

NAME	POSITION
Mile Šikić	Associate Professor, University of Zagreb, Faculty of Electrical Engineering and Computing (FER) Adjunct scientist, Bioinformatics Institute, A*STAR Singapore Co- founder and director, Oraclum Intelligence Systems Ltd, UK

## EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	YEAR	FIELD OF STUDY
University of Zagreb, FER	Ph.D	2008	Computer Science
University of Zagreb, FER	Ms sc EE	2002	Electrical Engineering
University of Zagreb, FER	Ms EE.	1996	Electrical Engineering

**A. Positions**

- 2009-2014 Assistant Professor, University of Zagreb, FER  
 2011-2012 Visiting scientist, Bioinformatics Institute, A\*STAR Singapore  
 1997-2009 IT and network consultant, Teaching Assistant, University of Zagreb, FER

**B. Awards**

- 2009-2014 Faculty of Electrical Engineering and Computing Science award for achieving globally recognized research result or innovation for his paper entitled "Identification of Patient Zero in Static and Temporal Networks: Robustness and Limitations", published in Physical Review Letters

**C. Recent grants**

- 2017-2022 Advanced methods and technologies in data science and cooperative systems (DATACROSS), activity leader for Multidisciplinary data intensive applications: biological sciences and health care - (5 000 000 Euros)  
 2014-2017 Algorithms for Genome Sequence Analysis by Croatian Science Foundation, principal investigator (100 000 Euros)  
 2014-2016 Identify pathogens from a stream of DNA sequences by ADRIS foundation, principal investigator (8 000 Euros)  
 2014-2015 Identify pathogens from a stream of RNA sequences by Business Innovation Croatian Agency (BICRO), principal investigator (30 000 Euros)  
 2012-2013 Complex network analysis of cis and trans chromatin interactions A\*STAR Joint Council Office, Singapore, leading investigator for Bioinformatics Institute (200 000 SGD)

**D. Invited talks**

- 2017 Methods of sequencing in precise medicine, Scientific colloquium Croatian academy of science and Croatian Science Foundation, Zagreb  
 2016 Is it a time for nanopore sequencing? University of Lausanne, Switzerland  
 2016 Is it a time for nanopore sequencing? A\*STAR, Singapore  
 2014 Stress test for de novo assemblers, A\*STAR, Bioinformatics Institute, Singapore  
 2013 Whether the time has come to overthrow BLAST? A\*STAR, Singapore

### **E. Academic Service**

2009 - Contributed > 30 peer-reviews for Nature Protocols, Bioinformatics, BMC Bioinformatics, Briefings in Bioinformatics, Scientific Reports, Plos One, IEEE Computational Biology and Bioinformatics, F1000, etc.

### **F. Teaching activities**

2017- Organizer/Lecturer, Computer science, Statistical data analysis  
2014- Organizer/Lecturer, Creative laboratory (course co-creator)  
2013- Organizer/Lecturer, Computer science, Bioinformatics (course co-creator)  
2009 - Lecturer, Computer science, Algorithms and data structures

### **G. Professional experience**

2017 Uber Croatia - UBER digital focus groups using our BASON method (team member)  
2014 - Oraclum Intelligence Systems Ltd. - New Facebook based method for election forecasting and market research. Our method correctly predicted outcomes of the UK referendum and the US presidential elections (team member)  
2015 Jutarnji list (Croatian's leading newspaper) – Mathematical analysis of the Croatian 2015 general elections (team member)  
2013-2014 Croatian Bank Association – Analysis of systemic risk using the network of reorganization proceedings in Croatia (team member)  
2010-2014 Artes Calculi (spin off) - Member of Supervisory board  
1997-2008 Croatian Government, consulting in various projects including: e-health, Open Archives Referral centres, Electronic data interchange (consultant and team leader)  
2005-2006 Kapsch Austria (one of Austria's most successful technology corporation)– development of various software solutions (SIP server, tariff tester, correlation engine) for telco operators (team leader)  
2000-2002 Telefonica (previously known as Orange Austria) – consulting in the field of mediation and provisioning for mobile phone users (team leader)

### **H. Staff and students supervised**

I supervised 1 postdoctoral student (Dr. Krešimir Križanović), 2 PhD students (Nino Antulov-Fantulin and Ivan Sović), and over 80 bachelor and master students.

### **I. Contact**

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Website <http://bioinfo.zesoi.fer.hr/>

## Mile Šikić – Publications from last 5 years

H-index: 14; Total # of publications: 63; Total # of citations: 797  
(Google Scholar, Feb 2018)

Asterisks (\*) indicate joint first or senior authorship.

