

# Wout Bittremieux

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## Employment

- 2019–... POSTDOCTORAL RESEARCHER (Pharmacy)  
**University of California San Diego**, La Jolla, CA, USA  
Advisor: Prof. Pieter C. Dorrestein
- 2017–2019 POSTDOCTORAL RESEARCHER (Genome Sciences)  
**University of Washington**, Seattle, WA, USA  
Advisor: Prof. William Stafford Noble
- 2017 POSTDOCTORAL RESEARCHER (Computer Science)  
**University of Antwerp**, Antwerp, Belgium  
Advisor: Prof. Kris Laukens
- 2016 VISITING RESEARCHER (Molecular Biology)  
**Stellenbosch University**, Cape Town, South Africa

## Education

- 2013–2017 PHD Computer Science  
**University of Antwerp**, Antwerp, Belgium  
Thesis: *Computational Solutions for Quality Control of Mass Spectrometry-based Proteomics*  
Co-advisors: Prof. Kris Laukens, Prof. Bart Goethals
- 2010–2012 MSc Computer Science – Great Distinction  
**Hasselt University**, Diepenbeek, Belgium  
Thesis: *Time Series Similarity Search*  
Thesis advisor: Prof. Marc Gyssens
- 2007–2010 BA Computer Science – Distinction  
**Hasselt University**, Diepenbeek, Belgium  
Thesis: *Extending a Web Browser With Additional Navigation Options*  
Thesis advisor: Prof. Jan Van den Bussche

## Awards

- 2020 American Society for Mass Spectrometry: Postdoctoral Career Development Award
- 2019 Research Foundation – Flanders: Travel award to attend the Human Proteome Organization – Proteomics Standards Initiative Spring Meeting 2019 in Cape Town, South Africa
- 2017 Research Foundation – Flanders: Travel award for a nine-month research stay at the University of Washington in Seattle, WA, USA

- 2017 Research Foundation – Flanders: Travel award to attend the annual conference of the American Society for Mass Spectrometry 2017 in Indianapolis, IN, USA
- 2016 Research Foundation – Flanders: Travel award for a three-month research stay at Stellenbosch University in Cape Town, South Africa
- 2016 Research Foundation – Flanders: Travel award to attend the annual conference of the American Society for Mass Spectrometry 2016 in San Antonio, TX, USA
- 2015 Benelux Bioinformatics Conference 2015: Best Oral Presentation Award

## Professional activities

### Referee

**Journals** Analytical Chemistry, Artificial Intelligence in Medicine, Bioinformatics, IEEE/ACM Transactions on Computational Biology and Bioinformatics, Journal of Proteome Research, Mass Spectrometry Reviews, Metabolites, PLOS ONE, PROTEOMICS, Scientific Reports

**Conferences** Annual International Conference on Research in Computational Molecular Biology, Conference on Intelligent Systems for Molecular Biology, International Workshop on Data Mining in Bioinformatics, Machine Learning in Computational Biology, NIPS Workshop on Machine Learning in Computational Biology

### Scientific meetings organized

- 2020 European Bioinformatics Community Developers' Meeting: Member of the organizing committee
- 2020 Intelligent Systems for Molecular Biology Conference, Mass Spectrometry & Proteomics Track: Co-chair
- 2019 European Bioinformatics Community Winter School: Member of the organizing committee
- 2019 Machine Learning in Computational Biology: PC member
- 2018 European Bioinformatics Community Developers' Meeting: Main organizer
- 2015 Benelux Bioinformatics Community: Member of the organizing committee
- 2014 Belgian Proteomics Association Symposium: Member of the local organizing committee

### Professional affiliations

- 2017–... European Bioinformatics Community: Member
- 2016–... Human Proteome Organization – Proteomics Standards Initiative: Secretary of the Quality Control Working Group
- 2013–... American Society of Mass Spectrometry: Member
- 2014–2015 International Society for Computational Biology: Member

