

eDNA, forensic ecologies and the barcoding of urban life

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The field of urban ecology is being transformed by advances in DNA barcoding, genomics and bioinformatics. The advent of environmental DNA (eDNA), in particular, moves beyond the identification of individual species towards the rapid assessment of entire ecosystems. Urban ecology is being transformed through new sampling and sequencing techniques that are reframing the city as an object of study. The increasing emphasis on eDNA presents a notable elaboration of systems-based conceptions of urban ecology but there has been little engagement with the wider implications of these developments for the conceptualization of urban space. Here I outline the prospects for an alternative conceptual synthesis that lies closer to the concerns of the social and historical sciences. I suggest that a closer engagement with the related field of forensic ecologies can provide a methodological bridge between new advances in DNA sequencing and post-positivist approaches to the study of cities.

The increasing emphasis on DNA analysis has substantial metaphorical resonance within urban research. As early as 2009, for example, the architect Bill Hillier, founder of the Space Syntax Laboratory at University College London, referred to the ‘genetic code of cities’. For Hillier, cities display underlying laws akin to DNA that predetermine both the pattern and function of urban space¹. More recently, Jose Martin Luna-Rivera and his colleagues elaborate on the ‘urban genome’ as ‘a set of reproducible strategies that organize infrastructure, governance and behavior’. Their proposed analytical framework, borrowing language directly from DNA laboratory protocols, includes ‘a five-step sequencing methodology for mapping and editing urban genes’². The possibility for enhancing urban resilience is compared with the field of gene editing in a clear reference to recent advances in the biomedical sciences. In a similar fashion, the geographer Elizabeth Delmelle refers to the use of ‘sequential pattern mining procedures’ that mimic aspects of DNA analysis for the study of neighborhood change in Chicago and Los Angeles³. Yet these contributions from architecture, geography, planning and other fields are not actually using DNA analysis to study urban space but are simply positing a series of scientific analogies. With recent advances in the analytical scope of eDNA, however, it is possible to expand the scope of urban bioinformatics in relation to material rather than merely metaphorical aspects to biological processes.

The use of DNA barcoding for the identification of species has been a well-established taxonomic tool since the early 1990s. Since

the early 2010s, however, there has been a surge of interest in eDNA to produce a genomic profile of more complex samples or even entire ecosystems⁴. The use of eDNA has substantially extended the scope of bioinformatics through an emerging emphasis on the sampling of much larger datasets derived from soil, water and, more recently, air. The focus on air, for example, reveals new dimensions to biodiversity that can extend far into the atmosphere^{5,6}. In the case of cities, interest in eDNA has focused attention on a wider diversity of urban biomes, including new ecologies of verticality, extending from soil to sky. A wealth of new data have been created, especially for less intensively studied taxonomic groups such as bacteria or fungi, which can provide novel insights into the ecological dynamics of urbanization⁷.

The collection of eDNA from urban surfaces, waste water and other sources has transformed our understanding of the microbial ecologies of the built environment as well as providing methodological synergies between bioinformatics, epidemiology and forensic science^{8–11}. DNA analysis of urban soils, for example, has revealed new facets to urban biodiversity that might be overlooked with a reliance on traditional field-based methods^{12,13}. In the case of New York’s Central Park, the DNA analysis of soil has demonstrated levels of biodiversity that are comparable with tropical rainforests¹⁴. A recent eDNA study of a bridge in New Jersey even reveals the complex assemblages of organisms living within the concrete structure¹⁵. Other examples include the rapid appraisal of the degree of ecological recovery for fire-damaged landscapes in

Los Angeles and other cities through the analysis of microbiomes present in soil samples¹⁶.

New data frontiers in the genomic city

The emerging literature highlights a series of perceived advantages for an increased use of eDNA in comparison with existing survey methods: the scale of data collection can provide an ecological snapshot of entire sites or ecosystems; the use of eDNA data is regarded as quicker, cheaper and less invasive than existing modes of environmental fieldwork; the detection of invasive species at low density can allow earlier interventions; eDNA can detect rare or endangered taxa that might be missed by other methods; the regular testing of waste-water samples can pick up viral traces of COVID-19, polio and other public health risks; the analysis of food or other kinds of complex products can identify additives that might pose a threat to consumer safety; and the use of diet analysis can further understanding of relations between species of ecological or epidemiological concern (also referred to as ingested DNA (iDNA))^{17–19}. In the case of public health research, the gut analysis of hosts and vectors can delineate ‘virus-sharing networks’ that are pivotal to understanding the ecological dynamics of emerging epidemiological threats^{20,21}. A recent example is the use of genomic analysis of mosquito guts to establish the presence of a locally specific strain of the West Nile virus that has become endemic in the Berlin metropolitan region, with further research now underway to establish the likely avian hosts²². We can also use eDNA to monitor both the spatial diffusion and evolutionary dynamics of viruses and other pathogens in real time^{23,24}. A new generation of tracking devices will be able to undertake continuous forms of eDNA monitoring in situ, including the development of underwater drones that can collect and sequence samples as they scour marine ecosystems. There will be emerging networks of integrated devices that can combine eDNA monitoring with bioacoustics, camera traps and other data sources to enable artificial intelligence (AI)-augmented forms of pattern recognition. In the case of public health, the automated monitoring of pathogens through continuous sampling technologies can be combined with predictive models to locate potential disease outbreaks ahead of time. In the final analysis, however, these emerging frontiers in bioinformatics do not in themselves advance our understanding of the causes of biodiversity decline or new landscapes of epidemiological risk (see below). The question is rather how these new data sources might inform different kinds of analytical configurations that can move beyond the existing parameters of urban science.

