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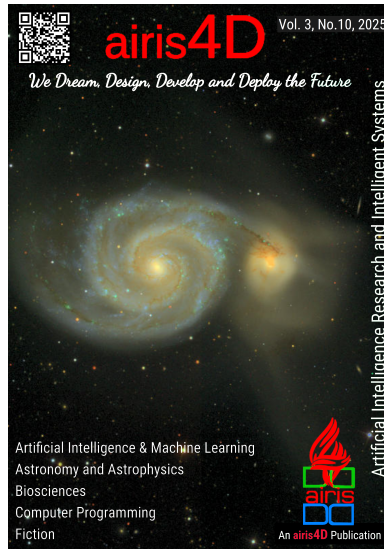
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Artificial Intelligence Research and Intelligent Systems

Artificial Intelligence & Machine Learning
Astronomy and Astrophysics
Biosciences
Computer Programming
Fiction



An **airis4D** Publication



Cover page

Image: M51, the "Whirlpool" galaxy in the constellation Canes Venatici, is about 30 million light years [10Mpc] away from our galaxy.

Read more: <https://www.astro.princeton.edu/~rhl/PrettyPictures/>

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Editorial

by Fr Dr Abraham Mulamoottil

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The October edition begins with the article “AlphaFold: Unlocking the Secrets of Life’s Building Blocks” by Dr Arun Aniyar, which highlights how Google DeepMind’s AlphaFold has revolutionised biology by solving the long-standing protein folding problem. Proteins, essential molecular machines of life, function based on their unique 3D structures, but determining these structures had traditionally been slow, costly, and complex. AlphaFold, using advanced deep learning and evolutionary data, can now predict protein shapes with remarkable accuracy, earning it the 2024 Nobel Prize in Chemistry. This breakthrough is transforming drug discovery, enabling faster understanding of disease mechanisms, designing new enzymes, advancing material science, and even paving the way for personalized medicine. While experimental validation remains important, AlphaFold has democratized access to structural biology, accelerating innovation across science and medicine. The article concludes that AlphaFold marks a new era of biological research, with AI set to play an ever-growing role in unlocking life’s deepest mysteries and driving a global scientific revolution.

The article “Entropy Across Scales: From Micro-Level Randomness to Macro-Level Order” by Jinsu Ann Mathew explores entropy as a unifying principle across physics, language, biology, and social systems. It explains how local randomness—whether in molecular motion, letter sequences, genetic mutations, or individual choices—scales up to produce predictable patterns and order at higher levels, such as thermodynamic laws, meaningful discourse, resilient ecosystems, and structured social dynamics. In physics,

entropy bridges molecular chaos and thermodynamic stability; in language, it balances predictability and creativity; in biology, it links genetic variation to ecosystem resilience; and in society, it connects individual unpredictability to collective patterns. The article concludes that entropy is not merely a measure of disorder but a universal framework that shows how small-scale uncertainty drives large-scale order, adaptability, and coherence across diverse domains.

Abishek’s article “Plasma Physics Comets” explores how plasma physics helps explain the dynamic behaviour of comets as they interact with the Sun and solar wind. Since plasma makes up most of the universe, its role in space environments—from solar flares to cometary activity—is crucial. Comets, originating from the Kuiper Belt and Oort Cloud, consist of nuclei of ice, dust, and rock that release gas and dust when heated by the Sun, forming comae, hydrogen envelopes, and distinct plasma and dust tails. The study details key plasma processes such as outgassing, ionisation, dust-plasma interactions, and solar wind coupling, which generate large-scale structures like bow shocks and ion tails. Insights from missions like Rosetta, Stardust, and Deep Impact have revealed complex plasma environments, comet morphology, and their role in delivering volatiles and organics to planets. While challenges remain in modelling dusty plasmas and capturing their evolving behaviour, upcoming missions like ESA’s Comet Interceptor promise breakthroughs. The article concludes that comets serve as natural laboratories for plasma physics, offering vital knowledge for planetary science, astrophysics, and understanding the early solar

system.

The article “X-ray Astronomy: Through Missions” by Aromal P. highlights the rapid progress in X-ray astronomy in the 2020s through landmark satellite missions. It begins with IXPE (Imaging X-ray Polarimetry Explorer), launched in 2021 by NASA and ASI, which pioneered X-ray polarimetry and revealed the magnetic field structures of black holes, magnetars, pulsars, and supernova remnants. XRISM, launched in 2023 by JAXA in collaboration with NASA and ESA, advanced high-resolution X-ray spectroscopy with its Resolve microcalorimeter and Xtend wide-field telescope, uncovering the complex dynamics in supernova remnants and microquasars. India’s XPoSat, launched in 2024, marked the country’s first dedicated X-ray polarimetry mission, equipped with POLIX and XSPECT instruments to study polarisation and spectral evolution of cosmic sources. China’s Einstein Probe, also launched in 2024, uses innovative lobster-eye optics and complementary telescopes to detect fast X-ray transients and contribute to multi-messenger astronomy. Together, these missions are revolutionising high-energy astrophysics by probing magnetic fields, plasma environments, and transient cosmic events, opening new frontiers in our understanding of the universe.

Robin Thomas discusses the article “Introduction: Galaxies in Motion”, how the environment shapes the evolution of barred galaxies, drawing on the study by Virginia Cuomo and collaborators on the Virgo Cluster and the surrounding cosmic web. Bars—elongated stellar structures in disk galaxies—play a crucial role in redistributing gas and stars, influencing star formation and galaxy dynamics. The study shows that galaxies in dense environments like the Virgo Cluster have shorter, less prominent bars due to tidal interactions, gas stripping, and dynamical friction, which hinder bar growth. In contrast, galaxies in filaments and especially in the field, where disruptive forces are weaker, retain more gas and form larger, more prominent bars. These findings highlight the significant role of the cosmic environment in determining galaxy morphology and evolution, offering deeper insights into how galaxies interact with the cosmic web over time.

Sindhu G explains in “Main Sequence Stars” the structure, classification, energy generation, and significance of stars on the main sequence—the stage where stars spend most of their lifetimes. A star’s position on the sequence is determined mainly by its mass, which dictates its temperature, luminosity, and lifespan. Massive O- and B-type stars are hot, luminous, and short-lived, while faint M-type red dwarfs are long-lived and form the majority of stars in the galaxy. Main sequence stars maintain stability through hydrostatic equilibrium, with energy produced by hydrogen fusion via the proton–proton chain in low-mass stars and the CNO cycle in massive stars. Energy is transported by radiation or convection, depending on stellar mass. Stars are classified into spectral types O, B, A, F, G, K, and M, each with distinct properties and lifetimes ranging from millions to trillions of years. Once core hydrogen is exhausted, stars evolve into red giants or more complex end stages. Main-sequence stars are vital for astrophysics, serving as standard candles, models for stellar evolution, and hosts for exoplanets. They remain central to understanding cosmic structure and the search for habitable worlds.

Geetha Paul highlights in the article “BLAST and FASTA: Cornerstones of Sequence Alignment in Biosciences”, the critical role of sequence alignment in bioinformatics and how heuristic tools like FASTA and BLAST transformed the field. Early exhaustive algorithms like Smith–Waterman were accurate but computationally impractical for large databases, leading to the development of faster, word-based methods. FASTA, introduced in the 1980s, was the first widely used heuristic alignment tool, known for its sensitivity in detecting distant sequence similarities. BLAST, developed in 1990, advanced the approach with greater speed, statistical rigor, and variants such as BLASTN, BLASTP, and BLASTX for different biological queries. While BLAST is typically faster and widely used in large-scale genome annotation and routine database searches, FASTA remains valuable for its sensitivity and versatility in research-focused analyses. Together, these tools underpin modern genomics, proteomics, evolutionary biology, and biomedical research by enabling efficient, accurate detection of functional and

evolutionary relationships among DNA, RNA, and protein sequences. Their enduring relevance makes them foundational in both laboratory practice and bioinformatics education. The article “Minimising Synchronisation Overhead in Parallel Computing” by Ajay Vibhute examines the performance challenges caused by synchronisation in multi-core and many-core systems. While synchronisation tools like locks, barriers, and critical sections are essential for correctness when threads share data, they often introduce contention, blocking, context switching, and idle time that hinder scalability. Issues such as false sharing and barrier synchronisation can further degrade efficiency, with Amdahl’s Law highlighting how even small synchronised sections cap overall speedup. To address this, the article outlines key strategies: avoiding shared state through data partitioning or message passing, using lock-free algorithms with atomic operations, reducing reliance on barriers, batching or merging synchronisation events, and applying fine-grained locking. These techniques maximise concurrency, reduce contention, and improve throughput, making parallel programs more scalable and easier to maintain. The article emphasises that careful synchronisation management is central to unlocking the full potential of parallel computing.

News Desk - airis4D mentoring session



The airis4D mentoring program started with Dr Balamurali, Distinguished Scientist, TCS research, Bangalore and the Dr Arun Kumar, Chief Architect, Deep Alert, UK leading the interactive sessions. Students from the Computer Science and Electronics departments of Ranni St Thomas College and Engineering College, Kalloopara participated.

Contents

Editorial	ii
I Artificial Intelligence and Machine Learning	1
1 AlphaFold: Unlocking the Secrets of Life's Building Blocks	2
1.1 Introduction	2
1.2 Protein Structure	2
1.3 Unfolding with AI	2
1.4 Applications	3
1.5 Conclusion	4
2 Entropy Across Scales: From Micro-Level Randomness to Macro-Level Order	6
2.1 Physics: From Molecules to Thermodynamics	6
2.2 Language: From Letters to Discourse	7
2.3 Biology: From Genes to Ecosystems	7
2.4 Social Systems: From Individual Choices to Collective Patterns	8
2.5 Conclusion	9
II Astronomy and Astrophysics	10
1 Plasma Physics & Comets	11
1.1 Introduction	11
1.2 Structure of Comet	11
1.3 Plasma processes in Comets	12
1.4 Observational Insights from Space Missions	13
1.5 Challenges and Opportunities	14
1.6 Conclusion	15
2 X-ray Astronomy: Through Missions	16
2.1 Satellites in 2020s	16
3 Introduction: Galaxies in Motion	20
3.1 Introduction	20
3.2 Examining the Role of Environment	20
3.3 Key Findings: Bars in Different Environments	21
3.4 What's Behind These Differences?	21
3.5 Connecting the Dots: Environmental Impact on Galaxy Evolution	22
3.6 Why Bars Matter	22
3.7 Conclusion: A Deeper Understanding of Galaxy Evolution	22
4 Main Sequence Stars	24

4.1	Introduction	24
4.2	The Hertzsprung - Russell Diagram and the Main Sequence	24
4.3	Stellar Structure and Energy Generation	25
4.4	Classification of Main Sequence Stars	25
4.5	Lifetimes of Main Sequence Stars	25
4.6	End of Main Sequence Phase	26
4.7	Importance of Main Sequence Stars	26
4.8	Conclusion	26
III	Biosciences	27
1	BLAST and FASTA: Cornerstones of Sequence Alignment in Biosciences and Bioinformatics:	28
1.1	Introduction	28
1.2	What is FASTA?	29
1.3	FASTA as a Format:	29
IV	Computer Programming	32
1	Minimizing Synchronization Overhead in Parallel Computing	33
1.1	Introduction	33
1.2	Why Synchronization Hurts Performance	33
1.3	Reducing Synchronization Overhead	34
1.4	Summary	36

Part I

Artificial Intelligence and Machine Learning

AlphaFold: Unlocking the Secrets of Life's Building Blocks

by Arun Aniyan

AIRIS4D, VOL.3, No.10, 2025

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1.1 Introduction

Imagine a world where we can understand diseases at their most fundamental level, design new medicines with unprecedented precision, and even create novel materials with properties never before seen. This might sound like science fiction, but thanks to groundbreaking advancements in artificial intelligence, particularly with tools like Google's AlphaFold, this future is rapidly becoming a reality. AlphaFold isn't just another tech gadget; it's a revolutionary leap in our ability to understand the very building blocks of life: proteins. AlphaFold also won the Nobel Prize for Chemistry in 2024.

