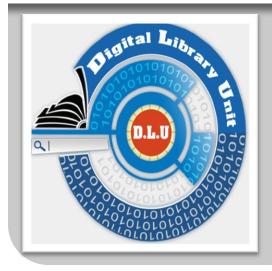
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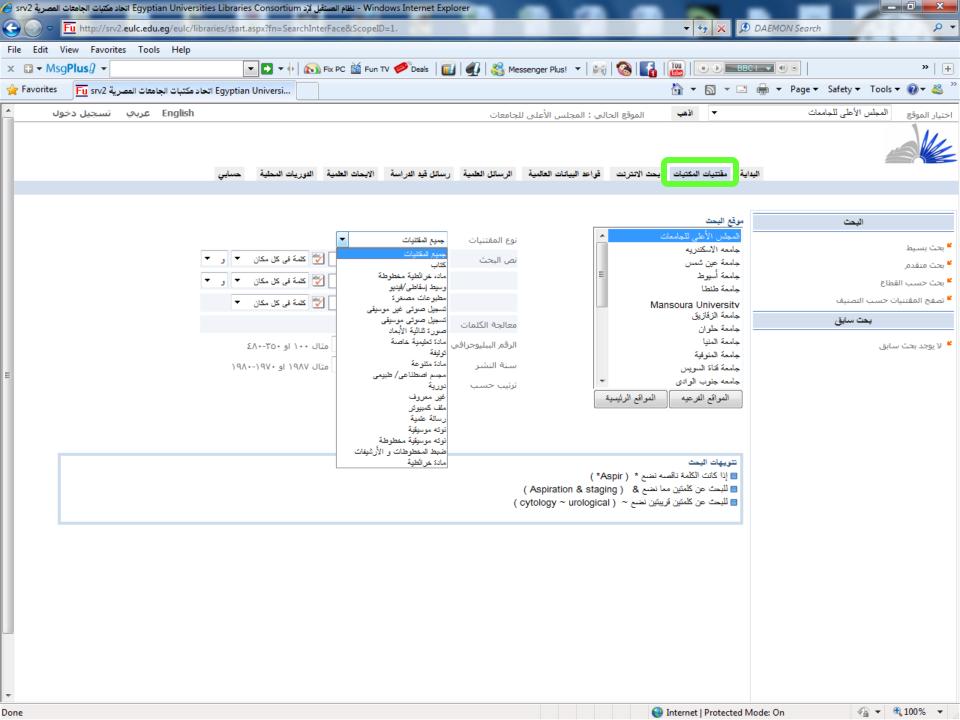
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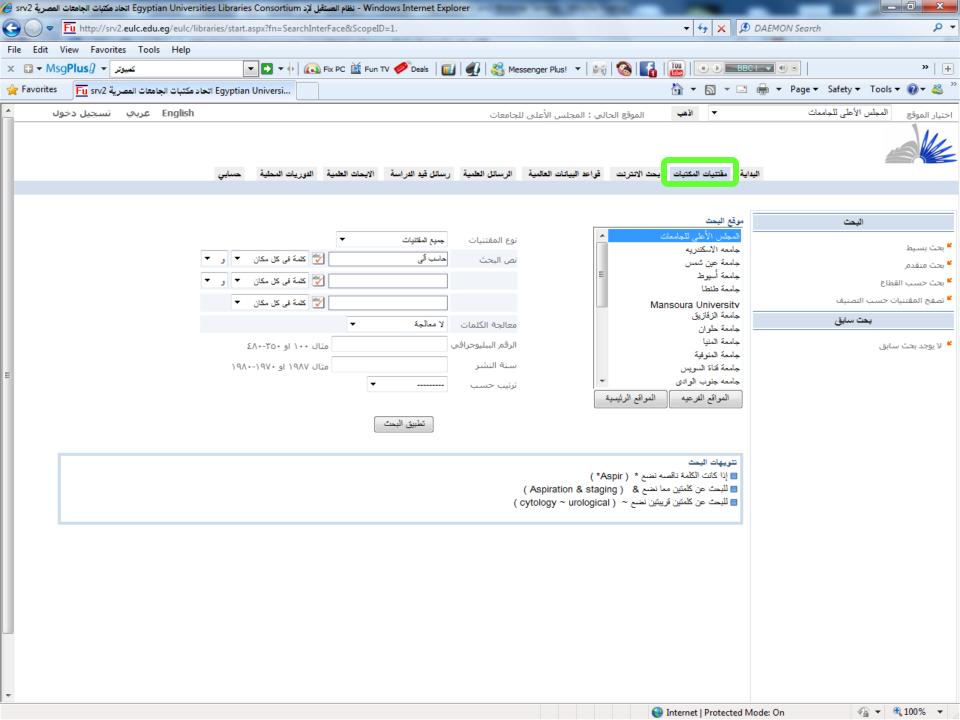
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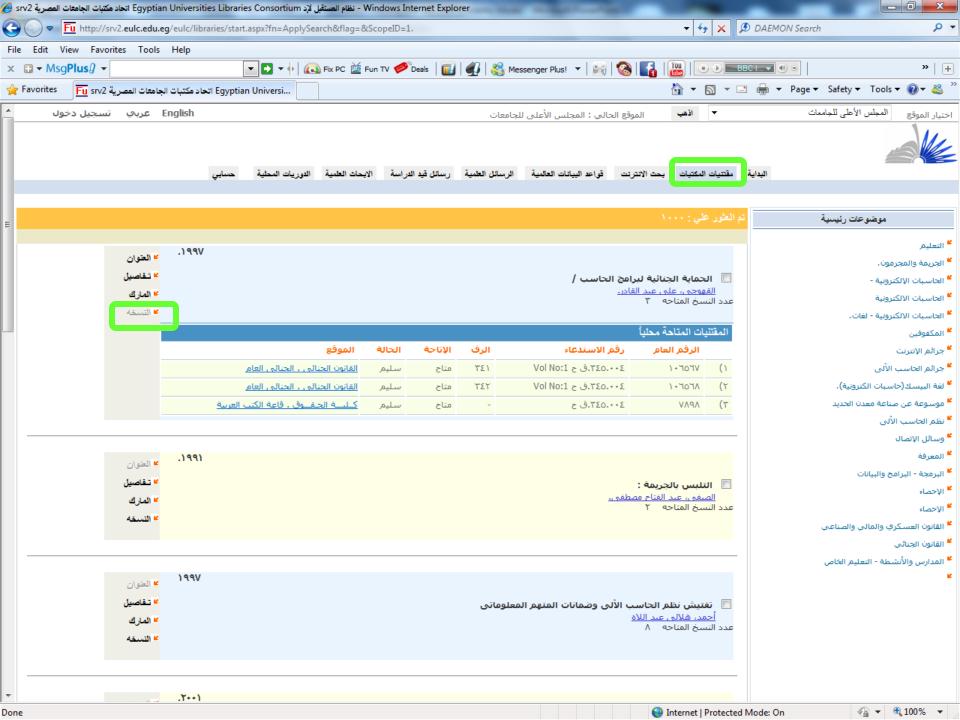
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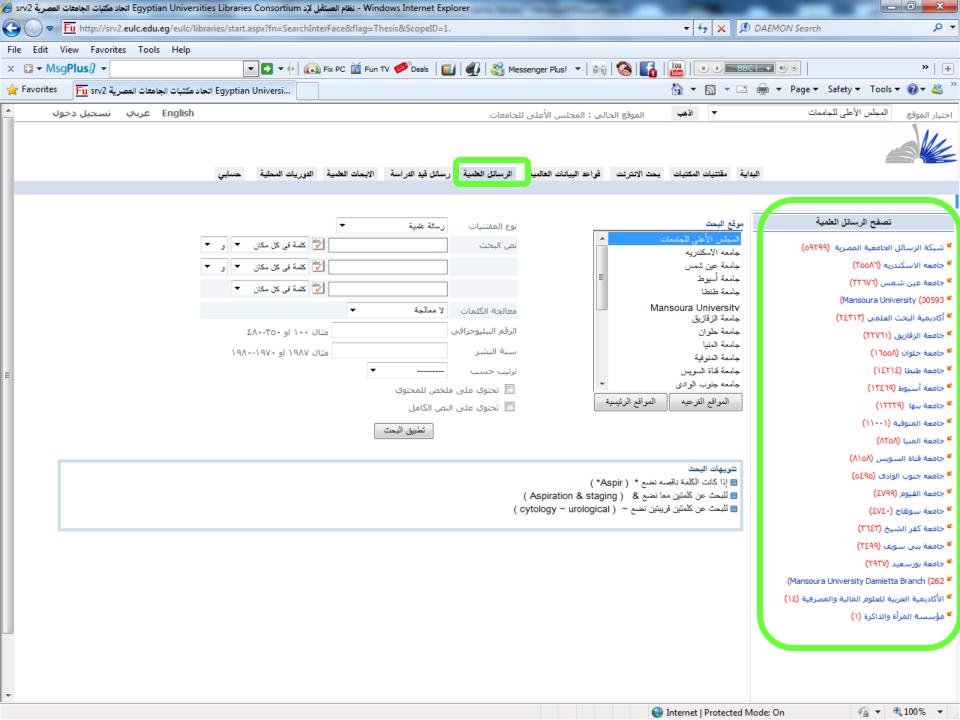
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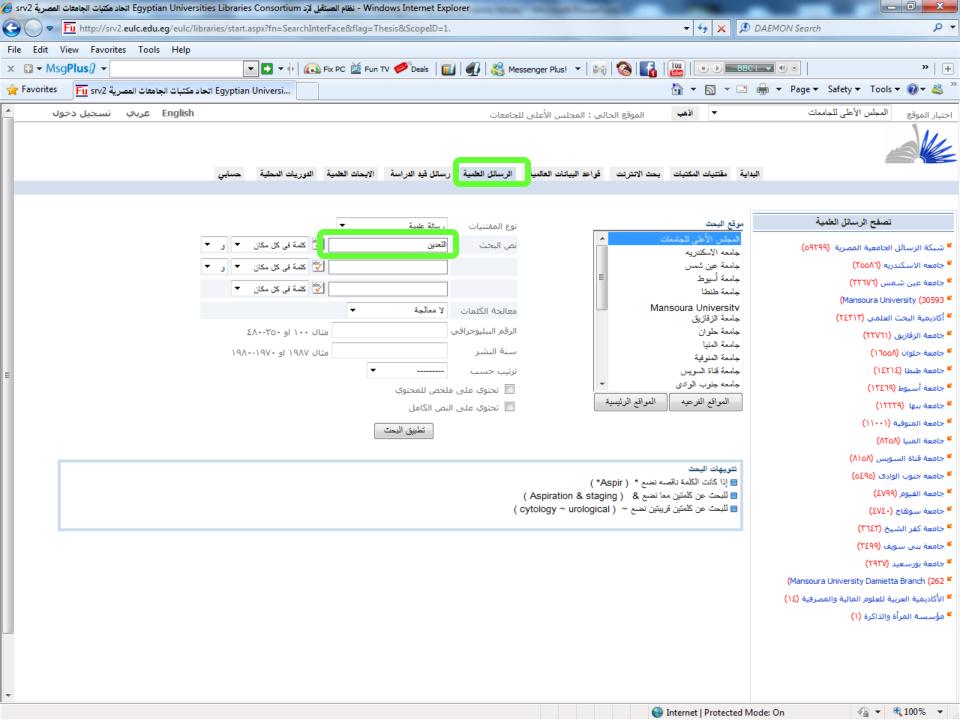


