The smart pixel

A digital camera can work with just a single light sensor and capture the information needed for high quality image

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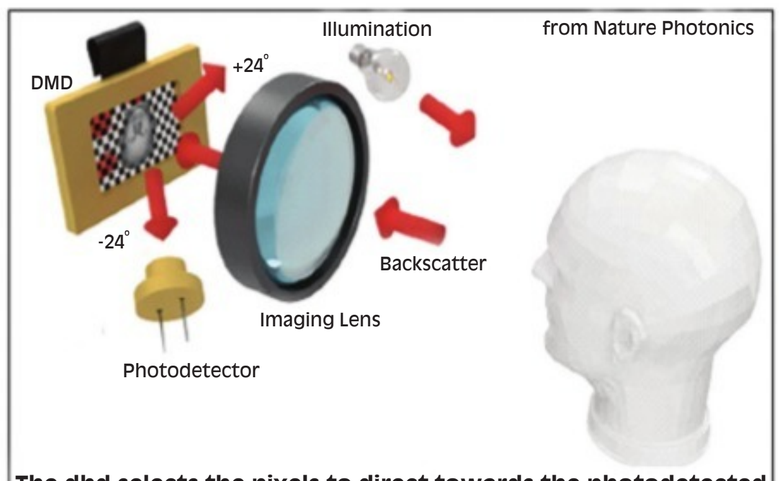
Megapixels, which mean millions of pixels, are the units in which the quality of cell phone cameras and professional cameras are measured. The pixel count is the number of discrete points of which an image consists. It is evident that the greater the number of pixels, the finer the grain, or the resolution of the picture. Digital cameras hence use an array of silicon chips in millions to get good images.

Matthew P Edgar, Graham M Gibson and Miles J Padgett, from the School of Physics and Astronomy, University of Glasgow, describe in the journal, Nature Photonics, a movement back to lesser pixels, just one pixel, in fact. This is not to say that the picture consists of lesser pixels. It is the camera, which scans the object with just one light sensor and captures the information needed for a high quality image. Using a single detector would be without several advantages of the current, multi-detector capability, but it would overcome limitations of the current technology in some applications.

The change, in a sense, is back to the way electronic images were first created. Photography started with capturing a whole image, at once, on film that consisted of specks of a light-sensitive chemical. The electronic counterpart, in the nineteenth century, was a single light-sensitive device, a photocell, which received the light, in succession, from different spots on an object to be imaged and then put them together.

The image was acquired by scanning the object using an arrangement called the Nipkov disk, a circular disk with pinholes in the form of a spiral. When the object was brightly illuminated and the disk was spun, it could be arranged that light from different "slices" of the object was received by a single photoreceptor on the other side of the disk. If the excitation of the receptor was made to control a light source, which was viewed through another Nipkov disk, the original image would be reproduced, and a fresh image created for every turn of the disc. This idea, the 1884 invention of Paul Gotlieb Nipkov (1860-1940), was made use of by John Logie Baird and Charles Francis Jenkins to develop the first mechanical television. We can appreciate that the quality of the image would depend on the diameter of the disc and the number of holes. As holes in greater numbers would need to be smaller, even just a pinhole, the illumination would need to be very bright. Sure enough, the arrangement was unwieldy and the quality was poor. The arrangement made it possible to transmit images, and movement, but not to capture good images.

In the meantime, the quality of normal photography improved by leaps and bounds and film with very fine grain became available. The electronics industry worked hard to match photo film by creating panels of multiple silicon based detectors, which captured the intensity of light at a large number of spots. Miniaturisation and advances in electronics led to panels that created very fine grained images, and then, methods to render the images captured. The technology has advanced and we now have low cost, hand held devices that pack millions of light gathering and emitting components and screens of liquid crystals or light emitting devices of very high resolution and accuracy.