1.2 Protein Structure

To truly appreciate the impact of AlphaFold, we first need to understand what proteins are and why their structure is so important. Think of proteins as the tiny, molecular machines that run our bodies. They are involved in almost every biological process imaginable, from digesting our food and fighting off infections to building our tissues and transmitting signals in our brains. Each protein is made up of a long chain of smaller units called amino acids, linked together like beads on a string. What makes proteins so remarkable is that these chains don't just stay straight; they fold into incredibly complex and specific three-dimensional shapes. It's this unique 3D shape that dictates a protein's function. If a protein isn't folded correctly, it

cannot perform its function, and this misfolding is often at the root of many diseases, including Alzheimer's, Parkinson's, and certain cancers.

For decades, scientists have been trying to figure out these intricate protein shapes. This challenge, known as the "protein folding problem," has been one of the grandest and most enduring mysteries in biology. Why is it so difficult? Because even though the chain of amino acids is linear, the number of ways it can theoretically fold is astronomically large – more possibilities than there are atoms in the universe! Traditionally, determining a protein's structure has been a painstaking and time-consuming process, relying on experimental techniques like X-ray crystallography or cryo-electron microscopy. These methods are expensive, require specialised equipment, and often take years to yield results for even a single protein. This bottleneck severely limited our understanding of countless proteins, hindering drug discovery and fundamental biological research.

1.3 Unfolding with AI

Enter AlphaFold, a game-changer developed by DeepMind, a subsidiary of Google. AlphaFold is an artificial intelligence system that can predict the 3D structure of a protein directly from its amino acid sequence with astonishing accuracy. This is like being able to look at a tangled piece of string and instantly know exactly how it will coil and fold into a specific, functional object. The implications of this ability are

profound.

So, how does AlphaFold work its magic? At its core, AlphaFold uses a deep learning approach, a type of artificial intelligence inspired by the structure and function of the human brain's neural networks. Imagine giving a computer millions of examples of protein sequences and their corresponding 3D structures. The computer then "learns" the complex relationships between the sequence of amino acids and how they fold.

More specifically, AlphaFold employs a sophisticated neural network architecture that combines several key ideas. One crucial aspect is its ability to reason about the physical and chemical constraints that govern protein folding. It doesn't just guess; it understands that certain amino acids attract or repel each other, and that proteins tend to settle into a state of lowest energy. The system considers all possible interactions between the amino acids in the chain, much like a meticulous puzzle solver.

A pivotal component of AlphaFold's success is its attention mechanism. In simple terms, this allows the AI to "focus" on different parts of the amino acid sequence simultaneously, understanding how distant parts of the chain might interact with each other to influence the overall fold. It's like having a hyper-attentive chef who can keep track of every ingredient and cooking step, even those that seem unrelated at first glance, to ensure the perfect final dish.

Furthermore, AlphaFold uses an "evoformer" module, which leverages evolutionary information. Proteins with similar functions often have similar structures, and by analysing how protein sequences have changed over millions of years of evolution, AlphaFold gains valuable clues about their likely 3D shapes. It's like looking at a family tree of proteins and noticing shared traits that reveal underlying structural similarities.

Finally, AlphaFold refines its predictions iteratively. It starts with an initial guess for the protein's structure and then continuously adjusts and optimises it, much like a sculptor refining a clay model until it perfectly matches their vision. This iterative refinement, combined with its deep understanding of biological principles, allows AlphaFold to produce incredibly

accurate and detailed protein structures.

1.4 Applications

The impact of AlphaFold on protein research and its relevance to humanity are immense. Here's a glimpse into the transformations it's already bringing about and promises to deliver

1.4.1 Accelerated Drug Discovery and Development

One of the most immediate and impactful applications of AlphaFold is in the pharmaceutical industry. Many drugs work by binding to specific proteins in the body, either to activate or inhibit their function. Knowing the precise 3D structure of these target proteins is crucial for designing drugs that fit perfectly, like a key in a lock. Before AlphaFold, determining these structures was a major bottleneck, often taking years and costing millions. Now, researchers can rapidly predict the structures of target proteins, enabling them to design new drug candidates much faster and more efficiently. This will lead to the development of novel treatments for a wide range of diseases, from cancer and infectious diseases to metabolic disorders and neurological conditions. For example, AlphaMissense, an AI tool developed using AlphaFold, can classify the effects of 71 million 'missense' mutations, accelerating research in genetics and making it easier to prioritise resources for studying diseases.

1.4.2 Understanding Disease Mechanisms

Many diseases, as mentioned earlier, are caused by misfolded proteins. With AlphaFold, scientists can now quickly predict the structures of both healthy and diseased proteins, allowing them to pinpoint precisely how misfolding occurs and how it disrupts normal biological processes. This deeper understanding of disease mechanisms is fundamental to developing effective therapies. Imagine being able to see exactly where a protein goes wrong in Alzheimer's disease; this insight could unlock entirely new avenues for treatment.

1.4.3 Designing New Enzymes and Industrial Catalysts

Proteins also act as enzymes, biological catalysts that speed up chemical reactions. By understanding protein structure, scientists can design new enzymes with enhanced efficiency or novel functions for various industrial applications, such as biofuels production, waste treatment, and even food processing. This opens up possibilities for more sustainable and efficient industrial processes.

1.4.4 Revolutionising Material Science

Proteins are incredibly versatile materials in nature, forming everything from the silk in a spiderweb to the collagen in our skin. By understanding and predicting protein structures, scientists can begin to design novel proteins with specific properties, potentially leading to the creation of new biomaterials for applications in medicine, engineering, and beyond. Imagine creating self-healing materials or biodegradable plastics with unprecedented strength.

1.4.5 Advancing Fundamental Biological Research

Beyond immediate applications, AlphaFold is fundamentally changing how biological research is conducted. It provides a powerful tool for generating hypotheses, designing experiments, and interpreting results. Scientists can now explore the structures of proteins that were previously impossible to study, unlocking new insights into the intricate workings of living organisms. This democratisation of structural biology will lead to a surge of new discoveries across all branches of biology.

1.4.6 Personalised Medicine

In the future, AlphaFold could play a role in personalised medicine. As we gain a deeper understanding of an individual's genetic makeup, we could use tools like AlphaFold to predict the structures of their unique proteins and identify any structural variations that might predispose them to certain diseases

or affect their response to particular medications. This could lead to highly tailored treatments, optimised for each patient.

1.4.7 AI Advancing Science

It's important to note that while AlphaFold is incredibly powerful, it's a computational tool. Experimental validation of its predictions is still crucial, and ongoing research continues to refine and expand its capabilities. However, the speed and accuracy it offers are unprecedented, transforming the pace and scope of scientific discovery.

The excitement surrounding AlphaFold is palpable within the scientific community. It's not just a technical achievement; it's a testament to the power of artificial intelligence to solve complex problems that have stumped humanity for decades. This tool is democratizing access to structural biology, empowering researchers worldwide to tackle challenges that were once considered insurmountable.

As we move forward, the synergy between AI advancements, like those seen in AlphaFold, and biological research will only grow stronger. The ability of AI models to understand the "deep structure" of language and to apply nuanced responses in complex scenarios hints at a future where AI can not only predict but also reason and innovate in scientific domains. The recent release of GPT-5, described as a "universal intelligence partner" with integrated thinking that automatically recognises when quick answers are sufficient and when more complex reasoning is required, further highlights the increasing sophistication of AI in handling intricate problems. These advancements suggest a future where AI tools will become even more seamless partners in scientific discovery, accelerating the pace of innovation.

1.5 Conclusion

In conclusion, AlphaFold represents a monumental achievement in scientific research, marking a new era in our understanding of proteins and their roles in life. It's a tool that empowers scientists to unlock the secrets

of biological systems, accelerate drug discovery, and tackle some of humanity's most pressing challenges. The potential of AlphaFold to revolutionise medicine, biotechnology, and our fundamental understanding of life itself is truly thrilling, and its impact will undoubtedly be felt for generations to come. We are standing at the precipice of a new biological revolution, driven by the incredible power of artificial intelligence.

References

- <https://deepmind.google/science/alphafold/>

About the Author



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Entropy Across Scales: From Micro-Level Randomness to Macro-Level Order

by Jinsu Ann Mathew

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www.airis4d.com

In our earlier explorations, entropy appeared first in physics, then in information theory, language, and networks. At each step, it revealed itself as more than just a measure of disorder—it became a way of connecting hidden structures and uncertainties across different domains. So far, we have looked at entropy within a given system: molecules in a gas, words in a sentence, or nodes in a network. But entropy's true power emerges when we step back and ask a deeper question: how does randomness at one scale shape order at another?

Entropy provides a bridge from the micro to the macro, turning local unpredictability into global regularity. Whether we are studying particles and thermodynamics, words and discourse, or individuals and societies, entropy links the small-scale fluctuations to the large-scale patterns that emerge from them. This article explores that scaling role of entropy, showing how the same principle unifies physics, biology, language, and social systems.

2.1 Physics: From Molecules to Thermodynamics

At the heart of physics lies a profound challenge: while the microscopic world of molecules is governed by strict physical laws, the sheer number of particles makes prediction impossible in practice. Imagine a box filled with gas. Each molecule moves according to Newton's laws, bouncing, colliding, and transferring

energy. If we tried to describe the system at this level, we would need to know the position and velocity of trillions of molecules—an impossible task.

This is where entropy steps in. Instead of tracking each molecule, entropy provides a statistical summary of the system's possible configurations (microstates). It tells us how many ways the molecules can be arranged while still producing the same overall, observable condition (macrostate). For example, we cannot know the exact motion of every air molecule in a room, but we can confidently say that the air has a temperature of 25 °C and a pressure of 1 atmosphere. These macroscopic properties are stable precisely because they emerge from the law of large numbers acting on countless microscopic events.

Entropy connects the two levels by counting possibilities:

Micro-level (molecular world): Each random arrangement of particles is a microstate.

Macro-level (thermodynamic world): Temperature, pressure, and volume are macrostates that summarize many microstates.

Example

Consider two rooms connected by a door, with all the gas molecules initially confined to one room. At this moment, the entropy is low, because there are few possible microstates (most molecules are in the same place). But once the door opens, molecules begin to spread out. The number of possible arrangements

skyrockets as molecules distribute between both rooms. The system naturally evolves toward this higher-entropy state, not because molecules “want” to, but because there are overwhelmingly more possible microstates corresponding to it. This illustrates the second law of thermodynamics: in an isolated system, entropy tends to increase, because high-entropy macrostates are vastly more probable than low-entropy ones.

Entropy, therefore, acts as the bridge between the random dance of molecules and the predictable flow of thermodynamics. While the micro-world is chaotic, the macro-world is regular: gases expand, heat flows from hot to cold, and equilibrium is reached. Entropy explains why these large-scale patterns emerge from countless small-scale uncertainties.

2.2 Language: From Letters to Discourse

At the smallest scale of language are the letters themselves. If we look closely at English, for example, we find that some letters appear often while others are rare. The letter e is the most common, while z or q appear only occasionally. This uneven distribution creates a characteristic entropy for the language. A random sequence of letters like xqzjpk has high entropy because it is difficult to predict the next symbol, whereas a monotonous sequence like aaaaaa has almost no entropy at all. Real words, such as apple or forest, lie somewhere in between: partly predictable because they follow the rules of spelling, yet varied enough to convey information.

When we move from letters to words, entropy takes on a richer meaning. Consider two short passages:

- “Yes, yes, yes, yes.”
- “The river bends quietly under the old stone bridge.”

The first passage uses only one word repeated, producing very low entropy—there is little variety or surprise. The second passage, by contrast, draws on a wider vocabulary. Here entropy captures the diversity of word choice, showing how language can scale from the dull repetition of a few tokens to the richness of

expressive imagery. At this level, entropy becomes a measure of lexical creativity and informational density.

Sentences introduce a new kind of structure. Words must fit into grammatical patterns, and this restricts how unpredictable they can be. A phrase such as “cat the chased dog the” is technically high in entropy because it defies expectations, but it fails to communicate meaning. On the other hand, a formulaic phrase like “I am fine, thank you” is highly predictable, with low entropy, but also limited in informational value. The sweet spot lies in the middle, where sentences like “The child chased the dog across the garden” follow grammar yet leave room for novelty. Here entropy highlights how syntax balances order and variation.

