MATERIALS CHEMISTRY

How soft is your nanomaterial?

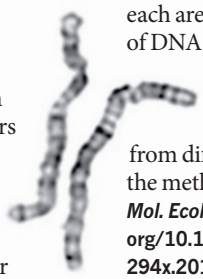
Materials scientists would love to be able to construct materials through rational design rather than the centuries-old method of trial and error. Moritz to Baben and his colleagues at RWTH Aachen University in Germany have furthered this quest by developing a computational approach based on dividing nanomaterials into subunit cells, in which a unit is the repeating entity that makes up the crystal.

The authors use their method to predict the bulk moduli —or softness — of several composite nanomaterials, something that has previously been done only at a macroscopic level. They apply the approach to materials with metallic, covalent and ionic bonding.

Scripta Materialia 65, **735–738 (2011)**

CELL BIOLOGY

DNA replication catastrophe



ELSEVIER

Faulty DNA replication can cause 'chromosome catastrophes' — extensive chromosomal rearrangements that can lead to genomic disorders if the catastrophe affects reproductive cells or hits during embryonic development.

James Lupski at Baylor College of Medicine in Houston, Texas, and his colleagues found single chromosomes (**pictured**) with multiple alterations, such as deletions, inversions, duplications, triplications and translocations, in 17 people with developmental delay and cognitive abnormalities. The DNA sequence around the chromosome breakpoints where the changes occurred revealed hallmarks of DNA replication gone wrong.

The authors say that similar chromosome-breakpoint features show up in the DNA of the 2–3% of human cancers that are characterized by multiple chromosomal changes, suggesting that the same mechanism might also underlie another type of chromosomal catastrophe, called chromothripsis, which can cause cancer.

Cell 146, **889–903 (2011)**

ECOLOGY METHODS

Dirt sequence for animal survey

The old-fashioned way to survey an area's fauna is to watch and wait, to trek and listen, and to examine tracks and scat. But in the era of cheap, rapid DNA sequencing, there's potentially an easier method: just sequence some soil and see what shows up. Animals urinate, defecate and shed skin flakes and hair, leaving traces of their DNA in the ground.

Eske Willerslev of the University of Copenhagen and his team trialled the method in areas where the species were a known quantity: zoos, safari parks and an ostrich farm. They found that dirt-DNA analysis could identify almost all of the animals living in each area, and that the amount of DNA of each species correlated well with its biomass. Taking multiple samples from different areas improved the method's accuracy.

Mol. Ecol. **http://dx.doi.org/10.1111/j.1365-294x.2011.05261.x (2011)**

CLIMATE

Ocean depths store heat

In spite of rising greenhouse-gas levels, global mean sea surface temperature has not increased notably during the past decade — and may even have dropped slightly. So what has happened to the surplus energy? According to researchers in Colorado, it has warmed the deep ocean.

Gerald Meehl and his team at the National Center for Atmospheric Research in Boulder ran a set of global atmosphere–ocean models to project twenty-first-century climate. The model runs yielded several roughly decade-long intervals with slightly negative trends in mean sea surface temperature but significantly enhanced ocean heat uptake.

Ocean warming during these periods was most pronounced in layers at a depth of more than 300 metres. Prolonged intervals with little or no surface warming, possibly linked to La Niña-like conditions, seem to be common in a warming climate, the team says.

Nature Clim. Change **http://dx.doi.org/10.1038/nclimate1229 (2011)**

GENOMICS

Sequencing a family affair

Individual genomes only reveal so much, so researchers have begun sequencing whole families. Such projects necessitate the development of new tools to analyse the large amount of data generated, as exemplified by one such project led by Euan Ashley of Stanford University in Palo Alto, California.

All the family members sequenced for the study are relatively healthy, but the analysis reveals their genetic risk factors for dozens of common diseases. For instance, the father, John West, and his daughter — but not his son — share a genetic risk for blood-clotting disorders, although it is not clear whether this contributed to a pulmonary embolism that West suffered in 2003.

The team also used the data to build a new human reference sequence by integrating them with data from the 1000 Genomes Project. West has now founded a company with some of the co-authors that aims to use the project's data-analysis tools to interpret whole-genome sequence data.

PLoS Genet. 7, **e1002280 (2011)**

COMMUNITY CHOICE

The most viewed papers in science

ANIMAL BEHAVIOUR

Woodlice and humidity, 74 years on

HIGHLY READ at jeb.biologists.org during August

Among the most-read papers at the *Journal of Experimental Biology* last month was a blast from the past — a 1937 paper about the humidity-seeking behaviour of the common woodlouse by D. L. Gunn of the University of Birmingham, UK. Gunn used specially built chambers to watch the crustaceans — which thrive on wet wood — avoid dryness, principally by hunkering down in humid places and staying still. Gunn looked for the location of the creature's humidity receptor by removing candidate regions of the body or blocking them with Vaseline or paraffin; he concluded that the relevant organs were not on the abdomen or head.

The journal's staff don't know why the research is suddenly popular, but guess that a class assignment might have boosted its download numbers. A recent *PLoS ONE* paper by Cédric Devigne of the University of Lille–North of France and his colleagues did cite the work. This group adds a twist to the tale with the finding that woodlice tend to form groups regardless of the prevailing conditions.

J. Exp. Biol. 14, **178–186 (1937); *PLoS ONE*** 6, **e17389 (2011)**

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