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2 **Modular strategies for spatial mapping of**
3 **diverse cell type data of the mouse brain**

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²³ **Abstract**

²⁴ Large-scale, international collaborative efforts by members of the BRAIN Initiative Cell
²⁵ Census Network (BICCN) consortium are aggregating the most comprehensive reference
²⁶ database to date for diverse cell type profiling of the mouse brain, which encompasses over
²⁷ 40 different multi-modal profiling techniques from more than 30 research groups. One cen-
²⁸ tral challenge for this integrative effort has been the need to map these unique datasets into
²⁹ common reference spaces such that the spatial, structural, and functional information from
³⁰ different cell types can be jointly analyzed. However, significant variation in the acquisition,
³¹ tissue processing, and imaging techniques across data types makes mapping such diverse
³² data a multifarious problem. Different data types exhibit unique tissue distortion and sig-
³³ nal characteristics that precludes a single mapping strategy from being generally applicable
³⁴ across all cell type data. Tailored mapping approaches are often needed to address the unique
³⁵ barriers present in each modality. This work highlights modular atlas mapping strategies
³⁶ developed across separate BICCN studies using the Advanced Normalization Tools Ecosys-
³⁷ tem (ANTsX) to map spatial transcriptomic (MERFISH) and high-resolution morphology
³⁸ (fMOST) mouse brain data into the Allen Common Coordinate Framework (AllenCCFv3),
³⁹ and developmental (MRI and LSFM) data into the Developmental Common Coordinate
⁴⁰ Framework (DevCCF). We discuss common mapping strategies that can be shared across
⁴¹ modalities and driven by specific challenges from each data type. These mapping strategies
⁴² include novel open-source contributions that are made publicly available through ANTSX.
⁴³ These include 1) a velocity flow-based approach for continuously mapping developmental
⁴⁴ trajectories such as that characterizing the DevCCF and 2) an automated framework for de-
⁴⁵ termining structural morphology solely through the leveraging of publicly resources. Finally,
⁴⁶ we provide general guidance to aid investigators to tailor these strategies to address unique
⁴⁷ data challenges without the need to develop additional specialized software.

⁴⁸ 1 Introduction

⁴⁹ Over the past decade there have been significant advancements in mesoscopic single-cell analysis of the mouse brain. It is now possible to track single neurons in mouse brains¹, observe whole brain developmental changes on a cellular level², associate brain regions and tissues with their genetic composition³, and locally characterize neural connectivity⁴. Much of these scientific achievements have been made possible due to breakthroughs in high resolution cell profiling and imaging techniques that permit submicron, multi-modal, 3-D characterizations of whole mouse brains. Among these include advanced techniques such as micro-optical sectioning tomography⁶, tissue clearing^{1,7}, spatial transcriptomics⁹, and single-cell genomic profiling¹⁰, which have greatly expanded the resolution and specificity of single-cell measurements in the brain.

⁵⁹ Recent efforts by the National Institutes of Health’s Brain Research Through Advancing Innovative Neurotechnologies (BRAIN) Initiative has pushed for large-scale, international collaborative efforts to utilize these advanced single-cell techniques to create a comprehensive reference database for high-resolution transcriptomic, epigenomic, structural and imaging data of the mouse brain. This consortium of laboratories and data centers, known as the BRAIN Initiative Cell Census Network (BICCN), has archived datasets encompassing over 40 different multi-modal profiling techniques from more than 30 research groups, each providing unique characterizations of distinct cell types in the brain¹¹. Several of these modalities have been further developed into reference atlases to facilitate spatial alignment of individual brains and different data types into a common coordinate framework (CCF), thus allowing diverse single-cell information to be analyzed in an integrated manner. The most notable of these atlases is the Allen Mouse Brain Common Coordinate Framework (AllenCCFv3)¹², which serves as a primary target coordinate space for much of the work associated with the BICCN. Other atlases include modality-specific atlases^{13–15}, and spatiotemporal atlases^{16,17} for the developing mouse brain.

⁷⁴ **1.1 Mouse brain mapping**

⁷⁵ The cross-modality associations that can be learned from mapping different cell type data
⁷⁶ into a CCF is critical for improving our understanding of the complex relationships between
⁷⁷ cellular structure, morphology, and genetics in the brain. However, finding an accurate map-
⁷⁸ ping between each individual mouse brain and a CCF is a challenging and heterogeneous
⁷⁹ task. There is significant variance in the imaging protocols across different cell type data
⁸⁰ as well as different tissue processing and imaging methods which can potentially introduce
⁸¹ tissue distortion and signal differences^{18,19}. Certain modalities can have poor intensity corre-
⁸² spondence with the CCF, negatively impacting image alignment accuracy. Studies targeting
⁸³ specific regions or cell types can lead to missing anatomical correspondences. Other consid-
⁸⁴ erations include artifacts such as tissue distortion, holes, bubbles, folding, tears, and missing
⁸⁵ sections in the data that often require manual correction²⁰⁻²³. Given the diversity of these
⁸⁶ challenges, it is unlikely any single mapping approach can be generally applicable across all
⁸⁷ cell type data. Diverse, and often specialized, strategies are needed to address the unique
⁸⁸ barriers present for mapping each modality.

⁸⁹ Existing solutions to address mapping cell type data into the AllenCCFv3 falls broadly into
⁹⁰ three main categories. The first consists of integrated processing platforms that directly
⁹¹ provide mapped data to the users. These include the Allen Brain Cell Atlas²⁴ for the Allen
⁹² Reference Atlas (ARA) and associated data, the Brain Architecture Portal²⁵ for combined ex
⁹³ vivo radiology and histology data, OpenBrainMap²⁶ for connectivity data, and the Image and
⁹⁴ Multi-Morphology Pipeline²⁷ for high resolution morphology data. These platforms provide
⁹⁵ users online access to pre-processed, multi-modal cell type data that are already mapped to
⁹⁶ the AllenCCFv3. The platforms are designed such that the data is interactively manipulated
⁹⁷ by users through integrated visualization software that allow users to spatially manipulate
⁹⁸ and explore each dataset within the mapped space. While highly convenient for investigators
⁹⁹ who are interested in studying the specific modalities provided by these platforms, these
¹⁰⁰ systems can be limited in flexibility, general applicability, and public availability. As a
¹⁰¹ result, investigators often find it difficult to apply the same mapping solutions to their own
¹⁰² data.

103 The second category comprises specialized approaches specifically designed for mapping one
104 or more modalities into a CCF. These approaches use combinations of specialized manual and
105 automated processes that address specific challenges in each modality. Examples include ap-
106 proaches for mapping histology^{28–30}, magnetic resonance imaging (MRI)³⁷, micro-computed
107 tomography (microCT)^{35,37}, light-sheet fluorescence microscopy (LSFM)^{34,36–39}, fluorescence
108 micro-optical sectioning tomography (fMOST)^{15,40} and transcriptomic data^{41–43}. As special-
109 ized approaches, these techniques tend to boast higher mapping accuracy, robustness, and
110 ease of use. Conversely, their specialized designs often rely on base assumptions regard-
111 ing the data type that can make them rigid and difficult to adapt for new modalities or
112 unexpected artifacts and distortions in the data. Adapting these specialize software tools
113 to use with new data can require significant development, validation time, and engineering
114 expertise that may not be readily available for all investigators.

115 The last category consist of modular mapping approaches constructed using general im-
116 age analysis toolkits, which are software packages that include modular image processing,
117 segmentation and registration tools that have been previously developed, and validated for
118 multiple application areas. Examples of such toolkits include elastix⁴⁴, Slicer3D⁴⁵, ANTsX⁴⁶,
119 and several others which have all been applied towards mouse brain spatial mapping. The
120 main challenge, in these mouse-specific study scenarios, is that tailored pipelines often need
121 be constructed from available software components. Investigators must therefore be familiar
122 with the these tools for formulating new or adapting existing pipelines. However, in com-
123 parison to previously described specialized mapping approaches, these approaches are often
124 easier to create and prone to robustness, being typically constructed from pipeline compo-
125 nents which have been previously vetted in other contexts. In this work, we highlight such
126 mapping strategies designed using the ANTsX framework to map distinct mouse cell type
127 data with different characteristics into existing CCFs.

128 1.2 Advanced Normalization Tools (ANTsX)

129 The Advanced Normalization Tools Ecosystem (ANTsX) has been used in a number of
130 applications for mapping mouse brain data as part of core processing steps in various

¹³¹ workflows^{30,47–50}, particularly its pairwise, intensity-based image registration capabilities⁵¹
¹³² and bias field correction⁵². Historically, ANTsX development is originally based on fun-
¹³³ damental approaches to image mapping^{53–55}, particularly in the human brain, which has
¹³⁴ resulted in core contributions to the field such as the widely-used Symmetric Normalization
¹³⁵ (SyN) algorithm⁵¹. Since its development, various independent platforms have been used
¹³⁶ to evaluate ANTsX image registration capabilities in the context of different application
¹³⁷ foci which include multi-site brain MRI data⁵⁶, pulmonary CT data⁵⁷, and most recently,
¹³⁸ multi-modal brain registration in the presence of tumors⁵⁸.

¹³⁹ Apart from its registration capabilities, ANTsX comprises additional functionality such
¹⁴⁰ as template generation⁵⁹, intensity-based segmentation⁶⁰, preprocessing^{52,61}, deep learning
¹⁴¹ networks⁴⁶, and other utilities relevant to brain mapping (see Table 1). The use of the toolkit
¹⁴² has demonstrated high performance in multiple application areas (e.g., consensus labeling⁶²,
¹⁴³ brain tumor segmentation⁶³, and cardiac motion estimation⁶⁴). Importantly, ANTsX is built
¹⁴⁴ on the Insight Toolkit (ITK)⁶⁵ deriving benefit from the open-source community of scientists
¹⁴⁵ and programmers as well as providing an important resource for algorithmic development,
¹⁴⁶ evaluation, and improvement.

¹⁴⁷ With respect to mouse cell type data, ANTsX provides a comprehensive toolset which serves
¹⁴⁸ as a basis for developing modular frameworks for mapping diverse image data into com-
¹⁴⁹ mon coordinate frameworks (CCFs). Herein, we highlight its application for mapping data
¹⁵⁰ from separate BICCN projects focused on distinct data types: morphology data using flu-
¹⁵¹ orescence micro-optical sectioning tomography (fMOST), spatial transcriptomics from mul-
¹⁵² tiplexed error-robust fluorescence in situ hybridization (MERFISH) data, and time-series
¹⁵³ developmental data using light sheet fluorescence microscopy (LSFM) and magnetic reso-
¹⁵⁴ nance imaging (MRI). We describe both shared and targeted strategies developed to address
¹⁵⁵ the specific challenges of these modalities.

