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Commentary

Shaping the future of exposome science through analytical and computational advances

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Abstract

The exposome, including the totality of environmental exposures throughout the lifespan, offers a comprehensive framework for investigating environmental contributions to disease risks. Although methods for environmental monitoring and statistical analysis have advanced in recent years, exposome research still faces key challenges in assessing complex exposures, integrating diverse data sources, and examining biological mechanisms. This paper summarizes progress in analytical approaches to exposomic data and discusses remaining challenges in current exposome research. We outline important future directions, including improved exposure identification, novel use of artificial intelligence tools to assist discovery, development of standard protocols, and enhanced collaboration across disciplines. These steps are essential to decipher the influence of the exposome on health, enabling a shift from descriptive association to causal inference and actionable prevention strategies in precision public health.

Key words: exposome; exposure biomonitoring; multi-omics integration; mixture modeling; precision medicine.

Introduction

The exposome, initially conceptualized by Wild in 2005,[1] represents the totality of environmental exposures experienced by an individual across their lifespan. The exposome complements genomic information by comprehensively incorporating external exposures (eg, environmental pollutants, diet, and lifestyle factors) and internal biological responses (eg, metabolomic profiles and inflammatory markers).[2] Although much attention has focused on genetic determinants of disease, environmental factors contribute to a majority of risks, with an estimated 70–90% of chronic disease risks attributable to environmental exposures.[3] This highlights the need to assess lifelong environmental exposures to elucidate the complex interplay between genetics and environment in disease etiology. To translate the conceptual framework of exposome into empirical evidence, large-scale population studies and methodological innovations have been instrumental. Early exposome studies relied on large-scale epidemiological data, such as the Human Early Life Exposome (HELIX) project,[4] which has systematically assessed early life environmental exposures and notably identified adverse impacts of diverse early life environmental exposures, including air pollution, environmental chemicals, and dietary patterns, on children's developmental health outcomes.[5] Building on this foundation, recent European initiatives such as the EXPANSE project have leveraged large population cohorts and advanced exposome analytics to integrate multi-omics data and digital health records. By linking environmental, lifestyle, and biological datasets, these projects aim to uncover how complex exposure mixtures shape molecular pathways and contribute to chronic disease development.[6] These integrative strategies have provided stronger support for causal inference and a deeper understanding of biological mechanisms underlying the adverse impact of environmental factors on disease etiology. For example, utilizing epigenomic data, one research found prenatal tobacco exposure was associated with accelerated biological aging in adulthood.[7] As the field progresses, there is a growing need for refined analytical tools and computational strategies to manage the scale and complexity of exposomic data and to support its application in precision public health.

Analytical methods in exposome research

Exposomic data are comprehensive in their nature. While the exposome also encompasses physical, behavioral, and social

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factors, the present commentary focuses specifically on the environmental chemical exposome.

Environmental monitoring

Remote sensing and exposure modeling

Exposome analysis employs advanced environmental monitoring methodologies that incorporate sophisticated sensors, geolocation technologies, and mathematical exposure models (Figure 1). Geographic information systems (GIS) and remote sensing platforms aggregate data from stationary monitors, mobile devices, and wearable technologies, enabling spatially resolved and personalized exposure assessments. For instance, satellite-based platforms such as Copernicus Sentinel-5P and ground-based monitors, offer fine-scale temporal and spatial data on key air pollutants, including particulate matter ($PM_{2.5}$), nitrogen oxides, volatile organic compounds, and polycyclic aromatic hydrocarbons.[8,9] In addition to sensor-based methods, environmental exposure estimation often relies on geostatistical and mechanistic models. Land-use regression models estimate local pollution levels based on land features and traffic patterns, while atmospheric transport models (eg, WRF-Chem and ECHAM5/MESSy) can simulate pollutant dispersion and concentration to enhance spatial and temporal exposure resolution.[10] More importantly, substantial studies have demonstrated that exposure biomarkers in biological samples (eg, urine, blood, and semen samples) exhibit considerable within-person variability.[11-14] Therefore, more and more cohort studies collected repeated biological samples from each participant over time, which not only improve exposure estimations, but also offer opportunities to explore susceptibility windows.[15,16]