## Publications

### Journal articles

- [24] Youzhong Liu, Aida Mrzic, Pieter Meysman, Thomas De Vijlder, Edwin P Romijn, Dirk Valkenburg, **Wout Bittremieux**, and Kris Laukens. "MESSAR: Automated Recommendation of Metabolite Substructures from Tandem Mass Spectra." *PLOS ONE* 15.1 (2020), e0226770. doi: [10.1371/journal.pone.0226770](https://doi.org/10.1371/journal.pone.0226770).
- [23] **Wout Bittremieux**. "Spectrum\_utils: A Python Package for Mass Spectrometry Data Processing and Visualization." *Analytical Chemistry* 92.1 (2020), pp. 659–661. doi: [10.1021/acs.analchem.9b04884](https://doi.org/10.1021/acs.analchem.9b04884).
- [22] Sofie Gielis, Pieter Moris, **Wout Bittremieux**, Nicolas De Neuter, Benson Ogunjimi, Kris Laukens, and Pieter Meysman. "Detection of Enriched T Cell Epitope Specificity in Full T Cell Receptor Sequence Repertoires." *Frontiers in Immunology* 10 (2019), p. 2820. doi: [10.3389/fimmu.2019.02820](https://doi.org/10.3389/fimmu.2019.02820).
- [21] Pieter Meysman, Yvan Saeys, Ehsan Sabaghian, **Wout Bittremieux**, Yves van de Peer, Bart Goethals, and Kris Laukens. "Mining the Enriched Subgraphs for Specific Vertices in a Biological Graph." *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 16.5 (2019), pp. 1496–1507. doi: [10.1109/TCBB.2016.2576440](https://doi.org/10.1109/TCBB.2016.2576440).
- [20] Lindsay Pino, Andy Lin, and **Wout Bittremieux**. "2018 YPIC Challenge: A Case Study in Characterizing an Unknown Protein Sample." *Journal of Proteome Research* 18.11 (2019), pp. 3936–3943. doi: [10.1021/acs.jproteome.9b00384](https://doi.org/10.1021/acs.jproteome.9b00384).
- [19] **Wout Bittremieux**, Kris Laukens, and William Stafford Noble. "Extremely Fast and Accurate Open Modification Spectral Library Searching of High-Resolution Mass Spectra Using Feature Hashing and Graphics Processing Units." *Journal of Proteome Research* 18.10 (2019), pp. 3792–3799. doi: [10.1021/acs.jproteome.9b00291](https://doi.org/10.1021/acs.jproteome.9b00291).
- [18] Charlie Beirnaert, Laura Peeters, Pieter Meysman, **Wout Bittremieux**, Kenn Foubert, Deborah Custers, Anastasia Van der Auwera, Matthias Cuykx, Luc Pieters, Adrian Covaci, and Kris Laukens. "Using Expert Driven Machine Learning to Enhance Dynamic Metabolomics Data Analysis." *Metabolites* 9.3 (2019), p. 54. doi: [10.3390/metabo9030054](https://doi.org/10.3390/metabo9030054).
- [17] **Wout Bittremieux**, Pieter Meysman, William Stafford Noble, and Kris Laukens. "Fast Open Modification Spectral Library Searching through Approximate Nearest Neighbor Indexing." *Journal of Proteome Research* 17.10 (2018), pp. 3463–3474. doi: [10.1021/acs.jproteome.8b00359](https://doi.org/10.1021/acs.jproteome.8b00359).
- [16] Sander Willems, David Bouyssié, Dieter Deforce, Viktoria Dorfer, Vladimir Gorshkov, Dominik Kopczynski, Kris Laukens, Marie Locard-Paulet, Veit Schwämmle, Julian Uszkoreit, Dirk Valkenburg, Marc Vaudel, and **Wout Bittremieux**. "Proceedings of the EuBIC Developer's Meeting 2018." *Journal of Proteomics* 187 (2018), pp. 25–27. doi: [10.1016/j.jprot.2018.05.015](https://doi.org/10.1016/j.jprot.2018.05.015).
- [15] Aida Mrzic, Pieter Meysman, **Wout Bittremieux**, Pieter Moris, Boris Cule, Bart Goethals, and Kris Laukens. "Grasping Frequent Subgraph Mining for Bioinformatics Applications." *BioData Mining* 11.20 (2018). doi: [10.1186/s13040-018-0181-9](https://doi.org/10.1186/s13040-018-0181-9).
- [14] **Wout Bittremieux**, David L Tabb, Francis Impens, An Staes, Evy Timmerman, Lennart Martens, and Kris Laukens. "Quality Control in Mass Spectrometry-Based Proteomics." *Mass Spectrometry Reviews* 37.5 (2018), pp. 697–711. doi: [10.1002/mas.21544](https://doi.org/10.1002/mas.21544).
- [13] Nicolas De Neuter, **Wout Bittremieux**, Charlie Beirnaert, Bart Cuypers, Aida Mrzic, Pieter Moris, Arvid Suls, Viggo Van Tendeloo, Benson Ogunjimi, Kris Laukens, and Pieter Meysman. "On the Feasibility of Mining CD8+ T-Cell Receptor Patterns Underlying Immunogenic Peptide Recognition." *Immunogenetics* 70.3 (2018), pp. 159–168. doi: [10.1007/s00251-017-1023-5](https://doi.org/10.1007/s00251-017-1023-5).

