A Parallel Distributed Genetic Algorithm Application for Feature Selection in Classification Problems

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What is this long title about??

- What is **feature selection**?
- What is a **genetic algorithm** (GA)?
  - Selection, Crossover, Mutation, Fitness
  - Furthermore what is a distributed GA (DGA)?
- How do you classify given a data set? …Well, in our case we use a Support Vector Machine, specifically the program **SVM**$^{\textbf{light}}$
- **MPI** as the message passing service…but why? …and what implementation to use?

Problem to solve

- Goal:
  - Create a program such that given a data set as input can output a subset of the features which provides a better accuracy during classification and reduces the data set size.
- Approach:
  - Use MPI to parallelize a DGA which will search for a solution to the subset problem across a network of machines increasing accuracy of our solution as well as improved running time.
  - We have used 11 machines in the SunLab to run our program in which they communicate with each other while running in parallel

Feature Selection

- **Definition:** a process used in machine learning for selecting a subset of the features that reduces number of features while increasing the accuracy
- **Why is it useful?**
  - Data reduction- saves resources collecting/storing data
  - Improves prediction accuracy- by removing noise features
  - Reduces training time and algorithm execution time
  - Can provide insight to the problem
- Other approaches based on Greedy forward/backward search, mutual information, simulated annealing, etc.

Message Passing Interface (MPI)

- We chose to use MPICH (Version 3.0)
  - Superior performance than Open MPI [3]
  - Updated to the MPI 3.0 standard which was introduced in late 2012 (which Open MPI has not done yet)
  - Exclusively used on 9 of the top 10 supercomputers including the word's fastest Tianhe-2 [1]
- Used to provide communication, a virtual topology, and synchronization between a set of processes
- Basic operations: MPI_Send, MPI_Recv

