

## **Ahmad Vaez, MD, PhD**

(Updated on February 4, 2017)

### **Email:**

a.vaez@umcg.nl

ahmad.vaez@gmail.com

**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. He then participated in a highly competitive written exam in 2008 held by the Ministry of Health and Medical Education of Iran through which, he was awarded a scholarship abroad. 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 (manuscript in preparation).

## 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)

## 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-present)
- Course titled “Personalized Medicine”, Isfahan University of Medical Sciences, Isfahan, Iran (2016-present)
- Course titled “Bioinformatics”, Isfahan University of Medical Sciences, Isfahan, Iran (2016-present)
- Course titled: “Health and Demography”, Shahin Shahr Health Services Center (2000-2003)

## **Work Experience**

- 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 (2015-2016)
- 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)

## **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

## **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.

## **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

- **Vaez A**, van der Most PJ, Prins BP, Snieder H, van den Heuvel E, Alizadeh BZ, Nolte IM. lodGWAS: A software package for genome-wide association analysis of biomarkers with a limit of detection. *Bioinformatics*. 2016;32(10):1552-4.
- Barban N, Jansen R, de Vlaming R, **Vaez A**, Mandemakers JJ, Tropf FC, Shen X, Wilson JF, Chasman DI, Nolte IM, Tragante V, van der Laan SW, Perry JR, Kong A; BIOS Consortium, Ahluwalia TS, Albrecht E, Yerges-Armstrong L, Atzmon G, Auro K, Ayers K, Bakshi A, Ben-Avraham D, Berger K, Bergman A, Bertram L, Bielak LF, Bjornsdottir G, Bonder MJ, Broer L, Bui M, Barbieri C, Cavadino A, Chavarro JE, Turman C, Concas MP, Cordell HJ, Davies G, Eibich P, Eriksson N, Esko T, Eriksson J, Falahi F, Felix JF, Fontana MA, Franke L, Gandin I, Gaskins AJ, Gieger C, Gunderson EP, Guo X, Hayward C, He C, Hofer E, Huang H, Joshi PK, Kanoni S, Karlsson R, Kiechl S, Kifley A, Kluttig A, Kraft P, Lagou V, Lecoeur C, Lahti J, Li-Gao R, Lind PA, Liu T, Makalic E, Mamasoula C, Matteson L, Mbarek H, McArdle PF, McMahon G, Meddens SF, Mihailov E, Miller M, Missmer SA, Monnereau C, van der Most PJ, Myhre R, Nalls MA, Nutile T, Kalafati IP, Porcu E, Prokopenko I, Rajan KB, Rich-Edwards J, Rietveld CA, Robino A, Rose LM, Rueedi R, Ryan KA, Saba Y, Schmidt D, Smith JA, Stolk L, Streeten E, Tönjes A, Thorleifsson G, Ulivi S, Wedenoja J, Wellmann J, Willeit P, Yao J, Yengo L, Zhao JH, Zhao W, Zhernakova DV, Amin N, Andrews H, Balkau B, Barzilai N, Bergmann S, Biino G, Bisgaard H, Bönnelykke K, Boomsma DI, Buring JE, Campbell H, Cappellani S, Ciullo M, Cox SR, Cucca F, Toniolo D, Davey-Smith G, Deary IJ, Dedoussis G, Deloukas P, van Duijn CM, de Geus EJ, Eriksson JG, Evans DA, Faul JD, Sala CF, Froguel P, Gasparini P, Grotto G, Grabe HJ, Greiser KH, Groenen PJ, de Haan HG, Haerting J, Harris TB, Heath AC, Heikkilä K, Hofman A, Homuth G, Holliday EG, Hopper J, Hyppönen E, Jacobsson B, Jaddoe VW, Johannesson M, Jugessur A, Kähönen M, Kajantie E, Kardia SL, Keavney B, Kolcic I, Koponen P, Kovacs P, Kronenberg F, Kutalik Z, La Bianca M, Lachance G, Iacono WG, Lai S, Lehtimäki T, Liewald DC; LifeLines Cohort Study, Lindgren CM, Liu Y, Luben R, Lucht M, Luoto R, Magnus P, Magnusson PK, Martin NG, McGue M, McQuillan R, Medland SE, Meisinger C, Mellström D, Metspalu A, Traglia M, Milani L, Mitchell P, Montgomery GW, Mook-Kanamori D, de Mutsert R, Nohr EA, Ohlsson C, Olsen J, Ong

