SynEcoSys® - a standardized single cell database for clinical translation

SynEcoSys® Database is the first comprehensive single cell knowledgebase that combines curated data from tens of millions of single cells with information on clinical translation and drug discovery. All provided datasets are processed with uniform standards of data analysis and cell type annotation to guarantee precision and comparability.

SynEcoSys® is also a one-stop single cell data visualization and mining platform with intuitive user interface to make single cell data accessible. CeleViz™ data visualization module is embedded into the database to offer elegant graphical data visualizations compatible with major scientific journal requirements. CeleLens™ module facilitates automated data analysis pipeline with tunable analysis parameters and annotation.

Figure 1. SynEcoSys clinical translation database interface.

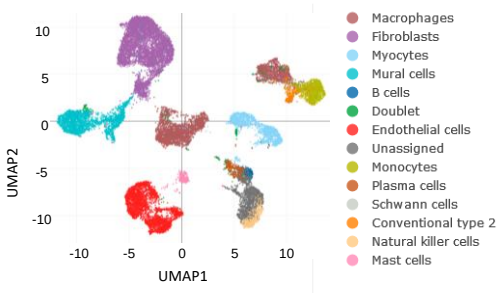


Figure 2. Example UMAP plot of single cell sequencing data with standardized and precise cell annotation.

Highlights

- **Clinical Translation Database:** first-in-the-field single cell database for clinical translation research
- **Proprietary cell type markers reference** built by professionals with years of literature curation
- **Core datasets for major disease models** integrated datasets that allow for an in-depth look at disease models
- **Automated Data Analysis**: input your own gene expression matrix for automatic analysis and annotation

Core datasets – pre-integrated disease samples across multiple datasets

Core datasets are pre-integrated cross-source single cell RNAseq data from major disease models (e.g., cancer types), obtained by integrative analysis of the most relevant single cell datasets. The automatic cell annotation is manually verified.

These datasets span a comprehensive coverage of clinically relevant information including disease stages, subtypes, mutations, treatment methods, and patient response. Differential Gene Expression (DGE) and Gene Ontology (GO) enrichment analysis can be performed with elegant visualisation of results in the form of heatmaps, dot plots, violin plots, histograms and pie charts.

SynEcoSys and its core datasets support clinical translation with molecular-level patient stratifications from multiple aspects, pathological and treatment records of sample donors, drug information for target genes and clinical biomarkers.

New core datasets are regularly added to the database.

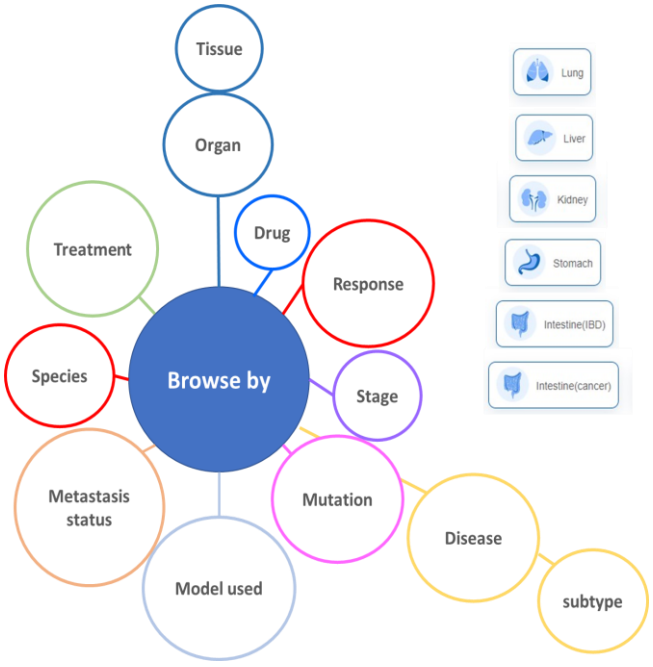


Figure 3. Direct comparison of clinical samples of different tissue origins from multiple sources in core datasets from SynEcoSys. The dataset can be filtered by parameters like age, gender, ethnicity, disease stage, treatment type, pre-conditions and responsiveness.

A comprehensive knowledge-base with accurate cell annotation

SynEcoSys® database has standardized ontology, allowing for direct comparison between the different datasets.
An in-house transcriptome-based cell annotation reference was built through meticulous literature curation by experienced professionals. This cell annotation reference allows for accurate cell annotation to match the populations found in the publications or discover novel cellular subtypes.

