1.

Record Nr.	UNINA9910452360703321
Autore	Michalis Maria <1969->
Titolo	Governing European communications : from unification to coordination / / Maria Michalis
Pubbl/distr/stampa	Lanham : , : Lexington Books, , [2007] ©2007
ISBN	0-7391-1736-X 0-7391-5571-7
Descrizione fisica	1 online resource (367 p.)
Collana	Critical media studies
Disciplina	302.2094
Soggetti	Communication policy - Europe - History - 20th century 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 (pages 303-337) and index.
Nota di contenuto	Title Page; Copyright Page; Contents; List of Figures and Tables; Acknowledgments; Abbreviations; 1 Introduction; 2 Origins of European Governance in Communications: The Formative Years (Late 1940s to Late 1960s); 3 The Crisis Years: National Capital and the Search for European Solutions and Identity (Late 1960s to Late 1970s); 4 Defensive Europeanization: Industrial Policy Moves to Europe (Late 1970s to Mid-/Late 1980s); 5 Liberalization and Re-regulation: The High Peak of European Governance? (Mid-/Late 1980s to Late 1990s) 6 Competitiveness, Knowledge Economy and Technological Convergence: Toward Policy Coordination (Late 1990s to Early 2007)7 Conclusions; Appendix; Bibliography; Index; About the Author
Sommario/riassunto	Governing European Communications provides a comprehensive and up-to-date account of the emergence, dynamics, and evolution of European-level communications governance in the post-war era, focusing on telecommunications and television policies and regulation, and their technological convergence. Concentrating on the EU, the book embeds governance within broader economic and political developments in a global context and demonstrates that European governance has been more about the character rather than the level of regulation.

2.

Record Nr.	UNINA9910480104203321
Autore	Lotz Amanda D (1974-).
Titolo	The television will be revolutionized / / Amanda D. Lotz
Pubbl/distr/stampa	London : , : New York University Press, , op. 2014 Baltimore, Md. : , : Project MUSE, , 2021 ©op. 2014
ISBN	1-4798-3007-0 1-4798-9039-1
Edizione	[2nd edition.]
Descrizione fisica	1 online resource (351 pages)
Disciplina	384.55/0973
Soggetti	Television broadcasting Television broadcasting - United States Television - Technological innovations Television broadcasting - Technological innovations Electronic books.
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Front matter -- Contents -- Preface -- Acknowledgments -- Introduction -- 1. Understanding television at the beginning of the post-network era -- 2. Television outside the box: the technological revolution of television -- 3. Making television: changes in the practices of creating television -- 4. Revolutionizing distribution: breaking open the network bottleneck -- 5. The new economics of television -- 6. Recounting the audience: measurement in the age of broadband -- 7. Television storytelling possibilities at the beginning of the post-network era: five cases -- Conclusion. Still watching television -- Notes -- Selected bibliography -- Index -- About the author
Sommario/riassunto	Go behind the TV screen to explore what is changing, why it is changing, and why the changes matters. Many proclaimed the “end of television” in the early years of the twenty-first century, as capabilities and features of the boxes that occupied a central space in American living rooms for the preceding fifty years were radically remade. In this revised, second edition of her definitive book, Amanda D. Lotz proves

that rumors of the death of television were greatly exaggerated and explores how new distribution and viewing technologies have resurrected the medium. Shifts in the basic practices of making and distributing television have not been hastening its demise, but are redefining what we can do with television, what we expect from it, how we use it—in short, revolutionizing it. Television, as both a technology and a tool for cultural storytelling, remains as important today as ever, but it has changed in fundamental ways. The Television Will Be Revolutionized provides a sophisticated history of the present, examining television in what Lotz terms the “post-network” era while providing frameworks for understanding the continued change in the medium. The second edition addresses adjustments throughout the industry wrought by broadband delivered television such as Netflix, YouTube, and cross-platform initiatives like TV Everywhere, as well as how technologies such as tablets and smartphones have changed how and where we view. Lotz begins to deconstruct the future of different kinds of television—exploring how“ prized content,” live television sports and contests, and linear viewing may all be “television,” but very different types of television for both viewers and producers. Through interviews with those working in the industry, surveys of trade publications, and consideration of an extensive array of popular shows, Lotz takes us behind the screen to explore what is changing, why it is changing, and why the changes matter.

