

- Predict Genes.
- Extract intergenic regions
- Create upstream regions database



- Group genes based on biochemical pathway / function



- Use MEME & AlignACE to find significant conserved, over-represented sequence motifs in upstream regions of genes within a group/ sub-set



- Conduct semi-quantitative RT-PCR for all genes in a group to establish co-regulation.
- Group genes into sub-sets based on expression profiles.

Repeat
Single iteration
on sub-sets

