

$$n = 3$$

Parameter inference with few experiments for a basic reaction network

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January 15, 2024

Presentation of the problem

Ideas explored

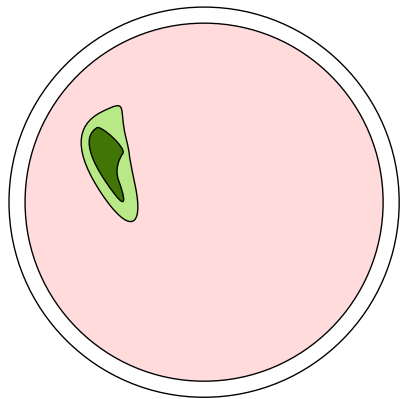
Bootstrapping

Discussions

References

The $n = 3$ problem

Context

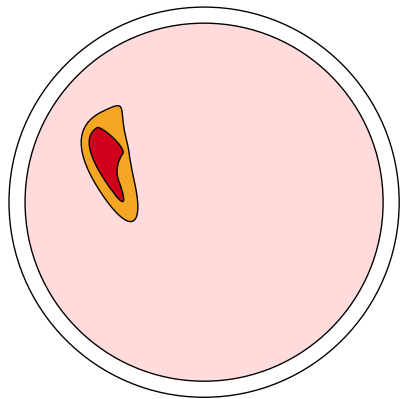


Experiment : Observe successive bacteria divisions over time

Figure: Petri dish with $k = 1$ bacterium

The $n = 3$ problem

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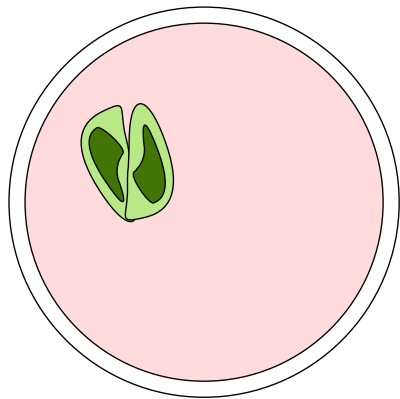


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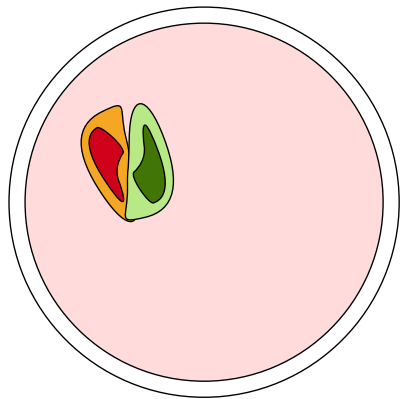


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The $n = 3$ problem

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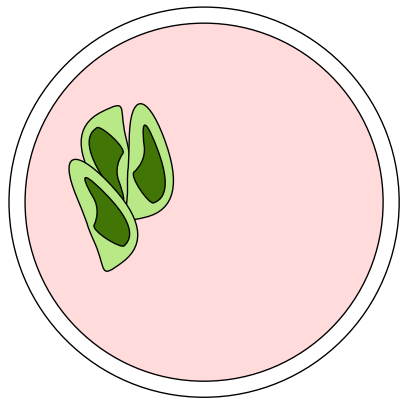


Experiment : Observe successive
bacteria divisions over time

Figure: Petri dish with $k = 1$
bacterium

The $n = 3$ problem

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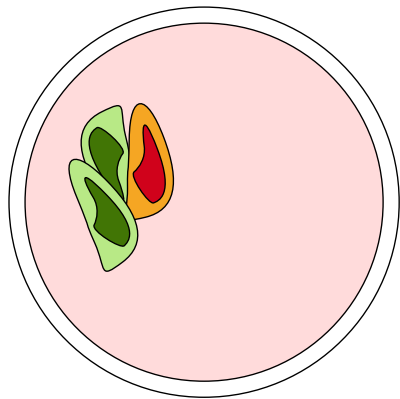


