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Dr. Dmitriy Drichel

Summary

Freelance data scientist based in Bonn, Germany, with a focus on big data, statistics, algorithms and software development. Working with a wide range of industries including biotech, pharma, and finance. Co-author of 35 peer-reviewed publications. Outstanding expertise and an excellent track record in solving real-world problems with cutting-edge methodology.

Key Skills and Interests

- Data science, statistics, machine learning, big data
- Genotyping, sequencing and imputation technology
- Anomaly detection, non-parametric analysis and taming the "dimensional explosion"
- Development of algorithms and methods
- Explorative and predictive analytics, statistical modelling and simulation
- System integration, analysis pipelines
- Software development (C/C++, Java, Python, R, Perl, awk, bash, ...)
- Project management and project development
- High-performance computing
- Communicating results, reporting and visualization

Work Experience

since 10.2018 Freelance data science consultant at Drichel Analytics

since 11.2015 Research associate (postdoc) at Cologne Center for Genomics (CCG), University of Cologne, department of Statistical Genetics and Bioinformatics

2010-2015 Research associate at the German Center for Neurodegenerative Diseases (DZNE), Bonn, in the research group Genomic Mathematics in Neuroepidemiology

2011-2013 Visiting scientist at the Max Planck Institute for Molecular Genetics, Berlin

2006-2010 Student assistant at the Institute for Theoretical Physics, Leibniz University Hannover

2006-2008 Student assistant at the Institute for Physiology, Hannover Medical School

Academic Education

2016 PhD in Epidemiology at the University Clinic Bonn, PhD thesis:
Association Analysis of Rare Genomic Variants

2003-2010 Studies of physics (focus on mathematical and statistical physics) at the Leibniz University of Hannover, diploma thesis at the Institute for Theoretical Physics (ITP), title:
Logarithmic Conformal Field Theory with Supersymmetry

2007-2008 Studies of mathematics and physics at the National University of Ireland, Maynooth and Trinity College, Dublin

Personal Details

01.09.1982	Born in Leningrad, Russia
	Languages: German, English, Russian
	Nationality: German

Professional Organizations and Official Positions

since 03.2016	German Association for Medical Informatics, Biometry and Epidemiology (GMDS)
	Full professional member
	Deputy leader of the working group "Human Genetics"
	MIBE ("GMS Medizinische Informatik, Biometrie und Epidemiologie"): member of the editorial board
2016-2018	International Genetic Epidemiology Society (IGES), member

Conference Presentations and Invited Talks

03.09.2018	"Personal Genomics Will Change Your Life, Whether You Get Tested or Not" annual conference of the GMDS, Osnabrück
07.12.2017	"Exhaustive Genomic Scans", invited talk, Biomedical Center Bonn
19.09.2017	"Update Epidemiology: Personal Genomics in the Age of Big Genomic Data", annual conference of the GMDS, Oldenburg
11.05.2016	"Beyond Exomes: a Nonparametric Collapsing Test for Joint Analysis of Rare Variants", European Mathematical Genetics Meeting (EMGM) Newcastle
18.03.2016	"Beyond Exomes: a Nonparametric Collapsing Test for Joint Analysis of Rare Variants", DAGStat Göttingen
10.07.2015	"Rare Variant Test COLL with Variable Bin Analysis", invited talk at IMBS Lübeck
17.04.2015	"Rare Variant Test COLL with Variable Bin Analysis", invited talk at CECAD Cologne
17.04.2015	"Rare Variant Test COLL with Variable Bin Analysis", European Mathematical Genetics Meeting (EMGM) Brest
05.03.2015	"Rare Variant Test COLL with Variable Bin Analysis", Biometrische Aspekte der Genomanalyse, Heidelberg
19.09.2012	"Genome-wide, Permutation-based Rare Variant Analysis with INTERSNP-RARE", annual conference of the GMDS, Braunschweig
13.04.2012	"Genome-wide, Permutation-based Rare Variant Analysis with INTERSNP-RARE", European Mathematical Genetics Meeting (EMGM) Göttingen

Publications

[1] Brian W Kunkle, Benjamin Grenier-Boley, Rebecca Sims, Joshua C Bis, Vincent Damotte, Adam C Naj, Anne Boland, Maria Vronskaya, Sven J van der Lee, Alexandre Amlie-Wolf, et al. "Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates Aβ, tau, immunity and lipid processing". In: *Nature Genetics* 51.3 (2019), p. 414.

