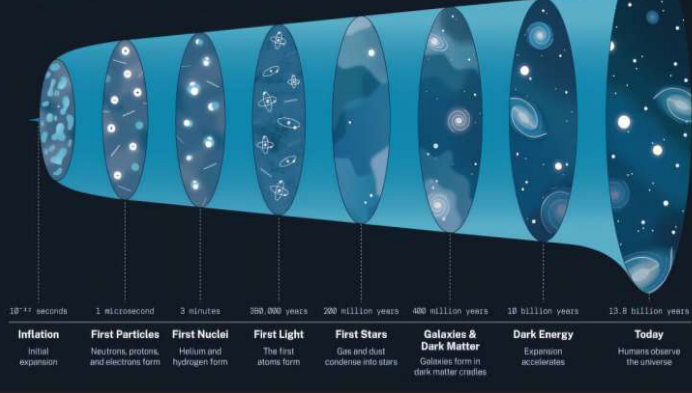


Study: Dark Energy Doesn't Actually Exist

History of the Universe



LONDON (Royal Astronomical Society) -- One of the biggest mysteries in science—dark energy—doesn't actually exist, according to researchers looking to solve the riddle of how the universe is expanding.

Their analysis has been published in the journal *Monthly Notices of the Royal Astronomical Society Letters*.

For the past 100 years, physicists have generally assumed that the cosmos is growing equally in all directions. They employed the concept of dark energy as a placeholder to explain unknown physics they couldn't understand, but the contentious theory has always had its problems.

Now a team of physicists and astronomers at the university of Canterbury in Christchurch, New Zealand are challenging the status quo, using improved analysis of supernovae light curves to show that the universe is expanding in a more varied, "lumpier" way.

The new evidence supports the "timescape" model of cosmic expansion, which doesn't have a need for dark energy because the differences in stretching light aren't the result of an accelerating universe but instead a consequence of how we calibrate time and distance.

It takes into account that gravity slows time, so an ideal clock in empty space ticks faster than inside a galaxy.

The model suggests that a clock in the Milky Way would be about 35 percent slower than the same one at an average position in large cosmic voids, meaning billions more years would have passed in voids. This would in turn allow more expansion of space, making it seem like the expansion is getting faster when such vast empty voids grow to dominate the universe.

Professor David Wiltshire, who led the study, said, "Our findings show that we do not need dark energy to explain why the universe appears to expand at an accelerating rate.

"Dark energy is a misidentification of variations in the kinetic energy of expansion, which is not uniform in a universe as lumpy as the one we actually live in."

He added, "The research provides compelling evidence that may resolve some of the key questions around the quirks of our expanding cosmos.

"With new data, the universe's biggest mystery could be settled by the end of the decade."

Dark energy is commonly thought to be a weak anti-gravity force which acts independently of matter and makes up around two thirds of the mass-energy density of the universe.

The standard Lambda Cold Dark Matter (ΛCDM) model of the universe requires dark energy to explain the observed acceleration in the rate at which the cosmos is expanding.

Scientists base this conclusion on measurements of the distances to supernova explosions in distant

galaxies, which appear to be farther away than they should be if the universe's expansion were not accelerating.

However, the present expansion rate of the universe is increasingly being challenged by new observations.

Firstly, evidence from the afterglow of the Big Bang—known as the Cosmic Microwave Background (CMB)—shows the expansion of the early universe is at odds with current expansion, an anomaly known as the "Hubble tension."

In addition, recent analysis of new high precision data by the Dark Energy Spectroscopic Instrument (DESI) has found that the ΛCDM model does not fit as well as models in which dark energy is "evolving" over time, rather than remaining constant.

Both the Hubble tension and the surprises revealed by DESI are difficult to resolve in models which use a simplified 100-year-old cosmic expansion law—Friedmann's equation.

This assumes that, on average, the universe expands uniformly—as if all cosmic structures could be put through a blender to make a featureless soup, with no complicating structure. However, the present universe actually contains a complex cosmic web of galaxy clusters in sheets and filaments that surround and thread vast empty voids.

Professor Wiltshire added, "We now have so much data that in the 21st century we can finally answer the question—how and why does a simple average expansion law emerge from complexity?"

"A simple expansion law consistent with Einstein's general relativity does not have to obey Friedmann's equation."

The researchers say that the European Space Agency's Euclid satellite, which was launched in July 2023, has the power to test and distinguish the Friedmann equation from the timescape alternative. However, this will require at least 1,000 independent high quality supernovae observations.

When the proposed timescape model was last tested in 2017, the analysis suggested it was only a slightly better fit than the ΛCDM as an explanation for cosmic expansion, so the Christchurch team worked closely with the Pantheon+ collaboration team who had painstakingly produced a catalog of 1,535 distinct supernovae.

They say the new data now provides "very strong evidence" for timescape. It may also point to a compelling resolution of the Hubble tension and other anomalies related to the expansion of the universe.

Further observations from Euclid and the Nancy Grace Roman Space Telescope are needed to bolster support for the timescape model, the researchers say, with the race now on to use this wealth of new data to reveal the true nature of cosmic expansion and dark energy.

Genomic Journey of Humans Older Than Thought

PADUA (Phys.org) -- Research conducted at the Department of Biology, University of Padova, has identified critical genomic milestones in the evolution of *Homo sapiens*, including key chromosomal rearrangements and specific gene variants that contributed to the development of current modern human traits.