¹⁵⁶ 1.3 Novel ANTsX-based open-source contributions

¹⁵⁷ We introduce two novel inclusions to the ANTsX toolset that were developed as part of
¹⁵⁸ the MRI mapping and analysis pipeline for the Developmental Common Coordinate Frame-

¹⁵⁹ work (DevCCF). Consistent with previous ANTsX development, newly introduced capa-
¹⁶⁰ bilities introduced below are available through ANTsX (specifically, via R and Python
¹⁶¹ ANTsX packages), and illustrated through self-contained examples in the ANTsX tuto-
¹⁶² rial (<https://tinyurl.com/antsxtutorial>) with a dedicated GitHub repository specific to this
¹⁶³ work (<https://github.com/ntustison/ANTsXMouseBrainMapping>). To complement stan-
¹⁶⁴ dard preprocessing steps (e.g., bias correction, brain masking), additional mouse brain spe-
¹⁶⁵ cific tools have also been introduced to the ANTsX ecosystem, such as section reconstruction
¹⁶⁶ and landmark-based alignment with corresponding processing scripts (<https://github.com/>
¹⁶⁷ [dontminchenit/CCFAAlignmentToolkit](https://github.com/dontminchenit/CCFAAlignmentToolkit)).

¹⁶⁸ **1.3.1 Continuously mapping the DevCCF developmental trajectory with a ve-**
¹⁶⁹ **locity flow model**

¹⁷⁰ Recently, the Developmental Common Coordinate Framework (DevCCF) was introduced to
¹⁷¹ the mouse brain research community as a public resource¹⁶ comprising symmetric atlases of
¹⁷² multi-modal image data and anatomical segmentations defined by developmental ontology.
¹⁷³ These templates sample the mouse embryonic days E11.5, E13.5, E15.5, E18.5 and postnatal
¹⁷⁴ days P4, P14, and P56. Modalities include LSFM and at least four MRI contrasts per
¹⁷⁵ developmental stage. Anatomical parcellations are also available for each time point and
¹⁷⁶ were generated from ANTsX-based mappings of gene expression and other cell type data.
¹⁷⁷ Additionally, the P56 template was integrated with the AllenCCFv3 to further enhance the
¹⁷⁸ practical utility of the DevCCF. These processes, specifically template generation and multi-
¹⁷⁹ modal image mapping, were performed using ANTsX functionality in the presence of image
¹⁸⁰ mapping difficulties such as missing data and tissue distortion.

¹⁸¹ Given the temporal gaps in the discrete set of developmental atlases, we also provide an
¹⁸² open-source framework for inferring correspondence within the temporally continuous do-
¹⁸³ main sampled by the existing set of embryonic and postnatal atlases of the DevCCF. This
¹⁸⁴ recently developed functionality permits the generation of a diffeomorphic velocity flow trans-
¹⁸⁵ formation model⁶⁶, influenced by previous work⁶⁷. The resulting time-parameterized veloc-
¹⁸⁶ ity field spans the stages of the DevCCF where mappings between any two continuous time

¹⁸⁷ points within the span bounded by the E11.5 and P56 atlases are determined by numerical
¹⁸⁸ integration of the optimized velocity field.

¹⁸⁹ **1.3.2 Automated structural parcellations of the mouse brain**

¹⁹⁰ In contrast to the pipeline development in human data⁴⁶, limited tools exist yet to cre-
¹⁹¹ ate adequate training data for automated parcellations of the mouse brain. In addition,
¹⁹² mouse brain data acquisition often has unique issues, such as lower data quality or sampling
¹⁹³ anisotropy which limits its applicability to high resolution resources (e.g., AllenCCFv3, De-
¹⁹⁴ vCCF), specifically with respect to the corresponding granular brain parcellations derived
¹⁹⁵ from numerous hours of expert annotation leveraging multi-modal imaging resources.

¹⁹⁶ Herein, we introduce a mouse brain parcellation pipeline for multi-modal MRI comprising
¹⁹⁷ two novel deep learning components: two-shot learning brain extraction from data augmen-
¹⁹⁸ tation of two ANTsX templates generated from two open datasets^{68,69} and single-shot brain
¹⁹⁹ parcellation derived from the AllenCCFv3 labelings mapped to the corresponding DevCCF
²⁰⁰ P56 template.

²⁰¹ Although we anticipate that this pipeline will be beneficial to the research community, this
²⁰² work demonstrates more generally how one can leverage ANTsX tools and other public
²⁰³ resources for developing quantitative mouse brain morphological tools. Evaluation is per-
²⁰⁴ formed on an independent open dataset⁷⁰ comprising longitudinal acquisitions of multiple
²⁰⁵ specimens.

206 **2 Results**

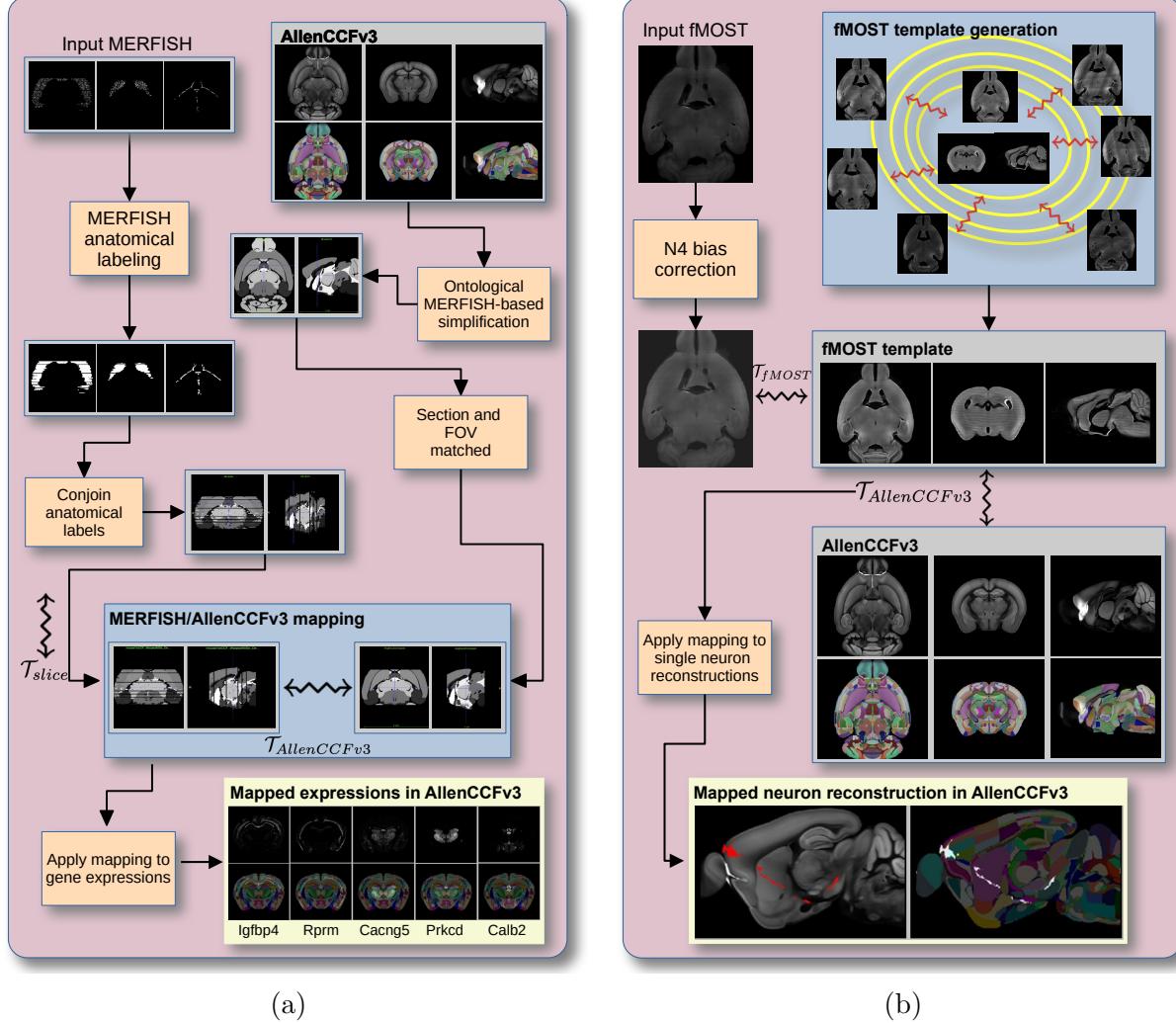


Figure 1: Diagram of the two ANTsX-based pipelines for mapping (a) MERFISH and (b)fMOST data into the space of AllenCCFv3. Each generates the requisite transforms, \mathcal{T} , to map individual images to the CCF.

207 **2.1 AllenCCFv3 brain image mapping**

208 **2.1.1 Mapping multiplexed error-robust fluorescence *in situ* hybridization
209 (MERFISH) data**

210 **Overview.** The ANTsX framework was used to develop a pipeline for mapping multiplexed
211 error-robust fluorescence *in situ* hybridization (MERFISH) spatial transcriptomic mouse

212 data onto the AllenCCFv3 (see Figure 1(a)). This pipeline, used recently in creating a
213 high-resolution transcriptomic atlas of the mouse brain⁵⁰, performs mappings by first gen-
214 erating anatomical labels from tissue related gene expressions in the MERFISH data, and
215 then spatially matching these labels to corresponding anatomical tissue parcellations in the
216 AllenCCFv3. The pipeline consists of MERFISH data specific preprocessing which includes
217 section reconstruction, mapping corresponding anatomical labels between AllenCCFv3 and
218 the spatial transcriptomic maps of the MERFISH data, and matching MERFISH sections
219 to the atlas space. Following preprocessing, two main alignment steps were performed: 1)
220 3-D global affine mapping and section matching of the AllenCCFv3 into the MERFISH data
221 and 2) 2-D global and deformable mapping between each MERFISH section and matched
222 AllenCCFv3 section. Mappings learned via each step in the pipeline are preserved and con-
223 catenated to provide point-to-point correspondence between the original MERFISH data
224 and AllenCCFv3, thus allowing individual gene expressions to be transferred into the Al-
225 lenCCFv3.

