why does mercury spins as it does?

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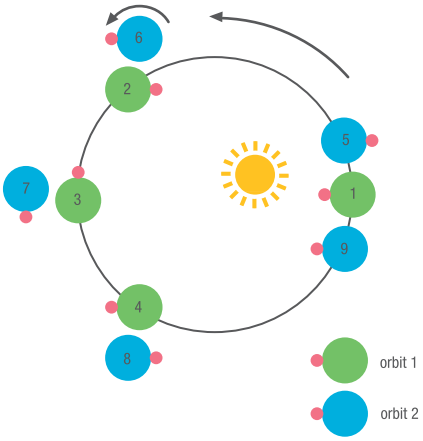
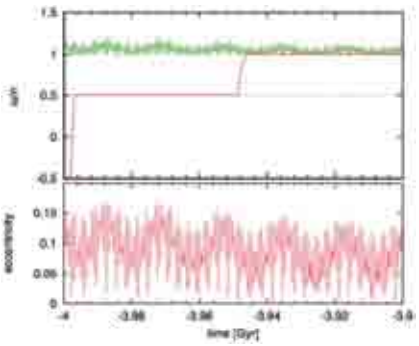


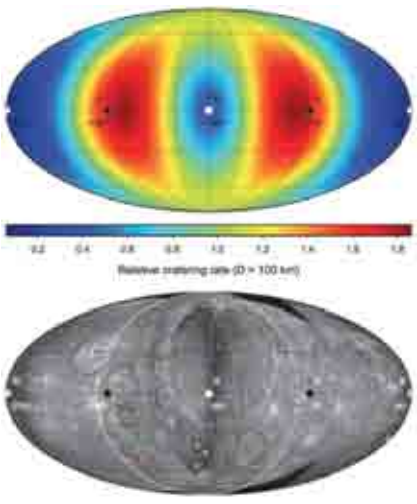
The rotation of Mercury is presently trapped in a 3/2 spin-orbit resonance. This means that the planet rotates three times about its spin axis for every two orbits about the Sun. However, recent observations with the Messenger spacecraft have shown that it was not always so. An international team of astronomers, including Alexandre Correia from the Physics Department, University of Aveiro, found strong evidence that the planet once rotated synchronously with the Sun (as the Moon does with the Earth). The team also explained how the present 3/2 configuration could be obtained due to impacts with large asteroids, starting from a retrograde rotation.

Using computer models that simulate the long-term evolution of Mercury's rotation, the team started the simulations by assuming that Mercury initially had a retrogade rotation (east-to-west) in the past instead of a prograde one (west-to-east). Current planet formation models suggest that the initial spin of terrestrial planets in the Solar System could have been either prograde or retrograde – with equal probability – so making such an assumption is not outlandish. In this situation, it was shown that Mercury evolves to the synchronous resonance naturally.

Moreover, in contrast to previous studies, the new model can make real predictions about the density and distribution of impact craters on the surface of Mercury. For a synchronous orbit, for example, the model implies that there should be more craters on the dark side of Mercury - that is, the side that does not face the Sun. This is exactly what astronomers observe today when they analyze Mercury's craters data from Messenger.

The calculations also suggest that a large asteroid impact may have disrupted this initial synchronous rotation. A giant impact like the one that formed the Caloris Basin unlocks the spin from the synchronous resonance and the planet subsequently evolves into the present 3/2 observed state. Researchers will now look for other evidence of the initial synchronous rotation, such as different thicknesses in the lithosphere (the rigid, outermost shell of a rocky planet) on the light and dark sides of Mercury. The Messenger probe, currently in Mercury's orbit, will hopefully provide further insights.





