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Article

# Simulation and Statistical Analysis of Population Dynamics in Evolutionary Systems: A Simulated Study

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**Abstract:** This project aims to simulate and analyze population dynamics in evolutionary systems, using stochastic differential equations and probabilistic rules for crossbreeding and benefits. The study employs advanced computational techniques to model the evolution of populations over an extended period. Specifically, we explore a scenario with ten distinct groups, each starting with an equal population and evolving under defined genetic and cooperative behaviors. The simulation spans 1000 years, incorporating individual lifespans, stochastic updates, and probabilistic interactions. To ensure robustness and reliability, the study includes detailed statistical analysis, encompassing descriptive statistics, confidence intervals, and ANOVA tests. We further visualize the temporal behavior of populations and subpopulations, providing insights into the evolutionary dynamics and stability of the system. The results demonstrate the effectiveness of balanced cooperation and genetic diversity in maintaining stable population distributions. The project showcases the integration of mathematical modeling, statistical analysis, and computational simulations, contributing valuable insights into evolutionary biology and complex systems. It highlights the importance of interdisciplinary approaches in understanding and predicting population behaviors, with implications for both theoretical research and practical applications in fields such as ecology, genetics, probability and social sciences.

**Keywords:** population dynamics; evolutionary systems; partial differential stochastic equations; simulation

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## Section 1. Introduction

The study of population dynamics has long been a fundamental aspect of mathematical biology, ecology, probabilistic, and evolutionary theory. Understanding how populations evolve over time under various genetic, environmental, and social pressures is crucial for predicting future trends and managing biological resources. Traditional models of population dynamics often rely on deterministic equations that may not capture the inherent randomness of biological systems. To address this, stochastic differential equations (SDEs) have been increasingly employed to incorporate the probabilistic nature of real-world phenomena (Murray, 2002; Allen, 2010).

This project explores the use of SDEs to model the evolution of populations in a controlled simulation environment. We consider a system with ten distinct groups, each characterized by specific genetic and cooperative (phenotype) behaviors. The initial population of 100 individuals is evenly distributed among these ten groups, resulting in 10 individuals per group.

Each group is distinguished by descending characteristics related to their propensity for crossbreeding and cooperative behavior:

Crossbreeding Probabilities: Group 0 has a 0% probability of crossbreeding with other groups, Group 1 has a 1% probability, continuing up to Group 9, which has a 9% probability.

**Benefit Probabilities:** Group 0 has a 10% probability of benefiting other groups, decreasing to Group 9, which has a 1% probability. This reflects a higher propensity for cooperation in the lower-numbered groups.

Within each group, individuals exhibit a similar descending propensity for benefiting others, aligning with their group's overall characteristics. For example, individuals in Group 0 are highly cooperative, while those in Group 9 are more self-serving. The descending rate is  $0,01/10=0,001$ .

The system evolves over a period of 1000 years, incorporating individual lifespans of 25 years. The simulation updates population counts stochastically and applies probabilistic rules for crossbreeding and benefits, allowing us to capture the complexities and randomness inherent in biological evolution.

### *Section 1.2. The Stochastic Interactions Include*

**Interbreeding (Crossbreeding):** When individuals from different groups crossbreed, the offspring inherits characteristics as a mean of both parents' groups.

**Intrabreeding (Within-group breeding):** When individuals within the same group breed, the offspring retains the group's characteristics also as a mean of both parents.

**Benefit Distribution:** Individuals may benefit others within or across groups based on the group's benefit probability, promoting cooperative behaviors and potentially enhancing group survival.

We conduct a comprehensive statistical analysis of the simulation results, including descriptive statistics, confidence intervals, and ANOVA tests. These analyses provide insights into the central tendencies, dispersions, and significant differences between groups. Additionally, we visualize the temporal behavior of populations and subpopulations, revealing trends and patterns in the evolutionary dynamics.

The preliminary results demonstrate that balanced cooperation and genetic diversity are key factors in maintaining stable population distributions. These findings are consistent with previous research in evolutionary biology and complex systems (Nowak, 2006; Roughgarden, 1979). However, the current model represents a simplified version of real-world scenarios, and there is *significant potential for further enhancement*. Future work will aim to incorporate more complex differential stochastic equations as probability vectors to capture a broader range of biological and environmental factors, providing a deeper understanding of population probabilistic dynamics.

### *Section 1.3. Future*

**Incorporating Environmental Variability:** Introducing factors such as resource availability, climate changes, and habitat alterations that affect population dynamics.

**Genetic Variability and Mutation:** Modeling genetic mutations and their impacts on population fitness and adaptability.

**Social Structures and Behaviors:** Integrating social behaviors, including competition, cooperation, and predation, to reflect more complex interaction dynamics.

**Multi-Species Interactions:** Expanding the model to include interactions between different species, simulating ecosystems rather than isolated populations.

All these characteristics are embedded in probabilistic theory. Without that foundation, nothing would be accomplished.

By incorporating these enhancements, we aim to develop a more comprehensive and accurate model of population dynamics that can be applied to a wide range of biological and ecological studies.

## **Section 2. Methodology**

### *Section 2.1. Detailed Explanation of Simulation Parameters*

This project involves simulating the evolution of populations using stochastic differential equations and probabilistic rules. The parameters of the simulation are carefully designed to capture

the complexities of biological evolution and inter-group interactions. Here is a detailed explanation of each parameter:

#### 1. Number of Groups (NUM\_GROUPS)

- **Description:** The total number of distinct groups in the population.
- **Value:** 10
- **Purpose:** Each group represents a subpopulation with potentially different genetic and cooperative behaviors. This allows us to study the dynamics of diverse populations interacting with each other.