226 **Data.** MERFISH mouse brain data was acquired using a previously detailed procedure⁵⁰.
227 Briefly, a brain of C57BL/6 mouse was dissected according to standard procedures and
228 placed into an optimal cutting temperature (OCT) compound (Sakura FineTek 4583) in
229 which it was stored at -80°C. The fresh frozen brain was sectioned at 10 μm on Leica 3050
230 S cryostats at intervals of 200 μm to evenly cover the brain. A set of 500 genes were imaged
231 that had been carefully chosen to distinguish the ~5200 clusters of our existing RNAseq
232 taxonomy. For staining the tissue with MERFISH probes, a modified version of instructions
233 provided by the manufacturer was used⁵⁰. Raw MERSCOPE data were decoded using
234 Vizgen software (v231). Cells were segmented based on DAPI and PolyT staining using
235 Cellpose^{71,72}. Segmentation was performed on a median z-plane (fourth out of seven) and
236 cell borders were propagated to z-planes above and below. To assign cluster identity to each
237 cell in the MERFISH dataset, we mapped the MERFISH cells to the scRNA-seq reference
238 taxonomy.

239 **Evaluation.** Alignment of the MERFISH data into the AllenCCFv3 was qualitatively as-
240 sessed by an expert anatomist at each iteration of the registration using known correspon-

²⁴¹ dence of gene markers and their associations with the AllenCCFv3. As previously reported⁵⁰,
²⁴² further assessment of the alignment showed that, of the 554 terminal regions (gray matter
²⁴³ only) in the AllenCCFv3, only seven small subregions were missed from the MERFISH
²⁴⁴ dataset: frontal pole, layer 1 (FRP1), FRP2/3, FRP5; accessory olfactory bulb, glomerular
²⁴⁵ layer (AOBgl); accessory olfactory bulb, granular layer (AOBgr); accessory olfactory bulb,
²⁴⁶ mitral layer (AOBmi); and accessory supraoptic group (ASO).

²⁴⁷ 2.1.2 Mapping fluorescence micro-optical sectioning tomography (fMOST) data

²⁴⁸ **Overview.** We developed a pipeline for mapping fluorescence micro-optical sectioning to-
²⁴⁹ mography (fMOST) mouse brain images into the AllenCCFv3 (see Figure 1(b)). The pipeline
²⁵⁰ is adapted from previously developed frameworks for human brain mapping⁵⁹, and uses a
²⁵¹ modality specific (fMOST) average atlas to assist in the image registration and mapping.
²⁵² This approach has been well validated in human studies^{73–75}, and successfully used in other
²⁵³ mouse data^{12,15,34}. Briefly, we construct an intensity- and shape-based average fMOST atlas
²⁵⁴ using 30 fMOST images to serve as an intermediate registration target for mapping fMOST
²⁵⁵ images from individual specimens into the AllenCCFv3. Preprocessing steps include down-
²⁵⁶ sampling to match the $25\mu m$ isotropic AllenCCFv3, acquisition-based stripe artifact removal,
²⁵⁷ and inhomogeneity correction⁵². Preprocessing also includes a single annotation-driven reg-
²⁵⁸ istration to establish a canonical mapping between the fMOST atlas and the AllenCCFv3.
²⁵⁹ This step allows us to align expert determined landmarks to accurately map structures
²⁶⁰ with large morphological differences between the modalities, which are difficult to address
²⁶¹ using standard approaches. Once this canonical mapping is established, standard intensity-
²⁶² based registration is used to align each new fMOST image to the fMOST specific atlas.
²⁶³ This mapping is concatenated with the canonical fMOST atlas-to-AllenCCFv3 mapping to
²⁶⁴ further map each individual brain into the latter without the need to generate additional
²⁶⁵ landmarks. Transformations learned through this mapping can be applied to single neuron
²⁶⁶ reconstructions from the fMOST images to evaluate neuronal distributions across different
²⁶⁷ specimens into the AllenCCFv3 for the purpose of cell census analyses.

²⁶⁸ **Data.** The high-throughput and high-resolution fluorescence micro-optical sectioning to-

269 mography (fMOST)^{76,77} platform was used to image 55 mouse brains containing gene-defined
270 neuron populations, with sparse transgenic expression^{78,79}. In short, the fMOST imaging
271 platform results in 3-D images with voxel sizes of $0.35 \times 0.35 \times 1.0 \mu\text{m}^3$ and is a two-channel
272 imaging system where the green channel displays the green fluorescent protein (GFP) labeled
273 neuron morphology and the red channel is used to visualize the counterstained propidium
274 iodide cytoarchitecture. The spatial normalizations described in this work were performed
275 using the red channel, which offered higher tissue contrast for alignment, although other
276 approaches are possible including multi-channel registration.

277 **Evaluation.** Evaluation of the canonical fMOST atlas to Allen CCFv3 mapping was per-
278 formed via quantitative comparison at each step of the registration and qualitative assess-
279 ment of structural correspondence after alignment by an expert anatomist. Dice values were
280 generated for the following structures: whole brain, 0.99; fimbria, 0.91; habenular com-
281 missure, 0.63; posterior choroid plexus, 0.93; anterior choroid plexus, 0.96; optic chiasm,
282 0.77; caudate putamen, 0.97. Similar qualitative assessment was performed for each fMOST
283 specimen including the corresponding neuron reconstruction data.

284 2.2 Continuously mapping the DevCCF developmental trajectory 285 with a velocity flow model

286 The DevCCF is an openly accessible resource for the mouse brain research community¹⁶. It
287 consists of multi-modal MRI and LSFM symmetric ANTsX-generated templates⁵⁹ sampling
288 the mouse brain developmental trajectory, specifically the embryonic (E) and postnatal (P)
289 days E11.5, E13.5, E15.5, E18.5 P4, P14, and P56. Each template space includes structural
290 labels defined by a developmental ontology. Its utility is also enhanced by a coordinated
291 construction with AllenCCFv3. Although this work represents a significant contribution,
292 the gaps between time points potentially limit its applicability which could be addressed
293 through the development of the ability to map not only between time points but also within
294 and across time points.

295 To continuously generate transformations between the different stages of the DevCCF atlases,

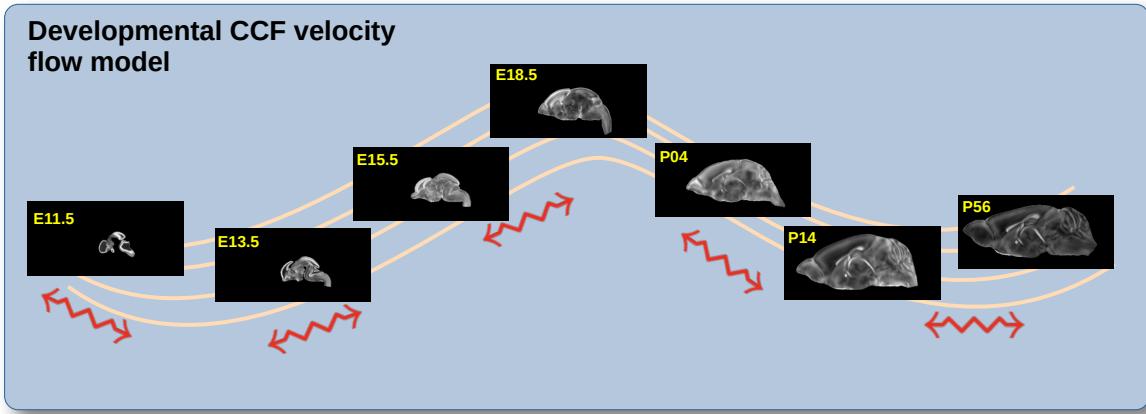


Figure 2: The spatial transformation between any two time points within the continuous DevCCF longitudinal developmental trajectory is available through the use of ANTsX functionality for generating a velocity flow model.

we developed a general velocity flow model approach which we apply to DevCCF-derived data. We also introduce this functionality into both the ANTsR and ANTsPy packages (for the latter, see `ants.fit_time_varying_transform_to_point_sets(...)`) for potential application to this and other analogous scenarios (e.g., modeling the cardiac and respiratory cycles). ANTsX, being built on top of ITK, uses an ITK image data structure for the 4-D velocity field where each voxel contains the x , y , z components of the field at that point.

2.2.1 Data

Labeled annotations are available as part of the original DevCCF and reside in the space of each developmental template which range in resolution from $31.5 - 50\mu\text{m}$. Across all atlases, the total number of labeled regions exceeds 2500. From these labels, a common set of 26 labels (13 per hemisphere) across all atlases were used for optimization and evaluation. These simplified regions include: terminal hypothalamus, subpallium, pallium, peduncular hypothalamus, prosomere, prosomere, prosomere, midbrain, prepontine hindbrain, pontine hindbrain, pontomedullary hindbrain, medullary hindbrain, and tracts (see Figure 3).

Prior to velocity field optimization, all data were rigidly transformed to DevCCF P56 using the centroids of the common label sets. In order to determine the landmark correspondence

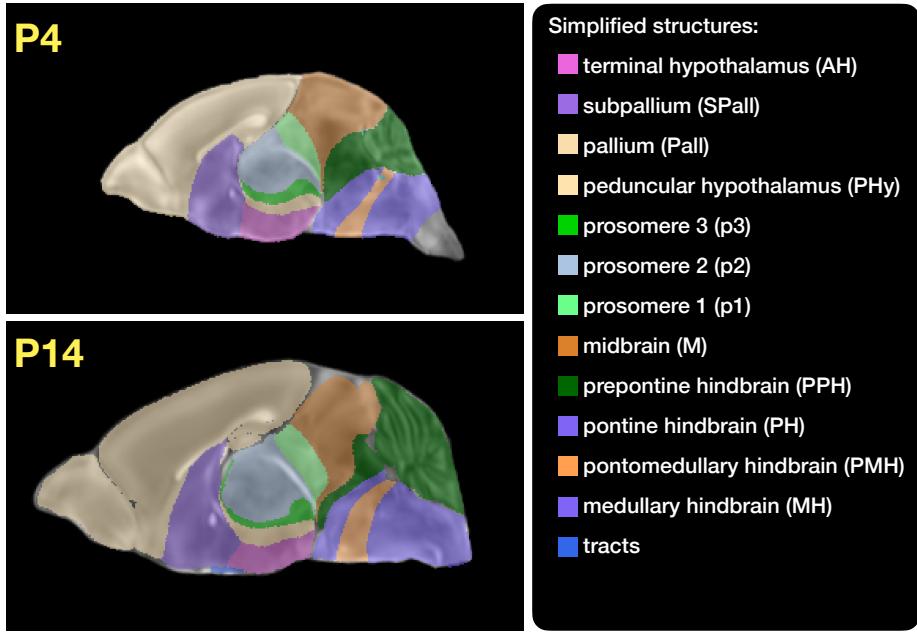


Figure 3: Annotated regions representing common labels across developmental stages which are illustrated for both P4 and P14.

