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Register

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Conference Program (8th December)

9:00-10:00 • Smurfit institute of genetics - Atrium

Sign in and coffee/pastries

10:00-10:15 • Hamilton building - MacNeill theatre

Welcome and opening remarks

10:15-11:00 • Hamilton building - MacNeill theatre

Keynote 1: Dr Nikolaos Vakirlis - Chair Amy Ó Brolcháin

11:00-12:00 • Hamilton building - MacNeill theatre

Session 1: Evolution and population genetics - Chair Dr Elle Loughran

From Similarity to Specificity: Dissecting Functional and Mutational Landscapes of Paralogous Genes

Olivier Dennler | 11:00-11:12

Gene gain, sequence evolution, and synteny shape the diversification of Lepidoptera

Peter Mulhair | 11:12-11:24

Genomic testing of hypotheses on the origins of the Grecìa Salentina population and language

Martina Gulì | 11:24-11:36

Genomic characterisation of recurrent Mycobacterium avium isolates from chronically infected patients reveals patterns of within-host evolution

Aaron Walsh | 11:36-11:42

What's in a Name? Tracing the Structural and Functional Evolution of the Ligand of Numb Protein X Family

Leah Gabrielle Erwin | 11:42-11:48

Evolution of histone mRNA 3' end processing machinery in eukaryotes

Bin Zhao | 11:48-11:54

CloudCIX talk

11:54-12:00

12:00-12:10

Break

12:10-13:10 • Hamilton building - MacNeill theatre

Session 2: Medical genetics - Chair Corey Alwell

The presence of a secondary species alters P. aeruginosa ciprofloxacinresistance evolution in the cystic fibrosis lung

Sadhbh Dodd | 12:10-12:22

Blood DNA Methylation Modifications in Response to Opioid Exposure in a Rodent Model

Nicole Glendinning | 12:22-12:34

Development of a blood-based transcriptional biosignature for the detection of cattle infected with Mycobacterium bovis, which causes bovine tuberculosis

David MacHugh | 12:34-12:46

Single-Cell Transcriptomic Decoding of B Cell Diversity in IgA Vasculitis Reveals a Glycosylation-Dysregulated Naïve Subset.

Joao Carlos Batista-Liz | 12:46-12:52

Quantifying Haploinsufficiency in Tumour Suppressor Genes: a Cancer Hallmarks-Based Functional Screen

Elle Loughran | 12:52-13:58

Transcriptomic Dysregulation of Bone Marrow Mesenchymal Stromal Cells in Type 2 Diabetes Mellitus

Jingyan Wang | 12:58-13:04

Concurrent session: Posters

13:05-14:30 • Smurfit institute of genetics - Atrium: Evolution and population genetics

Posters and coffee/lunch

13:05-14:30 • Moyne institute: Medical genomics & Methods and tools

Posters and coffee/lunch

Concurrent session: ELIXIR

13:30-14:30 • Smurfit institute of genetics - Dawson room

VIBE & ELIXIR-IE breakout session

14:35-15:20 • Hamilton building - MacNeill theatre

Keynote 2: Dr. María Ávila-Arcos - Chair Catherine Butt

15:20-16:20 • Hamilton building - MacNeill theatre

Session 3: Evolution and population genetics - Chair Tomas Gomes

Characterisation of diverse global ancestries among participants of the UK Biobank illustrates the immigration history of Great Britain in the 20th century

Fiona Pantring | 15:20-15:32

Homology-Based miRNA Annotation and Evolution Across Mammals

Sarahjane Power | 15:32-15:44

Building a Placenta: Roles for Syncytin-Like Retroviral Envelopes of Livebearing Fish

Amy Ó Brolcháin | 15:44-16:56

Natural knock-outs of human genes are more frequently observed in genes with paralogs.

Carlos Vivas Rodríguez | 15:56-16:02

A Duplicate-Resolved Paddlefish Genome Provides Insights into the Mechanisms of Rediploidization and Hox Cluster Evolution

Dearbhaile Casey | 16:02-16:08

The Genomics of an Irish Hunter-Gatherer Community

Corey Alwell | 16:08-16:14

Developing research infrastructure to empower Irish genetics and genomics innovation under EHDS

Aedín Culhane | 16:14-16:20

16:20-16:30

Break

16:30-17:30 • Hamilton building - MacNeill theatre

Session 4: Methods and Tools - Chair Róisín Long

Development of a Nextflow Pipeline for Consensus MHC Class I Genotyping within a Cloud-Based Neoantigen Prediction Workflow

Kevin Ryan | 16:30-16:42

AMRcast: A machine learning framework to predict AMR phenotypes from genomic functional annotations

Lucy Dillon | 16:42-17:54

PyamilySeq: Transparent and interpretable gene (re)clustering and pangenomic inference highlights the fragility of conventional methods

Nicholas Dimonaco | 16:54-17:06

CarbaSnake: a clinically orientated, open-source workflow for the genomic characterisation of Carbapenemase-producing Enterobacterales (CPE)

Emily Cronin | 17:06-17:12

A predicted cancer dependency map for paralog pairs

Narod Kebabci | 17:12-17:18

Predicting drug resistance to synthetic lethal therapies in cancer

Metin Yazar | 17:18-17:24

Evaluation of partitioning algorithms for trustworthy out-of-distribution evaluation of machine learning models in biochemistry

Raúl Fernández Díaz | 17:24-17:30

17:30-17:40 • Hamilton building - MacNeill theatre

Closing remarks and awards - Chair Dr Máire Ní Leathlobhair

18:00 • The Pav

Social event with Roots in Tune

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