Probabilistic embedding and clustering with alignment for spatial transcriptomics data integration with PRECAST

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Abstract

Spatially resolved transcriptomics are a set of emerging technologies that enable the transcriptomic profiling of tissues with the physical location of expressions. Although a variety of methods have been developed for data integration, most of them are for single-cell RNA-seq datasets without a consideration of spatial information. Thus, methods that are capable of integrating spatial transcriptomics data from multiple tissue slides, possibly from multiple individuals, are sincerely needed. Here, we present PRECAST, an efficient data integration method for multiple spatial transcriptomics data with non-cluster-relevant effects such as the complex batch effects. PRECAST unifies spatial factor analysis simultaneously with spatial clustering and embedding alignment, while requiring only partially

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shared cell/domain clusters across datasets. We showed that PRECAST effectively integrates multiple tissue slides with spots mixed across datasets and cell/domain clusters separated using both simulated datasets and four spatial transcriptomics datasets from either low- or near-single-cell-resolution sequencing. The method demonstrates improved cell/domain detection with outstanding visualization, and the estimated embeddings and cell/domain labels facilitate many downstream analyses. Using a hepatocellular carcinoma Visium dataset, PRECAST detected two cell lineages in tumor/normal epithelium via spatial RNA velocity analysis using its estimated embeddings and domain labels. We further showed the scalability of PRECAST with a mouse olfactory bulb Slide-seqV2 dataset for 16 slides with ∼600,000 spots.

Keywords— Data integration, spatially resolved transcriptomics, joint dimension reduction and spatial clustering, high-resolution spatial map

Introduction

Spatially resolved transcriptomics (SRT) encompass a set of recently developed technologies that characterize the gene expression profiles of tissues while retaining information on their physical location. The methodologies used for resolving spatial gene expression are primarily categorized into *in situ* hybridization (ISH) technologies (e.g., MERFISH [1–3], seqFISH [4, 5], seqFISH+ [6]), and *in situ* capturing technologies (e.g., HDST [7], Slide-seq [8, 9] and 10x Genomics Visium [10]) [11]. The *in situ* capturing technologies are unbiased and involve transcriptome-wide expression measurements, while ISH-based methods are targeted and require prior knowledge of the genes of interest. These technologies have provided extraordinary new opportunities for researchers to characterize the transcriptomic landscape within a spatial context; explore how cells influence and are influenced by the cells around them [12]; identify genes with spatial variations other than cell/domain differences, e.g., cell morphology [13]; and identify spatial trajectories or RNA velocity in tissues [14, 15], among other applications [16].

The importance of data integration is particularly relevant to SRT datasets from multiple slides due to the following reasons. First, multiple slides/arrays are required to cover each region of interest due to the tiny size of a single slide/array. Second, SRT profiles across multiple individuals, e.g., 12 tissue slides from three adult donors in human cortex [17], can be characterized, and the conclusions made based on transcriptomic differences among spatial cell/domain clusters across multiple individuals should be robust to chance variations occurring in only one replicate. Third, using multiple spatially slides along an axis from tissues/organs would allow the recovery of the organization of a tissue/organ map, e.g., multiple sections from a mouse olfactory bulb (OB) that are equally distributed along the anterior-posterior axis of the same mouse [18]. Moreover, when multiple SRT datasets from multiple clinical/biological conditions are available, integrative analysis to estimate shared embeddings representing variations among cell/domain clusters can provide the first step towards detecting genes that are differentially expressed between conditions [19]. Thus, it is important to develop rigorous methods that are capable of performing data integration across multiple SRT datasets via aligning shared the embeddings of cluster-relevant biological effects while accounting for non-cluster-relevant effects, such as complex batch effects [20].

Similar to domain adaption in the field of image analysis [21, 22], the major goal of data integration of SRT datasets from multiple slides is to align gene expression among multiple datasets on separable cell types. An ideal data integration method for SRT datasets should be capable of the following three tasks: (1) estimating the shared low-dimensional embeddings across SRT datasets,

accounting for locally shared microenvironments (spatial dimension reduction); (2) aligning the shared embeddings that capture the biological differences among cell/domain clusters across datasets with heterogeneous non-cluster-relevant effects (data alignment); (3) clustering the aligned embeddings to obtain cell/domain clusters across datasets that promote spatial smoothness (spatial clustering). Most existing data integration methods, including MNN [20], Scanorama [23], Seurat V3 [24], Harmony [19], scVI [25], and scGen [26], have been developed for scRNA-seq datasets. More recently, MEFISTO was proposed as a way to analyze datasets with repeated spatio-temporal measurements [27], and PASTE was proposed as a method able to stack and/or integrate SRT data from multiple adjacent tissue slices into a single slide, but it is not applicable to the integration of tissue sections from different individuals [28]. In addition, most existing methods perform data integration in low-dimensional space using the principal components (PCs) of conventional dimension reduction, e.g., principal component analysis (PCA), without considering the consistent loss functions of dimension reduction, alignment across datasets, and spatial clustering.

To address the challenges presented by SRT data integration and facilitate the downstream analyses of combinations of multiple tissue slides, we propose the use of a unified and principled probabilistic model, PRECAST, to simultaneously estimate cluster-relevant low-dimensional embeddings, perform spatial clustering, and more importantly, align embeddings across multiple SRT datasets. With its unique features, PRECAST builds hierarchical factor models that can jointly perform spatial dimension reduction and clustering while aligning embeddings for normalized gene expression matrices from multiple tissue slides. More importantly, PRECAST provides the framework that supports unified data integration of SRT datasets using simple projections. As a result, PRECAST can resolve the aligned representations, provide outstanding visualizations, and achieve higher spatial clustering accuracy in the combined tissue slides. The resolved representations and estimated labels from PRECAST can be used for multiple downstream analyses, e.g., removing batch effects, identifying differentially expressed genes under different conditions/stages, detecting spatially variable genes that are not due to cell/domain differences, and recovering spatial trajectories/RNA velocity, etc. We illustrate the benefits of PRECAST through extensive simulations and a diverse range of example datasets collated with different spatial transcriptomics technologies: 10x Visium datasets of 12 human dorsolateral prefrontal cortex (DLPFC) samples, four hepatocellular carcinoma samples, and Slide-seqV2 datasets from two mouse hippocampus tissue slides and 16 OB tissue slides.

Results

Spatial transcriptomics data integration using PRECAST

PRECAST takes as input the normalized gene expression matrices from multiple tissue slides, factorizes the input to each matrix into a latent factor with a shared distribution for each cell/domain cluster while performing spatial dimension reduction and spatial clustering, and aligning and estimating joint embeddings across multiple tissue slides (Fig. 1a). In the dimension-reduction step, we used an intrinsic conditional autoregressive (CAR) component to capture the spatial dependence induced by neighboring microenvironments while in the spatial-clustering step, we used a Potts model to promote spatial smoothness within spot neighborhoods in the space of cluster labels. PRECAST applies a simple projection strategy to non-cluster-relevant effects, e.g., batch effects, other than those of biological differences among cell/domain clusters, and implicitly accounts for shifts in the centroid of each cluster using the intrinsic CAR component in the dimension-reduction step (see Methods). These considerations of PRECAST mimic some of the recent explorations into self-supervised learning and

domain adaptation in deep learning but in a parametric manner. Unlike other integration methods that take as input the top (spatial) PCs and apply multiple steps to remove batch effects and merge the data, PRECAST is a unified approach, taking as input high-dimensional normalized gene expression matrices to simultaneously perform spatial dimension reduction and clustering while aligning shared cluster-relevant embeddings across multiple tissue slides. We show that PRECAST outperforms existing data integration methods by more successfully aligning similar clusters across multiple tissue slides while separating clusters with outstanding visualization.

PRECAST can be applied to SRT datasets of various resolutions. By increasing the resolution for SRT datasets, PRECAST can reveal fine-scale cell-type distributions. In Visium, the spots, which are 100 μm apart and 55 μm in diameter, are arranged in a hexagonal grid, while in Slide-seqV2, randomly barcoded beads 10 μm in diameter are deposited for mRNA capture, achieving near-single-cell resolution. In the following analysis, datasets in Slide-seqV2 with near-single-cell resolution present spatial patterns with much more "noise" than those of Visium due to the heterogeneity of the cell-type distributions. When we merged nearby beads in the Slide-seqV2 datasets, the recovered spatial patterns resembled those from Visium.

We use the estimated cell/domain labels and the finely aligned embeddings to showcase some downstream analyses, as depicted in Fig. 1b. First, users can visualize the inferred low-dimensional embeddings using two components from either tSNE [29] or UMAP [30]. Second, because embeddings obtained from PRECAST only carry information on the biological differences among cell/domain clusters, we provide a module to recover the gene expression matrices with batch effects removed and further identify genes differentially expressed either across different cell/domain clusters and/or under different conditions. Third, using these embeddings, we can identify genes whose spatial variability is not just due to biological differences among cell/domain clusters. Fourth, with the aligned embeddings estimated by PRECAST, we can perform trajectory inference/RNA velocity analysis to determine either the pseudotime or the pattern of dynamics in spatial spots across multiple tissue slides.

Validation using simulated data

We performed comprehensive simulations to evaluate the performance of PRECAST and compare it with that of several other methods (Fig. 1c and Supplementary Fig. S1-S2). Specifically, we considered the following eight integration methods: Harmony [19], Seurat V3 [24], fastMNN [20], scGen [26], Scanorama [23], scVI [25], MEFISTO [27] and PASTE [28], all of which except PASTE can be used to estimate the aligned low-dimensional embeddings among samples but PASTE can only estimate the embeddings of the center slice. The simulation details are provided in the Methods section. Briefly, we simulated either the normalized or count matrices of gene expression to compare PRECAST with other methods in terms of performance for data integration, dimension reduction, and spatial clustering. To mimic real data, we also considered the two ways to generate spatial coordinates and cell/domain labels, i.e., Potts models and real data in three DLPFC Visium slices. In total, we considered five scenarios: (1) Potts + logCount; (2) Potts + Count; (3) DLPFC (different donors) + logCount; (4) DLPFC (different donors)+ Count; and (5) DLPFC (same donors) + Count. Scenario 5 was designed to compare with PASTE since it can only handle SRT data from multiple adjacent tissue slices (see Methods).

In Scenarios 1-4, PRECAST achieved the best performance for data integration, with the highest F1 scores for the average silhouette coefficients, and in Scenario 5, PRECAST is comparable with PASTE (Fig. 1c, top panel). Moreover, PRECAST was able to merge spots within common cell/domain clusters across datasets, while separating spots from different cell/domain clusters (small cLISI, Supplementary Fig. S1a, top panel) and, at the same time, maintaining a sufficient mix of different

samples (large iLISI, Supplementary Fig. S1a, bottom panel). In contrast, the existing integration methods were either sensitive to the data generation process or failed to recover the spatial structure during integration (Fig. 1c and Supplementary Fig. S1a). Then, we evaluated the performance of the models in obtaining low-dimensional embeddings. For the average canonical correlation between the estimated embeddings and the true latent features, PRECAST ranked the highest in most scenarios (Supplementary Fig. S1b, top panel), suggesting the embeddings estimated by PRECAST were more accurate. We also showed that Pearson's correlation coefficients between the observed expression and the estimated cell/domain labels conditioned with the embeddings from PRECAST were lower than those from other methods (Supplementary Fig S1b, bottom panel), suggesting PRECAST captures more relevant information regarding cell/domain clusters and, thus, facilitates downstream analysis. Next, we compared the clustering performance of each method. As a unified method, PRECAST simultaneously estimate low-dimensional embeddings and cluster labels. For the other methods, we sequentially performed spatial clustering based on each of the estimated embeddings using SC-MEB/Louvain, except for Seurat V3, which has its own clustering pipeline based on Louvain. PRECAST achieved the highest adjusted Rand index (ARI) and normalized mutual information (NMI) in all considered scenarios (Fig. 1c, bottom panel, and Supplementary Fig. S2a), while other methods, such as Seurat V3 and Harmony, were sensitive to the data generation process. Moreover, we observed that all methods correctly chose the number of clusters. Finally, we showed that PRECAST was computationally efficient and scalable to large sample sizes, and it only took $\sim$6 hours to analyze a dataset with 2,000 genes and 600,000 spots for a fixed number of clusters (Supplementary Fig. S2b).

Application to human dorsolateral prefrontal cortex Visium data

We applied PRECAST and other methods to analyze four published datasets obtained via either Visium or Slide-seqV2 technologies (see Methods). By obtaining the estimated aligned embeddings and cluster labels from PRECAST, we can perform many downstream analyses using all tissue slides. Here, we showcase the differential expression (DE) analyses across detected domains, spatial variation analysis (SVA) adjusting for aligned embeddings as covariates, and trajectory inference/RNA velocity analysis. To examine the performance of clustering with low-resolution data, we performed deconvolution analysis to infer the cell compositions of the domains detected by PRECAST.