[2] Ben Krause-Kyora, Marcel Nutsua, Lisa Boehme, Federica Pierini, Dorthe Dangvard Pedersen, Sabin-Christin Kornell, **Dmitriy Drichel**, Marion Bonazzi, Lena Möbus, Peter Tarp, et al. "Ancient DNA study reveals HLA susceptibility locus for leprosy in medieval Europeans". In: *Nature communications* 9.1 (2018), p. 1569.

[3] Antonio F Pardiñas, Peter Holmans, Andrew J Pocklington, Valentina Escott-Price, Stephan Ripke, Noa Carrera, Sophie E Legge, Sophie Bishop, Darren Cameron, Marian L Hamshere, et al. "Common schizophrenia alleles are enriched in mutation-intolerant genes and in regions under strong background selection". In: *Nature genetics* 50.3 (2018), p. 381.

[4] Friederike Flachsbart, Janina Dose, Liljana Gentschew, Claudia Geismann, Amke Caliebe, Carolin Knecht, Marianne Nygaard, Nandini Badarinarayan, Abdou ElSharawy, Sandra May, Anne Luzius, Guillermo G. Torres,

Marlene Jentzsch, Michael Forster, Robert Häsler, Kathrin Pallauf, Wolfgang Lieb, Céline Derbois, Pilar Galan, **Dmitriy Drichel**, et al. "Identification and characterization of two functional variants in the human longevity gene FOXO3". In: *Nature communications* 8.1 (2017), p. 2063.

[5] Sukanya Horpaopan, Jutta Kirfel, Sophia Peters, Michael Kloth, Robert Hüneburg, Janine Altmüller, **Dmitriy Drichel**, Margarete Odenthal, Glen Kristiansen, Christian Strassburg, et al. "Exome sequencing characterizes the somatic mutation spectrum of early serrated lesions in a patient with serrated polyposis syndrome (SPS)". In: *Hereditary cancer in clinical practice* 15.1 (2017), p. 22.

[6] AK Hoebel, **D Drichel**, M van de Vorst, AC Böhmer, S Sivalingam, N Ishorst, J Klamt, L Gölz, M Alblas, A Maaser, et al. "Candidate genes for nonsyndromic cleft palate detected by exome sequencing". In: *Journal of dental research* 96.11 (2017), pp. 1314–1321.

[7] Stefanie Heilmann-Heimbach, Christine Herold, Lara M Hochfeld, Axel M Hillmer, Dale R Nyholt, Julian Hecker, Asif Javed, Elaine GY Chew, Sonali Pechlivanis, **Dmitriy Drichel**, et al. "Meta-analysis identifies novel risk loci and yields systematic insights into the biology of male-pattern baldness". In: *Nature Communications* 8 (2017), p. 14694.

[8] A Mobascher, A Diaz-Lacava, M Wagner, J Gallinat, TF Wienker, **D Drichel**, T Becker, M Steffens, N Dahmen, G Gründer, et al. "Association of common polymorphisms in the nicotinic acetylcholine receptor alpha4 subunit gene with an electrophysiological endophenotype in a large population-based sample". In: *PloS one* 11.4 (2016), e0152984.

[9] Isabel Spier, Martin Kerick, **Dmitriy Drichel**, Sukanya Horpaopan, Janine Altmüller, Andreas Laner, Stefanie Holzapfel, Sophia Peters, Ronja Adam, Bixiao Zhao, et al. "Exome sequencing identifies potential novel candidate genes in patients with unexplained colorectal adenomatous polyposis". In: *Familial cancer* 15.2 (2016), pp. 281–288.

[10] Isabel Spier, **Dmitriy Drichel**, Martin Kerick, Jutta Kirfel, Sukanya Horpaopan, Andreas Laner, Stefanie Holzapfel, Sophia Peters, Ronja Adam, Bixiao Zhao, et al. "Low-level APC mutational mosaicism is the underlying cause in a substantial fraction of unexplained colorectal adenomatous polyposis cases". In: *Journal of medical genetics* 53.3 (2016), pp. 172–179.

[11] Valentina Escott-Price, Rebecca Sims, Christian Bannister, Denise Harold, Maria Vronskaya, Elisa Majounie, Nandini Badarinarayan, GERAD/PERADES, IGAP consortia, Kevin Morgan, et al. "Common polygenic variation enhances risk prediction for Alzheimer's disease". In: *Brain* 138.12 (2015), pp. 3673–3684.

[12] Søren D Østergaard, Shubhabrata Mukherjee, Stephen J Sharp, Petroula Proitsi, Luca A Lotta, Felix Day, John RB Perry, Kevin L Boehme, Stefan Walter, John S Kauwe, et al. "Associations between potentially modifiable risk factors and Alzheimer disease: a Mendelian randomization study". In: *PLoS medicine* 12.6 (2015), e1001841.

