



Developmental Cell Atlas: Charting Cellular Progression Across Embryogenesis and Tissue Formation

Julian Hartmann*

Department of Developmental Biology, Eastwood Institute of Life Sciences, Copenhagen, Denmark

DESCRIPTION

Developmental biology focuses on how a single fertilized cell gives rise to a complex organism composed of many specialized tissues and cell types. This process involves highly coordinated changes in gene expression, protein activity, cellular behavior, and spatial organization. A developmental cell atlas is a comprehensive reference framework that maps the identities, states, and transitions of cells throughout developmental stages. It provides a structured view of how cells emerge, differentiate, and organize into functional biological systems.

During embryonic development, cells undergo progressive specialization. Initially, cells possess broad developmental potential, allowing them to adopt multiple possible fates. As development proceeds, they gradually restrict their potential and acquire specific identities such as neural, muscular, epithelial, or immune-related lineages. These transitions are guided by tightly regulated molecular programs that control gene activity and cellular behavior. A developmental cell atlas captures these transitions by cataloging cell types and intermediate states across time and space.

Traditional approaches to studying development relied on fixed tissue samples and microscopy-based observations. While these methods provided foundational insights, they were limited in their ability to resolve molecular diversity within individual cells. Many intermediate states and transient populations could not be easily identified. The emergence of single-cell technologies has transformed this field by enabling high-resolution profiling of gene expression, protein abundance, and chromatin accessibility in individual cells.

Single-cell RNA sequencing plays a central role in constructing developmental cell atlases. By measuring gene expression profiles across thousands of individual cells, researchers can identify distinct cell populations and arrange them into developmental hierarchies. These data allow reconstruction of lineage relationships and identification of branching points where cells

commit to different fates. Such analyses provide a dynamic view of how tissues are formed during development.

In regenerative medicine, developmental cell atlases provide valuable reference information for guiding tissue repair strategies. By comparing injured or diseased tissues with developmental reference maps, researchers can identify which cellular programs need to be activated or restored. This approach supports the design of therapies aimed at reconstructing damaged tissues or enhancing natural repair mechanisms.

Cancer research also benefits from developmental perspectives. Tumors often reactivate developmental programs that are normally restricted to early life stages. These programs can contribute to uncontrolled growth, invasion, and cellular plasticity. By comparing tumor cells with developmental atlases, researchers can identify similarities between cancer progression and embryonic development, offering insight into disease mechanisms.

Building developmental cell atlases requires integration of large-scale datasets generated from multiple experimental platforms. Single-cell sequencing, spatial mapping, and computational modeling all contribute to constructing comprehensive references. These datasets must be carefully aligned and analyzed to ensure accurate representation of developmental trajectories.

Computational methods are essential for organizing developmental data. Algorithms are used to cluster cells, infer lineage relationships, and reconstruct developmental timelines. Machine learning approaches can identify subtle patterns in gene expression that correspond to early fate decisions.

Despite significant progress, challenges remain in constructing complete developmental atlases. Early developmental stages are often difficult to sample due to technical and ethical limitations. Additionally, rapid changes in cellular states can make it challenging to capture intermediate transitions. Variability between individuals and environmental influences further complicate atlas construction.

Correspondence to: Julian Hartmann, Department of Developmental Biology, Eastwood Institute of Life Sciences, Copenhagen, Denmark, USA, E-mail: julian.hartmann@eastwoodresearch.org

Received: 25-May-2026, Manuscript No. SCPM-26-31895; **Editor assigned:** 27-May-2026, PreQC No. SCPM-26-31895 (PQ); **Reviewed:** 10-Jun-2026, QC No. SCPM-26-31895; **Revised:** 17-Jun-2026, Manuscript No. SCPM-26-31895 (R); **Published:** 24-Jun-2026, DOI: 10.35248/2168-9431.26.15.109.

Citation: Hartmann J (2026). Developmental Cell Atlas: Charting Cellular Progression Across Embryogenesis and Tissue Formation. Single Cell Biol. 15:109.

Copyright: © 2026 Hartmann J. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution and reproduction in any medium, provided the original author and source are credited.

Another challenge lies in integrating data across different scales. Development involves molecular, cellular, tissue, and organism-level processes that must be connected to form a coherent understanding. Achieving this integration requires advanced computational models capable of linking diverse types of biological information.

CONCLUSION

Future developmental cell atlases are expected to incorporate multi-layered data, including gene expression, protein activity, chromatin structure, spatial organization, and intercellular communication. These integrated frameworks will provide increasingly detailed representations of how organisms develop from single cells into complex systems. Developmental cell atlases represent an important advancement in biological research because they provide structured, high-resolution maps of cellular formation and differentiation. By documenting how cells change over time and space, they contribute to a deeper understanding of development, disease origins, and tissue organization. Continued technological and computational improvements are expected to expand their scope and biological relevance. These computational frameworks allow researchers to interpret complex datasets and generate biologically meaningful maps.

REFERENCE

1. Newman AM, Liu CL, Green MR, Gentles AJ, Feng W, Xu Y, et al. Robust enumeration of cell subsets from tissue expression profiles. *Nature methods*. 2015 ;12(5):453-457.
2. Papalexi E, Mimitou EP, Butler AW, Foster S, Bracken B, Mauck III WM, et al. Characterizing the molecular regulation of inhibitory immune checkpoints with multimodal single-cell screens. *Nature genetics*. 2021 ;53(3):322-331.
3. Buenrostro JD, Wu B, Chang HY, Greenleaf WJ. ATAC-seq: a method for assaying chromatin accessibility genome-wide. *Current protocols in molecular biology*. 2015 ;109(1):21-29.
4. Rodriques SG, Stickels RR, Goeva A, Martin CA, Murray E, Vanderburg CR, et al. Slide-seq: A scalable technology for measuring genome-wide expression at high spatial resolution. *Science*. 2019 ;363(6434):1463-1467.
5. Datlinger P, Rendeiro AF, Schmidl C, Krausgruber T, Traxler P, Klughammer J, et al. Pooled CRISPR screening with single-cell transcriptome readout. *Nature methods*. 2017 ;14(3):297-301.
6. Hanna RE, Hegde M, Fagre CR, DeWeirdt PC, Sangree AK, Szegletes Z, et al. Massively parallel assessment of human variants with base editor screens. *Cell*. 2021 ;184(4):1064-1080.
7. Katti A, Diaz BJ, Caragine CM, Sanjana NE, Dow LE. CRISPR in cancer biology and therapy. *Nature Reviews Cancer*. 2022;22(5):259-279.
8. Klein AM, Mazutis L, Akartuna I, Tallapragada N, Veres A, Li V, et al. Droplet barcoding for single-cell transcriptomics applied to embryonic stem cells. *Cell*. 2015;161(5):1187-201.
9. Macosko EZ, Basu A, Satija R, Nemesh J, Shekhar K, Goldman M, et al. Highly parallel genome-wide expression profiling of individual cells using nanoliter droplets. *Cell*. 2015 ; 161(5):1202-14.
10. Schürch CM, Bhate SS, Barlow GL, Phillips DJ, Noti L, Zlobec I, et al. Coordinated cellular neighborhoods orchestrate antitumoral immunity at the colorectal cancer invasive front. *Cell*. 2020 ;182(5):1341-1359.