At the largest scale—paragraphs and whole texts—entropy describes the flow of ideas. A story that repeats the same statement again and again quickly collapses into redundancy, like a system with entropy approaching zero. But a story that leaps chaotically between topics, never returning to a coherent theme, has entropy that is too high, making it confusing to follow. The best writing maintains a balance: each new sentence introduces some uncertainty, some novelty, yet remains tied to the context established before. A novel that develops its plot gradually, or a scientific article that builds argument upon argument, achieves this balance, moving from local unpredictability to global coherence.

Thus, just as molecules in motion give rise to the thermodynamic laws of heat, the small-scale unpredictability of letters and words accumulates into the large-scale order of discourse. Entropy is the thread that connects these levels, showing how language evolves from the randomness of characters to the structured richness of human communication.

2.3 Biology: From Genes to Ecosystems

Biological systems, like networks, reveal the interplay between local randomness and global order. At the genetic level, mutations occur unpredictably. A single nucleotide change in DNA might seem like a minor, random event with little immediate

consequence. Yet these small variations accumulate across generations, producing genetic diversity within a population. For example, in a population of fruit flies, some individuals may randomly acquire mutations that confer resistance to a particular pathogen. While each mutation is a local, stochastic event, collectively these variations provide the raw material for natural selection and adaptation. Entropy at this micro-level captures the unpredictability of genetic changes and the richness of possible traits in a population.

When we scale up to populations and communities, the effects of genetic entropy become visible in ecosystem-level patterns. Diverse traits within species increase the resilience of populations, allowing them to survive environmental fluctuations. In coral reef ecosystems, for instance, genetic variability among corals and their symbiotic algae determines how well the reef can recover from bleaching events caused by temperature changes. Similarly, the diversity of plant species in a rainforest ensures that some species will thrive under different conditions, stabilizing the ecosystem as a whole. Even though individual organisms behave unpredictably, the aggregation of these micro-level variations produces robust, adaptive systems.

Entropy thus provides a lens to understand biology across scales. At the gene level, it measures the uncertainty of mutations; at the species and ecosystem level, it quantifies the resulting diversity and resilience. Micro-level randomness does not imply chaos; rather, it underlies the emergence of structured, functional systems. This scaling—from stochastic mutations to the stability of entire ecosystems—illustrates a core principle: disorder at small scales fuels order and adaptability at large scales, making life both dynamic and robust.

2.4 Social Systems: From Individual Choices to Collective Patterns

Human societies are complex networks of interactions, where individual actions combine to create patterns that are often surprising and highly structured.

At the micro-level, each person's decisions—whether to buy a stock, share a social media post, or vote in an election—carry uncertainty. These decisions are influenced by personal preference, available information, social influence, and sometimes sheer chance. From the perspective of a single individual, behavior may appear unpredictable. Entropy captures this local uncertainty by quantifying the diversity and unpredictability of choices within a population. A market with many equally plausible investment decisions, for example, has high local entropy, while a tightly coordinated or heavily influenced population would show lower local entropy.

When aggregated across millions of individuals, these local uncertainties give rise to predictable patterns at the macro-level. In financial markets, while individual trades are largely random, the collective activity produces measurable volatility, trends, and cycles. In social media, seemingly random decisions to share content can generate viral phenomena, where a few posts spread rapidly through networks while most remain largely unseen. Similarly, in elections, the unpredictability of individual votes contrasts with the emergence of clear majority outcomes at the population level. This aggregation illustrates how local randomness is not chaos; rather, it feeds into emergent order.

Entropy provides the framework to connect these scales. By measuring the uncertainty of individual choices and comparing it to the variability of collective outcomes, researchers can better understand how micro-level behavior translates into macro-level social dynamics. For instance, entropy can help identify which individuals or groups have disproportionate influence—"opinion leaders" in social networks, or key investors in financial markets—whose actions significantly shape the system's global behavior. In this way, entropy bridges the gap between the unpredictability of single agents and the patterns that define societies, markets, and cultural evolution, demonstrating once again that local disorder often underlies large-scale order.

2.5 Conclusion

From the motion of particles and the structure of language to genetic diversity and human societies, entropy reveals a consistent principle: local unpredictability fuels global order. Whether through molecular randomness, word choice, genetic variation, or individual decisions, small-scale uncertainty accumulates to produce structure, diversity, and resilience at higher scales. This cross-domain perspective highlights entropy as a universal measure of complexity, showing how disorder at one level can generate emergent patterns, adaptability, and coherence at another. By examining entropy across these layers, we gain a deeper understanding of the hidden structures that shape the natural and social world.

References

- [Entropy - Physics](#)
- [Entropy Is Universal Rule of Language](#)
- [Universal Entropy of Word Ordering Across Linguistic Families](#)
- [Entropy and Information Approaches to Genetic Diversity and its Expression: Genomic Geography](#)
- [Information entropy as a measure of genetic diversity and evolvability in colonization](#)
- [Social Entropy and Normative Network](#)

About the Author



Jinsu Ann Mathew is a research scholar in Natural Language Processing and Chemical Informatics. Her interests include applying basic scientific research on computational linguistics, practical applications of human language technology, and interdisciplinary work in computational physics.

Part II

Astronomy and Astrophysics

Plasma Physics & Comets

by Abishek P S

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1.1 Introduction

In space science, plasma physics plays a foundational role in understanding the behaviour of the universe at both large and small scales. Since plasma constitutes over 99% of the visible universe, it is the dominant medium through which energy and matter interact in space. From the solar wind and planetary magnetospheres to interstellar clouds and galactic jets, plasma governs the dynamics of cosmic environments[1]. One of the most critical applications is in the study of space weather is the interaction between solar plasma and Earth's magnetic field. Solar flares and coronal mass ejections release vast amounts of plasma that can disrupt satellite operations, GPS systems, and even terrestrial power grids. Plasma physics helps model these events using magnetohydrodynamics (MHD) and kinetic theory, allowing scientists to predict and mitigate their effects

Comets are icy, small celestial bodies that orbit the Sun, often originating from the distant reaches of the solar system such as the Kuiper Belt and the Oort Cloud. Composed primarily of frozen gases, dust, and rocky material, they are sometimes described as “dirty snowballs.” When a comet approaches the Sun, solar heat causes its ices to sublimate, releasing gas and dust that form a glowing coma and often two distinct tails, one of dust and one of ionized plasma. These spectacular features make comets some of the most visually striking objects in the night sky[2]. Plasma processes in comets are central to understanding how these icy bodies interact with their space environment, especially as they approach the Sun. When a comet

nears the Sun, solar radiation heats its nucleus, causing volatile gases to sublimate and escape into space. These gases, once released, become ionized by ultraviolet radiation and collisions with solar wind particles, forming a plasma environment around the comet.

1.2 Structure of Comet

The structure of comets is a fascinating and multilayered system that reflects both their primordial origins and their dynamic interactions with the solar environment. Comets are composed of five primary components: the nucleus, coma, hydrogen envelope, plasma (ion) tail, and dust tail, each playing a distinct role in the comet's behaviour and evolution[2,3]. The nucleus is the solid core of the comet and the source of all observable activity. It is typically irregular in shape and composed of a mixture of volatile ices (primarily water ice, but also CO[2082?], CO, CH[2084?], and NH[2083?]), silicate dust, and organic compounds. These materials are thought to be remnants from the early solar system, making comet nuclei valuable archives of primordial matter. Nuclei range in size from a few hundred meters to tens of kilometres. Their surfaces are often covered in a dark, carbon-rich crust that insulates the interior and influences sublimation patterns.

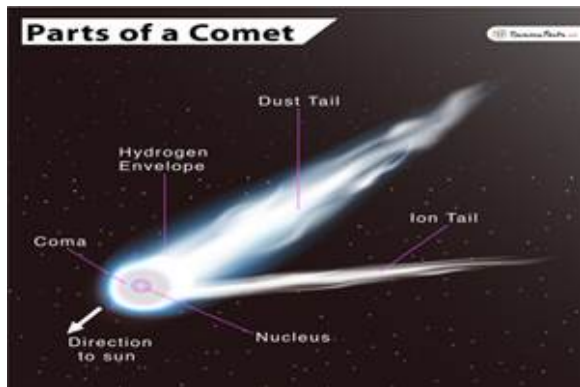


Fig. 1: Structure of Comet

Image courtesy :Parts of a Comet: Name, Composition, & Labelled Diagram

As the comet approaches the Sun, solar heating causes the ices in the nucleus to sublime, releasing gas and dust that form a surrounding atmosphere known as the coma. This region can extend thousands of kilometres and contains neutral molecules, radicals, and dust particles. The coma is the visible “head” of the comet and serves as the transition zone between the solid nucleus and the external environment. Surrounding the coma is an extended cloud of neutral hydrogen atoms, formed when solar ultraviolet radiation dissociates water molecules. This hydrogen envelope can stretch millions of kilometres and is detectable only in ultraviolet wavelengths. It plays a key role in the comet’s interaction with solar radiation and helps trace the water content of the nucleus.

The plasma tail forms when ionized gas from the coma interacts with the solar wind. Charged particles like CO^+ and H_2O^+ are swept away by the Sun’s magnetic field, creating a tail that points directly away from the Sun. This tail can extend tens of millions of kilometres and often glows blue due to emissions from ionized carbon monoxide. The structure of the plasma tail includes features like bow shocks, contact surfaces, and cometopauses, which are shaped by the solar wind’s pressure and magnetic field lines. The dust tail consists of small solid particles released from the nucleus. These particles are pushed outward by solar radiation pressure, forming a curved tail that follows the comet’s orbital path. The dust tail reflects sunlight and typically appears yellowish-white. It contains larger particles than the plasma tail and can persist long after the comet has passed perihelion.

1.3 Plasma processes in Comets

1.3.1 Outgassing and Ionization

Outgassing and ionization are two fundamental plasma processes that govern the dynamic behaviour of comets as they interact with the solar environment. As a comet approaches the Sun, solar heating causes the volatile ices within its nucleus, primarily water (H_2O), carbon dioxide (CO_2), and carbon monoxide (CO) to sublime, releasing neutral gas and dust into space. This process, known as outgassing, forms the coma, a vast and expanding atmosphere surrounding the nucleus. The density and composition of the coma vary with the comet’s proximity to the Sun and its intrinsic activity[4]. Once released, the neutral molecules in the coma are exposed to intense ultraviolet radiation from the Sun, which ionizes them through photoionization and charge exchange processes. This transformation marks the beginning of the comet’s plasma environment, as neutral atoms become charged particles, electrons and ions that respond to electromagnetic forces. The newly formed plasma interacts with the solar wind, a stream of charged particles emitted by the Sun, leading to the development of large-scale structures such as bow shocks, magnetic pile-up regions, and the ion tail. These interactions are not static; they evolve as the comet’s activity changes, offering researchers a rare opportunity to study both collisional and collisionless plasma regimes in a naturally occurring setting. Missions like ESA’s *Rosetta* have provided high-resolution measurements of these processes, revealing how plasma boundaries form, shift, and dissipate in response to solar wind conditions and cometary outgassing rates. Through these observations, scientists gain critical insights into the physics of ionized gases, the behaviour of dusty plasmas, and the mechanisms that shape cometary evolution and solar system dynamics.

