General Information

Nothnagel, Michael, Professor of Statistical Genetics and Bioinformatics (W2)
Professor Dr. rer. medic., Dipl. Mathematician, *22.07.1971, male
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University training and degree

1991-1999	Mathematics & Biology, Humboldt University Berlin
Degree:	Diploma of Mathematics 1999 (Prof. Olaf Bunke)

Scientific Degrees

Habilitation:	Medical Statistics, Christian-Albrechts University, Kiel, 2012 (Prof. Michael Krawczak)
Dissertation:	Statistical Genetics, Charité – Universitätsmedizin Berlin, 2005 (Prof. Jens G. Reich)

Professional Career

2012-present	Professor & Head of group	Dept. of Statistical Genetics and Bioinformatics, CCG, UoC, Germany
2005 - 2012	Scientist	Christian-Albrechts University, Institute of Medical Informatics and Statistics, Kiel, Germany
2003	Predoctoral Fellow	Baylor College of Medicine (BCM), Laboratory of Molecular and Human Genetics, Houston, TX, U.S.A.
2002 - 2005	Scientist	Max Delbrück Center for Molecular Medicine, Dept. of Bioinformatics, Berlin, Germany
2001	Visiting Student	The Rockefeller University, Laboratory of Statistical Genetics, New York, NY, U.S.A.

Miscellaneous

2018 - present	Guest Editor, *Human Genetics*
2018	Guest Editor, *PLoS Genetics*
2018 - present	West German Genome Center (WGGC), Speaker of SIG 6
2016 - present	Editorial Board, *Human Heredity*
2015 - present	Publication Committee, International Genetic Epidemiological Society (IGES)
2015 - present	Faculty, Graduate School for Biological Sciences (GSfBS), University of Cologne
2009 - present	Editorial Board, *Human Genetics*
2009 - 2012	DFG Cluster of Excellence *Inflammation at Interfaces*

Selected Publications

1. May P, Girard S, Harrer M, Bobbili DR, Schubert J, Wolking S, Becker F, Lachance-Touchette P, Meloche C, Gravel M, Niturad CE, Knaus J, De Kovel C, Toliat M, Polvi A, Iacomino M, Guerrero-López R, Baulac S, Marini C, Thiele H, Altmüller J, Jabbari K, Ruppert AK, Jurkowski W, Lal D, Rusconi R, Cestèle S, Terragni B, Coombs ID, Reid CA, Striano P, Caglayan H, Siren A, Everett K, Møller RS, Hjalgrim H, Muhle H, Helbig I, Kunz WS, Weber YG, Weckhuysen S, Jonghe P, Sisodiya SM, Nabbout R, Franceschetti S, Coppola A, Vari MS, Kasteleijn-Nolst Trenité D, Baykan B, Ozbek U, Bebek N, Klein KM, Rosenow F, Nguyen DK, Dubeau F, Carmant L, Lortie A, Desbiens R, Clément JF, Cieuta-Walti C, Sills GJ, Auce P, Francis B, Johnson MR, Marson AG, Berghuis B, Sander JW, Avbersek A, McCormack M, Cavalleri GL, Delanty N, Depondt C, Krenn M, Zimprich F, Peter S, Nikanorova M, Kraaij R, van Rooij J, Balling R, Ikram MA, Uitterlinden AG, Avanzini G, Schorge S, Petrou S, Mantegazza M, Sander T, LeGuern E, Serratosa JM, Koeleman BPC, Palotie A, Lehesjoki AE, **Nothnagel M**, Nürnberg P, Maljevic S, Zara F, Cossette P, Krause R, Lerche H; Epicure Consortium; EuroEPINOMICS CoGIE Consortium; EpiPGX Consortium (2018). Rare coding variants in genes encoding GABAA receptors in genetic generalised epilepsies: an exome-based case-control study. ***Lancet Neurol***, 17(8):699-708. doi: 10.1016/S1474-4422(18)30215-1.

