

Implementation of a Gene Pool Simulator and Computational Demonstration of Bergmann’s Rule

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Abstract

This paper presents the implementation of a gene pool simulator designed to model evolutionary dynamics. The simulation is utilized to demonstrate Bergmann’s Rule, illustrating how environmental temperature influences body size adaptation in homeotherms through natural selection. By defining specific metabolic and environmental parameters, the study verifies the stabilization of gene pools and the emergence of size-dependent survival traits.

1 Introduction

Richard Dawkins’ *The Selfish Gene* elucidates evolution by applying Darwinian concepts of “survival of the fittest” and “natural selection” to the genetic level. Fundamental concepts of heredity—including genes, natural selection, and meiosis—suggest that organisms function as survival mechanisms for their genetic material.

The manifestation of various phenotypic traits and the process of speciation are driven by fluctuations within the gene pool. Motivated by these principles, this study employs a computational approach to simulate gene pool dynamics.

Specifically, this research aims to demonstrate “Bergmann’s Rule,” a prominent principle of biological adaptation. Bergmann’s Rule posits that within homeothermic (warm-blooded) species, populations residing in colder climates exhibit larger body sizes, whereas those in warmer climates possess smaller body sizes.

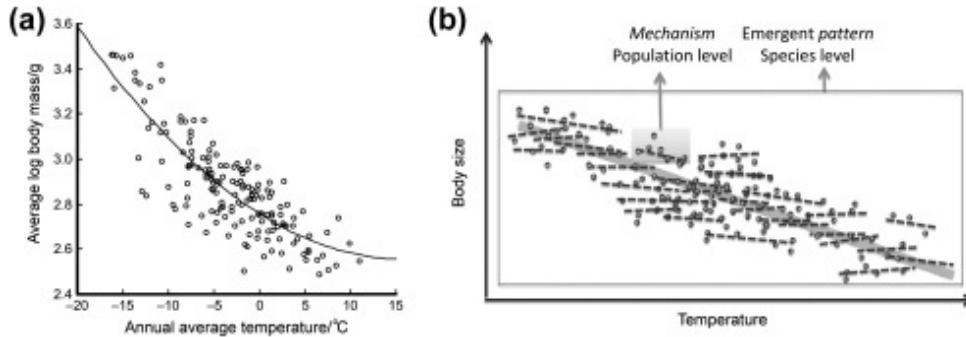


Figure 1: Illustration of Bergmann’s Rule demonstrating body size adaptation to latitude [5].

While Bergmann’s Rule can be rationalized through the physics of heat production and dissipation, relying solely on rational explanations to describe existing ecosystems is

insufficient. Evolutionary adaptations are strictly filtered by survival; for instance, while posterior eyes might theoretically aid predator avoidance, such traits do not persist in mammalian lineages.

Consequently, this simulation seeks to verify that genes associated with maladaptive body sizes relative to climatic conditions are eliminated from the gene pool, while genes facilitating adaptation survive and proliferate.

2 Methodology

2.1 Definition of Ecosystem

To demonstrate Bergmann's Rule, the simulated ecosystem is defined with a specific temperature attribute. The population size is initialized to be sufficiently large to mitigate the effects of genetic drift.

2.2 Simulation Premises

The simulation is established upon the following premises:

- The experimental subject is defined as a virtual, cube-shaped homeotherm.
- Metabolic rate is assumed to be proportional to volume, with the metabolic rate per unit volume referenced from human physiology.
- The organism's ideal body temperature is set at 35°C; survival probability decreases as the expected body temperature deviates from this ideal.
- Daily heat generation is assumed to equal daily heat dissipation.
- Mating within the population occurs randomly.
- Height is modeled as a polygenic trait, increasing in proportion to the number of growth genes present.
- Genes are located on distinct chromosomes and are inherited independently.

The specific constants and values utilized are detailed in Table 1.

