

Research Report
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Mapping the Mouse Brain Before It Becomes One: The Spatiotemporal Logic of Neural Development

Baran Bahari
Bachelor of Science in Microengineering, EPFL

Supervised by Yingjian Li, Alessandro Valente, and Gioele La Manno

La Manno Laboratory of Brain Development
and Biological Data Science

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Abstract

The embryonic mouse brain develops as a neural tube divided along its length into 19 segments called neuromeres. Within each segment, stem cells differentiate from radial glia into neuroblasts, into neurons. However, which specific population produces which remains largely unknown, because measuring the genes a cell expresses destroys the tissue so no cell can be followed through time and every developmental stage must be read from different embryos.

This research focused on developing a pipeline to reconstruct lineage relationships from data collected at different developmental stages. More than four million cells from 14 embryos were analyzed across six stages, from embryonic day 9.5 to day 15.5, each registered into the reference atlas of its own stage so that cells from different embryos share one anatomical frame. Common candidate parent-child relationships found by two independent methods were filtered based on different criteria.

As a result, the pipeline returns 17 complete lineage trees, of which eight are new, seven match an earlier doctoral study in the same laboratory, and the remaining two match relationships already reported in the published literature. It also recovers all 11 individual parent-child relationships established in the published literature. Alongside this, distinct differentiation profiles across brain regions revealed the spatiotemporal trajectory of neural development, which was further supported by anatomical and functional evidence.

1 Introduction

The embryonic mouse brain develops over a pregnancy of 19 to 21 days. The brain begins as a developing neural tube, divided along its length into 19 segments called *neuromeres*, arranged sequentially along the anterior–posterior (rostral–caudal) axis, each giving rise to distinct brain regions.^[1]

Within each neuromere, cells evolve through the same three-stage developmental sequence, forming a lineage from progenitors to neurons. *Radial glia*, the stem cells of the neural tube, divide both to self-renew and to produce other cell types. They give rise to *neuroblasts*, partially differentiated but still immature cells that can either generate additional neuroblasts or further differentiate into *neurons*, the mature cells responsible for brain activity.

That lineage has long been established. What remains unclear is not that radial glia become neurons, but which radial glial population gives rise to which neuronal population. The developing mouse brain holds dozens of transcriptionally distinct subcategories of each class, and the lineage tree connecting them remains largely unknown. As a matter of fact, reading which genes a cell expresses requires chemically processing the tissue, which destroys it, so each embryo can be analyzed exactly once. A radial glial cell cannot be labelled at day 10 and revisited at day 13, because the embryo examined at day 10 would have been destroyed and can no longer develop to reach day 13. Lineage must therefore be deduced by matching populations across samples from different individuals, which is the challenge this project aims to solve.

A small number of these developmental links have been established independently using experimental lineage-tracing approaches and can therefore serve as validation references. A method that cannot recover known links does not provide reliable new ones.

2 Research Design

The aim of this research was to develop a pipeline that takes data from embryonic brain tissue and returns lineage developmental trees, finding for a given radial glial population which neuroblasts it