The dhd selects the pixels to direct towards the photodetected

Alongside improvements in camera quality, there were advances in recording and transmission of the huge data that the millions of pixels collected. Apart from improvements in the capacity of the channels of transmission, there was data compression, or codes that reduced the quantity of data. It is well known that all digital data is expressed in binary codes, or codes that work with only the digits, 0 and 1. Thus, the code for the letter, A is 065, rendered in binary as, 01000001 and the word, CAT, is rendered as, 010000110100000101010100. We can see that there several stretches of repeated characters. These are necessary for coding the text, but need not all be recorded or transmitted, if we have a "shorthand" to express the series of 0s and 1s more economically. This becomes all the more true when transmitting the pixel distribution of an image. If there is dark line, for instance, rendered by a series of 10,000 pixels, we need not transmit them all, we can just say, 10,000 dark pixels.

For all this, conventional, multiple sensor methods have limitations in certain applications. For one, there are serious limitations of the ordinary panel of detectors in wavelengths outside the visible range. For another, very high sensitivity and speed photography are not possible with the miniaturised detectors. The development reported from Glasgow addresses these needs, by making use of a piece of hardware called a Spatial Light Modulator, essentially a high speed scanning device, along with methods to compress data.

The scanning arrangement consists of an array of nearly a million closely packed mirrors, some tenth of the width of human hair, called the Digital Micromirror Device. The angle of tilt of the mirrors can be controlled and the DMD can either focus light on a particular (micro) spot on the object or direct light from a particular spot on the object to the detector. The DMD thus works to illuminate or to bring light from different points on the object to the detector, in rapid succession, to enable building the image. The single pixel detector can have very high sensitivity and speed and the limitation is only how fast the DMD can scan the object. This limitation, the Glasgow paper explains, is overcome by scanning larger regions of the object at the same time and data compressing techniques where the image is reconstructed with collection of the least possible data. The method is akin to the game of "twenty question", the paper explains. In "twenty question", a player is allowed to twenty questions, of the kind that can be answered with "yes" or "no", to identify a person the other player has in mind. If one starts by asking, "is it a man?" for instance, the answer narrows the field to half. Further questions, of qualities that are shared by nearly half the target group, would repeatedly reduce the field to half. Doing this twenty times reduces the field a million-fold.

Using computational techniques that work like this, the limitations of the DMD are overcome and the single pixel camera has been shown to work in unusual situations. One of these is the detection of leaking methane, an invisible gas. Methane absorbs light at a particular, low, Infra Red frequency. The single pixel camera was used to display a methane pipeline, illuminated by light alternately of this specific frequency and then another one. The result was a pair of images, one showing the leak (when there is one) and the other with no leak.

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Unravelling the genes

The emerging field of bioinformatics merges computer science and biology in an attempt to make sense of the torrential data of human genomes and proteomes

TAPAN KUMAR MAITRA

Sequencing the human genome has been one of the crowning achievements of modern biology, not only because of its sheer scale but also because of its potential impact on our understanding of human evolution, physiology, and disease. And yet, unraveling the sequence of bases was the "easy" part. Now comes the hard part of figuring out the meaning of this sequence of 3 billion A's, G's, C's, and T's.

The prospect of analysing such a vast torrent of data has led to the identification of a new discipline, called bioinformatics, which merges computer science and biology in an attempt to make sense of it all. For example, computer programmes that analyse DNA for stretches that could code for amino acid sequences are used to estimate the number of protein-coding genes. Such analyses suggest the presence of about 30,000 protein-coding genes in the human genome, half of which were not known to exist. The fascinating thing about this estimate is that it means humans may have only about twice the number of genes as do worms or files! Computer analysis has also revealed that only about one to two per cent of the human genome actually codes for proteins. While the remaining DNA contains some important regulatory elements as well as some genes that code for RNA products instead of proteins, most of it appears to consist of "junk" DNA with no apparent function.

Because the function of most genes is to produce proteins which are responsible for most cellular functions, scientists are now looking beyond it to study proteome — the structure and properties of every protein produced by a genome. The complexity of an organism's proteome is considerably greater than that of its genome. For example, the roughly 30,000 genes found in human cells are thought to produce somewhere between 200,000 and a million or more proteins. This is why cells can produce so many proteins from a smaller number of genes.

In essence, it reflects the fact that an individual gene can be "read" in multiple ways to produce multiple versions of its protein product. The resulting proteins are subject to biochemical modifications that can significantly alter their structural and functional properties.

