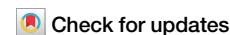


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Urban genome: a new paradigm for sustainable cities



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This article introduces an innovative paradigm in urban planning that goes beyond conventional methodologies by addressing the complex, multi-dimensional nature of contemporary cities. Drawing inspiration from living organisms, it presents the *Urban Genome (Urbanome)* framework, which posits that cities possess their own ‘DNA’—a coded set of service protocols, infrastructural designs and governance rules that guide development, functionality and adaptation. Leveraging advanced sensing, data-integration and artificial-intelligence (AI) technologies, among others, the Urbanome seeks to decode this urban DNA and integrate diverse data streams into a cohesive and dynamic model. The approach enables predictive analytics, adaptive planning and cross-sector integration to support long-term urban transformation. More than a metaphor, the Urban Genome offers as a blueprint for designing sustainable, resilient and inclusive urban environments, directly tackling the pressing challenges cities face worldwide. By providing a comprehensive and adaptable framework, it shifts practice from static sectoral models to a dynamic, systems-integrated strategy for sustainable cities urban futures.

Conceptual analogies have long shaped the way we understand cities, providing heuristic lenses that render their complexity more tractable. By framing urban complexity (its form, functions and interactions) in familiar biological, mechanical or cybernetic terms, they provide intuitive ‘shortcuts’ that guide data collection, model building and policy design. Several recurring metaphorical frameworks can be identified in the contemporary literature, each offering a distinct angle of interpretation. These include views of the city as a *machine*, an *organism*, an *ecosystem*, or a *network of adaptive flows*, each highlighting particular dimensions of urban life and informing planning paradigms accordingly.

Classic machine or *cyber-physical* frameworks privilege efficiency, control and feedback loops, underpinning many smart-city dashboards and optimisation models^{1,2}. The *city as organism* metaphor and its derivative *urban metabolism* explain urban material and energy cycles by analogy to biological processes^{3,4}. Ecosystem metaphors embed cities within broader socio-ecological dynamics, stressing co-evolution with climate and biodiversity⁵. Complexity science, meanwhile, portrays the city as a network of adaptive agents that self-organises through local interactions^{6,7}. Recent studies extend the analogy to *brain-like* or *cognitive* cities capable of learning from massive data streams^{8–10}. Nonetheless, each analogy elucidates only a limited domain of the urban organism. The metabolic perspective deciphers the city’s ‘digestive tract’—its material and energy flows—while neglecting, for instance, neural, immune and circulatory functions. The machine

metaphor optimises the skeletal hardware and control loops but underestimates processes of socio-cultural evolution and learning. Complex-systems framings map interaction topologies, yet rarely specify the underlying functional modules. Brain or cognitive city models focus on urban ‘neurons’ and data streams, detached from the physical tissues and historical path-dependencies that sustain the system. What remains absent is a comprehensive blueprint that, like a genome, codifies every subsystem and their cross-talk—a holistic framework that is simultaneously modular, transferable and evolvable.

Despite these conceptual gaps, urban policy has continued to evolve, but largely in a fragmented manner, through a broad menu of sustainability strategies: green-infrastructure and nature-based solutions that enhance biodiversity and thermal comfort¹¹; compact-city design and active-mobility programmes that reduce sprawl and emissions^{12,13}; energy-positive buildings and circular-economy pilots that cut resource footprints^{14–16}; and resilience planning that prepares cities for climate shocks and health crises^{17,18}. While each initiative delivers tangible benefits, it is typically framed through a single metaphorical lens, addressing one subsystem while leaving cross-domain feedbacks unexplored.

The smart-city agenda^{19,20} has meanwhile deployed IoT sensor networks and data platforms^{1,2}, AI analytics^{21–24}, Mobility-as-a-Service platforms²⁵, digital twins^{26,27} and the Internet of Behaviour²⁸ to optimise traffic, energy and public services in real-time. Citizen-engagement tools

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and tactical-urbanism apps further widen participation^{29,30}. Yet these technologies are still limited by partial metaphors: cyber-physical dashboards fine-tune discrete assets, brain-city models mine behavioural data and network approaches simulate flows, but none relates technological layers to social practice and long-term urban evolution in a unified schema.

Breakthroughs in genetics, from the rediscovery of Mendel's laws to the elucidation of the DNA double helix and, more recently, the Human Genome Project³¹, demonstrate how modular code governs growth, maintenance and adaptation. By analogy, cities can be thought of as possessing an urban genome: a set of reproducible strategies that organise infrastructure, governance and behaviour. *We therefore propose the Urban Genome Framework* as a paradigm shift for understanding and steering contemporary and future cities. In this concept, a city has its own 'DNA': a structured code of *urban genes* that represent foundational components such as mobility systems, water networks, energy grids, institutional rules and behavioural norms. Like genes in biology, these elements interact to produce observable *urban expressions*, the day-to-day services, patterns and externalities that constitute the *urban phenotype*. Genes also combine into higher-order *urban pathways* that cut across sectors, explaining why a modification in waste collection can ripple through health outcomes, logistics efficiency and carbon emissions. With nearly 70 % of the global population projected to live in cities by 2050³², planners require integrative approaches that bridge separate sectors and keep pace with rapid socio-technical change; the Urbanome offers such an integrative, modular and evolvable blueprint. Figure 1 offers a didactic side-by-side analogy: just as gene therapy targets a specific genetic disorder, a 'city-therapy' intervention targets air-quality genes, illustrating how modular code can drive precision solutions in both medicine and urban planning.

In this paper, we aim to: (1) present the Urban Genome as a coherent conceptual framework; (2) lay out a five-step sequencing methodology for mapping and editing urban genes; and (3) illustrate its practical application through a real-world air-quality case in Mexico City. Building on these objectives, the Urbanome introduces four key capabilities that address persistent gaps in existing frameworks. *First, modularity*: individual urban genes (defined as baseline units of infrastructure, governance, or behaviour) can be isolated, sequenced and deliberately edited through policy or

technology. *Second, transferability*: once sequenced, these urban genetic patterns can be benchmarked and compared across cities, supporting evidence-based learning. *Third, evolvability*: transformations (mutations) triggered by crises or strategic interventions can be traced over time, enabling planners to anticipate trajectory shifts. *Fourth, evidence synthesis*: by combining long-term historical patterns with real-time data streams, the framework overcomes the static and fragmented nature of sectoral models, delivering continuous, multi-scale insights. Collectively, these capabilities position the Urbanome as a holistic, evolutionary perspective on urban complexity. It marks a decisive shift from static, sector-specific toolkits toward a dynamic and integrated strategy for sustainable urban planning, one that can evolve as cities themselves evolve.

