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Jan Aerts - <http://vda-lab.io>

Personal Information

Date of birth: December 4, 1974
Place of birth: Turnhout, Belgium
Nationality: Belgian
Civil state: married

Interests

- data visualisation and visual analytics
- data science
- topological data analysis
- omics and bioinformatics
- process of knowledge acquisition
- tool development for science

Education and career

2022-present: **Guest Professor** Biological Data Visualisation, TU Eindhoven, Netherlands
2022-present: **Guest Professor** Visual Data Analysis, UHasselt, Belgium
2015-present: **Associate Professor** Visual Data Analysis, KU Leuven, Belgium
2019-2021: **Full Professor** Visual Data Analysis, UHasselt, Belgium
2019-2021: **Director** Data Science Institute, UHasselt, Belgium
2010-2015: **Assistant Professor** Visual Data Analysis, KU Leuven, Belgium
2008-2010: **Senior Bioinformatician**, Wellcome Trust Sanger Institute, Hinxton, UK
2005-2008: **Postdoctoral researcher** Bioinformatics, Roslin Institute, Roslin, Scotland
2001-2005: **PhD research** in Chicken Genomic Resources, Wageningen University, Wageningen, Netherlands
2000-2001: **Research Scientist** Pharmacogenomics, Janssen Pharmaceuticals, Beerse, Belgium
1999-2000: **Advanced Studies** in Cellular Biotechnology, KU Leuven, Belgium
1998-1999: **Data Management Analyst** at Computer Task Group (Diegem) for Janssen Pharmaceuticals
1992-1998: **MSc** Agricultural and Applied Biological Sciences, KU Leuven, Belgium
Major: phytotechnology; minor: cell- & gene biotechnology

Teaching experience

Since 2010, I have taught Master-level courses across different disciplines, including:

- data science and informatics: relational databases, NoSQL databases, lambda architecture, data structures, programming paradigms, topological data analysis, python, HTML/CSS/javascript, ...
- data visualisation and visual analytics: visual design, visualisation libraries (D3, processing, svelte, ...), ...

In addition, I have organised a yearly 1-week workshop on biological data visualisation at the European Bioinformatics Institute (EBI, UK) since 2015, and teach a yearly 1-day workshop on visualisation in evolutionary biology at the University of Leipzig and Berlin since 2011.

Awards

- VAST challenge 2021: Award for Strong Support for Visual Exploration
- VAST challenge 2016: Award - Robust Support for Visual Anomaly Detection
- Winner of VAST challenge 2015
- Winner Data Contest Award Biovis 2014
- Honourable Mention Data Challenge Biovis 2013
- Honourable Mention Redesign Challenge Biovis 2013
- Winner Data Visualization Challenge biovis 2011
- Winner ISMB 2013 best artwork

PhD students (promoter P / co-promoter CP)

- Alejandro Sifrim: Interpretation and Prioritization of Genomic Single-Nucleotide Variation (P; 2016)
- Ryo Sakai: Biological Data Visualization - Analysis and Design (P; 2016)
- Raf Winand: Messy Data in Life Sciences - A Discussion based on Case Studies (P; 2016)
- Parveen Kumar: Bioinformatics for single-cell genome sequence analyses to study genome instability and intra-tumour genetic heterogeneity at high resolution (CP; 2016)
- Amin Ardeshtirdavani: A Development Framework for Data Analytics in Genomics (CP; 2017)
- Daniel Alcaide Villar: Gaining insight in high-dimensional structures - A visual analytics approach (P; current)
- Thomas DeBodt: Visual analytics to support insight generation in dynamic geospatial data (P)
- Thomas Moerman: Scalable Software Solutions for Visualization and Analysis of Complex Data (P)
- Georgia Panagiotidou: Cross-disciplinary sensemaking via data visualization for the archaeological research project of Sagalassos (CP; current)
- Houda Lamqaddam: Information Visualization for Art History Research (CP; current)
- Danai Kafetzaki: Back to basics, with a twist. Applying visual and data analytics to constructing typology and chronology of material culture at ancient Sagalassos and for the discipline of Archaeology (P; current)
- Jelmer Bot: Topological Data Analysis for Sleep Apnea (P; current)
- Jannes Peeters: Visual Analytics for Microbiome Research (P; current)
- Alejandro Correa Rojo: Bioinformatic Analysis of Whole-Genome Data for Precision Health (CP; current)
- Dries Heylen: Omics Data Integration in the IAmFrontier project (CP; current)

