Paper outline:

Ideas:

* Do we want to create some simulated DEX data and run the same experiment using simulated data? Jesse: I think we want to be more generic: we want both over-expression data and under-expression data. I think it will be interesting to see which is more expressive. DEX itself is done by only a handful of labs.
* Introduction
	+ Paragraph about the task of inferring networks from noisy
	+ Paragraph about many different data types and analyses
	+ Intro paragraph to our approach
* Previous work
	+ (Does this need its own section or should we roll it into the intro?) whatever feels more comfortable for you. I’ll do the editing.
	+ Steady-state algorithms
	+ Time-series algorithms
	+ Clustering
	+ Pipelines
* Methods
	+ Depends on what actually ends up working, but for now the current pipeline where we are using the steady-state data and time-series data, with priors augmented by DEX. Right. Should be same number of genome wide assays no matter what (e.g. 60) and we should vary numbers of genes and noise.
* Results
	+ Compare to naïve and to other algorithms alone both from network architecture point of view and from prediction point of view.
	+ Image of the generated network
	+ Analysis of the subnetworks from a biological standpoint (i.e., do the subnetworks we infer actually make sense to biologist?) Since it’s simulated, why would it make sense?
* Conclusions