

Branching Models in Practice: Tackling Real-Life Challenges Beyond Theoretical Constructs Using Python Programming

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Abstract

The mathematical modeling of branching processes finds its origin in attempts to model reproduction patterns in species. For systems with replicating and dying components (like cells or particles), branching process theory provides the mathematical tools for understanding their probabilistic progression.. They are used to describe random systems such as chain reactions, survival of family names, pest eradication, population development and gene propagation. This study showcases clear illustrations of the likelihood of extinction, the duration until extinction, and the probability related to the entire offspring. Observations of past elite families often highlight their eventual decrease, leading to myriad speculations. Through Python-based modeling, it was found that if every person, on average, yields slightly over one offspring, there is no absolute guarantee of family extinction. However, if the mean number of offspring per individual μ is one or less, the process is guaranteed to become extinct.

Keywords: Branching process; Epidemiology, Size of population; Population-dependence; Extinction time

INTRODUCTION

A branching process is a mathematical construct used primarily to describe the reproduction of individuals in a population. The framework has been exploited in various fields to study phenomena that exhibit branching-like behavior. The branching process offers a streamlined and refined approach to modeling population expansion (Abdulazeez, 2021). The Galton-Watson Process, named after the foundational correspondence between Galton and Watson highlighted by Klebaner (1985), is a cornerstone in the mathematical modeling of systems. It efficiently depicts the probabilistic behavior of entities, whether they are cells or broader organisms, as they live and reproduce before meeting their end. (Becker, 1989), (Farrington & Grant, 1999), (Haccou *et al*, 2005), (Diekmann & Heesterbeek, 2000), (Lyons & Peres, 2016).

Using the branching process model, we observe an initial particle count expand as particles birth more of their kind or different types. As this creation sequence persists, the system's progression is steered by distinct probability laws. In a branching process time is measured discretely, particles are considered to behave independently and there exist a certain probability of producing new particles (Bagley, 1986).

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The decay of the families of men who occupied conspicuous positions in past times has been a subject of frequent remark, and has given rise to various conjectures (Gonzalez & Molina,1998).

Some entities, whether they are humans, bacteria through biological processes, or even neutrons in a chain reaction, have the capability to produce more of their kind. When the original group produces offspring, they become the first generation. The subsequent generation they produce is the second, and the sequence goes on. It is essential to note that this generational process is subject to random occurrences. We have employed the simplest mathematical model to depict this situation in our work. This corresponds to the model of Galton and Watson (Hefferman; Smith. & Wahl, 2005), (Abdulazeez, 2021), (Lyons & Peres, 2016).

According to Galton (1891) in his book “Hereditary genius” he treated the different social groups (such as nobility and judges), which he ascribed the biological reasons causing reduced fertility. Based on their population's law, a percentage of adult males in each generation don't have male descendants reaching adulthood; some have one, others have two, and so on until a few have five. This poses the question: after 'r' generations, what fraction of family names would no longer exist? And how often would certain surnames appear 'm' times? The statistical intricacies of this issue remained elusive, prompting attempts with numerical samples. However, Galton's re-exploration of family extinction, inspired by De Candolle's book, brought a fresh perspective. It is noteworthy that the loss of family names and the end of family lines essentially depict the same phenomenon.

Galton thought to himself that one could compute “using the laws of probability” the percentage of family that dies out and that consequently, one should be able to determine whether or a given number of family died out because of reduced fertility (Albertsen,1995) Citing historical examples of Galton-Watson process is complicated due to the history of family names often deviating significantly from the theoretical model. New family names can arise, while current ones might undergo changes throughout an individual's life. Historically, it was not uncommon for people to take on names of unrelated individuals, especially from noble backgrounds. So, the scarcity of some surnames today does not inherently point to their extinction over generations or the eradication of family lines. For such conclusions, one must verify that there were more diverse names before and that their absence now is due to lineage endings, not other reasons for name alterations.

