1. Pre-processing

- ORF extraction from translated genomic sequence
- ORF extraction from GFF3 file (optional)
- Pre-built / user-provided family alignments
- Building family-specific HMMs
- Hmmsearch against translated genome
- Hmmsearch against proteome (optional)
- Tiling search results, building “extended hits”

2. Motif Mining

3. Model Prediction

- Augustus (evidence mode)
- GeneWise + SplicePredictor
- GlimmerHMM (optional)
- GeneScan (optional)
- GeneMark (optional)
- ... 

4. Model Evaluation & Selection

- Evaluating alternative models (MSA score, HMM score, SignalP score, etc.)
- Removing low-confidence models & picking best model
- Building sub-family alignments
- Collecting & refining gene models