312 across DevCCF stages, the multi-metric capabilities of `ants.registration(...)` were used.
 313 Instead of performing intensity-based pairwise registration directly on these multi-label im-
 314 ages, each label was used to construct a separate fixed and moving image pair resulting in a
 315 multi-metric registration optimization scenario involving 24 binary image pairs (each label
 316 weighted equally) for optimizing diffeomorphic correspondence between neighboring time
 317 point atlases using the mean squares metric and the symmetric normalization transform⁵¹.
 318 To generate the set of common point sets across all seven developmental atlases, the label
 319 boundaries and whole regions were sampled in the P56 atlas and then propagated to each
 320 atlas using the transformations derived from the pairwise registrations. We selected a sam-
 321 pling rate of 10% for the contour points and 1% for the regional points for a total number
 322 of points being per atlas being 173303 ($N_{contour} = 98151$ and $N_{region} = 75152$). Regional
 323 boundary points were weighted twice as those of non-boundary points during optimization.

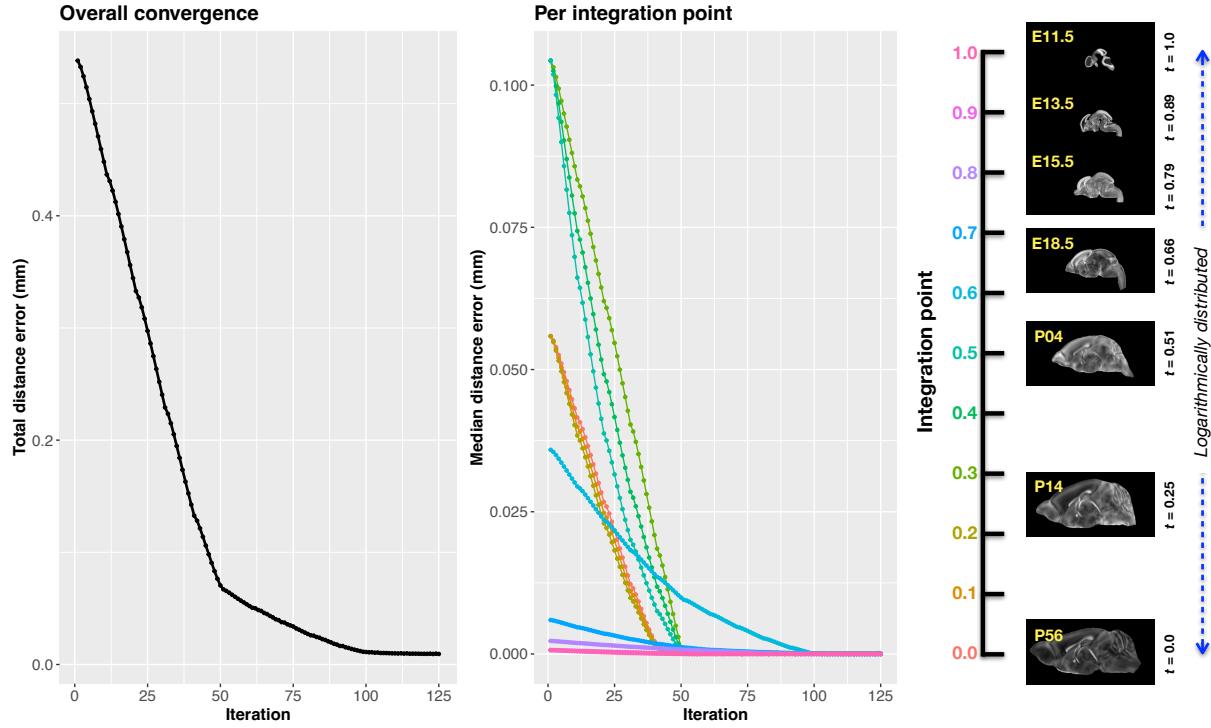


Figure 4: Convergence of the optimization of the velocity field for describing the transformation through the developmental stages from E11.5 through P56. Integration points in diagram on the right are color-coordinated with the center plot and placed in relation to the logarithmically situated temporal placement of the individual DevCCF atlases.

³²⁴ 2.2.2 Velocity field optimization

³²⁵ The velocity field was optimized using the input composed of the seven corresponding point
³²⁶ sets and their associated weight values, the selected number of integration points for the
³²⁷ velocity field ($N = 11$), and the parameters defining the geometry of the spatial dimensions
³²⁸ of the velocity field. Thus, the optimized velocity field described here is of size [256, 182, 360]
³²⁹ ($50\mu\text{m}$ isotropic) $\times 11$ integration points for a total compressed size of a little over 2 GB.

³³⁰ This choice represented weighing the trade-off between tractability, portability, and accuracy.
³³¹ However, all data and code to reproduce the results described are available in the dedicated
³³² GitHub repository.

³³³ The normalized time point scalar value for each atlas/point-set in the temporal domains $[0, 1]$
³³⁴ was also defined. Given the increasingly larger gaps in the postnatal time point sampling,
³³⁵ we made two adjustments. Based on known mouse brain development, we used 28 days for

336 the P56 data. We then computed the log transform of the adjusted set of time points prior
337 to normalization between 0 and 1 (see the right side of Figure 4). This log transform, as
338 part of the temporal normalization, significantly improves the temporal spacing of data.

339 The maximum number of iterations was set to 200 with each iteration taking approximately
340 six minutes on a 2020 iMac (processor, 3.6 GHz 10-Core Intel Core i9; memory, 64 GB 2667
341 MHz DDR4) At each iteration we looped over the 11 integration points. At each integration
342 point, the velocity field estimate was updated by warping the two immediately adjacent
343 point sets to the integration time point and determining the regularized displacement field
344 between the two warped point sets. As with any gradient-based descent algorithm, this field
345 was multiplied by a small step size ($\delta = 0.2$) before adding to the current velocity field.
346 Convergence is determined by the average displacement error over each of the integration
347 points. As can be seen in the left panel of Figure 4, convergence occurred around 125
348 iterations when the average displacement error over all integration points is minimized. The
349 median displacement error at each of the integration points also trends towards zero but at
350 different rates.

351 2.2.3 The velocity flow transformation model

352 Once optimized, the resulting velocity field can be used to generate the deformable transform
353 between any two continuous points within the time interval bounded by E11.5 and P56. As
354 a demonstration, in Figure 5, we transform each atlas to the space of every other atlas
355 using the DevCCF transform model. Additionally, one can use this transformation model
356 to construct virtual templates in the temporal gaps of the DevCCF. Given an arbitrarily
357 chosen time point within the normalized time point interval, the existing adjacent DevCCF
358 atlases on either chronological side can be warped to the desired time point. A subsequent
359 call to one of the ANTsX template building functions then permits the construction of the
360 template at that time point. In Figure 6, we illustrate the use of the DevCCF velocity flow
361 model for generating two such virtual templates for two arbitrary time points. Note that
362 both of these usage examples can be found in the GitHub repository previously given.

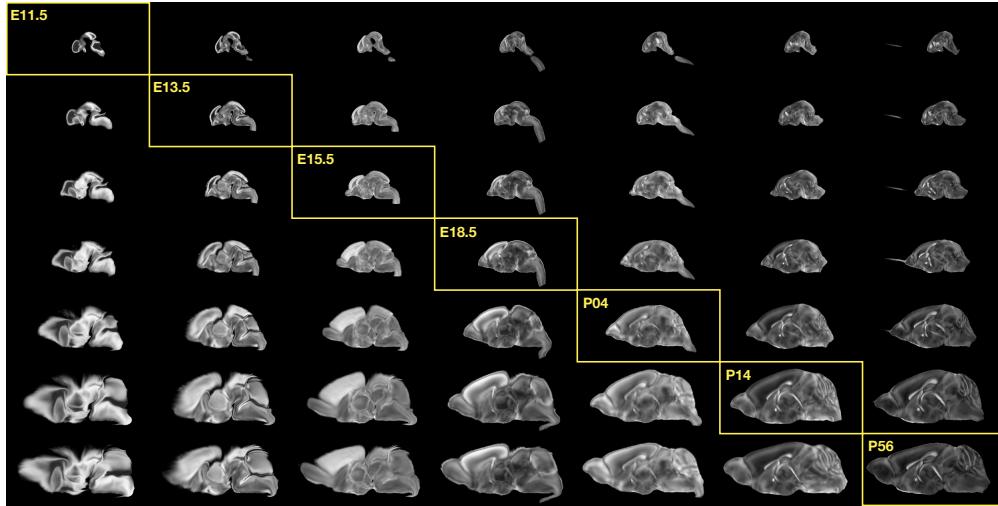


Figure 5: Mid-sagittal visualization of the effects of the transformation model in warping every developmental stage to the time point of every other developmental stage. The original images are located along the diagonal. Columns correspond to the warped original image whereas the rows represent the reference space to which each image is warped.

