# Transcriptome Data Supporting Early Prediction of Carcass Merit in Young Beef Cattle

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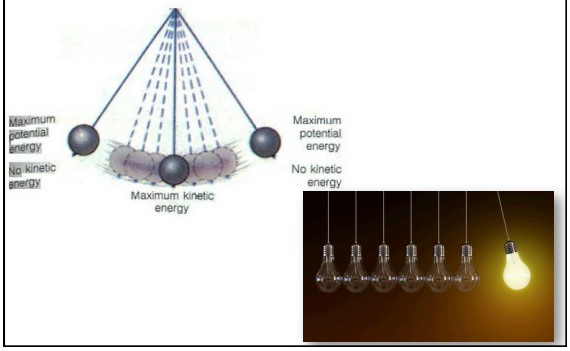
## Shift the paradigm back

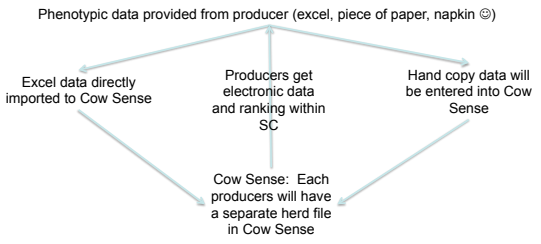
- Collection and reporting of phenotypic production data
- How do we facilitate this collection and analysis of data
- We have to fill a void, but make sure to not get run over




## Benchmarking Database

- Utilize Cow Sense software to aid in the collection and dissemination of data
- Facilitate the collection of phenotypic data from commercial producers
- Establish benchmark's for production traits within the state of South Carolina (southeast)
- What does this look like?

## Data Management




## Genome vs. Transcriptome

***Genome***
- Bovine genome is one of largest sequenced
- All **DNA** in the species
- Data is the same regardless of tissue source
- Not all genes are expressed

***Transcriptome***
- All **RNA** in the species
- Data varies based on the tissue samples
- All of these genes are expressed
- $$$

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## Work Flow for Data Collection

- Sample collection
- Total RNA isolation
- RNAseq library preparation
- Transcription sequencing using Illumina
- Multivariant analysis
- Data interpretation

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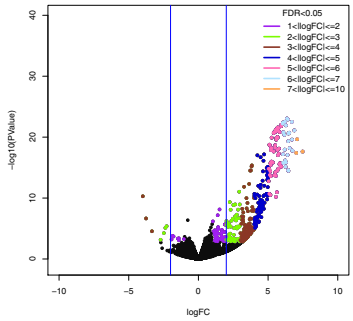
**Differential Gene Expression – Volcano Plot**

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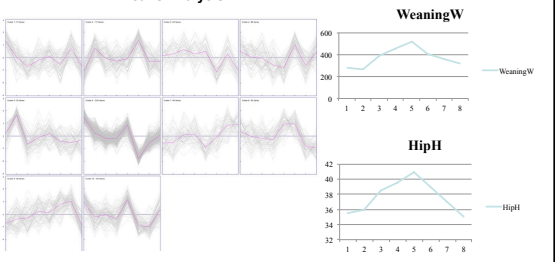
**K-Means Analysis**

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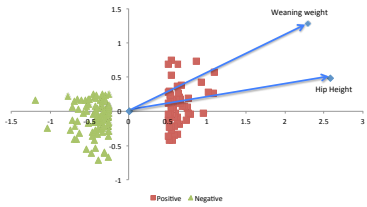
## Canonical Correspondence Analysis

**CCA Predictors**

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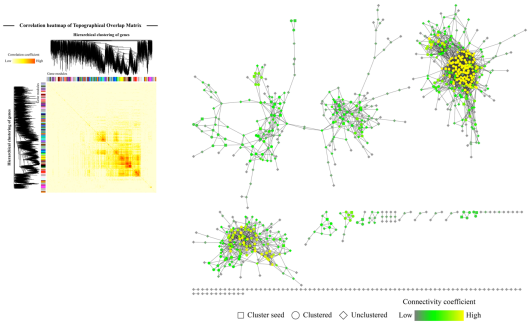
**Weighted Gene Co-expression Network Analysis**



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