



Mastering Perl for Bioinformatics

James D. Tisdall

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Historically, programming hasn't been considered a critical skill for biologists. But now, with access to vast amounts of biological data contained in public databases, programming skills are increasingly in strong demand in biology research and development. Perl, with its highly developed capacities in string handling, text processing, networking, and rapid prototyping, has emerged as the programming language of choice for biological data analysis. *Mastering Perl for Bioinformatics* covers the core Perl language and many of its module extensions, presenting them in the context of biological data and problems of pressing interest to the biological community. This book, along with *Beginning Perl for Bioinformatics*, forms a basic course in Perl programming. This second volume finishes the basic Perl tutorial material (references, complex data structures, object-oriented programming, use of modules--all presented in a biological context) and presents some advanced topics of considerable interest in bioinformatics. The range of topics covered in *Mastering Perl for Bioinformatics* prepares the reader for enduring and emerging developments in critical areas of bioinformatics programming such as:

- Gene finding
- String alignment
- Methods of data storage and retrieval (SML and databases)
- Modeling of networks (graphs and Petri nets)
- Graphics (Tk)
- Parallelization
- Interfacing with other programming languages
- Statistics (PDL)
- Protein structure determination
- Biological models of computation (DNA Computers)

Biologists and computer scientists who have conquered the basics of Perl and are ready to move even further in their mastery of this versatile language will appreciate the author's well-balanced approach to applying Perl's analytical abilities to the field of bioinformatics. Full of practical examples and real-world biological problem solving, this book is a must for any reader wanting to move beyond beginner level Perl in bioinformatics.

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