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SpatioTemporal Omics Consortium: a global effort for biological discovery across species, space and time

Lipin Loo, Keke Xia, Nicola Crosetto, Magda Bienko, Chang Xu, Jinmiao Chen, Anna Pascual Reguant, Chengyu Li, Ji Wang, Xiaofeng Wei, Longqi Liu, Shiping Liu, Lei Han, Ivano Legnini, Craig Glastonbury, Alok Sharma, Yutaka Suzuki, Nir Yosef, Boxiang Liu, Grace Yeo, Mu-ming Poo, Holger Heyn, Fabian Theis, Partha Majumder, Jan Mulder, Ido Amit, Piero Carninci, Xun Xu, Weibin Liu & Quan Nguyen

In this Comment we introduce the SpatioTemporal Omics Consortium (STOC), a global, open network collaborating to integrate spatial and temporal omics across species, development, disease and evolution.

The pace of innovation in spatial technologies has been extraordinary, rapidly transforming our ability to study biological systems within their native tissue environments. Throughout the history of biology, major advances have occurred when new measurement technologies meet conceptual frameworks that allow data to be compared, integrated and generalized. From early microscopy to the Human Genome Project and, more recently, single-cell genomics, transformative progress has followed moments when scale, standardization and coordination have enabled unprecedented discovery beyond the capability of any individual laboratory[1]. Spatial omics represents the next inflection point, extending molecular measurements into their native tissue contexts and revealing how cellular states, interactions and functions are organized in space.

Sequencing-based, imaging-based and affinity-based platforms now routinely profile transcripts, proteins, metabolites, epigenetic states and signaling events within intact tissues[2,3]. Resolution has improved from multicellular to subcellular scales while throughput continues to rise and costs are declining[3]. As a result, spatial profiling is becoming increasingly accessible, with more data generated across multiple biological disciplines ranging from neuroscience, immunology and developmental biology to plant science (Fig. 1).

Why spatiotemporal omics now demands global coordination

As spatial datasets grow in size and diversity, the limiting factor is no longer data generation, but integration, interpretation and generalization across studies. Spatial omics data are produced with heterogeneous technological platforms, with varying resolutions, coverage and sampling strategies, and are analyzed using diverse pipelines. Temporal context, whether developmental stage, disease progression, treatment response or environmental perturbation, is often inconsistently captured or omitted. Variability in metadata, annotations and descriptors makes even technically comparable datasets challenging to meaningfully align across studies or species.

This fragmentation has practical consequences. Without shared reference and standardization frameworks, comparisons and integration across laboratories, cohorts and organisms remain ad hoc. Findings from individual tissues or timepoints are difficult to generalize. As a result, spatial omics risks becoming a collection of detailed, context-specific snapshots rather than a cumulative resource for understanding biological processes that unfold in space and time.

This limitation mirrors earlier phases in genomics, where accumulation of complex data outpaced the development of standards required for reproducibility and synthesis[4]. In spatial biology, the risk is amplified because biological interpretation depends not only on omics profiles but also on spatial relationships and temporal context. As a consequence, the field faces a choice between continued fragmentation, yielding increasingly detailed but siloed atlases, or coordinated approaches that enable integrative discovery. Resolving this tension requires field-wide consensus on how spatial and temporal information is represented, annotated and aligned, such that heterogeneity becomes a source of insight rather than an obstacle to interpretation. Machine learning and integrative modeling compound the problem. These methods depend on diverse, well-annotated datasets to separate biological signal from technical variation, but poorly aligned heterogeneity degrades predictive performance[5].

Addressing these limitations requires coordination at a scale no single institute, country or sector can achieve alone. Biological diversity, disease burden, agricultural systems and environmental pressures span continents, species and evolutionary histories. To realize the full potential of spatial omics, the field must move beyond isolated advances toward shared, globally coordinated frameworks that enable integration, reuse and discovery at scale. To address this need, 270 participants representing 163 institutions across 40 countries convened in Singapore on 8–9 July 2024 and announced the establishment of the SpatioTemporal Omics Consortium (STOC). More information about STOC and its membership is available at https://sto-consortium.org/.