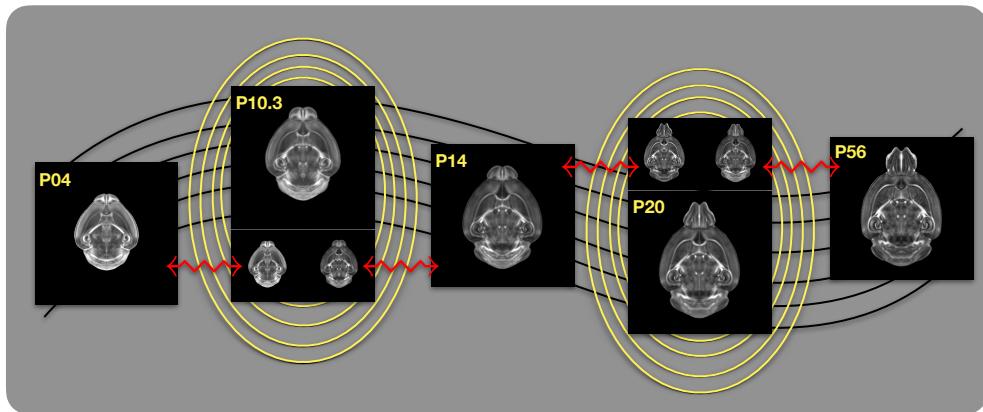


Figure 6: Illustration of the use of the velocity flow model for creating virtual templates at continuous time points not represented in one of the existing DevCCF time points. For example, FA templates at time point P10.3 and P20 can be generated by warping the existing temporally adjacent developmental templates to the target time point and using those images in the ANTsX template building process.

363 2.3 Automated structural parcellations of the mouse brain

364 Brain parcellation strategies for the mouse brain are pivotal for understanding the complex
365 organization and function of murine nervous system⁸⁰. By dividing the brain into distinct
366 regions based on anatomical, physiological, or functional characteristics, researchers can
367 investigate specific areas in isolation and identify their roles in various behaviors and pro-

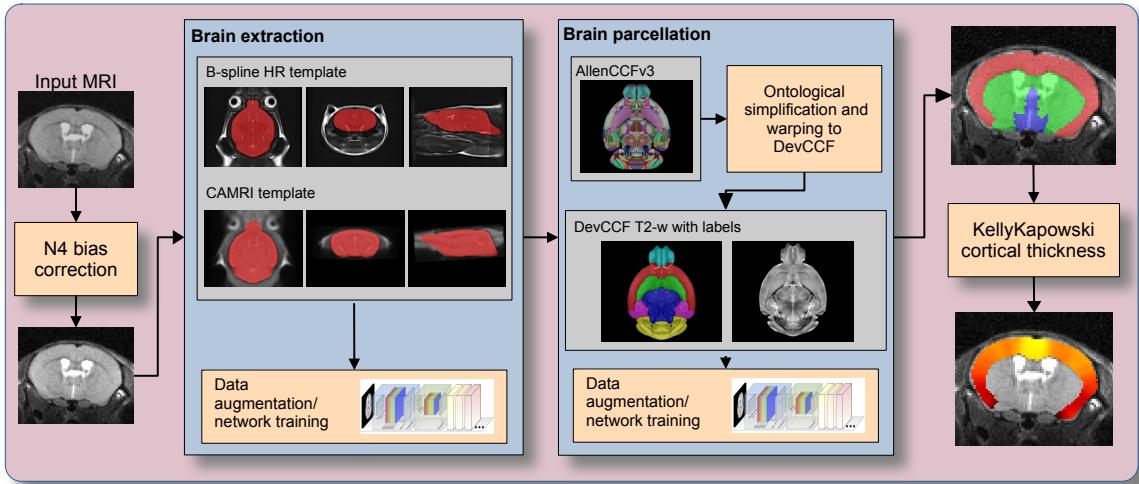


Figure 7: The mouse brain cortical parcellation pipeline integrating two deep learning components for brain extraction and brain parcellation prior to estimating cortical labels. Both deep learning networks rely heavily on aggressive data augmentation on templates built from open data and provide an outline for further refinement and creating alternative parcellations for tailored research objectives. Possible applications include voxelwise cortical thickness measurements.

cesses. For example, such parcellation schemes can help elucidate the spatial distribution of gene expression patterns⁸¹ as well as identify functional regions involved in specific cognitive tasks⁸².

Although deep learning techniques have been used to develop useful parcellation tools for human brain research (e.g., SynthSeg⁸³, ANTsXNet⁴⁶), analogous development for the mouse brain is limited. In addition, mouse data is often characterized by unique imaging issues such as extreme anisotropic sampling which are often in sharp contrast to the high resolution template-based resources available within the community, e.g., AllenCCFv3 and DevCCF. We demonstrate how one can use the ANTsX tools to develop a complete mouse brain structural morphology pipeline as illustrated in Figure 7 and detailed below.

2.3.1 Few-shot mouse brain extraction network

In order to create a generalized mouse brain extraction network, we built whole-head templates from two publicly available datasets. The Center for Animal MRI (CAMRI) dataset⁶⁸ from the University of North Carolina at Chapel Hill consists of 16 T2-w MRI volumes of

382 voxel resolution $0.16 \times 0.16 \times 0.16 mm^3$. The second high-resolution dataset⁶⁹ comprises
383 88 specimens each with three spatially aligned canonical views with in-plane resolution of
384 $0.08 \times 0.08 mm^2$ with a slice thickness of $0.5 mm$. These three orthogonal views were used
385 to reconstruct a single high-resolution volume per subject using a B-spline fitting algorithm
386 available in ANTsX⁸⁴.

387 From these two datasets, two ANTsX templates⁵⁹ were generated. Bias field simulation,
388 intensity histogram warping, noise simulation, random translation and warping, and random
389 anisotropic resampling in the three canonical directions were used for data augmentation
390 in training an initial T2-w brain extraction network. This network was posted and the
391 corresponding functionality was immediately made available within ANTsXNet, similar to
392 our previous contributions to the community.

393 User interest led to a GitHub inquiry regarding possible study-specific improvements (<https://github.com/ANTsX/ANTsPyNet/issues/133>). This interaction led to the offering of a
394 user-made third template and extracted brain mask generated from T2-w ex-vivo data with
395 isotropic spacing of $0.08 mm$ in each voxel dimension. This third template, in conjunction
396 with the other two, were used with the same aggressive data augmentation to refine the
397 network weights which were subsequently posted and made available through ANTsPyNet
398 using the function `antspynet.mouse_brain_extraction(...)`.

400 2.3.2 Single-shot mouse brain parcellation network

401 AllenCCFv3 and its hierarchical ontological labeling, along with the DevCCF, provides the
402 necessary data for developing a tailored structural parcellation network for multi-modal
403 imaging. The `allensdk` Python library permits the creation of any gross parcellation based
404 on the AllenCCFv3 ontology. Specifically, using `allensdk` we coalesced the labels to the
405 following six major structures: cerebral cortex, cerebral nuclei, brain stem, cerebellum, main
406 olfactory bulb, and hippocampal formation. This labeling was mapped to the P56 component
407 of the DevCCF for use with the T2-w template component.

408 The T2-w P56 DevCCF and labelings, in conjunction with the data augmentation
409 described previously for brain extraction, were used to train the proposed brain

410 parcellation network. This is available in ANTsXNet (e.g. in ANTsPyNet using
 411 `antspynet.mouse_brain_parcellation(...)`). Note that other brain parcellation
 412 networks have also been trained using alternative regions and parcellation schemes and are
 413 available in the same ANTsXNet functionality. One usage note is that the data augmenta-
 414 tion used to train the network permits a learned interpolation in 0.08 mm isotropic space.
 415 Since the training data is isotropic and data augmentation includes downsampling in the
 416 canonical directions, each of the two networks learns mouse brain-specific interpolation such
 417 that one can perform prediction on thick-sliced images, as, for example, in these evaluation
 418 data, and return isotropic probability and thickness maps (a choice available to the user).
 419 This permits robust cortical thickness estimation even in the case of anisotropic data (see
 420 `antspynet.mouse_cortical_thickness(...)`).

421 2.3.3 Evaluation

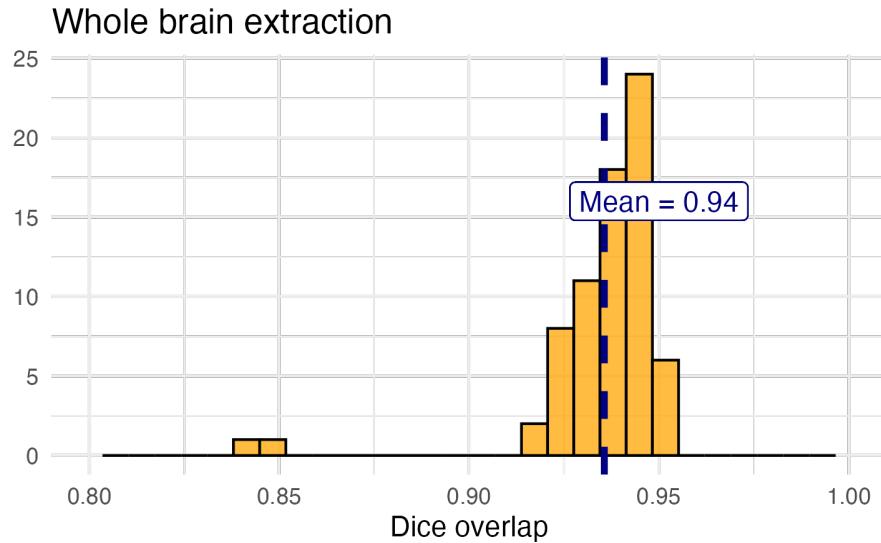
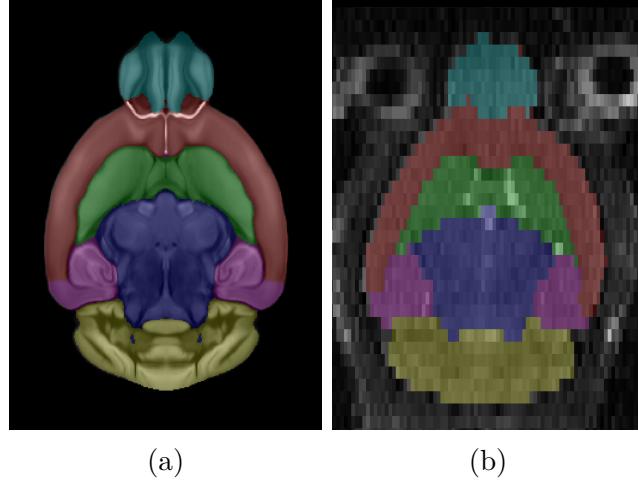


Figure 8: Evaluation of the ANTsX mouse brain extraction on an independent, publicly available dataset consisting of 12 specimens \times 7 time points = 84 total images. Dice overlap comparisons with the user-generated brain masks provide good agreement with the automated results from the brain extraction network.

