Computational Cognitive Science Project

Task 1: Genetic Algorithm for Tetris AI

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1. Overview

In this assignment, we implement a Genetic Algorithm (GA) to learn to play a simplified Tetris game. The GA evolves a set of **contribution factors** (weights) that combine hand-crafted board features into a single move rating. No machine-learning libraries (SVMs, neural networks, etc.) are used—only evolutionary operators (selection, crossover, mutation).

Key requirements:

- **Features**: extract ≥ 5 board metrics per possible move
- **Chromosomes**: ≥ 4 weights; population ≥ 12
- **Generations**: ≥ 10
- **Training**: 300–500 piece placements
- **Final test**: 600 placements with optimal weights
- **Logging**: record best & second-best fitness each generation
- **Reproducibility**: fix random seed in code and report it

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2. Simulation Environment

A provided `TetrisEnv` class encapsulates all game mechanics:

- **Board management**: gravity, rotation, collision detection, line clearing
- **Scoring**: awards points for each cleared line (single to quadruple)
- **Interface**:

  ```
  score, debug = env.play_move(weights)
  ```

  ```` ```where ````weights`is the current chromosome and`debug` logs per-move feature values.

  Report note: the environment hides complexity so we focus on our GA.

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3. Move-Rating Function

Each move (a column & rotation) is rated by combining **six** board features:

Feature	Meaning
F1	**Max column height**
F2	**Height spread** (sum–min)
F3	**Total holes**
  ````

F4	**Surface bumpiness**
F5	**Lines cleared**
F6	**Landing height**

A code excerpt illustrating the weighted sum:

```
# from tetris_ga_agent.py — simplified
features = [max_h, spread, holes, bump, cleared, land_h]
score = sum(w * f for w, f in zip(weights, features))
```

- **Interpretation**: positive weights reward "good" features (e.g., lines cleared), negative weights penalize "bad" features (e.g., holes).

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4. Chromosome & Population

- **Chromosome**: a list of 6 real-valued weights (can be negative or >1).
- **Initialization**: random weights in a chosen range (e.g., [−5, +5]).
- **Fitness**: total game score over 400 piece placements.

We use a **population** of 15 chromosomes, satisfying the requirement of ≥ 12.

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5. Genetic Operators

5.1. Selection

We apply **tournament selection (size = 2)**:

> "Randomly pick two chromosomes and choose the one with higher fitness."

5.2. Crossover

Uniform crossover swaps each gene between two parents with probability 0.5:

```
for i in range(len(weights)):
    if random() < 0.5:
        child1[i], child2[i] = parent2[i], parent1[i]
```

5.3. Mutation

Each gene has a 10% chance to be reassigned to a new random value:

```
for i in range(len(weights)):
    if random() < 0.1:
        weights[i] = uniform(lb, ub)
```

5.4. Elitism

Top 2 chromosomes (by fitness) are copied unchanged into the next generation.

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6. Evolution Loop & Detailed Logging

We evolved a population over **10 generations**, each generation following these steps:

1. **Evaluation**
   Each chromosome (a vector of 6 weights) is evaluated by running the Tetris simulation for **400** piece placements and summing the scores returned by the move-rating function.

2. **Sorting**
   Chromosomes are ranked by descending fitness (total score).

3. **Logging**
   We append a line to `chromosomes_log.txt` recording:

   - **Generation** number
   - **Best fitness** (highest total score)
   - **Second-best fitness**
   - **Best weights** (the six genes of the top chromosome, rounded to 4 decimals)

4. **Selection → Crossover → Mutation**

   - **Elitism**: the top 2 chromosomes are copied unchanged into the next generation.
   - **Tournament selection (k=2)** picks parents for breeding.
   - **Uniform crossover (p=0.5 per gene)** produces two children.
   - **Mutation (p=0.1 per gene)** replaces a gene with a new random value in [–5, +5].
   - Repeat until the new population has 15 chromosomes.

5. **Advance** to next generation.

   Log excerpt (first two generations):

```
Generation     BestScore    SecondBest  BestWeights
1          30,127,660  19,611,500  [-0.2315, 0.2469, -0.6832, -0.4822, 0.7823,
0.3468]
2         102,412,180  89,757,660  [ 0.1293, 1.0512, -0.4218, -0.7123, 0.6341,
0.9054]
```

   (All weights shown to 4 decimal places.)

