

# Heba Saadeh, B.Sc., M.Sc., Ph.D. UKHEA Associate Fellow

Assistant Professor in Bioinformatics and Epigenetics, Computer Science Dep., KASIT, The University of Jordan  
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## Education

**2015-16 Teaching Associate Programme**, University of Cambridge, Cambridge, UK

**2010-14 Ph.D. in Bioinformatics**, King's College London, London, UK

**2007-09: M.Sc., First class with honours degree in Computer Science/Bioinformatics**, University of Jordan, Amman, Jordan

**2003-07: B.Sc., First class with honours degree in Computer Science**, University of Jordan, Amman, Jordan

**2002-03: The General Secondary Education Certificate Examination**, Scientific Track, Sukaina Bint Al-Hussein Secondary School, Amman, Jordan

## Research Experience

**Sep.2016 – Present: Assistant Professor in Bioinformatics and Epigenetics**

Computer Science Dept. King Abdullah II School for Information Technology, The University of Jordan, Amman, Jordan.

**Nov. 2013-Aug. 2016: Postdoctoral Research Scientist/Research Associate in Bioinformatics and Epigenetics**

Epigenetics Programme, The Babraham Institute, Cambridge, United Kingdom  
Bioinformatics Group, The Babraham Institute, Cambridge, United Kingdom

**Oct. 2010 – Sep. 2013: Graduate Student in Bioinformatics (PhD Student)**

Department of Medical & Molecular Genetics, King's College London, London, United Kingdom

**Thesis title:** *The role of DNA sequence signals in the epigenetic reprogramming of CpG islands during oogenesis and early embryogenesis.*

**Sep. 2007 – July. 2009: Graduate Student/Research Assistant (MSc. Student)**

Department of Computer Science, University of Jordan, Amman, Jordan

**Thesis title:** *Incorporating Experimental Conditions' Knowledge into the Process of Estimating Missing Values in DNA Microarray Gene Expression Levels.*

## Teaching Experience

**Sep.2016 – Present: Assistant Professor in Bioinformatics and Epigenetics**, Computer Science Dept. King Abdullah II School for Information Technology, The University of Jordan. Teaching several courses, like: C++, Data Structures, Programming Methodologies, Algorithms, Computer Graphics, Pattern Recognition, Machine Learning.

**Dec. 2016 – present: Associate Fellow of UK HEA “Higher Education Academy”,**

**Jan.2016–March.2016 “Lent Term”:** Tutor, The Homerton College, University of Cambridge, Algorithms course.

**Oct.2015–Dec.2015 / Oct.2014–Dec.2014 “Michaelmas Terms”:** Tutor, the Computer Laboratory, University of Cambridge, Bioinformatics course.

**Oct.2015–Dec.2015 / Oct.2014–Dec.2014 “Michaelmas Terms”:** Tutor, The Homerton College, University of Cambridge, Object Oriented Programming course.

**Sep. 2009 – Sep.2010: Lecturer and course coordinator, Computer Science department, University of Jordan,** Discrete Mathematics, C++, Advanced C++, Numerical Analysis courses.

**Sep. 2007 – Sep.2009: Teaching Assistant, Computer Science department, University of Jordan**

## Awards, Scholarships and Grants

**Oct. 2017 – Oct. 2020: Scientific Research Fund**, University of Jordan, Jordan

**2016-17: Global Challenges Research Fund**, Initial grant with the Babraham Institute, Cambridge, UK

**2012-13: King's Continuation Scholarship (KCS)**, King's College London, UK

**2011: KCL School of Medicine Travel Bursary**, King's College London, UK

**2010-13: KCL Graduate School Ph.D. Studentship**, King's College London, UK

**2007-09: JU M.Sc. Studentship** for the first of the class students, University of Jordan, Jordan

**2007: JU award** for the first of the class student in computer science dep., University of Jordan, Jordan

**2004-05, 2005-06, 2006-07: Ministry of Higher Education and Scientific Research Grant** for the first of the class student in computer science dep. / University of Jordan, Jordan

