

IMMUNOINFORMATICS: BRIDGING PERSPECTIVES FROM THE SHLARC AND THE SIP

SCIENTIFIC PROGRAM



8:30-8:45	<p>Registration & Coffee</p> <p>Venue: MSH Ange Guépin – Hall</p>
8:50-9:00	<p>Welcome and Opening remarks</p> <p>Nicolas Vince (SHLARC, CR2TI UMR1064, Inserm, Nantes Université) Martin Maiers (SIP, NMDP, USA)</p>
9:00-9:30	<p>Session I “Advancing HLA Genomics”</p>
9:00-9:30	<p>“Building reference panels for admixed population: the impact of diversity on HLA imputation”</p> <p>Nayane Brito Silva (Ph.D. student, SHLARC, CR2TI UMR1064, Inserm, Nantes Université, France)</p>
9:30-10:00	<p>“Qatar genome: Insights on HLA and genomics from the Middle East”</p> <p>Christophe Demay (Researcher, Qatar Genome Program, Qatar)</p>
10:00-10:30	<p>“Tools and Methods for HLA Research”</p> <p>Steven Mack (Professor, University of California, San Francisco, San Francisco, CA, United States)</p>
10:30-11:00	<p>Coffee break</p>
11:00-12:30	<p>Session II “Innovations in Genomic Sequencing: Aligning MHC and LRC with Next-Generation Algorithms”</p>
11:00-11:30	<p>“MHC-short read alignment-free calling”</p> <p>Kristen Wade (PostDoc, Weill Institute for Neurosciences, Department of Neurology, University of California San Francisco, San Francisco, California, USA)</p>
11:30-12:00	<p>“LRC-short read calling”</p> <p>Danillo Augusto (Ph.D., Associate Professor, The University of North Carolina at Charlotte, Charlotte, USA)</p>
12:00-12:30	<p>“New algorithms in NGSengine 3.0 for accurate long-read sequencing-based typing”</p> <p>Loes van de Pasch (Ph.D., Director Bioinformatics at GenDx, Utrecht, Netherlands)</p>
12:30-13:45	<p>LUNCH</p>

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14:00-12:30	Session III “Population Genetics: Frontiers in Genomic Analysis”
14:00-14:30	<p>“Current methods in statistical imputation: going beyond missing genotypes”</p> <p>Anthony Herzig (Ph.D., Researcher INSERM, Bretagne Occidentale University, Brest, France)</p>
14:30-15:00	<p>“Immunogenetics of infectious diseases in Benin: collaborative research with local Scientists”</p> <p>Laure Gineau (Ph.D., Researcher IRD, University of Paris, Paris, France)</p>
15:00-15:30	<p>“Are identical HLA alleles identical by descent?”</p> <p>Diogo Meyer (Professor, The University of São Paulo, São Paulo, Brazil)</p>
15:30-16:00	Coffee break
16:00-17:30	Session IV “Latest advancements in HLA typing and genomic analysis”
16:00-16 :30	<p>“MHC Graph Assembly”</p> <p>Stephan Scholtz (Ph.D. student., Institute of Medical Microbiology and Hospital Hygiene, Heinrich Heine University Düsseldorf, Düsseldorf, Germany)</p>
16:30-17:00	<p>“Gene feature enumeration: how to improve HLA alleles description”</p> <p>Martin Maiers (Ph.D., NMDP, Minneapolis, MN, USA)</p>
17:00-17:30	<p>“Expanding the Genotype List String grammar for HLA and KIR genotypes”</p> <p>Jürgen Sauter (Ph.D., DKMS German Bone Marrow Donor Center, Germany)</p>
17 :30-18:00	Closing Remarks