In the concept of branching theory, initially our focus is on monitoring the magnitude of each subsequent generation, rather than pinpointing the birth timing of individual entities or understanding their specific familial ties. Suppose we denote by X_0, X_1, X_2, \dots the number in the 0th, first, second, ... generations (we sometimes can interpret X_0, X_1, X_2, \dots as a size of population at a sequence of point in time). Furthermore, we make the following assumptions

- a) If the size of the nth generation is known, then the probability law governing the later generations does not depend on the sizes of generation preceding the nth generation. In other words, X_0, X_1, X_2, \dots is a form of Markov chain. We shall always make additional assumption that the transitional probability does not vary with time.
- b) The Markov chain considered in this context have a very special property corresponding to the assumption that different objects do not interfere with one

another. The number of children born to an object does not depend on how many objects are present.

When we think of the branching process in action, the preservation of family names often stands out as a prime example.

Surnames are passed down exclusively through male lineage. Each man yields a variable number of sons, who in turn have an unpredictable number of sons themselves. This cascade of descendants epitomizes the "branching" concept.

Lotka (1931) used the theory of branching process to address a problem of survival of family names. In attempting to mirror the offspring spread of the 1920s male American populace, he turned to the zero modified geometric distribution. Within this distribution, the chance factor that a father has j sons is:

$$P_j = bp^{j-1}, \quad j = 1, 2, 3, \dots \dots$$

Lotka assumed $b = \frac{1}{5}$ and $p = \frac{1}{2}$. Therefore the probability of having no sons is $p_0 = \frac{1}{2}$, the probability of having one son is $p_1 = \frac{1}{5}$, following this progression, the structure of the offspring probability is outlined as

$$G(s) = p_0 + p_1s + p_2s^2 + \dots + \dots = p_0 + \sum_{j=1}^{\infty} bp^{j-1}s^j = p_0 + \frac{bs}{1-ps}$$

$$= \frac{1}{2} + \frac{s}{5-3s}$$

The mean of the offspring is $m = g'(1) = \frac{5}{4} > 1$. According to the fundamental case $\mu > 1$ there is a positive probability of survival. $1 - q^N$, where N is the initial number of males, applying the fundamental theorem, the number q is a fixed point of g , that is a number such that $g(q) = q$ and $0 < q < 1$. the fixed point of g are found by solving the following equation;

$$\frac{1}{2} + \frac{q}{5-3q} = q$$

There are two solutions $q = 1$ and $q = \frac{5}{6}$ but only one solution satisfies $0 < q < 1$, namely $q = \frac{5}{6}$ and it should be noted that $q = 1$ will always be one solution to $g(q) = q$ due to one of the properties of the probability generating function, $g(1) = 1$

To address the question about the probability of survival of family, it follows that one male has a probability of $\frac{5}{6}$ that his line of descent becomes extinct and a probability of $\frac{1}{6}$, that his descendants will continue forever. The concept that families can fade away over time is deeply rooted in theory, with a significant amount of subsequent writings delving into it. Our research zeroes in on the statistical indications of family line extinctions.

METHODOLOGY

Let us assume that an individual produces a random number ξ of offspring at a given time and produce no further offspring. In turn these descendants each produce further descendants at the next subsequent time at the same chance and let

$$P(\xi = k) = P_k \quad \text{where } k = 0, 1, 2, \dots \dots \dots \quad (1)$$

be the probability mass function of the number of offsprings generated by each individual. When every individual procreates without any dependence on others, then the scenario unfolds as ξ is independently and identically distributed for each individual within a

generation time n . In the n^{th} generation, the X_n independently produce other $\xi_1^{(n)}, \xi_2^{(n)}, \dots, \xi_k^{(n)}$. Consequently, the aggregate count of individuals emerging in the $(n+1)^{\text{th}}$ generation is

$$X_{(n+1)} = \xi_1^{(n)} + \xi_2^{(n)} + \dots + \xi_k^{(n)} \dots \dots (2)$$

And this makeup the fundamental branching process equation.

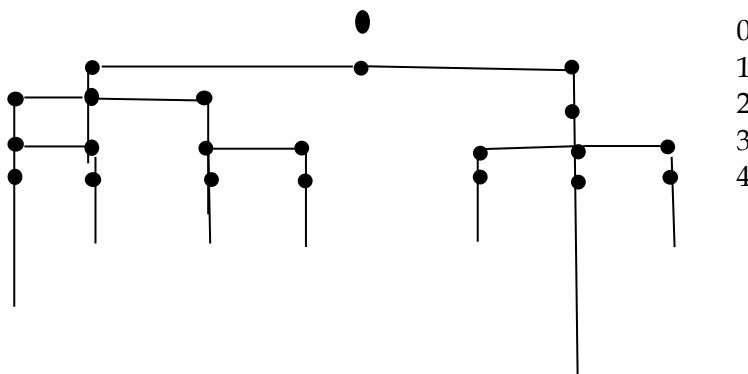


Fig 1.0 Picture of the branching process

Fig.1.0 above demonstrates the standard increase associated with the branching process. A dot indicates a birth of an individual $X_0 = 1$ implies that there is a single individual in the initial generation, $X_1 = 3$ which produces only three(3) individuals in the next generation. It shows that this continues indefinitely or until extinction.