Table 1: Simulation Constants and Parameters

Parameter	Source Code Identifier	Value
Population Size	NUMBER_OF_INDIVIDUALS	22,000
Growth per Gene	GROWTH_PER_GROWTH_HORMONE	20 cm
Base Height	BASE_HEIGHT	0 cm
Minimum Height	MINIMUM_HEIGHT	1 cm
Metabolic Rate per cm ³	METABOLIC_RATE_PER_CUBIC _CENTIMETER	0.02328 kcal/cm ³ (Based on 70kg human: 1680kcal/day, density 0.97g/cm ³)
Heat Transfer Coefficient	HEAT_TRANSFER_COEFFICIENT	0.01164 (Calibrated for 60cm height at 15°C env. to reach 35°C body)
Evolutionary Pressure	EVOLUTIONARY_PRESSURE	0.0003 or 0.0001
Ideal Body Temp	IDEAL_BODY_TEMPERATURE	35°C

2.3 Expected Body Temperature Calculation

Body temperature is estimated using Newton’s Law of Cooling:

$$Q = h \cdot A \cdot (T_{body} - T_{env}) \quad (1)$$

Where h represents the heat transfer coefficient. The value of h is calibrated such that a specific height is optimal for a specific climate. A denotes the heat transfer surface area, equivalent to the organism’s total surface area. Based on the established premises, the metabolic rate and surface area are derived to calculate the expected body temperature.

2.4 Gamete Formation and Progeny Generation

Gamete formation involves the random selection of one chromosome from each homologous pair. In the simulation, new individuals are generated by combining gametes from two randomly selected parents.

The following code demonstrates the initialization of the first generation. Genes are initialized as recessive (lowercase), and a specified number are converted to dominant growth genes (uppercase).

```

1 static createRandomOrganism(numberOfDominantGenes: number) {
2   const genes: [string, string][] = Array.from(Array(5).keys()).map((n)
3     => [
4       String.fromCharCode(97 + n),
5       String.fromCharCode(97 + n),
6     ]
7   );
8   Array.from(Array(10).keys())
9     .sort(() => Math.random() - 0.5)
10    .slice(0, numberOfDominantGenes)
11    .forEach((n) => {
12      genes[Math.floor(n/2)][n % 2] =
13        genes[Math.floor(n/2)][n % 2].toUpperCase();
14    });
15 }

```

```

14
15     return new Organism(genes);
16 }

```

Listing 1: Initialization of Random Organism

The gamete generation function selects one allele from each homologous pair to form a haploid set.

```

1 getGamete() {
2     // [[a, A], [B,b], [c,c], [D,D], [E,e]] => [a,B,C,D,E] selection
3     return this.genes.map((gene) => gene[Math.random() > 0.5 ? 1 : 0]);
4 }

```

Listing 2: Gamete Generation Method

2.5 Viability Determination

2.5.1 Biometric Calculations

The height function determines the organism's size based on the count of growth genes. Subsequent functions calculate surface area and volume. The metabolism function derives the metabolic rate by multiplying the volume by the metabolic rate per cubic centimeter.

```

1 getHeight() {
2     if (this.numberofGrowthHormoneGenes === 0) return Co.MINIMUM_HEIGHT;
3     return (
4         Co.BASE_HEIGHT +
5         Co.GROWTH_PER_GROWTH_HORMONE_GENE *
6         this.numberofGrowthHormoneGenes
7     );
8 }
9
10 getVolume() {
11     const height = this.getHeight();
12     return height * height * height;
13 }
14
15 getSurfaceArea() {
16     const height = this.getHeight();
17     return height * height * 6;
18 }
19
20 getMetabolism() {
21     return this.getVolume() * Co.METABOLIC_RATE_PER_CUBIC_CENTIMETER;
22 }

```

Listing 3: Biometric Calculation Methods

2.5.2 Thermal Estimation

Using Newton's Law of Cooling, the expected body temperature is calculated by integrating the metabolic rate and surface area with the external temperature.

```

1 getEstimatedBodyTemperature(externalTemperature: number) {
2     return (
3         externalTemperature +
4         this.getMetabolism() /

```

```

5      Co.HEAT_TRANSFER_COEFFICIENT /
6      this.getSurfaceArea()
7  );
8  }

```

Listing 4: Body Temperature Estimation

2.5.3 Survivability Logic

Survivability is modeled as a quadratic function peaking at (35, 1) with a negative leading coefficient. This maps the expected body temperature (x) to a survival probability (y).

```

1  static survivability(t: number) {
2      // Returns 1 when expected body temp equals ideal temp.
3      // Probability decreases as temperature deviates.
4      return (
5          -1 *
6          Co.EVOLUTIONARY_PRESSURE *
7          (t - Co.IDEAL_BODY_TEMPERATURE) *
8          (t - Co.IDEAL_BODY_TEMPERATURE) +
9          1
10     );
11 }
12
13 isViable(externalTemperature: number) {
14     // Determine viability based on calculated probability.
15     const EBT = this.getEstimatedBodyTemperature(externalTemperature);
16     const survivability = Organism.survivability(EBT);
17     return Math.random() <= survivability;
18 }