absent words in genomic sequences

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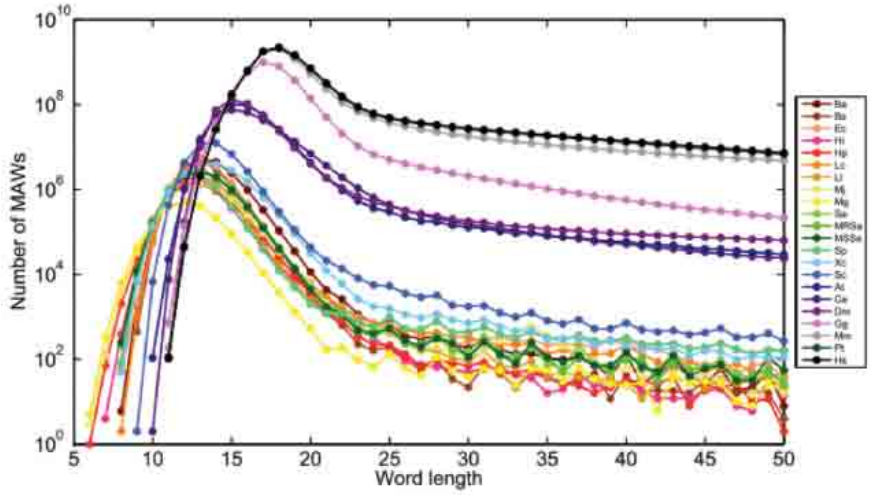
Genomes can be abstracted as a sequence of four letters representing the nucleotides. The convenience of this simplification goes beyond representation, to exploring properties of finite-sized strings over finite alphabets in genome analysis. One such property is the existence of a set of absent words. Absent words in genomic sequences are surprising because of the typically large size of the sequence (approximately 6 billion letters in the haploid human genome), the small alphabet size (4 letters), and the small size of the shortest absent words (11 letters in the reference human genome). The set of all words not present in a genome is of limited biological interest. Hence, we have introduced a new class of absent words designated minimal absent words. By definition, minimal absent words have at least three letters and the removal of their left- or rightmost character uncovers a word that is present in the sequence. For illustration, consider sequence ACGGCGGCTTC. Its set of minimal absent words is {ACT, CGC,CTC,GGG,TCG,TCT,TTT,ACGGC T,GCGGCG}. Consider word ACT from this set. This word does not occur in the sequence. However, words AC and CT do occur. Hence, ACT is a minimal absent word of the sequence above. The core of a minimal absent word, that is, the word that remains after removing the left- and rightmost characters (for example, CGGC in the minimal absent word ACGGCT), is



a maximal exact repeat. Maximal exact repeats are key for seeding alignment of sequencing reads from massively parallel methodologies in genome assembly, and as anchor points in comparisons of closely related genomes.
Minimal absent words have been ubiquitously computed in genomes of organisms from all domains of life. The figure displays the number of minimal absent words (MAWs) as a function of the length of the minimal absent word in the genomes of 22 organisms. These include one archaeota (Mj), thirteen bacteria (Ba, Bs, Ec, Hi, Hp, Lc, Ll, Mg, Sa, MRSa, MSSa, Sp, Xc), and eight case-study eukaryotes (Sc, At, Ce, Dm, Gg, Mm, Pt, Hs). Though here not displayed, these genomes contain many more and much larger minimal absent words.
We have investigated if the hypothesis of mutational biases (namely, the hypermutability of CpGs) as an explanation for the absence of the shortest absent words in vertebrates is valid for larger minimal absent words and in other organisms, but found no evidence supporting it. We have also investigated the hypothesis of the inheritance of minimal absent words through common ancestry, in addition to lineage specific inheritance, and found this inheritance may be exclusive to vertebrates.
As minimal absent words are intrinsically related to maximal exact repeats in the genome and not bound to protein-coding regions, they may be useful for inferring de novo genomic homology and uncovering new information on the evolution of genomes. Such strategy would overcome the failure to detect homology when there is considerable sequence divergence by current genomic homology inference methods, as well as, their typical disregard for the non-protein-coding regions of the genome. This might prove particularly useful in genomes with high repeat content, such as the human genome, where more than half of the sequence remains 'dark matter', with only _1.5% exons and _44% repetitive sequences presently annotated.

designing nanoparticles for electronics

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Researchers from the I3N – Institute for Nanostructures, Nanomodelling and Nanofabrication have recently proposed alternative ways to tweak the properties of silicon nanoparticles (DOI: 10.1103/PhysRevB.84.125437). These particles, of the scale of a few nanometers, have been object of intense study in recent years and regarded as a possible material for future solar cell technology.
Solar cells however, as many other electronic devices, are based on p-n junctions, sharp junctions between a material that is rich in electrons and a material that is poor in electrons, or in other words, that is rich in holes. Thus, solid state electronics and optoelectronics rely on the ability to control the excess or deficiency of electrons in a material and the flow of electrons between different materials. In bulk silicon, this is commonly achieved by introducing dopants in the material, but this method has limited success in small silicon nanoparticles.
Since small nanoparticles have a large surface-to-volume ratio, an alternative is to use surface manipulation as a means to modify the electronic properties of the nanoparticles. We have proposed that organic molecules in contact with the nanoparticles can be used to extract electrons from them. For example, first-principles calculations show that the adsorption of F_4 – TCNQ (7,7,8,8 – Tetracyano – 2,3,5,6 – tetrafluoroquinodimethane), an organic molecule with an extraordinarily high affinity for electrons, on the surface of silicon nanocrystals, leads to the formation of a hybrid electronic state shared by both moieties and results in the displacement of the electron density towards the adsorbed molecule. With a coverage ratio of just three F_4 – TCNQ molecules per silicon nanocrystal, it is possible to extract one electron charge from 2 nm nanocrystals. Thus, F_4 – TCNQ can be used as a surface dopant alone, or in conjunction with other p-type dopants, to increase the hole density in the proximity of the surface. This opens up new ways to control the properties of the nanoparticles from the exterior.