Using the Cell Type Knowledge Explorer

The Cell Type Knowledge Explorer (CTKE) is an interactive tool for exploring data from transcriptomic taxonomies. The CTKE features three transcriptomic taxonomies (from sc-and snRNAseq data): mouse, human, and marmoset primary motor cortex. The CTKE also features an integrated taxonomy of the three species taxonomies, which shows cross-species cell type homologies. Within the mouse taxonomy, there are also patch-seq data to show electrophysiological characteristics and morphological reconstructions at the subclass and cell type levels. In the human L5 ET subclass, there are patch-seq data as well.
1. Go to brain-map.org https://knowledge.brain-map.org/celltypes to find the Cell Type Knowledge Explorer (CTKE) landing page.
   a. On the landing page, there are three sunburst plots on the right. The three plots represent three transcriptomic taxonomies from the primary motor cortex of marmoset (callithrix jacchus), human (homo sapiens), and mouse (mus musculus). Clicking on the green buttons will take you to the landing page of that species’ taxonomy.
   b. On the left side of the landing page, there is dendrogram that shows an integrated taxonomy, created by combining the three motor cortex taxonomies from the different species.
2. After clicking on one of the green species buttons in step 1a, you will find the species landing page. This page shows an enlarged sunburst plot, representing the primary motor cortex transcriptomic taxonomy of that species. The entire plot is interactive, and any portion can be clicked on to learn more about those specific cell types.

   a. The innermost ring is the broadest level of the taxonomy, showing four classes of cell types. GABAergic cells are red, glutamatergic are blue, non-neuronal cells are grey, and non-neural cells are dark green.

   b. The next layer of the plot shows subclasses of cells that belong to the four classes defined in 2a. Warm colors denote subclasses of cells within the GABAergic class, while cool colors denote subclasses within the glutamatergic class. Brown tones denote subclasses of cells belonging to the non-neuronal or non-neural classes.

   c. The outermost layer of the ring shows individual transcriptomic cell types that belong within the corresponding subclasses and classes.

   d. To learn more about this project, read through the information on the lefthand panel which includes a link to the publications associated with these data.
3. After clicking on one of the classes (GABAergic, glutamatergic, non-neuronal, or non-neural) in the plot, you will find the page for that cell class. This page includes summary data about that cell class and transcriptomic data.

   a. In the gene expression panel, marker genes for the class are colored green. To expand plots, click on the double-edged arrow in the upper righthand corner of the plot. To find out more information about the plot being shown, hover the mouse over the “info” button.

   b. On the lefthand panel, you will find the subclasses within the class listed. To view all of the subclasses, click on the drop-down arrow.
4. After clicking on a subclass in step 3b, you will find the page for that specific subclass. The top of this page features a summary of the subclass, along with a reference in the upper righthand corner.

a. Next, you will find the gene expression data and the marker genes (in green) used to define cells belonging to this subclass. To find out more information about the plot being shown, hover the mouse over the “info” button. To access the raw data, click on the “MORE DATA” button.
b. Below the transcriptomic data, we have morphological data of cells within this subclass. On the left, we have a histogram which shows the distribution of axonal and dendritic segments throughout the cortical layers, and the distribution of cell bodies (open circles). On the right, we have morphological reconstructions of different cell types within this subclass. Below these panels, we have morphological reconstruction of a cell from this cell subclass compared to other cells from other cell subclasses.
Next, we have electrophysiological data. On the left, we have panels comparing electrophysiological characteristics of this cell type compared to other cell types within the same subclass. On the right, we have example traces from a cell within this cell type.

d. Below that we have spatial transcriptomics data. On the lefthand side, the distribution of this subclass as a fraction of its class is shown throughout the cortical layers. On the righthand side, there is an example tissue section and the spatial transcriptomics data, showing the distribution of cells in this subclass.
e. On the left panel at the top of the page, we have information about our subclass. To view the cell types within the subclass, click on the drop-down arrow.

Lamp5-like

**CLASS**
- **Accession**: CS202002013_125
- **Taxonomy**: CCN202002013
- **Ontology ID**: PCL:0011125
- **Ontology symbol**: Lamp5-like MOp (Mouse)
- **Ontology name**: Lamp5-like primary motor cortex GABAergic interneuron (Mus musculus)

**NEIGHBORHOOD**
- GABAergic
- Lamp5-like

**ANATOMY**
- Primary motor cortex (M)

**SUBJECT**
- **Species**: Mus
- **Age**: Young Adult (P56-P63)
- **Sex**: Both
5. After clicking on a cell type, you will find the main page for that cell type. Here we have a summary of data about the cell type, and references to the data in the upper righthand corner.

<table>
<thead>
<tr>
<th>Accession</th>
<th>CS202002013_8</th>
</tr>
</thead>
<tbody>
<tr>
<td>Taxonomy</td>
<td>CCN202002013</td>
</tr>
<tr>
<td>Ontology ID</td>
<td>PCL:0011008</td>
</tr>
<tr>
<td>Ontology symbol</td>
<td>Lamp5 Lhx6 MOp (Mouse)</td>
</tr>
<tr>
<td>Ontology name</td>
<td>Lamp5 Lhx6 primary motor cortex GABAergic interneuron (Mus musculus)</td>
</tr>
</tbody>
</table>

a. Below the summary, you will find transcriptomic data for this cell type, with marker genes listed in green. To find out more information about the plot being shown, hover the mouse over the “info” button. To access the raw data, click on the “MORE DATA” button.
b. Below the transcriptomic data, we have morphological data of cells within this cell type. On the left, we have a histogram which shows the distribution of axonal and dendritic segments throughout the cortical layers, and the distribution of cell bodies (open circles). On the left, we have morphological reconstructions of different cells within this cell type. Below these panels, we have morphological reconstruction of a cell from this cell type, compared to other cell types within the same subclass.
c. Below the morphological data, we have the electrophysiological data. On the left, we have panels comparing electrophysiological characteristics of this cell type compared to other cell types within the same subclass. On the right, we have example traces from a cell within this cell type.

![Electrophysiology Diagram](image1)

d. After the electrophysiological data, we have heatmaps; these heatmaps show homologous cell types between the three species (mouse, marmoset, and human) based on the integrated taxonomy featured on the CTKE landing page in step 1. Darker color on the heatmap indicates higher similarity and homologous cell types are outlined in black squares. To view homologous cell types in other species, click directly on the portion of the heat map corresponding to a homologous cell type, which will lead you to the page for that species cell type.

![Cross-Species Cell Types Heatmap](image2)