1.	Record Nr.	UNINA9910828791803321
	Autore	Fernandez Hermana Luis Angel <1946->
	Titolo	Historia Viva de Internet : Los anos de En. red. ando (2002-2004) / / Luis Angel Fernandez Hermana
	Pubbl/distr/stampa	Barcelona : , : Editorial UOC, , [2012] ©2012
	ISBN	84-9029-636-7
	Descrizione fisica	1 online resource (535 p.)
	Collana	Manuales ; ; 218
	Disciplina	004.678
	Soggetti	Internet - History Internet - Social aspects
	Lingua di pubblicazione	Spagnolo
	Formato	Materiale a stampa
	Livello bibliografico	Monografia
	Note generali	Bibliographic Level Mode of Issuance: Monograph
	Sommario/riassunto	En este volumen (2002-2004), se analizan las inquietantes consecuencias -dentro y fuera de la Red- del atentado terrorista contra las Torres Gemelas y las subsiguientes guerras en Irak y Afganistán, el impacto de estos acontecimientos en España, así como el ascenso imparable de la omnipresencia de Internet a pesar de las secuelas del desastre de la burbuja tecnológica. Educación, ciencia, medios de comunicación, nuevas formas de aprender y de relacionarse, estructuras virtuales insólitas para generar y gestionar conocimiento en red, la maduración del diseño, desarrollo y gestión de redes sociales virtuales de conocimiento, la emergencia de nuevos perfiles profesionales y el cultivo de las competencias correspondientes relacionadas con esta evolución de Internet, son algunos de los temas recurrentes en los editoriales de estos años. En julio de 2004, Enredando.com cerró definitivamente sus puertas digitales.

2.

Record Nr.	UNINA9910220037803321
Autore	David S. Needleman
Titolo	Emerging Approaches for Typing, Detection, Characterization, and Traceback of Escherichia coli
Pubbl/distr/stampa	Frontiers Media SA, 2017
Descrizione fisica	1 online resource (170 p.)
Collana	Frontiers Research Topics
Soggetti	Microbiology (non-medical)
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Sommario/riassunto	Pathogenic Escherichia coli strains cause a large number of diseases in humans, including diarrhea, hemorrhagic colitis, hemolytic uremic syndrome, urinary tract infections, and neonatal meningitis, while in animals they cause diseases such as calf scours and mastitis in cattle, post-weaning diarrhea and edema disease in pigs, and peritonitis and airsacculitis in chickens. The different E. coli pathotypes are characterized by the presence of specific sets of virulence-related genes. Therefore, it is not surprising that pathogenic E. coli constitutes a genetically heterogeneous family of bacteria, and they are continuing to evolve. Rapid and accurate molecular methods are critically needed to detect and trace pathogenic E. coli in food and animals. They are also needed for epidemiological investigations to enhance food safety, as well as animal and human health and to minimize the size and geographical extent of outbreaks. The serotype of E. coli strains has traditionally been determined using antisera raised against the >180 different O- (somatic) and 53 H- (flagellar) antigens. However, there are many problems associated with serotyping, including: it is labor-intensive and time consuming; cross reactivity of the antisera with different serogroups occurs; antisera are available only in specialized laboratories; and many strains are non-typeable. Molecular serotyping targeting O-group-specific genes within the E. coli O-antigen gene clusters and genes that are involved in encoding for the different flagellar types offers an improved approach for determining the E. coli

O- and H-groups. Furthermore, molecular serotyping can be coupled with determination of specific sets of virulence genes carried by the strain offering the possibility to determine O-group, pathotype, and the pathogenic potential simultaneously. Sequencing of the O-antigen gene clusters of all of the known O-groups of E. coli is now complete, and the sequences have been deposited in the GenBank database. The sequence information has revealed that some E. coli serogroups have identical sequences while others have point mutations or insertion sequences and type as different serogroups in serological reactions. There are also a number of other ambiguities in serotyping that need to be resolved. Furthermore, new E. coli O-groups are being identified. Therefore, there is an essential need to resolve these issues and to revise the E. coli serotype nomenclature based on these findings. There are emerging technologies that can potentially be applied for molecular serotyping and detection and characterization of E. coli. On a related topic, the genome sequence of thousands of E. coli strains have been deposited in GenBank, and this information is revealing unique markers such as CRISPR (clustered regularly interspaced short palindromic repeats) and virulence gene markers that could be used to identify E. coli pathotypes. Whole genome sequencing now provides the opportunity to study the role of horizontal gene transfer in the evolution and emergence of pathogenic E. coli strains. Whole genome sequencing approaches are being investigated for genotyping and outbreak investigation for regulatory and public health needs; however, there is a need for establishing bioinformatics pipelines able to handle large amounts of data as we move toward the use of genetic approaches for non-culture-based detection and characterization of E. coli and for outbreak investigations.