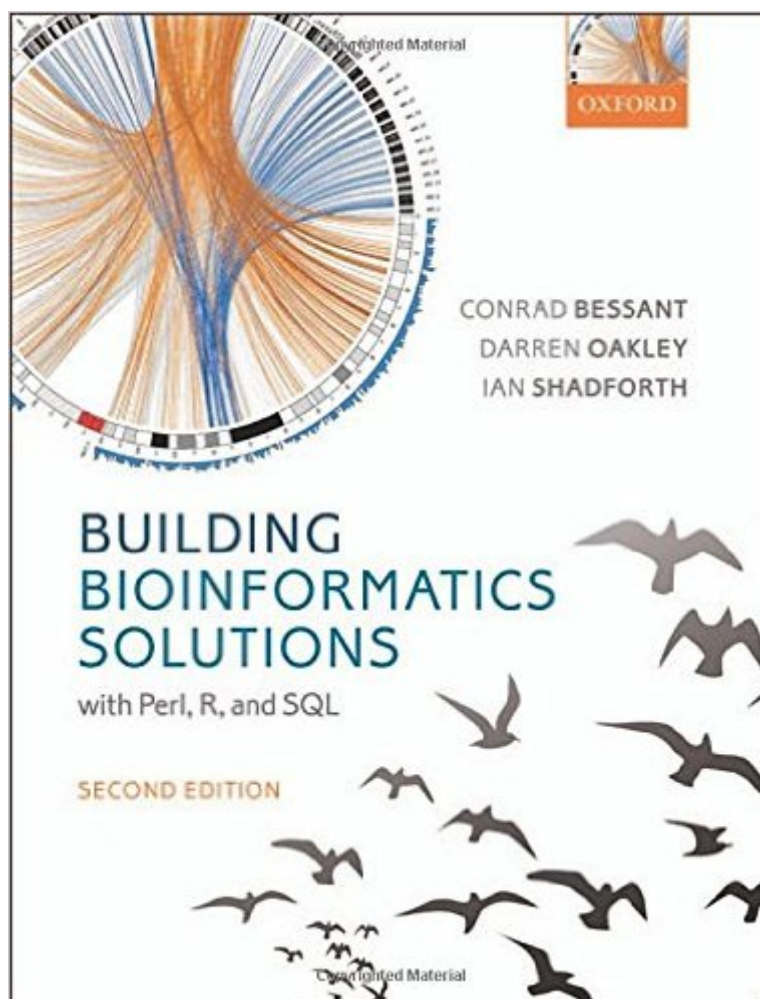# Building Bioinformatics Solutions 2nd Edition

Synopsis

Bioinformatics encompasses a broad and ever-changing range of activities involved with the management and analysis of data from molecular biology experiments. Despite the diversity of activities and applications, the basic methodology and core tools needed to tackle bioinformatics problems is common to many projects. This unique book provides an invaluable introduction to three of the main tools used in the development of bioinformatics software - Perl, R and MySQL - and explains how these can be used together to tackle the complex data-driven challenges that typify modern biology. These industry standard open source tools form the core of many bioinformatics projects, both in academia and industry. The methodologies introduced are platform independent, and all the examples that feature have been tested on Windows, Linux and Mac OS. Building Bioinformatics Solutions is suitable for graduate students and researchers in the life sciences who wish to automate analyses or create their own databases and web-based tools. No prior knowledge of software development is assumed. Having worked through the book, the reader should have the necessary core skills to develop computational solutions for their specific research programmes. The book will also help the reader overcome the inertia associated with penetrating this field, and provide them with the confidence and understanding required to go on to develop more advanced bioinformatics skills.

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