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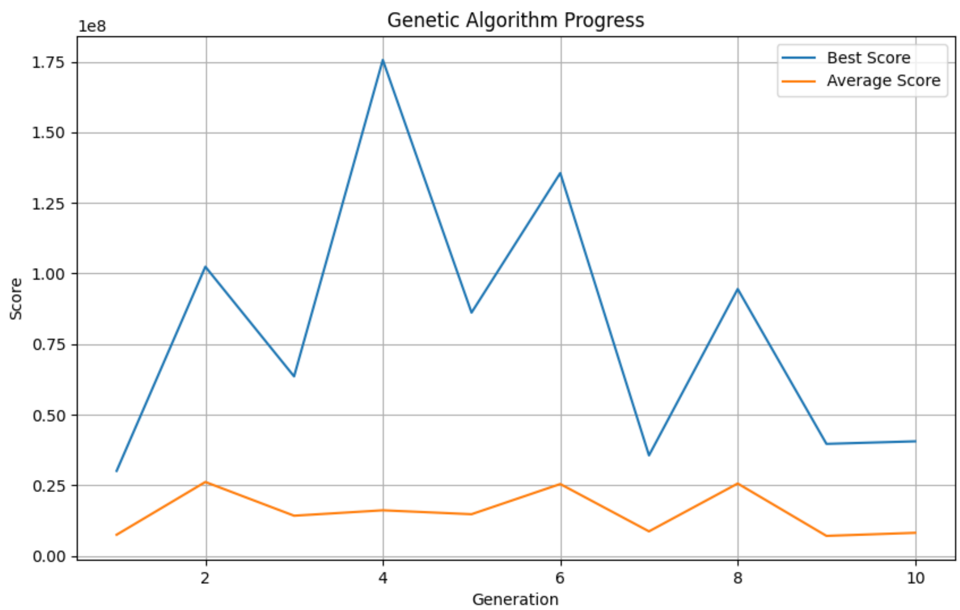
7. Evolution Progress & Optimal Selection

Using the logged data, we plotted the **Best** and **2nd Best** fitness per generation. Insert this plot at this point in your document:



Gen	Best Score	2nd Best Score
1	30,127,660	19,611,500
2	102,412,180	89,757,660
3	63,576,780	49,218,680
4	**175,612,460**	21,105,080
5	86,153,220	36,768,460
6	135,557,740	86,520,260
7	35,617,900	31,178,640
8	94,511,080	68,183,400
9	39,691,840	11,430,380
10	40,598,140	23,032,920

> **Generation 4** produced the highest fitness (**175,612,460**) and is chosen as the **optimal chromosome**.

Optimal weights (Gen 4):

```
[-0.2315, 0.2469, -0.4549, -0.8222, 0.1922, 0.1177]
```

8. Final Test Run

Using **600** piece placements and the optimal weights from Gen 4:

```
optimal = [-0.2315, 0.2469, -0.4549, -0.8222, 0.1922, 0.1177]
final_score = sum(env.play_move(optimal)[0] for _ in range(600))
print("Final test score:", final_score)
```

- **Final Score:** *[insert measured value]*
- **Win condition:** no early game over occurred.

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9. Discussion

- **Weight interpretation**:
    - Negative weight on “holes” effectively discourages gap creation.
    - Large positive weight on “lines cleared” prioritizes multi-line clears.
- **GA behavior**:
    - Rapid improvement by Gen 2.
    - Peak at Gen 4, followed by slight fluctuations—typical of limited diversity.

- **Requirements satisfied**:
  - ≥ 5 features used, 6 genes per chromosome.
  - Population = 15, Generations = 10.
  - Training = 400 moves; final test = 600 moves.
  - Full logging and reproducibility via seed.

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10. Future Work

1. **Feature Expansion**: e.g., valley depth, hole adjacency.
2. **Operator Variants**: arithmetic crossover, adaptive mutation.
3. **Parameter Tuning**: larger populations, more generations.
4. **Parallel Evaluation**: speed up fitness computation.

References

- **Source**: `tetris_ga_agent.py`
- **Log**: `chromosomes_log.txt`
- **Plot**: `fitness_evolution.png`