

## Lecture 6

# Genetic Algorithms Model Ensembles

## Genetic Algorithms

- Evolutionary computation
- Prototypical GA
- An example: GABIL
- Schema theorem
- Genetic programming
- The Baldwin effect

## Evolutionary Computation

1. Computational procedures patterned after biological evolution
2. Search procedure that probabilistically applies search operators to set of points in the search space

## Biological Evolution

Lamarck:

- Species “transmute” over time

Darwin:

- Consistent, heritable variation among individuals in population
- Natural selection of the fittest

Mendel/Genetics:

- A mechanism for inheriting traits
- Mapping: Genotype  $\rightarrow$  Phenotype

$GA(Fitness, Fitness\_threshold, p, r, m)$

- *Initialize*:  $P \leftarrow p$  random hypotheses
- *Evaluate*: for each  $h$  in  $P$ , compute  $Fitness(h)$
- While  $[\max_h Fitness(h)] < Fitness\_threshold$ 
  1. *Select*: Randomly select  $(1 - r)p$  members of  $P$  to add to  $P_s$ .  $Pr(h_i) = \frac{Fitness(h_i)}{\sum_{j=1}^p Fitness(h_j)}$
  2. *Crossover*: Randomly select  $\frac{r}{2}p$  pairs of hypotheses from  $P$ . For each pair  $(h_1, h_2)$ , produce two offspring by crossover. Add all offspring to  $P_s$ .
  3. *Mutate*: Invert random bit in  $mp$  random hyps.
  4. *Update*:  $P \leftarrow P_s$
  5. *Evaluate*: for each  $h$  in  $P$ , compute  $Fitness(h)$
- Return hypothesis from  $P$  with highest fitness.

## Representing Hypotheses

Represent

$(Outlook = Overcast \vee Rain) \wedge (Wind = Strong)$

by

Outlook	Wind
011	10

Represent

IF  $Wind = Strong$  THEN  $PlayTennis = yes$

by

Outlook	Wind	PlayTennis
111	10	10



### GABIL Extensions

Add new genetic operators, also applied probabilistically:

1. *AddAlternative*: generalize constraint on  $a_i$  by changing a 0 to 1
2. *DropCondition*: generalize constraint on  $a_i$  by changing every 0 to 1

And add new field to bitstring to determine whether to allow these

$a_1$	$a_2$	$c$	$a_1$	$a_2$	$c$	$AA$	$DC$
01	11	0	10	01	0	1	0

So now the learning strategy also evolves!

### Schemas

How to characterize evolution of population in GA?

Schema = string containing 0, 1, \* ("don't care")

- Typical schema: 10\*\*0\*
- Instances of above schema: 101101, 100000, ...

Characterize population by number of instances representing each possible schema

- $m(s, t) = \#$  instances of schema  $s$  in pop, at time  $t$

### Consider Just Selection

- $\bar{f}(t)$  = average fitness of pop. at time  $t$
- $m(s, t)$  = instances of schema  $s$  in pop. at time  $t$
- $\hat{u}(s, t)$  = average fitness of instances of  $s$  at time  $t$

Probability of selecting  $h$  in one selection step

$$\begin{aligned} \Pr(h) &= \frac{f(h)}{\sum_{i=1}^n f(h_i)} \\ &= \frac{f(h)}{nf(t)} \end{aligned}$$

Probability of selecting an instance of  $s$  in one step

$$\begin{aligned} \Pr(h \in s) &= \sum_{h \in s \cap p_t} \frac{f(h)}{nf(t)} \\ &= \frac{\hat{u}(s, t)}{nf(t)} m(s, t) \end{aligned}$$

Expected number of instances of  $s$  after  $n$  selections

$$E[m(s, t + 1)] = \frac{\hat{u}(s, t)}{\bar{f}(t)} m(s, t)$$

### Schema Theorem

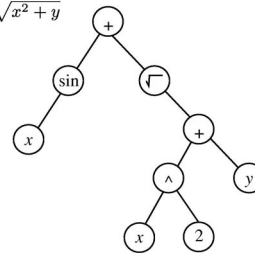
$$E[m(s, t + 1)] \geq \frac{\hat{u}(s, t)}{\bar{f}(t)} m(s, t) \left(1 - p_c \frac{d(s)}{l - 1}\right) (1 - p_m)^{o(s)}$$

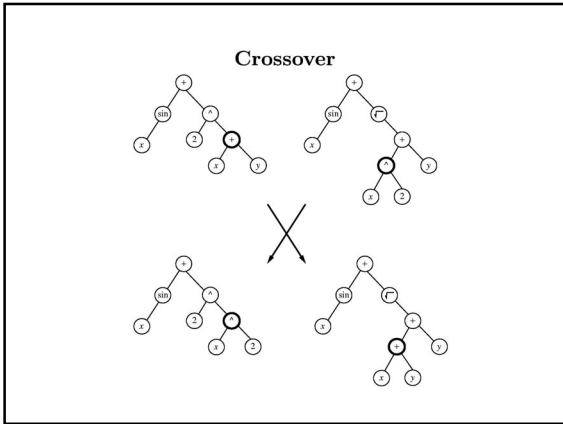
- $m(s, t)$  = instances of schema  $s$  in pop at time  $t$
- $\bar{f}(t)$  = average fitness of pop. at time  $t$
- $\hat{u}(s, t)$  = ave. fitness of instances of  $s$  at time  $t$
- $p_c$  = probability of single point crossover operator
- $p_m$  = probability of mutation operator
- $l$  = length of single bit strings
- $o(s)$  = number of defined (non "\*" bits) in  $s$
- $d(s)$  = dist. between left & rightmost defined bits in  $s$

### Genetic Programming

Population of programs represented by trees

E.g.:  $\sin(x) + \sqrt{x^2 + y}$





**Example: Electronic Circuit Design**

- Individuals are programs that transform beginning circuit to final circuit, by adding/subtracting components and connections
- Use population of 640,000, run on 64-node parallel processor
- Discovers circuits competitive with best human designs

**Biological Evolution**

Lamarck (19th century)

- Believed individual genetic makeup was altered by lifetime experience
- But current evidence contradicts this view

What is the impact of individual learning on population evolution?

