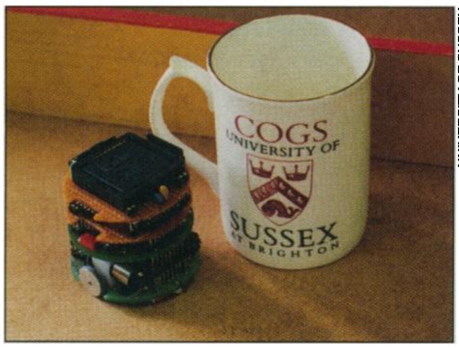
MEETING BRIEFS

Artificial Life Gets Real as Scientists Meet in Japan

The mathematicians and computer scientists who form the core of artificial-life enthusiasts have long thought their evolution-inspired computer techniques can model reality—and even create it. Their enthusiasm was much in evidence at A-Life V, held 16 to 18 May in Nara, Japan, where 500 attendees heard about efforts to evolve useful circuit designs and a model of runaway sexual selection.

Programs Beget Real Circuits

Artificial life has gone full circle, from reality to models and back again. The genetic algorithms at the heart of the field strive to mimic the evolutionary process by putting populations of software solutions to a problem through an electronic version of recombination and natural selection to yield improved answers to complex problems. But now this evolution-in-a-computer is moving into something real, namely, designing microelectronic circuits.



UNIVERSITY OF SUSSEX

On a roll. Programmable circuits help this tiny robot avoid bumping into objects.

The latest products of this effort to create what is being called evolvable hardware were discussed at the meeting, and some were even on display. They include artificially evolved circuit designs for use in stereos, radar devices, and pint-sized robots that can navigate among obstacles. As yet, the fittest microelectronics don't measure up to what human designers turn out. But John Koza, consulting professor in computer science at Stanford University, thinks that within 3 years genetic techniques will be yielding useful circuit designs. Visionaries even see autonomous robots evolving their own control circuits while on the job.

The process begins with simulated embryonic circuits with the desired number of inputs and outputs and the basic features needed for a simple working circuit, explains Forrest Bennett, a visiting scholar working with Koza. A circuit-constructing program then randomly modifies the wiring layout and adds components such as resistors, capacitors, and inductors. The resulting population of circuits is tested for performance in a circuit-simulation program. For a frequency filter in a stereo, for example, the test might be how well a circuit separates the tweeter and woofer signals.

Better performance increases the chance that a circuit's design will be passed on to the next generation. That evolution takes three forms: reproduction without modification; an exchange of subcircuits or components—the genetic programming analog of recombination—or mutation, in which the circuit is modified by the circuit-construction program. The operation is repeated until it yields a circuit with the desired characteristics.

Koza's original benchmarks were circuits designed in the 1950s. After succeeding in matching those designs, his group is trying to reproduce a circuit patented in 1990. "If we're successful we'll claim we've moved up 40 years in terms of solving [circuit design] problems," he says.

A team at the Advanced Telecommunications Research Institute International (ATR) near Kyoto is taking a different approach. Rather than evolve circuits directly, ATR scientists want to evolve circuit behaviors by performing genetic operations such as crossover, mutation, and gene duplication on "structured rules," which then feed into programs that describe circuits. Instead of evolving the "genes" of microelectronics—the circuits—says ATR's Katsunori Shimohara, he and his colleagues are evolving the proteins those genes code for: the rules. Each rule is linked to one clause of a special-purpose programming language that can be converted into a circuit diagram. By refining the rules, he and his colleagues hope to develop libraries of subcircuits with defined functions that could be linked to form complex circuits. Their goal is to avoid one large and nearly indecipherable genomelike circuit.

So far, these and other groups have only simulated their circuits. But a hardware breakthrough now allows researchers to conduct real-world fitness tests using a type of integrated circuit called a field programmable gate array (FPGA). In effect, FPGA users can wire up their own circuits. This process once took several hours, but the latest FPGAs can be rewritten almost instantaneously, giving the hardware evolvers a versatile test bed for circuit designs.