Taken together, the Urban Genome Framework offers a systematic map of how urban responses are encoded, transmitted and expressed, spanning policies, infrastructures and individual behaviour. By framing the city as a living system with editable 'DNA,' it helps planners pinpoint leverage points for greater resilience and sustainability. The framework is also grounded on historical patterns of adaptation: just as evolution fixes beneficial traits, cities embed successful strategies as 'urban genetic' blueprints. Copenhagen's long-standing commitment to cycling, energy-efficient buildings and climate adaptation, set in motion by the 1970s oil crisis, shows how such traits can be written into a city's genome. Decades later, the 2008 financial crisis led many cities, from Madrid to Detroit, to adopt low-cost tactical-urbanism schemes, green-retrofit programmes and innovative financing models, illustrating yet another pathway through which adaptive traits become encoded in an Urban Genome. These precedents demonstrate that urban knowledge can be encoded, shared and refined, enabling cities to learn from their own past and from one another. The sections that follow formalise the framework, introduce an illustrative air-quality gene and show how this approach can support resilient, inclusive urban development.

Results

This section formalises the Urban Genome not only as a conceptual but also as a methodological framework. It outlines the overall structure and internal logic of the Urbanome, detailing its core functional layers and introducing

Fig. 1 | From gene therapy to 'city therapy': a didactic analogy. *Left:* A genetic disorder (*medical problem*) is treated through targeted gene therapy (*biological solution*), yielding improved health (*health outcome*). *Right:* Severe urban air pollution (*urban problem*) is tackled with a sensor-AI-driven air-quality management system (*tech solution*), producing cleaner air and public-health gains (*urban outcome*). The panel is illustrative only, highlighting the conceptual bridge between precision medicine and precision urban intervention; quantitative results appear later in the paper.



City DNA as the digital tool underpinning them. It then describes the key components of the framework and illustrates how these can be applied in practice through the case of Mexico City's strategies for improving air quality. Together, these elements highlight the Urbanome's potential to analyse, compare and guide urban strategies in a consistent and transferable way.

We begin by presenting the core structure of the framework and its biological metaphor. Figure 2 visualises the Urban Genome paradigm, portraying the city as a living system whose modular 'DNA' encodes recurring strategies for growth, function and adaptation. Translating this idea into an operational model, the Urbanome framework organises urban information into four functional layers:

1. *Urban genes*—modular code units (e.g. mobility, energy, waste);
2. *Urban Gene expressions*—the operational translation of each gene into services and data flows;
3. *Urban pathways*—recurrent multi-gene routines that cut across sectors;
4. *Urban phenotype*—observable city outcomes such as health, emissions or safety.

The *City DNA* illustrated at the base of Fig. 2 represents the shared digital architecture that underpins the four functional layers of the Urbanome. More than a data repository, it provides the structural logic, operational mechanisms and integrity safeguards needed to encode, track and evolve strategies across Genes, Expressions, Pathways and Phenotype. It shapes how encoded strategies materialise as measurable services, coordinated routines and city-wide outcomes. A detailed description of this architecture appears in the Methods section.

Elements of the Urbanome

Having outlined the overall structure, we now examine each functional layer in detail.

Urban genes. Just as the human genome contains tens of thousands of genes, a fully mapped Urbanome would comprise a large, yet still undefined, number of modular 'city genes'. For illustration we depict six representative families (water, mobility, energy, waste, governance and health), each treated as an addressable unit that can be read, compared or edited. These exemplars show the principle: every distinct service, rule-set or behavioural pattern can, in principle, be encoded as a gene and combined with others to build higher-level functions. Importantly, when a gene is 'mutated' or edited, say by changing a policy or technology, those changes instantly appear in the expression layer and then feed into the pathways that link multiple genes together.

Gene expressions. Analogous to protein synthesis in biology, an urban gene is 'expressed' whenever its encoded rules and assets materialise as measurable services or resource flows. Typical manifestations range from vehicle-kilometres travelled (mobility gene) and litres of water per capita (water gene) to participation rates in e-governance portals. Although the examples in Fig. 2 are illustrative, any service metric or behavioural signal can, in principle, serve as a gene expression.

Once a gene is expressed, those rules crystallise into *urban proteins*: operational service protocols such as bus timetables generated from the mobility gene, optimised refuse-collection routes from the waste gene, or dynamic congestion-charge algorithms from the governance gene. These proteins drive the day-to-day routines that knit individual expressions into the multi-gene pathways described next.

Urban pathways. Individual expressions rarely act in isolation. Recurrent combinations such as *circular-waste loop* that couples waste collection, energy recovery and governance enforcement form urban pathways, the functional analogue of metabolic pathways in biology, where multiple gene expressions interact to carry out coordinated tasks. The catalogue of possible pathways is open-ended; the three-gene cluster

highlighted in the figure (ENE, WST, GOV) merely exemplifies the concept.

Urban phenotype. At the system level, multiple pathways converge to produce observable city outcomes. The aggregate indicators - carbon footprint, respiratory morbidity rate, congestion index, perceived safety - represent the urban phenotype. Fig. 2 also marks three dominant interaction patterns: (a) *regulatory links* where governance genes modulate physical genes; (b) *feedback loops* driven by real-time data, enabling rapid mutation; and (c) *cross-pathway coupling*, whereby action in one sector reverberates across others.

Together, these four functional layers provide a structured logic for interpreting how cities generate, combine and adapt key operational capacities, linking infrastructure, governance and behavioural signals across scales. These layers rest on a shared digital foundation, the *City DNA*, whose structural architecture runs from Urban Nucleotides through Genes and Chromatin, up to the cloud-based Urban Nucleus, with a blockchain-enabled 'Double Helix' ensuring integrity and traceability. A detailed technical description of this architecture appears in Methods.

