Ghada Badr

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Education

Doctor of Philosophy, Computer Science

April 2006 Carleton University School of Computer Sciences, Ottawa, ON

- *Dissertation Topic*: Tries in Data Retrieval and Syntactic Pattern Recognition.
- *Won* ***Senate Medal*** *for "Outstanding Research Achievements" for faculty of science, Carleton University.*

M.Sc in Engineering (Computer Science and Automatic Control)

March 2001 Alexandria University Faculty of Engineering, Alexandria, EGYPT

- *Dissertation Topic*: An Accurate Copy Detection Server for Digital Documents.
- *Graduated with Distinction (Degree of Honor).*

B.Sc. in Engineering (Computer Science and Automatic Control)

May 1996 Alexandria University Faculty of Engineering, Alexandria, EGYPT

- *Graduation Project*: The Alex Object-Oriented Database Management System.
- *Graduated with Distinction (Degree of Honor).*

Research interests

Bioinformatics: Motifs (Localization and discovery, sequential and structural), Genome Scale (big data) sequence and structural analysis, RNA pairwise structure alignment, Genome Rearrangement, Sorting by Reversals, RNA-RNA secondary structure interaction, microarray gene expression, Next Generation Sequencing, Structural Variation.

Data Mining: classification, feature selection, frequent pattern mining, Hidden Markov Models, sequence alignment, structure alignment, text mining.

Pattern Recognition: Syntactic Pattern Recognition (PR), Approximate String Matching (ASM), Efficient Sequence Alignment techniques for dictionary-based models, Exact String Matching.

Artificial Intelligence: Search techniques, Blind Search, Heuristic Search, Branch and Bound techniques.

Advanced Data Structures: The design and analysis of many advanced data structures, Designing and implementing algorithms that use these advanced data-structures. Most data structures used or updated are used for storing strings and sequences. Design an efficient data structure for storing and retrieving Genome data. Self-adjusting data structures.

Information Retrieval: The design and analysis of information retrieval algorithms, Self-adjusting search techniques. Update these algorithms to be used efficiently for strings.

Machine learning and Machine Translation: Phrase-based statistical machine translation, decoding techniques, filtering techniques for models, learning techniques for optimizing weights in log-linear models..

Database: Relational and Object Oriented Databases.

Work experience

Assistant Professor

http://fac.ksu.edu.sa/ghbadr/home
Computer Science Department
9/2011-current King Saud University

Coordinator of the Bioinformatics Research Group (BioInG)

http://bioinformaticksurg.blogspot.com/
2/2013-current King Saud University
College of computers and information systems (CCIS)
Riyadh, KSA

Postdoctoral Fellow

10/2007-3/2011 University of Ottawa
School of Information Technology and Engineering (SITE)
Laboratory for Innovation in Bioinformatics (Leader: David Sankoff)
Ottawa, ON, Canada

Research Associate

9/2006-9/2007 National Research Council of Canada (NRC)
Interactive Language Technologies, Gatineau, QC, Canada

Postdoctoral Fellow

5/2006– 9/2006 Carleton University
School of Computer Sciences (SCS), Ottawa, ON, Canada

Research Assistant

2001 – 4/2006 Carleton University
School of Computer Sciences (SCS), Ottawa, ON, Canada

Research Assistant

1997 – 2001 Alexandria University
Computer Science Department, Alexandria, Egypt

Research Assistant

1996 – 1997 Alexandria University, Faculty of Engineering
Computer Science Department, Alexandria, Egypt

Quest lecturer

Winter 2011 University of Ottawa
Department of Math and Statistics, Ottawa, ON, Canada

Quest lecturer

Fall 2009/2010 University of Ottawa
School of Information Technology and Engineering (SITE), Ottawa, ON, Canada

Instructor

Winter 2007 Carleton University
School of Computer Sciences (SCS), Ottawa, ON, Canada

Instructor

Summer 2006 Carleton University
School of Computer Sciences (SCS), Ottawa, ON, Canada

Teaching Assistant

1/2001– 4/2006 Carleton University
School of Computer Sciences (SCS), Ottawa, ON

Personal	Date of birth: 14th October, 1973 Citizen: Canadian Citizen. Marital Status: Married with three children. Languages: English (fluent), Arabic(fluent), French (basic-intermediate proficiency)

Scholarships, Funds and awards

Small Research Group from RC center at KSU
9/2014-9/2015 RC center at KSU,
Amount: ~ 70,000 RS

NPST Research Grant – (Project No. 12-BIO2605-02)
9/2012-9/2014 The National Plan for Science and Technology,
Amount: ~ 1,200,000 RS ~ 315,000 $

