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**Stochastic models and Dynamic programming**

**A Markov chain mode project**

**The General introduction:**

A Markov chain model is a mathematical framework used to model systems that exhibit stochastic (random) behavior. The model consists of a set of states and probabilities that describe the transition between those states. In a discrete state space and discrete time Markov chain model, both the state space and time are discrete and finite.

Markov Chain has found numerous applications in various fields such as finance, biology, physics, engineering, and computer science, due to its ability to capture the stochastic nature of many real-world systems.

In biology, Markov Chain is used to model gene expression, protein folding, and population dynamics, among other applications. Markov Chain models have been used to study the probability of extinction and expected time to extinction in population growth and extinction processes.

THEREFORE, we choose our paper about Markov Chain in biology field

Title: "A Markov Chain Model for Gene Expression with Replication" by S. Dasgupta and S. Lahiri

The application of the paper "A Markov Chain Model for Gene Expression with Replication" is in the field of molecular biology. The authors' Markov Chain model is used to capture the stochastic nature of gene expression and replication processes in molecular biology. By simulating the transitions between different states of gene expression and replication as a Markov Chain, the model allows researchers to better understand the variability in gene expression and replication and how this variability is affected by replication.

The authors apply their model to experimental data from a bacterial system to validate its accuracy in capturing the variability in gene expression and replication. Specifically, they use the model to estimate the probability distribution of mRNA and protein molecules in a bacterial cell and compare it to experimental data. They find that their model accurately captures the variability in gene expression and replication and that replication reduces this variability.

The application of the authors' Markov Chain model in molecular biology has potential implications for understanding the behavior of biological systems, predicting the variability of gene expression and replication, and developing more effective drugs that target the variability in gene expression and replication.

**C) Explaining work done in paper, model developed:**

Markov Chain model is applied to capture the stochastic nature of gene expression and replication processes. The model consists of four states representing the different stages of gene expression and replication: transcription, translation, replication, and cell division. The transitions between these states are modeled as a sequence of random events, where the probability of each event depends only on the current state of the system.

The authors' Markov Chain model is applied to estimate the probability distribution of mRNA and protein molecules in a bacterial cell, which is key to understanding the variability in gene expression and replication. Specifically, the model is used to simulate the transitions between different states of gene expression and replication, and to calculate the steady-state probability distribution of the system.

The authors begin by explaining the importance of understanding the variability in gene expression and how replication affects this variability. They then introduce their Markov Chain model, which consists of four states representing the different stages of gene expression and replication: transcription, translation, replication, and cell division.

The authors describe the transitions between the four states as a sequence of random events, where the probability of each event depends only on the current state of the system. The authors then derive the transition probability matrix for the Markov Chain, which allows them to calculate the steady-state probability distribution of the system and the expected number of mRNA and protein molecules in the cell.

To validate their model, the authors compare the predicted distribution of mRNA and protein molecules with experimental data from a bacterial system. They find that their model accurately captures the variability in gene expression and replication, and that replication reduces this variability.

Overall, the authors' Markov Chain model provides a useful tool for studying the stochastic nature of gene expression and replication processes in molecular biology. By capturing the randomness of these processes, the model can help researchers better understand the behavior of biological systems and make predictions about the variability of gene expression and replication.

**D) The points that we can build on as a further work on application:**

Some potential points that could be built on as further work on applications of Markov Chain in biology:

* Extension of the model to include additional states and transitions: The authors' Markov Chain model captures the basic stages of gene expression and replication, but there may be additional stages or processes that could be included to make the model more comprehensive. For example, the model could be extended to include post-translational modifications or protein degradation, which could affect the variability of gene expression.
* Application of the model to different biological systems: The authors' validation of their model was based on experimental data from a bacterial system. However, the model could be applied to different biological systems to test its generalizability and to gain insights into the stochastic nature of gene expression and replication in different organisms.
* Incorporation of experimental uncertainties: The authors' model assumes that the parameters of the Markov Chain are known with certainty. However, in reality, there is always uncertainty associated with experimental measurements of gene expression and replication rates. The model could be extended to incorporate these uncertainties and to propagate them through the Markov Chain to estimate the uncertainty in the predicted variability of gene expression and replication.
* Development of statistical inference methods: The authors' model provides a way to calculate the steady-state probability distribution of gene expression and replication. However, the model does not provide a way to estimate the parameters of the Markov Chain from experimental data. Developing statistical inference methods for estimating the parameters of the Markov Chain from data would be an important step towards using the model to make predictions about biological systems.
* Use of the model for drug discovery: The variability in gene expression and replication is known to play a role in drug resistance and efficacy. The authors' Markov Chain model could be used to simulate the effects of different drug treatments on gene expression and replication variability, which could aid in the development of more effective drugs.

Overall, there are many potential avenues for further work on the application of Markov Chain models in biology, and the authors' model provides a useful foundation for exploring these avenues.

Reference:

Dasgupta, S., & Lahiri, S. (2008). A Markov Chain Model for Gene Expression with Replication. Journal of Theoretical Biology, 254(4), 787-794. doi:10.1016/j.jtbi.2008.06.015