Experiment : Observe successive bacteria divisions over time

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The $n = 3$ problem

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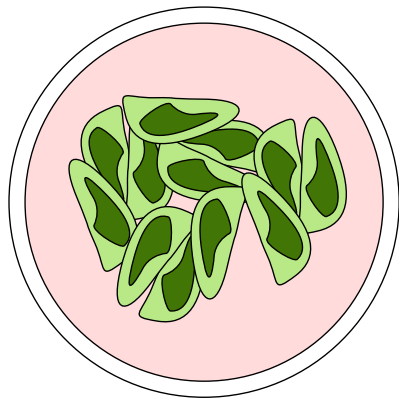


Experiment : Observe successive bacteria divisions over time

Figure: Petri dish with $k = 1$ bacterium

The $n = 3$ problem

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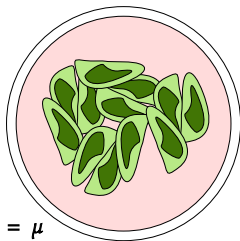


Experiment : Observe successive bacteria divisions over time

Figure: Petri dish with $k = 1$ bacterium

The $n = 3$ problem

Context



rate of division = μ

Figure: Petri dish with $k = 1$
bacterium

Experiment : Observe successive
bacteria divisions over time

The $n=3$ Problem

Question

How to estimate μ **reliably** with as few experiments as possible?

How many experiments are required to have a 95% confidence in our estimation?

The $n = 3$ problem

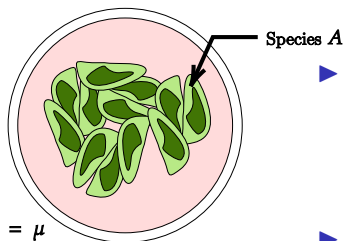
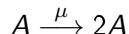


Figure: Petri dish with $k = 1$ bacterium

- ▶ System can be modeled by a *Reaction Network*



- ▶ μ is the rate parameter :
depends on the environment

The $n = 3$ problem

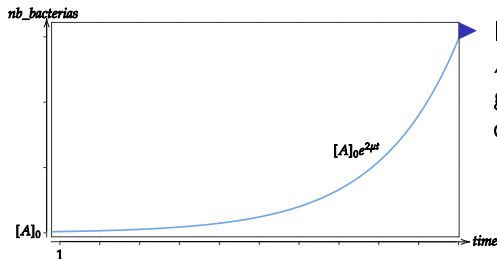


Figure: Petri dish with $k = 1$ bacterium

From the reaction network $A \xrightarrow{\mu} 2A$, we can derive a general expression for the quantity of cells:

- ▶ $\frac{d[A]}{dt} = 2\mu [A] \implies [A](t) = [A](0)e^{2\mu t}$
- ▶ so $\mu = \frac{1}{2t} \ln \left(\frac{1}{A_0} A(T) \right)$
- ▶ Doesn't work because it now a deterministic process

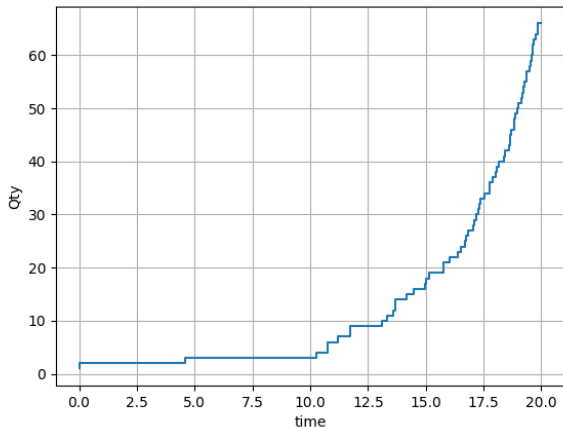
Ideas explored

- ▶ Mathematical brute-force
- ▶ Using Cross-Entropy method

New Idea (Thanks Matthias!:D)

Simplifying assumption

We now assume that we have access to the whole trace of an experiment: we know the number of cells in the dish at every moment t