3. Record Nr.	UNINA9910484497103321
Titolo	Research in Computational Molecular Biology : 21st Annual International Conference, RECOMB 2017, Hong Kong, China, May 3-7, 2017, Proceedings / / edited by S. Cenk Sahinalp
Pubbl/distr/stampa	Cham : , : Springer International Publishing : , : Imprint : Springer, , 2017
ISBN	3-319-56970-8
Edizione	[1st ed. 2017.]
Descrizione fisica	1 online resource (XIV, 406 p. 104 illus.)
Collana	Lecture Notes in Bioinformatics, , 2366-6331 ; ; 10229
Disciplina	572.80113
Soggetti	Bioinformatics Biomathematics Artificial intelligence Computer vision Database management Computational and Systems Biology Mathematical and Computational Biology Artificial Intelligence Computer Vision Database Management
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di contenuto	Boosting alignment accuracy by adaptive local realignment -- A concurrent subtractive assembly approach for identification of disease associated sub-meta-genomes -- A flow procedure for the linearization of genome variation graphs -- Dynamic alignment-free and reference-free read compression -- A fast approximate algorithm for mapping long reads to large reference databases -- Determining the consistency of resolved triplets and fan triplets -- Progressive calibration and averaging for tandem mass spectrometry statistical confidence estimation: Why settle for a single decoy -- Resolving multi-copy duplications de novo using polyploid phasing -- A Bayesian active learning experimental design for inferring signaling networks -- BBK* (Branch and Bound over K*): A provable and efficient ensemble-

	based algorithm to optimize stability and binding affinity over large sequence spaces -- Super-bubbles, ultra-bubbles and cacti -- EPR-dictionaries: A practical and fast data structure for constant time searches in unidirectional and bidirectional FM indices -- A Bayesian framework for estimating cell type composition from DNA methylation without the need for methylation reference -- Towards recovering Allele-specific cancer genome graphs -- Using stochastic approximation techniques to efficiently construct confidence intervals for heritability -- Improved search of large transcriptomic sequencing databases using split sequence bloom trees -- All some sequence bloom trees -- Longitudinal genotype-phenotype association study via temporal structure auto-learning predictive model -- Improving imputation accuracy by inferring causal variants in genetic studies -- The copy-number tree mixture deconvolution problem and applications to multi-sample bulk sequencing tumor data -- Quantifying the impact of non-coding variants on transcription factor-DNA binding -- aBayesQR: A Bayesian method for reconstruction of viral populations characterized by low diversity -- BeWith: A between-within method for module discovery in cancer using integrated analysis of mutual exclusivity, co-occurrence and functional interactions -- K-mer Set Memory (KSM) motif representation enables accurate prediction of the impact of regulatory variants -- Network-based coverage of mutational profiles reveals cancer genes -- Ultra-accurate complex disorder prediction: case study of neurodevelopmental disorders -- Inference of the human polyadenylation Code -- Folding membrane proteins by deep transfer learning -- A network integration approach for drug-target interaction prediction and computational drug repositioning from heterogeneous information -- Epistasis in genomic and survival data of cancer patients -- Ultra-fast identity by descent detection in biobank-scale cohorts using positional burrows-wheeler transform -- Joker de Bruijn: sequence libraries to cover all k-mers using joker characters -- GATTACA: Lightweight metagenomic binning using kmer counting -- Species tree estimation using ASTRAL: how many genes are enough.-Reconstructing antibody repertoires from error-prone immune-sequencing datasets -- NetREX: Network rewiring using EXpression - Towards context specific regulatory networks -- E pluribus unum: United States of single cells -- ROSE: a deep learning based framework for predicting ribosome stalling. .
Sommario/riassunto	This book constitutes the proceedings of the 21th Annual Conference on Research in Computational Molecular Biology, RECOMB 2017, held in Hong Kong, China, in May 2017. The 22 regular papers presented in this volume were carefully reviewed and selected from 184 submissions. 16 short abstracts are included in the back matter of the volume. They report on original research in all areas of computational molecular biology and bioinformatics.