2. Krause-Kyora B, Nutsua M, Boehme L, Pierini F, Pedersen DD, Kornell SC, Drichel D, Bonazzi M, Möbus L, Tarp P, Susat J, Bosse E, Willburger B, Schmidt AH, Sauter J, Franke A, Wittig M, Caliebe A, **Nothnagel M**, Schreiber S, Boldsen JL, Lenz TL, Nebel A (2018). Ancient DNA study reveals HLA susceptibility locus for leprosy in medieval Europeans. ***Nat Commun***, 9(1):1569. doi: 10.1038/s41467-018-03857-x.
3. Kanoungi G, **Nothnagel M** (2018). Pathway-induced allelic spectra of diseases in the presence of strong genetic effects. ***Hum Genet***, 137(3):215-230. doi: 10.1007/s00439-018-1872-5.
4. Flachsbart F, Dose J, Gentschew L, Geismann C, Caliebe A, Knecht C, Nygaard M, Badarinarayan N, ElSharawy A, May S, Luzius A, Torres GG, Jentzsch M, Forster M, Häsler R, Pallauf K, Lieb W, Derbois C, Galan P, Drichel D, Arlt A, Till A, Krause-Kyora B, Rimbach G, Blanché H, Deleuze JF, Christiansen L, Christensen K, **Nothnagel M**, Rosenstiel P, Schreiber S, Franke A, Sebens S, Nebel A (2017). Identification and characterization of two functional variants in the human longevity gene FOXO3. ***Nat Commun***, 8(1):2063. doi: 10.1038/s41467-017-02183-y.
5. **Nothnagel M**, Fan G, Guo F, He Y, Hou Y, Hu S, Huang J, Jiang X, Kim W, Kim K, Li C, Li H, Li L, Li S, Li Z, Liang W, Liu C, Lu D, Luo H, Nie S, Shi M, Sun H, Tang J, Wang L, Wang CC, Wang D, Wen SQ, Wu H, Wu W, Xing J, Yan J, Yan S, Yao H, Ye Y, Yun L, Zeng Z, Zha L, Zhang S, Zheng X, Willuweit S, Roewer L (2017). Revisiting the male genetic landscape of China: a multi-center study of almost 38,000 Y-STR haplotypes. ***Hum Genet***, 136(5):485-497. doi: 10.1007/s00439-017-1759-x. Epub 2017 Jan 30.
6. Ng M, Thakkar D, Southam L, Werker P, Ophoff R, Becker K, **Nothnagel M**, Franke A, Nürnberg P, Espirito-Santo AI, Izadi D, Hennies HC, Nanchahal J, Zeggini E, Furniss D (2017). A genome-wide association study of Dupuytren disease reveals 17 additional variants implicated in fibrosis. ***Am J Hum Genet***, 101(3):417-427.
7. Buch S*, Stickel F*, Trépo E*, Way M, Herrmann A, Nischalke HD, Brosch M, Rosendahl J, Berg T, Ridinger M, Rietschel M, McQuillin A, Frank J, Kiefer F, Schreiber S, Lieb W, Soyka M, Semmo N, Aigner E, Datz C, Schmelz R, Brückner S, Zeissig S, Stephan AM, Wodarz N, Devière J, Clumeck N, Sarrazin C, Lammert F, Gustot T, Deltenre P, Völzke H, Lerch MM, Mayerle J, Eyer F, Schafmayer C, Cichon S, Nöthen MM, **Nothnagel M**, Ellinghaus D, Huse K, Franke A, Zopf S, Hellerbrand C, Moreno C, Franchimont D*, Morgan MY*, Hampe J* (2015) A two-stage genome-wide association study confirms *PNPLA3* and identifies *TM6SF2* and *MBOAT7* as risk loci for alcohol-related cirrhosis. ***Nat Genet***, 47(12):1443-8. (* equal contribution)
8. Syrbe S, Hedrich UBS, Riesch E, Djémié T, Müller S, Møller RS, Maher B, Hernandez-Hernandez L, Synofzik M, Caglayan HS, Arslan M, Serratosa JM, **Nothnagel M**, May P, Krause R, Löffler H, Detert K, Dorn T, Vogt H, Krämer G, Schöls L, Mullis PE, Linnankivi T, Lehesjoki AE, Sterbova K, Craiu DC, Hoffman-Zacharska D, Korff CM, Weber YG, Steinlin M, Gallati S, Bertsche A, Bernhard MK, Merkenschlager A, Kiess K, EuroEPINOMICS RES consortium, Gonzalez M, Züchner S, Palotie A, Suls A, De Jonghe P, Helbig I, Biskup S, Wolff M, Maljevic S, Schüle R, Sisodiya SM, Weckhuysen S, Lerche H, Lemke JR (2015). Hyperexcitability or electrical silencing: de novo loss- or gain-of-function mutations in *KCNA2* cause epileptic encephalopathy. ***Nat Genet***, 47(4):393-9.
9. Siegert S, Wolf A, Cooper DN, Krawczak M*, **Nothnagel M*** (2015). Mutations causing complex disease may under certain circumstances be protective in an epidemiological sense. ***PLoS One***, 10(7):e0132150.
10. Lemke JR, Lal D, Reinthaler EM, Steiner I, **Nothnagel M**, Alber M, Geider K, Laube B, Schwake M, Finsterwalder K, Franke A, Schilhabel M, Jähn JA, Muhle H, Boor R, Van Paesschen W, Caraballo R, Fejerman N, Weckhuysen S, De Jonghe P, Larsen J, Møller RS, Hjalgrim H, Addis L, Tang S, Hughes E, Pal DK, Veri K, Vaher U, Talvik T, Dimova P, Guerrero López R, Serratosa JM, Linnankivi T, Lehesjoki AE, Ruf S,