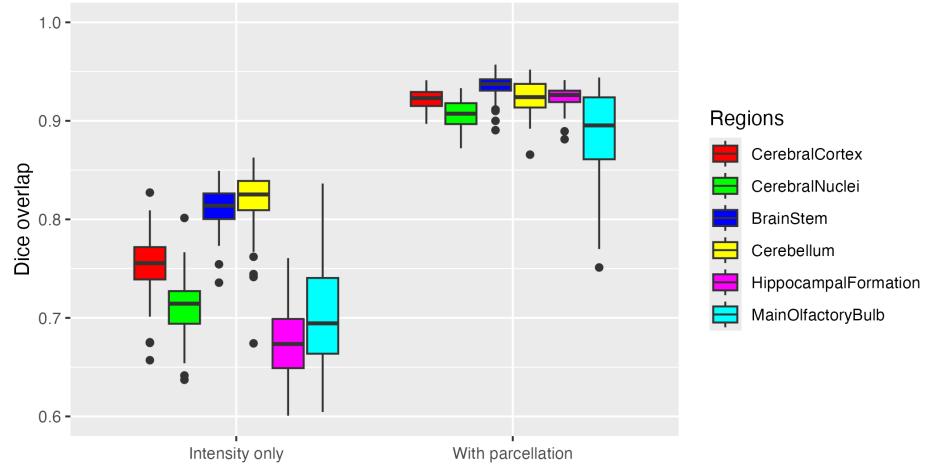
422 For evaluation, we used an additional publicly available dataset⁷⁰ that is completely inde-
 423 pendent from the data used in training the brain extraction and parcellation networks. Data
 424 includes 12 specimens each imaged at seven time points (Day 0, Day 3, Week 1, Week 4,



(a)

(b)

Normalization to AllenCCFv3



(c)

Figure 9: Evaluation of the ANTsX mouse brain parcellation on the same dataset. (a) T2-w DevCCF P56 with the described parcellation consisting of the cerebral cortex, nuclei, brain stem, cerebellum, main olfactory bulb, and hippocampal formation. (b) Sample subject (NR5 Day 0) with the proposed deep learning-based segmentation. (c) Dice overlap for comparing the regional alignments between registration using intensity information only and using intensity with the given parcellation scheme.

425 Week 8, Week 20) with in-house-generated brain masks for a total of 84 images. Spacing is
426 anisotropic with an in-plane resolution of $0.1 \times 0.1 mm^2$ and a slice thickness of $0.5 mm$.

427 Figure 8 summarizes the whole brain overlap between the provided segmentations for all
428 84 images and the results of applying the proposed network. Also, since mapping to the
429 AllenCCFv3 atlas is crucial for many mouse studies, we demonstrate the utility of the second
430 network by leveraging the labeled regions to perform anatomically-explicit alignment using
431 ANTsX multi-component registration instead of intensity-only registration. For these data,
432 the whole brain extraction demonstrates excellent performance across the large age range.
433 And although the intensity-only image registration provides adequate alignment, intensity
434 with the regional parcellations significantly improves those measures.

435 **3 Discussion**

436 The diverse mouse brain cell type profiles gathered through BICCN and associated efforts
437 provides a rich multi-modal resource to the research community. However, despite significant
438 progress, optimized leveraging of these valuable resources is ongoing. A central component
439 to data integration is accurately mapping novel cell type data into CCFs for subsequent
440 processing and analysis. To meet these needs, tools for mapping mouse cell type data must
441 be both generally accessible to a wide audience of investigators, and capable of handling
442 distinct challenges unique to each data type. In this work, we described modular ANTsX-
443 based pipelines developed to address the needs of three BICCN projects that cover distinct
444 cell type data, including spatial transcriptomic, morphological, and developmental data. We
445 highlighted how a modular toolbox like ANTsX can be tailored to address problems unique
446 to each modality through leveraging a variety of ready-to-use powerful tools that have been
447 previously validated in multiple application scenarios.

448 Our MERFISH pipeline provides an example of how to map high-resolution spatial transcripto-
449 mic data into the AllenCCFv3. While the techniques employed for mapping the sectioned
450 data can be generally applicable to spatially transform other serial histology images, much
451 of the pipeline was designed to specifically address known alignment challenges in the MER-
452 FISH data. Thus pipeline shows how general ANTsX tools can be adapted to target highly
453 specialized problems in mouse cell type data.

454 In contrast to the MERFISH pipeline, our fMOST pipeline was designed to be a more general
455 solution that can be employed in other modalities. The pipeline primarily uses previously
456 developed ANTsX preprocessing and atlasing tools to map fMOST data into the AllenCCFv3.
457 The key component of the pipeline is the use of a fMOST-specific average shape and intensity
458 atlas to most effectively address image registration in this context. The mapping between
459 the fMOST atlas is generated once and reused for each new fMOST image. Lastly, ANTsX
460 provides point set transformation tools to allow the mappings found through the pipeline to
461 be directly applied to associated single-cell reconstructions from the fMOST data to study
462 neuronal morphology.

463 The pipeline for continuously mapping the DevCCF data is also available in ANTsX and
464 is generally applicable for spatio-temporal mapping. With specific application to the De-
465 vCCF, despite the significant expansion of available developmental age templates beyond
466 what existed previously, there are still temporal gaps in the DevCCF which can be poten-
467 tially sampled by future research efforts. However, pioneering work involving time-varying
468 diffeomorphic transformations allow us to continuously situate the existing templates within
469 a velocity flow model. This allows one to determine the diffeomorphic transformation from
470 any one temporal location to any other temporal location within the time span defined by
471 the temporal limits of the DevCCF. This functionality is built on multiple ITK components
472 including the B-spline scattered data approximation technique for field regularization and
473 velocity field integration. This velocity field model permits intra-template comparison and
474 the construction of virtual templates where a template can be estimated at any continuous
475 time point within the temporal domain. This novel application can potentially enhance our
476 understanding of intermediate developmental stages.

477 We also presented a mouse brain morphological pipeline for brain extraction and brain
478 parcellation using single-shot and few-shot learning with aggressive data augmentation. This
479 approach attempts to circumvent (or at least minimize) the typical requirement of large
480 training datasets as with the human ANTsX pipeline analog. However, even given our initial
481 success on independent data, we anticipate that refinements will be necessary. Given that the
482 ANTsX toolkit is a dynamic effort undergoing continual improvement, we manually correct
483 cases that fail and use them for future training and refinement of network weights as we have
484 done for our human-based networks. And, as demonstrated, we welcome contributions from
485 the community for improving these approaches which, generally, provide a way to bootstrap
486 training data for manual refinement and future generation of more accurate deep learning
487 networks in the absence of other applicable tools.

488 The ANTsX ecosystem is a powerful framework that has demonstrated applicability to di-
489 verse cell type data in the mouse brain. This is further evidenced by the many software
490 packages that use various ANTsX components in their own mouse-specific workflows. The
491 extensive functionality of ANTsX makes it possible to create complete processing pipelines

⁴⁹² without requiring the integration of multiple packages or lengthy software development.
⁴⁹³ These open-source components not only perform well but are available across multiple plat-
⁴⁹⁴ forms which facilitates the construction of tailored pipelines for individual study solutions.
⁴⁹⁵ These components are also supported by years of development not only by the ANTsX
⁴⁹⁶ development team but by the larger ITK community.

497 **4 Methods**

498 The following methods are all available as part of the ANTsX ecosystem with analogous
499 elements existing in both ANTsR (ANTs in R) and ANTsPy (ANTs in Python) with an
500 ANTs/ITK C++ core. However, most of the development for the work described below was
501 performed using ANTsPy. For equivalent calls in ANTsR, please see the ANTsX tutorial at
502 <https://tinyurl.com/antsxtutorial>.

503 **4.1 General ANTsX utilities**

504 Although they focus on distinct data types, the three pipelines presented share common
505 components that are generally applicable when mapping mouse cell type data. These include,
506 addressing intensity biases and noise in the data, image registration to solve the mapping,
507 creating custom templates and atlases from the data, and visualization of the results. Table
508 1 provides a brief summary of key general functionalities in ANTsX for addressing these
509 challenges.

510 **4.1.1 Preprocessing: bias field correction and denoising**

511 Bias field correction and image denoising are standard preprocessing steps in improving over-
512 all image quality in mouse brain images. The bias field, a gradual spatial intensity variation
513 in images, can arise from various sources such as magnetic field inhomogeneity or acquisition
514 artifacts, leading to distortions that can compromise the quality of brain images. Correct-
515 ing for bias fields ensures a more uniform and consistent representation of brain structures,
516 enabling more accurate quantitative analysis. Additionally, brain images are often suscep-
517 tible to various forms of noise, which can obscure subtle features and affect the precision
518 of measurements. Denoising techniques help mitigate the impact of noise, enhancing the
519 signal-to-noise ratio and improving the overall image quality. The well-known N4 bias field
520 correction algorithm⁵² has its origins in the ANTs toolkit which was implemented and intro-
521 duced into the ITK toolkit, i.e. `ants.n4_bias_field_correction(...)`. Similarly, ANTsX

Table 1: Sampling of ANTsX functionality

<i>ANTsPy: Preprocessing</i>	
bias field correction	<code>n4_bias_field_correction(...)</code>
image denoising	<code>denoise_image(...)</code>
<i>ANTsPy: Registration</i>	
image registration	<code>registration(...)</code>
image transformation	<code>apply_transforms(...)</code>
template generation	<code>build_template(...)</code>
landmark registration	<code>fit_transform_to_paired_points(...)</code>
time-varying landmark reg.	<code>fit_time_varying_transform_to_point_sets(...)</code>
integrate velocity field	<code>integrate_velocity_field(...)</code>
invert displacement field	<code>invert_displacement_field(...)</code>
<i>ANTsPy: Segmentation</i>	
MRF-based segmentation	<code>atropos(...)</code>
Joint label fusion	<code>joint_label_fusion(...)</code>
diffeomorphic thickness	<code>kelly_kapowski(...)</code>
<i>ANTsPy: Miscellaneous</i>	
Regional intensity statistics	<code>label_stats(...)</code>
Regional shape measures	<code>label_geometry_measures(...)</code>
B-spline approximation	<code>fit_bspline_object_to_scattered_data(...)</code>
Visualize images and overlays	<code>plot(...)</code>
<i>ANTsPyNet: Mouse-specific</i>	
brain extraction	<code>mouse_brain_extraction(...modality="t2"...)</code>
brain parcellation	<code>mouse_brain_parcellation(...)</code>
cortical thickness	<code>mouse_cortical_thickness(...)</code>
super resolution	<code>mouse_histology_super_resolution(...)</code>

ANTsX provides state-of-the-art functionality for processing biomedical image data. Such tools, including deep learning networks, support a variety of mapping-related tasks. A more comprehensive listing of ANTsX tools with self-contained R and Python examples is provided as a gist page on GitHub (<https://tinyurl.com/antsxtutorial>).

