1. Record Nr. UNISA990003532850203316

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| Autore | PLA, Josep |
| Titolo | El cuaderno gris / Josep Pla |
| Pubbl/distr/stampa | Barcelona, : Austral, 2010 |
| ISBN | 978-84-322-4824-5 |
| Descrizione fisica | 800 p. ; 19 cm |
| Collana | Contemporánea , Narrativa |
| Disciplina | 849.935 |
| Collocazione | VI.5.A. 887 |
| Lingua di pubblicazione | Spagnolo |
| Formato | Materiale a stampa |
| Livello bibliografico | Monografia |
| Note generali | Sul frontespizio: Destino<br>Sul dorso: 683 |

2. Record Nr. UNINA9910569197503321

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| Autore | Husi Holger |
| Titolo | Computational Biology |
| Pubbl/distr/stampa | Australia, : Exon Publications, 2019 |
| Descrizione fisica | 1 online resource (194 p.) |
| Soggetti | MBF |
| Lingua di pubblicazione | Inglese |
| Formato | Materiale a stampa |
| Livello bibliografico | Monografia |
| Sommario/riassunto | Our understanding of biology has undergone a revolution in the past 20 years, driven by our ability to capture, store, interrogate and analyze the ever-increasing volumes of 'omics' data. Computational Biology, an integrated approach employing high performance computers, state-of-the art software and algorithms, mathematical modeling and statistical analyses have enabled us to unravel the seemingly impenetrable complexity of biological systems. This book draws together many of the latest cutting-edge developments in the field of Computational Biology. Each chapter draws on the expertise of leading researchers in the field to highlight the utility of specific technologies. The breadth of the text is impressive - from integrative biology in human diseases through the various branches of epigenomics, metabolomics and proteomics to biological sequencing and deep learning. Computational biology approaches for image-based analysis of multicellular spheroids, feature selection using entropy and cellular cryo-electron tomography structural pattern mining are covered. In addition, the key role of statistics in the analysis of high-dimensional multiset omics data and RNA sequencing are discussed in dedicated chapters. This book would have broad appeal to anyone with an interest in cutting edge computational biology. |