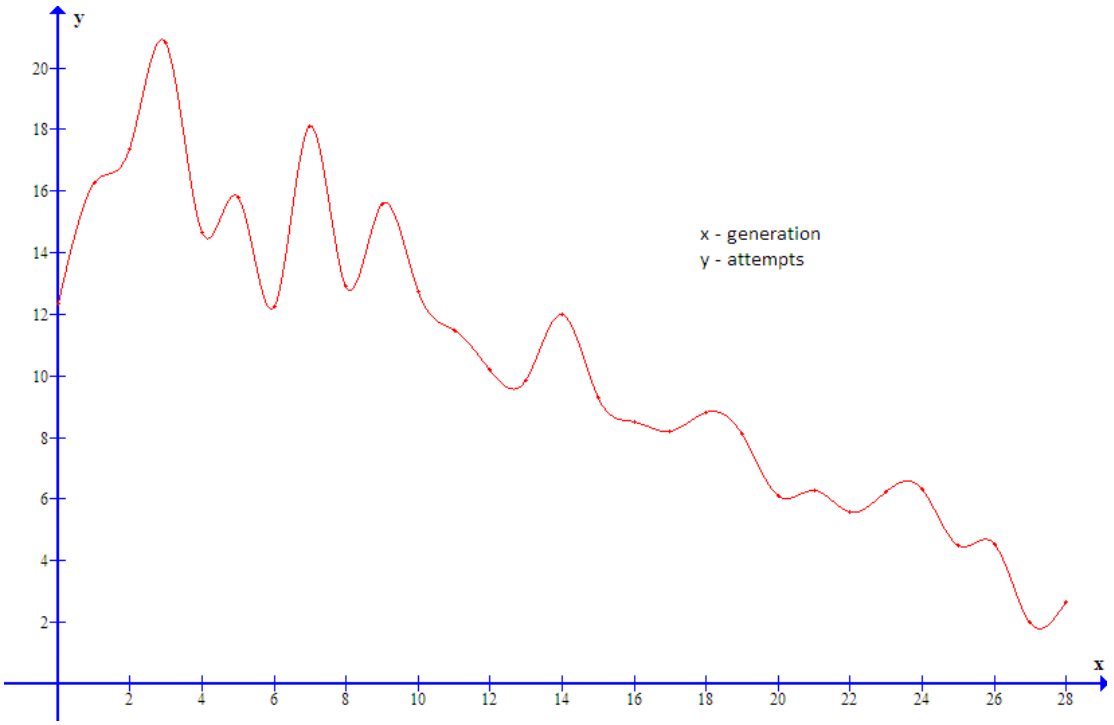
Hinton and Nowlan's Simulation of Life Time Learning

The pattern is "11111".

