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Shaking off genome fatigue

In the wake of the hoopla surrounding the publication of the rough draft of the human genome, the potential emergence of 'genome fatigue' in the media, and even among scientists, is understandable. The genome remains a work in progress, and has not yet produced any of the promised medical panaceas. Many of the jobs that policy-makers said would be in demand as a result of the stepped-up effort — production, finishing and annotation — seem like old news and, although important, are hardly glamorous.

And once the obvious organisms — mouse, chimpanzee, zebrafish — are done, then what? It's hard to imagine debates about the utility of sequencing the duck-billed platypus as opposed to the spotted owl generating much passion outside limited circles or leading to incredible new job opportunities.

Perhaps one reason for genome fatigue, beyond simple fallout from the hype, is that discussions about jobs in genomics focus too much on sequence production. It seems almost churlish to cavil at this: the increase in throughput and the rapid rise in the number of genomes in the sequencing pipeline are nothing short of amazing. It is, perhaps, even more astounding that many take this progress for granted.

But now that the hype about the sequence has died down, the genome itself is becoming intellectually interesting again. Instead of merely devising ever-faster ways to produce data, scientists are thinking about creative ways to use the existing information. A haplotype-mapping project aimed at producing a map of complex genetic variations is one idea (see *Naturejobs*, page 4). Such projects will create jobs that demand sophisticated sets of skills.

So the draft human genome should not generate complacency but continue to re-energize scientific opportunity.

Paul Smaglik
Naturejobs editor

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