To quantitatively show that PRECAST outperforms existing data integration methods, we first analyzed LIBD human dorsolateral prefrontal cortex (DLPFC) data generated using 10x Visium [17], which contained 12 tissue slices from three adult donors, comprising four tissue slices from each donor. In all 12 tissue slices, the median number of spots was 3,844, and the median number of genes was 1,716 per spot. The original study provided manual annotations of the tissue layers based on the cytoarchitecture that allowed us to evaluate the performance of both data integration and the accuracy of spatial domain detection by taking the manual annotations as ground truth. For each method, we summarized the inferred low-dimensional embeddings using three components from either tSNE or UMAP and visualized the resulting tSNE/UMAP components with red/green/blue (RGB) colors in the RGB plot (Fig. 2a, right-top panel, and Supplementary Fig. S3a&b-S5a&b). The resulting RGB plots from PRECAST show the laminar organization of the human cerebral cortex and present smoother transitions across neighboring spots and spatial domains than those from other methods. For each of the other methods, we further performed clustering analysis to detect spatial domains using different methods with the inferred low-dimensional embeddings (Fig. 2a, right-bottom panel, and Supplementary Fig. S3c-S5c). Not surprisingly, the patterns between the corresponding spatial heatmaps of the cluster assignments and the RGB plot were similar across the 12 slices, whereas those from PRECAST had stronger laminar patterns, and the estimated embeddings carried more

information about the domain labels (Supplementary Fig. S6a).

PRECAST can offer outstanding data visualization compared with other methods. We visualized the inferred low-dimensional embeddings using two components from tSNE for each method (Fig. 2b and Supplementary Fig. S6b). The tSNE plots for PRECAST show that spots from different slices were well mixed (Fig. 2b, top panel) while the domain clusters were well segregated (Fig. 2b, bottom panel), and there were significant improvements in visualization over other methods including the method with no corrections. To quantify the performance of the data integration, we calculated the F1 scores of the average silhouette coefficients, which summarize two similar metrics of silhouette coefficients into a single quantity, and two versions of the local inverse Simpsons Index (LISI): integration LISI (iLISI) and cell-type LISI (cLISI). iLISI was employed to assess integration mixing, while cLISI was employed to assess the separation of each domain cluster. Supplementary Fig. S6c shows PRECAST achieved the best F1 scores, iLISI, and cLISI. To evaluate clustering accuracy, we used both the ARI and NMI. As shown in Fig. 2c and Supplementary Fig. S6d&e, PRECAST achieved the highest ARI and NMI: the median ARI was 0.434 for PRECAST, 0.382 for Scanorama, and 0.406 for scVI. A heatmap of Pearson's correlation coefficients among the detected domains shows good separation of the estimated embeddings across domains (Fig. 2d) and that the correlations between deeper layers were high, e.g., there were high correlations between layers 5 and 6, and between layer 5 and layer 3/4, while correlations among the separated layer were low.

A key benefit of PRECAST is its ability to estimate aligned domain-relevant embeddings and joint labels for all slides. We performed DE analysis for the combined 12 slices (see Methods). In total, we detected 1,331 DE genes with adjusted p-values of less than 0.001 among the 10 spatial domains identified by PRECAST, with 314 genes being specific to Domain 5, which corresponded to white matter (Supplementary Table S1). Many of these genes were reported to be enriched in different layers of DLPFC, i.e., *Pcp4* (Domain 2, layer 5) [31], *Hopx* (Domain 1, layer 1/3), and *Enc1* (Domain 4, layer 2/3) [32] (Fig. 2e and Supplementary Fig. S7-S9). Next, we performed trajectory inference using the low-dimensional embeddings and domain labels estimated by PRECAST (Supplementary Fig. S10). In total, we identified 858 genes associated with the estimated pseudotime with adjusted p-values of less than 0.001. Among them, 373 were identified as DE genes in at least one domain (Fig. 2f and Supplementary Table S2). We further found that the pseudotime-associated genes identified by PRECAST were significantly enriched for nervous system development (Fig. 2g).

To further show that the estimated embeddings from PRECAST were well aligned across tissue slides, we performed SVA analysis with the embeddings from PRECAST as covariates for each slice to identify spatially variable genes (SVGs) with nonlaminar patterns. A detailed list of genes identified at a false discovery rate (FDR) of 1% is available in Supplementary Table S3. Interestingly, many of the identified genes were related to immune function. For example, *Isg15* is a ubiquitin-like molecule induced by type I interferon (IFN), and *Isg15* deficiency increases antiviral responses in humans [33, 34]. Many studies in the literature have highlighted the importance of immunebrain interactions to the development of many disorders of the central nervous system [35, 36]. Further enrichment analysis showed these genes from each slice to be highly enriched in many common pathways, suggesting the embeddings were aligned well by PRECAST (Fig. 2h and Supplementary Fig. S11-S15).

Application to hepatocellular carcinoma Visium data

To study dynamics of tumorigenesis in tumors and tumor-adjacent tissues, we further analyzed four slides of in-house hepatocellular carcinoma (HCC) data generated using the 10x Visium platform, with two from tumors (HCC1 and HCC2) and two from tumor-adjacent tissues (HCC3 and HCC4) from an HCC patient. The median number of spots was 2,748, and the median number of genes

was 3,635 per spot. Fig. 3a shows a histology image (top panel) with the manual annotations for tumor/normal epithelium (TNE) and stroma by a pathologist (bottom panel). Consistent with the DLPFC data, the RGB plots generated by PRECAST clearly segregated the tissue slices into multiple spatial domains (Fig. 3b, top panel), with neighboring spots and spots in the same domain across multiple slides sharing similar RGB colors more successfully than those generated by other methods (Supplementary Fig. S16a&b). Similarly, the spatial heatmaps of cluster assignments for four tissue slides resembled the corresponding RGB plots and presented more spatial patterns across the tissue slides than those from the other methods (Fig. 3b, bottom panel; Supplementary Fig. S16c). We further visualized the inferred low-dimensional embeddings using two components from tSNE for each method (Fig. 3c and Supplementary Fig. S17a), in which the tSNE plots by PRECAST showed the spots from different slices were well mixed (Fig. 3c, top panel), while the domain clusters were well segregated (Fig. 3c, bottom panel), with significant improvements in visualization. A heatmap of Pearson's correlation coefficients among the detected domains shows good separation of estimated embeddings across domains (Supplementary Fig. S17b), in which correlations between regions in TNE were high, and correlations between regions for TNE and stroma were low.

To characterize the transcriptomic properties of the spatial domains identified by PRECAST, we performed DE analysis for the combined four tissue slides (see Methods). In total, we detected 2,093 DE genes with adjusted p-values of less than 0.001 in all nine spatial domains detected by PRECAST, with 539 genes being specific to Domains 1-5, which correspond to regions in TNE (Supplementary Table S4). A heatmap and ridge plots of the findings showed good separation of the DE genes across different spatial domains (Supplementary Fig. S18-S22). In TNE regions (Domains 1-5), we further found that genes specific to Domains 1 and 5 are highly enriched in pathways of chemical carcinogenesis DNA adducts and chemical carcinogenesis receptor activation. Genes specific to Domain 4 were enriched in the pathways of signaling by RAF1 mutants and signaling by RAS mutants, and genes specific to Domains 2 and 3 were highly enriched in complement and coagulation cascade pathways (Supplementary Fig. S23). Genes specific to Domains 6-9 were enriched in the angiogenesis pathway, and we found 40 out of 427, 34 out of 606, 25 out of 281, and 18 out of 240 angiogenesis signature genes, respectively, in Domains 6, 7, 8, and 9, from multiple studies [37–40]. Interestingly, Domains 1-3 were only present in tumor tissues (HCC1 and HCC2), and Domain 5 was only present in tumor-adjacent tissues (HCC3 and HCC4), while Domain 4 was shared across tumor and tumor-adjacent tissues.

To identify SVGs other than those that are merely relevant to domain differences, we performed SVA analysis with the embeddings estimated by PRECAST as covariates for each slice. A detailed list of genes identified at an FDR of 1% is available in Supplementary Table S5. By performing functional enrichment analysis of these SVGs, we detected SVGs adjusted for domain-relevant covariates to be highly enriched in many common pathways in four HCC slices, e.g., cytoplasmic translation, and cytosolic ribosome (Supplementary Fig. S24-S25).

Next, to examine cell compositions of each spatial domain detected by PRECAST, we performed cell-type deconvolution analysis of all four HCC slides using scRNA-seq data as the reference panel (see Methods). The scRNA-seq reference panel consisted of malignant and tumor microenvironment cells, including cancer-associated fibroblasts (CAFs), tumor-associated macrophages (TAMs), tumor-associated endothelial cells (TECs), cells with an unknown entity but expressing hepatic progenitor cell markers (HPC-like), and immune cells [41]. As shown in Fig. 3d&e and Supplementary Fig. S26a, proportions of the malignant cells were substantially higher in Domains 1-5, while HPC-like cells were seen at higher proportions in Domain 7. In Domain 6, we observed an increased proportion of TAMs and immune cells and genes specific to this domain include *Tgfb1*, and *Mmp2*, which have been used for the classification of TAMs [42, 43].

The estimated aligned embeddings and cluster labels can also be used in RNA velocity analysis to investigate the directed transcriptional dynamics of tumorigenesis when spliced and unspliced mRNA is available (see Methods). Interestingly, two cell lineages were identified, with one that originated in Domain 2 (TNE) and spread to Domains 4 and 5 (TNE), followed by Domains 6, 7, and 9 (stroma), and the other that originated in Domains 1 and 3 (TNE) and spread to Domain 8 (stroma). The TNE regions in Domain 2 residing in HCC1 may play a key role in tumorigenesis with Domain 4 (TNE) shared among four slides and Domain 5 (TNE) in tumor-adjacent tissues (Fig. 3f and Supplementary Fig. S26b). To infer cell states in the identified TNE, we further performed RNA velocity analysis using the spots identified in Domains 1-5. Fig. 3g shows an expression heatmap of the top genes associated with cell states with induction close to 0 and repression close to 1 (see Methods). The TNEs in Domains 1 and 2 tended to be transcriptionally active, while TNEs in Domains 4 and 5 tended to be repressed and showed no transcription. The top genes associated with cell states included *Spink1*, *Rlp30*, and *IL32*, which highlights the importance of genes associated with cell states in HCC [44–46].

Application to mouse olfactory bulb Slide-seqV2 data

In Visium, barcoded beads 55 μm in diameter and with a center-to-center distance of 100 μm are used to capture mRNA with an average of 1-10 cells per spot [10]. The Slide-seq technique was recently developed for high-resolution SRT using 10-μm barcoded beads with an average of 13 cells per spot [8, 9], and Slide-seqV2 further improved the detection sensitivity. To show the scalability of PRECAST, we analyzed a mouse OB dataset generated using Slide-seqV2 technology [18]. In this dataset, spatial transcriptomic information was obtained from a total of 20 OB sections distributed evenly along the anteriorposterior axis. Due to the quality of the sections from the end of the mouse OB region, we removed four slides and analyzed 16 containing 21,571 genes on average from over a total of 693,863 spots using PRECAST and other methods. After quality control, we obtained data of a lower resolution ($\sim$4,000 spots) by collapsing nearby spots in each slide (see Methods), and the resulting resolution was similar to that of Visium (average 10 cells per spot). To further examine the structure of mouse OB, we relied on the structural annotation in the Allen Brain Atlas [47] (Fig. 4a). With near-single-cell resolution, the identified embeddings and cluster labels both showed more fine-scale cell-type distribution patterns in the mouse OB [48]. In comparison, when we lowered the resolution, PRECAST estimated embeddings and cluster labels with smoother spatial patterns at the expense of less detailed local spatial information (Fig. 4b and Supplementary Fig. S27-S30). Moreover, the resulting RGB plots of PRECAST showed the laminar organization of the mouse OB and presented smoother transitions across neighboring spots and spatial domains than other methods (Supplementary Fig. S27a&b-S30a&b). We next visualized the inferred embeddings using two components from tSNE from each method (Fig. 4c and Supplementary Fig. S31) and showed that, by using PRECAST, the spatial spots were well mixed across the 16 slides, while the cell/domain clusters were well segregated, suggesting PRECAST is more effective at spatial data integration.

Using reduced resolution, PRECAST detected 12 spatial domains with laminar organization, including rostral migratory stream (RMS, Domain 1), granule cell layer (GCL, Domain 2), GCL/inner plexiform layer (GCL/IPL, Domain 3), mitral cell layer (MCL, Domain 4), outer plexiform layer (OPL, Domain 5), glomerular layer (GL, Domains 6-7), and olfactory nerve layer (ONL, Domains 8), with Domains 9-12 belonging to low-quality regions or experiment artifacts. To characterize the transcriptomic properties of the spatial domains identified by PRECAST, we performed DE analysis for the combined 16 tissue slides (see Methods). In total, we detected 4,131 DE genes with adjusted p-values of less than 0.001 in all 12 spatial domains detected by PRECAST (Supplementary Table S6), including representative genes that define particular cellular layers in the mouse OB, e.g., *Sox2ot*

and *Sox11* (RMS) [49, 50]. The heatmap of the findings shows good separation of the DE genes across different spatial domains (Supplementary Fig. S32), and we found genes specific to Domain 1 (RMS) were enriched for myelin sheath and structural constituents of myelin sheath (Supplementary Fig. S33). Compared with the reduced resolution data, when near-single-cell level resolution was used, PRECAST identified 24 cell clusters, including fine-scale cell-type clusters. To better visualize each detected cell cluster, we plotted a heatmap of each cluster assignment for all 16 slides in the Supplementary Fig. S34-S35. A heatmap of DE genes across different cell clusters showed Clusters 1-3 were subtypes of granule cells, and Clusters 4-6 belonged to cells in MCL and GL (Supplementary Fig. S36).

