Genpax IDEM

Next Generation Infection Surveillance

IDEM Technical & Performance Guide

IDEM Insight Series: Document 4 of 6 - Advancing Infection Prevention and AMR Surveillance

About This Document

This is Document 4 of 6 in the IDEM Insight Series, designed to guide you from understanding the power of Whole Genome Sequencing (WGS) in infection prevention and control through to the benefits, performance, and practical use of IDEM.

The full IDEM Insight Series includes:

1. **The Power of WGS –** Transforming Infection Control and Public Health.
2. **IDEM Introduction –** Next-Generation Genomic Surveillance.
3. **IDEM Performance Overview –** How Accuracy, Resolution, and Connectivity Drive Results.
4. **IDEM Technical Validation Guide –** In-Depth Data and System Design.
5. **Health Economic Impact –** How Proactive WGS Saves Lives and Costs.
6. **IDEM Instructions for Use (IFU).**

For more information, visit www.genpax.co or contact support@genpax.co.

Insight Series Progress

[■] 1. The Power of WGS → [■] 2. IDEM Intro → [■] 3. Why IDEM Works → [■] 4. Technical Guide → [□] 5. Health Economics → [□] 6. IFU

Introduction This document provides a detailed technical overview of IDEM, highlighting how its capabilities support proactive infection prevention and control (IPC). IDEM's performance has been validated through extensive real-world studies, demonstrating its accuracy, resolution, and ability to track pathogen transmission. These validations include large-scale hospital outbreak data, same-patient infection tracking, and multi-site comparative studies, ensuring IDEM's effectiveness in clinical and public health settings. It aligns key technical elements from IDEM's existing solutions with the core goals of the team that developed it, demonstrating how IDEM's technology transforms pathogen genomics for IPC applications.

IDEM is designed to process and analyse over 100 clinically relevant bacterial and fungal pathogens, covering 99.9% of human bacterial infections and supporting infection prevention efforts across multiple healthcare and public health settings. Our goal is to continuously expand this coverage, with plans to include viral and further fungal pathogens in future developments.

Background and Team Expertise IDEM was developed by **Genpax**, a research and commercial innovation-driven company specialising in clinical pathogen genomics. Since 2021, the Genpax team has been dedicated to building a new generation of analytical tools for infection prevention and control.

- **Expert Team**: Comprising bioinformaticians, microbiologists, and infectious disease specialists with over a century of collective experience in pathogen genomics.
- **Research-Driven Approach**: The Genpax team includes experts with hundreds of peer-reviewed publications in the field of pathogen genomics, demonstrating our deep expertise in the area.
- **Focus on AMR and Emerging Pathogens**: IDEM was designed to address critical gaps in traditional pathogen genomics, ensuring rapid and accurate analysis for healthcare and public health applications.

Goals in Developing IDEM

ACCURACY

- Deliver a near-zero error rate to make genomic data truly actionable for IPC.
- Overcome the limitations of existing sequencing methods, which introduce substantial errors when analysing bacterial genomes.
- Ensure consistency in clinical replicates, identical strains from common sources, and ring-trial samples, allowing reliable cross-site comparisons.
- Avoid reference-based biases by implementing a **natural reference-free approach** using the Codex.

RESOLUTION

- Maximise the amount of genomic information extracted from each sample.
- Ensure high-resolution outbreak detection without compromising on scalability.
- Capture all relevant genomic variations, including **single nucleotide variations (SNVs), recombination events, and (soon) insertions and deletions (indels).**
- Enable genome-wide comparisons across highly diverse bacterial strains without loss of resolution over time.

CONNECTIVITY

- Enable hospitals, public health agencies, and research institutions to **compare and track strains across both time and geographic locations**.
- Provide an automated, scalable analysis pipeline that allows real-time outbreak detection and monitoring.
- Allow unrestricted comparison of all previously analysed strains, linking genomic insights across different sites and healthcare environments.
- Implement a **One Health approach** that connects human and food-associated bacterial genomics for a fully integrated surveillance strategy.

Note: QR codes are included throughout the following pages, allowing you to quickly access additional information by scanning them. Alternatively, you can click directly on the in-text links to view the same resources.

