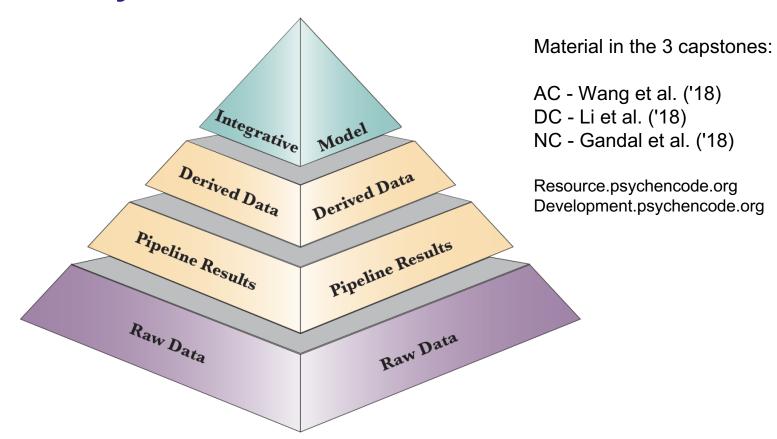
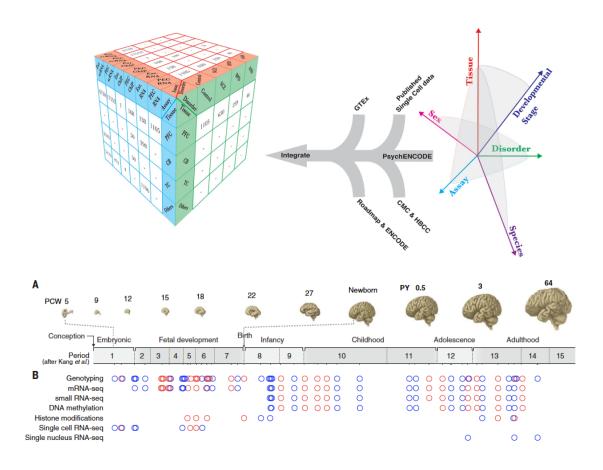
Review of the Phase 1 PsychENCODE capstone resource: Layers of distributed information



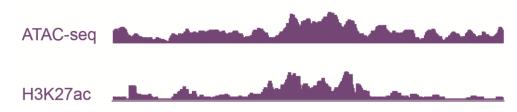
Base Data Layer

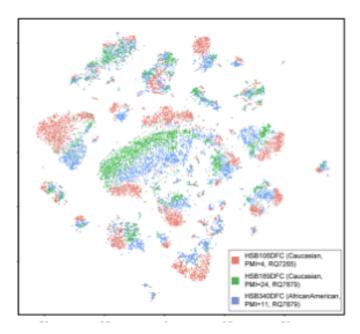


Organizing Metaphors

- New "Axes" ?
- New sets to merge (GTEx v8, HCA)?
- Reference brain ?

Pipeline Results

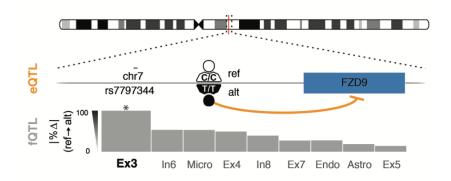


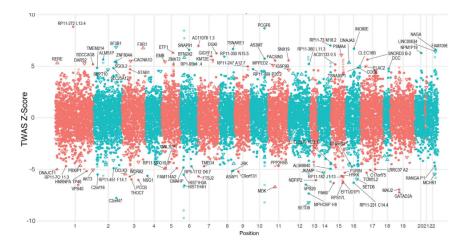


- ChIP-seq & Me
 - signal tracks & peaks
 - o Differential H3K27ac & Me peaks
- Bulk RNA-seq quantifications
- Single-cell
 - Quantifications
 - Cell-type signatures & fractions
- Imputed genotypes
- Hi-C matrix & TADs

- ATAC-seq pipeline? sc-ATAC?
- More cell types
- WGS vs. imputed genotypes

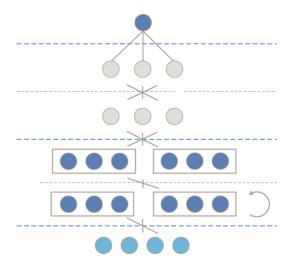
Derived Results

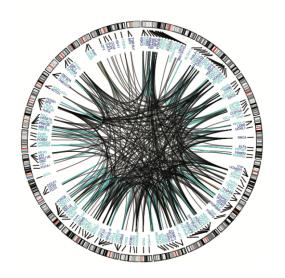




- DEX genes & co-expr. modules
 - Across development, regions & conditions
 - Differential splicing
- PFC QTLs
 - cis-eQTLs ~2M (sat'd)
 - o fQTL, cQTLs
- Enhancers (init. PFC & CBC)

- Trans QTLs? More regions?
- Starr-seq enhancers?





Integrative Models

- Integ. Regulatory Networks
 - Activity+Hi-C+QTL
 - Double overlap high-conf. linkages (eg A+H)
- Init. disease prediction model (DSPN)

- Better networks? Single-cell?
- How to distribute models?