- [12] Eric W Deutsch, Sandra Orchard, Pierre-Alain Binz, **Wout Bittremieux**, Martin Eisenacher, Henning Hermjakob, Shin Kawano, Henry Lam, Gerhard Mayer, Gerben Menschaert, Yasset Perez-Riverol, Reza M Salek, David L Tabb, Stefan Tenzer, Juan Antonio Vizcaíno, Mathias Walzer, and Andrew R Jones. "Proteomics Standards Initiative: Fifteen Years of Progress and Future Work." *Journal of Proteome Research* 16.12 (2017), pp. 4288–4298. doi: [10.1021/acs.jproteome.7b00370](https://doi.org/10.1021/acs.jproteome.7b00370).
- [11] Juan Antonio Vizcaíno, Mathias Walzer, Rafael C Jiménez, **Wout Bittremieux**, David Bouyssié, Christine Carapito, Fernando Corrales, Myriam Ferro, Albert JR Heck, Peter Horvatovich, Martin Hubalek, Lydie Lane, Kris Laukens, Fredrik Levander, Frederique Lisacek, Petr Novak, Magnus Palmblad, Damiano Piovesan, Alfred Pühler, Veit Schwämmle, Dirk Valkenburg, Merlijn van Rijswijk, Jiri Vondrasek, Martin Eisenacher, Lennart Martens, and Oliver Kohlbacher. "A Community Proposal to Integrate Proteomics Activities in ELIXIR [Version 1; Referees: 2 Approved]." *F1000Research* 6 (2017), p. 875. doi: [10.12688/f1000research.11751.1](https://doi.org/10.12688/f1000research.11751.1).
- [10] **Wout Bittremieux**, Mathias Walzer, Stefan Tenzer, Weimin Zhu, Reza M Salek, Martin Eisenacher, and David L Tabb. "The Human Proteome Organization–Proteomics Standards Initiative Quality Control Working Group: Making Quality Control More Accessible for Biological Mass Spectrometry." *Analytical Chemistry* 89.8 (2017), pp. 4474–4479. doi: [10.1021/acs.analchem.6b04310](https://doi.org/10.1021/acs.analchem.6b04310).
- [9] **Wout Bittremieux**, Dirk Valkenburg, Lennart Martens, and Kris Laukens. "Computational Quality Control Tools for Mass Spectrometry Proteomics." *PROTEOMICS* 17.3-4 (2017), p. 1600159. doi: [10.1002/pmic.201600159](https://doi.org/10.1002/pmic.201600159).
- [8] Evelyne Maes, Pieter Kelchtermans, **Wout Bittremieux**, Kurt De Grave, Sven Degroeve, Jef Hooyberghs, Inge Mertens, Geert Baggerman, Jan Ramon, Kris Laukens, Lennart Martens, and Dirk Valkenburg. "Designing Biomedical Proteomics Experiments: State-of-the-Art and Future Perspectives." *Expert Review of Proteomics* 13.5 (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 Valkenburg, and Kris Laukens. "Unsupervised Quality Assessment of Mass Spectrometry Proteomics Experiments by Multivariate Quality Control Metrics." *Journal of Proteome Research* 15.4 (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, Kris Laukens, and Dirk Valkenburg. "iMonDB: Mass Spectrometry Quality Control through Instrument Monitoring." *Journal of Proteome Research* 14.5 (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, Wim Vanden Berghe, Bart Goethals, and Kris Laukens. "A Primer to Frequent Itemset Mining for Bioinformatics." *Briefings in Bioinformatics* 16.2 (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, Filip Lemièrre, and Kris Laukens. "Efficient Reduction of Candidate Matches in Peptide Spectrum Library Searching Using the Top k Most Intense Peaks." *Journal of Proteome Research* 13.9 (2014), pp. 4175–4183. doi: [10.1021/pr401269z](https://doi.org/10.1021/pr401269z).
- [3] Mathias Walzer, Lucia Espona Pernas, Sara Nasso, **Wout Bittremieux**, Sven Nahnsen, Pieter Kelchtermans, Peter Pichler, Henk W P van den Toorn, An Staes, Jonathan Vandenbussche, Michael Mazanek, Thomas Taus, Richard A Scheltema, Christian D Kelstrup, Laurent Gatto, Bas van Breukelen, Stephan Aiche, Dirk Valkenburg, Kris Laukens, Kathryn S Lilley, Jesper Velgaard Olsen, Albert J R Heck, Karl Mechtler, Ruedi Aebersold, Kris Gevaert, Juan Antonio Vizcaino, Henning Hermjakob, Oliver Kohlbacher, and Lennart Martens. "qcML: An Exchange Format for Quality Control Metrics from Mass Spectrometry Experiments." *Molecular & Cellular Proteomics* 13.8 (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, and Kris Laukens. "jqcML: An Open-Source Java API for Mass Spectrometry Quality Control Data in the qcML Format." *Journal of Proteome Research* 13.7 (2014), pp. 3484–3487. doi: [10.1021/pr401274z](https://doi.org/10.1021/pr401274z).

