economy was the 43% increase in what Power calls "footloose income"—investment and retirement income. "This is money that follows its recipient and is not tied to employment opportunities," says Power, "and it can leave the area just as easily as it arrived." One telling statistic concerning the footloose dollars was that while wages and salaries in the area fell by almost $80 million a year from 1978 to 1987, investment and retirement income soared by $240 million a year.

Power argues that residents of the greater Yellowstone area do not face a choice between sacrificing their environment and watching their economy go down the tubes. "A new, more stable economy has developed here that depends not on the ongoing destruction of the area's unique natural systems but, rather, on their preservation." People won't retire or move to Yellowstone or start businesses, he argues, if clear-cutting, strip-mining, and over-grazing degrade the ecosystem's natural beauty.

Ecologists couldn't agree more—because the same policies that preserve natural beauty would help sustain endangered species like grizzlies, pronghorn antelopes, and elk. What those species need, say the biologists, are unified, ecologically sound policies from state and federal agencies, overcoming contradictions such as the fact that hunting is prohibited in the national parks but is allowed in the neighboring national forests. What the animals need, says Joel Berger, a biologist at the Smithsonian Institution's Conservation and Resource Center who has studied local wolf populations, is one governmental body overseeing management of the entire ecosystem that ignores political boundaries in favor of ecological limits.

Perhaps surprisingly, given the infighting that characterizes most bureaucracies, the agencies involved agree. Last year managers of the U.S. Forest Service, the Park Service, and the Fish and Wildlife Service, along with their state counterparts, developed a comprehensive set of coordinated management goals that the Greater Yellowstone Coalition and many environmental organizations applauded. That plan, called "Vision for the Future" was abandoned, however, in the face of intense lobbying by regional livestock, timber, mining, and agricultural interests.

"We opposed the Vision document because it attempted to set forth a land-use plan that takes the preservation philosophy that the National Park Service has toward Yellowstone Park and apply it to nonmanagement areas outside the park," says Gary Langley, director of the Montana Mining Association, an opponent of management coordination plans. "Basically, they're trying to turn the whole Greater Yellowstone area into one big protected place." The Wyoming legislature went so far as to pass a resolution asking Congress to order the Interior and Agriculture Departments to withdraw the document.

Dennis Glick has harsh words for the groups that scuttled the management plan. "What they want is business as usual," he says, "but business as usual is going to have an adverse effect on all who live here—humans and wildlife." And in their efforts to forestall those adverse effects ecologists and economists are—for once—on the same side of the divide. ■ JOSEPH ALPER

"African Eve" Backers Beat a Retreat

Is the African ground getting shaky under the feet of mitochondrial Eve? Could be. Mitochondrial Eve is the popular name for a common ancestor of modern humanity that the late Allan Wilson and his colleagues at the University of California at Berkeley announced they had found in 1987. The Wilson team claimed that by analyzing DNA from the energy-producing organelles called mitochondria, which are purely maternally inherited, they had traced the maternal lineage of all humans back to a single woman who lived in Africa about 200,000 years ago.

But that claim wasn't received with a quiet murmur of consensus. In fact, it kicked up a storm of controversy. Some paleoanthropologists argued that the finding couldn't be right—the fossil record, they said, ruled out a common ancestor more recent than a million years ago. Others criticized the group's methods for DNA analysis, their choice of study subjects, and their means of finding and dating the tree's roots.

Last September, the group published a followup paper in Science dealing with many of the methodological criticisms. That paper seemed to nail the African Eve hypothesis more firmly into place. Now, however, several of those newly hammered nails have been pulled out—and the root of the human tree has been thrown open to question once again.

Two technical comments in this issue of Science (page 737)—one co-authored by Mark Stoneking, a key member of the Wilson team—and an article in press in Systematic Biology, by a team led by David Maddison of Harvard, undermine the Science paper by showing its conclusions to be statistically flawed. "We're not saying...that [the origin] is definitely non-African, but rather that you can't tell," says Harvard anthropologist Maryellen Ruvolo, one of the authors of the Systematic Biology paper.

The new critiques focus on a central issue in all the mitochondrial Eve studies: how to build a reliable family tree from variations in mitochondrial DNA (see box on facing page). The underlying principle is straightforward. You simply examine the nucleotide

Radical skepticism. *Alan Templeton doubts mitochondrial DNA analysis can identify the root of the human family tree.*

sequences of several regions of the DNA from a wide variety of people, then calculate the relatedness of those individuals by seeing how similar the sequences are. That sounds simple, but even with small numbers of people and DNA sites, it requires decisions that can be made only by sophisticated computer analysis. And with 100 people or more—the size of the samples used by the Wilson group—the analysis can take weeks of main-frame computer time.

The Wilson team used a program written by David Swofford, a systematist with the Illinois Natural History Survey in Champaign. The program, PAUP, or Phylogenetic Analysis Using Parsimony, strives to find the most "parsimonious" tree—a tree that traces everyone's lineage back to a common ancestor with a minimum number of mutations along the way. That "shortest path" is considered most likely to reflect what happened during evolution. Unfortunately, PAUP doesn't often offer just one most parsimonious tree for each sample. Indeed there may be millions of equally good trees. After each computer run a number of possible trees pop out—and it's up to the researchers to decide how many computer runs to do, and how many hundreds or thousands of trees to ask the computer to save after each run for later analysis.