The missing dimensions: from data to insight in spatiotemporal and cross-species biology

Existing large-scale initiatives have catalogued molecular states at cellular and tissue resolution and have reshaped our understanding of cellular heterogeneity and tissue organization[1,5,6]. These efforts represent a major advance for the field and provide an essential foundation for future discovery. However, most remain constrained along at least one key dimension; many are focused on single species, predominantly

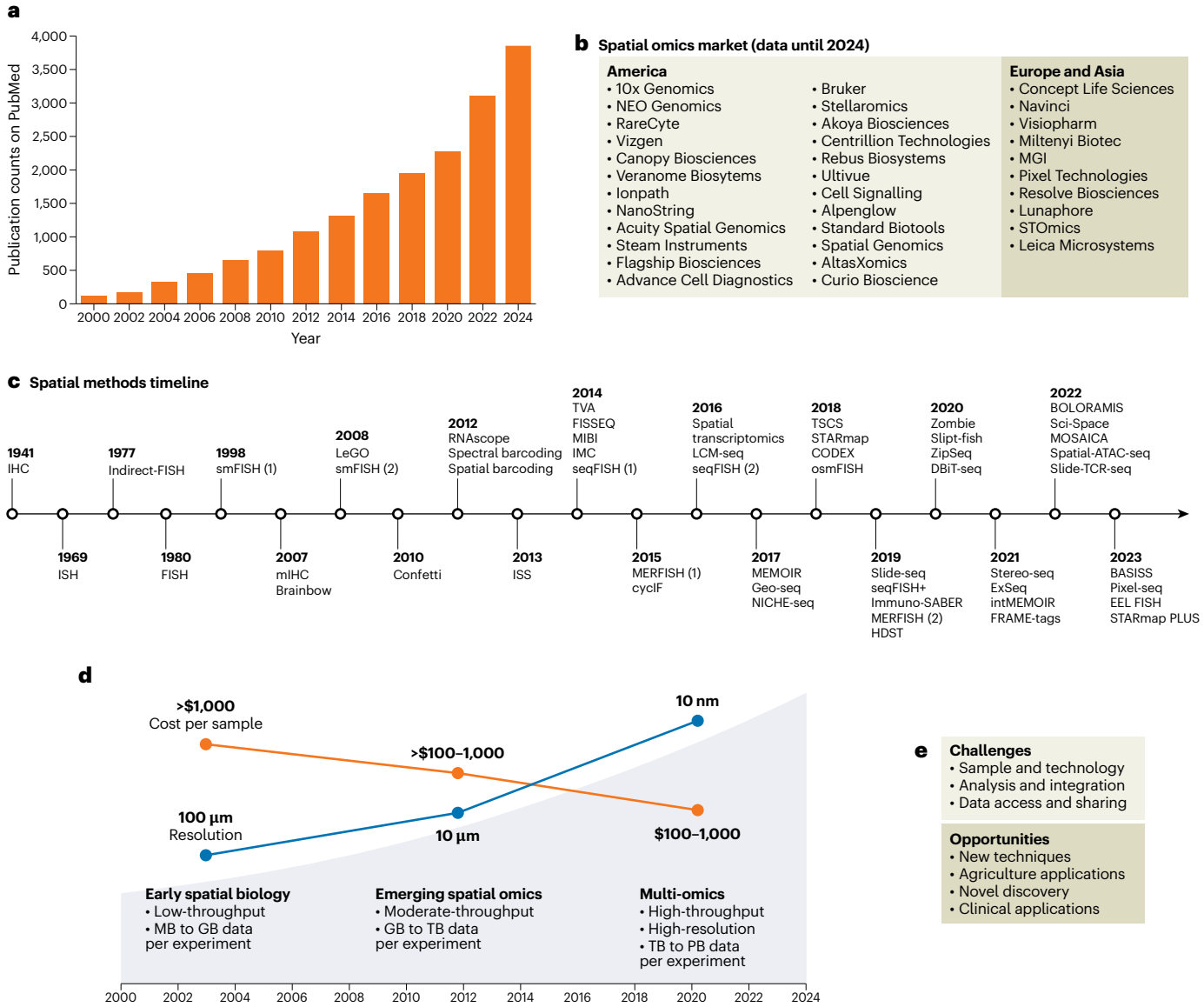

Fig. 1 | The evolution and landscape of spatial omics technologies. a, Growth in spatial omics publications from 2000 to 2024, illustrating the rapid expansion of the field. **b**, Overview of the spatial omics market, listing major companies and platforms active as of 2024. **c**, Timeline of major spatial profiling methods, from early techniques (IHC, ISH, FISH) to advanced high-throughput and multiplexed platforms, annotated by year of introduction. **d**, Comparison of costs and resolution for early, emerging, and high-throughput spatial omics experiments. **e**, Summary of key challenges and opportunities in the field.

human or mouse[5,6], limiting their ability to distinguish conserved biological principles from lineage-specific adaptations. Others emphasize static snapshots rather than dynamic trajectories, limiting insight into development, aging and disease progression[4,7]. As a result, essential biological questions that inherently span space, time and evolution remain only partially addressed.

