Overview of cellular and molecular changes across the primate dlPFC

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Evaluate species-specificity in this study

plot.auc.arhgap18.R
plot.auc.astro.R
plot.auc.immune.R
plot.auc.syt10.R

Plot the expression of representative markers of species-specific subtypes

plot.marexpr.vln.arhgap18.R
plot.marexpr.vln.rAstro.R
plot.marexpr.vln.syt10.R

Evaluate species-specificity in motor cortex

plot.syt10.motor.dlPFC.R
plot.arhgap18.motor.dlPFC.R

Cell type proportion comparisons (scCODA)

- Prepare data for scCODA analysis
  prep_sccoda_v1.R

- scCODA analysis
  calc_sccoda_v2_defref.py
  plot.sccoda.hres.fdr02.v2.R

- Plot pie summary for scCODA results
  plot.sccoda.summary.R

- Plot subtype proportions
  plot.prop.R

- Plot main figure network plot
  source functions:
  network.fun.v2.R

- visualization:
  plot.MF2B.R

Transcriptomic heterogeneity

- Entropy analysis
  calc.heter.fun.v3.R
  vis.heter.fun.R
  calc.bin.entropy.v4.R
  vis.dif.entropy.v4.R

- Bootstrap PCA analysis calc.bootstrap.fun.R
  calc.bootstrap.pca.R
  calc.boot.meandist.v1.R
  vis.boot.pca.v1.R

Transcriptomic divergence

- Transcriptomic divergence
  Different types: balanced HVGs from each class; top HVGs across all cells;
  subset cell
  get_hvg_byctp.R
  get_hvg_noctp.R
  calc.subset.avg.R
  plot.cor.bal.ctp.v2.R
  plot.cor.nobal.v2.R
  plot.cor.subset.v2.R

- Plot # DEGs
  plot.ndex.R