Analytical chemistry platforms for exposure profiling

High-resolution mass spectrometry (HRMS) has expanded environmental analysis by enabling sensitive and comprehensive profiling of chemical exposures, including non-targeted and suspect screening of previously uncharacterized compounds (Figure 1). Liquid chromatography-tandem mass spectrometry (LC-MS/MS) and gas chromatography-mass spectrometry (GC-MS/MS) are primarily applied for targeted quantification of known contaminants and can also be used in certain non-targeted workflows with less mass accuracy and limited structural resolution. In addition, recent studies have applied single-cell mass cytometry (CyTOF) to measure exogenous metals in spermatozoa and immune cells.[17,18] Recent advances such as ion mobility mass spectrometry (IM-MS) further enhance chemical identification by offering an orthogonal separation dimension and collision cross-section (CCS) values, which improve resolution of isomeric compounds and strengthen confidence in annotation.[19] Together, these analytical technologies support both targeted measurement and broader untargeted chemical exploration in exposome research.[20]

Bioinformatics and statistical methods

Single-pollutant and screening approaches

While environmental monitoring technologies provide increasingly granular data on external exposures, interpreting these data in relation to health outcomes requires robust statistical frameworks capable of handling their complexity. Advanced statistical and bioinformatics methodologies are indispensable for analyzing complex exposomic datasets (Figure 2). Exposome-wide association studies (ExWAS), analogous to genome-wide association studies (GWAS), allow a non-directed screening of associations between multiple environmental exposures and health outcomes.[21,22] While effective for high-throughput discovery, ExWAS faces limitations of multiple testing issues, mixing variables with differential degrees of exposure misclassification, and the inability to fully account for exposure correlations.[23]

Mixtures, dimension reduction, and variable-selection methods

To address these limitations, mixture-based models such as weighted quantile sum (WQS) regression and Bayesian kernel machine regression (BKMR) have emerged,[20,24] among others.[25] WQS regression estimates the joint effect of chemical mixtures by assigning weights to each exposure under the assumption of linearity and a common direction of effect. In contrast, BKMR can investigate a mixture of exposures showing opposing directions of association, along with accommodating nonlinear and non-additive relationships among exposures and outcomes, allowing for exploration of potential interactions, albeit with higher computational demands and reduced interpretability.

Other dimension reduction and variable selection tools, such as principal component analysis (PCA), sparse partial least squares (sPLS), least absolute shrinkage and selection operator (LASSO), elastic net (ENET), and the Bayesian model Genome Utilizing ESSential Setup (GUESS), have also been widely used.[25]

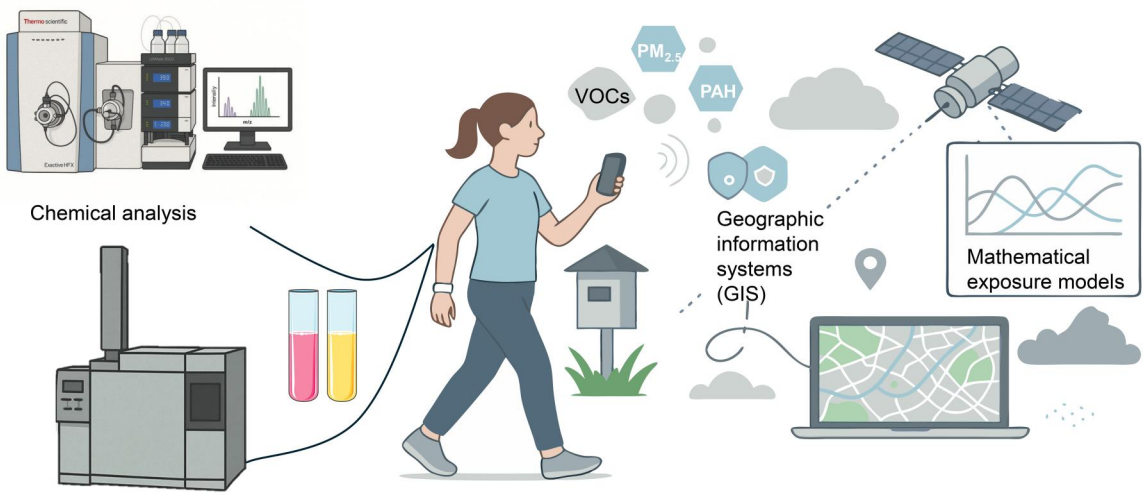

Figure 1. Advancing exposome assessment through integration of external monitoring technologies and internal chemical analysis.

