

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 (Mi), 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.

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 - Tetracvano - 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 F₄ – TCNQ molecules per silicon nanocrystal, it is possible to extract one electron charge from 2 nm nanocrystals. Thus, F₄ – 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.



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