

# Yasser EL-Manzalawy

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RESEARCH INTERESTS	Bioinformatics, Immunoinformatics, Machine Learning, Artificial Intelligence, Data Mining and Knowledge Discovery.	
TEACHING INTERESTS	Graduate and undergraduate level Bioinformatics, Artificial Intelligence, Machine Learning and Data Mining courses.	
EDUCATION	<b>Ph.D., Iowa State University, Computer Science</b> , Ames, IA, US Thesis Topic: Machine Learning Approaches for Epitope Prediction Advisor: Professor Vasant Honavar	2004-2008
	<b>M.S., Al-Azhar University, Systems &amp; Computer Engineering</b> , Egypt Thesis Topic: ATM Systems Design Advisor: Professor Hani Harb	1998-2000
	<b>B.S., Al-Azhar University, Systems &amp; Computer Engineering</b> , Egypt	1990-1995
PROFESSIONAL EXPERIENCE	<b>Postdoctoral Research Associate</b> . Center for Computational Intelligence, Learning, & Discovery, Iowa State University under Professor Vasant Honavar's supervision. Projects: Epitope prediction, Analysis of biological networks, protein functional site prediction.	2008-present
	<b>Research Assistant</b> . Center for Computational Intelligence, Learning, & Discovery, Iowa State University under Professor Vasant Honavar's supervision. Projects: Epitope prediction, Multiple-instance learning algorithms.	2008
	<b>AI Group Research Member</b> . Conducting research in various areas of Machine Learning and their applications in Bioinformatics and Immunoinformatics.	2004-2008
	<b>Freelance Technical Writer</b> . <a href="http://www.developer.com">www.developer.com</a> . Published tutorials on java language, aspect-oriented programming, and application frameworks.	2004
	<b>Java Programmer and Web Developer</b> . <a href="http://www.mindwork.com">www.mindwork.com</a> .	1999-2000
	<b>Teaching and Lecture Assistant</b> . Systems & Computer Engineering, Al-Azhar University, Egypt. Courses: database, software engineering, data structure and algorithms, computer architecture, computer networking, and artificial intelligence.	1997-2004
	<b>Programming Language Instructor</b> . Languages: C, C++, Visual C++, Visual Basic, and Java. Education centers: IBM authorized education centers, Computek Integrated Systems, and TRI-TECH.	1997-2004

HONORS AND AWARDS	Iowa State University Research Excellence Award	2008
	Research assistantship funded by the ISU Graduate College	2008
	Egyptian Government Fellowship	2004-2008
	Ranked nation's second best high school graduated student, Egypt	1990
RESEARCH PROJECTS	<b>Epitopes Toolkit (EpiT)</b> . A platform for developing epitope prediction tools. An EpiT developer can distribute his predictor as a serialized Java object (model file). This allows other EpiT users to use his predictor on their own machines, rebuild the predictor on other data sets, or combine the predictor with other predictors to obtain a customized hybrid or consensus predictor. URL: <a href="http://ailab.cs.iastate.edu/epit/">http://ailab.cs.iastate.edu/epit/</a>	2009
	<b>Repository for Epitope Datasets (RED)</b> . A large collection of epitope data sets published by our group and other publicly available data sets in Weka (ARFF) format. These data sets can be used with EpiT (Epitopes Toolkit) for developing epitope prediction tools. URL: <a href="http://ailab.cs.iastate.edu/red/">http://ailab.cs.iastate.edu/red/</a>	2009
	<b>Repository for Epitope Predictors (REP)</b> . A collection of epitope predictors as Java Serialized objects (model files). These model files can be used with EpiT (Epitopes Toolkit) for predicting potential epitopes in antigenic sequences. URL: <a href="http://ailab.cs.iastate.edu/rep/">http://ailab.cs.iastate.edu/rep/</a>	2009
	<b>MHCIPREDS</b> . A tool for predicting major histocompatibility complex (MHC) class I binding using several prediction methods covering the major approaches for predicting MHC-I binding peptides. URL: <a href="http://ailab.cs.iastate.edu/mhcipreds/">http://ailab.cs.iastate.edu/mhcipreds/</a>	2008
	<b>MHCMIR</b> . A tool for predicting major histocompatibility complex (MHC) class II binding affinity using multiple-instance regression. URL: <a href="http://ailab.cs.iastate.edu/mhcmir/">http://ailab.cs.iastate.edu/mhcmir/</a>	2008
	<b>BCPREDS</b> . A resource for linear B-cell epitope prediction. Current implementation supports three different methods for predicting linear B-cell epitopes and the benchmark datasets used to build the classifiers. URL: <a href="http://ailab.cs.iastate.edu/bcpreds/">http://ailab.cs.iastate.edu/bcpreds/</a>	2007
	<b>Weka LibSVM (WLSVM)</b> . A wrapper for integrating libsvm tool into Weka framework. WLSVM has been fully integrated into Weka 3.5. URL: <a href="http://www.cs.iastate.edu/~yasser/wlsvm.html">http://www.cs.iastate.edu/~yasser/wlsvm.html</a>	2005
	<b>JPLAN</b> . A Java implementation of the GraphPlan algorithm, a fast domain independent planner. URL: <a href="http://sourceforge.net/projects/jplan/">http://sourceforge.net/projects/jplan/</a>	2004
PUBLICATIONS	<b>Ph.D. Thesis</b> EL-Manzalawy, Y. (2008). Machine learning approaches for epitope prediction. Iowa State University.	