The predicted acceleration of DNA sequencing capacity under the so-called Carlson curve, coined back in 2003, is the genomic equivalent to Moore’s law in the computational realm (based on an approximate doubling of semiconductor capacity every two years²⁵). However, the Carlson curve has already been surpassed since 2008 under the transition to post-Sanger sequencing technologies. Advances such as next-generation sequencing can now process millions of fragments of DNA simultaneously, thereby speeding up laboratory analysis and lowering costs. Much of the necessary equipment, such as benchtop sequencers, has also become steadily cheaper in real terms. These technological developments are contributing to the wider accessibility of DNA analysis, including trends towards ‘garage biology’ and the use of DNA testing kits at home^{26,27}. The wider availability of bioinformatics has also enhanced the potential scope for citizen science²⁸. Indeed, the extensive use of polymerase chain reaction (PCR) tests during the COVID-19 pandemic opened a window into the wider application of these new scientific developments.

False positives and other anomalies

The increasing use of eDNA poses a range of practical challenges in relation to the sampling, storage and handling of DNA materials²⁹. Analytical protocols must contend with contaminated or degraded traces of DNA, often drawing on skills needed for archeological, paleoecological

or forensic modes of investigation^{30,31}. The increasing interest in forensic ecologies in particular connects long-established aspects of crime scene investigations with an emerging emphasis on counter-hegemonic methodologies led by the forensic architecture program at Goldsmiths, University of London³². A major exhibition held in 2014 at the Haus der Kulturen der Welt in Berlin, entitled *Forensis*, curated by Anselm Franke and Eyal Weizman, asks ‘How do mortal remains, DNA samples, and satellite images become forensic evidence?’³³ Different forms of DNA evidence can contribute to a wider post-positivist field of evidentiary materialism in which the political and institutional dimensions to research design are made explicit from the outset³⁴. In this sense, DNA analysis forms part of a suite of potential methodologies that can contribute towards critical forms of social and ecological analysis.

The claims of greater precision associated with eDNA need to be set alongside a range of analytical and conceptual challenges. A key limitation concerns any scaling up from the presence or absence of genetic traces towards a more systematic assessment of population size. Indeed, the shift of emphasis from individual organisms to entire ecosystems amplifies existing uncertainties over the role of genomic data within environmental research. Anomalies can emerge in the laboratory such as the unintentional generation of chimeric sequences (novel combinations of DNA for organisms that do not exist). In addition, a range of statistical methods are now used to address sampling errors that can reduce the representativeness or comparability of results³⁵. The connection between eDNA and bioinformatics implies a degree of analytical uniformity across disparate scientific fields as well as underlying probabilistic assumptions about the spatial characteristics of environmental phenomena. In some cases, Bayesian inference has been used to enhance the predictive capacity of environmental models based on eDNA data³⁶. In this sense there is at least an acknowledgment that the research field connects with an a priori set of assumptions about likely probabilities that can be modulated in the light of further data collection³⁷. Yet claims for the accuracy of eDNA-based models must be set alongside the need to better understand the historical and political dimensions of the urban arena (see below). Neo-positivist analytical frameworks that seek to elucidate universal laws or patterns remain limited in their explanatory scope despite the incorporation of ever larger datasets. In spite of these shortcomings, however, some of the recent literature displays a degree of impatience in relation to the wider use of eDNA analysis. The biologist Zacchaeus G. Compson and his colleagues, for instance, highlight ‘methodological conservatism’ as one of the barriers to the more extensive adoption of eDNA within the environmental sciences³⁸. Yet this kind of epistemological boosterism needs to be considered in relation to the wider implications of ‘big data’ and the rise of algorithmic modes of urban and environmental governmentality³⁹.

The increasing use of eDNA aligns with an emerging emphasis on ‘urban science’ as an interdisciplinary neo-positivist approach to the study of cities. Leading proponents for urban science such as Marina Alberti have emphasized how access to ever larger datasets might enable the discovery of ‘universal rules by which cities work and innovate’⁴⁰. Luis Bettencourt, for instance, drawing on elements of archeology, complexity theory, cognitive psychology and spatial science, stresses the need to uncover the ‘fundamental processes’ that have driven accelerating patterns of urbanization at a global scale. Taking an integrative approach, Bettencourt stresses the need to identify the processes ‘that are facilitated and, in many cases, unleashed for the first time by urban life’. And in a nod towards the potential for bioinformatics and next-generation sequencing, Bettencourt notes that ‘a more comprehensive empirical basis for urban science is necessarily predicated on harnessing new and better data as well as embracing more powerful technologies and methods’. He characterizes cities as ‘complex adaptive systems’ derived from the interaction between multiple processes with varying degrees of ‘circular causality’.

'These properties of cities as complex systems', suggests Bettencourt, 'will force us to frame urban science in a way that goes beyond existing theory in any particular discipline [...]'.⁴¹ Yet the emphasis on urban science as inherently interdisciplinary, extending all the way from the biophysical sciences to the arts, still lacks a clear sense of what a deeper level of interdisciplinary engagement might entail in both conceptual and methodological terms. Michele Acuto, Sue Parnell and Karen Seto, in a recent intervention for the journal *Nature Sustainability*, rightly suggest that many scientists have difficulty incorporating the political dynamics of urban space into existing models⁴². At the same time, however, we also encounter blind spots within the social and historical sciences in relation to recent developments in the biophysical sciences⁴³.