1.3.2 Dust Plasma Interactions

Dust-plasma interactions in comets represent a critical and complex aspect of cometary physics, offering unique insights into how charged particles and

solid grains behave in space. As a comet approaches the Sun, solar heating causes volatile gases to sublimate from the nucleus, entraining dust particles in the outflow. These dust grains, composed of silicates, carbonaceous material, and ice, become immersed in the surrounding plasma formed by ionized gas molecules. Through processes such as photoelectric charging, collisions with electrons and ions, and secondary electron emission, the dust particles acquire electric charges, transforming the cometary environment into a dusty plasma, a medium where both charged particles and charged dust grains interact dynamically [4,5]. This charged dust influences the local electric fields, modifies plasma wave propagation, and contributes to the formation of large-scale structures like the bow shock and plasma tail. Studies from missions like *Rosetta* and *Stardust* have shown that dust-plasma coupling affects the morphology of the coma and tail, alters particle trajectories, and can even lead to the formation of filamentary structures and jets. Moreover, the presence of dust changes the energy balance and conductivity of the plasma, making cometary environments ideal for studying non-equilibrium plasma behaviour. These interactions are not only vital for understanding comet evolution but also have broader implications for planetary ring systems, interplanetary dust dynamics, and astrophysical plasmas

1.3.3 Solar Wind Interaction

Solar wind interaction is one of the most critical plasma processes in comets, shaping their ion environment and revealing fundamental physics about mass-loaded plasmas in space. As a comet approaches the Sun, its nucleus begins to sublimate, releasing neutral gases into the coma. These gases are subsequently ionized by solar ultraviolet radiation and collisions with solar wind particles, forming a plasma-rich atmosphere. The solar wind, a continuous stream of charged particles emitted by the Sun encounters this expanding plasma, leading to a dynamic and complex interaction. This process results in the formation of large-scale structures such as bow shocks, magnetic pile-up regions, and the cometopause, which marks the boundary between solar wind-dominated

and cometary plasma-dominated regions. Observations from ESA's *Rosetta* mission at comet 67P/Churyumov–Gerasimenko showed that as the comet moved from 3.6 AU to 2.0 AU from the Sun, the number of water ions accelerated by the solar wind increased dramatically, with daily rates rising by a factor of 10,000 [6,7]. These ions, once formed, are swept away by the solar wind's electric and magnetic fields, contributing to the formation of the comet's ion tail. Additionally, solar wind particles can penetrate the coma and strike the comet's surface, causing sputtering, a process that liberates atoms from the surface into space, further enriching the plasma environment. The interaction is highly variable and depends on factors such as solar activity, the comet's outgassing rate, and its distance from the Sun. This variability allows researchers to study transient plasma phenomena, including wave-particle interactions and magnetic reconnection, in a naturally evolving system. Comets, therefore, offer a unique opportunity to observe how solar wind interacts with non-magnetized, mass-loading bodies, advancing our understanding of plasma physics in both planetary and astrophysical contexts.



Fig. 2: 67P/Churyumov–Gerasimenko

1.4 Observational Insights from Space Missions

Observational insights from cometary missions have revolutionized our understanding of these ancient bodies, transforming them from enigmatic wanderers into well-characterized laboratories of solar system science. Spacecraft such as ESA's *Rosetta*, NASA's *Deep Impact*, *Stardust*, and *Giotto* have provided unprecedented in situ data on cometary nuclei, comae,

and plasma environments. For instance, *Rosetta*'s multi-year study of comet 67P/Churyumov–Gerasimenko revealed a bilobate nucleus with complex surface morphology, including cliffs, pits, and jets, as well as seasonal changes in outgassing and dust activity. Instruments aboard *Rosetta* measured variations in plasma density, ion composition, and magnetic field strength, offering real-time insights into how solar wind interacts with a non-magnetized, mass-loading body. Similarly, *Stardust* returned samples from comet Wild, allowing laboratory analysis of mineral grains and organic compounds that confirmed the presence of high-temperature materials, suggesting that comets contain components formed in diverse regions of the early solar nebula. More recently, NASA's James Webb Space Telescope and Hubble have collaborated to study interstellar comet 3I/ATLAS, revealing a carbon dioxide-dominated gas coma and providing clues about the chemistry of objects formed outside our solar system[8]. These missions have also enabled remote sensing of nucleus properties such as size, rotation, albedo, and fragmentation behaviour, with radar and infrared surveys expanding our catalogue of cometary characteristics. Collectively, these observational campaigns have deepened our understanding of cometary evolution, plasma interactions, and the role of comets in delivering volatiles and organics to planetary surfaces, making them indispensable to planetary science and astrophysics.



Fig. 3: Rosetta spacecraft

1.5 Challenges and Opportunities

Studying plasma processes in comets presents a rich landscape of scientific challenges and opportunities,

especially as we move toward more sophisticated missions and modelling techniques. One of the foremost challenges lies in modelling dusty plasmas, which requires the integration of fluid dynamics with electromagnetic theory. Unlike conventional plasmas, cometary environments contain charged dust grains that interact with ions and electrons, altering the local electric fields and wave propagation. This coupling introduces nonlinearities and multi-scale behaviour that are difficult to simulate accurately. Researchers must account for grain charging mechanisms, particle collisions, and electromagnetic feedback, often relying on hybrid models that combine kinetic and fluid approaches to capture the full complexity of the system.

Another major challenge is the temporal evolution of plasma properties. As a comet travels through its orbit, its proximity to the Sun changes dramatically, leading to variations in outgassing rates, ionization levels, and solar wind interaction. These changes can transform the plasma environment from a weakly ionized, collisional regime into a highly dynamic, collisionless one. Instruments aboard ESA's *Rosetta* mission revealed that comet 67P/Churyumov–Gerasimenko exhibited significant variability in plasma density, magnetic field strength, and boundary formation as it approached perihelion. This temporal evolution complicates data interpretation and demands continuous monitoring to understand how plasma structures form, evolve, and dissipate.

Comparative studies across different comets further highlight the diversity of plasma behaviour. While earlier flyby missions provided snapshots of cometary environments, *Rosetta* offered long-term, close-up observations that revealed unexpected complexity. For example, 67P displayed asymmetric outgassing, localized jets, and a highly structured plasma tail, challenging pre-existing models that assumed more uniform behaviour. These findings underscore the need for multi-comet studies to identify universal plasma processes versus those that are comet-specific, shaped by factors such as nucleus composition, rotation, and orbital dynamics.

Looking ahead, future missions like ESA's *Comet Interceptor* promise to open new frontiers in cometary

plasma research. Scheduled for launch in 2029, this mission will target a dynamically new comet, one that has never entered the inner solar system before. By intercepting such a pristine object, scientists hope to observe plasma interactions in an environment untouched by previous solar exposure. The mission's innovative design includes multiple spacecraft that will perform simultaneous measurements from different vantage points, enabling three-dimensional mapping of plasma structures and real-time analysis of solar wind interaction. This multi-point approach will help resolve longstanding questions about plasma boundary formation, dust charging dynamics, and the role of comets in shaping heliospheric conditions.

1.6 Conclusion

The study of cometary plasmas is entering a transformative era. While modelling and observational challenges remain, the opportunities for discovery, especially with next-generation missions are vast and deeply promising for both planetary science and fundamental plasma physics.

References

- [1] Francis, F, Chen., (2015). Introduction to Plasma Physics and Controlled Fusion (3rd ed.). Springer Cham.<https://doi.org/10.1007/978-3-319-22309-4>
- [2]Greenberg, J. M. (1998). "Making a comet nucleus." *Astronomy and Astrophysics*. v. 330, p. 375-380, 330, 375-380.
- [3] Klaude, M., Eriksson, S., Nygren, J., & Ahnström, G. (1996). "The comet assay: mechanisms and technical considerations." *Mutation Research/DNA Repair*, 363(2), 89-96.
- [4] Galeev, A. A., & Lipatov, A. S. (1984). "Plasma processes in cometary atmospheres." *Advances in Space Research*, 4(9), 229-237.
- [5] Gombosi, T. I. (1991). "The plasma environment of comets." *Reviews of Geophysics*, 29(S2), 976-984.
- [6] Altwegg, K., Balsiger, H., Bar-Nun, A., Berthelier, J. J., Bieler, A., Bochsler, P., ... & Wurz, P. (2015). "67P/Churyumov-Gerasimenko, a Jupiter family comet with a high D/H ratio." *Science*, 347(6220), 1261952..
- [7] Sierks, H., Barbieri, C., Lamy, P. L., Rodrigo, R., Koschny, D., Rickman, H., ... & Paetzold, M. (2015). "On the nucleus structure and activity of comet 67P/Churyumov-Gerasimenko." *Science*, 347(6220), aaa1044.
- [8] Loeb, A. (2025). "3I/ATLAS is Smaller or Rarer than It Looks." *Research Notes of the AAS*, 9(7), 178.

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X-ray Astronomy: Through Missions

by Aromal P

AIRIS4D, VOL.3, No.10, 2025

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2.1 Satellites in 2020s

The last decade has marked a giant leap forward in astrophysics with the advent of X-ray polarimetry. Previously, our understanding of cosmic X-ray sources was limited to what we could learn from images, spectra, and timing analysis. Now, thanks to the groundbreaking success of the Imaging X-ray Polarimeter Experiment (IXPE), we can study the polarization of X-rays. This powerful new window into the high-energy universe provides invaluable information about the magnetic field geometry around extreme cosmic objects.

Although the first attempts to measure X-ray polarization date back to the 1970s, the dream was long hindered by technological hurdles. The primary challenge is that polarimetry is a "photon-hungry" technique, requiring long observations (often over 80,000 seconds) to gather enough data for a meaningful measurement. IXPE's innovative design has finally overcome this barrier, revolutionizing our ability to study the most energetic phenomena in the cosmos.

2.1.1 IXPE

Imaging X-ray Polarimetry Explorer (IXPE) is a game-changer for X-ray astronomy. As the first observatory built specifically for X-ray polarimetry, this joint NASA and Italian Space Agency (ASI) mission gives us a whole new way to see the universe. It adds polarization measurements to the traditional toolkit of images, timing, and spectroscopy, capturing all of this data at the same time. IXPE was successfully launched on December, 2021, aboard a SpaceX Falcon 9 rocket. The spacecraft operates in a circular low

Earth orbit (LEO) at an altitude of 600 km with an inclination of approximately 0 degrees. The mission's main goal is to look for cosmic features that have a specific direction or structure, which can't be seen with regular X-ray telescopes. This includes things like organized magnetic fields, lopsided clouds of matter, and the warping effects of intense gravity predicted by general relativity. Mission had a lifetime of 2 years and it is begin to start its fifth year operation in space. IXPE uses three identical mirror assemblies (MMA) to focus X-rays. Each mirror assembly converges the X-rays onto a detector placed exactly 4 meters away.

The real power of IXPE comes from its three advanced Gas Pixel Detectors, the result of over two decades of dedicated work by Italian research teams. When an incoming X-ray photon strikes a gas atom inside a detector, it knocks an electron free, creating a tiny, tell-tale track. This track is immediately captured by a custom-designed, highly sensitive chip. By analyzing the track's specific shape and direction, scientists can measure not only the X-ray's energy and origin but, for the first time, its polarization. MMA have an effective area of 590 cm² at 4 keV with a field of view of 12.9 arcminutes squared. It also had a temporal resolution of 100 microsecond and a spectral resolution of 0.57 keV at 2 keV.

Since it began its mission in 2022, IXPE has delivered a stream of groundbreaking discoveries across the cosmos. By studying supernova remnants, it mapped the average magnetic field of Cassiopeia A and, in a first for X-ray polarimetry, confirmed that the magnetic field wraps around the shockwave rim of RX J1713.7-3946. In a landmark observation of the black hole

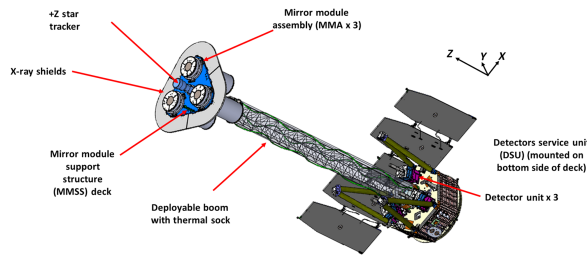


Figure 1: The IXPE Observatory highlighting the key scientific payload elements (credit:[1])

Cygnus X-1, IXPE provided the first direct proof that the swirling disk of matter falling in is what launches the powerful jets shooting out. The observatory also gave us our first-ever polarized view of magnetars, including 4U 0142+61, revealing the structure of their intense magnetic fields. On top of this, by watching over a dozen pulsars spin, it has shown that their magnetic environments are complex and change dramatically with every rotations

2.1.2 XRISM

The X-Ray Imaging and Spectroscopy Mission (XRISM) is an international X-ray astronomy satellite created to advance our knowledge of the hot universe through high-resolution X-ray spectroscopy. It serves as the replacement for the ASTRO-H (Hitomi) satellite, whose mission ended unexpectedly in 2016 after just one month, despite collecting valuable scientific data. XRISM was launched successfully on September, 2023, from the JAXA Tanegashima Space Center on an H-IIA rocket. The satellite is a cooperative mission between the Japan Aerospace Exploration Agency (JAXA) and the National Aeronautics and Space Administration (NASA), with contributions from the European Space Agency (ESA) and other international groups. XRISM circles the earth in a low-Earth orbit of radius 575 km and inclination of 31° specifically chosen to enhance scientific output and reduce background interference. XRISM carries two complementary advanced X-ray instruments that together provide comprehensive observational capabilities which works in the energy band 0.3-13 keV in total.

