

GENETIC ALGORITHMS

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The Genetic Algorithms (GA)

- ❖ Based on the mechanics of biological evolution.
- ❖Initially developed by John Holland, University of Michigan (1970's)
 - •To understand processes in natural systems.
 - To design artificial systems retaining the robustness and adaptation properties of natural systems.
- ❖ Provide efficient techniques for optimization and machine learning applications.
- ❖It is a stochastic algorithm.
- ❖It does not use gradient information.
- ❖ Widely used in business, science and engineering.



Genetic Algorithms: basic idea

- ❖ Start with a population of candidate solutions.
- ❖ Variation: Introduce variation by applying two operators: crossover and mutation.
- Survival of the fittest: Use a fitness criterion to bias the evolution towards desired features.

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Genetic Algorithms Techniques

- ❖GAs are a particular class of evolutionary algorithms. The techniques common to all GAs are: •Inheritance - offspring acquire characteristics
 - •Mutation change, to avoid similarity
 - •Natural Selection -variations improve survival

 - •Crossover recombination
- ❖GAs are best used when the objective function is:
 - •Discontinuous
 - •Highly nonlinear
 - •High dimension
 - Stochastic
 - •Has unreliable or undefined derivatives



Biological Terminology

❖Gene – a single encoding of part of the solution space, i.e. either single bits or short blocks of adjacent bits that encode an element of the candidate solution

❖Chromosome – a string of genes that represents a solution
1 0 1 1 0

❖Population – the number of chromosomes available to test

		:// A		4.50 - 11
0	1	1	0	1
1	1	0	0	1
1	0	1	0	1
1	0	1	0	1
1	0	0	0	1
0	0	1	1	1

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Features of Genetic Algorithms

- Not too fast but cover large search space
 - Capable of quickly finding promising regions of the search space but may take a relatively long time to reach the optimal solution.
- ❖ Good heuristics for combinatorial problems
- Usually emphasize combining information from good parents (crossover)
- ❖ Different GAs use different
 - Representations
 - Mutations
 - Crossovers
 - Selection mechanisms





Representation

- ❖ GAs on primarily two types of representations:
 - Binary Coded

[0110, 0011, 1101,]

· Real Coded

 $[13.2, -18.11, 5.72, \ldots]$

- ❖ Binary-Coded (genotype) GAs must decode a chromosome into a real value (phenotype), for evaluating the fitness value.
- * Real-Coded GAs can be regarded as GAs that operate on the actual real value (phenotype).
 - For Real-Coded GAs, no genotype-to-phenotype mapping is needed.

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Selection

- ❖A proportion of the existing population is selected to bread a new bread of generation.
- ❖ Parents with better fitness have better chances to produce offspring.

Rank selection

- * Rank selection first ranks the population and then every chromosome receives fitness from this ranking.
 - Selection is based on this ranking rather than absolute differences in fitness.
 - The best will have fitness 1, second best 2 etc. and the worst will have fitness *N* (number of chromosomes in population).

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Tournament selection

Runs a "tournament" among a few individuals chosen at random from the population and selects the winner (the one with the best fitness) for crossover

- Two entities are picked out of the pool, their fitness is compared, and the better is permitted to reproduce.
- Selection pressure can be easily adjusted by changing the tournament
- Deterministic tournament selection selects the best individual in each tournament.



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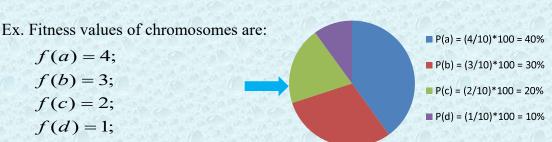
Roulette-wheel selection

- •Assign each individual part of the wheel according to proportion of fitness value.
- ✓ The probability that a individual will be selected is given by the ratio of its fitness to the sum of fitness of all individuals of the current population.

$$P(h_i) = \frac{f(h_i)}{\sum_{j=1}^{N} f(h_j)}$$

where h_i is the i^{th} individual of current population and size of population is N.

•Spin wheel (N) times to select (N) individuals





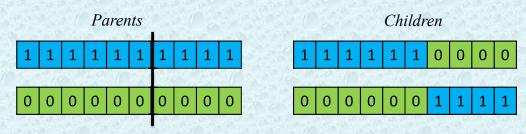
Crossover

Crossover is a genetic operator that combines (mates) two individuals (parents) to produce two new individuals (Childs).