The enhanced computational capacity for eDNA analysis obscures a series of epistemological tensions. Indeed, the mooted extension of research on the social behavior of insects or other organisms as part of a DNA-enhanced 'bio-urban' model illustrates an elaboration of earlier unsatisfactory attempts to build a socio-biological analytical framework^{44,45}. There is an emphasis on the algorithmic modeling of non-human forms of collective behavior that connects with simplistic assumptions about the influence of architectural form and the built environment on human culture. The city itself is widely characterized in the bio-urban literature as a 'constructed niche' to be further elucidated by a merger between evolutionary and complexity theory. The study of biomorphic growth patterns is extrapolated across disparate disciplinary domains to develop a modular model of urbanization that is based on a series of intersecting subsystems. It is instructive, for example, that many proponents of urban science draw on a variety of neo-positivist approaches that have long been abandoned within the critical social sciences. As the geographer Rob Kitchin notes, an urban science that is underpinned by urban informatics rests on a 'computational understanding of city systems'. This approach to urban research is not only rooted in neo-positivist conceptions of knowledge but also draws on a form of 'inductive empiricism' that makes use of machine learning to generate hypotheses directly from digital data sources⁴⁶.

How might eDNA alter conceptions of urban nature? The use of eDNA can reveal a degree of bias in relation to what is routinely considered interesting or noteworthy on the basis of ecological fieldwork. A recent study of mammals in urban parks in Detroit, for example, reveals substantial differences between species detected by eDNA analysis and iNaturalist records based on direct forms of observation⁴⁷. It seems that people, dogs and rats are routinely ignored by human observers whilst eDNA in turn can throw up odd results such as the presence of montane mammals that are most probably attributable to their genetic proximity to other species or to anomalies in existing databases.

The accuracy of eDNA, like single-species DNA barcoding, is ultimately dependent on the scope, quality and accessibility of existing genomic databases. There is a contrast, for example, between curated and non-curated genetic databases, notably between BOLD (Barcode of Life Data Systems) and the larger GenBank repository⁴⁸. There is an additional challenge of incomplete coverage for many taxa such as bacteria, fungi and insects. Indeed, a recent study suggests that some 86% of the estimated 8.7 million species on Earth have yet to be described^{49,50}. These data deficiencies are even greater for marine ecosystems and many biodiversity hotspots in the Global South. The future development of eDNA will rest to a notable extent on the degree of adherence to open data-sharing protocols such as FAIR (findability, accessibility, interoperability and reusability) and the input of organizations such as the Global Biodiversity Information Facility that seek to make data freely available rather than hoarded for profit^{23,51}. Furthermore, the geographically uneven coverage of existing DNA databases will contribute to a further divergence between computational and relational ecologies so that less-studied regions or taxa are likely to become increasingly dependent on the use of bioinformatics.

A reliance on eDNA alone cannot illuminate key aspects of behavior, population dynamics, or longer-term environmental change. Rates of DNA shedding vary greatly between organisms and cannot provide a reliable indicator of population size. If the use of eDNA is presented as a panacea for under-funded forms of environmental fieldwork then this has wider implications for the kind of data that are being collected. An increasing reliance on genomic data clearly challenges the status of existing ecological methods such as camera traps, transects and other forms of field observation. Yet a recent study of fish in Hong Kong harbor that compared the use of eDNA with underwater camera traps discovered that most species were only detected by either survey method alone—32.3% of species were only found through the use of an underwater visual census whilst 39.6% were only recorded via eDNA analysis—a finding that corroborates some of the pioneering eDNA studies of terrestrial mammals^{52,53}.

The use of eDNA can also record traces of species contained in bird or animal feces that may have originated from other sites^{23,54}. Indeed, eDNA can generate 'false positives' that might lead to extreme biosecurity measures such as the destruction of entire ecosystems^{23,55–57}. A growing reliance on eDNA, especially for biodiversity hotspots in the Global South, also risks the further marginalization of Indigenous knowledge^{23,58}. Indeed, a recent review article suggests that the use of eDNA might be easier in 'developing countries, which are not encumbered by historical precedents and legislation related to biomonitoring' in a worrying formulation that ignores existing cultural and institutional inequalities³⁸.

The increasing role of DNA analysis within the ecological sciences marks part of a wider shift towards post-Linnaean taxonomies where species are defined on the basis of measurable forms of genetic distance. The earlier taxonomic focus on individual species has expanded to encompass a wider set of scientific objectives including 'species-indifferent measures of diversity'³⁴. The field of eDNA is now moving from a focus on operational taxonomic units (OTUs) towards amplicon sequence variants (ASVs) as a statistical measure of genetic distance that can assign species more accurately for many taxonomic groups. But how can these new mathematical measures be reconciled with the existing taxonomic emphasis on diagnostic characters? Rob DeSalle, Mary G. Egan, and Mark Siddall, for example, at an early stage in the DNA barcoding debate, advocated for an integration between taxonomic and molecular approaches to enable more rigorous outcomes³⁹. Some key groups of urban organisms such as mosquitoes illustrate the practical limitations of a narrow reliance on DNA analysis, including the appropriate choice of primers to produce accurate results^{60–62}. In the case of the *Culex* genus of mosquitoes, for example, we not only contend with a 'species complex' but also with organisms that are undergoing rapid rates of epigenetic and evolutionary change. Indeed, mosquitoes are among those groups of organisms that are experiencing accelerated rates of evolution in urban environments^{63–66}.

The reframing of biodiversity as a series of DNA inventories marks a notable shift in how nature is conceptualized. The relational emphasis of observational fieldwork is being supplanted by a more abstract assessment of genetic variation. The analytical challenge is amplified within urban environments because socio-ecological systems are even less amenable to neo-positivist analytical frameworks than ecosystems with more limited degrees of human impact. Cities, in other words, are complex kinds of socio-ecological assemblages that develop in a very different way to ostensibly 'natural' ecosystems with minimal forms of human intervention. Recent research, however, casts doubt on existing assumptions about many ecosystems that might previously have been considered 'natural' or at least more amenable to a range of neo-positivist assumptions about causal relations. New studies of the Amazon basin, for example, emphasize the degree to which these ecosystems are better interpreted as cultural landscapes that include a variety of more dense settlement patterns, including archeological

traces of early cities^{67,68}. Although urban dimensions to environmental change clearly pre-date modernity there is a need to historicize specific dimensions to capitalist urbanization, including the influence of successive waves of colonial and neo-colonial expansion within the global economy.

