

**Erasmus University Rotterdam, the Netherlands**  
**CSC PhD 2015 Project Description**

<b>School/Department:</b>	<i>Department of Forensic Molecular Biology Erasmus University Medical Center Rotterdam, Rotterdam, The Netherlands.</i>
<b>Project Title:</b>	<i>Methodological approaches to predicting human externally visible characteristics from DNA variants</i>
<b>Abstract:</b>	<p>In many species, particularly humans, a large number of single-nucleotide polymorphism (SNP) has been detected to be significantly associated with heritable traits and diseases through genome-wide association studies (GWASs). There is increasing interest in making predictions of complex trait phenotypes from genotype data for individuals. High-performance prediction models have a wide range of potential applications in multiple disciplines such as in plant and animal breeding, personalized medicine, human population genetics, genetic epidemiology, and even forensic genetics.</p> <p>In the past several years, the Department of Forensic Molecular Biology at Erasmus University Medical Center identified a number of SNPs with various predictive values on a set of human externally visible characteristics, such as pigmentation traits and facial shape features, and established highly accurate prediction models for predicting human eye and hair colors. Some of the models and associated DNA test systems have already entered forensic practice in the emerging field of Forensic DNA Phenotyping, which the department has pioneered.</p> <p>The successful candidate will be developing high-performance prediction models for predicting human externally visible characteristics from SNP genotypes with a methodological focus. The candidate will be focusing on improving prediction accuracy and develop new algorithms to deal with large numbers of SNP predictors and their interactions by means of simulation. The candidate will also have opportunities to apply newly developed methods to real human phenotype data such as pigmentation traits, body height, and facial shape features in thousands of individuals for whom dense microarray SNP data are available.</p> <p>The successful candidate will obtain a PhD in 4 years.</p>
<b>Requirements of candidate:</b>	<p>Master degree: Yes</p> <p>Essential requirements  The candidate is required to have background in any of the following disciplines, at best more than one: biostatistics, bioinformatics, computer science, epidemiology, or public health.</p>

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	<p>The candidate is required to have excellent programming and computing skills. Note that there might be an exam about programming and computing.</p> <p>Desired pluses  Knowledge in genetics and human disease; Experience in dealing with large datasets; Experience in software package development; Authorship on science citation indexed (SCI) publications.</p> <p>IELTS Grade: 7.0 (<i>minimal 6.0 per component</i>)  or  TOEFL: 100 (<i>minimal 20 per component</i>)</p>
<b>Supervisor information:</b>	<p><i>The candidate will be under direct supervision by</i></p> <p><i>Professor Dr. Manfred Kayser</i>  Head, Dept. of Forensic Molecular Biology, Erasmus MC  P.O. Box 2040, 3000 CA Rotterdam, The Netherlands  Visiting address: Wytemaweg 80, 3015 CN Rotterdam, The Netherlands, room Ee1067  Email: <a href="mailto:m.kayser@erasmusmc.nl">m.kayser@erasmusmc.nl</a>  Tel: +31 10 703 80 73  <a href="http://www.erasmusmc.nl">www.erasmusmc.nl</a>   <a href="http://www.erasmusmc.nl/fmb">www.erasmusmc.nl/fmb</a></p> <p><i>and</i></p> <p><i>Assistant Professor Dr. Fan Liu</i>  Group leader, Dept. of Forensic Molecular Biology, Erasmus MC  P.O. Box 2040, 3000 CA Rotterdam, The