- Resolve(High-Resolution X-ray Microcalorimeter) is the main science payload on the XRISM satellite. At its heart is a special

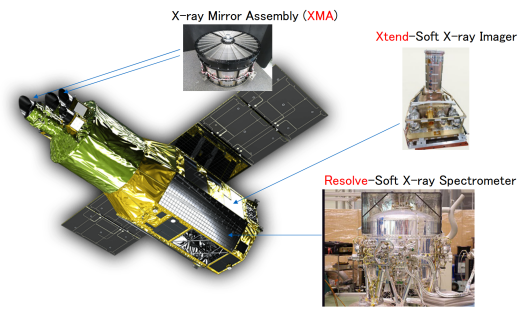


Figure 2: Schematic view of the XRISM satellite (credit: [12])

36-pixel sensor that works like a super-sensitive X-ray camera. To detect the tiny energy from a single X-ray, this sensor must be cooled to an extreme temperature of 50 millikelvin, which is just a fraction of a degree above absolute zero. The instrument's key feature is its incredible energy resolution of about 5 eV, which is even better than the original design goal. This ability is crucial because it lets scientists clearly see individual "spectral lines. It has a field of view of 3×3 arcminute and Resolve can detect X-rays from 0.3 to 12 keV energy range. Resolve have a timing resolution of 1 milliseconds.

- Xtend is a wide-field X-ray telescope that pairs a specialized CCD-camera (the Soft X-ray Imager, or SXI) with a mirror assembly (XMA). Its has is an exceptionally large field of view covering a 38.5×38.5 arcminute area of the sky, the biggest of any X-ray telescope. It is highly sensitive, with an effective collection area of 420 cm^2 for X-rays at an energy of 1.5 kilo-electron volts (keV). The instrument detects X-rays in the 0.4 to 13 keV energy range and can distinguish between their energies with a precision of 170-180 electron volts (eV) when observing X-rays at 6 keV.

High-resolution X-ray studies using XRISM revealed the complex dynamics of several key galactic objects. In the supernova remnant W49B, astronomers found the first kinematic proof of two-sided, or bipolar, flows of ejected material. Another study of MAXI J1744-294 detected intricate iron line structures for the first time, with coexisting emission and absorption

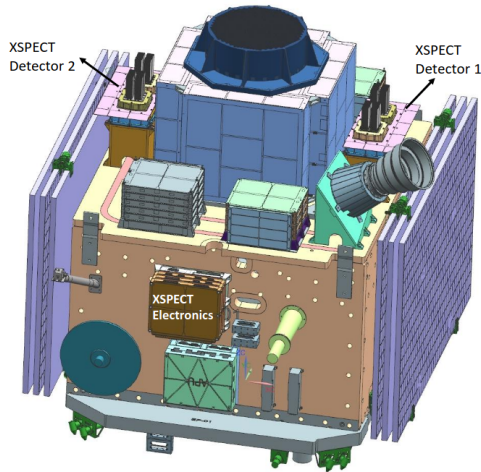


Figure 3: XPoSat satellite (credit: URSC, RRI, ISRO)

features that suggest a layered and turbulent medium is reprocessing the X-rays. Finally, a significant discovery was made around the microquasar V4641 Sgr, where a large cloud of extended X-ray emission was detected, confirming more activity around this powerful particle accelerator.

2.1.3 XPoSat

X-ray Polarimeter Satellite (XPoSat) is India's first dedicated X-ray polarimetry mission, a significant achievement that makes it only the second country to deploy such a specialized observatory in space. Launched successfully by ISRO on New Year's Day 2024, the satellite now operates from a 650-kilometer low Earth orbit. Its primary goal is to advance our understanding of high-energy astrophysical phenomena, like black holes, by conducting detailed studies of the polarization and spectroscopic characteristics of their X-ray emissions. XPoSat carries two co-aligned scientific instruments that work in tandem to provide comprehensive X-ray observations in the energy range 0.2-30 keV.

- Polarimeter Instrument in X-rays (POLIX) is an X-ray polarimeter designed to study cosmic sources in the 8-30 keV energy range. Its design features a central scatterer made of a low-atomic-mass material, which is surrounded by four X-ray proportional counters. Incoming polarized X-rays hit the scatterer and are

anisotropically scattered—a process known as Thomson scattering—allowing their polarization to be measured. To ensure that only a single bright source is observed at a time, a collimator restricts the instrument's field of view to 3×3 degrees. As the first payload dedicated to polarimetry in the medium X-ray band.

- The X-Ray Spectroscopy and Timing (XSPECT) instrument, a key payload on the XPoSat mission, is designed to monitor the long-term spectral evolution of select celestial sources in the soft X-ray band. Operating from 0.8 to 15 keV, it utilizes passively cooled Swept Charge Devices (SCDs) to ensure a large detection area and high-quality spectral data. The instrument is equipped with collimators offering two distinct fields of view (2×2 and 3×3 degrees) and boasts a fine spectroscopic resolution of under 200 eV at 6 keV, along with a respectable timing precision of 2 milliseconds.

2.1.4 Einstein Probe

The Einstein Probe (EP) is a Chinese-led space mission dedicated to time-domain high-energy astrophysics. Launched on January 9, 2024, via a Long March 2C rocket from the Xichang Satellite Launch Center, the mission is a collaborative effort between the Chinese Academy of Sciences (CAS), the European Space Agency (ESA), the Max Planck Institute for Extraterrestrial Physics (MPE), and the French National Centre for Space Studies (CNES). The satellite operates in a sun-synchronous circular orbit at an altitude of 592 kilometers, featuring an orbital period of 97 minutes. EP carries two complementary X-ray telescopes, works in 0.5-4 keV X-ray energy range.

- The Wide-field X-ray Telescope (WXT) utilizes innovative lobster-eye micro-pore optics (MPO), a biomimetic design where thousands of square microscopic channels are arranged in a square-packed array pointing to a common spherical center. The instrument is composed of 12 identical modules, each functioning as a complete telescope with its own optics and

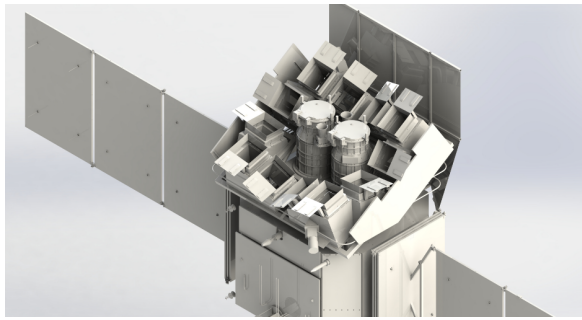


Figure 4: Layout of the payloads and spacecraft of the Einstein Probe satellite. The two FXT units are placed at the centre, surrounded by the twelve WXT modules (credit: IAMC, CAS)

a complementary metal-oxide-semiconductor (CMOS) detector. With a focal length of 375 mm, the optics are optimized for the 0.5-4 keV energy range. The complete 12-module system provides an instantaneous field-of-view of 3,600 square degrees and achieves a spatial resolution of 4-7 arcminutes FWHM, with a median of 4.2 arcminutes across the field.

- The Follow-up X-ray Telescope (FXT) comprises two identical Wolter-I type telescopes, FXT-A and FXT-B, each functioning as a complete X-ray imaging system. The telescopes feature a focal length of 1,600 mm and a combined effective area of approximately 600 cm^2 . They achieve a spatial resolution with a point spread function half-energy width (PSF HEW) under 20 arcseconds on-axis at 1.49 keV and provide an individual field of view of about 1 degree in diameter. Operating across the 0.3-10 keV energy range, the FXT offers broader spectral coverage than the WXT, facilitating comprehensive spectroscopic analysis.

Since beginning operations, the Einstein Probe has revolutionized the study of fast X-ray transients and multi-messenger astronomy. In its first year, the mission detected 72 high signal-to-noise fast X-ray transients (FXTs), discoveries which have provided unprecedented insights into this mysterious class of extragalactic phenomena

We have covered the major X-ray astronomical missions. We will explore the world of X-ray astronomy in upcoming articles.

References

- [1] Weisskopf et al., 2022, J. Astron. Telesc. Instrum. Syst., doi:10.1117/1.JATIS.8.2.026002
- [2] Mercuri et al., 2025, ApJ, doi: 10.3847/1538-4357/adcedb
- [3] Ferrazzoli et al., 2024, ApJL, doi:10.3847/2041-8213/ad4a68
- [4] Steiner et al., 2024, ApJL, doi:10.3847/2041-8213/ad58e4
- [5] Terada et al., 2024, SPIE, doi:10.1117/12.3019329
- [6] XRISM Collaboration, 2025, PASJ, doi:10.1093/pasj/psae111
- [7] XRISM Collaboration, 2025, ApJL, doi:10.3847/2041-8213/ade138
- [8] Chatterjee et al., 2025, arXiv, doi:10.48550/arXiv.2506.22964
- [9] Suzuki et al., 2024, arXiv, doi:10.48550/arXiv.2412.08089
- [10] Radhakrishna et al., 2025, J. Astron. Telesc. Instrum. Syst., doi:10.1117/1.JATIS.11.3.035001
- [11] Cheng et al., 2025, arXiv, doi:10.48550/arXiv.2505.18939
- [12] Team, XRISM Science, 2022, arXiv, doi:10.48550/arXiv.2202.05399
- [13] Aryan et al., 2025, arXiv, doi:10.48550/arXiv.2504.21096

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Introduction: Galaxies in Motion

by Robin Thomas

AIRIS4D, VOL.3, No.10, 2025

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3.1 Introduction

This article explores the findings of the study **”Properties of Barred Galaxies with the Environment: II. The case of the Cosmic Web around the Virgo cluster”** by Virginia Cuomo and collaborators (Cuomo et al. 2025). The research investigates how environmental factors affect the size and prominence of bars in disk galaxies, comparing galaxies located in the dense Virgo Cluster, surrounding filaments of the Cosmic Web, and in the field.

Galaxies are constantly evolving within the vast cosmic web—a complex network of filaments, clusters, and voids that shapes the universe’s large-scale structure. Just as our planet’s environment influences life on Earth, the environment surrounding galaxies plays a crucial role in determining their properties. In the research article **”Properties of Barred Galaxies with the Environment: II. The case of the Cosmic Web around the Virgo cluster”**, Virginia Cuomo and collaborators explore how different cosmic environments impact the formation and evolution of bars in disk galaxies.

A galactic bar is a central, elongated structure made up of stars, typically seen in spiral galaxies. These bars can affect the galaxy’s rotation, star formation, and gas dynamics. Understanding how bars form and evolve in different environments is essential for deciphering galaxy evolution at large. In this study, the authors focused on barred galaxies in various environments: the dense core of the **Virgo Cluster**, the surrounding **filaments of the Cosmic Web**, and the **field**—regions far from dense clusters.