Research Group Fund
2/2013 Bioinformatics Research Group (BioInG), King Saud University, Riyadh, KSA. Amount: 20,000 RS
http://bioinformaticksurg.blogspot.com/

Best poster Award
5/2012 The International Symposium on Bioinformatics Research and Applications (*ISBRA*), Dallas, USA

NSERC PDF Award
9/2007-3/2011 Ottawa University Amount: 40,000 / year
Laboratory for Innovation in Bioinformatics

Senate Medal for Outstanding Research Achievements
3/2006 Carleton University

Wilkes Best Paper Awards
3/2006 The Computer Journal, British Computer Society

Technology Related Grant
2/2006 C.I.T.O. Amount: 45,000

Research Assistant Scholarship
9/2002 – 4/2006 Carleton University Amount: 6,000 / year

University's Honor List
9/1996 – 6/1997 Alexandria University

Distinct High School Student
9/1991 - 6/1996 Alexandria University

Research Contributions

Bioinformatics and data mining

I am actively working in that field since 2007, some of my selected contributions are:

- Working on devising new techniques for Structural Variations for single paired reads in Next Generation Sequencing Data.
- I am actively working now in projects for microarray data analysis using bio-inspired algorithms for gen selection, when applied to support vector machine for classification.
- Devised a new algorithm for pairwise alignment for RNA secondary structures, when a component-based representation is used. The algorithm is efficient and the preliminary results prove high accuracy. This is the first attempt to solve this problem fully and efficiently, where algorithms in literature are only partial structural alignment approaches. This should have a good impact in comparing predicted structure to real structures in a fast and accurate way. *In progress*.
- Devised a new algorithm for sequential motif discovery when an HMM is used to represent motifs. The algorithm showed good results when applied on simulated data. *In progress*.
- Devised a new algorithm for the reversal median problem using Genetic Algorithms. The algorithm is efficient and the results prove high accuracy. A manuscript is under preparation for submission.
- Devised a new algorithm for sequential motif discovery using a modified Apriori data mining approach when sequences are stored in an efficient data structure, Tries, that allows us to simultaneously look for similar sequences. The work was accepted and published in ISBRA'12 and an extended work is accepted for publication in IJDMB'13.
- Devised a new algorithm for Motif discovery for RNA secondary structures when represented as a dot bracket notation, incremental structural motif discovery. Accepted for publication in ISBRA'13. A complete survey with extensive comparison for different previous approaches is accepted for publication in BMC'13. A lot of extensions are in progress and a manuscript is under preparation to be submitted for a journal publication in JBCB. (Collaborators: Dr. Marcel Turcotte)
- Devised, implemented, and tested a new representation for RNA secondary structures (interacting and non-interacting), A component-based representation along with the search algorithm. The algorithm showed a high performance when compared to the available backtracking approach. An efficient data structure was used to store sequences. The performance of the algorithms is illustrated with an application for locating RNA elements in a Diplonemid genome and is published in ISBRA'11. The work has been extended in KSU to an extended component-based representation and Published in ISBRA'13. A tool is also built and tested. A manuscript is under preparation and to be submitted for publication. (Collaborators: Dr. Marcel Turcotte)
- Devised, implemented, and tested a new framework for solving the all-sorting sequences by reversal (ASSR) problem. The new framework

enhanced all current algorithms for solving the problem including the best-known algorithm. Good results were recently obtained and published in RECOMB 2010. The work has been recently extended and published in Journal of algorithms for Molecular Biology, in 2012 by Sagot and Baudet University of Villeurbanne, France, so that to include partial solutions. (Collaborators: Dr. David Sankoff and Dr. Krister M. Swenson)

- Devised, implemented, and tested an average O(n^2) algorithm or counting all sorting reversals for a given permutation. The new algorithm beats the best known O(n^3) algorithm by Seipel. Theoretical analysis was recently obtained and published in WABI 2010. (Collaborators: Dr. David Sankoff and Dr. Krister M. Swenson)

Artificial Intelligence

- Have devised extremely efficient AI-enhanced trie-based syntactic pattern recognition schemes. (*IEEE T:SMC* 2006, *Proc. ICAPR* 2005). *These results were presented as a plenary talk* at the conference in Bath, UK. The results are also patent protected.
- Most work done below involves efficient AI techniques, but I will classify them according to the application in which they are used.

Sequence-Based Syntactic PR

- Applied the new AI Heuristic Search scheme I devised (see above) for sequence-based Syntactic PR. This work is also included in the patent protection.
- Devised an efficient *look-ahead* trie-based syntactic pattern recognition scheme. (*PAA* 2006, *Proc. CORES* 2005).
- Devised an optimized trie-based dynamic programming technique for edit-distance computations.
- Devised a fast trie-based syntactic pattern recognition scheme of strings, using the ``Linked List of Prefixes'' data structure. (*PAA* 2006, *Proc. S+SSPR* 2004).

