Connectivity among neurons reveals patterns. Neuronal connectivity patterns such as the rich club phenomenon and feedforward motif appear after analysis of simulations of digital circuits in the rodent neocortex.

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Mouse long-range connectome recipe format

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1 Recipe format

The recipe is yaml-formatted. It consists of five sections that together parameterize how projections are to be built. Three of the sections define various types, i.e. neuron populations, synapse types, and layer profile types. The other two sections then use the defined types to specify the spatial structure of projections (section "projections") and the "logic" of single axon targeting (section "p-types").

1.1 Section "populations"

This section defines a number of groups of neurons by specifying the brain region they are in and a number of other properties in terms of "filters" they have to pass. Such filters can be in term of their synapse class, electrical type, morphological types, etc.

Figure 1: Exemplary entry in the section "populations"

- name: MOS 6
  atlas_region: MOS
  name: MOS
  subregions: ['16']
  filters: {'synapse_type': 'EXC'}

This is the name the defined neuron population will be known as. Used in the other sections of the recipe.

- Specifies where the population can be found.
- The brain region according to the Allen Common Coordinate Framework.
- List of subregions of the specified region. In neocortex, this means layers.

Additional constraints the neurons of the population have to fulfill. Here, they need to be excitatory. Looking at the rest of the recipe you will find that this is because the population is going to be the source of a projection.

1.2 Section "layer profiles"

This specifies the layer-specific density profiles of projection synapses in the target region. Densities in the prototypical patterns are given relative to the overall average density that is parameterized elsewhere. In other words, the profile yields the peaks and troughs and is to be scaled up or down to the specified mean value.

Figure 2: Exemplary entry in the section "layer profiles"

- name: profile 1
  relative_densities:
  - layers: [11]
    value: 2.639020
  - layers: [12, 13]
    value: 1.655240
  - layers: [14]
    value: 0.394960
  - layers: [15]
    value: 0.351513
  - layers: [16]
    value: 0.351513

Name of the layer profile, used in the section "projections"

List of the relative densities in various layers. Relative to the mean density specified in the section "projections". i.e. this vector of densities is scaled, such that the overall mean density from the bottom of L6 to the top of L1 is the specified mean density.
1.3 Section "synapse types"

In this section the physiology of synapses can be placed, i.e. a number of synapse types can be specified and associated with stochastic distributions for the model parameters. The parameters themselves will depend on the model to be used. The example depicted here uses the stochastic version of the Tsodyks-Markram model with multi-vesicular release. Note: In the current version of the recipe (v1.15), the section is merely a placeholder for physiological information to be parameterized from biological data or the literature in the future.

![Figure 3: Exemplary entry in the section "synapse types"

- **name**: type_1
  - **physiology**:
    - **phys parameter**: 0
      - **distribution**:
        - **type**: truncated_gaussian
          - **dist parameters**:
            - mean: 0.46
            - std: 0.26
    - **phys parameter**: D
      - **distribution**:
        - **type**: truncated_gaussian
          - **dist parameters**:
            - mean: 671.0
            - std: 17.0
    - **phys parameter**: F
      - **distribution**:
        - **type**: truncated_gaussian
          - **dist parameters**:
            - mean: 17.0
            - std: 5.0
    - **phys parameter**: gsyn
      - **distribution**:
        - **type**: truncated_gaussian
          - **dist parameters**:
            - mean: 0.85
            - std: 0.44
    - **phys parameter**: nrrp
      - **distribution**:
        - **type**: uniform_int
          - **dist parameters**:
            - min: 1
            - max: 4
    - **phys parameter**: dtc
      - **distribution**:
        - **type**: truncated_gaussian
          - **dist parameters**:
            - mean: 1.74
            - std: 0.425

Name of the synapse type, used in the section "projections"

The physiology is parameterized in terms of distributions for parameters of the used synapse model. Here, we are using the stochastic Tsodyks-Markram model with multi-vesicular release.

For each parameter we specify the type of distribution along with the required parameters (usually mean and std).
1.4 Section "projections"

Figure 4: Exemplary entry in the section "projections"

This is the most important part of the recipe. It has one entry per projection, defining their source and target populations, the type of topographical mapping between them, the layer profile of synapse density to use in the target region and the type of synapse physiology to use. The topographical mapping is defined by specifying local coordinate systems in the source and target region and assuming that neurons at corresponding locations in the coordinate systems are mapped (=connected) together. However, this mapping is not simply point-to-point, but point-to-region. This is implemented by specifying a "mapping variance" in the target region coordinate system. We then assume that a neuron at $x, y, z$ in the source coordinate system is mapped to a gaussian kernel at $x, y, z$ in the target coordinate system with the specified variance.

Note that the mapping is performed in the "Allen Dorsal Flatmap", a 2d projected version of a brain coordinate system. Transformation from the Allen Common Coordinate Framework to the dorsal flatmap is part of their "mouse connectivity models" package that can be found at https://github.com/AllenInstitute/mouse_connectivity_models.git
1.5 Section "p-types"

Figure 5: Exemplary entry in the section "p-types"

This section constrains the targeting of brain regions by individual axons of a source population. It first specifies the first order probability that a randomly picked neuron of the source population actually projects to the target region. It further specifies statistical interactions between target region in the form of an increased probability to innervate region B, once one knows that region A is innervated by the axon.