

scLTdb tutorial

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Introduction

This tutorial give users a brief introduction to how to visualize and analyze single cell lineage tracing datasets in scLTdb. If you have any suggestions or find bugs, please feel free to contact us.

Search & query datasets

The search page on scLTdb offers the functionality to search and query datasets based on several features, namely: ‘Species’, ‘Tissue source’, ‘Technology’, ‘Modality’, and ‘Barcode type’. To illustrate, when you click on the drop-down box located under the **Technology** feature and choose **Larry**, the interactive table will present all datasets that have **Larry** as their designated **Technology**.

Dataset overview

Type to search...

Species	Tissue source	Technology	Modality	Barcode type
Nothing selected				

Show 10 entries

Study	Dataset	Species	Tissue source	Technology	Modality	Barcode type	Pubmed ID	Accession		
Spanjaard_2018_NatureBiotechnology	Spanjaard_2018_NatureBiotechnology	<i>Danio rerio</i>	Fin	LINNAEUS	cellfate,scRNA	PMID29644996	GSE106121			
Raj_2018_NatureBiotechnology	Raj_2018_NatureBiotechnology	<i>Danio rerio</i>	Brn	scGESTALT	cellfate,scRNA	PMID29608178	GSE105010			
Alemany_2018_Nature	Alemany_2018_Nature_R1_wkm	<i>Danio rerio</i>	He	multi-purpose molecular recorder	cellfate,scRNA	PMID29590089	GSE102990			
Alemany_2018_Nature	Alemany_2018_Nature_R1_head	<i>Danio rerio</i>	Bn	Chen et al.	cellfate,scRNA	PMID29590089	GSE102990			
Alemany_2018_Nature	Alemany_2018_Nature_R2_wkm	<i>Danio rerio</i>	He	Carlén	cellfate,scRNA	PMID29590089	GSE102990			
Alemany_2018_Nature	Alemany_2018_Nature_R3_head	<i>Danio rerio</i>	Bn	unwagITracer	cellfate,scRNA	PMID29590089	GSE102990			
Alemany_2018_Nature	Alemany_2018_Nature_R4_wkm	<i>Danio rerio</i>	Brn	Darlin	cellfate,scRNA	PMID29590089	GSE102990			
Alemany_2018_Nature	Alemany_2018_Nature_R4_fin	<i>Danio rerio</i>	He	APTracer	cellfate,scRNA	PMID29590089	GSE102990			
Alemany_2018_Nature	Alemany_2018_Nature_R5_fin	<i>Danio rerio</i>	Cat	Itzquierdo et al.	cellfate,scRNA	PMID29590089	GSE102990			
Alemany_2018_Nature	Alemany_2018_Nature_R5_fin	<i>Danio rerio</i>	Cat	TracerSeq	cellfate,scRNA	PMID29590089	GSE102990			
Chan_2019_Nature	Chan_2019_Nature_embryo1	<i>Mus musculus</i>	Fin	Cat	ScarTrace	cellfate,scRNA	PMID29590089	GSE102990		
Chan_2019_Nature	Chan_2019_Nature_embryo1	<i>Mus musculus</i>	Fin	Larry	cellfate,scRNA	PMID29590089	GSE102990			
Chan_2019_Nature	Chan_2019_Nature_embryo1	<i>Mus musculus</i>	Fin	Space-TREX	cellfate,scRNA	PMID29590089	GSE102990			
Chan_2019_Nature	Chan_2019_Nature_embryo1	<i>Mus musculus</i>	Fin	STICR	cellfate,scRNA	PMID29590089	GSE102990			
Showing 1 to 10 of 106 entries	Explore dataset...	Previous	1	2	3	4	5	...	11	Next

We begin by selecting the **Li_2023_Cell** dataset and proceed to click on the **Explore dataset** option. Subsequently, scLTdb will redirect us to the analysis result page specific to the **Li_2023_Cell** dataset.

Dataset overview

Type to search...

