



BRANCHING PROCESS MODELLING: A TOOL FOR DECIPHERING COMPLEX REAL-WORLD PHENOMENA USING R PROGRAMMING

Abdulazeez, Sikiru Adeyinka

Department of Mathematical Sciences, Kaduna State University, Kaduna..Kaduna State, Nigeria

*Corresponding authors' email: ysabdu194@gmail.com

ABSTRACT

The reproduction of organisms such as human beings, cells or neutrons can be modeled via branching processes. The theory of branching processes offers suitable mathematical models to depict the chance-based progression of systems, where elements like cells, particles, or general individuals replicate and perish over a certain lifespan. These models are employed to illustrate stochastic systems like chain reactions, lineage continuation of surnames, elimination of pests, population growth, and gene spread. This study clearly showcases the likelihood of extinction, its timing, and the odds of complete offspring through vivid examples. The decline of prominent families from history has often been observed and has sparked numerous speculations. The branching process is a very useful tool in many real life problems (non-deterministic problems) and random phenomenon. Research indicates that when the average number of descendants for each entity exceeds 1 (meaning individuals reproduce at a rate slightly higher than self-replacement), the branching process doesn't necessarily cease. On the other hand, if this average number is 1 or lower, the process will inevitably face extinction.

Keywords: Branching process, Mathematical Modelling Population-dependence, Extinction time, R Programming

INTRODUCTION

Branching processes have been deeply entrenched in the modeling of numerous phenomena across disciplines. It originated in biology, tracing their roots to the study of family names and the probabilities of them dying out (Galton & Watson, 1874). From there, the model has branched out to a myriad of applications. The branching process is a straightforward yet sophisticated model for understanding population expansion. Often referred to as the Galton-Watson Process, its name and initial theoretical findings can be traced back to the letters exchanged between Sir Francis Galton and Reverend Henry William Watson Klebaner (1985). In its simplest form, a branching process deals with entities that reproduce or "branch" into multiple other entities. In population genetics, Branching processes can model the number of copies of a particular allele (or gene variant) within a population. Understanding how certain alleles proliferate or diminish is crucial for studying evolutionary dynamics and predicting future genetic makeup. The theory of branching processes offers mathematical models aptly tailored to depict the chance-driven progression of systems. In these systems, components—be they cells, particles, or individuals at large—multiply and then perish after a certain lifespan (Becker, 1989; Farrington & Grant, 1999; Haccou, Jagers & Vatutin, 2005; Diekmann & Heesterbeek, (2000), Lyons & Peres (2016)).

A branching process starts with a set number of particles, which give rise to more particles, either of the same or different kind. These newly formed particles, in turn, generate others, with the system's growth being guided by specific probability rules. In this process, time is marked in discrete units, each particle acts independently, and there's a defined likelihood that they will produce additional particles (Bagley, 1986; Abdulazeez, 2021).

The decline of prominent families from historical times has often been noted and has led to a myriad of speculations (Gonzalez & Molina, 1998).

There are objects that can generate additional objects of the same kind; these could be men or bacteria reproduced by

familiar biological methods or neutrons in a chain reaction. An initial set of objects which we call the 0th generation have children that are called the first generation: their children are the second generation and so on. The process is affected by chance event. In this work, we choose the simplest possible mathematical description of such a situation corresponding to the model of Galton and Watson (Hefferman; Smith & Wahl, 2005, Lyons & Peres (2016)).

According to Galton (1891) in his book "Hereditary genius" he treated the different social groups (such as nobility and judges). He attributed the decline to biological factors that led to decreased fertility. According to their population law, in each generation a certain percentage of adult males don't have male offspring who survive to adulthood, some have one, others have two, and a few might have up to five. How many surnames would vanish after r generations? And how many times would a particular surname be shared by m individuals? The statistical complexity of the issue was ambiguous, prompting them to delve into specific numerical examples. However, upon encountering De Candolle's book, Galton felt compelled to re-examine the family extinction issue and approach it from a fresh perspective. It's worth noting that the fading of family names and the extinction of families essentially describe the same phenomenon.