Towards an alternative conceptual synthesis

The next phase of eDNA research is set to explore the adaptive potential of both populations and ecosystems through a greater emphasis on epigenetic and evolutionary pathways^{69,70}. But how can emerging insights into temporal aspects of eDNA analysis be related to existing studies of urban space? And how might the latest advances in eDNA research be integrated into existing kinds of longitudinal datasets for the monitoring of environmental change? The increasing use of eDNA marks a notable extension to the existing dominance of system-based analytical approaches within urban ecology, which in themselves do not get us any closer to an understanding of the historical specificities of capitalist urbanization. There is an intellectual tension between new advances in (predictive) modeling enabled by bioinformatics and the wider conceptual framing for socio-ecological transitions. The influential Vienna school of social ecology, for example, with its emphasis on large-scale energy transitions, illustrates the difficulties in extending systems-based analytical approaches to the historical realm⁷¹. A narrow focus on technological innovation can only ever offer a partial account of capitalist urbanization as a historically and geographically specific set of developments. By contrast, structuralist approaches such as urban political ecology emphasize how the capitalist mode of production has generated a distinctive 'social metabolic order' within which underlying tensions between capital and ecology have steadily intensified^{72,73}. A key challenge, therefore, is how the use of eDNA might enrich rather than obscure alternative analytical approaches within the social and historical sciences. How, for example, are differences between biological and cultural forms of evolution to be conceptualized? If eDNA becomes a kind of neo-positivist explanatory syntax in its own right, then other aspects of socio-ecological change will be displaced from the analytical frame.

The increasing interest in eDNA has led to a surge in demand for laboratory work that has facilitated the emergence of new actors, including hedge-fund-backed forms of bio-capital (important players include EDF Pulse Ventures, BNP Paribas, Monaco ReOcean Fund and Ananda Impact Ventures). The global market value of DNA sequencing is predicted to rise from an estimated US \$4.69 billion in 2022 to nearly US \$17 billion by 2030. More broadly, there are stark disparities in global laboratory capacity to undertake genomic analysis, as was starkly revealed during the COVID-19 pandemic, with ongoing implications for the monitoring of public health threats as well as biodiversity research⁷⁴.

Biodiversity surveys that might previously have been carried out by trained ecologists are now being offered by commercial monitoring services that are reliant on laboratory-based DNA analysis. A range of companies, such as NatureMetrics, Jonah Ventures, SimplexDNA, Genidaqs and Smith-Root, now provide eDNA services for fields such as fisheries management and environmental impact assessment⁷⁵. In early 2025, for example, a new collaboration was announced between the Minderoo Foundation's OceanOmics program and the International Union for Conservation of Nature (IUCN) to monitor marine biodiversity⁷⁶. These developments, including a diversion of government investment towards eDNA and related fields, threaten to exacerbate the ongoing funding crisis facing taxonomic research in museums and also the use of existing field-based expertise for ecosystem monitoring.

Furthermore, the data-processing requirements of eDNA clearly connect with the environmental impact of digital capitalism. These huge amounts of data require an enhanced energy-intensive infrastructure with an ecological impact that unsettles the 'non-disturbance' argument in comparison with more traditional modes of ecological

fieldwork⁷⁷⁻⁷⁹. Indeed, DNA sequencing itself forms part of the impetus towards emerging biotechnology (bio-tech)-driven patterns of urbanization in Cambridge (UK), Copenhagen, Hyderabad, Leiden, Munich, San Diego, Shenzhen and a number of other cities.

What aspects of biodiversity are highlighted by the use of eDNA? In the place of field-based surveys, including the direct observation of living organisms, we have a variety of more abstract quantitative indices. The taxonomic reliance on measures of genetic distance such as OTUs and ASVs aligns with a shift of emphasis towards generic aspects of nature rather than a focus on more fragile kinds of ecological specificity. Terms such as 'biodiversity net gain', 'biodiversity offsetting' and 'compensation landscapes' are indicative of a perceived interchangeability of nature that mirrors the wider adoption of policy instruments such as carbon trading^{80,81}. These new measures have a conceptual affinity with resilience discourse under the adaptive Anthropocene (also referred to as 'eco-modernism' in some of the literature) and wider forms of skepticism towards the loss of biodiversity as new species are continually emerging over geological timeframes⁸².

The advent of eDNA is clearly contributing to the interdisciplinary impetus of bioinformatics and urban science. But what kind of interdisciplinarity might be enabled by eDNA, or conversely, what possibilities might become more difficult through the relative exclusion of other data sources or epistemological frameworks? The full potential of eDNA will be furthered by an innovative combination of different methods—both genomic and non-genomic—as part of a more critically reflexive approach to environmental research. In this way, eDNA can contribute to the emergence of new perspectives rather than merely replicate (or amplify) existing approaches. The use of eDNA can be incorporated into collaborative modes of interpretation that extend to urban political ecology, critical toxicology and other fields. In this case, the technical contributions of eDNA analysis are less likely to become overextended into neo-positivist epistemological frameworks.

