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## PERSONAL INFORMATION

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

## IN BRIEF

- +20 years experience in Data Management and Governance; expert in Data Visualisation and Visual Analytics
- +10 years teaching experience at Master level (including molecular biology, data management, data visualisation)
- Performed data integration in large international whole-genome sequencing projects
- Supervised a team leading to several awards on the topic of data visualisation and visual analytics
- >100 scientific publications (h-index: 37; <https://orcid.org/0000-0002-6416-2717>)
- Language skills: fluent in English and Dutch, intermediate level of French, elementary level of German
- Master in Bioscience Engineering
- PhD in Animal Sciences

## INTERESTS

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

## AIM

First, it is my firm belief that we need to put the human back in the loop of data analysis, in order to gain deeper insights in complex datasets and define new hypotheses through visual data exploration. This requires both advances in data transformation (“how do we transform the original data such that we can visualise it”) as in visual design research

(“what does a visualisation look like”). Bringing my experience to this question, I aim to help experts explore their data and analysis results in context (e.g. in combination with raw data and/or effects of changes in parameter space). This helps to build trust in those results and give the experts a deeper insight than what a single summary statistic can do. In addition, data visualisation is a strong tool for the data analyst and statistician to clean their data, and to identify issues with that data as well as unexpected trends in the projects. Finally, visualisation is an excellent tool for supporting business operations through dashboarding.

In addition, my deep experience in data management and integration supports organisations in thinking strategically about the different data sources they have and how they could or should be managed. My expertise helps in defining and tackling data security, avoiding data corruption, ensuring data quality, preventing data decline, keeping track of data provenance, organising data stewardship, and setting up systems for data integration across projects and groups.

## EDUCATION AND CAREER

2022: **Research Fellow** Amador Bioscience, Hasselt, Belgium

2022-present: **Guest Professor** Visual Data Analysis, UHasselt, Belgium

2022-present: **Guest Professor** Visual Data Analysis, KU Leuven, 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- & genebiotechnology

## 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, ...), ...
- life sciences: omics technologies, bioinformatics, cellular biologie, ...

In addition, I organise 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

## WORKING VISITS ABROAD

June-July 2003 - Washington University School of Medicine, StLouis, MO, USA

October 2003 - Washington University School of Medicine, StLouis, MO, USA

## JOURNAL AND CONFERENCE PUBLICATIONS

(selection out of >100; 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)
- 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](https://doi.org/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)

- Faria R, Triant D, Perdomo-Sabogal A et al. Introducing evolutionary biologists to the analysis of big data: guidelines to organize extended bioinformatics training courses. *Evolution: Education and Outreach*. 11(1):8 (2018)
- 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)
- Verbeiren T, Sakai R & Aerts J. A Pragmatic Approach to Biases in Visual Data Analysis. *DECISIVE : Workshop on Dealing with Cognitive Biases in Visualisations*, IEEE VIS2014. Nov 9th 2014, Paris.
- 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>
- 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)
- 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)
- 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).
- The DBCLS BioHackathon Consortium. The DBCLS BioHackathon: standardization and interoperability for bioinformatics web services and workflows. *Journal of Biomedical Semantics* 1(1):8 (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)
- The Bovine HapMap Consortium. Genome-wide survey of SNP variation uncovers the genetic structure of cattle breeds. *Science* 324(5926):528-532 (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)

## 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
- 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 ISMB
- General co-chair BioVis 2016 at VIS
- Organizing Committee & Session Chair Beyond the Genome 2014
- Co-organizer VIZBI 2014
- Organizing Committee IEEE VIS - biovis 2013

- Session chair Eurovis/VMLS 2013
- Session chair ISMB 2013
- Session chair VIZBI 2014
- Program Committee ISMB 2013
- 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 ECCB2012
- 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, Norrkoping, Sweden, 2012

## PATENTS

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

## LANGUAGES

Dutch: mother tongue

English: fluent

French: moderate

German: moderate