomic Prediction of Resistance

Reference: The CRyPTIC Consortium WGS Database Analysis

Target Organism



M. tuberculosis is notoriously slow-growing, traditionally requiring weeks for culture-based AST.

Algorithm

WGS Data
(SNPs & Pan-genome)



Gradient Boosting
Machine Learning
Discovery of non-obvious
epistatic interactions

Performance & Impact

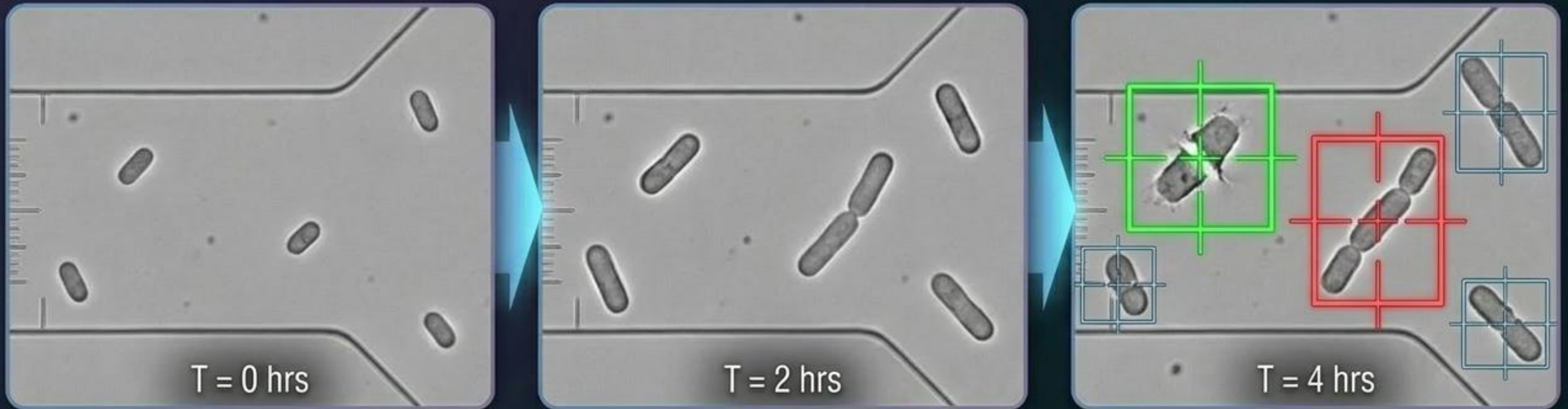
>90% Accuracy for First-Line Drugs



Clinical Impact: Replaces weeks of mycobacterial culturing with rapid genomic AST, halting MDR-TB transmission.

Study Profile: Deep Learning for Phenotypic AST

Reference: Single-cell imaging diagnostics (Lancet Digital Health)



The Methodology

Deep learning models track micro-morphological changes (elongation, lysis) of single cells exposed to antibiotics long before human eyes can detect visible colonies.

Clinical Impact & Limits

Delivers highly accurate phenotypic AST results in under 4 hours. Current limitation: Requires highly specialized microfluidic and microscopic imaging hardware.

AI Integration: Opportunities and Criticalities

Diagnostic Comparison Matrix

Systemic Strengths

Unmatched Speed

Bypasses biological incubation bottlenecks.

Data Synthesis

Holistic integration of multi-omics and epidemiology.

Proactive Support

Shifts workflows from reactive detection to predictive forecasting.

Critical Friction Points

The 'Black Box'

Lack of algorithm explainability hinders trust in life-or-death clinical decisions.

