

Resume – Thomas Abeel, PhD

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Name

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Contact:

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Professional appointments

- **Delft University of Technology**, 11/2014-present, *Delft, Netherlands*
Assistant Professor Bioinformatics
- **Broad Institute of MIT and Harvard**, 1/2011-present, *Cambridge, MA, USA*
Visiting scientist (11/2014-present)
Postdoctoral fellow, mentors A. Earl and J. Galagan (1/2011 – 10/2014)
- **VIB-Ghent University**, 10/2010-11/2014, *Gent, Belgium*
Postdoctoral fellow, mentor Y. Van de Peer
- **Broad Institute of MIT and Harvard**, 2/2009-12/2009, *Cambridge, MA, USA*
Visiting graduate student, mentor J. Galagan
- **VIB-Ghent University**, 7/2005-9/2010, *Gent, Belgium*
PhD candidate, mentors Y. Van de Peer and Y. Saeys

Education

- **Massachusetts Institute of Technology**, 2/2009-12/2009, *Cambridge, MA, USA*
- **VIB-Ghent University**, PhD in Biotechnology, 7/2005-9/2010, *Ghent, Belgium*
- **Ghent University**, Master in Computer Sciences, 10/2003-8/2005, *Ghent, Belgium*
- **Ghent University**, Bachelor in Computer Sciences, 10/2001-8/2003, *Ghent, Belgium*

Publications

Full list: http://scholar.google.com/citations?user=eCS5_oAAAAAJ

Google scholar: 46 publications, 1381 citations, 16 h-index

Key papers

- 1) Desjardins, C., Cohen, K., Munsamy, V., **Abeel, T.**, Maharaj, K., Walker, B., Shea, T., Almeida, D., Manson, A., Salazar, A., Padayatchi, N., O'Donnell, M., Mlisana, K., Wortman, J., Birren, B., Grosset, J., Earl, A., Pym, A. 2016. Genomic and functional analyses of Mycobacterium tuberculosis strains implicate ald in d-cycloserine resistance. *Nature Genetics*. 201 (6): 544–551
- 2) Cohen*, K., **Abeel***, T., Manson McGuire, A., Desjardins, C., Munsamy, V., Shea, T., Walker, B., Bantubani, N., Almeida, D., Alvarado, L., Chapman, S., Mvelase, N., Duffy, E., Fitzgerald, M., Govender, P., Gujja, S., Hamilton, S., Howarth, C., Larimer, J., Maharaj, K., Pearson, M., Priest, M., Zeng, Q., Padayatchi, N., Grosset, J., Young, S., Wortman, J., Mlisana, K., O'Donnell, M., Birren, B., Bishai, W., Pym+, A., Earl+, A. 2015. Evolution of extensively drug-resistant tuberculosis over four decades: whole genome sequencing and dating analysis of Mycobacterium tuberculosis isolates from KwaZulu-Natal. *PLOS Medicine*. 12 (9): e1001880
- 3) Walker*, B., **Abeel***, T., Shea, T., Priest, M., Abouelliel, A., Sakthikumar, S., Cuomo, C., Zeng, Q., Wortman, J., Young, S., Earl, A. 2014. Pilon: an integrated tool for comprehensive microbial variant detection and genome assembly improvement. *PLOS One*. 9 (11): e112963
- 4) Galagan, J., Minch, K., Peterson, M., Lyubetskaya, A., Azizi, E., Sweet, L., Gomes, A., Rustad, T., Dolganov, G., Glotova, I., **Abeel, T.**, Mawhinney, C., Kennedy, A., Allard, R., Brabant, W., Krueger, A., Jaini, S., Honda, B., Yu, W., Hickey, M., Zucker, J., Garay, C., Weiner, B., Sisk, P., Stolte, C., Camacho, D., Dreyfuss, J., Liu, Y., Dorhoi, A., Mollenkopf, H., Drogaris, P., Lamontagne, J., Zhou, Y., Piquenot, J., Tae Park, S., Raman, S., Kaufmann, S., Mohny, R., Chelsky, D., Moody, B., Sherman, D., Schoolnik, G., Van de Peer, Y., Iazzetti, P., Winkler, J. 2013. The Mycobacterium tuberculosis Regulatory Network and the Hypoxic Response. *Nature*. 499 (7457): 178–183
- 5) **Abeel, T.**, Van Parys, T., Saeys, Y., Galagan, J., Van de Peer, Y. 2011. GenomeView: a next-generation genome browser. *Nucleic Acids Research*. doi: 10.1093/nar/gkr995
- 6) **Abeel, T.**, Helleputte, T., Van de Peer, Y., Dupont, P., Saeys, Y. 2010. Robust biomarker identification for cancer diagnosis with ensemble feature selection methods. *Bioinformatics*. 26 (3): 392–398

Education and supervision

- Supervision: 5 interns, 16 Bachelor graduation projects, 8 Master thesis projects, 5 PhD, 3 postdoc/staff
- Education:
 - Lecturer of 3 undergraduate courses, currently: Context projects (TI2806), Datamining (TI2736-C)
 - Lecturer of 2 graduate courses, currently: Advanced Bioinformatics (IN4329)
 - Lecturer of 2 postgraduate courses

Community service

- **Open Source Project manager**, several open source projects: Java-ML, GenomeView and several smaller projects. Several thousands of downloads a month, >100,000 lines of code. (9/2006-present)
- **Co-founder, vice-chair**, Broad Next-Gen association for post-docs and graduate students (10/2012-9/2013)
- **Director**, Student Representative to the International Society for Computational Biology Board of Directors (2/2011-12/2012)
- **Chaired 3 international meetings**: Workshop track at ECCB 2016, Den Haag, The Netherlands; 6th ISCB Student Council Symposium at ISMB 2010, Boston, USA; 1st European Student Council Symposium at ECCB 2010, Gent, Belgium
- **Co-organized 11 international meetings**
- **Reviewed for 20+ internationally recognized journals and conferences**

Software

- GenomeView is an award-winning interactive genome browser and annotation editor that can deal with a multitude of sequencing and (comparative) genomics data sets. (15000+ users)
- Java-ML is a collection of machine learning algorithms aimed at software engineers and programmers. It has well documented source code and provides plenty of code samples and tutorials with a focus on clustering and feature selection. (25000+ downloads)
- Pilon: integrated variant caller
- Peacock: phylogenetic tree visualization library
- EP3, ProSOM, pppBenchmark : Eukaryote core promoter prediction programs and benchmarks

Presentations

I have presented over 50 oral and poster presentations at international conferences, research institutes and universities. Selected presentations:

- Machine learning methods for genotype-phenotype association in bacterial genomes, ISMB 2013
- Presenting your science visually. 9th ISCB Student Council Symposium
- Visualizing the next generation of sequencing data with GenomeView, 14th Annual Bioinformatics Open Source Conference (BOSC 2013), VIB seminar 2012, Illumina iDEA conference, ABRF 2011