**Intro:**

* Mass spec data effected by systematic bias (sample prep, temp, unknown)
* Normalization: statistical method to adjust
* Make sample more comparable while preserving signal
* Adequate normalization is important for given data set
* Incorrect normalization can introduce new artificial patterns
* Inspired this tool: streamline evaluation of normalization methods

**Data:**

* Peptides and Proteins (from MaxQuant)
* Protein = sum of peptides for given protein
* Peptide level about the same for given Protein
* Top3 peptide method
* Meta data (treatments/batch)

**Filter:**

* Focus on ER/PR+, HER2 and control
* With and without Hydroxyurea treatment
* 3 replicates / 2 batches
* PCA Protein: cell lines + treatment cluster (treatment/batch)
* PCA Peptide: cluster by treatment/batch below

**Normalization:**

* Different methods work for different data sets
* Popular normalization methods
* PCV/PMAD/PEV: small good
* Cor: within group; high good
* Heatmap: Cluster by: Treatment groups, cell lines, batch/treatment
* Log2 ratio: distribution of log2 ratios of all treatment group combinations; centered around 0
* NA: for imputation method selection (missing at random (MAR) or missing not at random (MNAR))

**DAtest:**

* Select normalization and imputation method
* LIMMA does not require imputation
* DAtest: comparison of different differential abundance/expression methods
* Automatically selects appropriate tests [**RUN**]
* Ranking of tests
* Log LIMMA best

**DAtest power:**

* Power evaluation over a range of effect sizes for a given test