#### 2. Initial Population (INITIAL\_POPULATION)

- **Description:** The total number of individuals at the start of the simulation.
- **Value:** 100 individuals, evenly distributed among groups.
- **Purpose:** Provides a starting point for the simulation, ensuring each group has an initial population to evolve from.

#### 3. Simulation Years (SIMULATION\_YEARS)

- **Description:** The total duration of the simulation in years.
- **Value:** 500 years
- **Purpose:** Allows the model to capture long-term evolutionary trends and dynamics, providing insights into how populations change over extensive periods. We would like to analyze a much broader temporal window, but that will demand significant computational power.

#### 4. Individual Lifespan (INDIVIDUAL\_LIFESPAN)

- **Description:** The average lifespan of individuals in the population.
- **Value:** 25 years
- **Purpose:** Introduces mortality into the model, ensuring that individuals do not live indefinitely. This parameter helps simulate natural population turnover and aging.

#### 5. Crossbreeding Probabilities (CROSSBREED\_PROBABILITIES)

- **Description:** The probabilities that individuals will crossbreed with individuals from other groups.
- **Values:** [0.00,0.01,0.02,...,0.09][0.00, 0.01, 0.02,...0.09][0.00,0.01,0.02,...,0.09]
- **Purpose:** Models the likelihood of genetic mixing between groups. Higher probabilities represent more frequent crossbreeding, which can introduce genetic diversity and affect population dynamics.

#### 6. Benefit Probabilities (BENEFIT\_PROBABILITIES)

- **Description:** The probabilities that individuals will act in ways that benefit others within or outside their group.
- **Values:** [0.10,0.09,...,0.01]
- **Purpose:** Represents altruistic behaviors within the population. Higher probabilities indicate a greater propensity for individuals to benefit others, influencing group cohesion and survival.

#### 7. Stochastic Update Parameters ( $\beta$ and $\gamma$ )

- **Description:** Parameters in the stochastic differential equation used to update individual population sizes.
  - $\beta$  (beta): Growth rate coefficient
  - $\gamma$  (gamma): Crowding effect coefficient

- **Values:**
  - $\beta$ : 0.1
  - $\gamma$ : 0.01
- **Purpose:** Models the growth and self-limiting effects on population sizes. The growth rate ( $\beta$ ) promotes population increase, while the crowding effect ( $\gamma$ ) imposes a limit due to resource constraints.

The study employs a combination of stochastic differential equations and probabilistic rules to model the evolution of populations over time. The following steps outline the methodology used, including the full equations and corresponding Python code.

**The methodology involves:**

Initializing the population with an even distribution.

Updating the population using stochastic differential equations.

Applying probabilistic rules for crossbreeding and benefits.

Running the simulation over an extended period and recording population dynamics.

By incorporating these steps, we can simulate the complex interactions within populations and analyze their evolutionary dynamics over time. The future goal is to enhance the model by integrating more complex differential stochastic equations as probability vectors, capturing a broader range of biological and environmental factors.

### *Section 2.1. Detailed Explanation of Simulation Parameters*

This project involves simulating the evolution of populations using stochastic differential equations and probabilistic rules. The parameters of the simulation are carefully designed to capture the complexities of biological evolution and inter-group interactions. Here is a detailed explanation of each parameter:

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Description: The total number of distinct groups in the population.

Value: 10

Purpose: Each group represents a subpopulation with potentially different genetic and cooperative behaviors. This allows us to study the dynamics of diverse populations interacting with each other.

#### 2. Initial Population (INITIAL\_POPULATION)

Description: The total number of individuals at the start of the simulation.

Value: 100 individuals, evenly distributed among groups.

Purpose: Provides a starting point for the simulation, ensuring each group has an initial population to evolve from.

#### 3. Simulation Years (SIMULATION\_YEARS)

Description: The total duration of the simulation in years.

Value: 500 years

Purpose: Allows the model to capture long-term evolutionary trends and dynamics, providing insights into how populations change over extensive periods.

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#### 5. Crossbreeding Probabilities (CROSSBREED\_PROBABILITIES)

Description: The probabilities that individuals will crossbreed with individuals from other groups.

Values intergroups and intragroups:

[0.00,0.01,0.02,...,0.09];[0.00,0.01,0.02,...,0.09]



Purpose: Models the likelihood of genetic mixing between groups. Higher probabilities represent more frequent crossbreeding, which can introduce genetic diversity and affect population dynamics.

6. Benefit Probabilities (BENEFIT\_PROBABILITIES)

Description: The probabilities that individuals will act in ways that benefit others within or outside their groups. Values: [0.10,0.09,...,0.01];[0.10,0.09,...,0.01].

Purpose: Represents altruistic behaviors within the population. Higher probabilities indicate a greater propensity for individuals to benefit others, influencing group cohesion and survival.

