Stanford

Laurens van de Wiel

Postdoctoral Scholar, Cardiovascular Medicine

Bio

BIO

Laurens van de Wiel is Dutch scientist from Berghem, The Netherlands. Laurens spent his undergrad in Software Development (BSc, Avans Hogeschool ‘s-Hertogenbosch) and Computing Science (MSc, Radboud University Nijmegen). Laurens continued his career at a start-up, where he created large-scale, real-time analytical software. Laurens continued on his academic trajectory at the Radboudumc in Nijmegen, where he started his PhD in bioinformatics.

During his PhD, Laurens integrated genetic data with protein 3D structures and protein domains. He utilized the skills he obtained before setting out on his academic trajectory; building large-scale, robust, reliable software. Exemplified by the MetaDome Web server (https://stuart.radboudumc.nl/metadome/). During his PhD, he developed novel methodologies for the interpretation of genetic variants of unknown clinical significance and, by integrating structural and evolutionary biology with genomics, Laurens identified 36 novel disease-gene associations for developmental disorders. These discoveries enabled diagnosis for over 500 families worldwide.

Laurens’ areas of expertise are (bioinformatic) software development, data integration of genetic variation with other omics, and his research aims are:
1.) Lessons long-learned in computer science aid computational biology
2.) Multi-omic data integration allows the impact measurement of genetic variation
3.) Diagnosing undiagnosed disorders will uncover novel insights into biology.
4.) International and multidisciplinary collaborations are key in diagnosing rare disorders.

At Stanford University, under guidance of Dr. Matthew Wheeler, he is conducting his postdoctoral studies in line with his research aims.

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

Research & Scholarship

LAB AFFILIATIONS

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

Publications

PUBLICATIONS

- **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. 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. 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. F., Dingemans, A. 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. 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**
  Wiel, L., Heskes, T., Levin, E., Japkowicz, N., Matwin, S.
  SPRINGER-VERLAG BERLIN.2015: 308-315