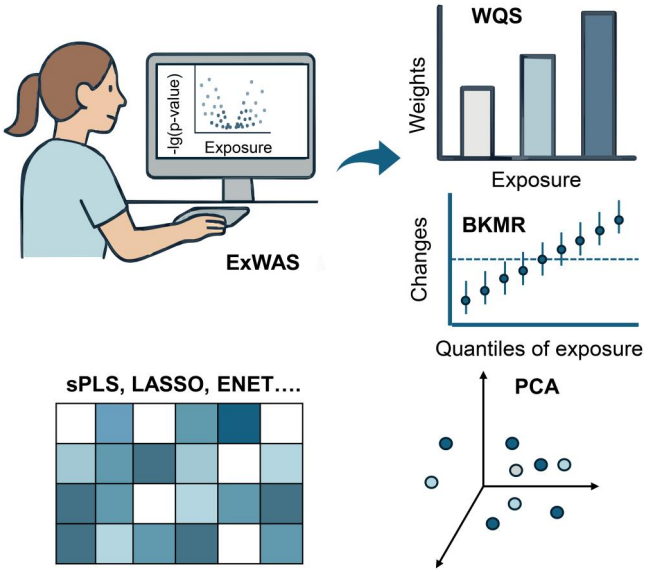

Figure 2. Statistical and bioinformatics frameworks for exposomic mixture analyses.

PCA summarizes exposures into orthogonal components to reduce multicollinearity, though this can obscure individual chemical contributions.[26] In contrast, sPLS provides supervised dimension reduction and simultaneous feature selection, and has been used to identify multi-pollutant exposure patterns associated with birth outcomes in the HELIX cohort.[25] LASSO uses an L1-penalty to perform simultaneous coefficient shrinkage and variable selection, making it well-suited for high-dimensional environmental health data. For example, Jedynak et al. applied an adjusted LASSO to screen 47 prenatal chemical biomarkers in relation to child behaviour outcomes in an exposome-based analysis.[27] ENET combines LASSO and ridge penalties to better manage correlated exposure mixtures. Lenters et al. applied ENET to a panel of prenatal phthalate metabolites, perfluoroalkyl acids, and organochlorines to identify chemicals jointly associated with term birth weight across three European birth cohorts.[28] GUESS is a Bayesian variable-selection framework that explores many competing exposure-outcome models in parallel, making it well suited for high-dimensional exposome settings. It has been applied to hair-derived exposome data from the nutrition, environment, and cardiovascular health (NESCAV) study to identify pollutants jointly associated with multiple cardiometabolic health traits.[29] Deletion substitution addition (DSA) has also emerged recently as a powerful tool for identifying key exposures in relation to specific phenotypes, offering enhanced classification and feature selection capabilities.[23] The integration of these approaches,[30] demonstrates their potential to enhance reproducibility, clarify mixture effects, and support mechanistic interpretations.

Ideally, statistical methods used in exposome research should be capable of handling a large set of time-varying exposures from different domains, while considering correlation structures and accounting for multiple comparisons. However, there is still no consensus on how to conduct longitudinal analyses using exposome data. The longitudinal nature of exposure data introduces further complexity, requiring decisions on how to model exposure trajectories, cumulative exposures, lagged effects, or windows of susceptibility. These issues are particularly relevant for pregnancy and birth cohort studies, which often repeatedly collect exposure measurements across critical developmental periods. Future simulation studies are needed to evaluate and compare statistical methods in this context. The EU Child Cohort Network, developed under the LifeCycle Project, offers a valuable platform for reproducible longitudinal exposome research from the prenatal period and onwards.[31]

Each statistical method offers unique advantages and limitations. By applying them in a complementary manner, researchers can more effectively navigate the complexity of exposomic data, improve accuracy in identifying critical exposures, and strengthen the validity of health outcome predictions.

