

– **Curriculum Vitae** –

Dr. Michael Sammeth



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GENERAL INFORMATION

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<b>Date of birth</b>	13. Jan 1976 (in Würzburg, Germany)
<b>Nationality</b>	German
<b>Additional languages</b>	English (fluent) French (high school level) Spanish (good writing and communication) Catalan (official level A)
<b>School training</b>	German "Abitur" 1995 at the Matthias-Grnewald-Gymnasium special subjects in final class Math and Latin final work about "Julia sets"
<b>University education</b>	2002 German diploma at the University of Würzburg subjects: biochemistry, genetics, computer science and virology final work "Web-based visualization of Multiple Alignments" at the Department of Computer Science 2, University of Würzburg  2005 PhD (German Doctor) at the Bielefeld University Title of the thesis: "Integrated multiple alignment"

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RESEARCH CAREER

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<b>1999</b>	lab course, Bayer AG, Uerdingen, Germany	"wet lab" research on single nucleotide polymorphisms
<b>2002</b>	Internship of the graduate school (Cebitec), Bielefeld University, Germany	Developing the QAlign Software
<b>2003</b>	Dept. of Genome Informatics, Bielefeld University, Germany	Fragment-based hyperspace alignments

collaboration with Dep. of Computer Science (2), University of Würzburg, Germany      Benchmarks and visualization of multiple alignment methods

project course *P-Tree*, Bielefeld University, Germany      Benchmarks and visualization of multiple alignment methods

## 2004

Integrated Bioinformatics, Vrije Universiteit Amsterdam, The Netherlands      Motif-constrained multiple alignment

Genome Informatics, Bielefeld University in coll. with UZKF Mnster, Germany      Sequence alignment with duplication and excision of tandem repeat copies

## 2005

Research Unit on Biomedical Informatics (GRIB), IMIM/ University Pompeu Fabra (UPF), Barcelona, Spain      Alignment of alternative splicing patterns

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## TEACHING

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### 2003

Bielefeld University      Exercises in "algorithms and data structures 2"

project course *P-Tree*, Bielefeld University      Benchmarks and visualization of multiple alignment methods

### 2004

University of Würzburg      supervising the diploma thesis of M. Pfeiffer "Algorithms to Visualize and Compare Multiple Alignments"

Bielefeld University      "Deep Java", application programming in JAVA  
several assistant classes in bioinformatics, algorithms and datastructure courses

### 2005

Universitat Pompeu Fabra      Master of Science "Bioinformatics for Health Sciences", classes

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PUBLICATIONS AND REPORTS

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D. Harmsen, J. Rothgänger, M. Sammeth, and J. Albert (2002) *Ribosomal Differentiation of Medical Microorganisms (RIDOM)*. **Nucl Acids Res** online database summary.

M. Sammeth, J. Rothgänger, W. Esser, J. Albert, J. Stoye, and D. Harmsen (2003) *QAlign: Quality Based Multiple Alignments with Dynamic Phylogenetic Analysis*. **Bioinformatics** 19 1592–1593.

M. Sammeth, B. Morgenstern, and J. Stoye (2003) *Divide-and-Conquer Alignment with Segment-Based Constraints*. **Bioinformatics**, II189-II195.

D. Harmsen, S. Dostal, A. Roth, S. Niemann, J. Rothgänger, M. Sammeth, J. Albert, M. Frosch, and E. Richter (2003) *RIDOM: Comprehensive and public sequence database for identification of Mycobacterium species*. **BMC Infectious Diseases** 3:26.

M. Pfeiffer supervised by M. Sammeth (2004) *Algorithms to visualize and compare multiple alignments*. Diploma thesis.

M. Sammeth, T. Weniger, D. Harmsen and J. Stoye (in prep.) *Alignment of tandem repeats with Excision, Duplication, Substitution and Indels (EDSI)*. **LNBI** 3692: 276-290.

M. Sammeth, and J. Stoye *Alignment of tandem repeats with Excision, Duplication, Substitution and Indels (EDSI)*. Bielefeld Univ., Technical Report 2005-05.

M. Sammeth *Integrated multiple sequence alignment* Bielefeld University, Thesis.

M. Sammeth, and J. Heringa *Global multiple alignment with repeats*. **Proteins: Structure, Functions and Genetics** 64: 263-274.

M. Sammeth, T. Griebel, F. Tille, and J. Stoye *Panta rhei (QAlign 2): an open graphical environment for sequence analysis*. **Bioinformatics** 22: 889-890.