KK, Paternoster L, Pattie A, Penninx BW, Perola M, Peyser PA, Pirastu M, Polasek O, Power C, Kaprio J, Raffel LJ, Rääkkönen K, Raitakari O, Ridker PM, Ring SM, Roll K, Rudan I, Ruggiero D, Rujescu D, Salomaa V, Schlessinger D, Schmidt H, Schmidt R, Schupf N, Smit J, Sorice R, Spector TD, Starr JM, Stöckl D, Strauch K, Stumvoll M, Swertz MA, Thorsteinsdottir U, Thurik AR, Timpson NJ, Tung JY, Uitterlinden AG, Vaccargiu S, Viikari J, Vitart V, Völzke H, Vollenweider P, Vuckovic D, Waage J, Wagner GG, Wang JJ, Wareham NJ, Weir DR, Willemsen G, Willeit J, Wright AF, Zondervan KT, Stefansson K, Krueger RF, Lee JJ, Benjamin DJ, Cesarini D, Koellinger PD, den Hoed M, Snieder H, Mills MC. Genome-wide analysis identifies 12 loci influencing human reproductive behavior. *Nat Genet.* 2016;48(12):1462-1472.

- Prins BP, Abbasi A\*, Wong A\*, **Vaez A\***, Nolte I, Franceschini N, Stuart PE, Gutierrez Achury J, Mistry V, Bradfield JP, Valdes AM, Bras J, Shatunov A; PAGE Consortium; International Stroke Genetics Consortium; Systemic Sclerosis consortium; Treat OA consortium; DIAGRAM Consortium; CARDIoGRAMplusC4D Consortium; ALS consortium; International Parkinson's Disease Genomics Consortium; Autism Spectrum Disorder Working Group of the Psychiatric Genomics Consortium; CKDGen consortium; GERAD1 Consortium; International Consortium for Blood Pressure; Schizophrenia Working Group of the Psychiatric Genomics Consortium; Inflammation Working Group of the CHARGE Consortium, Lu C, Han B, Raychaudhuri S, Bevan S, Mayes MD, Tsoi LC, Evangelou E, Nair RP, Grant SF, Polychronakos C, Radstake TR, van Heel DA, Dunstan ML, Wood NW, Al-Chalabi A, Dehghan A, Hakonarson H, Markus HS, Elder JT, Knight J, Arking DE, Spector TD, Koeleman BP, van Duijn CM, Martin J, Morris AP, Weersma RK, Wijmenga C, Munroe PB, Perry JR, Pouget JG, Jamshidi Y, Snieder H, Alizadeh BZ. Investigating the Causal Relationship of C-Reactive Protein with 32 Complex Somatic and Psychiatric Outcomes: A Large-Scale Cross-Consortium Mendelian Randomization Study. *PLoS Med.* 2016;13(6):e1001976.
- Joubert BR, Felix JF, Yousefi P, Bakulski KM, Just AC, Breton C, Reese S, Markunas C, Richmond RC, Xu C-J, Küpers L, Oh S, Hoyo C, Gruziova O, Söderhäll C, Salas LA, Baiz N, Zhang H, Lepeule J, Ruiz C, Ligthart S, Wang T,