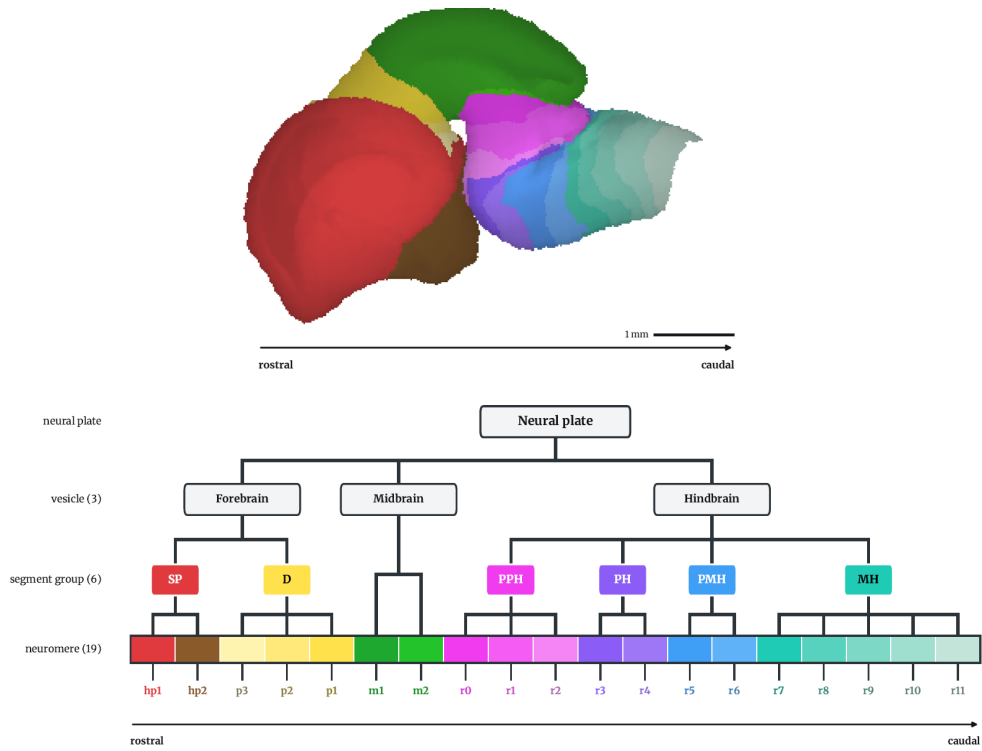


Figure 1. The mouse brain anatomical hierarchy at day 13.5 (embryonic day E13.5) by neuromere : Above, the brain coloured by neuromere, rostral at the left. Below, the same regions as a tree: neural plate, then forebrain, midbrain and hindbrain, then segment groups, then the 19 neuromeres from hp1 to r11.

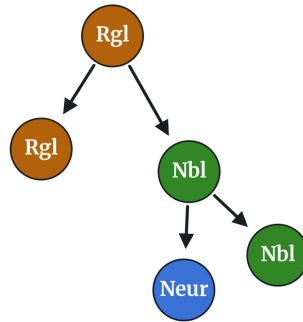


Figure 2. The lineage

produces and which neurons those become. As each stage comes from different embryos, it has to be worked out from separate samples.

To achieve this aim, the project was divided into two major parts. First, I needed a database in which cells from different embryos could be compared. Second, I needed a way to propose candidate relationships and then, remove those that were not sufficiently reliable. While proposing candidate relationships can be done easily using established methodologies, the main challenge was to develop a filtering system that evaluates and removes candidates based on several independent criteria.

2.1 Building the database

The dataset is based on brain tissue images generated using HybISS, or hybridization-based in situ sequencing.^[2] This method uses fluorescent probes that bind to selected transcripts, which are then identified through successive rounds of imaging. This preserves the positions of each transcript, allowing both the gene expression and the location within the tissue of each cell to be mapped. Instead

of removing cells from the tissue, HybISS detects RNA molecules directly within an intact brain section.

However, embryos differ in size, orientation, and how the tissue was cut. ABBA^[3] solves this by aligning each section to a reference atlas, through the four stages shown in Figure 3: the raw HybISS section from a specific timepoint (a); determining the x and y orientation of the cutting plane and finding the best-matching atlas section for each section (b); placing anchor points and either stretching or moving the section to match the atlas borders of each brain region (c); and, once the section has been aligned within these borders, every RNA molecule is now assigned to a named region (d).

