Stanford

Laurens van de Wiel

Postdoctoral Scholar, Cardiovascular Medicine

Bio

BIO

I am a post-doctoral researcher at Stanford University under supervision of Matthew Wheeler and Stephen Montgomery. My research focuses on understanding the entire spectrum of genetic variation effects on protein function and structure in order to decipher molecular mechanisms of disease.

My post-doctoral work centers on developing novel software methodologies which combine multi-omics data to interpret the functional impact of genetic variants in undiagnosed patients. I am part of the Undiagnosed Disease Network (UDN) at Stanford Center for Undiagnosed Diseases (CUD), Genomics Research to Elucidate the Genetics of Rare Diseases (GREGoR) consortium at GREGoR Stanford Site (GSS), and the Molecular Transducers of Physical Activity Consortium (MoTrPAC) at the Bioinformatics Center (BIC).

Before joining Stanford. I was received my Ph.D. in 2021 at the Radboud University Medical Center under supervision of Christian Gilissen, Gert Vriend, and Joris Veltman. I received my MSc degree in 2014 at Radboud University under supervision of Tom Heskes, Evgeni Levin, and Armand Paauw. Before my Ph.D, I worked as a Data Scientist at FLXone, where I developed machine learning solutions within a large-scale, real-time infrastructure.

Research

I am interested in a variety of topics in Bioinformatics and Computer Science. In particular, I am interested in the application of Artificial Intelligence and Statistical Modelling to analyse human (Rare) Mendelian Disease Genetics, Evolutionary Comparative Genomics, Protein Domain Homology, and Molecular Structures.

HONORS AND AWARDS

- Rubicon postdoctoral fellowship grant, The Netherlands Organisation for Scientific Research (NWO) (04/14/2022)
- Best master thesis in computing science of 2014, AIA Software / Radboud University Nijmegen, the Netherlands (2014)

PROFESSIONAL EDUCATION

- Doctor of Philosophy, Katholieke Universiteit Nijmegen (2021)
- Bachelor of Applied Science, Unlisted School (2010)
- Master of Science, Katholieke Universiteit Nijmegen (2014)
- Ph.D, Radboud University Medical Center , Bioinformatics (2021)
- MSc, Radboud University , Computing Science (2014)
- B.A.Sc, Avans University of Applied Science , Computer Science (2010)

STANFORD ADVISORS

- Matthew Wheeler, Postdoctoral Faculty Sponsor
- Matthew Wheeler, Postdoctoral Research Mentor

LINKS

- wiel.science - Personal Site: https://www.wiel.science

Research & Scholarship

LAB AFFILIATIONS

- Euan Ashley, Ashley Lab (10/1/2021)
- Stephen Montgomery, Montgomery Lab (10/1/2021)

Publications

PUBLICATIONS

- **Biallelic LAMP3 Variants in Five Families with Interstitial Lung Disease: Evidence of a Disease-Gene Association.** *Genetics in medicine : official journal of the American College of Medical Genetics*
  Keehan, L. A., Ono-Minagi, H., Hadhud, M., Rips, J., Hinds, D. M., Fischer, A. J., Bartlett, J. A., McCray, P. B., Qawasmi, N., Nathan, N., Louvrier, C., Desroziers, T., Damme, et al
  2026: 102531

- **GREGoR: accelerating genomics for rare diseases.** *Nature*
  Dawood, M., Heavner, B., Wheeler, M. M., Ungar, R. A., LoTempio, J., Wiel, L., Berger, S., Bernstein, J. A., Chong, J. X., Délot, E. C., Eichler, E. E., Lupski, J. R., Shojaie, et al
  2025; 647 (8089): 331-342

- **An optimized variant prioritization process for rare disease diagnostics: recommendations for Exomiser and Genomiser.** *Genome medicine*
  Cooperstein, I. B., Marwaha, S., Ward, A., Kobren, S. N., Carter, J. N., Wheeler, M. T., Marth, G. T.
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- **Scaled multidimensional assays of variant effect identify sequence-function relationships in hypertrophic cardiomyopathy.** *bioRxiv : the preprint server for biology*
  Yamamoto, Y., Chua, K., Ferrasse, A., Kirilova, A., De Jong, H. N., Floyd, B. J., Cadisch, C., Wiel, L., Wang, Q., O'Neill, M. J., Tabet, D., Staudt, D., Goryznski, et al
  2025

- **GREGoR: Accelerating Genomics for Rare Diseases.** *ArXiv*
  Dawood, M., Heavner, B., Wheeler, M. M., Ungar, R. A., LoTempio, J., Wiel, L., Berger, S., Bernstein, J. A., Chong, J. X., Délot, E. C., Eichler, E. E., Gibbs, R. A., Lupski, et al
  2024

- **Molecular adaptations in response to exercise training are associated with tissue-specific transcriptomic and epigenomic signatures.** *Cell genomics*
  Nair, V. D., Pincas, H., Smith, G. R., Zaslavsky, E., Ge, Y., Amper, M. A., Vasoya, M., Chikina, M., Sun, Y., Raja, A. N., Mao, W., Gay, N. R., Esser, et al
  2024: 100421

- **The mitochondrial multi-omic response to exercise training across rat tissues.** *Cell metabolism*
  Amar, D., Gay, N. R., Jimenez-Morales, D., Jean Beltran, P. M., Ramaker, M. E., Raja, A. N., Zhao, B., Sun, Y., Marwaha, S., Gaul, D. A., Hershman, S. G., Ferrasse, A., Xia, et al
  2024