While the Urbanome introduces a novel conceptual framework, its foundational logic reflects adaptive patterns already observed in real-world urban systems. These historical patterns resemble *genetic traits*, persistent responses that emerge from repeated challenges and become embedded in a city's operational fabric, much like heritable traits in biological systems. In Mexico City, for example, historical adaptive responses to air pollution such as driving restriction programmes (Hoy No Circula), transit expansion, green corridors and stricter fuel standards constitute a recognisable set of adaptive traits. Although these interventions reduced peak ozone and PM₁₀ levels by over 50% between 1990 and 2020³³, persistent PM_{2.5} exceedances suggest that these traits must *mutate* further to address ongoing challenges like population growth and climate change. Other cities show similar inherited adaptations, as seen in Dutch flood management and Singaporean water reuse strategies. The Urbanome formalises such traits as modular, addressable genes, enabling cities to identify, replicate and evolve successful patterns proactively rather than respond reactively.

Illustrative application: the air-quality gene

To demonstrate how the Urbanome sequencing protocol (Table 1, Methods) operates in practice, we illustrate the application of Steps 1–5 to an air-quality management challenge in the Mexico City Metropolitan Area (about 21.5 million inhabitants). The area is served by the Mexico City Air Quality Monitoring System (SIMAT), a network of 44 monitoring sites that measure criteria pollutants, surface meteorology and UV radiation in real-time^{34,35}. Thirty-four automatic stations report hourly concentrations of PM_{2.5}, PM₁₀, ozone (O₃), nitrogen dioxide (NO₂), carbon monoxide (CO), carbon dioxide (CO₂), sulfur dioxide (SO₂) and other regulated pollutants; the remaining sites provide complementary meteorological data. These measurements feed into public dashboards and underpin the metropolitan air-quality programme (PROAIRE)³⁶. In the example that follows, we focus on PM_{2.5} to illustrate each step of the workflow.

SIMAT³⁷ data show that the 2010–2019 annual mean of PM_{2.5} fluctuated around 24 µg m⁻³, well above the World Health Organization (WHO) guideline of 10 µg m⁻³ established in 2005 and the stricter 2021 updated revision of 5 µg m⁻³, underscoring the remaining gap³⁸. Although SIMAT monitors several pollutants, we focus on PM_{2.5} because it carries the strongest health evidence, the strictest WHO limits and serves as a practical proxy for the combined impact of transport, industry and waste-handling emissions.

Figure 3 shows how we specialised the generic five-step workflow (Table 1, Methods) to this air-quality challenge. The following step-wise cascade traces how a targeted policy 'edit' at the gene level propagates through expressions and pathways to produce a measurable phenotypic improvement:

1. **Scope.** Define the study boundary (Mexico City Metropolitan Area, about 21.5 million inhabitants), baseline period (2016–2020) and headline pollutant (PM_{2.5}).
2. **Gene identification.** The 2016 emission inventory for the Mexico City Metropolitan Area identified on-road transport as the ‘Energy Gene,’ since it accounts for roughly 60% of fossil-fuel consumption, drove the city’s primary energy flows and produced the largest shares of primary PM_{2.5} and PM₁₀. Diesel-powered waste-collection vehicles contributed roughly 10%, so transport and refuse traffic together were responsible for about 70% of particulate emissions documented in the valley³⁹. (The 2016 inventory remains the most recent official dataset released by the city government.)
3. **Expression mapping.** SIMAT operates 34 automatic monitoring stations that record hourly concentrations of PM_{2.5} and co-pollutant (PM₁₀, SO₂, CO, CO₂, NO₂ and O₃) across the metropolitan area³⁴. These measurements, combined with roadway traffic counts from loop detectors and GPS traces, form the real-time data streams that characterise gene expressions. A quality-assurance and quality-control (QA/QC) procedure removes any sensor records flagged for calibration drift or malfunction.
4. **Pathway formation.** In our five-step protocol, *urban mutation*—the targeted editing of an urban gene—occurs as part of pathway formation, where policy changes translate the conceptual edit into real-world routines. Under Mexico City’s long-standing PROAIRE air-quality framework (first launched in 2013 and extended through 2030)³⁶, cross-sector routines are operationalised by applying ‘genetic edits’ to the Energy and Waste genes through four key regulatory instruments:
 - (i) Mandatory ultra-low-sulphur diesel (<15 ppm) and Euro VI/Tier 4 emissions standards for new heavy-duty vehicles,
 - (ii) A central low-emission zone restricting high-emitting trucks and buses in the historic city center,
 - (iii) The *Basura Cero* (‘Zero-Waste’) initiative, which electrifies and optimises the routes of the municipal refuse-collection fleet.
 - (iv) Stricter industrial emissions controls and enhanced vehicle-inspection programmes.

These coordinated policy edits (urban mutations) produced rapid, measurable declines in PM_{2.5} (and other pollutants) at SIMAT monitoring sites, signalling the effectiveness of the Urbanome’s pathway interventions⁴⁰.

5. **Phenotypic shift.** By mid-2020, the coordinated air-quality interventions in the Mexico City Metropolitan Area experienced measurable system-level improvements: a 9% reduction in PM_{2.5}, 4% in PM₁₀ and NO₂, 3% in SO₂ and 2% in CO, demonstrating how targeted ‘gene’ edits can yield rapid, measurable gains in urban environmental health⁴¹.

Urban-metabolism models quantify material and energy flows but often overlook dynamic behavioural adaptations such as driver rerouting or household recycling that can significantly influence outcomes. Smart-city dashboards similarly optimise individual assets in isolation. In contrast, the Urbanome explicitly incorporates these behavioural responses as part of its multiscale analysis and captures cross-sector cascades, showing how interventions like low-emission zones not only improve air quality but also reshape logistics costs and waste-collection schedules. By identifying these actionable ‘genes,’ the framework enables urban planners to design, edit, monitor and benchmark targeted policies across diverse city contexts.

