HIGHLIGHTS

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EVOLUTION

Good arbitrations

independent versions of the story.

of conflicts - that is, incongruence

— between trees that are built using

single genes. On the basis of a con-

catenated data set of 106 genes that

were unambiguously orthologous among the genomes of seven

Saccharomyces species and a related

fungus, they built a tree in which

every relationship received the maxi-

mum possible level of statistical sup-

port. This is an unprecedented result

trees, but in their waking lives - in

which usually, at best, a few genes are

available --- they rarely get anywhere

near these consistent levels of sup-

port. In the absence of a time

machine, this tree is clearly the best

possible estimate of the evolutionary

relationships among these yeast

question of what would be the mini-

The authors went on to look at the

species.

Phylogeneticists dream of such

for a tree with so many taxa.

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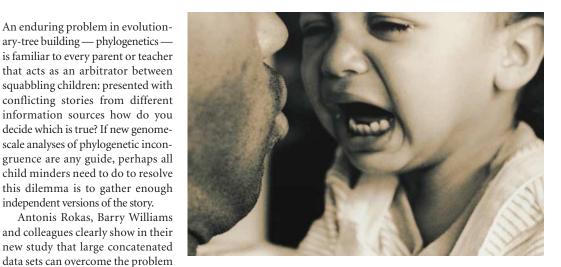
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mum number of genes that would lead to the correct tree being built with good statistical support for all relationships. By randomly resampling and concatenating variable numbers of genes from the complete data set and building trees from these, they showed that 20 genes would be sufficient.

However, the authors also showed that if the chosen genes are biased in the same direction, trees that strongly support the wrong relationships can result. This is important because one common strategy is to build trees from many genes that could be biased in the same direction: mitochondrial genes are the classic example.

These new results should raise the hopes of phylogeneticists while simultaneously raising the bar for them: the true tree is out there, but more than a few genes must be sampled to be sure that you have it.

The problem remains that for most researchers a few genes are all that they have or can afford to gather. The next few years might see the falling cost of high-throughput sequencing and the availability of a more diverse range of genomes make trees that are built with 20 or more genes the norm. However, until then there will still be many who, like the parent with only two versions of a juvenile dispute to work from, will be faced with the problem of how to resolve conflict in a non-arbitrary fashion.

Nick Campbell References and links

ORIGINAL RESEARCH PAPER Rokas, A. et al. Genome-scale approaches to resolving incongruence in molecular phylogenies. Nature **425**, 798-804 (2003)

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