[13] Fabian Hosp, Hannes Vossfeldt, Matthias Heinig, Djordje Vasiljevic, Anup Arumughan, Emanuel Wyler, Genetic and Environmental Risk for Alzheimer's Disease GERAD1 Consortium, Markus Landthaler, Norbert Hubner, Erich E. Wanker, Lars Lannfelt, Martin Ingelsson, Maciej Lalowski, Aaron Voigt, and Matthias Selbach. "Quantitative interaction proteomics of neurodegenerative disease proteins". In: *Cell Rep* 11.7 (May 2015), pp. 1134–1146.

[14] André Lacour, Vitalia Schüller, **Dmitriy Drichel**, Christine Herold, Frank Jessen, Markus Leber, Wolfgang Maier, Markus M Noethen, Alfredo Ramirez, Tatsiana Vaitsiakhovich, et al. "Novel genetic matching methods for handling population stratification in genome-wide association studies". In: *BMC bioinformatics* 16.1 (2015), p. 84.

[15] Stefanie Heilmann, **Dmitriy Drichel**, Jordi Clarimon, Victoria Fernández, André Lacour, Holger Wagner, Mathias Thelen, Isabel Hernández, Juan Fortea, Montserrat Alegret, et al. "PLD3 in non-familial Alzheimer's disease". In: *Nature* 520.7545 (2015), E3–E5.

[16] **Dmitriy Drichel**, Christine Herold, Andre Lacour, Alfredo Ramirez, Frank Jessen, Wolfgang Maier, Markus M. Noethen, Markus Leber, Tatsiana Vaitsiakhovich, and Tim Becker. "Rare Variant Testing of Imputed Data: An Analysis Pipeline Typified." In: *Hum Hered* 78.3-4 (Dec. 2014).

[17] Alfredo Ramirez, Wiesje M. van der Flier, Christine Herold, David Ramonet, Stefanie Heilmann, Piotr Lewczuk, Julius Popp, Andre Lacour, **Dmitriy Drichel**, Eva Louwersheimer, Markus P. Kummer, Carlos Cruchaga, Per Hoffmann, Charlotte Teunissen, Henne Holstege, Johannes Kornhuber, Oliver Peters, Adam C. Naj, Vincent Chouraki, Celine Bellenguez, Amy Gerrish, Reiner Heun, Lutz Frolich, Michael Hull, Lara Buscemi, Stefan Herms, Heike Kolsch, Philip Scheltens, Monique M. Breteler, Eckart Ruther, Jens Wiltfang, Alison Goate, Frank Jessen, Wolfgang Maier, Michael T. Heneka, Tim Becker, and Markus M. Nothen. "SUCLG2 identified as both a determinator of CSF Abeta1-42 levels and an attenuator of cognitive decline in Alzheimer's disease." In: *Hum Mol Genet* 23.24 (Dec. 2014), pp. 6644–6658.

[18] Mathias Thelen, Cristina Razquin, Isabel Hernandez, Ana Gorostidi, Raquel Sanchez-Valle, Sara Ortega-Cubero, Steffen Wolfsgruber, **Dmitriy Drichel**, Klaus Fliessbach, Tanja Duenkel, Marinella Damian, Stefanie Heilmann, Anja Slotosch, Martina Lennarz, Manuel Seijo-Martinez, Ramon Rene, Johannes Kornhuber, Oliver Peters, Christian Luckhaus, Holger Jahn, Michael Hull, Eckart Ruther, Jens Wiltfang, Elena Lorenzo, Jordi Gascon, Alberto Lleo, Albert Llado, Jaume Campdelacreu, Fermin Moreno, Hojjat Ahmadzadehfar, Juan Fortea, Begona Indakoetxea, Michael T. Heneka, Axel Wetter, Maria A. Pastor, Mario Riverol, Tim Becker, Lutz Frolich, Lluis Tarraga, Merce Boada, Michael Wagner, Frank Jessen, Wolfgang Maier, Jordi Clarimon, Adolfo Lopez de Munain, Agustin Ruiz, Pau Pastor, and Alfredo Ramirez. "Investigation of the role of rare TREM2 variants in frontotemporal dementia subtypes." In: *Neurobiol Aging* 35.11 (Nov. 2014), 2657.e13–19.