Acquired funding

- UHasselt BOF ADMIRE - Association, causality and biomarker Discovery in translational Microbiome REsearch
- FLAIR - Flanders AI Research Program
- Fonds Wetenschappelijk Onderzoek (FWO) Research Project Sagalassos - Applying visual and data analytics to constructing typology and chronology of material culture at ancient Sagalassos and for the discipline of Archaeology
- Program Financing Leuven University: SymBioSys II - From Variome to Phenome
- Agentschap voor Innovatie in Wetenschap en Technologie (IWT) O&O ExaScience Life
- iMinds ICON b-SLIM - A multi-source online super coach for sustainable weight loss
- iMinds ICON MECOVI - Medical Collaborative visualization
- iMinds ICON MyHealthData - Scenarios for a patient's use of healthcare data
- H2020 Virogenesis - Virus discovery and epidemic tracing from high throughput

- metagenomic sequencing
- Agentschap voor Innovatie en Wetenschap en Technologie (IWT) SBO
ACCUMULATE - Acquiring crucial medical information using language technology
- KU Leuven C1 CORAL - The coral reef of culture
- Vlaams Agentschap Innoveren en Ondernemen (VLAIO) Baekeland VISAGE - Visual Analytics to Support Insight Generation in Dynamic Geo-Spatial Data
- KU Leuven C1 - Sagalassos

Recent relevant roles (selection)

- Dagstuhl Seminar 21401 "Visualization of Biological Data - From Analysis to Communication", October 2021
- Panel Clustervisitatie Informatics TUEindhoven, Netherlands, September 2019
- Dagstuhl Seminar 19061 "Visual Analytics on Multi-Layer Networks", January 2019
- Organizing committee member f-TALES Big Data in the Life Science, September 2018
- Organizer Dagstuhl Seminar 18161 "Visualization of Biological Data - Crossroads" 15-20 April 2018
- Founding member Big Data @ KULeuven
- Founding member Leuven Institute Genome and Society (LIGAS)
- Assessment Committee Netherlands eScience Center (NLeSC) 2016
- General co-chair BioVis 2016 at VIS
- Co-organizer VIZBI 2014
- Organizing Committee IEEE VIS - biovis 2013
- Session chair Eurovis/VMLS 2013
- Session chair ISMB 2013
- Session chair VIZBI 2014
- Chair Visualization session BOSC 2013
- Consultant for television program "De Kruitfabriek" (Woestijnvis)
- Organizing Committee IEEE Visweek - biovis 2012
- Best Paper Committee IEEE Visweek - biovis 2012
- International Program Committee EuroGraphics - Visual Computing for Biology and Medicine 2012
- Program Committee 1st IEEE Symposium on Biological Data Visualization (biovis), 2011
- Review committee Bioinformatics Open Source Conference (BOSC) 2011
- Organizing Committee 2nd IEEE Symposium on Biological Data Visualization (biovis), 2012
- Organizing Committee Bioinformatics Open Source Conference (BOSC) 2012
- International Program Committee Eurographics Workshop on Visual Computing for Biology and Medicine, Norrköping, Sweden, 2012

Journal and Conference Publications

(selection; for full list, see <https://orcid.org/0000-0002-6416-2717>)

