

# PROGRAMME

	9:00 - 9:30	Registration
	9:30 - 9:40	Opening and Welcome
<b>Session I</b>	9:40 - 10:25	<p style="text-align: center;"><i>Invited Talk</i></p> <p style="text-align: center;"><b>Prof. Veli Mäkinen, University of Helsinki</b> Sparse Dynamic Programming on Variation Graphs</p>
	10:25-10:50	<p style="text-align: center;"><b>Edin Husic, London School of Economics</b> Reconstructing Perfect Phylogenies via Branchings in Digraphs</p>
	10:50 - 11:20	Morning Coffee Break
<b>Session II</b>	11:20 - 12:05	<p style="text-align: center;"><i>Invited Talk</i></p> <p style="text-align: center;"><b>Dr. Sophia Tsoka, King's College London</b> Informatics Approaches for Biological Network Analysis</p>
	12:05 - 12:30	<p style="text-align: center;"><b>Giuseppe Torrisi, King's College London</b> Mathematical Modelling of Gene Regulatory Network</p>
	12:30 - 14:30	Lunch
<b>Session III</b>	14:30 - 15:15	<p style="text-align: center;"><i>Invited Talk</i></p> <p style="text-align: center;"><b>Dr. Terry Meehan, European Bioinformatics Institute</b> Phenomics – An Emerging Field Informing Human Health</p>
	15:15 - 15:40	<p style="text-align: center;"><b>Victoria Carr, King's College London</b> Abundance and Diversity of Resistomes differ between Healthy Human Oral Cavities and Gut</p>
	15:40 - 16:10	Afternoon Coffee Break
<b>Session IV</b>	16:10-16:35	<p style="text-align: center;"><b>Graeme Benstead-Hume, University of Sussex</b> Biological Network Topology features predict Gene Dependencies in Cancer Cell Lines</p>
	16:35-17:00	<p style="text-align: center;"><b>Sarah Wooller, University of Sussex</b> Mutational Data Sheds Light on Mechanisms in Tumour Development</p>
	17:00 - 17:25	<p style="text-align: center;"><b>Dr. Jamie Alnasir, Institute of Cancer Research</b> Fostering Reproducibility, Standardisation, Fault-tolerance and Deployability in Computational Pipelines using Nextflow Workflow Language - Adoption and Training at the ICR.</p>
	17:25 - 17:30	Closing Remarks