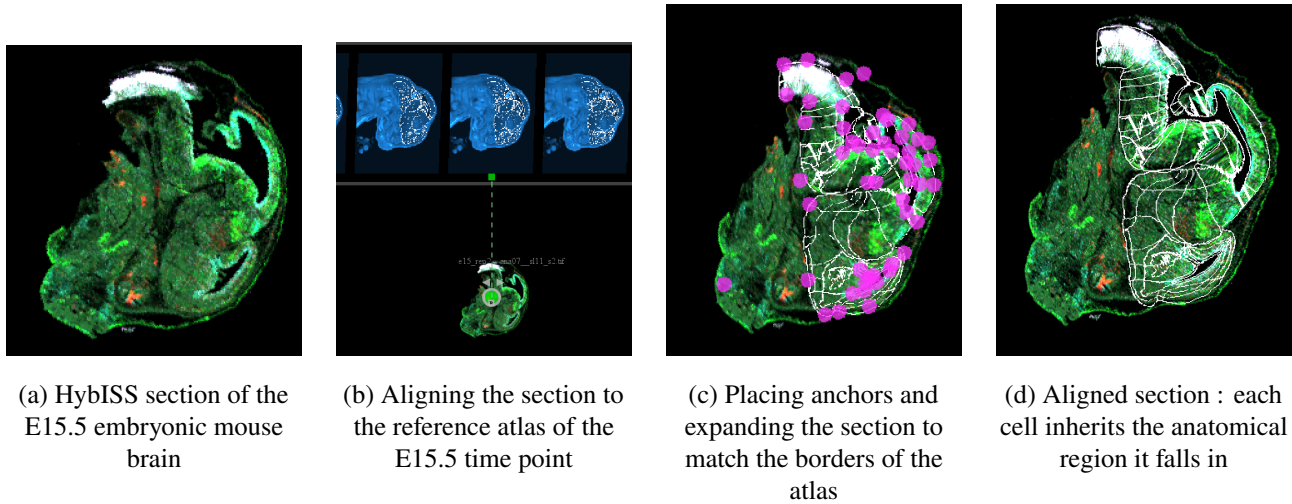


Figure 3. Aligning one section with ABBA

Each section is aligned to the atlas of its own timepoint. As the anatomy of the brain changes and new regions appear over time, each timepoint has its own atlas to which the sections can be aligned. Once all the sections of an embryo at a given timepoint are aligned, they are exported as a TIFF file, from which the coordinates of each RNA molecule can be read. As part of this project, 121 aligned sections from 14 embryos were used and analyzed.

2.2 The pipeline’s five steps

Several orders of steps were tried, and several methods at each one. They were judged on how much structure survived the filtering and how well what survived agreed with the published literature. The version below is the one that came out best.

1. **Aligning the sections and creating the dataset** After alignment, each section is a calibrated image in which cells are still represented as individual RNA reads. Pointillhist is a graph neural network developed in the lab.^[4] It assigns these cells to known populations. Because HybISS measures only about 200 genes and embryonic cells are small, individual cells often contain too little information to be identified on their own. Pointillhist therefore combines information at three scales: transcripts, cells, and local neighbourhoods, allowing each cell to be identified from both its own reads and the cells around it. The possible populations come from a single-cell RNA-seq reference atlas, and assignments are evaluated by how well they reproduce the observed gene expression while remaining coherent with known anatomy. The result is a table in which each cell is assigned one of about 300 population labels.
2. **Building and matching candidate transitions:** To create a first version of the database of parent–child candidates, we used two independent methods developed in previous studies. The

requirement for selecting these two methods was that they should rely on different processes and inputs to analyze the data and identify candidate transitions. Using independent methodologies means that when they agree on a candidate, that candidate has passed two separate and independent tests. This helps reduce errors and makes the results more reliable. Other methods were also reviewed as potential third confirmation but most of the other methods developed in previous studies shared part of their process or input with one or both of the two selected methods. These two are the most independent ones, providing the strongest confirmation when they agreed on a candidate transition.

The first method is *Optimal transport*^[5] that uses consecutive stages. It treats each stage as an amount of cell mass spread across its populations and sets a cost for moving mass from any population to any other. In other words, the cost is cheap between similar populations and expensive between dissimilar ones. Then, the cheapest overall way of moving the earlier stage onto the later one is selected. The idea is that cells do not change arbitrarily between stages, so the least costly transition is the most coherent one. The result is a table of flows, where pairs receiving a large flow become candidate transitions. The first matrix gives the cost of linking each pair of populations, based on the distance between their gene expression similarity. The second matrix gives the flow assigned to each pair by the optimal transport solution, which aims to minimize the total cost. Pairs receiving a large flow are therefore considered candidate transitions. Figure 4 shows these two matrices: the cost of linking each pair and the resulting flow between pairs.



Figure 4. How optimal transport chooses candidates: An example with five populations per stage. The flows in the second matrix are the resulting optimal transport solution based on the first.

The second method, *RNA velocity with CellRank*^[6,7], works within one stage, using a completely different process from optimal transport. When a gene is transcribed, newly produced RNA first contains introns and is therefore classified as *unspliced*; after the introns are removed, it becomes *spliced* RNA. The amounts of unspliced and spliced RNA provide information about recent changes in gene expression: an excess of unspliced RNA suggests that the gene is becoming more active, while a decrease in its production suggests that its expression is being reduced. Measuring that ratio across all genes gives each cell a direction of transition^[8], and CellRank turns those directions into probabilities that one population transforms into another. Figure 5 shows the three steps: the timing that makes it work, how a single gene is read, and how per-cell arrows become statements about populations.

