found, for the first time, that the factors Abf1 and Rpn4 are synergistic in the presence of DNA-damaging agents. By plotting these pairwise interactions as a graph, with the different conditions highlighted in colours, a map of motif-association can be constructed. This map shows that a relatively small number of transcription factors are responsible for many different expression patterns. Moreover, transcription factors with universal roles, such as Rap1, strike the eye by forming synergistic combinations with various motifs in each condition studied. A topological analysis of the map would probably reveal that it is another example of a scale-free network, besides, for example, maps of module-association in proteins, metabolic networks and protein–protein binding. There are highly connected 'hubs,' or nodes that might act as global signals, and sparsely connected nodes that are more gene-specific. The paper also addresses some more quantitative issues, such as whether for a particular synergistic motif pair, one motif is more crucial in determining the expression pattern than the other one. To this end, an integrated set of computational tools called Combinogram was developed and successfully employed.

The study by Pilpel *et al.* clearly shows that the immense diversity of the phenomena of life heavily relies on combinatorics (another prominent example being the diversity of immunoglobulins). Transcription factors can be regarded as 'words' that can be composed to form 'sentences' , which, in turn, regulate gene expression. This study appears to have promising applications in the definition of the genes regulated by each motif, in the annotation of new motifs and in the analysis of transcriptional regulatory networks. This is clearly relevant both in medicine and biotechnology.

1 Pilpel, Y. *et al.* (2001) Identifying regulatory networks by combinatorial analysis of promoter elements. *Nat. Genet.* 29, 153–159

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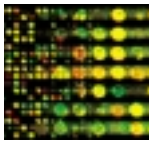
In Brief

Microarray production stopped



Incyte Genomics (San Francisco, CA, USA) announced that it would stop making microarrays and end its gene-expression analysis service as the operation was said to no longer be profitable (*Nature*, 8 November). Some Incyte users only learned of the company's decision from reporters. The reasons for the closure? Maintaining and replicating large collections of genes is expensive and also there has been a rapid proliferation of microarray facilities on almost every major research campus over the past two years. Alternatives are available for researchers in the middle of projects that are using Incyte's technology. The company says that microarrays using Incyte's gene collections will still be available through third-party providers. *DM*

NIEHS funds toxicogenomics

Grants totalling US$ 37m have been awarded by the US National Institute of Environmental Health Sciences (NIEHS) to study 'toxicogenomics' – the influence of environmental toxins on the development of genetic diseases (*bmn.com*, 9 November). Five institutions will each receive > US$ 7m over a five year period as part of a new toxicogenomics research consortium, and results will be collated in a 'Chemical Effects Biological Systems' database, which will be accessible to the public. One of the consortium members, Helmut Zarble (Fred Hutchinson Cancer Research Centre, Seattle, WA, USA), will use rat models and microarrays to pinpoint breast cancer oncogenes activated by environmental toxins. *MJD*

Seaweed bioremediation

Commercial cultivation of seaweed is big business – carageenan, agar, fertilisers and vitamins are all produced from seaweed extracts – and increasingly the environmental benefits of seaweed aquaculture are being exploited in other areas (*the-scientist.com*, 29 October). Intensive fish farming produces large quantities of effluent and food waste, which contributes to pollution and can trigger toxic algal blooms, but cultivating seaweed farms alongside fish stocks can bioremediate contaminated waters as the seaweed grow on the effluent. This 'polyculture' approach contributes to biodiversity and better management of marine resources while also producing a commercially valuable crop. Genetic engineering techniques are now being used to produce seaweed species with greatly increased growth rates, which can be rapidly cultivated in areas of coastal pollution. *MJD*

Nano Gram staining

Researchers have described how a sensor produced by acid etching on a silicon surface can be used to differentiate between Gram–positive and Gram–negative bacteria. Benjamin Miller and colleagues (University of Rochester, Rochester, NY, USA) coated the resulting nanocavities with molecules that have an affinity for groups on the surface of Gram-negative bacteria. When the bacteria are trapped in the cavities, a faint light is produced. In the absence of bacteria, the light emitted shifts wavelength. The team hopes that in the future they will be able to modify the sensor to identify specific bacterial species by using different molecular capture agents. This work is shortly to be published in the *Journal of the American Chemical Society*. *MJD*

Cancer cell typing

Using microarray technology, Arindam Bhattacharjee *et al.* (*PNAS*, 20 November) have divided lung cancers into new categories based on their expression signature rather than the cells' appearance under a microscope. One such signature identified a type of tumour, which on average would kill the sufferer earlier than a similar type of tumour with a different signature. Scientists also used the signatures to distinguish between tumours originating in the lung and those that had spread from elsewhere in the body – a distinction that can be impossible to make using current methods. *DM*