The challenge of interdisciplinary environmental research requires greater reflection on 'data ontologies', yet many scientists lack the time, resources or inclination to engage with such questions²³. The use of eDNA is now entrained in various forms of AI augmented scientific practices such as next-generation sequencing that are further widening the epistemological divide between neo-positivist approaches and alternative hermeneutic, critical realist and post-positivist forms of social and historical inquiry. A pixelated ontology derived from bioinformatics contrasts with relational dimensions to field-based ecology, including the kind of multispecies encounters explored in cultural anthropology, the environmental humanities and other fields^{83,84}. The history of urban ecology has been intimately related to the emergence of observational fields such as botany, lichenology and ornithology, in which the human observer develops an affective relation with their object of analysis. The rapid expansion of eDNA coincides with a period of enhanced public interest in urban ecology, especially through diverse kinds of direct contact with nature, including the use of pattern-recognition algorithms to assist with the identification of birdsong, plants or other organisms. In the case of taxonomically rich insect orders such as Lepidoptera, the compilation of a visual database of living specimens can enrich the scope of field surveys, notwithstanding the presence of cryptic species or those that cannot be reliably separated by morphological characteristics alone⁸⁵. These technologically augmented modes of fieldwork can operate independently from more abstract modes of computational analysis⁸⁶⁻⁸⁸. In this sense, bioinformatics is not reducible to a genomic or computational reading of nature.

An emphasis on eDNA highlights two very different conceptions of interdisciplinarity: on the one hand, there is the additive momentum of ever larger datasets that seek to combine social and environmental systems under a unified explanatory framework; and on the other hand, there are underexplored possibilities for a conceptual synthesis between forensic aspects to DNA analysis and historically framed

accounts of social and environmental change. This second strand rests on a form of evidentiary materialism in which DNA analysis can be used to complement other methodological tools and contribute to a more nuanced kind of explanatory framework that can take greater account of both geographical and historical specificities. Furthermore, an emphasis on forensic ecologies connects with the longstanding field of forensic entomology and the precise investigation of crime scenes, providing an analytical link between the emphasis on material traces and the use of DNA sequencing technologies⁸⁹. The key point is that a forensic approach can link empirical analysis of environmental phenomena such as biodiversity decline or emerging health threats to a post-positivist explanatory framework in which simplistic forms of data correlation or predictive modeling are replaced by an emphasis on evolving conceptions of the human subject, the exercise of social power, and the circulatory dynamics of capital. At root, there is a degree of epistemological tension between two different conceptions of the urban realm: in the first case there is an emphasis on intersecting systems that build a picture of urban space as a functional totality whilst in the second case the material characteristics of urban space, and even the definition of the urban itself, is recognized as historically constituted and socially contested.

The rise of eDNA transposes the earlier emphasis on the urban ecosystem as a measurable space of flows à la Paul Duvigneaud, Eugene Odum and other scholars towards a more abstract conception of urban space as a code-based series of multiscalar data correlations. Indeed, how is urban space conceptualized at all under eDNA? What kinds of zones, transitions or boundary effects can be incorporated into models based on DNA data sources? If we consider the multiscalar origins of zoonotic health threats such as dengue, Ebola or COVID-19, then eDNA techniques such as waste-water analysis can delineate emerging landscapes of epidemiological risk but not the structural dimensions to ongoing public health inequalities^{90,91}.

How might eDNA be used within a critical framework that is not rooted in neo-positivist variants of urban science? In other words, can there be a post-positivist use of eDNA that might contribute to an alternative conceptual synthesis? Systems-based approaches to ecology have always had an uneasy interface with the social and historical sciences just as alternative perspectives such as urban political ecology have had only a weakly articulated grasp of the latest advances in the biological sciences. Rather than an increased emphasis on reductive forms of interdisciplinarity we need to embrace new forms of epistemological complexity that can incorporate the latest methodological and theoretical advances across a wide spectrum of research fields.

If eDNA is regarded as an analytical tool rather than an epistemological framework in its own right then there are clearly possibilities to build an alternative kind of conceptual synthesis that is based on a more rigorous interface between biology and the social sciences. As we move from metaphors to materiality, from scientific analogies to systematic analysis, we can discern an alternative kind of interdisciplinary pathway for urban environmental research. Yet a more productive interface between biology and the social sciences in the urban arena will require substantial intellectual labor on both sides.

What, then, might an eDNA-enhanced field of post-positivist urban ecology look like? What kind of research questions or research programs might emerge? And what might be the wider implications for public policy or grassroots modes of engagement with scientific knowledge? If we move away from systems-based urban ecology, a series of new analytical vantage points come into view. A recognition of multiple temporalities underpins the epistemological distinction between the evolutionary and epigenetic development of organisms within urban ecosystems and the historically produced periodicities associated with capitalist urbanization, including the significance of both colonial and neo-colonial patterns of resource use and the relationship between urban growth and an array of often distant or hidden extractive frontiers.

The use of eDNA can provide a welter of novel empirical insights into urban ecosystems and the multispecies city (including the human body itself) but these computational advances are best conceived as a sophisticated form of pattern recognition that can complement rather than replace existing methodological tools, including the kind of interpretative and qualitative idioms that are widely deployed within the social and historical sciences. When evaluating alternative analytical approaches it is vital to make a distinction between the various forms of data correlation and the elucidation of underlying modes of causality: contra neo-positivist conceptions of the urban arena as a quantifiable space of flows, a post-positivist approach to urban ecology highlights more complex forms of agency, subjectivity and historical contingency, including the diverse kinds of spatial configurations or networks that constitute the urban realm. From this perspective, the field of urban ecology has evolved across a distinctive set of scientific milieus that reflect not only material aspects of urban environments but also the shifting cultural and institutional contexts for knowledge production itself. Indeed, as regulatory agencies struggle to ensure forms of environmental protection, the use of eDNA is being widely promoted as an alternative means to monitor ecological and epidemiological threats. Similarly, as museums and universities seek to nurture future taxonomic expertise, especially for species-rich but imperfectly known groups of organisms, they are becoming increasingly reliant on genomic analysis to delineate the tree of life.

