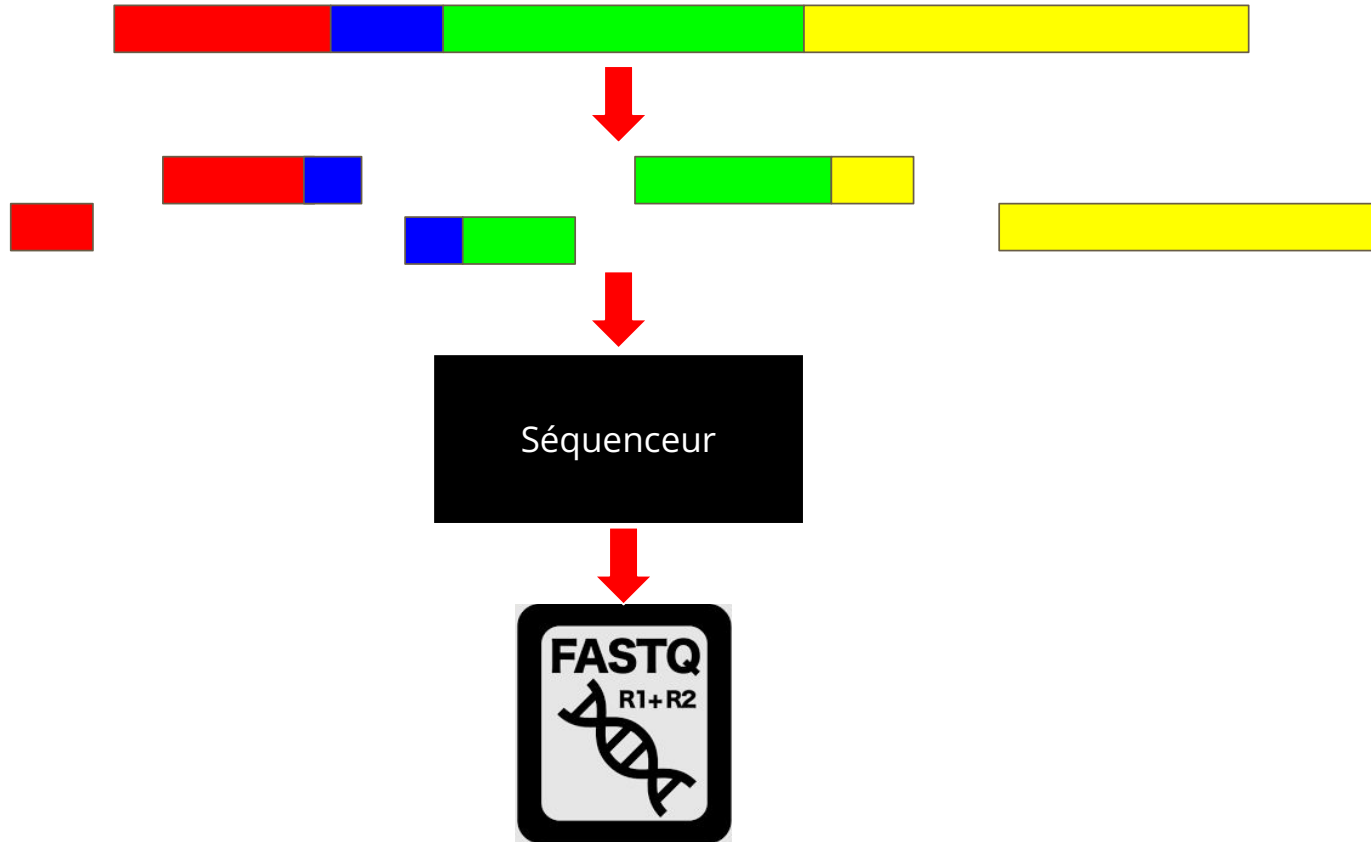

**Est ce que mieux,
— c'est toujours mieux? —**

Le Séquençage



Le stage

SoniQC:

