An Error Ananlysis of the Delayed Continous Time Markov Chain model

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ABSTRACT

Continuous-time Markov chains (CTMCs) with their rich theory and efficient simulation algorithms have been used successfully in modelling stochastic processes in diverse areas such as computer science, physics, and biology. However, systems that comprise non-instantaneous events cannot be accurately and efficiently modelled with CTMCs.

So, we develop the idea of delayed CTMCs and use it specifically in the study of Genetic Regulatory Circuits (GRCs).

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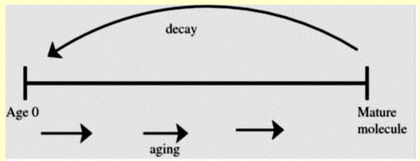
THE PROBLEM

- A new model to approximate computation of probability distributions
- Objective – to compute within an error bound.



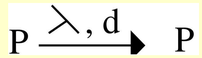
- Molecules available for reaction only at certain age
- Decay from mature state to 0-age state

- The two approximations:
  - Aging in discrete steps
    - State space with Δ-step discretization.
    - Decay from mature state to 0-age only at non-multiples of Δ.
  - Time with δ-step discretization

- lim δ→0 corresponds to continuous time

APPROACH

- Considered simple example – 1 molecule system



  - λ = decay rate for mature molecule
  - d = delay (time for maturing)
- Let d/Δ = n
  - ➢n+1 states, one for each age 0,1,2,….,n
  - ➢State 'i' corresponds to age 'i'.
- Δ/δ = N+1.
- Let S denote general system.
  - ➢ S_i : prob mass 1 in state 'i' at time 0.

- For S_0, whole prob mass in state x at time xΔ
- S_x at time t = S_0 at time (t+xΔ).
- Say we start with a probability vector $S=(\lambda_0,\lambda_1,\lambda_2,\ldots,\lambda_n)$.
- At time t, S is equivalent to the linear combination of results from systems $S_0,S_1,S_2\ldots,S_n$ with weights $\lambda_0,\lambda_1,\lambda_2,\ldots,\lambda_n$.
- So, we focus on the system S_0 now.

THE ANALYSIS

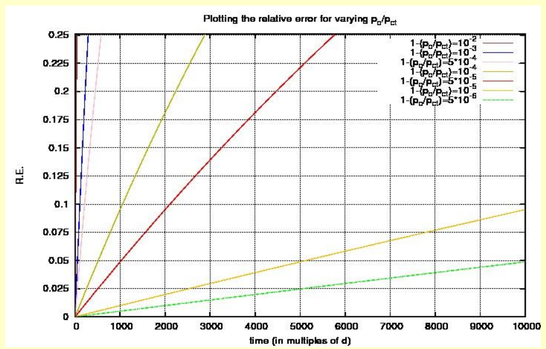
- At time *kd*, let prob. mass in state n be x
  - Time (*kd*+Δ) : state 0 has $(1-(1-\lambda\delta)^N)x$.
  - …..
  - Time (*kd*+(n-1) Δ) : state (n-1) has prob. mass $(1-(1-\lambda\delta)^N)x$.
- This mass re-enters n at *(k+1)d*.
- Prob. Mass that stays in 'n' throughout = $(1-\lambda\delta)^{n\,N}\,x$.

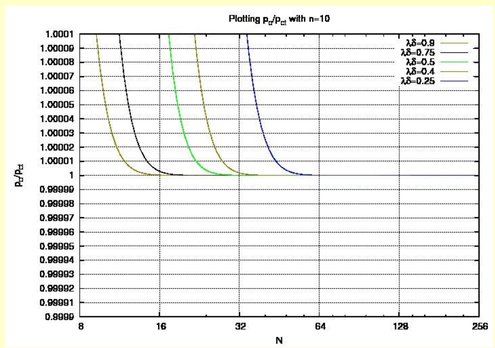
- So, prob. Mass in n at *(k+1)d* =
  $((1-\lambda\delta)^{n\,N} + (1-(1-\lambda\delta)^N))x = p_o x$ (say)
- For continuous-time, use
  $p_{ct} = \lim_{\delta\to 0} p_0 = e^{-\lambda d}+1-e^{-\lambda\Delta}$

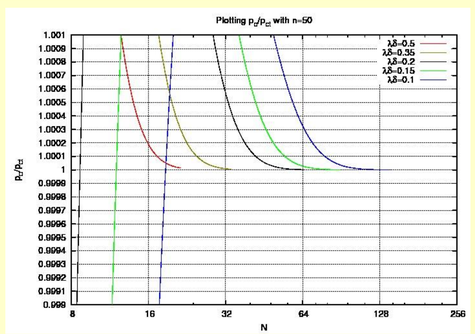
- Relative error = 1–(approx. / true value)

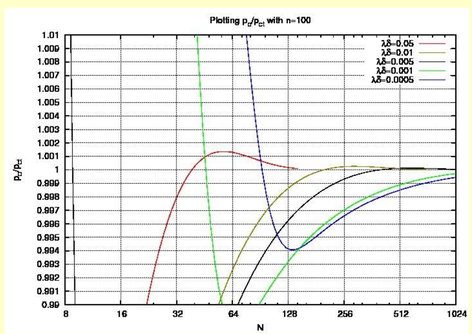
- At time *d*, relative error,
  R.E. = | $1 - (p_o/p_{ct})^{(k-1)}$ |

OBSERVATIONS









CONCLUSIONS

1. Shown that the delayed CTMC model computes within an error bound for simple 1-molecule system.
2. Optimum discretization exists both in ageing of molecule as well as time.
3. Wish to achieve such optimality points for more complex systems too.

REFERENCES

Delayed Continuous-Time Markov Chains for Genetic Regulatory Circuits
- Calin C. Guet, Ashutosh Gupta, Ali Sezgin, Thomas A. Henzinger, Maria Mateescu (IST Austria)