Machine Learning and Machine Translation

- Devised a new technique for learning weights for log-linear model in Phrase-based Machine Translation. Results showed improvements in score.
- Devised a new algorithms and techniques for calculating the edit distances over the lattice and over the n-best lists. This technique can be applied in many applications, including the decoding and rescoring processes in automatic machine translation.
- Devised a new variant for beam search, namely dynamic beam that is expected to be very helpful in speeding up the search process for a huge search space. This technique can be applied in many applications, including the decoding process in automatic machine translation.
- Designed more efficient way of applying Coverage Pruning in machine translation. Expect to have better evaluation scores.
- Devised, implemented and tested in a group based work, new filtering techniques for phrase-based machine translation models. These

techniques saved up to 30% memory requirement and increased the quality of translation results by giving the system the ability to load bigger models. The work had a high impact on the system performance and accuracy, where my name has been included as one of the co-inventors for their patent application. This work has been accepted and published in Computer Recognition Systems 2007.

- Designed, implemented and tested a speed up for a decoder used in machine translation when used in repeated processes (as in training the weights for the log-linear functions) by caching intermediate results. This technique has a speed up of almost 30% and great saving in memory requirements.

Data structures

- Designed and implemented a new data structure (namely, Dual-tries) that is very efficient for storing and retrieving Genomic data.
- Devised various self-adjusting techniques for the Ternary Search Tries (*The Comp. Journal* 2005). This paper was cited as being Most Meritorious, and was a winner of *one* of the **Wilkes Best Paper Awards** in 2006, from the journal The Computer Journal. The Computer Journal is the flagship journal of the **British Computer Society**..
- Devised new self-adjusting schemes for the newly invented variant of the trie structure, namely self-adjusting dual-tries.
- Devised a new self-adjusting scheme, the Scapegoat-Splay tree.

Information Retrieval

- Designed and implemented a lot of data structures that can help in speeding up dictionary and text-based information retrieval (see above). Most techniques I devised are very helpful in IR field.
- Designed and implemented an encyclopedia on the Egyptian Pharos, using text, audio and video components.
- Designed and implemented a visualization project for the Sphinx.

Databases

- Designed, implemented, and tested a full database for Canadian universities Using Oracle and SQL for queries implementation.
- Led a team in designing and developing an object-oriented database management system (ALEX). I was responsible for designing and implementing the memory management part of the system. This led to the design of a new data structure called the H-tree, useful for storing the objects and classes of the system.

Copy-Detection

- Developed a more accurate copy detection scheme between digital documents. This was done by developing a new data structure for storing the documents and a new algorithm to detect the similarity between the documents using the designed data structures. Currently enhancing the technique by adding semantic copy detection and also applying it for Arabic documents.

Publications

Patents

[1] **Ghada Badr** and B. John Oommen. Search-Enhanced Trie-Based Syntactic Pattern Recognition of Sequences. *Canada and U.S. U.S Patent No. 7,689,588 issued on March 30, 2010. Canadian Patent No. 2,608,772 issued on March 22nd, 2013.*

Journals Published or accepted for publication

[2] **Ghada Badr**, Isra Al-Turaiki, Marcel Turcotte, and Hassan Mathkour IncMD: Incremental Trie-Based Structural Motif Discovery Algorithm. *Journal of Bioinformatics and Computational Biology*, Vol. 12, No. 5 2014. (29 pages) (ISI: IF - 0.931)

[3] Hala Alshamlan, **Ghada Badr**, and Yousef Alohali,” The Performance of Bio-Inspired Evolutionary Gene Selection Methods for Cancer Classification Using Microarrays Gene Expression Profile”, International Journal of Bioscience, Biochemistry and Bioinformatics (IJBBB), Vol. 4, No. 3, May 2014

[4] Isra Al-Turaiki, **Ghada Badr**, and Hassan Mathkour. TrieAMD: A Scalable and efficient Apriori Motif Discovery Approach. *Accepted for publication in International Journal of Data Mining in Bioinformatics* 2014. (ISI: IF - 0.681)

[5] Al-Jaloud, Ebtisam S., Haifaa A. Al-Aqel, and Ghada H. Badr. "Comparative Performance Evaluation of Heap-Sort and Quick-Sort Algorithms." International Journal of Computing Academic Research (IJCAR), 3 (2): 39-57, April 2014.

