Predicting Exon/Intron using HMM, GA and NN

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Project Summary

- Previous work
  - Use GA to find HMM parameter
  - Drawbacks
    - Too few population
    - Too few training data
- Extend previous work by two ways
  - GA fine-tuning (or use ES)
  - Use HMM training algorithm as local optimization

System Overview

1. HMM + GA (1)
   - Chromosome: HMM parameter
   - Fitness: likelihood of each HMM
   - Evolve HMM parameter by GA (or ES)
2. HMM + GA (2)
   - Chromosome: HMM structure
   - Fitness: likelihood of each HMM
   - After training each HMM, evolve HMM structure by GA
3. HMM + NN
   - Train HMM for exon/intron
   - Train NN with HMM outputs

Data

- UCSC dataset
  - single_exon_GB.dat : 186 genes
  - Multi_exon_GB.dat : 304 genes