ACCURACY

Ensuring Reliable and Actionable Insights

Traditional sequencing methods introduce significant errors, leading to unreliable results when comparing bacterial genomes for IPC applications. IDEM's approach enhances accuracy by eliminating these sources of error through the following technical advancements:

- **Codex: A 'Natural Reference-Free' Solution**
  - The Codex provides a unique analysis tool that represents all variations within a species, overcoming the limitations of existing reference genomes.
  - Unlike previous approaches, it ensures comparability across diverse bacterial strains without introducing errors from reference selection.
- **Error Minimisation Strategies**
  - IDEM reduces assembly-induced errors by leveraging robust algorithms that minimise misinterpretation of genetic differences.
  - Error rates using established methods of **10s per million bases (many per genome) can be transformed to less than 1 in over 100 million bases compared**, indicating an improvement beyond a factor of 100.

Validation Studies

Calling Zero: A new foundation for diagnostic bacterial genomics.

IDEM's near-zero error rate has been demonstrated in **large-scale hospital outbreak** **WGS data for *Klebsiella pneumoniae***.

The novel genome comparison tool revealed false-positive and false-negative MRSA/MSSA identifications, showcasing the pitfalls of traditional methods.

Impact on IPC: IDEM's error minimisation and advanced genome comparison enable reliable outbreak detection and prevention, making sequencing data actionable for IPC teams.

UHD RESOLUTION

Maximising Information from Genomic Data

A major limitation of traditional sequencing approaches is the loss of valuable genetic information due to constrained resolution. IDEM's analytical framework ensures that every bit of useful genomic data is utilised effectively:

- **Comprehensive Genomic Coverage**
  - IDEM maximises usable genomic information by analysing all regions of the genome that can be reliably compared between samples, without limiting analysis to predefined core areas – while maintaining near-zero error rates for trusted results.
  - Unlike cgMLST or wgSNP methods that can introduce data loss, IDEM ensures full-spectrum genome comparison, maintaining integrity across diverse strains. **See limitations of sequence typing** for isolate inclusion in outbreak investigations.

- **Advanced Variant Detection**
  - IDEM identifies **single nucleotide variations (SNVs), recombination events, and (Soon) insertions and deletions (indels)**, providing superior resolution over existing approaches.
  - The Codex-based approach ensures that resolution does not degrade as more strains are analysed.

Demonstrated Performance Across Diverse Pathogens

Reference-free SNP-resolution analysis of *Campylobacter jejuni* validates IDEM's ability to analyse highly recombining bacteria.

High-resolution tracking of *Pseudomonas aeruginosa* outbreaks, overcoming limitations of standard methods.

Impact on IPC: The enhanced resolution allows IPC teams to distinguish between closely related strains and detect outbreak clusters with high precision, reducing unnecessary interventions and ensuring effective containment strategies.

CONNECTIVITY

Scalability and Cross-Site Comparability

A fundamental challenge in IPC genomics is the ability to connect sequencing data across time and geography. IDEM's design overcomes these challenges, enabling comprehensive tracking at both local and global scales:

- **Continuous, Cross-Site Comparisons**
  - Unlike traditional approaches that limit analysis to small batches of samples, IDEM allows **unrestricted comparisons between all previously analysed strains**.
  - Enables IPC teams to **track transmission routes across hospitals, reference labs, and public health settings** – while keeping identities confidential. Sites stay in control, sharing only through **mutual agreement.**
- **Unparalleled Analytical Scalability**
  - Traditional methods struggle with large datasets, limiting outbreak detection to short timeframes and small datasets.
  - IDEM's architecture allows **real-time analysis of thousands of strains over years**, providing long-term tracking capability.

Validation Studies

Listeria monocytogenes outbreak tracking demonstrated IDEM's ability to link strains from multiple laboratories.

Comprehensive One Health tracking of bacterial transmission across human and food environments, as validated through IDEM's comparative genomics approach.

Accurate infection tracking: IDEM differentiates persistent infections from new acquisitions, as demonstrated in **same-patient E. coli ST131 comparisons.**

Impact on IPC: IDEM's unmatched ability to connect genomic data across time and space ensures that transmission events are identified accurately, improving outbreak tracking, intervention strategies, and patient safety.