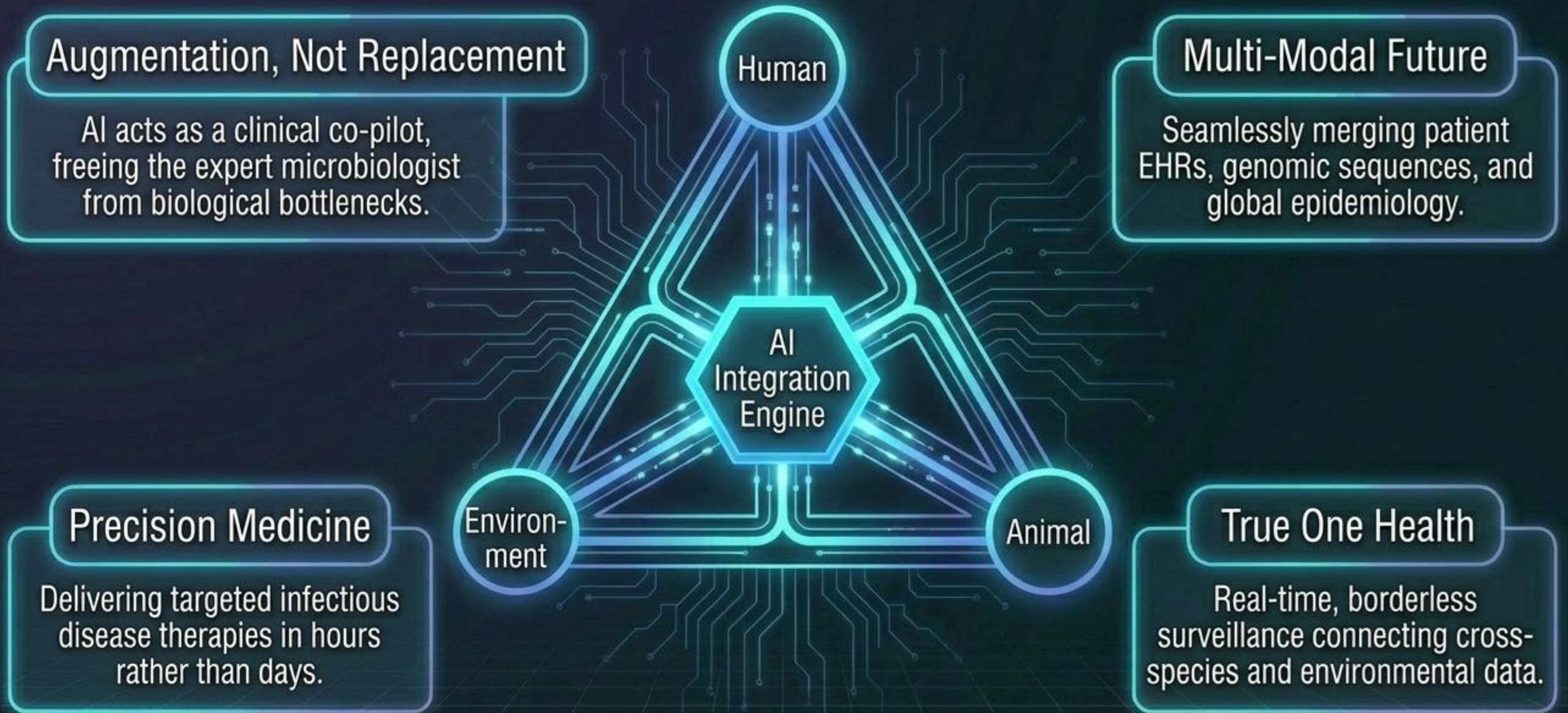
Geographic Data Bias

Models trained solely on Western datasets fail against Global South pathogen variants.

Regulatory Lag

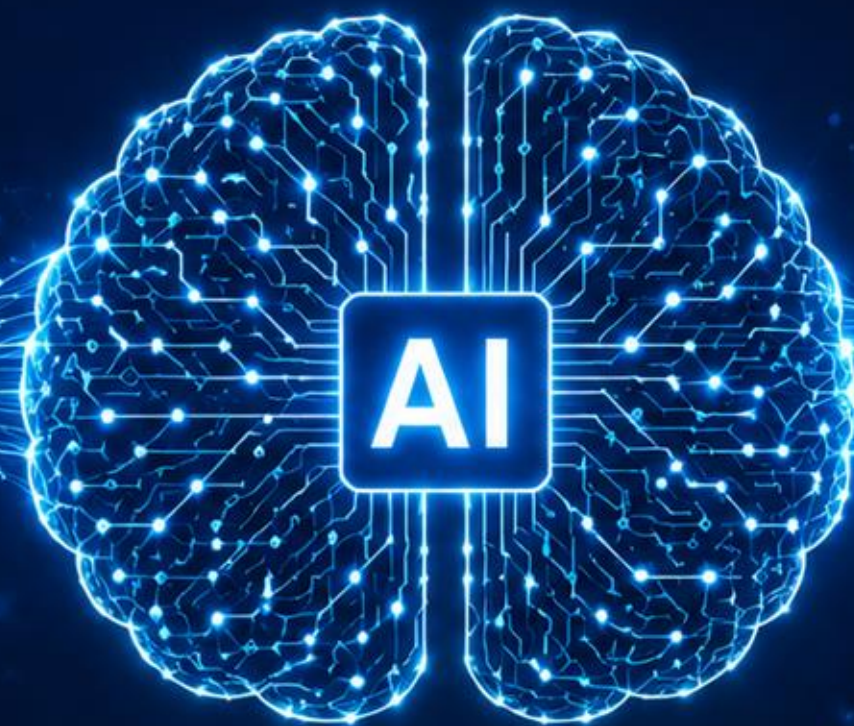
FDA/CE frameworks struggle to certify continuously learning algorithms and govern genomic data privacy.

Conclusions: Realizing the One Health Paradigm



THANK YOU FOR YOUR ATTENTION

Artificial Intelligence in Microbiology and Virology:
opportunities, innovation and the future of diagnostics



QUESTIONS?
Let's discuss!



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AMCLI – AI Working Group
Advancing AI in Laboratory Medicine