RNA-Seq

Variant calling in zebrafish (v10)

1. Analysis
   a. Pre-processing
      i. Map reads to reference
      ii. Mark duplicates
      iii. Recalibrate base quality scores
      iv. Indel-base realignment
   b. Variant discovery
      i. Calling cohorts
      ii. Recalibrate base quality scores
      iii. Genotype refinement
      iv. Annotation and variant evaluation

2. Retrieve data from experimental designs

3. Generalize into tools
Joint discovery to resolve bias issues

4. Assess the scope and limits