New Idea

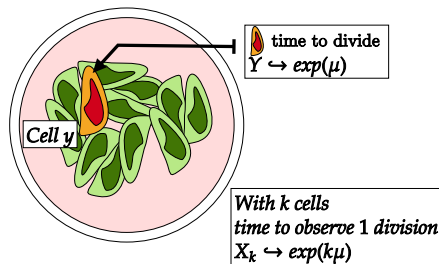
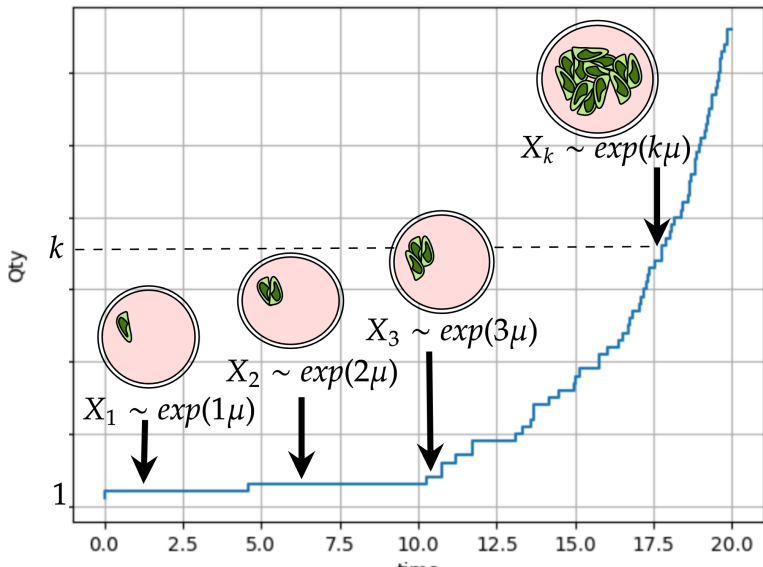


Figure: Petri dish with $k = 1$
bacterium

- ▶ When number of cell is large, the time that it takes for a each single cell to divide follows $\exp(\mu t)$
- ▶ So if there are k cells in the dish, the wait time follows $\exp(k\mu t)$

Modeling waiting time



Modeling waiting time

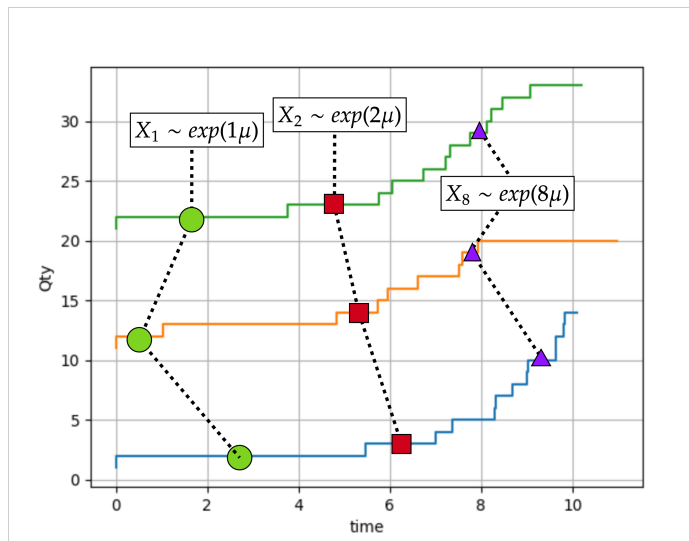


Figure: Petri dish with $k = 1$ bacterium

Estimating μ with Maximum Likelihood

- ▶ If given a set of samples $X = (x_1, \dots, x_n)$ drawn from a random variable $X_\lambda \hookrightarrow \exp(\lambda)$, we can estimate λ with maximum likelihood by

$$\hat{\lambda} := MLE(X) = \arg \max_{\lambda > 0} \prod_{x_i} \frac{1}{\lambda} e^{\lambda x_i}$$

- ▶ Confidence : $\sqrt{n} \left| \lambda - \hat{\lambda} \right| \longrightarrow \mathcal{N}(0, \text{some_cov_matrix}^*)^1$
- ▶ So the bias $B = \mathbb{E}(\lambda - \hat{\lambda}) = o\left(\frac{1}{\sqrt{n}}\right)$
- ▶ $n = 3$? ☹