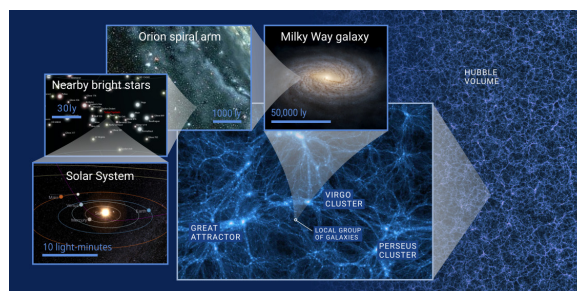


Figure 1: Comparison of scales showing our position in the Milky Way and the Local Group (top row) and the Local Group position in the nearby part of the Cosmic Web (bottom panel + background) on top of a theoretically modelled dark matter map of the nearby universe showing high density regions in bright color and low density regions in dark (Credits: The figure is based on adaptations of images of NASA, theskylive.com, GAIA and the CLUES project)

3.2 Examining the Role of Environment

The study uses a homogeneous sample of barred galaxies from the DESI Legacy Survey, ensuring that the sample is unbiased in terms of galaxy color and magnitude. The researchers then examined the bars’ properties by employing Fourier analysis and surface brightness fitting techniques. By comparing galaxies from three different environments, they aimed to uncover how the surrounding cosmic structure influences the size, prominence, and overall evolution of the bars.

3.3 Key Findings: Bars in Different Environments

The researchers found striking differences in the properties of bars depending on their environment. These differences provide crucial insights into the interplay between galaxies and their surroundings.

3.3.1 Bar Radii

The results revealed clear trends in the size of bars across different environments. Galaxies in the Virgo cluster, a high-density environment, tend to have smaller bars, with a median bar radius of 2.54 ± 0.34 kpc. In contrast, galaxies in filaments, which are the structures that connect galaxy clusters, exhibit slightly larger bars with a median radius of 3.29 ± 0.38 kpc. Galaxies located far from the influence of clusters or filaments, in the field, show the largest bars, with a median radius of 4.44 ± 0.81 kpc.

3.3.2 Bar Prominence

The prominence of the bars, which refers to how large they are relative to the overall galaxy disk, also varies significantly across the different environments. In the Virgo cluster, bars are less prominent, with a ratio of 1.26 ± 0.09 between the bar radius and disk scale length. The ratio increases in galaxies in filaments, where it reaches 1.72 ± 0.11 , indicating slightly more prominent bars. In field galaxies, bars are the most prominent, with a ratio of 2.57 ± 0.21 . These results show a clear trend: galaxies in dense environments, such as the Virgo cluster, tend to have shorter and less prominent bars, while those in the field, away from such environmental pressures, possess larger and more prominent bars.

3.4 What's Behind These Differences?

The observed differences in the size and prominence of bars across different environments suggest that the surrounding cosmic environment plays a significant role in shaping the structural properties of barred galaxies. Galaxies in different environments

experience distinct physical processes that influence their morphology and dynamics. These processes include tidal interactions, gas stripping, and the overall dynamical friction exerted by the surrounding environment. Let's delve deeper into each of these environmental factors and how they may hinder or facilitate the formation and growth of bars.

3.4.1 Tidal Interactions

In high-density environments such as the Virgo Cluster, galaxies are more likely to interact with neighboring galaxies. These interactions can lead to strong tidal forces, which can distort a galaxy's disk and alter its star formation. Tidal interactions often cause a redistribution of gas within the galaxy, which may prevent it from accumulating in the central regions and forming a strong bar. In the case of galaxies in the Virgo Cluster, the increased frequency of interactions may disrupt the growth of bars, leading to smaller and less prominent bars. These tidal forces can prevent the normal process of bar formation by scattering or redistributing the gas, making it difficult for the galaxy to develop a well-defined central bar structure.

3.4.2 Gas Stripping and Strangulation

In clusters like Virgo, galaxies are exposed to harsh environments that can strip away their gas through a process known as ram pressure stripping. This occurs when a galaxy moves through the hot gas of the intracluster medium, causing the galaxy's gas to be pushed out of its disk. Without sufficient gas, galaxies lose the fuel necessary for the growth of bars. Moreover, the removal of gas can lead to strangulation, a process in which star formation is suppressed due to the lack of fresh gas. In such cases, barred galaxies may experience slower bar evolution, resulting in shorter and less prominent bars compared to galaxies in the field or in filaments. This lack of gas availability significantly impacts the bar's growth and evolution, as the presence of gas is necessary for the angular momentum redistribution required for bar formation.

3.4.3 Dynamical Friction and Cluster Effects

Another factor at play in dense environments is dynamical friction. As galaxies interact with each other, the gravitational pull of one galaxy can cause another to lose energy, slowing its motion and allowing it to sink toward the center of the cluster. This can result in the formation of more compact and less defined bars. The Virgo Cluster, being a dense environment, promotes such processes, which could contribute to the observed trend of shorter bars in galaxies residing there. The accumulation of galaxies toward the cluster's center can cause more violent interactions, further hindering bar development by disrupting the dynamics of each individual galaxy's disk. As a result, the bars in these galaxies are often smaller and less prominent compared to their counterparts in less dense regions.

3.4.4 Filaments and Low-Density Environments

In contrast, galaxies in filaments, which are the web-like structures that connect clusters, experience less frequent and intense interactions. The gas content in these galaxies is also less likely to be stripped or disrupted, providing a more stable environment for the formation of bars. In these regions, galaxies can retain more of their gas, and the growth of bars is less hindered by the disruptive forces seen in dense clusters. As a result, galaxies in filaments tend to have moderately sized and more prominent bars compared to those in the cluster core.

Finally, galaxies in the field, where environmental influences are minimal, are free from the disruptive forces of tidal interactions and gas stripping. These galaxies are able to accumulate gas more easily, and the evolution of their bars can proceed without hindrance. In the field, galaxies enjoy an environment where their internal dynamics and gas content are largely unaffected by external forces, allowing the formation of large, prominent bars. These galaxies can evolve freely, with bar formation progressing over time without interference from surrounding galaxies or the intracluster medium.

3.5 Connecting the Dots:

Environmental Impact on Galaxy Evolution

The findings presented in this study align with previous research showing that **galaxies in clusters** often have shorter bars compared to those in the **field**. This study, however, provides new insights by offering a more homogenous and carefully selected sample, minimizing potential observational biases.

The fact that **bars in the Virgo cluster are shorter and less prominent** suggests that environmental factors like galaxy-galaxy interactions and gas stripping could play a critical role in **hindering the secular evolution of barred galaxies**. Conversely, galaxies in less dense environments, such as the field or cosmic web filaments, can evolve without such hindrances, allowing for the growth of more substantial and more prominent bars.

3.6 Why Bars Matter

Bars are not just structural features; they are **key players in the secular evolution** of galaxies. They act as mechanisms for redistributing gas and stars within galaxies, helping drive star formation and potentially influencing the central black hole growth. The study suggests that **bars in dense environments like the Virgo cluster** may evolve differently, impacting galaxy dynamics and even the potential for future star formation.

3.7 Conclusion: A Deeper Understanding of Galaxy Evolution

The study's findings underscore the **dynamic relationship between galaxies and their environments**. It highlights how the cosmic web—the network of filaments, clusters, and voids—can affect galaxy evolution on multiple scales. In particular, the way the environment influences bar formation could serve as a valuable tool for

understanding how galaxies in different regions of the universe evolve over cosmic timescales.

As we continue to explore the properties of barred galaxies, this research provides a crucial perspective on how the environment can shape galaxy structures. By studying the impact of environmental factors, we can improve our models of galaxy evolution and better understand the processes that shape the universe's large-scale structures.

References

Cuomo, V., Aguerri, J. A. L., Morelli, L., Choque-Challapa, N., & Zarattini, S. 2025, arXiv e-prints, arXiv:2509.23460

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Dr Robin is currently a Project Scientist at the Indian Institute of Technology Kanpur. He completed his PhD in astrophysics at CHRIST University, Bangalore, with a focus on the evolution of galaxies. With a background in both observational and simulation-based astronomy, he brings a multidisciplinary approach to his research. He has been a core member of CosmicVarta, a science communication platform led by PhD scholars, since its inception. Through this initiative, he has actively contributed to making astronomy research accessible to the general public.

Main Sequence Stars

by Sindhu G

AIRIS4D, VOL.3, No.10, 2025

www.airis4d.com

4.1 Introduction

Stars are the fundamental building blocks of galaxies and play a central role in cosmic evolution. Among the various stellar types, main sequence stars (Figure 1) represent the most common and longest-lasting phase of stellar evolution. During this stage, stars sustain themselves through the nuclear fusion of hydrogen into helium in their cores, producing the energy that makes them shine. The Hertzsprung–Russell (H-R) diagram (Figure 2), which plots stellar luminosity against surface temperature, clearly shows the main sequence as a diagonal band extending from hot, massive, blue stars to cool, low-mass, red stars.

This article provides a detailed overview of main sequence stars, including their physical characteristics, structure, classification, energy generation processes, and their significance in astrophysics.

4.2 The Hertzsprung - Russell Diagram and the Main Sequence

The H-R diagram is one of the most powerful tools in stellar astrophysics. When stars are plotted according to their absolute magnitude (or luminosity) versus spectral type (or temperature), they fall into distinct regions. The main sequence forms a continuous band running from the upper left (hot, luminous O-type stars) to the lower right (cool, faint M-type stars). Stars spend about 90% of their lifetimes on the main sequence.

The position of a star on the main sequence is

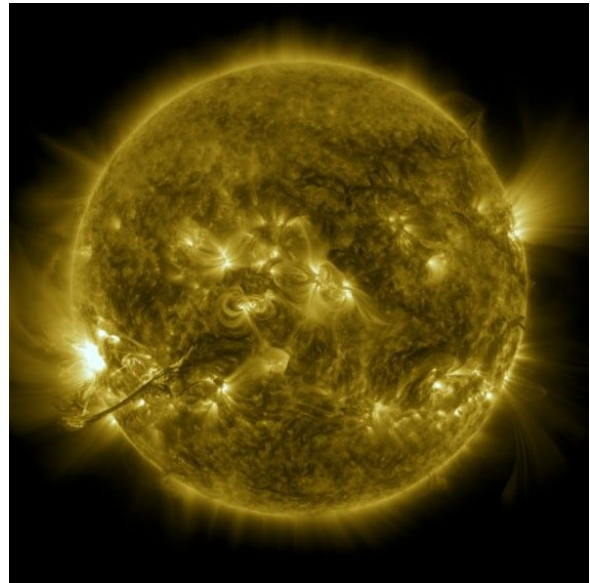


Figure 1: NASA's Solar Dynamics Observatory captured this image of our 4.6-billion-year-old Sun, a main sequence star. Scientists expect it will remain one for another 5 billion years before becoming a red giant.

Image Credit: NASA's Scientific Visualization Studio/SDO.

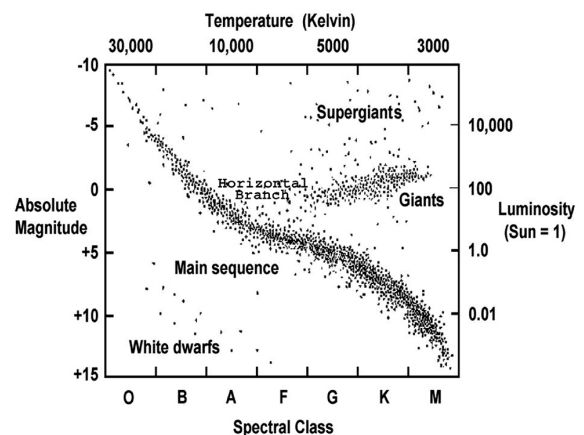


Figure 2: The H-R Diagram.

Image Credit: Chandra.

determined primarily by its mass, which governs its temperature, luminosity, and evolutionary timescale. Massive O- and B-type stars appear at the top left of the sequence: they are rare, short-lived, but extremely luminous. At the bottom right, M-type red dwarfs are faint but represent the majority of stars in the galaxy.

4.3 Stellar Structure and Energy Generation

4.3.1 Hydrostatic Equilibrium

A main sequence star maintains stability through hydrostatic equilibrium, where the inward pull of gravity is balanced by the outward pressure of hot gas produced by nuclear fusion in the core.

4.3.2 Energy Production

Main sequence stars generate energy by fusing hydrogen into helium. Two primary mechanisms dominate:

Proton-Proton (pp) Chain: Predominant in stars with masses up to about 1.5 solar masses (like the Sun). Hydrogen nuclei (protons) fuse through a series of reactions to form helium-4, releasing energy in the form of photons and neutrinos.

