

Phase 2 - ONT methylation calling pipeline

In this phase, you will be testing three ONT methylation calling tools and evaluate the results with respect to the results obtained in the WGBS calling pipeline. The data you will be using in this phase corresponds to the WGBS data from the previous stage.

The tools you will be evaluating are:

1. Tombo - statistics-based tool

Welcome to Tombo's documentation! - Tombo 1.5.1 documentation

Basic tombo installation (python 2.7 and 3.4+ support) This quick start guides the steps to perform some common modified base detection analyses using the Tombo command line interface. The first step in any Tombo analysis is to re-squiggle (raw signal to reference sequence alignment) raw nanopore reads.

<https://nanoporetech.github.io/tombo/>

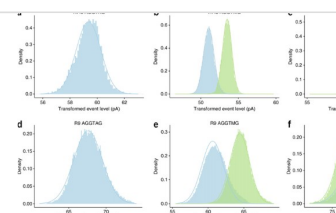
2. Nanopolish - machine learning-based tool

<https://github.com/jts/nanopolish>

Detecting DNA cytosine methylation using nanopore sequencing - Nature Methods

A hidden Markov model (HMM)-based tool enables detection of 5-methylcytosine (5-mC) from single-molecule nanopore-sequencing data generated directly from human genomic DNA without chemical treatment. In nanopore sequencing devices, electrolytic current signals

 <https://www.nature.com/articles/nmeth.4184>



3. Megalodon - deep learning-based tool

<https://github.com/nanoporetech/megalodon>

Once you obtain the methylation predictions from these three tools, compare all three tools to each other and evaluate them against WGBS results. Find pros and cons for each approach you've tested in this project.