Summary of results

The Urbanome converts the city as genome metaphor into a four-layer operational model: genes, expressions, pathways and phenotype, underpinned by a five-step sequencing workflow (scope, gene identification, expression mapping, pathway formation and mutation). Using an air-quality case, it shows how modular ‘genetic’ edits can produce integrated and measurable improvements, where traditional, sector-based approaches often fall short. To support these transformations, the Urbanome is enabled by a digital architecture, City DNA, that stores and organises its modular

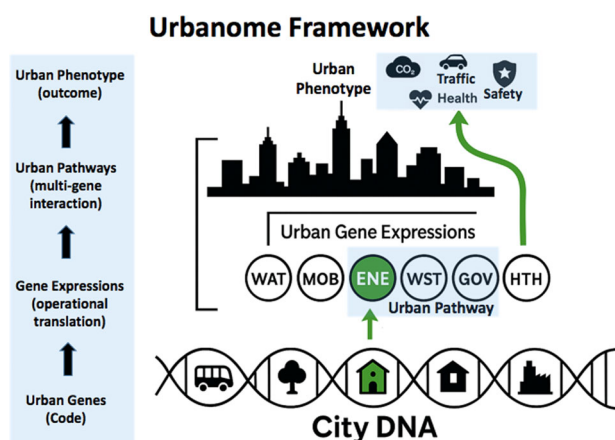


Fig. 2 | Functional flow within the Urbanome framework. The double helix (‘City DNA’) stores six illustrative urban genes: WAT (water), MOB (mobility), ENE (energy), WST (waste), GOV (governance) and HTH (health). When an individual gene is expressed (highlighted ENE), its service metrics merge with others to form a multi-gene *urban pathway*; interacting pathways then converge into the *urban pathway* (traffic, health, safety, CO₂). The figure therefore traces the complete chain *gene* → *expression* → *pathway* → *phenotype*, showing how a policy ‘edit’ at genetic level can propagate to city-wide outcomes.

Table 1 | Generic five-step protocol for applying the Urbanome Framework in any city

Step	Purpose	Typical inputs	Core methods / outputs
1. Scope	Define study boundary, priority challenge, baseline period	City boundary maps, census profiles, sustainable development goal or master-plan targets	Geographic study area; problem statement; baseline Key Performance Indicator (KPI) list
2. Gene ID	Catalogue modular <i>urban genes</i> and assign a unique ID to each (self-contained service units)	Sector inventories (transport, energy, waste, water), policy archives, asset registers	1. Identify one modular city function (e.g. mobility, energy, waste). 2. Map its governing rules and hard/soft assets (infrastructure, tariffs, main stakeholders). 3. Register the gene with a unique identifier and metadata tags (sector, scale, data owner).
3. Expression (Operationalisation)	Operationalise each gene into service workflows and data streams	IoT streams, open-data portals, administrative records, household or origin-destination surveys	Validated service workflows and data flows; standardized performance metrics (e.g. Vehicle-Kilometres Travelled, PM _{2.5}); data quality assurance/quality control
4. Pathways	Detect cross-sector routines and apply policy ‘mutations’	Multi-layer graphs, time-series of expressions	Network/sequence analysis → pathway motifs
5. Phenotype	Assess baseline phenotype; test edits	KPI dashboard, simple scenario or agent-based model	Baseline phenotype; simulated edits; sensitivity results

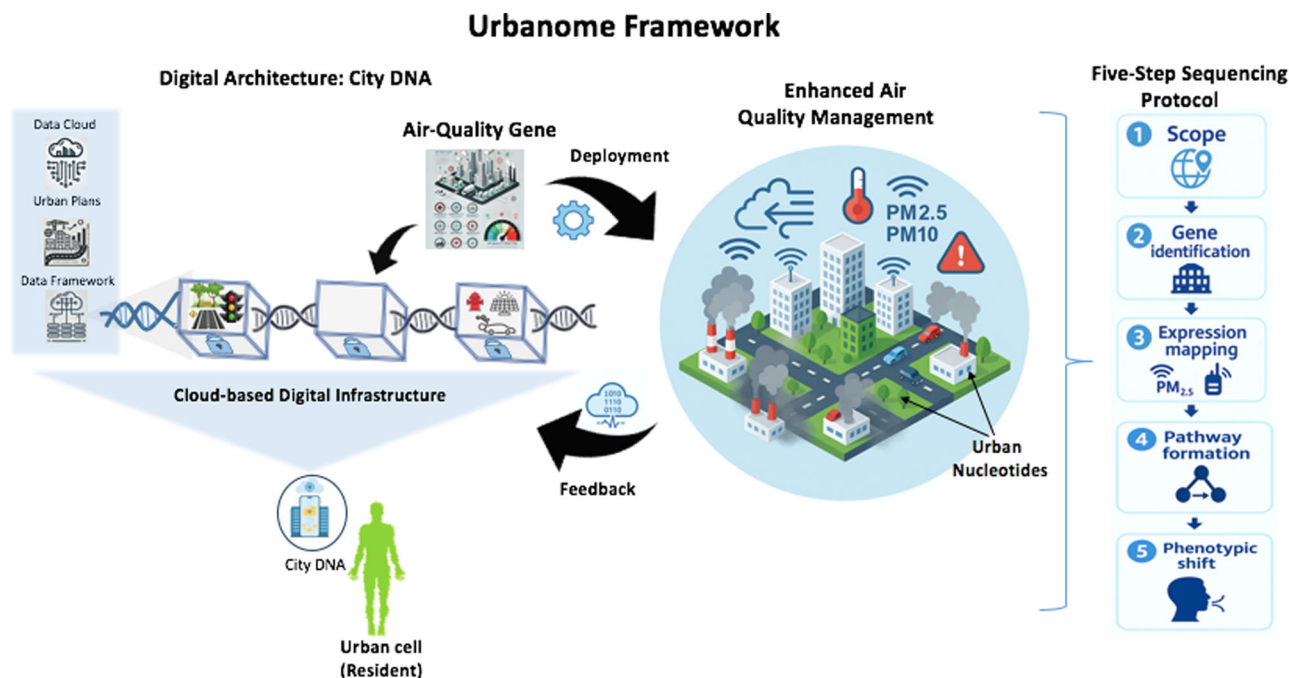


Fig. 3 | Illustrative application of the Urban Genome Framework to air-quality management in Mexico City. This diagram parallels medical gene therapy by showing how the Air-Quality Gene is digitally deployed, activated in the urban environment, and continuously monitored through feedback loops. Precision

targeting of PM_{2.5} emissions via tailored policy ‘edits’ demonstrates how data-driven planning can regulate environmental factors and deliver measurable improvements in air quality.

layers along with their operational logic. This architecture comprises key components, including *Urban Cells* (digitally enabled residents), the *Urban Nucleus*, *Urban Chromosomes*, *Urban Chromatin*, the *Urban Double Helix*, *Urban Genes* and *Urban Nucleotides*, which together enable the storage, organization and secure management of urban data and service logic. Their specific roles are detailed in *Methods*. The framework also introduces the notion of urban proteins, tangible actions (e.g. fleet electrification, networks logistics redesign) that carry out the instructions encoded in the Urbanome. These functional agents enact the genome’s edits, translating modular policy changes into systemic urban transformation.

