

Wout Bittremieux

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Work experience

University of Washington, Seattle, WA, USA

Visiting researcher

Sept. 2017 – current

Develop deep learning models for the analysis of mass spectrometry proteomics data.

University of Antwerp, Antwerp, Belgium

Postdoctoral researcher

Mar. 2017 – current

Investigate how machine learning can be used to solve bioinformatics challenges, with a special focus on mass spectrometry proteomics.

Stellenbosch University, Cape Town, South Africa

Visiting researcher

Sept. 2016 – Dec. 2016

Develop computational quality control techniques for mass spectrometry proteomics.

Education

University of Antwerp, Antwerp, Belgium

PhD in Computer Science

Mar. 2013 – Feb. 2017

PhD thesis: “Computational solutions for quality control of mass spectrometry-based proteomics”.

Hasselt University, Diepenbeek, Belgium

Master in Computer Science, completed with great honor

Sept. 2010 – Jun. 2012

Master thesis: “Time series similarity search”.

Bachelor in Computer Science, completed with honor

Sept. 2007 – Jun. 2010

Awards

- 2017 Research Foundation – Flanders (FWO): travel fellowship for a nine-month research stay at the University of Washington in Seattle, WA, USA
- 2017 Research Foundation – Flanders (FWO): travel fellowship to attend the annual conference of the American Society for Mass Spectrometry (ASMS) 2017 in Indianapolis, IN, USA
- 2016 Research Foundation – Flanders (FWO): travel fellowship for a three-month research stay at Stellenbosch University in Cape Town, South Africa
- 2016 Research Foundation – Flanders (FWO): travel fellowship to attend the annual conference of the American Society for Mass Spectrometry (ASMS) 2016 in San Antonio, TX, USA
- 2015 Benelux Bioinformatics Conference (BBC) 2015: best oral presentation award

Grants and fellowships

2017–2020 Research Foundation – Flanders (FWO): postdoctoral fellowship

Publications

Journal articles.....

- [15] Eric W Deutsch, Sandra Orchard, Pierre-Alain Binz, **Wout Bittremieux**, et al. “Proteomics Standards Initiative: Fifteen Years of Progress and Future Work”. In: *Journal of Proteome Research* Article ASAP (Aug. 29, 2017). DOI: [10.1021/acs.jproteome.7b00370](https://doi.org/10.1021/acs.jproteome.7b00370).
- [14] **Wout Bittremieux**, David L Tabb, Francis Impens, An Staes, et al. “Quality Control in Mass Spectrometry-Based Proteomics”. In: *Mass Spectrometry Reviews* Early view (Aug. 12, 2017). DOI: [10.1002/mas.21544](https://doi.org/10.1002/mas.21544).
- [13] Nicolas De Neuter, **Wout Bittremieux**, Charlie Beirnaert, Bart Cuypers, et al. “On the Feasibility of Mining CD8+ T-Cell Receptor Patterns Underlying Immunogenic Peptide Recognition.” In: *Immunogenetics* Early view (Aug. 4, 2017). DOI: [10.1007/s00251-017-1023-5](https://doi.org/10.1007/s00251-017-1023-5).
- [12] Juan Antonio Vizcaíno, Mathias Walzer, Rafael C Jiménez, **Wout Bittremieux**, et al. “A Community Proposal to Integrate Proteomics Activities in ELIXIR [Version 1; Referees: 2 Approved]”. In: *F1000Research* 6 (June 13, 2017), p. 875. DOI: [10.12688/f1000research.11751.1](https://doi.org/10.12688/f1000research.11751.1).
- [11] **Wout Bittremieux**, Mathias Walzer, Stefan Tenzer, Weimin Zhu, et al. “The Human Proteome Organization–Proteomics Standards Initiative Quality Control Working Group: Making Quality Control More Accessible for Biological Mass Spectrometry”. In: *Analytical Chemistry* 89.8 (Apr. 18, 2017), pp. 4474–4479. DOI: [10.1021/acs.analchem.6b04310](https://doi.org/10.1021/acs.analchem.6b04310).
- [10] **Wout Bittremieux**, Dirk Valkenborg, Lennart Martens, and Kris Laukens. “Computational Quality Control Tools for Mass Spectrometry Proteomics”. In: *PROTEOMICS* 17 (3-4 Feb. 2017), p. 1600159. DOI: [10.1002/pmic.201600159](https://doi.org/10.1002/pmic.201600159).
- [9] Pieter Meysman, Yvan Saeys, Ehsan Sabaghian, **Wout Bittremieux**, et al. “Mining the Enriched Subgraphs for Specific Vertices in a Biological Graph”. In: *IEEE/ACM Transactions on Computational Biology and Bioinformatics* Early access (June 7, 2016), p. 1. DOI: [10.1109/TCBB.2016.2576440](https://doi.org/10.1109/TCBB.2016.2576440).
- [8] Evelyne Maes, Pieter Kelchtermans, **Wout Bittremieux**, Kurt De Grave, et al. “Designing Biomedical Proteomics Experiments: State-of-the-Art and Future Perspectives”. In: *Expert Review of Proteomics* 13.5 (Apr. 25, 2016), pp. 495–511. DOI: [10.1586/14789450.2016.1172967](https://doi.org/10.1586/14789450.2016.1172967).
- [7] **Wout Bittremieux**, Pieter Meysman, Lennart Martens, Dirk Valkenborg, et al. “Unsupervised Quality Assessment of Mass Spectrometry Proteomics Experiments by Multivariate Quality Control Metrics”. In: *Journal of Proteome Research* 15.4 (Apr. 1, 2016), pp. 1300–1307. DOI: [10.1021/acs.jproteome.6b00028](https://doi.org/10.1021/acs.jproteome.6b00028).
- [6] **Wout Bittremieux**, Hanny Willems, Pieter Kelchtermans, Lennart Martens, et al. “iMonDB: Mass Spectrometry Quality Control through Instrument Monitoring”. In: *Journal of Proteome Research* 14.5 (May 1, 2015), pp. 2360–2366. DOI: [10.1021/acs.jproteome.5b00127](https://doi.org/10.1021/acs.jproteome.5b00127).