[6] **Ghada Badr**, Isra Al-Turaiki, and Hassan Mathkour. Classification and Assessment Tools for Structural Motif Discovery Algorithms. *Classification and assessment tools for structural motif discovery algorithms. BMC Bioinformatics, 14(Suppl 9):S4, 2013.* (ISI: IF – 2.67)

[7] **Ghada Badr,** Krister M. Swenson, David Sankoff. Listing all Parsimonious Reversal Sequences: New Algorithms and Perspectives. *Journal of Computational Biology,* 18(9): 1201–1210, 2011. (ISI: IF - 1.546). http://recombcg.uottawa.ca/Papers/JournalPublication/2011_Badr_Swenson.pdf

[8] Krister Swenson, **Ghada Badr**, and David Sankoff. Listing All Sorting Reversals in Quadratic Time. *Algorithms for Molecular Biology*, 6(11), 2011. (ISI: IF – 1.4). http://www.biomedcentral.com/content/pdf/1748-7188-6-11.pdf

[9] **Ghada Badr** and B. John Oommen. A Novel Look-Ahead Optimization Strategy for Trie-Based Approximate String Matching, *Pattern Analysis and Applications Journal (PAA)*, 9(2-3):77-187, October 2006 (ISI: IF - 0.739). http://www.springerlink.com/content/502r6pg2jv175221/

[10] B. John Oommen and **Ghada Badr**. Breadth-First Search Strategies for Trie-Based Syntactic Pattern Recognition. *Pattern Analysis and Applications Journal (PAA) Journal. 10(1):1-13, February,* 2007. (ISI: IF - 0.739). http://www.springerlink.com/content/j686387133hj1364/

[11]G**hada Badr** and B. John Oommen. On Optimizing Syntactic Pattern Recognition using Tries and AI-based Heuristic Search Strategies. To appear in *IEEE Transactions on Systems, Man and Cybernetics*, Part B. 36(3):611 – 622, June 2006. (ISI: IF - 2.123).

[12]**Ghada Badr** and B. John Oommen. Self-Adjusting of Ternary Search Tries Using Conditional Rotations and Randomized Heuristics. The *Computer Journal*. 48(2): 200-219, March 2005. Cited as being **Most Meritorious**, was a **winner** of *one* of the **Wilkes Best Paper Awards** in 2006. The Computer Journal is the flagship journal of the **British Computer Society**. (ISI: IF - 0.943)

Journals
In preparation
or submission

[13] Hala Alshamlan, **Ghada Badr**, and Yousef Alohali, An Artificial Bee Colony Algorithm for Microarray Gene Selection and Cancer Classification, in submission for publication in *BioData Mining*.

[14]**Ghada Badr** and Hessah Arraqibah. Extended Component-Based Motif Localization for Interacting RNA Structures." In submission for publication in *Algorithms in Molecular Biology*.

[15]Alraqibah, Hessah, and **Ghada Badr**. TrieSIML: Trie-Based Structural Interacting Motif Localization Tool. In preparation to be submitted for publication in *Bioinformatics-Application Notes*.

Conferences
(referred
contributions)

[16]**Ghada Badr** and Arwa Al-Turki. CompPSA: A Component-Based Pairwise RNA Secondary Structure Alignment Algorithm. Poster presentation RECOMB-CG, New york, US, 2014.

[17] **Ghada Badr** and Haifaa Alaqel. Genome Rearrangement for RNA Secondary Structure Using a Component-Based Representation: An Initial Framework. Poster presentation RECOMB-CG, New york, US, 2014.

[18]Najlaa AlHuwaishel, Maram AlAlwan and **Ghada Badr**. Finding the Frequent patterns in a Database: A Study on the Apriori Algorithm. Position Paper in the 6th International Conference on Knowledge Discovery and Information retrieval. Rome, Italy, 21st-24th October, 2014.

[19]Hala Alshamlan, **Ghada Badr**, and Yousef Alohali, The Performance of Bio-Inspired Evolutionary Gene Selection Methods for Cancer Classification Using Microarrays Gene Expression Profile, *The International Conference on Communication Systems and Computational intelligence (CCSCI 2014)*, Toronto, Canada, Jan, 2014.

[20]Hala Alshamlan, **Ghada Badr**, and Yousef Alohali, A Comparative Study of Cancer Classification Methods Using Microarray Gene Expression Profile, The First International Conference on Advanced Data and Information Engineering (DaEng-2013), Kuala Lumpor, Dec. 2013, Malaysia, Lecture Notes in Electrical Engineering (LNEE) 285, Springer Verlag. 2014.

[21]Isra Al-Turaiki, **Ghada Badr**, Marcel Turcotte, and Hassan Mathkour. Incremental Structural Motif Discovery, (short abstract) *poster presentation in 9th International Symposium on Bioinformatics Research and Applications*

ISBRA'13, Charlotte, USA, May 20-22, 2013.