CNO Cycle (Carbon-Nitrogen-Oxygen cycle): Dominates in stars more massive than the Sun. Hydrogen fusion occurs with carbon, nitrogen, and oxygen acting as catalysts. This process is highly temperature-sensitive, explaining why massive stars are much more luminous.

4.3.3 Energy Transport

Energy produced in the core is transported outward by radiation and convection:

- Low-mass stars → radiative cores, convective envelopes.
- High-mass stars → convective cores, radiative envelopes.
- Red dwarfs (very low mass) → fully convective, mixing fresh hydrogen into the core and prolonging their lifetimes.

4.4 Classification of Main Sequence Stars

Main sequence stars are classified by their spectral type and luminosity class V (Roman numeral five indicates a main sequence dwarf). The Morgan–Keenan (MK) system defines spectral classes: O, B, A, F, G, K, M, ranging from hottest to coolest.

- O-type: > 30,000 K, blue, very luminous, short-lived (few million years)
- B-type: 10,000–30,000 K, luminous, tens of millions of years
- A-type: 7,500–10,000 K, white, bright (e.g., Sirius A)
- F-type: 6,000–7,500 K, yellow-white
- G-type: 5,200–6,000 K, yellow (e.g., the Sun, G2V)
- K-type: 3,700–5,200 K, orange, moderately faint
- M-type: < 3,700 K, red dwarfs, extremely long-lived

The classification directly relates to surface temperature, luminosity, mass, and lifetime.

4.5 Lifetimes of Main Sequence Stars

The lifetime of a star on the main sequence is strongly dependent on its mass. The relationship can be approximated as:

$$t \propto \frac{M}{L}$$

where M is stellar mass and L is luminosity. Since luminosity increases steeply with mass ($L \propto M^{3.5}$), massive stars burn through their fuel very quickly.

- Massive stars (O, B types): lifetimes of a few million years
- Intermediate stars (A, F, G types): lifetimes of hundreds of millions to several billion years
- Low-mass stars (K, M types): lifetimes of tens to hundreds of billions of years

While massive stars dominate visually due to their brightness, the majority of stars in the Milky Way are faint red dwarfs that will outlive all others.

4.6 End of Main Sequence Phase

Once hydrogen in the core is depleted:

- The star can no longer maintain hydrostatic equilibrium.
- The core contracts and heats up, while the outer layers expand.
- The star leaves the main sequence and evolves into a red giant (for low- and intermediate-mass stars) or into more complex evolutionary stages (for high-mass stars).

This transition marks a fundamental turning point in stellar evolution.

our understanding of these stars continues to improve, offering deeper insights into both stellar physics and cosmic evolution.

References:

- [Main sequence stars: definition & life cycle](#)
- [The H-R Diagram](#)
- [Hertzsprung-Russell Diagram](#)
- [Main Sequence Stars](#)
- [Main sequence](#)
- [Main Sequence](#)
- [STARS, GALAXIES, THE UNIVERSE](#)

4.7 Importance of Main Sequence Stars

Main sequence stars are crucial to astrophysics for several reasons:

- **Standard candles:** Their predictable mass-luminosity relation makes them useful in distance measurements.
- **Galactic population studies:** Most stars in galaxies are main sequence stars, especially red dwarfs.
- **Stellar evolution models:** Studying their properties allows astronomers to understand how stars form, evolve, and die.
- **Habitability:** Many exoplanet-hosting stars are main sequence stars, making them critical to the search for life beyond Earth.

4.8 Conclusion

Main sequence stars are the backbone of stellar astrophysics. They provide the light and heat that shape planetary systems, and they serve as laboratories for understanding nuclear fusion, energy transport, and stellar lifetimes. From massive O-type stars that live fast and die young to red dwarfs that quietly persist for trillions of years, main sequence stars highlight the diversity and complexity of the Universe.

As observational techniques advance, especially with space telescopes like Gaia, Kepler, and TESS,

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Sindhu G is a research scholar in the Department of Physics at St. Thomas College, Kozhencherry. She is doing research in Astronomy & Astrophysics, with her work primarily focusing on the classification of variable stars using different machine learning algorithms. She is also involved in period prediction for various types of variable stars—especially eclipsing binaries—and in the study of optical counterparts of X-ray binaries.

Part III

Biosciences

BLAST and FASTA: Cornerstones of Sequence Alignment in Biosciences and Bioinformatics:

by Geetha Paul

AIRIS4D, VOL.3, No.10, 2025

www.airis4d.com

1.1 Introduction

Sequence alignment is a fundamental technique in bioinformatics that enables researchers to compare DNA, RNA, or protein sequences against known databases to detect regions of similarity. These similarities can indicate shared evolutionary ancestry, functional relationships, or structural conservation among biomolecules. With the surge in genomic and proteomic data over the past few decades, propelled by advances in sequencing technologies, the task of analysing and interpreting biological sequences has become increasingly complex and data-intensive. Consequently, the need for computational tools that can rapidly and accurately align sequences has become critical to biological research.

Historically, early methods for sequence comparison, such as the Smith-Waterman algorithm, employed exhaustive dynamic programming approaches that guaranteed optimal global or local alignments. While these methods provide highly precise alignments, their computational demand grows quadratically with sequence length, rendering them impractical for searching large-scale genomic databases that contain millions of sequences. To overcome this bottleneck, heuristic algorithms were developed that traded some accuracy for enormous gains in speed, enabling practical searches on modern genetic datasets.

In this context, two pioneering heuristic methods

developed in the late 1980s and early 1990s transformed the field: FASTA and BLAST. FASTA, introduced by David J. Lipman and William R. Pearson in 1985-1988, was the first widely adopted heuristic sequence alignment tool. It employed strategies that focused on identifying short, exact matches or hotspots between two sequences before extending them into longer alignments. This approach preserved much of the sensitivity of earlier algorithms while dramatically reducing computation time.

Building upon this foundation, Altschul and colleagues introduced BLAST (Basic Local Alignment Search Tool) in 1990, which further enhanced search speed and integrated rigorous statistical methods to assess the reliability of sequence matches. BLAST revolutionised sequence analysis by providing fast, statistically meaningful local alignments of nucleotide or protein sequences against large public and private databases. It rapidly gained popularity and remains one of the most widely used bioinformatics tools worldwide.

Both FASTA and BLAST have become indispensable in molecular biology, genomics, and evolutionary studies. They operate primarily by finding local regions of similarity, which allows researchers to detect conserved functional domains, gene families, and evolutionary relationships even in sequences with substantial divergence. While both tools employ heuristic word-based searching, they differ in algorithmic details, customisation options, and typical

applications. This article explores their underlying principles, comparative functionalities, and roles in modern bioinformatics workflows.

What is BLAST?

BLAST (Basic Local Alignment Search Tool) is a suite of programs developed by Stephen Altschul and colleagues at NCBI in 1990. It finds regions of local similarity between sequences and is widely used to compare nucleotide or protein sequences against databases. BLAST uses fixed-size words to search for high-scoring ungapped segments and then extends these for alignment. Its popularity stems from its speed, local alignment focus, and detailed statistical outputs, such as E-values, that help assess the likelihood of similarity occurring by chance. BLAST is not just a tool; it's a gateway to understanding the mysteries of life at the molecular level. As technology advances, BLAST will continue to play an important role in shaping the future of biology and medicine.

BLAST: Speed and Specificity

BLAST uses short word matches as seeds to rapidly find regions of high similarity, and then extends these alignments to produce local, statistically significant results. It is exceptionally useful for searching large databases, offering a practical balance between sensitivity and computational speed, and has various specialised variants for different types of sequence comparisons.

Example of BLAST Variants:

BLASTN: Used for nucleotide (DNA and RNA) sequence database searches. It compares a nucleotide query sequence against a nucleotide database.

BLASTP: Used for protein sequence database searches. It compares an amino acid query sequence against a protein sequence database -protein vs protein search.

BLASTX: Compares the six-frame conceptual translation products of a nucleotide query sequence (both DNA and RNA) against a protein sequence database. This is useful when you have a nucleotide sequence that might contain a coding region, and you want to find similar proteins.

TBLASTN: Compares a protein query sequence against a nucleotide sequence database dynamically

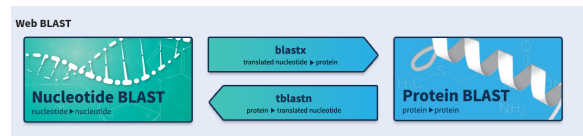


Figure 1: BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance. Image courtesy: https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Web&PAGE_TYPE=BLASTHome

translated in all six reading frames (both strands).

TBLASTX: Compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database. Given its nature, it's computationally intensive and less commonly used than the other BLAST types.

Each type of BLAST is designed for a specific purpose and can provide different insights, depending on the nature of the query sequence and the information sought by the researcher. Protein BLAST ClusteredNR is a collection of protein sequence clusters built from the current default database, nr. The representative sequence is chosen for each cluster, which is generally well-annotated and indicates the function of the proteins in the cluster, helping you focus on meaningful biological insights and decreasing redundant results.

1.2 What is FASTA?

FASTA is both a file format and the name of the first software tool developed for sequence similarity searching, preceding BLAST. The FASTA algorithm breaks the query sequence into smaller patterns called k-tuples or ktups (short sequence words), then searches for matches in the database. These initial matches are extended to generate full alignments. FASTA is known for sensitivity, especially in detecting similarities between less closely related sequences, though it may be slightly slower than BLAST with large protein databases.

1.3 FASTA as a Format:

The FASTA format is a universal sequence representation standard, beginning with a description line (>) followed by the sequence.

Table 1 BLAST vs FASTA: A Comparison

Feature	BLAST	FASTA
Main Use	Rapid database searching for local sequence similarity	Sensitive identification of homology, especially in less similar sequences
Algorithm	Uses fixed-size words and ungapped extensions	Searches with short k-tuples, then extends for alignment
Speed	Faster for large databases, especially for proteins	Can be slightly slower, but more sensitive in some contexts
Output	Detailed alignments, E-values, statistics	Detailed alignments, various scoring matrices
Typical application	Routine database searches and annotation pipelines	Research-focused, historical analyses, special cases

FASTA: Sensitivity and Versatility

FASTA, developed before BLAST, employs a hashing strategy and k-tuples (k-tups) to identify regions of similarity, often yielding greater sensitivity for certain types of searches, particularly nucleotide alignments. It produces optimised local alignments and is able to capture less obvious similarities between sequences, though it can be slower than BLAST for very large datasets.

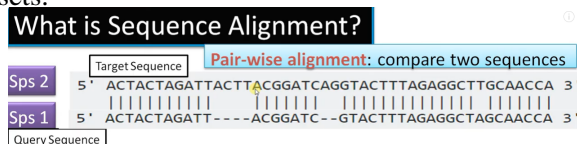


Fig. 2 Pair-wise sequence alignment finds regions of similarity between two biological sequences. By introducing gaps and aligning identical or similar residues in columns.

Image courtesy: https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Web&PAGE_TYPE=Blas

tHome

Sequence alignment facilitates the comparison of multiple sequences, distinguishing conserved regions, substitutions, and indels (insertions or deletions), which in turn helps interpret genetic information and analyse molecular evolution, gene function, and structural biology.

section How do we compare sequences?

Seq 1: CTGCACTA

Seq 2: CACTA

or C---ACTA

Scoring tries to approximate evolution: scores for substitutions and for gaps (insertions/deletions)

Scores = sum of terms for substitutions and for gaps (sequence as character string)

Simplest scoring: 1 for a match, 0 for no match, -1 for a gap.

CTGCACTA Score =5

CACTA

CTGCACTA Score =2

C---ACTA

Database Similarity Searching- BLAST and FASTA

Database similarity searching is the computational process of comparing a query biological sequence against a large repository of known sequences to identify and retrieve those with significant similarity, suggesting evolutionary, structural, or functional relationships. It employs sequence alignment algorithms like BLAST and FASTA, which use heuristics (words) to rapidly detect local regions of similarity, enabling efficient annotation, classification, and characterisation of unknown sequences within extensive biological databases. This method is fundamental for genome annotation, phylogenetic analysis, and molecular biology research, as it links novel sequences to known biological information through statistically validated alignments.

