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INTRODUCTION OF PARALLELISM IN RIBOSOMAL COMPUTING

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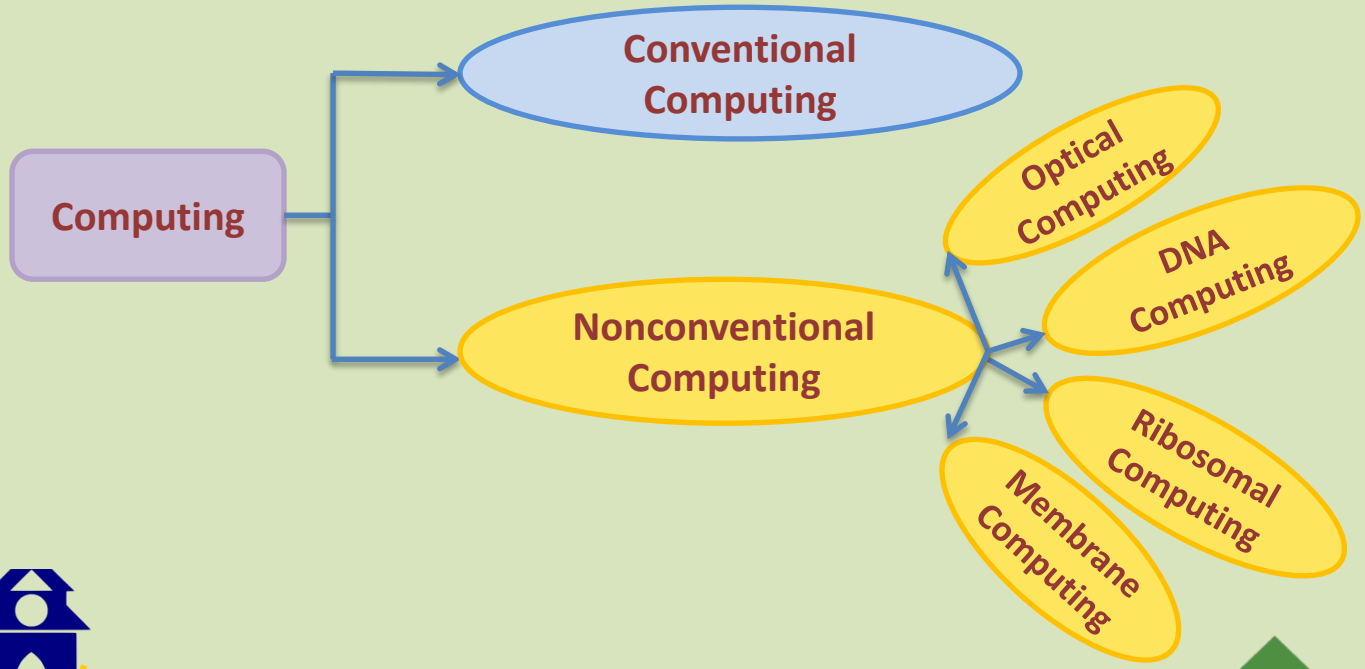
Introduction