This limitation is particularly evident for biological processes that are defined by dynamic change. Development, aging, disease progression and responses to external stimuli are biological trajectories shaped by spatial organization, cellular interactions and environmental context. Static atlases describe the molecular composition of tissues at individual timepoints but are poorly suited to reveal how those states emerge, transition and diverge. Without temporal alignment, spatial data risk over-representing stable or end-stage phenotypes while obscuring early, transient, or reversible biological programs. Equivalent biological states may vary at different species-specific timescales or developmental stages, making naive cross-sectional comparisons misleading. This challenge is particularly acute for translational research, where mechanistic insight derived from model organisms must be mapped onto human disease trajectories that unfold over much longer and more heterogeneous timescales.

Integrating temporal information with spatial organization therefore enables a shift from catalogs of discrete states toward process-aware representations of biology. Such representations make it

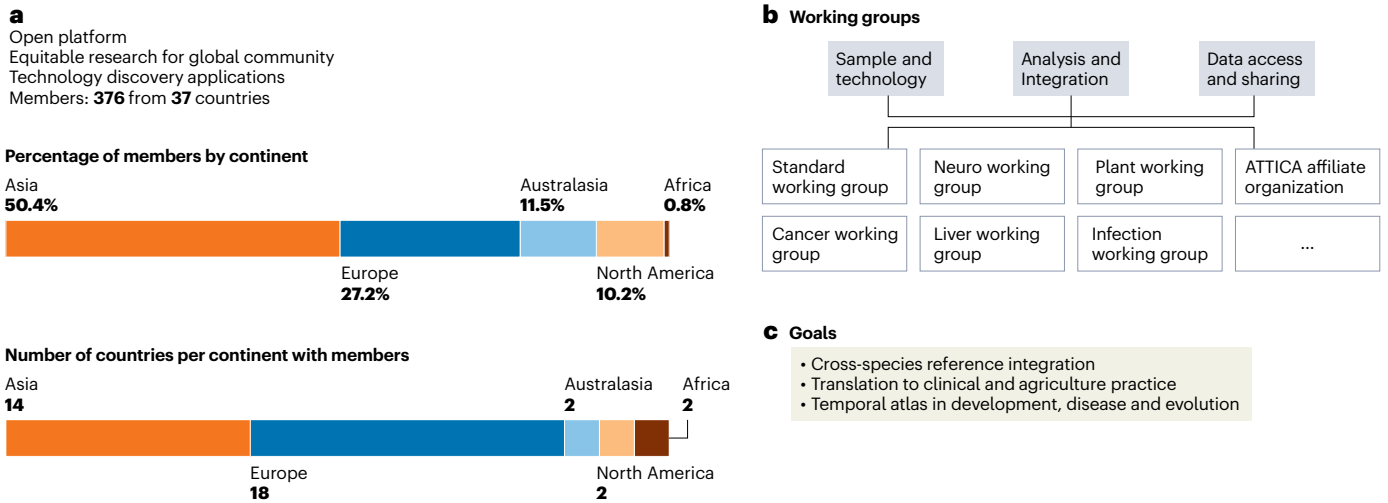

Fig. 2 | Structure and goals of the SpatioTemporal Omics Consortium (STOC). **a**, Geographic distribution of STOC members, showing participation from 376 researchers across 37 countries as of 2024. **b**, Schematic of STOC working groups, organized by focus area: sample and technology, analysis and integration, and data access and sharing. Standard, Neuro, Plant, Cancer, Liver and Infection working groups, as well as the ATTICA (Australian Spatial Sequencing Consortium for Clinical Translation) affiliate, are shown. **c**, Summary of STOC's goals: global collaboration and integration, cross-species reference integration, translation to clinical and agricultural practice, and development of temporal atlases in development, disease and evolution.

possible to align tissues and cellular states along comparable trajectories, rather than treating timepoints as independent observations. Without this shift, spatial omics risks remaining anchored to static descriptions, limiting its ability to inform mechanism, prediction and intervention.

