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# Multi-type branching process approximation to CTMC

MATH 8xyz – Lecture 24

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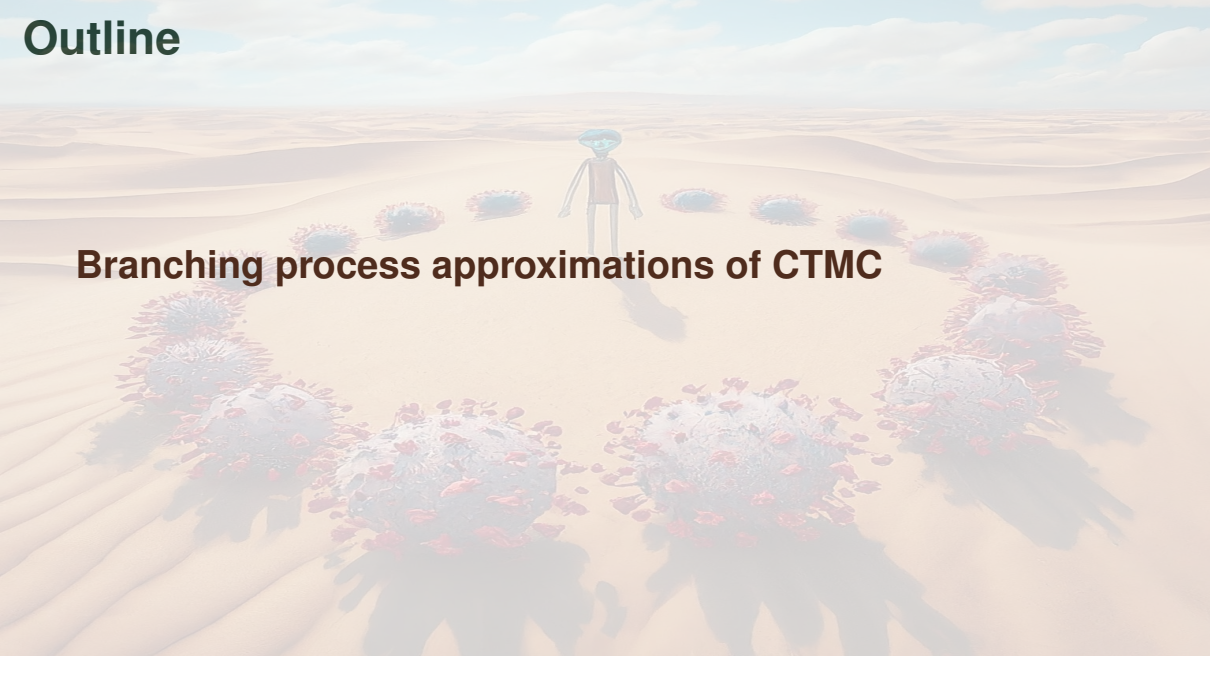
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**Winter 20XX**

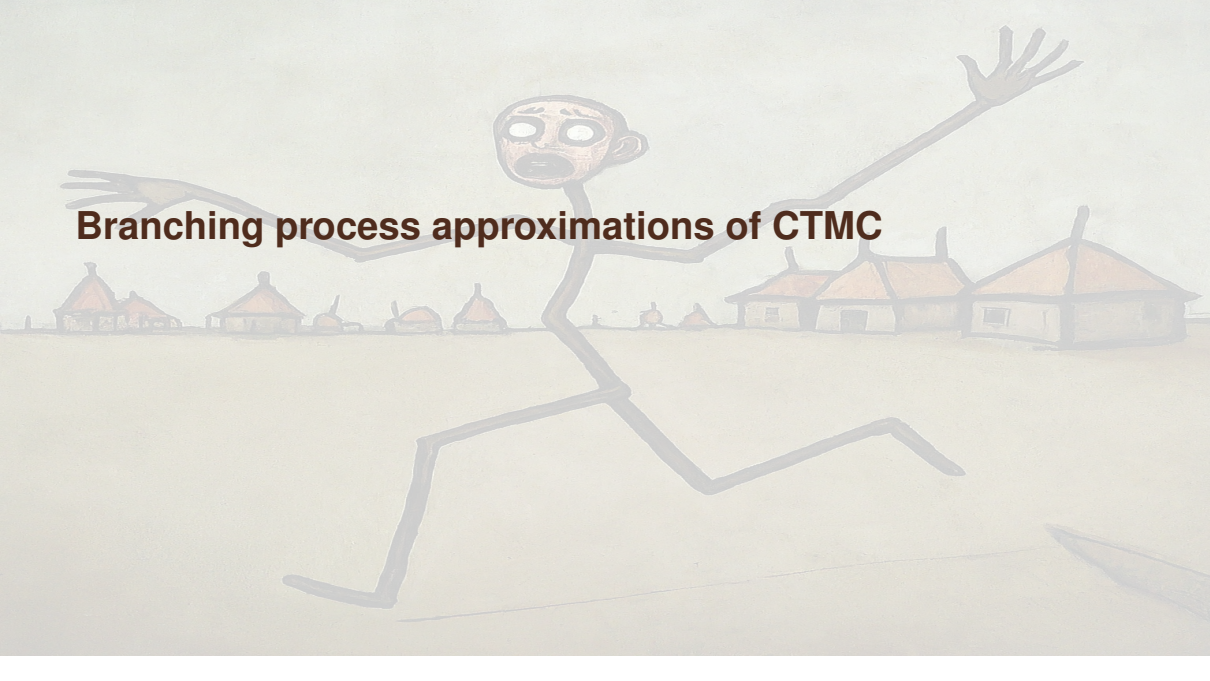
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# Outline

