



INDIAN ACADEMY OF SCIENCES

BENGALURU

Lectures in Physics, Biology and Engineering

(Convened by Professor K L Sebastian, Indian Academy of Sciences, Bengaluru)

Faculty Hall, Indian Institute of Science

29 JUNE 2017 (THURSDAY)
(1000-1310 hrs)

1000: The Mysterious Magnetic Personality of Our Sun
Arnab Rai Choudhuri
Department of Physics
Indian Institute of Science
Bengaluru

1100 Tea Break

1110: Transcription Complex and Silent Mutations
Dipankar Chatterji
Molecular Biophysics Unit
Indian Institute of Science
Bengaluru

1210: The Latent Power of Absurd Ideas
Jayant Haritsa
Department of Computer Science & Automation
Indian Institute of Science
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ABSTRACTS

The Mysterious Magnetic Personality of Our Sun

Arnab Rai Choudhuri, *Department of Physics, Indian Institute of Science, Bengaluru*

The Sun is the first astronomical object in which magnetic fields were discovered in 1908 by using the Zeeman effect. Even before this discovery of magnetic fields in sunspots, it was known that there is a 11-year cycle of sunspots, which could be identified as the magnetic cycle of the Sun after this discovery. The magnetic field of the Sun is also behind many other phenomena, such as the violent explosions known as solar flares, the corona much hotter than the solar surface and the solar wind. Only within the last few decades, major developments in plasma physics and magnetohydrodynamics (MHD) have at last provided a broad framework for the theoretical understanding of these phenomena connected with the solar magnetic fields. I shall give a general introduction to this field - with some emphasis on the research interests of our group. A more detailed account of this field can be found in my recently published popular science book. <http://www.amazon.in/Natures-Third-Cycle-Story-Sunspots/dp/0199674752/>

Transcription Complex and Silent Mutations

Dipankar Chatterji, *Molecular Biophysics Unit, Indian Institute of Science, Bengaluru*

Silent mutations are mutations that change the DNA and RNA sequence but not the amino acid sequence. They ascend from the degeneracy of the genetic code. For a long time, silent mutations were not considered to be of importance, but this perception is changing rapidly. However, the impact of silent mutation depends a lot on the distance between the two codons in the codon usage spectrum as well as on other factors. RNA polymerase that performs the essential function of gene transcription, is composed of a total of 6 subunits, which are as follows: two α , one β , one β' , one ω and one σ subunit. Information is available on the contribution of all the subunits in the primary functioning of bacterial RNA polymerase except the smallest subunit ω . In order to discover the role of ω in RNAP, we had isolated a dominant negative mutant of omega (ω_6), which is predominantly α helical and showed higher binding affinity to reconstituted core1 ($\alpha_2\beta\beta'$) compared to that with largely unstructured native. The interaction is driven by highly negative enthalpy and a small but unfavourable negative entropy term. Extensive structural alteration in ω_6 makes it more rigid, the plasticity of the interacting domain formed by ω_6 and core1 is compromised, which may be responsible for the entropic cost. Such tight binding of the structured mutant (ω_6) affects initiation of transcription. However, once pre-initiated, the complex elongates RNA chain efficiently. During the above study, we also obtained a silent mutant which was lethal and the mutant protein was found to have a helical structure. After establishing the role of flexibility in the structure of ω , next we wanted to ask why despite having the same amino acid sequence, silent mutant is structured. CD studies were done with the silent mutant as well as with the wild type protein. We observed that by mutation of a frequent codon to rare codon, structural change is observed in the protein. In vitro refolding experiments revealed that silent mutant refolds to the same structure as wild type protein. However, not all silent mutations affect the structure equally. Further silent mutants are being generated to see the effect of codon usage frequency and amino acid position on the protein expression and folding. Silent mutations are generated at different positions along the length of protein to see the impact of position of silent mutant on the ω protein folding.

The Latent Power of Absurd Ideas

Jayant Haritsa, *Department of Computer Science & Automation, Indian Institute of Science, Bengaluru*

A popular misconception about scientific breakthroughs is that they are predicated on brilliant schemes whose dazzling provenance is the exclusive preserve of quirky masterminds. This talk attempts to debunk the myth by demonstrating, to the contrary, that absurd and preposterous ideas, neglected and abandoned due to their manifest foolishness, can often lead to surprisingly potent results -- the key is to have several such ideas and to use them together! We will argue our case through a guided tour of a long-standing statistical estimation problem that has plagued, for over three decades, the effective operations of "database engines". These engines are the extremely complex and massive software systems that constitute the backbone of today's information-rich society, providing a congenial environment for handling enterprise data during its entire life cycle. In particular, we will show how a pair of seemingly irrational ideas, operating in tandem, can substantively address the statistical estimation problem. The end result is the first-ever provably robust database engine, thereby fulfilling a long-felt need of the information processing community.

All are welcome