Species	Tissue source	Technology	Modality	Barcode type
Nothing selected	Nothing selected	Larry	Nothing selected	Nothing selected

Show 10 entries

Study	Dataset	Species	Tissue source	Barcode type	Technology	Modality	Pubmed ID	Accession
Hurley_2020_CellStemCell	Hurley_2020_CellStemCell	<i>Homo sapiens</i>	Cell Line	Integration	Larry	cellfate,scRNA	PMID32004478	GSE137811
Weiurek_2020_Science	Weiurek_2020_Science	<i>Mus musculus</i>	Hematopoietic Progenitor Cells	Integration	Larry	cellfate,scRNA	PMID31974159	GSE140802
Rodriguez-Fraticelli_2020_Nature	Rodriguez-Fraticelli_2020_Nature_batch0	<i>Mus musculus</i>	Hematopoietic Progenitor Cells	Integration	Larry	cellfate,scRNA	PMID32669716	GSE134242
Rodriguez-Fraticelli_2020_Nature	Rodriguez-Fraticelli_2020_Nature_batch1	<i>Mus musculus</i>	Hematopoietic Progenitor Cells	Integration	Larry	cellfate,scRNA	PMID32669716	GSE134242
Rodriguez-Fraticelli_2020_Nature	Rodriguez-Fraticelli_2020_Nature_batch2	<i>Mus musculus</i>	Hematopoietic Progenitor Cells	Integration	Larry	cellfate,scRNA	PMID32669716	GSE134242
Showing 1 to 5 of 5 entries	Explore dataset...	Previous	1	Next				

Visualize & analyze datasets

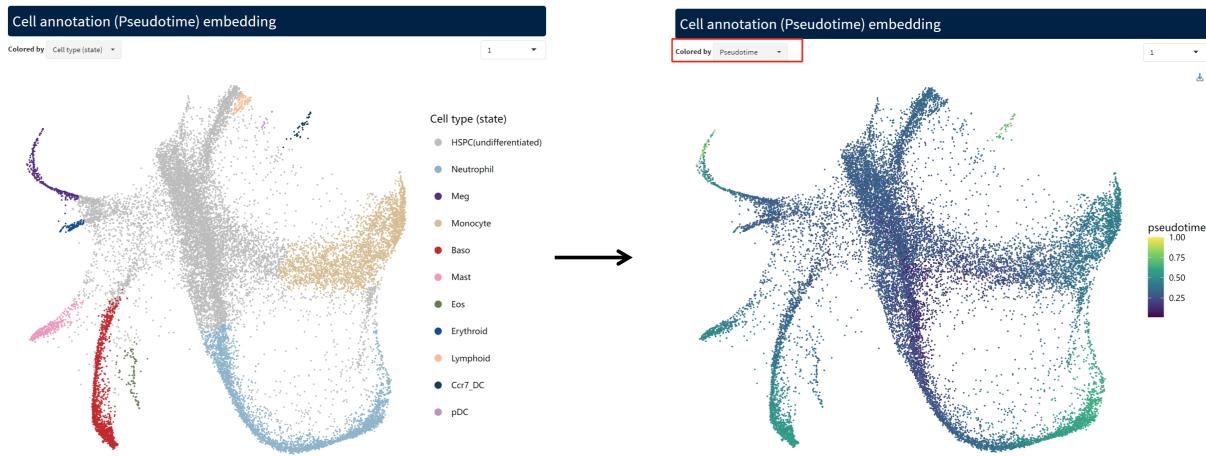
After clicking on the **Explore dataset** option, the user will be directed to the result page of the selected dataset. This result page provides three interactive modules for visualizing and analyzing single cell lineage tracing datasets.

single cell module

The single cell module of scLTdb offers an interactive interface that allows users to explore the transcriptome modality of the scLT dataset. Specifically, users can visualize cell annotation, cell pseudotime, cell type number, clone embedding, and gene expression within this module. In the following sections, I will demonstrate some of the interactive functions available in this module.

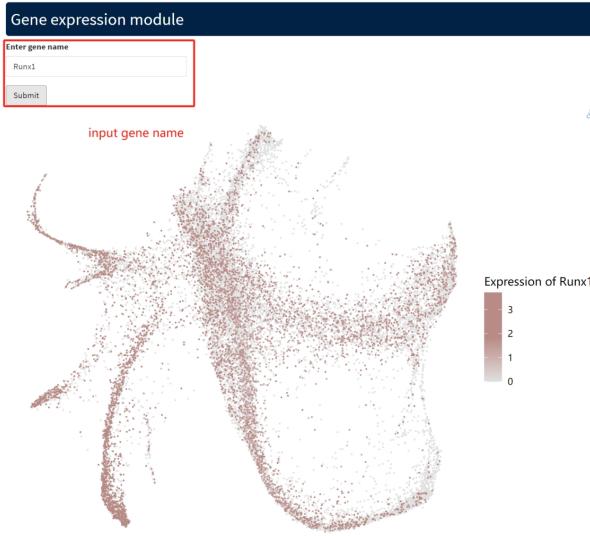
Visualize cell annotation and pseudotime

You can click **colored by** button in the **Cell annotation (Pseudotime) embedding** section to change cell color (colored by cell type or pseudotime).