Netherlands  Visiting address: Wytemaweg 80, 3015 CN Rotterdam, The Netherlands, room Ee1067  Email: <a href="mailto:f.liu@erasmusmc.nl">f.liu@erasmusmc.nl</a>  Tel: +31 10 704 29 96  <a href="http://www.erasmusmc.nl">www.erasmusmc.nl</a>   <a href="http://www.erasmusmc.nl/fmb">www.erasmusmc.nl/fmb</a></p> <p>Selected publications related to the topic last 5 years (1-2 pages)</p> <p>1) The Genome of the Netherlands Consortium: Francioli LC, Menelaou A, Pulit SL, van Dijk F, Palamara PF, Elbers CC, Neerincx PBT, Ye K, Guryev V, Kloosterman WP, Deelen P, Abdellaoui A, van Leeuwen EM, van Oven M, Vermaat M, Li M, Laros JFJ, Karssen LC, Kanterakis A, Amin N, Hottenga JJ, Lameijer E-W, Kattenberg M, Dijkstra M, Byelas H, van Setten</p>

	<p>J, van Schaik BDC, Bot J, Nijman IJ, Renkens I, Marschall T, Schönhuth A, Hehir-Kwa JY, Handsaker RE, Polak P, Sohail M, Vuzman D, Hormozdiari F, van Enckevort D, Mei H, Koval V, Moed MH, van der Velde K, Rivadeneira F, Estrada K, Medina-Gomez C, Isaacs A, McCarroll SA, Beekman M, de Craen AJM, Suchiman HED, Hofman A, Oostra B, Uitterlinden AG, Willemsen G, LifeLines Cohort Study, Platteel M, Veldink JH, van den Berg LH, Pitts SJ, Potluri S, Sundar P, Cox DR, Sunyaev SR, den Dunnen JT, Stoneking M, de Knijff P, <b>Kayser M</b>, Li Q, Li Y, Du Y, Chen R, Cao H, Li N, Cao N, Wang J, Bovenberg JA, Pe'er I, Slagboom PE, van Duijn CM, Boomsma DI, van Ommen GB, de Bakker PIW, Swertz MA, and Wijmenga C Whole-genome sequence variation, population structure and demographic history of the Dutch population. <b>Nature Genetics</b>, 46(8):818-825, <b>IF: 29.648, Ci: 0</b></p> <p>2) Jacobs LC, <b>Liu F</b>, Bleyen I, Gunn DA, Hofman A, Klaver CC, Uitterlinden AG, Neumann HAM, Bataille V, Spector TD, <b>Kayser M</b>, Nijsten T (2014) Intrinsic and extrinsic risk factors for sagging eyelids. <b>JAMA Dermatology</b>, Epub May 2014, doi:10.1001/jamadermatol.2014.27, <b>IF: 4.306, Ci: 0</b></p> <p>3) Pośpiech E, Wojas-Pelc A, Walsh S, <b>Liu F</b>, Maeda H, Ishikawa T, Skowron M, <b>Kayser M</b>, Branicki W (2014) The common occurrence of epistasis in the determination of human pigmentation and its impact on DNA-based pigmentation phenotype prediction. <b>Forensic Science International: Genetics</b>, 11:64-72, <b>IF: 3.202, Ci: 1</b></p> <p>4) Walsh S, Chaitanya L, Clarisse L, Wirken L, Draus-Barini J, Kovatsi L, Sijen T, de Knijff P, Branicki W, and <b>Kayser M</b> (2014) Developmental validation of the HirisPlex System: DNA-based eye and hair color prediction for forensic usage. <b>Forensic Science International: Genetics</b>, 9:150-161, <b>IF: 3.202, Ci: 0</b></p> <p>5) <b>Liu F</b>, Hendriks AEJ, Ralf A, Boot AM, Benyi E, Säwendahl L, Oostra BA, van Duijn C, Hofman A, Rivadeneira F, Uitterlinden AG, Drop SLS, and <b>Kayser M</b> (2014) Common DNA variants predict tall stature in Europeans. <b>Human Genetics</b>, 133(5):587-97, <b>IF: 4.522, Ci: 0</b></p> <p>6) Draus-Barini J, Walsh S, Pośpiech E, Kupiec T, Głąb H, Branicki W*, and <b>Kayser M*</b> (2013) Bona fide color: DNA prediction of human eye and hair color from ancient and modern skeletal remains, <b>Investigative Genetics</b>, 4:3, IF: -, Ci: - (not yet ISI-JRF listed)</p> <p>7) Jacobs LC, Wollstein A, Lao O, Hofman A, Vingerling JR,</p>