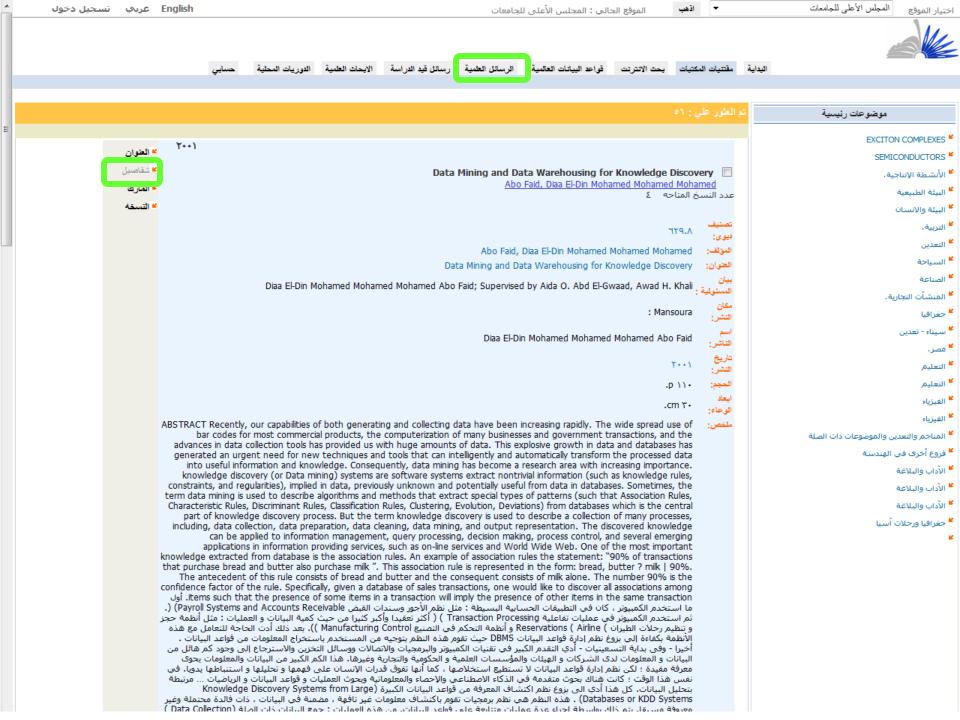


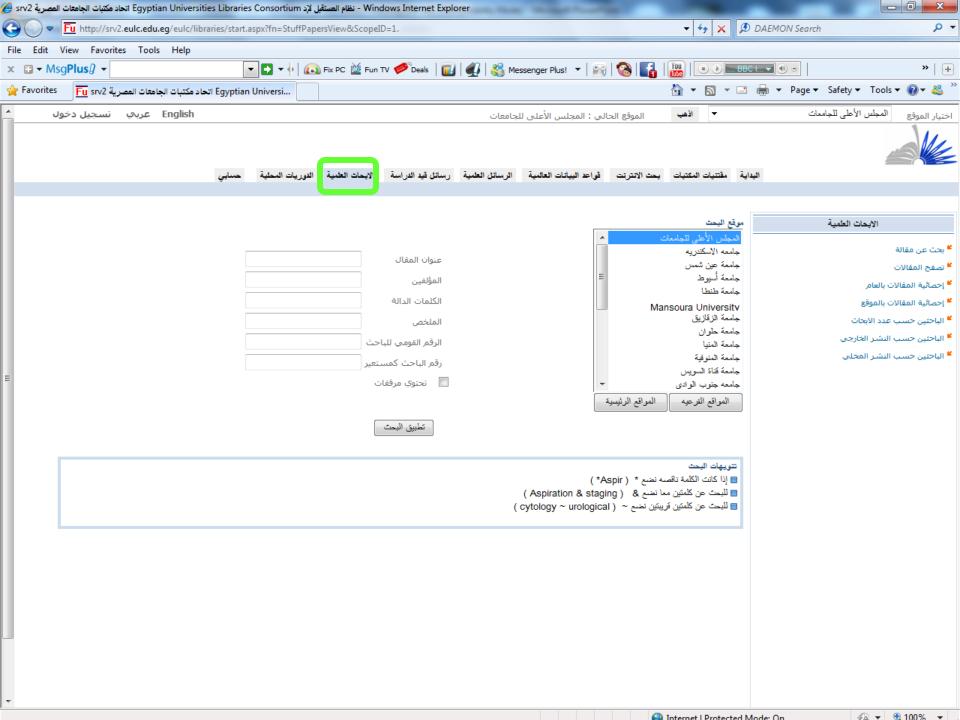


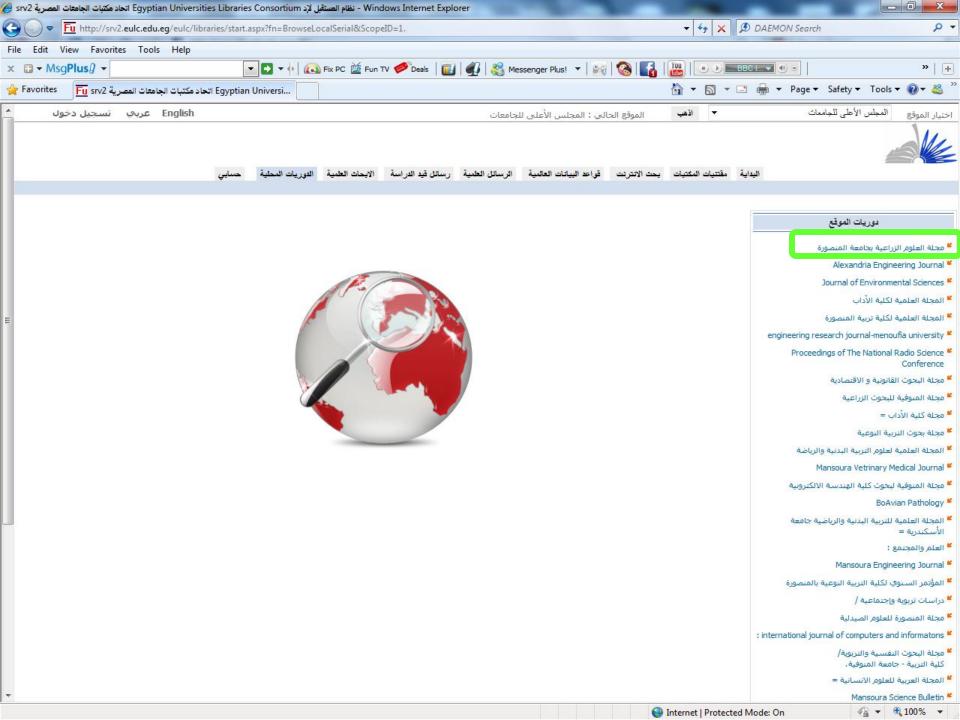


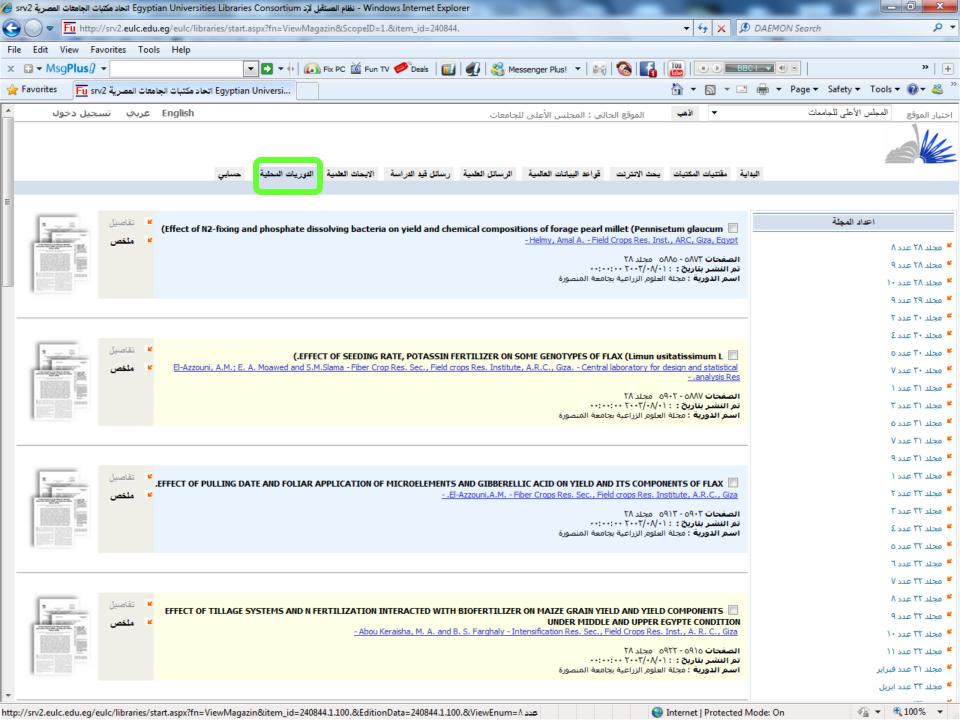














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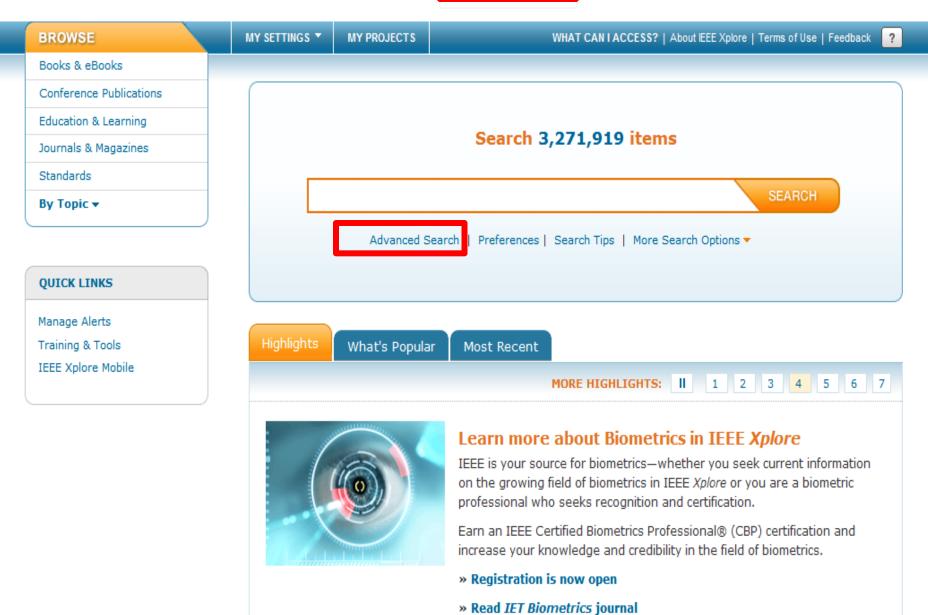
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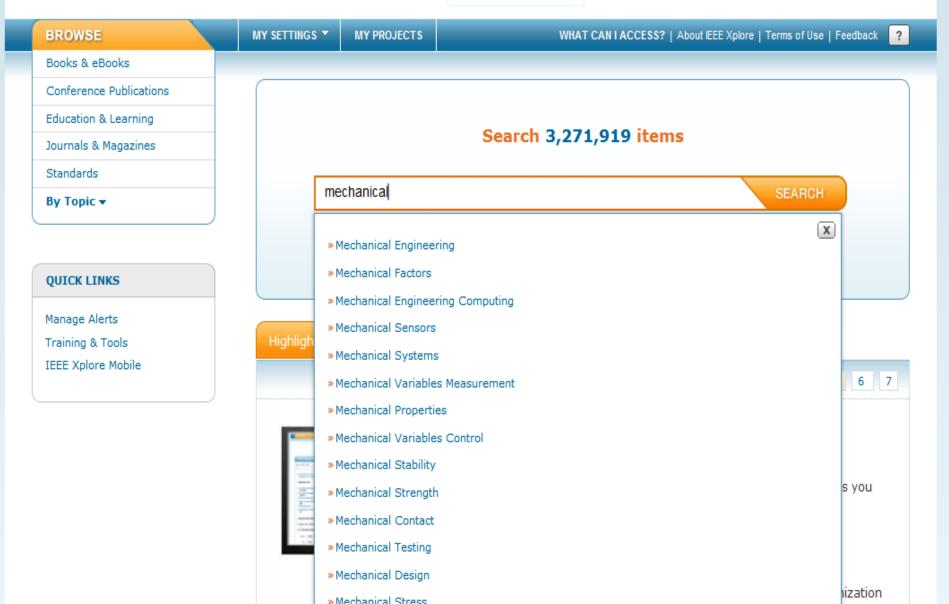


