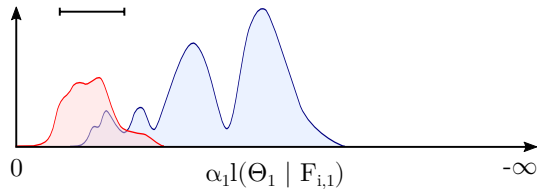
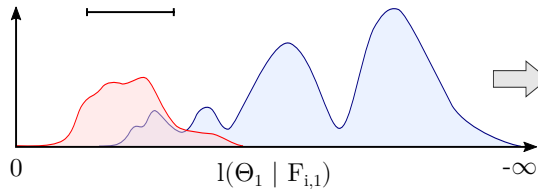


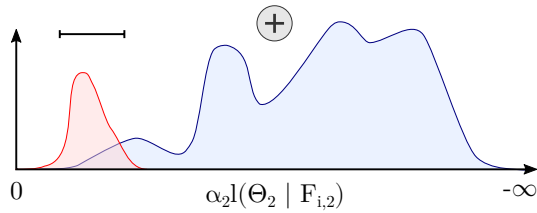
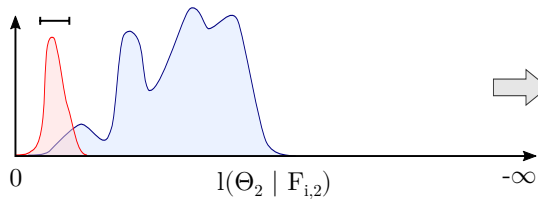
original log-likelihood

weighted log-likelihood

submodel 1



submodel 2



- genome (positive class)
- other genomes (negative class)
- positive class standard deviation

= aggregate log-likelihood