

NGS Goes Automatic : From library preparation to data quality control

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Due to the constant increase of second generation sequencers (as HiSeq or MiSeq) throughput and the multiplication of their applications, a challenge is to sequence, at the same time, in a single run, ever more samples of different types, while being able to verify the quality of the produced data. At the INRA GeT-PlaGe facility, we have automated both library production and data quality control steps, in partnership with the Genotoul Bioinformatics facility, for protocols such as whole genome sequencing, Amplicon sequencing (e.g. 16S sequencing on MiSeq for metagenomics studies), stranded RNA-seq, Mate-Pair or whole genome bisulfite sequencing.

Having acquired a solid expertise in library preparation and data quality control of short fragments, our challenge for the coming months will be to integrate data from 3rd generation sequencers in our automated quality control processes, dealing with the specificity of long fragments, in partnership with the bioinformatics community of Toulouse and France Genomique.



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