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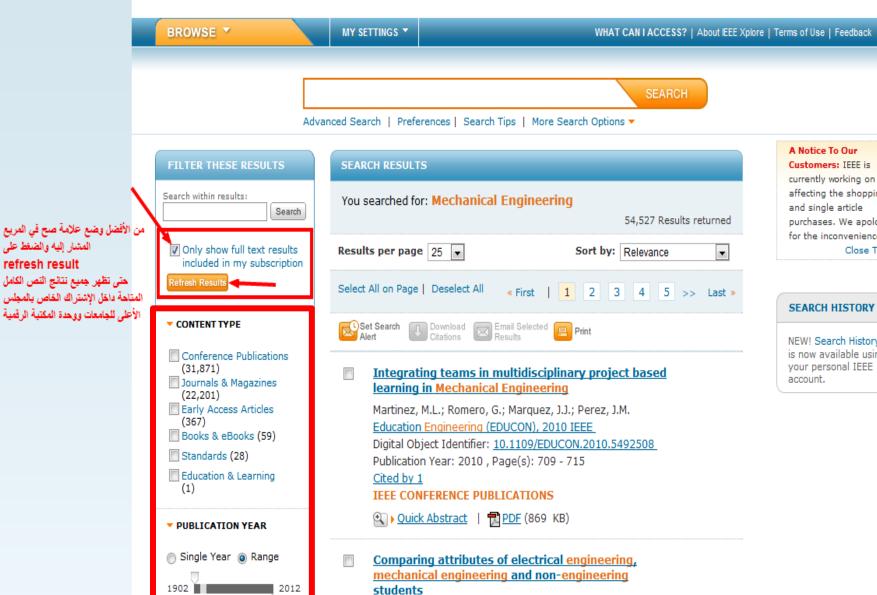


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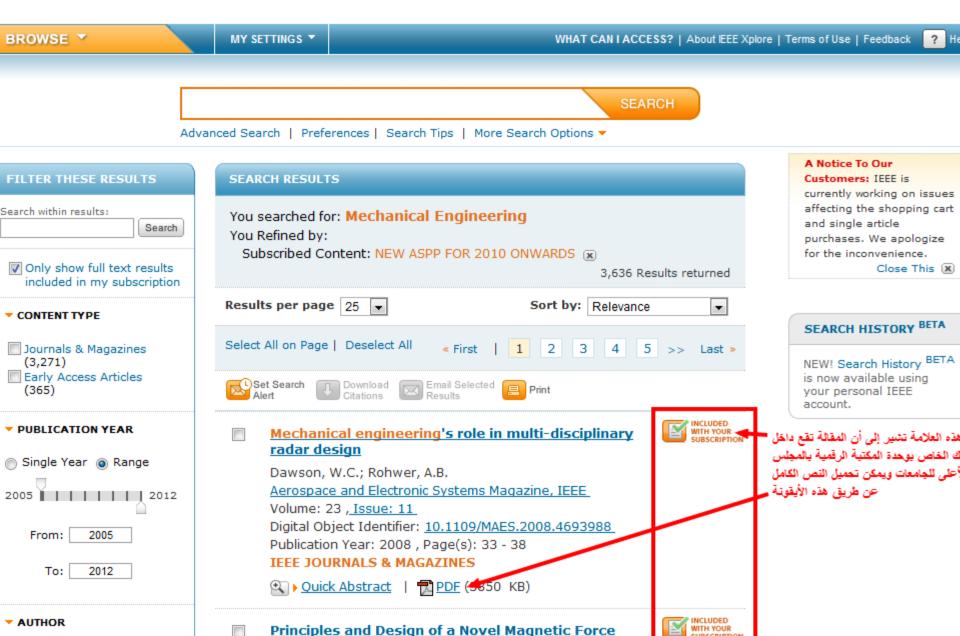
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### Discovering Functional Interdependence Relationship in PPI Networks for Protein Complex Identification

Winnie W. M. Lam\* and Keith C. C. Chan, Member, IEEE

Abstract—Protein molecules interact with each other in protein complexes to perform many vital functions, and different computational techniques have been developed to identify protein complexes in protein-protein interaction (PPI) networks. These techniques are developed to search for subgraphs of high connectivity in PPI networks under the assumption that the proteins in a protein complex are highly interconnected. While these techniques have been shown to be quite effective, it is also possible that the matching rate between the protein complexes they discover and those that are previously determined experimentally be relatively low and the "false-alarm" rate can be relatively high. This is especially the case when the assumption of proteins in protein complexes being more highly interconnected be relatively invalid. To increase the matching rate and reduce the false-alarm rate, we have developed a technique that can work effectively without having to make this assumption. The name of the technique called protein complex identification by discovering functional interdependence (PCIFI) searches for protein complexes in PPI networks by taking into consideration both the functional interdependence relationship between protein molecules and the network topology of the network. The PCIFI works in several steps. The first step is to construct a multiple-function protein network graph by labeling each vertex with one or more of the molecular functions it performs. The second step is to filter out protein interactions between protein pairs that are not functionally interdependent of each other in the statistical sense. The third step is to make use of an information-theoretic measure to determine the strength of the functional interdependence between all remaining interacting protein pairs. Finally, the last step is to try to form protein complexes based on the measure of the strength of functional interdependence and the connectivity between proteins. For performance evaluation, PCIFI was used to identify protein complexes in real PPI network data and the protein complexes it found were matched against those that were previously known in MIPS. The results show that PCIFI can be an effective technique for the identification of protein complexes.

#### I. INTRODUCTION

ROTEIN molecules in protein-protein interaction (PPI) networks interact with each other in subnetworks, called protein complexes [18], [21]. Since protein complexes can play important roles in the understanding of cellular organizations and functions, such as replication, transcription, and control of gene expression, etc. [16], much recent effort has been made to discover protein complexes experimentally. Unfortunately, as laboratory experiments are time consuming and expensive, the number of experimentally identified protein complexes is still far from complete [27]. To reduce costs and time, some attempts have been made to use computational techniques to search for protein complexes in PPI networks automatically so that biological experiments can be better directed [19]. These techniques are mostly graph clustering algorithms. Given a PPI network represented in a graph, these graph clustering algorithms can be used to discover densely connected regions. Under the assumption that the proteins in protein complexes are more highly interconnected, these regions are expected to have higher chance to correspond to known protein complexes.

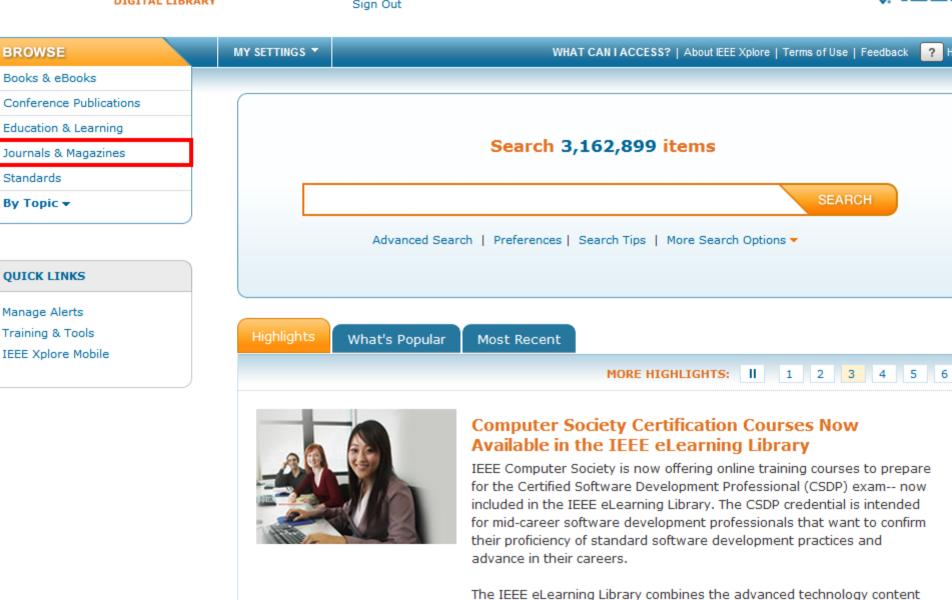
Among the graph clustering algorithms that have been used to discover protein complexes, MCODE [5] is one of the most popular. It discovers protein complexes based on the connectivity between protein molecules in a PPI network. Under the assumption that the proteins in a protein complex are more densely connected with each other [31], MCODE makes use of a local search algorithm that operates in three stages: vertex weighting, complex prediction, and postprocessing. Given a PPI network graph, MCODE first weights all its vertices based

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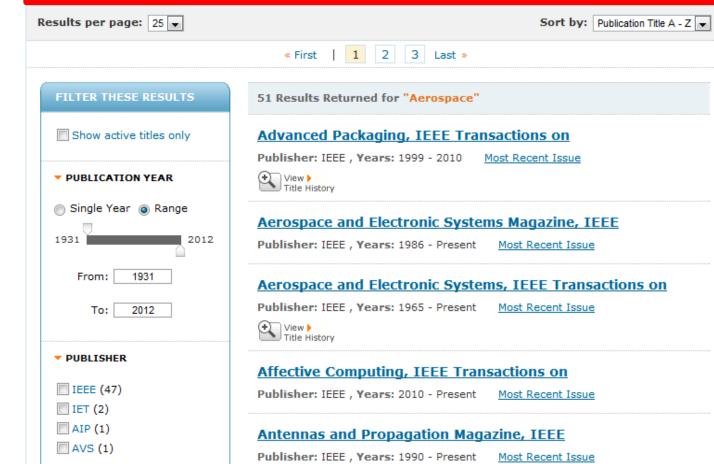
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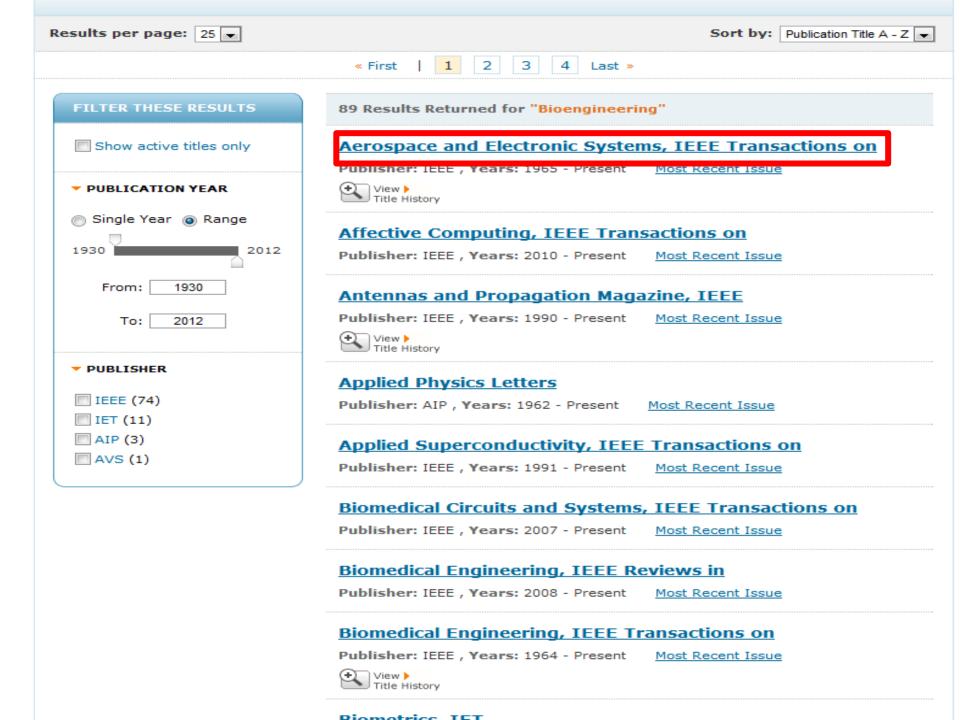
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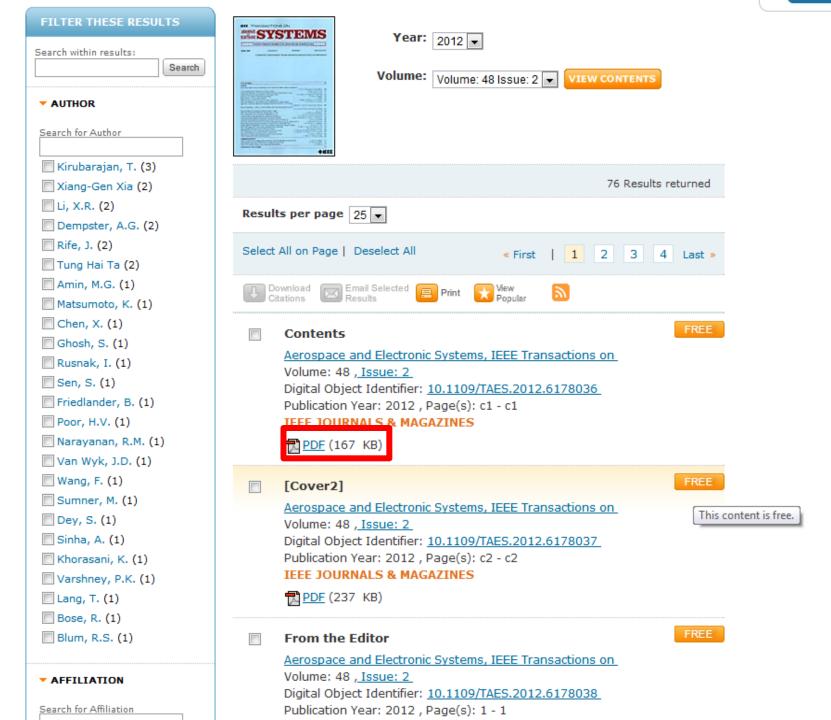
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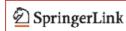
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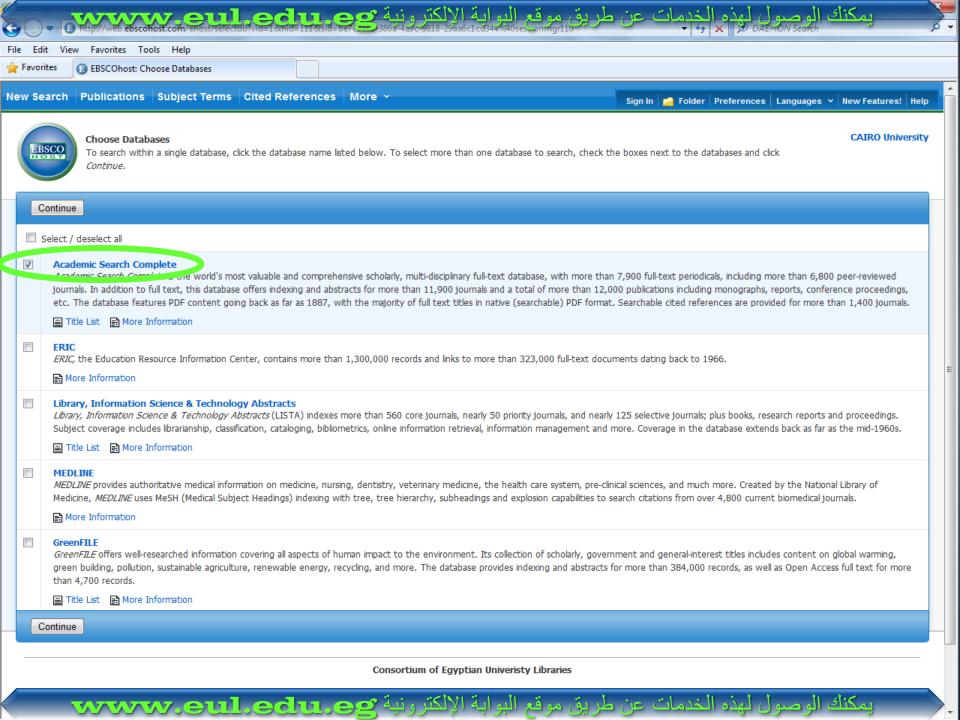


