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Chapter 5. SRS: An Integration Platform for Databanks and Analysis Tools in Bioinformatics; 5.1 Integrating Flat File Databanks; 5.2 Integration of XML Databases; 5.3 Integrating Relational Databases; 5.4 The SRS Query Language; 5.5 Linking Databanks; 5.6 The Object Loader; 5.7 Scientific Analysis Tools; 5.8 Interfaces to SRS; 5.9 Automated Server Maintenance with SRS Prisma; 5.10 Conclusion; References; Chapter 6. The Kleisli Query System as a Backbone for Bioinformatics Data Integration and Analysis; 6.1 Motivating Example 6.2 Approach6.3 Data Model and Representation; 6.4 Query Capability; 6.5 Warehousing Capability; 6.6 Data Sources; 6.7 Optimizations; 6.8 User Interfaces; 6.9 Other Data Integration Technologies; 6.10 Conclusions; References; Chapter 7. Complex Query Formulation Over Diverse Information Sources in TAMBIS; 7.1 The Ontology; 7.2 The User Interface; 7.3 The Query Processor; 7.4 Related Work; 7.5 Current and Future Developments in TAMBIS; Acknowledgments; References; Chapter 8. The Information Integration System K2; 8.1 Approach; 8.2 Data Model and Languages; 8.3 An Example; 8.4 Internal Language 8.5 Data Sources8.6 Query Optimization; 8.7 User Interfaces; 8.8 Scalability; 8.9 Impact; 8.10 Summary; Acknowledgments; References; Chapter 9. P/FDM Mediator for a Bioinformatics Database Federation; 9.1 Approach; 9.2 Analysis; 9.3 Conclusions; Acknowledgment; References; Chapter 10. Integration Challenges in Gene Expression Data Management; 10.1 Gene Expression Data Management: Background; 10.2 The GeneExpress System; 10.3 Managing Gene Expression Data: Integration Challenges; 10.4 Integrating Third-Party Gene Expression Data in GeneExpress; 10.5 Summary; Acknowledgments; Trademarks
References

Sommario/riassunto

Life science data integration and interoperability is one of the most challenging problems facing bioinformatics today. In the current age of the life sciences, investigators have to interpret many types of information from a variety of sources: lab instruments, public databases, gene expression profiles, raw sequence traces, single nucleotide polymorphisms, chemical screening data, proteomic data, putative metabolic pathway models, and many others. Unfortunately, scientists are not currently able to easily identify and access this information because of the variety of semantics, interfaces,