Current limitations and challenges in exposome research

Despite significant methodological progress, exposome research still faces key challenges. One of the most important limitations is the inability of current methods to fully capture the inherent complexity and variability of environmental exposures. Firstly, individuals are exposed to thousands of environmental exposures that fluctuate over time, space, intensity, and biological context. Capturing this dynamic and multifactorial exposure landscape with sufficient temporal resolution remains difficult, especially when relying on cross-sectional data or single-time point measurements.[10] Secondly, a large proportion of chemical signals detected in biospecimens remain structurally unidentified, primarily due to limitations in existing chemical libraries and reference standards. This is especially true for emerging pollutants and their transformation products, which complicates interpretation, reduces consistency across studies, and introduces uncertainty into exposure estimations.[32,33] Thirdly, mechanistic biomarkers of environmental exposures, such as inflammation, oxidative stress, and metabolic disruption markers, may be influenced by inherent biological heterogeneities within the population, which complicates the interpretation of causal relationships with external exposures.[30]

In addition to measurement difficulties, the interdisciplinary nature of exposome research (environmental science, analytical chemistry, epidemiology, and systems biology) also faces fundamental critical barriers related to data integration, standardization, and interpretation of biological meanings. Unified protocols and compatible data structures are needed to synthesize and interpret such data. Inconsistencies in metadata annotation, quality control procedures, and reporting standards hinder reproducibility and limit the potential for cross-study comparisons. Mechanistic understanding remains limited, and very few studies incorporate longitudinal designs, experimental validation or weight-of-evidence approaches to support causal interpretation.[24,34] Furthermore, there is no widely accepted framework for interpreting complex biological responses to environmental mixtures, which restricts the ability to translate internal signals into meaningful health insights.[33] Tackling these issues needs better coordination of data systems, stronger long-term cohort studies, and analysis approaches that are closely linked to biological mechanisms.

Future directions in exposome research

Future research needs to adopt a more integrated and harmonized approach. A key priority is improving chemical identification. Many detected environmental signals still lack structural annotation. Efforts should focus on expanding spectral databases, including more transformation products, and aligning mass spectrometry protocols across different studies to improve consistency and coverage.[35] Another important step is addressing the lack of temporal and contextual resolution in exposure

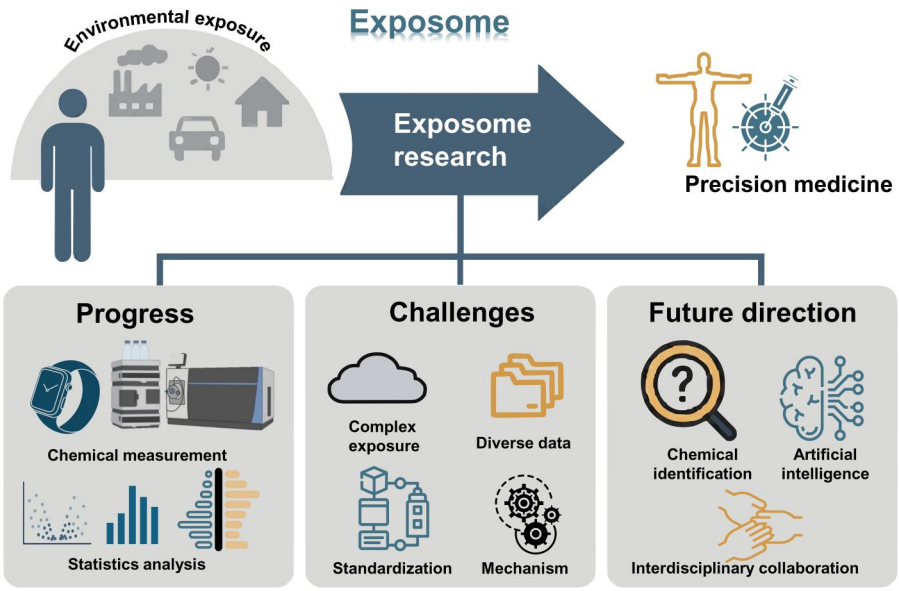

Figure 3. Conceptual framework of exposome research highlighting progress, challenges and future directions.