Probability of Extinction

Let $P[X_n = 0] = q_n$ Assume $P_0 > 0$

We are interested in knowing when the population would eventually die out, that is $\lim_{n \rightarrow \infty} q_n$. If q_n is non-decreasing, $\lim_{n \rightarrow \infty} q_n = \pi$ exists and $0 < \pi \leq 1$. It follows that, π is the smallest positive root of the equation $\phi(z) = z$ ($0 < z < 1$)

It follows that

$$q_0 = 0 \quad \text{since, } P(X_0 = 1) = 1 \text{ (by assumption)}$$

$$\phi(z) = \sum_{k=0}^{\infty} P(X_n = k) Z^k \quad \text{and} \quad P(X_n = 0) = q_n$$

Since

$$\phi_{n+1}(0) = \phi(\phi_n(0)) \quad \text{and} \quad q_{n+1} = \phi q_n \quad n = 0, 1, 2, \dots \quad (3)$$

Then

$$q_1 = \phi(q_0) > 0$$

$$= \phi(0) = P_0 \quad \text{(by assumption)}$$

Now

$$q_0 = 0 \quad \text{and} \quad \text{hence } q_1 > q_0$$

Suppose $q_{n-1} < q_n$ then

Since $\phi(z)$ is increasing in z ($0 < z \leq 1$)

We have

$$\phi(q_{n-1}) \leq \phi(q_n) \quad \dots \dots \dots (4)$$

Or

$q_n \leq q_{n+1}$ by (3) and (4) hence q_n is non- decreasing in n

$$q_{n+1} = \phi(q_n) \leq \phi(1) \quad \forall \quad n = 1, 2, 3, \dots \dots \dots$$

Therefore

$$\lim_{n \rightarrow \infty} q_n = \pi \quad (\text{say}) \quad \text{exists}$$

Now $q_1 > 0$ and $q_n > 0 \quad \forall \quad n$ and $\{q_n\}$ is non-decreasing and $\pi > 0$.

We have

$$q_{n+1} = \phi(q_n) \quad \text{taking the } \lim_{n \rightarrow \infty} \quad \text{on both sides we get}$$

$$\begin{aligned} \pi &= \lim_{n \rightarrow \infty} q_{n+1} = \lim_{n \rightarrow \infty} \phi(q_n) \quad (\phi(z)) \text{ is continuous} \\ &= \phi(\pi) \end{aligned}$$

Now $\phi(z) = z \rightarrow \pi$ is positive and hence π is positive root of $\phi(z) = z$

Assume that S_0 is another positive square root of $\phi(z) = z$

Then $q_0 = 0 < S_0$ assume $q_n < S_0$ and which implies

$$q_{n+1} \leq S_0 q_{n+1} = \phi(q_n) \leq \phi(S_0) = S_0 \dots \dots \dots \quad (5)$$

$$\text{Now} \quad \phi_n(0) = P(X_n = 0) = q_n \leq 1$$

It follows that on n, $q < S_0$ for $n = 0, 1, 2 \dots$

Hence

$$\lim_{n \rightarrow \infty} q_n = \pi \leq S_0$$

therefore π is the smallest positive root of $\phi(z) = z$

To show that $\phi(z) = z$ has a real root on $0 < z < 1$ iff $\mu > 1$

$\phi(z) = z$ has only $z = 1$ as root in $0 < z < 1$ iff $\mu \leq 1$

It is known that the generating function

$$\frac{\phi(z)}{z} = \frac{P_0}{z^2} + P_1 + P_2 z + P_3 z^2 + \dots \dots + \quad (0 < z < 1)$$