• The idea behind crossover is that the new chromosome may be better than both of the parents if it takes the best characteristics from each of the parents.

Single-Point Crossover

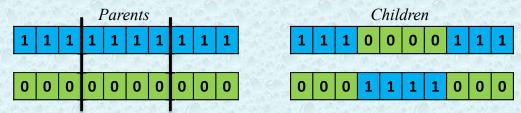
- •Choose a random point
- •Split parents at this crossover point
- •Create children by exchanging tails
- •Probability of crossover is typically in range (0.6, 0.9)



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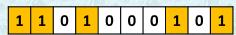
Two-Point Crossover

- •Choose two random points
- •Split parents at these crossover points
- •Create children by exchanging middle portion

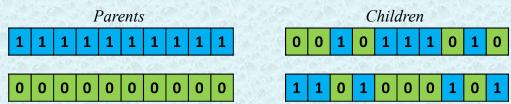


Uniform Crossover

•Randomly generated mask



•Create children by exchanging genes according to mask





Real value Crossover

- •Choose two parents randomly from the selected candidates.
- •Generate a random number (r) for each dimension of parents.
- •Create children by combining the weighted portion of both parents.

$$b = \begin{cases} (2*r)^{\left(\frac{1}{\mu+1}\right)} & \text{if } r \le 0.5\\ \left(\frac{1}{2*(1-r)}\right)^{\left(\frac{1}{\mu+1}\right)} & \text{if } r > 0.5 \end{cases}$$

$$child_1(j) = \frac{1}{2} ((1+b)*parent_1(j) + (1-b)*parent_2(j))$$

$$child_2(j) = \frac{1}{2} ((1-b)^* parent_1(j) + (1+b)^* parent_2(j))$$

where

- r is a random number $\{0,1\}$
- μ is a crossover operator
- child(j) represent jth dimension of child.

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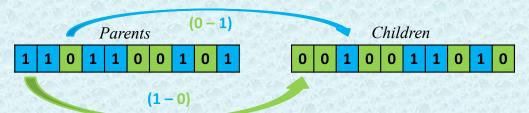
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Mutation

- **Autation** is a genetic operator used to maintain genetic diversity from one generation of a population of chromosomes to the next. It is analogous to biological mutation.
- * Mutation Probability determines how often the parts of a chromosome will be mutated.

Bit-reversal Mutation

- •Alter each gene independently
- Choose a random point
- •Create children by altering the gene of choosen point
- •Mutation probability is typically in range {(1/population size), (1/chromosome length)}





Polynomial Mutation

- •Select one parent randomly from the selected parents.
- •Generate a random number (r) for each dimension of parent.

$$d = \begin{cases} (2*r)^{\left(\frac{1}{\eta+1}\right)} - 1 & if \quad r \le 0.5\\ 1 - (2*(1-r))^{\left(\frac{1}{\eta+1}\right)} & if \quad r > 0.5 \end{cases}$$

$$child(j) = parent(j) + d$$

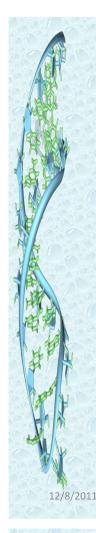
where

- r is a random number $\{0,1\}$
- η is a mutation operator
- child(j) represent j^{th} dimension of child.

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Fitness Function

- - ❖ A fitness function quantifies the optimality of a solution (chromosome) so that that particular solution may be ranked against all the other solutions.
 - ❖ It depicts the closeness of a given 'solution' to the desired result.
 - * Watch out for its speed.
 - * Most functions are stochastic and designed so that a small proportion of less fit solutions are selected. This helps keep the diversity of the population large, preventing premature convergence on poor solutions.



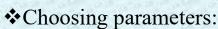
Termination

- ❖ A solution is found that satisfies minimum criteria
- ❖ Fixed number of generations found
- ❖ Allocated budget (computation, time/money) reached
- The highest ranking solution's fitness is reaching or has reached

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Issues with Genetic Algorithms



- •Population size
- •Crossover and mutation probabilities
- •Selection, deletion policies
- •Crossover, mutation operators, etc.
- •Termination criteria

*Performance:

- •Can be too slow but covers a large search space
- •Is only as good as the fitness function