To examine the cell compositions in each spatial domain detected by PRECAST at the reduced resolution, we performed cell-type deconvolution analysis of all 16 tissue slides using single-cell RNA-seq data from adult mouse OB as the reference panel [51]. As shown in Fig. 4d, Domain 1 (RMS) was enriched for myelinating oligodendrocyte cells, astrocytes, and immature neurons; astrocytes from the RMS are reported to be turned into neurons [52] and immature neurons migrate to the OB through RMS [53]. Not surprisingly, we found that Domains 2-3 (GCL) were dominated by two primary subtypes of granule cell, with a larger proportion of immature neurons in Domain 2 (inner), and an enrichment of mitral and tufted cells in Domain 4 (MCL). Domain 8 (ONL) was primarily enriched in olfactory ensheathing cells (OECs) and olfactory sensory neurons (OSNs). OECs are a unique class of vertebrate glial cells within the ONL of the OB [54], and OSNs express odorant receptors in the olfactory epithelium [55].

We performed trajectory inference to examine the cell lineages among the detected domains using aligned embeddings and estimated domain labels from PRECAST. In general, the estimated trajectory showed the "inside-out" sequence, consistent with the general understanding that OB neurons migrate from the subventricular zone along the RMS to OB, before migrating radially out of the RMS in an inside-out sequence [56] (Fig. 4e and Supplementary Fig. S37a). Further DE analysis identified genes along the pseudotime (Supplementary Fig. S37b).

Application to mouse hippocampus Slide-seqV2 data

To demonstrate the importance of using near-single-cell-resolution datasets and the effectiveness of PRECAST, we analyzed a mouse hippocampus dataset generated using Slide-seqV2 technology [9]. In this study, we analyzed two tissue slides from the mouse hippocampus that contained 22,860 genes measured on 43,664 spots on average. First, we examined the performance of data integration under both the original and reduced resolutions, the latter of which was similar to that of Visium (average 10 cells per spots). To further examine the structure of the mouse hippocampus, we relied on the structural annotations in the Allen Brain Atlas [47] (Fig. 5a, top panel). Fig. 5a (middle and bottom panels) shows both the RGB plots and spatial heatmaps of cluster assignments for two slices with two resolutions. Similar to mouse OB data, PRECAST recovered fine-scale cell-type distribution using Slide-seqV2 data at the original resolution (Fig. 5a, bottom panel). Compared with other methods, PRECAST can obtain the aligned embeddings and cluster labels with clearer spatial patterns at both the reduced and original resolutions (Supplementary Fig. S38-S39). By lowering the resolution to the level of 10x Visium, the spatial patterns became clearer at the expense of less detailed local information (Fig. 5a, middle panel). Next, we visualized the inferred low-dimensional embeddings at the reduced and original resolutions using two components from tSNE for each method (Fig. 5b and Supplementary Fig. S40). Again, the tSNE plots of PRECAST showed that the spots across two slices were well mixed while cell/domain clusters were well segregated.

At the reduced resolution, PRECAST detected 17 spatial domains including CA1 (Domain 1),

CA3 (Domain 2), dentate gyrus (DG; Domain 3), other hippocampus (Domains 4-8), third ventricle (Domain 9), thalamus regions (Domains 10-13), corpus callosum (CC; Domains 14-15), and cortical layers (layer 6, Domain 16; layer 5, Domain 17). To characterize the transcriptomic properties of the spatial domains identified by PRECAST, we performed DE analysis for the combined hippocampus slides (see Methods). In total, we detected 5,469 DE genes with adjusted p-values of less than 0.001 in all 17 spatial domains detected by PRECAST, with 436 genes being specific to CA1 (Supplementary Table S7). A heatmap of the findings shows good separation of the DE genes across different spatial domains (Fig. 5c). Many of these genes are markers that define particular hippocampal subregions, e.g., *Hpca* (CA1) [9], *Tomm34* (CA3) [57], *Pcdh20* (DG) [57] (Supplementary Fig. S41). Genes specific to DG were enriched for the GABAergic synapse pathway, and both genes specific to CA1 and CA3 were highly enriched in the glutamatergic synapse pathway (Supplementary Fig. S42a). In the spatial domains of the cortical layers, PRECAST detected marker genes for deep layers, e.g., *Pde1a* [58], that were enriched for neurotransmitter transport (Supplementary Fig. S43). We also observed good Pearson's correlations among spatial domains in the same regions, e.g., high correlations between Domains 4 and 5, and between Domains 16 and 17 (Supplementary Fig. S42b). In comparison, at the original near-single-cell level resolution, PRECAST identified 25 cell clusters. The major patterns that included principal cells from CA3, CA1, and DG (Clusters 1-3, respectively) were similar to those of the spatial domains detected under the reduced resolution but with improved fine-scale cell-type distribution (Fig. 5a, third row; Supplementary Fig. S44a). Further DE analysis revealed that genes specific to Clusters 12-14 included markers for oligodendrocytes and cells in myelin processes, e.g., *Mbp* and *Mog* [59], that were highly enriched for pathways related to the structural constituents of myelin sheaths, myelin sheaths, and myelination (Supplementary Table S8 and Fig. S45).

To examine the cell compositions of each spatial domain detected by PRECAST at the reduced resolution, we performed cell-type deconvolution analysis of both mouse hippocampus datasets using single-cell Drop-seq data for the adult mouse brain as the reference panel [60]. We found that CA1, CA3, DG, and cortical layer 5 and layer 6 were highly enriched in CA1, CA3, and dentate principal cells, and cortical layer 5 and layer 6 cells, respectively. The thalamus regions were enriched in medial habenula (MH), lateral habenula (LH), lateral geniculate nucleus (LGN), and lateral dorsal nucleus of thalamus (LD) cells, and the proportions of MH and LH cells decreased while those of LGN and LD cells increased from left to right in Domains 10-13 (Fig. 5d).

To examine the cell lineages in the detected domains, we performed trajectory inference using aligned embeddings and estimated domain labels from PRECAST. As shown in Fig. 5e, the thalamus regions (Domains 10-13) developed earlier in the pseudotime than hippocampal regions (Domains 1-8), consistent with our existing knowledge of mouse central nervous system development [61]. Within hippocampal regions, subregions in CA1 (Domain 1), CA3 (Domain 2), and dentate gyrus (Domain 3) developed later than other subregions (Domains 4-8). The heatmap of the top 20 most significant gene expressions (Supplementary Fig. S44b) suggested the occurrence of some interesting dynamic expression patterns over pseudotime. For example, *Prkcd*, *Tnnt1*, and *Tcf7l2* had higher expression levels in the early stage, but later their expression levels decreased substantially. *Prkcd* has been reported to be a positive regulator of PRKN-independent mitophagy [62].

Discussion

PRECAST takes, as input, matrices of normalized expression levels and the physical location of each spot across multiple tissue slides. The output of PRECAST comprises both aligned low-dimensional embeddings and estimated cluster labels. In contrast to other existing methods of data integration,

PRECAST is a unified and principled probabilistic model that simultaneously estimates cluster-relevant low-dimensional embeddings, performs spatial clustering, and more importantly, aligns the estimated embeddings across multiple tissue sections. Thus, we recommend applying PRECAST first before a comprehensive data analysis pipeline is deployed. By applying PRECAST, the aligned embeddings and estimated cluster labels can be used for many types of downstream analyses, such as visualization, trajectory analysis, SVA and DE analysis for the combined tissue slices. In detail, we developed a module to further remove batch effects across multiple tissue slides based on housekeeping genes, making expression data comparable for different cell/domain clusters. This module is also applicable to the examination of expressional differences caused by multiple conditions when such information on tissue slides is obtainable.

A unique feature of PRECAST is that it performs dimension reduction and spatial clustering while using simple projections to align embeddings. Recently, Liu et al. [63] showed that, compared with methods that perform dimension reduction and spatial clustering sequentially [31, 64, 65], joint methods can estimate cluster-relevant embeddings more efficiently while accounting for the uncertainty in obtaining low-dimensional features from sequential analysis. A similar strategy has been described in previous self-supervised learning literature [66, 67]. PRECAST also takes advantage of CAR to account for the local microenvironments of neighboring spots, and an intrinsic CAR component has been used to promote spatial smoothness in the observed expressions of SRT data [68]. We showed that, by projecting non-cluster-relevant effects onto the cluster-relevant space, different sample slides present a constant shift in the centroid of each cell/domain type. With the assistance of joint modeling, we can use a subclass of CAR, intrinsic CAR, to simultaneously account for both smoothness in neighboring embeddings and non-cluster-relevant effects, e.g., batch effects, across batches. To avoid over smoothing, PRECAST optimizes the smoothness parameter (β_r) and conditional covariance (Ψ_r), and further selects the number of cell/domain clusters in a data-driven manner.

With the advent of high-throughput technologies for SRT, data integration is particularly relevant for analyzing SRT datasets from multiple tissue slides. Analysis of a single section with current state-of-art techniques, e.g., 10x Visium and Slide-seqV2, only covers a tiny area in the region of interest, and it takes a few or dozens of slides to cover the whole tissue/organ. In this case, biological variations in cell/domain clusters are often confounded by factors related to data generation processes. Methods in data integration, which serve as the first step before downstream analyses, not only align the embeddings but also estimate the shared cell/domain clusters across samples [19, 20, 23, 24]. Most existing methods of data integration were designed to analyze single-cell RNA-seq data without considering additional spatial information in the SRT data.

We examined the SRT data generated by two major platforms, 10x Visium and Slide-seqV2, with different spatial resolutions. With 10x Visium, each spot captures the mRNA in an average of 1-10 cells, whereas Slide-seqV2 achieves a higher resolution with an average of 1-3 cells per spot. As common sense implies, with low-resolution datasets, PRECAST recovers embeddings and cluster labels with smoother spatial patterns while losing the detailed local spatial information. Whereas, at near-single-cell resolution, the identified embeddings and cluster labels show more fine-scale cell-type distribution patterns. Using four datasets, we demonstrated that PRECAST can successfully perform data integration with aligned embeddings across tissue sections, such that spots across different tissue sections are well mixed while cell/domain clusters are well segregated, and with outstanding improvements in visualization. When applied to an HCC dataset, PRECAST identified five spatial domains belonging to TNE cells that were consistent with both manual annotations and spatial deconvolution. We further performed RNA velocity analysis to show the potential velocity of spots in different regions, shedding light on the tumorigenesis in the context of the tissues. To demonstrate the scalability of PRECAST, we analyzed a Slide-seqV2 dataset of 16 slides equally distributed along

the anteriorposterior axis of the mouse OB.

PRECAST provides opportunities for new exciting research routes. Firstly, when SRT datasets of single-cell resolution are available, its use can be extended to the integration of multimodal single-cell data. For example, integrating single-cell ATAC-seq will allow users to examine cell-type-specific regulatory mechanisms in the spatial context of tissues. Secondly, it would be interesting to integrate single-cell-resolution SRT datasets with CITE-seq data, thus integrating spatial transcriptomics with immunophenotyping, in which surface proteins are detected by antibody-derived tags. This would enable the exploration of surface proteins not measured in SRT datasets.

Materials and Methods

Methods

PRECAST overview

Here, we present a basic overview of PRECAST, and further details are available in the Supplementary Notes. PRECAST is a data integration method for SRT data from multiple tissue slides. The proposed method involves simultaneous dimension reduction and spatial clustering built on a hierarchical model with two layers, as shown in Fig. 1a. The first layer, the dimension-reduction step, relates the gene expression to the latent low-dimensional embeddings, while the second layer, the spatial-clustering step, relates the latent embeddings and the spatial coordinates to the cluster labels. In the dimension-reduction step, an intrinsic CAR model captures the spatial dependence induced by neighboring microenvironments in the space of low-dimensional embeddings, while in the spatial-clustering step, a Potts model promotes spatial smoothness in the space of cluster labels. Using simple projections of non-cluster-relevant effects onto the space of biological effects among cell/domain clusters, PRECAST aligns clusters across multiple tissue slides with shared distributions of embeddings in each cell/domain and detects their cell/domain labels. With M SRT datasets, we observe an $n_r \times p$ normalized expression matrix $X_r = (\mathbf{x}_{r1}^{\mathrm{T}}, \cdots, \mathbf{x}_{ri}^{\mathrm{T}}, \cdots, \mathbf{x}_{rn_r}^{\mathrm{T}})^{\mathrm{T}}$ for each sample r $(= 1, \cdots, M)$, where $\mathbf{x}_{ri} = (x_{ri1}, \cdots, x_{rip})^{\mathrm{T}}$ is a p-dimensional normalized expression vector for each spot $s_{ri} \in \mathbb{R}^2$ of sample r on square or hexagonal lattices, among others; while the cluster label of spot s_{ri}, $y_{ri} \in \{1, \cdots, K\}$, and q-dimensional embeddings, $\mathbf{z}_{ri}$'s, are unavailable. Without loss of generality, we assume that, for each sample r, $\mathbf{x}_{ri}$ is centered, and PRECAST models the centered normalized expression vector $\mathbf{x}_{ri}$ with its latent low-dimensional feature, $\mathbf{z}_{ri}$, and class label, y_{ri}, as

$$\mathbf{x}_{ri} = W(\mathbf{z}_{ri} + \mathbf{v}_{ri}) + \boldsymbol{\varepsilon}_{ri}, \boldsymbol{\varepsilon}_{ri} \sim N(0, \Lambda_r), \tag{1}$$