Since this is a power series which is uniformly convergent

$$\begin{aligned} f'(z) &= -\frac{P_0}{z^2} + P_2 + 2P_3 z + \\ \text{and } f''(z) &= \frac{2P_0}{z^3} + 2P_3 \dots \dots \dots \quad (0 < z < 1) \\ \Rightarrow f'(z) \uparrow Z \quad \text{and} \quad f'(0+) &= -\infty \dots \dots \dots \quad (6) \end{aligned}$$

Case 1 $\mu > 1$

$$\begin{aligned} f'(1) &= -P_0 + P_2 + 2P_3 + \dots \dots + \\ f'(0) &= P_1 + 2P_2 + 3P_3 + \dots \dots + \\ &= \phi(1) > 0 \end{aligned}$$

Thus there exists $0 < \beta < 1$, such that $f'(\beta) = 0$ and which implies that $f'(z) < 0$ for $0 < z < \beta$. Hence $f'(z) \downarrow$ in z for $0 < z < \beta$ and $f'(z) \uparrow$ in z for $\beta < z < 1$

Now

$$f(1) = \frac{\phi(1)}{1} = \frac{1}{1} = 1 \qquad f(0+) = \infty \qquad \dots \qquad (7)$$

Therefore there exists $0 < a < 1$ such that $f(a) = 1$ that is $\phi(a) = a$

Case 2: $\mu \leq 1$

Since $\beta = 1$ it follows that, $f'(z) < 0$ in z for $0 < z < 1$

For $f(2) \downarrow f(0+) = \infty \qquad f(1) = 1$

Hence, there does not exist $0 < a < 1$ such that $f(a) = 1$ and hence $z = 1$ is the only root of $\phi(z) = z$

Method 1

$$P(\xi = 0) = v > 0, \quad P(\xi = 2) = \lambda > 0, \quad P(\xi = 1) = 1 - v - \lambda > 0$$

$$\text{Then } \phi(z) = v + (1 - v - \lambda)z + \lambda z^2$$

To find the solution of $\phi(z) = z$

We have

$$v + (1 - v - \lambda)z + \lambda z^2 = z$$

$$v + z - vz - \lambda z + \lambda z^2 = z$$

$$v - vz - \lambda z + \lambda z^2 = z - z$$

$$v - (v - \lambda)z + \lambda z^2 = 0$$

Thus $(z-1)(\lambda z - v) = 0 \Rightarrow z = 1 \text{ or } z = \frac{v}{\lambda}$

Then $\mu = \phi'(1) = 1 - v - \lambda + 2\lambda = 1 - v + \lambda$

Therefore $\mu > 1 \Rightarrow 1 - v + \lambda > 1 \text{ or } -v + \lambda > 0 \text{ or } \lambda > v$

Thus if $\mu > 1$, that is $\lambda > v$, the population dies out with probability of $\pi = \frac{v}{\lambda} < 1$ and if $\mu \leq 1$

That is $\lambda \leq v$, that is $\frac{v}{\lambda} > 1$

Then $\pi = 1$ that is, the population is to die out (Athreya & Ney, 1972), (Linda, 2011))

If $\mu > 1$ then with the probability π the population become extinct and with probability $1 - \pi$ the population explodes.

If $\mu \leq 1$ then with probability 1, the population becomes extinct [regardless of the actual value of the mean $E(X_1) = \mu > 1$, the probability that the n -th generation will consist of any positive finite number of individuals tend to zero as $n \rightarrow \infty$, with the probability of extinction tending to π . In this circumstance, we say that $X_n \rightarrow \infty$ as $n \rightarrow \infty$ with probability $1 - \pi$]. (Bruss, 1984)

Let T be the time till extinction (first passage time to state zero)

Then $[T = n] = [X_n = 0, X_{n-1} \neq 0]$

Hence, $P[T = n] = q_n - q_{n-1} = P[X_n = 0] - P[X_{n-1} = 0]$

$$E(T) = \sum_{n=1}^{\infty} n(q_n - q_{n-1})$$

Hence $= q_1 - q_0 + 2q_2 - 2q_1 + 3q_3 - 3q_2 + \dots +$

$$= -q_0 - q_1 - q_2 - q_3 - \dots < 0$$

This is because the series $\sum_{n=1}^{\infty} n(q_n - q_{n-1})$ is convergent in the rearrangement of the series.