At root, however, there remains a glaring disconnect between an urban science that is increasingly anchored to an augmented computational realm and the need for alternative post-positivist approaches within the social and historical sciences. We must ensure that an enhanced capacity for DNA sequencing contributes to new forms of methodological collaboration rather than a widening of existing epistemological asymmetries in the urban arena. A conceptual synthesis between the novel empirical insights derived from eDNA analysis and alternative approaches to environmental research such as forensic ecologies and urban political ecology will allow the development of a different kind of interdisciplinary framework to that offered by neo-positivist urban science.

References

- Hillier, B. in *Complexity Theories of Cities Have Come of Age: An Overview with Implications to Urban Planning and Design* (eds Portugali, J. et al.) 129–152 (Springer, 2012).
- Luna-Rivera, J. M., Rufo, J., Rabadan, J., Guerra, V. & Perez-Jimenez, R. Urban genome: a new paradigm for sustainable cities. *npj Urban Sustain.* **5**, 77 (2005).
- Delmelle, E. C. Mapping the DNA of urban neighborhoods: clustering longitudinal sequences of neighborhood socio-economic change. *Ann. Am. Assoc. Geogr.* **106**, 36–56 (2016).
- Giles, S. et al. *Environmental DNA: A Policy Explainer* (The Royal Society, 2025).
- Clare, E. L. et al. Measuring biodiversity from DNA in the air. *Curr. Biol.* **32**, 693–700 (2002).
- Goray, M. et al. Emerging use of air eDNA and its application to forensic investigations—a review. *Electrophoresis* **45**, 916–932 (2024).
- Senn, S. et al. The community structure of eDNA in the Los Angeles River reveals an altered nitrogen cycle at impervious sites. *Diversity* **15**, 823 (2023).
- Hsu, T. et al. Urban transit system microbial communities differ by surface type and interaction with humans and the environment. *Msystems* **1**, 10–1128 (2016).
- Mihajlovski, K. et al. SARS-CoV-2 surveillance with environmental surface sampling in public areas. *PLoS ONE* **17**, e0278061 (2022).
- Neves, C. & Zieger, M. ‘Total human DNA sampling’—forensic DNA profiles from large areas. *Forensic Sci. Int. Genet.* **67**, 102939 (2023).