$$\mathbf{z}_{ri} | y_{ri} = k \sim N(\mu_k, \Sigma_k), \tag{2}$$

where $\Lambda_r = \mathrm{diag}(\lambda_{r1}, \cdots, \lambda_{rp})$ is a diagonal matrix for residual variance, $W \in \mathbb{R}^{p \times q}$ is a loading matrix that transforms the p-dimensional expression vector into q-dimensional embeddings shared across M datasets, $\mu_k \in \mathbb{R}^{q \times 1}$ and $\Sigma_k \in \mathbb{R}^{q \times q}$ are the mean vector and covariance matrix for the kth cluster, respectively, and $\mathbf{v}_{ri}$ is a q-dimensional latent vector that captures the spatial dependence among neighboring spots and aligns embeddings across datasets. Eqn. (1) is related to the high-dimensional expression vector ($\mathbf{x}_{ri}$) in p genes with a low-dimensional feature ($\mathbf{z}_{ri}$) via a probabilistic PCA model [69] with consideration of spatial dependence while Eqn. (2) is a Gaussian mixture model (GMM) [70] for this latent feature among all spots across M datasets. To promote spatial smoothness in the space of cluster labels, we assume each latent class label, y_{ri}, is interconnected with the class labels of its neighborhoods via a discrete hidden Markov random field (HMRF). In detail, we use the

following Potts model for the latent labels,

$$P(\mathbf{y}_r) = C_r(\beta_r)^{-1} \exp\{-\frac{1}{2}\sum_i \sum_{i' \in N_{ri}} \beta_r(1 - \delta(y_{ri}, y_{ri'}))\}, \tag{3}$$

where $C_r(\beta_r)$ is a normalization constant that does not have a closed form, N_{ri} is the neighborhood of spot s_{ri} in sample r, and β_r is the sample-specific smoothing parameter that captures the label similarity among the neighboring spots. However, we assume a continuous multivariate HMRF for the vector, $\mathbf{v}_{ri}$, which captures spatial dependence in the embedding space. In detail, we assume an intrinsic CAR model [71] for $\mathbf{v}_{ri}$

$$\mathbf{v}_{ri}|\mathbf{v}_{[n_r]\setminus i} \sim N(\mu_{v_{ri}}, m_{ri}^{-1}\Psi_r), \tag{4}$$

where subscript $_{[n_r]\setminus i}$ denotes all spots but s_{ri} in sample r, m_{ri} is the number of neighbors of spot i in sample r, $\mu_{v_{ri}} = m_{ri}^{-1}\sum_{i' \in N_{ri}} \mathbf{v}_{ri'}$ is the conditional mean relevant to the neighbors of that spot s_{ri}, and Ψ_r is a $q \times q$ conditional covariance matrix for the elements of $\mathbf{v}_{ri}$. Conventionally, the joint distribution of the intrinsic CAR model is non-identifiable, as the mean of the joint distribution of intrinsic CAR is not zero. As shown in the next section, non-cluster-relevant effects, e.g., batch effects, from each slide can be projected onto the cluster-relevant embedding space, which can be corrected by the nonzero-mean property of intrinsic CAR.

Projections of non-cluster-relevant effects

For each tissue slide, we assume the normalized expressions in each sample r can be decomposed into additional parts with respect to non-cluster-relevant effects as follows:

$$\mathbf{x}_{ri} = W(\mathbf{z}_{ri} + \boldsymbol{\nu}_{ri}) + W_r\boldsymbol{\zeta}_{ri} + \boldsymbol{\varepsilon}_{ri}, \tag{5}$$

where $\boldsymbol{\nu}_{ri}$ is a q-dimensional vector that captures the spatial dependence among neighboring spots; $W_r \in \mathbb{R}^{p\times\tilde{q}}$ is a loading matrix for a factor related to non-cluster-relevant effects; and $\boldsymbol{\zeta}_{ri}$, independent of $(\mathbf{z}_{ri}, \boldsymbol{\nu}_{ri})$, is the corresponding $\tilde{q}$-dimensional vector. Assuming cluster-relevant biological space (W) and non-cluster-relevant biological space (W_r) are non-orthogonal, we can project W_rs onto the column spaces of W, i.e., $\widehat{W_r} = W(W^TW)^{-1}W^{\mathrm{T}}W_r$, and then rewrite the normalized expressions as the following

$$\mathbf{x}_{ri} \approx W(\mathbf{z}_{ri} + \boldsymbol{\nu}_{ri} + \widetilde{W}^{\mathrm{T}}W_r\boldsymbol{\zeta}_{ri}) + \boldsymbol{\varepsilon}_{ri},$$

where $\widetilde{W} = W(W^TW)^{-1}$. We denote $\mathbf{v}_{ri} = \boldsymbol{\nu}_{ri} + \widetilde{W}^{\mathrm{T}}W_r\boldsymbol{\zeta}_{ri}$, $\mu'_{v_{ri}} = E(\boldsymbol{\nu}_{ri}|\boldsymbol{\nu}_{[n_r]/i})$, $m_{ri}^{-1}\Psi'_r = \mathrm{var}(\boldsymbol{\nu}_{ri}|\boldsymbol{\nu}_{[n_r]/i})$, then the conditional mean and variance in the intrinsic CAR component can be written as

$$\begin{aligned}
\mathrm{E}(\mathbf{v}_{ri}|\mathbf{v}_{[n_r]/i}) &= \mu'_{v_{ri}} + \widetilde{W}^{\mathrm{T}}W_r\mathrm{E}(\boldsymbol{\zeta}_{ri}) \equiv \mu_{v_{ri}}, \\
\mathrm{var}(\mathbf{v}_{ri}|\mathbf{v}_{[n_r]/i}) &= m_{ri}^{-1}\Psi'_r + \widetilde{W}^{\mathrm{T}}W_r\mathrm{var}(\boldsymbol{\zeta}_{ri})W_r^{\mathrm{T}}\widetilde{W} \equiv m_{ri}^{-1}\Psi_r,
\end{aligned}$$

where we assume $\mathrm{var}(\boldsymbol{\zeta}_{ri}) = m_{ri}^{-1}\Psi''_r$. Then, the projected approximated model can be written as

$$\mathbf{x}_{ri} \approx W(\mathbf{z}_{ri} + \mathbf{v}_{ri}) + \boldsymbol{\varepsilon}_{ri}, r = 1, 2, \tag{6}$$

where $\mathbf{z}_{ri}|y_{ri} = k \sim N(\mu_k, \Sigma_k)$, and $\mathbf{v}_{ri}|\mathbf{v}_{[n_r]/i} \sim N(\mu_{v_{ri}}, m_{ri}^{-1}\Psi_r)$.

Recovery of comparable gene expression matrices

Once the estimated cluster labels are obtained by PRECAST, we can remove batch effects using a set of housekeeping genes as negative control genes that are not affected by other biological effects [72]. In this study, we used a set of mouse/human housekeeping genes from the Housekeeping and Reference Transcript Atlas [73]. First, we obtained vectors, $\tilde{\mathbf{x}}_{ri} = (\tilde{\mathbf{x}}_{ri1}, \cdots, \tilde{\mathbf{x}}_{hrL})$, of the expression of L housekeeping genes by matching the set of housekeeping genes and genes passing quality control for each dataset. By performing PCA, we obtained the top 10 PCs, $\widehat{\mathbf{m}}_{ri}$, as covariates to adjust for unwanted variation. One of the outputs of PRECAST, the posterior probability of y_{ri} ($\widehat{\mathbf{r}}_{ri} \in \mathbb{R}^K$), can be used as the design matrix to explain biological variation. Finally, we used linear model for the normalized gene expression vector

$$\mathbf{x}_{ri} = \widehat{\mathbf{r}}_{ri}^{\mathrm{T}}\boldsymbol{\alpha} + \widehat{\mathbf{m}}_{ri}^{\mathrm{T}}\boldsymbol{\gamma} + \varepsilon_{ri}, \tag{7}$$

where $\boldsymbol{\alpha}$ is a K-dimensional vector for biological effects and $\boldsymbol{\gamma}$ is a 10-dimensional vector of regression coefficients associated with the unwanted factors. After obtaining the parameter estimates in Eqn. (7), users can remove batch effects from the original normalized gene expression using

$$\widehat{\mathbf{x}}_{ri} = \mathbf{x}_{ri} - \widehat{\mathbf{m}}_{ri}^{\mathrm{T}}\widehat{\boldsymbol{\gamma}}.$$

This strategy can also be applied to samples from multiple biological conditions when such information is available. This can be achieved by adding additional covariates for biological conditions in Eqn. (7).

Differential expression analysis and enrichment analysis

After obtaining the batch corrected gene expression matrices for multiple slides, we performed DE analyses and enrichment analysis on all four datasets. In detail, we used the `FindAllMarkers` function in the R package *Seurat* with default settings to detect the differentially expressed genes for each domain detected by PRECAST. The DE analysis was considered to identify domain-specific DE genes with adjusted p-values of less than 0.001 and a log-fold change of greater than 0.25. After obtaining a set of genes specific to each domain, we performed gene set enrichment analysis (GSEA) on a set of detected DE genes using g:Profiler with the g:SCS multiple testing correction method and applying a significance threshold of 0.05 [74].

Conditional SVG analysis

After obtaining aligned embeddings and domain labels for DLPFC and HCC Visium data using PRECAST, we detected the SVGs by controlling the estimated domain-relevant embeddings as covariates to investigate the role of SVGs beyond domain-relevant differences. In detail, we used the function `spark.vc` in the R package *SPARK* to identify SVGs adjusted for domain-relevant covariates for each sample. Finally, an FDR of 1% was adopted to identify the significant SVGs.

Trajectory inference/RNA velocity analysis

To further investigate the development and differentiation of these identified spatial domains/cells by PRECAST, we used the aligned embeddings and domain clusters estimated by PRECAST to perform trajectory inference, or RNA velocity analysis if the splicing and unsplicing information was available. For the DLPFC Visium data and mouse OB and hippocampus Slide-seqV2 data, we conducted trajectory inference for the combined spots in all multiple tissue sections using Slingshot [75]. We inputted the aligned embeddings and domain clusters estimated by PRECAST into the function

`slingshot` in the R package *slingshot* for implementation. Because the splicing and unsplicing information was available for the HCC Visium dataset, we ran RNA velocity analysis using the `scvelo.tl.velocity` function in the Python module *scvelo* based on the splicing and unsplicing matrices, then the aligned embeddings and domain clusters estimated by PRECAST were used to visualize the inferred RNA velocity and latent time.

Cell-type deconvolution analysis

We performed deconvolution analysis using Robust Cell Type Decomposition (RCTD)[76], a supervised learning method used to decompose each spatial transcriptomics pixel into a mixture of individual cell types while accounting for platform effects. We leveraged the results of deconvolution analysis for better biological interpretation of the real data analysis.

For the HCC Visium data, we leveraged a droplet-based scRNA dataset collected from HCC and intra-hepatic cholangiocarcinoma patients to serve as the reference data for deconvolution [41]. After filtering out 92 cells of unclassified cell type, the reference data contained 5,023 cells belonging to seven cell types: B cells ($n = 598$), CAFs ($n = 724$), HPC-like cells ($n = 254$), malignant cells (702), T cells ($n = 1,429$), TAMs ($n = 437$), and TECs ($n = 879$). After acquiring the deconvolution results from the above-mentioned reference, we combined the proportions of B cells, T cells and TECs into a single set and referred to this as the immune cell proportion.

For the mouse OB Slide-seqV2 data, we used 10X Genomics Chromium scRNA-seq data collected from the wild-type OB [51]. The reference data included 17,453 cells belonging to 40 cell types: three astrocyte types (Astro1: $n = 1087$; Astro2: $n = 129$; Astro3: $n = 599$), two endothelial types (EC1: $n = 897$ and EC2: $n = 445$), two mesenchymal types (Mes1: $n = 200$ and Mes2: $n = 65$), three microglials (MicroG1: $n = 255$; MicroG2: $n = 766$; MicroG3: $n = 294$), monocytes ($n = 238$), two murals (Mural1: $n = 43$ and Mural2: $n = 272$), myelinating-oligodendrocyte cells ($n = 294$), macrophages ($n = 197$), five olfactory ensheathing cell types (OEC1: $n = 812$; OEC2: $n = 664$; OEC3:$n = 1073$; OEC4: $n = 1083$; OEC5: $n = 281$), oligodendrocyte progenitor cells (OPC: $n = 137$), red blood cells (RBCs: $n = 103$), and 18 neural subtypes (OSNs: $n = 467$; PGC-1: $n = 437$; PGC-2: $n = 146$; PGC-3 $n = 106$; GC-1: $n = 540$; GC-2: $n = 1245$; GC-3: $n = 96$; GC-4: $n = 80$; GC-5: $n = 516$; GC-6: $n = 89$; GC-7: 293; Immature: $n = 1150$; Transition: $n = 733$; Astrocyte-Like: $n = 1078$; M/TC-1: $n = 24$; M/TC-2: $n = 44$; M/TC-3: $n = 411$; EPL-IN: $n = 64$). For more details of the cell types, referred to Tepe et al. [51].

