Algorithms and analysis of human disease genomics

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LIST OF PUBLICATIONS

* indicates joint first authors

1. Jallow M, Teo YY, Small KS, Rockett KA, Deloukas P, Clark TG, Kivinen K, Bojang KA, Conway DJ, Pinder M, Sirugo G, Sisay-Joof F, Usen S, Auburn S, Bumpstead SJ, Campino S, Coffey A, Dunham A, Fry AE, Green A, Gwilliam R, Hunt SE, **Inouye M**, Jeffreys AE, Mendy A, Palotie A, Potter S, Ragoussis J, Rogers J, Rowlands K, Somaskantharajah E, Whittaker P, Widden C, Donnelly P, Howie B, Marchini J, Morris A, Sanjoaquin M, Achidi EA, Agbenyega T, Allen A, Amodu O, Corran P, Djimde A, Dolo A, Doumbo OK, Drakeley C, Dunstan S, Evans J, Farrar J, Fernando D, Hien TT, Horstmann RD, Ibrahim M, Karunaweera N, Kokwaro G, Koram KA, Lemnge M, Makani J, Marsh K, Michon P, Modiano D, Molyneux ME, Mueller I, Parker M, Peshu N, Plowe CV, Puijalon O, Reeder J, Reyburn H, Riley EM, Sakuntabhai A, Singhasivanon P, Sirima S, Tall A, Taylor TE, Thera M, Troye-Blomberg M, Williams TN, Wilson M, Kwiatkowski DP; Wellcome Trust Case Control Consortium; Malaria Genomic Epidemiology Network. (2009) Genome-wide and fine-resolution association analysis of malaria in West Africa. Nature Genetics 41, 657 – 665.

2. Soranzo N, Rivadeneira F, Chinappen-Horsley U, Malkina I, Richards JB, Hammond N, Stolk L, Nica A, **Inouye M**, Hofman A, Stephens J, Wheeler E, Arp P, Gwilliam R, Jhamai PM, Potter S, Chaney A, Ghori MJ, Ravindrarajah R, Ermakov S, Estrada K, Pols HA, Williams FM, McArdle WL, van Meurs JB, Loos RJ, Dermitzakis ET, Ahmadi KR, Hart DJ, Ouwehand WH, Wareham NJ, Barroso I, Sandhu MS, Strachan DP, Livshits G, Spector TD, Uitterlinden AG, Deloukas P. (2009) Meta-analysis of genome-wide scans for human adult stature identifies novel Loci and associations with measures of skeletal frame size. PLoS Genet. 5(4):e1000445.

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CURRICULUM VITAE

Michael Inouye was born on 23 March 1981 in Livingston, New Jersey, USA. He graduated in 1999 from Newport Senior High School (Bellevue, Washington, USA) and, later that year, enrolled at the University of Washington (Seattle, Washington, USA). As a freshman at the University of Washington (UW) studying toward degrees in biochemistry and economics, his interest in bioinformatics was piqued by a summer internship at Zymogenetics, Inc. Much of his time was spent mining the sequence data still being produced by the Human Genome Sequencing Consortium, analysis which consequently led to a long and fruitful Mary Gates fellowship with Prof. Ram Samudrala in the Computational Genomics Group at the UW Microbiology department. The fellowship was undertaken concurrent to his university studies. With Prof. Samudrala, his first peer-reviewed scientific work was published: an algorithm to differentiate biologically native and non-native protein structures. He was also awarded the Erling J. Ordal prize for best undergraduate research in the department for work on adaptive evolution and sequence-based gene finding. In 2004, he attained his undergraduate degrees and, in 2005, he completed a Masters degree in biochemistry from the University of California at Los Angeles, specializing in protein crystallography and synthetic biochemistry.

He returned to bioinformatics research in late 2005 by moving to the Wellcome Trust Sanger Institute (Cambridge, United Kingdom) where, during the next 4 years, he worked in the groups of Dr. Panos Deloukas and Prof. Leena Peltonen. Throughout this time, his research was primarily in genome-wide association studies (GWAS), leading to many high-profile publications identifying genetic variants underlying bone mineral density and osteoporosis, celiac disease, obesity, and several other complex diseases and phenotypes. However, his main expertise was in the analysis and algorithms used to identify these genetic variants. This included genotype calling algorithms and the statistical, end-point assessment of laboratory protocols (like the whole-genome amplification of DNA). In 2008, he began his PhD studies by splitting his research between the groups of Prof. Peltonen and Prof. Van Ommen in the Department of Human Genetics at Leiden University Medical Center (the Netherlands). In addition to GWAS, his studies during this time were in both clinical genome sequencing and transcriptomics. In particular, he became interested in the

statistical approaches used to dissect biological networks. Using these approaches, he uncovered a novel co-expression network linking inflammation and lipid metabolism, potentially providing a molecular explanation for the role the immune system plays in atherosclerosis.

Currently, he is applying genomics approaches to problems in immunology including the generation of a transcriptional roadmap for the differentiation of the B lymphoblast into an antibody secreting cell.