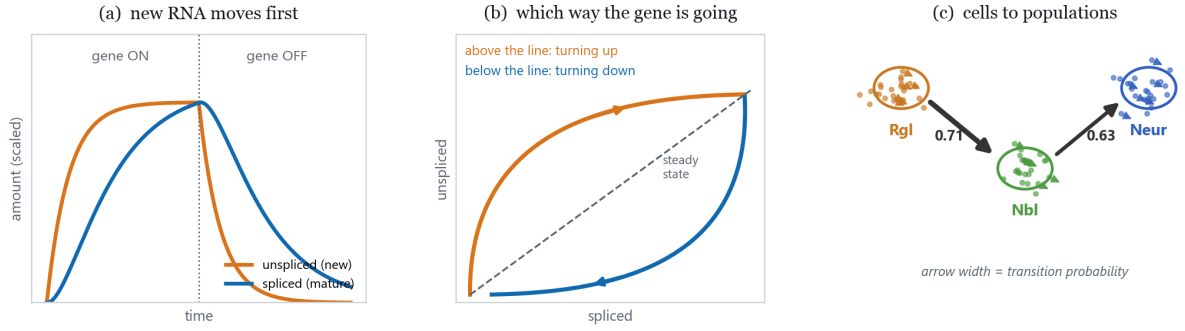


Figure 5. How RNA velocity and CellRank propose candidates: (a) When a gene becomes active, unspliced RNA increases first; when it becomes less active, unspliced RNA decreases first. (b) Comparing unspliced and spliced RNA shows whether a cell is increasing or decreasing the gene’s activity. (c) These changes are then combined to estimate transition probabilities between cell populations.

While Optimal transport uses population composition across stages, RNA velocity uses splicing within one stage and never compares two stages. Nothing makes them fail in the same way, so a transition found by both has passed two unrelated tests.

3. **Filtering, keeping only coherent transitions:** The candidates cannot be used as they are, for a simple reason: both methods always return an answer. Optimal transport will always find some cheapest way of moving one stage onto the next, whether or not a real relationship exists, and RNA velocity will always give every cell some direction, even when the signal is mostly noise. Neither has a way of saying no reliable transition was found. Furthermore, with hundreds of populations there are tens of thousands of possible pairs, so even a one-in-a-thousand coincidence will turn up dozens of times. The 4,360 candidates are a starting list for filtering, not a result. Therefore, the transitions are scored statistically. The first formula measures how strong a transition is:

$$E_{ij} = \frac{f_{ij}}{c_j}$$

- i and j are a population at one stage and a population at the next
- f_{ij} is the proportion of i ’s outgoing flow that goes to j
- c_j is the share of everything arriving at that stage that lands on j , in other words how popular j is as a destination
- $E = 1$ is chance level, and $E = 3$ means three times the expected flow

A big population receives cells from everywhere just because it is big, so counting raw arrivals would make the largest populations look like everyone’s children. Dividing by c_j asks instead whether i prefers j more than an average source would.

The second formula asks whether a transition like that could have come up by chance:

$$p_{ij} = \frac{1 + \#\{b : E_{ij}^* \geq E_{ij}\}}{B + 1}$$

- E_{ij}^* is the enrichment expected by chance, calculated after randomly reassigning the connections between parent and child cells while keeping the population sizes and total number of cells unchanged

- $B = 200$ is the number of randomised copies generated for each case
- $\#\{\cdot\}$ counts how many of those copies match or beat the real enrichment
- The added 1 floors the result at $1/201$, as 200 draws cannot support a p-value of zero

Finally, transitions with less than 2% of a parent's weight are not considered, because a relationship can be statistically reliable and still be too small to mean anything, and the surviving p-values are corrected with the Benjamini–Hochberg procedure^[9] to hold the false discovery rate below 0.05. That means no more than one in twenty of the relationships kept is expected to be a false positive.

4. Checking and testing biological coherence:

A transition can be statistically strong but still make no biological sense. This step checks whether the transitions as a whole are coherent with the embryonic development. Each of four properties was compared with a random set of transitions where connections are reassigned, while each population keeps the same number of connections. This tests whether the observed patterns are stronger than expected from the lineage relationships alone.

- **Do parent and child share a neuromere?** Cells rarely cross between segments of the neural tube, so parent and child should belong to the same neuromere. They should also be close along the rostrocaudal axis, rather than being separated by a large distance.
- **Is the parent nearer the ventricle?** Cells move away from the ventricle as they mature, so the parent should be closer to the ventricle than the child. As a matter of fact, you can see in Figure 6 the spatial distribution of cells while they mature. This also follows the normal lineage order from radial glia to neuroblasts to neurons.