Therefore, shared reference frameworks are required to contextualize spatial datasets across time, biological scale and evolutionary distance. Addressing this gap requires coordinated approaches that explicitly integrate spatial organization with temporal dynamics and comparative biology. Without such integration, spatial omics risks remaining a collection of detailed but disconnected snapshots, rather than a coherent resource for understanding biological processes as they unfold across space, time and species (Fig. 2).

What STOC uniquely enables

STOC is established to address these missing dimensions as a global, open-science framework dedicated to integrating spatial and temporal omics across species and biological contexts. Rather than a single centralized project or atlas, STOC is designed as a platform for coordination, interoperability and community-driven discovery that complements and connects existing initiatives rather than duplicating them[1,7]. A detailed description of the STOC working groups, including their visions, their roadmaps and the challenges they aim to address, is provided in the Supplementary Note.

A scope that spans species, scales and stages. A defining feature of STOC is its explicit cross-species perspective. In addition to human biology, STOC engages with a broad range of organisms, including non-model animals, plants, microbes and agriculturally relevant species[8]. Many fundamental biological principles, including tissue organization, stress responses, regeneration and adaptation, are most clearly revealed through comparative analysis. Conversely, reliance on a small number of model organisms can obscure lineage-specific constraints and adaptive solutions that underlie robustness and diversity in biological systems. The inclusion of non-model organisms is increasingly important as biology confronts questions shaped by environmental change, ecological pressure and evolutionary adaptation. Many organisms exhibit remarkable resilience, regenerative capacity or stress tolerance that is absent or attenuated in traditional model systems. Understanding the spatial and temporal organization underlying these traits through an evolutionary lens can reveal biological strategies that are otherwise inaccessible.

STOC also prioritizes temporal dynamics, including developmental trajectories, aging, disease progression, environmental exposure or experimental perturbation[9,10]. By aligning spatial organization with temporal context, the consortium seeks to move beyond descriptive atlases toward dynamic representations of tissue function. This temporal perspective enables the mapping of causal processes that are not otherwise captured by static correlations and the identification of early or transient programs that may be invisible in end-stage snapshots.

Comparative analysis across species provides a natural framework for identifying biological features that are robust, conserved and functionally essential, as well as those that are adaptive or context-dependent[11]. Aligning spatial and temporal datasets across species can reveal shared organizational principles that determine biological functions and show how tissues and cellular circuits are adapted across evolutionary timescales. Such insights are difficult to obtain from single-species atlases alone.

The absence of integrated spatiotemporal and cross-species frameworks also limits the interpretability of spatial data in translational contexts. Biomarkers or cellular signatures identified at a single timepoint or in a single organism may fail to generalize across disease stages, treatment conditions or populations[12]. Therapeutic interventions often perturb tissues dynamically, yet prediction of their effects requires models trained on temporally resolved data. In agriculture, plant development and stress responses are fundamentally time-dependent and environmentally contingent, challenging efforts to translate molecular profiling into predictive breeding strategies.

STOC also operates across levels of biological organization, from subcellular localization to organ-scale architecture. Biological function emerges from interactions across these spatial hierarchies, yet most current datasets capture only a narrow slice of this complexity. Coordinated reference frameworks enable these scales to be connected rather than treated independently, supporting integrative analyses that more faithfully reflect how tissues function in vivo.

Standardization as an enabler of discovery. A central principle of STOC is that standardization should enable, not constrain, scientific innovation. STOC does not prescribe specific technologies or workflows; rather, it harmonizes metadata, quality benchmarks and representational frameworks that allow diverse datasets to be compared and integrated. This distinction is critical in a rapidly evolving field where methodological diversity is both inevitable and scientifically valuable.

Standardized and interoperable representations of spatial coordinates, temporal variables and biological context reduce technical variability that obscures biological signal while preserving the richness of heterogeneous data. Such standards function as invisible infrastructure that does not dictate how data are generated, but determines whether datasets can be meaningfully reused, reinterpreted and combined[13].

From atlases to predictive models. Large, harmonized spatiotemporal data across species and conditions provide the substrate for machine-learning models that capture complex tissue organization and dynamics[4,9]. Such models benefit not only from depth within a single system but also from diversity across biological contexts. Exposure to variation across species, developmental stages and perturbations allows models to learn more generalizable representations of biological structure and function.

STOC envisions a progression from reference atlases toward predictive, AI-driven frameworks that can infer unmeasured states, simulate perturbations and generate hypotheses that guide experimental design for mechanistic understanding. These models are not intended to replace experiments, but to complement or guide them, enabling in silico exploration of biological scenarios that are difficult, slow or impractical to test directly. By grounding computational approaches in diverse, well-annotated spatiotemporal data, STOC aims to accelerate both fundamental discovery and translation.

