

## SUMMARY

I'm Effie - I've worked on basic research, evolutionary genetics, -omics and my PhD in RNA therapeutics & viral vectors @ The University of Edinburgh.

I care about making human bodies more robust and long lasting, well-designed multiomics pipelines and maximising thinking time for scientists by automating tedious research tasks.

### What I can do in a nutshell:

- Design, perform & analyse -omics projects from start (cell culture & sample collection) to finish (viz & interpretation)
- WGS, ChIP, RNA-seq (bulk, small, single cell, ATAC)
- Coding, computational biology, pipeline development & ML (Unix/NextFlow, R, Python + various libraries)
- Functional genomics (GWAS, eQTL)
- Experience with cells & tissue: vascular smooth muscle & endothelial cells, embryonic stem cells, HEK293T, HeLa, S. pombe, plasmid/siRNA/miRNA transfections, nucleofection, human vein tissue dissection and culture
- Experience on the bench: RNA extraction, PCR, RT-qPCR, immunohistochemistry, immunofluorescence, western blot, X-gal staining, flow cytometry. Numerous phenotypic/functional assays
- Adenoviral vector production, viral transduction of primary cells & cell lines
- I can also make web apps & visualisations using TS/React/D3.js - taught myself how to build biology software products

## EXPERIENCE

**Doctoral Researcher** | Queen's Medical Research Institute, University of Edinburgh (Oct 2019 - Dec 2023)

**Niche: Research at the intersection of wet and dry lab, transcriptomics, vascular biology, RNA biology.**

**Focus: *in silico* transcriptomics & data science**

### 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. Selected candidates.
- Evaluated the top candidates as potential therapeutics & studied their mechanism of action (*in vitro* / *ex vivo* / *RNAseq*)
- Testing adenoviral delivery systems in the vasculature & identified the most efficient

### Project 2: Studying endogenous miRNA loci that become deregulated in response to injurious stimuli in vascular smooth muscle cells *in silico* & *in vitro*

- Developed transcriptomics & genomics pipelines with R, Python, Unix and NextFlow
- Analysis of time-series data (ML & non-ML methods)
- Analysis of in-house & public RNA-sequencing datasets (bulk, small & single cell)
- Functional genomics-based evaluation of the loci of interest using GWAS/eQTL

### 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 identify the most optimal miRNAs that make the most sense to research and work with for translational projects

### Also involved in:

- A project on extracellular vesicles derived from a stem cell-derived endothelial cell product whose potent angiogenic effect could be harnessed for blood supply restoration in the infarcted heart
- Extracellular vesicle isolation and RNA-sequencing analysis (small & bulk)
- Teaching new lab members (students and post-doctoral)

**BBSRC CASE internship** | Batavia Biosciences B.V., Leiden, NL (June – August 2023)

- Training on the generation of clinical-grade Adenovirus 5-based vectors for miRNA therapy.

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

### Project: 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 (Jun - 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.

## EDUCATION

**PhD Vascular Biology** | Queen's Medical Research Institute, University of Edinburgh (Oct 2019 - Dec 2023)

**BSc Genetics** | School of Life Sciences, University of Sussex (Sept 2016 - Jun 2019)

- Genetics society: Chair (Sept 2017 - Jun 2018); President (Sept 2018 - Jun 2019)

## MANUSCRIPTS & PUBLICATIONS

**“Functional screening identifies novel miRNAs inhibiting Vascular Smooth Muscle Cell proliferation”**; 1<sup>st</sup> author, Manuscript submitted (2023)

**“Vascular smooth cell function and dysfunction controlled by non-coding RNA”** Invited review article, submitted (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"**; 5<sup>th</sup> author, Manuscript submitted (2023)

*Two more manuscripts in development*

## CODING

**I can code in:** Python, R, Bash, SQL, Typescript, HTML5/CSS.

**Tools/platforms:** Git/Github, NextFlow, Snakemake, Puppeteer, Conda/Mamba, FastAPI, AWS

## PERSONAL PROJECTS

**Drylab Inc, maximizing time spent on thinking for scientists** | To be launched in 2023

I am interested in task automation and “autopiloting” aspects of biology research so I can use the time saved on thinking and planning, & keen to share what I have made with the community.

Currently building a minimalistic but advanced and easy-to-use genome browser. Next.js/React-based frontend and a python backend, using the Ensembl REST API. Optimising for high-speed and very easy, fast browsing using the touch bar/mouse and keyboard shortcuts.

**I am including:**

- connection to genomic/transcriptomic data repositories to view alignments (IGV fails at this)
- features for easy download of annotation data in multiple formats, including high-quality, customisable images for publication (all current browsers fail at this)
- a log-in feature, through which the user can access their own old browser searches, data downloads, and images

## CONFERENCES · TALKS · PRESENTATIONS

**Keystone Symposia “Small Regulatory RNAs: From Bench to Bedside”** | Santa Fe, NM (2022)

Title: “Investigating miRNAs regulating vascular smooth muscle cell proliferation”; 1<sup>st</sup> author

**Cardiovascular Research Institute Maastricht invited talk** | Virtually (2023)

“Functional screening identifies novel miRNAs inhibiting Vascular Smooth Muscle Cell proliferation” (2023)