**Branching process approximations of CTMC**



# Branching process approximations of CTMC



# What is a Branching Process?

## The Core Idea

A branching process is a mathematical model for a population where individuals produce a random number of offspring and then die.

- ▶ Think of bacteria splitting, a virus spreading, or even the survival of family surnames.
- ▶ We start with an initial population,  $Z_0$ .
- ▶ Each individual in generation  $n$  produces a number of offspring for generation  $n + 1$ .
- ▶ This "number of offspring" is a random variable. All individuals produce offspring according to the same probability distribution, independently of each other.

# The Galton-Watson Process

Let  $Z_n$  be the size of the population in generation  $n$ . We typically start with  $Z_0 = 1$ . The population evolves according to the rule:

$$Z_{n+1} = \sum_{i=1}^{Z_n} X_{n,i}$$

- ▶ The term  $X_{n,i}$  represents the number of offspring produced by the  $i$ -th individual in generation  $n$ .
- ▶ The variables  $\{X_{n,i}\}$  are assumed to be **independent and identically distributed (i.i.d.)** integer-valued random variables.
- ▶ We call their common distribution  $\{p_k\}_{k=0}^{\infty}$  the **offspring distribution**, where  $p_k = P(X = k)$ .

## The Fundamental Questions

1. What is the long-term expected size of the population?
2. What is the probability that the population eventually dies out?

# Mean Offspring

The fate of the population hinges on a single parameter: the mean of the offspring distribution

$$\mu = E[X] = \sum_{k=0}^{\infty} k \cdot p_k$$

## Expected Population Size

Using the law of total expectation, we find the expected size of the next generation:

$$E[Z_{n+1}|Z_n] = E\left[\sum_{i=1}^{Z_n} X_{n,i} \middle| Z_n\right] = Z_n E[X] = Z_n \mu$$

Taking the expectation again, we get a simple recurrence:

$$E[Z_{n+1}] = \mu E[Z_n]$$

# The Three Regimes of Population Growth

The behavior of  $E[Z_n] = Z_0\mu^n$  suggests three distinct cases:

## Subcritical ( $\mu < 1$ )

$E[Z_n] \rightarrow 0$ . The population is expected to shrink. It goes extinct with probability 1.

## Critical ( $\mu = 1$ )

$E[Z_n] = Z_0$ . The population is expected to remain stable. Surprisingly, it still goes extinct with probability 1.

## Supercritical ( $\mu > 1$ )

$E[Z_n] \rightarrow \infty$ . The population is expected to grow exponentially. It has a non-zero probability of surviving forever.

# Tool: The Probability Generating Function

To find the extinction probability, we need a powerful tool: the **probability generating function (PGF)** of the offspring distribution  $X$ .

$$G(s) = E[s^X] = \sum_{k=0}^{\infty} p_k s^k \quad \text{for } |s| \leq 1$$

## Key Properties

- ▶  $G(1) = \sum p_k = 1$
- ▶ The mean can be found from the derivative:  $G'(1) = \sum k p_k = \mu$ .
- ▶ The PGF of  $Z_n$  is the  $n$ -th iterate of  $G(s)$  with itself. If  $G_n(s)$  is the PGF of  $Z_n$ , then  $G_{n+1}(s) = G(G_n(s))$ .