- Vranckx M, Faes C, Molenberghs G, Hens N, Beutels P, Van Damme P, Aerts J & Petrof O. A Joint Spatial Model to Analyse Self-Reported Survey Data of COVID-19 Symptoms and Lagged Surveillance-Based COVID-19 Incidence Data, *Biometrical Journal* (2022)
- Panagiotidou G, Poblome J, Aerts J & Vande Moere A, *Interdisciplinary Data Visualisation: Acknowledging the Frictions between Different Epistemologies* (2021)
- Peeters J, Thas O, Shkedy, et al. Exploring the Microbiome Analysis and Visualisation Landscape. *Frontiers in Bioinformatics*. Accepted for publication.
- Aerts J, Peeters J, Bot J, Kafetzaki D & Lamqaddam H. Remote Instruction for Data Visualization Design - a Report from the Trenches, in *IEEE Computer Graphics & Applications* (2021) doi: <https://doi.org/10.1109/MCG.2021.3116042>.
- Alcaide D, Aerts J. A visual analytic approach for the identification of ICU patient

- subpopulations using ICD diagnostic codes. *PeerJ Computer Science* 7:e430 <https://doi.org/10.7717/peerj-cs.430> (2021)
- Neyens N et al. Can COVID-19 symptoms as reported in a large-scale online survey be used to optimise spatial predictions of COVID-19 incidence risk in Belgium? *Spatial and Spatio-temporal Epidemiology*, 35:100379 (2020) <https://doi.org/10.1016/j.sste.2020.100379>
 - Panagiotidou G, Aerts J & Vande Moere A. GoCo: A Gamified Activity for Winnowing Visualization Projects with Interdisciplinary Experts. *IEEE VIS Workshop on Data Vis Activities* (2020)
 - Molenberghs G et al. Belgian COVID-19 mortality, excess deaths, number of deaths per million, and infection fatality rates (8 March - 9 May 2020). Preprint at <https://doi.org/10.1101/2020.06.20.20136234> (2020).
 - Alcaide D & Aerts J. Spanning Trees as Approximation of Data Structures. *IEEE Transactions on Visualization and Computer* 27(10): 3994-4008 (2021) doi: 10.1109/TVCG.2020.2995465.
 - Brosens K, Aerts J, Alen K, Beerens RJ, Cardoso B *et al.* Slow Digital Art History in Action: Project Cornelia's Computational Approach to Seventeenth-century Flemish Creative Communities. *Visual Resources* 1-20 (2019)
 - Knudsen S, Aerts J, Archambault D, Chang R, Fekete J-D et al. Unifying the framework of Multi-Layer Network and Visual Analytics. *Visual Analytics of Multilayer Networks Across Disciplines*, 9 (2), pp.19-23, Dagstuhl Reports (2019)
 - Lamqaddam H, Brosens K, Verbert K & Aerts J. NAHR: A Visual Representation of Social Networks as Support for Art History Research. *Nordic Forum for Human-Computer Interaction (nordiCHI)*, 634-641 (2018)
 - Kyndt E & Aerts J. Op maat matchen. Een wicked probleem dat een innovatieve aanpak vraagt. In: *Leren Duaal Leren*. Eds Dekocker V & Sodermans AK (2018)
 - Alcaide D & Aerts J. MCLEAN: Multilevel Clustering Exploration As Network. *PeerJ Computer Science* 4:e145 <https://doi.org/10.7717/peerj-cs.145> (2018)
 - Brosens, K., Aerts, J., Alen, K., Slegten, A., & Truyen, F. (2017). Visualizing and Analyzing Complex and Dynamic Networks of Flemish Tapestry Entrepreneurs (1640–1720). *Leonardo*, 50(5), 503-503.
 - Lamqaddam H & Aerts J. InViTe - Towards Intuitive Visualization of Iterations over Text. *Eurographics Conference on Visualization (EuroVis) Posters Track* (2016)
 - Aerts J, Marai GE, Nieselt K, Nielsen C, Streit M & Weiskopf D. Highlights from the 5th Symposium on Biological Data Visualization: Part 1. *BMC Bioinformatics* 16(Suppl 11):S1 (2015)
 - Aerts J, Marai GE, Nieselt K, Nielsen C, Streit M & Weiskopf D. Highlights from the 5th Symposium on Biological Data Visualization: Part 2. *BMC Bioinformatics* 16(Suppl 11):S1 (2015)
 - Sakai R & Aerts J. Card sorting techniques for domain characterization in problem-driven visualization research. *Eurographics Conference on Visualization (EuroVis)* 2015. DOI: 10.2312/eurovisshort.20151136
 - Chua, A., Sakai, R., Aerts, J., & Vande Moere, A. (2015). A three step process to design visualisations for GeoTemporal analysis (VAST 2014 Mini Challenge 2). 2014 IEEE Conference on Visual Analytics Science and Technology, VAST 2014 - Proceedings, 349–350. <http://doi.org/10.1109/VAST.2014.7042560>
 - Sakai R & Aerts J. 2014. "Sequence Diversity Diagram for Comparative Analysis of Multiple Sequence Alignments." *BMC Proceedings* 8 (Suppl 2 Proceedings of the 3rd Annual Symposium on Biological Data Visualization) (January): S9. doi:10.1186/1753-6561-8-S2-S9.
 - Katayama T, Wilkinson MD, Aoki-Kinoshita KF, Kawashima S, Yamamoto Y, Yamaguchi A, Okamoto S, Kawano S, Kim JD, Wang Y et al. BioHackathon series in 2011 and 2012: penetration of ontology and linked data in life science domains. *Journal of Biomedical Semantics* 5:5 (2014)
 - Sakai R, Moisse M, Reumers J & Aerts J. Pipit: visualizing functional impacts of

