



Fikrat Talibli

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Email: fikrattalibli@gmail.com

Work permit: German **Gender:** Male **Date of birth:** 26/10/1994 **Place of birth:** Baku, Azerbaijan **Nationality:** German

WORK EXPERIENCE

University of Stuttgart

City: Stuttgart | **Country:** Germany

[01/12/2020 – Current]

PhD, Researcher

Topic: **Graph-based algorithms for CRISPR-Cas analyses**

Tools: C++, CMakeLists, Python, HMMER, HMM file, MegaHit assembly tool for succinct data structure/succinct de Bruijn graph, OpenMP, edlib for edit distance calculations, pyhmmer, MegaGTA.

Skills:

- graph algorithms
 - bounded cycle enumeration algorithm on directed graphs
 - succinct data structures
 - Viterbi, A* algorithms for pathfinding
- advanced memory management techniques in a multi-threaded environment, e.g., data structures and prefetching techniques in HPC
- gene detection using hmmer;

Taught Machine Learning in Biology for master students, and worked with Neural Ordinary Differential Equations and Neural CDEs

Libelle AG

City: Stuttgart | **Country:** Germany

[01/2018 – 01/07/2018]

Web developer

Responsibilities:

- Develop a communication module using Node.js
- Redesign the web platform with React.js
- Document the developed software and web apps

Azerbaijan State Oil and Industry University

City: Baku | **Country:** Azerbaijan

[15/09/2016 – 28/05/2017]

Teaching assistant in higher education

R.I.S.K. Company <https://risk.az/>

[01/11/2013 – 01/09/2016]

Junior Developer and Technical Support

- Collaborated with clients across diverse countries and age groups, ensuring clear communication and tailored support.
- Delivered software presentations and provided comprehensive technical assistance.
- Designed and developed user-focused helper applications in C#.
- Created detailed software manuals and documentation to enhance user experience.

PUBLICATIONS

[**Metagenomic CRISPR Array Analysis Tool: a novel graph-based approach to finding CRISPR arrays in metagenomic datasets**](#)

[2025]

Reference: microLife, part of FEMS (Federation of European Microbiological Societies)

MCAAT - Metagenomic CRISPR Array Analysis Tool: a highly sensitive algorithm for finding CRISPR Arrays in unassembled metagenomic data. It takes advantage of the properties of CRISPR arrays that form multicycles in de Bruijn graphs. We are developing the successor to the method that aims to identify and enumerate phage sequences.

Github: <https://github.com/RNABioInfo/mcaat>

Docker: <https://hub.docker.com/r/feeka94/mcaat>

Authors: Fikrat Talibli, Björn Voß | **Journal Name:** microLife | **Volume, Issue and Pages:** Volume 6 | **Publisher:** Oxford University Press

EDUCATION AND TRAINING

[16/10/2017 – 01/08/2020]

M.Sc. INFOTECH

University of Stuttgart https://www.infotech.uni-stuttgart.de/about_us/

City: Stuttgart | **Country:** Germany | **Field(s) of study:** Information and Communication Technologies (ICTs)

[15/09/2013 – 15/06/2017]

B.Sc. Computer Engineering

Azerbaijan State Oil and Industry University <https://asoiu.edu.az/>

City: Baku | **Country:** Azerbaijan | **Field(s) of study:** Computer Engineering

LANGUAGE SKILLS

Mother tongue(s): Azerbaijani

Other language(s):

English

LISTENING C2 READING C1 WRITING C1

SPOKEN PRODUCTION C1 SPOKEN INTERACTION C1

Russian

LISTENING C2 READING C2 WRITING C1

SPOKEN PRODUCTION C1 SPOKEN INTERACTION C1

German

LISTENING B2 READING B2 WRITING B2

SPOKEN PRODUCTION B2 SPOKEN INTERACTION B2

French

LISTENING B2 READING B2 WRITING B1

SPOKEN PRODUCTION B1 SPOKEN INTERACTION B1

Levels: A1 and A2: Basic user - B1 and B2: Independent user - C1 and C2: Proficient user

SKILLS

write scientific publications | prepare presentation material | tutor students | algorithms | C+ + | Python (computer programming) | linux shell scripting | HPC basics | neural networks | operate open source software | perform project management | assess students | promote the transfer of knowledge | supervise practical courses | PyTorch, Keras | Python (NumPy, Pandas, NLTK, Matplotlib, sklearn, TensorFlow)