[19] Tatsiana Vaitsiakhovich, **Dmitriy Drichel**, Christine Herold, Andre Lacour, and Tim Becker. "METAINTER: meta-analysis of multiple regression models in genome-wide association studies." In: *Bioinformatics* (Sept. 2014).

[20] Alfredo Ramirez, Stefanie Heilmann, **Dmitriy Drichel**, Isabel Hernandez, Alberto Lleó, André Lacour, Maitée Rosende-Roca, Ana Mauleon, Susana Ruiz, Montse Alegret, et al. "Role of PLD3 rare variants in european sporadic Alzheimer's disease patients". In: *Alzheimer's & Dementia: The Journal of the Alzheimer's Association* 10.4 (2014), P319–P320.

[21] Tatsiana Vaitsiakhovich, **Dmitriy Drichel**, Marina Angisch, Tim Becker, Christine Herold, and Andre Lacour. "Analysis of the progression of systolic blood pressure using imputation of missing phenotype values." In: *BMC Proc* 8.Suppl 1 (2014).

[22] Rima Nuwaihyd, Silke Redler, Stefanie Heilmann, **Dmitriy Drichel**, Sabrina Wolf, Pattie Birch, Kathy Dobson, Gerhard Lutz, Kathrin A. Giehl, Roland Kruse, Rachid Tazi-Ahnini, Sandra Hanneken, Markus Bohm, Anja Miesel, Tobias Fischer, Hans Wolff, Tim Becker, Natalie Garcia-Bartels, Ulrike Blume-Peytavi, Markus M. Nothen, Andrew G. Messenger, and Regina C. Betz. "Investigation of four novel male androgenetic alopecia susceptibility loci: no association with female pattern hair loss." In: *Arch Dermatol Res* 306.4 (May 2014), pp. 413–418.

[23] S. Redler, P. Birch, **Drichel, D.**, P. Hofmann, K. Dobson, A. C. Bohmer, J. Becker, K. A. Giehl, R. Tazi-Ahnini, R. Kruse, H. Wolff, A. Miesel, T. Fischer, M. Bohm, R. Nuwayhid, N. Garcia Bartels, G. Lutz, T. Becker, U. Blume-Peytavi, M. M. Nothen, A. G. Messenger, and R. C. Betz. "The oestrogen receptor 2 (ESR2) gene in female-pattern hair loss: replication of association with rs10137185 in German patients." In: *Br J Dermatol* 170.4 (Apr. 2014), pp. 982–985.

[24] Christine Herold, Alfredo Ramirez, **Dmitriy Drichel**, Andre Lacour, Tatsiana Vaitsiakhovich, Markus M. Nothen, Frank Jessen, Wolfgang Maier, and Tim Becker. "A one-degree-of-freedom test for supra-multiplicativity of SNP effects." In: *PLoS One* 8.10 (2013).

[25] J. C. Lambert et al. "Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease." In: *Nat Genet* 45.12 (Dec. 2013), pp. 1452–1458.

[26] Silke Redler, Kathy Dobson, **Dmitriy Drichel**, Stefanie Heilmann, Sabrina Wolf, Felix F. Brockschmidt, Rachid Tazi-Ahnini, Pattie Birch, Peter Tessmann, Kathrin A. Giehl, Roland Kruse, Gerhard Lutz, Natalie Garcia Bartels, Sandra Hanneken, Hans Wolff, Markus Bohm, Tim Becker, Ulrike Blume-Peytavi, Markus M. Nothen, Andrew G. Messenger, and Regina C. Betz. "Investigation of six novel susceptibility loci for male androgenetic alopecia in women with female pattern hair loss." In: *J Dermatol Sci* 72.2 (Nov. 2013), pp. 186–188.

[27] Christina Rohr, Martin Kerick, Axel Fischer, Alexander Kuhn, Karl Kashofer, Bernd Timmermann, Andriani Daskalaki, Thomas Meinel, **Dmitriy Drichel**, Stefan T. Borno, Anja Nowka, Sylvia Krobitsch, Alice C. McHardy, Christina Kratsch, Tim Becker, Andrea Wunderlich, Christian Barmeyer, Christian Viertler, Kurt Zatloukal, Christoph Wierling, Hans Lehrach, and Michal R. Schweiger. "High-throughput miRNA and mRNA sequencing of paired colorectal normal, tumor and metastasis tissues and bioinformatic modeling of miRNA-1 therapeutic applications." In: *PLoS One* 8.7 (2013).