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The Basic Genetic Algorithm

```
% Generate random population of chromosomes
Initialize population;
% Evaluate the fitness of each chromosome in the population
Evaluate population;
                                                          [Fitness]
% Create, accept and test a new population:
while Termination Criteria Not Satisfied
    % Select according to fitness
    Select parents for reproduction;
                                                          [Selection]
    % With a crossover probability perform crossover or copy parents
    Perform crossover;
                                                          [Crossover]
    % With a mutation probability mutate offspring at each position in chromosome
    Perform mutation;
                                                          [Mutation]
    Accept new generation;
    Evaluate population;
                                                          [Fitness]
```

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$Minimize - f(x) = \sin(x),$

where $0 < x < (2 * \pi)$

Initialize population:

- Search space is of single dimension (given).
- Let population size (N) = 10
- Initialize population with 10 chromosomes having single dimensioned real value.
- These values are randomly distributed in between $[0,2*\pi]$.

X

2.620

4.526

0.001

1.900

0.922

0.580

1.170

2.171

_ ---

2.493

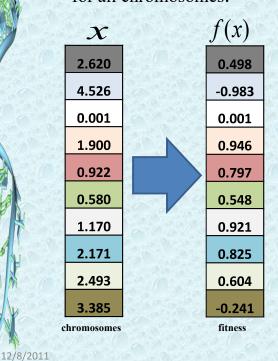
3.385

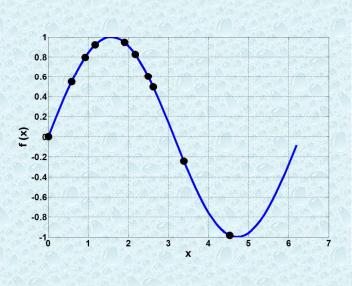
chromosomes



Evaluate function:

• Find out objective function values (fitness values) for all chromosomes.



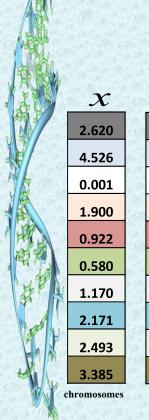


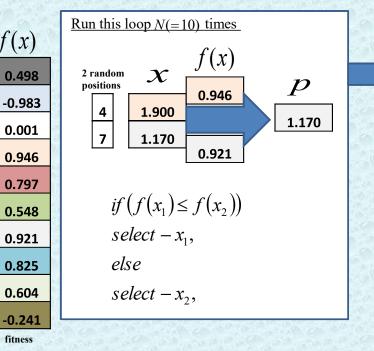
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Tournament Selection:

f(x)

-0.241fitness





p							
	1.170						
	4.526						
	2.620	-					
100	0.580						
	4.526						
250	3.385						
	0.001						
P	2.620	9					
	4.526						
256	2.620						
	parents						



P

1.170

4.526

2.620

0.580

4.526

3.385

0.001

2.620

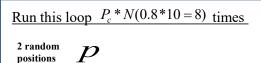
4.526

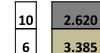
2.620

parents

Crossover:

Select Probability of Crossover $P_c = 0.8$ Distribution index for Crossover $(\mu)=20$





2.611 3.394

 C_c

2.611 3.394

Generate random number -(r)

$$b = \begin{cases} (2*r)^{\left(\frac{1}{\mu+1}\right)} & \text{if} & r \le 0.5\\ \left(\frac{1}{2*(1-r)}\right)^{\left(\frac{1}{\mu+1}\right)} & \text{if} & r > 0.5 \end{cases}$$

$$c_{c1} = \frac{1}{2} ((1+b)*p_1 + (1-b)*p_2)$$

$$c_{c2} = \frac{1}{2} ((1-b)*p_1 + (1+b)*p_2)$$

4.196 2.625

0.330

 C_c

4.521

1.146

4.469

children

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Mutation:

Select Probability of Mutation $P_m = 0.2$

Distribution index for Mutation $(\eta) = 20$



2.611

3.394

0.330

4.196

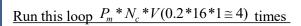
2.625

4.521

1.146

4.469

children



1 random position

2.625

 C_{m}

2.594 2.751

2.200

0.010

Mutated children

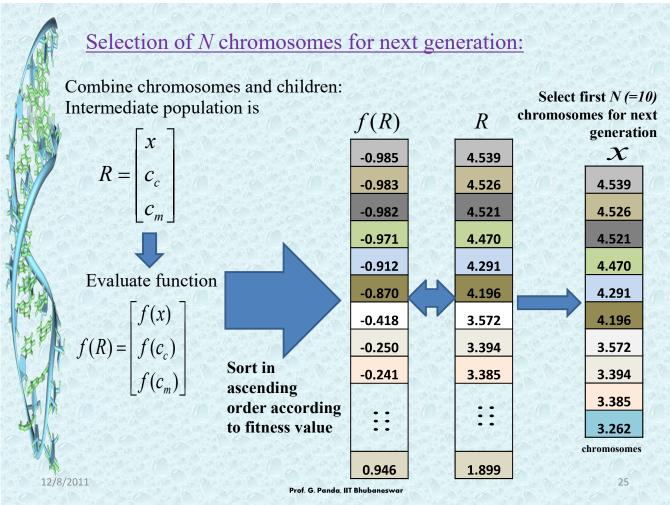
 $d = \begin{cases} (2*r)^{\left(\frac{1}{\eta+1}\right)} - 1 & \text{if } r \le 0.5\\ 1 - (2*(1-r))^{\left(\frac{1}{\eta+1}\right)} & \text{if } r > 0.5 \end{cases}$

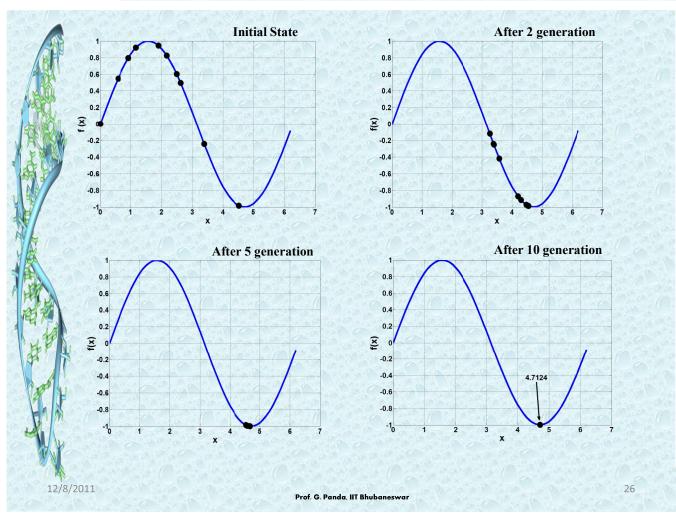
Generate random number -(r)

 $c_m = c_c + d$

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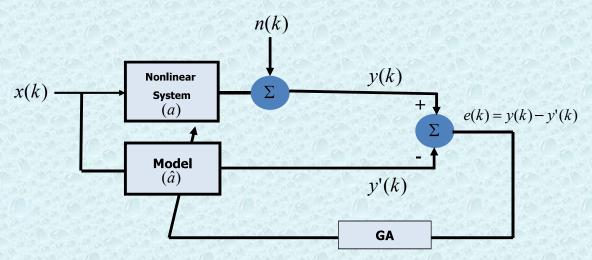
Applications of Genetic Algorithms

- •Optimization-numerical and combinatorial optimization problems, e.g. travelling salesman, routing, graph colouring and partitioning
- •Robotics—trajectory planning
- •Machine learning—designing neural networks, classification and prediction, e.g. prediction of weather or protein structure
- •Signal processing-filter design
- •Design-semiconductor layout, aircraft design, communication networks
- •Automatic programming-evolve computer programs for specific tasks, design cellular automata and sorting networks
- •Economics—development of bidding strategies, emergence of economics markets
- •Immune systems—model somatic mutations
- Ecology-model symbiosis, resource flow

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Schematic Block diagram of an adaptive identification system



- x represents the random input sequence lie in between [-0.5,0.5]
- y represents the desired output sequence.
- represents estimated output sequence.
- is additive white Gaussian noise.
- a represent coefficients of system.

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Genetic Algorithm For System Identification

 \bullet Coefficients of the model (\hat{a}) are initially chosen from a population of M - chromosomes.

 \clubsuit Each chromosome constitutes (Q*L) number of random binary bits where each sequential group of L - bits represent one coefficient of the adaptive model, where Q is the number of parameters of the model.