For mouse hippocampus Slide-seqV2 data, we used Drop-seq scRNA-seq data collected from the mouse hippocampus and adjacent areas in the posterior cortex and thalamus as reference data [60]. The reference data contained 72,845 cells that belonged to 33 cell types: anterior subiculum, proximal to CA1 ($n = 1,556$), astrocyte ($n = 7,503$), CA1 principal ($n = 2,489$), CA1 principle anterior ($n = 3,088$), CA2 ($n = 330$), CA3 ($n = 5,623$), Cajal Retzius ($n = 336$), choroid plexus ($n = 22$), deep layer subiculum ($n = 509$), dentate hilum ($n = 530$), dentate principal ($n = 13,265$), endothelial stalk ($n = 1,903$), endothelial tip ($n = 296$), entorhinal cortex ($n = 1,580$), entorhinal cortex (IEG) ($n = 27$), ependymal ($n = 337$), interneuron ($n = 3,035$), lateral CA3 principal ($n = 649$), lateral dorsal thalamic nuclei (LD) ($n = 680$), lateral geniculate nucleus (LGN) ($n = 722$), lateral habenula ($n = 26$), Layer 5 ($n = 14,875$), Layer 6 ($n = 5,068$), macrophages ($n = 78$), medial habenula ($n = 171$), medial habenular, lateral portion ($n = 188$), microglia ($n = 467$), mural ($n = 705$), myelin processes ($n = 227$), neurogenesis ($n = 458$), neurons ($n = 3,087$), oligodendrocytes ($n = 1,969$), polydendrocyte ($n = 1,046$).

Comparisons of methods

We conducted comprehensive simulation and real data analyses to compare PRECAST with existing methods of data integration and clustering.

We applied the following single-cell integration methods to benchmark the data integration performance of PRECAST: (1) Seurat V3 [24]; (2) Harmony [19] implemented in the R package *harmony*; (3) fastMNN [20] implemented in the R package *batchelor*; (4) Scanorama [23] implemented in the Python module *scanorama*. (5) scGen [26]; (6) scVI [25] implemented in the Python module *scvi*; (7) MEFISTO [27] implemented in the Python module *mofax*; and (8) PASTE [28] implemented in the Python module *paste*.

The first six methods were designed for scRNA-seq integration, while MEFISTO can be used for scRNA-seq and SRT data integration, and PASTE is designed for integrating SRT data from multiple adjacent tissue slices into a single slice. In detail, the Seurat V3 method is based on finding the mutual nearest neighbors. First, anchor pairs between different batches were obtained using the function `FindIntegrationAnchors` in the *Seurat* R package. Then, the `IntegrateData` function in *Seurat* was used to integrate the datasets based on the anchor pairs and their confidence scores. Finally, we obtained the 15-dimensional batch-corrected embeddings using the function `RunPCA` in *Seurat*. Compared with the original MNN method, fastMNN is a faster version based on PCA and is used to find mutual nearest neighbors, greatly increasing the computational efficiency. We used `fastMNN` in the R package *batchelor* with the top 15 PCs and other default parameters and obtained the 15-dimensional batch-corrected embeddings. Another PCA-based method, Harmony corrects batch-contaminated PCs by iteratively performing maximum diversity clustering and linear mixture model correction. For the analysis, we first obtained the 15-dimensional PCs by performing PCA on the combined normalized expression matrix, then took the obtained PCs and batch information as the input using the function `HarmonyMatrix` in the R package *harmony*, and lastly, obtained 15-dimensional batch-corrected embeddings as the output. Scanorama is a generalization of mutual nearest-neighbor matching used to find similar elements among many datasets. Instead of searching for similar elements in high-dimensional gene space, Scanorama applies randomized singular value decomposition to extract low-dimensional embeddings from the combined cell-by-gene expression matrix. We conducted the analysis following the author's pipeline `https://scanpy-tutorials.readthedocs.io/en/latest/spatial/integration-scanorama.html` and set the parameter *dimred=15* in function `correct_scanpy` to extract 15-dimensional batch-corrected embeddings. The pipelines for scGen and scVI, which are two deep-learning-based methods, were followed using the two respective links, `https://scgen.readthedocs.io/en/latest/tutorials/scgen_batch_removal.html` and `https://docs.scvi-tools.org/en/stable/tutorials/notebooks/tabula_muris.html`, and we set the number of latent embeddings to 15 for both methods in the analysis. MEFISTO is a factor-model-based integration method that integrates multiple datasets by simultaneously identifying and aligning the underlying patterns of variation. To implement this, we followed the author's pipeline provided at `https://github.com/bioFAM/MEFISTO_tutorials/blob/master/MEFISTO_microbiome.ipynb` and `https://github.com/bioFAM/MEFISTO_tutorials/blob/master/MEFISTO_ST.ipynb`, and set the number of factor to be 15. PASTE is pairwise alignment method that integrates adjacent slices based on transcriptional and spatial similarity using optimal transport and nonnegative matrix factorization, and we followed the author's pipeline `https://github.com/raphael-group/paste/blob/main/docs/source/notebooks/getting-started.ipynb` for implementation and set the number of low-dimensional representation of center slice to 15.

To evaluate the clustering performance, we considered the following two clustering methods that use extracted low-dimensional embeddings as input. (1) SC-MEB implemented in the R package

SC.MEB [65] and (2) Louvain implemented in the R package *igraph* [77]. SC-MEB was recently developed to perform spatial clustering based on a discrete Markov random field [65], while Louvain is a conventional non-spatial clustering algorithm based on community detection in large networks [77]. In the implementation, we set the default values for SC-MEB and Louvain clustering in the respective packages, except that the 15-dimensional embeddings and spatial coordinates were used as input for SC-MEB while only the embeddings were the input for Louvain. Similar to PRECAST, SC-MEB uses MBIC [78] to determine the number of clusters in a data-driven manner, while Louvain uses a community-modularity maximizing rule [77].

Evaluation metrics

We evaluated the methods' performances in batch correction, obtaining cluster-relevant embeddings, and spatial clustering using the following metrics.

Local inverse Simpson's index. To assess the performance of batch-effect removal, we used the cell-type/integration local inverse Simpson's index, cLISI and iLISI [19] to quantify the performance in merging the shared cell populations among tissue slides and mixing spots from M tissue slides. cLISI assigns a diversity score to each spot that represents the effective number of cell types in the neighborhoods of that spot. For M datasets with a total of K cell types, accurate integration should maintain a cLISI value close to 1, reflecting the purity of the unique cell types in the neighborhood of each spot, as defined in the low-dimensional embeddings. Erroneous embedding would include neighborhoods with a cLISI of more than 1, while the worst case has cLISI close to K, suggesting that neighbors have K different types of cells. iLISI has a similar form and interpretation as cLISI but is based on a sample index set rather than clusters of cell types. Thus, a larger iLISI value means the different samples have more sufficient mixing.

Silhouette coefficient. To simultaneously evaluate the separation of each cell/domain cluster and mixing of multiple datasets, we calculated the average silhouette coefficient of the SRT datasets using two different groupings: (1) grouping using known cell types as the cell/domain-type silhouette coefficient ($\text{silh}_{cluster}$) and (2) grouping using different datasets as the batch silhouette coefficient (silh_{batch}). In the data integration, a larger value of $\text{silh}_{celltype}$ indicates better preservation of the cluster-relevant biological signals, while a smaller value of silh_{batch} suggests better mixing of datasets. These two metrics can be summarized using the F1 score as follows [79]:

$$\text{F1_score_silh} = \frac{2(1-\text{silh}'_{\text{batch}})\text{silh}'_{\text{cluster}}}{\text{silh}'_{\text{cluster}} + (1-\text{silh}'_{\text{batch}})} \in [0,1],$$

where $\text{silh}'_{\text{batch}} = \frac{1+\text{silh}_{\text{batch}}}{2}$ and $\text{silh}'_{\text{cluster}} = \frac{1+\text{silh}_{\text{cluster}}}{2}$. A larger F1 score suggests better data integration that preserves the cluster-relevant biological variations while removing other non-cluster-relevant variations across multiple tissues.

Canonical correlation coefficients and/or conditional correlation. For dimension reduction, we applied two measurements to assess the performance of true latent feature recovery in the simulation studies. The first is the mean canonical correlation between the estimated features and the true one, defined as

$$\text{CCor} = \frac{1}{q}\sum_{l=1}^{q} \zeta_l(\mathbf{z}_i, \hat{\mathbf{z}}_i),$$

where ζ_l is the l-th canonical correlation coefficient. The second measure is the mean conditional correlation between gene expression $\mathbf{x}_i$ and cell type label y_i given the estimated latent features $\hat{\mathbf{z}}_i$,

defined as

$$\text{ConCor} = \frac{1}{p}\sum_{j=1}^{p} corr(y_i, resid_{ij}),$$

where $resid_i$ is the residual of x_{ij} regressing on $\widehat{\mathbf{z}}_i$, and $corr(y_i, resid_{ij})$ is the Pearson correlation coefficient between y_i and $resid_{ij}$.

Adjusted Rand index and/or normalized mutual information. To evaluate the performance of spatial clustering, we used ARI [80] and NMI [81]. ARI is the corrected version of the Rand index (RI) [82] that is used avoid some drawbacks of RI [80]. The ARI measures the similarity between two different partitions and ranges from -1 to 1. A larger value of ARI means a higher degree of similarity between two partitions. ARI takes a value of 1 when the two partitions are equal up to a permutation. Whereas, NMI is a variant of the mutual information (MI) that normalizes the value of MI to a range from zero to one. When the two partitions are equal up to a permutation, the NMI takes a value of 1.

Simulations

Scenario 1. Normalized gene expression data: domain labels and spatial coordinates from Potts model. For this scenario, we generated the normalized gene expression data for three samples as well as spatial coordinates based on Potts models with four neighborhoods. All quantities, such as the labels y_{ri}s and latent features $\boldsymbol{\nu}_{ri}$s for spots, were randomly simulated from the generative model (5). In detail, we generated the class label y_{ri} for each $r = 1, 2, 3$ and $i = 1, \cdots, n_r$ with $n_r \in \{65 \times 65, 60 \times 60, 60 \times 60\}$ corresponding to rectangular lattices from a K-state (K=7) Potts model with the smoothing parameter $\beta_r = 0.8 + 0.2(r-1)$ using the function `sampler.mrf` in R package *GiRaF*. Then, we generated latent features $\boldsymbol{\nu}_{ri}$s from the CAR model with the same N_{ri} as defined in the Potts model and covariance matrix $\Psi'_r = (\sigma_{r,ij})$ with $\sigma_{r,ij} = r(0.2r)^{|i-j|}$ using the function `rmatrixnorm` in R package *LaplacesDemon*. We set different values for the smoothing parameter β_r and covariance matrices Ψ'_r across r to mimic the heterogeneity of three samples. The domain labels y_{ri}s and latent features $\boldsymbol{\nu}_{ri}$s were fixed once they were obtained.

Then, we generated domain-related latent low-dimensional features $\mathbf{z}_{ri}$ in the model (5) from the conditional Gaussian, such that $\mathbf{z}_{ri}|y_{ri} = k \sim (\mu_k, \Sigma_k)$, where $\mathbf{z}_{ri} \in R^q$ with $q = 10$ and structures for μ_k and Σ_k are shown in Supplementary Table S9. Next, we generated $\widetilde{W} = (\widetilde{w}_{ij}, i \le p, j \le q)$ with each $\widetilde{w}_{ij} \overset{i.i.d.}{\sim} N(0,1)$, performed QR decomposition on $\widetilde{W}$ such that $\widetilde{W} = \widetilde{Q}\widetilde{R}$, and assigned $W = \widetilde{Q}$, which is a column orthogonal matrix. Then, we generated a batch-loading matrix W_r by generating $\bar{W}_r = \bar{W} + \bar{E}_r$ with $\bar{W} = (\bar{w}_{ij}, i \le p = 2{,}000, j \le q_r), q_r = 2$ and $\bar{w}_{ij} \overset{i.i.d.}{\sim} N(0,1)$ and $\bar{E}_r = (\bar{e}_{rij}, i \le p, j \le q_r)$ and $\bar{e}_{rij} \sim N(0, \bar{\sigma}_r^2)$ with $\bar{\sigma}_1 = 0.5, \bar{\sigma}_2 = 0.8, \bar{\sigma}_3 = 1$. Similar to the generation of W, we performed orthogonalization of $\bar{W}_r$ to generate W_r. Next, we generated $\boldsymbol{\zeta}_{ri}$ in the model (5) by $\boldsymbol{\zeta}_{ri} = (\zeta_{ri1}, \cdots, \zeta_{riq_r})^{\mathrm{T}}$ such $\zeta_{rik} \overset{i.i.d.}{\sim} N(0, \sigma_r^2)$ with $\sigma_1 = 1, \sigma_2 = 2$ and $\sigma_3 = 0.5$. Finally, we generated a high-dimensional normalized expression matrix using $\mathbf{x}_{ri} = W(\mathbf{z}_{ri} + \boldsymbol{\nu}_{ri}) + W_r\boldsymbol{\zeta}_{ri} + \boldsymbol{\varepsilon}_{ri}, \boldsymbol{\varepsilon}_{ri} \sim N(\mathbf{0}, \Lambda_r)$, where $\Lambda_r = \text{diag}(\lambda_{rj}), j = 1, \ldots, p$, $\lambda_{1j} = 2(1 + 1.5|z_{1j}|)$ with $z_{1j} \overset{i.i.d.}{\sim} N(0,3)$; $\lambda_{2j} = 2(1 + z_{2j})$ with $z_{2j} \overset{i.i.d.}{\sim} U[0,1]$; and $\lambda_{3j} = 2(1 + 2z_{3j})$ with $z_{3j} \overset{i.i.d.}{\sim} U[0,1]$.