Identifying the vast number of proteins produced by a genome has been facilitated by mass spectrometry, a high speed, extremely sensitive technique that utilises magnetic and electric fields to separate proteins or protein fragments based on differences in mass and charge. One application of mass spectrometry has been to identify the peptides derived from proteins separated by gel electrophoresis and then digested with specific proteases, such as trypsin. By comparing the resulting data to the predicted masses of peptides that would be produced by DNA sequences present in genomic databases, the proteins produced by newly discovered genes can be identified. Other techniques make it feasible to study the interactions and functional properties of the vast number of proteins found in a proteome. For example, it is possible to immobilise thousands of different proteins (or other molecules that bind to specific proteins) as tiny spots on a piece of glass smaller than a microscope slide. The resulting protein microarrays can then be used to study a variety of protein properties, such as the ability of each individual spot to bind to other molecules added to the surrounding solution.

Another important feature of the human genome is the way in which its base sequence differs from person to person. The published human genome sequence is actually a mosaic obtained from the DNA isolated from 10 different individuals. In practice, about 99.7 per cent of the bases in genome will match perfectly with this published sequence, or with the DNA base sequence of your next-door neighbour. But the remaining 0.3 per cent of the bases can vary from person to person, creating features that make individuals unique. These variations are called single nucleotide polymorphisms, or SNPs. 0.3 per cent multiplied by the 3.2 billion bases in the human genome yields roughly 10 million SNPs. Scientists have already created a database containing most of the common SNPs, which are thought to be important because these tiny genetic variations may influence how likely you are to become afflicted with a particular disease or how well you might respond to a particular treatment.

The impact of this growing body of genetic data is already becoming apparent as discoveries regarding the genetic basis of many human diseases - from breast cancer and colon cancer to diabetes and Alzheimer's disease - are being reported at rapidly increasing pace.

Such discoveries promise to revolutionise the future practice of medicine, because the ability to identify disease genes and investigate their function makes it possible to devise medical interventions for alleviating and even preventing disease.

But the ability to identify potentially harmful genes also raises ethical concerns, because all of us are likely to carry genes that place us at risk. Such information could be misused. To alter people's genes, not only to correct diseases in malfunctioning body tissues but also to change genes in sperm and eggs, and hence to alter the genetic makeup of future generations. What use to make of these abilities and how they should be regulated are clearly questions that concern not only the scientific community but society also.

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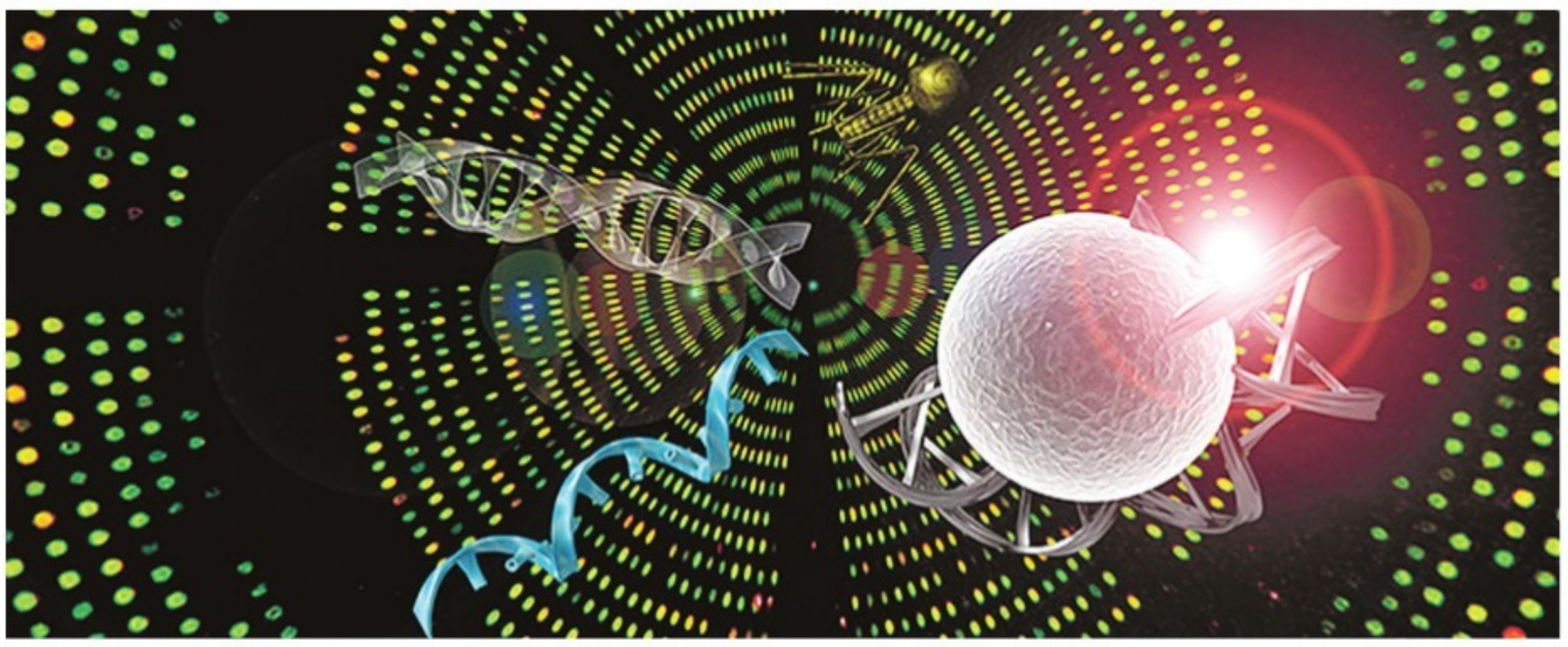