			←	L							Q	\rightarrow
0	1	1	1	0	1	1	0	1	1	\hat{a}_1^1	\hat{a}_2^1	\hat{a}_3^1
0	1	1	1	0	1	1	0	1		\hat{a}_1^2	\hat{a}_2^2	\hat{a}_3^2
0	1	1	1	0	1	1	0	1	M	\hat{a}_1^3	\hat{a}_2^3	\hat{a}_3^3
0	1	1	1	0	1	1	0	1		\hat{a}_1^4	\hat{a}_2^4	\hat{a}_3^4
0	1	1	1	0	1	1	0	1	$\Big] \bigvee$	\hat{a}_1^5	\hat{a}_2^5	\hat{a}_3^5
	Chromosomes									Mode	1 Coef	ficient

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Noise vector System Coefficient Time delay Desired Output vector Input matrix * * Time delay Model Coefficient Estimated Mean Square Input matrix Output vector Error (MSE) $\widetilde{X} = \begin{bmatrix} x_1 & x_2 & x_3 & \dots & x_K \\ 0 & x_1 & x_2 & \dots & x_{K-1} \\ 0 & 0 & x_1 & \dots & x_{K-2} \end{bmatrix} \qquad \begin{aligned} \vec{Y} &= [y_1, y_2, y_3, \dots, y_K] \\ \vec{N} &= [n_1, n_2, n_3, \dots, n_K] \\ E_m &= mse(e_1^m, e_2^m, \dots, e_K^m) \end{aligned}$



Simulation & Results

- ❖ Input Signal (x):- zero mean uniformly distributed random sample lying between [-0.5, 0.5]
- \bullet Noise (N):- White & Gaussian distributed random samples
- \bullet Coefficients of the FIR filter (Q):- 3
- ❖ Number of input signal samples (K):- 500
- ❖Binary coded GA is used
 - •Number of chromosomes taken (M):- 60
 - •Number of bits in each chromosome (Q*L):- 60
 - •Using one point cross over
 - •Using Tournament selection
 - •Probability of Crossover (Pc) :- 0.8
 - •Probability of Mutation (Pm) :- 0.1

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Systems

Linear System

$$A(z) = 0.3040 + 0.9029z^{-1} + 0.3040z^{-2}$$
$$NSR = -30dB & NSR = -20dB$$

Nonlinear System

For simulation purpose the Nonlinear system can be obtained by passing the output of the linear system through various nonlinearity functions.

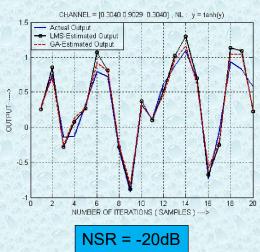
$$Y = \tanh(Y)$$
,

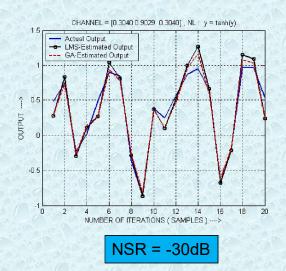
$$Y = Y + 0.2Y^2 - 0.1Y^3$$

V



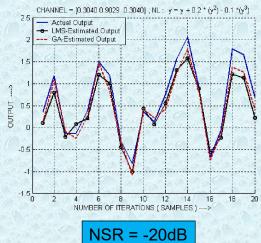
Comparison of output response of (Exp-1) at -20dB NSR & -30dB NSR

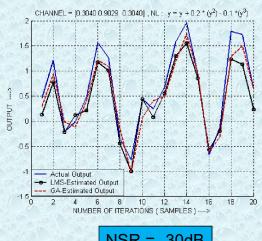




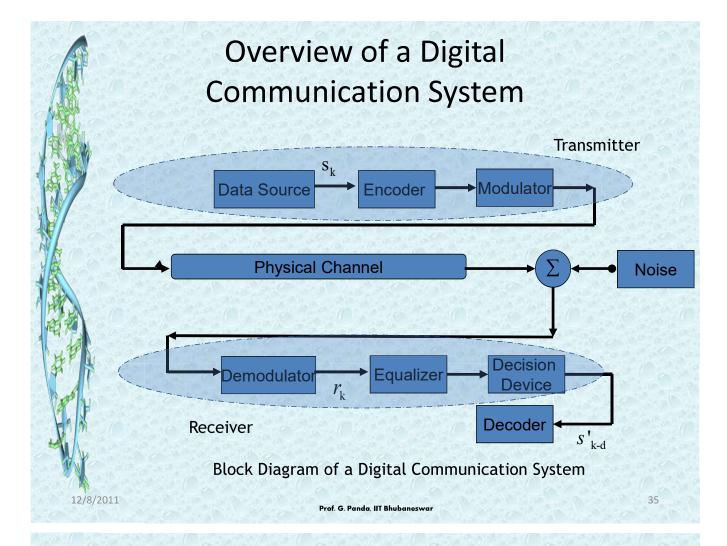
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Comparison of output response of (Exp-2) at -20dB NSR & -30dB NSR





