Cell Composition

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[1]

Abstract

Cell density and cell-type diversity in reconstructed brain region are analyzed and validated against experimental data.

Introduction

Cell densities are an essential input to building a realistic brain-region circuit. Cell density varies widely across the cortex. Layer boundaries are determined experimentally by locating transitions in cell densities and soma-sizes. Accordingly, a reconstruction of a brain region should have the same cell densities in its various sub-regions as that observed experimentally, and reproduce the input values.

Individual neurons show a lot of morphological and electro-physiological diversity. A brain reconstruction must also reproduce experimentally observed neuronal diversity across the modeled regions. In this report we analyze cell densities and cell type diversity across the modeled brain regions:

- Overall cell density by layer
- Fraction of inhibitory neurons by layer
- Fractions for different cell *mtype*s.

[1] This report was written using DMT.

Methods

We perform statistical tests in order to compare the *in-silico* means against the *in-experimentum* means. The null-hypothesis is that the *in-silico* mean and the *in-experimentum* mean are the same. The alternative hypothesis is that the two means are different.

Statistical Testing: The *in-silico* value is assumed to be a realization of a random variable from a normal distribution with the mean and standard deviation estimated from biological data. This assumption results in the test statistic: $\frac{X-\bar{x}}{\bar{s}}$. The test statistic follows a normal distribution with zero mean and standard deviation 1. When a given dataset contains multiple data points, *e.g.* cell density across layers, a pooled p-value is computed as $-2\sum_{i=1}\log p_i$ according to Fischer's method.

Measurements

- **Cell Density**: To mimic an experimental measurement of cell density, cells were counted in random regions of interest (ROIs). For each set of parameters (*i.e.* regions and layers in the model), 100 ROIs in the shape of cuboids of side 50 μm were sampled. Cell density was determined as the count of cells in each ROI divided by it's volume.

- **Cell Density By Mtype**: Cell densities of a given mtype was computed in the same way as overall cell density except that only the subset of cells with the given mtype were counted.

- **Inhibitory Fraction**: To mimic an experimental measurement of inhibitory fraction, cells were counted in random regions of interest (ROIs). For each set of parameters (*i.e.* regions and layers in the model), 100 ROIs in the shape of cuboids of side 50 μm were sampled. Inhibitory fraction was measured as the number of inhibitory cells in each ROI divided by the number of total cells in that ROI.

- **Mtype Fraction**: Fraction of cells of a given mtype were computed over all the cells in a layer.

- **Cell Density By Depth**: Cells were counted in random regions of interest (ROI). Several ROIs were sampled for each depth. Because only the center of an ROI was required to lie in a layer, it may overlap a neighboring layer. For such ROIs cell density measurement would be an overlap of those of the two neighboring layers that the ROI covers.

Results

Results are presented as figures.

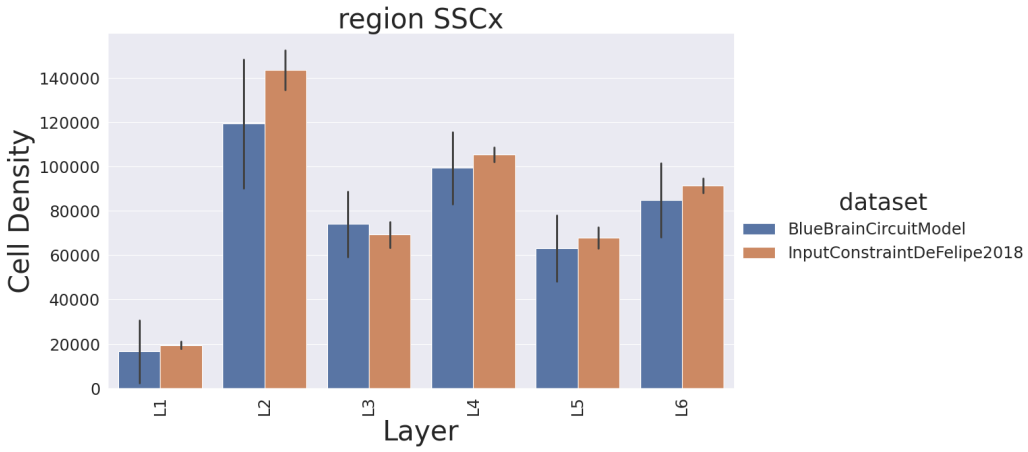


Figure 1: Cell density by layer.

