Robert Bakarić
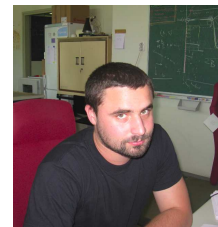
Curriculum Vitae

EMAIL **rbakaric@irb.hr**
PHONE **+385915320625**
COUNTRY **Croatia**

Education

GRADUATE STUDIES

2014–today	Max Planck Institute, Ploen, Germany / Christian-Albrechts-Universitat, Kiel, Germany / Ruder Boskovic Institute, Zagreb, Croatia. **Field: Bioinformatics, Genomics of gene loss and horizontal gene transfer in Eukaryotes**
2011–2014	International Max Planck Research School, MPI-Ploen/CAU-Kiel, Germany. **Field: Bioinformatics, Alignment free sequence comparison**
2008–2011	University of Zagreb, Faculty of Science, Division of Biology, Zagreb, Croatia. **Field: Computational biology, Genomic phylostratigraphy**

UNDERGRADUATE STUDIES

2003–2008	Diploma/MSc in Molecular Biology, University of Zagreb, Faculty of Science, Division of Biology, Zagreb, Croatia. **Title: Functional Characteristics of Orphan Genes in Caenorhabditis elegans**

Professional Experience

2014–today	**Bioinformatic consultant:** Exaltum (exaltum.eu), Vrbik 13, Zagreb, Croatia.
2008–today	**Research Assistant:** "Ruder Bosković" Institute, Division of Molecular Biology, Laboratory of evolutionary Genetics, Group for Genomic Phylostratigraphy, Zagreb, Croatia. *Involved in:* **Scientific software development:** PhyloStrat software, Linux shell emulators, lightweight job distributors, development of database mining tools and tools for statistical analysis **Linux system administration:** HPC cluster and web/storage server administration, shell scripting (bash, Perl), database administration, software installation and development
2005–2008	**Volunteering:** "Ruder Boskovic" Institute, Division of Molecular Biology, Zagreb, Croatia. Involved in the orphan genes research project (project leader dr.Tomislav Domazet-Loso).

Technical skills/Computer skills

Programming language(s)	**Perl**, **C++**, **C**	-	ADVANCE
	SQL, **R**	-	BASIC TO ADVANCE
	bash, **HTML**	-	BASIC

Libraries (ToolKits)	**boost, STL, SeqAn, ncbi-c++**	-	ADVANCE
	ncbi-c	-	BASIC TO ADVANCE
	GEM	-	BASIC

Database(s)	**SQLite**	-	ADVANCE
	MySQL	-	BASIC TO ADVANCE
	MsSQL,**MsAcc.**	-	BASIC

Operating system(s)	**Linux/Unix** - administration: Debian, Ubuntu, CentOs (Rocks). **Windows**

Additional software	**VMD, NAMD**, **NGS tools** (bowtie, Cufflinks, BWA, …), **Alignment tools** (BLAST, MUSCLE, Clustal, Mummer …) **Latex**

Languages

Croatian	**Mother tongue**
English	Fluent
German	Basic

Soft skills/Communication skills

ORAL PRESENTATIONS

4/2012	Oral presentation: "Efficient computation of minimal mappable read lengths", Max Planck Institute for Evolutionary Biology, Ploen, Germany.
9/2011	Oral presentation: "Efficient computation of minimal mappable read lengths", Institute for genetics, University of Cologne, Cologne, Germany.
4/2011	Oral presentation: "Efficient computation of minimal mappable read lengths", Max Planck Institute for Evolutionary Biology, Ploen, Germany.
7/2009	Oral presentation: "PhyloStrat: An algorithmic approach to genome stratification", Max Planck Institute for Evolutionary Biology, Ploen, Germany

POSTERS PRESENTATIONS

09/2014	Poster presentation: Vojvoda Zeljko, Tanja; Bakarić, Robert; Plohl, Miroslav. "Interweaving of satellite DNAs and mobile elements in the Pacific oyster Crassostrea gigas (Thunberg, 1793)", 20th International Chromosome Conference, Canterbury, Kent, UK.
09/2014	Poster presentation: Vojvoda Zeljko, Tanja; Bakarić, Robert; Plohl, Miroslav. "MITE - like elements with internal tandem repeats in the Pacific oyster Crassostrea gigas (Thunberg, 1796)", The Interplay of Biomolecules, HDBMB 2014. Congress of the Croatian Society of Biochemistry and Molecular Biology, Zadar, Croatia.
06/2013	Poster presentation: Bakarić, Robert, "Efficient quantification of sequencing reed mappability", EMBL-EBI-Wellcome Trust Summer School in Bioinformatics 2013, Hinxton, Cambridge.
11/2011	Poster presentation: Bakarić, Robert, "Efficient quantification of sequencing reed mappability", Evolution at the sea, 3rd Status Symposium in Evolutionary biology, Zylt, Germany.
9/2008	Poster presentation with short talk: Bakarić, Robert , "Phylostratigraphy of *Caenorhabditis elegans* genome reveals depletion of anatomy related mutant phenotypes among Nematoda specific genes", 12th Evolutionary Biology Meeting in Marseilles, Marseilles, France

