

## Journée bioinfo biostat – 04 Octobre 2019 – INRA Auzerville

<b>08h45 - 09h00</b>	<b>Accueil</b>
<b>09h00 - 09h15</b>	<b>Le mot de Genotoul et des plateformes</b>
	<b>Session 1</b>
<b>09h15 – 10h05</b>	Conférencier invité : <u>Franklin Delehelle</u> (CNRS AMIS/AGES) <b>ASGART – cartographie de novo des duplications segmentaires ; application aux dynamiques des chromosomes sexuels</b>
<b>10h05 – 10h25</b>	<u>Veronique Decroocq</u> (INRA, UMR1332 BFP, Villenave d'Ornon) Evolutionary and comparative genomics of long-lived perennial species of the section Armeniaca
<b>10h25 – 10h45</b>	<u>Andreea Dreau</u> (INRA, MIAT) Construction of individual recombination maps using linked-read sequencing data
<b>10h45 – 11h20</b>	<b>Pause et session poster (hall d'entrée)</b>
	<b>Session 2</b>
<b>11h20 – 11h40</b>	<u>Pancaldi Vera</u> (CRCT) GARDEN-NET: A tool for chromatin 3D interaction network visualization
<b>11h40 – 12h00</b>	<u>Raphaël Mourad</u> (CNRS, LBCMCP) TADreg : A versatile regression framework for TAD identification, differential analysis and predictions
<b>12h00 – 12h20</b>	<u>Cyril Kurylo</u> (INRA, GenPhySE) Détection et comparaison de compartimentation génomique
<b>12h20 – 14h00</b>	<b>Déjeuner (hall génome)</b>
	<b>Session 3</b>
<b>14h00 – 14h50</b>	Conférencière invitée : <u>Andrea Rau</u> (INRA GABI) <b>Integrative methods for multi-omic data reveal multi-level gene regulation</b>
<b>14h50 – 15h10</b>	<u>Jérôme Mariette</u> (INRA, MIAT) Unsupervised variable selection for kernel methods in systems biology
<b>15h10 – 15h30</b>	<u>Matthias Zytnicki</u> (INRA, MIAT) Finding differentially expressed sRNA-Seq regions with srnadb
<b>15h30 – 16h10</b>	<b>Pause et session poster (hall d'accueil)</b>
	<b>Session 4</b>
<b>16h10 – 16h30</b>	<u>Dimeglio Chloé</u> (CHU Toulouse, PTI) THETA: a new genotypic approach for predicting HIV-1 CRF02-AG coreceptor usage
<b>16h30 – 16h50</b>	<u>Annie Robic</u> (INRA, GenPhySE) Commentaires sur l'identification des ARN circulaires
<b>16h50 – 17h10</b>	<u>Pablo Rodriguez</u> (INRA, Toxalim) Ignoring the optimal set of context-specific metabolic networks can bias the interpretation of data
<b>17h10</b>	<b>Clôture de la journée</b>