- structural variations. *Bioinformatics* 29(17):2206-2207 (2013)
- Pavlopoulos GA, Oulas A, Iacucci E, Sifrim A, Moreau Y, Schneider R, Aerts J & Iliopoulos I. Unraveling genomic variation from next generation sequencing data. *BioData Min.* 6(1):13 (2013)
 - Sakai R, Sifrim A, Reumers J, Moreau Y & Aerts J. TrioVis - using visualization to investigate the effect of filter settings on genotype concordance in trios. *BMC Bioinformatics* 29(14):1801-1802 (2013)
 - Pavlopoulos GA, Kumar P, Sifrim A, Sakai R, Lin ML, Voet T, Moreau Y & Aerts J. Meander: visually exploring the structural variome using space-filling curves. *Nucleic Acids Res.* 11:1-9 (2013) doi:10.1093/nar/gtk254
 - Katayama T, Wilkinson M, Micklem G, Kawashima S, Yamaguchi A, Belleau F, Nakao M, Yamamoto Y, Oouchida K, Chun HW et al. The 3rd DBCLS BioHackathon: Improving life science data integration with Semantic Web technologies. *Journal of Biomedical Semantics* 4(1):6 (2013)
 - Sifrim A, Van Houdt JKJ, Tranchevent L-C, Nowakowska B, Sakai R, Pavlopoulos GA, Devriendt K, Vermeesch JR, Moreau Y & Aerts J. Interpretation of single nucleotide variation in human disease: a Swiss-knife approach to annotation and analysis. *Genome Medicine* 4(9):73 (2012)
 - Mishima H, Aerts J, Katayama T, Bonnal RJP & Yoshiura KI. The Ruby UCSC API: accessing the UCSC genome database using Ruby. *BMC Bioinformatics* 13:240 (2012).
 - Thomas Boogaerts, Léon-Charles Tranchevent, Georgios A. Pavlopoulos, Jan Aerts and Joos Vandewalle. Visualizing High Dimensional Datasets Using Parallel Coordinates: Application to Gene Prioritization. *Proc. 12th IEEE international conference on bioinformatics and bioengineering BIBE* (2012)
 - Neylon C, Aerts J, Brown CT, Lemire D, Millman J, Murray-Rust P, Perez F, Saunders N, Smith A, Varoquaux G & Willighagen E. Changing computational research. The challenges ahead. *Source Code for Biology and Medicine* 7:2 (2012)
 - Bartlett C, Cheong SY, Hou L, Paquette J, Lum PY, Jaeger G, Battke F, Vehlouw C, Heinrich J, Nieselt K, Sakai R, Aerts J & Ray WC. An eQTL biological data visualization challenge and approaches from the visualization community. *BMC Bioinformatics* 13(Suppl 8):S8 (2012)
 - Secrier M, Pavlopoulos GA, Aerts J & Schneider R. Arena3D: visualizing time-driven phenotypic differences in biological systems. *BMC Bioinformatics* 13:45 (2012) [Highly accessed]
 - Bonnal RJP, Aerts J, Githinji G, Goto N, MacLean D, Miller CA, Mishima H, Pagani M, Ramirez-Gonzalez R, Smant G et al. Biogem: an effective tool based approach for scaling up open source software development in bioinformatics. *Bioinformatics* 28(7):1035-1037 (2012)
 - Pavlopoulos GA, Hooper SD, Sifrim A, Schneider R & Aerts J. Medusa: A tool for exploring and clustering biological networks. *BMC Research Notes* 4:384 (2011)
 - Katayama T, Wilkinson MD, Vos R, Kawashima T, Kawashima S, Nakao M, Yamamoto Y, Chun HW, Yamaguchi A, Kawano S, Aerts J et al. The 2nd DBCLS BioHackathon: interoperable bioinformatics Web services for integrated applications. *Journal of Biomedical Semantics* 2:4 (2011)
 - Pavlopoulos G, Secrier M, Moschopoulos CN, Soldatos TG, Kossida S, Aerts J, Schneider R & Bagos PG. Using graph theory to analyze biological networks. *BMC BioData Mining* 4:10 (2011) - highly accessed
 - Strozzi F & Aerts J. A Ruby interface to query the Ensembl database for genomic features. *Bioinformatics* 27(7):1013-1014 (2011)
 - Kettner C, Field D, Sansone S, Taylor C, Aerts J, Binns N, Black A, Britten CM, de Marco A, Fostel J et al. Meeting report from the second "Minimum Information for Biological and Biomedical Investigations" (MIBBI) workshop. *Standards in Genomic Sciences* 3(3):259-266 (2010)
 - Goto N, Prins P, Nakao M, Bonnal R, Aerts J & Katayama T. BioRuby: *Bioinformatics*