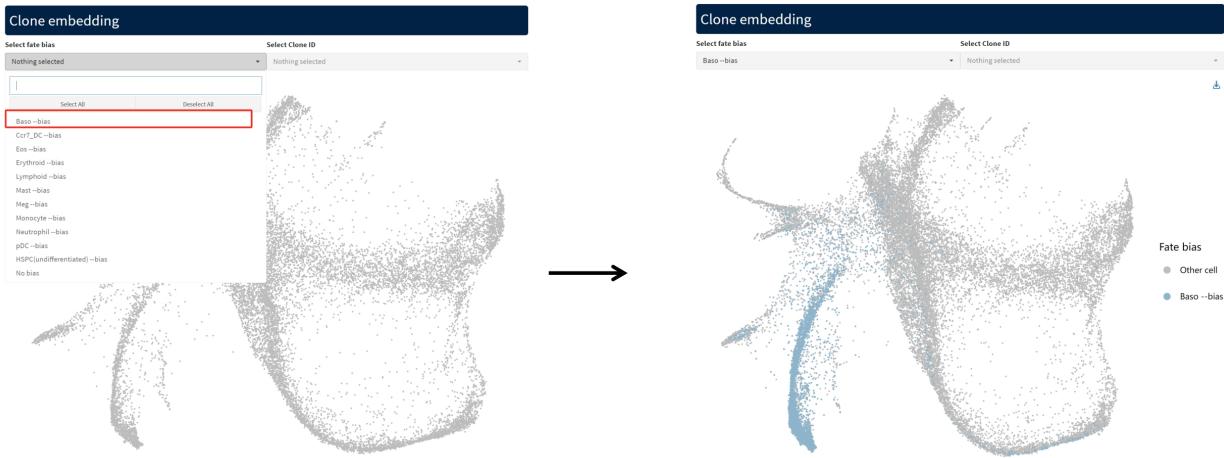
Visualize gene expression

To visualize gene expression on the embedding plot, you can input interested gene name in the **Enter gene name** box

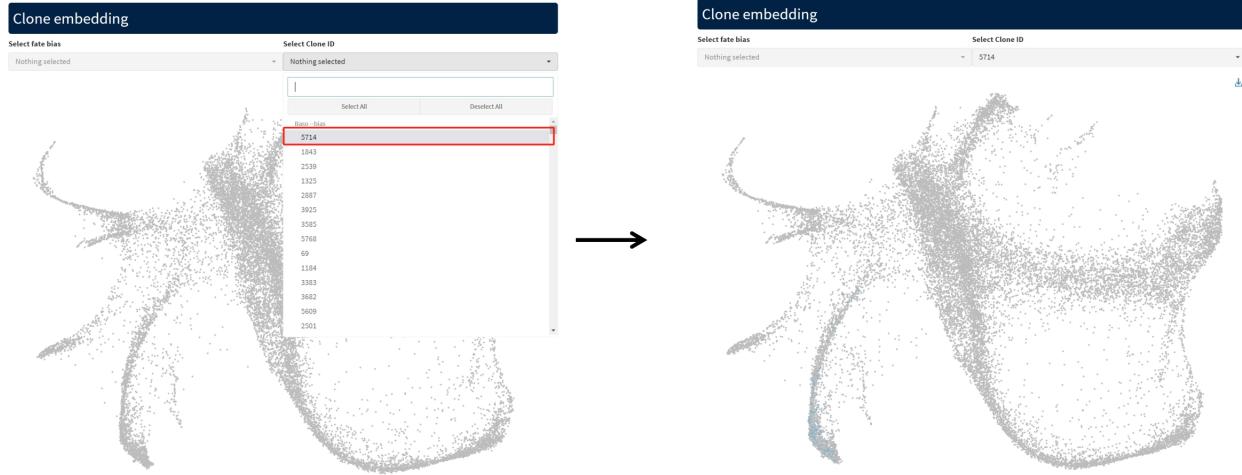


Visualize clone embedding

To visualize a set of clones with the same fate bias, you can click the 'select fate bias' button in the clone embedding section.



In a similar way, you can visualize single clone by clicking **select clone id** button.