11. Sorg, A., Gouy, A., Tiede, C. C. & Zieger, M. Human background DNA on stones in an urban environment. *Forensic Sci. Int. Genet.* **65**, 102880 (2023).
12. Fan, K. et al. Soil biodiversity supports the delivery of multiple ecosystem functions in urban greenspaces. *Nat. Ecol. Evol.* **7**, 113–126 (2023).
13. Weber, C. et al. Urban pavements as a novel habitat for wild bees and other ground-nesting insects. *Urban Ecosyst.* **27**, 2453–2467 (2024).
14. Ramirez, K. S. et al. Biogeographic patterns in below-ground diversity in New York City's Central Park are similar to those observed globally. *Proc. R. Soc. B Biol. Sci.* **281**, 20141988 (2014).
15. Kiledal, E. A., Shaw, M., Polson, S. W. & Maresca, J. A. Metagenomic analysis of a concrete bridge reveals a microbial community dominated by halophilic Bacteria and Archaea. *Microbiol. Spectrum* **11**, e05112-22 (2023).
16. Senn, S. et al. The functional biogeography of eDNA metacommunities in the post-fire landscape of the Angeles National Forest. *Microorganisms* **10**, 1218 (2022).
17. Frigerio, J. et al. Early molecular detection of invasive alien plants in urban and peri-urban areas. *Diversity* **16**, 647 (2024).
18. Staley, Z. R. et al. Fecal source tracking and eDNA profiling in an urban creek following an extreme rain event. *Sci. Rep.* **8**, 14390 (2018).
19. Villalta, I. et al. A DNA barcode-based survey of wild urban bees in the Loire Valley, France. *Sci. Rep.* **11**, 4770 (2021).
20. Konstantinidis, K. et al. Defining virus-carrier networks that shape the composition of the mosquito core virome of a local ecosystem. *Virus Evol.* **8**, veac036 (2022).
21. Wang, J. et al. Individual bat virome analysis reveals co-infection and spillover among bats and virus zoonotic potential. *Nat. Commun.* **14**, 4079 (2023).
22. Ruscher, C. et al. Ecological and clinical evidence of the establishment of West Nile virus in a large urban area in Europe, Berlin, Germany, 2021 to 2022. *Eurosurveillance* **28**, 2300258 (2023).
23. Perrin, S. eDNA & accuracy: overcoming the challenges. *The Biologist* https://biologist.rsb.org.uk/edna_and_accuracy.html (2023).
24. Gardy, J. L. & Loman, N. J. Towards a genomics-informed, real-time, global pathogen surveillance system. *Nat. Rev. Genet.* **19**, 9–20 (2018).
25. George, A. K., Kunnummal, I. O., Alazzawi, L. & Singh, H. Design of DNA digital circuits. *IEEE Potentials* **39**, 35–40 (2020).
26. Delfanti, A. *Tweaking Genes in your Garage: Biohacking between Activism and Entrepreneurship* (Innsbruck Univ. Press, 2012).
27. Meyer, M. Domesticating and democratizing science: a geography of do-it-yourself biology. *J. Mater. Culture* **18**, 117–134 (2013).
28. Zhang, H., Yang, J., Zhang, L., Gu, X. & Zhang, X. Citizen science meets eDNA: a new boom in research exploring urban wetland biodiversity. *Environ. Sci. Ecotechnol.* **16**, 100275 (2023).
29. Sepulveda, A. J., Hutchins, P. R., Forstchen, M., McKeefry, M. N. & Swigris, A. M. The elephant in the lab (and field): contamination in aquatic environmental DNA studies. *Front. Ecol. Evol.* **8**, 609973 (2020).
30. Tiedge, T. M., Love, K. R. & Meiklejohn, K. A. Utilizing eDNA from bacteria, fungi, plants and arthropods associated with mock geologic evidence for sample-to-sample comparisons and study site separation: a feasibility study. *Forensic Sci. Int. Genet.* **78**, 103284 (2025).
31. Wiltshire, P. in *Crime Scene to Court: the Essentials of Forensic Science* (ed. White, P. C.) 63–107 (Royal Society of Chemistry, 2024).
32. Fuller, M. & Weizman, E. *Investigative Aesthetics: Conflicts and Commons in the Politics of Truth* (Verso Books, 2021).
33. HKW. Forensis. https://archiv.hkw.de/https://archiv.hkw.de/de/programm/projekte/2014/forensis/ausstellung_forensis/forensis.php (2014).
34. Waterton, C., Ellis, R. & Wynne, B. *Barcoding Nature: Shifting Cultures of Taxonomy in an Age of Biodiversity Loss* (Routledge, 2013).
35. Olson, N. D. et al. Metagenomic assembly through the lens of validation: recent advances in assessing and improving the quality of genomes assembled from metagenomes. *Brief. Bioinform.* **20**, 1140–1150 (2019).
36. Graham, S. E., Chariton, A. A. & Landis, W. G. Using Bayesian networks to predict risk to estuary water quality and patterns of benthic environmental DNA in Queensland. *Integr. Environ. Assess. Manag.* **15**, 93–111 (2019).
37. Longo, A. in *Contemporanea: a Glossary for the Twenty-First Century* (eds Marder, M. & Tusa, G.) 289–292 (MIT Press, 2024).
38. Compson, Z. G., McClenaghan, B., Singer, G. A., Fahner, N. A. & Hajibabaei, M. Metabarcoding from microbes to mammals: comprehensive bioassessment on a global scale. *Front. Ecol. Evol.* **8**, 581835 (2020).
39. Amoore, L. *Cloud Ethics: Algorithms and the Attributes of Ourselves and Others* (Duke Univ. Press, 2020).
40. Alberti, M. Grand challenges in urban science. *Front. Built Environ.* **3**, 6 (2017).
41. Bettencourt, L. *Introduction to Urban Science: Evidence and Theory of Cities as Complex Systems* (MIT Press, 2021).
42. Acuto, M., Parnell, S. & Seto, K. C. Building a global urban science. *Nat. Sustain.* **1**, 2–4 (2018).
43. Gandy, M. Urban political ecology: a critical reconfiguration. *Prog. Human Geogr.* **46**, 21–43 (2022).
44. Ireland, T. & Garnier, S. Architecture, space and information in constructions built by humans and social insects: a conceptual review. *Philos. Trans. R. Soc. B Biol. Sci.* **373**, 20170244 (2018).
45. Roberts, P. et al. Connecting the general and particular in interdisciplinary urban research. *Nat. Cities* <https://doi.org/10.1038/s44284-026-00461-9> (2026).
46. Kitchin, R. The ethics of smart cities and urban science. *Phil. Trans. R. Soc. A Math. Phys. Eng. Sci.* **374**, 20160115 (2016).
47. Hallam, J. & Harris, N. C. Network dynamics revealed from eDNA highlight seasonal variation in urban mammal communities. *J. Animal Ecol.* **94**, 1587–1602 (2025).
48. Cheng, Z., Li, Q., Deng, J., Liu, Q. & Huang, X. The devil is in the details: problems in DNA barcoding practices indicated by systematic evaluation of insect barcodes. *Front. Ecol. Evol.* **11**, 1149839 (2023).
49. Mora, C., Tittensor, D. P., Adl, S., Simpson, A. G. & Worm, B. How many species are there on Earth and in the ocean?. *PLoS Biol.* **9**, e1001127 (2011).
50. Stork, N. E. How many species of insects and other terrestrial arthropods are there on Earth? *Annu. Rev. Entomol.* **63**, 31–45 (2018).
51. Stammnitz, M. R., Scholz, A. H. & Duffy, D. J. Environmental DNA without borders: let's embrace decentralised genomics to meet the UN's biodiversity targets. *EMBO Rep.* **25**, 4095–4099 (2024).
52. Chung, A., Kam, Y. C., Shea, S. K. & Schunter, C. Detecting fish diversity in urban-impacted ecosystems: a comparative approach of eDNA metabarcoding and UVC. *Environ. DNA* **6**, e70048 (2024).
53. Leempoel, K., Hebert, T. & Hadly, E. A. A comparison of eDNA to camera trapping for assessment of terrestrial mammal diversity. *Proc. R. Soc. B* **287**, 20192353 (2020).
54. Zhan, A. Overlooked eDNA contamination in human-influenced ecosystems: a call to manage large-scale false positives in biodiversity assessments. *Water Biol. Security* **4**, 100374 (2025).
55. Darling, J. A., Jerde, C. L. & Sepulveda, A. J. What do you mean by false positive?. *Environ. DNA* **3**, 879–883 (2021).
56. Burian, A. et al. Improving the reliability of eDNA data interpretation. *Mol. Ecol. Resources* **21**, 1422–1433 (2021).

