1.	Record Nr.	UNINA9910299953103321
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	Titolo	Optimized Cloud Based Scheduling / / by Rong Kun Jason Tan, John A. Leong, Amandeep S. Sidhu
	Pubbl/distr/stampa	Cham : , : Springer International Publishing : , : Imprint : Springer, , 2018
	ISBN	3-319-73214-5
	Edizione	[1st ed. 2018.]
	Descrizione fisica	1 online resource (XIII, 99 p. 33 illus.)
	Collana	Data, Semantics and Cloud Computing, , 2524-6593 ; ; 759
	Disciplina	004.6782
	Soggetti	Computational intelligence
		Artificial intelligence
		Application software
		Information Systems Applications (incl. Internet)
	Lingua di pubblicazione	Inglese
	Formato	Materiale a stampa
	Livello bibliografico	Monografia
	Nota di bibliografia	Includes bibliographical references.
	Nota di contenuto	Introduction Background Benchmarking Computation of Large Datasets Optimized Online Scheduling Algorithms.
	Sommario/riassunto	This book presents an improved design for service provisioning and allocation models that are validated through running genome sequence assembly tasks in a hybrid cloud environment. It proposes approaches for addressing scheduling and performance issues in big data analytics and showcases new algorithms for hybrid cloud scheduling. Scientific sectors such as bioinformatics, astronomy, high-energy physics, and Earth science are generating a tremendous flow of data, commonly known as big data. In the context of growing demand for big data analytics, cloud computing offers an ideal platform for processing big data tasks due to its flexible scalability and adaptability. However, there are numerous problems associated with the current service provisioning and allocation models, such as inefficient scheduling algorithms, overloaded memory overheads, excessive node delays and improper error handling of tasks, all of which need to be addressed to enhance the performance of big data analytics.