Discussion

The Urban Genome marks a paradigm shift in city planning, offering a coherent framework to understand and manage the complexity of today’s urban ecosystems. This bio-inspired approach moves beyond fragmented strategies by mapping a city’s ‘genetic code’ to reveal replicable traits, adaptive behaviours and cross-sector synergies. Borrowing from systems biology, we conceptualise residents as urban cells; through their collective activity, these cells give rise to *urban tissues*, the networks and spaces, such as roads, water and energy grids, healthcare facilities, parks, that assemble into *urban organs* (mobility, energy, health subsystems) which in turn integrate into *urban organ systems* (e.g., the transport system or the metabolic-energy system). Thus, these elements constitute the city as an organism, mirroring the familiar hierarchy used in life sciences (cell → tissue → organ → systems → organism). This integrated, systems-biology lens clarifies how interventions at one scale ripple through others, grounding the Urban Genome’s four functional layers in a rigorously layered view of urban form and function. In doing so, Urban Genome supplies a unifying vocabulary for comparative research and positions cities as laboratories where genetic traits can be sequenced, benchmarked and deliberately evolved. Bioinformatics methods, in turn, supply the data-fusion and pattern-detection tools that make such multiscale analysis operational.

Optimising transit through *Urban Mobility Genes*, cooling neighbourhoods via *Urban Green-Infrastructure Genes* and redirecting resources with *Urban Social-Equity Genes*, demonstrate the Urban Genome’s day-to-

day utility. Conceptually, the framework advances urban theory by introducing a modular, evolvable ‘genetic’ lens that bridges physical infrastructure, human behaviour and governance. Unlike urban-metabolism models, which follow material and energy flows, or smart-city architectures that foreground sensor integration and real-time analytics, the Urban Genome captures infrastructure and historical behaviour, adaptability and planning logic, treating each as an *editable gene* that can be tested, replicated and evolved across cities, thereby shifting practice from static zoning toward dynamic, data-informed governance.

Equally important is the framework’s historical grounding. By analysing consistent responses to past challenges, such as environmental crises (air-quality crises, flood events, wildfires) or infrastructure failures (energy shortages, transportation network breakdowns, bridge or road collapses), the framework identifies *urban genetic traits*: adaptive patterns such as low-emission zones, sponge-city drainage or tactical green spaces. Embedding these responses in a city’s genome provides a foundation for understanding urban evolution but also enables cities to proactively apply time-tested ‘genes’ solutions, enhancing resilience and sustainability.

Central to the framework is its human-centred design. By decoding urban genes, the Urban Genome translates systemic complexity into tangible improvements in citizens’ lives. Mapping mobility genes can shorten commutes and reduce emissions while improving accessibility and mental well-being. Green-infrastructure genes could mitigate urban heat and foster community cohesion and psychological health, whereas social-equity genes realign resource flows toward underserved districts. Such targeted interventions extend to housing, health and energy and beyond, enabling cities to evolve on the basis of lived experience rather than abstract technological fixes, offering a practical blueprint for healthier, more inclusive and sustainable cities.

Together, the Urban Genome attributes (modularity, transferability, evolvability and rigorous evidence synthesis) reframe the city not as a static artefact or a collection of isolated subsystems, but as a living organism whose ‘DNA’ can be sequenced, compared and deliberately steered toward equitable, sustainable futures.

While the Urban Genome introduces an innovative paradigm for urban planning, its implementation faces several conceptual and operational challenges that must be addressed to ensure its viability:

- **Complexity of Mapping an Urban Genome:** The process of identifying and codifying a city's 'genetic traits' requires sophisticated analytical tools and methodologies that may not yet exist or are in early stages of development. For instance, accurately mapping relationships between urban systems, such as transportation networks and air quality, necessitates a level of computational modelling and data integration that is both resource-intensive and technically demanding.
- **Data Availability and Standardization:** A critical barrier lies in compiling and standardizing historical and real-time data across diverse urban contexts. Cities vary significantly in their capacity to collect, process and maintain comprehensive datasets. Inconsistent or incomplete data could limit the framework's accuracy and its ability to identify meaningful patterns or 'genetic traits.'
- **Equity and Inclusivity Risks:** Data-driven approaches, while promising, carry the inherent risk of reinforcing existing inequalities. Vulnerable populations or underserved communities may be inadvertently excluded if data is biased or incomplete. For example, areas with limited technological infrastructure may not have sufficient representation in the datasets used to inform Urban Genome strategies.
- **Practical Implementation Challenges:** Translating genomic insights into actionable urban policies demands a high level of coordination across sectors, including urban planning, governance and community engagement. Long-term commitment and interdisciplinary collaboration are required, yet these can be difficult to achieve in the face of political or economic constraints.
- **Cultural and Educational Shifts:** The framework requires a paradigm shift that challenges conventional urban planning methodologies. Urban planners, policymakers and citizens must embrace a dynamic, systems-thinking approach that views cities as evolving organisms rather than static entities. This cultural transition may be met with resistance.
- **Balancing Conceptual and Practical Contributions:** While the framework offers a robust theoretical foundation, its success ultimately depends on its ability to translate into actionable strategies. Ensuring that the framework remains grounded in real-world applicability is critical to its adoption and long-term impact.

Proactively addressing these issues is essential to ensure that the Urbanome evolves as a tool that is not only visionary, but also implementable and inclusive. This critical assessment not only highlights potential risks but also underscores the opportunities for innovation and collaboration, ensuring that the framework delivers tangible benefits to cities and their inhabitants.

The Urban Genome concept opens new possibilities for research and practice not only in urban planning, management and governance but also in technology development, data science applications, infrastructure engineering and real-time environmental monitoring. By examining the fundamental components and 'genetic code' of urban systems, we can better understand urban dynamics and how cities have historically responded to environmental, infrastructural and social stressors. This historical perspective provides a foundation for understanding urban evolution while enabling cities to proactively apply proven solutions, enhancing resilience and sustainability.

Investigating the practical applications of the framework, such as 'urban proteins,' could lead to innovative solutions in infrastructure, community engagement and environmental sustainability. In analogy with biological proteins, urban proteins are the executable service protocols—traffic-control algorithms, water-treatment workflows, emergency-response procedures—that carry out the instructions encoded by Urban Genes. Mapping, cataloguing and testing these proteins in live environments will close the design-implementation gap, ensuring that pathway edits translate into measurable improvements in city performance and

equity. Addressing the scalability and complexity of mapping the Urbanome will be crucial, alongside developing robust methodologies to implement it effectively.

