



DeepSpaceDB: a spatial transcriptomics atlas for interactive in-depth analysis of tissues and tissue microenvironments

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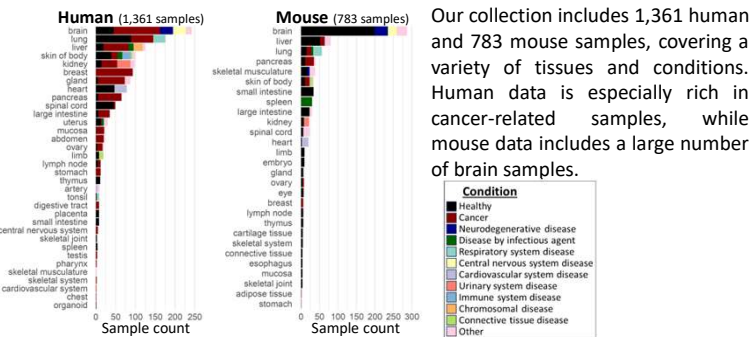
Summary

Spatial transcriptomics enables researchers to study the spatial organization of cells and gene expression patterns within tissues. However, this technology requires considerable financial resources and bioinformatics experience. Here, we present DeepSpaceDB (www.DeepSpaceDB.com), a spatial transcriptomics atlas that enables in-depth exploration of public spatial data. The public version of DeepSpaceDB now contains 2,144 Visium samples. We added new tools for comparing between 2 different samples, for searching the whole database with a query gene of interest, and others.

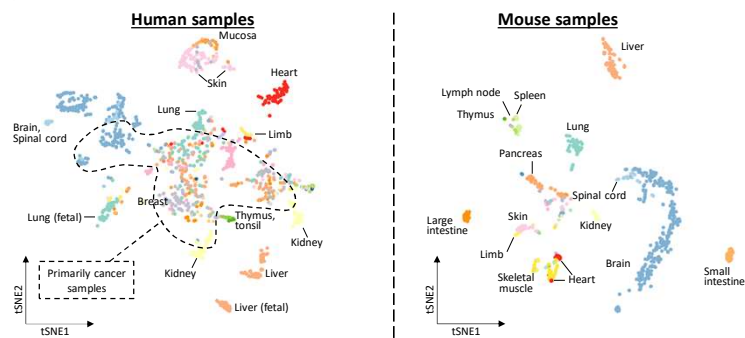
We have also collected and processed >500 Xenium samples. We are currently exploring ways for storing this data and preparing a database interface. This part has not yet been made public.

Overview of Visium data

Version 1.1 of DeepSpaceDB contains 2,144 spatial transcriptomics samples of the 10x Genomics Visium platform from multiple sources.

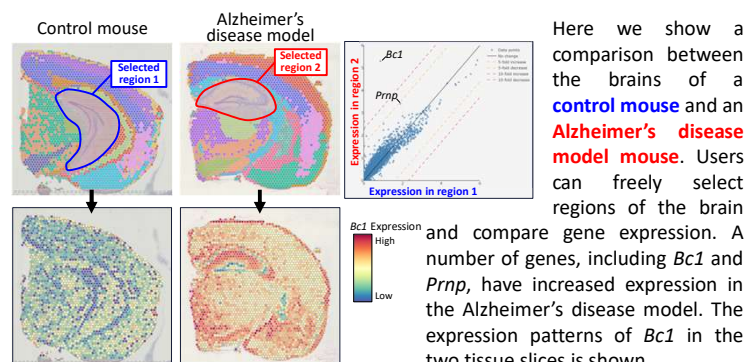


To evaluate the biological validity of the collection of samples, we converted each tissue slice into a “pseudo-bulk” sample, and visualized these in a 2D embedding. We confirmed that samples from similar tissues group together, even if they were generated by different studies.



New analysis tools

Previously, we implemented a tool that allows users to compare gene expression between freely selected regions **within a sample**. Recently, we added a new tool which allows comparison **between 2 different samples**.