[22] Hessah Arraqibah and **Ghada Badr**. Extended Component-Based Motif Localization for Interacting RNA Structures. (short abstract) *poster presentation in ISBRA'13,* Charlotte, US, 2013..

[23] Hala Alshamlan, **Ghada Badr**, and Yousef Alohali. A Study for Effective Binary Classification Approaches for Cancer Microarray Gene Expression Profile. (short abstract) *poster presentation in ISBRA'13,* Charlotte, US, 2013.

[24] Hala Alshamlan, **Ghada Badr**, and Yousef Alohali. A Study of Cancer Microarray Gene Expression Profile: Objectives and Approaches. *World congress in Engineering, the 2013 International Conference of Systems Biology and Bioengineering (ICSBB'13),* London, U.K., 3-5 July, 2013.

[25] Aljohara Alhassan, Ashwaq Alfawwaz, Ebtesam Alghamdi, Rand Albrahim, Rawabi Alsharif, **Ghada Badr**. TrieAMDT: A Data Mining Tool for Sequential Motif Discovery*. Poster presentation and is a winner of the annual Research Poster Competition for undergraduate at* King Abdullah University of Science and Technology (KAUST), January 2013.

[26] Isra Al-Turaiki, **Ghada Badr** and Hassan Mathkour, Structural Motif Discovery Algorithms: Classification and Benchmarks. (short abstract) *poster presentation at the 8th International Symposium on Bioinformatics Research and Applications ISBRA 2012,* Dallas, TX, USA. May 21-23, 2012. *(**Winner of the best poster award**, 2nd position)*

[27] Isra Al-Turaiki, **Ghada Badr**, and Hassan Mathkour. Trie-based Apriori Motif Discovery Approach*. Bioinformatics Research and Application (ISBRA'12, Dallas, US), Lecture Notes in Computer Science* 7292, Springer Berlin Heidelberg, p:1-12, January 2012.

[28] **Ghada Badr,** Marcel Turcotte. Component-Based Matching for Multiple interacting RNA Sequences. *Bioinformatics Research and Applications* (J. Chen, J. Wang, and A. Zelikovsky, eds.), vol. 6674 of Lecture Notes in Computer Science, pp. 73–86, Springer Berlin / Heidelberg, 2011. 10.1007/978-3-642-21260-4 11.

[29] **Ghada Badr,** Krister M. Swenson, David Sankoff. Listing all Parsimonious Reversal Sequences: New Algorithms and Perspectives. *RECOMB CG, Lecture Notes in Computer Science* 6398, Ottawa, Canada, October 2010.

[30] **Ghada Badr,** Krister M. Swenson, David Sankoff. Listing All Sorting Sequences by Reversals Problem Revisited with a New Framework. WABI Posters, Liverpool, England, September 2010.

[31] Krister M. Swenson, **Ghada Badr**, and David Sankoff. Listing All Sorting Reversals in Quadratic Time*. WABI, Lecture Notes in Computer Science* 6293, Liverpool, England, September 2010.

[32] **Ghada Badr,** Eric Joanis, Samuel Larkin, and Roland Kuhn. "Manageable Phrase-based Statistical Machine Translation Models". *Computer Recognition Systems 2.* 437-444, Poland, Warsaw, October 2007.

[33] **Ghada Badr**. Optimized Similarity Measure Over Trie. *MLDM Posters,* 236-250, German, July 2007.

[34] **Ghada Badr** and B. John Oommen. Enhancing Trie-Based Syntactic Pattern Recognition Using AI Heuristic Search Strategies. Invited paper in *ICAPR*, Bath, United Kingdom 22-25 August, 2005. This was a *plenary* talk of the conference.

[35] **Ghada Badr** and B. John Oommen. A Look-Ahead Branch and Bound Pruning Scheme for Trie-Based Approximate String Matching. Proceedings of the 4th *International Conference on Computer Recognition Systems CORES'05.* Rydzyna Castle (Poland), 87-94, May 2005.

[36] **Ghada Badr** and B. John Oommen. On Using Conditional Rotations and Randomized Heuristics for Self-Organizing Ternary Search Tries. Proceedings of *ACMSE'2005, the 2005 ACM South Eastern Conference*. Kennesaw, Georgia, 1:109—115, March 2005.

[37] John Oommen, **Ghada Badr**: Dictionary-Based Syntactic Pattern Recognition Using Tries. Proceedings of *SSSPR-2004, the 2004 International Symposium on Structural, Syntactic and Statistical Pattern Recognition,* Lisbon, Portugal, 251-259, 2004.