Future research should focus on applying the Urban Genome concept across diverse urban settings and scales. This includes exploring how urban genes and proteins can be customized to address specific challenges, such as traffic congestion, pollution, social inequality and housing shortages. Collaborative efforts among urban planners, data scientists, environmentalists and community organizations will be essential for advancing this approach. These efforts aim to redefine urban planning as a dynamic process, fostering cities that are more responsive to human and environmental needs. For example, successful strategies from one city could be replicated in others, creating scalable and adaptable models of urban management.

Building on this potential for cross-city learning, the Urban Genome Framework positions cities as dynamic, intelligent and adaptive systems capable of addressing the complex and evolving needs of their inhabitants. By leveraging real-time data and historical insights, this approach envisions urban environments that optimize resource use, enhance quality of life, and promote sustainability.

This work serves as an introduction to a transformative paradigm in urban planning. Much like the impact of the Human Genome Project on biology and medicine, the Urban Genome Framework lays the foundation for a comprehensive approach to urban management. It redefines cities as interconnected ecosystems that are resilient and responsive to social, environmental and technological challenges. This vision holds the promise of urban spaces that are as dynamic and adaptable as living organisms—sustainable, equitable and aligned with the long-term well-being of their inhabitants and ecosystems.

Methods

This section defines and justifies the *Urbanome Framework* as the conceptual groundwork for an eventual 'Urban Genome Project' that would catalogue a city's full set of modular urban genes, much as the Human Genome Project sequenced human DNA, focusing on methodological development rather than on empirical or experimental results. At this exploratory stage the task is to craft the vocabulary, logic and workflow from which such a mapping effort could grow. To illustrate the framework's potential, we apply it to publicly available Mexico-City air-quality data. This illustrative case serves only as a didactic demonstration, not a comprehensive empirical evaluation. In short, the study prepares the conceptual foundation, showing how existing datasets can already be viewed through an Urbanome lens while acknowledging that large-scale mapping will require future, coordinated data and standards.

The Urbanome idea emerged inductively from a decade of IoT- and AI projects run by the authors. Each project followed a recurring loop (sense → feedback → policy adjustment) that echoed genetic regulation observed in biomedical work on autoimmune disorders. The analogy suggested that cities, like organisms, store reusable 'instructions' for adaptation. To formalise this metaphor, we performed a critical review of existing urban planning paradigms, combining a traditional literature survey with an interdisciplinary synthesis of urban planning, biology and systems science (see Introduction). This examination revealed persistent gaps, fragmentation across sectoral models, weak integration of historical learning and limited modularity for cross-domain interventions, motivating the search for a unifying, modular framework: the Urbanome.

Defining the Urbanome

Cities, like living organisms, rely on an underlying 'instruction set' that governs growth, coordination and adaptation. The *Urbanome* frames this instruction set as an urban analogue of DNA: a coded ensemble of service protocols, infrastructural designs and governance rules that together shape a city's structural, functional and cultural identity, as well as its patterns of human behaviour. By treating cities as dynamic, evolving systems—with inherited traits shaped by past crises and innovations ('genetic traits')—the framework offers a structured yet flexible lens for decoding urban

complexity and anticipating future change. Grounding the model in documented historical responses ensures that the Urbanome remains a practical, evidence-based tool rather than a purely conceptual construct.

The Urbanome is defined as a four-tier hierarchy: *genes* encode modular service logic, *expressions* render that logic measurable, *pathways* weave expressions into cross-sector routines, and the *phenotype* aggregates city-wide outcomes. These tiers are stored in a digital ‘City DNA’ architecture composed of Urban Nucleotides, Genes organised into Chromosomes, packaged as Chromatin, housed in the Urban Nucleus, and secured by a blockchain-enhanced Double Helix. Figure 4 depicts this structural stack, showing how Urban Nucleotides aggregate into Genes, which are encapsulated within Chromosomes and Chromatin, secured by a blockchain-enhanced Double Helix, and governed through the Urban Nucleus.

To operationalise the Urbanome in practice, we translate its four functional layers into concrete analytic tasks, identifying genes, measuring their expressions, uncovering cross-gene pathways and assessing the resulting phenotype, and then condense the full workflow into a five-step protocol that any city can follow.

Table 1 presents a compact workflow for ‘sequencing’ an Urbanome. It begins by asking the analyst to stake out the study’s boundary, choosing the geographic study area (e.g., a neighbourhood, district or metropolitan region), a baseline year and the headline indicators against which success will later be judged. With that scope fixed, attention shifts to one service domain at a time, treating it as a candidate gene: its rules, physical assets and principal stakeholders are mapped so that the gene can be referenced unambiguously in subsequent work. Those rules come alive in the next step, where raw sensor streams or survey records are transformed into validated service workflows and data flows that operationalise each gene; these processes constitute the gene’s expressions. Patterns that cut across domains emerge when these expressions are overlaid in time and space, revealing stable multi-gene routines or pathways that cities rely on for day-to-day functioning. Finally, pathway outputs are rolled up into city-level outcomes (defining the urban phenotype), such as carbon emissions, road-safety

scores or respiratory-health statistics. Comparing those outcomes against the baseline closes the loop, signalling which genes need reinforcement, which pathways merit replication elsewhere and where policy ‘edits’ should be trialled next.

In parallel to these edits, the service protocols that put those ‘edits’ into action (traffic-control algorithms, water-treatment workflows and emergency-response procedures) are what we term ‘urban proteins.’ By mapping, cataloguing and testing these proteins alongside the KPI changes, we capture how genotypic recommendations become phenotypic improvements in city performance and equity.

The DNA concept in urban complexity

The City DNA concept serves as a metaphor for biological DNA, representing an intricate yet full blueprint that guides the growth, operation and governance of urban environments. Urban DNA encapsulates the entirety of the city’s planning, operational guidelines and policies, forming the blueprint that defines its structural, functional and cultural identity. Just as biological DNA supports development and resilience, City DNA contains the instructions a city needs to withstand disruptions, evolve over time and achieve long-term sustainability.