Translation without centralization. Spatiotemporal omics holds enormous potential for accelerating translational applications in health and agriculture. Global initiatives must balance scientific coordination with regulatory, ethical and sovereignty considerations. STOC addresses this tension through a deliberately flexible, domain-specific approach that recognizes fundamental differences between human health data, agricultural datasets, and ecological or biodiversity resources.

For human health applications, STOC operates firmly within a research context. The consortium does not define clinical diagnostic standards, establish regulatory criteria or replace national or regional oversight bodies[14]. Instead, STOC enables the generation of harmonized, high-quality spatiotemporal datasets and analytical frameworks that support translational research conducted independently in each jurisdiction while allowing for subsequent integration of appropriate data. This distinction is essential for maintaining trust, protecting participants, and ensuring that scientific coordination does not overstep clinical or legal boundaries.

Recognizing that sensitive or identifiable types of human data are subject to diverse regulatory regimes and ethical norms, STOC supports such data types remaining within their countries of origin or local jurisdictions while safe summary objects such as standardized metadata, analytical outputs and learned models may be agreed to be sharable internationally[14]. Sensitive data handling, analysis or collaboration should prioritize infrastructure that allows researchers to easily access data while strictly respecting data privacy and data sovereignty rules. One example is federated approaches, which offer scientific advantages despite their tendency to be framed as regulatory compromises. Cross-cohort analysis at scale reduces biases from centralized curation and improves reproducibility across independent populations. In so doing, federated analysis aligns robust science with responsible data stewardship.

By contrast, for agricultural, ecological and biodiversity data, centralized global resources are often both feasible and strategically advantageous to support data generation and integration. Coordinated spatiotemporal atlases of crops and livestock across developmental stages and environmental conditions can inform predictive breeding, resilience strategies and sustainable food systems[8]. Similarly, spatial datasets collected from diverse ecosystems provide a basis for understanding adaptation and environmental response at a systems level. In these domains, centralization can accelerate discovery while complementing federated approaches used in human research.

Across all contexts, the unifying principle is translation through coordination for integration rather than control. By aligning data structures, analytical representations and conceptual frameworks while respecting domain-specific constraints, STOC enables insights to be learned and tested across species and systems, and supports applications without imposing a single model of data ownership or governance.

A call for coordinated global action

The trajectory of spatiotemporal omics mirrors earlier phases in genomics and single-cell biology, where initial technological breakthroughs were followed by the recognition that coordination, scale and openness were essential for sustained progress. STOC represents a collective response to ensure that the vast potential of spatiotemporal biology is realized through inclusive, global collaboration rather than fragmented, parallel advances.

STOC is designed to complement and collaborate with existing consortia[1,7] by aligning and sharing standards, reference frameworks, data representations and infrastructure so that ongoing initiatives are amplified rather than duplicated. The consortium provides a platform for engagement across academia, industry, healthcare, agriculture and technological and computational science, reflecting the inherently interdisciplinary nature of spatiotemporal biology. Failure to coordinate at this stage carries real risks. Without shared spatiotemporal and cross-species frameworks, spatial omics and its vast, diverse sources of funding may yield increasingly detailed yet irreproducible atlases whose insights do not generalize across systems, stages or populations[9]. Conversely, coordinated action can transform spatial data into integrative resources that economically accelerate discovery at scale and robust translation.

Equity and inclusivity are central to this vision. Many geographic regions, tissues, species and biological contexts remain underrepresented in spatial datasets, limiting the scope and generalizability of biological insight. By lowering barriers to participation and prioritizing diversity, STOC aims to enable equitable access to spatial biology and

ensure that its benefits are shared globally. We invite the scientific community to participate in shaping the next phase of biological discovery: one that integrates space, time and evolution to better understand life in all its complexity.

