

AHMAD VAEZ, MD, PHD

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AHMAD VAEZ was born on 11 May 1973 in Isfahan, a beautiful historic city in the center of Iran. After graduating with a medical degree (MD) from the Isfahan University of Medical Sciences in 1999, he worked as a medical doctor, then as a lecturer, then as a researcher, then as a research officer, and then as a chief research officer. He also served as an officer of the regional bioethics research committee, Isfahan University of Medical Sciences, Iran. In September 2010, he started his PhD research program at the Unit of Genetic Epidemiology and Bioinformatics, Department of Epidemiology, University of Groningen, the Netherlands, under the supervision of Prof. Harold Snieder.

AHMAD has been interested in using bioinformatics-based approaches to unravel the multifaceted genomic mechanisms controlling complex traits or diseases. During his PhD trajectory, he tried to provide a comprehensive walk-through of the classic steps of genomic association mapping using bioinformatics tools and approaches. Also, in parallel to the successful completion of his PhD trajectory, he has been leading one of the largest international consortia of meta-analysis of Genome-Wide Association studies (GWAS), including more than 200,000 samples from more than 70 centers, designed to explore genomic determinants of C-reactive protein (CRP). This mega-scale project has successfully identified a large number of novel genomic markers underlying serum levels of CRP.

EDUCATION

- PhD in Bioinformatics, University of Groningen, Groningen, the Netherlands (2010-2015)

- Summer Institute in Statistical Genetics, University of Washington, Seattle, Washington, United States (2011)
- MD in Medicine: Faculty of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran (1991 - 1999)

WORK EXPERIENCE

- Department Head and Assistant Professor of Bioinformatics, Department of bioinformatics, school of advanced technologies in medicine, Isfahan University of Medical Sciences, Isfahan, Iran (2017-present)
- Assistant Professor of Bioinformatics, Department of genetics and molecular biology, school of medicine, Isfahan University of Medical Sciences, Isfahan, Iran (2016-present)
- Postdoctoral Researcher, University of Groningen, Groningen, the Netherlands (2015-present)
- PhD Fellow, University of Groningen, Groningen, the Netherlands (2010-2015)
- Chief Research Officer, Head of Department of Research Officers, Isfahan University of Medical Sciences, Isfahan, Iran (2008-2010)
- Co-head of the Research Administration Office, Isfahan University of Medical Sciences, Isfahan, Iran (2008-2010)
- Research Officer, Isfahan University of Medical Sciences, Isfahan, Iran (2004-2008)
- General Physician, Isfahan University of Medical Sciences, Isfahan, Iran (1999-2004)

TEACHING EXPERIENCE

- Course titled “Advances in Genetic Epidemiological Research and Data Analysis”, University of Groningen (2013-present)
- Course titled “Genetic Epidemiology”, Isfahan University of Medical Sciences, Isfahan, Iran (2017-present)
- Course titled “Epidemiology”, Isfahan University of Medical Sciences, Isfahan, Iran (2016-present)

- Course titled “Population Genetics”, Isfahan University of Medical Sciences, Isfahan, Iran (2016)
- Course titled “Personalized Medicine”, Isfahan University of Medical Sciences, Isfahan, Iran (2016)
- Course titled “Bioinformatics”, Isfahan University of Medical Sciences, Isfahan, Iran (2016)

PHD THESIS

- Bioinformatics of Genomic Association Mapping. ISBN: 978-90-367-8202-9 (print). ISBN: 978-90-367-8201-2 (e-book). Sep 2015. University of Groningen, the Netherlands.

LANGUAGES

- Persian (Farsi): native language
- English: holding a score of 6.5 in the IELTS exam (and 7.5 in its writing module)

ACHIEVEMENTS AND AWARDS

- Awarded a scholarship from the University of Washington, Seattle, Washington, United States, to attend Summer Institute in Statistical Genetics; 2011
- Accepted for a scholarship position overseas, available for a PhD program in Bioinformatics, by a highly competitive entrance exam which was held by the ministry of health and medical education, Tehran, Iran; 2008
- Accepted for a job position as a research officer in the Vice Chancellery for Research, Isfahan University of Medical Sciences, Isfahan, Iran, by a competitive entrance exam; 2006

SOFTWARE PACKAGES

- lodGWAS: Genome-Wide Association Analysis of a Biomarker Accounting for Limit of Detection (2015). Publicly available at: <https://cran.r-project.org/web/packages/lodGWAS>.

- QCGWAS: Quality Control of Genome Wide Association Study results (2012). Publicly available at: <https://cran.r-project.org/web/packages/QCGWAS>.

