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Figure 1
(b) Draw experimental design and rejection
- Run @BCexperimentProcedureRejection.m (in /BipolarCellTerminal)

(d-e) Dendritic and axonal Quantification
- Run @PlotMorphologyClassification

(f) Plot confocal GFP intensity as a functionIPL depth
- Run @ProcessIPLData (in /BC diversity morphology data)

(g) Depth correlation coefficient between paired bipolar cells
- In the same scripts as it documented in Fig3e

Figure 2
(a-c) Plot the averaged responses to different frequency-modulated spots, and plot the summary results and test statistics
- Run @BlockFreqAnalysis_BipolarCellTerminal (in /BlockFreq)
- Run @BlockFreqAnalysis_SummaryPlot

Figure 3
(a-d) Plot the averaged responses to varied-size spots, summary heatmap and swarmchat for cell type difference in transience and surround strength and response correlation of spot responses
- Run @Response_BCPlexusComparison (in /Spot/Analysis) to collect the data
- Run @IdentifiedBCComparison (in /Spot/Analysis) to plot the figures

(e-g) Plot the morphological bipolar cell classification with or without depth information and its closest assigned cell types, and summary response heatmap
- Run @DirectDistanceDataAugmentationTypeComparison
- Use @PlotMorphologyIdentifiedBCResults

Figure 4
(a) Plot the schematics for augmentation process
- Run @DirectDistanceDataAugmentationTypeComparison (in /Spot/Analysis)
- Run @DrawAugmentedProcess

(b) Scatter plot for each types
- Run @DirectDistanceDataAugmentationTypeComparison
- Run @DisplayMultidimensionalScaling

(c) Heatmap and permutation test on bipolar cell type difference in the primary encoding space
- Run @DirectDistanceDataAugmentationTypeComparison
- Run @DisplayMultidimensionalScaling
- Run @DifferenceBetweenBCType_Spot

(d-e) Left: Encoding features of surround strength and transience in the encoding space.
- Run @DirectDistanceDataAugmentationTypeComparison
- Run @DisplayMultidimensionalScaling

Top right: Histogram of feature alignment in the primary encoding space

- Run @DirectDistanceDataAugmentationTypeComparison
- Run @DisplayMultidimensionalScaling
- Run @ShowFeatureAlignment

Bottom right: Explained variance of each coordinates to encoding features

- Run @DirectDistanceDataAugmentationTypeComparison
- Run @DisplayMultidimensionalScaling
- Run @DrawFeatureAxisAlignment_Spot

Figure 5

(a-e) General steps, and plot averaged response traces to different movie clips and scatter plot for distribution of different bipolar cell types in the encoding space by the multidimensional scaling

- Run @BCTerminalNatMovResponse_TypeComparison_Augmented (in /NaturalSceneVideo/Analysis)
- Run @DisplayMultidimensionalScaling_NatMov

(b) Bar chart for explained variance for each type by the luminance encoding and comparison to repeat reliability

- Run @TestFeatureXcorr

(c, e) Heatmap and statistic test for difference in paired bipolar cell types

- Run @DifferenceBetweenBCType_NaturalMovie

Figure 6

(a-e) General steps, and scatter plots for each encoding features in the encoding space by the multidimensional scaling

- Run the followings to get extracted signals for each encoding features (in /NaturalSceneVideo/Analysis)
    - EstimateRFCenterSurround_NatMov
    - EstimateRFTransienceHP_NatMov
    - PrepareAvi4OpticalFlow
    - GenerateExpectedGC6fResponsetoNatMov_Positions
- Run @BCTerminalNatMovResponse_TypeComparison_Augmented (in NaturalSceneVideo)
- Run @DisplayMultidimensionalScaling_NatMov

(a) Trace of extracted encoding features of each movie clip

- Run @TestFeatureXcorr

(b-e) Bottom middle: Alignment of each encoding feature in the primary encoding space