Galton believed that through the principles of probability, one could calculate the proportion of families that become extinct. Therefore, it should be possible to ascertain if a specific number of families faded away due to decreased fertility (Albertsen, 1995)

Using historical instances to illustrate the Galton-Watson process is challenging since the evolution of family names often diverges from the theoretical model. Notably, new surnames can emerge, individuals might change their names during their lives, and historically, many have adopted the names of unrelated figures, especially from the aristocracy. Hence, having only a few surnames today doesn't necessarily indicate the extinction of names over the years. To draw such a conclusion, there should be evidence that a greater variety of names existed in the past and their reduction was primarily

due to the end of lineage, rather than name changes for other reasons Iglehart, (1976).

In the concept of branching theory, first we keep track of the size of the successive generation not the time which individual objects are born or their individual family relationships. 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 examined in this scenario possesses a unique characteristic. This stems from the presumption that different objects don't influence each other: the quantity of offspring an object produces isn't affected by the number of objects currently present.

A typical example of the application of the branching process pertains to the endurance of family surnames.

Only sons inherit family names. Throughout his life, a man may have a varied number of male descendants. These sons, in turn, have a random number of male children in following generations. This succession of descendants is what we refer to as branching.

Lotka (1931) used the theory of branching process to address a problem of survival of family names. The following is his approach;

He used a zero-modified geometric distribution to align with the offspring pattern of the American male population from the 1920s. In this distribution, the likelihood that a father has 'j' sons is described as:

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

Lotka assumed $b = \frac{1}{5}$ and $p = \frac{1}{2}$ Hence, the likelihood of not having any sons is $p_0 = 1/2$, The likelihood of having a single son is $p_1 = 1/5$ and so on. Consequently, the offspring probability takes the subsequent shape

$$G(s) = p_0 + p_1s + p_2s^2 + \dots$$

$$= p_0 + \sum_{j=1}^{\infty} bp^{j-1}s^j = p_0 + bs / (1 - ps)$$

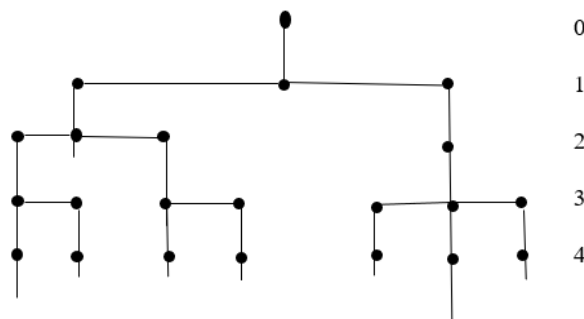


Figure 1: Picture of the branching process

Figure 1 above illustrates the general growth in branching process. A dot indicates a birth of an individual $X_0 = 1$ implies that there is one individual in the initial generation, $X_1 = 3$ which produces three (3) individuals in the next generation. Thus it continues indefinitely or until extinction. Linda (2011)

Probability of Extinction

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

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

The average number of offspring is $m = g'(1) = 5/4 > 1$.

Based on the primary scenario $\mu > 1$ there's a favorable chance of survival. $1 - q^N$, where N is the initial count of males and using the primary theorem, the figure is 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 $q = 5/6$ but only one solution satisfies $0 < q < 1$, namely $q = 5/6$ and it should be observed that $q = 1$ there will invariably be a single solution to $g(q) = q$ owing to a characteristic of the probability generating function., $g(1) = 1$

To answer the query regarding the likelihood of a family's continuity, it's evident that a single male has a probability of $5/6$ meaning his lineage comes to an end, and there's a probability of $1/6$, indicating that his lineage will persist indefinitely. The concept that families become extinct stems from theoretical foundations, and extensive literature has been produced on this issue. This study primarily focuses on the statistical indications related to family extinction.

