EFFIE KLIMI

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SKILLS

Programming: R (tidyverse, Bioconductor + more), Python (Pandas, NumPy + more), Bash scripting, NextFlow, Node.js, React, D3, Typescript

Raw sequencing pre-processing: WGS/WGBS, ChIP-seq, ATAC-seq, bulk/small/single cell RNA-seq analysis

Genomics: Variant calling (SNPs/indels & structural variants), GWAS/eQTL analyses

Epigenomics: Differentially methylated region analysis, ChIP- & ATAC-seq peak calling & downstream analysis, HOMER-based TF analyses

Transcriptomics: Differential expression analysis, single cell RNA-seq clustering/marker identification/integration, gene set enrichment analyses

Computational structural biology: Protein tertiary structure modelling (PyMOL), RNA secondary structure modelling (RNAfold)

Culturing of vascular smooth muscle & endothelial cells, embryonic stem cells, HeLa, HEK293T, human vein tissue, *S. pombe*

Wet lab: RNA extraction, RT-qPCR, cloning, transfections, nucleofections, immuno-histochemistry/fluorescence, western blot, X-gal staining, FACS

EXPERIENCE

PhD Research | Queen's Medical Research Institute, University of Edinburgh, UK (Oct 2019 - Nov 2023)

Project 1: Identification of novel therapeutic miRNAs for vein graft failure – *in vitro* & *in silico*

- Assessed the effect of 2000+ miRNAs on proliferation & viability via a high-throughput screen
- Evaluated the top candidates as potential therapeutics & studied their mechanism of action (*in vitro* / *ex vivo* / RNA-seq)
- Testing adenoviral delivery systems in the vasculature

Project 2: Studying endogenous miRNA loci dysregulated in response to injurious stimuli in vascular smooth muscle cells – *in vitro* & *in silico*

- Developed transcriptomics & genomics pipelines with R, Python, Unix and NextFlow
- Analysis of time-series data (ML & non-ML methods)

Project 3: Evaluation of all human miRNAs by predicting processing efficiency – *in silico*

I used sequence and structural determinants associated with Drosha recognition and subsequent increased mature miRNA expression to identified the most optimal miRNAs that make the most sense to research and work with for translational projects

Also involved in:

- A project on pro-angiogenic extracellular vesicles derived from a stem cell-derived endothelial cell product
- Extracellular vesicle isolation and RNA-seq analysis of their contents

Multiomics pipeline development for cancer precision medicine | Collab with AI Forge, London, UK (Sep - Oct 2023)

- Constructed multimodal multiomics pipelines including genomics, epigenomics, transcriptomics and proteomics datasets

Virology training | Batavia Biosciences B.V., Leiden, NL (July - Oct 2023)

- Generation of clinical-grade Adenovirus 5-based vectors

Honours Project | Genome Damage and Stability Centre, University of Sussex, UK (Sept 2018 – Feb - 2019)

- Structure-function analysis of the DNA helicase factor Cdc45 in *Saccharomyces pombe*
- *S. pombe* culture and Cre-lox-mediated insertion of Cdc45 mutants generated by error-prone PCR & tertiary protein structure modelling of temperature-sensitive Cdc45 mutants (PyMOL)

Junior Research Associate | Evolution, Behaviour and Environment Department, University of Sussex, UK (June – Sept 2018)

- Used single nucleotide polymorphism data (from the 1000 genomes project) and *de novo* mutation data (from multiple studies) to estimate the variation of the effective population size across the human genome

TALKS · PRESENTATIONS

Keystone Symposia "Small Regulatory RNAs: From Bench to Bedside" with Scholarship by the NIH | Santa Fe, NM (2022)
Title: "Investigating miRNAs regulating vascular smooth muscle cell proliferation"; 1st author

Cardiovascular Research Institute Maastricht invited talk | Virtually (2023)
"Functional screening identifies novel miRNAs inhibiting Vascular Smooth Muscle Cell proliferation" (2023)

MANUSCRIPTS · PUBLICATIONS

Functional screening identifies novel miRNAs inhibiting Vascular Smooth Muscle Cell proliferation 1st author, manuscript in development (2023)

Vascular smooth cell function and dysfunction controlled by non-coding RNA Invited review article, joint 1st author, invited review (2023)

Extracellular vesicles from a human embryonic stem cell-derived endothelial cell product induce angiogenesis with high efficiency at very low input and contain miRNAs with novel proangiogenic function 5th author, in review (2023)