¹The inverse of the Fischer Information Matrix

A solution: Bootstrapping

- ▶ Technique for data re-sampling, when true distribution is unknown
- ▶ **Assumption**: Consider the observed data as representative of the true distribution F
- ▶ If F is the real distribution, \hat{F} is the empirical distribution :
 - ▶ $X \hookrightarrow \hat{F}$ means $P(X = x_i) = \frac{1}{n}$
- ▶ Idea : Do stats with \hat{F} as we would with F

Illustration of the Bootstrapping process

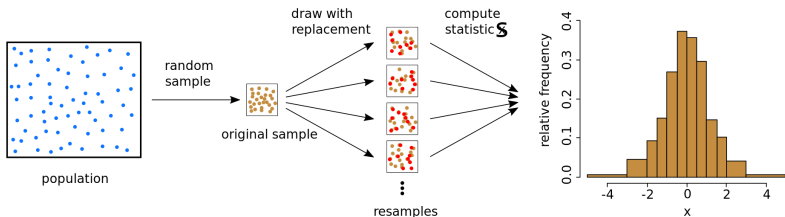


Figure: Petri dish with $k = 1$ bacterium

WARNING

WARNING : Assumption to use Bootstrapping

We consider the observed data as representative of the true distribution F

- ▶ How to quantify the “closeness” of the observed distribution to the real one?
- ▶ Introduce a metric: *Statistical distance*



$$\Delta(X, Y) = \int_{\mathcal{D}} P(X = \omega) - P(Y = \omega) d\omega$$

- ▶ Need to be thought through...
- ▶ Assume for now that the assumption is satisfied...

Bootstrap confidence interval of $\hat{\mu} = MLE(X)$

- ▶ We want a confidence interval on the value of μ , $\hat{\mu}$
- ▶ Need to estimate the *Standard Error* on our Bootstrapped samples

Bootstrap confidence interval of $\hat{\mu} = MLE(X)$

Estimation of the Standard Error

- ▶ Double Bootstrap : let X_1^*, \dots, X_R^* be R replications of our original sample $y_1, \dots, y_n \hookrightarrow \exp(\mu)$
- ▶ Bootstrap Replicate B times each X_i^* : Gives $R \times B$ samples $X^{**} = X_{1,1}^{**}, \dots, X_{1,Q}^{**}, X_{2,1}^{**}, \dots, X_{2,Q}^{**}, \dots, X_{R,1}^{**}, \dots, X_{R,Q}^{**}$.

$$\widehat{se}^2 = \frac{1}{n-1} \sum \left(\hat{\mu}(X_i^{**}) - \overline{\hat{\mu}(X_i^{**})} \right)^2$$

- ▶ $\text{var}(\widehat{se}) = \frac{O(1)}{n^2} + \frac{O(1)}{nB}$

Bootstrap confidence interval of $\hat{\mu} = MLE(X)$

Conf. Interv. Bounds

- ▶ We want a $1 - \alpha$ confidence interval on $\hat{\mu}$, that is, a and b st



$$P(a < |\hat{\mu} - \mu| < b) = 1 - \alpha$$

- ▶ Idea : Studentize $\hat{\mu}$

Bootstrap confidence interval of $\hat{\mu} = MLE(X)$

Conf. Interv. Bounds \rightarrow Studentized variable



$$Z = \frac{\hat{\mu} - \mu}{\sigma_{\hat{\mu}}} \equiv \frac{\hat{\mu}^* - \hat{\mu}}{\hat{se}} \hookrightarrow \mathcal{N}(0, 1)$$

- ▶ So after computations², we get a $1 - 2\alpha$ confidence interval for $\hat{\mu}$:

$$low = \hat{\mu} - \hat{se} \cdot z_{(1-\alpha)(R+1)}^* \quad high = \hat{\mu} + \hat{se} \cdot z_{\alpha(R+1)}^*$$

