

Application of high-end sequencing technologies

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Abstract

Advancements of sequencing technologies enable us to obtain genomic sequences for a reduced cost. Genomic approaches are now a big trend in many research areas. Accordingly, sequencing generates now a big market. Companies who provide sequencing platforms or devices often advertise only strong points without telling the limitations or difficulties. Thus, in this presentation, I will discuss several high-end sequencing technologies from my direct experiences, including Illumina HiSeq, Illumina NovaSeq, Oxford nanopore MinIon, Pacbio, Hi-C, and 10X chromium sequencing. I used these technologies for genome assembling, resequencing, and phylogenomics studies from several non-model insect species. I believe that Oxford nanopore and NovaSeq will replace Pacbio and HiSeq, respectively. Importantly, de novo whole genome assembling is now a remarkably simple task. Lastly, I will show how these sequencing techniques can change the way of research, with an example of a phylogenetic analysis.

Biography

researcher at INRA;

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