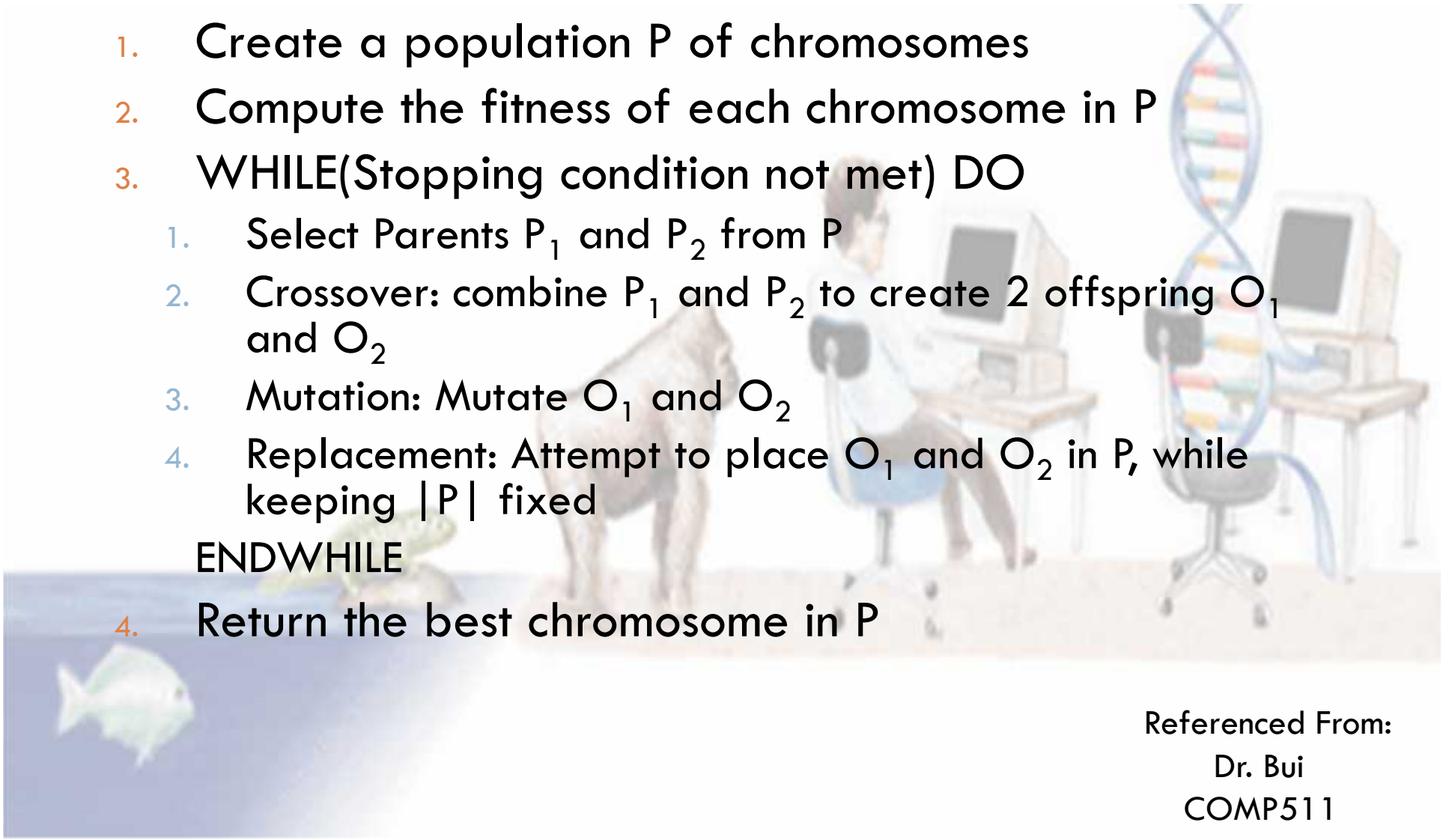
Background for GAs

- **Chromosome-** encoding of a solution to the given problem (i.e. a subset of features)
- **Genes** of a chromosome- encode whether or not we include a feature from our data set in our classification process
  - Ex. If C1 has genes = [1, 1, 0, 0, 1] this means that out of 5 features for the given data set this chromosome will only use features 1,2, and 5 for classification
- **Fitness** of a chromosome- the measure of how fit the given chromosome is in relation to the problem
  - Fitness = accuracy value returned by SVM^{light} after running the modified data set which corresponded to the chromosome's genes

Generic Scheme for a GA

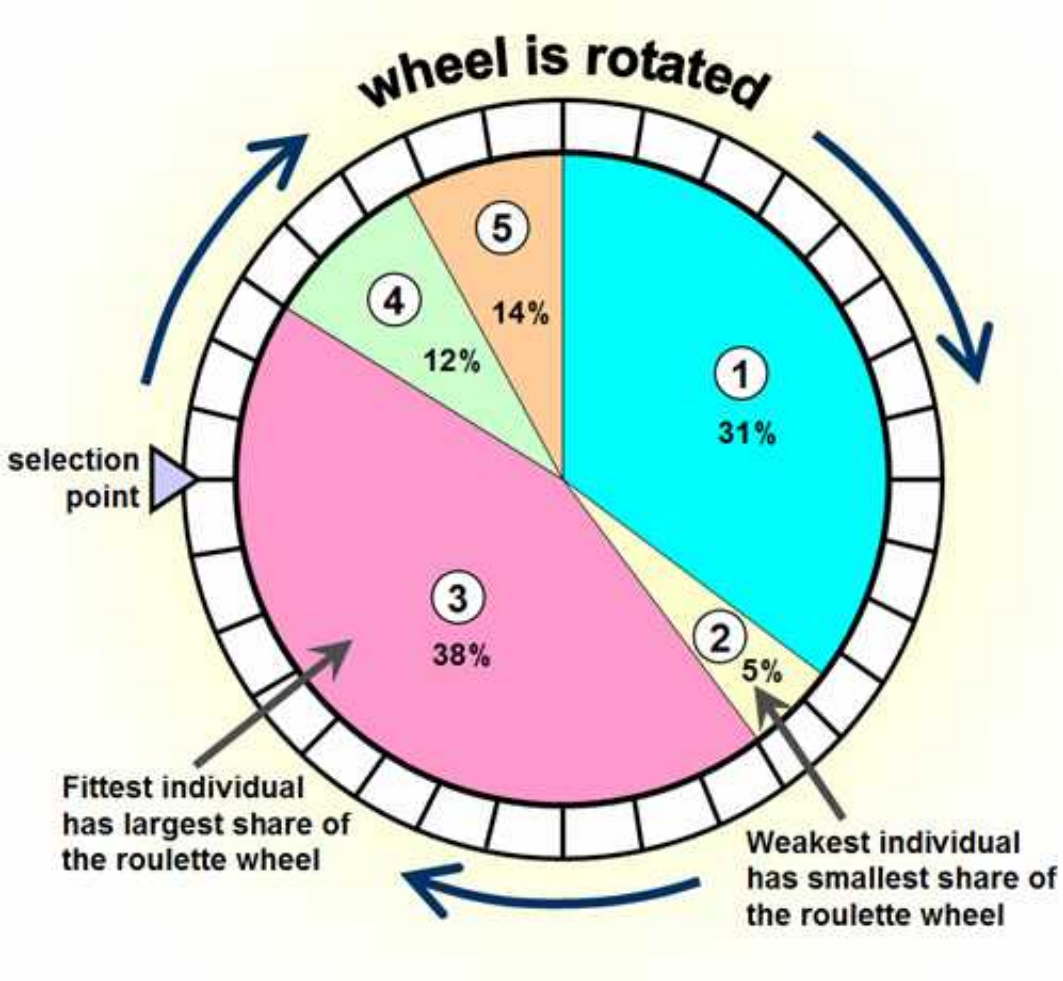
1. Create a population P of chromosomes
2. Compute the fitness of each chromosome in P
3. WHILE(Stopping condition not met) DO
   1. Select Parents P_1 and P_2 from P
   2. Crossover: combine P_1 and P_2 to create 2 offspring O_1 and O_2
   3. Mutation: Mutate O_1 and O_2
   4. Replacement: Attempt to place O_1 and O_2 in P, while keeping |P| fixed