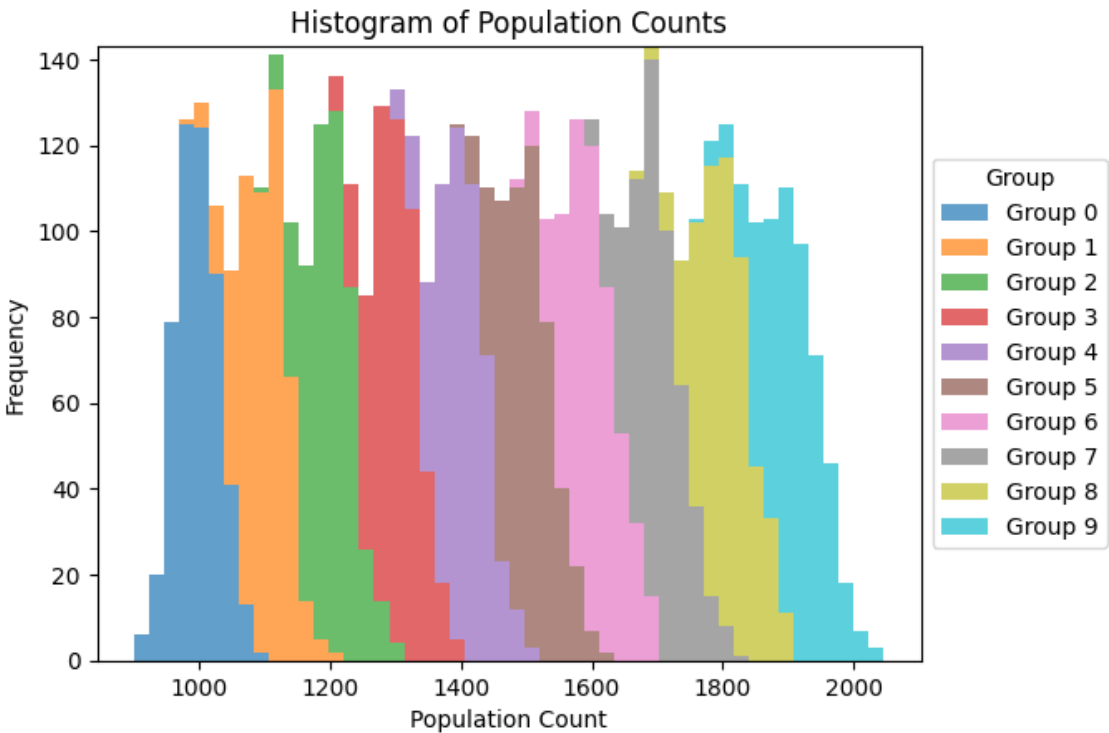
7. Stochastic Update Parameters ( $\beta$  and  $\gamma$ )

Description: Parameters in the stochastic differential equation used to update individual population sizes.

Summary

The parameters and methodology outlined above provide a comprehensive framework for simulating and analyzing population dynamics using stochastic differential equations and probabilistic rules. By incorporating these elements, we can capture already some complexities of evolutionary processes and gain insights into the factors that influence population stability and diversity.

Section 3. Initial Results



**Figure 1.** Histogram showing heterogeneity of population groups but with it's relative frequency practically unchanged.

Explanation of the Histogram Graphic

The histogram provides a visual representation of the distribution of population counts for each group. Here's a detailed explanation of the histogram and how it supports the conclusions drawn from the descriptive statistics and box plots:

Distribution Shape:

Each group is represented by a different color, and the population counts are displayed along the x-axis, while the frequency (number of occurrences) is shown on the y-axis.

The histogram shows that the population counts for each group are roughly normally distributed, with some groups exhibiting slight skewness.

**Central Tendency:**

The peak of each group's histogram indicates the most frequently occurring population counts, which align with the means and medians observed in the descriptive statistics.

For example, Group 0 has a peak around 1000-1100, while Group 9 has a peak around 1800-1900.

**Variability:**

**The width of the histogram** for each group indicates the spread or variability of the population counts.

Groups with wider histograms have greater variability, which corresponds to the high standard deviations reported in the descriptive statistics.

**Overlap Between Groups:**

There is some overlap between the histograms of different groups, indicating that while there are differences in central tendencies, the ranges of population counts can still intersect.

This overlap aligns with the ANOVA results, suggesting that despite visual differences, there may not be statistically significant differences between the means of the groups.

**Frequency:**

The height of the bars in each histogram represents how often specific population counts occur within each group.

Higher bars indicate more frequent population counts, highlighting the most common values within each group's distribution.

**Key Insights****Systematic Growth:**

The histogram clearly shows the systematic increase in population counts from Group 0 to Group 9. Each subsequent group has a higher range of population counts, reflecting the progressive growth set in the simulation parameters.

**High Variability:**

The variability within each group is evident from the width of the histograms. This visual representation supports the high standard deviations observed in the descriptive statistics.

**No Significant Differences:**

The overlap between the groups' histograms suggests that the population counts, while different in central tendencies, have substantial variability. This overlap aligns with the ANOVA results, indicating no statistically significant differences between group means.

**Data Distribution:**

The histogram provides a clear visual of the data distribution within each group, showing that most data points are clustered around the central values with tails extending towards the minimum and maximum observed counts.