WORKSHOPS

10/2009	Organization of "Introduction to Genomic Phylostratigraphy" course held by Croatian Society for Theoretical and Mathematical Biology, Zagreb, Croatia.
6/2009	Involved in organization of "Practical course: Introduction to Bioinformatics", organized by prof. dr. Kristian Vlahovicek, University of Zagreb, Faculty of Science, Zagreb, Croatia.
8/2007	2nd Opatija Meeting on Computational Solutions in the Life Science. Participating in organization of Bioinformatic workshop.
7/2007	Involved in organization of "Practical course: Introduction to Bioinformatics", organized by prof. dr. Kristian Vlahovicek, University of Zagreb, Faculty of Science, Zagreb, Croatia.
6–7/2001	"Conflict resolution SC program in Cyprus". In organization: "UWC (United World College) Association", Nicosia, Cyprus.
7–8/2000	CAD/HAD - "Language and cultural learning program" Los Angeles, USA.

Publications

2014	Ivica Rubelj, Tomislav Domazet-Lošo, Robert Bakarić, Milena Ivanković, Nikolina Skrobot Vidaček and Andrea Čukšić Kalajžić, 2014. Method of determination of neutral dna sequences in the genome, system for targeting sequences obtained thereby and methods for use thereof, WO 2013144663 A3, WO 2013144663 A2, filed Mar 26, 2013, and issued Apr 17, 2014.
2013	Šestak MS, Božičević V, Bakarić R, Dunjko V, Domazet-Lošo T. 2013. Phylostratigraphic profiles reveal a deep evolutionary history of the vertebrate head sensory systems. Frontiers in Zoology, 10:18
in prep.	Bakarić R, Šestak MS, Domazet-Lošo T. PhyloStrat: Genomic phylostratigraphy editor
in prep.	Bakarić R, Šestak MS, Domazet-Lošo T. Long-term patterns of gain and loss of genes in evolution of eukaryote species

Awards

2011–2014	International Max Planck Research School fellowship. Ploen, Germany
2004–2008	Scholarship for excellent students. Croatian Ministry of Science, Education and Sports, Zagreb, Croatia.

Professional memberships

2010–2012	Acting secretary of the "Croatian Society for Theoretical and Mathematical Biology"
2009-2010	Leader of "Young Researchers", section of "Croatian Society of Natural Sciences"

Selected finished and ongoing projects

PhyloStrat	**Genomic phylostratigraphy editor** **Project leader:** dr. Tomislav Domazet-Lošo, "Ruder Boškoviš" Institute,Zagreb **Description:** Command driven interactive software for genomic phylostratigraphy. Software is composed of a set of procedures for: taxonomy editing, sequence editing, genome stratification, statistical analysis, local and grid BLAST-ing and data visualization all reachable through custom made unix shell (physh).
physh	**Custom designed Unix shell environment for PhyloStrat** **Project leader:** dr. Tomislav Domazet-Lošo, "Ruder Bošković" Institute,Zagreb,Croatia **Description:** Unix shell environment designed for parallelization, job distribution and communication with PhyloStrat software.
GenomicDeserts	**Software for identifying of non-functional genomic regions** **Project leader:** dr. Ivica Rubelj, "Ruder Bošković" Institute,Zagreb,Croatia **Description:** Project required developing a software tool for identifying non-functional genomic regions based on a functional significance of the underlying sequence.
ABI_analyzer	**Software for analysing data from ABI sequencing machines** **Project leader:** Robert Bakaric, "Ruder Bošković" Institute,Zagreb,Croatia **Description:** Software for extracting and analysing data from chromatogram files generated by Applied Biosystems (ABI) automated DNA sequencing machine. Project required creating an algorithm for identifying SNPs and predicting a potential length of a repetitive sequence based on the intensity of the signal.
mmrl	**Collection of tools for identifying and analysing repetitions in genomic sequences** **Project leader:** dr. Bernhard Haubold, Max Planck Institute for evolutionary Biology, Ploen, Germany **Description:** Collection of tools for identifying repetitions in genomic sequences, computing minimum mappable read lengths and analysing next-generation sequencing data (ChIP and RNA sequencing).
PhyloToolBox	**Collection of tools for identifying and analysing gene loss and horizontal gene transfer events in Eukaryote genomes** **Project leader:** dr. Diethard Tautz, Max Planck Institute for evolutionary Biology, Ploen, Germany dr. Tomislav Domazet-Lošo, "Ruder Bošković" Institute, Zagreb, Croatia

	Description: Project included developing new strategies for alignment based parsimony identification of gene loss events across Eukaryote species.
GitHub-projects	**Collection of various software tools for processing string/graph based data** **Project leader:** Robert Bakarić, "Ruder Bošković" Institute, Zagreb, Croatia **Description:** Project includes developing new strategies and implementing various theoretical solutions to problems involving processing string data: https://github.com/RobertBakaric.

Professional Interest

COMPUTER SCIENCE

Search algorithms
Sequence alignment
Alignment free sequence comparison
Scientific computing
Parallel programming

BIOLOGY

Evolution
Geniomic phylostratigraphy
Orphan genes
Next-generation sequencing