- [1] Pieter Kelchtermans, **Wout Bittremieux**, Kurt De Grave, Sven Degroeve, Jan Ramon, Kris Laukens, Dirk Valkenburg, Harald Barsnes, and Lennart Martens. "Machine Learning Applications in Proteomics Research: How the Past Can Boost the Future." *PROTEOMICS* 14.4-5 (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**, Yves Van de Peer, Bart Goethals, and Kris Laukens. "Discovery of Significantly Enriched Subgraphs Associated with Selected Vertices in a Single Graph." *Proceedings of the 14th International Workshop on Data Mining in Bioinformatics - BIODDD '15*. Sydney, Australia, 2015, p. 8.

## Book sections

- [1] Sofie Gielis, Pieter Moris, **Wout Bittremieux**, Nicolas De Neuter, Benson Ogunjimi, Kris Laukens, and Pieter Meysman. "Identification of Epitope-Specific T Cells in T-Cell Receptor Repertoires." *Bioinformatics for Cancer Immunotherapy*. Ed. by Sebastian Boegel. Vol. 2120. New York, NY: Springer US, 2020, pp. 183–195. doi: [10.1007/978-1-0716-0327-7\\_13](https://doi.org/10.1007/978-1-0716-0327-7_13).

## Other publications

- [2] Alexander A Aksenov, Ivan Laponogov, Zheng Zhang, Sophie LF Doran, Ilaria Belluomo, Dennis Veselkov, **Wout Bittremieux**, Louis Felix Nothias, Mélissa Nothias-Esposito, Katherine N Maloney, Biswapriya B Misra, Alexey V Melnik, Kenneth L Jones, Kathleen Dorrestein, Morgan Panitchpakdi, Madeleine Ernst, Justin JJ van der Hooft, Mabel Gonzalez, Chiara Carrazzone, Adolfo Amézquita, Chris Callewaert, James Morton, Robert Quinn, Amina Bouslimani, Andrea Albarracín Orío, Daniel Petras, Andrea M Smania, Sneha P Couvillion, Meagan C Burnet, Carrie D Nicora, Erika Zink, Thomas O Metz, Viatcheslav Artsev, Elizabeth Humston-Fulmer, Rachel Gregor, Michael M Meijler, Itzhak Mizrahi, Stav Eyal, Brooke Anderson, Rachel Dutton, Raphaël Lugan, Pauline Le Boulch, Yann Guitton, Stephanie Prevost, Audrey Poirier, Gaud Dervilly, Bruno Le Bizec, Aaron Fait, Noga Sikron Persi, Chao Song, Kelem Gashu, Roxana Coras, Monica Guma, Julia Manasson, Jose U Scher, Dinesh Barupal, Saleh Alseekh, Alisdair Fernie, Reza Mirnezami, Vasilis Vasiliou, Robin Schmid, Roman S Borisov, Larisa N Kulikova, Rob Knight, Mingxun Wang, George B Hanna, Pieter C Dorrestein, and Kirill Veselkov. "Algorithmic Learning for Auto-Deconvolution of GC-MS Data to Enable Molecular Networking within GNPS." *bioRxiv* (2020). doi: [10.1101/2020.01.13.905091](https://doi.org/10.1101/2020.01.13.905091).
- [1] **Wout Bittremieux**. "Computational Solutions for Quality Control of Mass Spectrometry-Based Proteomics." Antwerp, Belgium: Universiteit Antwerpen, 2017. 129 pp.