   ENDWHILE
4. Return the best chromosome in P



Referenced From:
Dr. Bui
COMP511

GA-Selection Roulette Wheel



We sum up the fitness values then assign each chromosome a proportion of the wheel based on their individual fitness

GA- Crossover & Mutation

- Best explained in an example:

  Selected parents P_1 and P_2

  $P_1=[1,0,1,0,1,0]$ & $P_2=[0,0,0,1,1,1]$

  Offspring O_1 and O_2 after one-point crossover

  $O_1=[1,0,1,1,1,1]$ & $O_2=[0,0,0,0,1,0]$

  Offspring O_1 and O_2 after mutation

  $O_1=[1,0,1,1,1,0]$ & $O_2=[0,1,0,0,1,0]$

GA- Replacement

- We want to possibly bring the offspring into our population, but while keeping the overall size fixed

- One possible replacement is as follows:
  - If an offspring is more fit than any of the chromosomes in our current population, we replace them

Implementation – Coded in C

- Master/Worker relationship with 11 computers
  - 10 worker processes (islands) & 1 master process
- Use DGA such that each island runs a separate GA and occasionally send chromosomes to each other to increase diversity
- Bank Marketing Data Set from the UCI repository[4]
  - Number of Instances: 45,211 Number of Features: 16
  - Binary classification: Y/N whether a client will open a term deposit (data taken from a Portuguese bank)
- How to determine fitness for chromosome C?
  - Create a temporary data set which only contains the subset of features that C represents
  - Train a model based on the temporary data set using SVM ^{light} and obtain a test accuracy
  - C's fitness = obtained accuracy value

Structure of our DGA

WORKER-Island

```
//START WORKER
1.WHILE( Master says Work) DO:
   a. Run 5 Generations of GA:
      *Selection
      *Crossover
      *Mutation
      *Fitness  <-> SVM^light
      *Replacement
   b. Migration:
      *Send migrants to Master
      *Receive immigrants
      *Replacement of immigrants
//END WHILE
2.Send Best Chromosome to Master
//END WORKER
```

WORKER-Island

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   a. Run 5 Generations of GA:
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      *Mutation
      *Fitness  <-> SVM^light
      *Replacement
   b. Migration:
      *Send migrants to Master
      *Receive immigrants
      *Replacement of immigrants
//END WHILE
2.Send Best Chromosome to Master
//END WORKER
```

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MASTER

```
//START MASTER
1.Randomize data set
2.DO
    *Tell Workers to Work
    *Wait for migrants from all islands
    *Mutate migrants
    *Shuffle migrant ordering
    *Randomly send migrants to each island
  WHILE( ! Stopping Condition)
3.Tell Workers to STOP working
4.Receive Best Chromosome from each island
5.Output the best overall Chromosome
//END MASTER
```

Results & Analysis

Running times and Results:

- 10 migration rounds, 5 GA generations between migration rounds, each island has population 50
  - Full data set (≈45k): Estimated 4-5 days (currently running)
    - Unknown results
  - Small data set (≈4.5k): ~8-10 hours
    - Produces a few different subsets with same accuracy ≈ 91%
- 3 migration rounds, 2 GA generations between migration rounds, each island has population 25
  - Very small data set (50): < 10 minutes
    - You will see in the upcoming demo

structure.c