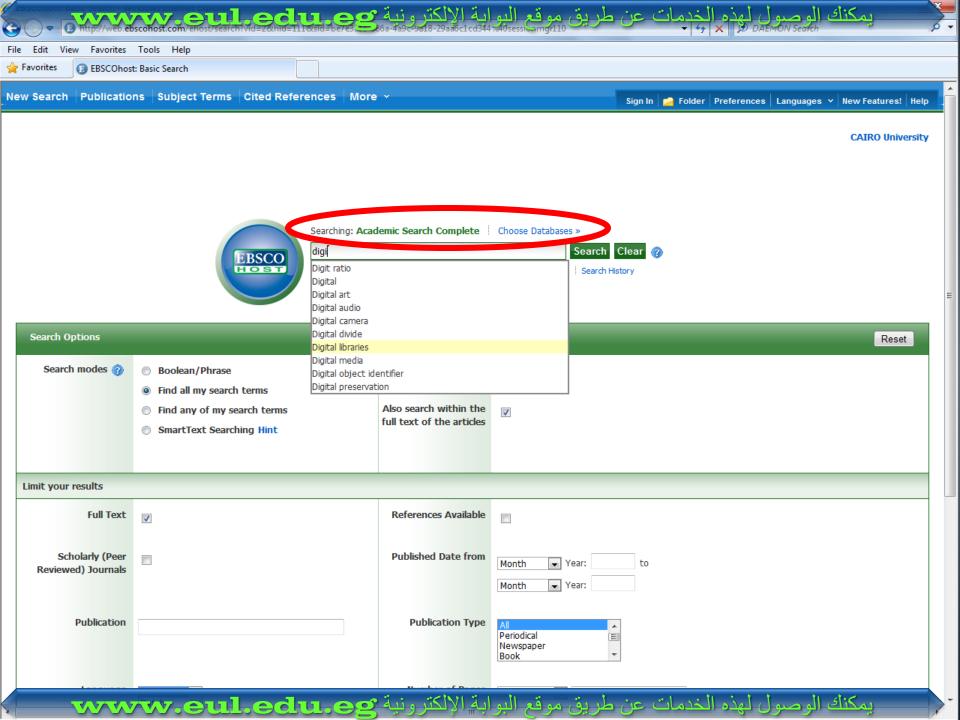
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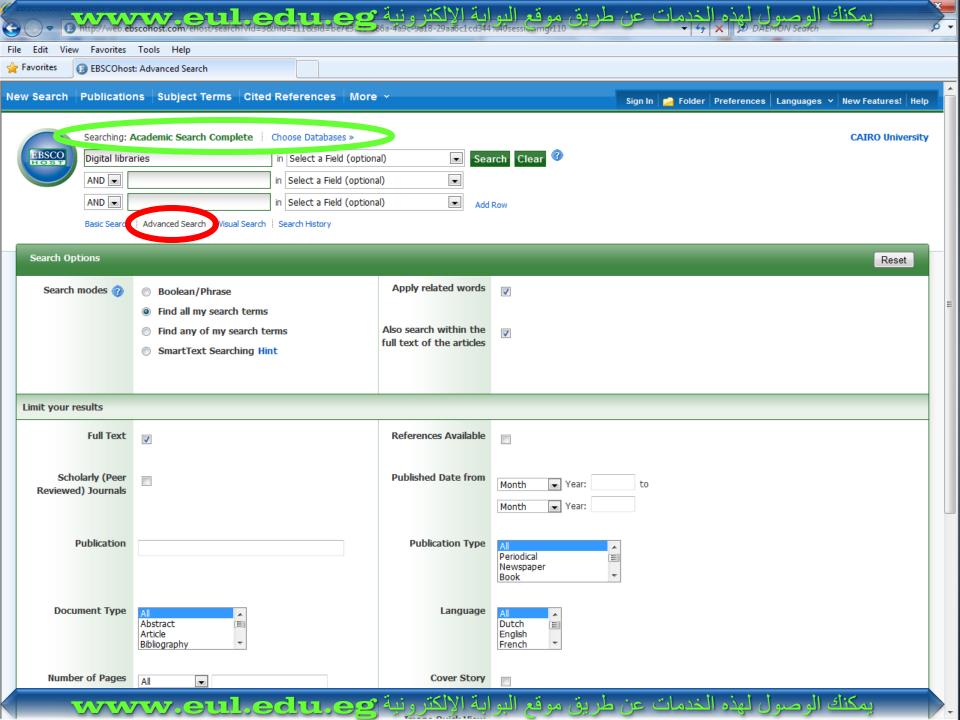
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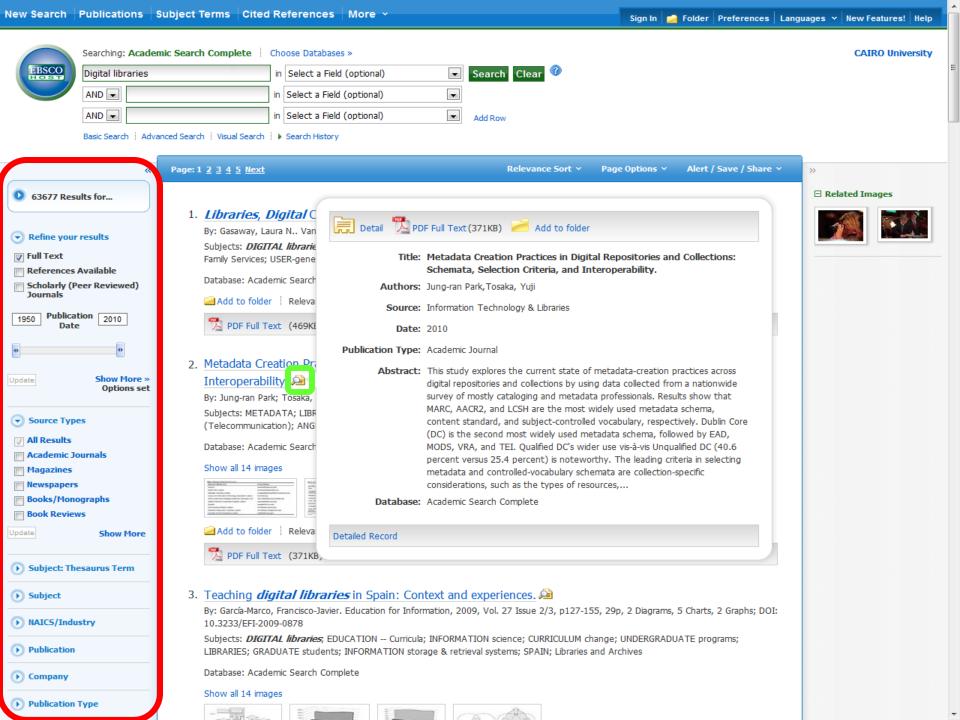
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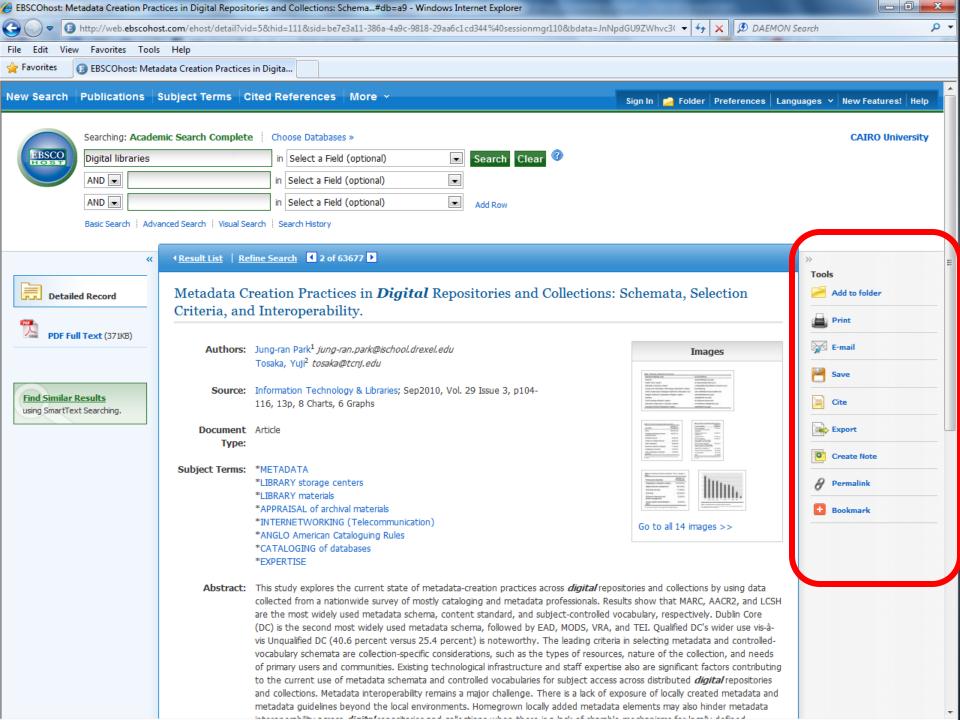
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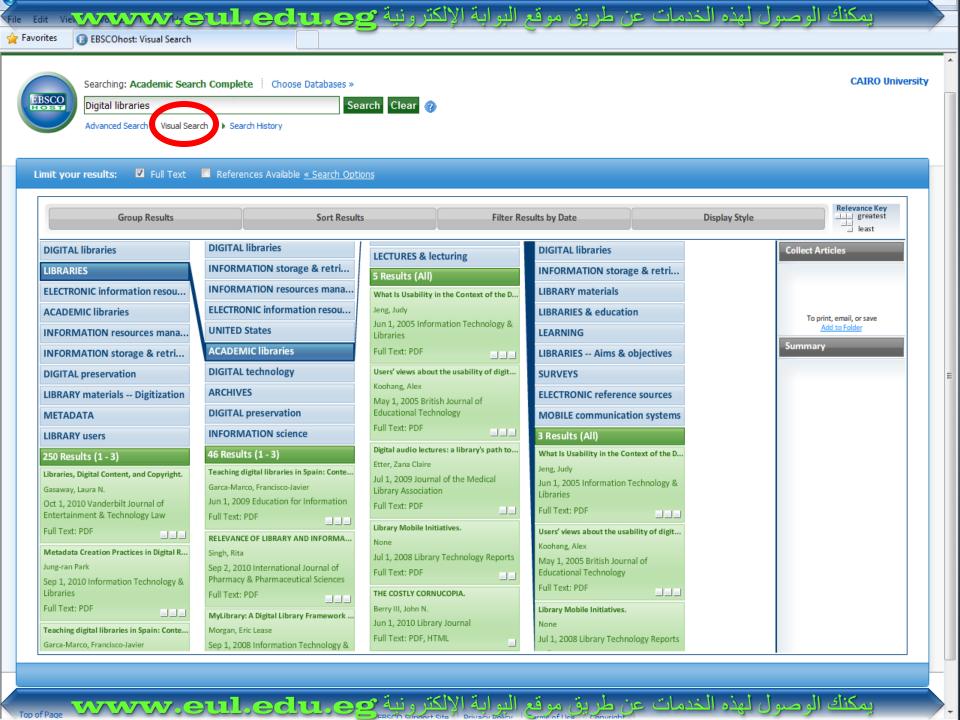














