

FULL DE RESUM DEL TREBALL DE FI DE GRAU DEL BDBI (ESCI-UPF)

TÍTOL DEL PROJECTE: Best Practices for the Analysis of Oxford Nanopore Direct RNA Sequencing Data	
AUTOR/A: José Miguel Ramírez	NIA: 102772
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TUTOR/S: Eva Novoa	
PARAULES CLAU (mínim 3)	
<ul style="list-style-type: none"> • Català: • Castellà: • Anglès: RNA modifications, Epitranscriptomics, Oxford Nanopore Technologies, Direct RNA sequencing, N6-methyladenosine,, pseudouridine, 5-methylcytosine, 5-hydroxymethylcytosine 	
RESUM DEL PROJECTE (extensió màxima: 100 paraules per llengua)	
<ul style="list-style-type: none"> • Català: • Castellà: • Anglès: RNA modifications have recently emerged as key regulators in many biological processes. However, current methods to genome-wide map RNA modifications using next-generation sequencing (NGS) are only available for 5 % of the known modifications, among other drawbacks. A new method is the direct RNA sequencing platform developed by Oxford Nanopore Technologies, which is able to sequence native RNA molecules. Here, we systematically compare state-of-the-art base-calling and mapping algorithms, as well as their ability to detect and distinguish RNA modifications using systematic base-calling 'errors'. We find that Guppy 3.0.3 produces the highest accuracy and qualities, being also able to detect RNA modifications with the highest accuracy, and that GraphMap performs better than minimap2. However, distinguishing between different types of RNA modifications that modify the same ribonucleotide, such as 5-methylcytosine and 5-hydroxymethylcytosine, still remains a challenge. 	