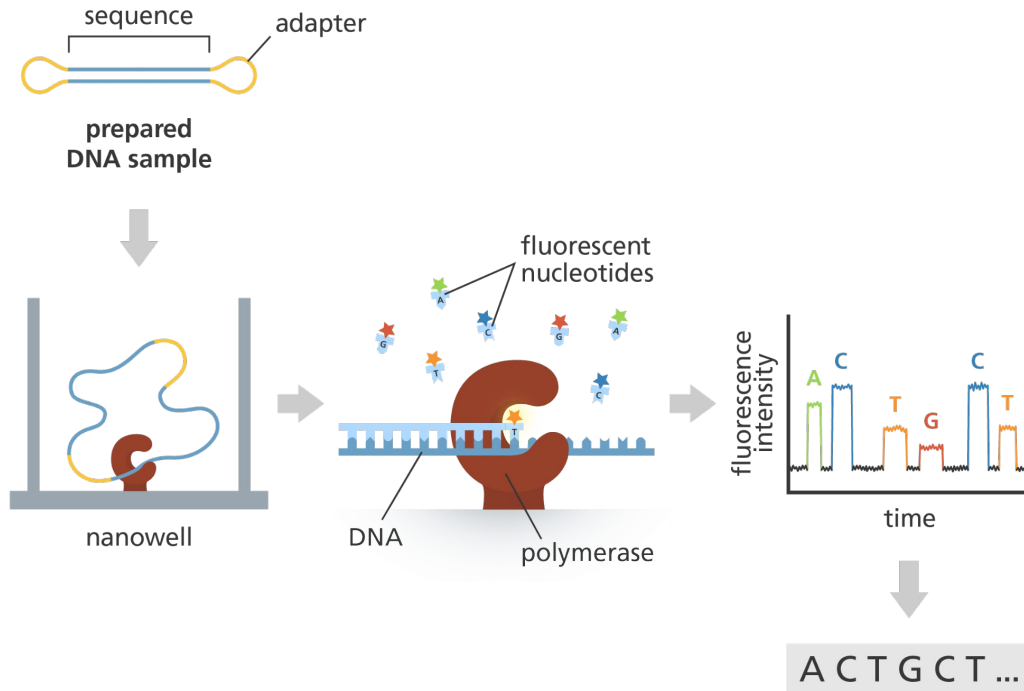
Développement et mise en production
d'un logiciel de contrôle de la qualité
des lots de séquences longues lectures



UMR GENOSCOPE
METABOLIC GENOMICS

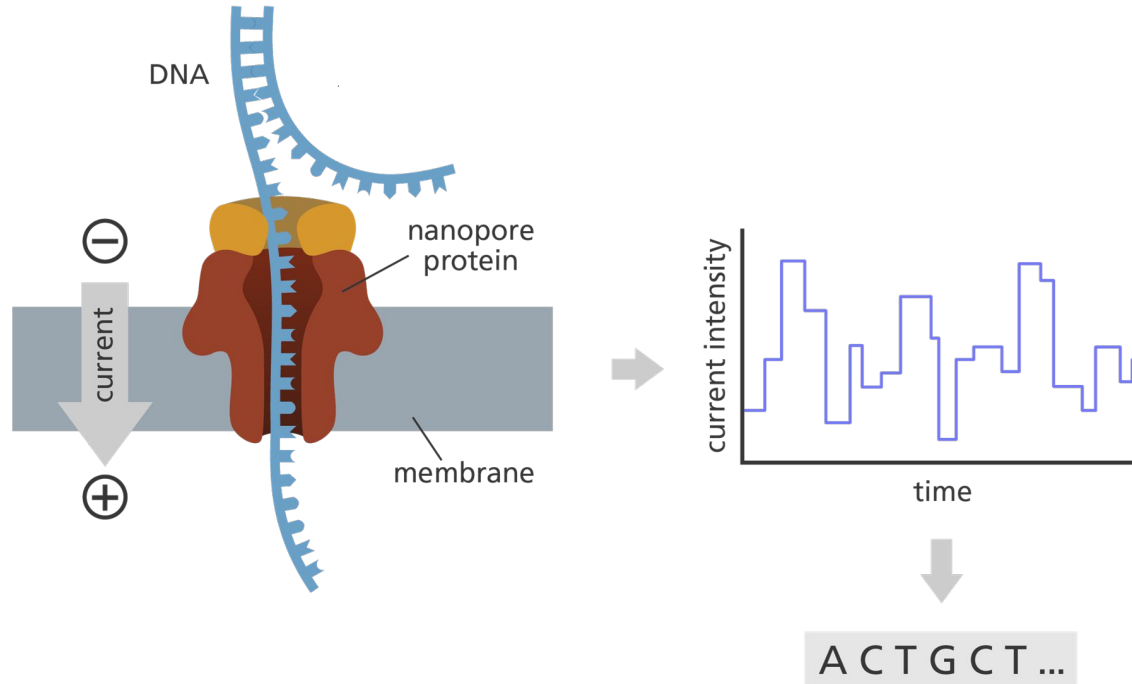


Technologies de séquençage long reads (PacBio)