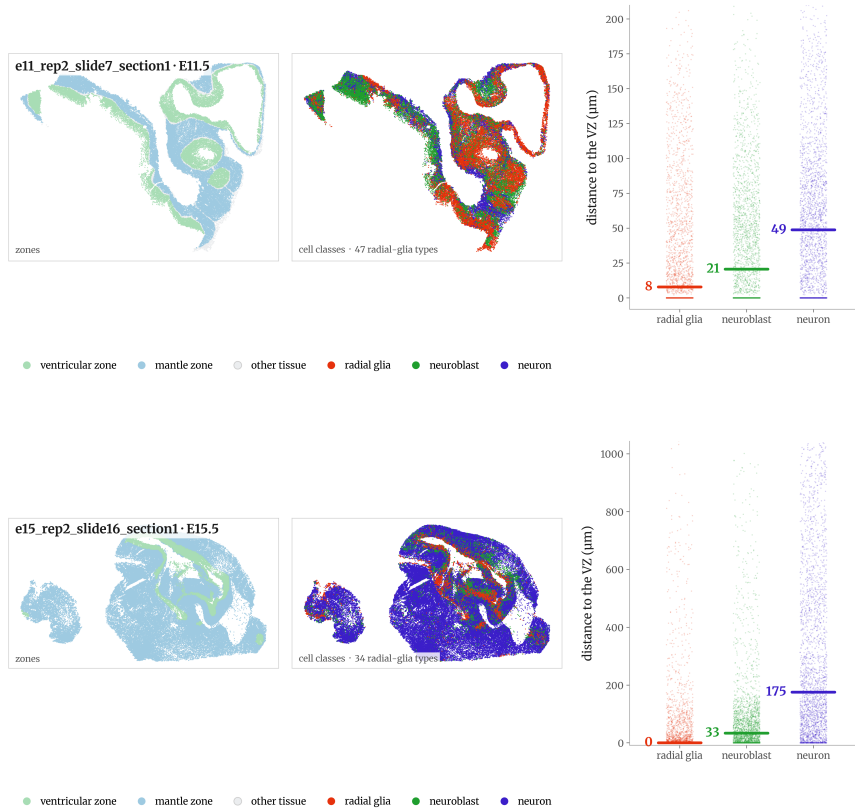


Figure 6. Differentiating cells progressively move away from the ventricular zone: Distance from the ventricular zone, by cell-type, for two sections from two different time points

- **Does the transition follow the developmental order?** This property is not compared with the random set, because it is imposed earlier: candidates are only called between consecutive stages and between different classes, and every tree is assembled as radial glia → neuroblast → neuron, so the order cannot be violated.
- **Does the parent peak no later than the child?** A parent population should increase and peak before its child. If the parent is still increasing after the child has peaked, the relationship is biologically unlikely.

5. **Validation against existing work.** Finally, what survived was compared against two outside sources: published research from other laboratories, which supplies the established relationships of mouse neural development, and the doctoral thesis of Irina Khven^[4], a PhD student in this same laboratory who built her own lineage trees from the same tissue using different methods. Neither was used anywhere earlier in the pipeline.

3 Analysis and Findings

3.1 The final dataset

The aligned database has more than four million cells from 14 embryos and 121 sections, spread unevenly across the six stages. Cells were sorted into 60 subclasses from radial glia through neuroblasts to neurons, and 2.8% could not be correctly identified.

Figure 7 shows three of them, each cell drawn where the atlas places it and coloured by subclass along the scale underneath, warm for radial glia through green for neuroblasts to blue for neurons. At day 9.5 the brain is almost entirely orange and yellow. By day 12.5 the picture has split, the rostral end still warm while the caudal end has turned blue. By day 15.5 almost everything is blue or violet. Reading across gives the conversion of a progenitor sheet into a neuronal organ; reading within a panel gives the second result, that the change does not arrive everywhere at once.

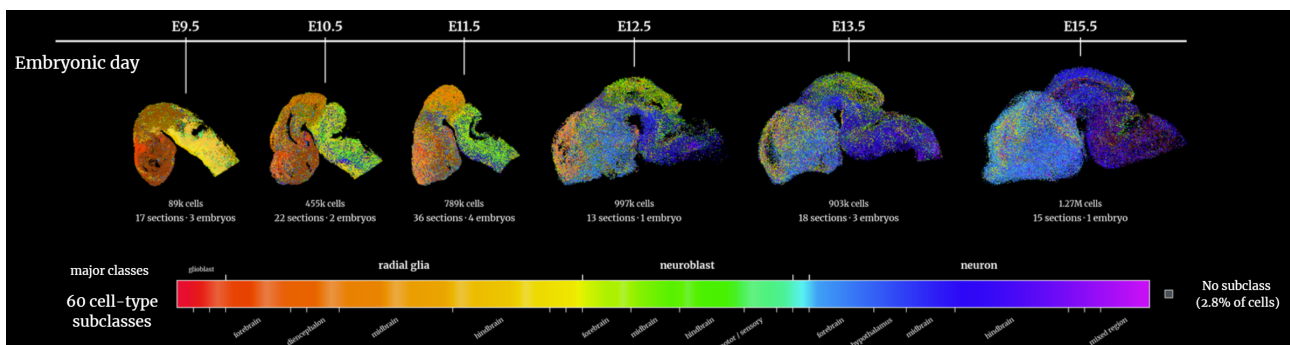


Figure 7. Cell-type distribution across the 6 developmental stages, obtained using Napari

3.2 The logic of neural development: a caudal-to-rostral wave

All segments follow the same lineage order, but at different rates. At each stage, the segment with the highest proportion of neurons is the most advanced one temporally, revealing the order of development that can be justified based on the spatial location of the neuromere or its functional or anatomical importance.