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	<p>Uitterlinden AG, Nijsten T, <b>Kayser M</b>, <b>Liu F</b> (2013) Comprehensive candidate gene study highlights <i>UGT1A</i> and <i>BNC2</i> as new genes determining continuous skin color variation in Europeans. <b>Human Genetics</b>, 132:147–158, <b>IF: 4.522, Ci: 6</b></p> <p>8) Walsh S, <b>Liu F</b>, Wollstein A, Kovatsi L, Ralf A, Kosiniak-Kamysz A, Branicki W, and <b>Kayser M</b> (2013) The HlrisPlex System for simultaneous prediction of hair and eye color from DNA. <b>Forensic Science International: Genetics</b>, 7:98–115, <b>IF: 3.202, Ci: 24</b></p> <p>9) <b>Liu F</b>, van der Lijn F, Schurmann C, Zhu G, Chakravarty MM, Hysi PG, Wollstein A, Lao O, de Bruijne M, Ikram MA, van der Lugt A, Rivadeneira F, Uitterlinden AG, Hofman A, Niessen WJ, Homuth G, de Zubiceray G, McMahon KL, Thompson PM, Daboul A, Puls R, Hegenscheid K, Bevan L, Pausova Z, Medland SE, Montgomery GW, Wright MJ, Wickiing C, Boehringer S, Spector TD, Paus T, Martin NG, Biffar R, and <b>Kayser M</b> on behalf of the International Visible Trait Genetics (VisiGen) Consortium (2012) A genome-wide association study identifies five loci influencing facial morphology in Europeans. <b>PLoS Genetics</b>, 8(9):e1002932, , <b>IF: 8.167, Ci: 27</b></p> <p>10) Walsh S, Wollstein A, Liu F, Chakravarthy U, de Jong PTVM, Rahu M, Seland JH, Soubrane G, Tomazzoli L, Topouzis F, Vingerling JR, Vioque J, Fletcher AE, Ballantyne KN, and <b>Kayser M</b> (2012) DNA-based eye color prediction across Europe with the IrisPlex system. <b>Forensic Science International: Genetics</b>, 6:330–340, <b>IF: 3.202, Ci: 16</b></p> <p>11) <b>Liu F</b>, Struchalin MV, van Duijn K, Hofman A, Uitterlinden AG, Aulchenko YS, and <b>Kayser M</b> (2011) Detecting low frequent loss-of-function alleles in genome-wide association studies with red hair color as example. <b>PLoS One</b>, 6(11):e28145, <b>IF: 3.534, Ci: 6</b></p> <p>12) Walsh S, Lindenberg A, Zuniga SB, Sijen T, de Knijff P, <b>Kayser M</b>, and Ballantyne KN (2011) Developmental validation of the IrisPlex System: Determination of blue and brown iris color for forensic intelligence. <b>Forensic Science International: Genetics</b>, 5:464–471, <b>IF: 3.202, Ci: 26</b></p> <p>13) Boehringer S, van der Lijn F, <b>Liu F</b>, Günther M, Sinigerova S, Birnbaum S, Ludwig KU, Herberz R, Klein S, Hofman A, Uitterlinden AG, Niessen WJ, Breteler MMB, van der Lugt A, Wurtz RP, Nöthen MM, Horsthemke B, Wieczorek D, Mangold</p>
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	<p>E<sup>+</sup>, <b>Kayser M</b><sup>+</sup> (2011) Genetic determination of human facial morphology: links between cleft-lips and normal variation. <b><i>European Journal of Human Genetics</i></b>, 19:1192-1197, <b>IF: 4.225, Ci: 17</b></p> <p>14) Walsh S, <b>Liu F</b>, Ballantyne K, van Oven M, Lao O, <b>Kayser M</b> (2011) IrisPlex: a sensitive DNA tool for accurate prediction of blue and brown eye color in the absence of ancestry information. <b><i>Forensic Science International: Genetics</i></b>, 5:170-180, <b>IF: 3.202, Ci: 41</b></p> <p>15) Branicki W, <b>Liu F</b>, van Duijn K, Draus-Barini J, Pośpiech E, Walsh S, Kupiec T, Wojas-Pelc A, and <b>Kayser M</b> (2011) Model-based prediction of human hair color using DNA variants. <b><i>Human Genetics</i></b>, 129:443–454, <b>IF: 4.522, Ci: 31</b></p> <p>16) Zubakov D, <b>Liu F</b>, van Zelm MC, Vermeulen J, Oostra BA, van Duijn CM, Driessen GJ, van Dongen JJM, <b>Kayser M</b><sup>+</sup>, Langerak AW<sup>+</sup> (2010) Estimating human age from T cell DNA rearrangements. <b><i>Current Biology</i></b>, 20(22):R970, Featured in <i>Nature, Science</i>, <b>IF: 9.916, Ci: 28</b></p> <p>17) Lango Allen H, Estrada K, Lettre G, Berndt SI, Weedon MN, Rivadeneira F, Willer CJ, Jackson AU, Vedantam S, Raychaudhuri S, Ferreira T, Wood AR, Weyant RJ, Segrè AV, Speliotes EK, Wheeler E, Soranzo N, Park JH, Yang J, Gudbjartsson D, Heard-Costa NL, Randall JC, Qi L, Vernon Smith A, Mägi R, Pastinen T, Liang L, Heid IM, Luan J, Thorleifsson G, Winkler TW, Goddard ME, Sin Lo K, Palmer C, Workalemahu T, Aulchenko YS, Johansson A, Carola Zillikens M, Feitosa