## Presentations

### Oral presentations

- [9] **Wout Bittremieux**, Pieter Meysman, William Stafford Noble, and Kris Laukens. "Fast Open Modification Spectral Library Searching through Approximate Nearest Neighbor Indexing." *Cascadia Proteomics Symposium* Seattle, WA, USA (2018). doi: [10.5281/zenodo.1319035](https://doi.org/10.5281/zenodo.1319035).

- [8] **Wout Bittremieux**. “Shedding Light on Complex Mass Spectrometry Proteomics Processes through Advanced Data Mining.” *Faculty of Science Research Day* Antwerp, Belgium (2017). doi: [10.5281/zenodo.242392](https://doi.org/10.5281/zenodo.242392).
- [7] **Wout Bittremieux**. “Git: How Version Control Can Power Your Research.” *Biomina Lunch Talks* Antwerp, Belgium (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.” *ASMS Annual Conference* San Antonio, TX, USA (2016). doi: [10.5281/zenodo.55999](https://doi.org/10.5281/zenodo.55999).
- [5] **Wout Bittremieux**, Pieter Meysman, Lennart Martens, Bart Goethals, Dirk Valkenburg, and Kris Laukens. “Approaches for Mass Spectrometry Quality Control.” *Biomina Research Day* Antwerp, Belgium (2015). doi: [10.5281/zenodo.56004](https://doi.org/10.5281/zenodo.56004).
- [4] **Wout Bittremieux**, Pieter Meysman, Lennart Martens, Bart Goethals, Dirk Valkenburg, and Kris Laukens. “Analysis of Mass Spectrometry Quality Control Metrics.” *Benelux Bioinformatics Conference* Antwerp, Belgium (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.” *Benelux Bioinformatics Conference Student Council Symposium* Antwerp, Belgium (2015). doi: [10.5281/zenodo.56002](https://doi.org/10.5281/zenodo.56002).
- [2] **Wout Bittremieux**, Emmanuel Müller, Dirk Valkenburg, Lennart Martens, Bart Goethals, and Kris Laukens. “Pattern Mining of Mass Spectrometry Quality Control Data.” *Benelux Bioinformatics Conference* Luxembourg, Luxembourg (2014). doi: [10.5281/zenodo.56000](https://doi.org/10.5281/zenodo.56000).
- [1] **Wout Bittremieux**, Pieter Kelchtermans, Dirk Valkenburg, Lennart Martens, and Kris Laukens. “Collecting and Mining Mass Spectrometry Quality Control Data.” *Biomina Research Day* Antwerp, Belgium (2014). doi: [10.5281/zenodo.56003](https://doi.org/10.5281/zenodo.56003).

## Poster presentations

- [11] **Wout Bittremieux**, Damon H May, Jeffrey Bilmes, and William Stafford Noble. “A Learned Embedding for Efficient Joint Analysis of Millions of Mass Spectra.” *Machine Learning in Computational Biology* Vancouver, BC, Canada (2019). doi: [10.5281/zenodo.3576516](https://doi.org/10.5281/zenodo.3576516).
- [10] **Wout Bittremieux**, Kris Laukens, and William Stafford Noble. “ANN-SoLo: Extremely Fast and Accurate Open Modification Spectral Library Searching.” *ASMS Annual Conference* Atlanta, Georgia, USA (2019). doi: [10.5281/zenodo.3242687](https://doi.org/10.5281/zenodo.3242687).
- [9] **Wout Bittremieux**, Pieter Meysman, William Stafford Noble, and Kris Laukens. “Fast Open Modification Spectral Library Searching through Approximate Nearest Neighbor Indexing.” *Department of Genome Sciences Retreat* Leavenworth, WA, USA (2018). doi: [10.5281/zenodo.1418397](https://doi.org/10.5281/zenodo.1418397).
- [8] **Wout Bittremieux**, Dirk Valkenburg, and Kris Laukens. “Towards the Smart Lab: A Comprehensive Approach to Mass Spectrometry Quality Control.” *ASMS Annual Conference* Indianapolis, IN, USA (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?” *ASMS Annual Conference* Indianapolis, IN, USA (2017). doi: [10.5281/zenodo.584067](https://doi.org/10.5281/zenodo.584067).
- [6] **Wout Bittremieux**, Pieter Meysman, Lennart Martens, Dirk Valkenburg, and Kris Laukens. “Automatic Quality Assessment of Mass Spectrometry Experiments by Multivariate Quality Control Metrics.” *ASMS Annual Conference* San Antonio, TX, USA (2016). doi: [10.5281/zenodo.55998](https://doi.org/10.5281/zenodo.55998).