A robotics group at the University of Sussex in Great Britain demonstrated how it works with a tiny two-wheeled robot displayed at the Nara conference. The robot's task was to wander aimlessly and avoid obstacles. Two sonar sensors provide the input to the robot's FPGA brain, while the output controls motors that drive the wheels.

The Sussex group began its exercise in robot evolution by loading a "population" of 40 different control-circuit designs into the FPGA one by one, then giving each one a fitness score based on its ability to avoid obstacles. The designs were then mutated and recombined in a computer, then retested in the robot. Twenty-five generations later, a control circuit emerged that avoided obstacles. Phil Husbands, a lecturer in artificial intelligence at Sussex, says the work could be a first step toward autonomous robots that modify their own control circuits in real time.

The next challenge for scientists is to apply the approach to more complex circuits. Koza says one major problem with the evolutionary approach is a decrease over time in circuit diversity as crossover operations win out over mutations. And as biologists know well, without a constant supply of new variants, evolution grinds to a halt.

The Tale of a Peacock's Tail

The perennial challenge for mathematicians and computer scientists who hope to apply their evolution-inspired computer techniques to the study of evolution itself is to show that their simulations are true to life. Last month, artificial-life enthusiasts heard evidence that they may be on the right path, even if they aren't blazing the trail.

Gregory Werner, a doctoral candidate in computer science at the University of California, Los Angeles, who recently joined the Max Planck Institute for Psychological Research in Munich, Germany, examined runaway sexual selection, in which a male trait detrimental to survival becomes exaggerated because of female preferences. A prime example is the peacock's tail, just the kind of structure Werner had in mind when he constructed a computer model of sexual selection based on genetic algorithm techniques. The model generates many software "individuals" and then replicates them depending on how well they meet some criterion of "fitness."

In Werner's model, each individual carried "genes" for heritable traits—some beneficial, some detrimental—that were tied to fitness scores. The higher an individual's fitness score, the greater its chance of reproducing. Individuals also carried "genes" for heritable mating preferences. Each female was paired with the male that most closely matched her preferences from among a random group of candidates. Standard genetic algorithm techniques allowed for random mutations.

After conducting numerous simulations with varying parameters, Werner found that males would accept extremely high fitness handicaps to win in sexual-selection competition. What kept runaway sexual selection from getting too far out of hand was another heritable trait—limits on females' willingness to put time and energy into looking for males with desirable traits. Werner concluded that, based on his simulation exercises, the cost to females of evaluating males "is what limits the growth of maladaptive traits."


JAN HALSKA/PHOTO RESEARCHERS

Checkout time. Computer model finds female peacocks limit time spent on choosing a mate.

That result is accepted wisdom among evolutionary biologists, says Andrew Pomiankowski, an evolutionary biologist at University College, London, "but I'm glad to hear he's confirming it." And Pomiankowski thinks that Werner's approach, despite its belated conclusion, can augment work based on the more traditional analytical methods used by biologists. "There's plenty of work to be done," he says.

Werner intends to refine his model to study more general population trends by adding in such factors as parental investment in offspring and mate choice. He is also collaborating with colleagues in looking at how sexual selection may facilitate speciation. In the end, he and his colleagues hope the results will speed the process by which artificial life evolves into a useful biological tool.

–Dennis Normile

DEVELOPMENTAL BIOLOGY

Corn: A Lot of Change From a Little DNA

NASHVILLE, TENNESSEE—If wolves can give rise to poodles and Pekingese, perhaps it's not so hard to believe that corn growing "as high as an elephant's eye"—as songwriters Rodgers and Hammerstein put it—is the domesticated version of a bushy and inedible weed called teosinte. Yet the two plants are incredibly different. In addition to the shape disparity, corn ears—the flowers of the domesticated plant—are covered with hundreds of soft, edible kernels, while teosinte flowers are studded with just a dozen or so, all firmly encased in armor. At the national meeting of the Society for Developmental Biology 3 weeks ago in Nashville, however, scientists heard that the plants are not only close relatives, but many of the features that make corn ears so bountiful could result from mutations in just one small stretch of teosinte DNA.