Taylor J, Duijts L, Sharp GC, Jankipersadsing SA, Nilsen RM, **Vaez A**, Fallin MD, Hu D, Litonjua AA, Fuemmeler BF, Huen K, Kere J, Inger Kull, Munthe-Kaas MC, Gehring U, Bustamante M, Saurel-Coubizolles MJ, Quraishi BM, Ren J, Tost J, Gonzalez JR, Peters MJ, Håberg SE, Xu Z, van Meurs JB, Gaunt TR, Kerkhof M, Corpeleijn E, Feinberg AP, Eng C, Baccarelli AA, Neelon SEB, Bradman A, Merid SK, Bergström A, Herceg Z, Hernandez-Vargas H, Brunekreef B, Pinart M, Heude B, Ewart S, Yao J, Lemonnier L, Franco OH, Wu MC, Hofman A, McArdle W, Van der Vlies P, Falahi F, Gillman MW, Barcellos LF, Kumar A, Wickman M, Guerra S, Charles M, Holloway J, Auffray C, Tiemeier HW, Davey Smith G, Postma D, Hivert M, Eskenazi B, Vrijheid M, Arshad H, Antó JM, Dehghan A, Karmaus W, Annesi-Maesano I, Sunyer J, Ghantous A, Pershagen G, Holland N, Murphy S, DeMeo DL, Burchard EG, Ladd-Acosta C, Snieder H, Nystad W, Koppelman GH, Relton CL, Jaddoe VWV, Wilcox A, Melén E, London SJ. DNA methylation in newborns and maternal smoking in pregnancy: Genome-wide consortium meta-analysis. *Am J Hum Genet.* 2016;98:680-696.

- Ehret GB, Ferreira T, Chasman DI, Jackson AU, Schmidt EM, Johnson T, Thorleifsson G, Luan J, Donnelly LA, Kanoni S, Petersen AK, Pihur V, Strawbridge RJ, Shungin D, Hughes MF, Meirelles O, Kaakinen M, Bouatia-Naji N, Kristiansson K, Shah S, Kleber ME, Guo X, Lyytikäinen LP, Fava C, Eriksson N, Nolte IM, Magnusson PK, Salfati EL, Rallidis LS, Theusch E, Smith AJ, Folkersen L, Witkowska K, Pers TH, Joehanes R, Kim SK, Lataniotis L, Jansen R, Johnson AD, Warren H, Kim YJ, Zhao W, Wu Y, Tayo BO, Bochud M; CHARGE-EchoGen Consortium; CHARGE-HF Consortium; Wellcome Trust Case Control Consortium, Absher D, Adair LS, Amin N, Arking DE, Axelsson T, Baldassarre D, Balkau B, Bandinelli S, Barnes MR, Barroso I, Bevan S, Bis JC, Bjornsdottir G, Boehnke M, Boerwinkle E, Bonnycastle LL, Boomsma DI, Bornstein SR, Brown MJ, Burnier M, Cabrera CP, Chambers JC, Chang IS, Cheng CY, Chines PS, Chung RH, Collins FS, Connell JM, Döring A, Dallongeville J, Danesh J, de Faire U, Delgado G, Dominiczak AF, Doney AS, Drenos F, Edkins S, Eicher JD, Elosua R, Enroth S, Erdmann J, Eriksson P, Esko T, Evangelou E, Evans A, Fall T, Farrall M, Felix JF, Ferrières J, Ferrucci L, Fornage M, Forrester T, Franceschini N, Franco OH, Franco-Cereceda A, Fraser RM, Ganesh SK, Gao H, Gertow K, Gianfagna F, Gigante B, Giulianini F, Goel A, Goodall AH, Goodarzi MO, Gorski M, Gräßler J, Groves CJ, Gudnason V, Gyllensten U,