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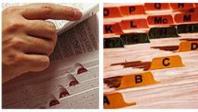
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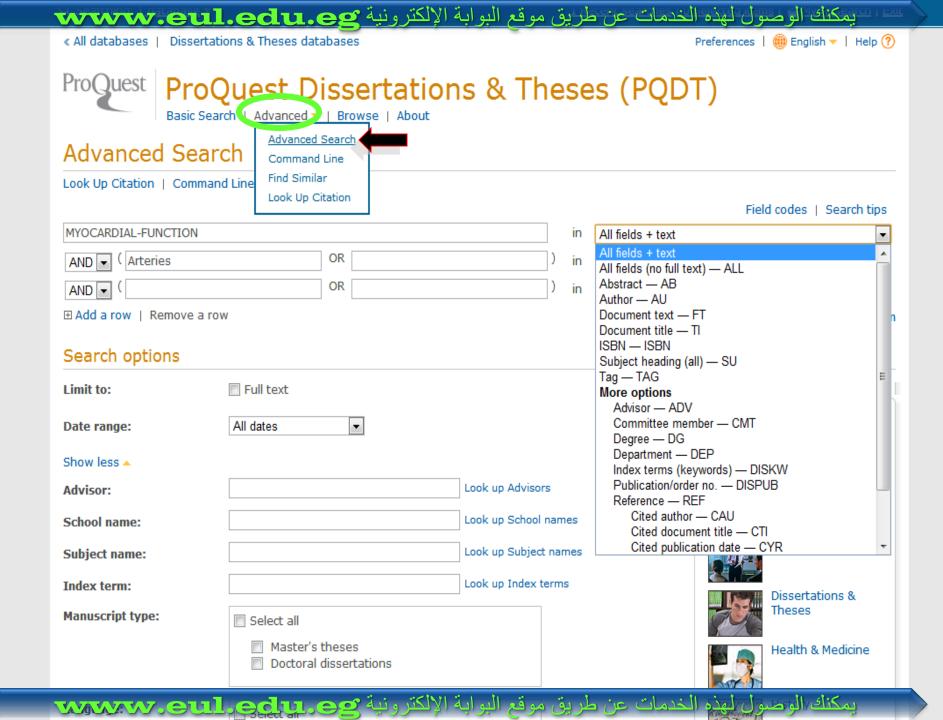


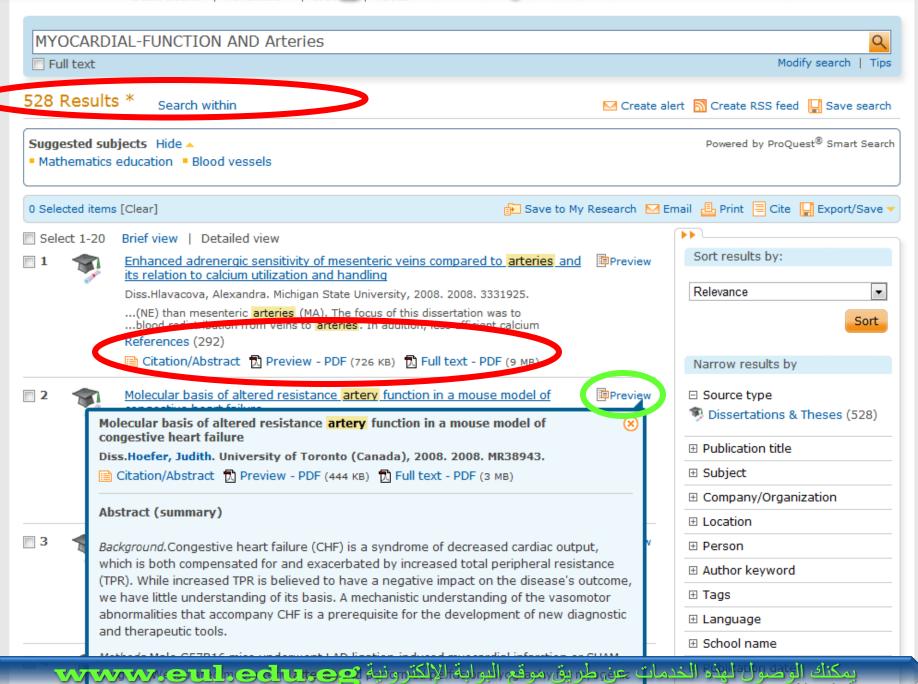


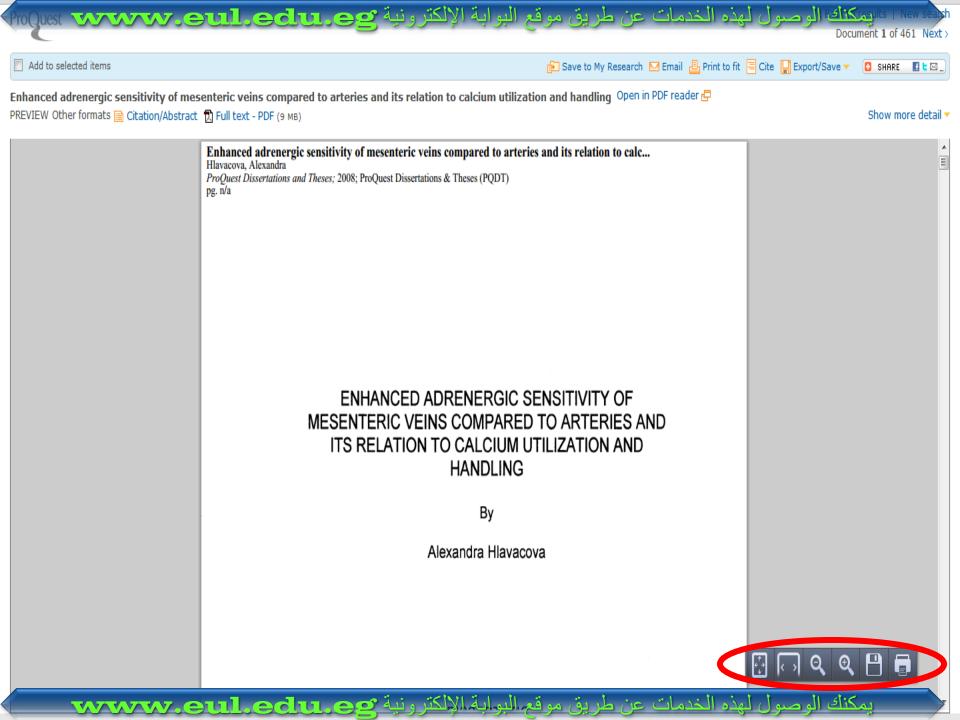
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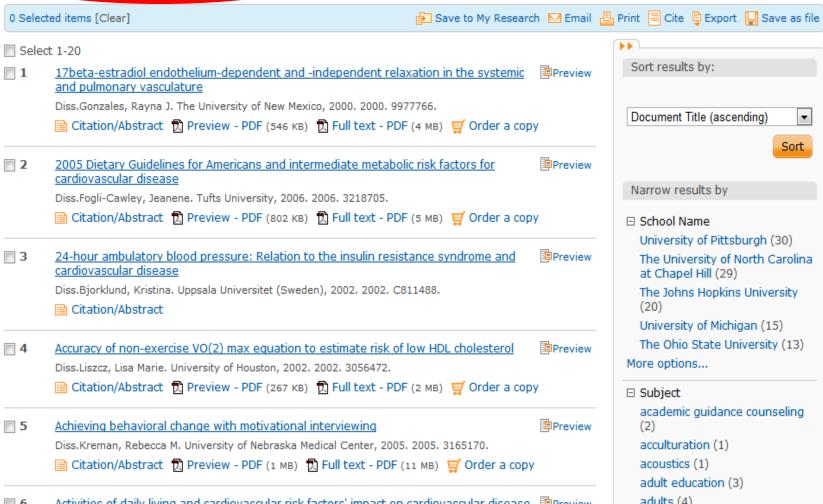
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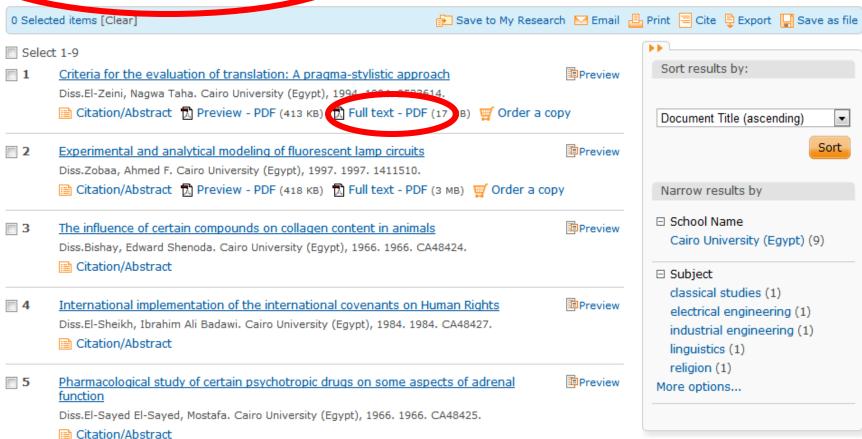
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# A Scalable Middleware for Web Databases

Athman Bouguettaya, Virginia Tech., USA

Zaki Malik, Virginia Tech., USA

Abdelmounaam Rezgui, Virginia Tech., USA

Lori Korff, Virginia Tech., USA

#### **ABSTRACT**

The emergence of Web databases has introduced new challenges related to their organization, access, integration, and interoperability. New approaches and techniques are needed to provide across-the-board transparency for accessing and manipulating Web databases irrespective of their data models, platforms, locations, or systems. In meeting these needs, it is necessary to build a middleware infrastructure to support flexible tools for information space organization.