Jane Dorweiler, a graduate student at the University of Minnesota, reported that giving teosinte a single portion of corn's chromosome 4 altered the basic process of flower development, and teosinte seeds became exposed kernels just like those on corn—or maize, as it's known to botanists. The hybrid is "what teosinte may have looked like during one of the morphological steps in its evolution toward maize" some 7000 to 10,000 years ago, when archaeologists believe teosinte was domesticated in what is now Mexico, Dorweiler says.

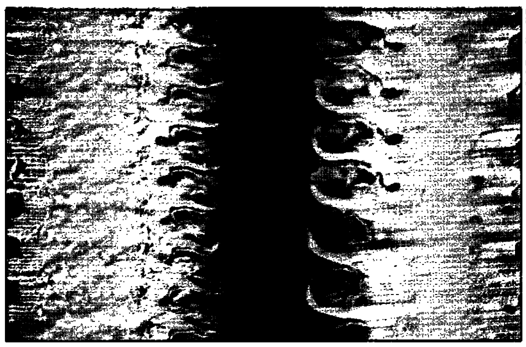
One such archaeologist, Bruce Smith of the Smithsonian Institution's Museum of Natural History, agrees. "How you get the morphology of the corn cob out of teosinte ... has been the big puzzle remaining to be described," he says. "Having biologists move closer in on that is really of great value and interest." And plant developmental geneticist Scott Poethig of the University of Pennsylvania adds that the work supports the growing notion that minor genetic changes can result in large evolutionary leaps. Dorweiler and her colleagues think it may even point toward a way of engineering similar improvements in other cereal or grain plants.

Dorweiler's investigation follows work done in 1991 by Minnesota's John Doebley and others, who used genetic markers on maize's 10 chromosomes to track several important traits that distinguish it from teosinte. They led to five "quantitative trait loci" or QTLs, the regions where the genes producing these characteristics are presumed to be (*Science*, 28 June 1991, p. 1792). Changes in one QTL, named *tga1*, seemed to account for the diminishment of the fruit case, or glume, that surrounds the seeds in teosinte, where it is "lignified" or hardened enough to crack the teeth of even the most ardent corn lover.

Dorweiler took that work a step further, watching how glume structures developed in teosinte hybrids with one copy of *tga1*. The glumes ended up shorter than in wild-type teosinte, did not completely encase the kernels, and were much softer, apparently because they contained less silica. Glumes were feebler still in teosinte carrying two copies of *tga1*—a sure sign that the locus contained a gene or genes regulating the trait.

Doebley speculates that maize may have first emerged when ancient humans cultivated a mutant teosinte strain in which the functions of genes within *tga1* were somehow attenuated, an idea that is "certainly reasonable," says Poethig. "Until you can make [corn] edible, there isn't much point in harvesting it." The researchers have yet to clone genes from the locus. But because it seems to guide several disparate aspects of glume architecture, Doebley and Dorweiler suspect that the genes may regulate very early events in ear development.

The Minnesota group's finding further strengthens the argument, made by Harvard University paleontologist Stephen Jay Gould and others, that small evolutionary changes can produce drastic—and sometimes advantageous—differences in an organism's architecture. Moreover, Doebley says, if QTLs corresponding to *tga1* can be found in other cereal crops or even noncrop plants, then knowledge about maize evolution could be used to bring other hidden fruits into the open.


J. DORWEILER

All ears. Exposed kernels make standard corn easy to harvest *(left)*. But in corn carrying a small stretch of DNA from its wild relative teosinte, kernels are protected by a hard case *(right)*.

–Wade Roush