522 contains an implementation of a well-performing patch-based denoising technique⁶¹ and is
523 also available as an image filter to the ITK community, `ants.denoise_image(...)`.

524 **4.1.2 Image registration**

525 The ANTs registration toolkit is a complex framework permitting highly tailored solutions
526 to pairwise image registration scenarios⁸⁵. It includes innovative transformation models
527 for biological modeling^{51,67} and has proven capable of excellent performance^{56,86}. Vari-
528 ous parameter sets targeting specific applications have been packaged with the different
529 ANTsX packages, specifically ANTs, ANTsPy, and ANTsR⁴⁶. In ANTsPy, the function
530 `ants.registration(...)` is used to register a pair of images or a pair of image sets where
531 `type_of_transform` is a user-specified option that invokes a specific parameter set. For ex-
532 ample `type_of_transform='antsRegistrationSyNQuick[s]'` encapsulates an oft-used pa-
533 rameter set for quick registration whereas `type_of_transform='antsRegistrationSyN[s]'`
534 is a more aggressive alternative. Transforming images using the derived transforms is per-
535 formed via the `ants.apply_transforms(...)` function.

536 Initially, linear optimization is initialized with center of (intensity) mass alignment typically
537 followed by optimization of both rigid and affine transforms using the mutual information
538 similarity metric. This is followed by diffeomorphic deformable alignment using symmetric
539 normalization (SyN) with Gaussian⁵¹ or B-spline regularization⁶⁷ where the forward trans-
540 form is invertible and differentiable. The similarity metric employed at this latter stage is
541 typically either neighborhood cross-correlation or mutual information. Note that these pa-
542 rameter sets are robust to input image type (e.g., light sheet fluorescence microscopy, Nissl
543 staining, and the various MRI modalities) and are adaptable to mouse image geometry and
544 scaling. Further details can be found in the various documentation sources for these ANTsX
545 packages.

546 **4.1.3 Template generation**

547 ANTsX provides functionality for constructing templates from a set (or multi-modal sets) of
548 input images as originally described⁵⁹ and recently used to create the DevCCF templates¹⁶.

549 An initial template estimate is constructed from an existing subject image or a voxelwise
550 average derived from a rigid pre-alignment of the image population. Pairwise registration
551 between each subject and the current template estimate is performed using the Symmetric
552 Normalization (SyN) algorithm⁵¹. The template estimate is updated by warping all subjects
553 to the space of the template, performing a voxelwise average, and then performing a “shape
554 update” of this latter image by warping it by the average inverse deformation, thus yielding
555 a mean image of the population in terms of both intensity and shape. The corresponding
556 ANTsPy function is `ants.build_template(...)`.

557 4.1.4 Visualization

558 To complement the well-known visualization capabilities of R and Python, e.g., `ggplot2`
559 and `matplotlib`, respectively, image-specific visualization capabilities are available in the
560 `ants.plot(...)` function (Python). These are capable of illustrating multiple slices in
561 different orientations with other image overlays and label images.

562 4.2 Mapping fMOST data to AllenCCFv3

563 4.2.1 Preprocessing

- 564 • *Downsampling*. The first challenge when mapping fMOST images into the AllenCCFv3
565 is addressing the resolution scale of the data. Native fMOST data from an individual
566 specimen can range in the order of terabytes, which leads to two main problems. First,
567 volumetric registration methods (particularly those estimating local deformation) have
568 high computational complexity and typically cannot operate on such high-resolution
569 data under reasonable memory and runtime constraints. Second, the resolution of
570 the AllenCCFv3 atlas is much lower than the fMOST data, thus the mapping process
571 will cause much of the high-resolution information in the fMOST images to be lost
572 regardless. Thus, we perform a cubic B-spline downsampling of the fMOST data to
573 reduce the resolution of each image to match the isotropic $25 \mu\text{m}$ voxel resolution of the
574 AllenCCFv3 intensity atlas using `ants.resample_image(...)`. An important detail

575 to note is that while the fMOST images and atlas are downsampled, the mapping
576 learned during the registration is assumed to be continuous. Thus, after establishing
577 the mapping to the AllenCCFv3, we can interpolate the learned mapping and apply it
578 directly to the high-resolution native data directly to transform any spatially aligned
579 data (such as the single-cell neuron reconstructions) into the AllenCCFv3.

- 580 • *Stripe artifact removal.* Repetitive pattern artifacts are a common challenge in fMOST
581 imaging where inhomogeneity during the cutting and imaging of different sections can
582 leave stripes of hyper- and hypo-intensity across the image. These stripe artifacts
583 can be latched onto by the registration algorithm as unintended features that are
584 then misregistered to non-analogous structures in the AllenCCFv3. We address these
585 artifacts by fitting a 3-D bandstop (notch) filter to target the frequency of the stripe
586 patterns and removing them prior to the image registration.
- 587 • *Inhomogeneity correction.* Regional intensity inhomogeneity can also occur within
588 and between sections in fMOST imaging due to staining or lighting irregularity during
589 acquisition. Similar to stripe artifacts, intensity gradients due to inhomogeneity
590 can be misconstrued as features during the mapping and result in matching of non-
591 corresponding structures. Our pipeline addresses these intensity inhomogeneities using
592 N4 bias field correction⁵², `ants.n4_bias_field_correction(...)`.

593 4.2.2 Steps for spatial normalization to AllenCCFv3

- 594 1. *Average fMOST atlas as an intermediate target.* Due to the preparation of the mouse
595 brain for fMOST imaging, the resulting structure in the mouse brain has several large
596 morphological deviations from the AllenCCFv3 atlas. Most notable of these is an en-
597 largement of the ventricles, and compression of cortical structures. In addition, there is
598 poor intensity correspondence for the same anatomic features due to intensity dissim-
599 ilarity between imaging modalities. We have found that standard intensity-base reg-
600 istration is insufficient to capture the significant deformations required to map these
601 structures correctly into the AllenCCFv3. We address this challenge in ANTsX by
602 using explicitly corresponding parcellations of the brain, ventricles and surrounding

603 structures to directly recover these large morphological differences. However, generating
604 these parcellations for each individual mouse brain is a labor-intensive task. Our
605 solution is to create an average atlas whose mapping to AllenCCFv3 encapsulates these
606 large morphological differences to serve as an intermediate registration point. This has
607 the advantage of only needing to generate one set of corresponding annotations which
608 is used to register between the two atlas spaces. New images are first aligned to the
609 fMOST average atlas, which shares common intensity and morphological features and
610 thus can be achieved through standard intensity-based registration.

611 2. *Average fMOST atlas construction.* An intensity and shape-based contralaterally sym-
612 metric average of the fMOST image data is constructed from 30 images and their
613 contralateral flipped versions. We ran three iterations of the atlas construction using
614 the default settings. Additional iterations (up to six) were evaluated and showed mini-
615 mal changes to the final atlas construction, suggesting a convergence of the algorithm.

616 3. *fMOST atlas to AllenCCFv3 alignment.* Alignment between the fMOST average atlas
617 and AllenCCFv3 was performed using a one-time annotation-driven approach. Label-
618 to-label registration is used to align 7 corresponding annotations in both atlases in
619 the following: 1) brain mask/ventricles, 2) caudate/putamen, 3) fimbria, 4) posterior
620 choroid plexus, 5) optic chiasm, 6) anterior choroid plexus, and 7) habenular com-
621 missure. The alignments were performed sequentially, with the largest, most relevant
622 structures being aligned first using coarse registration parameters, followed by other
623 structures using finer parameters. This coarse-to-fine approach allows us to address
624 large morphological differences (such as brain shape and ventricle expansion) at the
625 start of registration and then progressively refine the mapping using the smaller struc-
626 tures. The overall ordering of these structures was determined manually by an expert
627 anatomist, where anatomical misregistration after each step of the registration was
628 evaluated and used to determine which structure should be used in the subsequent it-
629 eration to best improve the alignment. The transformation from this one-time expert-
630 guided alignment is preserved and used as the canonical fMOST atlas to AllenCCFv3
631 mapping in the pipeline.

- 632 4. *Alignment of individual fMOST mouse brains.* The canonical transformation between
633 the fMOST atlas and AllenCCFv3 greatly simplifies the registration of new individ-
634 ual fMOST mouse brains into the AllenCCFv3. Each new image is first registered
635 into the fMOST average atlas, which shares intensity, modality, and morphologi-
636 cal characteristics. This allows us to leverage standard, intensity-based registration
637 functionality⁸⁵ available in ANTsX to perform this alignment. Transformations are
638 then concatenated to the original fMOST image to move it into the AllenCCFv3 space
639 using `ants.apply_transforms(...)`.
- 640 5. *Transformation of single cell neurons.* A key feature of fMOST imaging is the ability
641 to reconstruct and examine whole-brain single neuron projections⁷⁹. Spatial mapping
642 of these neurons from individual brains into the AllenCCFv3 allows investigators to
643 study different neuron types within the same space and characterize their morphology
644 with respect to their transcriptomics. Mappings found between the fMOST image
645 and the AllenCCFv3 using our pipeline can be applied in this way to fMOST neuron
646 reconstruction point set data using `ants.apply_transforms_to_points(..)`.