Now, $\lim_{n \rightarrow \infty} q_n = \pi > 0 \Rightarrow q_n = d > 0$ therefore $\sum nq_n$ is divergent. (Lyons & Peres, 2016)

Method 2

$$\phi(z) = P_0 + P_1 Z, \quad 0 < P_0 < 1 \quad \text{and} \quad P_0 + P_1 = 1$$

then

$$\phi_2(z) = P_0 + P_1(P_0 + P_1 Z) = P_0 + P_0 P_1 + P_1^2 Z$$

thus

$$\phi_n(z) = P_0 + P_0 P_1^2 + \dots + P_0 P_1^{n-1} + P_1^n Z \quad (\text{By iteration})$$

$$= P_0 \frac{1 - P_1^n}{1 - P_1} + P_1^n Z$$

$$= P_0 \frac{1 - P_1^n}{P_0} + P_1^n Z$$

$$= (1 - P_1^n) + P_1^n Z$$

Hence

$$q_n = P(X_n = 0) = 1 - P_1^n, \rightarrow 1 \quad \text{as} \quad n \rightarrow \infty$$

Also

$$\phi(z) = Z = P_0 + P_1 Z = Z(1 - P_1) = P_0 \Rightarrow Z = 1$$

That is population will surely die out

Here

$P(T = n) = q_n = q_{n-1} = 1 - P_1^n - 1 + P_1^{n-1} = P_0 P_1^{n-1}$ that is, the population is alive with geometric distribution:

$$\begin{aligned} (T) &= \sum_{n=1}^{\infty} n P_0 P_1^{n-1} = P_0 \sum_{n=1}^{\infty} n P_1^{n-1} \\ &= P_0 \frac{1}{(1 - P_1)^2} = \frac{P_0}{(P_0)^2} = \frac{1}{P_0} \end{aligned}$$

The aggregate of descendants amounts to $Y_{\infty} = \sum_{n=0}^{\infty} z_n$ from the extinction likelihood

$$P(Y_{\infty} < \infty) = q$$

and putting $Y_n = \sum_{k=0}^n z_k$

We obtained,

$$(Y_n) = \frac{1 - \mu^{n+1}}{1 - \mu} \quad \text{if} \quad \mu \neq 1$$

and if $\mu = 1$

$$E(Y_n) = n + 1$$

If $P_{jk} = P(Z_{nb+1} = k | Z_n = j)$ then verily, it can be shown that for any $j \leq k$

$$P(Y_{\infty} = k) = \frac{j}{k} P_{K, k-j}$$

Here is the python program that simulates and models the branching processes

```
import random
```

```
def simulate_spread(initial_infected, generation_limit, reproduction_number):
```

```
    """ Simulates the spread of a disease using a simple branching process model.
```

```
        :param initial_infected: Initial number of infected individuals.
```

```
        :param generation_limit: Limit to the number of generations to simulate.
```

```
        :param reproduction_number: Expected number of people an infected person will infect.
```

```

:return: List of number of infected individuals for each generation.
"""
generations = [initial_infected]
for i in range(generation_limit):
    new_infected = sum([random.poisson(reproduction_number) for _ in
range(generations[-1])])
    if new_infected == 0:
        # Disease has died out.
        break
    generations.append(new_infected)
return generations
if __name__ == "__main__":
    initial_infected = 1
    generation_limit = 10
    reproduction_number = 1.5
    result = simulate_spread(initial_infected, generation_limit, reproduction_number)
    for gen, num_infected in enumerate(result, 1):
        print("Generation {gen}: {num_infected} infected individuals.")

```

This program models the disease spread using a branching process. Starting with an initial infected individual, it simulates how many new people get infected in each generation. It assumes that the number of people each infected individual infects follows a Poisson distribution centered around a given reproduction number. Upon running the program, it displays the count of affected persons in each generation until either the ailment ceases or the generation cap is met. Adjusting the '**reproduction number**' helps us understand the impact of varying disease transmissibility levels.