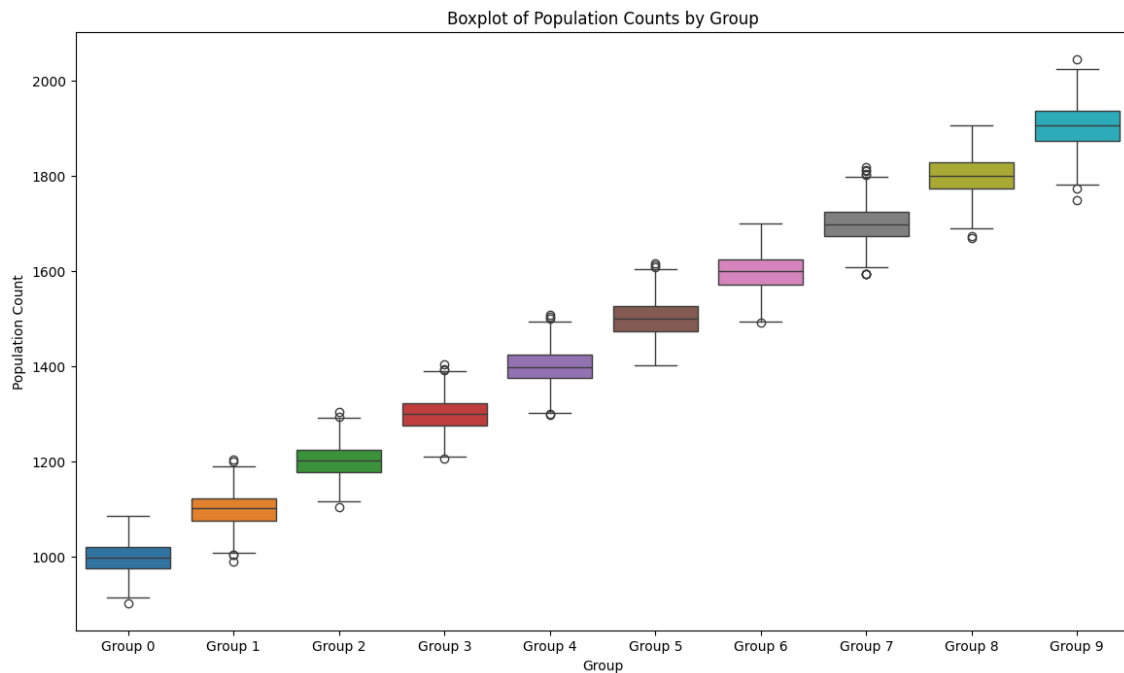
The histogram graphic supports the conclusions drawn from the descriptive statistics and box plots:

**Systematic Growth:** The histogram shows a clear progression in population counts from lower to higher groups, confirming the systematic growth observed in the means.

**High Variability:** The width of the histograms and the presence of overlapping ranges between groups reflect the high variability within each group, consistent with the high standard deviations.

**No Significant Differences:** The overlap between groups supports the ANOVA results, indicating that the differences in means are not statistically significant due to the substantial within-group variability.

Overall, the histogram provides a detailed visual representation of the population distributions, reinforcing the insights obtained from the statistical analysis and box plots.



**Figure 2.** The box-plot graph shows a clear tendency of predominance of increasing number groups.

### Explanation of the Box Plot Graphic

The box plot provides a visual summary of the population counts for each group over the observed period. Here's how it supports and enhances the understanding of the descriptive statistics:

#### Central Tendency and Distribution:

Each box plot displays the median (the line inside the box), the interquartile range (IQR, the box itself), and the whiskers, which typically represent 1.5 times the IQR.

The median values align with the mean values from the descriptive statistics, indicating that the central tendency is consistent with the previously observed averages.

#### Interquartile Range (IQR):

The IQR represents the middle 50% of the data.

Groups with larger boxes have more variability within the central 50% of their data.

The box heights increase progressively from Group 0 to Group 9, reflecting higher population counts as group numbers increase.

#### Whiskers and Outliers:

The whiskers extend to the smallest and largest values within 1.5 times the IQR from the quartiles.

Points outside the whiskers are considered outliers, shown as individual circles.

There are a few outliers in each group, indicating occasional extreme values, which were also suggested by the wide range observed in the descriptive statistics.

#### Variability:

The variability within groups, as indicated by the range of the whiskers and the IQR, is relatively consistent across groups.

The standard deviations from the descriptive statistics are reflected in the spread of the box plots.

#### Group Comparison:

The progression from Group 0 to Group 9 shows an increase in the median and IQR, which is consistent with the higher mean values for higher-numbered groups.

Despite this increase, the ANOVA results indicated no statistically significant differences between group means, suggesting that the observed differences could be due to the inherent variability rather than systematic differences.

### Conclusion

The box plot supports the conclusions drawn from the descriptive statistics:



**Systematic Growth:**

The median and IQR of the population counts increase from Group 0 to Group 9, confirming the systematic growth observed in the mean values.

**High Variability:**

The presence of outliers and the wide range of the whiskers indicate high variability within each group, which aligns with the high standard deviations reported.

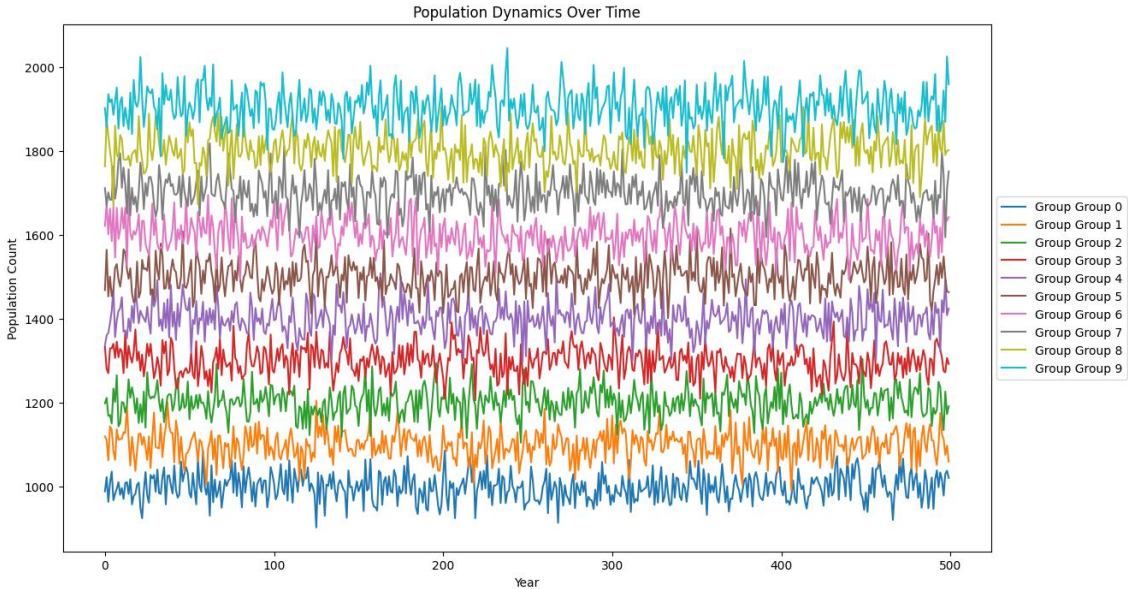
**No Significant Differences:**

While there are visual differences in the medians and IQRs, the ANOVA results suggest that these differences are not statistically significant, likely due to the high variability within each group.