```

Listing 5: Survivability Determination

2.6 Generational Turnover

Generational replacement proceeds by selecting two parents from the current population to produce offspring. The offspring's viability is tested against the environmental temperature. Surviving offspring are added to the subsequent generation. This cycle repeats until the population size is restored, at which point the new generation replaces the old.

```

1  const newPopulation: Organism[] = [];
2  this.individualsByGH = this.initialIndividualsByGH.slice();
3  let growthHormoneGene = 0;
4
5  while (newPopulation.length < Co.NUMBER_OF_INDIVIDUALS) {
6      // Random selection of parents
7      const organism1 = this.population[Math.floor(Math.random() * this.
8      population.length)];
9      const organism2 = this.population[Math.floor(Math.random() * this.
10     population.length)];
11
12     const gamete1 = organism1.getGamete();
13     const gamete2 = organism2.getGamete();
14
15     // Offspring creation
16     const newOrganism = Organism.fromTwoGametes(gamete1, gamete2);

```

```

16 // Natural Selection Check
17 if (!newOrganism.isViable(this.temperature)) continue;
18
19 // Survivor Registration
20 growthHormoneGene += newOrganism.numberOfGrowthHormoneGenes;
21 this.individualsByGH[newOrganism.numberOfGrowthHormoneGenes]++;
22 newPopulation.push(newOrganism);
23 }
24 this.population = newPopulation;

```

Listing 6: Generational Loop

2.7 Stabilization Criteria

The simulation tracks the average number of growth genes per generation. Stabilization is declared when the difference between the average of the most recent 10 generations and the preceding 10 generations falls below 0.01.

```

1 if (Math.abs(prevAvg - prevPrevAvg) < Co.STABILITY_THRESHOLD) {
2     this.isStabilized = true;
3 }

```

Listing 7: Stabilization Check

3 Results

3.1 Gene Pool Shifts under Natural Selection

The simulation demonstrated that over successive generations, the distribution of growth genes shifted toward an optimum for the given environment. At 25°C, individuals possessing a high count of dominant growth genes (resulting in larger size) exhibited reduced survival rates. Consequently, dominant genes were purged from the gene pool, leading to an increased prevalence of recessive genes and smaller individuals.

- **2nd Generation:** Gene count distribution spans 0-10.
- **5th Generation:** Distribution shifts slightly toward lower counts.
- **9th Generation:** Distribution centers significantly around lower numbers.
- **Stabilized (89th Generation):** A distinct distribution curve is established around a low gene count.

3.2 Temperature-Dependent Gene Distribution

Results indicate an inverse relationship between environmental temperature and the frequency of growth genes. As illustrated in the generated graphs (represented below), a climate of 25°C resulted in a distribution centered around 1 growth gene. Conversely, a climate of −25°C shifted the center to approximately 9 growth genes. The distributions consistently formed a normal curve around the optimal gene count for each climatic condition.

