HIDI: Genomics, Metagenomics & Data Analysis

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HIDI Day
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Medical Sciences Training Centre
University of Oxford
HIDI Aims

Facilitate access to immunological expertise in the form of:

1. funding,
2. experimental equipment and expert advice, and
3. data management, analysis and cross-platform analyses to improve
   • immunological capability in Oxford,
   • communication & collaboration in Oxford,
   • new discoveries, &
   • patient outcomes.
The HIDI Platforms

- **Deep Immune Phenotyping**: Immune cell phenotyping, cytokine staining, immunoassays
- **Genomics, Metagenomics & Data Analysis**: Immunogenomics (DNA/RNA/TCR-BCR/protein analysis), Viromics/Microbiomics pipeline (sequencing + analysis), Metabolomics (mass spectrometry)
- **Immune Imaging**: Chip cytometry, multi-spectral imaging, electron microscopy, micron advanced bioimaging unit, live-cell super-resolution microscopy
- **Proteomics**
- **Immunopeptidomics**
Genomics, Metagenomics & Data Analysis

Calli Dendrou
Group Leader, WHG

- Immune-mediated diseases
- Primary human immune cell genotype-to-phenotype analyses
- Disease gene regulation
- Immune gene expression dynamics

Camilla Ip
Bioinformatician, Dendrou Group

- Bioinformatics pipelines
- Microbial genomics
  - ModMedMicro Consortium
  - WHG Bioinformatics Core
  - STOP-HCV Consortium
- Data management
- Databases
- Nanopore data analysis
Experimental design

Data analysis comes last but do contact us from the start - before you begin experiments

No question is too trivial

• How to choose the right technology?
• How many samples/cells for appropriate power?
• How many replicates?
• How to design experiments to minimise artefacts in resulting data?
• How to mine and make use of available data sets?
• How to maximise output given funds available?
Techniques supported

- Whole exome sequencing
- Whole genome sequencing
- Targeted gene sequencing
- Genotyping
- DNA/RNA metagenomics – species identification
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- ChIP-Seq
- Bisulfite-Seq
- Chromatin conformation capture
- Data mining
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- Single-cell V(D)J-Seq +/- 5’ mRNA-Seq
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- 3’/5’ scRNA-Seq
- CITE-Seq
- Demultiplexing & deconvolution
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- Proteome lists to guide MS interpretation
- Proteome characterisation from MS

HIDI
Facilitating access to immunological expertise
Additional expertise

Next Gen Sequencing
• Oxford Genomics Centre (David Buck, Helen Lockstone, Rory Bowden, WHG)

Single-Cell Genomics
• Oxford Single Cell Consortium (Neil Ashley, WIMM; Rory Bowden, WHG)

Oxford Viromics Pipeline
• David Bonsall (BDI); Rory Bowden (WHG)

Microbiomics
• Claire Pearson (Kennedy)

Metabolomics
• James McCullagh (Chemistry)

Proteomics
• Nicola Ternette (Jenner/TDI)
Data analysis across multiple platforms

Data management
• Initial storage and pre-processing of raw data
• Integration of data from multiple platforms

Cross-platform analyses

Collaboration and documentation tools
• HIDIbook : *LabArchives* notebook for project documentation and collaboration
• HIDIproject : *Slack* workspace for team messaging and teleconferencing
• HIDIcode : *GitHub* repository for code distribution