Matthew Crown

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EDUCATION

Northumbria University   Newcastle, UK
PhD in Bioinformatics (submitted)   *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 chemoinformatics 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.