Orientation specific cells in V1 organize themselves in either swaths of similar-orientation preferring clusters (iso-orientation domains) or in distinctive singularities where cells representing 180-degrees of orientation specificity center themselves about a blob (pinwheels). The gradient (0 to 180-degrees) of the orientation-specific cells are organized in either a clockwise or counterclockwise direction. However, pinwheels and iso-orientation domains develop with some level of stochasticity, which many computational models have attempted to explain. While many good models exist, our goal was to develop a biologically plausible model incorporating a three-layer approach (representing retina, LGN, and cortex), presynaptic competition for resources, diffusive cooperation of near neighbor cells and corresponding lateral connections, maintenance of retinotopic mapping, and a capped synaptic load per neuron.

We use a Self-Organizing Map as the basis for each of the layers, and a Hebbian-style approach for reinforcing link weights between layer sub-networks. We train our network with an iterative presentation of randomly sized and oriented Gabors. Our data set contained 10 maps of each iteration level: 3500, 5000, 10000. We compare our maps against both real maps and synthetic maps produced via other methods.

We also aim to develop meaningful metrics for comparing maps. In addition to counting clockwise and counterclockwise pinwheels, we use graph theoretic approaches to compute distances between pinwheels and estimate the coefficient of variance for those distances. Pooled distance variance across maps indicates the 10000-map to be closest to the real map. Our method also maintains a counterclockwise/clockwise pinwheel ratio most similar to that in the real map with increasing number of iterations.

Our approach, we think, proposes both a biologically relevant model of pinwheel organization and more statistically relevant methods for making comparisons across maps.

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