- [5] **Wout Bittremieux**, Hanny Willems, Lennart Martens, Dirk Valkenburg, and Kris Laukens. "Mass Spectrometry Quality Control: Instrument Monitoring and Pattern Mining Insights." *ASMS Annual Conference* St. Louis, MO, USA (2015). doi: [10.5281/zenodo.55992](https://doi.org/10.5281/zenodo.55992).
- [4] **Wout Bittremieux**, Hanny Willems, Lennart Martens, Bart Goethals, Dirk Valkenburg, and Kris Laukens. "A Comprehensive Approach to Mass Spectrometry Quality Control." *Two-day Symposium of the Belgian Proteomics Association* Brussels, Belgium (2014). doi: [10.5281/zenodo.55990](https://doi.org/10.5281/zenodo.55990).
- [3] **Wout Bittremieux**, Dirk Valkenburg, Aida Mrzic, Hanny Willems, Bart Goethals, and Kris Laukens. "Pattern Mining of Mass Spectrometry Quality Control Data." *European Conference on Computational Biology* Strasbourg, France (2014). doi: [10.5281/zenodo.55989](https://doi.org/10.5281/zenodo.55989).
- [2] **Wout Bittremieux**, Pieter Kelchtermans, Dirk Valkenburg, Lennart Martens, Bart Goethals, and Kris Laukens. "Mining Mass Spectrometry Quality Control Data." *ASMS Annual Conference* Baltimore, MD, USA (2014). doi: [10.5281/zenodo.55988](https://doi.org/10.5281/zenodo.55988).
- [1] **Wout Bittremieux**, Pieter Kelchtermans, Dirk Valkenburg, Lennart Martens, and Kris Laukens. "jqcML: An Open-Source Java API for Mass Spectrometry Quality Control Data in the qcML Format." *Benelux Bioinformatics Conference* Brussels, Belgium (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." *Methods and Tools for Intra- and Inter-experiment LC MS Performance Tracking Workshop, ASMS Annual Conference* St. Louis, MO, USA (2015).

### Student supervision

- 2020 **Charlotte Adams**, MSc student, Bioengineering, University of Antwerp  
Thesis: *Investigation of the Human Interactome Using Open Modification Searching to Reveal the Role of Post-translational Modifications on Protein-protein Interactions*
- 2019 **Charlotte Adams**, MSc student, Bioengineering, University of Antwerp  
Internship: *Investigating the Advantages of Open Modification Searching to Identify Modified Proteins*
- 2019 **Stephen Blaskowski**, PhD student, Molecular Engineering, University of Washington  
Internship: *Using Machine Learning to Speed Up Calibration of Tandem Mass Spectrometry Database Search*
- 2017 **Joeri Reyns**, MSc student, Computer Science, University of Antwerp  
Thesis: *Protein Identification Using Deep Neural Networks*
- 2017 **Keerthana Sanala Prakash**, MSc student, Computer Science, University of Antwerp  
Internship: *Temporal Mining of Mass Spectrometry Quality Control Data*
- 2016 **Phui San Cheong**, MSc student, Computer Science, University of Antwerp  
Internship: *Implement Frequent Itemset-based Clustering in pyGCluster*
- 2016 **Robin Verachtert**, BA student, Computer Science, University of Antwerp  
Internship: *Automatic Discovery of Artefacts in Mass Spectrometry Data*

## Teaching

- 2017 Bachelor of Computer Science – Introduction to Computational Biology: Teaching Assistant
- 2016 Bachelor of Mathematics – Project Work: Teaching Assistant
- 2014–2015 Master of Biochemistry and Biotechnology – Data Mining: Teaching Assistant
- 2015 Master of Computer Science – Data Mining: Guest Lecturer

## Funding acquired

- 2019–2023 University of Antwerp – University Research Fund  
Project: *Transferable Deep Learning for Sequence Based Prediction of Molecular Interactions*  
Role: Co-investigator Funding: € 205 000
- 2018–2019 Belgian American Educational Foundation  
Project: *Prediction of Mass Spectrometry Spectral Libraries*  
Role: Postdoctoral Fellow Funding: \$ 45 000
- 2017–2022 Research Foundation – Flanders  
Project: *Intelligent Quality Control for Mass Spectrometry-based Proteomics*  
Role: Postdoctoral Fellow Funding: € 265 300