software for the Ruby programming language. *Bioinformatics* 26(20):2617-1619 (2010)

- The Wellcome Trust Case Control Consortium. Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. *Nature* 464:713-720 (2010)
- Conrad D, Pinto D, Redon R, Feuk L, Gokumen O, Zhang Y, Aerts J, Andrews D, Barnes C, Campbell P et al. Origins and functional impact of copy number variation in the human genome. *Nature* 464:704-712 (2010)
- Aerts J & Tyler-Smith C. Structural variation in Great Ape genomes. In: *Encyclopedia of Life Sciences*. John Wiley & Sons, Ltd. Chichester (2009)
- The Bovine Genome Sequencing and Analysis Consortium, Elsik CG, Tellam RL & Worley KC. The genome sequence of taurine cattle: a window to ruminant biology and evolution. *Science* 324(5926):522-528 (2009)
- Taylor CF, Field D, Sansone SA, Aerts J, Apweiler R, Ashburner M, Ball CA, Binz PA, Bogue M, Booth T et al. Promoting coherent minimum reporting requirements for biological and biomedical investigations: The MIBBI Project. *Nature Biotechnol* 26:889-896 (2008)
- International Chicken Genome Sequencing Consortium. Sequencing and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. *Nature* 432:695-716 (2004)
- Wallis JW, Aerts J, Groenen M, Crooijmans R, Layman D, Graves T, Scheer D, Kremitzki C, Higgenbotham J, Gaige T et al. A physical map of the chicken genome. *Nature* 432:761-764 (2004)

Patents

USPTO 20030190649: Data Mining of SNP Databases for the Selection of Intragenic SNPs

Languages

Dutch: mother tongue

English: fluent

French: moderate

German: moderate