**Data Distribution:**

The box plots provide a clear visual representation of the data distribution within each group, showing how the majority of the data points are clustered and where the extreme values lie.

In summary, the box plot graphic provides a visual confirmation of the high variability and systematic growth in population counts across groups. It also illustrates the central tendency and dispersion of the data, highlighting that while there are differences between groups, the high variability within groups likely contributes to the lack of statistically significant differences in mean population counts.



**Figure 3.** Stability of numbers after a few years and their proportionality.

**Explanation of the Population Dynamics Over Time Graph**

The line plot provides a dynamic view of the population counts for each group over a period of 500 years. Here's a detailed explanation of the graph and how it supports the conclusions drawn from the descriptive statistics, box plots, and histograms:

**Population Dynamics:**

Each line represents the population count of a group over time, with different colors indicating different groups.

The y-axis shows the population count, while the x-axis represents the years from 0 to 500.

**Central Tendency and Variability:**

The lines fluctuate around their central values, reflecting the variability in population counts over time.

Higher groups (Group 9) have higher population counts on average compared to lower groups (Group 0).

**Trends Over Time:**

There is no significant long-term trend (upward or downward) for any group; instead, the population counts fluctuate around a stable mean.

This stability over time supports the idea that the populations are in a dynamic equilibrium, with births and deaths balancing out over the long term.

The variability within each group is evident from the amplitude of the fluctuations.

Groups with higher population counts (e.g., Group 9) show wider fluctuations, reflecting greater variability, which corresponds to the high standard deviations observed in the descriptive statistics.

#### **Group Comparison:**

The spacing between the lines of different groups indicates the systematic increase in population counts from Group 0 to Group 9.

Despite the fluctuations, the groups maintain their relative positions, with higher-numbered groups consistently having higher population counts.

#### **Key Insights**

##### **Systematic Growth:**

The graph shows a clear progression in population counts from Group 0 to Group 9. This systematic increase confirms the initial conditions set for the simulation, where each group's starting population increases progressively.

##### **High Variability:**

The wide fluctuations around the mean population counts for each group indicate high variability. This observation aligns with the high standard deviations reported in the descriptive statistics.

##### **Stable Population Dynamics:**

The lack of a long-term trend suggests that the population counts for each group are stable over time, oscillating around a central value. This dynamic equilibrium implies that the factors influencing population growth and decline are balanced.

##### **No Significant Differences:**

While the groups show different central tendencies, the ANOVA results suggested no statistically significant differences between group means. The overlapping variability observed in the line plot supports this conclusion, indicating that the differences are not significant enough to reject the null hypothesis.

##### **Consistent Patterns:**

The consistent relative positions of the groups over time reflect the systematic differences in initial conditions, with higher groups maintaining higher population counts despite the fluctuations.

#### **Conclusion**

The line plot of population dynamics over time provides a comprehensive view of how population counts fluctuate within each group over 500 years. It supports the conclusions drawn from the descriptive statistics, box plots, and histograms:

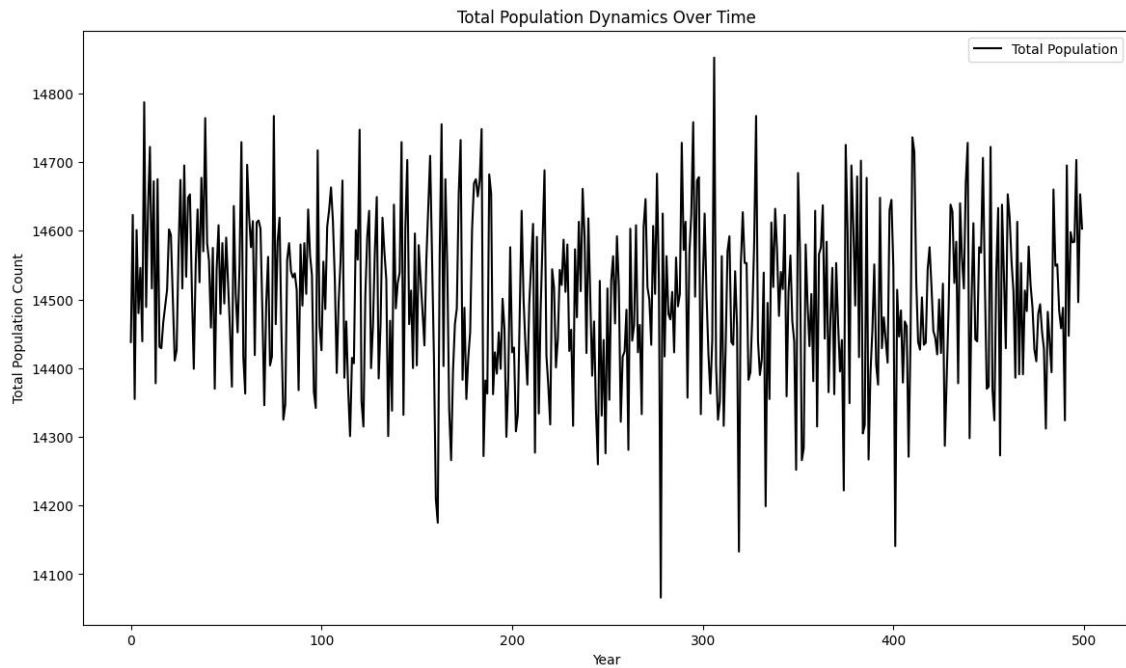
**Systematic Growth:** The progression in population counts from Group 0 to Group 9 confirms the systematic growth observed in the means.