Lipin Loo[1], Keke Xia[2], Nicola Crosetto[3,4], Magda Bienko[3,4], Chang Xu[5], Jinmiao Chen[6,7,8], Anna Pascual Reguant[9,10], Chengyu Li[11], Ji Wang[12], Xiaofeng Wei[12], Longqi Liu[13], Shiping Liu[13], Lei Han[13], Ivano Legnini[3], Craig Glastonbury[3,14], Alok Sharma[15,16,17,18], Yutaka Suzuki[18], Nir Yosef[19], Boxiang Liu[5,20,21], Grace Yeo[7,20,22], Mu-ming Poo[23], Holger Heyn[9,10,24], Fabian Theis[25,26,27], Partha Majumder[28], Jan Mulder[29], Ido Amit[19], Piero Carninci[3,15], Xun Xu[12], Weibin Liu[30] ✉ & Quan Nguyen[31] ✉

[1]Charles Perkins Centre, School of Life and Environmental Sciences, University of Sydney, Sydney, New South Wales, Australia. [2]BGI Research, Beijing, China. [3]Human Technopole, Milan, Italy. [4]Department of Microbiology, Tumor and Cell Biology, Karolinska Institute, Stockholm, Sweden. [5]Department of Pharmacy and Pharmaceutical Sciences, Faculty of Science, National University of Singapore, Singapore, Singapore. [6]Centre for Biomedical Data Science and Program in Cancer and Stem Cell Biology, Duke-NUS Medical School, Singapore, Singapore. [7]Bioinformatics Institute (BII), Agency for Science, Technology and Research (A*STAR), Singapore, Singapore. [8]Immunology Translational Research Program, Department of Microbiology and Immunology, Yong Loo Lin School of Medicine, National University of Singapore (NUS), Singapore, Republic of Singapore. [9]Centro Nacional de Análisis Genómico (CNAG), Barcelona, Spain. [10]Universitat de Barcelona (UB), Barcelona, Spain. [11]Lingang Laboratory, Shanghai, China. [12]State Key Laboratory of Genome and Multi-omics Technologies, BGI Research, Shenzhen, China. [13]State Key Laboratory of Genome and Multi-omics Technologies, BGI Research, Hangzhou, China. [14]Nuffield Department of Medicine, University of Oxford, Oxford, UK. [15]RIKEN Center for Integrative Medical Sciences, RIKEN Yokohama Campus, Yokohama, Japan. [16]College of Informatics, Korea University, Seoul, South Korea. [17]University of the South Pacific, Suva, Fiji. [18]University of Tokyo, Tokyo, Japan. [19]Department of Systems Immunology, Weizmann Institute, Rehovot, Israel. [20]Genome Institute of Singapore (GIS), Agency for Science, Technology and Research (A*STAR), Singapore, Republic of Singapore. [21]Department of Biomedical Informatics, Yong Loo Lin School of Medicine, National University of Singapore, Singapore, Singapore. [22]Division of Medical Oncology, National Cancer Centre, Singapore, Singapore. [23]Institute of Neuroscience, Chinese Academy of Sciences, Shanghai, China. [24]ICREA, Barcelona, Spain. [25]Institute of Computational Biology, Helmholtz Center, Munich, Germany. [26]TUM School of Computation, Information and Technology, Technical University of Munich, Munich, Germany. [27]TUM School of Life Sciences, Technical University of Munich, Munich, Germany. [28]John C. Martin Centre for Liver Research and Innovations, Kolkata, India. [29]Department of Neuroscience, Karolinska Institute, Stockholm, Sweden. [30]BGI, Shenzhen, China. [31]QIMR Berghofer and The University of Queensland, Brisbane, Queensland, Australia.

✉e-mail: liuweibin@genomics.cn; quan.nguyen@qimrb.edu.au

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Author contributions

Q.N., L. Loo. and W.L. conceived and coordinated the consortium whitepaper. L. Loo, K.X., N.C., M.B., C.X., J.C., A.P.R., C.L., J.W., X.W., L. Liu, S.L., L.H., I.L., C.G., Alok Sharma, Y.S., N.Y., B.L., G.Y., M.-m.P., H.H., F.T., P.M., J.M., I.A., P.C., X.X., W.L. and Q.N. contributed to the writing, editing and critical review of the manuscript. J.W. and Q.N. generated the figures. All authors contributed intellectual input to the development of the STOC framework, participated in working groups and approved the final version of the manuscript.

Competing interests

L. Loo is co-founder of an RNA therapeutics company, Enhanced Analgesics. H.H. is co-founder and chief scientific officer of Omniscope, is a scientific advisory board member at Nanostring and Mirxes, is a consultant for Moderna and has received honoraria from Genentech. F.J.T. consults for Immunai, CytoReason, Genbio, Valinor Industries, Bioturing and Phylo Inc., and has ownership interest in RN.AI Therapeutics, Dermagnostix and Cellarity.

Additional information

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