```c
/* MPI Derived Data Type Structure Example */
#include <stdio.h>
#include <stdlib.h>
#include "mpi.h"
#define MESSAGE_TAG 1
#define NUM_FEATURES 16
#define NUM_MIGRANTS 1
typedef struct
{
    char genes[NUM_FEATURES];
    double fitness;
} Chromosome;

int main (int argc, char *argv[])
{
    int rank, size, i;
    MPI_Init (&argc, &argv);                /* Initialization of MPI operations */
    MPI_Comm_rank (MPI_COMM_WORLD, &rank);  /* To get the rank of the process */
    MPI_Comm_size (MPI_COMM_WORLD, &size);  /* To get the number of processes */
    MPI_Status status;                      /* Stores the message tag, error status and source of message being sent */

/* Creating Derived Data Type */
    MPI_Datatype migrant;                   /* Name of new data type */
    MPI_Datatype types[2]={MPI_DOUBLE,MPI_CHAR};
    int blocklengths[2]={1,16};             /* Number of variables of each MPI data type */

    MPI_Aint displacements[2];              /* Holds the starting position of each variable of the struct */
    MPI_Aint doubleex;
    MPI_Type_extent(MPI_DOUBLE,&doubleex);
    displacements[0]= (MPI_Aint) 0;         /* Set the displacement of fitness to 0 since its the first variable of the struct */
    displacements[1]=doubleex;              /* Set the displacement of the genes array to be after fitness in our MPI derived data type */

    MPI_Type_struct(2,blocklengths,displacements,types,&migrant); /* Constructing the above components to create our migrant derived data type */
    MPI_Type_commit(&migrant);              /* Committing the data type so it can be used in our program */
/* END Creating Derived Data Type */

    if (rank==0) /* Master Process */
    {
        Chromosome wiggle;
        MPI_Recv(&wiggle,NUM_MIGRANTS,migrant,MPI_ANY_SOURCE,MPI_ANY_TAG,MPI_COMM_WORLD,&status);
        printf("Chromosome fitness is %f and genes are: ", wiggle.fitness);
        for(i=0; i<NUM_FEATURES; i++)
            printf("%c",wiggle.genes[i]);
        printf("\n");
    }
    else /* Worker Processes - ranks other than zero */
    {
        Chromosome jiggle;
        jiggle.fitness = .314159;
        for(i=0; i < NUM_FEATURES; i++)
        {
            if(i%2)
                jiggle.genes[i] = '0';
            else
                jiggle.genes[i] = '1';
        }
        MPI_Send(&jiggle,NUM_MIGRANTS,migrant,0,MESSAGE_TAG,MPI_COMM_WORLD);
    }
    MPI_Finalize();
}
```

Terminal

```
galois:                    Our hidden directory location :)        mpicc structure.c -o struct
galois:                                                            mpiexec -f machinefile -n 2 ./struct
Chromosome fitness is 0.314159 and genes are: 1010101010101010
galois:
```

Our Struct and Initializing MPI

```
#define MESSAGE_TAG 1
#define NUM_FEATURES 16
#define NUM_MIGRANTS 1
typedef struct
{
    char genes[NUM_FEATURES];
    double fitness;
} Chromosome;
```

```
int main (int argc, char *argv[])
{
        int rank, size, i;
        /* Initialization of MPI operations */
        MPI_Init (&argc, &argv);
        /* To get the rank of the process */
        MPI_Comm_rank (MPI_COMM_WORLD, &rank);
        /* To get the number of processes */
        MPI_Comm_size (MPI_COMM_WORLD, &size);
        /* Stores the message tag, error status
           and source of message being sent */
        MPI_Status status;
```

MPI Derived Data Type

```
#define MESSAGE_TAG 1
#define NUM_FEATURES 16
#define NUM_MIGRANTS 1
typedef struct
{
    char genes[NUM_FEATURES];
    double fitness;
} Chromosome;
```

```
/* Creating Derived Data Type */
        /* Name of new data type */
        MPI_Datatype migrant;
        MPI_Datatype types[2]={MPI_DOUBLE,MPI_CHAR};
        /* Number of variables of each MPI data type */
        int blocklengths[2]={1,16};

        /* Holds the starting position of each variable of the struct */
        MPI_Aint displacements[2];
        MPI_Aint doubleex;
        MPI_Type_extent(MPI_DOUBLE,&doubleex);
        /* Set the displacement of fitness to
           0 since its the first variable of the struct */
        displacements[0]= (MPI_Aint) 0;
        /* Set the displacement of the genes array
           to be after fitness in our MPI derived data type */
        displacements[1]=doubleex;