- **Day 9.5** Almost all cells are still radial glia. The leading segment (hp2) has reached only 6% neurons, and the segments barely differ from one another.

- **Day 10.5** The first leader appears at the caudal end, where r9 reaches 31% neurons. Its position explains why: it sits next to the developing spine and musculature and picks up early maturation signals from them, so what happens here is not decided inside the brain alone.
- **Day 11.5** Segment r5 reaches 33%. It makes neurons for eye movement, a function needed early in life, so finishing early makes sense.
- **Day 12.5** The hindbrain still leads, with r10 at the junction with the spinal cord furthest along at about 76% neurons.
- **Day 13.5** The leader is now p3, at 79%. It started late for a reason that can be named: the signalling centre that instructs it only switches on around day 10.5, two days after the equivalent centres further back. The delay is in the instructions, not the cells.
- **Day 15.5** The rostral end finishes last. Segment hp2 reaches 89% while its neighbour hp1 lags behind, which is informative rather than odd: hp1 contains the telencephalon, the future cerebral cortex, and is still holding on to a progenitor pool long after other regions have run theirs down.

Together these describe the order of maturation moving from the caudal side of the brain towards the rostral side over about six days.

3.3 Lineage trees returned by the pipeline

Optimal transport proposed 1,687 parent-child connections and RNA velocity with CellRank proposed 3,530 so only 857 were found by both.

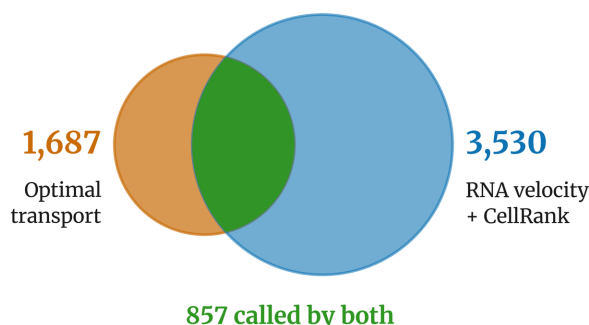


Figure 8. Relationships proposed by each method

The challenging part was finding reliable direction. Of the 4,360 candidate relationships, 2,414 could be assigned a clear direction: from one population to another. In many cases, the data showed that two populations were related, but did not provide enough evidence to tell which one came first. This is because a connection can be detected even when the differences between the two populations are too small or too noisy to determine which is the parent and which is the child. Therefore, the main limitation of the results is not finding possible relationships, but finding their direction.

Filtering and checking brought the candidates down to 17 complete trees, each with a radial glial origin, the neuroblasts it produces and the neurons those become. Eight of them are new, and of the rest, seven match trees in Khven's thesis^[4] and the remaining two match relationships already reported in the published literature.

The 17 are whole trees, each assembled from eight to twelve individual parent-child relationships. The pipeline also recovered all 11 relationships established in the published literature, but those are single links sitting inside trees.

The eight new trees are situated in four neuromeres, and Figures 9 and 10 show them: the circles mark where each lineage is concentrated. Two are in hp1 at the rostral part and one in p2 behind it, three in the midbrain part m1, and two in r1 at the front of the hindbrain. The concentration of relationships in m1 and hp1 is mainly because we have more data from these regions.

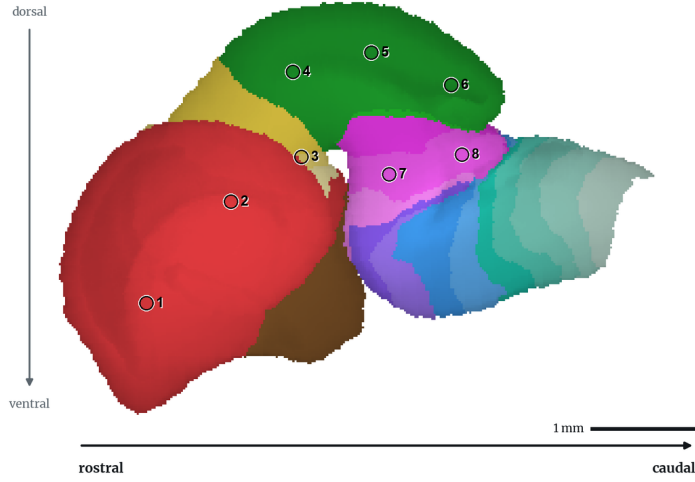


Figure 9. Where the eight new lineages are within the brain's neuromeres: Circles mark the neuromere each lineage is concentrated in