NSR = -30dB

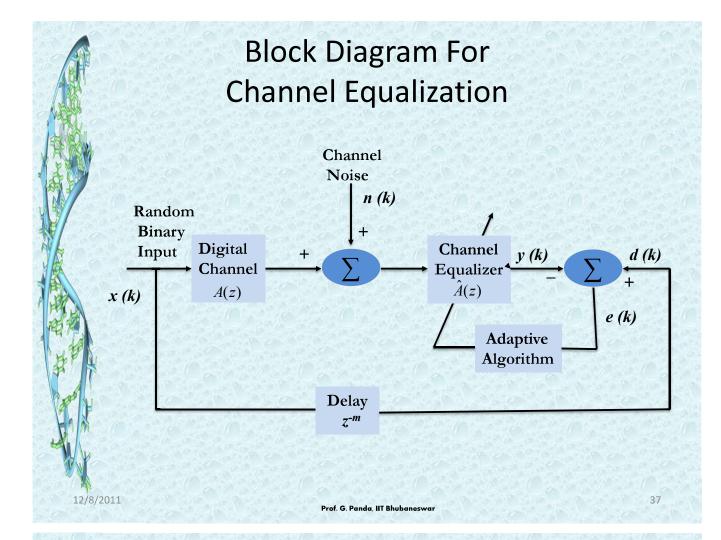


Digital Channel Equalizers

- ❖Located in the front end of the receivers (in series with the channel)
- ❖ Inverse system of the channel model (Transfer function of the equalizer is inverse to the transfer function of the channel)

Use to reduce: -

- •Inter-Symbol Interference (ISI)
- •Inter User Interference in the form of Co-channel Interference (CCI)
- •Adjacent Channel Interference (ACI) in the presence of Additive White Gaussian Noise (AWGN).



Simulation & Results



- ❖Binary coding is used
- \bullet Number of chromosomes taken (M):- 60
- Number of bits used for each parameter (L):- 20
- ❖One point cross over is used
- ❖ Tournament selection is used
- ArrProbability of Crossover (Pc) :- 0.8
- ightharpoonup Probability of Mutation (Pm) :- 0.1
- ❖ Experiments on Nonlinear Channel



Nonlinear Channels

Linear System

$$A(z) = 0.3040 + 0.9029z^{-1} + 0.3040z^{-2}$$
$$NSR = -10dB$$

Nonlinear System

For simulation purpose the Nonlinear system can be obtained by passing the output of the linear system through various nonlinearity functions.

•EXP : - 1

$$r(k) = r(k) + 0.2 r^{2}(k) - 0.1 r^{3}(k),$$

•EXP : - 2

$$r(k) = r(k) + 0.2 \cdot r^2(k) - 0.1 \cdot r^3(k) + 0.5 \cdot \cos(\pi \cdot r),$$

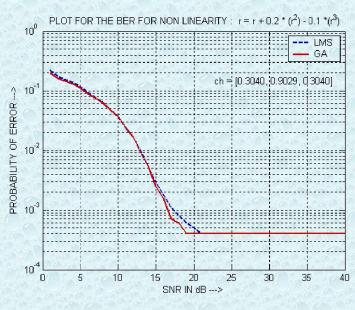
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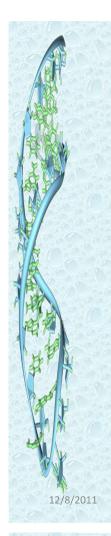
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Comparison of BER of Nonlinear Channel NCH1 between LMS & GA based Equalizer at -10dB noise

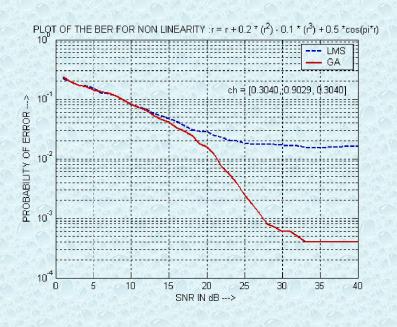




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Comparison of BER of nonlinear Channel NCH2 between LMS & GA based equaliser at -10dB noise



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