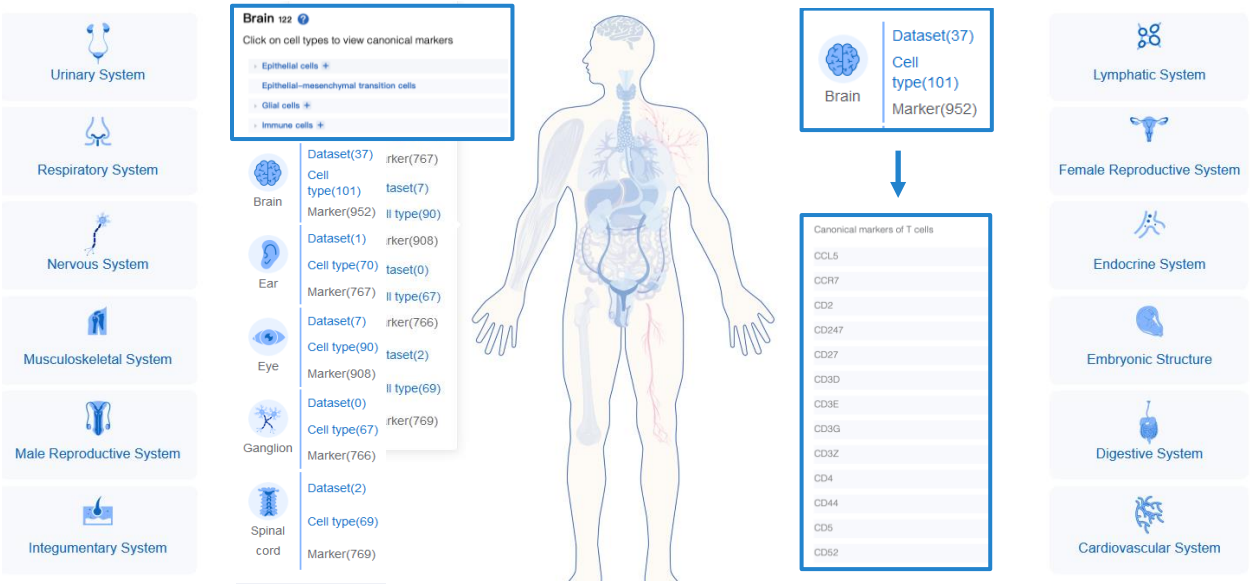
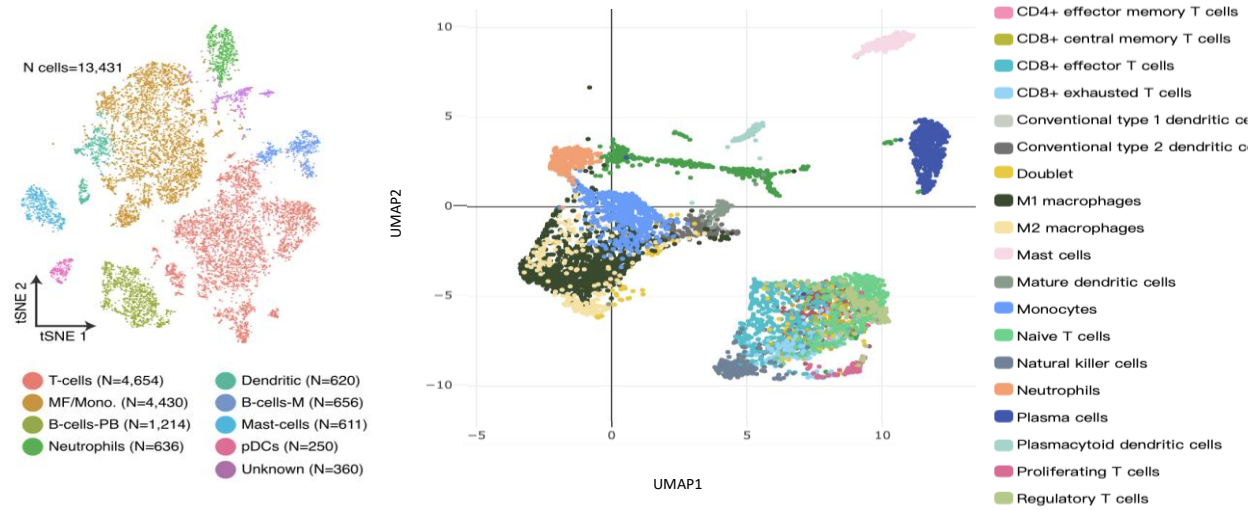


Figure 4. SynEcoSys database currently comprises 470+ single cell RNAseq datasets from 6700+ samples; 300+ cell types; 3500+ sets of marker genes, 70+ tissue types, and more than 25 million cells sequenced, and is regularly updated with new public data.