Because that the City DNA code is vast, we introduce a *hierarchy of urban needs*, shown in Fig. 5, adapted from Maslow’s classic pyramid⁴². The hierarchy acts as a navigational aid, helping planners locate which ‘genes’ and which expressions, require attention at different stages of urban evolution. This hierarchy comprises five layers:

- *Foundational layer.* Basic infrastructure and services (water, power, waste, food, mobility) mirror Maslow’s physiological tier, providing the metabolism on which all higher functions rest.
- *Safety and security layer.* Policing, firefighting and healthcare secure the urban organism against acute threats, much as immune responses protect living cells.
- *Social-community layer.* Inclusive public space, recreation and cultural networks nurture belonging and esteem, ensuring socio-spatial cohesion.

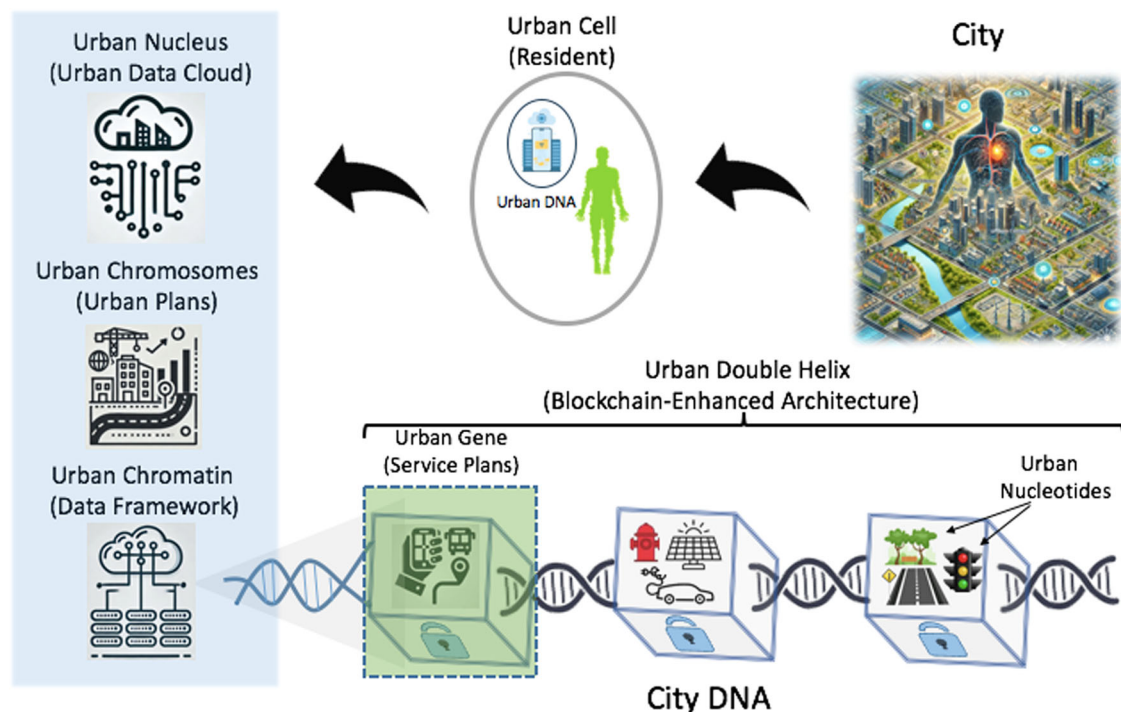


Fig. 4 | Illustration of the Urban Genome Framework. The diagram maps Urban Nucleotides → Genes → Chromosomes → Chromatin within a blockchain-enhanced Double Helix architecture, governed via the Urban Nucleus (Urban Data

Cloud). It draws an analogy with the hierarchical structure of human DNA, showing how the framework deciphers and organizes key urban components—from the Urban Cell (resident) to the city scale.

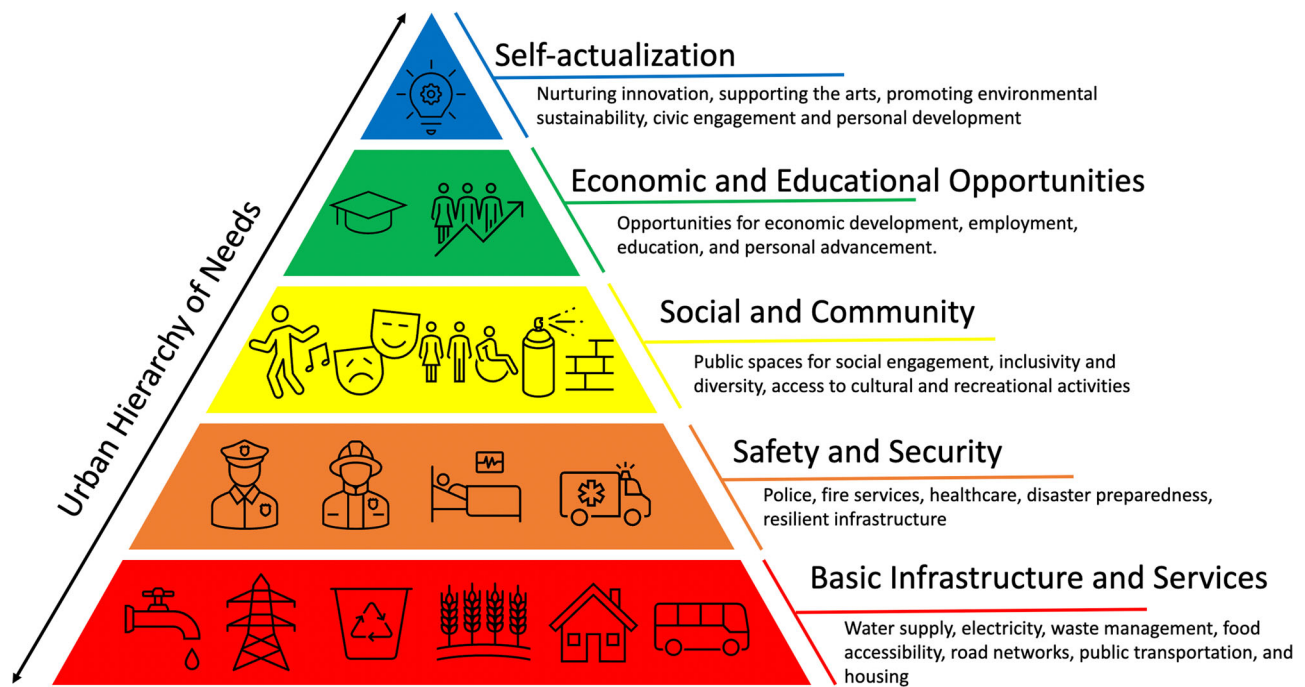


Fig. 5 | Urban hierarchy of needs. This figure visually represents a revised approach to urban planning, structuring city requirements from basic infrastructure to cultural and personal fulfilment goals. The hierarchy highlights the progressive development of urban environments to ensure sustainability and well-being.