Scenario 2. Raw gene expression count data: domain labels and spatial coordinates from Potts model. In Scenario 2, we generated the raw gene expression data. The class label y_{ri}, loading matrices W, W_r, latent features $\boldsymbol{\nu}_{ri} and \mathbf{z}_{ri}$, and error term $\boldsymbol{\varepsilon}_{ri}$ were generated in the same as in Scenario 1, except that μ_k had a different value (Supplementary Table S9). The other difference was we generated normalized gene expressions $\mathbf{x}_i$ using $\mathbf{x}_{ri} = \tau_r + W(\mathbf{z}_{ri} + \boldsymbol{\nu}_{ri}) + W_r\boldsymbol{\zeta}_{ri} + \boldsymbol{\varepsilon}_{ri}, \tau_{rj} \sim N(0,4)$

and raw gene expressions $\tilde{\mathbf{x}}_i$ by using $\tilde{x}_{rij} \sim Poisson(exp(x_{rij}))$, where τ_{rj} is the j-th element of τ_r. The term $\boldsymbol{\varepsilon}_{ri}$ makes the distribution of $\tilde{\mathbf{x}}_{rij}$ over-dispersed, which can better imitate the properties of count expression. In this scenario, for each sample r, we only observed raw gene expression $\tilde{x}_{rij}$ of gene j and spot i and spatial coordinates s_{ri} for spot i.

Scenario 3. Normalized gene expression data: domain labels and spatial coordinates from DLPFC data. To validate the generality of PRECAST, we also generated data based on three DLFPC datasets (ID: 151507, 151669 and 151673) from three donors (Visium platform). The domain labels y_{ri}s for spots were obtained from the expert annotations from Maynard et al. [17] together with the spatial coordinates. To generate the latent features $\boldsymbol{\nu}_{ri}$s, PRECAST was used to fit the three datasets, then we used the estimated features $\hat{\boldsymbol{\nu}}_{ri}$s as input. The cluster labels y_{ri}s and latent features $\boldsymbol{\nu}_{ri}$s were fixed once they were obtained. The other quantities were generated in the same way as in Scenario 1 but with a different μ_k (Supplementary Table S9).

Scenario 4. Raw gene expression data: domain labels and spatial coordinates from DLPFC data. In this scenario, we also generated the raw gene expression data. The class label y_{ri}, loading matrices W, W_r, latent features $\boldsymbol{\nu}_{ri}$ and $\mathbf{z}_{ri}$ were generated as in Scenario 3. The only difference was we generated normalized gene expression $\mathbf{x}_i$ using $\mathbf{x}_{ri} = \tau_r + W(\mathbf{z}_{ri} + \boldsymbol{\nu}_{ri}) + W_r\boldsymbol{\zeta}_{ri} + \boldsymbol{\varepsilon}_{ri}, \tau_{rj} \sim N(0, 4)$ and $\boldsymbol{\varepsilon}_{ri} \sim N(\mathbf{0}, \Lambda_r)$, where $\Lambda_r = \text{diag}(\lambda_{rj}), j = 1, \ldots, p$, $\lambda_{1j} = 2(1 + 0.5|z_{1j}|)$ with $z_{1j} \overset{i.i.d.}{\sim} N(0, 3)$; $\lambda_{2j} = 2(1 + 0.2z_{2j})$ with $z_{2j} \overset{i.i.d.}{\sim} U[0, 1]$; and $\lambda_{3j} = 2(1 + z_{3j})$ with $z_{3j} \overset{i.i.d.}{\sim} U[0, 1]$. Then the raw gene expressions $\tilde{\mathbf{x}}_i$ using $\tilde{x}_{rij} \sim Poisson(exp(x_{rij}))$, where τ_{rj} is the j-th element of τ_r. The term $\boldsymbol{\varepsilon}_{ri}$ makes the distribution of $\tilde{\mathbf{x}}_{rij}$ over-dispersed, which can better imitate the properties of count expression.

Scenario 5. Raw gene expression data: count matrix, domain labels and spatial coordinates and from DLPFC data. To make PASTE comparable with other methods, we obtained the raw gene expressions, domain labels and spatial coordinates from all three tissue slides (ID: 151673, 151674 and 151675) in the last donor, where the domain labels were from the expert annotations in Maynard et al. [17]. In this case, the true low-dimensional embeddings are unknown, so we did not evaluate the canonical correlation. Similar to Zeira et al. [28], to generate count matrix, we randomly added a pseudocount for each raw count from a binomial distribution with size three and probability parameter 0.3. Finally, we obtained the count matrix as well as spatial coordinates as input for compared methods. The domain labels were used to evaluate ARI and cLISI.

Data resources

Human dorsolateral prefrontal cortex Visium data

We downloaded spatial transcriptomic data obtained on the 10x Visium platform for human DLPFC from `https://github.com/LieberInstitute/spatialLIBD`. These data were collected from 12 human postmortem DLPFC tissue sections from three independent neurotypical adult donors, and the raw expression count matrix contained 33,538 genes for each sample, with a total of 47,681 spatial locations. Before conducting the analysis, we first performed quality control (QC) on each sample to filter out genes with non-zero expression levels for fewer than 20 spots and the spots with nonzero expression levels on less than 20 genes. The filtering step led to sets of 14,535 genes on average in a total of 47,680 spatial locations. For each sample, we performed log-normalization, followed by

centering, and selected the top 2,000 SVGs using SPARK [83]. Next, we prioritized genes based on the number of times they were selected as SVGs in all 12 samples and chose the top 2,000 genes as the input for the analysis. The annotated spatial domains in all 12 samples based on the cytoarchitecture in the original study [17] were layer 1 (n=5,321), layer 2 (n=2,858), layer 3 (n= 17,587), layer 4 (n=3,547), layer 5 (n=7,300), layer 6 (n=6,201), white matter (n=4,514), and undetermined spots (n=352). In the analysis, we treated these manual annotations as the ground truth to evaluate the clustering performance of the different methods.

Human hepatocellular carcinoma Visium data

These data were from two tissue sections from each tumor and tumor-adjacent region from an HCC patient, and contained 36,601 genes from over a total of 9,813 spatial locations. In the QC steps, we first filtered out genes with non-zero expression levels in fewer than 20 spots and spots with non-zero expression levels for fewer than 20 genes. The filtering step led to a set of 14,851 genes on average from a total of 9,813 locations. For each tissue section, we performed log-normalization, followed by centering, and selected the top 2,000 SVGs using SPARK. Next, we prioritized genes based on the number of times they were selected as SVGs in all four samples, and we chose the top 2,000 genes as the input for the analysis. In this data, we provided manual annotations for the TNE and stroma regions annotated by a pathologist with the Visium companion H&E images. We further performed spatial deconvolution to examine the spatial distribution of malignant cells using RCTD [76].

Mouse olfactory bulb Slide-seqV2 data

We obtained the data for 20 mouse OB Slide-seqV2 sections in replicate 2 from CNBI with accession number GSE169021 `https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE169021`. We used the first 16 slides because of the low quality of the last four slides. The data contained 21,571 genes on average over all 693,863 spatial locations across 16 sections, which were are equally distributed along the anterior-posterior axis of the same mouse. In the QC steps, we first filtered out genes with non-zero expression levels in fewer than 20 spots and spots with non-zero expression levels for fewer than 20 genes. The filtering step led to a set of 14,307 genes on average at a total of 594,890 locations. For each tissue slide, we performed log-normalization followed by centering, and selected the top 2,000 SVGs using SPARK-X [84] for computational efficiency. Next, we prioritized genes based on the number of times they were selected as SVGs in all 16 tissue slides, and we chose the top 2,000 genes as input for the analysis. To evaluate the impact of spatial resolution, we further collapsed nearby spots in each tissue slide using square grids of size 70×70. Then, the same QC steps were performed to obtain the normalized expression for the analysis. To examine the structure of the mouse OB, we relied on the structural annotation in the Allen Brain Atlas [47] and used the results of downstream analyses to determine the specific regions of OB.

Mouse hippocampus Slide-seqV2 data

We downloaded the two sets of mouse hippocampus Slide-seqV2 data, "Puck_191204_01" and "Puck_200115_08", from `https://singlecell.broadinstitute.org/single_cell/study/SC`

P815/highly-sensitive-spatial-transcriptomics-at-near-cellular-resolution-with-slide-seqv2#/. The two datasets contained 22,457/23,264 genes measured over 34,035/53,208 spatial spots. In the QC steps, we first filtered out genes with non-zero expression levels in fewer than 20 spots and spots with non-zero expression levels for fewer than 20 genes. The filtering step led to a set of 15,301 genes on average from a total of 82,876 locations. For each tissue slide, we performed log-normalization, followed by centering, and selected the top 2,000 SVGs using SPARK-X. Next, we prioritized genes based on the number of times they were selected as SVGs in both two datasets, and chose the top 2,000 genes as the input for the analysis. To evaluate the impact of spatial resolution, we further collapsed nearby spots for each tissue slide using square grids of size 70×70. Then, the same QC steps were performed to obtain the normalized expression for the analysis. To examine the structure of the mouse hippocampus, we relied on the structural annotation in the Allen Brain Atlas [47] and used results from the downstream analyses to determine the specific regions of mouse hippocampus.

Data availability

All datasets used in this study are publicly available. These include the 12 human dorsolateral prefrontal cortex Visium datasets (https://github.com/LieberInstitute/spatialLIBD), four human hepatocellular carcinoma Visium datasets (access available upon reviewer's request), 16 mouse OB Slide-seqV2 datasets (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE169021) and two mouse hippocampus Slide-seqV2 datasets (https://singlecell.broadinstitute.org/single_cell/data/public/SCP815/sensitive-spatial-genome-wide-expression-profiling-at-cellular-resolution#study-summary).

Code availability

The PRECAST methods are implemented in an open-source, publicly available R package that is available at https://cran.r-project.org/package=PRECAST and https://github.com/feiyoung/PRECAST. The code to reproduce the analysis can be found at https://github.com/feiyoung/PRECAST_Analysis.

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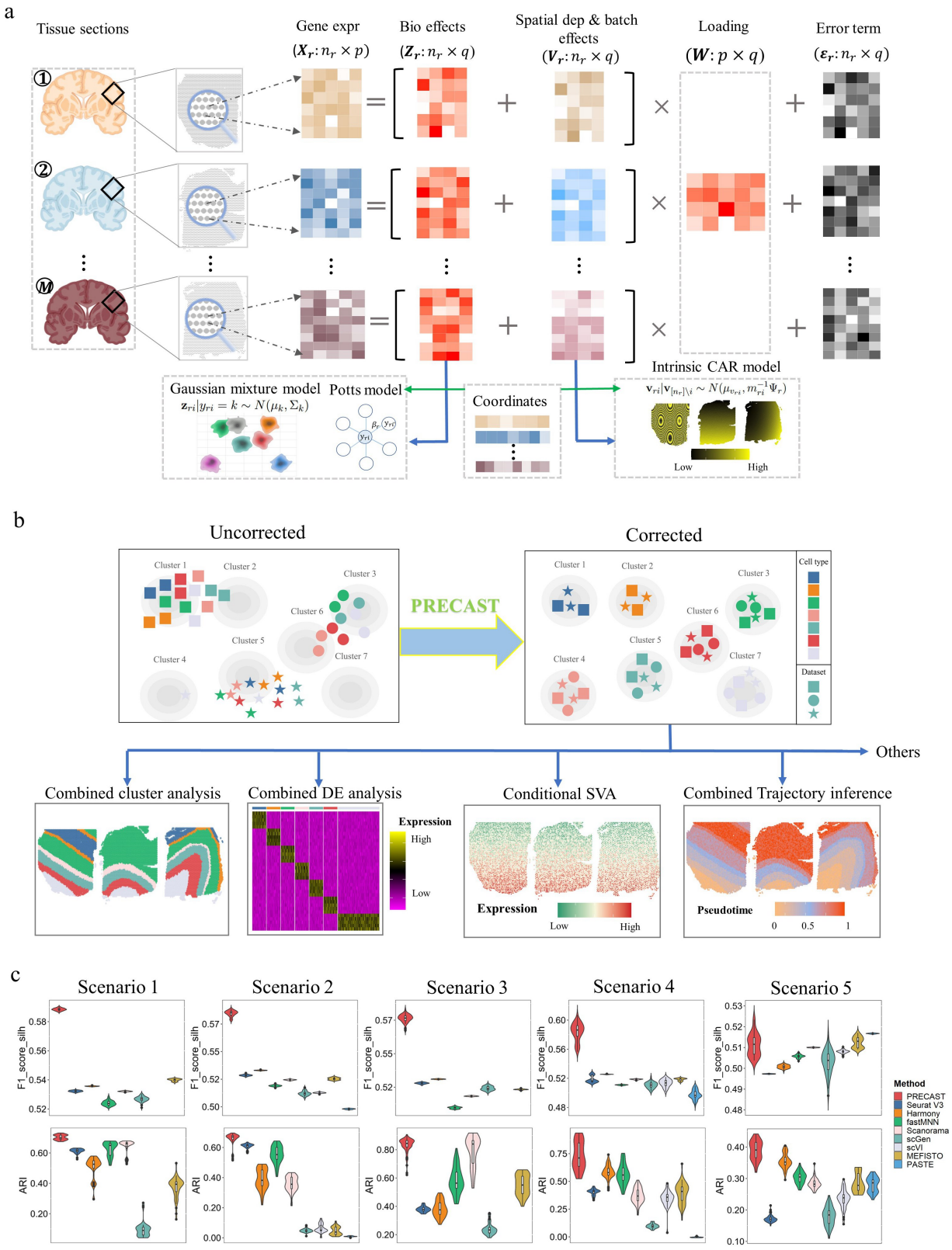
a
Tissue sections
Gene expr
$(\boldsymbol{X_r}: n_r \times p)$
Bio effects
$(\boldsymbol{Z_r}: n_r \times q)$
Spatial dep & batch effects
$(\boldsymbol{V_r}: n_r \times q)$
Loading
$(\boldsymbol{W}: p \times q)$
Error term
$(\boldsymbol{\varepsilon_r}: n_r \times q)$
Gaussian mixture model
$\mathbf{z}_{ri}|y_{ri} = k \sim N(\mu_k, \Sigma_k)$
Potts model
Coordinates
Intrinsic CAR model
$\mathbf{v}_{ri}|\mathbf{v}_{[n_r]\setminus i} \sim N(\mu_{v_{ri}}, m_{ri}^{-1}\Psi_r)$
Low
High
b
Uncorrected
Cluster 1
Cluster 2
Cluster 3
Cluster 4
Cluster 5
Cluster 6
Cluster 7
PRECAST
Corrected
Cell type
Dataset
Others
Combined cluster analysis
Combined DE analysis
Expression
High
Low
Conditional SVA
Expression
Low
High
Combined Trajectory inference
Pseudotime
0
0.5
1
c
Scenario 1
Scenario 2
Scenario 3
Scenario 4
Scenario 5
F1_score_silh
ARI
Method
PRECAST
Seurat V3
Harmony
fastMNN
Scanorama
scGen
scVI
MEFISTO
PASTE