[38] Mohamed Ismail, Amani Saad, and **Ghada Badr**. An accurate copy Detection server for digital documents, *Alexandria Engineering Journal*, 40(4): 505-519. July 2001.

[39] Amani Saad and **Ghada Badr**. The Alex Object Manager**.** Proceedings of *the 2nd IEEE Symposium on Computers and Communications (ISCC '97)*, page 200-204, July 1997.

Technical Reports/ Contributions

[40] **Badr, G.,** Joanis, E., Larkin, S. R. Kuhn, R. Manageable Phrase-based Statistical Machine Translation Models – with Pseudo-code and Proofs. *Technical Report, NRCC#* 49304, NPArC# 9183591. Interactive Language Technologies Group, NRC Institute for Information Technology, National Research Council Canada, 2007.

[41] **Ghada Badr**, "*The Alex Object oriented database management system* ", B.Sc. Final Project, Alexandria University, Department of Computer Science and automatic control, Alexandria University, Alexandria, Egypt, June 1996.

Thesis

[42] **G. Badr.** *Tries in Data Retrieval and Syntactic Pattern Recognition*. Ph.D. Thesis, School of Computer Science, Carleton University, Ottawa, Canada, April 2006. Winner of **Senate Medal** for outstanding research achievements.

[43] M. Ismail, A. Saad, and **G. Badr**. *An Accurate Copy Detection Server for Digital Documents*, Master's thesis, Department of Computer Science and automatic control, Alexandria University, Alexandria, Egypt, March 2001.

Supervision

Ph.D

Isra Al-Turaiki "Computational Motif discovery Approaches", Ph.D program, CS Department, KSU.
(Fall 2011- Fall 2013) (graduated)
(***Winner of the 3rd position for an outstanding research achievement award, over all science specialities, KSU***)

Hala Al-Shamlan "A Novel Cancer Classification Model for Microarray Gene Expression Profile", Ph.D program, CS Department, KSU.
(2012 – expected to graduate Fall 2014)

Eman Alzayed "Next generation structural variation and copy number variation analysis", Ph.D program, CS Department, KSU.
(2013 – expected to graduate Winter 2016)

Master Thesis

Lena Al-Mutair "Component-Based RNA Secondary Structure for Phylogeny construction. (Co-supervisor: Dr. Manar Hosny). Expected Fall 2014.

Master projects

Haifa'a Al-Aqel "Genome Rearrangement for RNA Secondary Structures" Winter/Fall 2014

Maram Al-ALwan "Copy detection between Arabic Documents" Winter/Fall 2014

Arwa M Alturki "Component Based Pair-wise RNA Secondary Structure Alignment Algorithm". Regular Master program, CS Department, KSU. (Co-supervisor Dr Hafida Benhidour) (Winter 2013-Fall 2013)

Al-Hanouf Al-Amr "The Median problem: A hybrid approach with application in bioinformatics". Parallel Master program, CS Department, KSU. (Co-supervisor: Dr Manar Hosny) (Fall 2012-Winter 2013)

Aseel Al-Hadlaq "Trie-based Sequential Motif Localization (TrieSeqML) Tool". Parallel Master program, CS Department, KSU. (Co-supervisor Dr Areej El-Wabil) (Winter 2012-Winter 2013)

Hessah Arraqibah "Trie-based Structural Interacting Motif Localization (TrieSIML)Tool ". Regular Master program, CS Department, KSU. (Winter 2012-Fall 2012)

Undergraduate projects

Aljohara Alhassan, Ashwaq Alfawwaz, Ebtesam Alghamdi, Rand Albrahim, Rawabi Alsharif "TrieAMDT: An Apriori Motif Discovery Tool". IT Department, KSU. (Fall 2012-Winter 2013)

Hanan and Sarah "A Web-Based Tool for the Visualization of RNA Secondary Structures". IT Department, KSU. (Winter 2012-Fall 2012)

Examination Committees

Involved in many Examination committees for Master projects (Project 1 and project 2). Computer Science Department. King Saud University. (2012-now).

Committees

Head of the CCIS lab Committee (convener) (Female Section) (Fall 2013/winter 2014/Fall 2014)

Head of Quality unit for CS Female section (convener) (Winter 2012/Fall 2012/Winter 2013/fall 2013/Winter 2014/Fall 2014)

Equipment committee CS. (member) (Fall 2013/winter 2014)

Travelling abroad advising committee. (convener) (Winter 2012) (member) (Fall 2012/Winter 2013/Fall 1013/Winter 2014)

Student advisor for master program CS. (Winter 2012/Fall 2012/Winter 2013/fall 2013/winter 2014)

Recruiting committee CS. (member) (Winter 2012/ Fall 2012/Winter 2013)

Master committee CS. (member) (Fall 2012/Winter 2013)

Curriculum committee CS. (member) (Winter 2012/Fall 2013/Fall 2014)

Bioinformatics master program committee. (convener) (Winter 2012) (designed and proposed a master program in the CS department in Bioinformatics, pending university approval)

Workshops

Organization

Workshops organized at King Saud University:

Ist Bioinformatics Scientific meeting, May 4th, BioSM-2014 http://bioinformaticksurg.blogspot.com/p/bio-sm.html

Choose-Post-Win poster competition May 4th, 2014.