PLUS POINTS

Graveyard of continents

The eastern section of Antarctica is buried beneath a thick ice sheet. Some scientists simply assumed that under that cold mass there was nothing more than a "frozen tectonic block".

But with the help of data from a discontinued European satellite, scientists have now found that east Antarctica is in fact a graveyard of continental remnants. They have created stunning 3D maps of the southernmost continent's tectonic underworld and found that the ice has been concealing the wreckage of an ancient supercontinent's spectacular destruction.

The researchers, led by Jörg Ebbing, a geophysicist at Kiel University, Germany, reported their discovery recently in Scientific Reports.

The findings relied on data from the gravity field and Steady-state Ocean Circulation Explorer (GOCE) satellite, which orbited earth just 155 miles above the surface until late 2013, when it re-entered the atmosphere at the end of its mission. Called the "ferrari of space", this sleek instrument could measure the gravitational fields weaving through Earth's crust and mantle.

GOCE's eye revealed that east Antarctica is a jigsaw puzzle of at least three geological titans named cratonic provinces. One craton has geological similarities with some of Australia's bedrock, while another resembles part of India's. The third is an amalgamation of pieces of old seafloors.

The pieces may have been assembled one billion years ago, when the supercontinent Rodinia was built, or 500 million years ago, when another supercontinent, Gondwana, came together. Either way, what has been found beneath Antarctica is part of what was left after Gondwana's dissolution, around 160 million years ago.

The independent

Easy to detect cancer

Worried you may have cancer? One day, you could take a 10-minute test with a 90 per cent success rate.

The cheap and simple test uses a colour-changing fluid to reveal the presence of malignant cells anywhere in the body and provides results in less than 10 minutes, according to a new study published in the journal Nature communications.

The test was made possible by the Queensland team's discovery that cancer DNA and normal DNA stick to metal surfaces in markedly different ways.

This allowed them to develop a test that distinguishes between healthy cells and cancerous ones, even from the tiny traces of DNA that find their way into the bloodstream. The DNA sample is added to water containing gold nanoparticles.

DNA from cancer cells sticks to the nanoparticles, making the water's colour stay pink; DNA from healthy cells binds to the particles differently and turns the water blue.

The researchers have run the test on 200 human cancer samples and healthy DNA with 90 per cent accuracy.

The test has been used to detect only breast, prostate, bowel and lymphoma cancers so far, but researchers are confident that the results can be replicated with other types of the disease.

"We certainly don't know yet whether it's the Holy Grail for all cancer diagnostics, but it looks really interesting as an incredibly simple universal marker of cancer, and as an accessible and inexpensive technology that doesn't require complicated lab-based equipment like DNA sequencing," Trau said.

The test has yet to be used on humans and large clinical trials are needed before it can be used on prospective patients.

The straits times/ann