Species Coverage

Species	Type	Species	Type	Species	Type
Acinetobacter baumannii	HD	*Campylobacter coli*	HD	*Enterobacter kobei*	HD
Acinetobacter calcoaceticus	SD	*Campylobacter jejuni*	HD	*Enterobacter ludwigii*	HD
Acinetobacter lwoffii	SD	*Campylobacter lari*	HD	*Enterobacter roggenkampii*	HD
Aeromonas hydrophila	SD	*Candida auris*	SD	*Enterococcus casseliflavus*	SD
Aliarcobacter butzleri	SD	*Capnocytophaga canimorsus*	SD	*Enterococcus faecalis*	HD
Bacillus anthracis	SD	*Citrobacter freundii*	SD	*Enterococcus faecium*	HD
Bordetella holmesii	SD	*Clostridioides difficile*	HD	*Enterococcus gallinarum*	SD
Bordetella parapertussis	SD	*Clostridium butyricum*	SD	*Escherichia albertii*	SD
Bordetella pertussis	SD	*Clostridium perfringens*	SD	*Escherichia coli*	HD
Brucella melitensis	SD	*Corynebacterium diphtheriae*	SD	*Gardnerella vaginalis*	SD
Burkholderia arboris	SD	*Corynebacterium pseudotuberculosis*	SD	*Haemophilus influenzae*	SD
Burkholderia cenocepacia	SD	*Corynebacterium silvaticum*	SD	*Haemophilus parainfluenzae*	SD
Burkholderia cepacia	SD	*Corynebacterium striatum*	SD	*Helicobacter pylori*	SD
Burkholderia contaminans	SD	*Corynebacterium ulcerans*	SD	*Klebsiella aerogenes*	SD
Burkholderia dolosa	SD	*Coxiella burnetii*	SD	*Klebsiella africana*	SD
Burkholderia lata	SD	*Cronobacter sakazakii*	SD	*Klebsiella oxytoca*	HD
Burkholderia multivorans	SD	*Cutibacterium acnes*	SD	*Klebsiella pneumoniae*	HD
Burkholderia pseudomallei	SD	*Elizabethkingia anophelis*	SD	*Klebsiella quasipneumoniae*	HD
Burkholderia pyrrocinia	SD	*Enterobacter asburiae*	HD	*Klebsiella variicola*	HD
Burkholderia seminalis	SD	*Enterobacter bugandensis*	SD	*Legionella pneumophila*	SD

Burkholderia stagnalis	SD	*Enterobacter cloacae (and subspecies)*	HD	*Leptospira interrogans*	SD
Burkholderia ubonensis	SD	*Enterobacter hormaechei (and subspecies)*	HD	*Listeria monocytogenes*	HD
Moraxella catarrhalis	SD	*Nocardia farcinica*	SD	*Staphylococcus capitis*	SD
Moraxella osloensis	SD	*Pasteurella multocida*	SD	*Staphylococcus epidermidis*	SD
Mycobacteroides abscessus	SD	*Proteus mirabilis*	SD	*Staphylococcus lugdunensis*	SD
Mycobacteroides chelonae	SD	*Proteus vulgaris*	SD	*Stenotrophomonas maltophilia*	SD
Mycobacterium avium	SD	*Pseudomonas aeruginosa*	HD	*Streptococcus agalactiae*	SD
Mycobacterium intracellulare	SD	*Raoultella ornithinolytica*	SD	*Streptococcus dysgalactiae*	SD
Mycobacterium kansasii	SD	*Raoultella planticola*	SD	*Streptococcus equi*	SD
Mycobacterium tuberculosis	HD	*Salmonella enterica*	HD	*Streptococcus pneumoniae*	SD
Mycolicibacterium fortuitum	SD	*Serratia liquefaciens*	SD	*Streptococcus pyogenes*	SD
Mycoplasmopsis bovis	SD	*Serratia marcescens*	SD	*Vibrio alginolyticus*	SD
Mycoplasmoides genitalium	SD	*Shigella boydii*	HD	*Vibrio cholerae*	SD
Mycoplasmoides pneumoniae	SD	*Shigella dysenteriae*	HD	*Vibrio parahaemolyticus*	SD
Neisseria gonorrhoeae	SD	*Shigella flexneri*	HD	*Vibrio vulnificus*	SD
Neisseria lactamica	SD	*Shigella sonnei*	HD	*Yersinia enterocolitica*	SD
Neisseria meningitidis	SD	*Staphylococcus aureus*	HD		

HD = High-definition SD = Standard Definition

While SD codexes provide an industry-standard level of resolution, HD codexes offer enhanced granularity, better than SNP analysis with an outbreak lineage reference.

Conclusion: A Unified Solution for IPC Genomics

IDEM transforms pathogen surveillance, providing a powerful, fully connected, and actionable solution for healthcare, public health, and food safety applications.

Get Started with IDEM Today

- **Contact us**
- **Learn More**
- **Schedule a Demo**

EMAIL: support@genpax.co

Next in the IDEM Document Series:

➡️ *Health Economic Impact – How Proactive WGS Saves Lives and Costs*

Previous in the IDEM Document Series:

⬅️ *IDEM Performance Overview – How Accuracy, Resolution, and Connectivity Drive Results.*

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