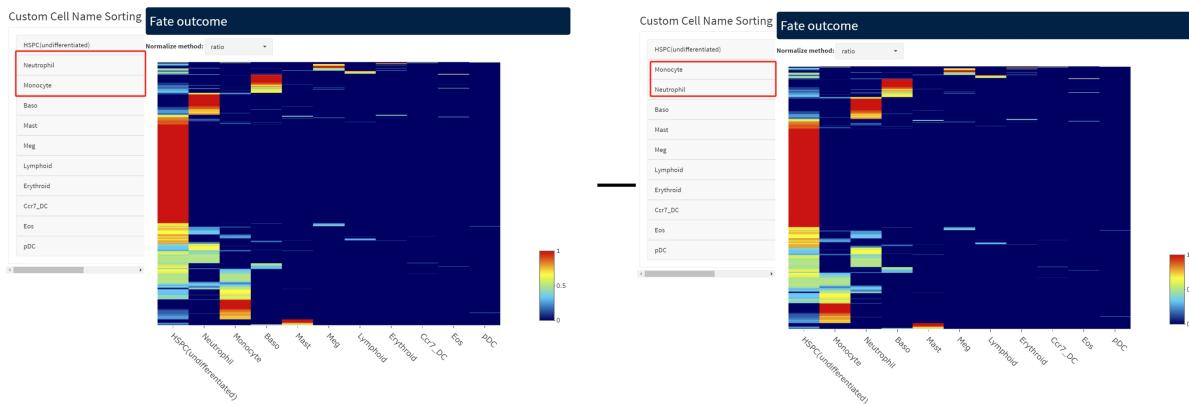


Lineage tracing module

The lineage tracing module of the scLTdb offers an interactive interface that allows users to explore the lineage tracing modality of the scLT datasets. I will demonstrate some of the interactive functions available in this module.

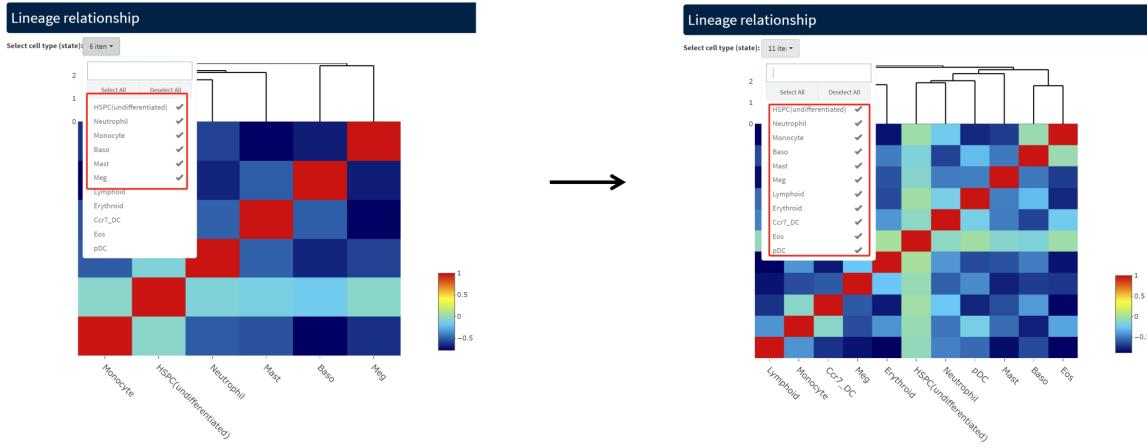
Fate outcome

This section presents a heatmap illustrating the clone enrichment for each cell type (state). Users have the ability to modify the column order of the heatmap by adjusting the position of the cell type box on the left side of the heatmap. In addition, user can change the barcode normalization method by clicking the **Normalize method** button.



