

Matthew Crown

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EDUCATION

Northumbria University

Newcastle, UK

PhD in Bioinformatics

Sep. 2020 – Oct. 2024

- Thesis Title: "Global, viral and protein scale functional annotation tools for -omics and structural bioinformatics". See projects section for more information on projects developed during PhD.

Newcastle University

Newcastle, UK

BSc. (Hons) Biochemistry

Sep. 2016 – Jun. 2020

- Dissertation title: "Proteomic analysis of the E3-ubiquitin ligase DTX3L interactome"
- Graduated with First Class Honours and awarded the Gus Lienhard Prize for Biochemistry.

EMPLOYMENT AND EXPERIENCE

Senior Research Assistant

Newcastle, UK

COVID19 Sequencing Group, Northumbria University

Oct. 2021 – Sep. 2022

- Part of the COVID19 Genomics Consortium (COG-UK) Sequencing efforts at Northumbria University and developed a novel structural and functional annotation tool for SARS-CoV-2 proteins (see Projects).
- Undertook routine analysis of SARS-CoV-2 sequencing data as part of the sequencing efforts, including running and troubleshooting Nextflow pipelines, handling sensitive metadata linkage, and developing SOPs.

Industrial Placement

Stevenage, UK

Exploratory Biomarker Assay Group, GlaxoSmithKline

Sep. 2018 – Aug. 2019

- 1-year industrial placement. The focus of work was development and optimisation of assays to support preclinical/clinical safety and efficacy studies of large and small molecule drugs.
- Utilised commercial immunoassay and flow cytometry platforms and performed downstream data analysis.

RESEARCH PROJECTS

AlphaCognate | *Python, GEMMI, Nextflow, Git*

May. 2024 – Present

- Developed a tool for transplantation of cognate ligands to predicted protein structures, which integrates annotation data from ProCogGraph (see below) through a Snakemake pipeline, and uses the GEMMI package for structural superposition of predicted and known protein structures.

ProCogGraph | *neo4j, Python, RDKit, Arpeggio, Nextflow, Git*

Jan. 2023 – Jun. 2024

- Developed a graph database (neo4j) of enzyme domain-ligand interactions and cognate ligand mapping.
- The database is built using a Nextflow pipeline, and integrates cheminformatics ligand similarity matching and protein contact analysis.

OMEinfo | *Docker, Python, Rasterio, Rio-Cogeo, Git*

Jan. 2023 – Sep. 2023

- Developed a metadata annotation tool to automatically and consistently annotate locations with geospatial features, which allows non-expert users to integrate specialist geospatial data formats (GeoTIFF) into their metadata.

SPEAR | *Python, Snakemake, minimap2, Plotly, Bash, Git*

Oct. 2021 – Sep. 2022

- Developed a pipeline for rapid structural and functional annotation of SARS-CoV-2 proteins, including antibody escape potential and conformational dynamics.
- The tool includes a report feature which allows easy comprehension of complex structural/functional features of the virus for non-expert decision makers.

For a full list of publications, see my Google Scholar profile: [Google Scholar](#)

TECHNICAL SKILLS

Languages: Python, R, Bash, Cypher, HTML/CSS

Reproducible Workflow & DevOps Tools: Snakemake, Nextflow, Git, Docker

Bioinformatics Tools: Biopython, GEMMI, RDKit, Pymol,

Generic Tools and Libraries: neo4j, pandas, NumPy, Matplotlib, scikit-learn

PERSONAL INTERESTS

Outside of work, I am a keen runner, having recently completed my first Great North Run for charity. I also enjoy the physical challenge and problem solving of bouldering. Whilst my work focusses on bioinformatics, I also have a passion for technology and enjoy learning about and tinkering with the latest new hardware and software.