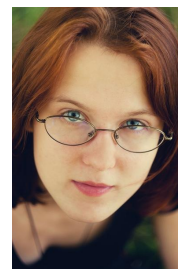


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Education:

10/2016 — 04/2020 Ph.D. student, Bielefeld University, Bielefeld, Germany.
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09/2009 — 06/2014 Lomonosov Moscow State University, Moscow, Russia, Department of Bioengineering and Bioinformatics, Specialist degree in bioengineering, Diploma with honors. GPA 4.85/5.0

Professional experience:

5/2021 — present Associated junior group leader of Computational Systems Medicine group at the chair of Computational Systems Biology at University of Hamburg development of novel biclustering method for patient stratification and disease subtyping; development of privacy-aware tools for bioinformatics; multi-omics data integration and network-based analysis

5/2020 — present Research Employee, Technical University of Munich, Freising, Germany.
analysis of MS data from [CLINSPECT-M](#) project; developing federated ML methods for [FeatureCloud.eu](#)

10/2016 — 9/2019 Research Employee, Bielefeld University, Bielefeld, Germany.
Data integration for investigation of the molecular basis of comorbidity between asthma and hypertension. Developing the method for the identification of network-constrained differentially expressed network-constrained biclusters.

03-12/2018 Visiting researcher, Simon Fraser University, Burnaby, Canada.
Developing the method for the identification of network-constrained differentially expressed network-constrained biclusters. Multi-omics data preprocessing, harmonization, and analysis for the project on drug response prediction.

08/2015 — 9/2016 Analyst, BostonGene, Moscow, Russia.
Developing pipelines for NGS data processing and analysis, testing of bioinformatics software, preparing patent applications, and literature reviews in the field of cancer omics.

09/2014 — 01/2016 Junior Researcher, Laboratory of Evolutionary Genomics, Department of Human Genetics and Genomics, Vavilov Institute of General Genetics, Moscow, Russia.
Developing software for finding disease-specific patterns of allelic imbalance in ChIP-seq data. Searching for complex genetic interactions e.g. epistasis on WGS data.

Awards and Scholarships:

- 2020** Doctorate Completion Scholarship from Bioinformatics/Medical Informatics Department of Bielefeld University
- 2014** CUDA Center of Excellence MSU Scholarship for the project «Nucleic acid conformational ensembles from Markov state models»

Patents:

- 2017** International Application No.: PCT/US2017/026723
CONSTRUCTION AND METHODS OF USE OF A THERAPEUTIC CANCER VACCINE LIBRARY COMPRISING FUSION-SPECIFIC VACCINES

Publications:



- 2021**
- **O. Zolotareva**, R. Nasirigerdeh, J. Matschinske, R. Torkzadehmahani, et al. Flimma: a federated and privacy-aware tool for differential gene expression analysis. *arXiv* preprint <https://arxiv.org/abs/2010.16403>
 - H. Sharifi-Noghabi, P.A. Harjandi, **O. Zolotareva**, C.C. Collins, M. Ester. Velodrome: Out-of-Distribution Generalization from Labeled and Unlabeled Gene Expression Data for Drug Response Prediction, *bioRxiv* preprint doi: 10.1101/2021.05.25.445658.
- 2020**
- **O. Zolotareva**, S. Khakabimamaghani, O. Isaeva, Z. Chervontseva, A. Savchik, and M. Ester. Identification of Dysregulated Gene Modules in Heterogeneous Diseases. *Bioinformatics* (2020) Dec 16, doi: 10.1093/bioinformatics/btaa1038.
 - H. Sharifi-Noghabi, S. Peng, O. Zolotareva, C.C. Collins, M. Ester. AITL: Adversarial Inductive Transfer Learning with input and output space adaptation for pharmacogenomics. (2020) *Bioinformatics*, doi: 10.1093/bioinformatics/btaa442
- 2019**
- H. Sharifi-Noghabi, **O. Zolotareva**, C. Collins, and M. Ester. “MOLI: Multi-Omics Late Integration with deep neural networks for drug response prediction”. *Bioinformatics*, 35(14), 2019. doi:10.1093/bioinformatics/btz318
 - **O. Zolotareva**, and M. Kleine. “A survey of gene prioritization tools for Mendelian and complex human diseases”. *J Integr Bioinform*. 2019 Sep 9;16(4).
 - **O. Zolotareva**, O. Saik, C. Königs, E. Bragina, I. Goncharova, M. Freidin, V. Dosenko, V. Ivanisenko, and R. Hofestädt. Comorbidity of asthma and hypertension may be mediated by shared genetic dysregulation and drug side effects. *Scientific Reports* 2019 Nov 8;9(1):16302.
 - O Snow, H Sharifi, J Lu, **O Zolotareva**, M Lee, M Ester. BDKANN-Biological Domain Knowledge-based Artificial Neural Network for drug response prediction. *bioRxiv*, 840553
- 2018**
- A. Shoshi, R. Hofestädt, **O. Zolotareva**, M. Friedrichs, A. Maier, V. A. Ivanisenko, V. E. Dosenko, E. Yu. Bragina. GenCoNet - A Graph Database for the Analysis of Comorbidities by Gene Networks. *J Integr Bioinform*, 15(4), 2018. doi: 10.1515/jib-2018-0049
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2017

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- Smirnov IV, Golovin AV, Chatziefthimiou SD, Stepanova AV, Peng Y, **Zolotareva OI**, Belogurov AA Jr, Kurkova IN, Ponomarenko NA, Wilmanns M, Blackburn GM, Gabibov AG, Lerner RA. Robotic QM/MM-driven maturation of antibody combining sites. *Science Advances*, 2016 Oct 19;2(10):e1501695. doi: 10.1126/sciadv.1501695
- Andreeva TV, Tyazhelova TV, Rykalina VN, Gusev FE, Goltsov AY, **Zolotareva OI**, Aliseichik MP, Borodina TA, Grigorenko AP, Reshetov DA, Ginter EK, Amelina SS, Zinchenko RA, Rogaev EI. Whole exome sequencing links dental tumor to an autosomal-dominant mutation in ANO5 gene associated with gnathodiaphyseal dysplasia and muscle dystrophies. *Scientific Reports*, 2016 May 24;6:26440. doi: 10.1038/srep26440.