

Robert Bakarić

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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 | **CTO / Bioinformatic consultant:** Exaltum (exaltum.eu), Zagreb, Croatia.
- 2008–2016 | **Research Assistant:** "Ruder Bosković" Institute, Division of Molecular Biology, Laboratory of evolutionary Genetics, Group for Genomic Phylostratigraphy, Zagreb, Croatia.
In charge of projects involving:
Algorithm/software development: PhyloStrat-ToolKit, Linux shell emulators, lightweight job distributors, database mining tools (ENSEMBL, NCBI, KEGG, Reactome, UCSC, etc.) and software for statistical analysis
Linux system administration: HPC cluster administration (phylostrat.irb.hr, pikaia.zmb.irb.hr) and web/storage server administration (epistasis.irb.hr), shell scripting (bash, Perl), database administration (PhyloDb), software maintenance and development
- 2005–2008 | **Volunteering:** "Ruder Bosković" Institute, Division of Molecular Biology, Zagreb, Croatia.
Involved in the orphan genes research project (project leader dr.Tomislav Domazet-Lošo).

Technical skills/Computer skills

Programming language(s)	Perl, C++, C SQL, R bash, HTML	- ADVANCE - BASIC TO ADVANCE - BASIC
Libraries (ToolKits)	boost, STL, SeqAn, ncbi-c++ ncbi-c GEM	- ADVANCE - BASIC TO ADVANCE - BASIC
Database(s)	SQLite MySQL MsSQL, MsAcc.	- ADVANCE - BASIC TO ADVANCE - 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, Doxygen, Galaxy	

Languages

Croatian	Mother tongue
English	Fluent
German	Basic

Soft skills/Communication skills

ORAL PRESENTATIONS

- 6/2016 Oral presentation: "Statistical Inference", Exaltum, Zagreb, Croatia.
- 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 read mappability", EMBL-EBI-Wellcome Trust Summer School in Bioinformatics 2013, Hinxton, Cambridge.
- 11/2011 Poster presentation: Bakarić, Robert, "Efficient quantification of sequencing read 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

- 6/2016 Organization and talk participation "Bioinformatic and Statistics for Next Generation Sequencing data analysis", Exaltum, Zagreb, Croatia.
- 3/2016 Organized and held "A gentle introduction to statistical inference with R" course at Ruder Bosković Institute, Zagreb, Croatia.
- 10/2009 Organized and held "Introduction to Genomic Phylostratigraphy" course as part of Croatian Society for Theoretical and Mathematical Biology workshops/course series, 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

Scientific

- 2016 | Domazet-Lošo T, Carvunis A-R, Alba MM, Sestak MS, Bakarić R, Neme R, Tautz D. 2016. No evidence for phylostratigraphic bias impacting inferences on patterns of gene emergence and evolution. doi: <http://dx.doi.org/10.1101/060756>
- 2016 | Hanschen ER, Marriage TN, Ferris PJ, Hamaji T, Toyoda A, Fujiyama A, Neme R, Noguchi H, Minakuchi Y, Suzuki M, Kawai-Toyooka H, Smith DR, Sparks H, Anderson J, Bakarić R, Luria V, Karger A, Kirschner MW, Durand PM, Michod RE, Nozaki H, Olson BJ 2016. The *Gonium pectorale* genome demonstrates co-option of cell cycle regulation during the evolution of multicellularity. *Nature Communications*,7:11370
- 2014 | Rubelj I, Domazet-Lošo T, Bakarić R, Ivanković M, Skrobot Vidaček N, and Čukšić Kalajžić A, 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, Mitrikeski PT, Šimatović A, Seitz WA, Brčić-Kostić K. Complexity and mixedness of genes reflect the strength of natural selection.
- in prep. | Bakarić R, Mitrikeski PT, Šimatović A, Brčić-Kostić K, Seitz WA. Mixing character and the emergence of orphan genes.
- in prep. | Bakarić R, Šestak MS, Domazet-Lošo T. Long-term patterns of gain and loss of genes in evolution of eukaryote species
- in prep. | Bakarić R. eMap: High resolution gene age computation tool

CPAN

- 2015 | Robert Bakarić, 2015. Longest Common Prefix Computation Algorithms. <http://search.cpan.org/dist/LCP/>, Package v0.01
- 2016 | Robert Bakarić, 2016. Simple Burrows - Wheeler transform Library. <http://search.cpan.org/dist/BWT/>, Package v0.01

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 Bošković" 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

	<p>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.</p>
mmrl	<p>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).</p>
PhyloToolBox	<p>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.</p>
GitHub-projects	<p>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.</p>

Professional Interest

COMPUTER SCIENCE

- Bioinformatics
- Information Theory
- Search algorithms
- Sequence alignment / Alignment free sequence comparison
- Scientific computing
- Statistics

BIOLOGY

- Evolution (Macroscopic)
- Phylostratigraphy
- Gene Gain / Gene Loss
- Next-generation sequencing