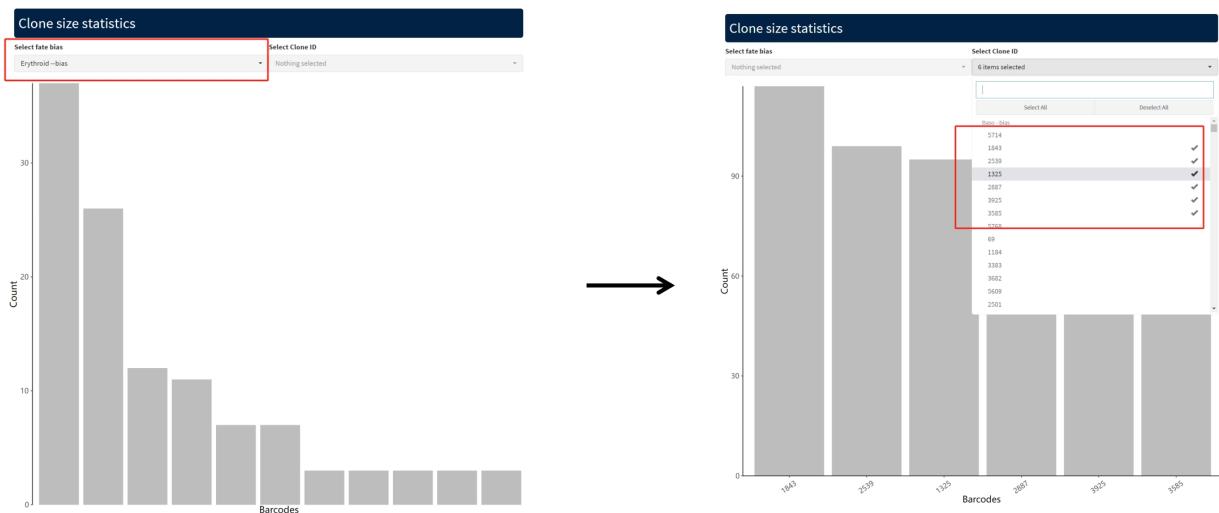
Lineage relationship

This section enables users to calculate the lineage similarity between cell types (states). User can select cell type by the **Select cell type (state)** button.



Clone size statistic

This section provides interactive functions to browse clone size (cell number count of single clone).



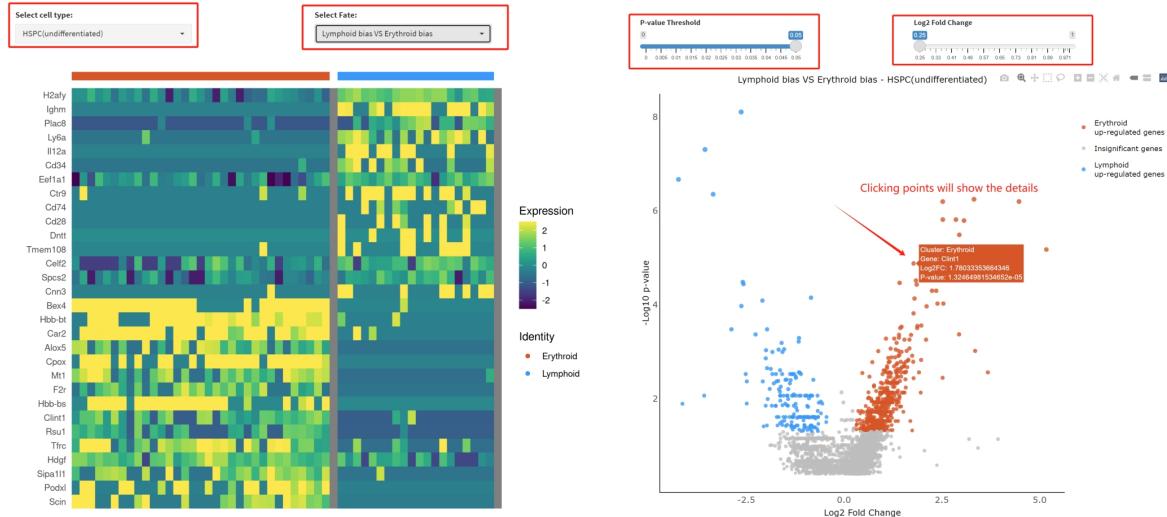
Integration module

The integrative module of scLTdb presents the integrative analysis result of both scRNA-seq data and lineage tracing data, such as fate bias DEGs, and clone DEGs.

Clone DEGs and fate bias DEGs

This section provides the differentially expressed genes analysis for cells within different clones, or cell with different fate bias. For example, we want to analyze the transcriptome heterogeneity between **Lymphoid biased HSPC** and **Erythroid biased HSPC**, we select cell type as **HSPC**, and fate bias as **Lymphoid bias vs Erythroid bias**.

For the volcano plot, you can play the slide windows of **P-value Threshold** and **Log2 Fold Change** to set the significant genes.



Violin plot of gene with different fate bias

scLTdb also provides function for users to visualize gene expression in different cell fate. For example, we want to visualize the expression of Gata2 among different **HSPC fate bias**. We firstly need to select cell type **HSPC**, then type **Gata2** at the **Enter gene name** box.