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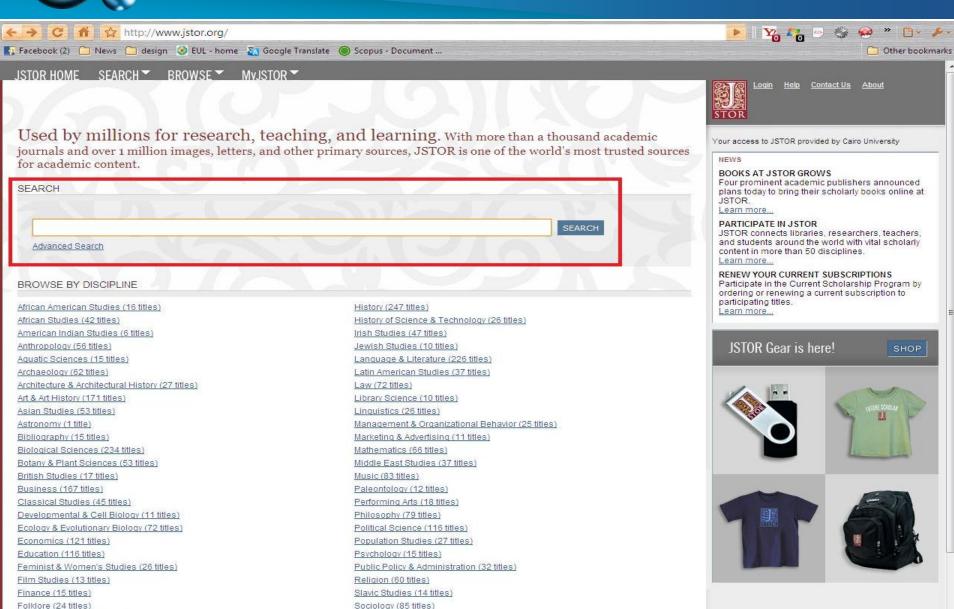
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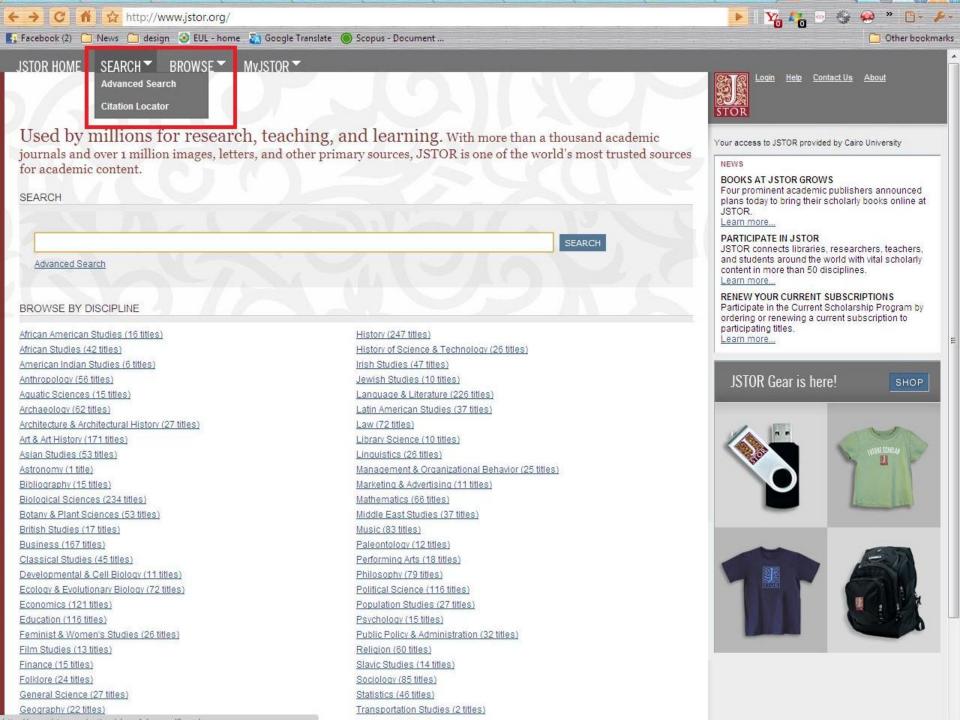
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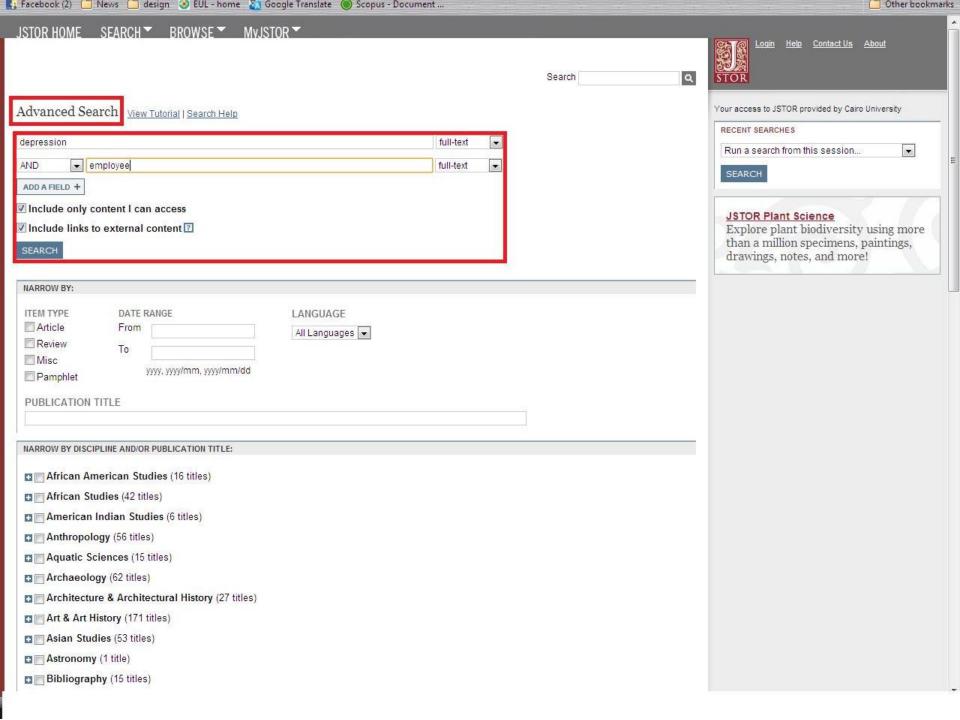
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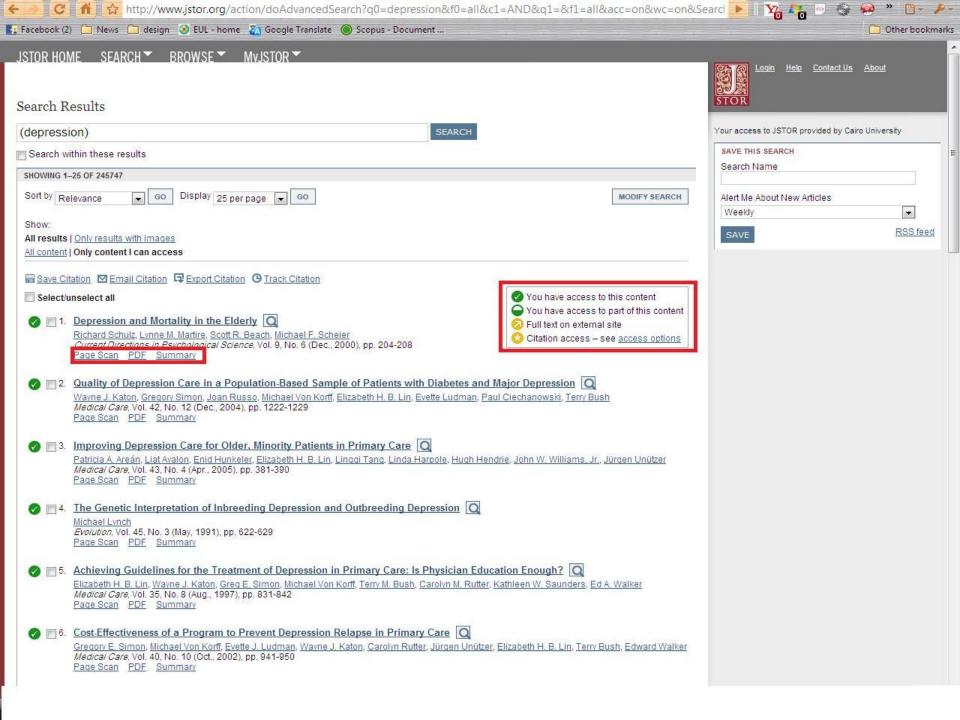


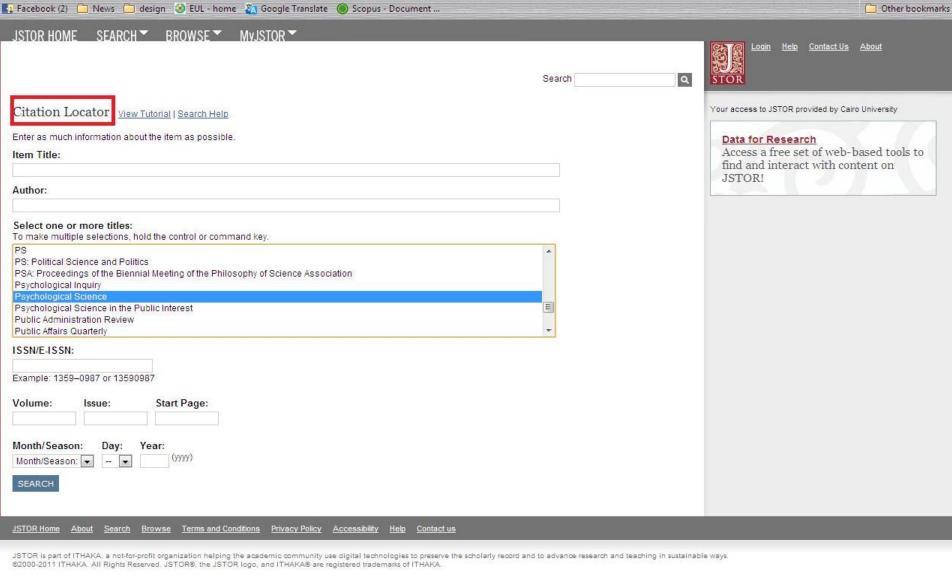
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Evolution, 45(3), 1991, pp. 622-629

Page 622 01 622-629

#### THE GENETIC INTERPRETATION OF INBREEDING DEPRESSION AND OUTBREEDING DEPRESSION

MICHAEL LYNCH

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Abstract. —Inbreeding with close relatives and outbreeding with members of distant populations can both result in deleterious shifts in the means of fitness-related characters, most likely for very different reasons. Such processes often occur simultaneously and have important implications for the evolution of mating systems, dispersal strategies, and speciation. They are also relevant to the design of breeding strategies for captive populations of endangered species. A general expression is presented for the expected phenotype of an individual under the joint influence of inbreeding and crossbreeding. This expression is a simple function of the inbreeding coefficient, of source and hybridity indices of crossbreeding, and of specific forms of gene action. Application of the model may be of use in identifying the mechanistic bases for a number of evolutionary phenomena such as the shift from outbreeding enhancement to outbreeding depression that occurs with population divergence.

Key words. - Inbreeding depression, outbreeding depression.