Hallmans G, Hartikainen AL, Hassinen M, Havulinna AS, Hayward C, Hercberg S, Herzig KH, Hicks AA, Hingorani AD, Hirschhorn JN, Hofman A, Holmen J, Holmen OL, Hottenga JJ, Howard P, Hsiung CA, Hunt SC, Ikram MA, Illig T, Iribarren C, Jensen RA, Kähönen M, Kang HM, Kathiresan S, Keating BJ, Khaw KT, Kim YK, Kim E, Kivimäki M, Klopp N, Kolovou G, Komulainen P, Kooner JS, Kosova G, Krauss RM, Kuh D, Kutalik Z, Kuusisto J, Kvaløy K, Lakka TA, Lee NR, Lee IT, Lee WJ, Levy D, Li X, Liang KW, Lin H, Lin L, Lindström J, Lobbens S, Männistö S, Müller G, Müller-Nurasyid M, Mach F, Markus HS, Marouli E, McCarthy MI, McKenzie CA, Meneton P, Menni C, Metspalu A, Mijatovic V, Moilanen L, Montasser ME, Morris AD, Morrison AC, Mulas A, Nagaraja R, Narisu N, Nikus K, O'Donnell CJ, O'Reilly PF, Ong KK, Paccaud F, Palmer CD, Parsa A, Pedersen NL, Penninx BW, Perola M, Peters A, Poulter N, Pramstaller PP, Psaty BM, Quertermous T, Rao DC, Rasheed A, Rayner NW, Renström F, Rettig R, Rice KM, Roberts R, Rose LM, Rossouw J, Samani NJ, Sanna S, Saramies J, Schunkert H, Sebert S, Sheu WH, Shin YA, Sim X, Smit JH, Smith AV, Sosa MX, Spector TD, Stančáková A, Stanton AV, Stirrups KE, Stringham HM, Sundstrom J, Swift AJ, Syvänen AC, Tai ES, Tanaka T, Tarasov KV, Teumer A, Thorsteinsdóttir U, Tobin MD, Tremoli E, Uitterlinden AG, Uusitupa M, **Vaez A**, Vaidya D, van Duijn CM, van Iperen EP, Vasan RS, Verwoert GC, Virtamo J, Vitart V, Voight BF, Vollenweider P, Wagner A, Wain LV, Wareham NJ, Watkins H, Weder AB, Westra HJ, Wilks R, Wilsgaard T, Wilson JF, Wong TY, Yang TP, Yao J, Yengo L, Zhang W, Zhao JH, Zhu X, Bovet P, Cooper RS, Mohlke KL, Saleheen D, Lee JY, Elliott P, Gierman HJ, Willer CJ, Franke L, Hovingh GK, Taylor KD, Dedoussis G, Sever P, Wong A, Lind L, Assimes TL, Njølstad I, Schwarz PE, Langenberg C, Snieder H, Caulfield MJ, Melander O, Laakso M, Saltevo J, Rauramaa R, Tuomilehto J, Ingelsson E, Lehtimäki T, Hveem K, Palmas W, März W, Kumari M, Salomaa V, Chen YD, Rotter JI, Froguel P, Jarvelin MR, Lakatta EG, Kuulasmaa K, Franks PW, Hamsten A, Wichmann HE, Palmer CN, Stefansson K, Ridker PM, Loos RJ, Chakravarti A, Deloukas P, Morris AP, Newton-Cheh C, Munroe PB. The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nat Genet. 2016;48(10):1171-84.

- Ligthart S, **Vaez A**, Hsu YH, Inflammation Working Group of the CHARGE Consortium, PMI-WG-XCP, LifeLines Cohort Study, Stolk R, Uitterlinden



AG, Hofman A, Alizadeh BZ, Franco OH, Dehghan A. Bivariate genome-wide association study identifies novel pleiotropic loci for lipids and inflammation. BMC Genomics. 2016;17(1):443.

