

progression², and these processes are not mutually exclusive. Over time, it is the balance between enhancers and suppressors of metastasis that will determine the rate of tumour progression (see Fig. 1).

Microarray technology has revolutionized our ability to detect the temporal molecular changes that occur as cancers progress towards metastasis. Combining this technology with advances in bioinformatics provides growing sophistication for analysing such molecular patterns. What is commendable about Varambally and colleagues' approach³ is that, in addition to conducting complex pattern analysis, they have gone on to investigate the potential functions of individual genes. In the study described here, they selected one promising candidate for more intensive investigation using the tools of contemporary molecular and cellular biology. Their results provide new insight into the role of one particular protein, EZH2, in tumour biology, and in so doing reveal a potential new mechanism underlying tumour progression.

Could prostate-cancer patients benefit from this finding? Quite possibly. Although blood levels of the prostate-specific antigen (PSA) protein allow physicians to diagnose prostate cancer, this test is less useful for

prognosis. What is needed is a way of distinguishing prostate cancers that are, or will become, metastatic from those that will remain localized to the prostate. The best prognostic indicators would be molecules whose levels fall or rise during the transition to metastasis — as is the case with EZH2. Significantly, Varambally and colleagues' data³ also indicate that the presence of EZH2 at the time of diagnosis correlates with future tumour recurrence. So this protein, along with other molecules such as thymosin beta 15 (ref. 8) and PTEN⁹, may offer physicians new predictive tools with which to guide decisions about how and when to treat prostate-cancer patients. ■

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Nanotechnology

Beyond the silicon roadmap

Neil Mathur

Silicon will eventually fail to satisfy the 'smaller, faster, cheaper' drive in technology. Nanoscale techniques could take over, and a recent conference reviewed the prospects for computing and electronics.

When and how will nanotechnology make computers work better? At a conference held last month*, Jim Hutchby (Semiconductor Research Co.) predicted that nanoscale electronics would appear on the International Technology Roadmap for Semiconductors¹ in 2011–2016 — and would tear it up by 2050.

Existing silicon-based CMOS technology in computers cannot navigate the roadmap as far as the nanoscale. At that scale, quantum effects start to become significant, and even if silicon components were shrunk to these dimensions the result would not be a 'quantum computer': heat dissipation (around 100 W cm⁻², according to L. Manchanda, Semiconductor Research Co.) would not only lead to the decoherence of fragile quantum states, it would melt the silicon substrate. So what does the science of today suggest about the computing of tomorrow?

In the short term, the existing von

Neumann architecture of today's computers should survive and carry silicon a little beyond its natural shelf-life, thanks to spectacular advances in molecular electronics. For example, binary information can be written into an 'atomic switch' between crossed and nearby nanometre-size wires of platinum and silver if the latter are coated with the solid electrolyte Ag₂S (M. Aono, RIKEN). The silver in this material is mobile², and a few atoms can be electrically induced to migrate to the platinum wire and close the switch. It is possible to combine switches such as these to form logic gates,



Figure 1 The conference logo writ small. Carbon nanotubes such as these could make both the computers and displays of tomorrow. (Image courtesy Kenneth Teo, Manish Chhowalla, Gehan Amaratunga and Bill Milne, Univ. Cambridge.)

*Trends in Nanotechnology, Santiago de Compostela, Spain, 9–13 September 2002.

many possible routes to quantum computing have been suggested, but the most promising are solid-state implementations — most famously, nuclear spins of phosphorus atoms in a silicon matrix¹⁰ — because they can be scaled up to generate the massive parallelism required for useful computation.

The counter-intuitive rules of quantum mechanics imply that, unlike classical computers, quantum computers should perform best with a slow clock speed¹¹ (in other words, the devices within them should switch slowly). This necessarily suggests that rapid decoherence of the quantum states encoding information is unacceptable. Entanglement between two solid-state quantum bits, or qubits, was reported for the first time at this conference — albeit with a rather rapid decoherence time of 300 picoseconds (J. S. Tsai, NEC). The qubits used were based on low-temperature superconducting tunnel junctions. Perhaps this breakthrough indicates where the future of quantum computing actually lies.