[28] Fanggeng Zou, Olivia Belbin, Minerva M. Carrasquillo, Oliver J. Culley, Talisha A. Hunter, Li Ma, Gina D. Bisceglio, Mariet Allen, Dennis W. Dickson, Neill R. Graff-Radford, Ronald C. Petersen, the Genetic and Environmental Risk for Alzheimer's disease (GERAD1) Consortium, Kevin Morgan, and Steven G. Younkin. "Linking protective GAB2 variants, increased cortical GAB2 expression and decreased Alzheimer's disease pathology." In: *PLoS One* 8.5 (2013).

[29] Stefanie Heilmann, Amy K. Kiefer, Nadine Fricker, **Dmitriy Drichel**, Axel M. Hillmer, Christine Herold, Joyce Y. Tung, Nicholas Eriksson, Silke Redler, Regina C. Betz, Rui Li, Ari Karason, Dale R. Nyholt, Kijoung Song, Sita H. Vermeulen, Stavroula Kanoni, George Dedoussis, Nicholas G. Martin, Lambertus A. Kiemeney, Vincent Mooser, Kari Stefansson, J. Brent Richards, Tim Becker, Felix F. Brockschmidt, David A. Hinds, and Markus M. Nothen. "Androgenetic alopecia: identification of four genetic risk loci and evidence for the contribution of WNT signaling to its etiology." In: *J Invest Dermatol* 133.6 (June 2013), pp. 1489–1496.

[30] Hassnaa Mahmoudi, Silke Redler, Pattie Birch, **Dmitriy Drichel**, Kathy Dobson, Rachid Tazi-Ahnini, Peter Tessmann, Kathrin A. Giehl, Roland Kruse, Gerhard Lutz, Sandra Hanneken, Hans Wolff, Ulrike Blume-Peytavi, Tim Becker, Markus M. Nothen, Andrew G. Messenger, Markus Bohm, and Regina C. Betz. "Selected variants of the melanocortin 4 receptor gene (MC4R) do not confer susceptibility to female pattern hair loss." In: *Arch Dermatol Res* 305.3 (Apr. 2013), pp. 249–253.

[31] Christian Meesters, Markus Leber, Christine Herold, Marina Angisch, Manuel Mattheisen, **Dmitriy Drichel**, Andre Lacour, and Tim Becker. "Quick, "imputation-free" meta-analysis with proxy-SNPs." In: *BMC Bioinformatics* 13 (2012).

[32] Silke Redler, Rachid Tazi-Ahnini, **Dmitriy Drichel**, Mary P. Birch, Felix F. Brockschmidt, Kathy Dobson, Kathrin A. Giehl, Melanie Refke, Nadine Kluck, Roland Kruse, Gerhard Lutz, Hans Wolff, Markus Bohm, Tim Becker, Markus M. Nothen, Regina C. Betz, and Andrew Messenger. "Selected variants of the steroid-5-alpha-reductase isoforms SRD5A1 and SRD5A2 and the sex steroid hormone receptors ESR1, ESR2 and PGR: no association with female pattern hair loss identified." In: *Exp Dermatol* 21.5 (May 2012), pp. 390–393.

[33] Christine Herold, Manuel Mattheisen, Andre Lacour, Tatsiana Vaitsiakhovich, Marina Angisch, **Dmitriy Drichel**, and Tim Becker. "Integrated genome-wide pathway association analysis with INTERSNP." In: *Hum Hered* 73.2 (2012).

[34] S. Redler, F. F. Brockschmidt, R. Tazi-Ahnini, **D. Drichel**, M. P. Birch, K. Dobson, K. A. Giehl, S. Herms, M. Refke, N. Kluck, R. Kruse, G. Lutz, H. Wolff, M. Bohm, T. Becker, M. M. Nothen, A. G. Messenger, and R. C. Betz. "Investigation of the male pattern baldness major genetic susceptibility loci AR/EDA2R and 20p11 in female pattern hair loss." In: *Br J Dermatol* 166.6 (June 2012), pp. 1314–1318.

[35] S. Redler, M. P. Birch, **D. Drichel**, K. Dobson, F. F. Brockschmidt, R. Tazi-Ahnini, K. A. Giehl, N. Kluck, R. Kruse, G. Lutz, H. Wolff, T. Becker, M. M. Nothen, A. G. Messenger, and R. C. Betz. "Investigation of variants of the aromatase gene (CYP19A1) in female pattern hair loss." In: *Br J Dermatol* 165.3 (Sept. 2011), pp. 703–705.

[36] **Dmitriy Drichel** and Michael Flohr. "Correlation Functions in N= 3 Superconformal Theory". In: *arXiv preprint arXiv:1006.3346* (2010).