Figure 1: Schematic overview of PRECAST and simulation results. (a) PRECAST is a unified probabilistic factor model that simultaneously estimates the aligned embeddings and cluster labels with consideration of spatial smoothness in both the cluster label and low-dimensional embedding spaces. It takes, as input, the normalized gene expression matrices from multiple tissue slides. (b) Examples of PRECAST downstream analyses. (c) In the simulations, we considered two ways to generate gene expression, continuous or count matrix, followed by log-normalization. We also considered two ways to generate spatial coordinates and cell/domain labels: Potts model and three cortex tissues from the DLPFC data. Lastly, we considered a scenario favored in PASTE. We evaluated the performance of the data integration, estimation of aligned embeddings, and spatial clustering using F1 scores of average silhouette coefficients and the adjusted Rand index (ARI), respectively, and the displayed ARIs for other methods were evaluated based on the results of the spatial clustering method SC-MEB. PRECAST outperformed all other data integration methods according to these assessments in Scenario 1-4 and is comparable with PASTE in Scenario 5. It is noted that scVI and PASTE are only applicable to Scenario 2, 4 and 5 with count matrix.

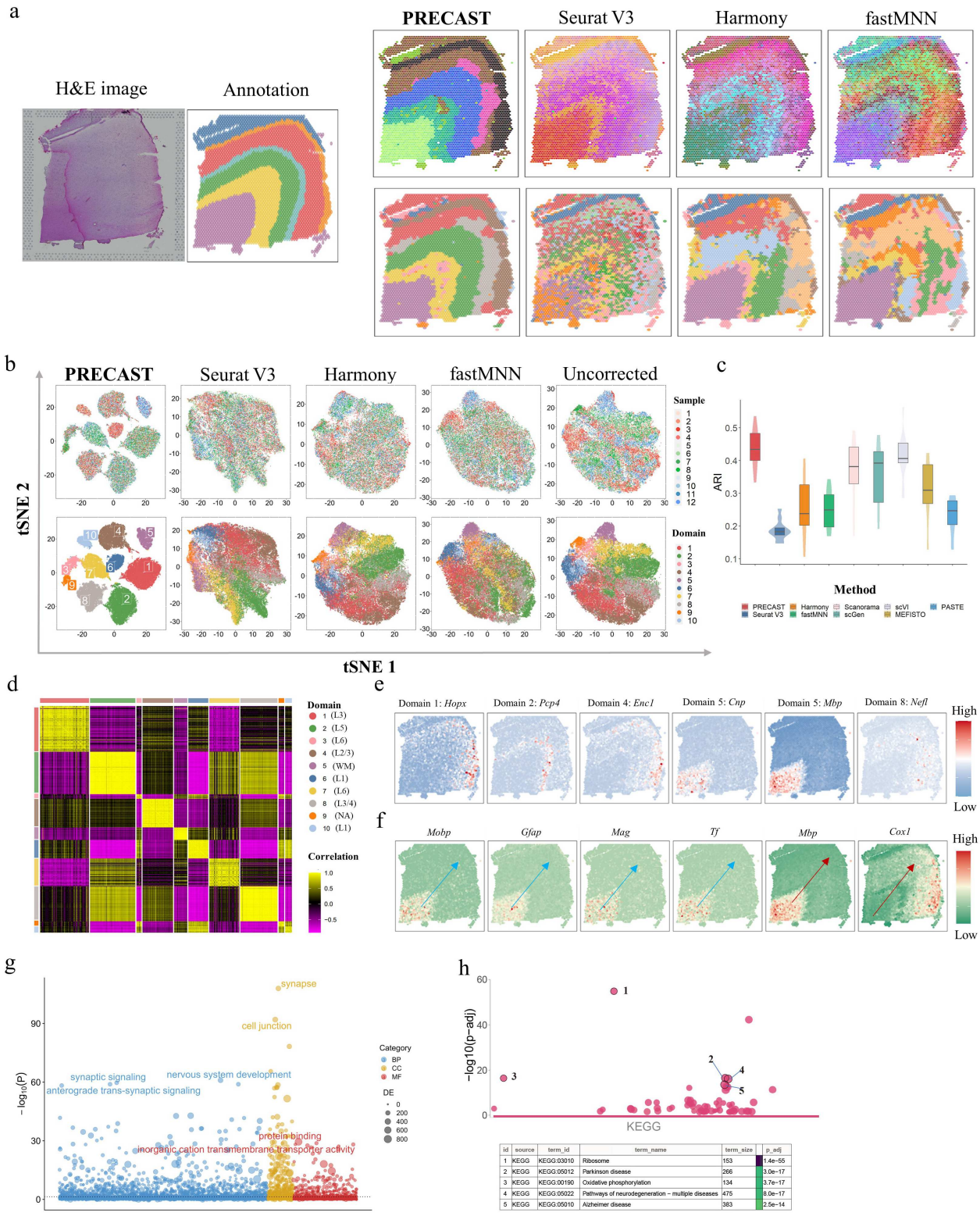
a
H&E image
Annotation
PRECAST
Seurat V3
Harmony
fastMNN
b
PRECAST
Seurat V3
Harmony
fastMNN
Uncorrected
tSNE 2
tSNE 1
Sample
Domain
c
ARI
Method
PRECAST
Seurat V3
Harmony
fastMNN
Scanorama
scGen
scVI
MEFISTO
PASTE
d
Domain
1 (L3)
2 (L5)
3 (L6)
4 (L2/3)
5 (WM)
6 (L1)
7 (L6)
8 (L3/4)
9 (NA)
10 (L1)
Correlation
e
Domain 1: Hopx
Domain 2: Pcp4
Domain 4: Enc1
Domain 5: Cnp
Domain 5: Mbp
Domain 8: Nefl
High
Low
f
Mobp
Gfap
Mag
Tf
Mbp
Cox1
High
Low
g
synapse
cell junction
synaptic signaling
nervous system development
anterograde trans-synaptic signaling
protein binding
inorganic cation transmembrane transporter activity
Category
BP
CC
MF
DE
h
KEGG
id source term_id term_name term_size p_adj
1 KEGG KEGG:03010 Ribosome 153 1.4e−55
2 KEGG KEGG:05012 Parkinson disease 266 3.0e−17
3 KEGG KEGG:00190 Oxidative phosphorylation 134 3.7e−17
4 KEGG KEGG:05022 Pathways of neurodegeneration − multiple diseases 475 8.0e−17
5 KEGG KEGG:05010 Alzheimer disease 383 2.5e−14

Figure 2: Analysis of data for 12 human DLPFC sections. (a) Left panel: H&E image and manual annotation of sample ID151674. Top panel: UMAP RGB plots of sample ID151674 for PRECAST, Seurat V3, Harmony, and fastMNN. Bottom panel: Clustering assignment heatmaps for these four methods. Color scheme used in clustering assignment heatmap for PRECAST is the same with (b) and (d). (b) tSNE plots for these four data integration methods with right-most column showing the analysis without correction; domains are labeled as in (d). (c) Box/violin plot of ARI values for PRECAST and other methods; SC-MEB was used in the other methods for clustering based on their low-dimensional embeddings. (d) Heatmap of Pearson's correlation coefficients among detected domains. (e) Spatial expression patterns of DE genes for Domain 1 (*Hopx*), Domain 2 (*Pcp4*), Domain 4 (*Enc1*), Domain 5 (*Cnp*), Domain 5 (*Mbp*), and Domain 8 (*Nefl*) for sample ID151674. (f) Spatial expression patterns of genes associated with pseudotime: *Mobp*, *Gfap*, *Mag*, *Tf*, *Mbp*, and *Cox1*, where the arrow represents the direction of the increased pseudotime. (g) Bubble plot of -log10(P-values) for GO enrichment analysis of genes associated with pseudotime. (h) Bubble plot of -log10(P-values) for KEGG enrichment analysis of SVGs while controlling domain-relevant embeddings by PRECAST for sample ID151674.

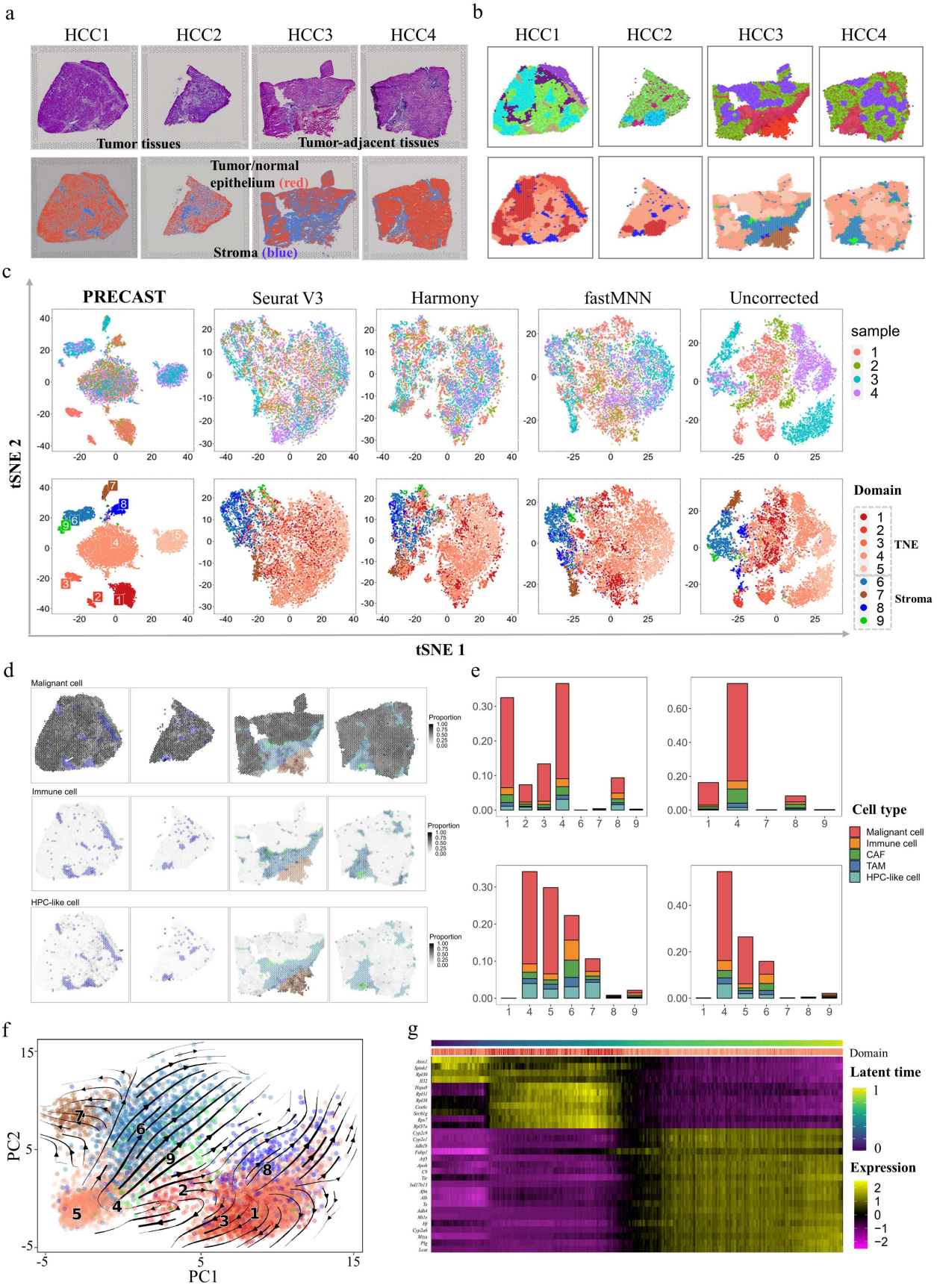
a
HCC1
HCC2
HCC3
HCC4
Tumor tissues
Tumor-adjacent tissues
Tumor/normal epithelium (red)
Stroma (blue)
b
HCC1
HCC2
HCC3
HCC4
c
PRECAST
Seurat V3
Harmony
fastMNN
Uncorrected
sample
1
2
3
4
Domain
TNE
Stroma
tSNE 2
tSNE 1
d
Malignant cell
Immune cell
HPC-like cell
Proportion
e
Cell type
Malignant cell
Immune cell
CAF
TAM
HPC-like cell
f
PC1
PC2
g
Domain
Latent time
Expression

Figure 3: Analysis of data for four human HCC sections. (a) Top panel: H&E images from four tissue slides. Bottom panel: Manual annotation by a pathologist of four tissue slides. (b) Top panel: UMAP RGB plots of PRECAST for four tissue slides. Bottom panel: Clustering assignment heatmaps for four tissue sections by PRECAST. Color scheme for clustering assignment heatmap in PRECAST is the same as in (c), (f), and (g). (c) tSNE plots for four data integration methods with the right-most column showing analysis without correction; domains are labeled as in (e) and (f). TNE, tumor/normal epithelium. (d) Spatial heatmap of deconvoluted cell proportions in malignant cells, immune cells, and HPC-like cells. (e) Percentage of different cell types in each domain detected by PRECAST, with (left panel) or without (right panel) scaling to the summation of all cell types across all domains equal to 100%. (f) PC plot of estimated RNA velocity. (g) Heatmap of genes with expression change in the latent time.