PUBLICATIONS

- Amare AT*, **VAEZ A***, Hsu Y-H, Direk N, Kamali Z, Howard DM, McIntosh AM, Tiemeier H, Bültmann U, Snieder H, Hartman CA. Bivariate genome-wide association analyses of the broad depression phenotype combined with major depressive disorder, bipolar disorder or schizophrenia reveal eight novel genetic loci for depression. *Mol Psychiatry*. 2019;
- Thio CHL, Reznichenko A, van der Most PJ, Kamali Z, **VAEZ A**, Smit JH, Penninx BWJH, Haller T, Mihailov E, Metspalu A, Damman J, de Borst MH, van der Harst P, Verweij N, Navis GJ, Gansevoort RT, Nolte IM, Snieder H, Cohort Study group L. Genome-Wide Association Scan of Serum Urea in European Populations Identifies Two Novel Loci. *Am J Nephrol*. 2019;49:193–202.
- Ligthart S, **VAEZ A**, Vösa U, Stathopoulou MG, de Vries PS, Prins BP, Van der Most PJ, Tanaka T, Naderi E, Rose LM, Wu Y, Karlsson R, Barbalic M, Lin H, Pool R, Zhu G, Macé A, Sidore C, Trompet S, Mangino M, Sabater-Lleal M, Kemp JP, Abbasi A, Kacprowski T, Verweij N, Smith AV, Huang T, Marzi C, Feitosa MF, Lohman KK, Kleber ME, Milaneschi Y, Mueller C, Huq M, Vlachopoulou E, Lyytikäinen L-P, Oldmeadow C, Deelen J, Perola M, Zhao JH, Feenstra B, Alizadeh BZ, Boezen HM, Franke L, van der Harst P, Navis G, Rots M, Snieder H, Swertz M, Wolffenbuttel BHR, Wijmenga C, Amini M, Benjamin E, Chasman DI, Dehghan A, Ahluwalia TS, Meigs J, Tracy R, Alizadeh BZ, Ligthart S, Bis J, Eiriksdottir G, Pankratz N, Gross M, Rainer A, Snieder H, Wilson JG, Psaty BM, Dupuis J, Prins B, Vaso U, Stathopoulou M, Franke L, Lehtimäki T, Koenig W, Jamshidi Y, Siest S, Abbasi A, Uitterlinden AG, Abdollahi M, Schnabel R, Schick UM, Nolte IM, Kraja A, Hsu Y-H, Tylee DS, Zwicker A, Uher R, Davey-Smith G, Morrison AC, Hicks A, van Duijn CM, Ward-Caviness C, Boerwinkle E, Rotter J, Rice K, Lange L, Perola M, de Geus E, Morris AP, Makela KM, Stacey D, Eriksson J, Frayling TM, Slagboom EP, Lahti J, Schraut KE, Fornage M, Suktitipat B, Chen W-M, Li X, Nutile T, Malerba G, Luan J, Bak T, Schork N, Del Greco M. F, Thiering E, Mahajan A, Marioni RE, Mihailov E, Eriksson J, Ozel AB, Zhang W, Nethander M, Cheng Y-C, Aslibekyan S, Ang W, Gandin I, Yengo L, Portas L, Kooperberg C, Hofer E, Rajan KB, Schurmann C, den Hollander W, Ahluwalia TS, Zhao J, Draisma HHM, Ford I, Timpson N, Teumer A, Huang H, Wahl S, Liu Y, Huang J, Uh H-W, Geller F, Joshi PK, Yanek LR, Trabetti E, Lehne B, Vozzi D, Verbanck M, Biino G, Saba Y, Meulenbelt I, O'Connell JR, Laakso M, Giulianini F, Magnusson PKE, Ballantyne CM, Hottenga JJ, Montgomery GW, Rivadineira F, Ruedi R, Steri M, Herzig K-H, Stott DJ, Menni C, Frånberg M, St. Pourcain B, Felix SB, Pers TH, Bakker SJL, Kraft P, Peters A, Vaidya D, Delgado G, Smit JH, Großmann V, Sinisalo J, Seppälä I, Williams SR, Holliday EG, Moed M, Langenberg C, Rääkkönen K, Ding J, Campbell H, Sale MM, Chen Y-DI, James AL, Ruggiero D, Soranzo N, Hartman CA, Smith EN,

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* Equal contribution

H-INDEX

Citation analysis in Web of Science shows a steep increase in the number of citations in the last few years. **Ahmad's h-index is 12** and **14** according to Web of Science and Google Scholar, respectively (June 1, 2019).

