

BIOINFORMATICS AND COMPUTATIONAL BIOLOGY



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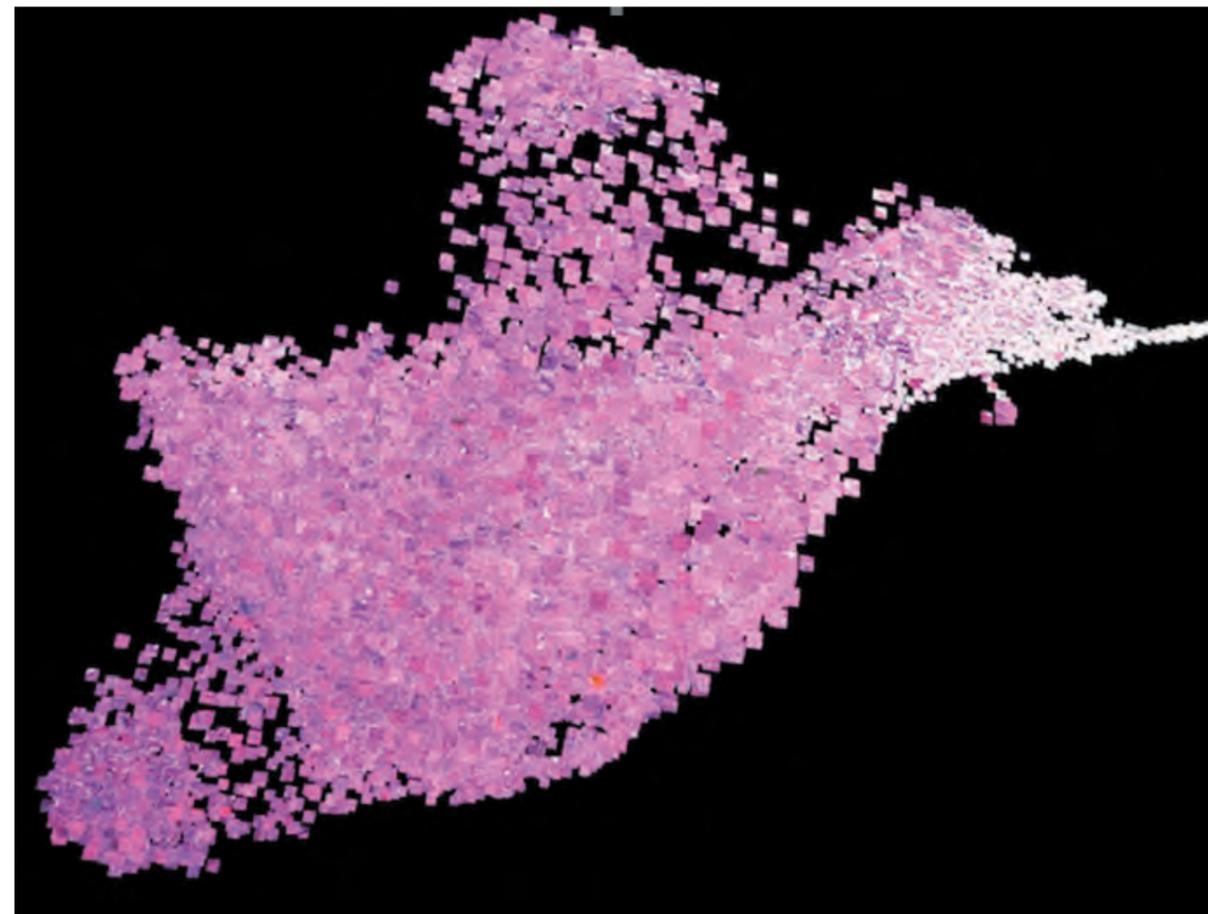
The Bioinformatics and Computational Biology unit provides numerical expertise across the Institute. A major aspect of our work continues to centre on the analysis of high-throughput 'omics data, including a wide range of next-generation sequencing, proteomics and metabolomics datasets. Our remit also includes mathematical modelling, and a growing focus has been on the application of these techniques to imaging data.

Our team focuses on exploratory data analysis, and our ultimate goal is to provide insights that enhance our understanding of cancer biology. The need for DNA and RNA sequencing analyses has continued to grow, and this has been accompanied by continued interest in using computational and machine learning approaches to interpret imaging and proteomics data.

A major aspect of our work continues to be the analysis of single-cell sequencing data and we have been developing workflows that use a mixture of specific packages, such as Seurat, along with other software tools and packages from the Bioconductor project. We are particularly interested in establishing standardised workflows for initial pre-processing and up-stream analysis of single-cell datasets in order to automate the more routine parts of the analysis.

Data analysis and modelling is performed using a variety of open-source software environments, programming languages and scripting tools, including R, Bioconductor, KNIME, Fortran, Bash, PHP and Perl. We frequently make use of analytical routines that have been developed in-house, and/or in collaboration with our colleagues from the areas of mathematics, statistics, computer science and biology. We use a mixture of academic software tools for functional annotation, clustering, enrichment, ontology and pathway analysis, as well as commercial tools including OncoPrint Research Premium Edition, Ingenuity Pathway Analysis and GeneGo MetaCore.

The unit also provides support and guidance to graduate students and postdocs in other research groups who are using computational approaches to analyse their data. This includes advice on R scripting (by appointment), experimental design and data presentation. We have introduced an experimental design course and continue to operate a regular internal bioinformatics forum to provide a central point of contact to bring together bioinformaticians, researchers and students who are applying computational biology and numerical approaches to their data. Our team also participates in delivering part of the postgraduate Cancer Sciences MSc programme at the University of Glasgow.



This image shows colon tumours (each little square is a cancer image) being classified by self-supervised learning. Image by Rob Insaall