



Comparison of ligand-receptor interactions predicted by six methods capable of predicting cell-cell interactions (SpaOTsc, Giotto, CellChat, ICELLNET, NicheNet, and SingleCellSignalR). a, The number of overlapped ligand-receptor interactions of these methods between L2/3 eNeuron and L4 eNeuron in dataset 4. b-d, The numbers of ligand-receptor interactions found by different methods for each cell-type pair in dataset 1 (seqFISH; Fluidigm c1; mouse gastrulation) (b), dataset 4 (seqFISH+; Smart-seq; mouse cortex) (c), and dataset 41 (Slide-seqV2; Drop-seq; mouse hippocampus) (d). For all the methods, we used the expression metrics of the spatial transcriptomics data as the inputs.