

# Michał WOŹNIAK



## PERSONAL DATA

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NATINALITY: Polish  
DATE OF BIRTH: 5 April 1985  
E-MAIL: [mw219725@gmail.com](mailto:mw219725@gmail.com)  
GITHUB: <https://github.com/mimowo>

## EXPERIENCE

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APRIL 2022-(CURRENT) **Software engineer** at Google  
• Support for batch workloads in Kubernetes

MAY 2015-APRIL 2022 **Software engineer** at RD Projekt  
• Programming in Java, C++  
• Semantic web languages: RDF, RDFS, SKOS, SKOSXL, OWL  
• Semantic web technologies: triplestore, SPARQL  
• Performance reporting, analysis and optimization

JUNE 2015 **PhD studies in Computer Science** (WITH DISTINCTION)  
University of Warsaw, Poland  
Thesis title: Computational aspects of the presence of drug resistance mechanisms  
Advisors: prof. Jerzy Tiuryn and prof. Limsoon Wong  
• Programming in Python, R  
• Application of computational and statistical methods in biology

2007 AND 2008 SUMMERS **Software engineer** in Comarch  
programming in Java, C#, SQL

## EDUCATION

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JUNE 2015 | **PhD studies in Computer Science** (WITH DISTINCTION)  
University of Warsaw, Poland  
Thesis title: Computational aspects of the presence of drug resistance mechanisms  
Advisors: prof. Jerzy Tiuryn and prof. Limsoon Wong

SEP 2010 | **Master's degree in Computer Science**  
University of Warsaw, Poland  
Advisor: prof. Jerzy Tiuryn

SEP 2009 | **Master's degree in Mathematics**  
University of Warsaw, Poland  
Advisor: prof. Włodzimierz Waluś

2004-2010 | **Double Degree Program in Computer Science and Mathematics**  
University of Warsaw, Poland

## SCIENTIFIC VISITS

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SEP 2010 - SEP 2011 **Research Assistant** under supervision of prof. Limsoon Wong  
AND SEP 2012 - SEP 2013 National University of Singapore

## SKILLS AND INTERESTS

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Programming: JAVA, PYTHON, C++, PHP, SQL, HTML,  $\LaTeX$   
Languages: Polish (native), English (fluent)  
Interests: computational biology  
Other: analytical thinking, Polish Mensa member  
Hobbies: orienteering, logical puzzles, chess

## SCIENTIFIC PUBLICATIONS (H-INDEX=4)

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- BMC GENOMICS 2014 GWAMAR: Genome-wide assessment of mutations associated with drug resistance in bacteria  
**Michał Woźniak**, Jerzy Tiuryn, Limsoon Wong
- BMC BIOINFORMATICS 2014 eCAMBer: efficient support for large-scale comparative analysis of multiple bacterial strains  
**Michał Woźniak**, Limsoon Wong, Jerzy Tiuryn
- BMC SYSTEMS BIOLOGY 2013 Stringent DDI-based prediction of *H. sapiens*-*M. tuberculosis* H37Rv protein-protein interactions  
Hufeng Zhou, Javad Rezaie, Willy Hugo, Shangzhi Gao, Jingjing Jin, Mengyuan Fan, Chern-Han Yong, **Michał Woźniak**, Limsoon Wong
- BMC SYSTEMS BIOLOGY 2012 IntPath—an integrated pathway gene relationship database for model organisms and important pathogens.  
Hufeng Zhou, Jingjing Jin, Haojun Zhang, Bo Yi, **Michał Woźniak**, Limsoon Wong
- BMC GENOMICS 2012 An approach to identifying drug resistance associated mutations in multiple bacterial strains  
**Michał Woźniak**, Jerzy Tiuryn, Limsoon Wong
- BIOINFORMATICS 2011 CAMBerVis: visualization software to support comparative analysis of multiple bacterial strains  
**Michał Woźniak**, Limsoon Wong, Jerzy Tiuryn
- BMC BIOINFORMATICS 2011 CAMBer: an approach to support comparative analysis of multiple bacterial strains  
**Michał Woźniak**, Limsoon Wong, Jerzy Tiuryn
- BIOINFORMATICS 2011 MODEVO: exploring modularity and evolution of protein interaction networks  
**Michał Woźniak**, Janusz Dutkowski, Jerzy Tiuryn