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| APPOINTMENTS | <i>Senior Research Associate</i> Cambridge, UK Group Leader – Computational Proteomics Unit | University of Cambridge October 2013 – |
| | <i>Visiting Scientist</i> Cambridge, UK Member of the Proteomics identifications database (PRIDE) team. | EMBL/EBI January 2010 – |
| | Software Sustainability Institute Fellow 2014. Software Carpentry Instructor. Bioconductor project, associated member. | |
| PREVIOUS APPOINTMENTS | <i>Post-Doctoral Research Associate</i> University of Cambridge, Cambridge, UK | Jan 2010 – Sept 2013 |
| | <i>Bioinformatician, Project Leader</i> DNAVision, Gosselies, Belgium | Aug 2006 – Dec 2009 |
| EDUCATION | 2000 – 2006 (viva 2006-07-27) <i>PhD</i> in Science (Molecular Biology Department) Free University of Brussels (ULB), Belgium 2000 – 2001 Master of Advanced Studies (DEA) in Sciences Free University of Brussels (ULB), Belgium 1997 – 2000 Masters in Biology (highest honors) Free University of Brussels (ULB), Belgium | |
| SELECTED PUBLICATIONS (OUT OF 26) | Huber W. <i>et al.</i> , Orchestrating high-throughput genomic analysis with Bioconductor , Nat Methods 2015 Jan 29;12(2):115-21. Gatto L. , Breckels LM, Burger T, Wiczorek S and Lilley KS Mass-spectrometry based spatial proteomics data analysis using pRoloc , Bioinformatics , 2014 May 1;30(9):1322-4. Gatto L. , Christoforou A. <i>Using R and Bioconductor for proteomics data analysis</i> . Biochim Biophys Acta 2014 Jan;1844(1 Pt A):42-51. Chambers M. <i>et al.</i> <i>A Cross-platform Toolkit for Mass Spectrometry and Proteomics</i> , Nature Biotechnology , 30, 918 – 920, 2012. | |

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| | <p>Gatto L. and Lilley K.S. <i>MSnbase – an R/Bioconductor package for isobaric tagged mass spectrometry data visualisation, processing and quantitation</i>, Bioinformatics, 28(2), 288-289, 2012.</p> |
| SELECTED SOFTWARE DEVELOPMENT | <p>Manipulating and exploring protein and proteomics data, 2014.</p> <p>pRolocGUI: Interactive visualisation of organelle (spatial) proteomics data, 2014.</p> <p>rpx: An R interface to the ProteomeXchange repository, 2014.</p> <p>pRoloc: A unifying bioinformatics framework for organelle proteomics, 2012.</p> <p>hpar: A simple interface to and data from the Human Protein Atlas project, 2012.</p> <p>rols: An R interface to the Ontology Lookup Service, 2012.</p> <p>MSnbase: Base Functions and Classes for MS-based Proteomics, 2011.</p> <p>mzR: Raw mass-spectrometry data parsig library.</p> |
| SELECTED ORAL COMMUNICATIONS (INVITED TALKS) | <p>Gatto L. <i>Spatial proteomics: Combining experimental and annotation data to predict protein sub-cellular localisation</i>. 13 Jan 2015, European Bioconductor Developer meeting, EMBL, Heidelberg.</p> <p>Gatto L. <i>An overview of the (growing) R/Bioc ecosystem for mass spectrometry and proteomics</i>, MRC Clinical Sciences Centre, Imperial College London, 5 December 2014, London.</p> <p>Gatto L. <i>Computational Challenges in Mass Spectrometry-Based Spatial Proteomics</i>, HUPO meeting, Computational Mass Spectrometry Initiative, 8 Oct 2014, Madrid.</p> |
| CURRENT GRANTS | <p>May 2014 – Oct. 2015 BBSRC Tools and Resources Development Fund (£144,112). <i>Automated identification of optimal data-specific organelle clusters using freely available protein annotations</i>. PI Laurent Gatto, University of Cambridge.</p> <p>March 2014 – February 2018 BBSRC Strategic Longer and Larger grant. <i>A spatio-temporal map of the developmental fly interactome</i>. Research co-investigator, with PI Professor Simon Hubbard, University of Manchester.</p> <p>March 2013 – November 2015 Addenbrookes Charitable Trust. <i>Protein biomarkers for vascular calcification in end-stage renal disease</i>. Co-applicant, with PI Dr Thomas Hiemstra, University of Cambridge.</p> |
| TEACHING | <p>I am regularly teaching at national and international workshops on computational biology, scientific programming and Software Carpentry Bootcamps. My teaching at the University of Cambridge (such as in the MPhil in Computational Biology in 2012-2014) are on a voluntary basis.</p> |
| REVIEWING ACTIVITIES | <p>Journals: Proteomics, Bioinformatics, BMC Genomics, BMC Research Notes, Expert Reviews in Proteomics, Journal of Proteomics, F1000Research, PeerJ, Journal of Open Research Software.</p> <p>Conferences: ISMB/ECCB. Funding agencies: Medical Research Council.</p> |