



## Editor's Note

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*Genome Res.* 1998 8: 159

Access the most recent version at doi:[10.1101/gr.8.3.159](https://doi.org/10.1101/gr.8.3.159)

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Cold Spring Harbor Laboratory Press

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This issue of *Genome Research* focuses on informatics. As the amount of data coming out of genetic research and the complexity of the questions asked increases, the need for faster computer programs with increasingly complex analysis capabilities grows. Informatics handling is required to enable faster and higher quality sequencing, to assess sequencing systems as a whole, and to promote better ability to analyze long sequences for identification of genes—by recognizing potential open reading frames, splice sites, and promoters—and for predicting potential gene function. Evolutionary analyses using phylogeny analysis programs enables both an understanding of change in gene and gene families over time, but also opens the door to greater means of assessing the function of unknown genes as well as a greater general understanding of an organism's history. Disease gene identification for Mendelian and complex disorders can be enhanced by a variety of programs including appropriate software for complex pedigree design and analysis. In addition to all of these individual programs addressing specific questions there are program suites that interlock several programs, creating additional capacity for analyses as well as the means for the noncomputational biologist to access and make the best use of the available power generated by the latest program venture.

The papers presented in this issue cover a variety of these issues. In some cases, they represent the culmination of years of work that has already been tested in many laboratories; others exemplify the beginnings of newer analyses for areas of research that will be developing over the upcoming years. Simply reading the introduction of the papers contained within this issue should give the more general reader excellent insight into the reasons behind the development of these programs and illuminate some of the problems that still need to be overcome to make the best use of all the data being generated by current studies.

The work that has been done and is currently being done in the informatics field is vital to the future success of ongoing biological studies. It is incumbent on all researchers to take full advantage of the wide range of powerful tools coming out of this area. Both researchers who consider themselves computational biologists and those who do not need to continue to make strides to work together to address those issues in biology that can best be met using the amazing computational capabilities being developed.

*Laurie Goodman*