Findings challenge traditional models that attribute certain genetic innovations exclusively to modern *Homo sapiens*. Similarities observed in both modern and archaic human genomes suggest many hallmarks of the *Homo sapiens* genetic landscape arose before the lineages split.

Homo sapiens evolved through a series of significant genetic events. A population bottleneck approximately 900,000 years ago is thought to coincide with genomic rearrangements, the fusion of chromosome 2 and the translocation of the pseudoautosomal region 2 (PAR2).

About 650,000 years ago, modern humans diverged from Neanderthals and Denisovans. Interbreeding events have occurred more than once, providing opportunities for shared genetic traits. At least one modern human-Neanderthal event occurred as early as 350,000 years ago.

In the study, "Partitioning the Genomic Journey to Becoming *Homo sapiens*," published Dec. 9 on the bioRxiv preprint server, genomic sequences from modern humans, Neanderthals, and Denisovans were analyzed for genetic divergences and pinpointing human-specific genomic regions.

The researchers employed coalescence analyses, mutation rate estimates, and examination of archaic admixture signatures to partition the human genome and trace the



emergence of these key variants. Molecular clock assessments provided a minimum age estimate for the PAR2 translocation, while phylogenetic methods tracked the timing and frequency changes of shared variants among modern and archaic populations.

Researchers focused on three key events: a bottleneck 900,000 years ago (Event 1), the divergence of modern and archaic humans 650,000 years ago (Event 2), and interbreeding between *Homo sapiens* and Neanderthals 350,000 years ago (Event 3).

Event 1 marked a critical reduction in ancestral human populations. This event is thought to coincide with significant chromosomal rearrangements, including the fusion of chromosome 2 and the translocation of the pseudoautosomal region 2 (PAR2) from chromosome X to Y.

Analysis of male Denisovan and Neanderthal genomes demonstrated that PAR2 was present on both X and Y as in modern humans. Rearrangement had to occur before the split between archaic and modern lineages, which the researchers estimate to be around 856,000 to 1.3 million years ago, potentially pushing back the estimated age of a shared PAR2 ancestor by 400,000

years.

During their analysis, the team identified 11 single nucleotide variants (SNVs) in the PAR2 regions of male chromosome X, which were mostly absent in females. The gender-specific distribution suggests that these mutations were likely incorrectly mapped in previous analyses. Importantly, these SNVs appeared to have arisen after the common ancestor of all Y-PAR2 sequences had diverged from the X-PAR2 gene pool.

By applying a Y chromosome mutation rate of 3×10^{-8} mutations per base pair per generation, they calculated that the ancestor of all Y-PAR2 sequences diverged from the X-PAR2 gene pool approximately 518,000 years ago. This timeframe represents the period between the translocation event (856,000 to 1.3 million years ago) and the most recent common ancestor of all modern human Y chromosomes, dating to around 338,000 years ago.

For Event 2, when modern humans diverged from Neanderthals and Denisovans, scientists examined the genetic history of "Human650 regions" through coalescence events and variants appearing exclusively in modern hu-

mans. They identified recent functional variants in 56 genes in modern humans, 24 of which are associated with brain functions and skull morphology. These genetic changes emerged soon after the divergence and are believed to underpin key aspects of modern human biology and behavior.

Researchers observed that the Altai Neanderthal genome exhibited more regions with coalescence events occurring within the last 650,000 years compared to the Denisova genome. Variants uniquely associated with the modern human lineage were not widely found in Neanderthal populations during Event 3.

This suggests that when *Homo sapiens* and Neanderthals interbred in Event 3, approximately 350,000 years ago, certain ancestral variants were reintroduced, potentially enhancing their Neanderthal genetic diversity.

Specific gene variants have a tendency to drop out of small population sizes, with inbreeding over long timeframes leading to less genetically diverse populations. Due to this drifting, certain genetic variants previously present in Neanderthal populations were lost.

When modern humans first intermingled with Neanderthal genomes, the effect was not so much an introduction to novel genes as a reintroduction of previously lost genetic variants finding their way back into the Neanderthal gene pool.

The study offers great new insights into the rich tapestry of archaic and modern human genome history. They would meet yet again around 50,000 to 65,000 years ago, continuing the braided stream of human genetic and cultural collaborations.

Chennai Festival Awards 'In the Arms of the Tree'

TEHRAN – Directed by Iranian filmmaker Babak Khajepasha, the movie "In the Arms of the Tree" was awarded at the 22nd Chennai International Film Festival in India.

In the Arms of the Tree is a 2023 Iranian drama film written and directed by Babak Khajepasha, and produced by Muhammad Reza Mesbah and Sajjad Nasrollahi Nasab. It premiered in February 2023 at the 41st Fajr International Film Festival.

The Chennai International Film Festival provides a common platform for the film fraternity to show its expression through films; understand other cultures and project the excellence of this art form; contribute to the understanding and appreciation of film cultures of the different nations in the context of the social and cultural ethos; and promote friendship and cooperation among peoples of the world.

The festival has been organized since 2003. It show-

cases international as well as Indian feature films. In the ongoing edition, a total of 123 films chosen from 50 countries were screened by the end of the festival which was closed on December 19.



Picture of the Day



Snow at Imam Reza (AS) Shrine in Mashhad.