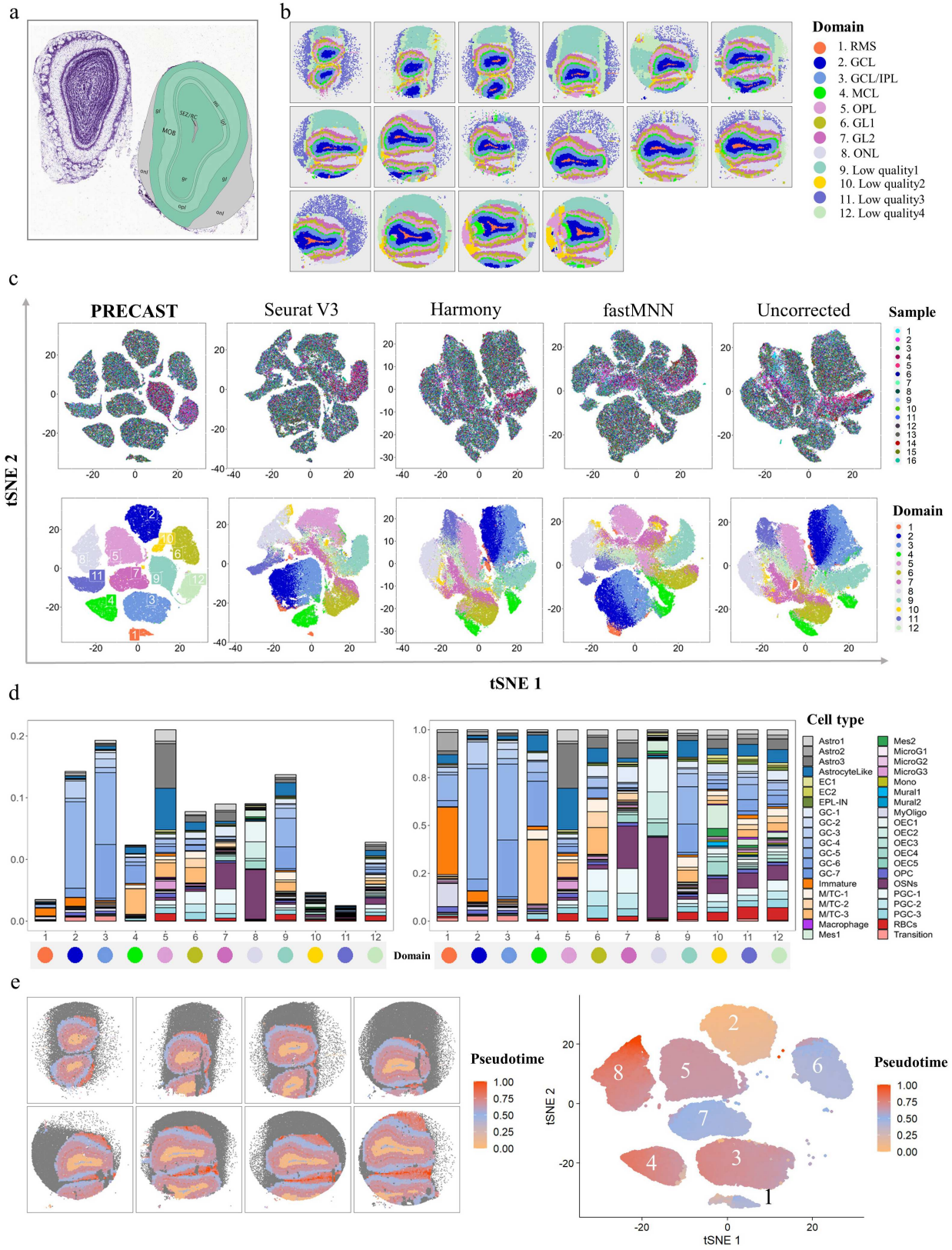
a
b
Domain
1. RMS
2. GCL
3. GCL/IPL
4. MCL
5. OPL
6. GL1
7. GL2
8. ONL
9. Low quality1
10. Low quality2
11. Low quality3
12. Low quality4
c
PRECAST
Seurat V3
Harmony
fastMNN
Uncorrected
Sample
Domain
tSNE 2
tSNE 1
d
Cell type
Astro1
Astro2
Astro3
AstrocyteLike
EC1
EC2
EPL-IN
GC-1
GC-2
GC-3
GC-4
GC-5
GC-6
GC-7
Immature
M/TC-1
M/TC-2
M/TC-3
Macrophage
Mes1
Mes2
MicroG1
MicroG2
MicroG3
Mono
Mural1
Mural2
MyOligo
OEC1
OEC2
OEC3
OEC4
OEC5
OPC
OSNs
PGC-1
PGC-2
PGC-3
RBCs
Transition
Domain
e
Pseudotime
1.00
0.75
0.50
0.25
0.00
tSNE 2
tSNE 1

Figure 4: Analysis of data for 16 mouse olfactory bulb sections. (a) Structure of the mouse olfactory bulb annotated using the Allen Brain Atlas. (b) Clustering assignment heatmaps for 16 tissue slides by PRECAST, where the first row shows samples 1 to 6, the second row samples 7 to 12, and last row samples 13 to 16 (RMS, rostral migratory stream; GCL, granule cell layer; IPL, inner plexiform layer; MCL, mitral cell layer; OPL, outer plexiform layer; GL, glomerular layer; ONL, olfactory nerve layer). Color scheme for domains detected in PRECAST is as in (c) and (d), and the order of domain labels in (b) is the same as in (c), (d), and (e). (c) tSNE plots for four data integration methods with the right-most column showing analysis without correction. (d) Percentage of different cell types in each domain detected by PRECAST with (left panel) or without (right panel) scaling to the summation of all cell types across all domains equal to 100%. (e) Visualization of the trajectory inferred by PRECAST in spatial heatmap for samples 1-8 (left panel) and tSNE plot of all samples(right panel).

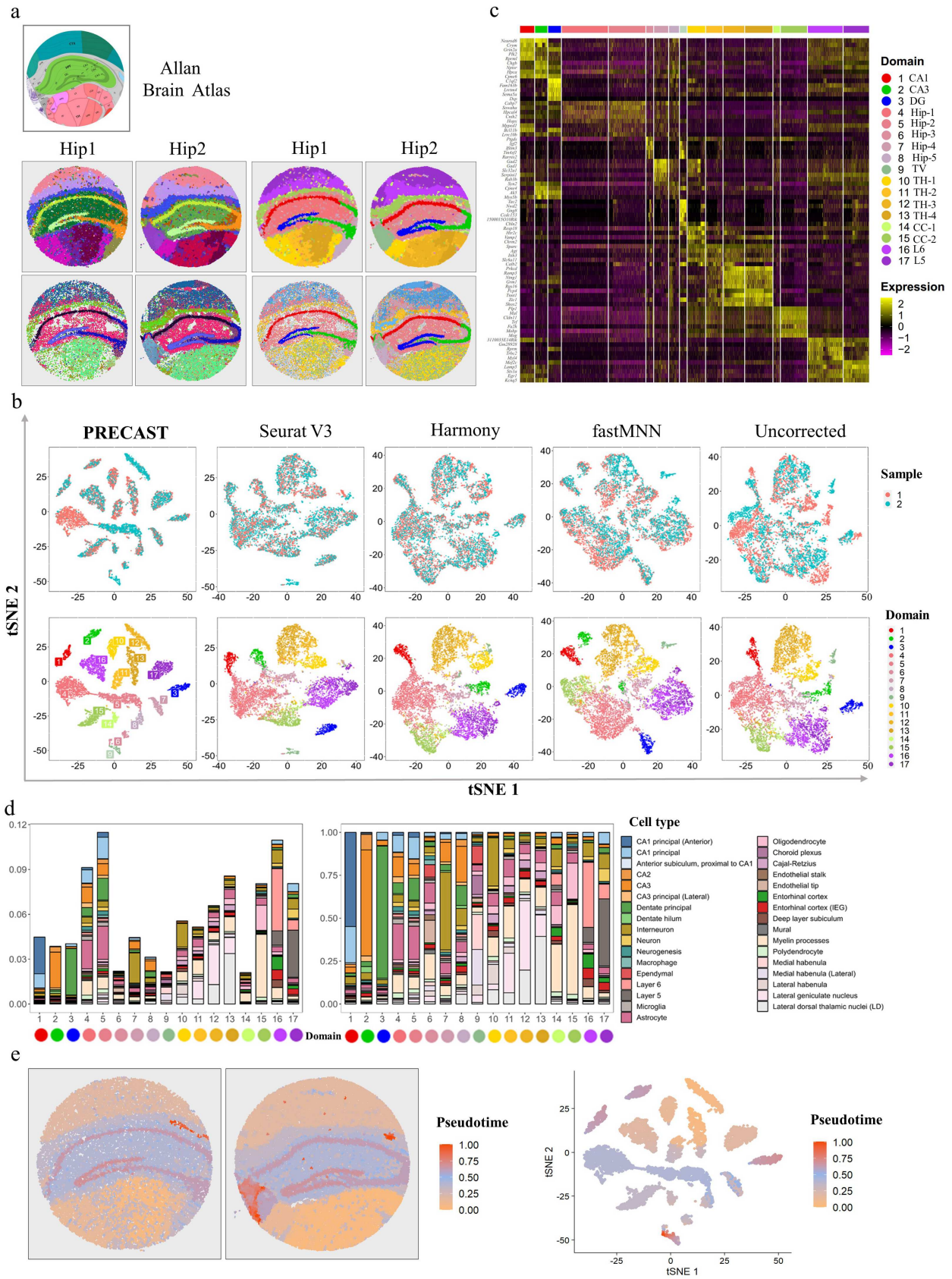
a
Allan
Brain Atlas
Hip1
Hip2
Hip1
Hip2
c
Domain
1 CA1
2 CA3
3 DG
4 Hip-1
5 Hip-2
6 Hip-3
7 Hip-4
8 Hip-5
9 TV
10 TH-1
11 TH-2
12 TH-3
13 TH-4
14 CC-1
15 CC-2
16 L6
17 L5
Expression
b
PRECAST
Seurat V3
Harmony
fastMNN
Uncorrected
Sample
Domain
tSNE 2
tSNE 1
d
Cell type
CA1 principal (Anterior)
CA1 principal
Anterior subiculum, proximal to CA1
CA2
CA3
CA3 principal (Lateral)
Dentate principal
Dentate hilum
Interneuron
Neuron
Neurogenesis
Macrophage
Ependymal
Layer 6
Layer 5
Microglia
Astrocyte
Oligodendrocyte
Choroid plexus
Cajal-Retzius
Endothelial stalk
Endothelial tip
Entorhinal cortex
Entorhinal cortex (IEG)
Deep layer subiculum
Mural
Myelin processes
Polydendrocyte
Medial habenula
Medial habenula (Lateral)
Lateral habenula
Lateral geniculate nucleus
Lateral dorsal thalamic nuclei (LD)
Domain
e
Pseudotime
Pseudotime
tSNE 2
tSNE 1

Figure 5: Analysis of data for two mouse hippocampus sections. (a) Top panel: Structure of the mouse hippocampus annotated using the Allen Brain Atlas. Middle panel: UMAP RGB plots (first two) and clustering assignment heatmaps (latter two) for PRECAST analysis of low-resolution data. Bottom panel: RGB plots (frst two) and clustering assignment heatmaps (latter two) for PRECAST analysis of data at the original resolution. Color scheme of clustering assignment heatmap for the reduced resolution for PRECAST is the same as in (b), (c), and (d) while color scheme of clustering assignment heatmap at the original resolution can be found in the Supplementary Fig. S44.(b) tSNE plots for four data integration methods, with the right-most column showing analysis without correction. (c) Heatmap of differentially expressed genes for each domain identified by PRECAST. (d) Percentage of different cell types in each domain detected by PRECAST, with (left panel) or without (right panel) scaling to the summation of all cell types across all domains equal to 100%. (e) Visualization of the trajectory inferred by PRECAST in spatial heatmap (left panel) and tSNE plot (right panel).