        /* Constructing the above components to create
           our migrant derived data type */
        MPI_Type_struct(2,blocklengths,displacements,types,&migrant);
        /* Committing the data type so it can be used in our program */
        MPI_Type_commit(&migrant);
/* END Creating Derived Data Type */
```

Basic Communication

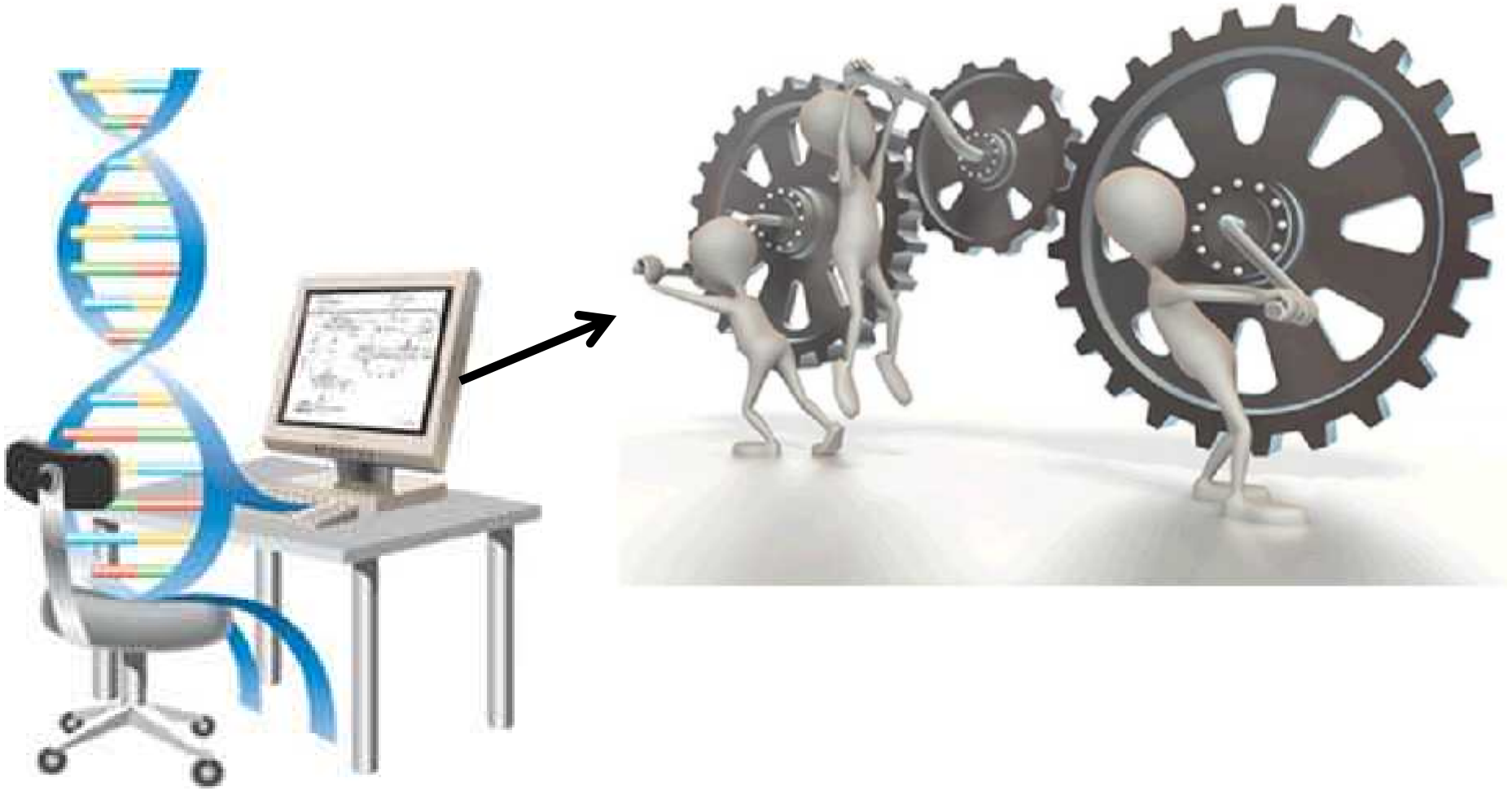
```
        /* Master Process */
        if (rank==0)
        {
                Chromosome wiggle;
                MPI_Recv(&wiggle,NUM_MIGRANTS,migrant,MPI_ANY_SOURCE,MPI_ANY_TAG,MPI_COMM_WORLD,&status);
                printf("Chromosome fitness is %f and genes are: ", wiggle.fitness);
                for(i=0; i<NUM_FEATURES; i++)
                        printf("%c",wiggle.genes[i]);
                printf("\n");
        }
        /* Worker Processes - ranks other than zero */
        else
        {
                Chromosome jiggle;
                jiggle.fitness = .314159;
                for(i=0; i < NUM_FEATURES; i++)
                {
                        if(i%2)
                                jiggle.genes[i] = '0';
                        else
                                jiggle.genes[i] = '1';
                }
                MPI_Send(&jiggle,NUM_MIGRANTS,migrant,0,MESSAGE_TAG,MPI_COMM_WORLD);
        }
        MPI_Finalize();
}
```

