

# Hugh WARDEN

Machine Learning | Data Science | Statistics | Bioimage Analysis | Bioinformatics

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I am a PhD student at the Institute of Genetics and Cancer, part of the University of Edinburgh. I am very passionate about using my background in machine learning, data science and statistics in a more applied setting, working with a wide range of geneticists and biologists to solve real world problems. Some details of my work may have been omitted if they pertain to unpublished research.

## EDUCATION

### August 2025 | April 2022 | PhD Genetics, KHAMSEH LAB - INSTITUTE OF GENETICS AND CANCER, University of Edinburgh

I am currently studying for my PhD with the Khamseh Lab at the Institute of Genetics and Cancer. I will be using machine learning and cell painting to investigate how cancer affects cellular morphology. I am currently using Paquo to create a preprocessing pipeline to carry out machine learning on whole slide bioimages that interacts with already established QuPath projects. By doing this I am hoping to leverage the power of Python to carry out powerful analysis, but having all of the results output into a QuPath project that is easy to interpret.

Machine Learning   QuPath   Paquo   Python   Groovy   Bash   R   Cell Painting   Cancer   Genetics

### March 2022 | January 2022 | Rotation Project, KUDLA LAB - INSTITUTE OF GENETICS AND CANCER, University of Edinburgh

I completed a 3 month rotation under the supervision of Grzegorz Kudla and Diego Oyarzún using machine learning to investigate the transcriptomic and morphological effects of certain mutations. As well as producing the computational pipelines for analysis, I also got hands on with the wet lab work. As part of this rotation I spent a lot of time in the tissue culture lab observing how to look after cells, as well as looking after some of my own cells independently.

Machine Learning   R   Python   Cell Painting   CellProfiler   Genetics   Cancer

### December 2021 | September 2021 | Rotation Project, KHAMSEH LAB - INSTITUTE OF GENETICS AND CANCER, University of Edinburgh

I spent 3 months working with Ava Khamseh producing a preprocessing pipeline for whole slide images to curate labelled data sets for machine learning. I worked in QuPath to understand how tools could be used to select various parts of images based on their immunohistochemistry. I then pulled this pipeline out of the GUI and into a groovy script so that it could be run on multiple images via the command line. After this, I worked on writing all of the meta scripts needed to submit these analyses as a job on the high performance cluster for fast analysis. I am now continuing this work as part of my PhD.

Bioimage Analysis   QuPath   Groovy   Bash   R   Python   Cancer   Genetics

### September 2016 | August 2021 | MMath Mathematics, UNIVERSITY OF SOUTHAMPTON,

I graduated from my Integrated Master of Mathematics (MMath) at the University of Southampton with first class honours. I gained an insight into all areas of maths, however I leaned towards the statistical and computational tracks. In the last two years of my degree I focused my studies on machine learning, data science and hypergraph theory, specifically their applications in the analysis of biological systems.

Machine Learning   Data Science   Statistics   Hypergraph Theory   R   Python   Java   Maths   Biology   Genetics

## </> PROGRAMMING LANGUAGES

R	●	●	●	●	●
Python	●	●	●	●	○
Groovy	●	●	●	○	○
Julia	●	●	○	○	○
SQL	●	●	○	○	○
Java	●	●	○	○	○

## </> FAMILIAR WITH

- > Version Control :
  - > Git
  - > GitHub/GitLab
- > Bash
- > Environment Managers :
  - > Conda
- > BioImage Analysis :
  - > QuPath
  - > CellProfiler
- >  $\text{\LaTeX}$

## 🎵 PERSONAL INTERESTS

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I am a keen trumpet player, having played for almost 18 years. On top of this I also play drums, piano, guitar, bass and trombone. I am a member of multiple bands playing anything from classical or baroque to jazz or show tunes. Over many years I have held multiple roles on the committees for my ensembles, gaining experience in organisation as well as event planning.

As well as participating in multiple ensembles, I also spent a lot of time organising music events. During my undergraduate studies I spent one year as the Performing Arts Music Representative, organising events for 17 ensembles. I also spent one year as the Performing Arts Officer chairing a committee overseeing the running of all 42 of the University's performing arts societies. For both of these years I was a Strategic Board Member for the Turner Sims Concert Hall.

I have played badminton for over 15 years. During my undergraduate studies I was a member of the Recreational Badminton Society (one year of which I was treasurer) including travelling to and participating in multiple International Student Badminton Tournaments.

## 💻 PERSONAL PROJECTS

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### RHYPE : A PACKAGE FOR WORKING WITH HYPERGRAPHS IN R

2021 - PRESENT

<https://www.hwarden.com/project/rhype/working-with-hypergraphs-in-r-using-rhype/> [github.com/hwarden162/rhype](https://github.com/hwarden162/rhype)  
I built my own R package for working with hypergraphs in R. It has multiple functions to turn data structures into an R6 hypergraph environment and then multiple functions for manipulating and analysing the hypergraph object. It is currently available to install from CRAN and the development version is available from GitHub.

R Package Development CRAN Hypergraphs

### CREATING DIGITAL TEXT ART USING JAVASCRIPT

MARCH 2022

<https://www.hwarden.com/project/creating-text-art-using-javascript/>

I used the p5.js JavaScript library and some of my own cell painting photos to create a striking cover photo for an upcoming presentation.

p5.js JavaScript Text Art

### USING NLP TO CLASSIFY GENES AS GOF/LOF FROM PUBMED ARTICLES

JUNE 2022

[Initial Blog Post](#) [github.com/hwarden162/mutation\\_nlp](https://github.com/hwarden162/mutation_nlp)

I used Python to gather abstracts from PubMed articles referencing known gain of function or loss of function (GOF/LOF) genes. After this, I used various techniques in R to analyse these abstracts to tell the difference between ones referencing GOF and LOF genes.

R Python Machine Learning NLP Genetics

## “ REFERENCES

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#### Ava Khamseh

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