CHAD A. HIGHFILL, PhD

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SUMMARY OF QUALIFICATIONS

Over eight years of experience in project design/management, molecular biology and data analysis. Proven ability to independently design and execute new research projects and succeed under pressure. Have ability to program and manipulate big data in Bash, R, SAS, and Python. Can quickly acquire and implement new knowledge and skills. Many publications in peer-review journals. Can quickly establish connections in diverse environments, fluent in English with N5 Japanese fluency.

CORE COMPETIENCIES

- **Management/Leadership**: Managed technicians, graduate students and undergraduates on multiple projects with successful deliverables.
- **Project planning and Coordination**: collecting preliminary data for grant proposal, defining potential budget, time lines and outcomes, ordering supplies and coordinating work of subordinates.
- **Programming Skills***:* R (Base R (Plotting and Statistical), ggplot, Bioconductor, Limma, DESeq2, rlme), Python (resting API and very basic utilization), Bash (Unix Shell), SAS (Statistical Analysis – Mixed Model ANOVAs)
- **Bioinformatics Tools**: Bioconductor, Bed tools, Sam tools, bwa, fastqc, Picard tools, STAR, MAGMA
- **Machine Learning**: Classification (Random Forest – R), WGCNA Clustering, NeoPulse (AI), IBM WATSON
- **Big Data**: DNA Analysis, Transcriptomics, Metabolomics (limited experience), Proteomics (limited experience), scRNAseq
- **Public Data Utilization**: Open Targets, CEL files (NCBI), GTEx, GWAS summary datasets
- **Open Source Software:** Cytoscape, DAVID, Panther GO, STRING, IPA, NEO PULSE, IBM WATSON
- **Reproducible Research**: R notebook, Github
- **Wet-Lab Skills**: DNA/RNA extraction, SANGER seq, NGS workflows, CRISPR workflow, PCR, qRT-PCR, Western Blots, Microscopy (Confocal and TEM), Cell Culture
- **Basic Computer Skills**: Microsoft packages, Adobe packages, Cytoscape

EMPLOYMENT HISTORY

RNA Biologist @ Exicure (February 2021 – Present)

- Managed three separate projects via internal and external collaborations.
    - Malat1 Target identification, determine if SNAs can cause upregulation, creation of bispecific SNAs
        - Found three new Malat1 sites
        - Successfully created bispecific SNAs with synergetic effects
        - Upregulation via SNAs is still under investigation
    - Brought RNAseq into Exicure in conjunction with Watershed strength indications
    - Helped find key assay for FXN target
    - In charge of all insilico target design at Exicure.

System's Biologist @ Takeda Pharmaceutical (April 2019 – February 2021)

- Managed and lead five separate projects via internal and external collaborations.
    - New Target Identification, CRISPR screen ID, Deep Learning AI, AMED Project, COCKP-T Project
    - Datasets utilized for projects:
        - Transcriptomics (bulk and scRNAseq), metabolomics, proteomics, public microarray, public GWAS data, and data platforms (GTEx, OPEN TARGETS)
- Developed custom scripts and statistical pipelines
    - CRISPR screening scoring and ranking of genetic targets

        - Safety screen, expression presence, DEGs, machine learning (IBM WATSONs) for prediction, tissue specificity/enrichment, pathway analysis, gene ontology, WGCNA, network construction
        - Resulted in 10 viable targets
    - Combined different Affymetrix platforms for clinical microarray analysis.
        - Quantile normalization, Average Probes, limma (linear regression)
        - pathway analysis, gene ontology, WGCNA, network construction
        - Resulted in 3 new potential targets
- Developed and managed deep learning AI project.
    - Utilized AI (NeoPulse platform) to help find new targets for ataxia's
    - Utilized FRONTEO to help discover new biological targets for FTLD.

Postdoctoral Researcher @ Trudy Mackay's Lab (August 2016 – March 2019)

- Managed a team of 10 undergraduates screening the DGRP for cocaine and meth addiction.
- Mentored and trained 1 undergraduate student from Surrey University, UK.
- Mentored and trained 2 graduate students.
- Developed cocaine and methamphetamine consumption assays.
- Performed GWAS to identify SNPs associated with cocaine and meth addiction and assembled genetic networks using Cytoscape.
- Performed RNAi to validated GWAS genes and used SAS and R for statistical analysis.
- Performed RNAseq and analyzed data through Bash Scripts.
- Developed method to improve CRISPR efficiency using small molecules.
- Used CRISPR to induce the same mutation over multiple genetic backgrounds.
- Used Big Dye, DNA sequencing, and Bash Scripting to confirm mutations.

PhD Graduate Researcher @ Stuart J. Macdonald's Lab (August 2012 – July 2016)

- Lead a team of 3 undergraduates on validation of nicotine resistance candidate genes.
- Obtained hands on experience in genetics and programming (R and python) to analysis big data generated through DNA/RNA sequencing.
- Developed lifespan assay and screened a mapping panel for novel QTL.
- Validated nicotine resistance genes via RNAi, over-expression, CRISPR.
- Performed DNA/RNA sequencing on caffeine resistance flies.
- PCR

Lab Tech Researcher/ Lab Manager @ Liang Xu's Lab (August 2011 – July 2012)

- In charge of ordering supplies and fixing lab equipment.
- In charge of standard operating procedures for the lab.
- Helped with qRT-PCR and western blots.
- Developed novel methods to screen nanoparticles using electron microscopy.
- Worked with many cancer cell lines (culturing cells).

Masters Graduate Researcher @ Kyoungtae Kim's Lab (August 2010 – July 2011)

- Obtained hands of experience in yeast genetics and molecular biology techniques and spinning confocal microscopy.

EDUCATION

PhD in Molecular, Cellular, and Developmental Biology University of Kansas 2016

MS in Biology Missouri State University 2011

PUBLICATIONS

List of 10 published papers can be found at:
https://scholar.google.com/citations?user=ZsnRDPIAAAAJ&hl=en

REFERENCES

References are available upon request