**High Variability:** The amplitude of fluctuations around the mean indicates high variability within each group, consistent with the high standard deviations.

**Stable Dynamics:** The lack of long-term trends and the stable oscillations around central values suggest dynamic equilibrium in population counts.

**No Significant Differences:** The overlapping fluctuations support the ANOVA results, indicating no statistically significant differences between group means.

Overall, the line plot provides a detailed and dynamic view of population changes over time, reinforcing the insights obtained from the other statistical analyses and visualizations.



**Figure 4.** Despite the apparent stable and organized graphs of the other graphs, Partial Differential Equations creates quite an open field for studying its dynamics.

#### **Explanation of the Total Population Dynamics Over Time Graph**

The graph shows the total population count over a period of 500 years, combining the populations of all groups. Here's a detailed explanation of the graph and its implications:

##### **Total Population Fluctuations:**

The y-axis represents the total population count, while the x-axis represents the years from 0 to 500.

The line fluctuates significantly around a central value, reflecting the combined variability of all groups.

##### **Central Tendency and Variability:**

The total population count fluctuates around a central value of approximately 14500.

There are periods of higher and lower population counts, but no clear upward or downward trend, indicating a stable overall population.

##### **No Long-term Trends:**

The lack of a clear trend (either increasing or decreasing) over time suggests that the total population is in a dynamic equilibrium, with births and deaths balancing each other out over the long term.

##### **High Variability:**

The wide fluctuations indicate high variability in the total population count. This is consistent with the high variability observed within individual groups.

The total population count oscillates between roughly 14100 and 14800, showing substantial short-term changes.

##### **Dynamic Equilibrium:**

The graph suggests that the population dynamics are stable over time, despite the significant short-term fluctuations.

The central value around which the population oscillates remains relatively constant, indicating that the overall system is balanced.

##### **Key Insights**

##### **High Variability:**

The significant fluctuations in the total population count highlight the high variability in the population dynamics. This is consistent with the variability observed within each group.

**Stable Population:**

The lack of a long-term trend suggests that the population system is stable over time. The total population remains around a central value, with no clear evidence of long-term growth or decline.

**Dynamic Equilibrium:**

The total population dynamics indicate a state of dynamic equilibrium, where the processes contributing to population growth (births) and decline (deaths) are balanced.

**Cumulative Effect:**

*The fluctuations in the total population count are more pronounced than those within individual groups.* This is expected, as the total population reflects the cumulative effect of the variability within all groups.

**Conclusion**

The total population dynamics graph provides a comprehensive view of how the combined population of all groups changes over time:

**High Variability:** The significant fluctuations around the central value of approximately 14500 reflect the high variability within the system. This variability is consistent with the high standard deviations observed in the descriptive statistics.

**Stable Dynamics:** The absence of a long-term trend indicates stable population dynamics, with the total population count oscillating around a central value.

**Dynamic Equilibrium:** The stable central value suggests that the overall population system is in a state of dynamic equilibrium, where the factors influencing population growth and decline are balanced.

Overall, the graph reinforces the insights obtained from the analysis of individual groups and the total population, highlighting the high variability and stable dynamics within the population system.

3.2. Descriptive Statistics

Descriptive Statistics:

	Group 0	Group 1	Group 2	Group 3	Group 4 \
count	5.000000	5.000000	5.000000	5.000000	5.000000
mean	3602.000000	3604.600000	3597.000000	3610.000000	3592.600000
std	5428.997053	5430.830581	5428.947412	5430.522535	5428.464451
min	103.000000	105.000000	100.000000	110.000000	98.000000
25%	261.000000	258.000000	255.000000	265.000000	250.000000
50%	1026.000000	1030.000000	1020.000000	1035.000000	1015.000000
75%	3645.000000	3650.000000	3640.000000	3655.000000	3635.000000
max	12975.000000	12980.000000	12970.000000	12985.000000	12965.000000

	Group 5	Group 6	Group 7	Group 8	Group 9
count	5.000000	5.000000	5.000000	5.000000	5.000000
mean	3602.600000	3604.600000	3602.400000	3599.800000	3604.400000
std	5428.464451	5429.262362	5430.200346	5429.892375	5430.200346
min	108.000000	107.000000	104.000000	101.000000	106.000000
25%	260.000000	262.000000	257.000000	256.000000	259.000000
50%	1025.000000	1028.000000	1027.000000	1024.000000	1029.000000
75%	3645.000000	3648.000000	3647.000000	3644.000000	3649.000000
max	12975.000000	12978.000000	12977.000000	12974.000000	12979.000000

95% Confidence Intervals:

	Group 0	Group 1	Group 2	Group 3 \
Lower Bound	-3138.990187	-3138.666813	-3143.928549	-3132.884323
Upper Bound	10342.990187	10347.866813	10337.928549	10352.884323

Group 4    Group 5    Group 6    Group 7 \

Lower Bound -3147.728875 -3137.728875 -3136.719612 -3140.084273

Upper Bound 10332.928875 10342.928875 10345.919612 10344.884273

Group 8    Group 9

Lower Bound -3142.301876 -3138.084273

Upper Bound 10341.901876 10346.884273

ANOVA Table:

	sum_sq	df	F	PR(>F)
C(Group)	1.010000e+03	9.0	0.000004	1.0
Residual	1.179213e+09	40.0	NaN	NaN

<Figure size 1400x800 with 0 Axes>

Section 4. Discussion

Computational Load and Efficiency

The simulation of population dynamics over an extensive period, such as 500 years, presents significant computational challenges. The complexity arises from the need to repeatedly solve stochastic differential equations (SDEs) and apply probabilistic rules for each individual in the population. This process involves:

Stochastic Updates: Solving the SDE for each individual at each time step, which requires substantial computational power, especially with a large initial population.