RESULTS AND DISCUSSION

Illustration 1

Ponder upon a male progenitor whose reproductive capacity is limited to birthing a maximum of two male descendants in his lifetime. We only consider male offspring based on the fact that family names are maintained by sons only. The probabilities of the male offspring produced are as follows:

Likelihood of having no male is: $P_0 = 0.1$

Likelihood of having one male is: $P_1 = 0.6$

Likelihood of having two males is: $P_2 = 0.3$

and

$$\sum_{k=0}^2 P_k = P_0 + P_1 + P_2 = 0.1 + 0.6 + 0.3 = 1$$

The likelihood of extinction in each generation is given by

$$q_n = P_0 + P_1 q_{n-1} + P_2 (q_{n-1})^2$$

With $q = 0$, here the extinction probability is calculated from generation one (X_1) to generation 30 (X_{30})

$$P(X_1) = 0.1 + 0.6(0) + 0.3(0)^2 = 0.1$$

$$P(X_2) = 0.1 + 0.6(0.1) + 0.3(0.1)^2 = 0.163$$

$$P(X_3) = 0.1 + 0.6(0.163) + 0.3(0.163)^2 = 0.2058$$

$$\dots$$

$$P(X_{28}) = 0.1 + 0.6(0.3328) + 0.3(0.3328)^2 = 0.3329$$

$$P(X_{29}) = 0.1 + 0.6(0.3329) + 0.3(0.3329)^2 = 0.3330$$

$$P(X_{30}) = 0.1 + 0.6(-0.3330) + 0.3(0.3330)^2 = 0.3$$

Table 1

GENERATION	PROBABILITY OF EXTINCTION	GENERATION	PROBABILITY OF EXTINCTION
1	0.1	16	0.3277
2	0.163	17	0.3288
3	0.2058	18	0.3297
4	0.2063	19	0.3304
5	0.2584	20	0.331
6	0.2751	21	0.3315
7	0.2878	22	0.319
8	0.2975	23	0.3322
9	0.3053	24	0.3324
10	0.3111	25	0.3326
11	0.3157	26	0.3327
12	0.3193	27	0.3328
13	0.3222	28	0.3329
14	0.3245	29	0.3330
15	0.3263	30	0.3331

Hence, the likelihood of extinction q_n is non- decreasing and as n increases, it tends to one (1) or the probability of extinction tends to the ultimate probability of extinction as time goes on. It can be concluded that all families are to die out as stated by the earlier pioneers of branching process (Karlin & Kaplan, 1973), (Hull, 1982), (Alsmeyer & Osler, 2002), (Gonzalez, 2009).

Illustration 2

From example 1, suppose we let the probability for the number of offspring to be as follows:

Likelihood of having no son (male offspring) is $P_0 = 0.2$

Likelihood of having one male offspring is $P_1 = 0.5$

Likelihood of having two male offspring is $P_2 = 0.3$

and $\sum_{k=0}^2 p_k = 0.2 + 0.5 + 0.3 = 1$

Then the likelihood of extinction would be given by

$$q_n = P_0 + P_1 q_{n-1} + P_2 (q_{n-1})^2$$

With $q_0 = 0$.

In this case we would consider calculating the probability of extinction from generation one (X_1) to generation 20 (X_{20})

$$P(X_1) = 0.2 + 0.3(0) + 0.5(0)^2 = 0.2$$

$$P(X_2) = 0.2 + 0.3(0.2) + 0.5(0.2)^2 = 0.28$$

$$\dots$$

$$P(X_{17}) = 0.2 + 0.3(0.3994) + 0.5(0.3994)^2 = 0.3996$$

$$P(X_{18}) = 0.2 + 0.3(0.3996) + 0.5(0.3996)^2 = 0.3997$$

$$P(X_{19}) = 0.2 + 0.3(0.3997) + 0.5(0.3997)^2 = 0.3998$$

$$P(X_{20}) = 0.2 + 0.3(0.3998) + 0.5(0.3998)^2 = 0.3999$$

Table 2

GENERATION	PROBABILITY OF EXTINCTION	GENERATION	PROBABILITY OF EXTINCTION
1	0.2	11	0.3962
2	0.28	12	0.3973
3	0.3232	13	0.3981
4	0.3492	14	0.3987
5	0.3657	15	0.3991
6	0.3766	16	0.3994
7	0.3839	17	0.3996
8	0.3889	18	0.3997
9	0.3923	19	0.3998
10	0.3946	20	0.3999

Thus by inspection, the probability of extinction q_n is non-decreasing and as n increases it tends to 1 as time goes on. It follows that all family names are to die out in the long run. This result is in line with the generalization of the classical branching process which is used to describe the evolution of population size at each generation.