Another departure from conventional computing philosophy would be to work with light rather than electrons. Whereas the periodicity of the structure of crystalline materials is comparable to the wavelength of mobile electrons, advanced materials techniques enable periodic structures to be produced in which the repeating unit matches the wavelength of light — these are photonic band-gap materials. Complex structures formed with these advanced techniques (for example, ref. 12) could be used to manipulate light and form computer logic gates. Indeed, computer simulations suggest that light can bend around cleverly constructed corners with no discernible energy loss (S. John, Univ. Toronto).

The conference was also presented with some aspects of nanotechnology that could have an indirect impact on tomorrow's computers. For example, the issue of heat dissipation mentioned earlier could be locally monitored using a 75-nm-diameter carbon nanotube containing the liquid-metal gallium, which would act like a nanoscale mercury thermometer¹³ in the 50–500 °C range (Y. Bando, National Institute for Materials Science, Tsukuba). Or perhaps computerized devices such as gas-specific sensors will rely on specially adapted nanotube elements — such devices can detect as little as 0.02% H₂ (G. Gruner, Nanomix, Inc. and UCLA). Or perhaps computer display devices will use electron emission from nanotubes (P. Legagneux, Thales) such as those shown in Fig. 1 — in fact, Samsung have this year reported a proof-of-principle display unit¹⁴.

So where will it all end? The graphics of S. John were reminiscent of the best that Hollywood can achieve, and the many talks relating to biology could at times make this

physicist feel that he had come to the wrong conference. The nanoscale therefore seems to be the length scale at which science has become truly interdisciplinary. The question is, will it reconcile science fact with science fiction? ■

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Ecology

Biodiversity in the scales

Nicholas J. Gotelli

Scaling coefficients can reveal nonlinear relationships among biological variables. The approach has now proved fruitful in exploring the relationship between diversity at different taxonomic levels.

Species diversity is central to ecological studies. But it is a challenging parameter to measure because diversity is organized hierarchically: individual organisms are classified into species, species into genera, genera into families, and so on. As a consequence, patterns of diversity at one level (genera, for instance) are linked statistically and by evolutionary history to the patterns at higher and lower levels (such as families and species). On page 610 of this issue¹, Enquist and colleagues describe tight scaling relationships between species richness and diversity among the higher taxa (genera or families), in both living and fossil plant communities. These patterns should eventually help in understanding how species diversity is controlled and how total biomass is partitioned among coexisting species.

Enquist *et al.*¹ used allometric scaling equations that have traditionally been applied to problems of body size and relative growth. In mammals, for example, a power function² describes the relationship between brain size (x) and body size (y):

$$\text{Brain size} \propto \text{constant} \times (\text{body size})^z.$$

The exponent z is the scaling coefficient, and describes whether y is increasing faster ($z > 1$) or more slowly ($z < 1$) than x . On a log–log scale, these relationships plot as straight lines for which the scaling coefficient is the slope. In previous work, Enquist and colleagues^{3–5} successfully applied allometric models to general patterns of biomass, body size and growth form in plant and animal assemblages. Here, they extend this approach to describe patterns of taxonomic and biomass partitioning in different tree

communities. They analysed a high-quality global data set, collected by the late Alwyn H. Gentry, that includes 227 sites, each one-tenth of a hectare in area, from six continents. A database of plant fossil communities from the Tertiary period included 29 samples from sites in western North America.

For both the living and fossil tree communities, Enquist *et al.* plotted the logarithm of the number of higher taxa against the logarithm of the number of species, and discovered a tight relationship that explained more than 90% of the variance (although the fit to the Gentry data was not strictly linear). In other words, the number of higher taxa in a community is highly predictable from the number of lower taxa. In one sense, this is not new. Ecologists and biogeographers established long ago that the diversity of higher taxa changed predictably in large communities compared with small ones⁶. As more species are drawn randomly from a regional source pool, the number of higher taxa rises steeply at first as common taxa are added, and then more slowly as progressively rarer taxa are added⁷. The power function transforms this sampling curve into an approximately linear allometric relationship over limited regions of the curve.

Could taxonomic scaling be the inevitable consequence of random sampling from a large regional or global species pool? The answer seems to be no: the exponents for randomly constructed communities were consistently larger than those found by Enquist and colleagues. This result means that higher-level diversity in communities accumulates relatively slowly. Put another way, communities consist of slightly more species per genus or species per family than