Wolff M, Buerki S, Wohlrab G, Kroell J, Datta AN, Fiedler B, Kurlemann G, Kluger G, Hahn A, Haberlandt DE, Kutzer C, Sperner J, Becker F, Weber YG, Feucht M, Steinböck H, Neophythou B, Ronen GM, Gruber-Sedlmayr U, Geldner J, Harvey RJ, Hoffmann P, Herms S, Altmüller J, Toliat MR, Thiele H, Nürnberg P, Wilhelm C, Stephani U, Helbig I, Lerche H, Zimprich F, Neubauer BA, Biskup S, von Spiczak S (2013). Mutations in *GRIN2A* cause idiopathic focal epilepsy with rolandic spikes. ***Nat Genet*** 45(9):1067-72.

11. **Nothnagel M**, Wolf A, Herrmann A, Szafranski K, Vater I, Brosch M, Huse K, Siebert R, Platzer M, Hampe J, Krawczak M (2011). Statistical inference of allelic imbalance from transcriptome data. ***Hum Mutat***,32:98-106.
12. Dolmans GH, Werker PM, Hennies HC, Furniss D, Festen EA, Franke L, Becker K, van der Vlies P, Wolffenbuttel BH, Tinschert S, Toliat MR, **Nothnagel M**, Franke A, Klopp N, Wichmann HE, Nürnberg P, Giele H, Ophoff RA, Wijmenga C; Dutch Dupuytren Study Group; German Dupuytren Study Group; LifeLines Cohort Study; BSSH-GODD Consortium (2011). Wnt signaling and Dupuytren's disease. ***N Engl J Med***, 365(4):307-17.
13. **Nothnagel M***, Herrmann A*, Wolf A, Schreiber S, Platzer M, Siebert R, Krawczak M, Hampe J (2011). Technology-specific error signatures in the 1000 Genomes Project data. ***Hum Genet***, 130(4):505-16.
14. **Nothnagel M**, Lu TT, Kayser M, Krawczak M (2010). Genomic and geo¬gra¬phic distri¬bu-tion of SNP-defined runs of homozygosity in Europeans. ***Hum Mol Genet***, 19(15):2927-35.
15. Helbig I, Mefford HC, Sharp AJ, Guipponi M, Fichera M, Franke A, Muhle H, de Kovel C, Baker C, von Spiczak S, Kron KL, Steinich I, Kleefuß-Lie AA, Leu C, Gaus V, Schmitz B, Klein KM, Reif PS, Rosenow F, Weber Y, Lerche H, Zimprich F, Urak L, Fuchs K, Feucht M, Genton P, Thomas P, Visscher F, de Haan GJ, Møller RS, Hjalgrim H, Luciano D, Wittig M, **Nothnagel M**, Elger CE, Nürnberg P, Romano C, Malafosse A, Koeleman BPC, Lindhout D, Stephani U, Schreiber S, Eichler EE, Sander T (2009). 15q13.3 microdeletions increase risk of idiopathic generalized epilepsy. ***Nat Genet***, 41(2):160-2.
16. Lao O*, Lu TT*, **Nothnagel M**, Junge O, Freitag-Wolf S, Caliebe A, Balascakova M, Bertranpetit J, Bindoff LA, Comas D, Holmlund G, Kouvatsi A, Macek M, Mollet I, Parson W, Palo J, Ploski R, Sajantila A, Tagliabracci A, Gether U, Werge T, Rivadeneira F, Hofman A, Uitterlinden AG, Gieger C, Wichmann HE, Rüther A, Schreiber S, Becker C, Nürnberg P, Nelson MR, Krawczak M*, Kayser M* (2008). Correlation between genetic and geographic structure in Europe. ***Curr Biol***, 18(16):1241-1248.
17. Nothnagel M, Rohde K (2005). The effect of single-nucleotide polymorphism marker selection on patterns of haplotype blocks and haplotype frequency estimates. ***Am J Hum Genet***, 77(6):988-98.