data. This can be achieved by designing longitudinal studies that extensively collect repeated biological samples over time, as some exposome cohorts are beginning to conduct. The use of wearable devices and location-tracking technologies can help capture more detailed information about personal exposures at different life stages.[10,36] Moreover, artificial intelligence (AI) and exposome intelligence (EI) tools offer a transformative opportunity for scaling exposome science. EI refers to the use of AI-driven analytical frameworks to systematically identify, characterize, and prioritize environmental exposures across complex datasets.[37] Methods such as machine learning, network analysis, and causal modeling can be used to identify patterns, explore possible mechanisms, and improve predictions of health outcomes.[38] For example, AI-assisted molecular network analysis has already shown promise in identifying unknown environmental compounds and helping prioritize those that may require further investigations.[39,40] Finally, it is critical to build stronger connections between different scientific fields. Bringing together expertise from environmental health, data science, biology, and public health will be essential for training researchers who can interpret exposome data and apply it to real-world health problems. As the field moves toward a large-scale Human Exposome Project, similar in scope to the Human Genome Project, international cooperation, open data sharing, and stable funding will be necessary to realize its full impact on public health and disease prevention.[33]

Conclusion

The exposome offers a valuable and comprehensive framework for understanding how environmental factors influence human health (Figure 3). Although methods for exposure assessment and data analysis have improved, researchers still face important challenges, including the limited ability to identify unknown chemicals, the difficulty of capturing exposure information over long periods, and the complexity of combining diverse datasets to uncover causal relationships. Addressing these gaps will require closer collaboration across disciplines, improved standardization of data collection and analysis, and the thoughtful use the application of novel tools such as wearable sensors and data-driven approaches. With continued progress, exposome research can go beyond identifying descriptive associations to understand how the total environment affects human health, which is critical for developing more effective disease prevention and health promotion strategies.

Author contributions

Min Nian (Conceptualization [equal], Funding acquisition [equal], Methodology [equal], Visualization [lead], Writing—original draft [lead], Writing—review & editing [equal]), Mustieles Vicente (Conceptualization [equal], Methodology [equal], Writing—review & editing [equal]), Liang Wang (Conceptualization [equal], Methodology [equal], Supervision [equal], Writing—review & editing [equal]), Yu Zhang (Methodology [equal], Writing—original draft [equal], Writing—review & editing [equal]), and Yixin Wang (Conceptualization [equal], Funding acquisition [equal], Supervision [equal], Writing—review & editing [lead]).

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Conflict of interest

The authors have no conflicts of interest to disclose.

Data availability

No new data were generated or analyzed in support of this research.

References

1. Wild CP. Complementing the genome with an "exposome": the outstanding challenge of environmental exposure measurement in molecular epidemiology. *Cancer Epidemiol Biomarkers Prev*. 2005;14(8):1847–1850. https://doi.org/10.1158/5–9965.EPI-5–0456