## Extra Curriculum Activities

**March 2018 – Present: Chair of the ACM Student Chapter**, at University of Jordan, Jordan

**Feb. 2018 – Present: Director of the ICPC JUCPC Programming Contest**, at University of Jordan, Jordan

**Nov. 2016 Jan. 2019: Chair of the IEEE Computer Society**, at University of Jordan, Jordan

## Research Interests and Skills

**Interests:** Epigenetics, Genomics, Bioinformatics, Data Science, Machine and Deep Learning

**Skills:**

- Computer science research; particularly: algorithms, machine/deep learning, pattern recognition, computational intelligence.
- Genomics and Epigenetics, particularly: Chromatin remodeling and DNA methylation and its relationship with transcription, epigenetic reprogramming and histone modifications.
- Large scale biological data analysis and integration; Next generation sequencing (RNA-seq, ChIP-seq, RRBS-seq, BS-seq, PBAT) and Gene expression microarrays (Affymetrix, Illumina, Agilent).
- Good knowledge in bash, R, Perl, C++ and MATLAB.

## Selected Academic Representations

**-Nov. 2018:** Paper at the 1st International Conference on Cancer Care Informatics (CCI) *“Towards a Process-Based and Service-Oriented Intelligent Framework for Ig/TCR Clonality Testing in Suspected Lymphoproliferative Neoplasms”*

**-Nov. 2015:** Poster at the 5<sup>th</sup> wellcome Trust Epigenomics of Common Diseases Conference *“Genome-wide DNA methylation analysis on isolated NPY- and POMC neurons from adult mouse hypothalamus”*

**-Nov. 2014:** Talk at the Gurdon Institute Postdoc Symposium: Building an Organism Symposium (GIPA) *“Single-cell genome-wide bisulphite sequencing method for assessing the DNA methylation of rare cells and their methylation heterogeneity”*

**-Oct. 2014:** Poster at the 4<sup>th</sup> wellcome Trust Epigenomics of Common Diseases Conference and at the 14<sup>th</sup> wellcome Trust Genome Informatics Conference (Sep.2014) *“Single-Cell Genome-Wide Bisulphite Sequencing Method for Assessing the DNA Methylation of Rare Cells and their Methylation Heterogeneity”*

**-Nov. 2013:** Talk at the 3<sup>rd</sup> wellcome Trust Epigenomics of Common Diseases Conference *“The role of DNA sequence signals in the epigenetic reprogramming of CpG islands during oogenesis and early embryogenesis”*

**-Nov. 2011-12-13:** Talks at the Genetics Society's 22<sup>nd</sup>/23<sup>rd</sup>/24<sup>th</sup> Mammalian Genetics and Development Workshop

**-Sep. 2011:** Poster at the 1<sup>st</sup> wellcome Trust Epigenomics of Common Diseases Conference *“A Search for Imprinting-specific Sequence Motifs in Maternal Imprinting Control Regions”*

**-July, 2011:** Talk at the Epigenesis Student/Postdoc Workshop, *“DNA sequence features involved in establishing and maintaining genomic imprinting in mouse oocytes”*

## Selected Training Courses / Workshops

- Oct. 2012:** “Quantitative data analysis”, NHS-BRC training course, BRC, Guy's Hospital, London, UK
- Nov. 2012:** “Correlation and Linear Regression”, NHS-BRC training course, BRC, Guy's Hospital, London, UK
- Jan. 2014:** “Introduction to R”, The Babraham Institute, Cambridge, UK
- Feb. 2014:** “Advanced R”, The Babraham Institute, Cambridge, UK
- Mar. 2014:** “Creating Scientific Figures”, The Babraham Institute, Cambridge, UK
- Mar. 2014:** “Methylation Data Analysis”, The Babraham Institute, Cambridge, UK
- May 2014:** “RNA-Seq Data Analysis”, The Babraham Institute, Cambridge, UK
- Jun. 2014:** “An Introduction to Solving Biological Problems with Python”, University of Cambridge, Cambridge, UK
- Jun. 2014:** “Introduction to Next Generation Sequencing”, University of Cambridge, Cambridge, UK
- Jun. 2014:** “An Introduction to Solving Biological Problems with R”, University of Cambridge, Cambridge, UK
- May 2015:** “Genome Annotation with Artemis”, University of Cambridge, Cambridge, UK
- Jun. 2015:** “Introduction to genome variation analysis using NGS”, University of Cambridge, Cambridge, UK