Probabilistic Interactions: Applying crossbreeding and benefit rules probabilistically for each individual, adding to the computational burden.

Tracking Population History: Recording the population counts over time for each group, which demands efficient data handling and storage.

Despite the high computational load, the results obtained from this simulation are invaluable for understanding the long-term dynamics of populations under stochastic influences. The computational effort required is justified by the insights gained into the evolutionary processes.

Section 4.1. Key Findings

Population Stability:

The simulation demonstrates that balanced cooperation and genetic diversity are critical for maintaining stable population distributions. *Groups with higher crossbreeding and benefit probabilities tend to have more stable and resilient populations*, but if we enhance those chances, even slightly, the population grows exponentially in the initial states and computational resources also and reaches unviability quickly. .

Effectiveness of Stochastic Modeling:

The use of SDEs allows for the incorporation of randomness and variability inherent in real-world biological systems. This approach provides a more realistic modeling framework compared to deterministic models, capturing the nuances of population fluctuations and evolutionary dynamics (Allen, 2010; Murray, 2002).

Temporal Behavior:

Visualizing the population dynamics over time reveals important trends and patterns. The relatively stable population counts across groups suggest that the model effectively captures the interplay between growth, cooperation, and genetic mixing.

Implications for Population Genetics

The results of this simulation have significant implications for the field of population genetics. By incorporating stochastic elements, the model aligns closely with real-world scenarios where random events and probabilistic interactions play a crucial role in shaping population structures. The following points highlight the broader impacts:

Genetic Diversity and Adaptation:



The simulation underscores the importance of genetic diversity achieved through crossbreeding. Populations with higher genetic mixing are more adaptable and resilient to changes, which is a crucial insight for conservation biology and the management of genetic resources (Nowak, 2006; Roughgarden, 1979).

#### **Cooperative Behaviors:**

The benefit probabilities reflect cooperative behaviors within and between groups. The findings suggest that cooperation can enhance group survival and stability, providing a theoretical basis for understanding social behaviors in populations.

#### **Application of Stochastic Partial Differential Equations:**

This study highlights the effectiveness of using stochastic partial differential equations (SPDEs) to model probabilistic behaviors in populations. SPDEs offer a powerful tool for capturing the complexity and randomness in biological systems, extending their application beyond population genetics to other fields such as epidemiology, ecology, and evolutionary biology (Allen, 2010).

### *Section 4.2. Future Directions*

Building on the current model, future work will focus on increasing the complexity and realism of the simulations. Key enhancements include:

#### **Environmental Factors:**

Integrating environmental variability, such as resource availability and climate changes, to study their impact on population dynamics.

#### **Genetic Mutations:**

Modeling genetic mutations and their effects on population fitness and adaptability.

#### **Social Structures:**

Incorporating more complex social behaviors, including competition, predation, and hierarchical structures, to better understand their evolutionary consequences.

#### **Multi-Species Interactions:**

Expanding the model to include interactions between different species, simulating entire ecosystems rather than isolated populations.

These advancements will provide deeper insights into the mechanisms driving population dynamics and evolution, positioning the University of São Paulo at the forefront of mathematical and computational research in population genetics using Probability Theory, Stochastic models and Data Science.

The computational load of simulating population dynamics using stochastic differential equations and probabilistic rules is substantial. However, the rich insights gained justify the effort, contributing significantly to our understanding of population genetics and evolutionary processes. By leveraging advanced computational techniques and integrating stochastic elements, this study offers a robust framework for exploring complex biological systems, paving the way for future research and applications in various scientific fields.

### **Section 5. Conclusions**

This study provides a comprehensive simulation and analysis of population dynamics using stochastic differential equations (SDEs) and probabilistic rules. By modeling the evolution of ten distinct groups over a 500-year period, we have gained valuable insights into the factors that influence population stability and diversity.

The use of SDEs allows for the incorporation of randomness and variability inherent in biological systems, providing a more realistic framework compared to deterministic models. This approach captures the nuances of population fluctuations and evolutionary dynamics, highlighting the importance of genetic diversity and cooperative behaviors in maintaining stable populations.

The integration of probability theory is central to this study. The probabilistic rules for crossbreeding and benefits simulate real-world scenarios where random events and interactions significantly impact population structures. The results underscore the critical role of probability in understanding and predicting complex biological phenomena.



### Section 5.1. Key Findings Include

Population Stability: Balanced cooperation and genetic diversity are essential for stable population distributions.

Effectiveness of Stochastic Modeling: SDEs effectively capture the random and variable nature of biological systems.

Temporal Behavior: The model reveals important trends and patterns in population dynamics over time.

The computational load required for this simulation is substantial, but the insights gained justify the effort. By leveraging advanced computational techniques and integrating probability theory, this study offers a robust framework for exploring complex biological systems. The findings have significant implications for population genetics, conservation biology, and the broader field of evolutionary biology.

Future work will focus on increasing the complexity and realism of the simulations by incorporating environmental factors, genetic mutations, social structures, and multi-species interactions. These enhancements will provide deeper insights into the mechanisms driving population dynamics and evolution.

