National University of Computer and Emerging Sciences, Islamabad FAST School of Computer Science



CS2002-Artificial Intelligence Project

Submitted by:

1. Syed Saifullah Rizwan (21I-0830)

Submitted to: Ma'am Labiba Fahad

DATA SET GENERATION:

For starters we needed a data set to generate well a timetable or a chromosome of a timetable: For this purpose I made Panda DataFrames for each { professors, courses, sections, rooms, timeslots, days}

Each dataframe has specific information relevant to them. However, each of them have a column name of 'Enc' which is used for binary encoding of the chromosome later on.

Here is the Complete Data Set:

Professors:

Enc	Name	ProfessorID	
000	Kashif Munir	1	0
001	Mukhtaar Ullah	2	1
010	Naveed Ahmed	3	2
011	Farukh Bashir	4	3
100	Amina Ashfaq	5	4

Courses:

	CourseID	Name	IsLab	ProfessorID	Enc
0	1	OS	False	1	000
1	2	OS Lab	True	1	001
2	3	AI	False	3	010
3	4	AI Lab	True	3	011
4	5	CNET	False	5	100
5	6	Network Security	False	5	101

Rooms:

	RoomID	Capacity	Floor	Enc
0	1	60	1	000
1	2	120	1	001
2	3	60	2	010
3	4	60	2	011
4	5	60	3	100
5	6	120	3	101
6	7	60	0	110
7	8	120	0	111
8	9	60	1	000
9	10	60	1	001
10	11	60	0	010
11	12	120	0	011
12	13	60	1	100
13	14	60	1	101
14	15	120	2	110

Sections:

	SectionID	CourseID	Capacity	Enc
0	1	1	50	000
1	1	6	50	001
2	2	2	25	010
3	3	3	55	011
4	4	4	20	100
5	5	5	60	101
6	5	1	60	110

```
TimeSlots:
```

```
TimeSlotID Timings Enc

0 1 (8.3, 9.5) 000

1 2 (10, 11.2) 001

2 3 (11.3, 12.5) 010

3 4 (13, 14.2) 011

4 5 (14.3, 15.5) 100

5 6 (16, 17.2) 101
```

Days:

```
Day Enc
Monday 000
Tuesday 001
Wednesday 010
Thursday 011
Friday 100
```

CHROMOSOME GENERATION:

To generate Chromosomes for the timetable I defined a function:

```
def generate_chromosome(courses, sections, professors, rooms, timeslots, days):
    which takes all the dataframes of input data and makes a chromosome tuple:
    detailed_chromosome = [] (Chromosome Containing Meaningful Data)
    encoded_chromosome = [] (Chromosome Containing Binary Encoded Data)
    it iterates through the section dataset and for every row ( needed for multiple)
```

it iterates through the section dataset and for every row (needed for multiple courses for same section) calculates and stores the data for the required course, professor, room. Picks a random day and timeslot (checking not pick the last

possible one (for lab as it needs 2)).

Then it converts the Tuple of Timeslots to string by:

```
# Convert timeslot tuple to string format for detailed chromosome
first_timeslot_str= f"{first_timeslot['Timings'][0]:.2f},
{first_timeslot['Timings'][1]:.2f}"
```

So that it is easier to manipulate later on when we make separate timetables for separate days.

After this Both the encoded gene and the detailed gene are constructed:

```
# Detailed gene construction
            detailed gene = {
               'Course': course['Name'],
                'Type': 'Lab' if course['IsLab'] else 'Theory',
                'Section': row['SectionID'],
                'Capacity': row['Capacity'],
                'Professor': professor['Name'],
                'First Lecture Day': first day['Day'],
                'First Lecture Timeslot': first_timeslot_str,
                'First Lecture Room': room['RoomID'],
                'First Lecture Room Capacity': room['Capacity']
            # Encoded gene construction using binary strings
            encoded gene = {
                'Course': course['Enc'],
                'Type': '1' if course['IsLab'] else '0',
                'Section': row['Enc'],
                'Capacity': format(row['Capacity'], '07b'),
                'Professor': professor['Enc'],
```

As I forgot and didn't make a new dataframe for the Section Strength I added it as a field in Section named Capacity, For Binary encoding I added

```
'Capacity': format(row['Capacity'], '07b')
```

Which just converts the Capacity to Binary and pads it.