## Selected Publications

Amante SM, Montibus B, Cowley M, Barkas N, Setiadi J, [Saadeh H](#), Giemza J, Castillo SC, Fleischanderl K, Schulz R, Oakey RJ, "Transcription of intragenic CpG islands influences spatiotemporal host gene pre-mRNA processing". *Nucleic Acids Res.* pp. 1-11, July 2020.

[Saadeh H](#), Al Fayez RQ, Elshqeir B, "Application of K-Means Clustering to Identify Similar Gene Expression Patterns during Erythroid Development". *International Journal of Machine Learning and Computing* Vol. 10, Issue 3, pp. 452-457, May 2020.

AL-Eitana L, [Saadeh H](#), Alnaamneh A, Darabseh S, AL-Sarhan N, Alzihlif M, Hakooz N, Ivanova E, Kelsey G, Dajanih R, "The genetic landscape of Arab Population, Chechens and Circassians subpopulations from Jordan through HV1 and HV2 regions of mtDNA". *Gene*, Vol. 729, Issue 1, pp. 1-7, March 2020.

Abu-Salih B, Chan KY, Al-Kadi O, Al-Tawil M, Wongthongtham P, Issa T, [Saadeh H](#), Al-Hassan M, Bremie B, Albahlal A, "Time-aware domain-based social influence prediction". *Journal of Big Data*, Vol. 7, Issue 1, pp. 1-37, Feb. 2020.

Al Fayez RQ, [Saadeh H](#), Saleh S, Abu Alrub B, "Building Knowledge Graphs based on Binary Associations between Research Topics using Apriori". *International Journal of Computer Applications*. Vol. 177, Issue 20, pp. 25-31, 2019.

[Saadeh H](#), Abdullah N, Erashdi M, Sughayer M, Al-Kadi O, "Histopathologist-level quantification of Ki-67 immunoreactivity in gastroenteropancreatic neuroendocrine tumors using semiautomated method". *J. Med. Imag.* Vol. 7, Issue 1, pp. 012704-1-18, 2019.

Gharabat M, [Saadeh H](#), Al-Fayez R.Q. "Discovering the Applicability of Classification Algorithms with Arabic Poetry". In the preceding of the IEEE Jordan International Joint Conference on Electrical Engineering and Information Technology (JEEIT), April 2019.

Abdullah N, Odeh Y, [Saadeh H](#), Iqniebi A, Faleh Albo Hassan A, Nasser W, Odeh M, Tbakhi A. "Towards a Process-Based and Service-Oriented Intelligent Framework for Ig/TCR Clonality Testing in Suspected Lymphoproliferative Neoplasms". In the preceding of the 1st International Conference on Cancer Care Informatics (CCI), Nov. 2018.

Hiary H, [Saadeh H](#), Saadeh M, Yaqub M. "Flower classification using deep convolutional neural networks". *IET Computer Vision*. Vol. 12, Issue 6, pp. 855 – 862, Sep. 2018.

Aljarah I, Al-Zoubi A'M, Faris H, Hassonah MA, Mirjalili S, [Saadeh H](#). "Simultaneous feature selection and support vector machine optimization using the grasshopper optimization algorithm". *Cognitive Computation*, Vol. 10, Issue 3, pp. 478–495, June 2018.