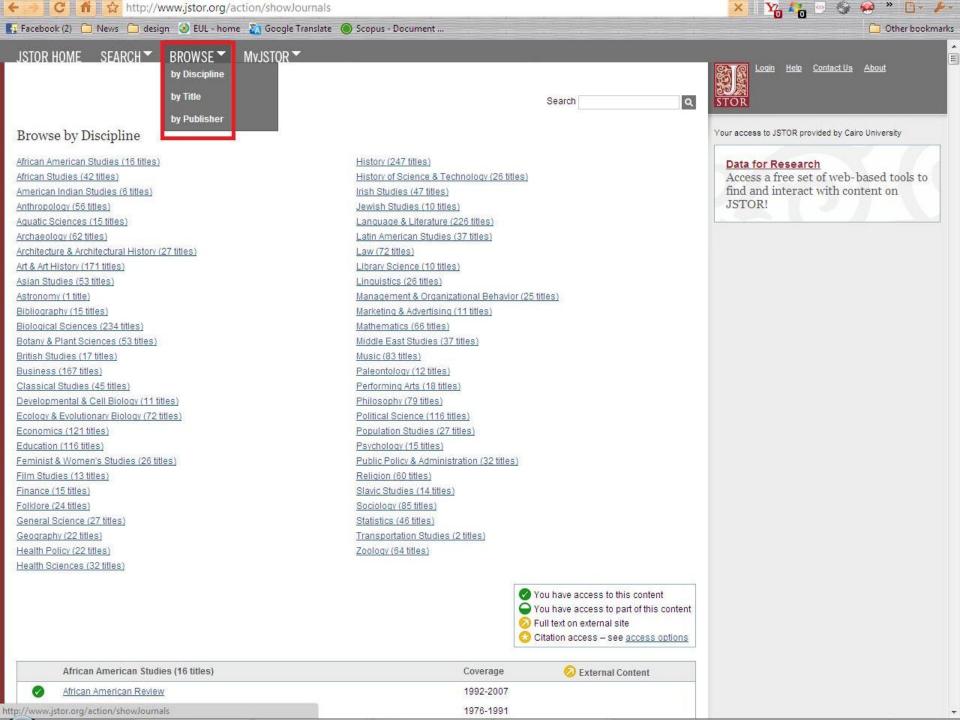
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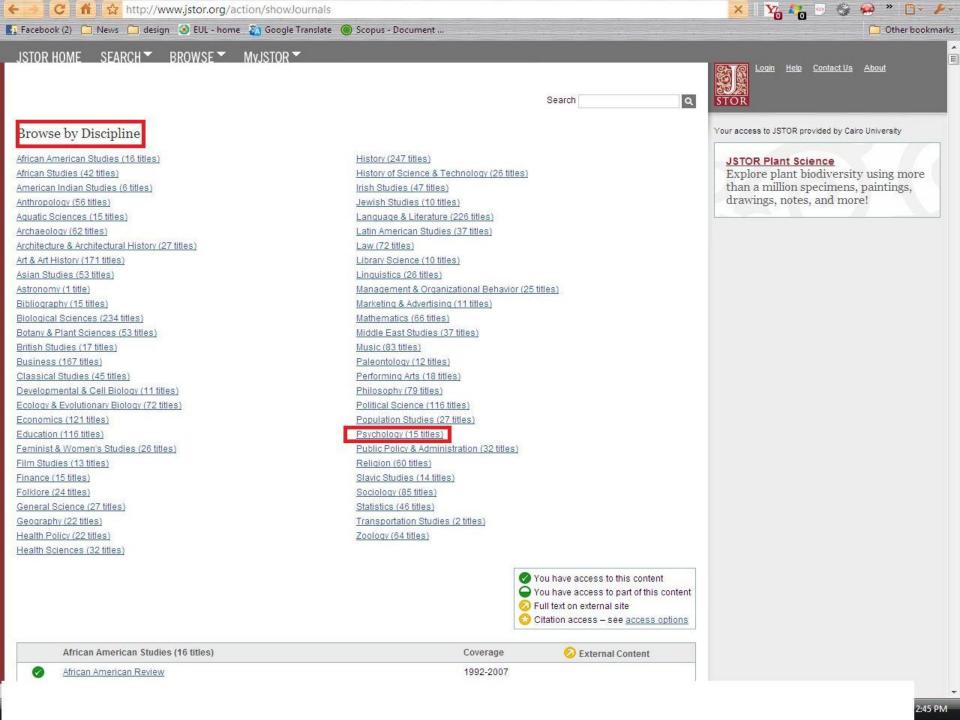
Two topics of fundamental importance to many areas in evolutionary biology are the consequences of inbreeding within populations and of outcrossing between populations. With almost no exception, empirical studies indicate that inbreeding causes a shift in mean phenotypes in a direction that causes a reduction in fitness (Wright, 1977; Shields, 1982; Charlesworth and Charlesworth, 1987; Ralls et al., 1988; Lynch, 1989). On the other hand, crossbreeding between populations often has positive effects on fitness-related traits (Darwin, 1877; Sheridan, 1981; Turton, 1981; Sprague, 1983; Levin, 1984). It is frequently argued that this response to outcrossing is simply the recovery from inbreeding depression that is expected to result from random genetic drift in isolated populations. One problem with this argument is that outcrossing does not always enhance fitness. Crosses between different species usually lead to substantial or complete inviability or infertility in the  $F_1$  or  $F_2$  generations (Barton and Hewitt, 1981; Templeton, 1981; Covne and Orr, 1989), and

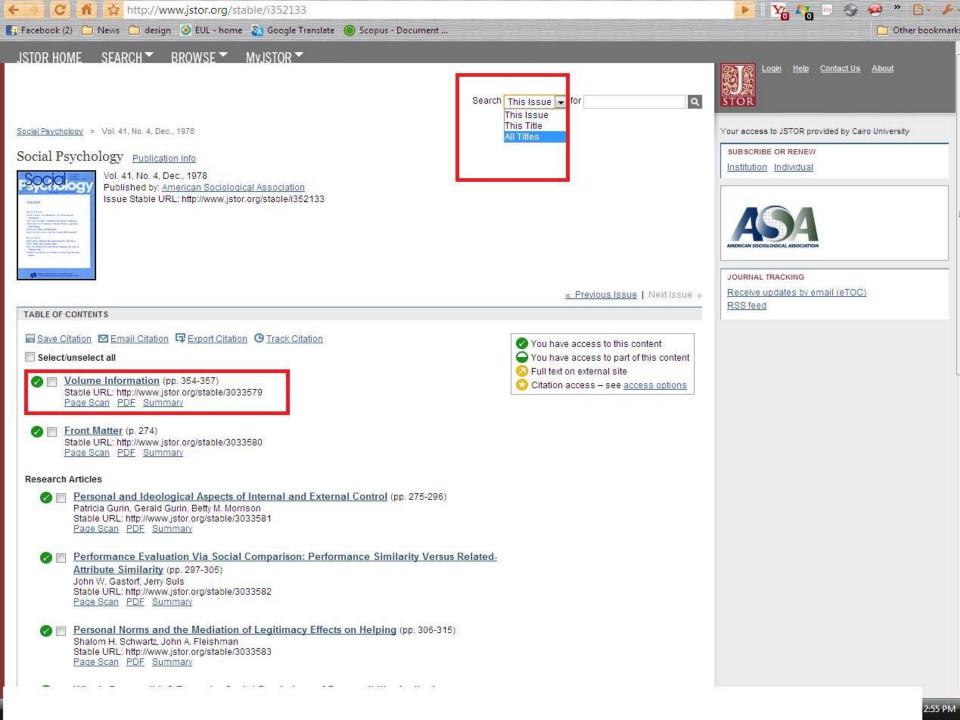
tions as mates become more and more distantly related, and has led to the suggestion that there is an optimal degree of outbreeding (Price and Waser, 1979; Shields, 1982; Bateson, 1983; Waser and Price, 1983). Dominance is generally believed to be the primary agent of inbreeding depression (Crow, 1948, 1952; Lande and Schemske, 1985; Charlesworth and Charlesworth, 1987). On the other hand, the decline in fitness under outcrossing is usually attributed to a breakup of coadapted gene complexes or favorable epistatic relationships (Mayr, 1963; Shields, 1982; Templeton, 1987). Thus, in proceding from theories of inbreeding depression to those of outbreeding depression, there is a shift in emphasis from interactions within loci to interactions between loci.

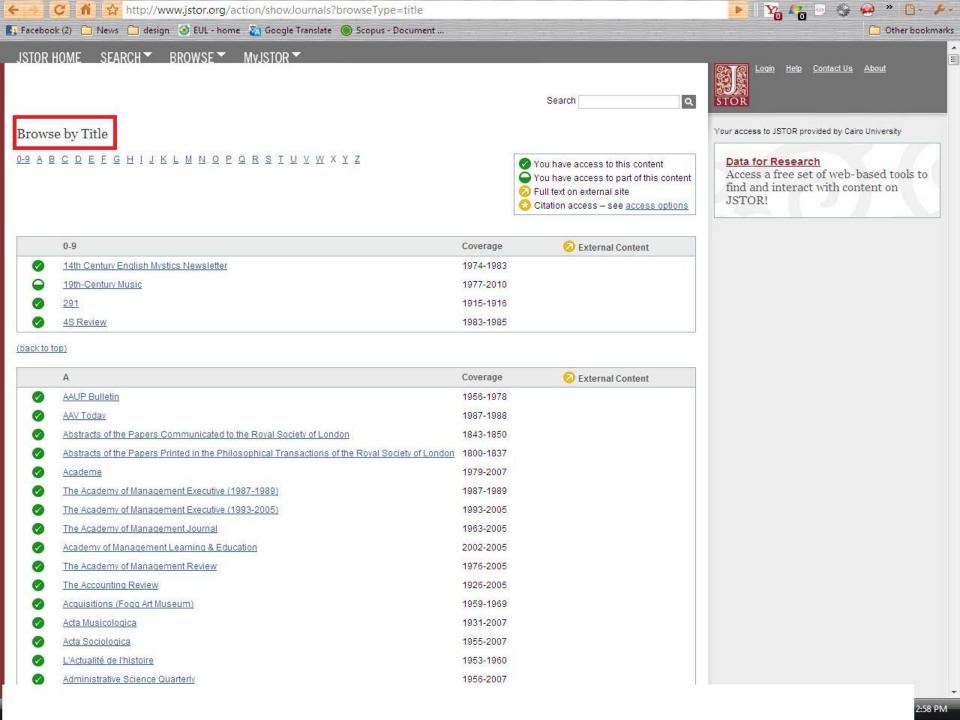
Unfortunately, this dichotomy is not so clearcut. For example, although it has received little attention from empiricists, epistasis can contribute to inbreeding depression (Kempthorne, 1957; Bulmer, 1980; Hill, 1982). Moreover, the possibility that overdominance between alleles of closely