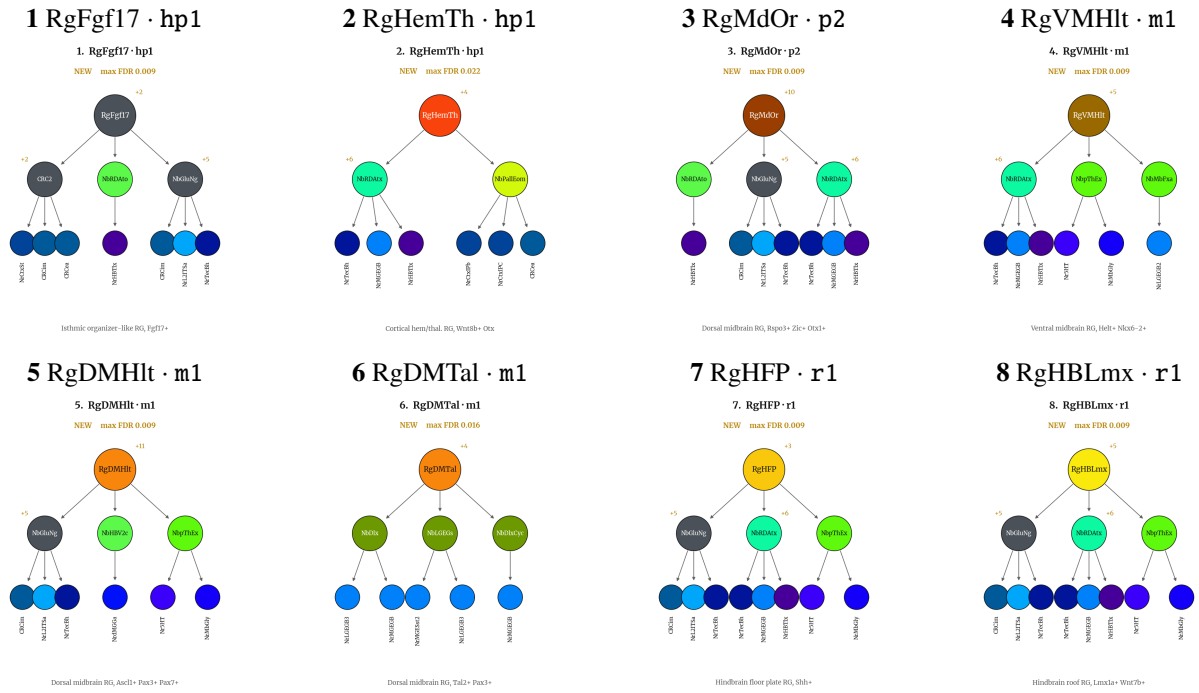


Figure 10. The eight new trees, numbered as in Figure 9: the highest false discovery rate (the statistically weakest link) is written under each root (+n : further children exist but are not drawn)

4 Conclusion

The result of this project is a new method for reconstructing lineage relationships in the embryonic brain from single-cell transcriptomic data, placed in space by the spatial measurements and tested against evidence. It returns 17 complete trees, eight of them new, seven matching earlier work in

the same laboratory^[4] and the remaining two matching the published literature, and recovers all 11 individual parent-child relationships established in the literature.

Through the analysis, we could also observe that the brain's segments differentiate on distinctly different schedules, developing from caudal to rostral. Those differences track the anatomical organization of the neural tube, and in several cases the reason for a segment's timing can be easily found, from proximity to the developing spine for r9 to the prolonged construction of the cerebral cortex for hp1.

4.1 Limitations

There are four main limitations to the current pipeline. Each also represents an opportunity for improvement.

Too few transcripts per cell: Only about four genes are reliably detected per cell. This limits how well similar populations can be distinguished. As a result, some of the 60 subclasses may contain different cell populations, making the resulting trees partly unreliable. Increasing the number of genes measured per cell would therefore improve the method.

Direction is missing for most pairs: For 45% of possible connections the pipeline can find that a relationship exists but not which way it runs. The reason is the same lack of transcripts: RNA velocity needs enough unspliced RNA to measure a direction, and below that level it finds nothing usable. Until direction can be found for the majority of transitions, the trees are partial lineage representations rather than complete ones.

Few validation tests: Recovering 11 of 11 literature relationships is relevant, but 11 is a small number against 4,360 candidates, and those eleven are the best lineages found in the brain.