The Wilson group drew its conclusions after looking at 100 trees from only a single

run. "They shouldn't have stopped at 100," says Swofford, who joined Maddison and Ruvulo in writing the *Systematic Biology* paper. "That's a very nonrandom sample of the trees that are considered equally good by the program." The group should have looked at trees from many different runs, he adds, because all the trees produced on any one run are related (see box). In their reanalysis, the Maddison team looked at trees from thousands of runs, and found a mixture of African and non-African roots.

Swofford says he doesn't want to condemn the Wilson group for not using his complicated program to its best advantage, but he nevertheless felt compelled to point out the weaknesses in their analysis. Ruvolo agrees that the lesson is a general one: "I think a lot of molecular workers haven't fully appreciated that...you have to search through [the trees] in a particular way, so you can actually give yourself the chance to reveal the trees that are most different."

Anyone who didn't realize that before should now. The authors of all three reanalyses found trees shorter than the one published in the *Science* paper—and some of them don't have African roots. Washington University geneticist Alan Templeton, author of one of the technical comments, says he stumbled onto better trees—with non-African roots—in his very first run. "I just wanted to test whether the hypothesis that the common female ancestor lived in Africa is justifiable by the current data," he says, "and one run was sufficient to say no."

The third reevaluation was done by Blair Hedges and his colleagues in the laboratory of Masatoshi Nei at Pennsylvania State University. They averaged results from 50,000 trees generated by PAUP, and found that the trees varied too widely to be of any use. Hedges told Stoneking, who is now at Penn State's Institute of Molecular Evolutionary Genetics, about the finding, and Stoneking agreed to sign the group's letter to *Science*.

And where does all this leave African Eve? Perhaps reeling under the weight of criticism—but not by any means dead. Hedges' team also used a second method, called neighbor joining, that uses a different algorithm than PAUP to build a single likely tree, and got a tree with African roots. The statistical significance of the result was low, however. Stoneking and Hedges say it nevertheless suggests African origins, though Stoneking concedes that "we can't say with a high degree of confidence that that is the case." But according to Harvard's Maddison, the lack of statistical support implies that "the
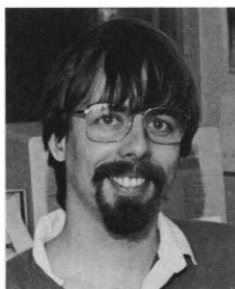
contrary hypothesis is basically just as good."

Templeton sounds an even gloomier note. In a review article in press in *American Anthropologist*, he presents calculations suggesting that low-level mixing among early human populations may have scrambled the DNA sequences sufficiently that it will never be possible to settle the question of an African origin on the basis of mitochondrial DNA trees. He also suggests the dating of Eve—something not challenged in the present exchange—may be so vague as to be meaningless as well.

But the notion that modern humanity originated in Africa wouldn't collapse without support from mitochondrial DNA, according to anthropologist Christopher Stringer of the

Natural History Museum in London. "There is plenty of other evidence in addition to the mitochondrial work," says Stringer, referring in part to his own fossil evidence that racial differentiation of modern humans did not begin until much less than 100,000 years ago, as well as studies of nuclear DNA in which "Africans seem to be splitting off first."

What's more, there is one piece of mitochondrial DNA evidence from the Wilson group that remains unchallenged, says Harvard's Ruvolo. That is the fact that Africans have greater diversity in their mitochondrial DNA than the inhabitants of any other continent. And that diversity, Ruvolo adds, is "the strongest piece of evidence for an African origin"—because it suggests that, to accumulate the largest number of mutations, humans must have lived longer in Africa than anywhere else. ■ MARCIA BARINAGA

David Maddison

A.E. COLEMAN, COURTESY OF THE MUSEUM OF COMPARATIVE ZOOLOGY, HARVARD

Choosing a Human Family Tree

In the debate over mitochondrial Eve a central problem has been how to use the nucleotide sequences in human DNA to construct a family tree that reveals human origins. There are several computer programs for building trees that show how individuals (or populations, or species) may be related, based on the similarity of their DNA. One

highly regarded method is "parsimony analysis," in which DNA sequences are sequentially arranged to build the most "parsimonious" family tree—the one that relates all the observed sequences and postulates the fewest mutations over the course of evolution.

But finding parsimonious trees isn't always a snap. The illustration shows some of the things a computer has to consider. Shown here are DNA sequences—five nucleotides long—for five people. In the third position, two people have an A nucleotide and three have a G. If comparison to an ancient sequence such as that of a chimpanzee suggests G was originally at that position, then it follows that a mutation must have given rise to the A. Of the two trees shown, the upper tree arranges the sequences in a way that requires only one mutation—and is therefore more parsimonious than the lower tree, which requires two mutations.

That seems easy, but it quickly becomes complicated, especially if the DNA contains conflicting information. For example, when the computer moves on to consider the fifth position, it will find information suggesting that I and II are more closely related than I and III. Following that information, the computer could create a different tree that is just as parsimonious as the upper tree shown here. Conflicts like these cause the number of equally parsimonious trees to rise rapidly: With conflict-riddled data for 100 people, the number of equally parsimonious trees may be in the millions.

PAUP, the parsimony-computing program developed by David Swofford of the Illinois Natural History Survey, goes about the process of finding the best solution by adding sequences to the tree one at a time and then swapping branches around to find better trees. The trees it finds on any one computer run are necessarily related to the starting tree, says Swofford, and the shape of that tree is influenced by the order in which the samples were added. To get the best idea of the range of possible trees, he says you need to sample trees from many runs, each with the samples added in a different, random order. ■ M.B.