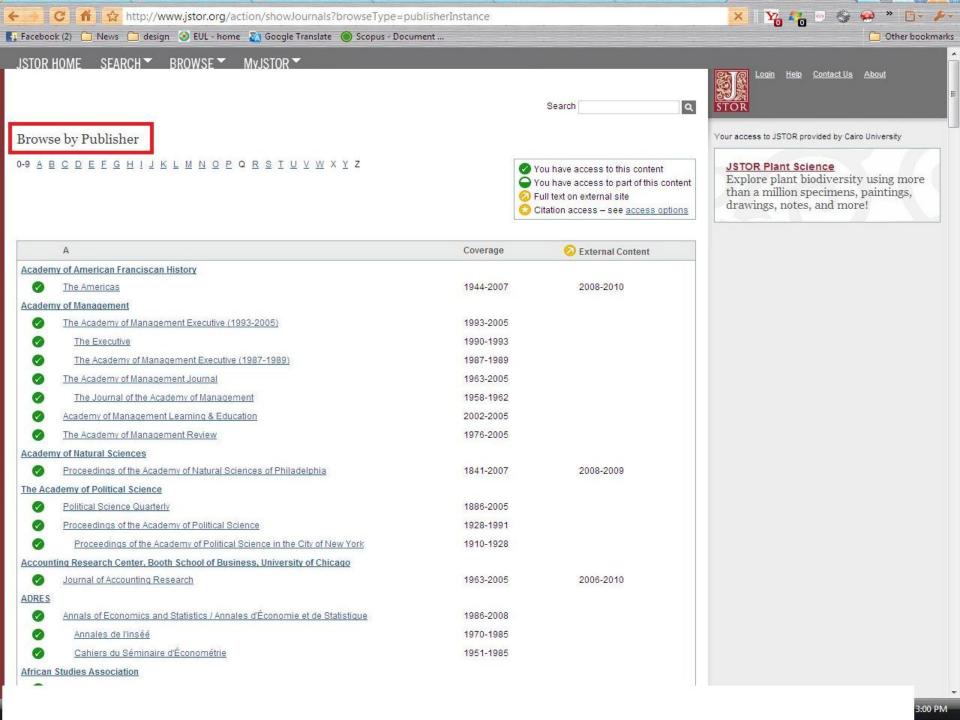
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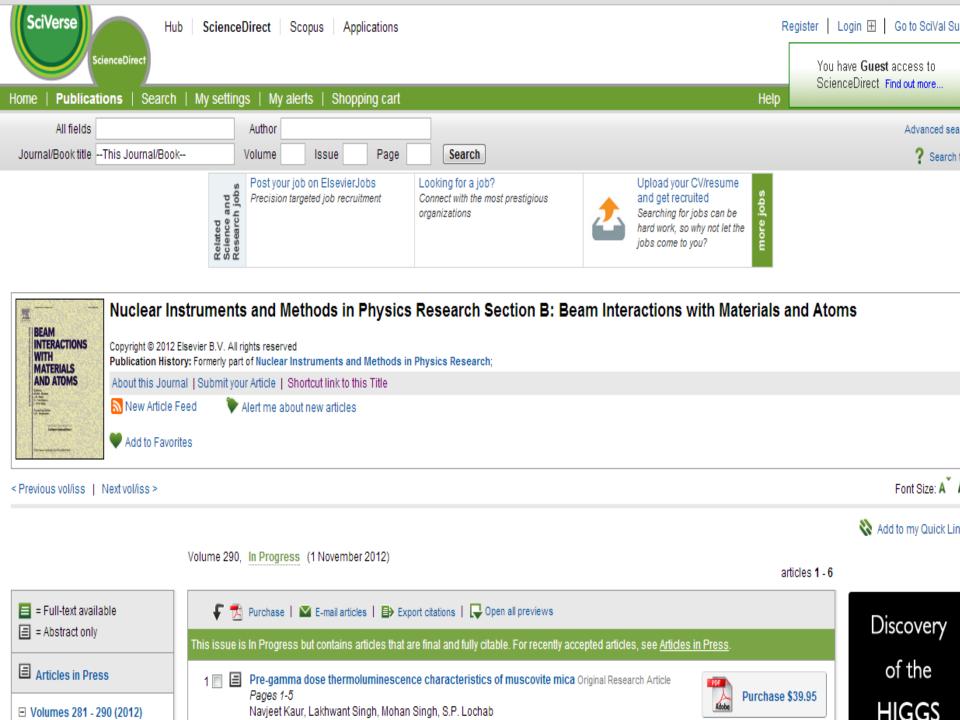
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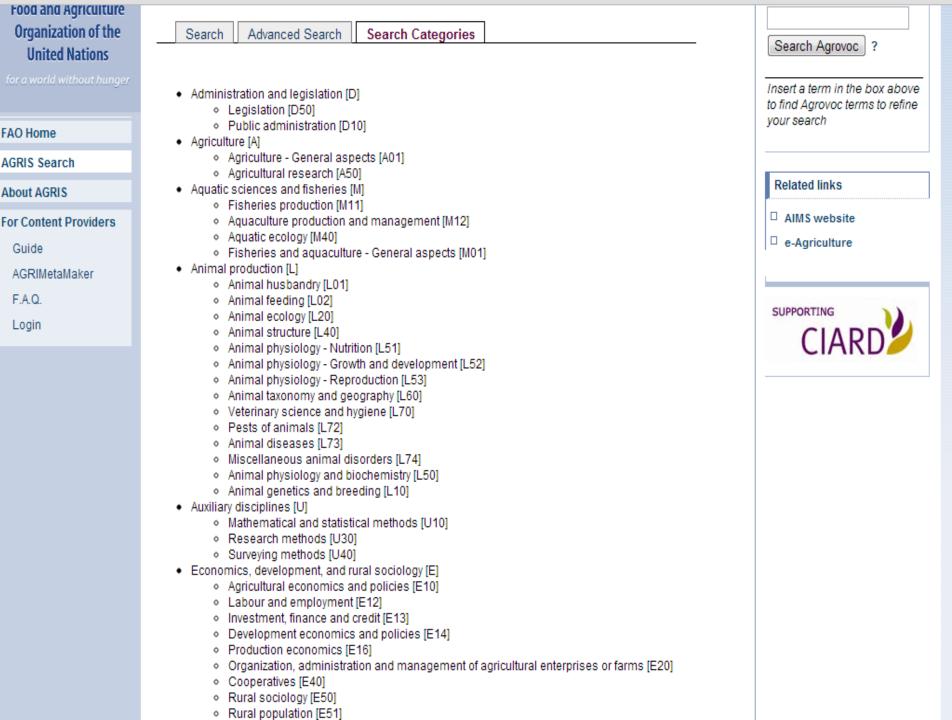
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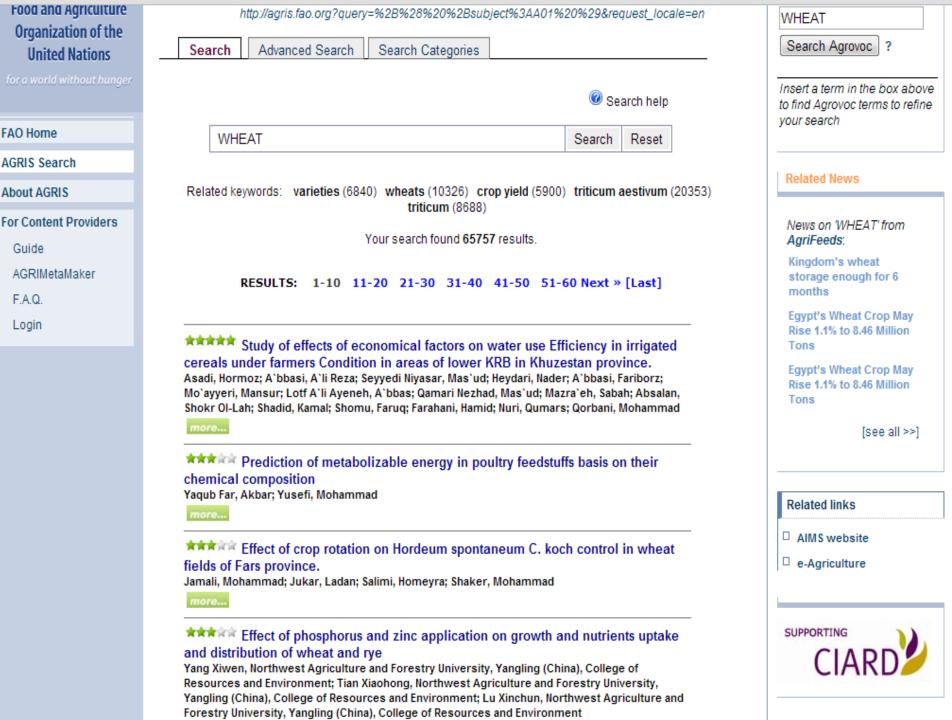
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efficiency and its comparison in salinity lands (Azadegan plain) and other lands (Sorkheh plain), Reaction of

sample farmers to some of quality indices. This study implemented in the Azadegan (DA) and Sorkheh (DS)

**Publisher** Seed and Plant Improvement Institute, Karaj (Iran) Date of publication 2009 **AGRIS Categories** 

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management

Watershed management; Water resources; Rivers; Iran islamic republic

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agricultural research in dry area(icarda), syria 31501

Language Farsi

Summaries (Fa. En ) Notes

69 p

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The purposes of this study were to: Socio-economic characteristics in target regions, Different water uses and water price for cereals in target regions, Situation of irrigated cereals in the Azadegan and Sorkheh plain, Socio-economic characteristics of sample farmers, determination of Profitability in irrigated cereals production between sample farmers. Determination of average Water use efficiency in irrigated cereals

Irrigation; Cereals; Water use; Efficiency; Economic value; On-farm research; Socioeconomic development;

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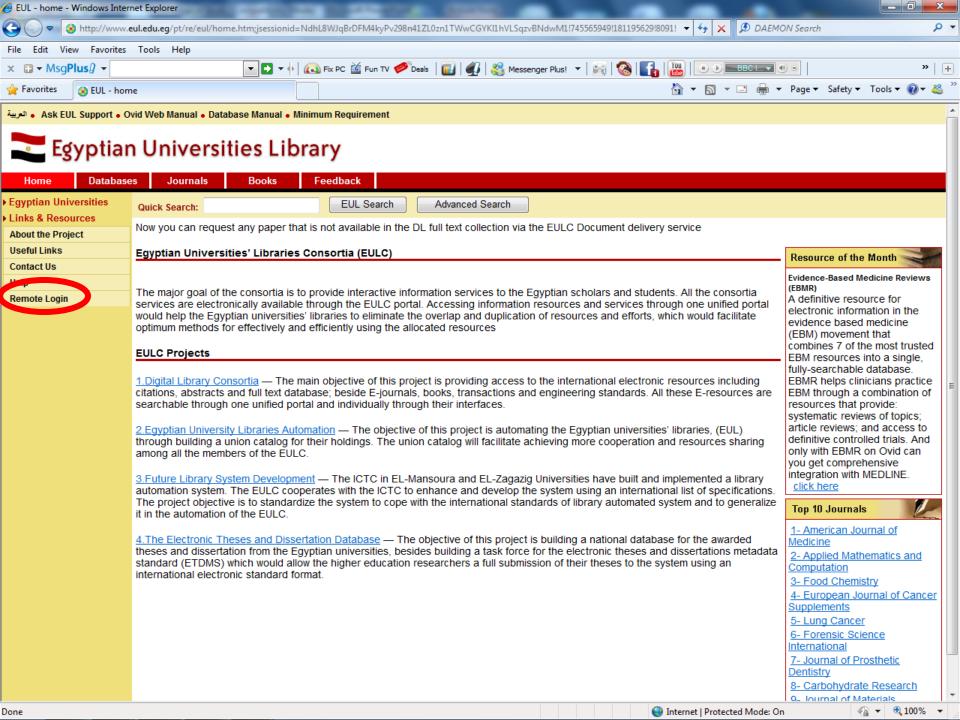
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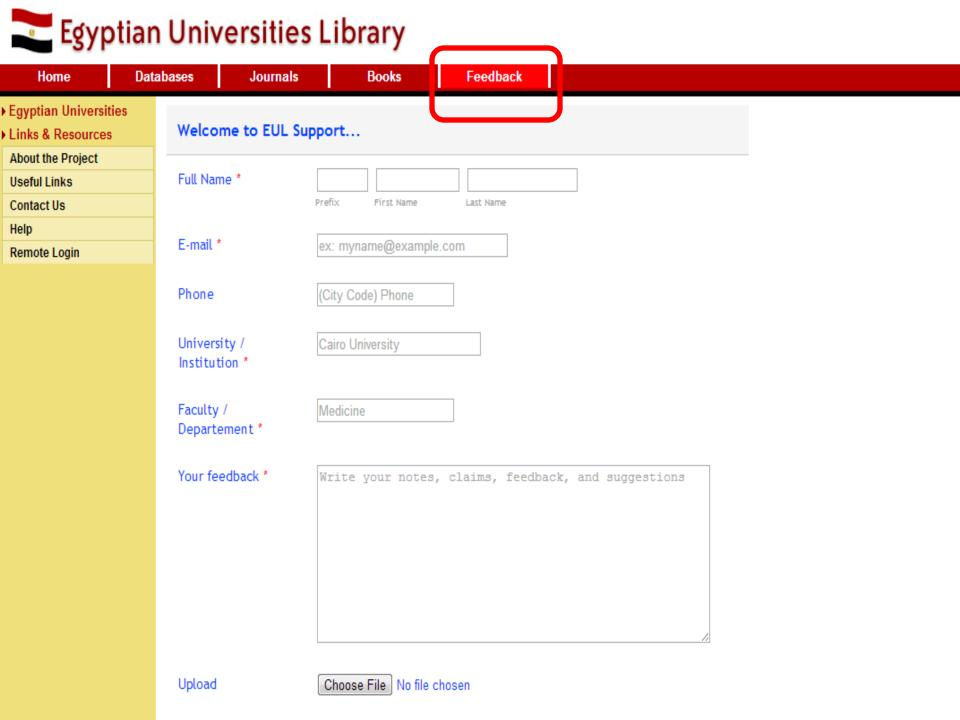
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