2. Fang M, Hu L, Chen D, *et al.* Exposome in human health: utopia or wonderland? *Innovation (Camb)*. 2021;2(4):100172. https://doi.org/10.1016/j.xinn.2021.100172
3. Rappaport SM, Smith MT. Epidemiology. Environment and disease risks. *Science*. 2010;330(6003):460–461. https://doi.org/10.1126/science.1192603
4. Vrijheid M, Slama R, Robinson O, *et al.* The human early-life exposome (HELIX): project rationale and design. *Environ Health Perspect*. 2014;122(6):535–544. https://doi.org/10.1289/ehp.1307204
5. Maitre L, Bustamante M, Hernandez-Ferrer C, *et al.* Multi-omics signatures of the human early life exposome. *Nat Commun*. 2022;13(1):7024. https://doi.org/10.1038/s41467-2–34422-2
6. Yu Z, Kress S, Blay N, *et al.* External exposome and incident asthma across the life course in 14 European cohorts: a prospective analysis within the EXPANSE project. *Lancet Reg Health Eur*. 2025;54:101314. https://doi.org/10.1016/j.lanepe.2025.101314
7. Cui F, Tang L, Li D, *et al.* Early-life exposure to tobacco, genetic susceptibility, and accelerated biological aging in adulthood. *Sci Adv*. 2024;10(18):eadl3747. https://doi.org/10.1126/sciadv.adl3747
8. Wang Y, Yuan Q, Li T, Tan S, Zhang L. Full-coverage spatiotemporal mapping of ambient PM(2.5) and PM(10) over China from Sentinel-5P and assimilated datasets: Considering the precursors and chemical compositions. *Sci. Total Environ* 2021;793:148535. https://doi.org/10.1016/j.scitotenv.2021.148535
9. Mamic L, Gasparovic M, Kaplan G. Developing PM(2.5) and PM(10) prediction models on a national and regional scale using open-source remote sensing data. *Environ. Monit. Assess* 2023;195(6):644. https://doi.org/10.1007/s10661-3–11212-x
10. Munzel T, Sorensen M, Hahad O, Nieuwenhuijsen M, Daiber A. The contribution of the exposome to the burden of cardiovascular disease. *Nat Rev Cardiol*. 2023;20(10):651–669. https://doi.org/10.1038/s41569-3–00873-3
11. Wang L, Luo D, Li X, *et al.* Temporal variability of organophosphate flame retardant metabolites in spot, first morning, and 24-h urine samples among healthy adults. *Environ Res*. 2021;196:110373. https://doi.org/10.1016/j.envres.2020.110373
12. Wang Y, Liu C, Chen Y, *et al.* Profiles, variability and predictors of concentrations of blood trihalomethanes and urinary haloacetic acids along pregnancy among 1760 Chinese women. *Environ Res*. 2019;172:665–674. https://doi.org/10.1016/j.envres.2019.03.017
13. Wang Y, Liu C, Shen Y, *et al.* Urinary levels of bisphenol A, F and S and markers of oxidative stress among healthy adult men: variability and association analysis. *Environ Int*. 2019;123:301–309. https://doi.org/10.1016/j.envint.2018.11.071
14. Wang Y, Feng W, Zeng Q, *et al.* Variability of metal levels in spot, first morning, and 24-hour urine samples over a 3-month period in healthy adult Chinese men. *Environ Health Perspect*. 2016;124(4):468–476. https://doi.org/10.1289/ehp.1409551
15. Li Y, Liu C, Mustieles V, *et al.* Organophosphate esters, sperm mitochondrial DNA copy number, and semen quality: a longitudinal study with repeated measurements. *Environ Sci Technol*. 2025;59(7):3388–3400. https://doi.org/10.1021/acs.est.4c09573
16. Sun Y, Wang Y, Liu C, *et al.* Trimester-specific blood trihalomethane and urinary haloacetic acid concentrations and adverse birth outcomes: identifying windows of vulnerability during pregnancy. *Environ Health Perspect*. 2020;128(10):107001. https://doi.org/10.1289/EHP7195
17. Liu N, Li G, Zhang G, *et al.* Exogenous metals indirectly affect human semen quality via immune cells at single-cell resolution. *Environ Health (Wash)*. 2025;3(9):1083–1093. https://doi.org/10.1021/envhealth.5c00082
18. Liu N, Chen H, Li Y, *et al.* Exogenous metals atlas in spermatozoa at single-cell resolution in relation to human semen quality. *Environ Sci Technol*. 2023;57(19):7358–7369. https://doi.org/10.1021/acs.est.2c08838
19. Paglia G, Astarita G. Metabolomics and lipidomics using traveling-wave ion mobility mass spectrometry. *Nat Protoc*. 2017;12(4):797–813. https://doi.org/10.1038/nprot.2017.013
20. You L, Kou J, Wang M, *et al.* An exposome atlas of serum reveals the risk of chronic diseases in the Chinese population. *Nat Commun*. 2024;15(1):2268. https://doi.org/10.1038/s41467-4–46595-z
21. Braun JM, Kalloo G, Kingsley SL, Li N. Using phenome-wide association studies to examine the effect of environmental exposures on human health. *Environ Int*. 2019;130:104877. https://doi.org/10.1016/j.envint.2019.05.071
22. Amine I, Guillien A, Philippat C, *et al.* Environmental exposures in early-life and general health in childhood. *Environ Health*. 2023;22(1):53. https://doi.org/10.1186/s12940-3–01001-x
23. Ding E, Deng F, Fang J, *et al.* Exposome-wide ranking to uncover environmental chemicals associated with dyslipidemia: a panel study in healthy older Chinese adults from the BAPE study. *Environ Health Perspect*. 2024;132(9):97005. https://doi.org/10.1289/EHP13864
24. Caporale N, Leemans M, Birgersson L, *et al.* From cohorts to molecules: adverse impacts of endocrine disrupting mixtures. *Science*. 2022;375(6582):eabe8244. https://doi.org/10.1126/science.abe8244
25. Agier L, Portengen L, Chadeau-Hyam M, *et al.* A systematic comparison of linear regression-based statistical methods to assess exposome-health associations. *Environ Health Perspect*. 2016;124(12):1848–1856. https://doi.org/10.1289/EHP172
26. Saucy A, Coloma F, Olmos S, *et al.* Socioeconomic inequalities in the external exposome in european cohorts: the EXPANSE project. *Environ Sci Technol*. 2024;58(37):16248–16257. https://doi.org/10.1021/acs.est.4c01509
27. Jedynak P, Maitre L, Guxens M, *et al.* Prenatal exposure to a wide range of environmental chemicals and child behaviour between 3 and 7 years of age - an exposome-based approach in 5 European cohorts. *Sci Total Environ*. 2021;763:144115. https://doi.org/10.1016/j.scitotenv.2020.144115
28. Lenters V, Portengen L, Rignell-Hydbom A, *et al.* Prenatal phthalate, perfluoroalkyl acid, and organochlorine exposures and term birth weight in three birth cohorts: multi-pollutant models based on elastic net regression. *Environ Health Perspect*. 2016;124(3):365–372. https://doi.org/10.1289/ehp.1408933
29. Wada R, Peng F, Lin C, *et al.* Hair-derived exposome exploration of cardiometabolic health: piloting a bayesian multitrait variable selection approach. *Environ Sci Technol*. 2024;58(12):5383–5393. https://doi.org/10.1021/acs.est.3c08739
30. Siroux V, Agier L, Slama R. The exposome concept: a challenge and a potential driver for environmental health research. *Eur Respir Rev*. 2016;25(140):124–129. https://doi.org/10.1183/16000617.4–2016
31. Santos S, Maitre L, Warembourg C, *et al.* Applying the exposome concept in birth cohort research: a review of statistical approaches. *Eur J Epidemiol*. 2020;35(3):193–204. https://doi.org/10.1007/s10654-0–00625-4
32. Escher BI, Stapleton HM, Schymanski EL. Tracking complex mixtures of chemicals in our changing environment. *Science*. 2020;367(6476):388–392. https://doi.org/10.1126/science.aay6636
33. Vermeulen R, Schymanski EL, Barabasi A, Miller GW. The exposome and health: where chemistry meets biology. *Science*. 2020;367(6476):392–396. https://doi.org/10.1126/science.aay3164

