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▶ **COVER:** 'Ascend/descend' by Patrick Morgan.


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A common rationale for funding genetic and genomic research is that it will ultimately lead to improvements in the quality of human lives. But how can this important output be maximized? Two articles in this issue discuss different ways of accelerating progress from basic research to public health benefit.

Given the increasingly vast amounts of information on genetic variation and disease, databases are vital tools for researchers and clinicians. But, as Anthony Brookes and colleagues discuss on p9, most databases are not geared up to cope with integrating multiple layers of genotype and phenotype data. If the goal is rapid translation of basic science to clinical applications, databases will ideally not only store information but also aid identification of new patterns and interpretations. Alongside the bioinformatic challenges are wider questions for the scientific community: who should curate integrated databases; how will contributing researchers be recognized; and who can access the information? If not addressed, these issues could impede realization of clinical progress from scientific advances. As discussed in a recent Policy Forum article in *Science* (Cotton, R. G. H. *et al. Science* **322**, 861–862), the efforts of the Human Variome Project (www.humanvariomeproject.org) to achieve global accessibility for information on human genetic variation demonstrate how such challenges might be tackled.

An alternative approach to accelerate the transition from laboratory to clinic is for research institutions to structure their organization with that goal in mind. In his Essay on p64, Edison Liu describes how the collaborative genomes-to-systems strategy at the Genome Institute of Singapore has maximized the clinical applicability of the research it carries out.

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