CONCLUSION

This kind of model proves instrumental in addressing various practical problems. The odds of it fading away hinge significantly on the value of μ , dictating the certainty with which the branching process will terminate. This will ensure that the branching process will die out with probability one. The assurance is such that the likelihood of dying out is firmly less than one. If the mean number of offspring per individual is more than 1, then generally speaking, individuals produce a bit more than just a replacement for themselves and the termination of the branching process is not assured. Yet, when considering the average number of descendants per individual, where μ is one or less, the process is guaranteed to become extinct.

This research solidifies the idea that the branching process is a potent method for handling unpredictable real-life situations. As such, it is recommended for tasks like modeling cell growth, understanding family name extinction, or examining nuclear reactions. It offers a fitting framework for a range of real-world problems.

REFERENCES

- Abdulazeez, S.A (2021). Application of Branching Process Modelling to Solve Real Life Challenges .*Lapai Journal of Applied and Natural Sciences (LAJANS)* VOL. 6(1), 101 - 107
- Albertsen, K. (1995). Extinction of family,. *International Statistical Institute (ISI)*,2, 234-239
- Alsmeyer, G., R & Osler, U.(2002). Asexual versus promiscuous bisexual Galton-Watson processes: the extinction probability ratio, *Annals of Applied Probability* **12**,125 142.
- Athreya, K.B. & Ney, P.E. (1972). *Branching Processes*; Springer-Verlag: Berlin, Germany.
- Bagley, J. H.(1986). On the asymptotic properties of a supercritical branching process, *Journal of Applied Probability*. **23**, 820 - 826.
- Becker, N.G (1989). *Analysis of Infectious Disease Data*; Chapman and Hall/CRC Press: Boca Raton, FL,USA.

- Bruss, F.T.(1984). A note on extinction criteria for bisexual Galton-Watson processes, *Journal of Applied Probability* **21**, , 915 - 919.
- Diekmann.O & Heesterbeek, J. A. P. (2000). *Mathematical Epidemiology of Infectious Diseases. Model Building, Analysis and Interpretation*; Wiley Series in Mathematical and Computational Biology. John Wiley, Ltd.: Chichester, UK.
- Farrington, C.P. & Grant, A.D.(1999). The distribution of time to extinction in subcritical branching processes: Applications to outbreaks of infectious disease. *Journal of Applied Probability.*, **36**, 771-779.
- Galton, F. (1891). *Hereditary genius* Second American edition. New York: Appleton and Co.
- Gonzalez, M. & Molina, M.(1998). On the partial and total progeny of a bisexual Galton - Watson branching process, *Applied Stochastic Models in Data Analysis* **13**,225- 232.
- Gonzalez, M., Molina, M. & Mota, M.(2000). Limit behavior for a subcritical bisexual Galton-Watson branching process with immigration, *Statistics and Probability Letters* **49**, 19 - 24.
- Haccou, P., Jagers, P. & Vatutin, V.A. (2005) . *Branching Processes Variation, Growth, and Extinction of Populations*; Cambridge Studies in Adaptive Dynamics: Cambridge, UK.
- Hefferman; J.M., Smith, R.J. . & Wahl, L M. (2005) . Perspectives on the basic reproductive ratio. *Journal of Royal Statistical Society*, , **2**, 281-293.
- Hull, D.M.(1982). A necessary condition for extinction in those bisexual Galton-Watson branching processes governed by super additive mating functions, *Journal of Applied Probability.* **19**, 847 - 850.
- Karlin, S. & Kaplan, N.(1993) . Criteria for extinction of certain population growth processes with interacting types, *Advanced Applied Probability* **5**, 183 - 199.
- Klebaner, F.C.(1985). A limit theorem for population-size-dependent branching processes, *Journal of Applied Probability* **22**, 48 - 57.
- Linda J.S(2011) : *An Introduction to Stochastic Processes with Applications to Biology*. 2nd Edition. CRC Press. New York
- Lotka, A.J.(1931). The extinction of families-I. *Journal of Washington Academy. Science* **21**, 377 - 380.
- Lyons R. & Peres Y.(2016). *Probability on trees and networks. Cambridge Series in Statistical and Probabilistic Mathematics.* **4**, 22 - 37
- Medhi, J.(2009): *Stochastic Processes*, New Age International Publishers, New Delhi