34. Mustieles V, Rolland M, Pin I, *et al.* Early-life exposure to a mixture of phenols and phthalates in relation to child social behavior: applying an evidence-based prioritization to a cohort with improved exposure assessment. *Environ Health Perspect.* 2023;131(8):87006. https://doi.org/10.1289/EHP11798
35. Wang X, Yu N, Jiao Z, *et al.* Machine learning-enhanced molecular network reveals global exposure to hundreds of unknown PFAS. *Sci Adv.* 2024;10(21):eadn1039. https://doi.org/10.1126/sciadv.adn1039
36. Shan G, Li X, Huang W. AI-enabled wearable and flexible electronics for assessing full personal exposures. *Innovation (Camb).* 2020;1(2):100031. https://doi.org/10.1016/j.xinn.2020.100031
37. Sillé FCM, Hartung T. AI: the Apollo guidance computer of the Exposome moonshot. *Front Artif Intell.* 2025;8:1632520. https://doi.org/10.3389/frai.2025.1632520
38. Hartung T. How AI can deliver the Human Exposome Project. *Nat Med.* 2025;31(6):1738. https://doi.org/10.1038/s41591-5–03749-w
39. He A, Yao Y, Chen S, *et al.* An enhanced protocol to expand human exposome and machine learning-based prediction for methodology application. *Environ Sci Technol.* 2025;59(7):3376–3387. https://doi.org/10.1021/acs.est.4c09522
40. Huang L, Duan Q, Liu Y, *et al.* Artificial intelligence: a key fulcrum for addressing complex environmental health issues. *Environ Int.* 2025;198:109389. https://doi.org/10.1016/j.envint.2025.109389

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