After this I check if the Course is a Lab, if so, I select the second timeslot to the next timeslot of the first one, then convert it to string and then accordingly update both the genes:

Then if it is not a Lab, I check the Soft Constraint of same or alternate days (will explain later on) by

```
# Ensure second lecture day is not the same or adjacent to the first
valid_days = days[~days['Day'].isin([first_day['Day'],
day_before(first_day['Day'], days), day_after(first_day['Day'], days)])]
```

This line of code filters out rows from the DataFrame days where the 'Day' column is not the same as the first lecture day or its adjacent days.

2 helper functions are used to calculate the valid days

```
def day_before(day, days_df):
def day_after(day, days_df):
```

day_before(day, days_df): Retrieves the day before the given day from the DataFrame days_df by finding its index and returning the corresponding value if it exists, otherwise returns None.

day_after(day, days_df): Retrieves the day after the given day from the DataFrame days_df by finding its index and returning the corresponding value if it exists, otherwise returns None.

Then using the valid days, I select a second day and choose a random timeslot and room where the capacity of the room is bigger than the capacity of the course section (Section studying that course).

```
second_day = valid_days.sample().iloc[0]
second_timeslot = timeslots.sample().iloc[0]
second_room = rooms[rooms['Capacity'] >= row['Capacity']].sample().iloc[0]
```

Then I update the both the Genes accordingly by adding details of Second Lecture. (Day, Timeslot, Room, Capacity)

Fitness Calculation:

To calculate the Fitness, I defined a function:

```
def calculate_fitness(detailed_chromosome, encoded_chromosome, timeslots, rooms,
days):
```

in which, I Constructs a dictionary **timeslot_dict** from the DataFrame **timeslots**, mapping each **'Enc'** value to its corresponding **'Timings'** value for quick lookup.

```
# Construct a dictionary from timeslot Enc to Timings for quick lookup
timeslot_dict = {ts['Enc']: ts['Timings'] for idx, ts in timeslots.iterrows()}
```

I will now be talking here mostly about how the chromosomes are constructed and which Hard and Soft Constraints I have applied and check here.

As for the Chromosomes, each chromosome whether detailed or encoded has n genes where n is the course_section meaning sum of courses for each section.

to check for classes a nested loop is applied to get 2 genes (1 course_section).

```
for i in range(len(encoded chromosome)):
   gene1 = encoded_chromosome[i]
   prof11, day11, slot11, room11 = gene1['Professor'],
                                   gene1['First LectureDay'],
                                   gene1['First Lecture Timeslot'],
                                   gene1['First Lecture Room']
  day12, slot12, room12 = gene1['Second Lecture Day'],
                          gene1['SecondLecture Timeslot'],
                          gene1['Second Lecture Room']
       for j in range(i + 1, len(encoded chromosome)):
           gene2 = encoded_chromosome[j]
           prof21, day21, slot21, room21 = gene2['Professor'],
                                           gene2['FirstLecture Day'],
                                           gene2['First Lecture Timeslot'],
                                           gene2['First Lecture Room']
           day22, slot22, room22 = gene2['Second Lecture Day'],
                                    gene2['SecondLecture Timeslot'],
                                    gene2['Second Lecture Room']
```

values of both genes are compared if there is a conflict a penalty of +10 is applied if timeslot clash or room clash (Hard Constraint)

and a +1 penalty is applied if a Lab is scheduled in Morning or A Theory class scheduled in evening.

Then the negative value of penalty is returned -> return -penalty

3 helper functions are defined to check for timeslot overlap and to calculate if the timeslot is in morning or afternoon:

```
def timeslot_overlap(timeslot1, timeslot2):
def in_morning(timeslot):
def in_afternoon(timeslot):
```

timeslot_overlap(timeslot1, timeslot2): Checks if two timeslots overlap by comparing their start and end times, returning True if there is an overlap, False otherwise.

in_morning(timeslot): Determines if the given timeslot falls within the morning session, assuming the morning session ends at 12:50.

in_afternoon(timeslot): Determines if the given timeslot falls within the afternoon session, assuming the afternoon session starts at 13:00.