- **The functional impact of rare variation across the regulatory cascade.** *Cell genomics*
  Li, T., Ferraro, N., Strober, B. J., Aguet, F., Kasela, S., Arvanitis, M., Ni, B., Wiel, L., Hershberg, E., Ardlie, K., Arking, D. E., Beer, R. L., Brody, et al
  2023; 3 (10): 100401

- **De novo mutation hotspots in homologous protein domains identify function-altering mutations in neurodevelopmental disorders.** *American journal of human genetics*
  Wiel, L., Hampstead, J. E., Venselaar, H., Vissers, L. E., Brunner, H. G., Pfundt, R., Vriend, G., Veltman, J. A., Gilissen, C.
  2022

- **Mind the Gap: The Complete Human Genome Unlocks Benefits for Clinical Genomics.** *Clinical chemistry*
  Kim, D. S., Wiel, L., Ashley, E. A.
  2022

- **Evidence for 28 genetic disorders discovered by combining healthcare and research data** *NATURE*
  Kaplanis, J., Samocha, K. E., Wiel, L., Zhang, Z., Arvai, K. J., Eberhardt, R. Y., Gallone, G., Lelieveld, S. H., Martin, H. C., McRae, J. F., Short, P. J., Torene, R. I., de Boer, et al
  2020; 586 (7831): 757-+

- **De novo CLTC variants are associated with a variable phenotype from mild to severe intellectual disability, microcephaly, hypoplasia of the corpus callosum, and epilepsy** *GENETICS IN MEDICINE*
  Sa, M., Venselaar, H., Wiel, L., Trimouille, A., Lasseaux, E., Naudion, S., Lacombe, D., Piton, A., Vincent-Delorme, C., Zweier, C., Reis, A., Trollmann, R., Ruiz, et al
  2020; 22 (4): 797-802

- **De Novo Variants in SPOP Cause Two Clinically Distinct Neurodevelopmental Disorders** *AMERICAN JOURNAL OF HUMAN GENETICS*
  Sa, M., El Tekle, G., de Brouwer, A. P. M., Sawyer, S. L., del Gaudio, D., Parker, M. J., Kanani, F., van den Boogaard, M. H., van Gassen, K., Van Allen, M., Wierenga, K., Purcarin, G., Elias, et al
  2020; 106 (3): 405-411

- **De Novo Variants Disturbing the Transactivation Capacity of POU3F3 Cause a Characteristic Neurodevelopmental Disorder** *AMERICAN JOURNAL OF HUMAN GENETICS*
  Blok, L., Kleefstra, T., Venselaar, H., Maas, S., Kroes, H. Y., Lachmeijer, A. M. A., van Gassen, K. L., Firth, H., Tomkins, S., Bodek, S., Study, T. D., Ounap, K., Wojcik, et al
  2019; 105 (2): 403-412

- **MetaDome: Pathogenicity analysis of genetic variants through aggregation of homologous human protein domains** *HUMAN MUTATION*
  Wiel, L., Baakman, C., Gilissen, D., Veltman, J. A., Vriend, G., Gilissen, C.
  2019; 40 (8): 1030-1038

- **De Novo and Inherited Pathogenic Variants in KDM3B Cause Intellectual Disability, Short Stature, and Facial Dysmorphism** *AMERICAN JOURNAL OF HUMAN GENETICS*
  Diets, I. J., van der Donk, R., Baltrunaite, K., Waanders, E., Reijnders, M. R. F., Dingemans, A. J. M., Pfundt, R., Vulto-van Silfhout, A. T., Wiel, L., Gilissen, C., Thevenon, J., Perrin, L., Afenjar, et al
  2019; 104 (4): 758-766

- **Heterozygous missense variants of LMX1A lead to nonsyndromic hearing impairment and vestibular dysfunction** *HUMAN GENETICS*
  Wesdorp, M., Gans, P., Schraders, M., Oostrik, J., Huynen, M. A., Venselaar, H., Beynon, A. J., van Gaalen, J., Piai, V., Voermans, N., van Rossum, M. M., Hartel, B. P., Lelieveld, et al
  2018; 137 (5): 389-400

- **Aggregation of population-based genetic variation over protein domain homologues and its potential use in genetic diagnostics** *HUMAN MUTATION*
  Wiel, L., Venselaar, H., Veltman, J. A., Vriend, G., Gilissen, C.
  2017; 38 (11): 1454-1463

- **Genome-scale detection of positive selection in nine primates predicts human-virus evolutionary conflicts** *NUCLEIC ACIDS RESEARCH*
  van der Lee, R., Wiel, L., van Dam, T. J. P., Huynen, M. A.
  2017; 45 (18): 10634-10648

- **Spatial Clustering of de Novo Missense Mutations Identifies Candidate Neurodevelopmental Disorder-Associated Genes** *AMERICAN JOURNAL OF HUMAN GENETICS*
  Lelieveld, S. H., Wiel, L., Venselaar, H., Pfundt, R., Vriend, G., Veltman, J. A., Brunner, H. G., Vissers, L. M., Gilissen, C.
  2017; 101 (3): 478-484

- **KeCo: Kernel-Based Online Co-agreement Algorithm**

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