Automated data annotation combined with an in-house built cell marker database allows for more precise annotations of different cell subtypes.

Furthermore, CeleViz™ allows you to choose between tSNE and UMAP dimensionality reduction plots as well as 2D and 3D interactive visualization for better visualization of cell types.



Original annotation ✓ SynEcoSys annotation is more precise

Figure 5. Standardization of data across all datasets allows for more precise annotation of different cell subtypes. (left) tSNE plot with original annotation. (right) UMAP plot with more precise annotation of cell subtypes.

SynEcoSys homogenizes public single-cell data for productive data mining

The biggest caveat of publicly available, clinically relevant single-cell data is the lack of comparability among different datasets due to the diversity in data analysis and cell type annotation, as well as the bioinformatic expertise needed to analyze and interpret raw data.

SynEcoSys® database integrates standardized, manually curated, high impact, publicly available single cell sequencing data with automated data analysis and visualization modules, CeleLens™, and Celeviz™, respectively. This enables deep mining of clinically relevant single-cell data to generate potential biomarkers and novel drug targets, with high consistency.

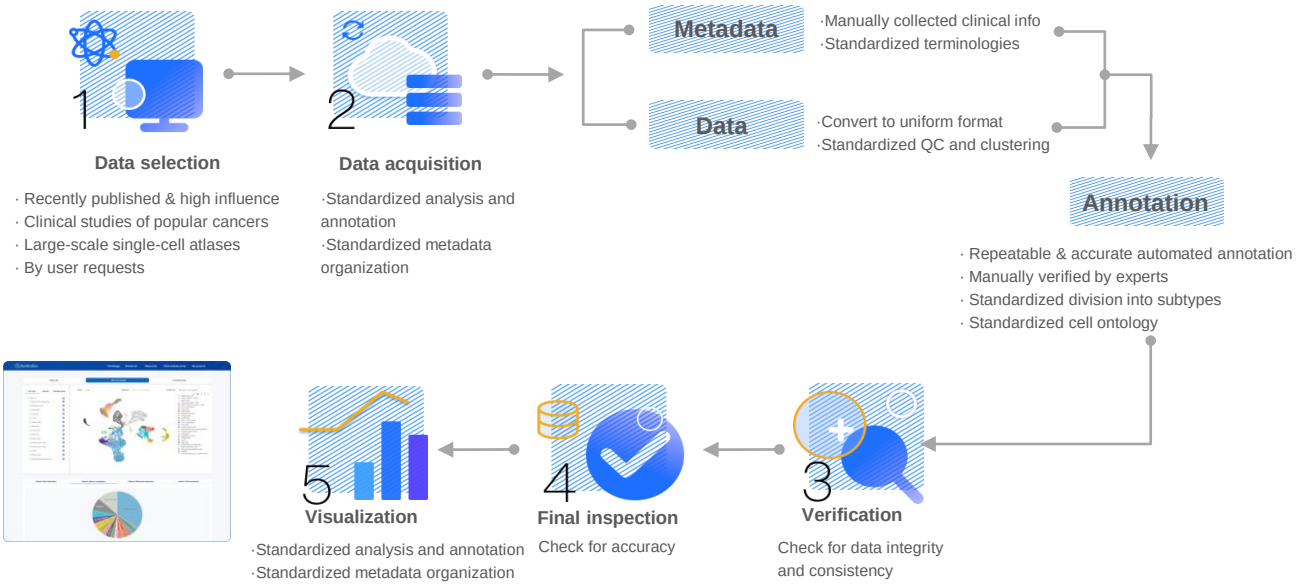


Figure 6. Overview of standardized SynEcoSys data curation and presentation workflow.