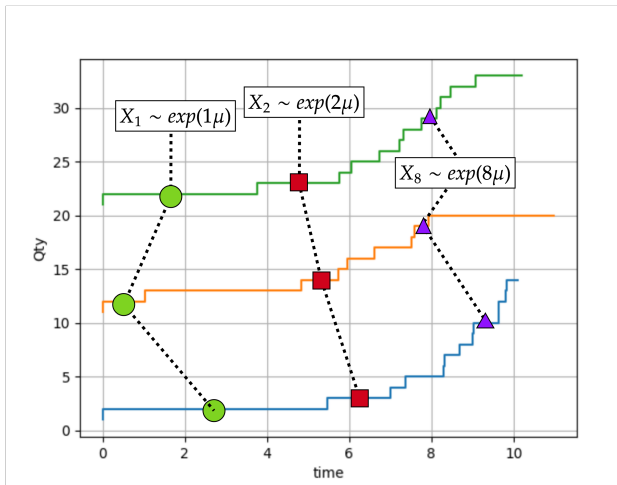
- ▶ with an error of $O\left(\frac{1}{nB} + \frac{1}{n^2}\right)$ for \hat{se} as per earlier.

²See [3]

Increasing reliability

Goal

If we have $n = 3$ traces, we have at most 3 samples from the same exponential distribution \rightarrow not enough for a reliable bootstrap estimation



Increasing reliability

Idea

Convert each independant $X_k \hookrightarrow \exp(k\mu)$ to one single $\tilde{X}_k \hookrightarrow \exp(\mu)$

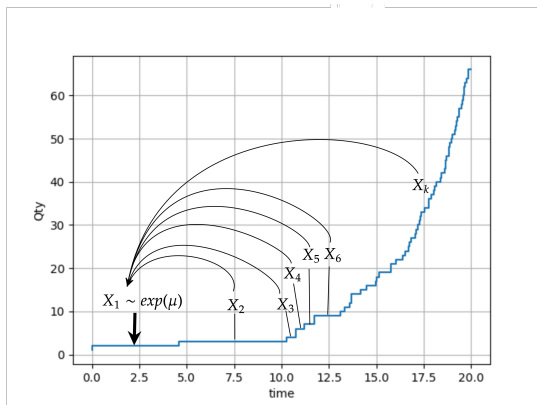


Figure: Petri dish with $k = 1$ bacterium

Increasing reliability

Theorem

If $X_0 \hookrightarrow \exp(\lambda_0)$, $X_1 \hookrightarrow \exp(\lambda_1)$, X_0 and $\frac{\lambda_1}{\lambda_0} X_1$ are identically distributed.

Proof.

- ▶ Let $X_0 \hookrightarrow \exp(\lambda_0)$, $X_1 \hookrightarrow \exp(\lambda_1)$, and
$$F_{X_0}^{-1}(x) = \int_{-\infty}^x \lambda_0 e^{-\lambda_0 t} dt = -\frac{1}{\lambda_0} \ln x.$$
- ▶ By using the inverse transform sampling relation, we have that $F_{X_0}^{-1}(U) \hookrightarrow \exp(\lambda_0)$ for U any uniformly distributed random variable.
- ▶ But $e^{-\lambda_1 X_1} \hookrightarrow \mathcal{U}([0, 1])$ ³
- ▶ so $F_{X_0}^{-1}(1 - e^{-\lambda_1 X_1}) = \frac{\lambda_1}{\lambda_0} X_1 \hookrightarrow \exp(\lambda_0)$
- ▶ So X_0 and $\frac{\lambda_1}{\lambda_0} X_1$ are identically distributed.

