



**Usage of High Throughput Sequencing in Virology**  
**Belgian Society for Virology**  
**Wednesday the 9<sup>th</sup> of September 2015**  
**Université de Liège, Tour GIGA, Batiment B34**  
**1 avenue de l'Hôpital, Sart-Tilman, Liège**

**9h00-9h20: Registration**, Tour GIGA B34, 5<sup>th</sup> Floor, L. Frédéricq auditorium

**9h20-9h45: Principles of High Throughput Sequencing Technology** - Wouter Coppieters (ULg, GIGA)

**9h50-10h15: Retroviral insertion site mapping and clonal abundance** - Gillet Nicolas (ULg-GIGA, ULg Gembloux Agro BioTech)

**10h20-10h45: Deep sequencing reveals abundant noncanonical retroviral microRNAs in B-cell leukemia/lymphoma** - Anne Van den Broeke (ULg-GIGA, Institut Bordet)

10h45-11h00 coffee break

**11h00-11h40:** to be determined

**11h45-12h30: Challenges for the transition from research use towards diagnostic tool: the case of plant virus diagnostic** - Sebastien Massart (ULg – Gembloux Agro BioTech)

12h30 – 14h00: sandwich lunch

**14h00-16h00: Virus discovery from HTS data**, practical training session (10 people max, a dedicated room with 10 computers will be available) – Sebastien Massart (ULg – Gembloux Agro BioTech)