5 bits

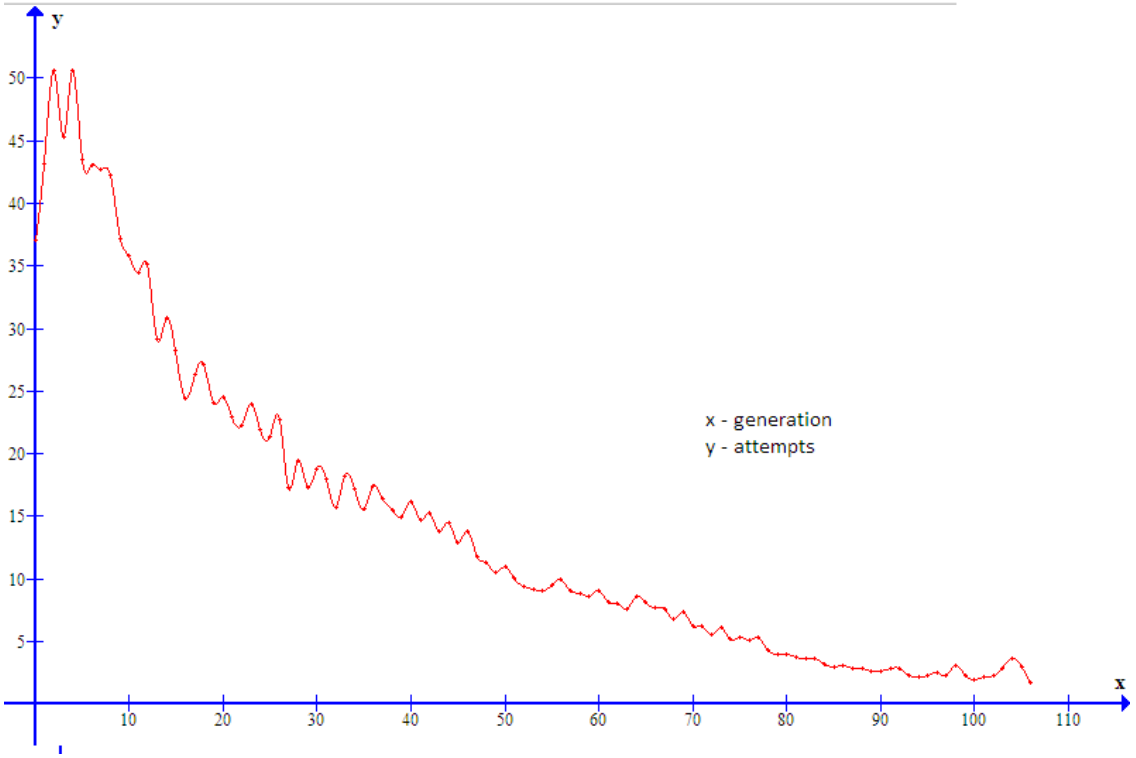
Results:



The pattern is "1111111111".

10 bits:

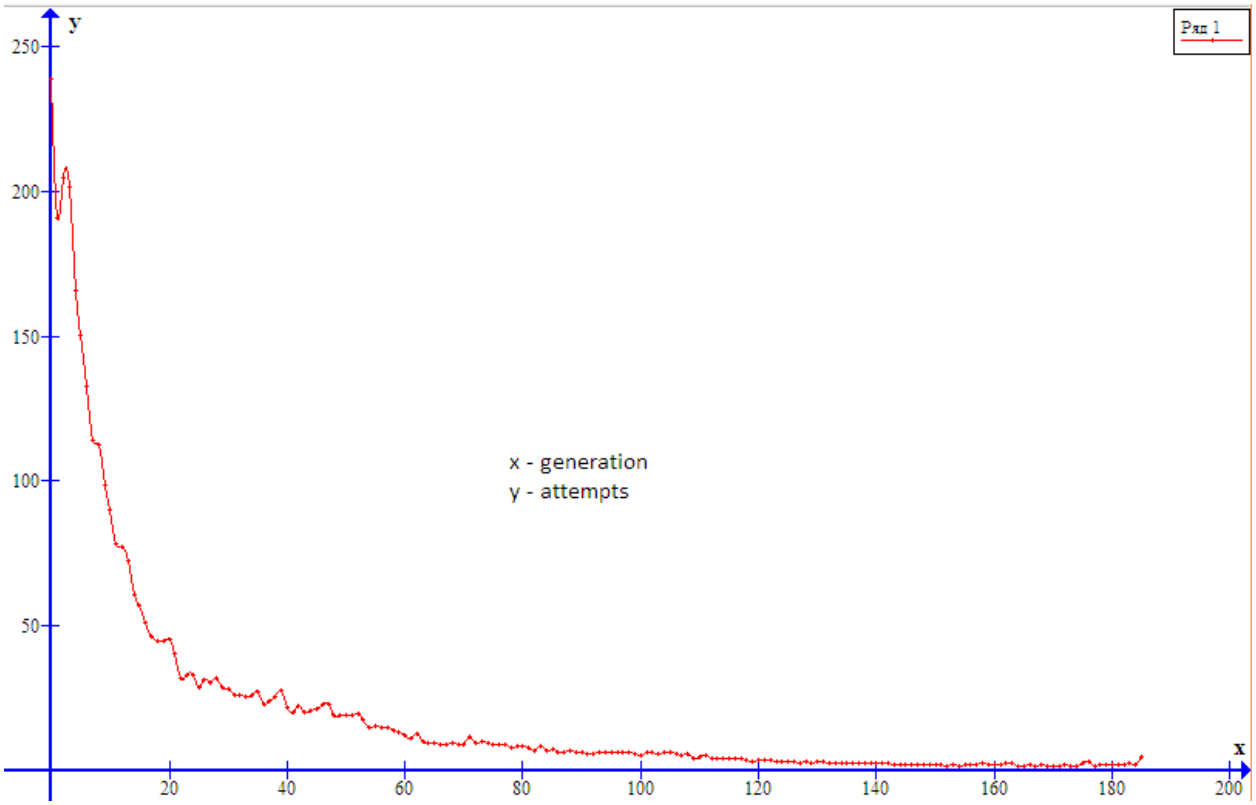
Results:



The pattern is “111111111111111”.

15 bits:

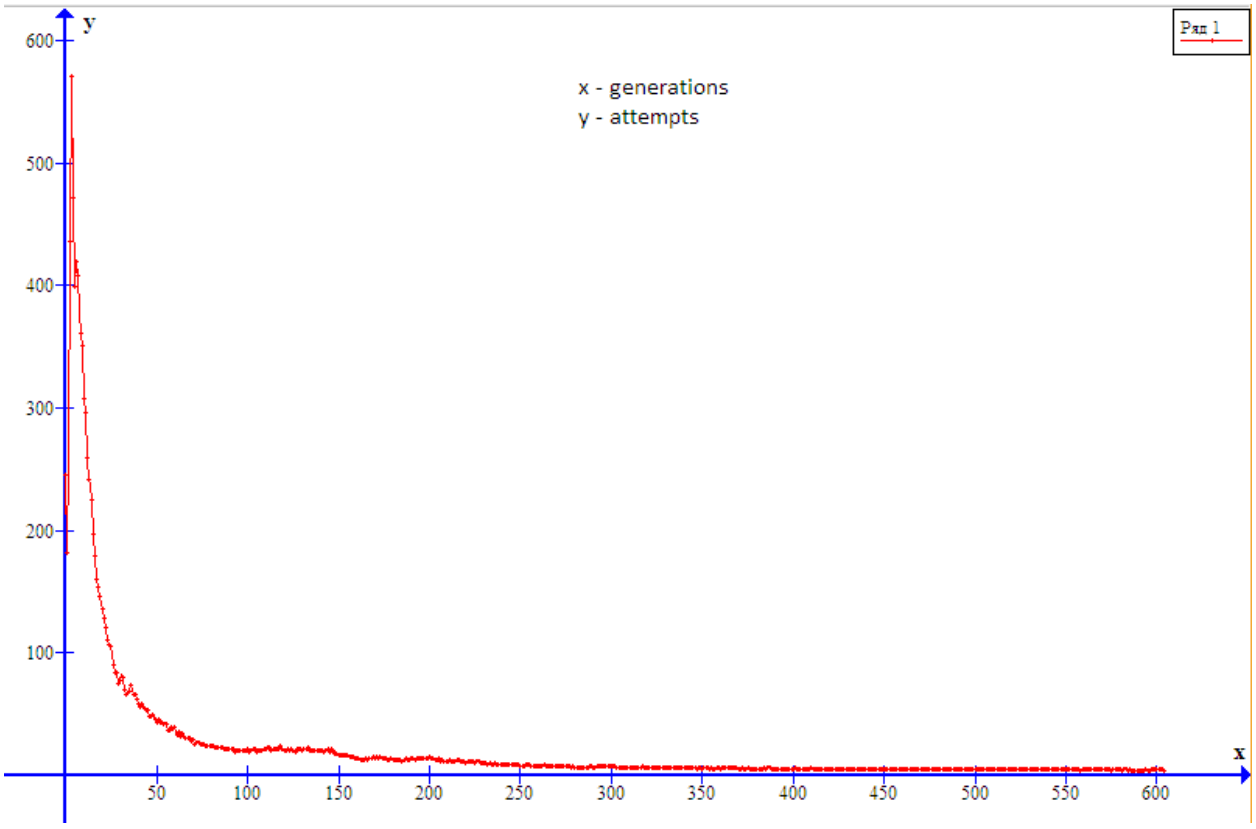
Results:



The pattern is “111111111111111111111111”.

