RT STATGEN : ANNUAL MEETING
Tuesday December 9, 8h30-18h30

8h30-9h00 Welcome Coffee

9h00-9h05 Introduction PDG Inserm, Emmanuelle Génin IT GGB & Robert Barouki IT SP

9h05-9h15 Program overview, Anne-Louise Leutenegger and Emmanuelle Bouzigon

Session 1: Statistics and genetic epidemiology

9h15-9h45: Keynote Speaker - Iuliana Ionita-Laza

9h45-10h05: Berrandou Takiy, Multi-trait genome-wide and gene-based analyses implicate coagulation and vascular smooth-muscle pathways in spontaneous coronary artery dissection

10h05-10h25: Huang Haibo, Genetic Correlations Between Asthma Subtypes and Neuropsychiatric Disorders

10h25-10h45: Fritsch Humblet Barbara, ATM, medical ionising radiation and breast cancer risk in high-risk women without pathogenic variants in BRCA1 and BRCA2

10h45-11h15 Coffee Break + Posters

11h15-11h35:Palmal Sagnik, Interactions with genetics in Alzheimer's disease

11h35-11h55: Schramm Catherine, Estimation oligogénique de la pénétrance de la maladie d'Alzheimer en fonction de l'Age pour les porteurs de variants rares

11h55-12h15: Foulon Sidonie, Fantasio: A Case-Control Approach To Detect Rare Recessive Variants In Multifactorial Diseases

12h15-12h35: Herzig Anthony, Impact of study sample composition on supervised admixture modelling

12h35-14h00 Lunch Break + Posters

Session 2: Bioinformatics and omics analysis

14h00-14h30: Keynote Speaker - Antonio Rausell

14h30-14h50: Asgari Yazdan, DNA Methylation and Breast Cancer Risk: An Epigenome-Wide Association Study within the French E3N-Generations Cohort

14h50-15h10: Perrin Aglaé, Assessing the association between human genetic variation and SARS-CoV-2 viral dynamics

15h10-15h40 Coffee Break + Posters

15h40-16h00: Chataigner Lucas, When Ancestry Matters: Visualizing and Profiling Missense Variants in Drug-Response Genes

16h00-16h20: Paes Gabriela, Population-Specific Diversity of KIR2DS1 and KIR2DS4 Activating Receptors: Copy Number Variation and Allelic Patterns Across Global Ancestries

16h20-16h40: Monlong Jean, Association tests in pangenome graphs with STOAT

16h40-16h45 Conclusion

16h45-18h30 Cocktail, discussion & networking

Poster Presentations

1. Abani Fatima-Zahra, Mise en place d'un pipeline d'analyse post-GWAS des variants de tous types à partir de génomes complets PacBio HiFi et application à la la maladie d'Alzheimer précoce
2. Barzine Mitra, Fine-mapping of human leukocyte antigen alleles associated with French anti-aquaporin-4 antibodies seropositive Neuromyelitis Optica Spectrum Disorder patients.
3. Brocard Simon, First genomic study of chronic lung allograft dysfunction discovers two novel associations
4. Bugnon Agathe, Description of molecular interaction networks involved in humoral rejection of kidney allograft
5. Conil Clément, A human YEATS4 variant confers resistance to TST and IGRA conversion despite Mycobacterium tuberculosis exposure
6. De Walsche Annaïg, Multitrait GWAS to Enhance Signal Detection for a Single Target Trait
7. Dowding Julien, Genome-wide association study of IgG response to Ebola virus antigens in survivors of Ebola virus disease
8. Durand Axelle, Caractérisation des facteurs génétiques associés à la protéinurie pédiatrique
9. Gélin Morgane, Identification of genetic susceptibility to develop invasive pneumococcal disease in children by whole-exome sequencing.
10. Ghestem Florence, Knowledge graph to dissect genotype phenotype association
11. Le Borgne Julie, Gene-sex interaction GWAS for Alzheimer's Disease risk for StatGen 2025
12. Park Seehyun, Large-scale association analysis identified new susceptibility risk loci for differentiated thyroid carcinoma by integrating the transcriptome and proteome
13. Pluntz Matthieu, Generalized Viterbi algorithm for identifying the multiple most likely paths of hidden states in a HMM and application to detection of homozygosity by descent
14. Martinez Jessica, Multi-trait analysis reveal new variants associated with cytokine levels in asthmatic families
15. Mauduit Vincent, Genome-wide survival study identifies a novel non-HLA donor-recipient genetic mismatch associated with kidney allograft survival
16. Morin Martin, PBMC mRNA/miRNA profiling identifies MMP9 as a putative non-invasive biomarker and therapeutic target in chronic kidney allograft rejection
17. Orsi Laurent, Gènes impliqués dans les voies liées à l'interleukine-6 dans l'asthme : méta-analyse de quatre études
18. Rioux Bastien, Re-evaluating the association between TREX1 variants, lupus and oligoprotein interferon signatures
19. Sugier Pierre-Emmanuel, Meta-Analysis models with group structure for pleiotropy detection at gene and variant level using summary statistics from multiple datasets