- [5] Stefan Naulaerts, Pieter Meysman, **Wout Bittremieux**, Trung Nghia Vu, et al. “A Primer to Frequent Itemset Mining for Bioinformatics”. In: *Briefings in Bioinformatics* 16.2 (Mar. 2015), pp. 216–231. DOI: [10.1093/bib/bbt074](https://doi.org/10.1093/bib/bbt074).
- [4] Trung Nghia Vu, **Wout Bittremieux**, Dirk Valkenburg, Bart Goethals, et al. “Efficient Reduction of Candidate Matches in Peptide Spectrum Library Searching Using the Top k Most Intense Peaks”. In: *Journal of Proteome Research* 13.9 (Sept. 5, 2014), pp. 4175–4183. DOI: [10.1021/pr401269z](https://doi.org/10.1021/pr401269z).
- [3] Mathias Walzer, Lucia Espona Pernas, Sara Nasso, **Wout Bittremieux**, et al. “qcML: An Exchange Format for Quality Control Metrics from Mass Spectrometry Experiments”. In: *Molecular & Cellular Proteomics* 13.8 (Aug. 1, 2014), pp. 1905–1913. DOI: [10.1074/mcp.M113.035907](https://doi.org/10.1074/mcp.M113.035907).
- [2] **Wout Bittremieux**, Pieter Kelchtermans, Dirk Valkenburg, Lennart Martens, et al. “jqcML: An Open-Source Java API for Mass Spectrometry Quality Control Data in the qcML Format”. In: *Journal of Proteome Research* 13.7 (July 3, 2014), pp. 3484–3487. DOI: [10.1021/pr401274z](https://doi.org/10.1021/pr401274z).
- [1] Pieter Kelchtermans, **Wout Bittremieux**, Kurt De Grave, Sven Degroeve, et al. “Machine Learning Applications in Proteomics Research: How the Past Can Boost the Future”. In: *PROTEOMICS* 14 (4-5 Mar. 2014), pp. 353–366. DOI: [10.1002/pmic.201300289](https://doi.org/10.1002/pmic.201300289).

Conference proceedings.....

- [1] Pieter Meysman, Yvan Saeys, Ehsan Sabaghian, **Wout Bittremieux**, et al. “Discovery of Significantly Enriched Subgraphs Associated with Selected Vertices in a Single Graph”. In: *Proceedings of the 14th International Workshop on Data Mining in Bioinformatics - BIODDD '15*. Sydney, Australia, Aug. 10, 2015, p. 8.

Other publications.....

