

# Hugh WARDEN

## Machine Learning | Data Science | Biostatistician

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I am a PhD Student working in the Human Genetics unit at the Institute of Genetics and Cancer, part of the University of Edinburgh. This is the online version of my CV, please contact me if you are interested in receiving a full copy.

## EDUCATION

<b>Present</b> <b>April 2022</b>	<b>PhD Genetics and Molecular Medicine, INSTITUTE OF GENETICS AND CANCER - UNIVERSITY OF EDINBURGH,</b> I am currently a rotation student working at the Human Genetics Unit at the Institute of Genetics and Cancer, a part of the University of Edinburgh. <div>Machine Learning</div>
<b>March 2022</b> <b>January 2022</b>	<b>Rotation Project, KUDLA LAB - INSTITUTE OF GENETICS AND CANCER - UNIVERSITY OF EDINBURGH,</b> I am currently spending 3 months working with Greg Kudla and Diego Oyarzún using explainable AI to investigate the effects of mutated P53. I am training machine learning models to classify P53 mutations from various biological/morphological data and then interrogating the models as to what predictors were the most useful. <div>Machine Learning   DeepLift   R   Python   TidyModels   Cancer   Genetics</div>
<b>December 2021</b> <b>September 2021</b>	<b>Rotation Project, KHAMSEH LAB - INSTITUTE OF GENETICS AND CANCER - UNIVERSITY OF EDINBURGH,</b> I spent 3 months working with Ava Khamseh to develop an automated image preprocessing pipeline for whole slide images of mouse livers. The algorithm was written in groovy and run using QuPath, it used cell detection and density mapping to find areas of high immune cell infiltration within a tissue. Within these areas, it would then use biological staining information as well as morphological features to detect neoplastic hepatocytes. These neoplastic hepatocytes were then exported as small image tiles labelled with meta data to train image based machine learning algorithms. <div>Machine Learning   QuPath   Groovy   R   Python   Cancer   Genetics   NextFlow</div>
<b>September 2016</b> <b>August 2021</b>	<b>MMath Mathematics, UNIVERSITY OF SOUTHAMPTON,</b> In my degree I focused on machine learning, statistical modelling and data science, especially their applications in biology. For my third year dissertation I investigated basic supervised machine learning techniques for the classification of cell type from scRNA-seq data. I built upon this for my masters by working with Raffaella Mulas to apply spectral hypergraph theory to the analysis of these classifications. As well as this I developed my own hypergraphic centrality metrics and their uses in analysis protein interaction networks. This work was then developed into the 'rhype' package now available on CRAN, with my other R package 'SCent'. <div>Machine Learning   Statistical Modelling   Hypergraph Theory   R   Python   Data Science   Stochastic Processes   Dynamic Systems</div>

## PROGRAMMING LANGUAGES

R	●	●	●	●	○
Python	●	●	○	○	○
C++	●	○	○	○	○
Groovy	●	○	○	○	○
Java	●	○	○	○	○

## FAMILIAR WITH

- > Version Control :
  - > Git
  - > GitHub/GitLab
- > Bash
- > Environment Managers :
  - > Conda
  - > REnv
- > BioImage Analysis :
  - > QuPath
  - > Cell Profiler
- > Workflow Managers :
  - > NextFlow
- >  $\LaTeX$