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| Record Nr. | UNINA9910456983703321 |
| Autore | DeHoyos Art <1959-> |
| Titolo | Is it true what they say about freemasonry? [[electronic resource] /] / Arturo de Hoyos and S. Brent Morris ; with a foreword and addendum by James T. Tresner II |
| Pubbl/distr/stampa | Lanham, Md., : M. Evans, c2010 |
| ISBN | 1-282-96096-2<br>9786612960963<br>1-59077-156-7 |
| Descrizione fisica | 1 online resource (285 p.) |
| Altri autori (Persone) | MorrisS. Brent |
| Disciplina | 366/.1 |
| Soggetti | Freemasonry<br>Freemasonry - United States<br>Anti-Masonic movements<br>Freemasonry - Religious aspects<br>Electronic books. |
| Lingua di pubblicazione | Inglese |
| Formato | Materiale a stampa |
| Livello bibliografico | Monografia |
| Note generali | Description based upon print version of record. |
| Nota di bibliografia | Includes bibliographical references. |
| Nota di contenuto | Contents; Acknowledgments; Foreword; Preface; Chapter 1; Chapter 2; Chapter 3; Chapter 4; Chapter 5; Chapter 6; Chapter 7; Chapter 8; Chapter 9; Chapter 10; Chapter 11; Appendix 1; Appendix 2; Appendix 3; Notes; Works Cited; About the Authors |
| Sommario/riassunto | For as long as there have been Freemasons, there has been a calculated effort to disparage and their practices. In this insightful text, masons de Hoyos and Morris explore the origins of the anti-Masonic mindset and delve into the falsehoods on which critics have based these perennial sentiments. Confronting opponents one at a time, the authors methodically debunk the myths that have surrounded Freemasonry since its establishment, investigating the motives and misconceptions that derive antagonists to spread deceit about Masonic traditions. |

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| Record Nr. | UNINA9910830644503321 |
| Autore | Moorhouse Michael |
| 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<br>9786610238682<br>0-470-02645-6<br>0-470-02057-1 |
| Descrizione fisica | 1 online resource (507 p.) |
| Altri autori (Persone) | BarryPaul <1966-> |
| Disciplina | 570.285<br>570.285571262 |
| Soggetti | Bioinformatics<br>Computational biology<br>Perl (Computer program language) |
| Lingua di pubblicazione | Inglese |
| Formato | Materiale a stampa |
| Livello bibliografico | Monografia |
| Note generali | Description based upon print version of record. |
| Nota di bibliografia | Includes bibliographical references (p. [461]-466) and index. |
| Nota di contenuto | Bioinformatics Biocomputing and Perl; Contents; Preface; 1 Setting the Biological Scene; 1.1 Introducing Biological Sequence Analysis; 1.2 Protein and Polypeptides; 1.3 Generalised Models and their Use; 1.4 The Central Dogma of Molecular Biology; 1.4.1 Transcription; 1.4.2 Translation; 1.5 Genome Sequencing; 1.5.1 Sequence assembly; 1.6 The Example DNA-gene-protein system we will use; Where to from Here; 2 Setting the Technological Scene; 2.1 The Layers of Technology; 2.1.1 From passive user to active developer; 2.2 Finding perl; 2.2.1 Checking for perl; Where to from Here<br>I Working with Perl3 The Basics; 3.1 Let's Get Started!; 3.1.1 Running Perl programs; 3.1.2 Syntax and semantics; 3.1.3 Program: run thyself!; 3.2 Iteration; 3.2.1 Using the Perl while construct; 3.3 More Iterations; 3.3.1 Introducing variable containers; 3.3.2 Variable containers and loops; 3.4 Selection; 3.4.1 Using the Perl if construct; 3.5 There Really is MTOWTDI; 3.6 Processing Data Files; 3.6.1 Asking getlines to do 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