- [2] Aida Mrzic, Pieter Meysman, **Wout Bittremieux**, and Kris Laukens. “Automated Recommendation of Metabolite Substructures from Mass Spectra Using Frequent Pattern Mining”. In: *bioRxiv* (May 4, 2017). DOI: [10.1101/134189](https://doi.org/10.1101/134189).
- [1] **Wout Bittremieux**. “Computational Solutions for Quality Control of Mass Spectrometry-Based Proteomics”. Antwerp, Belgium: Universiteit Antwerpen, Feb. 24, 2017. 129 pp.

Presentations

Oral presentations.....

- [8] **Wout Bittremieux**. “Shedding Light on Complex Mass Spectrometry Proteomics Processes through Advanced Data Mining”. In: *Faculty of Science Research Day* Antwerp, Belgium (Jan. 13, 2017). DOI: [10.5281/zenodo.242392](https://doi.org/10.5281/zenodo.242392).
- [7] **Wout Bittremieux**. “Git: How Version Control Can Power Your Research”. In: *Biomina Lunch Talks* Antwerp, Belgium (June 24, 2016). DOI: [10.5281/zenodo.56352](https://doi.org/10.5281/zenodo.56352).
- [6] **Wout Bittremieux**, Dirk Valkenburg, and Kris Laukens. “Optimized Open Modification Spectral Library Searching Using Approximate Nearest Neighbor Techniques”. In: *ASMS annual conference* San Antonio, TX, USA (June 9, 2016). DOI: [10.5281/zenodo.55999](https://doi.org/10.5281/zenodo.55999).

- [5] **Wout Bittremieux**, Pieter Meysman, Lennart Martens, Bart Goethals, et al. “Approaches for Mass Spectrometry Quality Control”. In: *Biomina Research Day* Antwerp, Belgium (Dec. 9, 2015). DOI: [10.5281/zenodo.56004](https://doi.org/10.5281/zenodo.56004).
- [4] **Wout Bittremieux**, Pieter Meysman, Lennart Martens, Bart Goethals, et al. “Analysis of Mass Spectrometry Quality Control Metrics”. In: *Benelux Bioinformatics Conference* Antwerp, Belgium (Dec. 7, 2015). DOI: [10.5281/zenodo.56001](https://doi.org/10.5281/zenodo.56001).
- [3] **Wout Bittremieux** and Kris Laukens. “Precursor-Free and Fast Spectral Library Search Using Approximate Nearest Neighbor Techniques”. In: *Benelux Bioinformatics Conference Student Council Symposium* Antwerp, Belgium (Dec. 6, 2015). DOI: [10.5281/zenodo.56002](https://doi.org/10.5281/zenodo.56002).
- [2] **Wout Bittremieux**, Emmanuel Müller, Dirk Valkenburg, Lennart Martens, et al. “Pattern Mining of Mass Spectrometry Quality Control Data”. In: *Benelux Bioinformatics Conference* Luxembourg, Luxembourg (Dec. 9, 2014). DOI: [10.5281/zenodo.56000](https://doi.org/10.5281/zenodo.56000).
- [1] **Wout Bittremieux**, Pieter Kelchtermans, Dirk Valkenburg, Lennart Martens, et al. “Collecting and Mining Mass Spectrometry Quality Control Data”. In: *Biomina Research Day* Antwerp, Belgium (Feb. 20, 2014). DOI: [10.5281/zenodo.56003](https://doi.org/10.5281/zenodo.56003).

Poster presentations.....