- *Economic-educational layer.* Access to employment, education, skills and innovation fuels the city's cognitive growth, echoing Maslow's esteem and cognitive needs.
- *Self-actualisation layer.* Cultural richness, experimentation and sustainability agendas let the city realise its highest collective aspirations.

By addressing urban needs sequentially, and revisiting them as new data arrive, the framework treats cities as living, evolving systems rather than static layouts. The resulting hierarchy is not merely descriptive: planners can use it as a diagnostic tool to prioritise initiatives, allocate resources and monitor progress toward balanced, humane urban development.

Digital architecture: City DNA

Building on the previous definition, the City DNA substrate implements coded protocols (service rules, infrastructural designs and governance logic) in a layered digital architecture that secures, updates and activates them as urban conditions change. Within the Urbanome Framework, this instruction set is stored in a digital architecture we call *City DNA*. Figure 4 sketches its structure, which packages data into Urban Nucleotides and Genes, gathers them into Chromosomes, protects them inside an Urban Nucleus and records changes on a blockchain 'Double Helix,' ensuring integrity while the city evolves.

This hierarchical framework provides a systematic method for analyzing urban systems, breaking them down into distinct components that form the foundation of the Urban Genome. These components include:

Structural stack of City DNA.

1. *Urban Nucleus (Data Cloud):* The central repository that stores and manages urban chromosomes (urban plans) and urban chromatin (data framework). This cloud-based repository ensures that urban data is accessible, secure and well-organized, reflecting the role of the cellular nucleus in managing genetic material.
2. *Urban Chromosomes (Urban Plans):* Analogous to biological chromosomes, Urban Chromosomes package Urban Genes into the city's planning policies and strategies that guide its development. These include master development plans, zoning regulations and sustainability initiatives, that together form a comprehensive blueprint for the city's growth and evolution.
3. *Urban Chromatin (Data Framework):* Urban Chromatin serves as the conceptual organizational layer that organizes complex urban plans, such as emissions reduction policies, public transportation strategies and green-infrastructure initiatives, into accessible and adaptable formats. This packaging process can leverage key technologies and methods, including: metadata-driven categorization, interactive dashboards, automated data pipelines, scenario-modelling tools, APIs for seamless integration and machine-learning algorithms to detect patterns and suggest adaptive solutions. Such an approach ensures that urban plans remain well-structured, easily navigable and responsive, mirroring chromatin's role in regulating gene accessibility and expression in biological systems.
4. *Urban Genes (Service Plans):* Analogous to biological genes, Urban Genes are detailed service plans for specific urban functionalities such as public transportation, waste management, or energy distribution. They encode the organizational and operational protocols for urban services, ensuring consistency and alignment with the city's objectives. For example, an urban gene for public transportation would define route designs, stop locations, schedules and fare rules and operational protocols, collectively shaping network efficiency and urban character.
5. *Urban Nucleotides (Fundamental Elements):* Representing the city's smallest operational elements such as traffic signals, streetlights, air-quality sensors, paving units, etc., Urban Nucleotides encode basic service logic and complex interactions across the urban ecosystem. When combined into larger assemblies, these nucleotides form systems analogous to 'genes,' such as transportation networks or environmental monitoring systems, that carry out essential urban functions.
6. *Urban Double Helix (Blockchain-Enhanced Architecture):* Reflecting the dual-stranded structure of DNA, this component is intended to store, secure and govern City DNA information through an immutable, auditable ledger. Implemented via blockchain technology, it:
 - (a) Records pollution levels, policy changes and interventions in tamper-proof blocks.
 - (b) Uses smart contracts to automate real-time responses (e.g. enforcing traffic restrictions during pollution spikes).

- (c) Provides transparent audit trails and stakeholder interfaces to support accountability, build trust and facilitate informed decision-making.

By maintaining a verifiable sequence of urban processes, the Urban Double Helix ensures the integrity, traceability and adaptability of critical urban data—enabling planners to replicate successful strategies and adapt policies based on historical effectiveness.

Cities ultimately exist for their residents. As illustrated in Fig. 4, *Urban Cells* (the city's residents) sit at the apex of the City DNA hierarchy, anchoring every digital layer to human needs. Acting as the fundamental units, akin to cells in a biological organism, residents carry the urban DNA and shape the overall health and functionality of the system. Their collective behaviours and requirements cascade through the stack—from Urban Nucleotides and Genes, through Chromosomes, Chromatin and the Nucleus, to the blockchain-enhanced Double Helix—ensuring that service rules, data frameworks and governance protocols are designed, executed and updated with people at the centre. This human-centric hierarchy unites macro-scale experience with micro-infrastructure, providing a coherent blueprint that links lived reality with infrastructure, governance and data, and forming the foundation for all subsequent analyses.

In conclusion, the Urban Genome framework is inherently scalable and adaptable, designed to accommodate the ever-evolving nature of urban development. Serving as both a foundational model and a flexible platform, it evolves in tandem with advancements in urban analysis, planning methodologies and technological innovation. By drawing inspiration from biological systems, the framework simplifies the complexities of urban ecosystems, offering a structured yet adaptable approach to decipher and manage the multifaceted challenges of modern cities. As research and practical applications continue to refine its principles, the Urban Genome is poised to foster a transformative era in urban planning—one that views cities not merely as physical spaces, but as dynamic, living systems capable of growth, adaptation and resilience.

Data availability

Data sharing is not applicable to this article as no datasets were generated or analysed during the current study.

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Author contributions

J.M.L.R. conceived the initial concept and directed the subsequent analysis, establishing the conceptual foundation of the study. J.R. (Julio Rufo), J.R. (Jose Rabadan), V.G. and R.P.J. collaborated extensively in the analysis and discussion of the concepts and methodology, enhancing the depth and scope of the research. All authors actively contributed to the final manuscript, providing essential feedback and intellectual contributions throughout the development process.

Competing interests

The authors declare no competing interests.

Additional information

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