

1. Record Nr.	UNINA9910715426403321
Titolo	Message from the President of the United States, transmitting copies of documents referred to in his communication of the seventeenth ultimo, in relation to the Seminole War, &c. December 3, 1818. Read and ordered to lie upon the table
Pubbl/distr/stampa	[Washington, D.C.] : , : [publisher not identified], , 1818
Descrizione fisica	1 online resource (165 pages) : tables
Collana	House document / 15th Congress, 2nd session. House ; ; no. 14 [United States congressional serial set] ; ; [serial no. 17]
Altri autori (Persone)	MonroeJames <1758-1831.>
Soggetti	Courts-martial and courts of inquiry Executions and executioners Communications, Military Military art and science Territories and possessions Seminole War, 1st, 1817-1818 Indians of North America - Wars - 1815-1875 Legislative materials. Spain Territories and possessions
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Batch processed record: Metadata reviewed, not verified. Some fields updated by batch processes. FDLP item number not assigned.

2. Record Nr.	UNINA9910261145903321
Autore	Marco Pellegrini
Titolo	Repetitive Structures in Biological Sequences: Algorithms and Applications
Pubbl/distr/stampa	Frontiers Media SA, 2016
Descrizione fisica	1 online resource (93 p.)
Collana	Frontiers Research Topics
Soggetti	History of engineering and technology
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Sommario/riassunto	<p>Repetitive structures in biological sequences are emerging as an active focus of research and the unifying concept of "repeatome" (the ensemble of knowledge associated with repeating structures in genomic/proteomic sequences) has been recently proposed in order to highlight several converging trends. One main trend is the ongoing discovery that genomic repetitions are linked to many biological significant events and functions. Diseases (e.g. Huntington's disease) have been causally linked with abnormal expansion of certain repeating sequences in the human genome. Deletions or multiple copy duplications of genes (Copy Number Variations) are important in the aetiology of cancer, Alzheimer, and Parkinson diseases. A second converging trend has been the emergence of many different models and algorithms for detecting non-obvious repeating patterns in strings with applications to genomic data. Borrowing methodologies from combinatorial pattern matching, string algorithms, data structures, data mining and machine learning these new approaches break the limitations of the current approaches and offer a new way to design better trans-disciplinary research. The articles collected in this book provides a glance into the rich emerging area of repeatome research, addressing some of its pressing challenges. We believe that these contributions are valuable resources for repeatome research and will stimulate further research from bioinformatic, statistical, and biological points of view.</p>