25 bits:

Results:



```
import java.util.*;
class Attempts
{
public int value;
public boolean changed;
public Attempts()
{
value = 0;
changed = false;
}
}
class Chromosome
{
private static int numberLearningAttempts = 1000;
private final boolean fixGenomeWhenSuccess = false;
private final double fitnessBoost = 19.;
private int[] genome;
private int ID;
public static void setNumberOfLearningAttempts(int numberLearningAttempts)
{
Chromosome.numberLearningAttempts = numberLearningAttempts;
}
public Chromosome(int ID, int[] genome)
{
this.ID = ID;
this.genome = genome;
}
public Chromosome(int ID, int size, int fixedElements, Random random)
{
this.ID = ID;
genome = new int[size];
ArrayList<Integer> positions = new ArrayList<>();
for(int i = 0; i < size; i++)
{
genome[i] = 2; // init as ?
positions.add(i);
}
Collections.shuffle(positions, random);
for(int i = 0; i < fixedElements; i++)
{
int pos = positions.get(i);
genome[pos] = random.nextInt(2);
}
}
@Override
public String toString()
{
if(genome == null)
return "";
return String.valueOf(ID) + '\t' + sequenceToString(genome);
}
public int[] getSequence()
{
return this.genome;
}
public static String sequenceToString(int[] genome)
{
if(genome == null)
```

```
return "";
StringBuilder s = new StringBuilder();
for(int aGenome : genome)
if(aGenome == 2)
s.append('?');
else
s.append(aGenome);
return s.toString();
}
public static Chromosome mate(int ID, Chromosome ind1, Chromosome ind2, Random rand)
{
int recPos = 1 + rand.nextInt(ind1.genome.length - 1);
int[] genomeNew = new int[ind1.genome.length];
System.arraycopy(ind1.genome, 0, genomeNew, 0, recPos);
System.arraycopy(ind2.genome, recPos, genomeNew, recPos, genomeNew.length - recPos);
return new Chromosome(ID, genomeNew);
}
public static int[] getCounts(int[] genome)
{
int[] cnts = new int[3];
for(int aGenome : genome)
cnts[aGenome]++;
return cnts;
}
public double liveLearnAndReturnFitness(Random random, Attempts att)
{
int len = genome.length;
if(getCounts(genome)[1] == len)
// this individual has correct sequence, no learning will happen
return 1 + fitnessBoost;
else if(getCounts(genome)[0] > 0)
// this individual has 0s in the sequence, will not learn right solution
return 1;
else
{
// do learning
int[] sequence = genome.clone();
ArrayList<Integer> positionOfQuestionMarks = new ArrayList<>();
for(int i = 0; i < sequence.length; i++)
if(sequence[i] == 2)
positionOfQuestionMarks.add(i);
int attempts = 1;
for(; attempts <= numberLearningAttempts; attempts++)
{
int[] learnedBits = getRandomBinaryString(positionOfQuestionMarks.size(), random);
for(int i = 0; i < positionOfQuestionMarks.size(); i++)
sequence[positionOfQuestionMarks.get(i)] = learnedBits[i];
if(getCounts(sequence)[1] == len)
{
if(fixGenomeWhenSuccess)
genome = sequence;
att.value = attempts;
att.changed = true;
return 1 + fitnessBoost * (numberLearningAttempts - attempts) / 1000.;
}
}
// could not learn
return 1;
```

```
}
}
public static int[] getRandomBinaryString(int len, Random random)
{
int[] s = new int[len];
for(int i = 0; i < len; i++)
s[i] = random.nextBoolean() ? 1 : 0;
return s;
}
public static Chromosome sampleIndividualPropToFitness(Random random, HashMap<Chromosome, Double>
largeFitness,
ArrayList<Chromosome> fitnessOne,