Performs automated data analysis and compares to public datasets

With CeleLens™ data analysis module, users can import their own dataset in the form of a gene expression matrix for automated data analysis and annotation with adjustable parameters. The user dataset can also be compared to other datasets in order to verify previous findings or discover new insights such as novel cell types, biomarkers, or drug targets.

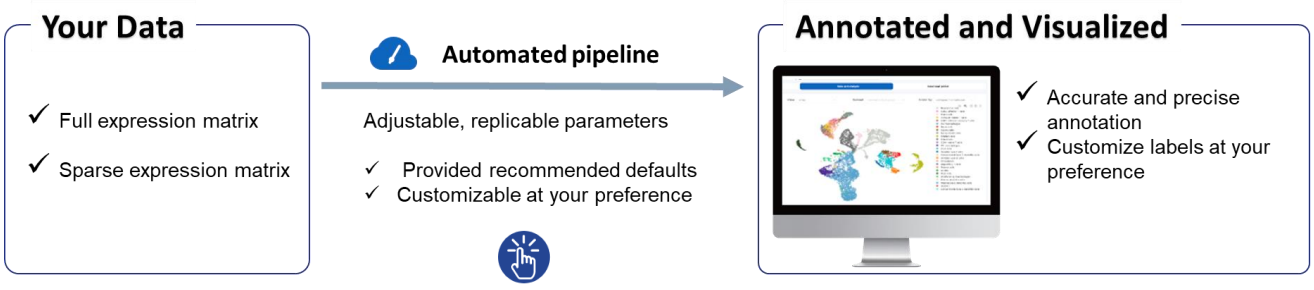


Figure 7. CeleLens™ module analyses user's own gene expression matrix data within an automated pipeline, meaning results can be obtained by adjusting parameters such as gene expression level, mitochondrial content and clustering resolution.

CeleViz – Explore clinical information in scRNAseq data

With CeleViz™, data visualization and exploratory analysis become easy with a user-friendly interface. No previous knowledge of scRNAseq data analysis is required.

For each dataset 5 modules of data visualization are offered:

- Gene Expression
- Cellular Composition
- Differential Expression
- Cell Interactions
- Trajectory Analysis

In every module the clinical and prognostic metadata can be used to perform comparisons and understand the impact of clinical differences in the cell transcriptome.

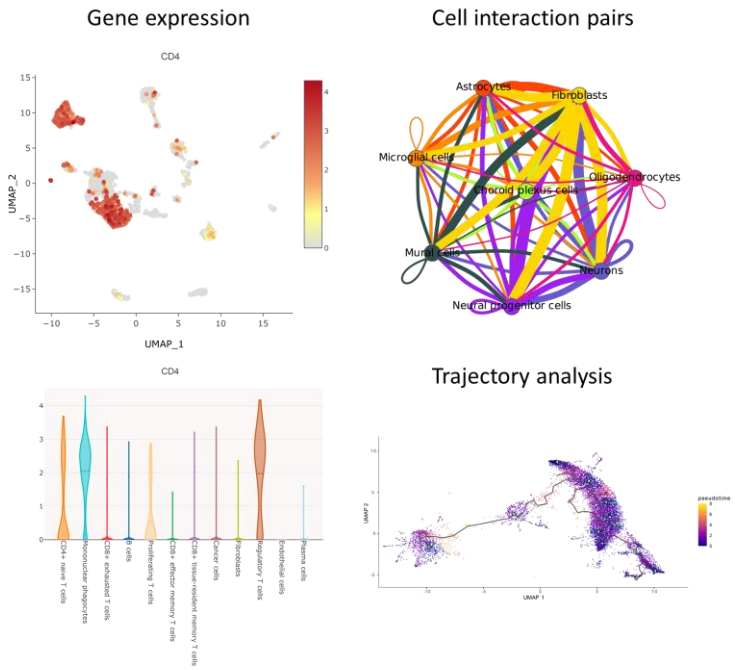


Figure 8. CeleViz™ visualization tool can be used for exploration of the SynEcoSys database. Take advantage of clinical information in the database to explore the clinical insights of transcriptome data and compare different datasets.

Ordering information:

Product	Catalog Number
SynEcoSys® Clinical Single Cell Database (1 year subscription)	8270060

Resources

Tutorial videos

https://www.youtube.com/channel/UCZeGRq83pQv4ebiy16Nc-Rw

Guidebook

www.synecosys.com

Free trial inquiry:

www.synecosys.com

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