HARD AND SOFT CONSTRAINTS:

- Classes can only be scheduled in free classrooms. ✓
- A classroom should be big enough to accommodate the section. There should be two categories of classrooms: classroom (60) and large hall (120).
- A professor should not be assigned two different lectures at the same time.
- The same section cannot be assigned to two different rooms at the same time. ✓
- A room cannot be assigned for two different sections at the same time.

- No professor can teach more than 3 courses.
- No section can have more than 5 courses in a semester.
- Each course would have two lectures per week not on the same or adjacent days. ✓
- Lab lectures should be conducted in two consecutive slots.
- 15 mins breaks allowed between consecutive classes to ensure that there is sufficient time for transitions between classes. ✓ (10 mins)

Soft Constraints:

- All the theory classes should be taught in the morning session and all the lab sessions should be done in the afternoon session. ✓
- Teachers/students may be facilitated by minimizing the number of floors they have to traverse. That is, as much as possible, scheduled classes should be on the same floor for either party.
- A class should be held in the same classroom across the whole week. X
- Teachers may prefer longer blocks of continuous teaching time to minimize interruptions and maximize productivity except when the courses are different.

GENETIC ALGORITHM:

To generate the population, I defined a function:

```
def generate_population(pop_size, courses, sections, professors, rooms,
timeslots, days):
    return [generate_chromosome(courses, sections, professors, rooms, timeslots,
days) for _ in range(pop_size)]
```

Which just calls the generate_chromosome(...) function pop_size times.

Then for selection I defined:

```
def select(population, fitness_scores, num_parents):
    # Tournament selection
    selected_indices = sorted(range(len(fitness_scores)),
    key=lambda i: fitness_scores[i], reverse=True)[:num_parents]
    return [population[i] for i in selected_indices]
```

In select(...) a specified number of parents from the population using tournament selection based on their fitness scores, returning their indices sorted in descending order of fitness scores.

Then For Crossover and Mutation I defined:

```
def crossover(parent1, parent2):
    def mutate(child, mutation_rate, timeslots):
```

crossover(...) does a one point crossover and produces 2 child Chromosomes
(encoded) then to generate the detailed part of the chromosome I defined a
function called:

```
def regenerate_detailed_from_encoded(encoded_chromosome, courses, professors,
rooms, timeslots, days):
```

Which basically takes the Encoded part of the chromosome and maps it to the original dataset to get the Detailed part. It checks for the alternate or same day constraint for Theory Courses as well, if the Second day is either the same or alternate then the First Day then it is fixed. It also checks if the course changed was a lab, then if its timing (2 consecutive slots) is correct. If they are not correct then it fixes the timing and then updates the changes in the Encoded Part of the chromosome as well so every change is recorded.

```
1 helper function def get adjacent days(current day, days df):
```

get_adjacent_days(current_day, days_df): Returns a list of adjacent days to the **current_day** from the DataFrame **days_df** to prevent scheduling on consecutive days for theory courses.

In mutate(...) if the random.random() returns a bigger value than the mutation rate
then it will change the timeslot then there is a chance if another random.random() is
bigger than 0.5 to change the room. After this regenerate_detailed_from_encoded(...)
Is called to generate the detailed part of the chromosome.

For the Actual function for genetic algorithm I defined:

```
def genetic_algorithm(courses, sections, professors, rooms, timeslots, days,
pop_size, num_generations, mutation_rate):
```

It generates a population, calculates the fitness and checks if the best fitness of the population is better than the best_fitness than its index is stored and the actual chromosome is saved to best_solution.

If Perfect Fitness has been reached (which is 0) indicating 0 conflicts with the Timetable then the loop breaks to print the output.

Else, number of parents are selected through selection. And then Crossover and Mutation is applied.