### **Refereed Journal Articles**

**EL-Manzalawy, Y., Dobbs, D., and Honavar, V. (2008).** Predicting linear B-cell epitopes using string kernels. *J. Mol. Recognit.*, 21:243-255.

**EL-Manzalawy, Y., Dobbs, D., and Honavar, V. (2008).** On Evaluating MHC-II binding peptide prediction methods. *PLoS ONE*, 3.

### **Refereed Conference Articles**

**EL-Manzalawy, Y. and Honavar, V. (2009).** MICCLLR: Multiple-Instance Learning using Class Conditional Log Likelihood Ratio. In: *Proceedings of the 12<sup>th</sup> International Conference on Discovery Science (DS 2009)*. In press.

**EL-Manzalawy, Y., Dobbs, D., and Honavar, V. (2008).** Predicting flexible length linear B-cell epitopes. *7th International Conference on Computational Systems Bioinformatics*, pages 121-131.

**EL-Manzalawy, Y., Dobbs, D., and Honavar, V. (2008).** Predicting protective linear B-cell epitopes using evolutionary information. *IEEE International Conference on Bioinformatics and Biomedicine*, pages 289-292.

### **Journal Articles under Review**

**EL-Manzalawy, Y., Dobbs, D., and Honavar, V. (2008).** Predicting MHC-II binding affinity using multiple-instance regression. Submitted to *IEEE/ACM Trans. Comput. Biol. Bioinform.*

**EL-Manzalawy, Y. and Honavar, V. (2008).** Qualitative versus quantitative approaches for predicting MHC-I peptides. Submitted to *Immunome Res.*

**EL-Manzalawy, Y. and Honavar, V. (2009).** EpiT: Software for developing epitope prediction tools. Submitted to *Bioinformatics*.

### **Abstracts and Posters**

**EL-Manzalawy, Y., Caragea, C., Dobbs, D., and Honavar, V. (2006).** On the quality of motifs for protein phosphorylation site prediction. Accepted to *The 14th Annual International Conference On Intelligent Systems For Molecular Biology (ISMB)*, Poster Program, Fortaleza, Brazil.

**EL-Manzalawy, Y., Caragea, C., Dobbs, D., Honavar, V. (2006).** Machine Learning versus Profile-Based Methods for Protein Phosphorylation Site Prediction, Accepted to *The Sixth Annual Joint Bioinformatics Symposium, Student Abstract and Poster Program*, Ames, Iowa.

### **Papers in Preparation**

**EL-Manzalawy, Y., Caragea, C., Honavar, V. (2009).** On assessing the performance of machine learning methods for residue-based macromolecular sequence labeling.

**EL-Manzalawy, Y., Dobbs, D., and Honavar, V. (2009).** On the Utility of Evolutionary Information in Predicting Linear B-cell Epitopes.

**EL-Manzalawy, Y. and Honavar, V. (2009).** AUC-optimized matrix method.

REFERENCES

Available upon request.