

Mercredi 21 septembre

- 10h00-10h30 **Accueil**
- 10h30-10h45 **Introduction**
- 10h45-11h40 **Nadia BESSOLTANE** *Small-variant calling by mapping reads to reference sequences.*
- 11h40-12h35 **Antoine LIMASSET** *De novo assembly, the good, the bad and the ugly.*
- 12h35-12h55 **Ludovic DUVAUX** *An automatic and reproducible PacBio HiFi based genome assembly workflow for pangenomic applications.*
- 12h55-14h30 **Déjeuner**
- 14h30-15h25 **Romuald LASO-JADART** *Reference-free population genomics using metagenomic data.*
- 15h25-15h45 **Sarah GAUTIER** *High quality phased assembly of grape genome offer new opportunities in chimera detection.*
- 15h45-16h15 **Pause café**
- 16h15-17h10 **Claire LEMAITRE** *Methodological challenges of Structural Variation characterization and the particular case of long insertions.*
- 17h10-17h30 **Claire MÉROT** *Structural variants and species differentiation in Lake Whitefish.*
- 17h30-17h50 **Hugues ROEST CROLLIUS** *ATLASEa : An atlas of marine genomes.*

Jeudi 22 septembre

- 10h10-11h05 **Mark BLAXTER** *Tree of Life Genomics: from specimens to reference genomes.*
- 11:05-11:35 **Pause café**
- 11h25-12h20 **Jean-Marc AURY** *De novo sequencing and assembly of complex genomes.*
- 12h20-12h40 **Ana ZOTTA** *So close yet so far: scaffolding and phasing highly similar copies from a triploid hybrid genome.*
- 12h40-13h00 **William MARANDE** *From seeds to genome : production of high quality plant genome at the CNRGV.*

13h00-14h30	Déjeuner
14h40-15h35	Romain KOSZUL <i>Hi-C applications for genomics.</i>
15h35-16h30	Céline BON <i>Challenges in NGS analyses of ancient DNA.</i>
16h15-16h45	Pause café
16h45-17h30	Stefano MONA <i>Population genomics in the wild: examples from some non-model species.</i>
17h30-17h40	Concluding words