³See Lemma

Increasing reliability

$$T(X) = [kx_k, k \in \llbracket 1, n \rrbracket]$$

Histogram distribution $e^{-\mu T(X)}$

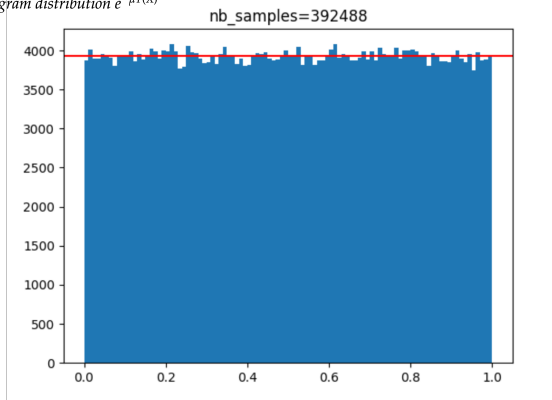


Figure: Petri dish with $k = 1$ bacterium

Increasing reliability

Lemma

$$e^{-\lambda_1 X_1} \hookrightarrow \mathcal{U}([0, 1])$$

Increasing reliability

- ▶ Since each $X_k \sim \exp(k\mu)$, $\frac{k\mu}{\mu}X_k = kX_k$ has the same distribution as $X_1 \sim \exp(\mu)$,
- ▶ We have effectively transformed our single trace from 1 experiment into nb_cells independant samples from $\exp(\mu)$!
- ▶ $n = 3 \rightarrow n = 3 \times nb_cells \approx 3.10^3$
- ▶ $\text{var}(\hat{se}) < C.10^{-6} \text{😊😊😊😊😊}$

Estimation of μ on simulations

- ▶ Simulations of the boolean network using a Gillespie-like algorithm:
- ▶ 3 Traces/ Experiments, duration =100 secs, $\mu = .5$, Initial Number of cells = 1

Estimation of μ on simulations

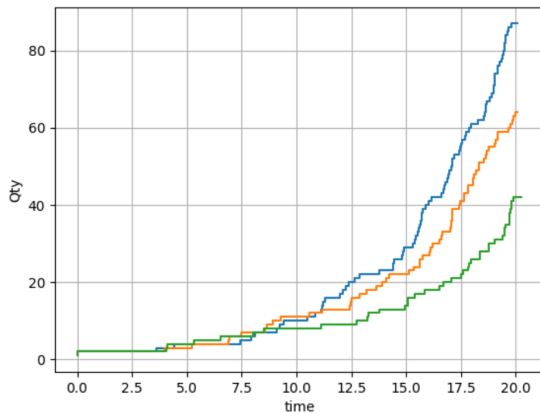


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Estimation of μ on simulations

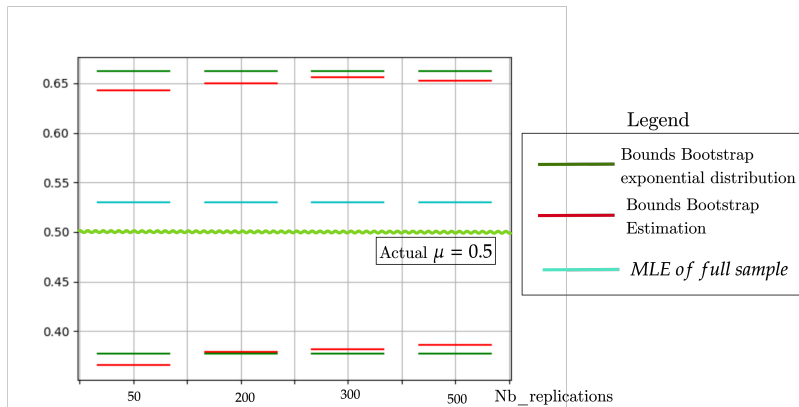






Figure: Petri dish with $k = 1$ bacterium

Discussions

1. Need to think over the assumption of "representativeness" of the empirical distribution
2. Need to be adapted to reality : Interpolation
3. We worked on a simple model : $A \xrightarrow{\mu} 2A$. More complex ones? Resource consumption model?

-  Stochastic Modelling for Systems Biology Third Edition Darren J. Wilkinson
-  Efron, B.; Tibshirani, R. (1993). An Introduction to the Bootstrap. Boca Raton, FL: Chapman & Hall/CRC
-  'Bootstrap Methods and their Application', by A. C. Davison and D. V. Hinkley Cambridge University Press, 1997
-  Stochastic Rate Parameter Inference Using the Cross-Entropy Method, Jeremy Revell and Paolo Zuliani