June 07th 2019,

NGS analysis is now already in use in several diagnostics labs in the field of hemato-oncology with the use of a variety of different kits and platforms.

The main challenge that clinical scientist are facing now is on the classification and interpretation of the detected variants.

For the autumn meeting of Molecular Diagnostics.be we would like to invite companies to present their solution on variant classification and interpretation starting from Fastq, Bam or Vcf files.

The purpose for each company would be to present an overview of their workflow in terms of:

- Annotation of the variants

- Biological classification of the variants

- Clinical interpretation of the variants

- Links with genomic database, prediction tools and scientific literature

- Links with clinical trials database

- Possibility to implement the Belgian variant interpretation algorithm (customization?)

- Potential use of a variant database

- Report output

- Other

We invite you to contact us via info@moleculardiagnostics or [Marie.LeMercier@uza.be](mailto:Marie.LeMercier@uza.be) to apply for a slot.

**Practical info:**

The meeting is planned on 28/11/2019 (afternoon) in Brussels.

Presentation slot: 20 min

All companies are allowed to attend the presentations, but questions will be limited to the members of Molecular Diagnostics.be.