Uber paper:

1. DEGs and orthology. Are DEGs enriched in orthology? **1 week.**
   1. Each species has one or more DEG-sets (different time points and/or different brain regions). For any pair of DEG-sets, from distinct species, count how many orthology pairs are included; test its significance empirically by considering pairs of random gene-sets. Repeat this for every pair of DEG-sets (Table). Figure shows Venn diagram.
2. Discovery of cross-species co-expression modules (ab initio). **1 week.**
   1. 3-species clustering using Potts model. (Use noise cluster, if it works.)
   2. Subject “cross-species clusters” to enrichment tests. Show that we gain (stronger enrichments) this way.
   3. Other performance evaluations (supplementary).
   4. Main results: discuss which biological processes show up significantly *only when* examining cross-species.
3. Are DEG-sets, separately defined in each species, strongly connected to common ‘features’? Use DRaWR to identify annotations/features that are associated with DEG sets in each species separately and then in a cross-species mode (discriminatively). **2 weeks.**
4. Temporal Waves of transcription that emphasize different biological themes.
   1. Subjecting clusters from (4) and (5) to linear model, identify clusters with significant temporal dependence (“waves”), characterize biological processes enriched in these waves, see if trends are shared across species.
5. DEGs and accessibility.
   1. Are DAPs next to the same genes in the three species? (Repeat analysis 1 with DEG-sets replaced by DAP-sets.) **Dave produces DAP gene sets in 2 weeks.**
   2. Is there a common trend of DEGs being enriched for baseline (region-specific) accessibility but not for differential accessibility? **Laura in 1 week.**
6. Conservation of regulation?
   1. Conservation of TF presence in promoters at a gene set level? (**Laura in 2 weeks**)
   2. Conservation of TF-target correlations in gene expression. Using TRNs in each species and orthology map, find TF-gene pairs shared in each species. **(Laura in 3 weeks)**
   3. Is TF presence in the promoters of an orthology group highly conserved? What are the TF-orthogroup pairs with strongest conservation? Using GxM maps and orthology map, find TF-orthogroup pair such that the motif is present in promoters of that orthogroup in all three species.