ORAL PRESENTATIONS

- Genomic architecture of complex diseases. Seminar on Systems Medicine and Bioinformatics, Tabriz University of Medical Sciences, Tabriz, Iran, May 2019. Invited keynote speaker.
- Bioinformatics of genomic association mapping: an A-to-Z walk-through. The 3rd Iranian Conference on Systems Biology, Tarbiat Modares University, Tehran, Iran, February 2018. Invited keynote speaker.
- Bioinformatics of genomic association mapping: an A-to-Z walk-through. Molecular medicine congress, Isfahan University of Medical Sciences, Isfahan, Iran, December 2016. Invited keynote speaker.
- lodGWAS: a software package for genome-wide association analysis of biomarkers accounting for Limit of Detection (LOD). University Medical Center Groningen, the Netherlands, June 2015. Invited speaker.
- An in silico post-GWAS analysis of C-reactive protein loci reveals an important role for interferons. Dept. Epidemiology, Erasmus University Medical Center, Rotterdam, the Netherlands, February 2015. Invited speaker.
- To understand the genetics of C-reactive protein (CRP): a mega meta-GWAS project. Dept. Epidemiology, Erasmus University Medical Center, Rotterdam, the Netherlands, February 2015. Invited speaker.

- An in silico post-GWAS analysis of C-reactive protein loci: a pipeline of sequential bioinformatics-based approaches. International genetics congress, Tehran, Iran, May 2014. Invited keynote speaker.
- A pipeline of sequential bioinformatics-based approaches for post-GWAS analysis of GWAS findings. University Medical Center Groningen, the Netherlands, January 2014. Invited speaker.
- Understanding the genetics of inflammatory markers: a meta-GWAS approach. CHARGE Investigator meeting, Reykjavik, Iceland, May 2012. Invited speaker.

POSTER PRESENTATIONS

- lodGWAS: a software package for genome-wide association analysis of biomarkers with a limit of detection (Abstract 4). CHARGE Investigator Meeting, Rotterdam, the Netherlands, April 2018.
- An in silico post-GWAS analysis of C-reactive protein loci: a pipeline of sequential bioinformatics-based approaches (Abstract 1541T). Annual Meeting of the American Society of Human Genetics (ASHG), San Diego, CA, October 2014.
- An in silico post-GWAS analysis of C-reactive protein loci reveals an important role for interferons. Netherlands Bioinformatics Conference (NBIC), Lunteren, the Netherlands, April 2014.
- A bioinformatics-based in silico post-GWAS analysis of CRP variants. CHARGE Investigator Meeting, Los Angeles, CA, January 2014.
- QCGWAS: a flexible R package for automated quality control of genome-wide association results files. Congress of the Netherlands Consortium for Healthy Ageing (NCHA), the Hague, the Netherlands, December 2013.
- A bioinformatics-based in silico post-GWAS analysis of CRP variants. Annual conference of the Netherlands epidemiology society (WEON), Utrecht, the Netherlands, June 2013.

TRAINING COURSES

- Project Management for Scientific Research (Groningen, the Netherlands)
- Publishing in English (Groningen, the Netherlands)

- English presentation course (Groningen, the Netherlands)
- The Basic Course in Human Genetics (Rotterdam, the Netherlands)
- Classical Methods in Data Analysis (Utrecht, the Netherlands)
- The SNP Course (Rotterdam, the Netherlands)
- The Basic Course on 'R' (Rotterdam, the Netherlands)
- From DNA variations to phenotype (Rotterdam, the Netherlands)
- Genetic Epidemiological Research and Data Analysis (Groningen, the Netherlands)
- Molecular Genetics and Genomics (Seattle, WA, USA)
- Regression and Analysis of Variance (Seattle, WA, USA)
- Population Genetics (Seattle, WA, USA)
- Human Association Mapping (Seattle, WA, USA)
- Human Quantitative Genetics (Seattle, WA, USA)
- GWAS Data Cleaning (Seattle, WA, USA)
- Introduction to Clinical and Public Health Genomics (Rotterdam, the Netherlands)
- Mixed Effects Models for Longitudinal and Cross Sectional Data (Groningen, the Netherlands)
- Bioinformatics Course: Browsing Genes and Genomes with Ensembl (Rotterdam, the Netherlands)
- Bioinformatics Course: High-throughput next-generation biology (Groningen, the Netherlands)
- Bioinformatics Course: NCBI & other open source software (Rotterdam, the Netherlands)