**Baldwin Effect**

Assume

- Individual learning has no direct influence on individual DNA
- But ability to learn reduces need to “hard wire” traits in DNA

Then

- Ability of individuals to learn will support more diverse gene pool, because learning allows individuals with various “hard wired” traits to be successful
- More diverse gene pool will support faster evolution of gene pool

⇒ Individual learning increases rate of evolution

**Baldwin Effect**

Plausible example:

1. New predator appears in environment
2. Individuals who can learn (to avoid it) will be selected
3. Increase in learning individuals will support more diverse gene pool
4. Resulting in faster evolution
5. Possibly resulting in new non-learned traits such as instinctive fear of predator

**Computer Experiments on Baldwin Effect**

Evolve simple neural networks:

- Some network weights fixed, others trainable
- Genetic makeup determines which are fixed, and their weight values

Results:

- With no individual learning, population failed to improve over time
- When individual learning allowed
  - Early generations: population contained many individuals with many trainable weights
  - Later generations: higher fitness, while number of trainable weights decreased

### Genetic Algorithms: Summary

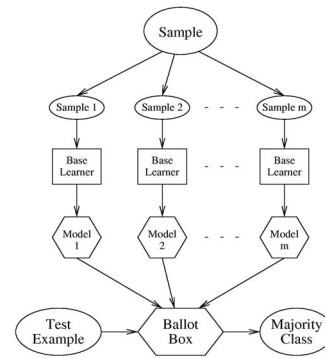
- Evolving algorithms by natural selection
- Genetic operators avoid (some) local minima
- Why it works: schema theorem
- Genetic programming
- Baldwin effect

### Model Ensembles

- **Basic idea:**  
Instead of learning one model,  
Learn several and combine them
- Typically improves accuracy, often by a lot
- **Many methods:**
  - Bagging
  - Boosting
  - ECOC (error-correcting output coding)
  - Stacking
  - Etc.

### Bagging

- Generate “bootstrap” replicates of training set by sampling with replacement
- Learn one model on each replicate
- Combine by uniform voting



### Boosting

- Maintain vector of weights for examples
- Initialize with uniform weights
- Loop:
  - Apply learner to weighted examples (or sample)
  - Increase weights of misclassified examples
- Combine models by weighted voting

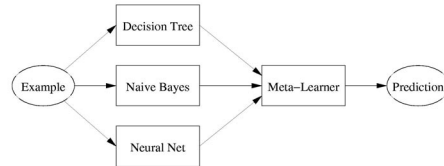
ADABOOST( $S, Learn, k$ )  
 $S$ : Training set  $\{(x_1, y_1), \dots, (x_m, y_m)\}$ ,  $y_i \in Y$   
 $Learn$ : Learner( $S$ , weights)  
 $k$ : # Rounds  
 For all  $i$  in  $S$ :  $w_1(i) = 1/m$   
 For  $r = 1$  to  $k$  do  
   For all  $i$ :  $p_r(i) = w_r(i) / \sum_i w_r(i)$   
    $h_r = Learn(S, p_r)$   
    $\epsilon_r = \sum_i p_r(i) \mathbf{1}[h_r(i) \neq y_i]$   
   If  $\epsilon_r > 1/2$  then  
      $k = r - 1$   
     Exit  
    $\beta_r = \epsilon_r / (1 - \epsilon_r)$   
   For all  $i$ :  $w_{r+1}(i) = w_r(i) \beta_r^{1 - \mathbf{1}[h_r(x_i) \neq y_i]}$   
 Output:  $h(x) = \operatorname{argmax}_{y \in Y} \sum_{r=1}^k (\log \frac{1}{\beta_r}) \mathbf{1}[h_r(x) = y]$

### Error-Correcting Output Coding

- **Motivation:**  
Applying binary classifiers to multiclass problems
- **Train:** Repeat  $L$  times:
  - Form a binary problem by randomly assigning classes to “superclasses” 0 and 1  
E.g.: A, B, D  $\rightarrow$  0; C, E  $\rightarrow$  1
  - Apply binary learner to binary problem
- Each class is represented by a binary vector
- **Test:**
  - Apply each classifier to test example, forming vector of predictions  $\mathbf{P}$
  - Predict class whose vector is closest to  $\mathbf{P}$  (Hamming)

### Stacking

- Apply multiple base learners  
(e.g.: decision trees, naive Bayes, neural nets)
- Meta-learner: Inputs = Base learner predictions
- Training by leave-one-out cross-validation:  
Meta-L. inputs = Predictions on left-out examples



### Model Ensembles: Summary

- Learn several models and combine them
- Bagging: Random resamples
- Boosting: Weighted resamples
- ECOC: Recode outputs
- Stacking: Multiple learners