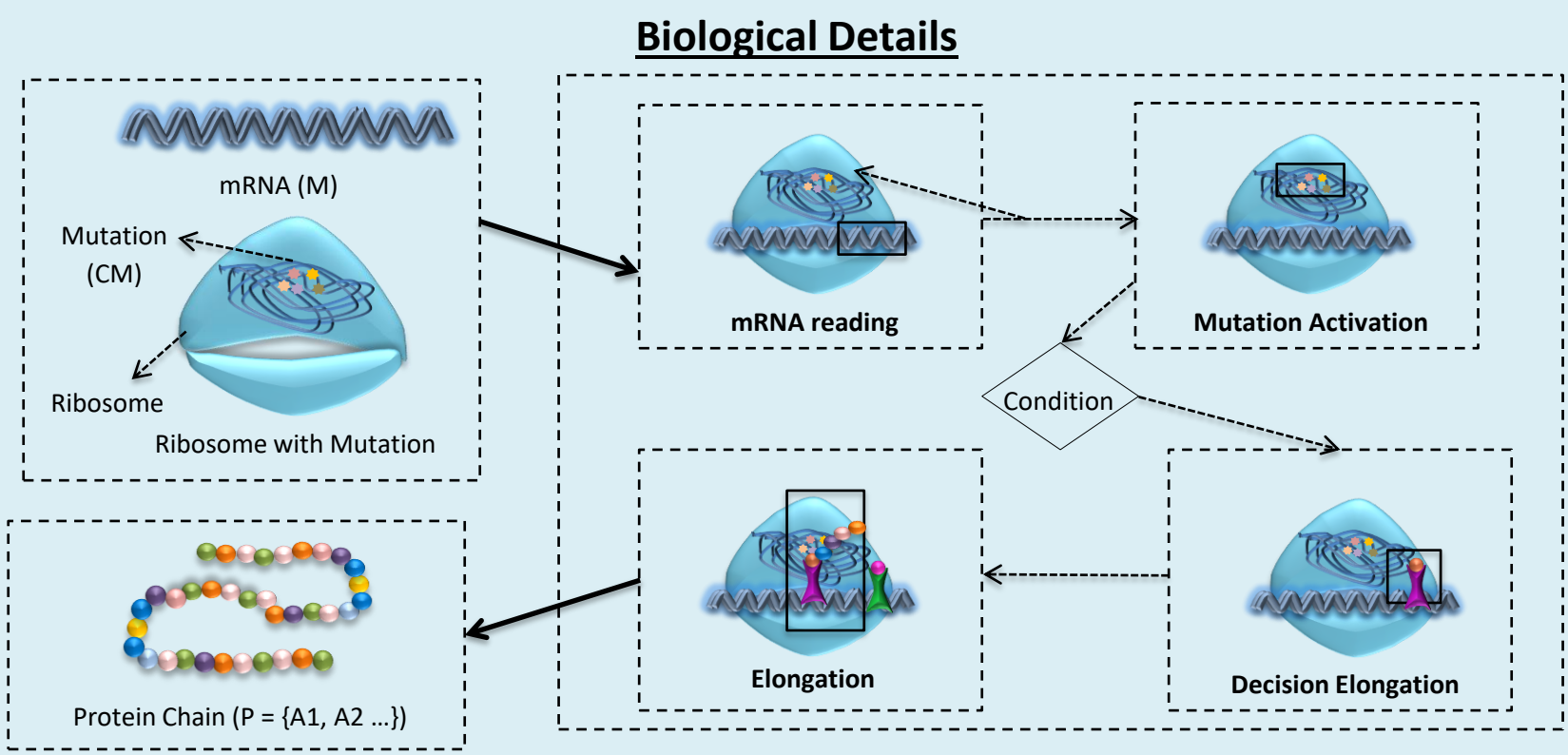
- Limitations of silicon based computing (such as miniaturize transistor size, lack of proper insulating material etc.) is the reason of raising the nonconventional approach
- Ribosomal computing is an automated biomolecular computing
- Ribosomal Computing imitates



Introduction

Ribosomal Computing:

- **Variables: mRNA, Ribosome, mutation**
- **Functions: mRNA reading**



Related Work

- Various mathematical and computational models of protein synthesis or translation have been reviewed in [1].
- Probabilistic Boolean Network (PBN) based approach for translation process have been used to analyze and compare these mathematical and computational modeling techniques systematically in [2].
- Ribosome in living cells have been simulated artificially as a small molecule machine for protein synthesis by [3].
- An artificial ribosome, oRibo-T that can perform much similar to the original ribosome, have organized in [4]. It is also clear from this work that gene mutations in various locations of oRibo-T can be performed to get desired operation.
- Performing Boolean logic operation in orthogonal ribosome-mRNA pair is shown in [5].

