PI profile

## Chris Holmes

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| https://www.well.ox.ac.uk/people/chris-holmes/@@haiku.profiles.portrait/fee55599059d4f6894d85df4c77bab59/@@images/image/w1140?76e4120c-dc1f-44bd-b239-7993349b1402 | **Professor Chris Holmes**  **Titles**: Professor of Biostatistics  **Location**: Department of Statistics  **Department**: Statistics  **Group**: Statistical and Population Genetics  **Webpage**: <http://www.stats.ox.ac.uk/all-people/chris-holmes/>  **Email**: cholmes@stats.ox.ac.uk  **PA**: Ann Hendy <ahendy@turing.ac.uk> |

### GMS themes:

* Genome biology (genomes and genetic variation)
* Genomics of disease
* Genomic analysis (bioinformatics and statistical genetics)

### Research Overview

Modern scientific applications in genetics and genomics produce data sets that continue to challenge conventional statistical methods. Our group is focussed on developing new scalable statistical methods and statistical foundations for robust, reproducible, analysis involving high-throughput genomics data particularly with multivariate outcome measurements (phenotypes). For instance, in recent work (de Angelis et al, Nature Genetics 2015) we developed techniques based on statistical “modularisation” to allow for scalable robust analysis of genomic data taken across multiple labs at multiple times. The modularisation allows for a global baseline model to be used with then multiple simple sub-models are used for testing. The statistical analysis pipeline in our paper was highlighted in the News and Views section of Nature Genetics entitled “Genetic differential calculus”. Genomics data is often complex and high dimensional such that it is difficult to construct an accurate probability model, or likelihood function, for the samples. In a recent paper (Bissiri et al 2015) we developed an extension of Bayesian statistics that allows for learning from data when models are misspecified. This provides for a way to fit simple Bayesian models to data and then “temper” (or anneal) the likelihood function to account for the approximation. Such methods have widespread appeal in modern biomedical applications and we are currently investigating them in the retrospective analysis of randomised trial data as part of an MRC Stratified Medicine consortium.

Project areas: Stratified medicine and statistical machine learning models for multi-view integrative genomics, particularly using Bayesian methods. Recent collaborations include MRC Stratified Medicine consortium, STOP-HCV and S-CORT, as well as working closely with UK Biobank.

### Specific project proposals:

Please contact directly for further information.

*These pages were reviewed/updated:* ***10/06/2022***

Project proposal

# **Title**: **[Project title here]**

Supervisors: [name and title of relevant individuals]

Wet/dry lab mix (approx): X% wet lab, X% dry lab

### Description:

[Write a ~ half-page page description of the project here].

### Training Opportunities:

[Write a brief description of the training opportunities the project will provide].

### Background reading / references:

Please include references as desired. Suggested format:

* [Surname] [Firstname], [other authors]… **(year in bold)** . [Title]. [Journal name], [other details]. Available at: [link]

Insert any additional project description(s) on subsequent pages if applicable. Please use the same template and use separate pages for each project.