**A**  
Yeast genome/transcriptome assembly

- BLAST with reference sequences
  - BLAST hits
    - 1. Combine hits
    - 2. Extend hitregion
    - 3. AUGUSTUS-PPX

Reference sequence(s)  
Gene predictions

- Reference sequence(s)
- Gene predictions

  - pair-wise (NW, SW, LCC, Gotoh)
  - add to existing MSA (MAFFT)

  - Alignment
    - 1. Compare aa
    - 2. Compare CUGs

  - CUG codon prediction
    - 1. Gene concatenation
    - 2. Gblocks
    - 3. FastTree (ML)

  - Phylogeny

- Identity of the tRNA_CAG
  - 1. BLAST against reference sequences
  - 2. add to existing MSA

**B**  
Yeast protein sequence  
Gene reconstruction

- Yeast protein sequence
  - WebScipio

- Gene reconstruction
  - Translation from reconstruction
  - Compare CUG translations