We have also added tools for inspection of manual image annotations for 69 breast cancer samples and for searching the whole database with a query gene of interest. Users can now also upload and analyze their own Visium data on DeepSpaceDB.

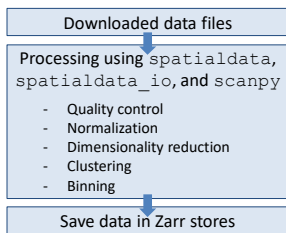
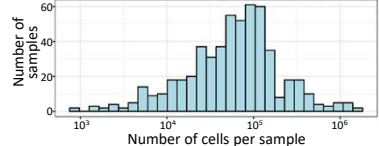
Overview of Xenium data

We collected samples of the 10x Genomics Xenium platform from multiple sources. After processing using a consistent pipeline, 548 Xenium samples remained. We are now conducting preliminary analysis and implementing analysis tools.

Of the samples, 445 use a small gene panel (between 90 and 500 genes), and 103 are Xenium Prime samples covering about 5,000 genes. Sample annotation is still ongoing, but the most frequent organs and tissues are shown in the tables below.

Human samples		Mouse samples	
Tissue	Samples	Tissue	Samples
Lung	48	Brain	48
Brain	29	Kidney	16
Pancreas	21	Skin	14
Adipose	12	Lung	10
Kidney	10	Nervous system	3
Others	36	Others	7
Total	156	Total	98

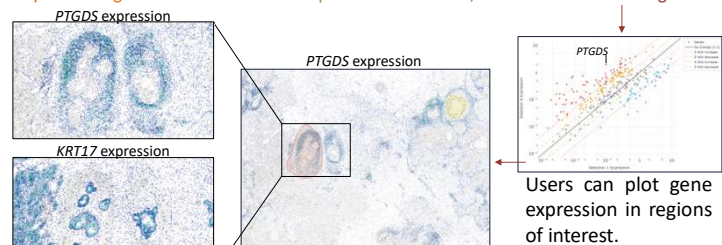
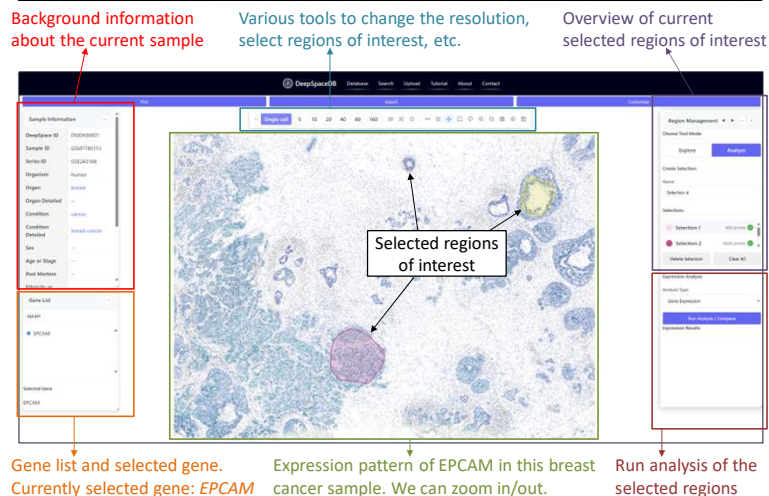
The number of cells per sample ranged from 919 to 1.7 million (mean: 118,545).



All samples were processed using a standard pipeline in Python. We attempted binning cells in bins of various sizes to speed up the access to the data.

Resulting data was stored in various Zarr stores to make it easily and quickly accessible from the database interface.

Xenium interface



Future plans

For Visium samples:

- We will continue regular updates to add newly published Visium samples.
- We are exploring alternative ways for tissue image data segmentation and LLM-based annotation.

For Xenium samples:

- We will add more Xenium samples in the near future, and add functions for inspecting cell types, spatial domains, and spatially variable genes.
- We will prepare a public version of the Xenium database.

We will explore other platforms to include in the database.