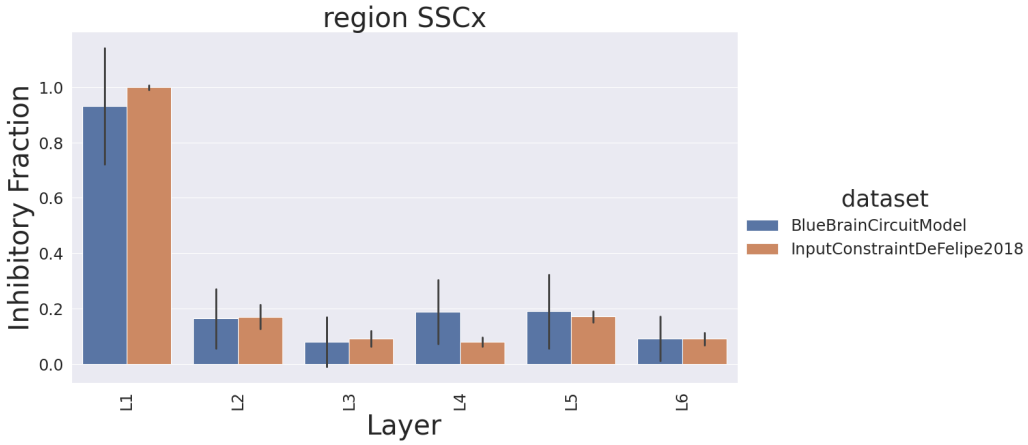
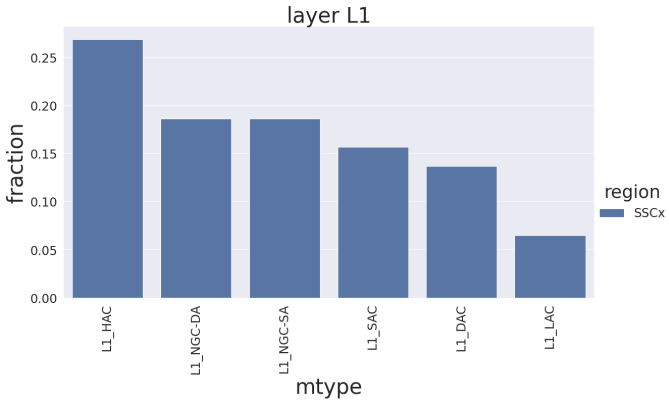
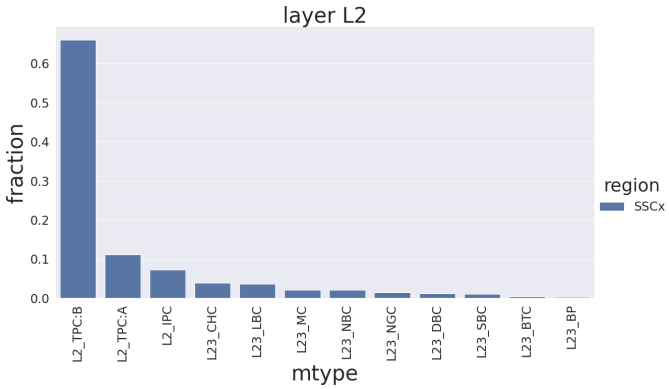


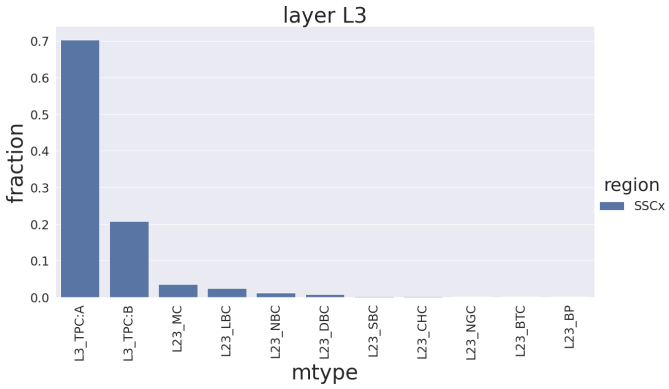
Figure 2: Cell density by layer.