After which a new population is made from

```
# Create the new generation
population = parents + children
```

As The output was so lengthy, It overlapped in the output window. So I store it into a text file.

```
# Define the file path to store the table
output_file_path = "output_table.txt"
# Write the table to the text file
with open(output_file_path, "w") as file:
    file.write(str(table))
```

Then to store in a separate file and print separate timetables for each day

```
["Monday", "Tuesday", "Wednesday", "Thursday", "Friday"]
```

I defined the following functions:

```
def generate_daily_timetables(detailed_chromosome):
def get_sort_key(time_slot):
```

```
def convert_to_twelve_hour(time_str):
def print_timetables(timetables):
def write_timetables_to_file(timetables, file_path):
```

generate_daily_timetables(detailed_chromosome): Generates daily timetables from the detailed chromosome, sorting lectures by time and formatting them into a dictionary of DataFrames for each day.

print_timetables(timetables): Prints timetables for each day in the **timetables** dictionary using PrettyTable for better visualization.

write_timetables_to_file(timetables, file_path): Writes timetables for each day in the timetables dictionary to a text file specified by file_path, using PrettyTable for formatting.

Best_chromosome(example) (fitness 0):

■ outpu	ıt_table.txt							
	Course	Туре	Section	Section Capacity	Professor	First Lecture Day	First Lecture Timeslot	First Lecture Room
	OS	Theory	1		Kashif Munir	Monday	8.30-9.50	1 1
	Network Security	Theory	1	50	Amina Ashfaq	Thursday	10.00-11.20	6
	OS Lab	Lab	2	25	Kashif Munir	Monday	13.00-14.20	6
	AI	Theory	3	55	Naveed Ahmed	Thursday	11.30-12.50	4
	AI Lab	Lab	4		Naveed Ahmed	Thursday	14.30-15.50	6
	CNET	Theory	5	60	Amina Ashfaq	Friday	8.30-9.50	6
	OS	Theory	5	69	Kashif Munir	Friday	8.30-9.50	7
11	+	+	+	+	+	+	+	++

: Lecture Room	First Lecture Room Capacity	Second Lecture Day	Second Lecture Timeslot	Second Lecture Room	Second Lecture Room Capacity
1	60	Thursday	11.30-12.50	15	120
6	120	Monday	11.30-12.50	6	120
6	120	Monday	14.30-15.50	6	120
4	60	Tuesday	10.00-11.20	8	120
6	120	Thursday	16.00-17.20	6	120
6	120	Monday	8.30-9.50	8	120
7	60	Wednesday	13.00-14.20	7	69

Timetable of the best chromosome:

	-+	-+	-+	+	-+		+
Time Slot	Course	Type	Section	Room		Professo	or
10:00 AM to 11:20 AM	AI Lab	Lab	4	8		aveed Al	
11:30 AM to 12:50 PM				8		aveed Al	
2:30 PM to 3:50 PM	CNE I		5 -+	6 -+		mina Asl	
imetable for Tuesday	_+						
Time Slot					ion	Room	Professor
10:00 AM to 11:20 AM	i	os	Theory	1			
11:30 AM to 12:50 PM						1 Kashif Mu	
1:00 PM to 2:20 PM				1 -+			Amina Ashfaq
imetable for Wednesda 	-	-+	-+	+	-+		+
Time Slot			Section			Professo	or
8:30 AM to 9:50 AM	AI	Theory	3	3	N	aveed Al	nmed
10:00 AM to 11:20 AM	CNET		5 - +			mina Asl	
imetable for Thursday							
Time Slot			Section		Pro	ofessor	+
+	05	Theory	4	o I	Kas	hif Muni	# in I
4:00 PM to 5:20 PM	03	medi y	1 1	9 1	Ku3		.
4:00 PM to 5:20 PM		+	+-	+			+
·+		+		9 +			+
·+	-+	ourse	+	.+		Room	
4:00 PM to 5:20 PM imetable for Friday Time Slot 8:30 AM to 9:50 AM	-+	ourse	+ Type	+ -+ Sect	ion	+	Professor
imetable for Friday Time Slot	-+	ourse	+ Type	 Sect -+	ion	Room	
imetable for Friday Time Slot 8:30 AM to 9:50 AM	Co	ourse k Securit	+	 Sect 1	ion	+ Room 	Professor Amina Ashfaq
Time Slot 8:30 AM to 9:50 AM 11:30 AM to 12:50 PM	Co	ourse k Securit	Type Theory	 Sect 1 5	ion	+ Room 6 3 8	Professor Amina Ashfaq