Record Nr.	UNINA9910142732603321
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Titolo	Bioinformatics, biocomputing and Perl [[electronic resource] ] : an introduction to bioinformatics computing skills and practice / / Michael Moorhouse, Paul Barry
Pubbl/distr/stampa	Chichester ; ; Hoboken, NJ, : Wiley, c2004
ISBN	1-280-23868-2 9786610238682 0-470-02645-6 0-470-02057-1
Descrizione fisica	1 online resource (507 p.)
Altri autori (Persone)	BarryPaul <1966->
Disciplina	570.285 570.285571262
Soggetti	Bioinformatics Computational biology Perl (Computer program language) Electronic books.
Literation of search C.B. 11	
Lingua di pubblicazione	Inglese
Lingua di pubblicazione Formato	Materiale a stampa
	Materiale a stampa Monografia
Formato	Materiale a stampa
Formato Livello bibliografico	Materiale a stampa Monografia

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	more; 3.7 Introducing Patterns; Where to from Here; The Maxims Repeated; 4 Places to Put Things; 4.1 Beyond Scalars; 4.2 Arrays: Associating Data with Numbers 4.2.1 Working with array elements4.2.2 How big is the array?; 4.2.3 Adding elements to an array; 4.2.4 Removing elements from an array; 4.2.5 Slicing arrays; 4.2.6 Pushing, popping, shifting and unshifting; 4.2.7 Processing every element in an array; 4.2.8 Making lists easier to work with; 4.3 Hashes: Associating Data with Words; 4.3.1 Working with hash entries; 4.3.2 How big is the hash?; 4.3.3 Adding entries to a hash; 4.3.4 Removing entries from a hash; 4.3.5 Slicing hashes; 4.3.6 Working with hash entries: a complete example; 4.3.7 Processing every entry in a hash; Where to from Here The Maxims Repeated5 Getting Organised; 5.1 Named Blocks; 5.2 Introducing Subroutines; 5.2.1 Calling subroutines; 5.3 Creating Subroutines; 5.3.1 Processing parameters; 5.3.2 Better processing of parameters; 5.3.3 Even better processing of parameters; 5.3.4 A more flexible drawline subroutine; 5.3.5 Returning results; 5.4 Visibility and Scope; 5.4.1 Using private variables; 5.4.2 Using global variables properly; 5.4.3 The final version of drawline; 5.5 In-built Subroutines; 5.6 Grouping and Reusing Subroutines; 5.6.1 Modules; 5.7 The Standard Modules; 5.8 CPAN: The Module Repository 5.8.1 Searching CPAN5.8.2 Installing a CPAN module manually; 5.8.3 Installing a CPAN module automatically; 5.8.4 A final word on CPAN modules; Where to from Here; The Maxims Repeated; 6 About Files; 6.1 I/O: Input and Output; 6.1.1 The standard streams: STDIN, STDOUT and STDERR; 6.2 Reading Files; 6.2.1 Determining the disk-file names; 6.2.2 Opening the named disk-files; 6.2.3 Reading a line from each of the disk-files; 6.2.4 Putting it all together; 6.2.5 Slurping; 6.3 Writing Files; 6.3.1 Redirecting output; 6.3.2 Variable interpolation; 6.4 Chopping and Chomping; Where to from Here The Maxims Repeated
Sommario/riassunto	Bioinformatics, Biocomputing and Perl presents a modern introduction to bioinformatics computing skills and practice. Structuring its presentation around four main areas of study, this book covers the skills vital to the day-to-day activities of today's bioinformatician. Each chapter contains a series of maxims designed to highlight key points and there are exercises to supplement and cement the introduced material. Working with Perl presents an extended tutorial introduction to programming through Perl, the premier programming technology of the bioinformatics community. Even t