M. Sammeth, and J. Stoye *Comparing tandem repeats with duplications and excisions of higher order*. **TCBB** invited paper (accepted).

M. Sammeth, and J. Heringa *The RAlign webserver* (submitted).

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CONFERENCE AND WORKSHOP TALKS

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**Oct 2002** Comparative Analysis of Protein Evolution (COPE). IZKF Mnster, Germany. *QAlign: a graphical tool for multiple alignments with dynamic phylogenetic analyses*.

**Dec 2002** Max-Planck-Institute for terrestrial Microbiology. Marburg, Germany. *QAlign: a graphical tool for constructing simultaneous multiple alignments*.

**Apr 2003** Bioinformatics Research and Education Workshop (BREW). Bielefeld, Germany. *The QAlign framework for multiple sequence analysis*. (long talk)

**Jun 2003** Forschungsschwerpunkt Mathematisierung (FSPM). Bielefeld, Germany. *QAlign: a graphical framework for multiple sequence analysis*.

- Jul 2003** New trends in phylogenetics and genomics workshop. ZBIT Tübingen, Germany. *The QAlign framework for multiple sequence analysis.*
- Sep 2003** European Conference on Computational Biology (ECCB), Paris, France. *The QAlign framework for multiple sequence analysis.*
- Oct 2004** DNA sequence-based typing of microbes and data analysis. DGHM workshop, Würzburg, Germany. *Multiple alignments and phylogenetic analysis.*
- Jun 2005** DNA Sequence Based Identification and Typing of Microbes: Generation and Analysis of Data and Interpretation of Results. ASM workshop together with E. Feil (UK), D. Roult (France) and D. Harmsen (Germany). Atlanta, USA. *Practical Phylogeny.*
- Oct 2005** 5th International Workshop, WABI 2005. Palma de Mallorca, Spain. *Alignment of tandem repeats with Excision, Duplication, Substitution and Indels (EDSI).*

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POSTERS AND OTHER CONFERENCE CONTRIBUTIONS

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- Nov 2001** Medica Media, Düsseldorf, Germany. *DNA sequence database for microbial identification.*
- May 2002** Genomics in Infectious Diseases (2nd Intl.), Würzburg, Germany. *Quality based multiple alignments of DNA sequences.*
- May 2002** ASM 102nd general meeting, Salt Lake City, USA. *QAlign: a quality based multiple alignment tool in the framework of the RIDOM project.*
- Jul 2002** Applications of biomics (genomics, proteomics and bioinformatics), PHLS London, UK. *QAlign: a quality based multiple alignment tool in the framework of the RIDOM project.*
- Oct 2002** Gegenwart und Zukunft der bakteriellen Genomforschung (BGF), Bielefeld, Germany. *QAlign: a graphical tool for constructing simultaneous multiple alignments.*
- Apr 2003** 7th conference on research in computational molecular biology (RECOMB), Berlin, Germany. *Introducing consistency-based hyperspace alignments.*
- May 2003** ASM 103rd general meeting, Washington DC, USA. *QAlign: a free software environment for graphical multiple alignment construction and phylogenetic analysis.*
- May 2004** ASM 104th general meeting, New Orleans, USA. *Ridom Tracer: an Accurate Base Quality Calling Algorithm that Smoothly Integrates into a DNA Diagnostic Software.*

<b>May 2004</b> ASM 104th general meeting, New Orleans, USA.	<i>Based upon repeat patterns (BURP): a new algorithm and implementation for clustering of sequences containing repeats.</i>
<b>Aug 2004</b> Intelligent Systems for Molecular Biology (ISMB), Glasgow, UK.	<i>QAlign: Quality-Based Multiple Alignments by Complementary Algorithms.</i>
<b>Sep 2005</b> European Conference on Computational Biology (ECCB), Madrid, Spain.	<i>Aligning intron-exon structures of alternatively spliced genes.</i>
<b>Mar 2006</b> Symposium on Alternate Transcript Diversity II (EMBL), Heidelberg, Germany.	<i>A general notation for alternative splicing.</i>

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SCHOLARSHIPS AND AWARDS

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<b>ASM Grant</b>	May 2002, ASM Corporate Student Travel Grant
<b>Cebitec Internship</b>	2002, 3 months Internship of the Graduate School of Bielefeld University
<b>EU Grant</b>	Apr 2003, Travel Grant of the European Union
<b>Schering Fellowship</b>	2003-2005, doctoral fellowship of the Ernst-Schering-Stiftung
<b>DAAD Fellowship</b>	2005-2006, post-doctoral fellowship of the German Academic Exchange Service (DAAD)