57. Darling, J. A., Pochon, X., Abbott, C. L., Inglis, G. J. & Zaiko, A. The risks of using molecular biodiversity data for incidental detection of species of concern. *Divers. Distrib.* **26**, 1116–1121 (2020).
58. Shen, E. W., Vandenberg, J. M. & Moore, A. Sensing inequity: technological solutionism, biodiversity conservation and environmental DNA. *BioSocieties* **19**, 501–525 (2024).
59. DeSalle, R., Egan, M. G. & Siddall, M. The unholy trinity: taxonomy, species delimitation and DNA barcoding. *Phil. Trans. R. Soc. B Biol. Sci.* **360**, 1905–1916 (2005).
60. Beebe, N. W. DNA barcoding mosquitoes: advice for potential prospectors. *Parasitology* **145**, 622–633 (2018).
61. Laurito, M., Oliveira, T. M. D., Almiron, W. R. & Sallum, M. A. M. COI barcode versus morphological identification of *Culex* (*Culex*) (Diptera: Culicidae) species: a case study using samples from Argentina and Brazil. *Mem. Inst. Oswaldo Cruz* **108**, 110–122 (2013).
62. Paiva, M. H. S. et al. An unsettling explanation for the failure of skatole-baited ovitraps to capture *Culex* mosquitoes. *Insect Sci.* **26**, 873–880 (2019).
63. Byrne, K. & Nichols, R. A. *Culex pipiens* in London Underground tunnels: differentiation between surface and subterranean populations. *Heredity* **82**, 7–15 (1999).
64. Johnson, M. T. & Munshi-South, J. Evolution of life in urban environments. *Science* **358**, 8327 (2017).
65. Haba, Y. & McBride, L. Origin and status of *Culex pipiens* mosquito ecotypes. *Curr. Biol.* **32**, R237–R246 (2022).
66. Fifer, J. E. et al. Genomics of urban adaptation and exaptation in mosquitoes and consequences for vectorial capacity. *Curr. Opin. Insect Sci.* **70**, 101384 (2025).
67. Iriarte, J. *The Archaeology of Amazonia: a Human History* (Bloomsbury, 2024).
68. Prümers, H., Betancourt, C. J., Iriarte, J., Robinson, M. & Schaich, M. Lidar reveals pre-Hispanic low-density urbanism in the Bolivian Amazon. *Nature* **606**, 325–328 (2022).
69. Balard, A., Baltazar-Soares, M., Eizaguirre, C. & Heckwolf, M. J. An epigenetic toolbox for conservation biologists. *Evol. Appl.* **17**, e13699 (2024).
70. Mathieu, C. et al. A systematic review of sources of variability and uncertainty in eDNA data for environmental monitoring. *Front. Ecol. Evol.* **8**, 135 (2020).
71. Fischer-Kowalski, M. On the mutual historical dynamics of societies' political governance systems and their sources of energy. The approach of the Vienna School of Social Ecology. *Hist. Soc. Res./Historische Sozialforschung* **48**, 170–189 (2023).
72. Mészáros, I. Dialectical transformations: teleology, history and social consciousness. *Sci. Soc.* **62**, 417–433 (1998).
73. Saito, K. *Marx in the Anthropocene* (Cambridge Univ. Press, 2022).
74. Smith, E. A., Fleming, D. F., Lackritz, E. M. & Ulrich, A. K. Inequities and global declines in SARS-CoV-2 genomic data availability hinder response to emerging variants. *npj Viruses* **4**, 13 (2026).
75. Ngila, F. Investment in DNA sequencing has a new focus: eDNA. *Quartz* (19 May 2019).
76. Navistrat Statistics. *eDNA Biomonitoring Market Size, Share and Trends Analysis*. Report Code: NA_00996 (accessed 19 November 2025).
77. Maak, N. *Servermanifest: Architektur der Aufklärung: Data Center als Politikmaschinen* (Hatje Cantz, 2022).
78. Tacheva, J. & Ramasubramanian, S. AI Empire: unraveling the interlocking systems of oppression in generative AI's global order. *Big Data Soc.* **10**, 20539517231219241 (2023).
79. Edwards, D. *Enduring Digital Damage: Rhetorical Reckonings for Planetary Survival* (Univ. Alabama Press, 2025).
80. Danneels, K. Compensation landscapes. *Landsc. Res.* **50**, 786–797 (2025).
81. Chapman, K. & Tait, M. Commodification, labor, abstraction: three key concepts to understand the many-headed hydra of biodiversity offsetting. *J. Political Ecol.* **32**, 6186 (2025).
82. Thomas, C. D. *Inheritors of the Earth: how Nature is Thriving in an Age of Extinction* (Allen Lane, 2017).
83. Bathla, N. *Researching Otherwise: Pluriversal Methodologies for Landscape and Urban Studies* (gta, 2024).
84. Van Dooren, T. *Flight Ways: Life and Loss at the Edge of Extinction* (Columbia Univ. Press, 2014).
85. Meier, R., Hartop, E., Pylatiuk, C. & Srivathsan, A. Towards holistic insect monitoring: species discovery, description, identification and traits for all insects. *Phil. Trans. R. Soc. B* **379**, 20230120 (2024).
86. Moss, T., Voigt, F. & Becker, S. Digital urban nature: probing a void in the smart city discourse. *City* **25**, 255–276 (2021).
87. Turnbull, J. et al. Digital ecologies: materialities, encounters, governance. *Prog. Environ. Geogr.* **2**, 3–32 (2023).
88. Ritts, M. Geographies of environmental data 1. *Prog. Environ. Geogr.* **5**, 111–121 (2026).
89. Gandy, M. *Natura Urbana: Ecological Constellations in Urban Space* (MIT Press, 2022).
90. Gandy, M. The zoonotic city: urban political ecology and the pandemic imaginary. *Int. J. Urban Reg. Res.* **46**, 202–219 (2022).
91. Brenner, N. & Ghosh, S. Between the colossal and the catastrophic: planetary urbanization and the political ecologies of emergent infectious disease. *Environ. Plan. A* **54**, 867–910 (2022).

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