- [8] **Wout Bittremieux**, Dirk Valkenburg, and Kris Laukens. “Towards the Smart Lab: A Comprehensive Approach to Mass Spectrometry Quality Control”. In: *ASMS annual conference* Indianapolis, IN, USA (June 8, 2017). DOI: [10.5281/zenodo.584052](https://doi.org/10.5281/zenodo.584052).
- [7] **Wout Bittremieux** and Kris Laukens. “Mass Spectrometry Proteomics: Ready for the Deep Learning (r)Evolution?” In: *ASMS annual conference* Indianapolis, IN, USA (June 8, 2017). DOI: [10.5281/zenodo.584067](https://doi.org/10.5281/zenodo.584067).
- [6] **Wout Bittremieux**, Pieter Meysman, Lennart Martens, Dirk Valkenburg, et al. “Automatic Quality Assessment of Mass Spectrometry Experiments by Multivariate Quality Control Metrics”. In: *ASMS annual conference* San Antonio, TX, USA (June 9, 2016). DOI: [10.5281/zenodo.55998](https://doi.org/10.5281/zenodo.55998).
- [5] **Wout Bittremieux**, Hanny Willems, Lennart Martens, Dirk Valkenburg, et al. “Mass Spectrometry Quality Control: Instrument Monitoring and Pattern Mining Insights”. In: *ASMS annual conference* St. Louis, MO, USA (June 2, 2015). DOI: [10.5281/zenodo.55992](https://doi.org/10.5281/zenodo.55992).
- [4] **Wout Bittremieux**, Hanny Willems, Lennart Martens, Bart Goethals, et al. “A Comprehensive Approach to Mass Spectrometry Quality Control”. In: *Two-day symposium of the Belgian Proteomics Association* Brussels, Belgium (Dec. 18, 2014). DOI: [10.5281/zenodo.55990](https://doi.org/10.5281/zenodo.55990).
- [3] **Wout Bittremieux**, Dirk Valkenburg, Aida Mrzic, Hanny Willems, et al. “Pattern Mining of Mass Spectrometry Quality Control Data”. In: *European Conference on Computational Biology* Strasbourg, France (Sept. 7, 2014). DOI: [10.5281/zenodo.55989](https://doi.org/10.5281/zenodo.55989).
- [2] **Wout Bittremieux**, Pieter Kelchtermans, Dirk Valkenburg, Lennart Martens, et al. “Mining Mass Spectrometry Quality Control Data”. In: *ASMS annual conference* Baltimore, MD, USA (June 16, 2014). DOI: [10.5281/zenodo.55988](https://doi.org/10.5281/zenodo.55988).
- [1] **Wout Bittremieux**, Pieter Kelchtermans, Dirk Valkenburg, Lennart Martens, et al. “jqcML: An Open-Source Java API for Mass Spectrometry Quality Control Data in the qcML Format”. In: *Benelux Bioinformatics Conference* Brussels, Belgium (Dec. 9, 2013). DOI: [10.5281/zenodo.55986](https://doi.org/10.5281/zenodo.55986).

Software demonstrations.....
[1] **Wout Bittremieux** and Dirk Valkenburg. “iMonDB: Mass Spectrometry Instrument Monitoring for Quality Control”. In: *Methods and tools for intra- and inter-experiment LC MS performance tracking workshop, ASMS annual conference* St. Louis, MO, USA (June 1, 2015).

Teaching

- 2017 Introduction to computational biology • Bachelor of Computer Science
teaching assistant
- 2016 Project work • Bachelor of Mathematics
teaching assistant
- 2014–2015 Data mining • Master of Biochemistry and Biotechnology
teaching assistant
- 2015 Data mining • Master of Computer Science
guest lecturer

Student supervision

- 2017 Joeri Reyns • Master of Computer Science: Thesis
“Protein identification using deep neural networks”
- 2017 Keerthana Sanala Prakash • Master of Computer Science: Research internship
“Temporal mining of mass spectrometry quality control data”
- 2016 Phui San Cheong • Master of Computer Science: Research internship
“Implement frequent itemset-based clustering in pyGCluster”
- 2016 Robin Verachtert • Bachelor of Computer Science: Research internship
“Automatic discovery of artefacts in mass spectrometry data”

Referee

Referee for: *Analytical Chemistry, International Workshop on Data Mining in Bioinformatics 2016 (BioKDD’16), Mass Spectrometry Reviews, NIPS Workshop on Machine Learning in Computational Biology 2017 (NIPS MLCB 2017)*.

Scientific meetings organized

- 2018 European Bioinformatics Community (EuBIC) developer’s meeting
main organizer

- 2015 [Benelux Bioinformatics Conference \(BBC\)](#)
member of the local organizing committee
- 2014 [Belgian Proteomics Association Symposium \(BePac\)](#)
member of the local organizing committee

Membership of scientific organizations

- 2017–... [European Bioinformatics Community \(EuBIC\)](#)
member
- 2016–... [Human Proteome Organization \(HUPO\) – Proteomics Standards Initiative \(PSI\)](#)
secretary of the Quality Control working group
- 2013–... [American Society of Mass Spectrometry \(ASMS\)](#)
member
- 2014–2015 [International Society for Computational Biology \(ISCB\)](#)
member