

Bioinformatics Computing

Bryan Bergeron, M.D.

In *Bioinformatics Computing*, Harvard Medical School and MIT faculty member Bryan Bergeron presents a comprehensive and practical guide to bioinformatics for life scientists at every level of training and practice. After an up-to-the-minute overview of the entire field, he illuminates every key bioinformatics technology, offering practical insight into the full range of bioinformatics applications—both new and emerging.

FEATURES INCLUDE:

Technologies that enable researchers to collaborate more effectively

Fundamental concepts, state-of-the-art tools, and "on-the-horizon" advances

Bioinformatics information infrastructure, including GENBANK and other Web-based resources

Very large biological databases: object-oriented database methods, data mining/warehousing, knowledge management, and more

3D visualization: exploring the inner workings of complex biological structures

Advanced pattern matching techniques, including microarray research and gene prediction

Event-driven, time-driven, and hybrid simulation techniques

Bioinformatics Computing combines practical insight for assessing bioinformatics technologies, guidance for using them effectively, and intelligent context for understanding their rapidly evolving roles.

ABOUT THE AUTHOR

BRYAN BERGERON, M.D., is a faculty member at both Harvard Medical School and Massachusetts Institute of Technology, editor-in-chief of *e.MD*, editorial board member of *Healthcare Informatics*, and Fellow of the American College of Medical Informatics. He has authored more than 300 publications on topics ranging from AI to computers in medicine.

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