Complete list of publications <https://scholar.google.com/citations?user=EK7apmcAAAAJ>

### Peer-reviewed publications

1. Piškorec, Matija; Antulov-Fantulin, Nino; Miholić, Iva; Šmuc, Tomislav; **Šikić, Mile**. *Modeling Peer and External Influence in Online Social Networks: Case of 2013 Referendum in Croatia*. Complex Networks 2017 Lyon 2017. 1015-1027
2. Križanović, Krešimir; Echchiki, Amina; Roux, Julien; **Šikić, Mile**. *Evaluation of tools for long read RNA-seq splice-aware alignment*. // Bioinformatics. btx668 (2017);
3. Ristov, Strahil; Vaser Robert; **Šikić Mile**. *Trade-offs in query and target indexing for the selection of candidates in protein homology searches* // Proceedings of The Prague Stringology Conference 2017 Prague 2017. 118-125
4. Križanović, Krešimir; Sović, Ivan; Krpelnic, Ivan; **Šikić, Mile**. *RNA Transcriptome Mapping with GraphMap* // Bioinformatics Research and Applications 13th International Symposium, ISBRA 2017
5. Šošić, Martin; **Šikić, Mile**. *Edlib: a C/C++ library for fast, exact sequence alignment using edit distance*. // Bioinformatics. 9 (2017); 1394-1395;
6. Vaser, Robert; Sović, Ivan; Nagarajan, Niranjana; **Šikić, Mile**. *Fast and accurate de novo genome assembly from long uncorrected reads*. // Genome research. 27 (2017); 737-746
7. Sović, Ivan; Križanović, Krešimir; Skala, Karolj; **Šikić, Mile**. *Evaluation of hybrid and non-hybrid methods for de novo assembly of nanopore reads*. // Bioinformatics. 32 (2016); 17; 2582-2589
8. Sović, Ivan; **Šikić, Mile\***; Wilm Andreas; Fenlon, Shannon Nicole; Chen, Swaine. // *Fast and sensitive mapping of nanopore sequencing reads with GraphMap*. // Nature Communications. 7 (2016); 11307-1-11307-11
9. Vaser, Robert; Adusumalli, Swarnaseetha; Ngak Leng, Sim; **Šikić, Mile**; Ng, Pauline C. *SIFT missense predictions for genomes*. // Nature Protocols. 11 (2016); 1-9
10. Križanović, Krešimir; Marinović, Mladen; Bulović, Ana; Vaser, Robert; **Šikić, Mile**. *TGTP-DB – a database for extracting genome, transcriptome and proteome data using taxonomy* // Proceedings of the 39th International Convention Mipro 2016, Distributed Computing, Visualization and Biomedical Engineering /DC VIS / Croatian Society for Information and Communication Technology, Electronics and Microelectronics - MIPRO, 2016. 472-476

11. Vaser, Robert; Pavlović, Dario; **Šikić, Mile**. *SWORD—a highly efficient protein database search*. // ECCB 2016: The 15th European Conference on Computational Biology, Bioinformatics. 32 (2016), 17; 680-684
12. Antulov-Fantulin, Nino; Lančić, Alen; Šmuc, Tomislav; Štefančić, Hrvoje; **Šikić, Mile**. *Identification of Patient Zero in Static and Temporal Networks: Robustness and Limitations*. // Physical Review Letters. 114 (2015) ; 248701-1-248701-5
13. Novak, Andrej; Križanović, Krešimir; Lančić, Alen; **Šikić, Mile**. *Some new results on assessment of Q-gram filter efficiency* // 9th International Symposium on Image and Signal Processing and Analysis (ISPA) 2015. proceedings. IEEE, 2015
14. Korpar, Matija; Šošić, Martin; Blažeka, Dino; **Šikić, Mile**. *SW#db: GPU-Accelerated Exact Sequence Similarity Database Search*. // PLoS One. 10 (2015) , 12;
15. Khoo, Aik-Aun; Ogrizek-Tomaš, Mario; Bulović, Ana; Korpar, Matija; Gurler, Ece; Slijepčević, Ivan; **Šikić, Mile**; Mihalek, Ivana. *ExoLocator—an online view into genetic makeup of vertebrate proteins*. // Nucleic acids research. 42 (2014), D1; 879-881
16. Antulov-Fantulin, Nino; Lančić, Alen; Štefančić, Hrvoje; **Šikić, Mile**. *FastSIR algorithm: A fast algorithm for the simulation of the epidemic spread in large networks by using the susceptible–infected–recovered compartment model*. // Information sciences. 239 (2013); 226-240
17. Korpar, Matija; **Šikić, Mile**. *SW#–GPU-enabled exact alignments on genome scale*. // Bioinformatics. 29 (2013), 19; 2494-2495
18. **Šikić, Mile**; Lančić, Alen; Antulov-Fantulin, Nino; Štefančić, Hrvoje. *Epidemic centrality — is there an underestimated epidemic impact of network peripheral nodes?* // European physical journal B: condensed matter physics. 86 (2013), 10; 440-1-440-13
19. Pavlović, Dario; Vaser, Robert; Korpar, Matija; **Šikić, Mile**. *Protein database search optimization based on CUDA and MPI*. Proceedings of the 36th International Convention on Information and Communication Technology, Electronics and Microelectronics MIPRO, 2013, Opatija, Croatia

## Reviews

1. Sović, Ivan; Skala, Karolj; **Šikić, Mile**. *Approaches to DNA de novo Assembly* Proceedings of the 36th International Convention on Information and Communication Technology, Electronics and Microelectronics MIPRO, 2013, Opatija, Croatia