Not enough embryos per stage, and no cell followed: Two of the six stages rest on a single embryo, so individual variation cannot be separated from developmental change, and day 9.5 contributes only 89,000 cells. More samples per stage would fix the first problem. The second problem cannot be solved with this dataset, in which lineage is deduced statistically rather than directly observed. The trees show the most likely relationships between populations, not confirmed ones.

4.2 Outlook

Beyond the limitations above, there are three ways to continue this study. The first is to bring position into the lineage question, asking how a cell's neuromere and its location within it shape development. The second is to separate proliferation from differentiation because the pipeline of this study treats them together. The third is a possible future application: if the development can be followed and mapped reliably, then lineage trees turn into a tool for identifying where and when development goes wrong in neurodevelopmental disorders.

5 Resources

References

Sources are numbered in order of first appearance; the marker ^[n] in the text points to the corresponding entry below.

1. Kronman, F.N., Liwang, J.K., Betty, R. *et al.* (2024) 'Developmental mouse brain common coordinate framework', *Nature Communications*, 15, 9072. doi:10.1038/s41467-024-53254-w.

The E13.5 and E15.5 reference atlases, and the prosomeric neuromere segmentation used in this report.

2. Gyllborg, D., Langseth, C.M., Qian, X., Choi, E., Salas, S.M., Hilscher, M.M., Lein, E.S. and Nilsson, M. (2020) ‘Hybridization-based in situ sequencing (HybISS) for spatially resolved transcriptomics in human and mouse brain tissue’, *Nucleic Acids Research*, 48(19), e112. doi:10.1093/nar/gkaa792. *The spatial transcriptomics method that produced the data.*
3. Chiaruttini, N., Castoldi, C., Requeie, L.M. *et al.* (2025) ‘ABBA+Brain, an integrated suite for whole-brain mapping, reveals brain-wide differences in immediate-early genes induction upon learning’, *Cell Reports*, 44(7), 115876. doi:10.1016/j.celrep.2025.115876. *Aligning Big Brains and Atlases, used to register every section to its stage-matched atlas.*
4. Khven, I. (2025) *Fine-grained mapping of neural progenitor subtypes in the embryonic brain unveils context-dependent roles of signalling on cell fate decisions.* PhD thesis. EPFL, Lausanne. *Source of the Pointillhist cell-typing framework and of the independent lineage trees used for comparison.*
5. Klein, D., Palla, G., Lange, M. *et al.* (2025) ‘Mapping cells through time and space with moscot’, *Nature*, 638(8052), pp. 1065–1075. doi:10.1038/s41586-024-08453-2. *The optimal transport framework used to propose candidate transitions between consecutive stages.*
6. La Manno, G., Soldatov, R., Zeisel, A. *et al.* (2018) ‘RNA velocity of single cells’, *Nature*, 560, pp. 494–498. doi:10.1038/s41586-018-0414-6. *The original spliced/unspliced formulation on which the direction of a transition is based.*
7. Lange, M., Bergen, V., Klein, M. *et al.* (2022) ‘CellRank for directed single-cell fate mapping’, *Nature Methods*, 19(2), pp. 159–170. doi:10.1038/s41592-021-01346-6. *Turns per-cell velocity directions into transition probabilities between populations.*
8. Lederer, A.R., Leonardi, M., Talamanca, L. *et al.* (2024) ‘Statistical inference with a manifold-constrained RNA velocity model uncovers cell cycle speed modulations’, *Nature Methods*, 21(12), pp. 2271–2286. doi:10.1038/s41592-024-02471-8. *A manifold-constrained velocity model developed in this laboratory.*
9. Benjamini, Y. and Hochberg, Y. (1995) ‘Controlling the false discovery rate: a practical and powerful approach to multiple testing’, *Journal of the Royal Statistical Society: Series B*, 57(1), pp. 289–300. *The multiple-testing correction applied to the permutation p-values.*

Methods and tools

- **HybISS**^[2]: hybridization-based in situ sequencing, used to read gene activity within intact tissue sections so that each cell retains its anatomical position.
- **ABBA**^[3]: Aligning Big Brains and Atlases, used to register each tissue section to the reference atlas corresponding to its own developmental stage.
- **Pointillhist**^[4]: the graph neural network used to assign each cell to one of about 300 reference populations from its own reads and those of its neighbours.
- **moscot**^[5]: the optimal transport framework used to propose candidate population-to-population transitions between consecutive stages.
- **RNA velocity and CellRank**^[6,7,8]: used to infer the direction of transitions from the balance of newly transcribed and processed gene copies within individual cells.

- **Napari:** the multidimensional image viewer used to render the cell-type maps of Figure 7.