This is not the end.
It is not even the beginning of the end.
But it is, perhaps, the end of the beginning.

—Sir Winston Churchill

To Sequence or Not To Sequence?

Critics noted that the portion of the human genome that actually codes for genes was thought to be less than 5 percent of the total. The remainder was dismissed as “junk” and not worth the cost of sequencing. Still, other scientists like Sydney Brenner pointed out that “We have the surprising result that most of the human genome is junk; junk and not garbage because there is a difference that everybody knows; junk is kept while garbage is thrown away” (Brenner 1990). Nobel laureate Paul Berg is another scientist who believes that junk DNA has many lessons to teach us. He once gave a talk at the Salk Institute where he described how the SV40 virus can produce two different RNA transcripts from the same DNA sequence. He predicted that this strategy of “alternate splicing” also would have application in mammalian genomes. Francis Crick disagreed, and the two made a bet of two cases of wine. Berg made similar bets with other colleagues and now has a well-stocked wine cellar (Davis 1990).

As the HGP moved forward, other scientists worried that the resultant torrent of sequence data would prove overwhelming and unintelligible. Robert Weinberg, who at the time was studying genes associated with retinoblastoma, lamented, “I fear . . . that the important discussions have already been made and that the great sequencing juggernaut will soon begin its inexorable forward motion, flooding our desks with oceans of data whose scope defies conception and our ability to interpret meaningfully” (Lee 1991). During the late 1980s when...