double totFitnessGreaterThanOne)
{
double totFitness = fitnessOne.size() + totFitnessGreaterThanOne;
if(random.nextDouble() < fitnessOne.size() / totFitness)
// sample from those with fitness = 1
return fitnessOne.get(random.nextInt(fitnessOne.size()));
else
{
// sample from those ith fitness > 1
double fitnessMark = random.nextDouble() * totFitnessGreaterThanOne;
double cumulativeFitness = 0.;
Chromosome sampledInd = null;
for(Chromosome ind : largeFitness.keySet())
{
cumulativeFitness += largeFitness.get(ind);
if(cumulativeFitness >= fitnessMark)
{
sampledInd = ind;
break;
}
}
return sampledInd;
}
}
public static boolean isFixated(ArrayList<Chromosome> inds)
{
int[] firstGenome = inds.get(0).genome;
for(Chromosome ind : inds)
if(!Arrays.equals(firstGenome, ind.genome))
return false;
return true;
}
public static double[] getGenomeProb(Collection<Chromosome> inds)
{
double[] res = new double[3];
for(Chromosome ind : inds)
{
int[] thisInd = getCounts(ind.genome);
res[0] += thisInd[0];
res[1] += thisInd[1];
res[2] += thisInd[2];
}
double sum = res[0] + res[1] + res[2];
res[0] /= sum;
res[1] /= sum;
res[2] /= sum;
```

```
return res;
}
}
public class Main
{
static long seed = System.currentTimeMillis();
public static void main(String[] args) throws InterruptedException
{
Random random = new Random(seed);
int numberOfSamples = 1000;
int len = 20;
int fixed = 10;
Chromosome.setNumberOfLearningAttempts(numberOfSamples);
ArrayList<Chromosome> inds = new ArrayList<>();
for(int i = 0; i < numberOfSamples; i++)
inds.add(new Chromosome(i, len, fixed, random));
int generation = 0;
double[] populationStats = Chromosome.getGenomeProb(inds);
while(!Chromosome.isFixated(inds))
{
HashMap<Chromosome, Double> largeFitness = new HashMap<>();
ArrayList<Chromosome> fitnessOne = new ArrayList<>();
double totFitnessGreaterThanOne = 0., totalAttempts = 0, bestAttempts = 1000;
int cnt = 0;
for(Chromosome ind : inds)
{
Attempts attempts = new Attempts();
double fitness = ind.liveLearnAndReturnFitness(random, attempts);
totalAttempts += attempts.value;
if(attempts.changed)
cnt++;
if(attempts.changed && attempts.value < bestAttempts)
bestAttempts = attempts.value;
if(fitness > 1)
{
largeFitness.put(ind, fitness);
totFitnessGreaterThanOne += fitness;
} else
fitnessOne.add(ind);
}
System.out.printf(
"GENERATION %4d\t\t0 --> %.6f\t\t\t1 --> %.6f\t\t\t? --> %.6f\t\t\taverage --> %3.6f\t\t\tbest --> %3.6f\n",
generation, populationStats[0], populationStats[1], populationStats[2], totalAttempts / cnt,
bestAttempts);
ArrayList<Chromosome> newGen = new ArrayList<>();
for(int i = 0; i < numberOfSamples; i++)
{
Chromosome samp1 = Chromosome.sampleIndividualPropToFitness(random, largeFitness, fitnessOne,
totFitnessGreaterThanOne);
Chromosome samp2 = Chromosome.sampleIndividualPropToFitness(random, largeFitness, fitnessOne,
totFitnessGreaterThanOne);
Chromosome newSamp = Chromosome.mate(i, samp1, samp2, random);
newGen.add(newSamp);
}
inds = newGen;
populationStats = Chromosome.getGenomeProb(inds);
generation++;
}
```

```
System.out.println("Done:\t" + Chromosome.sequenceToString(inds.get(0) .getSequence()) + "\t" +
populationStats[0] +
"\t" + populationStats[1] + "\t" + populationStats[2]);
Thread.sleep(1000);
}
}
```