(a) L1

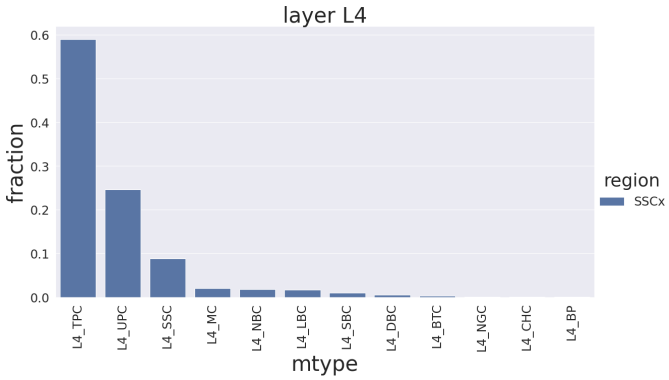


(b) L2

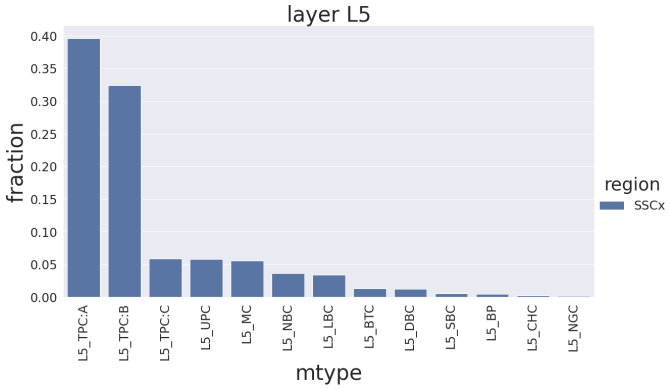


(c) L3

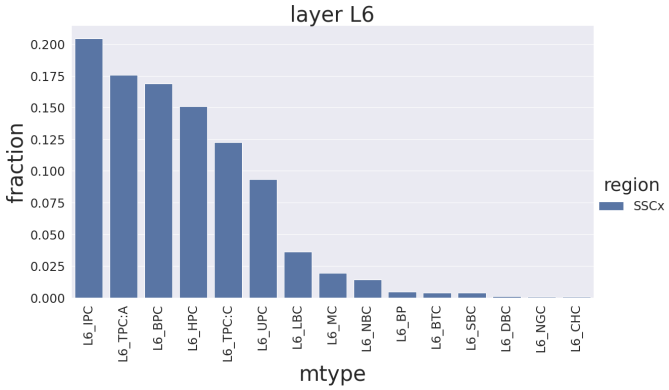
Figure 3: Cell density by mtype and layer.



(a) L4



(b) L5



(c) L6

Figure 4: Cell density by mtype and layer.

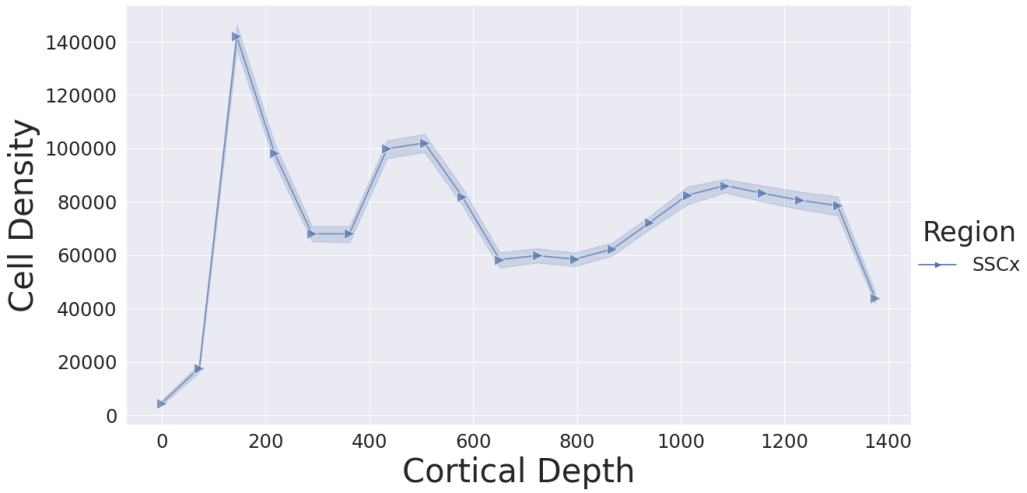


Figure 5: Cell density $[mm^3]$ plotted against depth $[\mu m]$.