MATERIALS AND METHODS

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 $P(\xi = k) = P_k$ where $k = 0, 1, 2, \dots$ (1)

be the probability mass function of the number of offsprings generated by each individual. If every individual independently produces descendants, then ξ is uniformly and independently distributed for each person within a generational span n. In the nth generation, the X_n independently produce other $\xi_1^{(n)}, \xi_2^{(n)}, \dots, \xi_k^{(n)}$ and consequently, the cumulative count of individuals generated in the (n+1)th generation is

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

And this makeup the fundamental branching process equation.

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 $0 < \pi \leq 1$. Moreover, π is the smallest positive root of the equation $\varphi(z) = z$ ($0 < z < 1$) It follows that

$q_0 = 0$ since $P(X_0 = 1) = 1$ (by assumption)

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

Since

$$\varphi_{n+1}(0) = \varphi(\varphi_n(0)) \text{ and } q_{n+1} = \varphi q_n, n = 0, 1, 2, \quad (3)$$

Then

$$q_1 = \varphi(q_0) > 0 \\ = \varphi(0) = P_0 \text{ (by assumption)}$$

Now

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

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

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

We have

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

Or

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

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

Therefore

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

Now

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

We have

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

$$\pi = \lim_{n \rightarrow \infty} q_{n+1} =$$

$$\lim_{n \rightarrow \infty} \varphi(q_n) = \varphi(\pi) \text{ (since } \varphi \text{ is continuous) } = \varphi(\pi)$$

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

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

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

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

Now $\varphi_n(0) = P(X_n = 0) = q_n \leq 1$

By building upon $n, q < S_0$ for $n = 0, 1, 2, \dots$

Hence

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

therefore π is the minimum positive root of $\varphi(z) = z$

To show that $\varphi(z) = z$ has a real root on $0 < z < 1$

iff $\mu > 1$

$\varphi(z) = z$ has only $z = 1$ as root in $0 < z < 1$

iff $\mu \leq 1$

It is known that the generating function

$$\frac{\varphi(z)}{z} = \frac{p_0}{z^2} + P_1 + P_2 z + P_3 z^2 + \dots + (0 < z < 1)$$

Since this is a power series which is uniformly convergent

$$f'(z) = -\frac{P_0}{z^2} + P_2 + 2P_3 z +$$

$$\text{and } f''(z) = \frac{2P_0}{z^3} + 2P_3 \dots (0 < z < 1)$$

$$\Rightarrow f'(z) \uparrow \text{ and } f''(0+) = -\infty \quad (6)$$

Case 1 $\mu > 1$

$$f'(1) = -P_0 + P_2 + 2P_3 + \dots +$$

$$f'(0) = P_1 + 2P_2 + 3P_3 + \dots +$$

$$= \varphi(1) > 0$$

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

$$f(1) = \frac{\varphi(1)}{1} = \frac{1}{1} = 1 \quad f(0+) = \infty. \quad (7)$$

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

Case 2: $\mu \leq 1$

Since $\beta = 1$ hence $f'(z) < 0$ in z for $0 < z < 1$

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

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

Method 1

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

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

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

We have

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

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

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

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

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

$$\text{Then } \mu = \varphi'(1) = 1 - v - \lambda + 2\lambda = 1 - v + \lambda$$

Therefore $\mu > 1 \Rightarrow 1 - v + \lambda > 1$ or $-v + \lambda > 0$ 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)

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

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

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

Hence

$$E(T) = \sum_{n=1}^{\infty} n(q_n - q_{n-1}) \\ = q_1 - q_0 + 2q_2 - 2q_1 + 3q_3 - 3q_2 + \dots \\ = -q_0 - q_1 - q_2 - q_3 - \dots < 0$$

This is because the series $\sum_{n=1}^{\infty} n(q_n - q_{n-1})$ is convergent in the rearrangement of the series Abdulazeez (2022).