## The Extinction Probability Equation

Let  $\pi_0$  be the probability of eventual extinction, starting with  $Z_0 = 1$ .

$$\pi_0 = P(\text{population dies out}) = \lim_{n \rightarrow \infty} P(Z_n = 0)$$

Since  $P(Z_n = 0) = G_n(0)$ , and  $G_{n+1}(0) = G(G_n(0))$ , in the limit the extinction probability  $\pi_0$  must satisfy the equation:

$$\pi_0 = G(\pi_0)$$

### Theorem 1

*The extinction probability  $\pi_0$  is the **smallest non-negative solution** to the equation  $s = G(s)$ .*

- ▶ If  $\mu \leq 1$ , the only solution in  $[0, 1]$  is  $s = 1$ . So  $\pi_0 = 1$ .
- ▶ If  $\mu > 1$ , there is a unique solution in  $[0, 1)$ , which is the extinction probability  $\pi_0 < 1$ .

# From Discrete to Continuous Time

## Limitation of Galton-Watson

Generations don't happen in synchronized steps in the real world. Individuals give birth and die at random times.

This leads us to **Continuous-Time Markov Chains (CTMCs)**.

- ▶ The state of the system is the population size,  $k \in \{0, 1, 2, \dots\}$ .
- ▶ Instead of generations, we have transition rates:
  - ▶  $\lambda_k$ : rate of birth when population is size  $k$  (moves to  $k + 1$ ).
  - ▶  $\delta_k$ : rate of death when population is size  $k$  (moves to  $k - 1$ ).
- ▶ Often, we assume these rates are linear:  $\lambda_k = k\lambda$  and  $\delta_k = k\delta$ . This means individuals act independently.

# Branching Process Approximation of a CTMC

## The Key Insight

At the beginning of an outbreak (or for a very large population), the dynamics caused by a single individual are largely independent of others.

This allows us to approximate the start of a CTMC population process with a branching process.

### Example: A Simple Epidemic (SIR Model)

- ▶  $S$ : Susceptible,  $I$ : Infected,  $R$ : Recovered.
- ▶ An infected person meets others at a certain rate. If they meet a susceptible, a new infection may occur (an "offspring").
- ▶ The infected person recovers (or dies) at another rate, ending their infectious period.
- ▶ **Question:** How many new infections does a single infected person cause on average?

## Case Study: The Basic Reproduction Number $\mathcal{R}_0$

Consider a single infected individual in a large population of susceptibles.

- ▶ Let  $\beta$  be the infection rate (rate of producing "offspring").
- ▶ Let  $\gamma$  be the recovery rate (rate of "dying").

The individual's infectious lifetime is an exponential random variable with mean  $1/\gamma$ .

The average number of secondary infections they cause is:

$$\mathcal{R}_0 = (\text{rate of infection}) \times (\text{average infectious period}) = \beta \times \frac{1}{\gamma} = \frac{\beta}{\gamma}$$

### The Connection

$\mathcal{R}_0$  is precisely the **mean offspring number**  $\mu$  for the embedded branching process that approximates the start of the epidemic.

# Applying Branching Theory to Epidemics

The fate of the epidemic's initial phase is determined by  $\mathcal{R}_0$ :

- ▶ If  $\mathcal{R}_0 \leq 1$  ( $\mu \leq 1$ ): The number of infected individuals is a subcritical or critical process. The epidemic will die out with probability 1.
- ▶ If  $\mathcal{R}_0 > 1$  ( $\mu > 1$ ): The process is supercritical. There is a positive probability that the epidemic takes off and causes a major outbreak.

We can even calculate the probability of a major outbreak! It is  $1 - \pi_0$ , where  $\pi_0$  is the extinction probability.

For this simple birth-death infection process, the PGF is  $G(s) = \frac{\gamma}{\beta + \gamma} + \frac{\beta}{\beta + \gamma}s$ . Solving  $s = G(s)$  gives the extinction probability:

$$\pi_0 = \frac{\gamma}{\beta} = \frac{1}{\mathcal{R}_0}$$

The probability of a major outbreak is  $1 - 1/\mathcal{R}_0$ .

# Summary

- ▶ **Branching Processes** model populations with i.i.d. offspring generation.
- ▶ The fate of the population is determined by the **mean offspring number**  $\mu$ . Extinction is certain if  $\mu \leq 1$ .
- ▶ The **extinction probability**  $\pi_0$  can be calculated as the smallest non-negative fixed point of the probability generating function  $G(s)$ .
- ▶ The initial stages of many large-scale **Continuous-Time Markov Chains** can be approximated by a branching process.
- ▶ This allows us to apply the theory to real-world problems, like calculating an epidemic's **basic reproduction number**  $\mathcal{R}_0$  and its probability of causing a major outbreak.

# Bibliography I