- Sequence alignment projects:
  1. Comparison of alignment programs on real data benchmarks
     - Study speed and/or accuracy
     - Protein, RNA, or genome alignment
     - Spliced alignment
     - Short read alignment
     - Sequence to structure alignment (also known as threading)
     - Profile alignment
  2. Implementation of a new alignment program
  3. Genome alignment
  4. Alignment to determine SNPs
  5. Expected accuracy alignment vs. HMM vs. Needleman-Wunsch

- Phylogeny reconstruction
  1. Study of phylogeny reconstruction methods on simulated data
     - Speed and/or accuracy
     - Protein, DNA, or RNA data
  2. Simultaneous alignment and phylogeny estimation: speed and/or accuracy
  3. Phylogenies from whole genome data

- Genome-wide association studies
  1. Comparison of univariate tests on simulated data
     - Chi-square vs. F-test vs. Pearson correlation
  2. Univariate vs multivariate methods
     - Chi-square, logistic regression, support vector machine

- Prediction of disease risk from genotype and/or phenotype
  1. Comparison of classifiers
     - Discriminative vs. generative
     - Different discriminative or generative classifiers
  2. Effect of SNP selection on accuracy of classification
  3. Simulated and/or real data

- Prediction of phenotype from genotype

- Population structure
  1. PCA and/or STRUCTURE analysis on publicly available data