MF, Esko T, Johnson T, Ketkar S, Kraft P, Mangino M, Prokopenko I, Absher D, Albrecht E, Ernst F, Glazer NL, Hayward C, Hottenga JJ, Jacobs KB, Knowles JW, Kutalik Z, Monda KL, Polasek O, Preuss M, Rayner NW, Robertson NR, Steinthorsdottir V, Tyrer JP, Voight BF, Wiklund F, Xu J, Hua Zhao J, Nyholt DR, Pellikka N, Perola M, Perry JR, Surakka I, Tammesoo ML, Altmaier EL, Amin N, Aspelund T, Bhangale T, Boucher G, Chasman DI, Chen C, Coin L, Cooper MN, Dixon AL, Gibson Q, Grundberg E, Hao K, Juhani Junttila M, Kaplan LM, Kettunen J, König IR, Kwan T, Lawrence RW, Levinson DF, Lorentzon M, McKnight B, Morris AP, Müller M, Suh Ngwa J, Purcell S, Rafelt S, Salem RM, Salvi E, Sanna S, Shi J, Sovio U, Thompson JR, Turchin MC, Vandenput L, Verlaan DJ, Vitart V, White CC, Ziegler A, Almgren P, Balmforth AJ, Campbell H, Citterio L, De Grandi A, Dominiczak A, Duan J,</p>
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	<p>Elliott P, Elosua R, Eriksson JG, Freimer NB, Geus EJ, Glorioso N, Haiqing S, Hartikainen AL, Havulinna AS, Hicks AA, Hui J, Igl W, Illig T, Jula A, Kajantie E, Kilpeläinen TO, Koiranen M, Kolcic I, Koskinen S, Kovacs P, Laitinen J, Liu J, Lokki ML, Marusic A, Maschio A, Meitinger T, Mulas A, Paré G, Parker AN, Peden JF, Petersmann A, Pichler I, Pietiläinen KH, Pouta A, Ridderstråle M, Rotter JI, Sambrook JG, Sanders AR, Oliver Schmidt C, Sinisalo J, Smit JH, Stringham HM, Bragi Walters G, Widen E, Wild SH, Willemsen G, Zagato L, Zgaga L, Zitting P, Alavere H, Farrall M, McArdle WL, Nelis M, Peters MJ, Ripatti S, van Meurs JB, Aben KK, Ardlie KG, Beckmann JS, Beilby JP, Bergman RN, Bergmann S, Collins FS, Cusi D, den Heijer M, Eiriksdottir G, Gejman PV, Hall AS, Hamsten A, Huikuri HV, Iribarren C, Kähönen M, Kaprio J, Kathiresan S, Kiemeny L, Kocher T, Launer LJ, Lehtimäki T, Melander O, Mosley Jr TH, Musk AW, Nieminen MS, O'Donnell CJ, Ohlsson C, Oostra B, Palmer LJ, Raitakari O, Ridker PM, Rioux JD, Rissanen A, Rivolta C, Schunkert H, Shuldiner AR, Siscovick DS, Stumvoll M, Tönjes A, Tuomilehto J, van Ommen GJ, Viikari J, Heath AC, Martin NG, Montgomery GW, Province MA, <b>Kayser M</b>, Arnold AM, Atwood LD, Boerwinkle E, Chanock SJ, Deloukas P, Gieger C, Grönberg H, Hall P, Hattersley AT, Hengstenberg C, Hoffman W, Mark Lathrop G, Salomaa V, Schreiber S, Uda M, Waterworth D, Wright AF, Assimes TL, Barroso I, Hofman A, Mohlke KL, Boomsma DI, Caulfield MJ, Adrienne Cupples L, Erdmann J, Fox CS, Gudnason V, Gyllenstein U, Harris TB, Hayes RB, Jarvelin MR, Mooser V, Munroe PB, Ouwehand WH, Penninx BW, Pramstaller PP, Quertermous T, Rudan I, Samani NJ, Spector TD, Völzke H, Watkins H, Wilson JF, Groop LC, Haritunians T, Hu FB, Kaplan RC, Metspalu A, North KE, Schlessinger D, Wareham NJ, Hunter DJ, O'Connell JR, Strachan DP, Wichmann HE, Borecki IB, van Duijn CM, Schadt EE, Thorsteinsdottir U, Peltonen L, Uitterlinden AG, Visscher PM, Chatterjee N, Loos RJ, Boehnke M, McCarthy MI, Ingelsson E, Lindgren CM, Abecasis GR, Stefansson K, Frayling TM, Hirschhorn JN. (2010) Hundreds of variants clustered in genomic loci and biological pathways affect human height. <b>Nature</b>, <b>467</b>:832-838, <b>IF: 42.351</b>, <b>Ci: 374</b></p> <p>18) <b>Liu F</b>, Wollstein A, Hysi PG, Ankra-Badu GA, Spector TD, Park D, Zhu G, Larsson M, Duffy DL, Montgomery GW, Mackey DA, Walsh S, Lao O, Hofman A, Rivadeneira F, Vingerling JR, Uitterlinden AG, Martin NG, Hammond CJ, and <b>Kayser M</b></p>
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	(2010) Digital quantification of human eye color highlights genetic association of three new loci. <b><i>PLoS Genetics</i></b> , 6 (5):e1000934, <b>IF: 8.167, Ci: 43</b>
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