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

Method 2

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

then

$$\varphi_2(z) = P_0 + P_1(P_0 + P_1 z) = P_0 + P_0 P_1 + P_1^2 z$$

thus

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

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

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

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

Hence

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

Also

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

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:

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

The entire lineage amounts to $Y_{\infty} = \sum_{n=0}^{\infty} Z_n$ from the extinction probability $P(Y_{\infty} < \infty) = q$

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 R program that simulates and models the branching processes

```
simulate_spread<- function(initial_infected, generation_limit, reproduction_number) {
  # Simulates the spread of a disease using a simple branching process model.
  #
  # Args:
  #   initial_infected: Initial number of infected individuals.
  #   generation_limit: Limit to the number of generations to simulate.
  #   reproduction_number: Expected number of people an infected person will infect.
  # Returns:
  #   Vector of number of infected individuals for each generation.
  generations <- c(initial_infected)

  for (i in 1:generation_limit) {
    new_infected<- sum(rpois(generations[length(generations)], reproduction_number))

    if (new_infected == 0) {
      # Disease has died out.
      break
    }

    generations <- c(generations, new_infected)
  }

  return(generations)
}
# Main execution
initial_infected<- 1
generation_limit<- 10
reproduction_number<- 1.5

result <- simulate_spread(initial_infected, generation_limit, reproduction_number)

for (gen in 1:length(result)) {
  cat(sprintf("Generation %d: %d infected individuals.\n", gen, result[gen]))
}
```

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.

When the program is executed, it will show the number of infected individuals in each generation until the disease dies out or until the generation limit is reached. Adjusting the reproduction_number allows us to see the effects of diseases with different contagious levels.

RESULTS AND DISCUSSION

Illustration 1

Consider a parent (male) that can produce a maximum of two male descendants in his lifetime. We focus solely on male descendants since family names are carried forward by sons.

The associated probabilities for the production of male offspring are:

$$\text{Probability of having no male is: } P_0 = 0.1$$

$$\text{Probability of having one male is: } P_1 = 0.6$$

$$\text{Probability of having two males is: } P_2 = 0.3$$

and

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

The probability 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})

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

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

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

$$\dots \quad \dots \quad \vdots \quad \dots \quad \dots \quad \dots \quad \dots$$

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

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

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

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 probability 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, Molina & Mota 2000)

$n \rightarrow \infty \quad q_n = 1$

Illustration 2

The state of the branching process at time n is z_n , where each z_n can take values $0, 1, 2, 3, \dots$. Note that $z_0 = 1$ always. z_n represents the size of the population at time n . Suppose we let the probability for the number of offspring to be as follows:

Likelihood of not having a 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 Likelihood of extinction from generation one (X_1) to generation 10 (X_{10})

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

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

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

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

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

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

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.

CONCLUSION

While branching processes provide a robust tool for modeling, it is essential to be aware that certain assumptions must be strictly adhered to. Assumptions such as homogeneous populations or constant branching probabilities might not hold true in complex real-world situations. Also, the model may not capture long-term behavior accurately, especially when external factors play a significant role.

A model of this sort is found useful in many real life problems. The Likelihood of extinction depends extensively on the value of μ which ensures that the branching process will die out with probability 1. There are values of μ that guarantee that the probability of extinction will be strictly less than 1. If the average number of offspring per individual is more than 1 (that is, on average, if individuals replace themselves with a bit extra), then the branching process is not guaranteed to die out. Yet, if the average offspring count for each individual is $\mu \leq 1$ or less, the process is certain to face extinction.

Based on the outcome of this research, it is established that non-deterministic real life problems can be tackled using branching process. Branching process is thus recommended

to serve as a suitable tool in solving problems such as: cell division, family extinction and nuclear chain reaction. It may be used to fit appropriate models for various real life problems.

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