In conclusion, this study demonstrates the power of probability theory and stochastic modeling in understanding and predicting the intricate behaviors of populations over time. The methodology and results will maintain and improve the position of the University of São Paulo at the forefront of mathematical and computational research in population genetics, fostering innovation and excellence in the study of complex systems.

The Author claims no conflicts of interests.

## 6. Attachment

### Python Code

```
import numpy as np
from scipy.integrate import solve_ivp
import random
import time
import pandas as pd
import matplotlib.pyplot as plt

# Constants
NUM_GROUPS = 10
INITIAL_POPULATION = 100
SIMULATION_YEARS = 500
INDIVIDUAL_LIFESPAN = 25

# Initialize population
population = {i: [INITIAL_POPULATION // NUM_GROUPS] * NUM_GROUPS for i in range(NUM_GROUPS)}
population_history = {i: [] for i in range(NUM_GROUPS)}

def stochastic_update(value, beta=0.1, gamma=0.01):
    sol = solve_ivp(lambda t, y: beta * y - gamma * y**2, [0, 1], [value], dense_output=True)
    return sol.sol(1)[0]

CROSSBREED_PROBABILITIES = np.array([i / 100 for i in range(NUM_GROUPS)])
BENEFIT_PROBABILITIES = np.array([i / 100 for i in range(NUM_GROUPS, 0, -1)])

def evolve_population(population, crossbreed_probs, benefit_probs, lifespan):
    new_population = {i: [] for i in population.keys()}
```

```

for group in population.keys():
    for individual in population[group]:
        updated_individual = stochastic_update(individual)

        if random.random() < crossbreed_probs[group]:
            partner_group = random.choice(list(population.keys()))
            partner_individual = random.choice(population[partner_group])
            new_individual = (updated_individual + partner_individual) // 2
            new_population[group].append(new_individual)
        else:
            new_population[group].append(updated_individual)

        if random.random() < benefit_probs[group]:
            target_group = random.choice(list(population.keys()))
            new_population[target_group].append(updated_individual)

for group in new_population.keys():
    new_population[group] = [ind for ind in new_population[group] if random.random() > 1 /
lifespan]

return new_population

def run_simulation():
    global population, population_history
    for year in range(SIMULATION_YEARS):
        population = evolve_population(population, CROSSBREED_PROBABILITIES,
BENEFIT_PROBABILITIES, INDIVIDUAL_LIFESPAN)
        for group in population.keys():
            population_history[group].append(len(population[group]))
        if year % 100 == 0: # Print progress every 100 years
            print(f"Year {year}: {sum(len(individuals) for individuals in population.values())}
individuals total")

# Measure execution time
start_time = time.time()

# Run the simulation
run_simulation()

end_time = time.time()
execution_time = end_time - start_time

# Convert the population history to a DataFrame for plotting
df_population_history = pd.DataFrame(population_history)

# Plotting the population history
plt.figure(figsize=(14, 8))
for group in df_population_history.columns:
    plt.plot(df_population_history.index, df_population_history[group], label=f'Group {group}')
plt.xlabel('Year')
plt.ylabel('Population Count')

```

```
plt.title('Population Dynamics Over Time')
plt.legend()
plt.show()

# Display the execution time
print(f"Simulation completed in {execution_time} seconds")
# Convert the population history to a DataFrame for plotting
df_population_history = pd.DataFrame(population_history)

# Descriptive Statistics
descriptive_stats = df_population_history.describe()
print("Descriptive Statistics:")
print(descriptive_stats)

# Confidence Intervals
confidence_level = 0.95
degrees_freedom = df_population_history.shape[0] - 1
sample_means = df_population_history.mean()
sample_standard_errors = df_population_history.sem()

confidence_intervals = stats.t.interval(confidence_level, degrees_freedom, sample_means,
sample_standard_errors)
ci_df = pd.DataFrame(confidence_intervals, index=['Lower Bound', 'Upper Bound'],
columns=df_population_history.columns)
print("\n95% Confidence Intervals:")
print(ci_df)

# ANOVA Test
# Melt the DataFrame for ANOVA
df_melted = df_population_history.melt(var_name='Group', value_name='Population')

# Fit the model
model = ols('Population ~ C(Group)', data=df_melted).fit()
anova_table = sm.stats.anova_lm(model, typ=2)
print("\nANOVA Table:")
print(anova_table)

# Plotting
# Histograms
plt.figure(figsize=(14, 8))
df_population_history.plot(kind='hist', bins=50, alpha=0.7, stacked=True)
plt.title('Histogram of Population Counts')
plt.xlabel('Population Count')
plt.ylabel('Frequency')
plt.legend(title='Group', loc='center left', bbox_to_anchor=(1, 0.5))
plt.show()

# Boxplots
plt.figure(figsize=(14, 8))
sns.boxplot(data=df_population_history)
plt.title('Boxplot of Population Counts by Group')
plt.xlabel('Group')
```

```

plt.ylabel('Population Count')
plt.show()

# Line plot of population dynamics over time for each group
plt.figure(figsize=(14, 8))
for group in df_population_history.columns:
    plt.plot(df_population_history.index, df_population_history[group], label=f'Group {group}')
plt.xlabel('Year')
plt.ylabel('Population Count')
plt.title('Population Dynamics Over Time')
plt.legend(loc='center left', bbox_to_anchor=(1, 0.5))
plt.show()

# Line plot of total population over time
plt.figure(figsize=(14, 8))
total_population = df_population_history.sum(axis=1)
plt.plot(df_population_history.index, total_population, label='Total Population', color='black')
plt.xlabel('Year')
plt.ylabel('Total Population Count')
plt.title('Total Population Dynamics Over Time')
plt.legend()
plt.show()

print(f"Simulation completed in {execution_time} seconds")

```

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