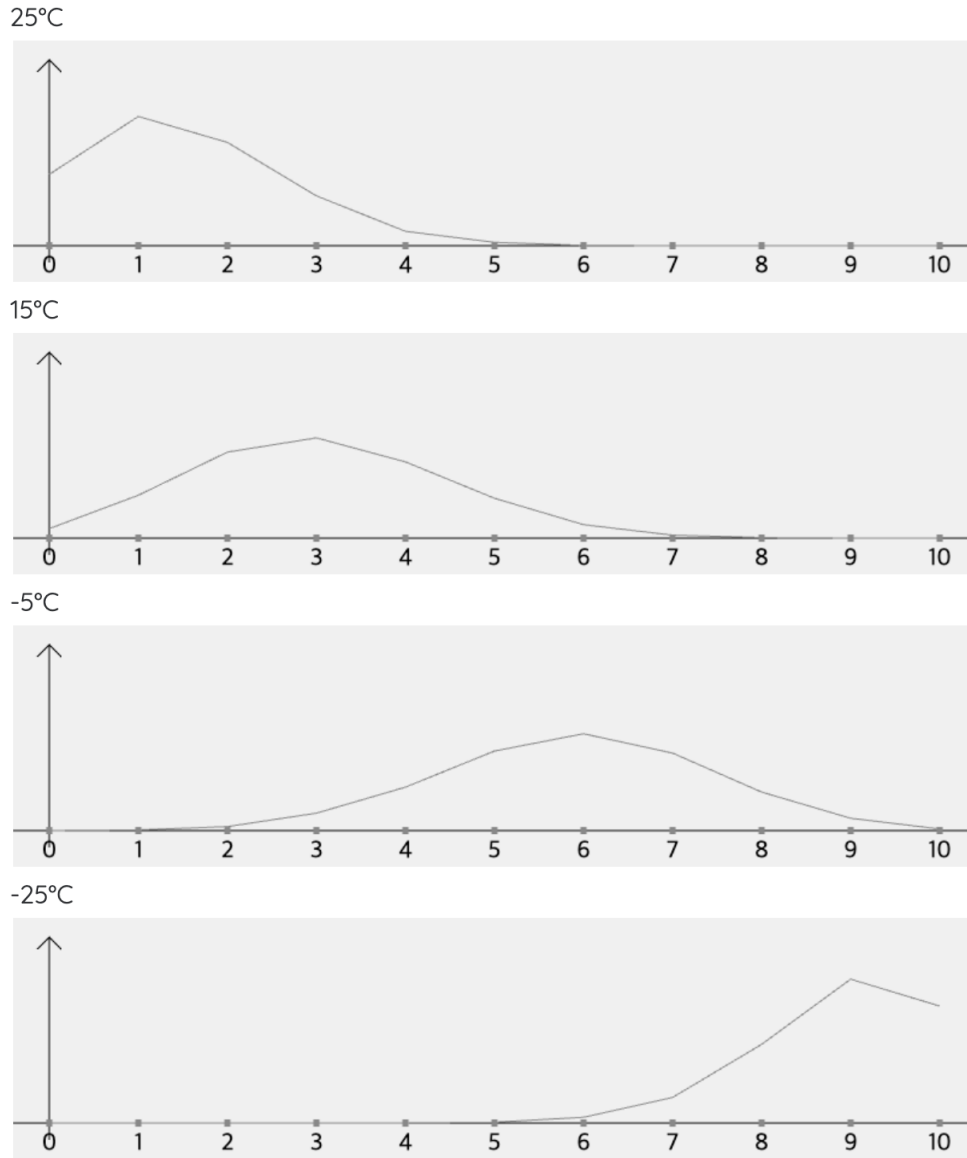


Figure 2: Gene Distribution Variance by Temperature

3.3 Evolutionary Pressure and Stabilization Time

Evolutionary pressure was modeled as the magnitude of the leading coefficient in the quadratic survival function. A larger absolute coefficient implies a steeper decline in survival probability for deviations from the ideal temperature, representing higher pressure.

It was observed that higher evolutionary pressure accelerated the stabilization of the gene pool across all tested temperatures. Specifically, a pressure coefficient of 0.0001 required approximately 1.5 times more generations to reach equilibrium compared to a coefficient of 0.0003.

Table 2: Generations to Equilibrium (Pressure = 0.0001)

Temp (°C)	1st	2nd	3rd	4th	5th	Avg
25	170	145	175	156	127	154.6
15	112	101	111	124	119	113.4
-5	81	71	66	58	71	69.4
-25	157	165	160	152	140	154.8

Table 3: Generations to Equilibrium (Pressure = 0.0003)

Temp (°C)	1st	2nd	3rd	4th	5th	Avg
25	94	92	103	91	83	92.6
15	73	68	82	67	66	71.2
-5	46	56	55	60	57	54.8
-25	96	115	108	100	93	102.4

4 Conclusion

The simulation confirms that differential survival probabilities inherent to specific environments drive alterations in the gene pool. These findings successfully demonstrate Bergmann’s Rule: colder regions correlated with an increase in growth genes (larger body size), while warmer regions showed a decrease. Additionally, the data suggests that increased evolutionary pressure expedites the arrival at a genetic equilibrium.

The modular nature of the simulation allows for further applications. By modifying the viability function, other ecological principles such as Allen’s Rule or Gloger’s Rule could potentially be modeled and verified.

5 References

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