Introduction to R, March 3rd, 2014

Introduction to Linux, February 23rd, 2014.

Bioinformatics Awareness day, February 15th, 2014.

Genome Rearrangements (Part 1), November 2nd, 2013.

“Bioinformatics Meeting Day: Next Generation Bioinformatics - Technology and Tools”. May 11th, 2013.

“I can! Apply my Computing Background in Bioinformatics”. April 6th, 2013.

“Hands on Experience in Bioinformatics”. (a) Databases in Bioinformatics, February 2^{3rd} and (b) Similarity Tools: BLAST, March ^{2nd}, 2013.

Seminars/ workshop participation

“Data Mining in Medical applications”“ invited speaker at the Medical diagnosis using ultrafast lasers workshop, Senatssitzungssaal, Leopold-Franzens Innsbruck University, Innsbruck, Austria, September 18th, 2014.

“BioInG in minutes”: Speaker at research day 2014, KSU, KSA.

“Neat-MLD project”: Speaker at BioSM-2014, KSU, KSA.

Poster presentation at ISBRA’13 conference, Charlotte, US, May 2013.

Algorithms in Bioinformatics and Molecular Biology. Seminar in the BioInG group at KSU. February 16th, 2013.

From DNA to protein. Seminar in the BioInG group at KSU. Dec 8th, 2012.

Introduction to Bioinformatics and all about BioInG. Seminar in the BioInG group at KSU. Nov 24th, 2012

Beyond a course syllabus: A broad minded students with different learning abilities. Best Teaching Practices in CCIS, Vice Dean of Student Affairs, King Saud University, March 21st, 2012.

"I Can!" Workshop on Mobile and Sensor Technologies for People with Special Needs, chaired by Dr. Eiman Kanjo, KSU. Oct. 8th, 2012. Facilitator for group: Portable technology for People with Hearing difficulties or Visually impaired.

Papers’ Presentations for ISBRA 2012 conference, Dallas, US, and ISBRA 2011 conference, Chungsha, China.

Seminar presentation at the University Health Network and the Cancer Research Institute (MARS), Toronto, Canada, 2011.

Paper presentation for RECOMB CG 2010 conference in Ottawa, Canada.

Paper and poster presentation for WABI 2010 conference in Liverpool, England 2010.

Paper presentation for SSPR’07 Structural and Syntactic Pattern Recognition conference Warsaw, Poland, October, 2007.

Seminar presentation at the Interactive Language Technologies (October 2006), NRC, to illustrate various ideas and proposals.

Seminar presentation at Toronto University (Cellular and Molecular Canter) (June 2006).

Seminar presentation at McGill University. (January 2006).

Presented various seminars at Carleton University, Ottawa

Active Participant in *Lets Talk Science*. (See below)

Teaching Record

Teaching

I

KSU (Fall 2011-now):

- Teaching undergraduate courses in the department of Information Technology, College of Computer and Information Sciences, King Saud University, Riyadh, Sauc Arabia:

- IT 434: Data warehouse and Data Mining (two sections, 70 students). (Fall 2011/Winter 2012)
  Contributions:
    - 3 groups were accepted for conference Poster presentations for URC workshop in Zayid University (April 18-19, 2012).
    - 3 groups participated with a poster presentation for the IT project fair (May 9th, 2012).
    - 1 group were accepted for conference Poster presentations for URC workshop in Zayid University (May 1-2, 2013).
- CSC 111: Teaching one section (20 students in IT department) and course coordinator for 4 sections (Math, Information Systems, and Information Technology departments) (7 TAs and Instructors with ~ 80 students) (Winter 2013) – Developed and updated the course with new slides, activities, markir schema, material, and teaching methodologies.
- CSC 111: teaching one section of first CS undergraduate students (23 student Couse coordinator for 9 sections including CS, IT and Math (Fall 2014).
- Contributions: Developed an e-course using LMS and Articulate Engage to be used for teaching the course for all sections over all departments at KSU.