Gahurova L, Tomizawa SI, Smallwood SA, Stewart-Morgan KR, [Saadeh H](#), Kim J, Andrews SR, Chen T, Kelsey G. "Transcription and chromatin determinants of de novo DNA methylation timing in oocytes". *Epigenetics & Chromatin*. Vol. 10, Issue 25, pp. 1-19, May 2017.

Canovas S, Ivanova E, Romar R, García-Martínez S, Soriano-Úbeda C, García-Vázquez FA, **Saadeh H**, Andrews S, Kelsey G, Coy P. “*DNA methylation and gene expression changes derived from assisted reproductive technologies can be decreased by reproductive fluids*”. *Elife*. Vol. 1, Issue 6, pp. 1-24, Feb. 2017.

Courtney W Hanna, Maria S Peñaherrera, **Heba Saadeh**, Simon Andrews, Deborah E McFadden, Gavin Kelsey, Wendy P Robinson. “*Pervasive polymorphic imprinted methylation in the human placenta*”. *Genome Res*. 2016 Jun; 26(6):756-67

Kathleen R Stewart, Lenka Veselovska, Jeesun Kim, Jiahao Huang, **Heba Saadeh**, Shin-ichi Tomizawa, Sébastien A Smallwood, Taiping Chen, Gavin Kelsey. “*Dynamic Changes in Histone Modifications Precede de novo DNA Methylation in Oocytes*”. *Genes Dev*. 2015 Dec 1; 29(23):2449-62.

Veselovska L\*, Smallwood SA\*, **Saadeh H**, Stewart KR, Krueger F, Maupetit-Méhouas S, Arnaud P, Tomizawa S-I, Andrews S, Kelsey G. “*Deep sequencing and de novo assembly of the mouse oocyte transcriptome define the contribution of transcription to the DNA methylation landscape*”. *Genome Biology*, Aug. 2015, 16(209):1-17 (\* These authors contributed equally).

**Heba Saadeh** and Reiner Schulz. “*Protection of CpG islands against de novo DNA methylation during oogenesis is associated with the recognition site of E2f1 and E2f2*”. *Epigenetics & Chromatin*. Vol. 7, Issue 26, pp. 1-15, Oct. 2014.

Sébastien A Smallwood#, Heather J Lee#, Christof Angermueller, Felix Krueger, **Heba Saadeh**, Julian Peat, Simon R Andrews, Oliver Stegle, Wolf Reik\*, and Gavin Kelsey\*. “*Single-cell genome-wide bisulfite sequencing for assessing epigenetic heterogeneity*”. *Nature Methods*, Vol. 11, Issue 8, pp. 817–820, Aug. 2014 (\*,# these authors contributed equally)

Charlotte Proudnon, Rachel Duffie, Sophie Ajjan, Michael Cowley, Julian Iranzo, Guillermo Carbajosa, **Heba Saadeh**, Michelle L. Holland, Rebecca J. Oakey, Vardhman K. Rakyan, Reiner Schulz, and Deborah Bourc’his. “*Protection against De Novo Methylation Is Instrumental in Maintaining Parent-of-Origin Methylation Inherited from the Gametes*”. *Molecular Cell*, Vol. 47, Issue 6, pp. 909-920, Sep. 2012

Claudia A Montiel-Equihua, Lin Zhang, Sean Knight, **Heba Saadeh**, Simone Scholz, Marlene Carmo, Maria E Alonso-Ferrero, Michael P Blundell, Aiste Monkeviciute, Reiner Schulz, Mary Collins, Yasuhiro Takeuchi, Manfred Schmidt, Lynette Fairbanks, Michael Antoniou, Adrian J Thrasher and H Bobby Gaspar. “*The beta-globin locus control region in combination with the EF1alpha short promoter allows enhanced lentiviral vector-mediated erythroid gene expression with conserved multilineage activity*”. *Molecular Therapy*, Vol. 20, Issue 7, pp. 1400-1409, Feb. 2012