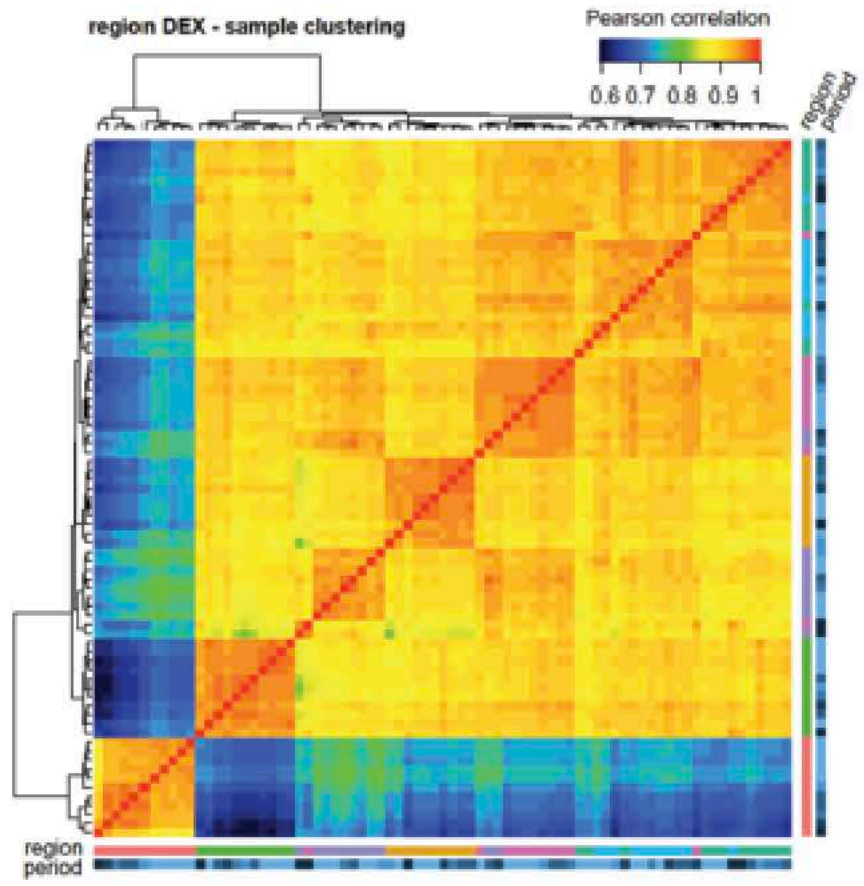
Exploring Post-transcriptional regulation in specific neuronal cell-types



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The immense intercellular and intracellular heterogeneity of the central nervous system presents major challenges for high-throughput omic analyses. Transcriptional, translational, and post-translational regulatory events are localized to specific neuronal cell types or subcellular compartments, resulting in discrete patterns of protein expression and activity. A spatial and quantitative knowledge of the neuroproteome is therefore critical to understanding both normal and pathological aspects of the functional genomics and anatomy of the CNS. We find that on a broad level, protein abundance differences between human brain regions are generally of a greater magnitude than mRNA. Moreover, even structurally similar cortical regions harbour significant differences in the abundance of receptor-associated and resident plasma membrane proteins that are not readily observed by mRNA. However, there are significant challenges in obtaining comprehensive neuroproteomic data with cell-type specificity. Here we illustrate how proteomics and translatomics can be exploited to enhance high-throughput functional genomic analysis of neural tissues at cell type-resolution.

Friday, October 6th, 4pm

Hess Seminar - Room B

WINE and CHEESE reception
5-7pm,Hess, 9th Flr.

Icahn School of Medicine at Mount Sinai

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