<https://www.yourgenome.org/theme/what-is-pacbio-smrt-sequencing/>

Technologies de séquençage long reads (Nanopore)



<https://www.yourgenome.org/theme/what-is-oxford-nanopore-technology-ont-sequencing/>

Qualité d'un read

$$Q_{base} =$$

Calcul en place: $Q_{read} = moy(Q_{base})?$

Qualité d'un read

$$Q_{base} = -10 \log_{10}(P)$$

Calcul en place: ~~$Q_{read} = \text{moy}(Q_{base})?$~~

"Bon" calcul: $Q_{read} = -10 \log(\text{moy}(P_{base}))$

Qualité d'un read

$$9 \times Q_{40} + 1 \times Q_0$$



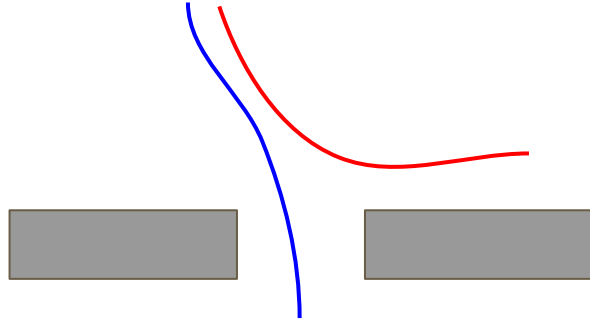
$Q_{\text{read}} = 36$



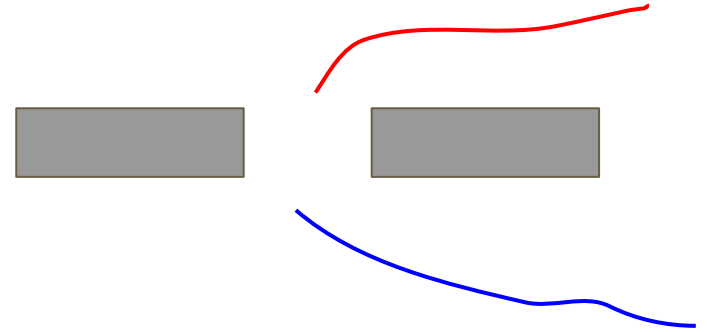
$Q_{\text{read}} \approx 11$

Reads chimériques (Nanopore)

Lecture Read

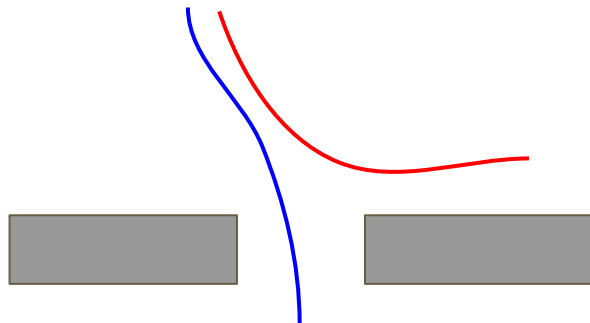


Lecture Read Complément

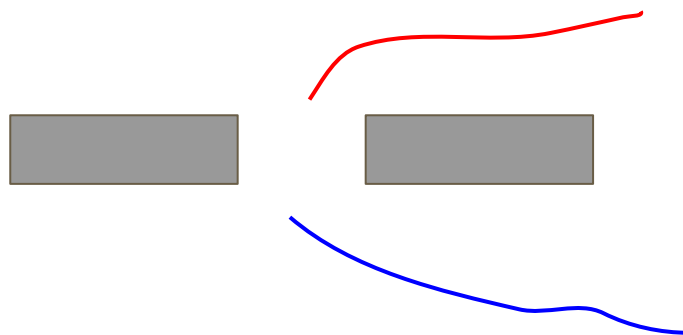


Reads chimériques (Nanopore)

Lecture Read



Lecture Read Complément



@29e24f1e-c334-49e5-aal-c-5a4b7bca1fc2_fail_PBE04124

CTAGAAAGGTGGAGGTGTCAAGGGTACCTTATGGGTGACAGTGGATATGGATGCCAAACATTCCTTATGACCCCTGTATTGGGTTCTGTTTCTATCAAGGAAAAAACTATAATGAACCACATGTAAAAACAAGAAATGTAATTGAGC
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GTGTGTGTGTGT