647 4.3 Mapping MERFISH data to AllenCCFv3

648 4.3.1 Preprocessing

- 649 • *Initial volume reconstruction.* Alignment of MERFISH data into a 3-D atlas space
650 requires an estimation of anatomical structure within the data. For each section,
651 this anatomic reference image was created by aggregating the number of detected
652 genetic markers (across all probes) within each pixel of a $10 \times 10 \mu\text{m}^2$ grid to match
653 the resolution of the $10 \mu\text{m}$ AllenCCFv3 atlas. These reference image sections are then
654 coarsely reoriented and aligned across sections using manual annotations of the most
655 dorsal and ventral points of the midline. The procedure produces an anatomic image
656 stack that serves as an initialization for further global mappings into the AllenCCFv3.
- 657 • *Anatomical correspondence labeling.* Mapping the MERFISH data into the AllenCCFv3
658 requires us to establish correspondence between the anatomy depicted in the MERFISH

and AllenCCFv3 data. Intensity-based features in MERFISH data are not sufficiently apparent to establish this correspondence, so we need to generate instead corresponding anatomical labelings of both images with which to drive registration. These labels are already available as part of the AllenCCFv3; thus, the main challenge is deriving analogous labels from the spatial transcriptomic maps of the MERFISH data. Toward this end, we assigned each cell from the scRNA-seq dataset to one of the following major regions: cerebellum, CTXsp, hindbrain, HPF, hypothalamus, isocortex, LSX, midbrain, OLF, PAL, sAMY, STRd, STRv, thalamus and hindbrain. A label map of each section was generated for each region by aggregating the cells assigned to that region within a $10 \times 10\mu m^2$ grid. The same approach was used to generate more fine grained region specific landmarks (i.e., cortical layers, habenula, IC). Unlike the broad labels which cover large swaths of the section these regions are highly specific to certain parts of the section. Once cells in the MERFISH data are labeled, morphological dilation is used to provide full regional labels for alignment into the AllenCCFv3.

- *Section matching.* Since the MERFISH data is acquired as sections, its 3-D orientation may not be fully accounted for during the volume reconstruction step, due to the particular cutting angle. This can lead to obliqueness artifacts in the section where certain structures can appear to be larger or smaller, or missing outright from the section. To address this, we first use a global alignment to match the orientations of the MERFISH sections to the atlas space. In our pipeline, this section matching is performed in the reverse direction by performing a global affine transformation of the AllenCCFv3 into the MERFISH data space, and then resampling digital sections from the AllenCCFv3 to match each MERFISH section. This approach limits the overall transformation and thus resampling that is applied to the MERFISH data, and, since the AllenCCFv3 is densely sampled, it also reduces in-plane artifacts that result from missing sections or undefined spacing in the MERFISH data.

685 **4.3.2 2.5D deformable, landmark-driven alignment to AllenCCFv3**

686 After global alignment of the AllenCCFv3 into the MERFISH dataset, 2D per-section de-
687 formable refinements are used to address local differences between the MERFISH sections
688 and the resampled AllenCCFv3 sections. Nine registrations were performed in sequence us-
689 ing a single label at each iteration in the following order: 1) brain mask, 2) isocortex (layer
690 2+3), 3) isocortex (layer 5), 4) isocortex (layer 6), 5) striatum, 6) medial habenula, 7) lateral
691 habenula, 8) thalamus, and 9) hippocampus. This ordering was determined empirically by
692 an expert anatomist who prioritized which structure to use in each iteration by evaluat-
693 ing the anatomical alignment from the previous iteration. Global and local mappings are
694 then all concatenated (with appropriate inversions) to create the final mapping between the
695 MERFISH data and AllenCCFv3. This mapping is then used to provide a point-to-point
696 correspondence between the original MERFISH coordinate space and the AllenCCFv3 space,
697 thus allowing mapping of individual genes and cell types located in the MERFISH data to
698 be directly mapped into the AllenCCFv3.

699 **4.4 DevCCF velocity flow transformation model**

700 Given multiple, linearly or non-linearly ordered point sets where individual points across the
701 sets are in one-to-one correspondence, we developed an approach for generating a velocity
702 flow transformation model to describe a time-varying diffeomorphic mapping as a variant of
703 the landmark matching solution. Integration of the resulting velocity field can then be used
704 to describe the displacement between any two time points within this time-parameterized
705 domain. Regularization of the sparse correspondence between point sets is performed using
706 a generalized B-spline scattered data approximation technique⁸⁴, also created by the ANTsX
707 developers and contributed to ITK.

708 **4.4.1 Velocity field optimization**

709 To apply this methodology to the developmental templates¹⁶, we coalesced the manual an-
710 notations of the developmental templates into 26 common anatomical regions (see Figure 3).

711 We then used these regions to generate invertible transformations between successive time
712 points. Specifically each label was used to create a pair of single region images resulting in 26
713 pairs of “source” and “target” images. The multiple image pairs were simultaneously used to
714 iteratively estimate a diffeomorphic pairwise transform. Given the seven atlases E11.5, E13.5,
715 E15.5, E18.5, P4, P14, and P56, this resulted in 6 sets of transforms between successive time
716 points. Approximately 10^6 points were randomly sampled labelwise in the P56 template
717 space and propagated to each successive atlas providing the point sets for constructing the
718 velocity flow model. Approximately 125 iterations resulted in a steady convergence based
719 on the average Euclidean norm between transformed point sets. Ten integration points were
720 used and point sets were distributed along the temporal dimension using a log transform for
721 a more evenly spaced sampling. For additional information a help menu is available for the
722 ANTsPy function `ants.fit_time_varying_transform_to_point_sets(...)`.

723 4.5 ANTsXNet mouse brain applications

724 4.5.1 General notes regarding deep learning training

725 All network-based approaches described below were implemented and organized in the
726 ANTsXNet libraries comprising Python (ANTsPyNet) and R (ANTsRNet) analogs using
727 the Keras/Tensorflow libraries available as open-source in ANTsX GitHub repositories.
728 For the various applications, both share the identically trained weights for mutual re-
729 producibility. For all GPU training, we used Python scripts for creating custom batch
730 generators which we maintain in a separate GitHub repository for public availability
731 (<https://github.com/ntustison/ANTsXNetTraining>). These scripts provide details such as
732 batch size, choice of loss function, and network parameters. In terms of GPU hardware, all
733 training was done on a DGX (GPUs: 4X Tesla V100, system memory: 256 GB LRDIMM
734 DDR4).

735 Data augmentation is crucial for generalizability and accuracy of the trained networks.
736 Intensity-based data augmentation consisted of randomly added noise (i.e., Gaussian, shot,
737 salt-and-pepper), simulated bias fields based on N4 bias field modeling, and histogram warp-

738 ing for mimicking well-known MRI intensity nonlinearities^{46,87}. These augmentation tech-
739 niques are available in ANTsXNet (only ANTsPyNet versions are listed with ANTsRNet
740 versions available) and include:

- 741 • image noise: `ants.add_noise_to_image(...)`,
- 742 • simulated bias field: `antspynet.simulate_bias_field(...)`, and
- 743 • nonlinear intensity warping: `antspynet.histogram_warp_image_intensities(...)`.

744 Shape-based data augmentation used both random linear and nonlinear deformations in
745 addition to anisotropic resampling in the three canonical orientations to mimic frequently
746 used acquisition protocols for mice brains:

- 747 • random spatial warping: `antspynet.randomly_transform_image_data(...)` and
- 748 • anisotropic resampling: `ants.resample_image(...)`.

749 4.5.2 Brain extraction

750 Similar to human neuroimage processing, brain extraction is a crucial preprocessing step
751 for accurate brain mapping. We developed similar functionality for T2-weighted mouse
752 brains. This network uses a conventional U-net architecture⁸⁸ and, in ANTsPyNet, this
753 functionality is available in the program `antspynet.mouse_brain_extraction(...)`.
754 For the two-shot T2-weighted brain extraction network, two brain templates were gen-
755 erated along with their masks. One of the templates was generated from orthogonal
756 multi-plane, high resolution data⁶⁹ which were combined to synthesize isotropic volu-
757 metric data using the B-spline fitting algorithm⁸⁴. This algorithm is encapsulated in
758 `ants.fit_bspline_object_to_scattered_data(...)` where the input is the set of voxel
759 intensity values and each associated physical location. Since each point can be assigned
760 a confidence weight, we use the normalized gradient value to more heavily weight edge
761 regions. Although both template/mask pairs are available in the GitHub repository
762 associated with this work, the synthesized volumetric B-spline T2-weighted pair is available
763 within ANTsXNet through the calls:

- 764 • template: `antspynet.get_antsxnet_data("bsplineT2MouseTemplate")` and
765 • mask: `antspynet.get_antsxnet_data("bsplineT2MouseTemplateBrainMask")`.

766 **4.5.3 Brain parcellation**

767 The T2-weighted brain parcellation network is also based on a 3-D U-net architecture and the
768 T2-w DevCCF P56 template component with extensive data augmentation, as described pre-
769 viously. Intensity differences between the template and any brain extracted input image are
770 minimized through the use of the rank intensity transform (`ants.rank_intensity(...)`).
771 Shape differences are reduced by the additional preprocessing step of warping the brain ex-
772 tracted input image to the template. Additional input channels include the prior probability
773 images created from the template parcellation. These images are also available through the
774 ANTsXNet `get_antsxnet_data(...)` interface.

775 **Data availability**

776 All data and software used in this work are publicly available. The DevCCF atlas is
777 available at <https://kimlab.io/brain-map/DevCCF/>. ANTsPy, ANTsR, ANTsPyNet, and
778 ANTsRNet are available through GitHub at the ANTsX Ecosystem ([https://github.com/](https://github.com/ANTsX)
779 [ANTsX](#)). Training scripts for all deep learning functionality in ANTsXNet can also be
780 found on GitHub (<https://github.com/ntustison/ANTsXNetTraining>). A GitHub reposi-
781 tory specifically pertaining to the AllenCCFv3 mapping is available at <https://github.com/>
782 [dontminchenit/CCFAAlignmentToolkit](#). For the other two contributions contained in this
783 work, the longitudinal DevCCF mapping and mouse cortical thickness pipeline, we refer the
784 interested reader to <https://github.com/ntustison/ANTsXMouseBrainMapping>.

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⁷⁹² **Author contributions**

⁷⁹³ N.T., M.C., and J.G. wrote the main manuscript text and figures. M.C., M.K., R.D., S.S.,
⁷⁹⁴ Q.W., L.G., J.D., C.G., and J.G. developed the Allen registration pipelines. N.T. and F.K.
⁷⁹⁵ developed the time-varying velocity transformation model for the DevCCF. N.T. and M.T.
⁷⁹⁶ developed the brain parcellation and cortical thickness methodology. All authors reviewed
⁷⁹⁷ the manuscript.

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