- Run @ShowFeatureAlignment_NatMov

Bottom: Explained variance of each encoding feature by the coordinates in the encoding space

- Run @DrawFeatureAxisAligment

Figure 7

(a, b) Representative trace for the selected ROIs

- Run @NaturalMovieHeterogeneityEncodingMapping (in /NaturalSceneVideo/Analysis)
- Run @VisualizeHeterogeneityResponses_NaturalMovie

- Run @GetPairPathDistance

(c, d) Representative plot for the relationship between repeat reliability and within- and cross-repeat between each paired ROIs in the movie clips

- Run @VisualizeHeterogeneityFunction_NaturalMovie_Batch (in /NaturalSceneVideo)
- Run @NaturalMovieHeterogeneity
- Run @GetRepresentiveData_Heterogeneity_NaturalMovies

(e, f) Summary plot for data fitting of each length constant based on the responses of image and path distance.

- Run @SummarySimulateLengthConstant_NatMov_byBCType

Figure 8

(a, b) Heatmap of representative response traces of morphological segmented ROIs by varied size spots.

- Run @GetPairROIDistancefromSkeleton (in /BipolarCellTeminal/Analysis)
- Run @VisualizeHeterogeineityResponse_Spot

(c, b) Get the relationships (scatter plots) between difference in spot response parameters (i.e., surround strength and transience) and paired ROI distances, including path and image measurement.

- Run @GetPairROIDistancefromSkeleton
- Run @GetSpotImageDistanceParameters
- Run @SummarySimulateLengthConstant_Spot_byCell

Supplementary figure 2: modeling GCaMP6f response to frequency-modulated spots

- Run @ModelFrequencyResponse (in /Simulation/GCaMP6f)

Supplementary figure 3

(a-c) Response to 800 μm spots, with varied modulating frequencies, plot averaged response, f1 power summary and phase shift between spot sizes

- Run @BlockFreqAnalysis_BipolarCellTerminal (in /BlockFreq)
- Run @BlockFreqAnalysis_SummaryPlot

Supplementary figure 4 (a-b) batch effect evaluation

Scatter plot and histogram

- Run @DirectDistanceDataAugmentationTypeComparison
- Run @DisplayMultidimensionalScaling

Supplementary figure 5: Explained variance of responses by the multidimensional scaling

(a) Encoding space of the varied-size spot stimuli

- Run @DirectDistanceDataAugmentationTypeComparison
- Run @DisplayMultidimensionalScaling

(b) Encoding space of the naturalistic stimuli

- Run @BCTerminalNatMovResponse_TypeComparison_Augmented (in /NaturalSceneVideo)
- Run @DisplayMultidimensionalScaling_NatMov

Supplementary figure 6: calculate and plot histogram of camera moving speeds

- Run @PhysicalMovingSpeed (in /NaturalSceneVideo)

Supplementary figure 7: receptive field alignment for in-center contrast by noise stimuli

- Run @RFMapping_RF_nonliearity_batch (in /Noise/Analysis)
- Run @DrawNoiseRFMappingIllustratioin and @DrawRFMap_SignalCorrelation separately

Supplementary figure 8: encoding feature difference of different bipolar cell types in swarm charts

- Run @BCTerminalNatMovResponse_TypeComparison_Augmented (in /NaturalSceneVideo)
- Run @DisplayMultidimensionalScaling_NatMov

Supplementary figure 9: encoding feature difference of different bipolar cell types in swarm charts

(a) for varied-size spots

- Run @DirectDistanceDataAugmentationTypeComparison
- Run @DisplayMultidimensionalScaling
- Run @ShowFeatureAlignment

(b-d) for natural movies

- Run @BCTerminalNatMovResponse_TypeComparison_Augmented (in /NaturalSceneVideo)
- Run @DisplayMultidimensionalScaling_NatMov
- Run @ShowFeatureAlignment_NatMov