Central Role in Biosciences

Both BLAST and FASTA continue to underpin critical workflows in the biosciences and bioinformatics, powering public databases, web-based tools, and research pipelines for a range of applications, from gene

annotation to evolutionary analysis and metagenomics. Their enduring influence and integration into nearly every molecular biology lab and bioinformatics curriculum validate their description as cornerstones in the field.

This article accurately reflects the significance of BLAST and FASTA in both their historical development and ongoing applications within the biosciences and bioinformatics.

References

<https://blast.ncbi.nlm.nih.gov/Blast.cgi>

https://ncbiinsights.ncbi.nlm.nih.gov/2025/05/22/faster-better-results-protein-blast/?utm_source=ncbi_linkedin&utm_medium=referral&utm_campaign=clusterednr-default-2025052

<https://pmc.ncbi.nlm.nih.gov/articles/PMC441573/>

<https://omicstutorials.com/essential-tools-and-software-in-bioinformatics-blast-fasta-and-clustal/>

About the Author



Geetha Paul is one of the directors of airis4D. She leads the Biosciences Division. Her research interests extend from Cell & Molecular Biology to Environmental Sciences, Odonatology, and Aquatic Biology.

Part IV

Computer Programming

Minimizing Synchronization Overhead in Parallel Computing

by Ajay Vibhute

AIRIS4D, VOL.3, No.10, 2025

www.airis4d.com

1.1 Introduction

In recent years, parallel computing has emerged as a cornerstone of high-performance software design. With the slowdown of Moore's Law and the proliferation of multi-core and many-core processors, software developers have increasingly turned to parallelism as the primary path toward improving execution speed and responsiveness. Whether it's scientific computing, machine learning, graphics rendering, or real-time data processing, the demand for scalable parallel systems is greater than ever.

At the heart of parallel programming lies a central tension: while dividing work across multiple processors can significantly accelerate computation, coordinating the actions of these processors often introduces overhead that can limit, or even negate, the benefits of parallel execution. This coordination—commonly referred to as synchronization—is essential to maintaining correctness when threads or processes interact with shared data. However, the cost of synchronization grows rapidly with the number of processors, especially when access patterns are not carefully managed.

Traditional synchronization mechanisms, such as mutexes, barriers, and critical sections, ensure consistency but also force threads to wait, serialize execution, or compete for shared resources. In high-contention scenarios, this can result in performance bottlenecks that dramatically reduce the overall efficiency of the system. Even finely tuned parallel algorithms may fail to scale as expected if

synchronization overhead is not minimized.

Understanding how to design parallel programs that reduce or avoid unnecessary synchronization is therefore a critical skill for developers working in high-performance and scalable computing. This involves more than just choosing the right tools—it requires a deep understanding of how parallel architectures behave, how memory is shared and accessed, and how threads interact under the hood.

This article explores the various forms of synchronization overhead encountered in parallel computing and introduces practical strategies for minimizing their impact. Through conceptual diagrams and real-world examples, we'll highlight common pitfalls and demonstrate how techniques such as data partitioning, lock-free programming, and asynchronous execution can lead to more scalable, efficient parallel systems.

1.2 Why Synchronization Hurts Performance

Parallel programming is fundamentally about maximizing concurrency while preserving correctness. To ensure that multiple threads or processes don't interfere with each other when accessing shared data, synchronization mechanisms—such as locks, mutexes, and barriers—are introduced. While these tools are necessary, they also become a major source of inefficiency in parallel systems.



Figure 1: Contention and Blocking: Only one thread can access the critical section at a time. Others must wait.

One of the primary performance costs arises from contention. When several threads attempt to access the same critical section, only one can proceed at a time, forcing others to wait, figure 1. This introduces serialization in what should be a concurrent program. As the number of threads increases, the time spent waiting often grows disproportionately, reducing the overall speedup and, in extreme cases, causing performance to degrade.

Synchronization can also trigger expensive context switches. When threads block while waiting for locks, the operating system may preempt them and switch execution to other threads. While this ensures system responsiveness, the frequent saving and restoring of thread states adds latency and consumes valuable CPU cycles, especially in high-contention scenarios.

Even in seemingly well-parallelized code, performance can suffer due to false sharing—when threads operate on different variables that reside on the same cache line. In such cases, writes from one thread can invalidate the cache lines of others, leading to increased memory traffic and degraded cache efficiency, despite the absence of explicit data sharing.

Another challenge is barrier synchronization. In many parallel algorithms, threads must wait at fixed synchronization points until all others reach the same state. If some threads complete their tasks earlier, they sit idle, waiting for the slowest thread. This imbalance—often caused by varying workloads or memory latency—reduces overall throughput and wastes computational resources.

Underlying all these effects is a limitation described by Amdahl’s Law: the speedup of a parallel program is bounded by the fraction of code that must

be executed sequentially. Every synchronized section effectively acts as serial code, creating bottlenecks that scale poorly as more cores are added. Even a small portion of synchronization can cap the theoretical maximum performance.

Lastly, synchronization adds complexity to parallel software design. It increases the risk of deadlocks, priority inversion, and non-deterministic behavior, making programs harder to develop, debug, and maintain. These hidden costs—combined with the direct performance penalties—make minimizing synchronization not just an optimization, but a necessity for building truly scalable parallel systems.

1.3 Reducing Synchronization Overhead

Synchronization is often a necessary evil in parallel programming, but its cost can be significantly reduced through careful design and strategy. By minimizing contention, reducing the frequency and duration of synchronization, and leveraging modern concurrency techniques, developers can improve the scalability and performance of their parallel applications. Below, we explore five key approaches to reducing synchronization overhead.

1.3.1 Avoid Shared State

One of the most effective ways to reduce synchronization is to avoid shared state whenever possible. By designing algorithms and data structures that allow threads to operate on independent, thread-local data, the need for coordination through locks or barriers diminishes, figure 2. This approach minimizes contention and eliminates many sources of synchronization-related delays.

Techniques such as data partitioning, functional programming paradigms (immutable data), or employing message passing instead of shared memory can help reduce or even eliminate shared mutable state. When threads don’t have to coordinate access to data, they can run truly concurrently, boosting throughput and scalability.

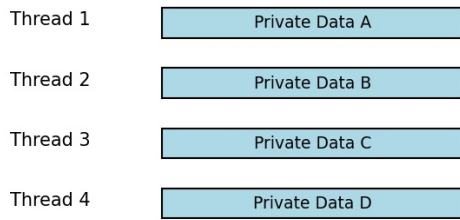


Figure 2: Thread-local storage: each thread operates on private data, avoiding the need for locks.

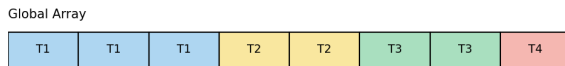


Figure 3: Partitioned access to shared array: different threads operate on disjoint segments.

1.3.2 Partition Data for Independent Access

When data cannot be fully private, it can often be partitioned so that each thread works on a separate region. This avoids contention while still enabling use of shared structures.

1.3.3 Use Lock-Free Techniques

When shared state cannot be avoided, lock-free programming offers an alternative to traditional locking mechanisms. Lock-free algorithms use atomic operations provided by modern CPUs—such as compare-and-swap (CAS)—to ensure consistency without putting threads to sleep or forcing them to wait.

Lock-free data structures like queues, stacks, and counters can dramatically reduce blocking and contention. Because threads can retry failed operations without holding locks, the overall system tends to be more responsive and scalable, especially under high concurrency.

However, lock-free programming requires careful design and understanding of memory models and atomicity guarantees, as it can introduce subtle correctness challenges such as the ABA problem. Nevertheless, for many performance-critical sections, it is a powerful technique to reduce synchronization overhead.

1.3.4 Minimize the Use of Barriers

Barriers ensure that all threads reach a synchronization point before any continue, but they can introduce significant idle time. To minimize this overhead, it is beneficial to reduce the number of barrier synchronizations in a program.

This can be achieved by restructuring algorithms to increase asynchronous execution, allowing threads to proceed independently as much as possible. For example, techniques like pipelining or overlapping communication with computation can help.

Additionally, replacing global barriers with more fine-grained synchronization mechanisms—such as point-to-point signals or lock-free queues—can improve resource utilization and reduce waiting times.

1.3.5 Delay or Merge Synchronization

In some cases, synchronization can be delayed or combined to amortize its cost over multiple operations. Instead of synchronizing after every small step, threads can perform a batch of operations independently and then synchronize once.

This batching approach reduces the frequency of synchronization events and the associated overhead. For example, instead of locking shared data for every update, threads can accumulate updates in local buffers and apply them collectively at synchronization points.

Merging synchronization operations can also improve cache locality and reduce contention hotspots by spreading updates over time, thus smoothing out bursts of synchronization activity.

1.3.6 Fine-Grained Synchronization

Finally, when synchronization is unavoidable, fine-grained synchronization can help improve performance compared to coarse-grained locking.

Instead of protecting large data structures or entire algorithms with a single lock, breaking the synchronization scope into smaller, more localized locks allows multiple threads to proceed concurrently when accessing different parts of the data. This reduces contention and increases parallelism.

However, fine-grained synchronization increases programming complexity and the risk of deadlocks or other concurrency bugs. Careful design, thorough testing, and the use of higher-level abstractions or frameworks can help manage this complexity.

1.4 Summary

Synchronization is essential for correctness in parallel programs but often limits scalability and performance. By adopting strategies such as avoiding shared state, employing lock-free techniques, minimizing barrier usage, delaying or merging synchronization events, and using fine-grained synchronization, developers can significantly reduce synchronization overhead. These approaches help maximize concurrency, reduce contention, and improve resource utilization, ultimately enabling parallel applications to achieve higher speedup and better scalability. Effective management of synchronization not only boosts performance but also simplifies debugging and maintenance, making it a cornerstone of efficient parallel computing design.

About the Author



Dr. Ajay Vibhute is currently working at the National Radio Astronomy Observatory in the USA. His research interests mainly involve astronomical imaging techniques, transient detection, machine learning, and computing using heterogeneous, accelerated computer architectures.

About airis4D

Artificial Intelligence Research and Intelligent Systems (airis4D) is an AI and Bio-sciences Research Centre. The Centre aims to create new knowledge in the field of Space Science, Astronomy, Robotics, Agri Science, Industry, and Biodiversity to bring Progress and Plenitude to the People and the Planet.

Vision

Humanity is in the 4th Industrial Revolution era, which operates on a cyber-physical production system. Cutting-edge research and development in science and technology to create new knowledge and skills become the key to the new world economy. Most of the resources for this goal can be harnessed by integrating biological systems with intelligent computing systems offered by AI. The future survival of humans, animals, and the ecosystem depends on how efficiently the realities and resources are responsibly used for abundance and wellness. Artificial intelligence Research and Intelligent Systems pursue this vision and look for the best actions that ensure an abundant environment and ecosystem for the planet and the people.

Mission Statement

The 4D in airis4D represents the mission to Dream, Design, Develop, and Deploy Knowledge with the fire of commitment and dedication towards humanity and the ecosystem.

Dream

To promote the unlimited human potential to dream the impossible.

Design

To nurture the human capacity to articulate a dream and logically realise it.

Develop

To assist the talents to materialise a design into a product, a service, a knowledge that benefits the community and the planet.

Deploy

To realise and educate humanity that a knowledge that is not deployed makes no difference by its absence.

Campus

Situated in a lush green village campus in Thelliyoor, Kerala, India, airis4D was established under the auspicious of SEED Foundation (Susthiratha, Environment, Education Development Foundation) a not-for-profit company for promoting Education, Research. Engineering, Biology, Development, etc.

The whole campus is powered by Solar power and has a rain harvesting facility to provide sufficient water supply for up to three months of drought. The computing facility in the campus is accessible from anywhere through a dedicated optical fibre internet connectivity 24×7.

There is a freshwater stream that originates from the nearby hills and flows through the middle of the campus. The campus is a noted habitat for the biodiversity of tropical Fauna and Flora. airis4D carry out periodic and systematic water quality and species diversity surveys in the region to ensure its richness. It is our pride that the site has consistently been environment-friendly and rich in biodiversity. airis4D is also growing fruit plants that can feed birds and provide water bodies to survive the drought.