-Teaching postgraduate courses in the department of Computer Science, College of Computer and Information Sciences, King Saud University, Riyadh, Saudi Arabia:

- CSC 696: Independent Study 1, Algorithms in Bioinformatics (Pathway analysis). (Fall 2013).
- CSC 687: Data Warehouse and Data Mining Systems (PhD students) 4 studer (Fall 2014).
- CSC 588: Data Warehouse and Data Mining systems (Master students). Teac it for regular program (10 students) (Winter 2012/Fall 2014)
- CSC 512: Algorithm Analysis and Design (Master students). Teach the course for both regular (10 students) and parallel program (10 students). (Winter 2012/Fall 2012/Winter 2013/Fall 2013/Winter 2014)
- CSC 696: Independent Study 1, Algorithms in Bioinformatics. (Fall 2013).
- CSC 697: Independent Study 2, Structural Variation in Next Generation Sequences (Winter 2014).

Canada (2001-2011):

- Instructor for two lectures in genome Rearrangement. This teaching was mentored an evaluated as a part of my course for Practicum in University teaching, (Ottawa University) (Fall 2010/Winter 2011).
- Instructor for graduate/undergraduate courses in Algorithm Analysis and Design (Carleton University) (Fall 2006).
- Instructor for a third year course in Algorithm Analysis and Design

(Carleton University) (Summer 2006).

- Teaching assistant for ten terms for discrete structures. (Carleton University) (2001-2006).

Egypt (1996-2000):

- Instructor for an introductory course in programming (Alexandria University) (Fall 1996).
- Instructor for an introductory course in Computer Science (EGC High School for an American Diploma) (Winter 1997).

Personal Development

Courses

Courses in Ottawa University arranged by the Center of University Teaching:

- ESG 5300 **Theory and Practice of Undergraduate Teaching**

Research and theory on undergraduate teaching. Development of practical teaching skills for university teaching (Winter 2010).
Ottawa University, Center for University Teaching

- ESG 8300 - **Practicum in University Teaching**

Workshops in university teaching practice, mentored practice teaching, teaching dossier preparation (60 to 66 hours) (2010/2011).

Ottawa University, Center for University Teaching

Courses in King Saud University

- *EMC Data Science and Big Data Analytics course 2014: An ‘open’ course to unleash the power of Big Data*

23 March 2014, 5 Days, 09:00 - 17:00, EMC Computer Systems, Saudi Arabia Branch King Fahad Road, Al-Mas Center, Riyadh

Workshops

Workshops attended in Ottawa University arranged by the Center of University Teaching:

- “Clickers in the Classroom” (9/18/2009)
- “Seven Principles for Good Practice in Undergraduate Education” (9/30/2009)
- “Active Learning and Large Classes: Is It Possible?” (10/6/2009)
- “How Acting Can Inform Teaching” (10/14/2009)
- “Beyond Content Learning: Creating and Maintaining an Effective Learning Environment” (10/21/2009)
- “Improving Learning Through Effective Feedback” (10/27/2009)
- “Effective Presentations” (11/18/2009)
- “The Essential Role of Planning in Teaching” (11/24/2009)
- “The First Class: The Key to Success!” (12/8/2009)
- “Different Roles, Same Goal: How to Build a Strong Teaching Team (1/19/2010)
- “How to Motivate Your Students: Useful Tools and Strategies” (2/25/2010)

- “Best Practices in Integrating Online Components into your Teaching” (3/3/2010)
- “Design and Delivery of a Video-Conference Course” (3/23/2010)

Workshops attended in King Saud University:

- “LMS Blackboard principles” (April, 2013)
- “Uploading your e-course in LMS” (April, 2013)
- “Virtual classrooms” (April, 2013)
- “Designing a course using storyboarding” (March, 2013)
- “Authoring Tools for e-course design” (March, 2013)
- “Social network” (2012)
- “Strategic planning” (2012)
- “Introduction to professional certificate in education and university teaching. Professional development department, King Saud University. February 11th, 2012.

Professional memberships/ social service

Established the Bioinformatics Research Group (BioInG) in Fall 2012 http://bioinformaticksurg.blogspot.com/ at King Saud University and attracted many students and colleagues to work in the filed and established collaborations with other research institutes through well funded projects. Coordinator for the group (2012-now).

Article Reviews for Current Bioinformatics 2104, Journal of Bio-informatics and Computational Biology 2013, Bioinformatics 2013, URC 2013, ISBRA 2012, SIAM Journal 2011 and the Journal of Bio-informatics and Computational Biology 2011, SSPR 2006.

Member of *ACM*, *IEEE*, Computer Society.

Volunteer in a well-known program called *Lets Talk Science* (LTS) that helps to increase the quality of science education in public/high schools.

Judge for two science fair competitions for local High Schools (February 2006).