Neuronal plaque formation halted

Plaque formation on the neurons of Parkinson's disease (PD) sufferers could

be halted by a new class of naturally occurring molecules discovered recently (*Sciencedaily.com,* 8 November). In work that was jointly funded by the National Institutes of Health and the Michael J Fox Foundation for Parkinson's Research, Eliezer Masriah and colleagues (University Of California, San Diego, CA, USA) found that molecules called beta-synucleins could untangle plaque-like aggregates formed by a related molecule known as alpha-synuclein, *in vitro*. In animal models, mice bred to overexpress alpha–synuclein displayed PD-like symptoms. Other mice bred with a normal ratio of beta- to alpha-synuclein displayed fewer symptoms. Although the mechanism of beta-synuclein action is unclear, the ratio of the alpha and beta forms is an important factor in controlling neuronal plaque formation. *MJD*

Bioweapons detection

The threat of bioterrorism, seen so vividly in the USA recently, has prompted an urgency to develop equipment capable of detecting harmful biological agents including anthrax. A team of researchers at Eastern Washington State University (Cheney, WA, USA) has developed a detector that uses photoacoustics to monitor airborne particles (*Chemweb.com,* 1 November). This device collects air samples using cyclone technology and concentrates particle in the size range of 1–10 microns. A pulsed laser-beam then irradiates the sample and produces an intense acoustic signal if any biological particles are present; each signal is unique to a particular species. Soot and dust particles produce only very low signals. The researchers envisage that sensors could be permanently mounted in 'high-risk' areas such as mail sorting offices, and an audible signal triggered if any harmful biological agents are detected. *MJD*

Pharmacogenomics news

The report by Kathryn Phillips *et al.* (*JAMA*, 14 November) sheds some new light on pharmacogenomics – the relationship between a patient's genetic make-up and the action of drugs. The work confirms that many harmful drug reactions, previously thought to be non-preventable, could now be averted using genetic information about patients to select their drug therapies. The study, the first systematic assessment of pharmacogenomics' potential, involved linking two independent systematic literature reviews – one reports adverse drug reactions and one concerns natural genetic variation (or variant alleles in genes for enzymes that metabolise drugs. The results highlight a strong potential link between the genetic variants and adverse drug reactions. *DM*

The lethal consequences of research

George Poste, who chairs a Department of Defence task force on bioterrorism and sits on its advisory Defence Science Board, told a pharmaceuticals-industry conference (London, UK, 6 November) that biology must 'lose its innocence'. He criticised biologists for what he regards as 'their naivety in failing to consider malign applications of data generated in legitimate projects', and urged them to start considering how access to such data could best be regulated. One of Poste's suggestions includes the vetting of manuscripts to determine whether 'sensitive' findings should be withheld from the open literature. Poste is particularly worried about things such as the creation of 'stealth' viruses that could evade the immune system (*Nature*, 15 November). *DM*

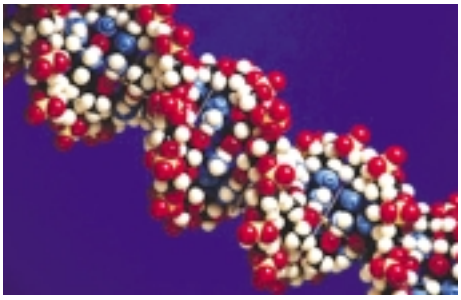
Growth factor vessels

Thomas Richardson *et al.* (*Nature Biotechnology*, November issue) report that a spongy, plastic material impregnated with two types of growth factor has been shown to encourage the formation of healthy new blood vessels in rats. Using microcapsules that dissolve over time, the approach allowed a controlled release of growth factors – crucial for the encouragement of cell growth. The polymer will allow the growth of new vessels on site with much less invasive surgery, and will melt away over time. *DM*

Sperm cell engineering

Makoto Nagano *et al.* (*PNAS*, 6 November) have successfully used a retrovirus to modify genes in spermatogonial stem cells in a mouse. This is the first time that a transgenic animal has been created by inserting a gene into male germ-line stem cells. The inserted gene (*lacZ*) subsequently appeared in ~4.5 % of offspring from mice transplanted with the altered stem cells, and was transmitted by mating to at least three succeeding generations. The work might facilitate the production of transgenic animals in a wide range of species. *DM*

DNA fits the picture



US company DNAPrint (Sarasota, FL, USA) has developed a genetic test that will predict a person's eye colour, and which could be used as a forensic tool to build up a photofit picture of a crime suspect (*Chemistry and Industry*, 19 November). The test identifies variations in genes involved in human tissue coloration by analysis of single nucleotide polymorphisms, subsets of which are linked to human eye colour. Tony Frukdakis, president and CEO of DNAPrint expects the technique might also be used to predict hair and skin colour. *MJD*

Many genome sequence bugs are not available

In the past few months, the publication of microbial genome sequences has emerged with almost monotonous regularity. It is therefore interesting to note a recent piece of correspondence to *Nature* (8 November) from Naomi Ward, Jonathan Eisen and Claire Fraser (The Institute for Genomic Research, Rockville, MD, USA). The authors argue that 'many prokaryotic strains used for genome sequencing projects are poorly documented and not generally available.' They go on to detail the lack of use of representative or type strains of particular species. A type strain is the standard by which other strains thought to be the same are compared. Only 51% of genomes sequenced are the actual type strains. Many of the organisms documented are not deposited in public culture collections, which guarantees the availability of the strain and allows cross-referencing of published data. *DM*

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