```
#define MESSAGE_TAG 1
#define NUM_FEATURES 16
#define NUM_MIGRANTS 1
typedef struct
{
    char genes[NUM_FEATURES];
    double fitness;
} Chromosome;
```

Executing the Above Example

- How to **compile** MPI programs:
  - mpicc example.c –o example
- How to **execute** MPI programs:
  - mpiexec –f machinefile –n 2 ./example
  - -f indicates we have a machine file
    - Machine file: Contains the IPs for each of the available machines we can connect to. In our case the names of the SunLab computers (i.e. Grace, Pascal, Galois, etc.)
  - -n is used to define how many processes to start

DEMONSTRATION



Problems We Faced

- For SVM^{light} we used C system(command) function
  - this **printed unnecessary statements** to the terminal and made it **convoluted to obtain the accuracy**
  - **Fix**: Use of popen(command, "r") to read and parse the output of SVM^{light}
- All islands were generating the **same chromosomes**!!
  - **Fix**: we seeded the rand() function with

    srand((island_ID + 1) * time(null)) as they have unique ids
- mpiexec command **needing ssh login password** for every machine being used on execution:
  - **Fix**: using ssh keygen we created a public key so that we can connect to any machine in the lab without a password
- MPI trying to use ports blocked in the Sun Lab
  - Fix: Set Environment Variable
    - MPIEXEC_PORT_RANGE = 6000:7000

Future thoughts…

- To create a GUI: Enable users to select a dataset file and choose input parameters such as: number of generations between migration, number of islands, mutation rate, etc.
- Using GPUs…
  - New research is being done to use MPI for communication between nodes, but also using CUDA or OpenACC to create MPI + OpenACC, CUDA-aware MPI, and MVAPICH2 systems
    - Increase performance by processing on several cores of a GPU rather than few of a CPU
- Implement failure handling through backup logs
  - MPI cannot handle machine failures or for you to add new machines during runtime

How OS Class Helped?

- Master/worker architecture (Client/Server)
- The examples from class with pipes in C
- Blocking/non-blocking send, receive, and broadcast
- Concurrency is handled using MPI and the use of MPI_Barrier allows for synchronization points
- Resource sharing- We use a shared folder for all processes
  - Shared data set: used in read mode (allows concurrency)
  - All process specific files append unique ID
- Scalability– no code changes needed…
  - MPI –n command to specify number of machines
  - TCP sockets only created when needed

Thank you Dr. Null ☺

If Time Travel Existed…

- SVM is a superior classifier…however very slow
  - Instead use a faster, less accurate classifier (e.g. Naïve Bayes)
- Choosing another data set for proof of concept
  - Our banking data set seems to be already refined
    - All features appear to be relevant after our investigation
  - Instead choose a more recent data set with more features that hasn't been refined by researchers

Conclusion

- Implementation of a parallel DGA to solve the feature selection problem encountered in machine learning classification problems
- Uses of MPICH: message passing, synchronization, resource sharing, and scalability
  - Allowed us to get a feel for distributed parallel computing and made it easier
- Learned that decision of data set is crucial

References

1. http://www.mpich.org/
2. http://archive.ics.uci.edu/ml/datasets/Bank+Marketing
3. McClements E., (2006). Performance Comparison of Open Source MPI Implementations. The-University of Edinburgh, Edinburgh. https://www.epcc.ed.ac.uk/sites/default/files/Dissertations/2005-2006/2688821-9h-dissertation1.1.pdf

Image/Figure sources:

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- https://computing.llnl.gov/tutorials/mpi/#Abstract

Thank You