

## Curriculum Vitae and Publication List

Dr. Roland Wittler  
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*Roland Wittler is a staff researcher in the Genome Informatics group at the Faculty of Technology, Bielefeld University, Germany. His research interest is the development of algorithms and software for the comparative analysis of genomic sequences with a focus on structural variation, pan-genomics and phylogenetics.*

### Academic background:

2002-2006 Diploma Studies of Informatics in the Natural Sciences at Bielefeld University, Germany  
2006-2010 Doctoral student at Bielefeld University, Germany  
02/2010 Dissertation at the Faculty of Technology, Bielefeld University, Germany;  
supervisors: Jens Stoye and Robert Giegerich

### Professional career:

2006-2009 PhD scholar, DFG Research Training Group "Bioinformatics", GRK 635  
2009-2010 Research assistant Bielefeld University, Germany  
03-12/2010 Research assistant at Simon Fraser University, Burnaby, BC, Canada  
2010-present Research assistant at Bielefeld University, Germany

### Theses advised:

16 Bachelor Theses  
6 Master Theses

### Administration:

2013-present Scientific Coordinator of "Computational Methods for the Analysis of the Diversity and Dynamics of Genomes", International DFG Research Training Group, GRK 1906  
2014-present Scientific Coordinator of doctoral degree program "Bioinformatics" at Bielefeld University, Germany

### 10 Most Relevant Publications (peer reviewed articles only):

#### **Scaffolding of Ancient Contigs and Ancestral Reconstruction in a Phylogenetic Framework**

Luhmann, N., Chauve, C., Stoye, J., Wittler, R.

[IEEE/ACM TCBB](#) (Accepted).

#### **Dynamic Alignment-Free and Reference-Free Read Compression**

Holley, G., Wittler, R., Stoye, J., Hach, F.

[Proceedings of RECOMB 2017](#). LNBI. 10229, 50-65, 2017.

**The SCJ Small Parsimony Problem for Weighted Gene Adjacencies**

*Luhmann, N., Lafond, M., Thévenin, A., Ouangraoua, A., Wittler, R., Chauve, C.*  
[IEEE/ACM TCBB](#) 14, 2017.

**Bloom Filter Trie: an alignment-free and reference-free data structure for pan-genome storage**

*Holley, G., Wittler, R., Stoye, J.*  
[Proceedings of WABI 2015](#). LNBI. 9289, 217-230, 2015.

**Repeat- and error-aware comparison of deletions**

*Wittler, R., Marschall, T., Schönhuth, A., Makinen, V.*  
[Bioinformatics](#) 31(18), 2947-2954, 2015.

**Unraveling overlapping deletions by agglomerative clustering**

*Wittler, R.*  
[BMC Genomics](#) 14(Suppl 1), S12, 2013.

**Linearization of ancestral multichromosomal genomes**

*Mañuch, J., Patterson, M., Wittler, R., Chauve, C., Tannier, E.*  
[BMC Bioinformatics](#) 13(Suppl. 19), 2012.

**Consistency of Sequence-Based Gene Clusters**

*Wittler, R., Mañuch, J., Patterson, M., Stoye, J.*  
[J. Comp. Biol.](#) 18(9), 1023-1039, 2011.

**Tractability results for the Consecutive-Ones Property with multiplicity**

*Chauve, C., Mañuch, J., Patterson, M., Wittler, R.*  
[Proceedings of CPM 2011](#). 6661, 90-103, 2011.

**A Unified Approach for Reconstructing Ancient Gene Clusters**

*Stoye, J., Wittler, R.*  
[IEEE/ACM TCBB](#) 6(3), 387-400, 2009.