- **Vaez A**, Jansen R\*, Prins BP\*, Hottenga J-J, Geus EJC de, Boomsma DI, Penninx BWJH, Nolte IM, Snieder H\*, Alizadeh BZ\*. In silico post genome-wide association studies analysis of C-reactive protein loci suggests an important role for interferons. Circ Cardiovasc Genet. 2015;8:487–497.
- Küpers LK, Xu X, Jankipersadsing SA, **Vaez A**, Gemert S la B, Scholtens S, Nolte IM, Richmond RC, Relton CL, Felix JF, Duijts L, van Meurs JB, Tiemeier H, Jaddoe VW, Wang X, Corpeleijn E, Snieder H. DNA methylation mediates the effect of maternal smoking during pregnancy on birthweight of the offspring. Int J Epidemiol. 2015;44:dyv048.
- van der Most PJ, **Vaez A**, Prins BP, Munoz ML, Snieder H, Alizadeh BZ, Nolte IM. QCGWAS: A flexible R package for automated quality control of genome-wide association results. Bioinformatics. 2014;30:1185–1186.
- Kraja AT, Chasman DI, North KE, Reiner AP, Yanek LR, Kilpelainen TO, Smith JA, Dehghan A, Dupuis J, Johnson AD, Feitosa MF, Tekola-Ayele F, Chu AY, Nolte IM, Dastani Z, Morris A, Pendergrass SA, Sun YV, Ritchie MD, **Vaez A**, Lin H, Ligthart S, Marullo L, Rohde R, Shao Y, Ziegler MA, Im HK, Schnabel RB, Jorgensen T, Jorgensen ME, Hansen T, Pedersen O, Stolk RP, Snieder H, Hofman A, Uitterlinden AG, Franco OH, Ikram MA, Richards JB, Rotimi C, Wilson JG, Lange L, Ganesh SK, Nalls M, Rasmussen-Torvik LJ, Pankow JS, Coresh J, Tang W, Linda Kao WH, Boerwinkle E, Morrison AC, Ridker PM, Becker DM, Rotter JI, Kardia SLR, Loos RJJ, Larson MG, Hsu Y-H, Province MA, Tracy R, Voight BF, Vaidya D, O'Donnell CJ, Benjamin EJ, Alizadeh BZ, Prokopenko I, Meigs JB, Borecki IB. Pleiotropic genes for metabolic syndrome and inflammation. Mol Genet Metab. 2014;112:317–338.
- Franceschini N\*, van Rooij FJA\*, Prins BP\*, Feitosa MF\*, Karakas M\*, Eckfeldt JH, Folsom AR, Kopp J, **Vaez A**, Andrews JS, Baumert J, Boraska V, Broer L, Hayward C, Ngwa JS, Okada Y, Polasek O, Westra H-J, Wang YA, Del Greco M. F, Glazer NL, Kapur K, Kema IP, Lopez LM, Schillert A, Smith AV, Winkler CA, Zgaga L, Bandinelli S, Bergmann S, Boban M, Bochud M, Chen YD, Davies G, Dehghan A, Ding J, Doering A, Durda JP, Ferrucci L,

Franco OH, Franke L, Gunjaca G, Hofman A, Hsu F-C, Kolcic I, Kraja A, Kubo M, Lackner KJ, Launer L, Loehr LR, Li G, Meisinger C, Nakamura Y, Schwienbacher C, Starr JM, Takahashi A, Torlak V, Uitterlinden AG, Vitart V, Waldenberger M, Wild PS, Kirin M, Zeller T, Zemunik T, Zhang Q, Ziegler A, Blankenberg S, Boerwinkle E, Borecki IB, Campbell H, Deary IJ, Frayling TM, Gieger C, Harris TB, Hicks AA, Koenig W, O'Donnell CJ, Fox CS, Pramstaller PP, Psaty BM, Reiner AP, Rotter JI, Rudan I, Snieder H, Tanaka T, van Duijn CM, Vollenweider P, Waeber G, Wilson JF, Witteman JCM, Wolffenbuttel BHR, Wright AF, Wu Q, Liu Y, Jenny NS, North KE, Felix JF, Alizadeh BZ, Cupples LA, Perry JRB, and Morris AP. Discovery and fine mapping of serum protein loci through transethnic meta-analysis. Am J Hum Genet. 2012;91:744–753.

\* Equal contribution

### Oral presentations

- Bioinformatics of genomic association mapping: an A-to-Z walk-through. Molecular medicine congress, Isfahan University of Medical Sciences, Isfahan, Iran, Dec 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**

- 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)