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Motivation

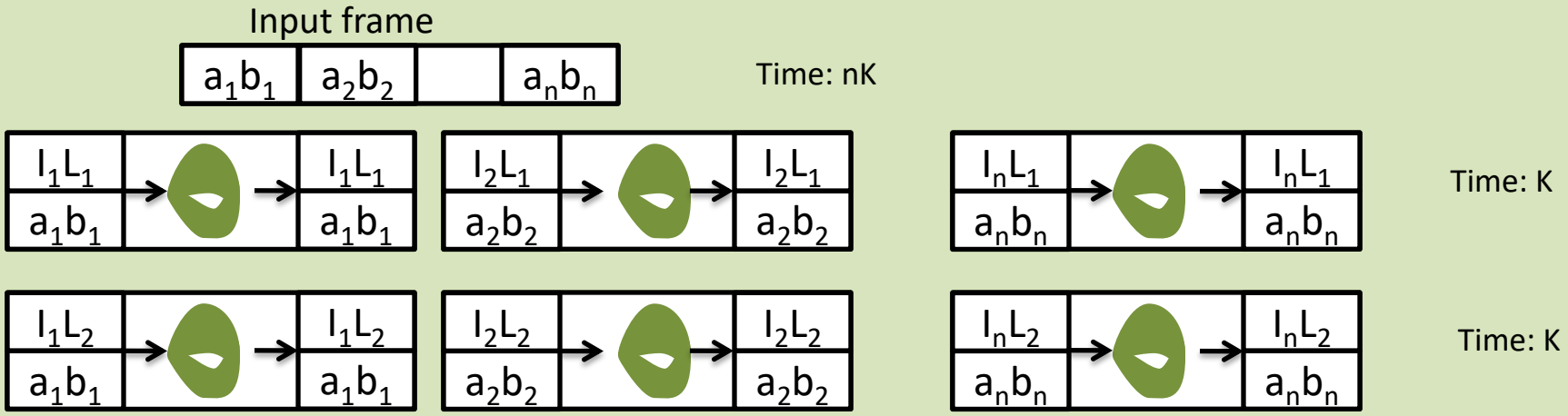
- **Limitations:**
  - Ribosomal computing is an automated bio-molecular computing.
  - Several computational works such as logic gate, arithmetic operations are already implemented using this computing method.
  - The ribosomal computing executes a computational operation in sequential manner.
  - The energy consumption for a computational operation in ribosomal computing is significantly low than other computing technique.
  - The time requirement of ribosomal computing is significantly high.
  - Introduction of parallelism can reduce the time.

Parallel Operation

- **Parallelism:**
  - In practical scenario, the concept of poly some carries the idea of parallel operation.
  - In the other hand multiple ribosome can operate on conjugate in cell environment.
  - We have combine these two technique and present two approaches for parallel operation on ribosomal computing.
  - The parallel operation speed up the execution of computational operation.

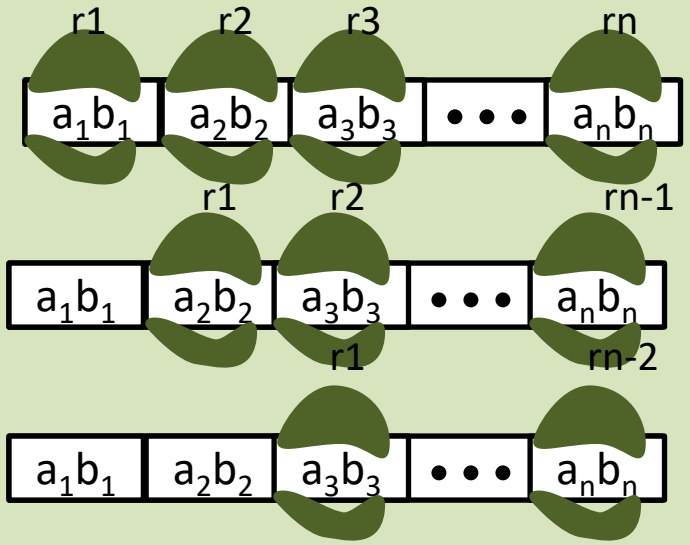
Parallelism (Approach-I)

- A single operation is performed on multiple operands.
- The complete task is divided into small sub-tasks, and each sub-task is performed in some non-identical units.
- This approach is applicable for a mutually independent data set.
- An example is presented here.
- The input frame is divided into several parts and each part executed parallel in different ribosome.



Parallelism (Approach-II)

- Multiple operations are performed on a single operand.
- A computational task is performed following the concept of polysome, i.e. multiple ribosomes operate on a single mRNA.
- Multiple operations are performed on a single data set.
- An example is illustrated below.



Time: nk

Time: (n-1)k

Time: k

Effect of Parallelism in Speed

- m number of codons are accessed on t time, here ($m \propto t$).
- We assume that the m number of the codons are accessed on the n number of the ribosome molecules and t_m time is required to access a codon. Therefore, $t_m \times m$ time is required for accessing m codon.
- Now, if p number of operations are performed and the consume time for one operation is t_p

❖ **Approach-I:** $t_p = (p \times t_m \times m)/(n \times p)$

❖ **Approach-II:** $t_p = ((t_m \times m) + (n - 1) \times m_{d)} /(p \times \text{n})$

Conclusion

- The ribosomal computing system performs operations in a sequential approach.
- In such a computing system, the time requirement is enormous as the sequential nature of codon access.
- We have presented two parallelism approaches with their best suitable application field and discussed the parallelism effect on reducing time.
- Thus, we can conclude that in ribosomal computing, the parallel approaches are time efficient over the sequential approach.

Bibliography

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